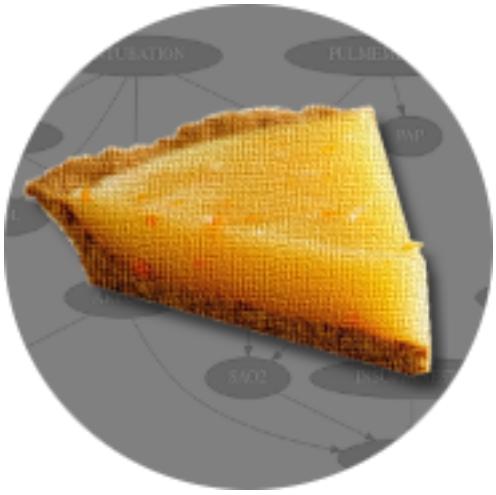

pyAgrum Documentation

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Pierre-Henri Wuillemin (Sphinx)

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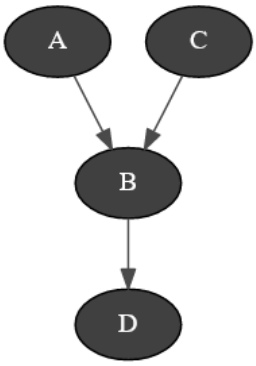
1-FUNDAMENTAL COMPONENTS

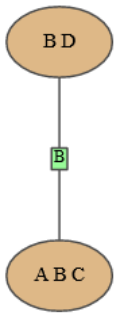
pyAgrum (http://agrum.org) is a scientific C++ and Python library dedicated to Bayesian networks (BN) and other Probabilistic Graphical Models. Based on the C++ aGrUM (https://agrum.lip6.fr) library, it provides a high-level interface to the C++ part of aGrUM allowing to create, manage and perform efficient computations with Bayesian networks and others probabilistic graphical models : Markov networks (MN), influence diagrams (ID) and LIMIDs, credal networks (CN), dynamic BN (dBN), probabilistic relational models (PRM).

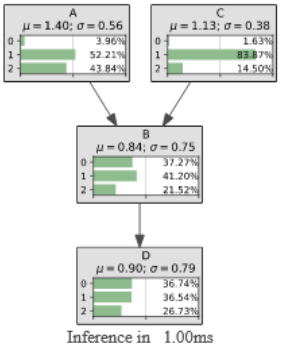
(http://agrum.org)

```
bn=gum.fastBN("A->B;C->B->D",3)
gnb.sideBySide(bn,
               bn.cpt("B"),
               gnb.getJunctionTree(bn),
               gnb.getInference(bn),
               captions=['a BN','a CPT : $P(B|A,C)$','a Junction Tree','an inference'])
```



		B		
C	A	0	1	2
0	0	0.3777	0.2394	0.3828
	1	0.5045	0.1455	0.3499
	2	0.1902	0.2699	0.5398
1	0	0.2354	0.4377	0.3270
	1	0.5313	0.3695	0.0991
	2	0.1253	0.5724	0.3023
2	0	0.2883	0.0806	0.6311
	1	0.4122	0.1077	0.4801
	2	0.7462	0.2097	0.0441





a BN | a CPT : $P(B|A,C)$ | a Junction Tree | an inference

The module is generated using the SWIG (http://www.swig.org) interface generator. Custom-written code was added to make the interface more user friendly.

pyAgrum aims to allow to easily use (as well as to prototype new algorithms on) Bayesian network and other graphical models.

pyAgrum contains :

- a *comprehensive API documentation* (page 3).
- *tutorials as jupyter notebooks* (page **??**).
- a gitlab repository (https://gitlab.com/agrumery/aGrUM).
- and a website (http://agrum.org).

CHAPTER

ONE

REFERENCE MANUAL

1.1 Graphs manipulation

In aGrUM, graphs are undirected (using edges), directed (using arcs) or mixed (using both arcs and edges). Some other types of graphs are described below. Edges and arcs are represented by pairs of int (nodeId), but these pairs are considered as unordered for edges whereas they are ordered for arcs.

For all types of graphs, nodes are int. If a graph of objects is needed (like *pyAgrum.BayesNet* (page 64)), the objects are mapped to nodeIds.

1.1.1 Edges and Arcs

Arc

class pyAgrum.**Arc**(**args*)

pyAgrum.Arc is the representation of an arc between two nodes represented by int : the head and the tail.

Arc(tail, head) -> Arc

Parameters:

- **tail** (int) – the tail
- **head** (int) – the head

Arc(src) -> Arc

Parameters:

- **src** (*Arc*) – the pyAgrum.Arc to copy

first()

Returns
the nodeId of the first node of the arc (the tail)
Return type
int

head()

Returns
the id of the head node
Return type
int

other(*id*)

Parameters
id (*int*) – the nodeId of the head or the tail
Returns
the nodeId of the other node

Return type
int

`second()`

Returns
the nodeId of the second node of the arc (the head)
Return type
int

`tail()`

Returns
the id of the tail node
Return type
int

Edge

`class pyAgrum.Edge(*args)`

pyAgrum.Edge is the representation of an arc between two nodes represented by int : the first and the second.

Edge(aN1,aN2) -> Edge

Parameters:

- **aN1** (int) – the nodeId of the first node
- **aN2** (int) – the nodeId of the secondnode

Edge(src) -> Edge

Parameters:

- **src** (*yAgrum.Edge*) – the Edge to copy

`first()`

Returns
the nodeId of the first node of the arc (the tail)
Return type
int

`other(id)`

Parameters
id (*int*) – the nodeId of one of the nodes of the Edge
Returns
the nodeId of the other node
Return type
int

`second()`

Returns
the nodeId of the second node of the arc (the head)
Return type
int

1.1.2 Directed Graphs

Digraph

class pyAgrum.**DiGraph**(**args*)

DiGraph represents a Directed Graph.

DiGraph() -> DiGraph
default constructor

DiGraph(src) -> DiGraph

Parameters:

- **src** (*pyAgrum.DiGraph*) – the digraph to copy

addArc(**args*)

Add an arc from tail to head.

Parameters
- **tail** (*int*) – the id of the tail node
- **head** (*int*) – the id of the head node

Raises
- *pyAgrum.InvalidNode* (page 291) –
- **If head or tail does not belong to the graph nodes.** –

Return type
None

addNode()

Returns
the new NodeId

Return type
int

addNodeWithId(*id*)

Add a node by choosing a new NodeId.

Parameters
id (*int*) – The id of the new node

Raises
- *pyAgrum.DuplicateElement* (page 289) –
- **If the given id is already used** –

Return type
None

addNodes(*n*)

Add n nodes.

Parameters
n (*int*) – the number of nodes to add.

Returns
the new ids

Return type
Set of int

arcs()

Returns
the list of the arcs

Return type
List

children(*id*)

Parameters
id (*int*) – the id of the parent

Returns
the set of all the children
Return type
Set

`clear`()

Remove all the nodes and arcs from the graph.
Return type
None

`connectedComponents`()

connected components from a graph/BN

Compute the connected components of a pyAgrum's graph or Bayesian Network (more generally an object that has *nodes*, *children*/*parents* or *neighbours* methods)

The firstly visited node for each component is called a 'root' and is used as a key for the component. This root has been arbitrarily chosen during the algorithm.
Returns
dict of connected components (as set of nodeIds (int)) with a nodeId (root) of each component as key.
Return type
dict(int,Set[int])

`empty`()

Check if the graph is empty.
Returns
True if the graph is empty
Return type
bool

`emptyArcs`()

Check if the graph doesn't contains arcs.
Returns
True if the graph doesn't contains arcs
Return type
bool

`eraseArc`(*n1*, *n2*)

Erase the arc between n1 and n2.
Parameters
- **n1** (*int*) – the id of the tail node
- **n2** (*int*) – the id of the head node

Return type
None

`eraseChildren`(*n*)

Erase the arcs heading through the node's children.
Parameters
n (*int*) – the id of the parent node
Return type
None

`eraseNode`(*id*)

Erase the node and all the related arcs.
Parameters
id (*int*) – the id of the node
Return type
None

eraseParents(*n*)

Erase the arcs coming to the node.

Parameters
n (*int*) – the id of the child node

Return type
None

existsArc(*n1*, *n2*)

Check if an arc exists bewteen n1 and n2.

Parameters
- **n1** (*int*) – the id of the tail node
- **n2** (*int*) – the id of the head node

Returns
True if the arc exists

Return type
bool

existsNode(*id*)

Check if a node with a certain id exists in the graph.

Parameters
id (*int*) – the checked id

Returns
True if the node exists

Return type
bool

hasDirectedPath(*_from*, *to*)

Check if a directedpath exists bewteen from and to.

Parameters
- **from** (*int*) – the id of the first node of the (possible) path
- **to** (*int*) – the id of the last node of the (possible) path
- **_from** (int) –

Returns
True if the directed path exists

Return type
bool

nodes()

Returns
the set of ids

Return type
set

parents(*id*)

Parameters
id (int) – The id of the child node

Returns
the set of the parents ids.

Return type
Set

size()

Returns
the number of nodes in the graph

Return type
int

sizeArcs()

Returns
the number of arcs in the graph

Return type
int

`toDot`()

Returns
a friendly display of the graph in DOT format
Return type
str

`topologicalOrder`(*clear=True*)

Returns
the list of the nodes Ids in a topological order
Return type
List
Raises
pyAgrum.InvalidDirectedCycle (page 290) – If this graph contains cycles
Parameters
clear (bool) –

Directed Acyclic Graph

`class pyAgrum.DAG`(**args*)

DAG represents a Directed Graph.

DAG() -> DAG
default constructor

DAG(src) -> DAG

Parameters:

- **src** (*pyAgrum.DAG*) – the digraph to copy

`addArc`(**args*)

Add an arc from tail to head.
Parameters
- **tail** (*int*) – the id of the tail node
- **head** (*int*) – the id of the head node

Raises
- *pyAgrum.InvalidNode* (page 291) – If head or tail does not belong to the graph nodes.
- **PyAgrum.InvalidDirectedCycle** – if the arc would create a cycle.

Return type
None

`addNode`()

Returns
the new NodeId
Return type
int

`addNodeWithId`(*id*)

Add a node by choosing a new NodeId.
Parameters
id (*int*) – The id of the new node
Raises
- *pyAgrum.DuplicateElement* (page 289) –
- **If the given id is already used** –

Return type
None

addNodes(*n*)

Add n nodes.

Parameters
n (*int*) – the number of nodes to add.
Returns
the new ids
Return type
Set of int

arcs()

Returns
the list of the arcs
Return type
List

children(*id*)

Parameters
id (*int*) – the id of the parent
Returns
the set of all the children
Return type
Set

clear()

Remove all the nodes and arcs from the graph.

Return type
None

connectedComponents()

connected components from a graph/BN

Compute the connected components of a pyAgrum's graph or Bayesian Network (more generally an object that has *nodes*, *children*/*parents* or *neighbours* methods)

The firstly visited node for each component is called a 'root' and is used as a key for the component. This root has been arbitrarily chosen during the algorithm.

Returns
dict of connected components (as set of nodeIds (int)) with a nodeId (root) of each component as key.
Return type
dict(int,Set[int])

dSeparation(**args*)

Return type
bool

empty()

Check if the graph is empty.

Returns
True if the graph is empty
Return type
bool

emptyArcs()

Check if the graph doesn't contains arcs.

Returns
True if the graph doesn't contains arcs
Return type
bool

eraseArc(*n1*, *n2*)

Erase the arc between n1 and n2.

Parameters
- **n1** (*int*) – the id of the tail node
- **n2** (*int*) – the id of the head node

Return type
None

eraseChildren(*n*)

Erase the arcs heading through the node's children.

Parameters
n (*int*) – the id of the parent node

Return type
None

eraseNode(*id*)

Erase the node and all the related arcs.

Parameters
id (*int*) – the id of the node

Return type
None

eraseParents(*n*)

Erase the arcs coming to the node.

Parameters
n (*int*) – the id of the child node

Return type
None

existsArc(*n1*, *n2*)

Check if an arc exists bewteen n1 and n2.

Parameters
- **n1** (*int*) – the id of the tail node
- **n2** (*int*) – the id of the head node

Returns
True if the arc exists

Return type
bool

existsNode(*id*)

Check if a node with a certain id exists in the graph.

Parameters
id (*int*) – the checked id

Returns
True if the node exists

Return type
bool

hasDirectedPath(*_from*, *to*)

Check if a directedpath exists bewteen from and to.

Parameters
- **from** (*int*) – the id of the first node of the (possible) path
- **to** (*int*) – the id of the last node of the (possible) path
- **_from** (int) –

Returns
True if the directed path exists

Return type
bool

`moralGraph`()

Return type
UndiGraph (page 12)

`moralizedAncestralGraph`(*nodes*)

Parameters
nodes (List[int]) –
Return type
UndiGraph (page 12)

`nodes`()

Returns
the set of ids
Return type
set

`parents`(*id*)

Parameters
id (int) – The id of the child node
Returns
the set of the parents ids.
Return type
Set

`size`()

Returns
the number of nodes in the graph
Return type
int

`sizeArcs`()

Returns
the number of arcs in the graph
Return type
int

`toDot`()

Returns
a friendly display of the graph in DOT format
Return type
str

`topologicalOrder`(*clear=True*)

Returns
the list of the nodes Ids in a topological order
Return type
List
Raises
pyAgrum.InvalidDirectedCycle (page 290) – If this graph contains cycles
Parameters
clear (bool) –

1.1.3 Undirected Graphs

UndiGraph

class pyAgrum.**UndiGraph**(**args*)

UndiGraph represents an Undirected Graph.

UndiGraph() -> UndiGraph
default constructor

UndiGraph(src) -> UndiGraph

Parameters!

- **src** (*UndiGraph*) – the pyAgrum.UndiGraph to copy

addEdge(**args*)

Insert a new edge into the graph.

Parameters
- **n1** (*int*) – the id of one node of the new inserted edge
- **n2** (*int*) – the id of the other node of the new inserted edge

Raises
pyAgrum.InvalidNode (page 291) – If n1 or n2 does not belong to the graph nodes.

Return type
None

addNode()

Returns
the new NodeId

Return type
int

addNodeWithId(*id*)

Add a node by choosing a new NodeId.

Parameters
id (*int*) – The id of the new node

Raises
pyAgrum.DuplicateElement (page 289) – If the given id is already used

Return type
None

addNodes(*n*)

Add n nodes.

Parameters
n (*int*) – the number of nodes to add.

Returns
the new ids

Return type
Set of int

clear()

Remove all the nodes and edges from the graph.

Return type
None

connectedComponents()

connected components from a graph/BN

Compute the connected components of a pyAgrum's graph or Bayesian Network (more generally an object that has *nodes*, *children*/*parents* or *neighbours* methods)

The firstly visited node for each component is called a 'root' and is used as a key for the component. This root has been arbitrarily chosen during the algorithm.

Returns
dict of connected components (as set of nodeIds (int)) with a nodeId (root) of each component as key.

Return type
dict(int,Set[int])

`edges()`

Returns
the list of the edges

Return type
List

`empty()`

Check if the graph is empty.

Returns
True if the graph is empty

Return type
bool

`emptyEdges()`

Check if the graph doesn't contains edges.

Returns
True if the graph doesn't contains edges

Return type
bool

`eraseEdge(n1, n2)`

Erase the edge between n1 and n2.

Parameters
- **n1** (*int*) – the id of the tail node
- **n2** (*int*) – the id of the head node

Return type
None

`eraseNeighbours(n)`

Erase all the edges adjacent to a given node.

Parameters
n (*int*) – the id of the node

Return type
None

`eraseNode(id)`

Erase the node and all the adjacent edges.

Parameters
id (*int*) – the id of the node

Return type
None

`existsEdge(n1, n2)`

Check if an edge exists bewteen n1 and n2.

Parameters
- **n1** (*int*) – the id of one extremity of the edge
- **n2** (*int*) – the id of the other extremity if tge edge

Returns
True if the arc exists

Return type
bool

existsNode(*id*)

Check if a node with a certain id exists in the graph.

Parameters
id (*int*) – the checked id

Returns
True if the node exists

Return type
bool

hasUndirectedCycle()

Checks whether the graph contains cycles.

Returns
True if the graph contains a cycle

Return type
bool

neighbours(*id*)

Parameters
id (*int*) – the id of the checked node

Returns
The set of edges adjacent to the given node

Return type
Set

nodes()

Returns
the set of ids

Return type
set

nodes2ConnectedComponent()

Return type
Dict[int, int]

partialUndiGraph(*nodes*)

Parameters
- **nodesSet** (*Set*) – The set of nodes composing the partial graph
- **nodes** (List[int]) –

Returns
The partial graph formed by the nodes given in parameter

Return type
pyAgrum.UndiGraph (page 12)

size()

Returns
the number of nodes in the graph

Return type
int

sizeEdges()

Returns
the number of edges in the graph

Return type
int

toDot()

Returns
a friendly display of the graph in DOT format

Return type
str

Clique Graph

class pyAgrum.**CliqueGraph**(**args*)

CliqueGraph represents a Clique Graph.

CliqueGraph() -> CliqueGraph
default constructor

CliqueGraph(src) -> CliqueGraph

Parameter

- **src** (*pyAgrum.CliqueGraph*) – the CliqueGraph to copy

addEdge(*first*, *second*)

Insert a new edge into the graph.

Parameters
- **n1** (*int*) – the id of one node of the new inserted edge
- **n2** (*int*) – the id of the other node of the new inserted edge
- **first** (int) –
- **second** (int) –

Raises
pyAgrum.InvalidNode (page 291) – If n1 or n2 does not belong to the graph nodes.

Return type
None

addNode(**args*)

Returns
the new NodeId

Return type
int

addNodeWithId(*id*)

Add a node by choosing a new NodeId.

Parameters
id (*int*) – The id of the new node

Raises
pyAgrum.DuplicateElement (page 289) – If the given id is already used

Return type
None

addNodes(*n*)

Add n nodes.

Parameters
n (*int*) – the number of nodes to add.

Returns
the new ids

Return type
Set of int

addToClique(*clique_id*, *node_id*)

Change the set of nodes included into a given clique and returns the new set

Parameters
- **clique_id** (*int*) – the id of the clique
- **node_id** (*int*) – the id of the node

Raises
- *pyAgrum.NotFound* (page 291) –
- **If clique_id does not exist** –
- *pyAgrum.DuplicateElement* (page 289) –
- **If clique_id set already contains the ndoe** –

Return type
None

`clear()`

Remove all the nodes and edges from the graph.

Return type
None

`clearEdges()`

Remove all edges and their separators

Return type
None

`clique(clique)`

Parameters
- **idClique** (*int*) – the id of the clique
- **clique** (int) –

Returns
The set of nodes included in the clique

Return type
Set

Raises
pyAgrum.NotFound (page 291) – If the clique does not belong to the clique graph

`connectedComponents()`

connected components from a graph/BN

Compute the connected components of a pyAgrum's graph or Bayesian Network (more generally an object that has *nodes*, *children*/*parents* or *neighbours* methods)

The firstly visited node for each component is called a 'root' and is used as a key for the component. This root has been arbitrarily chosen during the algorithm.

Returns
dict of connected components (as set of nodeIds (int)) with a nodeId (root) of each component as key.

Return type
dict(int,Set[int])

`container(idNode)`

Parameters
idNode (*int*) – the id of the node

Returns
the id of a clique containing the node

Return type
int

Raises
pyAgrum.NotFound (page 291) – If no clique contains idNode

`containerPath(node1, node2)`

Parameters
- **node1** (*int*) – the id of one node
- **node2** (*int*) – the id of the other node

Returns
a path from a clique containing node1 to a clique containing node2

Return type
List

Raises
pyAgrum.NotFound (page 291) – If such path cannot be found

edges()

Returns
the list of the edges
Return type
List

empty()

Check if the graph is empty.
Returns
True if the graph is empty
Return type
bool

emptyEdges()

Check if the graph doesn't contains edges.
Returns
True if the graph doesn't contains edges
Return type
bool

eraseEdge(*edge*)

Erase the edge between n1 and n2.
Parameters
- **n1** (*int*) – the id of the tail node
- **n2** (*int*) – the id of the head node
- **edge** (*Edge* (page 4)) –

Return type
None

eraseFromClique(*clique_id*, *node_id*)

Remove a node from a clique
Parameters
- **clique_id** (*int*) – the id of the clique
- **node_id** (*int*) – the id of the node

Raises
pyAgrum.NotFound (page 291) – If clique_id does not exist
Return type
None

eraseNeighbours(*n*)

Erase all the edges adjacent to a given node.
Parameters
n (*int*) – the id of the node
Return type
None

eraseNode(*node*)

Erase the node and all the adjacent edges.
Parameters
- **id** (*int*) – the id of the node
- **node** (int) –

Return type
None

existsEdge(*n1*, *n2*)

Check if an edge exists bewteen n1 and n2.
Parameters
- **n1** (*int*) – the id of one extremity of the edge
- **n2** (*int*) – the id of the other extremity if tge edge

Returns
True if the arc exists
Return type
bool

`existsNode`(*id*)

Check if a node with a certain id exists in the graph.
Parameters
id (*int*) – the checked id
Returns
True if the node exists
Return type
bool

`hasRunningIntersection`()

Returns
True if the running intersection property holds
Return type
bool

`hasUndirectedCycle`()

Checks whether the graph contains cycles.
Returns
True if the graph contains a cycle
Return type
bool

`isJoinTree`()

Returns
True if the graph is a join tree
Return type
bool

`neighbours`(*id*)

Parameters
id (*int*) – the id of the checked node
Returns
The set of edges adjacent to the given node
Return type
Set

`nodes`()

Returns
the set of ids
Return type
set

`nodes2ConnectedComponent`()

Return type
`Dict[int, int]`

`partialUndiGraph`(*nodes*)

Parameters
- **nodesSet** (*Set*) – The set of nodes composing the partial graph
- **nodes** (`List[int]`) –

Returns
The partial graph formed by the nodes given in parameter
Return type
pyAgrum.UndiGraph (page 12)

separator(*cliq1*, *cliq2*)

Parameters
- **edge** (pyAgrum.Edge (page 4)) – the edge to be checked
- **clique1** (*int*) – one extremity of the edge
- **clique** (*int*) – the other extremity of the edge
- **cliq1** (int) –
- **cliq2** (int) –

Returns
the separator included in a given edge

Return type
Set

Raises
pyAgrum.NotFound (page 291) – If the edge does not belong to the clique graph

setClique(*idClique*, *new_clique*)

changes the set of nodes included into a given clique

Parameters
- **idClique** (*int*) – the id of the clique
- **new_clique** (*Set*) – the new set of nodes to be included in the clique

Raises
pyAgrum.NotFound (page 291) – If idClique is not a clique of the graph

Return type
None

size()

Returns
the number of nodes in the graph

Return type
int

sizeEdges()

Returns
the number of edges in the graph

Return type
int

toDot()

Returns
a friendly display of the graph in DOT format

Return type
str

toDotWithNames(*bn*)

Parameters
- **bn** (pyAgrum.BayesNet (page 64)) –
- **network** (*a Bayesian*) –

Returns
a friendly display of the graph in DOT format where ids have been changed according to their correspondance in the BN

Return type
str

1.1.4 Mixed Graph

class pyAgrum.**MixedGraph**(**args*)

MixedGraph represents a graph with both arcs and edges.

MixedGraph() -> MixedGraph
default constructor

MixedGraph(src) -> MixedGraph

Parameters:

- **src** (*pyAgrum.MixedGraph*) –the MixedGraph to copy

addArc(*n1*, *n2*)

Add an arc from tail to head.

Parameters
- **tail** (*int*) – the id of the tail node
- **head** (*int*) – the id of the head node
- **n1** (int) –
- **n2** (int) –

Raises
pyAgrum.InvalidNode (page 291) – If head or tail does not belong to the graph nodes.

Return type
None

addEdge(*n1*, *n2*)

Insert a new edge into the graph.

Parameters
- **n1** (*int*) – the id of one node of the new inserted edge
- **n2** (*int*) – the id of the other node of the new inserted edge

Raises
pyAgrum.InvalidNode (page 291) – If n1 or n2 does not belong to the graph nodes.

Return type
None

addNode()

Returns
the new NodeId

Return type
int

addNodeWithId(*id*)

Add a node by choosing a new NodeId.

Parameters
id (*int*) – The id of the new node

Raises
pyAgrum.DuplicateElement (page 289) – If the given id is already used

Return type
None

addNodes(*n*)

Add n nodes.

Parameters
n (*int*) – the number of nodes to add.

Returns
the new ids

Return type
Set of int

adjacents(*id*)

adjacents nodes are neighbours (not oriented), children and parents

Parameters
id (*int*) – the id of the node
Returns
the set of node ids.
Return type
set

arcs()

Returns
the list of the arcs
Return type
List

children(*id*)

Parameters
id (*int*) – the id of the parent
Returns
the set of all the children
Return type
Set

clear()

Remove all the nodes and edges from the graph.

Return type
None

connectedComponents()

connected components from a graph/BN

Compute the connected components of a pyAgrum's graph or Bayesian Network (more generally an object that has *nodes*, *children*/*parents* or *neighbours* methods)

The firstly visited node for each component is called a 'root' and is used as a key for the component. This root has been arbitrarily chosen during the algorithm.

Returns
dict of connected components (as set of nodeIds (int)) with a nodeId (root) of each component as key.
Return type
dict(int,Set[int])

edges()

Returns
the list of the edges
Return type
List

empty()

Check if the graph is empty.

Returns
True if the graph is empty
Return type
bool

emptyArcs()

Check if the graph doesn't contains arcs.

Returns
True if the graph doesn't contains arcs
Return type
bool

emptyEdges()

Check if the graph doesn't contains edges.

Returns
True if the graph doesn't contains edges

Return type
bool

eraseArc(*n1*, *n2*)

Erase the arc between n1 and n2.

Parameters
- **n1** (*int*) – the id of the tail node
- **n2** (*int*) – the id of the head node

Return type
None

eraseChildren(*n*)

Erase the arcs heading through the node's children.

Parameters
n (*int*) – the id of the parent node

Return type
None

eraseEdge(*n1*, *n2*)

Erase the edge between n1 and n2.

Parameters
- **n1** (*int*) – the id of the tail node
- **n2** (*int*) – the id of the head node

Return type
None

eraseNeighbours(*n*)

Erase all the edges adjacent to a given node.

Parameters
n (*int*) – the id of the node

Return type
None

eraseNode(*id*)

Erase the node and all the related arcs and edges.

Parameters
id (*int*) – the id of the node

Return type
None

eraseParents(*n*)

Erase the arcs coming to the node.

Parameters
n (*int*) – the id of the child node

Return type
None

existsArc(*n1*, *n2*)

Check if an arc exists bewteen n1 and n2.

Parameters
- **n1** (*int*) – the id of the tail node
- **n2** (*int*) – the id of the head node

Returns
True if the arc exists

Return type
bool

existsEdge(*n1*, *n2*)

Check if an edge exists bewteen n1 and n2.

Parameters
- **n1** (*int*) – the id of one extremity of the edge
- **n2** (*int*) – the id of the other extremity if tge edge

Returns
True if the arc exists

Return type
bool

existsNode(*id*)

Check if a node with a certain id exists in the graph.

Parameters
id (*int*) – the checked id

Returns
True if the node exists

Return type
bool

hasDirectedPath(*_from*, *to*)

Check if a directedpath exists bewteen from and to.

Parameters
- **from** (*int*) – the id of the first node of the (possible) path
- **to** (*int*) – the id of the last node of the (possible) path
- **_from** (int) –

Returns
True if the directed path exists

Return type
bool

hasUndirectedCycle()

Checks whether the graph contains cycles.

Returns
True if the graph contains a cycle

Return type
bool

mixedOrientedPath(*node1*, *node2*)

Parameters
- **node1** (*int*) – the id form which the path begins
- **node2** (*int*) – the id to witch the path ends

Returns
a path from node1 to node2, using edges and/or arcs (following the direction of the arcs). If no path is found, the returned list is empty.

Return type
List

mixedUnorientedPath(*node1*, *node2*)

Parameters
- **node1** (*int*) – the id from which the path begins
- **node2** (*int*) – the id to which the path ends

Returns
a path from node1 to node2, using edges and/or arcs (not necessarily following the direction of the arcs). If no path is found, the list is empty.

Return type
List

neighbours(*id*)

Parameters
id (*int*) – the id of the checked node

Returns
The set of edges adjacent to the given node
Return type
Set

`nodes`()

Returns
the set of ids
Return type
set

`nodes2ConnectedComponent`()

Return type
`Dict[int, int]`

`parents`(*id*)

Parameters
id (`int`) – The id of the child node
Returns
the set of the parents ids.
Return type
Set

`partialUndiGraph`(*nodes*)

Parameters
- **nodesSet** (*Set*) – The set of nodes composing the partial graph
- **nodes** (`List[int]`) –

Returns
The partial graph formed by the nodes given in parameter
Return type
pyAgrum.UndiGraph (page 12)

`size`()

Returns
the number of nodes in the graph
Return type
int

`sizeArcs`()

Returns
the number of arcs in the graph
Return type
int

`sizeEdges`()

Returns
the number of edges in the graph
Return type
int

`toDot`()

Returns
a friendly display of the graph in DOT format
Return type
str

`topologicalOrder`(*clear=True*)

Returns
the list of the nodes Ids in a topological order
Return type
List

Raises
pyAgrum.InvalidDirectedCycle (page 290) – If this graph contains cycles
Parameters
clear (bool) –

1.2 Random Variables

aGrUM/pyAgrum is currently dedicated for discrete probability distributions.

There are 5 types of discrete random variables in aGrUM/pyAgrum: LabelizedVariable, DiscretizedVariable, IntegerVariable, RangeVariable and NumericalDiscreteVariable. The 5 types are mainly provided in order to ease modelization. Derived from DiscreteVariable, they share a common API. They essentially differ by the means to create, name and access to their modalities.

1.2.1 Common API for Random Discrete Variables

class pyAgrum.**DiscreteVariable**(**args*, ***kwargs*)

DiscreteVariable is the (abstract) base class for discrete random variables.

description()

Returns
the description of the variable
Return type
str

domain()

Returns
the domain of the variable
Return type
str

domainSize()

Returns
the number of modalities in the variable domain
Return type
int

empty()

Returns
True if the domain size < 2
Return type
bool

index(*label*)

Parameters
label (*str*) – a label
Returns
the indice of the label
Return type
int

label(*i*)

Parameters
i (*int*) – the index of the label we wish to return
Returns
the indice-th label

Return type
str
Raises
pyAgrum.OutOfBounds (page 292) – If the variable does not contain the label

`labels`()

Returns
a tuple containing the labels
Return type
tuple

`name`()

Returns
the name of the variable
Return type
str

`numerical`(*indice*)

Parameters
indice (*int*) – an index
Returns
the numerical representation of the indice-th value
Return type
float

`setDescription`(*theValue*)

set the description of the variable.
Parameters
theValue (*str*) – the new description of the variable
Return type
None

`setName`(*theValue*)

sets the name of the variable.
Parameters
theValue (*str*) – the new description of the variable
Return type
None

`stype`()

Returns
a description of its type
Return type
str

`toDiscretizedVar`()

Returns
the discretized variable
Return type
pyAgrum.DiscretizedVariable (page 31)
Raises
pyAgrum.RuntimeError – If the variable is not a DiscretizedVariable

`toIntegerVar`()

Return type
IntegerVariable (page 35)

`toLabelizedVar`()

Returns
the labelized variable

Return type
pyAgrum.LabelizedVariable (page 27)
Raises
pyAgrum.RuntimeError – If the variable is not a LabelizedVariable

`toNumericalDiscreteVar()`

Return type
NumericalDiscreteVariable (page 42)

`toRangeVar()`

Returns
the range variable
Return type
pyAgrum.RangeVariable (page 39)
Raises
pyAgrum.RuntimeError – If the variable is not a RangeVariable

`toStringWithDescription()`

Returns
a description of the variable
Return type
str

`varType()`

returns the type of variable
Returns

the type of the variable.

0: DiscretizedVariable, 1: LabelizedVariable, 2: IntegerVariable, 3: RangeVariable, 4:
Return type
int

1.2.2 Concrete classes for Random Discrete Variables

LabelizedVariable

`class pyAgrum.LabelizedVariable(*args)`

LabelizedVariable is a discrete random variable with a customizable sequence of labels.

LabelizedVariable(aName, aDesc='', nbrLabel=2) -> LabelizedVariable

Parameters:

- **aName** (str) – the name of the variable
- **aDesc** (str) – the (optional) description of the variable
- **nbrLabel** (int) – the number of labels to create (2 by default)

LabelizedVariable(aName, aDesc='', labels) -> LabelizedVariable

Parameters:

- **aName** (str) – the name of the variable
- **aDesc** (str) – the (optional) description of the variable
- **labels** (List[str]) – the labels to create

LabelizedVariable(aLDRV) -> LabelizedVariable

Parameters:

- **aLDRV** (*pyAgrum.LabelizedVariable*) – The pyAgrum.LabelizedVariable that will be copied

Examples

```
>>> import pyAgrum as gum
>>> # creating a variable with 3 labels : '0', '1' and '2'
>>> va=gum.LabelizedVariable('a','a labelized variable',3)
>>> print(va)
a:Labelized(<0,1,2>)
>>> va.addLabel('foo')
("pyAgrum.LabelizedVariable"@0x7fc4c840dd90) a:Labelized(<0,1,2,foo>)
>>> va.changeLabel(1,'bar')
>>> print(va)
a:Labelized(<0,bar,2,foo>)
>>> vb=gum.LabelizedVariable('b','b',0).addLabel('A').addLabel('B').
↪addLabel('C')
>>> print(vb)
b:Labelized(<A,B,C>)
>>> vb.labels()
('A', 'B', 'C')
>>> vb.isLabel('E')
False
>>> vb.label(2)
'C'
>>> vc=gum.LabelizedVariable('b','b',['one','two','three'])
>>> vc
("pyAgrum.LabelizedVariable"@0x7fc4c840c130) b:Labelized(<one,two,three>
↪)
```

addLabel(**args*)

Add a label with a new index (we assume that we will NEVER remove a label).

Parameters
aLabel (*str*) – the label to be added to the labelized variable

Returns
the labelized variable

Return type
pyAgrum.LabelizedVariable (page 27)

Raises
pyAgrum.DuplicateElement (page 289) – If the variable already contains the label

changeLabel(*pos*, *aLabel*)

Change the label at the specified index

Parameters
- **pos** (*int*) – the index of the label to be changed
- **aLabel** (*str*) – the label to be added to the labelized variable

Raises
- ***pyAgrum.DuplicateElement*** (page 289) – If the variable already contains the new label
- ***pyAgrum.OutOfBounds*** (page 292) – If the index is greater than the size of the variable

Return type
None

description()

Returns
the description of the variable

Return type
str

domain()

Returns
the domain of the variable as a string
Return type
str

domainSize()

Returns
the number of modalities in the variable domain
Return type
int

empty()

Returns
True if the domain size < 2
Return type
bool

eraseLabels()

Erase all the labels from the variable.
Return type
None

index(*label*)

Parameters
label (*str*) – a label
Returns
the indice of the label
Return type
int

isLabel(*aLabel*)

Indicates whether the variable already has the label passed in argument
Parameters
aLabel (*str*) – the label to be tested
Returns
True if the label already exists
Return type
bool

label(*i*)

Parameters
i (*int*) – the index of the label we wish to return
Returns
the indice-th label
Return type
str
Raises
pyAgrum.OutOfBounds (page 292) – If the variable does not contain the label

labels()

Returns
a tuple containing the labels
Return type
tuple

name()

Returns
the name of the variable
Return type
str

`numerical`(*index*)

Parameters
- **indice** (*int*) – an index
- **index** (int) –

Returns
the numerical representation of the indice-th value
Return type
float

`posLabel`(*label*)

Parameters
label (str) –
Return type
int

`setDescription`(*theValue*)

set the description of the variable.

Parameters
theValue (*str*) – the new description of the variable
Return type
None

`setName`(*theValue*)

sets the name of the variable.

Parameters
theValue (*str*) – the new description of the variable
Return type
None

`stype`()

Returns
a description of its type
Return type
str

`toDiscretizedVar`()

Returns
the discretized variable
Return type
pyAgrum.DiscretizedVariable (page 31)
Raises
pyAgrum.RuntimeError – If the variable is not a DiscretizedVariable

`toIntegerVar`()

Return type
IntegerVariable (page 35)

`toLabelizedVar`()

Returns
the labelized variable
Return type
pyAgrum.LabelizedVariable (page 27)
Raises
pyAgrum.RuntimeError – If the variable is not a LabelizedVariable

toNumericalDiscreteVar()

Return type
NumericalDiscreteVariable (page 42)

toRangeVar()

Returns
the range variable
Return type
pyAgrum.RangeVariable (page 39)
Raises
pyAgrum.RuntimeError – If the variable is not a RangeVariable

toStringWithDescription()

Returns
a description of the variable
Return type
str

varType()

returns the type of variable
Returns

the type of the variable.

0: DiscretizedVariable, 1: LabelizedVariable, 2: IntegerVariable, 3: RangeVariable, 4:
Return type
int

DiscretizedVariable

class pyAgrum.**DiscretizedVariable**(**args*)

DiscretizedVariable is a discrete random variable with a set of `ticks` defining intervals.

DiscretizedVariable(aName, aDesc ,ticks=None,is_empirical=False) -> DiscretizedVariable`

Parameters:

- **aName** (*str*) – the name of the variable
- **aDesc** (*str*) – the description of the variable
- ******ticks (*list[float]*) – the list of ticks to add
- **is_empirical** (***bool) – if False, raise an error if a value is out of bound.

DiscretizedVariable(aDDRV) -> DiscretizedVariable

Parameters:

- **aDDRV** (*pyAgrum.DiscretizedVariable*) – the pyAgrum.DiscretizedVariable that will be copied

Examples

```
>>> import pyAgrum as gum
>>> vX=gum.DiscretizedVariable('X','X has been discretized').addTick(1).
↪addTick(2).addTick(3).addTick(3.1415)
>>> print(vX)
X:Discretized(<[1;2[,[2;3[,[3;3.1415]>)
>>> vX.isTick(4)
False
>>> vX.labels()
('[1;2[', '[2;3[', '[3;3.1415]')
>>> # where is the real value 2.5 ?
>>> vX.index('2.5')
1
```

addTick(**args*)

Parameters
aTick (*float*) – the Tick to be added
Returns
the discretized variable
Return type
pyAgrum.DiscretizedVariable (page 31)
Raises
pyAgrum.DefaultInLabel (page 289) – If the tick is already defined

description()

Returns
the description of the variable
Return type
str

domain()

Returns
the domain of the variable as a string
Return type
str

domainSize()

Returns
the number of modalities in the variable domain
Return type
int

empty()

Returns
True if the domain size < 2
Return type
bool

eraseTicks()

erase all the Ticks
Return type
None

index(*label*)

Parameters
label (*str*) – a label
Returns
the indice of the label

Return type
int

`isEmpirical`()

Return type
bool

`isTick`(*aTick*)

Parameters
aTick (*float*) – the Tick to be tested
Returns
True if the Tick already exists
Return type
bool

`label`(*i*)

Parameters
i (*int*) – the index of the label we wish to return
Returns
the indice-th label
Return type
str
Raises
pyAgrum.OutOfBounds (page 292) – If the variable does not contain the label

`labels`()

Returns
a tuple containing the labels
Return type
tuple

`name`()

Returns
the name of the variable
Return type
str

`numerical`(*indice*)

Parameters
indice (*int*) – an index
Returns
the numerical representation of the indice-th value
Return type
float

`setDescription`(*theValue*)

set the description of the variable.
Parameters
theValue (*str*) – the new description of the variable
Return type
None

`setEmpirical`(*state*)

Parameters
state (bool) –
Return type
None

`setName`(*theValue*)

sets the name of the variable.

Parameters
theValue (*str*) – the new description of the variable
Return type
None

stype()

Returns
a description of its type
Return type
str

tick(*i*)

Indicate the index of the Tick

Parameters
i (*int*) – the index of the Tick
Returns
aTick – the index-th Tick
Return type
float
Raises
pyAgrum.NotFound (page 291) – If the index is greater than the number of Ticks

ticks()

Returns
a tuple containing all the Ticks
Return type
tuple

toDiscretizedVar()

Returns
the discretized variable
Return type
pyAgrum.DiscretizedVariable (page 31)
Raises
pyAgrum.RuntimeError – If the variable is not a DiscretizedVariable

toIntegerVar()

Return type
IntegerVariable (page 35)

toLabelizedVar()

Returns
the labelized variable
Return type
pyAgrum.LabelizedVariable (page 27)
Raises
pyAgrum.RuntimeError – If the variable is not a LabelizedVariable

toNumericalDiscreteVar()

Return type
NumericalDiscreteVariable (page 42)

toRangeVar()

Returns
the range variable
Return type
pyAgrum.RangeVariable (page 39)
Raises
pyAgrum.RuntimeError – If the variable is not a RangeVariable

toStringWithDescription()

Returns
a description of the variable
Return type
str

varType()

returns the type of variable
Returns

the type of the variable.

0: DiscretizedVariable, 1: LabelizedVariable, 2: IntegerVariable, 3: RangeVariable, 4:
Return type
int

IntegerVariable

class pyAgrum.**IntegerVariable**(**args*)

IntegerVariable is a discrete random variable with a customizable sequence of int.

IntegerVariable(aName, aDesc='', values) -> IntegerVariable

Parameters:

- **aName** (str) – the name of the variable
- **aDesc** (str) – the (optional) description of the variable
- **values** (List[int]) – the values to create

IntegerVariable(aIDRV) -> IntegerVariable

Parameters:

- **aIDRV** (*pyAgrum.IntegerVariable*) – The pyAgrum.IntegerVariable that will be copied

Examples

```
>>> import pyAgrum as gum
>>> # creating a variable with 3 values : 1,34,142
>>> va=gum.IntegerVariable('a','a integer variable',[1,34,142])
>>> print(va)
a:Integer(<1,34,142>)
>>> va.addValue(25)
(pyAgrum.IntegerVariable@000001E4F5D07490) a:Integer(<1,25,34,142>)
>>> va.changeLabel(34,43)
>>> print(va)
a:Integer(<1,25,43,142>)
>>> vb=gum.IntegerVariable('b','b').addValue(34).addValue(142).
↪addValue(1)
>>> print(vb)
b:Integer(<1,34,142>)
>>> vb.labels()
('1', '34', '142')
```

addValue(**args*)

Add a value to the list of values for the variable.

Parameters
value (*int*) – the new value
Returns
the Integer variable
Return type
pyAgrum.IntegerVariable (page 35)
Raises
pyAgrum.DuplicateElement (page 289) – If the variable already contains the value

changeValue(*old_value*, *new_value*)

Parameters
- **old_value** (*int*) – the value to be changed
- **new_value** (*int*) – the new value

Return type
None

description()

Returns
the description of the variable
Return type
str

domain()

Returns
the domain of the variable
Return type
str

domainSize()

Returns
the number of modalities in the variable domain
Return type
int

empty()

Returns
True if the domain size < 2
Return type
bool

eraseValue(*value*)

Parameters
value (*int*) – the value to erase. If the value is not in the domain, the function does nothing (no exception raised)
Return type
None

eraseValues()

Remove all the domain.
Return type
None

index(*label*)

Parameters
label (*str*) – a label
Returns
the indice of the label
Return type
int

integerDomain()

Returns
the list of integer values that form the domain of this variable
Return type
list[int]

isValue(*value*)

Parameters
value (*int*) – the value to look at.
Returns
True if the value is in the domain.
Return type
bool

label(*index*)

Parameters
- **i** (*int*) – the index of the label we wish to return
- **index** (int) –

Returns
the indice-th label
Return type
str
Raises
pyAgrum.OutOfBounds (page 292) – If the variable does not contain the label

labels()

Returns
a tuple containing the labels
Return type
tuple

name()

Returns
the name of the variable
Return type
str

numerical(*index*)

Parameters
- **indice** (*int*) – an index
- **index** (int) –

Returns
the numerical representation of the indice-th value
Return type
float

setDescription(*theValue*)

set the description of the variable.
Parameters
theValue (*str*) – the new description of the variable
Return type
None

setName(*theValue*)

sets the name of the variable.
Parameters
theValue (*str*) – the new description of the variable
Return type
None

stype()

Returns
a description of its type
Return type
str

toDiscretizedVar()

Returns
the discretized variable
Return type
pyAgrum.DiscretizedVariable (page 31)
Raises
pyAgrum.RuntimeError – If the variable is not a DiscretizedVariable

toIntegerVar()

Return type
IntegerVariable (page 35)

toLabelizedVar()

Returns
the labelized variable
Return type
pyAgrum.LabelizedVariable (page 27)
Raises
pyAgrum.RuntimeError – If the variable is not a LabelizedVariable

toNumericalDiscreteVar()

Return type
NumericalDiscreteVariable (page 42)

toRangeVar()

Returns
the range variable
Return type
pyAgrum.RangeVariable (page 39)
Raises
pyAgrum.RuntimeError – If the variable is not a RangeVariable

toStringWithDescription()

Returns
a description of the variable
Return type
str

varType()

returns the type of variable
Returns

the type of the variable.

0: DiscretizedVariable, 1: LabelizedVariable, 2: IntegerVariable, 3: RangeVariable, 4:
Return type
int

RangeVariable

class pyAgrum.**RangeVariable**(**args*)

RangeVariable represents a variable with a range of integers as domain.

RangeVariable(aName, aDesc,minVal, maxVal) -> RangeVariable

Parameters:

- **aName** (*str*) – the name of the variable
- **aDesc** (*str*) – the description of the variable
- **minVal** (int) – the minimal integer of the interval
- **maxVal** (int) – the maximal integer of the interval

RangeVariable(aName, aDesc='') -> RangeVariable

Parameters:

- **aName** (*str*) – the name of the variable
- **aDesc** (*str*) – the description of the variable

By default `minVal=0` and `maxVal=1`

RangeVariable(aRV) -> RangeVariable

Parameters:

- **aDV** (*RangeVariable*) – the pyAgrum.RangeVariable that will be copied

Examples

```
>>> import pyAgrum as gum
>>> vI=gum.RangeVariable('I','I in [4,10]',4,10)
>>> print(vI)
I:Range([4,10])
>>> vI.maxVal()
10
>>> vI.belongs(1)
False
>>> # where is the value 5 ?
>>> vI.index('5')
1
>>> vI.labels()
('4', '5', '6', '7', '8', '9', '10')
```

belongs(*val*)

Parameters
val (*int*) – the value to be tested
Returns
True if the value in parameters belongs to the variable's interval.
Return type
bool

description()

Returns
the description of the variable
Return type
str

domain()

Returns
the domain of the variable
Return type
str

domainSize()

Returns
the number of modalities in the variable domain
Return type
int

empty()

Returns
True if the domain size < 2
Return type
bool

index(*arg2*)

Parameters
arg2 (*str*) – a label
Returns
the indice of the label
Return type
int

label(*index*)

Parameters
- **indice** (*int*) – the index of the label we wish to return
- **index** (int) –

Returns
the indice-th label
Return type
str
Raises
pyAgrum.OutOfBounds (page 292) – If the variable does not contain the label

labels()

Returns
a tuple containing the labels
Return type
tuple

maxVal()

Returns
the upper bound of the variable.
Return type
int

minVal()

Returns
the lower bound of the variable
Return type
int

name()

Returns
the name of the variable
Return type
str

numerical(*index*)

Parameters
- **indice** (*int*) – an index
- **index** (int) –

Returns
the numerical representation of the indice-th value

Return type
float

setDescription(*theValue*)

set the description of the variable.

Parameters
theValue (*str*) – the new description of the variable

Return type
None

setMaxVal(*maxVal*)

Set a new value of the upper bound

Parameters
maxVal (*int*) – The new value of the upper bound

> **Warning:** An error should be raised if the value is lower than the lower bound.

Return type
None

setMinVal(*minVal*)

Set a new value of the lower bound

Parameters
minVal (*int*) – The new value of the lower bound

> **Warning:** An error should be raised if the value is higher than the upper bound.

Return type
None

setName(*theValue*)

sets the name of the variable.

Parameters
theValue (*str*) – the new description of the variable

Return type
None

stype()

Returns
a description of its type

Return type
str

toDiscretizedVar()

Returns
the discretized variable

Return type
pyAgrum.DiscretizedVariable (page 31)

Raises
pyAgrum.RuntimeError – If the variable is not a DiscretizedVariable

toIntegerVar()

Return type
IntegerVariable (page 35)

toLabelizedVar()

Returns
the labelized variable
Return type
pyAgrum.LabelizedVariable (page 27)
Raises
pyAgrum.RuntimeError – If the variable is not a LabelizedVariable

toNumericalDiscreteVar()

Return type
NumericalDiscreteVariable (page 42)

toRangeVar()

Returns
the range variable
Return type
pyAgrum.RangeVariable (page 39)
Raises
pyAgrum.RuntimeError – If the variable is not a RangeVariable

toStringWithDescription()

Returns
a description of the variable
Return type
str

varType()

returns the type of variable
Returns

the type of the variable.

0: DiscretizedVariable, 1: LabelizedVariable, 2: IntegerVariable, 3: RangeVariable, 4:
Return type
int

NumericalDiscreteVariable

class pyAgrum.**NumericalDiscreteVariable**(**args*)

addValue(**args*)

Add a value to the list of values for the variable.
Parameters
value (*float*) – the new value
Returns
the Integer variable
Return type
pyAgrum.IntegerVariable (page 35)
Raises
pyAgrum.DuplicateElement (page 289) – If the variable already contains the value

changeValue(*old_value*, *new_value*)

Parameters
- **old_value** (float) –
- **new_value** (float) –

Return type
None

closestIndex(*val*)

Parameters
val (float) –
Return type
int

closestLabel(*val*)

Parameters
val (float) –
Return type
str

description()

Returns
the description of the variable
Return type
str

domain()

Returns
the domain of the variable
Return type
str

domainSize()

Returns
the number of modalities in the variable domain
Return type
int

empty()

Returns
True if the domain size < 2
Return type
bool

eraseValue(*value*)

Parameters
value (float) –
Return type
None

eraseValues()

Return type
None

index(*label*)

Parameters
label (*str*) – a label
Returns
the indice of the label
Return type
int

isValue(*value*)

Parameters
value (float) –

Return type
bool

label(*index*)

Parameters
- **i** (*int*) – the index of the label we wish to return
- **index** (int) –

Returns
the indice-th label

Return type
str

Raises
pyAgrum.OutOfBounds (page 292) – If the variable does not contain the label

labels()

Returns
a tuple containing the labels

Return type
tuple

name()

Returns
the name of the variable

Return type
str

numerical(*index*)

Parameters
- **indice** (*int*) – an index
- **index** (int) –

Returns
the numerical representation of the indice-th value

Return type
float

numericalDomain()

Return type
object

setDescription(*theValue*)

set the description of the variable.

Parameters
theValue (*str*) – the new description of the variable

Return type
None

setName(*theValue*)

sets the name of the variable.

Parameters
theValue (*str*) – the new description of the variable

Return type
None

stype()

Returns
a description of its type

Return type
str

toDiscretizedVar()

Returns
the discretized variable
Return type
pyAgrum.DiscretizedVariable (page 31)
Raises
pyAgrum.RuntimeError – If the variable is not a DiscretizedVariable

toIntegerVar()

Return type
IntegerVariable (page 35)

toLabelizedVar()

Returns
the labelized variable
Return type
pyAgrum.LabelizedVariable (page 27)
Raises
pyAgrum.RuntimeError – If the variable is not a LabelizedVariable

toNumericalDiscreteVar()

Return type
NumericalDiscreteVariable (page 42)

toRangeVar()

Returns
the range variable
Return type
pyAgrum.RangeVariable (page 39)
Raises
pyAgrum.RuntimeError – If the variable is not a RangeVariable

toStringWithDescription()

Returns
a description of the variable
Return type
str

varType()

returns the type of variable
Returns

the type of the variable.

0: DiscretizedVariable, 1: LabelizedVariable, 2: IntegerVariable, 3: RangeVariable, 4:
Return type
int

1.3 Potential and Instantiation

pyAgrum.Potential (page 53) is a multi-dimensional array with a *pyAgrum.DiscreteVariable* (page 25) associated to each dimension. It is used to represent probabilities and utilities tables in aGrUMs' multidimensional (graphical) models with some conventions.

- The data are stored by iterating over each variable in the sequence.

```
>>> a=gum.RangeVariable("A","variable A",1,3)
>>> b=gum.RangeVariable("B","variable B",1,2)
>>> p=gum.Potential().add(a).add(b).fillWith([1,2,3,4,5,6])
```

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```
>>> print(p)
      ||  A                          |
B     ||1         |2         |3         |
------||----------|----------|----------|
1     || 1.0000  | 2.0000  | 3.0000  |
2     || 4.0000  | 5.0000  | 6.0000  |
```

- If a *pyAgrum.Potential* (page 53) with the sequence of *pyAgrum.DiscreteVariable* (page 25) X,Y,Z represents a conditional probability Table (CPT), it will be P(X|Y,Z).

```
>>> print(p.normalizeAsCPT())
      ||  A                          |
B     ||1         |2         |3         |
------||----------|----------|----------|
1     || 0.1667  | 0.3333  | 0.5000  |
2     || 0.2667  | 0.3333  | 0.4000  |
```

- For addressing and looping in a *pyAgrum.Potential* (page 53) structure, pyAgrum provides `Instantiation` class which represents a multi-dimensionnal index.

```
>>> I=gum.Instantiation(p)
>>> print(I)
<A:1|B:1>
>>> I.inc();print(I)
<A:2|B:1>
>>> I.inc();print(I)
<A:3|B:1>
>>> I.inc();print(I)
<A:1|B:2>
>>> I.setFirst();print(f"{I} -> {p.get(I)}")
<A:1|B:1> -> 0.16666666666666666
>>> I["B"]="2";print(f"{I} -> {p.get(I)}")
<A:1|B:2> -> 0.26666666666666666
```

- *pyAgrum.Potential* (page 53) include tensor operators (see for instance this notebook (http://www-desir.lip6.fr/~phw/aGrUM/docs/last/notebooks/potentials.ipynb.html)).

```
>>> c=gum.RangeVariable("C","variable C",1,5)
>>> q=gum.Potential().add(a).add(c).fillWith(1)
>>> print(p+q)
             ||  A                          |
C     |B     ||1         |2         |3         |
------|------||----------|----------|----------|
1     |1     || 1.1667  | 1.3333  | 1.5000  |
2     |1     || 1.1667  | 1.3333  | 1.5000  |
3     |1     || 1.1667  | 1.3333  | 1.5000  |
4     |1     || 1.1667  | 1.3333  | 1.5000  |
5     |1     || 1.1667  | 1.3333  | 1.5000  |
1     |2     || 1.2667  | 1.3333  | 1.4000  |
2     |2     || 1.2667  | 1.3333  | 1.4000  |
3     |2     || 1.2667  | 1.3333  | 1.4000  |
4     |2     || 1.2667  | 1.3333  | 1.4000  |
5     |2     || 1.2667  | 1.3333  | 1.4000  |
>>> print((p*q).margSumOut(["B","C"])) # marginalize p*q over B and C(using␣
↪sum)
  A                          |
1         |2         |3         |
```

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```
---------|---------|---------|
 2.1667  | 3.3333  | 4.5000  |
```

1.3.1 Instantiation

class pyAgrum.**Instantiation**(**args*)

Class for assigning/browsing values to tuples of discrete variables.

Instantiation is designed to assign values to tuples of variables and to efficiently loop over values of subsets of variables.

Instantiation() -> Instantiation
default constructor

Instantiation(aI) -> Instantiation

Parameters:

- **aI** (*pyAgrum.Instantiation*) – the Instantiation we copy

Returns

- *pyAgrum.Instantiation* – An empty tuple or a copy of the one in parameters
- *Instantiation is subscriptable therefore values can be easily accessed/modified.*

Examples

```
>>> ## Access the value of A in an instantiation aI
>>> valueOfA = aI['A']
>>> ## Modify the value
>>> aI['A'] = newValueOfA
```

add(*v*)

Adds a new variable in the Instantiation.

Parameters
v (pyAgrum.DiscreteVariable (page 25)) – The new variable added to the Instantiation

Raises
DuplicateElement (page 289) – If the variable is already in this Instantiation

Return type
None

addVarsFromModel(*model*, *names*)

From a graphical model, add all the variable whose names are in the iterable

Parameters
- **model** (*pyAgrum.GraphicalModel*) –
- **network** (*Markov*) –
- **network** –
- **Diagram** (*Influence*) –
- **etc.** –
- **names** (*iterable of strings*) –
- **string)** (*a list/set/etc of names of variables (as*) –

Returns
- *pyAgrum.Instantiation*
- *the current instantiation (self) in order to chain methods.*

chgVal(**args*)

Assign newval to v (or to the variable at position varPos) in the Instantiation.

Parameters

- **v** (pyAgrum.DiscreteVariable (page 25) *or string*) – The variable whose value is assigned (or its name)
- **varPos** (*int*) – The index of the variable whose value is assigned in the tuple of variables of the Instantiation
- **newval** (*int or string*) – The index of the value assigned (or its name)

Returns

The modified instantiation

Return type

pyAgrum.Instantiation (page 47)

Raises

- ***NotFound*** (page 291) – If variable v does not belong to the instantiation.
- ***OutOfBounds*** (page 292) – If newval is not a possible value for the variable.

clear()

Erase all variables from an Instantiation.

Return type

None

contains(**args*)

Indicates whether a given variable belongs to the Instantiation.

Parameters

v (pyAgrum.DiscreteVariable (page 25)) – The variable for which the test is made.

Returns

True if the variable is in the Instantiation.

Return type

bool

dec()

Operator –.

Return type

None

decIn(*i*)

Operator – for the variables in i.

Parameters

i (pyAgrum.Instantiation (page 47)) – The set of variables to decrement in this Instantiation

Return type

None

decNotVar(*v*)

Operator – for vars which are not v.

Parameters

v (pyAgrum.DiscreteVariable (page 25)) – The variable not to decrement in this Instantiation.

Return type

None

decOut(*i*)

Operator – for the variables not in i.

Parameters

i (pyAgrum.Instantiation (page 47)) – The set of variables to not decrement in this Instantiation.

Return type

None

decVar(*v*)

Operator – for variable v only.

Parameters
v (pyAgrum.DiscreteVariable (page 25)) – The variable to decrement in this Instantiation.

Raises
NotFound (page 291) – If variable v does not belong to the Instantiation.

Return type
None

domainSize()

Returns
The product of the variable's domain size in the Instantiation.

Return type
int

empty()

Returns
True if the instantiation is empty.

Return type
bool

end()

Returns
True if the Instantiation reached the end.

Return type
bool

erase(**args*)

Parameters
v (pyAgrum.DiscreteVariable (page 25)) – The variable to be removed from this Instantiation.

Raises
NotFound (page 291) – If v does not belong to this Instantiation.

Return type
None

fromdict(*dict*)

Change the values in an instantiation from a dictionary *{variable_name:value}* where value can be a position (int) or a label (string).

If a variable_name does not occur in the instantiation, nothing is done.

> **Warning:** OutOfBounds raised if a value cannot be found.

Parameters
dict (object) –

Return type
None

hamming()

Returns
the hamming distance of this instantiation.

Return type
int

inOverflow()

Returns
True if the current value of the tuple is correct

Return type
bool

`inc()`

Operator ++.

Return type
None

`incIn(i)`

Operator ++ for the variables in i.

Parameters
i (pyAgrum.Instantiation (page 47)) – The set of variables to increment in this Instantiation.

Return type
None

`incNotVar(v)`

Operator ++ for vars which are not v.

Parameters
v (pyAgrum.DiscreteVariable (page 25)) – The variable not to increment in this Instantiation.

Return type
None

`incOut(i)`

Operator ++ for the variables not in i.

Parameters
i (Instantiation (page 47)) – The set of variable to not increment in this Instantiation.

Return type
None

`incVar(v)`

Operator ++ for variable v only.

Parameters
v (pyAgrum.DiscreteVariable (page 25)) – The variable to increment in this Instantiation.

Raises
NotFound (page 291) – If variable v does not belong to the Instantiation.

Return type
None

`isMutable()`

Return type
bool

`nbrDim()`

Returns
The number of variables in the Instantiation.

Return type
int

`pos(v)`

Returns
the position of the variable v.

Return type
int

Parameters
v (pyAgrum.DiscreteVariable (page 25)) – the variable for which its position is return.

Raises
NotFound (page 291) – If v does not belong to the instantiation.

`rend()`

Returns
True if the Instantiation reached the rend.
Return type
bool

`reorder(*args)`

Reorder vars of this instantiation giving the order in v (or i).
Parameters
- **i** (pyAgrum.Instantiation (page 47)) – The sequence of variables with which to reorder this Instantiation.
- **v** (*list*) – The new order of variables for this Instantiation.

Return type
None

`setFirst()`

Assign the first values to the tuple of the Instantiation.
Return type
None

`setFirstIn(i)`

Assign the first values in the Instantiation for the variables in i.
Parameters
i (pyAgrum.Instantiation (page 47)) – The variables to which their first value is assigned in this Instantiation.
Return type
None

`setFirstNotVar(v)`

Assign the first values to variables different of v.
Parameters
v (pyAgrum.DiscreteVariable (page 25)) – The variable that will not be set to its first value in this Instantiation.
Return type
None

`setFirstOut(i)`

Assign the first values in the Instantiation for the variables not in i.
Parameters
i (pyAgrum.Instantiation (page 47)) – The variable that will not be set to their first value in this Instantiation.
Return type
None

`setFirstVar(v)`

Assign the first value in the Instantiation for var v.
Parameters
v (pyAgrum.DiscreteVariable (page 25)) – The variable that will be set to its first value in this Instantiation.
Return type
None

`setLast()`

Assign the last values in the Instantiation.
Return type
None

setLastIn(*i*)

Assign the last values in the Instantiation for the variables in i.

Parameters

i (pyAgrum.Instantiation (page 47)) – The variables to which their last value is assigned in this Instantiation.

Return type

None

setLastNotVar(*v*)

Assign the last values to variables different of v.

Parameters

v (pyAgrum.DiscreteVariable (page 25)) – The variable that will not be set to its last value in this Instantiation.

Return type

None

setLastOut(*i*)

Assign the last values in the Instantiation for the variables not in i.

Parameters

i (pyAgrum.Instantiation (page 47)) – The variables that will not be set to their last value in this Instantiation.

Return type

None

setLastVar(*v*)

Assign the last value in the Instantiation for var v.

Parameters

v (pyAgrum.DiscreteVariable (page 25)) – The variable that will be set to its last value in this Instantiation.

Return type

None

setMutable()

Return type

None

setVals(*i*)

Assign the values from i in the Instantiation.

Parameters

i (pyAgrum.Instantiation (page 47)) – An Instantiation in which the new values are searched

Returns

a reference to the instantiation

Return type

pyAgrum.Instantiation (page 47)

todict(*withLabels=True*)

Create a dictionary *{variable_name:value}* from an instantiation

Parameters

withLabels (*boolean*) – The value will be a label (string) if True. It will be a position (int) if False.

Returns

The dictionary

Return type

Dict[str,int]

unsetEnd()

Alias for unsetOverflow().

Return type

None

unsetOverflow()

Removes the flag overflow.

Return type
None

val(**args*)

Parameters
- **i** (*int*) – The index of the variable.
- **var** (pyAgrum.DiscreteVariable (page 25)) – The variable the value of which we wish to know

Returns
the current value of the variable.

Return type
int

Raises
NotFound (page 291) – If the element cannot be found.

variable(**args*)

Parameters
i (*int*) – The index of the variable

Returns
the variable at position i in the tuple.

Return type
pyAgrum.DiscreteVariable (page 25)

Raises
NotFound (page 291) – If the element cannot be found.

variablesSequence()

Returns
a list containing the sequence of variables

Return type
list

1.3.2 Potential

class pyAgrum.**Potential**(**args*)

Class representing a potential.

Potential() -> Potential
default constructor

Potential(src) -> Potential

Parameters:

- **src** (*pyAgrum.Potential*) – the Potential to copy

KL(*p*)

Check the compatibility and compute the Kullback-Leibler divergence between the potential and.

Parameters
p (pyAgrum.Potential (page 53)) – the potential from which we want to calculate the divergence.

Returns
The value of the divergence

Return type
float

Raises
- *pyAgrum.InvalidArgument* (page 290) – If p is not compatible with the potential (dimension, variables)

- *pyAgrum.FatalError* (page 289) – If a zero is found in p or the potential and not in the other.

abs()

Apply abs on every element of the container

Returns
a reference to the modified potential.

Return type
pyAgrum.Potential (page 53)

add(*v*)

Add a discrete variable to the potential.

Parameters
v (pyAgrum.DiscreteVariable (page 25)) – the var to be added

Raises
- *DuplicateElement* (page 289) – If the variable is already in this Potential.
- *InvalidArgument* (page 290) – If the variable is empty.

Returns
a reference to the modified potential.

Return type
pyAgrum.Potential (page 53)

argmax()

Returns
the list of positions of the max and the max of all elements in the Potential

Return type
Tuple[Dict[str,int],float]

argmin()

Returns
the list of positions of the min and the min of all elements in the Potential

Return type
Tuple[Dict[str,int],float]

contains(*v*)

Parameters
v (pyAgrum.Potential (page 53)) – a DiscreteVariable.

Returns
True if the var is in the potential

Return type
bool

domainSize()

Return type
int

draw()

draw a value using the potential as a probability table.

Returns
the index of the drawn value

Return type
int

empty()

Returns
Returns true if no variable is in the potential.

Return type
bool

entropy()

Returns
the entropy of the potential
Return type
float

`extract`(**args*)

create a new Potential extracted from self given a partial instantiation.

Parameters
- **inst** (*pyAgrum.instantiation*) – a partial instantiation
- **dict** (*Dict[str,str|int]*) – a dictionnary containing values for some discrete variables.

> **Warning:** if the dictionnary contains a key that is not the name of a variable in the *pyAgrum.Potential*, this key is just not used without notification. Then *pyAgrum.Potential.extract* concerns only the variables that both are in the Potential and in the dictionnary.

Returns
the new Potential
Return type
pyAgrum.Potential (page 53)

`fillWith`(**args*)

Automatically fills the potential with v.

Parameters
- **v** (*number or list of values or* pyAgrum.Potential (page 53)) – a value or a list/pyAgrum.Potential containing the values to fill the Potential with.
- **mapping** (*list|tuple|dict*) –

> **Warning:**
> - if *v* is a list, the size of the list must be the size of the potential
> - if *v* is a ref:pyAgrum.Potential, it must contain variables with exactly the same names and labels but not necessarily the same variables. If
> - If the second argument *mapping* is given, *mapping* explains how to map the variables of the potential source to the variables of the potential destination.
> - If *mapping* is a sequence, the order follows the same order as *destination.names*. If *mapping* is a dict, the keys are the names in the destination and the values are the names in the source.

Returns
a reference to the modified potentia
Return type
pyAgrum.Potential (page 53)
Raises
- ***pyAgrum.SizeError*** (page 292) – If v size's does not matches the domain size.
- ***pyAgrum.ArgumentError*** (page 292) – If anything wrong with the arguments.

`fillWithFunction`(*s*, *noise=None*)

Automatically fills the potential as a (quasi) deterministic CPT with the evaluation of the expression s.

The expression s gives a value for the first variable using the names of the last variables. The computed CPT is deterministic unless noise is used to add a 'probabilistic' noise around the exact value given by the expression.

Examples

```
>>> import pyAgrum as gum
>>> bn=gum.fastBN("A[3]->B[3]<-C[3]")
>>> bn.cpt("B").fillWithFunction("(A+C)/2")
```

Parameters
- **s** (*str*) – an expression using the name of the last variables of the Potential and giving a value to the first variable of the Potential
- **noise** (*list*) – an (odd) list of numerics giving a pattern of 'probabilistic noise' around the value.

Warning: The expression may have any numerical values, but will be then transformed to the closest correct value for the range of the variable.

Returns
a reference to the modified potential
Return type
pyAgrum.Potential (page 53)
Raises
- ***pyAgrum.InvalidArgument*** (page 290) –
- **If the first variable is Labelized or Integer, or if the len of the noise is not odd.** –

findAll(*v*)

Parameters
v (float) –
Return type
List[Dict[str, int]]

get(*i*)

Parameters
i (pyAgrum.Instantiation (page 47)) – an Instantiation
Returns
the value in the Potential at the position given by the instantiation
Return type
float

inverse()

Return type
Potential (page 53)

isNonZeroMap()

Returns
a boolean-like potential using the predicate *isNonZero*.
Return type
pyAgrum.Potential (page 53)

log2()

log2 all the values in the Potential

Warning: When the Potential contains 0 or negative values, no exception are raised but *-inf* or *nan* values are assigned.

Return type
Potential (page 53)

loopIn()

Generator to iterate inside a Potential.

Yield an pyAgrum.Instantiation that iterates over all the possible values for the pyAgrum.Potential

Examples

```
>>> import pyAgrum as gum
>>> bn=gum.fastBN("A[3]->B[3]<-C[3]")
>>> for i in bn.cpt("B").loopIn():
      print(i)
      print(bn.cpt("B").get(i))
      bn.cpt("B").set(i,0.3)
```

margMaxIn(*varnames*)

Projection using *max* as operation.

Parameters
varnames (*set*) – the set of vars to keep

Returns
the projected Potential

Return type
pyAgrum.Potential (page 53)

margMaxOut(*varnames*)

Projection using *max* as operation.

Parameters
varnames (*set*) – the set of vars to eliminate

Returns
the projected Potential

Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.InvalidArgument (page 290) – If varnames contains only one variable that does not exist in the Potential

margMinIn(*varnames*)

Projection using *min* as operation.

Parameters
varnames (*set*) – the set of vars to keep

Returns
the projected Potential

Return type
pyAgrum.Potential (page 53)

margMinOut(*varnames*)

Projection using *min* as operation.

Parameters
varnames (*set*) – the set of vars to eliminate

Returns
the projected Potential

Return type
pyAgrum.Potential (page 53)

Warning: InvalidArgument raised if varnames contains only one variable that does not exist in the Potential

margProdIn(*varnames*)

Projection using multiplication as operation.

Parameters
varnames (*set*) – the set of vars to keep

Returns
the projected Potential

Return type
pyAgrum.Potential (page 53)

margProdOut(*varnames*)

Projection using multiplication as operation.

Parameters
varnames (*set*) – the set of vars to eliminate

Returns
the projected Potential

Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.InvalidArgument (page 290) – If varnames contains only one variable that does not exist in the Potential

margSumIn(*varnames*)

Projection using sum as operation.

Parameters
varnames (*set*) – the set of vars to keep

Returns
the projected Potential

Return type
pyAgrum.Potential (page 53)

margSumOut(*varnames*)

Projection using sum as operation.

Parameters
varnames (*set*) – the set of vars to eliminate

Returns
the projected Potential

Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.InvalidArgument (page 290) – If varnames contains only one variable that does not exist in the Potential

max()

Returns
the maximum of all elements in the Potential

Return type
float

maxNonOne()

Returns
the maximum of non one elements in the Potential

Return type
float

Raises
pyAgrum.NotFound (page 291) – If all value == 1.0

min()

Returns
the min of all elements in the Potential

Return type
float

`minNonZero()`

Returns
the min of non zero elements in the Potential
Return type
float
Raises
pyAgrum.NotFound (page 291) – If all value == 0.0

`property names`

Returns
a list containing the name of each variables in the potential
Return type
list

> **Warning:** listed in the reverse order of the enumeration order of the variables.

`nbrDim(*args)`

Returns
the number of vars in the multidimensional container.
Return type
int

`newFactory()`

Erase the Potential content and create a new empty one.
Returns
a reference to the new Potential
Return type
pyAgrum.Potential (page 53)

`new_abs()`

Return type
Potential (page 53)

`new_log2()`

Return type
Potential (page 53)

`new_sq()`

Return type
Potential (page 53)

`noising(alpha)`

Parameters
alpha (float) –
Return type
Potential (page 53)

`normalize()`

Normalize the Potential (do nothing if sum is 0)
Returns
a reference to the normalized Potential
Return type
pyAgrum.Potential (page 53)

`normalizeAsCPT(varId=0)`

Normalize the Potential as a CPT

Returns
a reference to the normalized Potential
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.FatalError (page 289) – If some distribution sums to 0
Parameters
varId (int) –

pos(*v*)

Parameters
v (pyAgrum.DiscreteVariable (page 25)) – The variable for which the index is returned.
Return type
Returns the index of a variable.
Raises
pyAgrum.NotFound (page 291) – If v is not in this multidimensional matrix.

product()

Returns
the product of all elements in the Potential
Return type
float

putFirst(*varname*)

Parameters
- **v** (pyAgrum.DiscreteVariable (page 25)) – The variable for which the index should be 0.
- **varname** (str) –

Returns
a reference to the modified potential
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.InvalidArgument (page 290) – If the var is not in the potential

random()

Return type
Potential (page 53)

randomCPT()

Return type
Potential (page 53)

randomDistribution()

Return type
Potential (page 53)

remove(*var*)

Parameters
v (pyAgrum.DiscreteVariable (page 25)) – The variable to be removed
Returns
a reference to the modified potential
Return type
pyAgrum.Potential (page 53)

> **Warning:** IndexError raised if the var is not in the potential

Parameters
var (*DiscreteVariable* (page 25)) –

reorganize(**args*)

Create a new Potential with another order.

Returns
varnames – a list of the var names in the new order
Return type
list
Returns
a reference to the modified potential
Return type
pyAgrum.Potential (page 53)

scale(*v*)

Create a new potential multiplied by v.

Parameters
v (*float*) – a multiplier
Return type
a reference to the modified potential

set(*i*, *value*)

Change the value pointed by i

Parameters
- **i** (pyAgrum.Instantiation (page 47)) – The Instantiation to be changed
- **value** (*float*) – The new value of the Instantiation

Return type
None

property shape

Returns
a list containing the dimensions of each variables in the potential
Return type
list

Warning: *p.shape* and *p[:].shape* list the dimensions in different order

sq()

Square all the values in the Potential

Return type
Potential (page 53)

sum()

Returns
the sum of all elements in the Potential
Return type
float

property thisown

The membership flag

toarray()

Returns
the potential as an array
Return type
array

toclipboard(***kwargs*)

Write a text representation of object to the system clipboard. This can be pasted into spreadsheet, for instance.

`tolatex()`

Render object to a LaTeX tabular.

Requires to include *booktabs* package in the LaTeX document.

Returns
the potential as LaTeX string

Return type
str

`tolist()`

Returns
the potential as a list

Return type
list

`topandas()`

Returns
the potential as an pandas.DataFrame

Return type
pandas.DataFrame

`translate(v)`

Create a new potential added with v.

Parameters
v (*float*) – The value to be added

Return type
a reference to the modified potential

`property var_dims`

Returns
a list containing the dimensions of each variables in the potential

Return type
list

> **Warning:** This methods is deprecated. Please use gum.Potential.shape and note the change in the order !
>
> var_dims return a list in the reverse order of the enumeration order of the variables.

`property var_names`

Returns
a list containing the name of each variables in the potential

Return type
list

> **Warning:** This methods is deprecated. Please use gum.Potential.names and note the change in the order !
>
> var_names return a list in the reverse order of the enumeration order of the variables.

`variable(*args)`

Parameters
i (*int*) – An index of this multidimensional matrix.

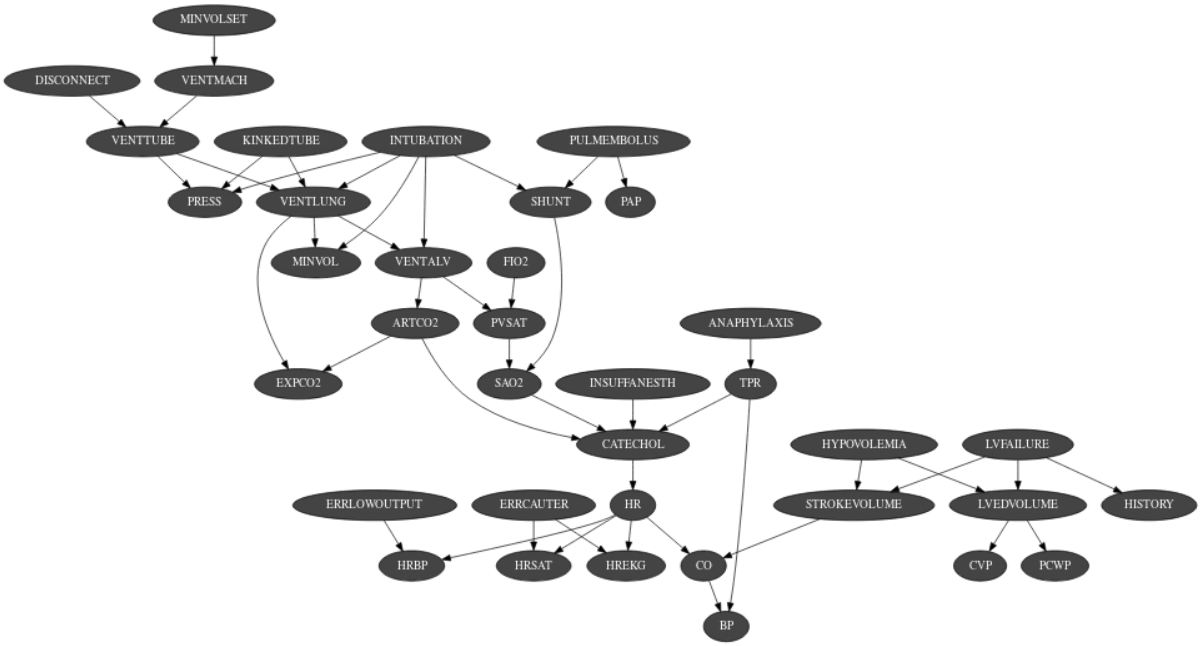
Return type
the varible at the ith index

Raises
pyAgrum.NotFound (page 291) – If i does not reference a variable in this multidimensional matrix.

`variablesSequence()`

Returns
a list containing the sequence of variables
Return type
list

1.4 Bayesian network



The Bayesian network is the main graphical model of pyAgrum. A Bayesian network is a directed probabilistic graphical model based on a DAG. It represents a joint distribution over a set of random variables. In pyAgrum, the variables are (for now) only discrete.

A Bayesian network uses a directed acyclic graph (DAG) to represent conditional independence in the joint distribution. These conditional independence allow to factorize the joint distribution, thereby allowing to compactly represent very large ones.

$$P(X_1, \cdots, X_n) = \prod_{i=1}^{n} P(X_i | Parents(X_i))$$

Moreover, inference algorithms can also use this graph to speed up the computations. Finally, the Bayesian networks can be learnt from data.

Tutorial

- Tutorials on Bayesian network

Reference

1.4.1 Model

class pyAgrum.**BayesNet**(**args*)

BayesNet represents a Bayesian network.

BayesNet(name='') -> BayesNet

Parameters:

- **name** (*str*) – the name of the Bayes Net

BayesNet(source) -> BayesNet

Parameters:

- **source** (*pyAgrum.BayesNet*) – the Bayesian network to copy

add(**args*)

Add a variable to the pyAgrum.BayesNet.

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable added
- **descr** (*str*) – the description of the variable (following *fast syntax* (page 281))
- **nbrmod** (*int*) – the number of modalities for the new variable
- **id** (*int*) – the variable forced id in the pyAgrum.BayesNet

Returns
the id of the new node

Return type
int

Raises
- ***pyAgrum.DuplicateLabel*** (page 289) – If variable.name() or id is already used in this pyAgrum.BayesNet.
- **pyAgrum.NotAllowed** – If nbrmod is less than 2

addAMPLITUDE(*var*)

Others aggregators

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable to be added
- **var** (*DiscreteVariable* (page 25)) –

Returns
the id of the added value

Return type
int

addAND(*var*)

Add a variable, it's associate node and an AND implementation.

The id of the new variable is automatically generated.

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – The variable added by copy.
- **var** (*DiscreteVariable* (page 25)) –

Returns
the id of the added variable.

Return type
int

Raises
pyAgrum.SizeError (page 292) – If variable.domainSize()>2

addArc(**args*)

Add an arc in the BN, and update arc.head's CPT.

Parameters
- **head** (*Union[int,str]*) – a variable's id (int) or name
- **head** – a variable's id (int) or name

Raises
- ***pyAgrum.InvalidEdge*** (page 290) – If arc.tail and/or arc.head are not in the BN.
- ***pyAgrum.DuplicateElement*** (page 289) – If the arc already exists.

Return type
None

addArcs(*listArcs*)

add a list of arcs in te model.

Parameters
listArcs (*List[Tuple[intstr,intstr]]*) – the list of arcs

addCOUNT(*var*, *value=1*)

Others aggregators

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable to be added
- **var** (*DiscreteVariable* (page 25)) –
- **value** (int) –

Returns
the id of the added value

Return type
int

addEXISTS(*var*, *value=1*)

Others aggregators

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable to be added
- **var** (*DiscreteVariable* (page 25)) –
- **value** (int) –

Returns
the id of the added value

Return type
int

addFORALL(*var*, *value=1*)

Others aggregators

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable to be added
- **var** (*DiscreteVariable* (page 25)) –
- **value** (int) –

Returns
the id of the added variable.

Return type
int

addLogit(**args*)

Add a variable, its associate node and a Logit implementation.

(The id of the new variable can be automatically generated.)

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – The variable added by copy
- **externalWeight** (*float*) – the added external weight
- **id** (*int*) – The proposed id for the variable.

Returns
the id of the added variable.
Return type
int
Raises
pyAgrum.DuplicateElement (page 289) – If id is already used

addMAX(*var*)

Others aggregators
Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable to be added
- **var** (*DiscreteVariable* (page 25)) –

Returns
the id of the added value
Return type
int

addMEDIAN(*var*)

Others aggregators
Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable to be added
- **var** (*DiscreteVariable* (page 25)) –

Returns
the id of the added value
Return type
int

addMIN(*var*)

Others aggregators
Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable to be added
- **var** (*DiscreteVariable* (page 25)) –

Returns
the id of the added value
Return type
int

addNoisyAND(**args*)

Add a variable, its associate node and a noisyAND implementation.

(The id of the new variable can be automatically generated.)
Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – The variable added by copy
- **externalWeight** (*float*) – the added external weight
- **id** (*int*) – The proposed id for the variable.

Returns
the id of the added variable.
Return type
int
Raises
pyAgrum.DuplicateElement (page 289) – If id is already used

addNoisyOR(**args*)

Add a variable, it's associate node and a noisyOR implementation.

Since it seems that the 'classical' noisyOR is the Compound noisyOR, we keep the addNoisyOR as an alias for addNoisyORCompound.

(The id of the new variable can be automatically generated.)

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – The variable added by copy
- **externalWeight** (*float*) – the added external weight
- **id** (*int*) – The proposed id for the variable.

Returns
the id of the added variable.

Return type
int

Raises
pyAgrum.DuplicateElement (page 289) – If id is already used

addNoisyORCompound(**args*)

Add a variable, it's associate node and a noisyOR implementation.

Since it seems that the 'classical' noisyOR is the Compound noisyOR, we keep the addNoisyOR as an alias for addNoisyORCompound.

(The id of the new variable can be automatically generated.)

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – The variable added by copy
- **externalWeight** (*float*) – the added external weight
- **id** (*int*) – The proposed id for the variable.

Returns
the id of the added variable.

Return type
int

Raises
pyAgrum.DuplicateElement (page 289) – If id is already used

addNoisyORNet(**args*)

Add a variable, its associate node and a noisyOR implementation.

Since it seems that the 'classical' noisyOR is the Compound noisyOR, we keep the addNoisyOR as an alias for addNoisyORCompound.

(The id of the new variable can be automatically generated.)

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – The variable added by copy
- **externalWeight** (*float*) – the added external weight
- **id** (*int*) – The proposed id for the variable.

Returns
the id of the added variable.

Return type
int

addOR(*var*)

Add a variable, it's associate node and an OR implementation.

The id of the new variable is automatically generated.

> **Warning:** If parents are not boolean, all value>1 is True

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – The variable added by copy
- **var** (*DiscreteVariable* (page 25)) –

Returns
the id of the added variable.
Return type
int
Raises
pyAgrum.SizeError (page 292) – If variable.domainSize()>2

addSUM(*var*)

Others aggregators
Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable to be added
- **var** (*DiscreteVariable* (page 25)) –

Returns
the id of the added value
Return type
int

addStructureListener(*whenNodeAdded=None*, *whenNodeDeleted=None*, *whenArcAdded=None*, *whenArcDeleted=None*)

Add the listeners in parameters to the list of existing ones.
Parameters
- **whenNodeAdded** (*lambda expression*) – a function for when a node is added
- **whenNodeDeleted** (*lambda expression*) – a function for when a node is removed
- **whenArcAdded** (*lambda expression*) – a function for when an arc is added
- **whenArcDeleted** (*lambda expression*) – a function for when an arc is removed

addVariables(*listFastVariables*, *default_nbr_mod=2*)

Add a list of variable in the form of 'fast' syntax.
Parameters
- **listFastVariables** (*List[str]*) – the list of variables in 'fast' syntax.
- **default_nbr_mod** (*int*) – the number of modalities for the variable if not specified following *fast syntax* (page 281). Note that default_nbr_mod=1 is mandatory to create variables with only one modality (for utility for instance).

Returns
the list of created ids.
Return type
List[int]

addWeightedArc(**args*)

Add an arc in the BN, and update arc.head's CPT.
Parameters
- **head** (*Union[int,str]*) – a variable's id (int) or name
- **tail** (*Union[int,str]*) – a variable's id (int) or name
- **causalWeight** (*float*) – the added causal weight

Raises
- *pyAgrum.InvalidArc* (page 290) – If arc.tail and/or arc.head are not in the BN.
- *pyAgrum.InvalidArc* (page 290) – If variable in arc.head is not a NoisyOR variable.

Return type
None

ancestors(*norid*)

Parameters
norid (object) –

Return type
object

arcs()

Returns
The lisf of arcs in the IBayesNet
Return type
list

beginTopologyTransformation()

When inserting/removing arcs, node CPTs change their dimension with a cost in time. begin Multiple Change for all CPTs These functions delay the CPTs change to be done just once at the end of a sequence of topology modification, begins a sequence of insertions/deletions of arcs without changing the dimensions of the CPTs.
Return type
None

changePotential(**args*)

change the CPT associated to nodeId to newPot delete the old CPT associated to nodeId.
Parameters
- **var** (*Union[int,str]*) – the current name or the id of the variable
- **newPot** (pyAgrum.Potential (page 53)) – the new potential

Raises
pyAgrum.NotAllowed – If newPot has not the same signature as __probaMap[NodeId]
Return type
None

changeVariableLabel(**args*)

change the label of the variable associated to nodeId to the new value.
Parameters
- **var** (*Union[int,str]*) – the current name or the id of the variable
- **old_label** (*str*) – the new label
- **new_label** (*str*) – the new label

Raises
pyAgrum.NotFound (page 291) – if id/name is not a variable or if old_label does not exist.
Return type
None

changeVariableName(**args*)

Changes a variable's name in the pyAgrum.BayesNet.

This will change the "pyAgrum.DiscreteVariable" names in the pyAgrum.BayesNet.
Parameters
- **var** (*Union[int,str]*) – the current name or the id of the variable
- **new_name** (*str*) – the new name of the variable

Raises
- *pyAgrum.DuplicateLabel* (page 289) – If new_name is already used in this BayesNet.
- *pyAgrum.NotFound* (page 291) – If no variable matches id.

Return type
None

check()

Return type
List[str]

children(*norid*)

Parameters
- **id** (*int*) – the id of the parent

- **norid** (object) –

Returns
the set of all the children

Return type
Set

clear()

Clear the whole BayesNet

Return type
None

completeInstantiation()

Return type
Instantiation (page 47)

connectedComponents()

connected components from a graph/BN

Compute the connected components of a pyAgrum's graph or Bayesian Network (more generally an object that has *nodes*, *children*/*parents* or *neighbours* methods)

The firstly visited node for each component is called a 'root' and is used as a key for the component. This root has been arbitrarily chosen during the algorithm.

Returns
dict of connected components (as set of nodeIds (int)) with a nodeId (root) of each component as key.

Return type
dict(int,Set[int])

cpt(**args*)

Returns the CPT of a variable.

Parameters
VarId (*Union[int,str]*) – a variable's id (int) or name

Returns
The variable's CPT.

Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.NotFound (page 291) – If no variable's id matches varId.

dag()

Returns
a constant reference to the dag of this BayesNet.

Return type
pyAgrum.DAG (page 8)

descendants(*norid*)

Parameters
norid (object) –

Return type
object

dim()

Returns the dimension (the number of free parameters) in this BayesNet.

Returns
the dimension of the BayesNet

Return type
int

empty()

Return type
bool

endTopologyTransformation()

Terminates a sequence of insertions/deletions of arcs by adjusting all CPTs dimensions. End Multiple Change for all CPTs.

Return type
pyAgrum.BayesNet (page 64)

erase(**args*)

Remove a variable from the pyAgrum.BayesNet.

Removes the corresponding variable from the pyAgrum.BayesNet and from all of it's children pyAgrum.Potential.

If no variable matches the given id, then nothing is done.

Parameters
var (*Union[int,str,*pyAgrum.DiscreteVariable (page 25)*]*) – the current name, the id of the variable or a reference to the variable

Return type
None

eraseArc(**args*)

Removes an arc in the BN, and update head's CTP.

If (tail, head) doesn't exist, the nothing happens.

Parameters
- **arc** (*pyAgrum.Arc when calling eraseArc(arc)*) – The arc to be removed.
- **head** (*Union[int,str]*) – a variable's id (int) or name for the head when calling eraseArc(head,tail)
- **tail** (*Union[int,str]*) – a variable's id (int) or name for the tail when calling eraseArc(head,tail)

Return type
None

exists(*node*)

Parameters
node (int) –

Return type
bool

existsArc(**args*)

Return type
bool

family(*norid*)

Parameters
norid (object) –

Return type
object

static fastPrototype(*dotlike*, *domainSize=2*)

Create a Bayesian network with a dot-like syntax which specifies:
- the structure 'a->b->c;b->d<-e;'.
- the type of the variables with different syntax:
  - by default, a variable is a pyAgrum.RangeVariable using the default domain size ([2])
  - with 'a[10]', the variable is a pyAgrum.RangeVariable using 10 as domain size (from 0 to 9)
  - with 'a[3,7]', the variable is a pyAgrum.RangeVariable using a domainSize from 3 to 7

- with 'a[1,3.14,5,6.2]', the variable is a pyAgrum.DiscretizedVariable using the given ticks (at least 3 values)
- with 'a{top|middle|bottom}', the variable is a pyAgrum.LabelizedVariable using the given labels.
- with 'a{-1|5|0|3}', the variable is a pyAgrum.IntegerVariable using the sorted given values.
- with 'a{-0.5|5.01|0|3.1415}', the variable is a pyAgrum.NumericalDiscreteVariable using the sorted given values.

Note:

- If the dot-like string contains such a specification more than once for a variable, the first specification will be used.
- the CPTs are randomly generated.
- see also pyAgrum.fastBN.

Examples

```
>>> import pyAgrum as gum
>>> bn=pyAgrum.BayesNet.fastPrototype('A->B[1,3]<-C{yes|No}->D[2,4]<-
↪E[1,2.5,3.9]',6)
```

Parameters
- **dotlike** (*str*) – the string containing the specification
- **domainSize** (*int*) – the default domain size for variables

Returns
the resulting Bayesian network

Return type
pyAgrum.BayesNet (page 64)

generateCPT(**args*)

Randomly generate CPT for a given node in a given structure.

Parameters
node (*Union[int,str]*) – a variable's id (int) or name

Return type
None

generateCPTs()

Randomly generates CPTs for a given structure.

Return type
None

hasSameStructure(*other*)

Parameters
pyAgrum.DAGmodel – a direct acyclic model

Returns
True if all the named node are the same and all the named arcs are the same

Return type
bool

idFromName(*name*)

Returns a variable's id given its name in the graph.

Parameters
name (*str*) – The variable's name from which the id is returned.

Returns
The variable's node id.

Return type
int

Raises
pyAgrum.NotFound (page 291) – If name does not match a variable in the graph

ids(*names*)

isIndependent(**args*)

Return type
bool

jointProbability(*i*)

Parameters
i (*pyAgrum.instantiation*) – an instantiation of the variables
Returns
a parameter of the joint probability for the BayesNet
Return type
float

> **Warning:** a variable not present in the instantiation is assumed to be instantiated to 0

loadBIF(**args*)

Load a BIF file.

Parameters
- **name** (*str*) – the file's name
- **l** (*list*) – list of functions to execute

Raises
- *pyAgrum.IOError* (page 290) – If file not found
- *pyAgrum.FatalError* (page 289) – If file is not valid

Return type
str

loadBIFXML(**args*)

Load a BIFXML file.

Parameters
- **name** (*str*) – the name's file
- **l** (*list*) – list of functions to execute

Raises
- *pyAgrum.IOError* (page 290) – If file not found
- *pyAgrum.FatalError* (page 289) – If file is not valid

Return type
str

loadDSL(**args*)

Load a DSL file.

Parameters
- **name** (*str*) – the file's name
- **l** (*list*) – list of functions to execute

Raises
- *pyAgrum.IOError* (page 290) – If file not found
- *pyAgrum.FatalError* (page 289) – If file is not valid

Return type
str

loadNET(**args*)

Load a NET file.

Parameters
- **name** (*str*) – the name's file
- **l** (*list*) – list of functions to execute

Raises
- *pyAgrum.IOError* (page 290) – If file not found

- *pyAgrum.FatalError* (page 289) – If file is not valid

Return type
str

loadO3PRM(**args*)

Load an O3PRM file.

> **Warning:** The O3PRM language is the only language allowing to manipulate not only DiscretizedVariable but also RangeVariable and LabelizedVariable.

Parameters
- **name** (*str*) – the file's name
- **system** (*str*) – the system's name
- **classpath** (*str*) – the classpath
- **l** (*list*) – list of functions to execute

Raises
- *pyAgrum.IOError* (page 290) – If file not found
- *pyAgrum.FatalError* (page 289) – If file is not valid

Return type
str

loadUAI(**args*)

Load an UAI file.

Parameters
- **name** (*str*) – the name's file
- **l** (*list*) – list of functions to execute

Raises
- *pyAgrum.IOError* (page 290) – If file not found
- *pyAgrum.FatalError* (page 289) – If file is not valid

Return type
str

log10DomainSize()

Return type
float

log2JointProbability(*i*)

Parameters
i (*pyAgrum.instantiation*) – an instantiation of the variables

Returns
a parameter of the log joint probability for the BayesNet

Return type
float

> **Warning:** a variable not present in the instantiation is assumed to be instantiated to 0

maxNonOneParam()

Returns
The biggest value (not equal to 1) in the CPTs of the BayesNet

Return type
float

maxParam()

Returns
the biggest value in the CPTs of the BayesNet

Return type
float

maxVarDomainSize()

Returns
the biggest domain size among the variables of the BayesNet
Return type
int

minNonZeroParam()

Returns
the smallest value (not equal to 0) in the CPTs of the IBayesNet
Return type
float

minParam()

Returns
the smallest value in the CPTs of the IBayesNet
Return type
float

minimalCondSet(**args*)

Returns, given one or many targets and a list of variables, the minimal set of those needed to calculate the target/targets.

Parameters
- **target** (*int*) – The id of the target
- **targets** (*List[int]*) – The ids of the targets
- **list** (*List[int]*) – The list of available variables

Returns
The minimal set of variables
Return type
Set[int]

moralGraph(*clear=True*)

Returns the moral graph of the BayesNet, formed by adding edges between all pairs of nodes that have a common child, and then making all edges in the graph undirected.

Returns
The moral graph
Return type
pyAgrum.UndiGraph (page 12)
Parameters
clear (bool) –

moralizedAncestralGraph(*nodes*)

Parameters
nodes (object) –
Return type
UndiGraph (page 12)

names()

Returns
The names of the graph variables
Return type
List[str]

nodeId(*var*)

Parameters
var (pyAgrum.DiscreteVariable (page 25)) – a variable
Returns
the id of the variable
Return type
int

Raises
pyAgrum.IndexError – If the graph does not contain the variable

nodes()

Returns
the set of ids
Return type
Set[int]

nodeset(*names*)

Parameters
names (Vector_string) –
Return type
List[int]

parents(*norid*)

Parameters
- **id** – The id of the child node
- **norid** (object) –

Returns
the set of the parents ids.
Return type
Set

reverseArc(**args*)

Reverses an arc while preserving the same joint distribution.
Parameters
- **tail** – (int) the id of the tail variable
- **head** – (int) the id of the head variable
- **tail** – (str) the name of the tail variable
- **head** – (str) the name of the head variable
- **arc** (pyAgrum.Arc (page 3)) – an arc

Raises
pyAgrum.InvalidArc (page 290) – If the arc does not exsit or if its reversal would induce a directed cycle.
Return type
None

saveBIF(*name*, *allowModificationWhenSaving=False*)

Save the BayesNet in a BIF file.
Parameters
- **name** (*str*) – the file's name
- **allowModificationWhenSaving** (*bool*) – False by default. if true, syntax errors are corrected when saving the file. If false, they throw a FatalError.

Return type
None

saveBIFXML(*name*, *allowModificationWhenSaving=False*)

Save the BayesNet in a BIFXML file.
Parameters
- **name** (*str*) – the file's name
- **allowModificationWhenSaving** (*bool*) – False by default. if true, syntax errors are corrected when saving the file. If false, they throw a FatalError.

Return type
None

saveDSL(*name*, *allowModificationWhenSaving=False*)

Save the BayesNet in a DSL file.
Parameters
- **name** (*str*) – the file's name

- **allowModificationWhenSaving** (*bool*) – False by default. if true, syntax errors are corrected when saving the file. If false, they throw a FatalError.

Return type
None

saveNET(*name*, *allowModificationWhenSaving=False*)

Save the BayesNet in a NET file.

Parameters
- **name** (*str*) – the file's name
- **allowModificationWhenSaving** (*bool*) – False by default. if true, syntax errors are corrected when saving the file. If false, they throw a FatalError.

Return type
None

saveO3PRM(*name*, *allowModificationWhenSaving=False*)

Save the BayesNet in an O3PRM file.

Warning: The O3PRM language is the only language allowing to manipulate not only DiscretizedVariable but also RangeVariable and LabelizedVariable.

Parameters
- **name** (*str*) – the file's name
- **allowModificationWhenSaving** (*bool*) – False by default. if true, syntax errors are corrected when saving the file. If false, they throw a FatalError.

Return type
None

saveUAI(*name*, *allowModificationWhenSaving=False*)

Save the BayesNet in an UAI file.

Parameters
- **name** (*str*) – the file's name
- **allowModificationWhenSaving** (*bool*) – False by default. if true, syntax errors are corrected when saving the file. If false, they throw a FatalError.

Return type
None

size()

Returns
the number of nodes in the graph

Return type
int

sizeArcs()

Returns
the number of arcs in the graph

Return type
int

property thisown

The membership flag

toDot()

Returns
a friendly display of the graph in DOT format

Return type
str

topologicalOrder(*clear=True*)

Returns
the list of the nodes Ids in a topological order

Return type
List
Raises
pyAgrum.InvalidDirectedCycle (page 290) – If this graph contains cycles
Parameters
clear (bool) –

variable(**args*)

Parameters
- **id** (*int*) – a variable's id
- **name** (*str*) – a variable's name

Returns
the variable
Return type
pyAgrum.DiscreteVariable (page 25)
Raises
pyAgrum.IndexError – If the graph does not contain the variable

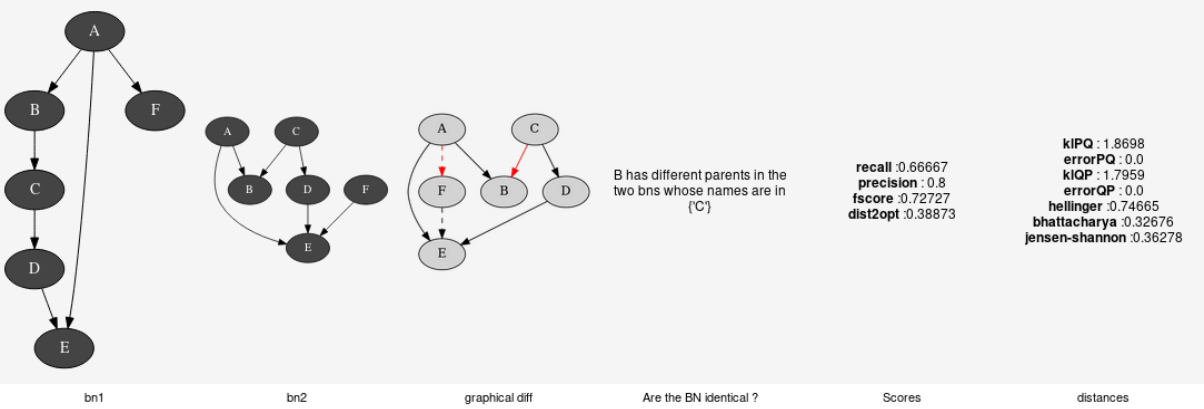
variableFromName(*name*)

Parameters
name (*str*) – a variable's name
Returns
the variable
Return type
pyAgrum.DiscreteVariable (page 25)
Raises
pyAgrum.IndexError – If the graph does not contain the variable

variableNodeMap()

Returns
the variable node map
Return type
pyAgrum.variableNodeMap

1.4.2 Tools for Bayesian networks



aGrUM/pyAgrum provide a set of classes and functions in order to easely work with Bayesian networks.

Generation of database

class pyAgrum.**BNDatabaseGenerator**(*bn*)

BNDatabaseGenerator is used to easily generate databases from a pyAgrum.BayesNet.

Parameters
bn (pyAgrum.BayesNet (page 64)) – the Bayesian network used to generate data.

bn()

Return type
BayesNet (page 64)

drawSamples(**args*)

Generate and stock a database generated by sampling the Bayesian network.

If *evs* is specified, the samples are stored only if there are compatible with these observations.

Returns the log2likelihood of this database.

Parameters
- **nbSamples** (*int*) – the number of samples that will be generated
- **evs** (*"pyAgrum.Instantiation" or Dict[intstr,intstr]*) – (optional) The evidence that will be observed by the resulting samples.

Warning: *nbSamples* is not the size of the database but the number of generated samples. It may happen that the evidence is very rare (or even impossible). In that cas the generated database may have only a few samples (even it may be empty).

Examples

```
>>> import pyAgrum as gum
>>> bn=gum.fastBN('A->B{yes|maybe|no}<-C->D->E<-F<-B')
>>> g=gum.BNDatabaseGenerator(bn)
>>> g.setRandomVarOrder()
>>> g.drawSamples(100,{'B':'yes','E':'1'})
-233.16554130404904
>>> g.to_pandas()
    D  E  C    B  F  A
0   1  1  0  yes  1  1
1   1  1  0  yes  1  0
2   1  1  1  yes  0  1
3   1  1  0  yes  0  0
4   1  1  0  yes  0  1
5   1  1  0  yes  1  0
6   1  1  0  yes  0  0
7   0  1  1  yes  1  1
8   1  1  0  yes  0  1
9   0  1  0  yes  1  1
10  1  1  0  yes  1  1
```

Return type
float

log2likelihood()

Return type
float

samplesAt(*row*, *col*)

Parameters

- **row** (int) –
- **col** (int) –

Return type
int

samplesLabelAt(*row*, *col*)

Parameters
- **row** (int) –
- **col** (int) –

Return type
str

samplesNbCols()

return the number of columns in the samples

Return type
int

samplesNbRows()

return the number of rows in the samples

Return type
int

setAntiTopologicalVarOrder()

Return type
None

setRandomVarOrder()

Return type
None

setTopologicalVarOrder()

Return type
None

setVarOrder(**args*)

Return type
None

setVarOrderFromCSV(**args*)

Return type
None

toCSV(**args*)

generates csv representing the generated database.

Parameters
- **csvFilename** (*str*) – the name of the csv file
- **useLabels** (*bool*) – whether label or id in the csv file (default true)
- **append** (*bool*) – append in the file or rewrite the file (default false)
- **csvSeparator** (*str*) – separator in the csv file (default ‘,’)

Return type
None

to_pandas(*with_labels=True*)

export the samples as a pandas.DataFrame.

Parameters
with_labels (*bool*) – is the DataFrame full of labels of variables or full of index of labels of variables

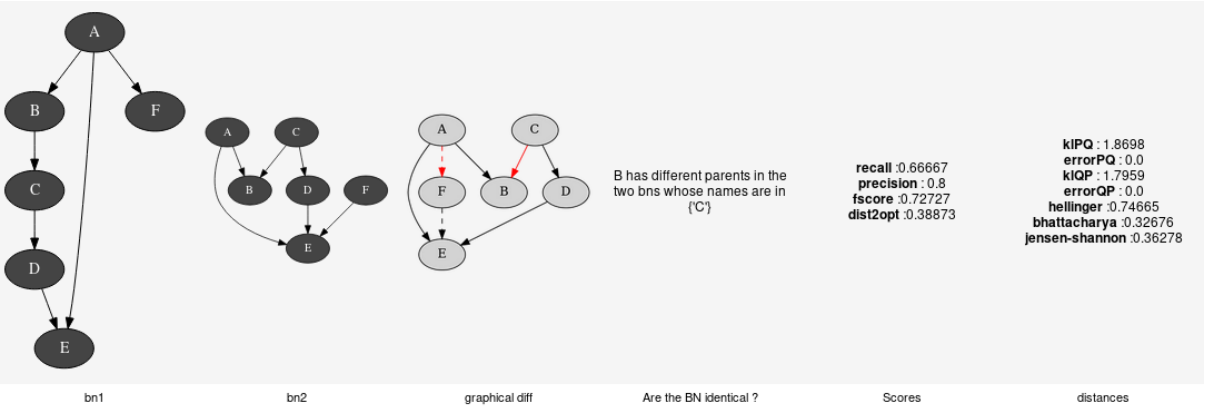
varOrder()

Return type
object

`varOrderNames`()

Return type
List[str]

Comparison of Bayesian networks



To compare Bayesian network, one can compare the structure of the BNs (see pyAgrum.lib.bn_vs_vb.GraphicalBNComparator). However BNs can also be compared as probability distributions.

`class` pyAgrum.`ExactBNdistance`(**args*)

Class representing exacte computation of divergence and distance between BNs

ExactBNdistance(P,Q) -> ExactBNdistance

Parameters:

- **P** (*pyAgrum.BayesNet*) a Bayesian network
- **Q** (*pyAgrum.BayesNet*) another Bayesian network to compare with the first one

ExactBNdistance(ebnd) -> ExactBNdistance

Parameters:

- **ebnd** (*pyAgrum.ExactBNdistance*) the exact BNdistance to copy

Raises
pyAgrum.OperationNotAllowed (page 292) – If the 2BNs have not the same domain size of compatible node sets

`compute`()

Returns
a dictionnary containing the different values after the computation.
Return type
Dict[str,float]

`class` pyAgrum.`GibbsBNdistance`(**args*)

Class representing a Gibbs-Approximated computation of divergence and distance between BNs

GibbsBNdistance(P,Q) -> GibbsBNdistance

Parameters:

- **P** (*pyAgrum.BayesNet*) – a Bayesian network
- **Q** (*pyAgrum.BayesNet*) – another Bayesian network to compare with the first one

GibbsBNdistance(gbnd) -> GibbsBNdistance

Parameters:

- **gbnd** (*pyAgrum.GibbsBNdistance*) – the Gibbs BNdistance to copy

Raises

pyAgrum.OperationNotAllowed (page 292) – If the 2BNs have not the same domain size of compatible node sets

`burnIn()`

Returns
size of burn in on number of iteration
Return type
int

`compute()`

Returns
a dictionnary containing the different values after the computation.
Return type
Dict[str,float]

`continueApproximationScheme(error)`

Continue the approximation scheme.
Parameters
error (*float*) –
Return type
bool

`currentTime()`

Returns
get the current running time in second (float)
Return type
float

`disableEpsilon()`

Disable epsilon as a stopping criterion.
Return type
None

`disableMaxIter()`

Disable max iterations as a stopping criterion.
Return type
None

`disableMaxTime()`

Disable max time as a stopping criterion.
Return type
None

`disableMinEpsilonRate()`

Disable a min epsilon rate as a stopping criterion.
Return type
None

`enableEpsilon()`

Enable epsilon as a stopping criterion.
Return type
None

`enableMaxIter()`

Enable max iterations as a stopping criterion.

Return type
None

enableMaxTime()

Enable max time as a stopping criterion.

Return type
None

enableMinEpsilonRate()

Enable a min epsilon rate as a stopping criterion.

Return type
None

epsilon()

Returns
the value of epsilon

Return type
float

history()

Returns
the scheme history

Return type
tuple

Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

initApproximationScheme()

Initiate the approximation scheme.

Return type
None

isDrawnAtRandom()

Returns
True if variables are drawn at random

Return type
bool

isEnabledEpsilon()

Returns
True if epsilon is used as a stopping criterion.

Return type
bool

isEnabledMaxIter()

Returns
True if max iterations is used as a stopping criterion

Return type
bool

isEnabledMaxTime()

Returns
True if max time is used as a stopping criterion

Return type
bool

isEnabledMinEpsilonRate()

Returns
True if epsilon rate is used as a stopping criterion

Return type
bool

`maxIter`()

Returns
the criterion on number of iterations
Return type
int

`maxTime`()

Returns
the timeout(in seconds)
Return type
float

`messageApproximationScheme`()

Returns
the approximation scheme message
Return type
str

`minEpsilonRate`()

Returns
the value of the minimal epsilon rate
Return type
float

`nbrDrawnVar`()

Returns
the number of variable drawn at each iteration
Return type
int

`nbrIterations`()

Returns
the number of iterations
Return type
int

`periodSize`()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

`remainingBurnIn`()

Returns
the number of remaining burn in
Return type
int

`setBurnIn`(*b*)

Parameters
b (*int*) – size of burn in on number of iteration
Return type
None

`setDrawnAtRandom`(*_atRandom*)

Parameters
_atRandom (*bool*) – indicates if variables should be drawn at random
Return type
None

setEpsilon(*eps*)
Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0
Return type
None

setMaxIter(*max*)
Parameters
max (*int*) – the maximum number of iteration
Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

setMaxTime(*timeout*)
Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0
Return type
None

setMinEpsilonRate(*rate*)
Parameters
rate (*float*) – the minimal epsilon rate
Return type
None

setNbrDrawnVar(*_nbr*)
Parameters
_nbr (*int*) – the number of variables to be drawn at each iteration
Return type
None

setPeriodSize(*p*)
Parameters
p (*int*) – number of samples between 2 stopping
Raises
pyAgrum.OutOfBounds (page 292) – If p<1
Return type
None

setVerbosity(*v*)
Parameters
v (*bool*) – verbosity
Return type
None

startOfPeriod()
Returns
True if it is a start of a period
Return type
bool

stateApproximationScheme()

Returns
the state of the approximation scheme
Return type
int

stopApproximationScheme()

Stop the approximation scheme.
Return type
None

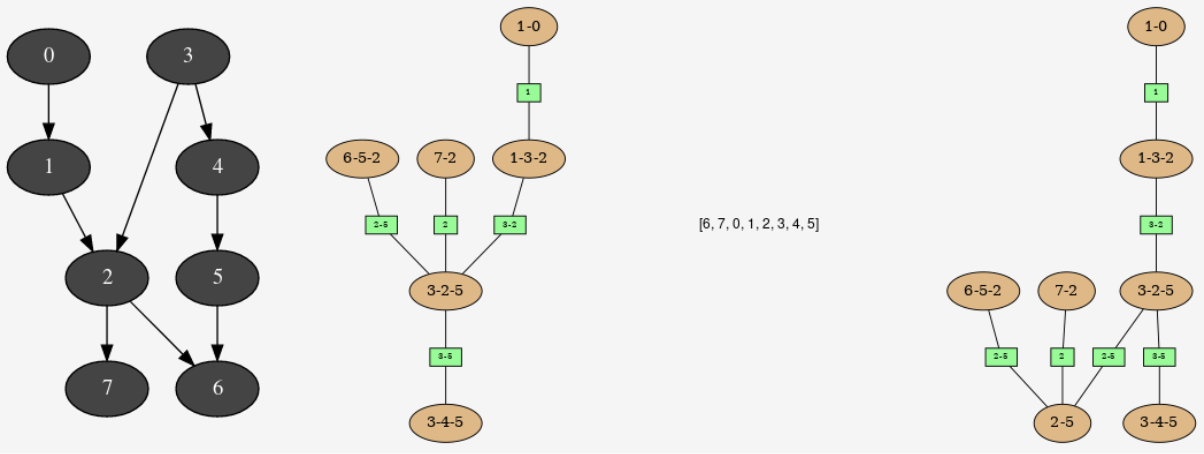
updateApproximationScheme(*incr=1*)

Update the approximation scheme.
Parameters
incr (int) –
Return type
None

verbosity()

Returns
True if the verbosity is enabled
Return type
bool

Explanation and analysis



This tools aimed to provide some different views on the Bayesian network in order to explore its qualitative and/or quantitave behaviours.

class pyAgrum.**JunctionTreeGenerator**

JunctionTreeGenerator is use to generate junction tree or binary junction tree from Bayesian networks.

JunctionTreeGenerator() -> JunctionTreeGenerator
default constructor

binaryJoinTree(**args*)

Computes the binary joint tree for its parameters. If the first parameter is a graph, the heurisitcs assume that all the node have the same domain size (2). If given, the heuristic takes into account the partial order for its elimination order.
Parameters
- **g** (pyAgrum.UndiGraph (page 12)) – a undirected graph
- **dag** (pyAgrum.DAG (page 8)) – a dag

- **bn** (pyAgrum.BayesNet (page 64)) – a BayesianNetwork
- **partial_order** (*List[List[int]]*) – a partial order among the nodeIDs

Returns
the current binary joint tree

Return type
pyAgrum.CliqueGraph (page 15)

eliminationOrder(**args*)

Computes the elimination for its parameters. If the first parameter is a graph, the heurisitcs assume that all the node have the same domain size (2). If given, the heuristic takes into account the partial order for its elimination order.

Parameters
- **g** (pyAgrum.UndiGraph (page 12)) – a undirected graph
- **dag** (pyAgrum.DAG (page 8)) – a dag
- **bn** (pyAgrum.BayesNet (page 64)) – a BayesianNetwork
- **partial_order** (*List[List[int]]*) – a partial order among the nodeIDs

Returns
the current elimination order.

Return type
pyAgrum.CliqueGraph (page 15)

junctionTree(**args*)

Computes the junction tree for its parameters. If the first parameter is a graph, the heurisitcs assume that all the node have the same domain size (2). If given, the heuristic takes into account the partial order for its elimination order.

Parameters
- **g** (pyAgrum.UndiGraph (page 12)) – a undirected graph
- **dag** (pyAgrum.DAG (page 8)) – a dag
- **bn** (pyAgrum.BayesNet (page 64)) – a BayesianNetwork
- **partial_order** (*List[List[int]]*) – a partial order among the nodeIDs

Returns
the current junction tree.

Return type
pyAgrum.CliqueGraph (page 15)

class pyAgrum.**EssentialGraph**(**args*)

Class building the essential graph from a BN.

Essential graph is a mixed graph (Chain Graph) that represents the class of markov equivalent Bayesian networks (with the same independency model).

EssentialGraph(m) -> EssentialGraph

Parameters:

- **m** (*pyAgrum.DAGmodel*) – a DAGmodel

arcs()

Returns
The lisf of arcs in the EssentialGraph

Return type
list

children(*id*)

Parameters
id (*int*) – the id of the parent

Returns
the set of all the children

Return type
Set

`connectedComponents`()

connected components from a graph/BN

Compute the connected components of a pyAgrum's graph or Bayesian Network (more generally an object that has *nodes*, *children*/*parents* or *neighbours* methods)

The firstly visited node for each component is called a 'root' and is used as a key for the component. This root has been arbitrarily chosen during the algorithm.

Returns
dict of connected components (as set of nodeIds (int)) with a nodeId (root) of each component as key.

Return type
dict(int,Set[int])

`edges`()

Returns
the list of the edges

Return type
List

`mixedGraph`()

Returns
the mixed graph

Return type
pyAgrum.MixedGraph (page 20)

`neighbours`(*id*)

Parameters
id (*int*) – the id of the checked node

Returns
The set of edges adjacent to the given node

Return type
Set

`nodes`()

Return type
`object`

`parents`(*id*)

Parameters
id (`int`) – The id of the child node

Returns
the set of the parents ids.

Return type
Set

`size`()

Returns
the number of nodes in the graph

Return type
int

`sizeArcs`()

Returns
the number of arcs in the graph

Return type
int

`sizeEdges`()

Returns
the number of edges in the graph

Return type
int

`sizeNodes`()

Returns
the number of nodes in the graph
Return type
int

`skeleton`()

Return type
UndiGraph (page 12)

`toDot`()

Returns
a friendly display of the graph in DOT format
Return type
str

class pyAgrum.`MarkovBlanket`(**args*)

Class building the Markov blanket of a node in a graph.

MarkovBlanket(m,n) -> MarkovBlanket

Parameters:

- **m** (*pyAgrum.DAGmodel*) – a DAGmodel
- **n** (int) – a node id

MarkovBlanket(m,name) -> MarkovBlanket

Parameters:

- **m** (*pyAgrum.DAGmodel*) – a DAGmodel
- **name** (*str*) – a node name

`arcs`()

Returns
the list of the arcs
Return type
List

`children`(*id*)

Parameters
id (*int*) – the id of the parent
Returns
the set of all the children
Return type
Set

`connectedComponents`()

connected components from a graph/BN

Compute the connected components of a pyAgrum's graph or Bayesian Network (more generally an object that has *nodes*, *children*/*parents* or *neighbours* methods)

The firstly visited node for each component is called a 'root' and is used as a key for the component. This root has been arbitrarily chosen during the algorithm.

Returns
dict of connected components (as set of nodeIds (int)) with a nodeId (root) of each component as key.
Return type
dict(int,Set[int])

dag()

Returns
a copy of the DAG
Return type
pyAgrum.DAG (page 8)

hasSameStructure(*other*)

Parameters
pyAgrum.DAGmodel – a direct acyclic model
Returns
True if all the named node are the same and all the named arcs are the same
Return type
bool

nodes()

Returns
the set of ids
Return type
set

parents(*id*)

Parameters
id (int) – The id of the child node
Returns
the set of the parents ids.
Return type
Set

size()

Returns
the number of nodes in the graph
Return type
int

sizeArcs()

Returns
the number of arcs in the graph
Return type
int

sizeNodes()

Returns
the number of nodes in the graph
Return type
int

toDot()

Returns
a friendly display of the graph in DOT format
Return type
str

Fragment of Bayesian networks

This class proposes a shallow copy of a part of Bayesian network. It can be used as a Bayesian network for inference algorithms (for instance).

class pyAgrum.**BayesNetFragment**(*bn*)

BayesNetFragment represents a part of a Bayesian network (subset of nodes). By default, the arcs and the CPTs are the same as the BN but local CPTs can be build to express different local dependencies. All the non local CPTs are not copied. Therefore a BayesNetFragment is a light object.

BayesNetFragment(BayesNet bn) -> BayesNetFragment

Parameters:

- **bn** (*pyAgrum.BayesNet*) – the bn refered by the fragment

Parameters
bn (IBayesNet) –

addArcs(*listArcs*)

add a list of arcs in te model.

Parameters
listArcs (*List[Tuple[intstr,intstr]]*) – the list of arcs

addStructureListener(*whenNodeAdded=None*, *whenNodeDeleted=None*, *whenArcAdded=None*, *whenArcDeleted=None*)

Add the listeners in parameters to the list of existing ones.

Parameters
- **whenNodeAdded** (*lambda expression*) – a function for when a node is added
- **whenNodeDeleted** (*lambda expression*) – a function for when a node is removed
- **whenArcAdded** (*lambda expression*) – a function for when an arc is added
- **whenArcDeleted** (*lambda expression*) – a function for when an arc is removed

addVariables(*listFastVariables*, *default_nbr_mod=2*)

Add a list of variable in the form of 'fast' syntax.

Parameters
- **listFastVariables** (*List[str]*) – the list of variables in 'fast' syntax.
- **default_nbr_mod** (*int*) – the number of modalities for the variable if not specified following *fast syntax* (page 281). Note that default_nbr_mod=1 is mandatory to create variables with only one modality (for utility for instance).

Returns
the list of created ids.
Return type
List[int]

ancestors(*norid*)

Parameters
norid (object) –
Return type
object

arcs()

Returns
The lisf of arcs in the IBayesNet
Return type
list

check()

Return type
List[str]

checkConsistency(**args*)

If a variable is added to the fragment but not its parents, there is no CPT consistant for this variable. This function checks the consistency for a variable of for all.

Parameters
n(*int, str (optional)*) – the id or the name of the variable. If no argument, the function checks all the variables.

Returns
True if the variable(s) is consistant.

Return type
boolean

Raises
- *pyAgrum.NotFound* (page 291) –
- **if the node is not found.** –

children(*norid*)

Parameters
- **id** (*int*) – the id of the parent
- **norid** (object) –

Returns
the set of all the children

Return type
Set

completeInstantiation()

Return type
Instantiation (page 47)

connectedComponents()

connected components from a graph/BN

Compute the connected components of a pyAgrum's graph or Bayesian Network (more generally an object that has *nodes*, *children*/*parents* or *neighbours* methods)

The firstly visited node for each component is called a 'root' and is used as a key for the component. This root has been arbitrarily chosen during the algorithm.

Returns
dict of connected components (as set of nodeIds (int)) with a nodeId (root) of each component as key.

Return type
dict(int,Set[int])

cpt(**args*)

Returns the CPT of a variable.

Parameters
- **VarId** (*int*) – A variable's id in the pyAgrum.IBayesNet.
- **name** (*str*) – A variable's name in the pyAgrum.IBayesNet.

Returns
The variable's CPT.

Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.NotFound (page 291) – If no variable's id matches varId.

dag()

Returns
a constant reference to the dag of this BayesNet.

Return type
pyAgrum.DAG (page 8)

descendants(*norid*)

Parameters
norid (object) –
Return type
object

dim()

Returns the dimension (the number of free parameters) in this BayesNet.
Returns
the dimension of the BayesNet
Return type
int

empty()

Return type
bool

exists(*node*)

Parameters
node (int) –
Return type
bool

existsArc(**args*)

Return type
bool

family(*norid*)

Parameters
norid (object) –
Return type
object

hasSameStructure(*other*)

Parameters
pyAgrum.DAGmodel – a direct acyclic model
Returns
True if all the named node are the same and all the named arcs are the same
Return type
bool

idFromName(*name*)

Returns a variable's id given its name in the graph.
Parameters
name (*str*) – The variable's name from which the id is returned.
Returns
The variable's node id.
Return type
int
Raises
pyAgrum.NotFound (page 291) – If name does not match a variable in the graph

ids(*names*)

installAscendants(**args*)

Add the variable and all its ascendants in the fragment. No inconsistant node are created.
Parameters
n (*int, str*) – the id or the name of the variable.

Raises
- *pyAgrum.NotFound* (page 291) –
- **if the node is not found.** –

Return type
None

installCPT(**args*)

Install a local CPT for a node. Doing so, it changes the parents of the node in the fragment.

Parameters
- **n** (*int, str*) – the id or the name of the variable.
- **pot** (Potential (page 53)) – the Potential to install

Raises
pyAgrum.NotFound (page 291) – if the node is not found.

Return type
None

installMarginal(**args*)

Install a local marginal for a node. Doing so, it removes the parents of the node in the fragment.

Parameters
- **n** (*int, str*) – the id or the name of the variable.
- **pot** (Potential (page 53)) – the Potential (marginal) to install

Raises
pyAgrum.NotFound (page 291) – if the node is not found.

Return type
None

installNode(**args*)

Add a node to the fragment. The arcs that can be added between installed nodes are created. No specific CPT are created. Then either the parents of the node are already in the fragment and the node is consistant, or the parents are not in the fragment and the node is not consistant.

Parameters
n (*int, str*) – the id or the name of the variable.

Raises
pyAgrum.NotFound (page 291) – if the node is not found.

Return type
None

isIndependent(**args*)

Return type
bool

isInstalledNode(**args*)

Check if a node is in the fragment

Parameters
n (*int, str*) – the id or the name of the variable.

Return type
bool

jointProbability(*i*)

Parameters
i (*pyAgrum.instantiation*) – an instantiation of the variables

Returns
a parameter of the joint probability for the BayesNet

Return type
float

> **Warning:** a variable not present in the instantiation is assumed to be instantiated to 0

log10DomainSize()

Return type
float

log2JointProbability(*i*)

Parameters
i (*pyAgrum.instantiation*) – an instantiation of the variables
Returns
a parameter of the log joint probability for the BayesNet
Return type
float

> **Warning:** a variable not present in the instantiation is assumed to be instantiated to 0

maxNonOneParam()

Returns
The biggest value (not equal to 1) in the CPTs of the BayesNet
Return type
float

maxParam()

Returns
the biggest value in the CPTs of the BayesNet
Return type
float

maxVarDomainSize()

Returns
the biggest domain size among the variables of the BayesNet
Return type
int

minNonZeroParam()

Returns
the smallest value (not equal to 0) in the CPTs of the IBayesNet
Return type
float

minParam()

Returns
the smallest value in the CPTs of the IBayesNet
Return type
float

minimalCondSet(**args*)

Returns, given one or many targets and a list of variables, the minimal set of those needed to calculate the target/targets.

Parameters
- **target** (*int*) – The id of the target
- **targets** (*List[int]*) – The ids of the targets
- **list** (*List[int]*) – The list of available variables

Returns
The minimal set of variables
Return type
Set[int]

moralGraph(*clear=True*)

Returns the moral graph of the BayesNet, formed by adding edges between all pairs of nodes that have a common child, and then making all edges in the graph undirected.

Returns
The moral graph

Return type
pyAgrum.UndiGraph (page 12)

Parameters
clear (bool) –

moralizedAncestralGraph(*nodes*)

Parameters
nodes (object) –

Return type
UndiGraph (page 12)

names()

Returns
The names of the graph variables

Return type
List[str]

nodeId(*var*)

Parameters
var (pyAgrum.DiscreteVariable (page 25)) – a variable

Returns
the id of the variable

Return type
int

Raises
pyAgrum.IndexError – If the graph does not contain the variable

nodes()

Returns
the set of ids

Return type
Set[int]

nodeset(*names*)

Parameters
names (Vector_string) –

Return type
List[int]

parents(*norid*)

Parameters
- **id** – The id of the child node
- **norid** (object) –

Returns
the set of the parents ids.

Return type
Set

property(*name*)

Parameters
name (str) –

Return type
str

propertyWithDefault(*name*, *byDefault*)

Parameters
- **name** (str) –
- **byDefault** (str) –

Return type
str

setProperty(*name*, *value*)

Parameters
- **name** (str) –
- **value** (str) –

Return type
None

size()

Returns
the number of nodes in the graph

Return type
int

sizeArcs()

Returns
the number of arcs in the graph

Return type
int

toBN()

Create a BayesNet from a fragment.

Raises
pyAgrum.OperationNotAllowed (page 292) – if the fragment is not consistent.

Return type
BayesNet (page 64)

toDot()

Returns
a friendly display of the graph in DOT format

Return type
str

topologicalOrder(*clear=True*)

Returns
the list of the nodes Ids in a topological order

Return type
List

Raises
pyAgrum.InvalidDirectedCycle (page 290) – If this graph contains cycles

Parameters
clear (bool) –

uninstallCPT(**args*)

Remove a local CPT. The fragment can become inconsistant.

Parameters
n (*int*, *str*) – the id or the name of the variable.

Raises
pyAgrum.NotFound (page 291) – if the node is not found.

Return type
None

uninstallNode(**args*)

Remove a node from the fragment. The fragment can become inconsistant.

Parameters
n (*int, str*) – the id or the name of the variable.

Raises
pyAgrum.NotFound (page 291) – if the node is not found.

Return type
None

variable(**args*)

Parameters
- **id** (*int*) – a variable's id
- **name** (*str*) – a variable's name

Returns
the variable

Return type
pyAgrum.DiscreteVariable (page 25)

Raises
pyAgrum.IndexError – If the graph does not contain the variable

variableFromName(*name*)

Parameters
name (*str*) – a variable's name

Returns
the variable

Return type
pyAgrum.DiscreteVariable (page 25)

Raises
pyAgrum.IndexError – If the graph does not contain the variable

variableNodeMap()

Returns
the variable node map

Return type
pyAgrum.variableNodeMap

whenArcAdded(*src*, *_from*, *to*)

Parameters
- **src** (object) –
- **_from** (int) –
- **to** (int) –

Return type
None

whenArcDeleted(*src*, *_from*, *to*)

Parameters
- **src** (object) –
- **_from** (int) –
- **to** (int) –

Return type
None

whenNodeAdded(*src*, *id*)

Parameters
- **src** (object) –
- **id** (int) –

Return type
None

whenNodeDeleted(*src*, *id*)

Parameters
- **src** (object) –
- **id** (int) –

Return type
None

1.4.3 Inference

Inference is the process that consists in computing new probabilistc information from a Bayesian network and some evidence. aGrUM/pyAgrum mainly focus and the computation of (joint) posterior for some variables of the Bayesian networks given soft or hard evidence that are the form of likelihoods on some variables. Inference is a hard task (NP-complete). aGrUM/pyAgrum implements exact inference but also approximated inference that can converge slowly and (even) not exactly but thant can in many cases be useful for applications.

1.4.4 Exact Inference

Lazy Propagation

Lazy Propagation is the main exact inference for classical Bayesian networks in aGrUM/pyAgrum.

class pyAgrum.**LazyPropagation**(**args*)

Class used for Lazy Propagation

LazyPropagation(bn) -> LazyPropagation

Parameters:

- **bn** (*pyAgrum.BayesNet*) – a Bayesian network

BN()

Returns
A constant reference over the IBayesNet referenced by this class.

Return type
pyAgrum.IBayesNet

Raises
pyAgrum.UndefinedElement (page 293) – If no Bayes net has been assigned to the inference.

H(**args*)

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation

Return type
float

I(**args*)

Parameters
- **X** (*int or str*) – a node Id or a node name
- **Y** (*int or str*) – another node Id or node name

Returns
- ------- –
- **float** – the Mutual Information of X and Y given the observation

Return type
float

VI(**args*)

Parameters
- **X** (*int or str*) – a node Id or a node name
- **Y** (*int or str*) – another node Id or node name

Returns
- **-------** –
- **float** – variation of information between X and Y

Return type
float

addAllTargets()

Add all the nodes as targets.

Return type
None

addEvidence(**args*)

Adds a new evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

addJointTarget(*targets*)

Add a list of nodes as a new joint target. As a collateral effect, every node is added as a marginal target.

Parameters
- **list** – a list of names of nodes
- **targets** (object) –

Raises
pyAgrum.UndefinedElement (page 293) – If some node(s) do not belong to the Bayesian network

Return type
None

addTarget(**args*)

Add a marginal target to the list of targets.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises
pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net

Return type
None

chgEvidence(**args*)

Change the value of an already existing evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

eraseAllEvidence()

Removes all the evidence entered into the network.

Return type
None

eraseAllJointTargets()

Clear all previously defined joint targets.

Return type
None

eraseAllMarginalTargets()

Clear all the previously defined marginal targets.

Return type
None

eraseAllTargets()

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).

Return type
None

eraseEvidence(**args*)

Remove the evidence, if any, corresponding to the node Id or name.

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

Return type
None

eraseJointTarget(*targets*)

Remove, if existing, the joint target.

Parameters
- **list** – a list of names or Ids of nodes
- **targets** (object) –

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network

- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

`eraseTarget`(**args*)

Remove, if existing, the marginal target.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

`evidenceImpact`(*target*, *evs*)

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)

Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

> **Warning:** if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)

Return type
pyAgrum.Potential (page 53)

`evidenceJointImpact`(**args*)

Create a pyAgrum.Potential for P(joint targets|evs) (for all instanciation of targets and evs)

Parameters
- **targets** (*List[intstr]*) – a list of node Ids or node names
- **evs** (*Set[intstr]*) – a set of nodes ids or names.

Returns
a Potential for P(target|evs)

Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.Exception – If some evidene entered into the Bayes net are incompatible (their joint proba = 0)

`evidenceProbability`()

Returns
the probability of evidence

Return type
float

`getNumberOfThreads`()

returns the number of threads used by LazyPropagation during inferences.

Returns
the number of threads used by LazyPropagation during inferences

Return type
int

`hardEvidenceNodes`()

Returns
the set of nodes with hard evidence

Return type
set

`hasEvidence`(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

`hasHardEvidence`(*nodeName*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

`hasSoftEvidence`(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

`isGumNumberOfThreadsOverriden`()

Indicates whether LazyPropagation currently overrides aGrUM's default number of threads (see method setNumberOfThreads).

Returns
A Boolean indicating whether LazyPropagation currently overrides aGrUM's default number of threads

Return type
bool

`isJointTarget`(*targets*)

Parameters
- **list** – a list of nodes ids or names.
- **targets** (`object`) –

Returns
True if target is a joint target.

Return type
bool

Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

`isTarget`(**args*)

Parameters

- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target
Return type
bool
Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

joinTree()

Returns
the current join tree used
Return type
pyAgrum.CliqueGraph (page 15)

jointMutualInformation(*targets*)

Parameters
targets (object) –
Return type
float

jointPosterior(*targets*)

Compute the joint posterior of a set of nodes.

Parameters
list – the list of nodes whose posterior joint probability is wanted

> **Warning:** The order of the variables given by the list here or when the jointTarget is declared can not be assumed to be used by the Potential.

Returns
a const ref to the posterior joint probability of the set of nodes.
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets
Parameters
targets (object) –

jointTargets()

Returns
the list of target sets
Return type
list

junctionTree()

Returns
the current junction tree
Return type
pyAgrum.CliqueGraph (page 15)

makeInference()

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later, the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.

Return type
None

nbrEvidence()

Returns
the number of evidence entered into the Bayesian network
Return type
int

nbrHardEvidence()

Returns
the number of hard evidence entered into the Bayesian network
Return type
int

nbrJointTargets()

Returns
the number of joint targets
Return type
int

nbrSoftEvidence()

Returns
the number of soft evidence entered into the Bayesian network
Return type
int

nbrTargets()

Returns
the number of marginal targets
Return type
int

posterior(**args*)

Computes and returns the posterior of a node.
Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

setEvidence(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.
Parameters
evidces (*dict*) – a dict of evidences
Raises
pyAgrum.InvalidArgument (page 290) – If one value is not a value for the node pyAgrum.InvalidArgument If the size of a value is different from the domain side of the node pyAgrum.FatalError If one value is a vector of 0s pyAgrum.UndefinedElement If one node does not belong to the Bayesian network

setMaxMemory(*gigabytes*)

sets an upper bound on the memory consumption admissible
Parameters
gigabytes (*float*) – this upper bound in gigabytes.

Return type
None

`setNumberOfThreads`(*nb*)

If the argument nb is different from 0, this number of threads will be used during inferences, hence overriding aGrUM's default number of threads. If, on the contrary, nb is equal to 0, the parallelized inference engine will comply with aGrUM's default number of threads.

Parameters
nb (*int*) – the number of threads to be used by ShaferShenoyMNInference
Return type
None

`setTargets`(*targets*)

Remove all the targets and add the ones in parameter.

Parameters
targets (*set*) – a set of targets
Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

`softEvidenceNodes`()

Returns
the set of nodes with soft evidence
Return type
set

`targets`()

Returns
the list of marginal targets
Return type
list

`property thisown`

The membership flag

`updateEvidence`(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).

Parameters
evidces (*dict*) – a dict of evidences
Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

Shafer Shenoy Inference

`class pyAgrum.ShaferShenoyInference`(**args*)

Class used for Shafer-Shenoy inferences.

ShaferShenoyInference(bn) -> ShaferShenoyInference

Parameters:

- **bn** (*pyAgrum.BayesNet*) – a Bayesian network

`BN`()

Returns
A constant reference over the IBayesNet referenced by this class.

Return type
pyAgrum.IBayesNet
Raises
pyAgrum.UndefinedElement (page 293) – If no Bayes net has been assigned to the inference.

H(**args*)

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation
Return type
float

I(**args*)

Parameters
- **X** (*int or str*) – a node Id or a node name
- **Y** (*int or str*) – another node Id or node name

Returns
- **-------** –
- **float** – the Mutual Information of X and Y given the observation

Return type
float

VI(**args*)

Parameters
- **X** (*int or str*) – a node Id or a node name
- **Y** (*int or str*) – another node Id or node name

Returns
- **-------** –
- **float** – variation of information between X and Y

Return type
float

addAllTargets()

Add all the nodes as targets.
Return type
None

addEvidence(**args*)

Adds a new evidence on a node (might be soft or hard).
Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

addJointTarget(*targets*)

Add a list of nodes as a new joint target. As a collateral effect, every node is added as a marginal target.

Parameters
- **list** – a list of names of nodes
- **targets** (object) –

Raises
pyAgrum.UndefinedElement (page 293) – If some node(s) do not belong to the Bayesian network

Return type
None

addTarget(**args*)

Add a marginal target to the list of targets.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises
pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net

Return type
None

chgEvidence(**args*)

Change the value of an already existing evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

eraseAllEvidence()

Removes all the evidence entered into the network.

Return type
None

eraseAllJointTargets()

Clear all previously defined joint targets.

Return type
None

eraseAllMarginalTargets()

Clear all the previously defined marginal targets.

Return type
None

eraseAllTargets()

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).

Return type
None

`eraseEvidence`(**args*)

Remove the evidence, if any, corresponding to the node Id or name.

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

Return type
None

`eraseJointTarget`(*targets*)

Remove, if existing, the joint target.

Parameters
- **list** – a list of names or Ids of nodes
- **targets** (object) –

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

`eraseTarget`(**args*)

Remove, if existing, the marginal target.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

`evidenceImpact`(*target*, *evs*)

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)

Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

> **Warning:** if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)

Return type
pyAgrum.Potential (page 53)

`evidenceJointImpact`(**args*)

Create a pyAgrum.Potential for P(joint targets|evs) (for all instanciation of targets and evs)

Parameters
- **targets** (*List[intstr]*) – a list of node Ids or node names
- **evs** (*Set[intstr]*) – a set of nodes ids or names.

Returns
a Potential for P(target|evs)
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.Exception – If some evidene entered into the Bayes net are incompatible (their joint proba = 0)

evidenceProbability()

Returns
the probability of evidence
Return type
float

getNumberOfThreads()

returns the number of threads used by LazyPropagation during inferences.
Returns
the number of threads used by LazyPropagation during inferences
Return type
int

hardEvidenceNodes()

Returns
the set of nodes with hard evidence
Return type
set

hasEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasHardEvidence(*nodeName*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasSoftEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

`isGumNumberOfThreadsOverriden()`

Indicates whether LazyPropagation currently overrides aGrUM's default number of threads (see method setNumberOfThreads).

Returns
A Boolean indicating whether LazyPropagation currently overrides aGrUM's default number of threads

Return type
bool

`isJointTarget(targets)`

Parameters
- **list** – a list of nodes ids or names.
- **targets** (object) –

Returns
True if target is a joint target.

Return type
bool

Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

`isTarget(*args)`

Parameters
- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target

Return type
bool

Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

`joinTree()`

Returns
the current join tree used

Return type
pyAgrum.CliqueGraph (page 15)

`jointMutualInformation(targets)`

Parameters
targets (object) –

Return type
float

`jointPosterior(targets)`

Compute the joint posterior of a set of nodes.

Parameters
list – the list of nodes whose posterior joint probability is wanted

> **Warning:** The order of the variables given by the list here or when the jointTarget is declared can not be assumed to be used by the Potential.

Returns
a const ref to the posterior joint probability of the set of nodes.

Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets
Parameters
targets (object) –

`jointTargets`()

Returns
the list of target sets
Return type
list

`junctionTree`()

Returns
the current junction tree
Return type
pyAgrum.CliqueGraph (page 15)

`makeInference`()

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later, the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.
Return type
None

`nbrEvidence`()

Returns
the number of evidence entered into the Bayesian network
Return type
int

`nbrHardEvidence`()

Returns
the number of hard evidence entered into the Bayesian network
Return type
int

`nbrJointTargets`()

Returns
the number of joint targets
Return type
int

`nbrSoftEvidence`()

Returns
the number of soft evidence entered into the Bayesian network
Return type
int

`nbrTargets`()

Returns
the number of marginal targets
Return type
int

`posterior`(**args*)

Computes and returns the posterior of a node.
Parameters

- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

setEvidence(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.
Parameters
evidces (*dict*) – a dict of evidences
Raises
pyAgrum.InvalidArgument (page 290) – If one value is not a value for the node pyAgrum.InvalidArgument If the size of a value is different from the domain side of the node pyAgrum.FatalError If one value is a vector of 0s pyAgrum.UndefinedElement If one node does not belong to the Bayesian network

setMaxMemory(*gigabytes*)

sets an upper bound on the memory consumption admissible
Parameters
gigabytes (*float*) – this upper bound in gigabytes.
Return type
None

setNumberOfThreads(*nb*)

If the argument nb is different from 0, this number of threads will be used during inferences, hence overriding aGrUM's default number of threads. If, on the contrary, nb is equal to 0, the parallelized inference engine will comply with aGrUM's default number of threads.
Parameters
nb (*int*) – the number of threads to be used by ShaferShenoyMNInference
Return type
None

setTargets(*targets*)

Remove all the targets and add the ones in parameter.
Parameters
targets (*set*) – a set of targets
Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

softEvidenceNodes()

Returns
the set of nodes with soft evidence
Return type
set

targets()

Returns
the list of marginal targets
Return type
list

property thisown

The membership flag

updateEvidence(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).

Parameters
evidces (*dict*) – a dict of evidences

Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

Variable Elimination

class pyAgrum.**VariableElimination**(**args*)

Class used for Variable Elimination inference algorithm.

VariableElimination(bn) -> VariableElimination

Parameters:

- **bn** (*pyAgrum.BayesNet*) – a Bayesian network

BN()

Returns
A constant reference over the IBayesNet referenced by this class.

Return type
pyAgrum.IBayesNet

Raises
pyAgrum.UndefinedElement (page 293) – If no Bayes net has been assigned to the inference.

H(**args*)

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation

Return type
float

addAllTargets()

Add all the nodes as targets.

Return type
None

addEvidence(**args*)

Adds a new evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node

- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

addJointTarget(*targets*)

Add a list of nodes as a new joint target. As a collateral effect, every node is added as a marginal target.

Parameters
- **list** – a list of names of nodes
- **targets** (object) –

Raises
pyAgrum.UndefinedElement (page 293) – If some node(s) do not belong to the Bayesian network

Return type
None

addTarget(**args*)

Add a marginal target to the list of targets.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises
pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net

Return type
None

chgEvidence(**args*)

Change the value of an already existing evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

eraseAllEvidence()

Removes all the evidence entered into the network.

Return type
None

eraseAllTargets()

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).

Return type
None

eraseEvidence(**args*)

Remove the evidence, if any, corresponding to the node Id or name.

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

Return type
None

eraseJointTarget(*targets*)

Remove, if existing, the joint target.

Parameters
- **list** – a list of names or Ids of nodes
- **targets** (object) –

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

eraseTarget(**args*)

Remove, if existing, the marginal target.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

evidenceImpact(*target*, *evs*)

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)

Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

> **Warning:** if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)

Return type
pyAgrum.Potential (page 53)

evidenceJointImpact(*targets*, *evs*)

Create a pyAgrum.Potential for P(joint targets|evs) (for all instanciation of targets and evs)

Parameters
- **targets** (*List[intstr]*) – a list of node Ids or node names
- **evs** (*Set[intstr]*) – a set of nodes ids or names.

Returns
a Potential for P(target|evs)

Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.Exception – If some evidene entered into the Bayes net are incompatible (their joint proba = 0)

getNumberOfThreads()

returns the number of threads used by LazyPropagation during inferences.
Returns
the number of threads used by LazyPropagation during inferences
Return type
int

hardEvidenceNodes()

Returns
the set of nodes with hard evidence
Return type
set

hasEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasHardEvidence(*nodeName*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasSoftEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

isGumNumberOfThreadsOverriden()

Indicates whether LazyPropagation currently overrides aGrUM's default number of threads (see method setNumberOfThreads).
Returns
A Boolean indicating whether LazyPropagation currently overrides aGrUM's default number of threads
Return type
bool

isJointTarget(*targets*)

Parameters
- **list** – a list of nodes ids or names.
- **targets** (object) –

Returns
True if target is a joint target.

Return type
bool

Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- ***pyAgrum.UndefinedElement*** (page 293) – If node Id is not in the Bayesian network

isTarget(**args*)

Parameters
- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target

Return type
bool

Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- ***pyAgrum.UndefinedElement*** (page 293) – If node Id is not in the Bayesian network

jointMutualInformation(*targets*)

Parameters
targets (object) –

Return type
float

jointPosterior(*targets*)

Compute the joint posterior of a set of nodes.

Parameters
list – the list of nodes whose posterior joint probability is wanted

> **Warning:** The order of the variables given by the list here or when the jointTarget is declared can not be assumed to be used by the Potential.

Returns
a const ref to the posterior joint probability of the set of nodes.

Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

Parameters
targets (object) –

jointTargets()

Returns
the list of target sets

Return type
list

junctionTree(*id*)

Returns
the current junction tree

Return type
pyAgrum.CliqueGraph (page 15)

`makeInference()`

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later, the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.

Return type
None

`nbrEvidence()`

Returns
the number of evidence entered into the Bayesian network

Return type
int

`nbrHardEvidence()`

Returns
the number of hard evidence entered into the Bayesian network

Return type
int

`nbrSoftEvidence()`

Returns
the number of soft evidence entered into the Bayesian network

Return type
int

`nbrTargets()`

Returns
the number of marginal targets

Return type
int

`posterior(*args)`

Computes and returns the posterior of a node.

Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node

Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

`setEvidence(evidces)`

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.

Parameters
evidces (*dict*) – a dict of evidences

Raises
pyAgrum.InvalidArgument (page 290) – If one value is not a value for the node pyAgrum.InvalidArgument If the size of a value is different from the domain side of the node pyAgrum.FatalError If one value is a vector of 0s pyAgrum.UndefinedElement If one node does not belong to the Bayesian network

setMaxMemory(*gigabytes*)

sets an upper bound on the memory consumption admissible

Parameters
gigabytes (*float*) – this upper bound in gigabytes.

Return type
None

setNumberOfThreads(*nb*)

If the argument nb is different from 0, this number of threads will be used during inferences, hence overriding aGrUM's default number of threads. If, on the contrary, nb is equal to 0, the parallelized inference engine will comply with aGrUM's default number of threads.

Parameters
nb (*int*) – the number of threads to be used by ShaferShenoyMNInference

Return type
None

setTargets(*targets*)

Remove all the targets and add the ones in parameter.

Parameters
targets (*set*) – a set of targets

Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

softEvidenceNodes()

Returns
the set of nodes with soft evidence

Return type
set

targets()

Returns
the list of marginal targets

Return type
list

property thisown

The membership flag

updateEvidence(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).

Parameters
evidces (*dict*) – a dict of evidences

Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

1.4.5 Approximated Inference

Loopy Belief Propagation

class pyAgrum.**LoopyBeliefPropagation**(*bn*)

Class used for inferences using loopy belief propagation algorithm.

LoopyBeliefPropagation(bn) -> LoopyBeliefPropagation

Parameters:

- **bn** (*pyAgrum.BayesNet*) – a Bayesian network

Parameters
bn (IBayesNet) –

BN()

Returns
A constant reference over the IBayesNet referenced by this class.
Return type
pyAgrum.IBayesNet
Raises
pyAgrum.UndefinedElement (page 293) – If no Bayes net has been assigned to the inference.

H(**args*)

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation
Return type
float

addAllTargets()

Add all the nodes as targets.
Return type
None

addEvidence(**args*)

Adds a new evidence on a node (might be soft or hard).
Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

addTarget(*args)

Add a marginal target to the list of targets.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises
pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net

Return type
None

chgEvidence(*args)

Change the value of an already existing evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

currentTime()

Returns
get the current running time in second (float)

Return type
float

epsilon()

Returns
the value of epsilon

Return type
float

eraseAllEvidence()

Removes all the evidence entered into the network.

Return type
None

eraseAllTargets()

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).

Return type
None

eraseEvidence(*args)

Remove the evidence, if any, corresponding to the node Id or name.

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network
Return type
None

eraseTarget(**args*)

Remove, if existing, the marginal target.
Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

evidenceImpact(*target*, *evs*)

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)
Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

> **Warning:** if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)
Return type
pyAgrum.Potential (page 53)

hardEvidenceNodes()

Returns
the set of nodes with hard evidence
Return type
set

hasEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasHardEvidence(*nodeName*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasSoftEvidence(*args)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

history()

Returns
the scheme history

Return type
tuple

Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

isTarget(*args)

Parameters
- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target

Return type
bool

Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

makeInference()

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later, the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.

Return type
None

maxIter()

Returns
the criterion on number of iterations

Return type
int

maxTime()

Returns
the timeout(in seconds)

Return type
float

messageApproximationScheme()

Returns
the approximation scheme message

Return type
str

minEpsilonRate()

Returns
the value of the minimal epsilon rate
Return type
float

nbrEvidence()

Returns
the number of evidence entered into the Bayesian network
Return type
int

nbrHardEvidence()

Returns
the number of hard evidence entered into the Bayesian network
Return type
int

nbrIterations()

Returns
the number of iterations
Return type
int

nbrSoftEvidence()

Returns
the number of soft evidence entered into the Bayesian network
Return type
int

nbrTargets()

Returns
the number of marginal targets
Return type
int

periodSize()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

posterior(**args*)

Computes and returns the posterior of a node.
Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

setEpsilon(*eps*)

Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0
Return type
None

setEvidence(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.

Parameters
evidces (*dict*) – a dict of evidences
Raises
pyAgrum.InvalidArgument (page 290) – If one value is not a value for the node pyAgrum.InvalidArgument If the size of a value is different from the domain side of the node pyAgrum.FatalError If one value is a vector of 0s pyAgrum.UndefinedElement If one node does not belong to the Bayesian network

setMaxIter(*max*)

Parameters
max (*int*) – the maximum number of iteration
Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

setMaxTime(*timeout*)

Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0
Return type
None

setMinEpsilonRate(*rate*)

Parameters
rate (*float*) – the minimal epsilon rate
Return type
None

setPeriodSize(*p*)

Parameters
p (*int*) – number of samples between 2 stopping
Raises
pyAgrum.OutOfBounds (page 292) – If p<1
Return type
None

setTargets(*targets*)

Remove all the targets and add the ones in parameter.

Parameters
targets (*set*) – a set of targets
Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

setVerbosity(*v*)

Parameters
v (*bool*) – verbosity
Return type
None

softEvidenceNodes()

Returns
the set of nodes with soft evidence
Return type
set

targets()

Returns
the list of marginal targets
Return type
list

property thisown

The membership flag

updateEvidence(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).
Parameters
evidces (*dict*) – a dict of evidences
Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

verbosity()

Returns
True if the verbosity is enabled
Return type
bool

Sampling

Gibbs Sampling

class pyAgrum.**GibbsSampling**(*bn*)

Class for making Gibbs sampling inference in Bayesian networks.

GibbsSampling(bn) -> GibbsSampling

Parameters:

- **bn** (*pyAgrum.BayesNet*) – a Bayesian network

Parameters
bn (IBayesNet) –

BN()

Returns
A constant reference over the IBayesNet referenced by this class.
Return type
pyAgrum.IBayesNet
Raises
pyAgrum.UndefinedElement (page 293) – If no Bayes net has been assigned to the inference.

H(*args)

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation

Return type
float

addAllTargets()

Add all the nodes as targets.

Return type
None

addEvidence(*args)

Adds a new evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

addTarget(*args)

Add a marginal target to the list of targets.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises
pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net

Return type
None

burnIn()

Returns
size of burn in on number of iteration

Return type
int

chgEvidence(*args)

Change the value of an already existing evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises

- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

currentPosterior(**args*)

Computes and returns the current posterior of a node.

Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the current posterior probability of the node

Return type
pyAgrum.Potential (page 53)

Raises
UndefinedElement (page 293) – If an element of nodes is not in targets

currentTime()

Returns
get the current running time in second (float)

Return type
float

epsilon()

Returns
the value of epsilon

Return type
float

eraseAllEvidence()

Removes all the evidence entered into the network.

Return type
None

eraseAllTargets()

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).

Return type
None

eraseEvidence(**args*)

Remove the evidence, if any, corresponding to the node Id or name.

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

Return type
None

eraseTarget(**args*)

Remove, if existing, the marginal target.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

evidenceImpact(*target*, *evs*)

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)

Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

> **Warning:** if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)

Return type
pyAgrum.Potential (page 53)

hardEvidenceNodes()

Returns
the set of nodes with hard evidence

Return type
set

hasEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasHardEvidence(*nodeName*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasSoftEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence

Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

history()

Returns
the scheme history
Return type
tuple
Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

isDrawnAtRandom()

Returns
True if variables are drawn at random
Return type
bool

isTarget(**args*)

Parameters
- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target
Return type
bool
Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

makeInference()

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later, the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.
Return type
None

maxIter()

Returns
the criterion on number of iterations
Return type
int

maxTime()

Returns
the timeout(in seconds)
Return type
float

messageApproximationScheme()

Returns
the approximation scheme message
Return type
str

minEpsilonRate()

Returns
the value of the minimal epsilon rate
Return type
float

nbrDrawnVar()

Returns
the number of variable drawn at each iteration
Return type
int

nbrEvidence()

Returns
the number of evidence entered into the Bayesian network
Return type
int

nbrHardEvidence()

Returns
the number of hard evidence entered into the Bayesian network
Return type
int

nbrIterations()

Returns
the number of iterations
Return type
int

nbrSoftEvidence()

Returns
the number of soft evidence entered into the Bayesian network
Return type
int

nbrTargets()

Returns
the number of marginal targets
Return type
int

periodSize()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

posterior(**args*)

Computes and returns the posterior of a node.
Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node
Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

setBurnIn(*b*)

Parameters
b (*int*) – size of burn in on number of iteration
Return type
None

setDrawnAtRandom(*_atRandom*)

Parameters
_atRandom (*bool*) – indicates if variables should be drawn at random
Return type
None

setEpsilon(*eps*)

Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0
Return type
None

setEvidence(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.
Parameters
evidces (*dict*) – a dict of evidences
Raises
pyAgrum.InvalidArgument (page 290) – If one value is not a value for the node pyAgrum.InvalidArgument If the size of a value is different from the domain side of the node pyAgrum.FatalError If one value is a vector of 0s pyAgrum.UndefinedElement If one node does not belong to the Bayesian network

setMaxIter(*max*)

Parameters
max (*int*) – the maximum number of iteration
Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

setMaxTime(*timeout*)

Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0
Return type
None

setMinEpsilonRate(*rate*)

Parameters
rate (*float*) – the minimal epsilon rate
Return type
None

setNbrDrawnVar(*_nbr*)

Parameters
_nbr (*int*) – the number of variables to be drawn at each iteration

Return type
None

setPeriodSize(*p*)

Parameters
p (*int*) – number of samples between 2 stopping
Raises
pyAgrum.OutOfBounds (page 292) – If p<1
Return type
None

setTargets(*targets*)

Remove all the targets and add the ones in parameter.

Parameters
targets (*set*) – a set of targets
Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

setVerbosity(*v*)

Parameters
v (*bool*) – verbosity
Return type
None

softEvidenceNodes()

Returns
the set of nodes with soft evidence
Return type
set

targets()

Returns
the list of marginal targets
Return type
list

property thisown

The membership flag

updateEvidence(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).

Parameters
evidces (*dict*) – a dict of evidences
Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

verbosity()

Returns
True if the verbosity is enabled
Return type
bool

Monte Carlo Sampling

class pyAgrum.**MonteCarloSampling**(*bn*)

Class used for Monte Carlo sampling inference algorithm.

MonteCarloSampling(bn) -> MonteCarloSampling

Parameters:

- **bn** (*pyAgrum.BayesNet*) – a Bayesian network

Parameters
bn (IBayesNet) –

BN()

Returns
A constant reference over the IBayesNet referenced by this class.
Return type
pyAgrum.IBayesNet
Raises
pyAgrum.UndefinedElement (page 293) – If no Bayes net has been assigned to the inference.

H(**args*)

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation
Return type
float

addAllTargets()

Add all the nodes as targets.
Return type
None

addEvidence(**args*)

Adds a new evidence on a node (might be soft or hard).
Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

addTarget(**args*)

Add a marginal target to the list of targets.
Parameters

- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises

pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net

Return type

None

chgEvidence(**args*)

Change the value of an already existing evidence on a node (might be soft or hard).

Parameters

- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises

- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type

None

currentPosterior(**args*)

Computes and returns the current posterior of a node.

Parameters

- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns

a const ref to the current posterior probability of the node

Return type

pyAgrum.Potential (page 53)

Raises

UndefinedElement (page 293) – If an element of nodes is not in targets

currentTime()

Returns

get the current running time in second (float)

Return type

float

epsilon()

Returns

the value of epsilon

Return type

float

eraseAllEvidence()

Removes all the evidence entered into the network.

Return type

None

eraseAllTargets()

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).

Return type
None

`eraseEvidence`(**args*)

Remove the evidence, if any, corresponding to the node Id or name.

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

Return type
None

`eraseTarget`(**args*)

Remove, if existing, the marginal target.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

`evidenceImpact`(*target*, *evs*)

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)

Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

> **Warning:** if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)

Return type
pyAgrum.Potential (page 53)

`hardEvidenceNodes`()

Returns
the set of nodes with hard evidence

Return type
set

`hasEvidence`(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

`hasHardEvidence`(*nodeName*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasSoftEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

history()

Returns
the scheme history

Return type
tuple

Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

isTarget(**args*)

Parameters
- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target

Return type
bool

Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

makeInference()

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later, the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.

Return type
None

maxIter()

Returns
the criterion on number of iterations

Return type
int

maxTime()

Returns
the timeout(in seconds)
Return type
float

`messageApproximationScheme`()

Returns
the approximation scheme message
Return type
str

`minEpsilonRate`()

Returns
the value of the minimal epsilon rate
Return type
float

`nbrEvidence`()

Returns
the number of evidence entered into the Bayesian network
Return type
int

`nbrHardEvidence`()

Returns
the number of hard evidence entered into the Bayesian network
Return type
int

`nbrIterations`()

Returns
the number of iterations
Return type
int

`nbrSoftEvidence`()

Returns
the number of soft evidence entered into the Bayesian network
Return type
int

`nbrTargets`()

Returns
the number of marginal targets
Return type
int

`periodSize`()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

`posterior`(**args*)

Computes and returns the posterior of a node.
Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

setEpsilon(*eps*)

Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0
Return type
None

setEvidence(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.
Parameters
evidces (*dict*) – a dict of evidences
Raises
pyAgrum.InvalidArgument (page 290) – If one value is not a value for the node pyAgrum.InvalidArgument If the size of a value is different from the domain side of the node pyAgrum.FatalError If one value is a vector of 0s pyAgrum.UndefinedElement If one node does not belong to the Bayesian network

setMaxIter(*max*)

Parameters
max (*int*) – the maximum number of iteration
Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

setMaxTime(*timeout*)

Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0
Return type
None

setMinEpsilonRate(*rate*)

Parameters
rate (*float*) – the minimal epsilon rate
Return type
None

setPeriodSize(*p*)

Parameters
p (*int*) – number of samples between 2 stopping
Raises
pyAgrum.OutOfBounds (page 292) – If p<1
Return type
None

setTargets(*targets*)

Remove all the targets and add the ones in parameter.

Parameters
targets (*set*) – a set of targets
Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

`setVerbosity`(*v*)

Parameters
v (*bool*) – verbosity
Return type
None

`softEvidenceNodes`()

Returns
the set of nodes with soft evidence
Return type
set

`targets`()

Returns
the list of marginal targets
Return type
list

`property thisown`

The membership flag

`updateEvidence`(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).
Parameters
evidces (*dict*) – a dict of evidences
Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

`verbosity`()

Returns
True if the verbosity is enabled
Return type
bool

Weighted Sampling

`class pyAgrum.WeightedSampling`(*bn*)

Class used for Weighted sampling inference algorithm.

WeightedSampling(bn) -> WeightedSampling

Parameters:

- **bn** (*pyAgrum.BayesNet*) – a Bayesian network

Parameters
bn (IBayesNet) –

BN()

Returns
A constant reference over the IBayesNet referenced by this class.
Return type
pyAgrum.IBayesNet
Raises
pyAgrum.UndefinedElement (page 293) – If no Bayes net has been assigned to the inference.

H(**args*)

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation
Return type
float

addAllTargets()

Add all the nodes as targets.
Return type
None

addEvidence(**args*)

Adds a new evidence on a node (might be soft or hard).
Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

addTarget(**args*)

Add a marginal target to the list of targets.
Parameters
- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises
pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net
Return type
None

chgEvidence(**args*)

Change the value of an already existing evidence on a node (might be soft or hard).
Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises

- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type

None

currentPosterior(**args*)

Computes and returns the current posterior of a node.

Parameters

- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns

a const ref to the current posterior probability of the node

Return type

pyAgrum.Potential (page 53)

Raises

UndefinedElement (page 293) – If an element of nodes is not in targets

currentTime()

Returns

get the current running time in second (float)

Return type

float

epsilon()

Returns

the value of epsilon

Return type

float

eraseAllEvidence()

Removes all the evidence entered into the network.

Return type

None

eraseAllTargets()

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).

Return type

None

eraseEvidence(**args*)

Remove the evidence, if any, corresponding to the node Id or name.

Parameters

- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises

pyAgrum.IndexError – If the node does not belong to the Bayesian network

Return type

None

eraseTarget(*args)

Remove, if existing, the marginal target.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

evidenceImpact(*target*, *evs*)

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)

Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

> **Warning:** if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)

Return type
pyAgrum.Potential (page 53)

hardEvidenceNodes()

Returns
the set of nodes with hard evidence

Return type
set

hasEvidence(*args)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasHardEvidence(*nodeName*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasSoftEvidence(*args)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

history()

Returns
the scheme history
Return type
tuple
Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

isTarget(**args*)

Parameters
- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target
Return type
bool
Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

makeInference()

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later, the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.
Return type
None

maxIter()

Returns
the criterion on number of iterations
Return type
int

maxTime()

Returns
the timeout(in seconds)
Return type
float

messageApproximationScheme()

Returns
the approximation scheme message
Return type
str

minEpsilonRate()

Returns
the value of the minimal epsilon rate

Return type
float

`nbrEvidence`()

Returns
the number of evidence entered into the Bayesian network
Return type
int

`nbrHardEvidence`()

Returns
the number of hard evidence entered into the Bayesian network
Return type
int

`nbrIterations`()

Returns
the number of iterations
Return type
int

`nbrSoftEvidence`()

Returns
the number of soft evidence entered into the Bayesian network
Return type
int

`nbrTargets`()

Returns
the number of marginal targets
Return type
int

`periodSize`()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

`posterior`(**args*)

Computes and returns the posterior of a node.
Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

`setEpsilon`(*eps*)

Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0

Return type
None

setEvidence(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.

Parameters
evidces (*dict*) – a dict of evidences
Raises
pyAgrum.InvalidArgument (page 290) – If one value is not a value for the node pyAgrum.InvalidArgument If the size of a value is different from the domain side of the node pyAgrum.FatalError If one value is a vector of 0s pyAgrum.UndefinedElement If one node does not belong to the Bayesian network

setMaxIter(*max*)

Parameters
max (*int*) – the maximum number of iteration
Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

setMaxTime(*timeout*)

Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0
Return type
None

setMinEpsilonRate(*rate*)

Parameters
rate (*float*) – the minimal epsilon rate
Return type
None

setPeriodSize(*p*)

Parameters
p (*int*) – number of samples between 2 stopping
Raises
pyAgrum.OutOfBounds (page 292) – If p<1
Return type
None

setTargets(*targets*)

Remove all the targets and add the ones in parameter.

Parameters
targets (*set*) – a set of targets
Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

setVerbosity(*v*)

Parameters
v (*bool*) – verbosity
Return type
None

softEvidenceNodes()

Returns
the set of nodes with soft evidence

Return type
set

`targets()`

Returns
the list of marginal targets
Return type
list

`property thisown`

The membership flag

`updateEvidence(evidces)`

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).
Parameters
evidces (*dict*) – a dict of evidences
Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

`verbosity()`

Returns
True if the verbosity is enabled
Return type
bool

Importance Sampling

`class pyAgrum.ImportanceSampling(bn)`

Class used for inferences using the Importance Sampling algorithm.

ImportanceSampling(bn) -> ImportanceSampling

Parameters:

- **bn** (*pyAgrum.BayesNet*) – a Bayesian network

Parameters
bn (IBayesNet) –

`BN()`

Returns
A constant reference over the IBayesNet referenced by this class.
Return type
pyAgrum.IBayesNet
Raises
pyAgrum.UndefinedElement (page 293) – If no Bayes net has been assigned to the inference.

`H(*args)`

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation

Return type
float

`addAllTargets()`

Add all the nodes as targets.

Return type
None

`addEvidence(*args)`

Adds a new evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

`addTarget(*args)`

Add a marginal target to the list of targets.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises
pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net

Return type
None

`chgEvidence(*args)`

Change the value of an already existing evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

`currentPosterior(*args)`

Computes and returns the current posterior of a node.

Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the current posterior probability of the node

Return type
pyAgrum.Potential (page 53)

Raises
UndefinedElement (page 293) – If an element of nodes is not in targets

currentTime()

Returns
get the current running time in second (float)

Return type
float

epsilon()

Returns
the value of epsilon

Return type
float

eraseAllEvidence()

Removes all the evidence entered into the network.

Return type
None

eraseAllTargets()

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).

Return type
None

eraseEvidence(**args*)

Remove the evidence, if any, corresponding to the node Id or name.

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

Return type
None

eraseTarget(**args*)

Remove, if existing, the marginal target.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

evidenceImpact(*target*, *evs*)

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)

Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

> **Warning:** if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)
Return type
pyAgrum.Potential (page 53)

hardEvidenceNodes()

Returns
the set of nodes with hard evidence
Return type
set

hasEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasHardEvidence(*nodeName*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasSoftEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

history()

Returns
the scheme history
Return type
tuple
Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

isTarget(**args*)

Parameters
- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target

Return type
bool

Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

makeInference()

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later, the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.

Return type
None

maxIter()

Returns
the criterion on number of iterations

Return type
int

maxTime()

Returns
the timeout(in seconds)

Return type
float

messageApproximationScheme()

Returns
the approximation scheme message

Return type
str

minEpsilonRate()

Returns
the value of the minimal epsilon rate

Return type
float

nbrEvidence()

Returns
the number of evidence entered into the Bayesian network

Return type
int

nbrHardEvidence()

Returns
the number of hard evidence entered into the Bayesian network

Return type
int

nbrIterations()

Returns
the number of iterations
Return type
int

`nbrSoftEvidence`()

Returns
the number of soft evidence entered into the Bayesian network
Return type
int

`nbrTargets`()

Returns
the number of marginal targets
Return type
int

`periodSize`()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

`posterior`(**args*)

Computes and returns the posterior of a node.
Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

`setEpsilon`(*eps*)

Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0
Return type
None

`setEvidence`(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.
Parameters
evidces (*dict*) – a dict of evidences
Raises
pyAgrum.InvalidArgument (page 290) – If one value is not a value for the node pyAgrum.InvalidArgument If the size of a value is different from the domain side of the node pyAgrum.FatalError If one value is a vector of 0s pyAgrum.UndefinedElement If one node does not belong to the Bayesian network

`setMaxIter`(*max*)

Parameters
max (*int*) – the maximum number of iteration

Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

setMaxTime(*timeout*)

Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0
Return type
None

setMinEpsilonRate(*rate*)

Parameters
rate (*float*) – the minimal epsilon rate
Return type
None

setPeriodSize(*p*)

Parameters
p (*int*) – number of samples between 2 stopping
Raises
pyAgrum.OutOfBounds (page 292) – If p<1
Return type
None

setTargets(*targets*)

Remove all the targets and add the ones in parameter.

Parameters
targets (*set*) – a set of targets
Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

setVerbosity(*v*)

Parameters
v (*bool*) – verbosity
Return type
None

softEvidenceNodes()

Returns
the set of nodes with soft evidence
Return type
set

targets()

Returns
the list of marginal targets
Return type
list

property thisown

The membership flag

updateEvidence(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).

Parameters
evidces (*dict*) – a dict of evidences
Raises

- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

verbosity()

Returns
True if the verbosity is enabled

Return type
bool

Loopy sampling

Loopy Gibbs Sampling

class pyAgrum.**LoopyGibbsSampling**(*bn*)

Parameters
bn (IBayesNet) –

BN()

Returns
A constant reference over the IBayesNet referenced by this class.

Return type
pyAgrum.IBayesNet

Raises
pyAgrum.UndefinedElement (page 293) – If no Bayes net has been assigned to the inference.

H(**args*)

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation

Return type
float

addAllTargets()

Add all the nodes as targets.

Return type
None

addEvidence(**args*)

Adds a new evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node

- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

addTarget(**args*)

Add a marginal target to the list of targets.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises
pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net

Return type
None

burnIn()

Returns
size of burn in on number of iteration

Return type
int

chgEvidence(**args*)

Change the value of an already existing evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

currentPosterior(**args*)

Computes and returns the current posterior of a node.

Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the current posterior probability of the node

Return type
pyAgrum.Potential (page 53)

Raises
UndefinedElement (page 293) – If an element of nodes is not in targets

currentTime()

Returns
get the current running time in second (float)

Return type
float

`epsilon()`

Returns
the value of epsilon
Return type
float

`eraseAllEvidence()`

Removes all the evidence entered into the network.
Return type
None

`eraseAllTargets()`

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).
Return type
None

`eraseEvidence(*args)`

Remove the evidence, if any, corresponding to the node Id or name.
Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network
Return type
None

`eraseTarget(*args)`

Remove, if existing, the marginal target.
Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

`evidenceImpact(target, evs)`

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)
Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

> **Warning:** if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)
Return type
pyAgrum.Potential (page 53)

`hardEvidenceNodes()`

Returns
the set of nodes with hard evidence
Return type
set

`hasEvidence`(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

`hasHardEvidence`(*nodeName*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

`hasSoftEvidence`(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

`history`()

Returns
the scheme history
Return type
tuple
Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

`isDrawnAtRandom`()

Returns
True if variables are drawn at random
Return type
bool

`isTarget`(**args*)

Parameters
- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target

Return type
bool
Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

makeInference()

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later, the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.

Return type
None

makeInference_()

Return type
None

maxIter()

Returns
the criterion on number of iterations
Return type
int

maxTime()

Returns
the timeout(in seconds)
Return type
float

messageApproximationScheme()

Returns
the approximation scheme message
Return type
str

minEpsilonRate()

Returns
the value of the minimal epsilon rate
Return type
float

nbrDrawnVar()

Returns
the number of variable drawn at each iteration
Return type
int

nbrEvidence()

Returns
the number of evidence entered into the Bayesian network
Return type
int

nbrHardEvidence()

Returns
the number of hard evidence entered into the Bayesian network

Return type
int

nbrIterations()

Returns
the number of iterations
Return type
int

nbrSoftEvidence()

Returns
the number of soft evidence entered into the Bayesian network
Return type
int

nbrTargets()

Returns
the number of marginal targets
Return type
int

periodSize()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

posterior(**args*)

Computes and returns the posterior of a node.
Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

setBurnIn(*b*)

Parameters
b (*int*) – size of burn in on number of iteration
Return type
None

setDrawnAtRandom(*_atRandom*)

Parameters
_atRandom (*bool*) – indicates if variables should be drawn at random
Return type
None

setEpsilon(*eps*)

Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0

Return type
None

setEvidence(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.

Parameters
evidces (*dict*) – a dict of evidences
Raises
pyAgrum.InvalidArgument (page 290) – If one value is not a value for the node pyAgrum.InvalidArgument If the size of a value is different from the domain side of the node pyAgrum.FatalError If one value is a vector of 0s pyAgrum.UndefinedElement If one node does not belong to the Bayesian network

setMaxIter(*max*)

Parameters
max (*int*) – the maximum number of iteration
Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

setMaxTime(*timeout*)

Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0
Return type
None

setMinEpsilonRate(*rate*)

Parameters
rate (*float*) – the minimal epsilon rate
Return type
None

setNbrDrawnVar(*_nbr*)

Parameters
_nbr (*int*) – the number of variables to be drawn at each iteration
Return type
None

setPeriodSize(*p*)

Parameters
p (*int*) – number of samples between 2 stopping
Raises
pyAgrum.OutOfBounds (page 292) – If p<1
Return type
None

setTargets(*targets*)

Remove all the targets and add the ones in parameter.

Parameters
targets (*set*) – a set of targets
Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

setVerbosity(*v*)

Parameters
v (*bool*) – verbosity

Return type
None

`setVirtualLBPSize`(*vlbpsize*)

Parameters
vlbpsize (*float*) – the size of the virtual LBP
Return type
None

`softEvidenceNodes`()

Returns
the set of nodes with soft evidence
Return type
set

`targets`()

Returns
the list of marginal targets
Return type
list

`property thisown`

The membership flag

`updateEvidence`(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).
Parameters
evidces (*dict*) – a dict of evidences
Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

`verbosity`()

Returns
True if the verbosity is enabled
Return type
bool

Loopy Monte Carlo Sampling

`class pyAgrum.LoopyMonteCarloSampling`(*bn*)

Parameters
bn (IBayesNet) –

`BN`()

Returns
A constant reference over the IBayesNet referenced by this class.
Return type
pyAgrum.IBayesNet
Raises
pyAgrum.UndefinedElement (page 293) – If no Bayes net has been assigned to the inference.

H(**args*)

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation

Return type
float

addAllTargets()

Add all the nodes as targets.

Return type
None

addEvidence(**args*)

Adds a new evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

addTarget(**args*)

Add a marginal target to the list of targets.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises
pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net

Return type
None

chgEvidence(**args*)

Change the value of an already existing evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s

- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

currentPosterior(**args*)

Computes and returns the current posterior of a node.

Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the current posterior probability of the node

Return type
pyAgrum.Potential (page 53)

Raises
UndefinedElement (page 293) – If an element of nodes is not in targets

currentTime()

Returns
get the current running time in second (float)

Return type
float

epsilon()

Returns
the value of epsilon

Return type
float

eraseAllEvidence()

Removes all the evidence entered into the network.

Return type
None

eraseAllTargets()

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).

Return type
None

eraseEvidence(**args*)

Remove the evidence, if any, corresponding to the node Id or name.

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

Return type
None

eraseTarget(**args*)

Remove, if existing, the marginal target.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network

- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

evidenceImpact(*target*, *evs*)

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)

Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

Warning: if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)

Return type
pyAgrum.Potential (page 53)

hardEvidenceNodes()

Returns
the set of nodes with hard evidence

Return type
set

hasEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasHardEvidence(*nodeName*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasSoftEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

history()

Returns
the scheme history

Return type
tuple
Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

`isTarget`(**args*)

Parameters
- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target
Return type
bool
Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

`makeInference`()

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later, the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.
Return type
None

`makeInference_`()

Return type
None

`maxIter`()

Returns
the criterion on number of iterations
Return type
int

`maxTime`()

Returns
the timeout(in seconds)
Return type
float

`messageApproximationScheme`()

Returns
the approximation scheme message
Return type
str

`minEpsilonRate`()

Returns
the value of the minimal epsilon rate
Return type
float

`nbrEvidence`()

Returns
the number of evidence entered into the Bayesian network

Return type
int

nbrHardEvidence()

Returns
the number of hard evidence entered into the Bayesian network
Return type
int

nbrIterations()

Returns
the number of iterations
Return type
int

nbrSoftEvidence()

Returns
the number of soft evidence entered into the Bayesian network
Return type
int

nbrTargets()

Returns
the number of marginal targets
Return type
int

periodSize()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

posterior(**args*)

Computes and returns the posterior of a node.
Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

setEpsilon(*eps*)

Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0
Return type
None

setEvidence(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.
Parameters
evidces (*dict*) – a dict of evidences

Raises
pyAgrum.InvalidArgument (page 290) – If one value is not a value for the node pyAgrum.InvalidArgument If the size of a value is different from the domain side of the node pyAgrum.FatalError If one value is a vector of 0s pyAgrum.UndefinedElement If one node does not belong to the Bayesian network

setMaxIter(*max*)

Parameters
max (*int*) – the maximum number of iteration
Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

setMaxTime(*timeout*)

Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0
Return type
None

setMinEpsilonRate(*rate*)

Parameters
rate (*float*) – the minimal epsilon rate
Return type
None

setPeriodSize(*p*)

Parameters
p (*int*) – number of samples between 2 stopping
Raises
pyAgrum.OutOfBounds (page 292) – If p<1
Return type
None

setTargets(*targets*)

Remove all the targets and add the ones in parameter.
Parameters
targets (*set*) – a set of targets
Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

setVerbosity(*v*)

Parameters
v (*bool*) – verbosity
Return type
None

setVirtualLBPSize(*vlbpsize*)

Parameters
vlbpsize (*float*) – the size of the virtual LBP
Return type
None

softEvidenceNodes()

Returns
the set of nodes with soft evidence
Return type
set

targets()

Returns
the list of marginal targets
Return type
list

property thisown

The membership flag

updateEvidence(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).
Parameters
evidces (*dict*) – a dict of evidences
Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

verbosity()

Returns
True if the verbosity is enabled
Return type
bool

Loopy Weighted Sampling

class pyAgrum.**LoopyWeightedSampling**(*bn*)

Parameters
bn (IBayesNet) –

BN()

Returns
A constant reference over the IBayesNet referenced by this class.
Return type
pyAgrum.IBayesNet
Raises
pyAgrum.UndefinedElement (page 293) – If no Bayes net has been assigned to the inference.

H(**args*)

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation
Return type
float

addAllTargets()

Add all the nodes as targets.
Return type
None

addEvidence(*args)

Adds a new evidence on a node (might be soft or hard).

Parameters

- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises

- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type

None

addTarget(*args)

Add a marginal target to the list of targets.

Parameters

- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises

pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net

Return type

None

chgEvidence(*args)

Change the value of an already existing evidence on a node (might be soft or hard).

Parameters

- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises

- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type

None

currentPosterior(*args)

Computes and returns the current posterior of a node.

Parameters

- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns

a const ref to the current posterior probability of the node

Return type
pyAgrum.Potential (page 53)
Raises
UndefinedElement (page 293) – If an element of nodes is not in targets

`currentTime`()

Returns
get the current running time in second (float)
Return type
float

`epsilon`()

Returns
the value of epsilon
Return type
float

`eraseAllEvidence`()

Removes all the evidence entered into the network.
Return type
None

`eraseAllTargets`()

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).
Return type
None

`eraseEvidence`(**args*)

Remove the evidence, if any, corresponding to the node Id or name.
Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network
Return type
None

`eraseTarget`(**args*)

Remove, if existing, the marginal target.
Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

`evidenceImpact`(*target*, *evs*)

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)
Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

Warning: if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)
Return type
pyAgrum.Potential (page 53)

hardEvidenceNodes()

Returns
the set of nodes with hard evidence
Return type
set

hasEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasHardEvidence(*nodeName*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasSoftEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence
Return type
bool
Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

history()

Returns
the scheme history
Return type
tuple
Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

isTarget(**args*)

Parameters
- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target
Return type
bool
Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

makeInference()

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later, the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.
Return type
None

makeInference_()
Return type
None

maxIter()
Returns
the criterion on number of iterations
Return type
int

maxTime()
Returns
the timeout(in seconds)
Return type
float

messageApproximationScheme()
Returns
the approximation scheme message
Return type
str

minEpsilonRate()
Returns
the value of the minimal epsilon rate
Return type
float

nbrEvidence()
Returns
the number of evidence entered into the Bayesian network
Return type
int

nbrHardEvidence()
Returns
the number of hard evidence entered into the Bayesian network
Return type
int

nbrIterations()

Returns
the number of iterations
Return type
int

`nbrSoftEvidence`()

Returns
the number of soft evidence entered into the Bayesian network
Return type
int

`nbrTargets`()

Returns
the number of marginal targets
Return type
int

`periodSize`()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

`posterior`(**args*)

Computes and returns the posterior of a node.
Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

`setEpsilon`(*eps*)

Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0
Return type
None

`setEvidence`(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.
Parameters
evidces (*dict*) – a dict of evidences
Raises
pyAgrum.InvalidArgument (page 290) – If one value is not a value for the node pyAgrum.InvalidArgument If the size of a value is different from the domain side of the node pyAgrum.FatalError If one value is a vector of 0s pyAgrum.UndefinedElement If one node does not belong to the Bayesian network

`setMaxIter`(*max*)

Parameters
max (*int*) – the maximum number of iteration

Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

`setMaxTime`(*timeout*)

Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0
Return type
None

`setMinEpsilonRate`(*rate*)

Parameters
rate (*float*) – the minimal epsilon rate
Return type
None

`setPeriodSize`(*p*)

Parameters
p (*int*) – number of samples between 2 stopping
Raises
pyAgrum.OutOfBounds (page 292) – If p<1
Return type
None

`setTargets`(*targets*)

Remove all the targets and add the ones in parameter.

Parameters
targets (*set*) – a set of targets
Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

`setVerbosity`(*v*)

Parameters
v (*bool*) – verbosity
Return type
None

`setVirtualLBPSize`(*vlbpsize*)

Parameters
vlbpsize (*float*) – the size of the virtual LBP
Return type
None

`softEvidenceNodes`()

Returns
the set of nodes with soft evidence
Return type
set

`targets`()

Returns
the list of marginal targets
Return type
list

`property thisown`

The membership flag

updateEvidence(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).

Parameters
evidces (*dict*) – a dict of evidences

Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

verbosity()

Returns
True if the verbosity is enabled

Return type
bool

Loopy Importance Sampling

class pyAgrum.**LoopyImportanceSampling**(*bn*)

Parameters
bn (IBayesNet) –

BN()

Returns
A constant reference over the IBayesNet referenced by this class.

Return type
pyAgrum.IBayesNet

Raises
pyAgrum.UndefinedElement (page 293) – If no Bayes net has been assigned to the inference.

H(**args*)

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation

Return type
float

addAllTargets()

Add all the nodes as targets.

Return type
None

addEvidence(**args*)

Adds a new evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises

- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

addTarget(**args*)

Add a marginal target to the list of targets.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises
pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net

Return type
None

chgEvidence(**args*)

Change the value of an already existing evidence on a node (might be soft or hard).

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises
- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

currentPosterior(**args*)

Computes and returns the current posterior of a node.

Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the current posterior probability of the node

Return type
pyAgrum.Potential (page 53)

Raises
UndefinedElement (page 293) – If an element of nodes is not in targets

currentTime()

Returns
get the current running time in second (float)

Return type
float

epsilon()

Returns
the value of epsilon
Return type
float

eraseAllEvidence()

Removes all the evidence entered into the network.
Return type
None

eraseAllTargets()

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).
Return type
None

eraseEvidence(**args*)

Remove the evidence, if any, corresponding to the node Id or name.
Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network
Return type
None

eraseTarget(**args*)

Remove, if existing, the marginal target.
Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

evidenceImpact(*target*, *evs*)

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)
Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

> **Warning:** if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)
Return type
pyAgrum.Potential (page 53)

hardEvidenceNodes()

Returns
the set of nodes with hard evidence
Return type
set

hasEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasHardEvidence(*nodeName*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasSoftEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

history()

Returns
the scheme history

Return type
tuple

Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

isTarget(**args*)

Parameters
- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target

Return type
bool

Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

makeInference()

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later,

the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.

Return type
None

makeInference_()

Return type
None

maxIter()

Returns
the criterion on number of iterations

Return type
int

maxTime()

Returns
the timeout(in seconds)

Return type
float

messageApproximationScheme()

Returns
the approximation scheme message

Return type
str

minEpsilonRate()

Returns
the value of the minimal epsilon rate

Return type
float

nbrEvidence()

Returns
the number of evidence entered into the Bayesian network

Return type
int

nbrHardEvidence()

Returns
the number of hard evidence entered into the Bayesian network

Return type
int

nbrIterations()

Returns
the number of iterations

Return type
int

nbrSoftEvidence()

Returns
the number of soft evidence entered into the Bayesian network

Return type
int

nbrTargets()

Returns
the number of marginal targets

Return type
int

periodSize()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

posterior(**args*)

Computes and returns the posterior of a node.
Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

setEpsilon(*eps*)

Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0
Return type
None

setEvidence(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.
Parameters
evidces (*dict*) – a dict of evidences
Raises
pyAgrum.InvalidArgument (page 290) – If one value is not a value for the node pyAgrum.InvalidArgument If the size of a value is different from the domain side of the node pyAgrum.FatalError If one value is a vector of 0s pyAgrum.UndefinedElement If one node does not belong to the Bayesian network

setMaxIter(*max*)

Parameters
max (*int*) – the maximum number of iteration
Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

setMaxTime(*timeout*)

Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0
Return type
None

setMinEpsilonRate(*rate*)

Parameters
rate (*float*) – the minimal epsilon rate
Return type
None

setPeriodSize(*p*)

Parameters
p (*int*) – number of samples between 2 stopping
Raises
pyAgrum.OutOfBounds (page 292) – If p<1
Return type
None

setTargets(*targets*)

Remove all the targets and add the ones in parameter.

Parameters
targets (*set*) – a set of targets
Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

setVerbosity(*v*)

Parameters
v (*bool*) – verbosity
Return type
None

setVirtualLBPSize(*vlbpsize*)

Parameters
vlbpsize (*float*) – the size of the virtual LBP
Return type
None

softEvidenceNodes()

Returns
the set of nodes with soft evidence
Return type
set

targets()

Returns
the list of marginal targets
Return type
list

property thisown

The membership flag

updateEvidence(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).

Parameters
evidces (*dict*) – a dict of evidences
Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

verbosity()

Returns
True if the verbosity is enabled
Return type
bool

1.4.6 Learning

pyAgrum encloses all the learning processes for Bayesian network in a simple class BNLearner. This class gives access directly to the complete learning algorithm and theirs parameters (such as prior, scores, constraints, etc.) but also proposes low-level functions that eases the work on developping new learning algorithms (for instance, compute chi2 or conditioanl likelihood on the database, etc.).

class pyAgrum.**BNLearner**(*filename*, *inducedTypes=True*)

Parameters:

- **source** (*str* or *pandas.DataFrame*) – the data to learn from
- **missingSymbols** (*List[str]*) – list of string that will be interpreted as missing values (by default : ['?'])
- **inducedTypes** (*Bool*) – whether BNLearner should try to automatically find the type of each variable

BNLearner(filename,src) -> BNLearner

Parameters:

- **source** (*str* or *pandas.DataFrame) – the data to learn from
- **src** (*pyAgrum.BayesNet*) – the Bayesian network used to find those modalities
- **missingSymbols** (*List[str]*) – list of string that will be interpreted as missing values (by default : ['?'])

BNLearner(learner) -> BNLearner

Parameters:

- **learner** (*pyAgrum.BNLearner*) – the BNLearner to copy

G2(**args*)

G2 computes the G2 statistic and pvalue for two columns, given a list of other columns.
Parameters
- **name1** (*str*) – the name of the first column
- **name2** (*str*) – the name of the second column
- **knowing** (*[str]*) – the list of names of conditioning columns

Returns
the G2 statistic and the associated p-value as a Tuple
Return type
statistic,pvalue

addForbiddenArc(**args*)

Return type
BNLearner (page 183)

addMandatoryArc(**args*)

Return type
BNLearner (page 183)

addPossibleEdge(**args*)

Return type
BNLearner (page 183)

chi2(**args*)

chi2 computes the chi2 statistic and pvalue for two columns, given a list of other columns.

Parameters
- **name1** (*str*) – the name of the first column
- **name2** (*str*) – the name of the second column
- **knowing** (*[str]*) – the list of names of conditioning columns

Returns
the chi2 statistic and the associated p-value as a Tuple

Return type
statistic,pvalue

correctedMutualInformation(**args*)

Return type
float

currentTime()

Returns
get the current running time in second (float)

Return type
float

databaseWeight()

Return type
float

domainSize(**args*)

Return type
int

epsilon()

Returns
the value of epsilon

Return type
float

eraseForbiddenArc(**args*)

Return type
BNLearner (page 183)

eraseMandatoryArc(**args*)

Return type
BNLearner (page 183)

erasePossibleEdge(**args*)

Return type
BNLearner (page 183)

fitParameters(*bn*)

Easy shortcut to LearnParameters method. fitParameters uses self to direcuptly populate the CPTs of bn.0

Parameters
bn (pyAgrum.BayesNet (page 64)) – a BN which will directly have its parameters learned.

getNumberOfThreads()

Return type
int

hasMissingValues()

Return type
bool

history()

Returns
the scheme history
Return type
tuple
Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

idFromName(*var_name*)

Parameters
var_name (str) –
Return type
int

isGumNumberOfThreadsOverriden()

Return type
bool

latentVariables()

> **Warning:** learner must be using 3off2 or MIIC algorithm

Returns
the list of latent variables
Return type
list

learnBN()

learn a BayesNet from a file (must have read the db before)
Returns
the learned BayesNet
Return type
pyAgrum.BayesNet (page 64)

learnDAG()

Return type
DAG (page 8)

learnEssentialGraph()

learnMixedStructure()

Return type
MixedGraph (page 20)

learnParameters(**args*)

learns a BN (its parameters) when its structure is known.
Parameters
- **dag** (pyAgrum.DAG (page 8)) –
- **bn** (pyAgrum.BayesNet (page 64)) –
- **take_into_account_score** (*bool*) – The dag passed in argument may have been learnt from a structure learning. In this case, if the score used to learn the structure has an implicit prior (like K2 which has a 1-smoothing prior), it is important to also take into account this implicit prior for parameter learning. By default, if a score exists, we will learn parameters by taking into account the prior specified by methods usePriorXXX () + the implicit prior of the score, else we just take into account the prior specified by usePriorXXX ()

Returns
the learned BayesNet

Return type
pyAgrum.BayesNet (page 64)
Raises
- **pyAgrum.MissingVariableInDatabase** – If a variable of the BN is not found in the database
- ***pyAgrum.UnknownLabelInDatabase*** (page 293) – If a label is found in the database that do not correspond to the variable

logLikelihood(**args*)

Return type
float

maxIter()

Returns
the criterion on number of iterations
Return type
int

maxTime()

Returns
the timeout(in seconds)
Return type
float

messageApproximationScheme()

Returns
the approximation scheme message
Return type
str

minEpsilonRate()

Returns
the value of the minimal epsilon rate
Return type
float

mutualInformation(**args*)

Return type
float

nameFromId(*id*)

Parameters
id (int) –
Return type
str

names()

Return type
List[str]

nbCols()

Return type
int

nbRows()

Return type
int

nbrIterations()

Returns
the number of iterations

Return type
int

periodSize()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

pseudoCount(*vars*)

access to pseudo-count (priors taken into account)
Parameters
vars (*list[str]*) – a list of name of vars to add in the pseudo_count
Return type
a Potential containing this pseudo-counts

rawPseudoCount(**args*)

Return type
List[float]

recordWeight(*i*)

Parameters
i (int) –
Return type
float

score(**args*)

Return type
float

setDatabaseWeight(*new_weight*)

Parameters
new_weight (float) –
Return type
None

setEpsilon(*eps*)

Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0
Return type
None

setForbiddenArcs(*set*)

Parameters
set (Set[Tuple[int, int]]) –
Return type
BNLearner (page 183)

setInitialDAG(*dag*)

Parameters
dag (pyAgrum.DAG (page 8)) – an initial DAG structure
Return type
BNLearner (page 183)

setMandatoryArcs(*set*)

Parameters
set (Set[Tuple[int, int]]) –

Return type
BNLearner (page 183)

setMaxIndegree(*max_indegree*)

Parameters
max_indegree (*int*) – the limit number of parents
Return type
BNLearner (page 183)

setMaxIter(*max*)

Parameters
max (*int*) – the maximum number of iteration
Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

setMaxTime(*timeout*)

Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0
Return type
None

setMinEpsilonRate(*rate*)

Parameters
rate (*float*) – the minimal epsilon rate
Return type
None

setNumberOfThreads(*nb*)

Parameters
nb (int) –
Return type
None

setPeriodSize(*p*)

Parameters
p (*int*) – number of samples between 2 stopping
Raises
pyAgrum.OutOfBounds (page 292) – If p<1
Return type
None

setPossibleEdges(*set*)

Parameters
set (Set[Tuple[int, int]]) –
Return type
BNLearner (page 183)

setPossibleSkeleton(*skeleton*)

Parameters
skeleton (*UndiGraph* (page 12)) –
Return type
BNLearner (page 183)

setRecordWeight(*i*, *weight*)

Parameters
- **i** (int) –

- **weight** (float) –

Return type
None

setSliceOrder(**args*)

Return type
BNLearner (page 183)

setVerbosity(*v*)

Parameters
v (*bool*) – verbosity

Return type
None

state()

Return type
object

use3off2()

Indicate that we wish to use 3off2.

Return type
BNLearner (page 183)

useAprioriBDeu()

Deprecated methods in BNLearner for pyAgrum>1.1.1

useAprioriDirichlet()

Deprecated methods in BNLearner for pyAgrum>1.1.1

useAprioriSmoothing()

Deprecated methods in BNLearner for pyAgrum>1.1.1

useBDeuPrior(*weight=1.0*)

Parameters
weight (float) –

Return type
BNLearner (page 183)

useDirichletPrior(**args*)

Use the Dirichlet prior.

Parameters
- **source** (*str*|pyAgrum.BayesNet (page 64)) – the Dirichlet related source (filename of a database or a Bayesian network)
- **weight** (*float (optional)*) – the weight of the prior (the 'size' of the corresponding 'virtual database')

Return type
BNLearner (page 183)

useEM(*epsilon*)

Indicates if we use EM for parameter learning.

Parameters
epsilon (*float*) – if epsilon=0.0 then EM is not used if epsilon>0 then EM is used and stops when the sum of the cumulative squared error on parameters is les than epsilon.

Return type
BNLearner (page 183)

useGreedyHillClimbing()

Indicate that we wish to use a greedy hill climbing algorithm.

Return type
BNLearner (page 183)

useK2(**args*)

Return type
BNLearner (page 183)

useLocalSearchWithTabuList(*tabu_size=100*, *nb_decrease=2*)

Parameters
- **tabu_size** (int) –
- **nb_decrease** (int) –

Return type
BNLearner (page 183)

useMDLCorrection()

Indicate that we wish to use the MDL correction for 3off2 or MIIC

Return type
BNLearner (page 183)

useMIIC()

Indicate that we wish to use MIIC.

Return type
BNLearner (page 183)

useNMLCorrection()

Indicate that we wish to use the NML correction for 3off2 or MIIC

Return type
BNLearner (page 183)

useNoApriori()

Deprecated methods in BNLearner for pyAgrum>1.1.1

useNoCorrection()

Indicate that we wish to use the NoCorr correction for 3off2 or MIIC

Return type
BNLearner (page 183)

useNoPrior()

Use no prior.

Return type
BNLearner (page 183)

useScoreAIC()

Indicate that we wish to use an AIC score.

Return type
BNLearner (page 183)

useScoreBD()

Indicate that we wish to use a BD score.

Return type
BNLearner (page 183)

useScoreBDeu()

Indicate that we wish to use a BDeu score.

Return type
BNLearner (page 183)

useScoreBIC()

Indicate that we wish to use a BIC score.

Return type
BNLearner (page 183)

useScoreK2()

Indicate that we wish to use a K2 score.

Return type
BNLearner (page 183)

useScoreLog2Likelihood()

Indicate that we wish to use a Log2Likelihood score.

Return type
BNLearner (page 183)

useSmoothingPrior(*weight=1*)

Use the prior smoothing.

Parameters
weight (*float*) – pass in argument a weight if you wish to assign a weight to the smoothing, otherwise the current weight of the learner will be used.

Return type
BNLearner (page 183)

verbosity()

Returns
True if the verbosity is enabled

Return type
bool

1.5 Influence Diagram

An influence diagram is a compact graphical and mathematical representation of a decision situation. It is a generalization of a Bayesian network, in which not only probabilistic inference problems but also decision making problems (following the maximum expected utility criterion) can be modeled and solved. It includes 3 types of nodes : action, decision and utility nodes (from wikipedia (https://en.wikipedia.org/wiki/Influence_diagram)).

PyAgrum's so-called influence diagram represents both influence diagrams and LIMIDs. The way to enforce that such a model represent an influence diagram and not a LIMID belongs to the inference engine.

Tutorial

- *Tutorial on Influence Diagram* (page 365)

Reference

1.5.1 Model for Decision in PGM

class pyAgrum.**InfluenceDiagram**(**args*)

InfluenceDiagram represents an Influence Diagram.

InfluenceDiagram() -> InfluenceDiagram
default constructor

InfluenceDiagram(source) -> InfluenceDiagram

Parameters:

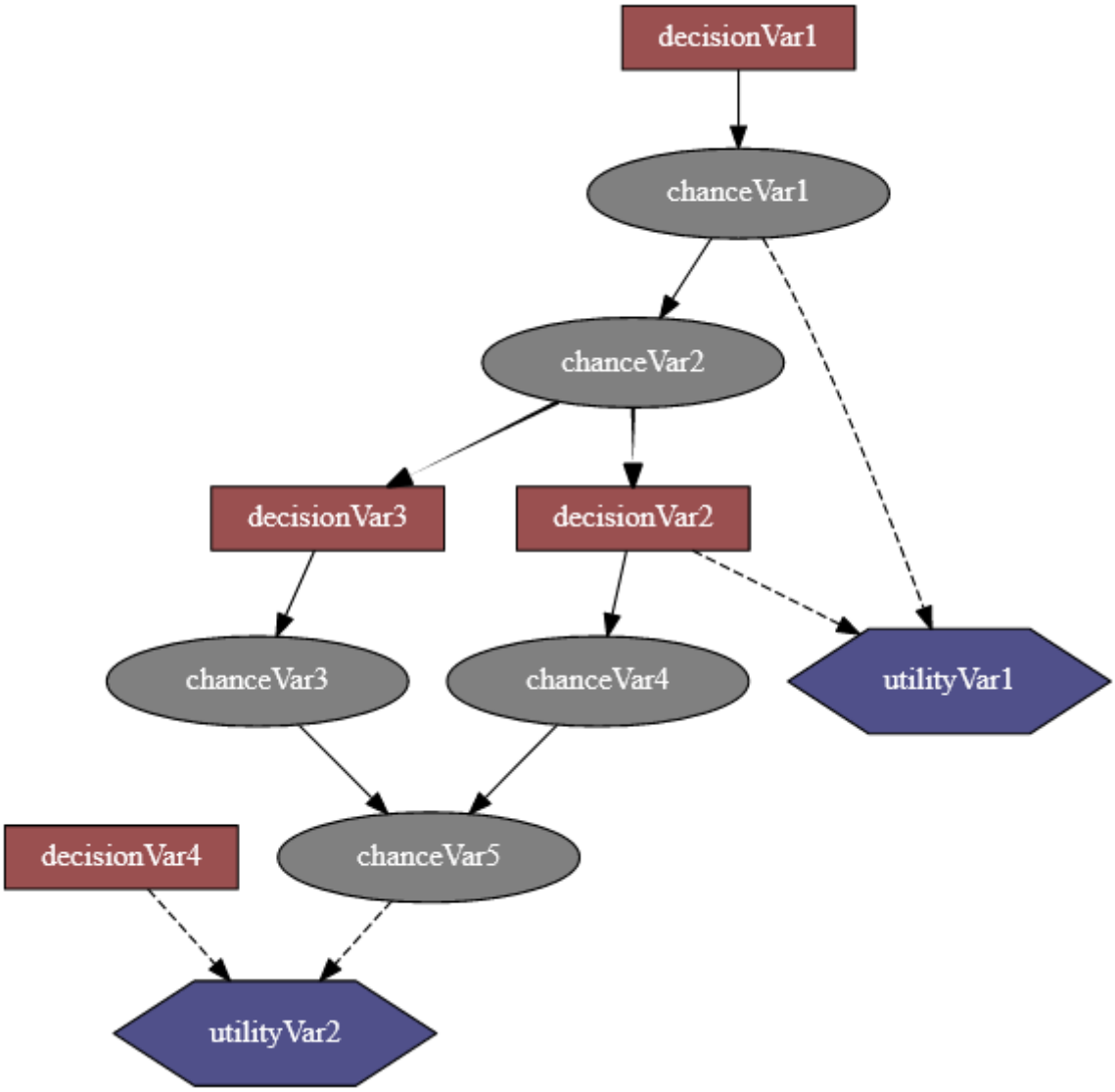
- **source** (*pyAgrum.InfluenceDiagram*) – the InfluenceDiagram to copy

add(**args*)

Add a variable, it's associate node and it's CPT.

The id of the new variable is automatically generated.

Parameters


decisionVar1
chanceVar1
chanceVar2
decisionVar3
decisionVar2
chanceVar3
chanceVar4
utilityVar1
decisionVar4
chanceVar5
utilityVar2

- **variable** (pyAgrum.DiscreteVariable (page 25)) – The variable added by copy that will be a chance node.
- **descr** (*str*) – the descr of the variable following *fast syntax* (page 281) extended for *pyAgrum.fastID()* (page 282).
- **nbr_mod_or_id** (*int*) – if the first argument is *variable*, this set an optional fixed id for the node. If the first argument is *descr*, this gives the default number of modalities for the variable. Note that if a utility node is described in *descr*, this value is overriden by 1.

Returns
the id of the added variable.
Return type
int
Raises
pyAgrum.DuplicateElement (page 289) – If already used id or name.

addArc(**args*)

Add an arc in the ID, and update diagram's potential nodes cpt if necessary.
Parameters
- **tail** (*Union[int,str]*) – a variable's id (int) or name
- **head** (*Union[int,str]*) – a variable's id (int) or name

Raises
- *pyAgrum.InvalidEdge* (page 290) – If arc.tail and/or arc.head are not in the ID.
- *pyAgrum.InvalidEdge* (page 290) – If tail is a utility node

Return type
None

addArcs(*listArcs*)

add a list of arcs in te model.
Parameters
listArcs (*List[Tuple[int,int]]*) – the list of arcs

addChanceNode(**args*)

Add a chance variable, it's associate node and it's CPT.

The id of the new variable is automatically generated.
Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable added by copy.
- **id** (*int*) – the chosen id. If 0, the NodeGraphPart will choose.

Warning: give an id (not 0) should be reserved for rare and specific situations !!!

Returns
the id of the added variable.
Return type
int
Raises
pyAgrum.DuplicateElement (page 289) – If id(<>0) is already used

addDecisionNode(**args*)

Add a decision variable.

The id of the new variable is automatically generated.
Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable added by copy.
- **id** (*int*) – the chosen id. If 0, the NodeGraphPart will choose.

Warning: give an id (not 0) should be reserved for rare and specific situations !!!

Returns
the id of the added variable.
Return type
int
Raises
pyAgrum.DuplicateElement (page 289) – If id(<>0) is already used

addStructureListener(*whenNodeAdded=None*, *whenNodeDeleted=None*, *whenArcAdded=None*, *whenArcDeleted=None*)

Add the listeners in parameters to the list of existing ones.

Parameters
- **whenNodeAdded** (*lambda expression*) – a function for when a node is added
- **whenNodeDeleted** (*lambda expression*) – a function for when a node is removed
- **whenArcAdded** (*lambda expression*) – a function for when an arc is added
- **whenArcDeleted** (*lambda expression*) – a function for when an arc is removed

addUtilityNode(**args*)

Add a utility variable, it's associate node and it's UT.

The id of the new variable is automatically generated.

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable added by copy
- **id** (*int*) – the chosen id. If 0, the NodeGraphPart will choose

Warning: give an id (not 0) should be reserved for rare and specific situations !!!

Returns
the id of the added variable.
Return type
int
Raises
- *pyAgrum.InvalidArgument* (page 290) – If variable has more than one label
- *pyAgrum.DuplicateElement* (page 289) – If id(<>0) is already used

addVariables(*listFastVariables*, *default_nbr_mod=2*)

Add a list of variable in the form of 'fast' syntax.

Parameters
- **listFastVariables** (*List[str]*) – the list of variables following *fast syntax* (page 281) extended for *pyAgrum.fastID()* (page 282).
- **default_nbr_mod** (*int*) – the number of modalities for the variable if not specified in the fast description. Note that default_nbr_mod=1 is mandatory to create variables with only one modality (for utility for instance).

Returns
the list of created ids.
Return type
List[int]

ancestors(*norid*)

Parameters
norid (object) –
Return type
object

arcs()

Returns
the list of all the arcs in the Influence Diagram.
Return type
list

chanceNodeSize()

Returns
the number of chance nodes.
Return type
int

changeVariableName(**args*)

Parameters
- **var** (*Union[int,str]*) – a variable's id (int) or name
- **new_name** (*str*) – the name of the variable

Raises
- *pyAgrum.DuplicateLabel* (page 289) – If this name already exists
- *pyAgrum.NotFound* (page 291) – If no nodes matches id.

Return type
None

children(*norid*)

Parameters
- **var** (*Union[int,str]*) – a variable's id (int) or name
- **norid** (*object*) –

Returns
the set of all the children
Return type
Set

clear()

Return type
None

completeInstantiation()

Return type
Instantiation (page 47)

connectedComponents()

connected components from a graph/BN

Compute the connected components of a pyAgrum's graph or Bayesian Network (more generally an object that has *nodes*, *children*/*parents* or *neighbours* methods)

The firstly visited node for each component is called a 'root' and is used as a key for the component. This root has been arbitrarily chosen during the algorithm.

Returns
dict of connected components (as set of nodeIds (int)) with a nodeId (root) of each component as key.
Return type
dict(int,Set[int])

cpt(**args*)

Returns the CPT of a variable.

Parameters
var (*Union[int,str]*) – a variable's id (int) or name
Returns
The variable's CPT.
Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.NotFound (page 291) – If no variable's id matches varId.

dag()

Returns
a constant reference to the dag of this BayesNet.
Return type
pyAgrum.DAG (page 8)

decisionNodeSize()

Returns
the number of decision nodes
Return type
int

decisionOrder()

decisionOrderExists()

Returns
True if a directed path exist with all decision node
Return type
bool

descendants(*norid*)

Parameters
norid (object) –
Return type
object

empty()

Return type
bool

erase(**args*)

Erase a Variable from the network and remove the variable from all his childs.

If no variable matches the id, then nothing is done.
Parameters
- **id** (*int*) – The id of the variable to erase.
- **var** (*Union[int,str,pyAgrum.DiscreteVariable* (page 25)*]*) – a variable's id (int) or name or th reference on the variable to remove.

Return type
None

eraseArc(**args*)

Removes an arc in the ID, and update diagram's potential nodes cpt if necessary.

If (tail, head) doesn't exist, the nothing happens.
Parameters
- **arc** (*pyAgrum.Arc* (page 3)) – The arc to be removed whn calling eraseArc(arc)
- **tail** (*Union[int,str]*) – a variable's id (int) or name when calling eraseArc(tail,head)
- **head** (*Union[int,str]*) – a variable's id (int) or name when calling eraseArc(tail,head)

Return type
None

exists(*node*)

Parameters
node (int) –

Return type
bool

existsArc(**args*)

Return type
bool

existsPathBetween(**args*)

Returns
true if a path exists between two nodes.
Return type
bool

family(*norid*)

Parameters
norid (object) –
Return type
object

static fastPrototype(*dotlike*, *domainSize=2*)

Create an Influence Diagram with a dot-like syntax which specifies:

- the structure 'a->b<-c;b->d;c<-e;'.
- a prefix for the type of node (chance/decision/utiliy nodes):
  - *a* : a chance node named 'a' (by default)
  - *$a* : a utility node named 'a'
  - **a* : a decision node named 'a'
- the type of the variables with different syntax as postfix:
  - by default, a variable is a pyAgrum.RangeVariable using the default domain size (second argument)
  - with *'a[10]'*, the variable is a pyAgrum.RangeVariable using 10 as domain size (from 0 to 9)
  - with *'a[3,7]'*, the variable is a pyAgrum.RangeVariable using a domainSize from 3 to 7
  - with *'a[1,3.14,5,6.2]'*, the variable is a pyAgrum.DiscretizedVariable using the given ticks (at least 3 values)
  - with *'a{top|middle|bottom}'*, the variable is a pyAgrum.LabelizedVariable using the given labels.
  - with 'a{-1|5|0|3}', the variable is a pyAgrum.IntegerVariable using the sorted given values.
  - with 'a{-0.5|5.01|0|3.1415}', the variable is a pyAgrum.NumericalDiscreteVariable using the sorted given values.

Note:

- If the dot-like string contains such a specification more than once for a variable, the first specification will be used.
- the potentials (probabilities, utilities) are randomly generated.
- see also pyAgrum.fastID.

Examples

```
>>> import pyAgrum as gum
>>> bn=pyAgrum.fastID('A->B[1,3]<-*C{yes|No}->$D<-E[1,2.5,3.9]',6)
```

Parameters
- **dotlike** (*str*) – the string containing the specification
- **domainSize** (*int*) – the default domain size for variables

Returns
the resulting Influence Diagram

Return type
pyAgrum.InfluenceDiagram (page 191)

getDecisionGraph()

Returns
the temporal Graph.

Return type
pyAgrum.DAG (page 8)

hasSameStructure(*other*)

Parameters
pyAgrum.DAGmodel – a direct acyclic model

Returns
True if all the named node are the same and all the named arcs are the same

Return type
bool

idFromName(*name*)

Returns a variable's id given its name.

Parameters
name (*str*) – the variable's name from which the id is returned.

Returns
the variable's node id.

Return type
int

Raises
pyAgrum.NotFound (page 291) – If no such name exists in the graph.

ids(*names*)

isChanceNode(**args*)

Parameters
varId (*int*) – the tested node id.

Returns
true if node is a chance node

Return type
bool

isDecisionNode(**args*)

Parameters
varId (*int*) – the tested node id.

Returns
true if node is a decision node

Return type
bool

isIndependent(**args*)

Return type
bool

isUtilityNode(**args*)

Parameters
varId (*int*) – the tested node id.
Returns
true if node is an utility node
Return type
bool

loadBIFXML(**args*)

Load a BIFXML file.
Parameters
name (*str*) – the name's file
Raises
- *pyAgrum.IOError* (page 290) – If file not found
- *pyAgrum.FatalError* (page 289) – If file is not valid

Return type
bool

log10DomainSize()

Return type
float

moralGraph(*clear=True*)

Returns the moral graph of the BayesNet, formed by adding edges between all pairs of nodes that have a common child, and then making all edges in the graph undirected.
Returns
The moral graph
Return type
pyAgrum.UndiGraph (page 12)
Parameters
clear (bool) –

moralizedAncestralGraph(*nodes*)

Parameters
nodes (object) –
Return type
UndiGraph (page 12)

names()

Returns
The names of the InfluenceDiagram variables
Return type
List[str]

nodeId(*var*)

Parameters
var (pyAgrum.DiscreteVariable (page 25)) – a variable
Returns
the id of the variable
Return type
int
Raises
pyAgrum.IndexError – If the InfluenceDiagram does not contain the variable

nodes()

Returns
the set of ids
Return type
set

nodeset(*names*)

Parameters
names (Vector_string) –
Return type
List[int]

parents(*norid*)

Parameters
- **var** (*Union[int,str]*) – a variable's id (int) or name
- **norid** (object) –

Returns
the set of the parents ids.
Return type
set

saveBIFXML(*name*)

Save the BayesNet in a BIFXML file.
Parameters
name (*str*) – the file's name
Return type
None

size()

Returns
the number of nodes in the graph
Return type
int

sizeArcs()

Returns
the number of arcs in the graph
Return type
int

property thisown

The membership flag

toDot()

Returns
a friendly display of the graph in DOT format
Return type
str

topologicalOrder(*clear=True*)

Returns
the list of the nodes Ids in a topological order
Return type
List
Raises
pyAgrum.InvalidDirectedCycle (page 290) – If this graph contains cycles
Parameters
clear (bool) –

utility(**args*)

Parameters
var (*Union[int,str]*) – a variable's id (int) or name
Returns
the utility table of the node
Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.IndexError – If the InfluenceDiagram does not contain the variable

utilityNodeSize()

Returns
the number of utility nodes
Return type
int

variable(**args*)

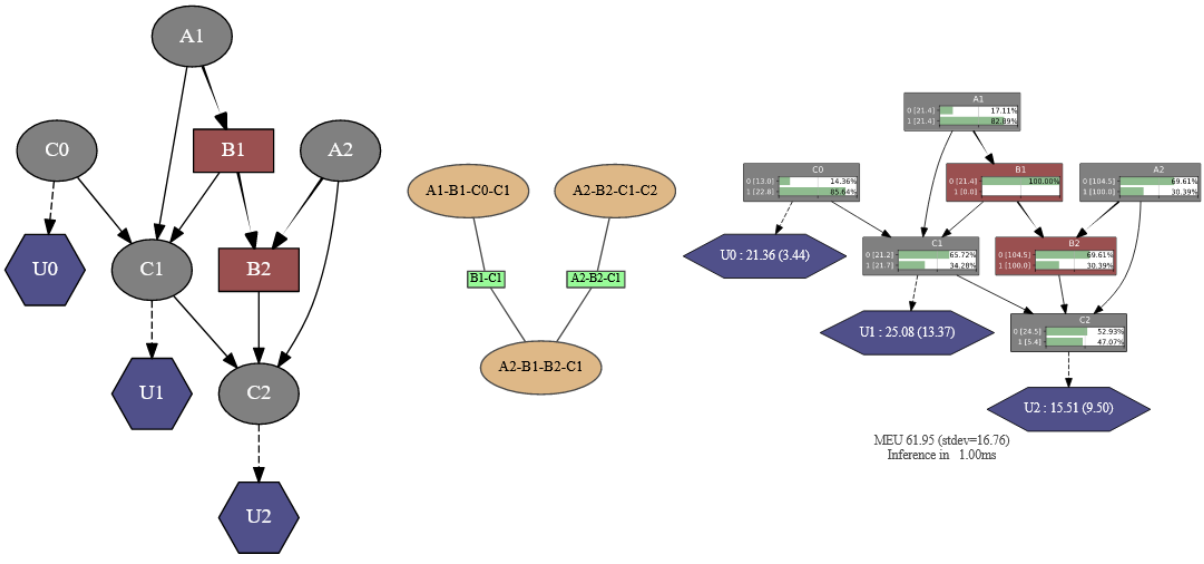
Parameters
id (*int*) – the node id
Returns
a constant reference over a variabe given it's node id
Return type
pyAgrum.DiscreteVariable (page 25)
Raises
pyAgrum.NotFound (page 291) – If no variable's id matches the parameter

variableFromName(*name*)

Parameters
name (*str*) – a variable's name
Returns
the variable
Return type
pyAgrum.DiscreteVariable (page 25)
Raises
pyAgrum.IndexError – If the InfluenceDiagram does not contain the variable

variableNodeMap()

1.5.2 Inference for Influence Diagram



An influence diagram | Its reduced Junction Tree | The inference

	B1	
A1	0	1
0	1.0000	0.0000
1	1.0000	0.0000

Optimal decision for B_1

	B2	
A2	0	1
0	1.0000	0.0000
1	0.0000	1.0000

Optimal decision for B_2

class pyAgrum.**ShaferShenoyLIMIDInference**(*infDiag*)

This inference considers the provided model as a LIMID rather than an influence diagram. It is an optimized implementation of the LIMID resolution algorithm. However an inference on a classical influence diagram can be performed by adding a assumption of the existence of the sequence of decision nodes to be solved, which also implies that the decision choices can have an impact on the rest of the sequence (Non Forgetting Assumption, cf. pyAgrum.ShaferShenoyLIMIDInference.addNoForgettingAssumption).

Parameters
infDiag (*InfluenceDiagram* (page 191)) –

MEU(**args*)

Returns maximum expected utility obtained from inference.

Raises
pyAgrum.OperationNotAllowed (page 292) – If no inference have yet been made

Return type
object

addEvidence(**args*)

Return type
None

addNoForgettingAssumption(**args*)

Return type
None

chgEvidence(**args*)

Return type
None

clear()

Return type
None

eraseAllEvidence()

Removes all the evidence entered into the diagram.

Return type
None

eraseEvidence(**args*)

Parameters
evidence (pyAgrum.Potential (page 53)) – the evidence to remove

Raises
pyAgrum.IndexError – If the evidence does not belong to the influence diagram

Return type
None

hardEvidenceNodes()

Return type
object

hasEvidence(**args*)

Return type
bool

hasHardEvidence(*nodeName*)

Parameters
nodeName (str) –

Return type
bool

hasNoForgettingAssumption()

Return type
bool

hasSoftEvidence(**args*)

Return type
bool

influenceDiagram()

Returns a constant reference over the InfluenceDiagram on which this class work.

Returns
the InfluenceDiagram on which this class work

Return type
pyAgrum.InfluenceDiagram (page 191)

isSolvable()

Return type
bool

junctionTree()

makeInference()

Makes the inference.

Return type
None

meanVar(**args*)

Return type
object

nbrEvidence()

Return type
int

nbrHardEvidence()

Return type
int

nbrSoftEvidence()

Return type
int

optimalDecision(**args*)

Returns best choice for decision variable given in parameter (based upon MEU criteria)

Parameters
decisionId (*int*, *str*) – the id or name of the decision variable

Raises
pyAgrum.OperationNotAllowed (page 292) – If no inference have yet been made

pyAgrum.InvalidNode
If node given in parmaeter is not a decision node

Return type
Potential (page 53)

posterior(**args*)

Return type
Potential (page 53)

posteriorUtility(**args*)

Return type
Potential (page 53)

reducedGraph()

Return type
DAG (page 8)

reducedLIMID()

Return type
InfluenceDiagram (page 191)

reversePartialOrder()

setEvidence(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.

Parameters
evidces (*dict*) – a dict of evidences

Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the influence diagram

softEvidenceNodes()

Return type
object

updateEvidence(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).

Parameters
evidces (*dict*) – a dict of evidences

Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

1.6 Credal Network

Credal networks are probabilistic graphical models based on imprecise probability. Credal networks can be regarded as an extension of Bayesian networks, where credal sets replace probability mass functions in the specification of the local models for the network variables given their parents. As a Bayesian network defines a joint probability mass function over its variables, a credal network defines a joint credal set (from Wikipedia (https://en.wikipedia.org/wiki/Credal_network)).

Tutorial

- *Tutorial on Credal Networks* (page 377)

Reference

1.6.1 CN Model

class pyAgrum.**CredalNet**(**args*)

Constructor used to create a CredalNet (step by step or with two BayesNet)

CredalNet() -> CredalNet
default constructor

CredalNet(src_min_num,src_max_den) -> CredalNet

Parameters

- **src_min_num** (*str or* pyAgrum.BayesNet (page 64)) – The path to a BayesNet or the BN itself which contains lower probabilities.
- **src_max_den** (*str or* pyAgrum.BayesNet (page 64)) – The (optional) path to a BayesNet or the BN itself which contains upper probabilities.

NodeType_Credal = 1

NodeType_Indic = 3

NodeType_Precise = 0

NodeType_Vacuous = 2

addArc(*tail*, *head*)

Adds an arc between two nodes

Parameters
- **tail** (int) – the id of the tail node
- **head** (*int*) – the id of the head node

Raises
- **pyAgrum.InvalidDirectedCircle** – If any (directed) cycle is created by this arc
- *pyAgrum.InvalidNode* (page 291) – If head or tail does not belong to the graph nodes
- *pyAgrum.DuplicateElement* (page 289) – If one of the arc already exists

Return type
None

addVariable(*name*, *card*)

Parameters
- **name** (*str*) – the name of the new variable
- **card** (*int*) – the domainSize of the new variable

Returns
the id of the new node

Return type
int

approximatedBinarization()

Approximate binarization.

Each bit has a lower and upper probability which is the lowest - resp. highest - over all vertices of the credal set. Enlarge the orignal credal sets and may induce huge imprecision.

Warning: Enlarge the orignal credal sets and therefor induce huge imprecision by propagation. Not recommended, use MCSampling or something else instead

Return type
None

bnToCredal(*beta*, *oneNet*, *keepZeroes=False*)

Perturbates the BayesNet provided as input for this CredalNet by generating intervals instead of point probabilities and then computes each vertex of each credal set.

Parameters

- **beta** (*float*) – The beta used to perturbate the network
- **oneNet** (*bool*) – used as a flag. Set to True if one BayesNet if provided with counts, to False if two BayesNet are provided; one with probabilities (the lower net) and one with denominators over the first modalities (the upper net)
- **keepZeroes** (*bool*) – used as a flag as whether or not - respectively True or False - we keep zeroes as zeroes. Default is False, i.e. zeroes are not kept

Return type

None

computeBinaryCPTMinMax()

Return type

None

credalNet_currentCpt()

> **Warning:** Experimental function - Return type to be wrapped

Returns

a constant reference to the (up-to-date) CredalNet CPTs.

Return type

tbw

credalNet_srcCpt()

> **Warning:** Experimental function - Return type to be wrapped

Returns

a constant reference to the (up-to-date) CredalNet CPTs.

Return type

tbw

currentNodeType(*id*)

Parameters

id (*int*) – The constant reference to the choosen NodeId

Returns

the type of the choosen node in the (up-to-date) CredalNet __current_bn if any, __src_bn otherwise.

Return type

pyAgrum.CredalNet (page 205)

current_bn()

Returns

Returs a constant reference to the actual BayesNet (used as a DAG, it's CPTs does not matter).

Return type

pyAgrum.BayesNet (page 64)

domainSize(*id*)

Parameters

id (*int*) – The id of the node

Returns

The cardinality of the node

Return type

int

epsilonMax()

Returns
a constant reference to the highest perturbation of the BayesNet provided as input for this CredalNet.

Return type
float

epsilonMean()

Returns
a constant reference to the average perturbation of the BayesNet provided as input for this CredalNet.

Return type
float

epsilonMin()

Returns
a constant reference to the lowest perturbation of the BayesNet provided as input for this CredalNet.

Return type
float

fillConstraint(**args*)

Set the interval constraints of a credal set of a given node (from an instantiation index)

Parameters
- **id** (*int*) – The id of the node
- **entry** (*int*) – The index of the instantiation excluding the given node (only the parents are used to compute the index of the credal set)
- **ins** (pyAgrum.Instantiation (page 47)) – The Instantiation
- **lower** (*list*) – The lower value for each probability in correct order
- **upper** (*list*) – The upper value for each probability in correct order

Warning: You need to call intervalToCredal when done filling all constraints.

Warning: DOES change the BayesNet (s) associated to this credal net !

Return type
None

fillConstraints(*id*, *lower*, *upper*)

Set the interval constraints of the credal sets of a given node (all instantiations)

Parameters
- **id** (*int*) – The id of the node
- **lower** (*list*) – The lower value for each probability in correct order
- **upper** (*list*) – The upper value for each probability in correct order

Warning: You need to call intervalToCredal when done filling all constraints.

Warning: DOES change the BayesNet (s) associated to this credal net !

Return type
None

get_binaryCPT_max()

> **Warning:** Experimental function - Return type to be wrapped

Returns
a constant reference to the upper probabilities of each node X over the 'True' modality
Return type
tbw

`get_binaryCPT_min()`

> **Warning:** Experimental function - Return type to be wrapped

Returns
a constant reference to the lower probabilities of each node X over the 'True' modality
Return type
tbw

`hasComputedBinaryCPTMinMax()`

Return type
`bool`

`idmLearning(s=0, keepZeroes=False)`

Learns parameters from a BayesNet storing counts of events.

Use this method when using a single BayesNet storing counts of events. IDM model if s > 0, standard point probability if s = 0 (default value if none precised).

Parameters
- **s** (*int*) – the IDM parameter.
- **keepZeroes** (*bool*) – used as a flag as whether or not - respectively True or False - we keep zeroes as zeroes. Default is False, i.e. zeroes are not kept.

Return type
`None`

`instantiation(id)`

Get an Instantiation from a node id, usefull to fill the constraints of the network.

bnet accessors / shortcuts.

Parameters
id (*int*) – the id of the node we want an instantiation from
Returns
the instantiation
Return type
pyAgrum.Instantiation (page 47)

`intervalToCredal()`

Computes the vertices of each credal set according to their interval definition (uses lrs).

Use this method when using two BayesNet, one with lower probabilities and one with upper probabilities.

Return type
`None`

`intervalToCredalWithFiles()`

> **Warning:** Deprecated : use intervalToCredal (lrsWrapper with no input / output files needed).

Computes the vertices of each credal set according to their interval definition (uses lrs).

Use this method when using a single BayesNet storing counts of events.

Return type
None

`isSeparatelySpecified()`

Returns
True if this CredalNet is separately and interval specified, False otherwise.

Return type
bool

`lagrangeNormalization()`

Normalize counts of a BayesNet storing counts of each events such that no probability is 0.

Use this method when using a single BayesNet storing counts of events. Lagrange normalization. This call is irreversible and modify counts stored by __src_bn.

Doest not performs computations of the parameters but keeps normalized counts of events only. Call idmLearning to compute the probabilities (with any parameter value).

Return type
None

`nodeType(id)`

Parameters
id (*int*) – the constant reference to the choosen NodeId

Returns
the type of the choosen node in the (up-to-date) CredalNet in __src_bn.

Return type
pyAgrum.CredalNet (page 205)

`saveBNsMinMax(min_path, max_path)`

If this CredalNet was built over a perturbed BayesNet, one can save the intervals as two BayesNet.

to call after bnToCredal(GUM_SCALAR beta) save a BN with lower probabilities and a BN with upper ones

Parameters
- **min_path** (*str*) – the path to save the BayesNet which contains the lower probabilities of each node X.
- **max_path** (*str*) – the path to save the BayesNet which contains the upper probabilities of each node X.

Return type
None

`setCPT(*args)`

> **Warning:** (experimental function) - Parameters to be wrapped

Set the vertices of one credal set of a given node (any instantiation index)

Parameters
- **id** (*int*) – the Id of the node
- **entry** (*int*) – the index of the instantiation (from 0 to K - 1) excluding the given node (only the parents are used to compute the index of the credal set)
- **ins** (pyAgrum.Instantiation (page 47)) – the Instantiation (only the parents matter to find the credal set index)
- **cpt** (*tbw*) – the vertices of every credal set (for each instantiation of the parents)

> **Warning:** DOES not change the BayesNet(s) associated to this credal net !

Return type
None

`setCPTs`(*id*, *cpt*)

> **Warning:** (experimental function) - Parameters to be wrapped

Set the vertices of the credal sets (all of the conditionals) of a given node

Parameters
- **id** (*int*) – the NodeId of the node
- **cpt** (*tbw*) – the vertices of every credal set (for each instantiation of the parents)

> **Warning:** DOES not change the BayesNet (s) associated to this credal net !

`src_bn`()

Returns
Returns a constant reference to the original BayesNet (used as a DAG, it's CPTs does not matter).

Return type
pyAgrum.BayesNet (page 64)

1.6.2 CN Inference

`class pyAgrum.CNMonteCarloSampling`(*credalNet*)

Class used for inferences in credal networks with Monte Carlo sampling algorithm.

CNMonteCarloSampling(cn) -> CNMonteCarloSampling

Parameters:

- **cn** (*pyAgrum.CredalNet*) – a credal network

Parameters
credalNet (*CredalNet* (page 205)) –

`CN`()

Return type
CredalNet (page 205)

`currentTime`()

Returns
get the current running time in second (float)

Return type
float

`dynamicExpMax`(*varName*)

Get the upper dynamic expectation of a given variable prefix.

Parameters
varName (*str*) – the variable name prefix which upper expectation we want.

Returns
a constant reference to the variable upper expectation over all time steps.

Return type
float

dynamicExpMin(*varName*)

Get the lower dynamic expectation of a given variable prefix.

Parameters
varName (*str*) – the variable name prefix which lower expectation we want.

Returns
a constant reference to the variable lower expectation over all time steps.

Return type
float

epsilon()

Returns
the value of epsilon

Return type
float

history()

Returns
the scheme history

Return type
tuple

Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

insertEvidenceFile(*path*)

Insert evidence from file.

Parameters
path (*str*) – the path to the evidence file.

Return type
None

insertModalsFile(*path*)

Insert variables modalities from file to compute expectations.

Parameters
path (*str*) – The path to the modalities file.

Return type
None

makeInference()

Starts the inference.

Return type
None

marginalMax(**args*)

Get the upper marginals of a given node id.

Parameters
- **id** (*int*) – the node id which upper marginals we want.
- **varName** (*str*) – the variable name which upper marginals we want.

Returns
a constant reference to this node upper marginals.

Return type
list

Raises
pyAgrum.IndexError – If the node does not belong to the Credal network

marginalMin(**args*)

Get the lower marginals of a given node id.

Parameters
- **id** (*int*) – the node id which lower marginals we want.
- **varName** (*str*) – the variable name which lower marginals we want.

Returns
a constant reference to this node lower marginals.
Return type
list
Raises
pyAgrum.IndexError – If the node does not belong to the Credal network

maxIter()

Returns
the criterion on number of iterations
Return type
int

maxTime()

Returns
the timeout(in seconds)
Return type
float

messageApproximationScheme()

Returns
the approximation scheme message
Return type
str

minEpsilonRate()

Returns
the value of the minimal epsilon rate
Return type
float

nbrIterations()

Returns
the number of iterations
Return type
int

periodSize()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

setEpsilon(*eps*)

Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0
Return type
None

setMaxIter(*max*)

Parameters
max (*int*) – the maximum number of iteration
Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

setMaxTime(*timeout*)

Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0

Return type
None

setMinEpsilonRate(*rate*)

Parameters
rate (*float*) – the minimal epsilon rate

Return type
None

setPeriodSize(*p*)

Parameters
p (*int*) – number of samples between 2 stopping

Raises
pyAgrum.OutOfBounds (page 292) – If p<1

Return type
None

setRepetitiveInd(*flag*)

Parameters
flag (*bool*) – True if repetitive independence is to be used, false otherwise. Only usefull with dynamic networks.

Return type
None

setVerbosity(*v*)

Parameters
v (*bool*) – verbosity

Return type
None

verbosity()

Returns
True if the verbosity is enabled

Return type
bool

class pyAgrum.**CNLoopyPropagation**(*cnet*)

Class used for inferences in credal networks with Loopy Propagation algorithm.

CNLoopyPropagation(cn) -> CNLoopyPropagation

Parameters:
- **cn** (*pyAgrum.CredalNet*) – a Credal network

Parameters
cnet (*CredalNet* (page 205)) –

CN()

Return type
CredalNet (page 205)

InferenceType_nodeToNeighbours = 0

InferenceType_ordered = 1

InferenceType_randomOrder = 2

currentTime()

Returns
get the current running time in second (float)

Return type
float

dynamicExpMax(*varName*)

Get the upper dynamic expectation of a given variable prefix.

Parameters
varName (*str*) – the variable name prefix which upper expectation we want.

Returns
a constant reference to the variable upper expectation over all time steps.

Return type
float

dynamicExpMin(*varName*)

Get the lower dynamic expectation of a given variable prefix.

Parameters
varName (*str*) – the variable name prefix which lower expectation we want.

Returns
a constant reference to the variable lower expectation over all time steps.

Return type
float

epsilon()

Returns
the value of epsilon

Return type
float

eraseAllEvidence()

Erase all inference related data to perform another one.

You need to insert evidence again if needed but modalities are kept. You can insert new ones by using the appropriate method which will delete the old ones.

Return type
None

history()

Returns
the scheme history

Return type
tuple

Raises
pyAgrum.OperationNotAllowed (page 292) – If the scheme did not performed or if verbosity is set to false

inferenceType(**args*)

Returns
the inference type

Return type
int

insertEvidenceFile(*path*)

Insert evidence from file.

Parameters
path (*str*) – the path to the evidence file.

Return type
None

insertModalsFile(*path*)

Insert variables modalities from file to compute expectations.

Parameters
path (*str*) – The path to the modalities file.

Return type
None

makeInference()

Starts the inference.

Return type
None

marginalMax(**args*)

Get the upper marginals of a given node id.

Parameters
- **id** (*int*) – the node id which upper marginals we want.
- **varName** (*str*) – the variable name which upper marginals we want.

Returns
a constant reference to this node upper marginals.

Return type
list

Raises
pyAgrum.IndexError – If the node does not belong to the Credal network

marginalMin(**args*)

Get the lower marginals of a given node id.

Parameters
- **id** (*int*) – the node id which lower marginals we want.
- **varName** (*str*) – the variable name which lower marginals we want.

Returns
a constant reference to this node lower marginals.

Return type
list

Raises
pyAgrum.IndexError – If the node does not belong to the Credal network

maxIter()

Returns
the criterion on number of iterations

Return type
int

maxTime()

Returns
the timeout(in seconds)

Return type
float

messageApproximationScheme()

Returns
the approximation scheme message

Return type
str

minEpsilonRate()

Returns
the value of the minimal epsilon rate

Return type
float

nbrIterations()

Returns
the number of iterations
Return type
int

periodSize()

Returns
the number of samples between 2 stopping
Return type
int
Raises
pyAgrum.OutOfBounds (page 292) – If p<1

saveInference(*path*)

Saves marginals.
Parameters
path (*str*) – The path to the file to save marginals.
Return type
None

setEpsilon(*eps*)

Parameters
eps (*float*) – the epsilon we want to use
Raises
pyAgrum.OutOfBounds (page 292) – If eps<0
Return type
None

setMaxIter(*max*)

Parameters
max (*int*) – the maximum number of iteration
Raises
pyAgrum.OutOfBounds (page 292) – If max <= 1
Return type
None

setMaxTime(*timeout*)

Parameters
- **tiemout** (*float*) – stopping criterion on timeout (in seconds)
- **timeout** (float) –

Raises
pyAgrum.OutOfBounds (page 292) – If timeout<=0.0
Return type
None

setMinEpsilonRate(*rate*)

Parameters
rate (*float*) – the minimal epsilon rate
Return type
None

setPeriodSize(*p*)

Parameters
p (*int*) – number of samples between 2 stopping
Raises
pyAgrum.OutOfBounds (page 292) – If p<1
Return type
None

setRepetitiveInd(*flag*)

Parameters
flag (*bool*) – True if repetitive independence is to be used, false otherwise. Only usefull with dynamic networks.
Return type
None

setVerbosity(*v*)

Parameters
v (*bool*) – verbosity
Return type
None

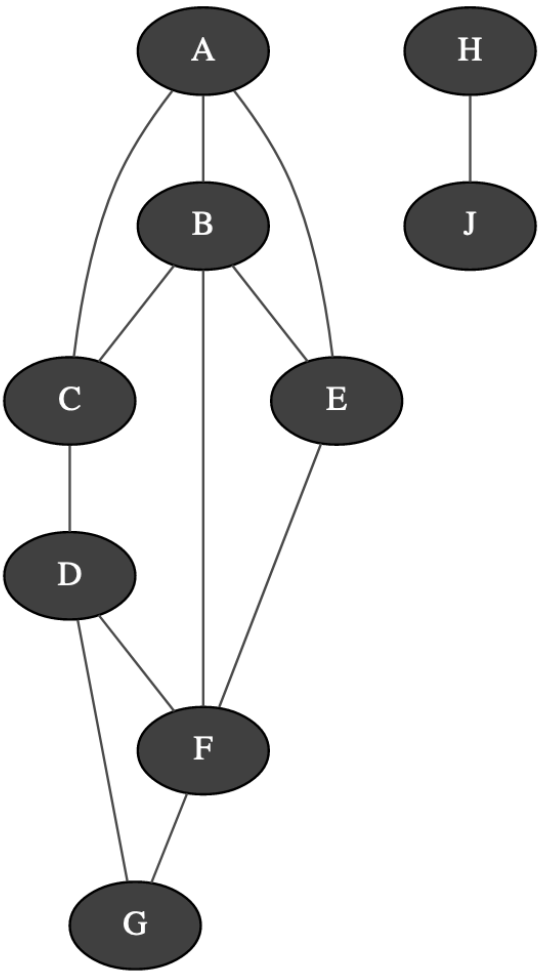
property thisown

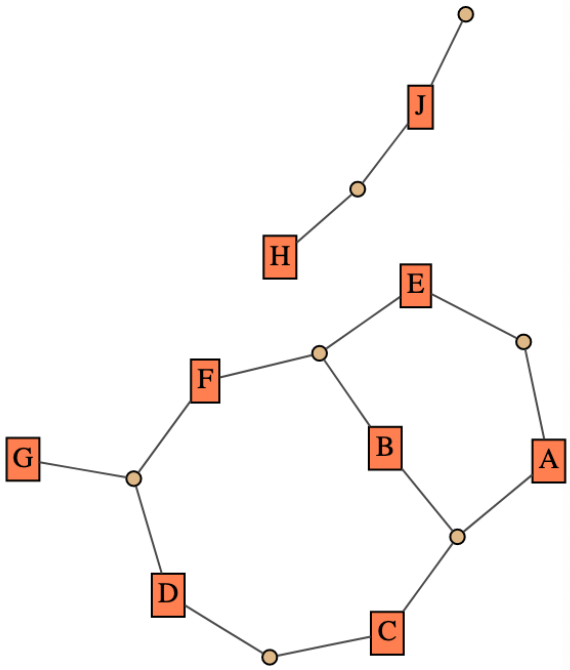
The membership flag

verbosity()

Returns
True if the verbosity is enabled
Return type
bool

1.7 Markov Network





A Markov network is a undirected probabilistic graphical model. It represents a joint distribution over a set of random variables. In pyAgrum, the variables are (for now) only discrete.

A Markov network uses a undirected graph to represent conditional independence in the joint distribution. These conditional independence allow to factorize the joint distribution, thereby allowing to compactly represent very large ones.

$$P(X_1, \cdots, X_n) \propto \prod_{i=1}^{n_c} \phi_i(C_i)$$

Where the ϕ_i are potentials over the n_c cliques of the undirected graph.

Moreover, inference algorithms can also use this graph to speed up the computations.

Tutorial

- *Tutorial on Markov Network* (page 372)

Reference

1.7.1 Undirected Graphical Model

class pyAgrum.**MarkovNet**(**args*)

MarkovNet represents a Markov Network.

MarkovNet(name='') -> MarkovNet

Parameters:

- **name** (*str*) – the name of the Bayes Net

MarkovNet(source) -> MarkovNet

Parameters:

- **source** (*pyAgrum.MarkovNet*) – the Markov network to copy

add(**args*)

Add a variable to the pyAgrum.MarkovNet.

Parameters
- **variable** (pyAgrum.DiscreteVariable (page 25)) – the variable added
- **name** (*str*) – the variable name
- **nbrmod** (*int*) – the number of modalities for the new variable
- **id** (*int*) – the variable forced id in the pyAgrum.MarkovNet

Returns
the id of the new node

Return type
int

Raises
- *pyAgrum.DuplicateLabel* (page 289) – If variable.name() is already used in this pyAgrum.MarkovNet.
- **pyAgrum.NotAllowed** – If nbrmod is less than 2
- *pyAgrum.DuplicateElement* (page 289) – If id is already used.

addFactor(**args*)

Add a factor from a list or a set of id or str. If the argument is a set, the order is the order of the IDs of the variables

Parameters
seq (*sequence (list or set) of int or string*) – The sequence (ordered or not) of node id or names

Return type
Potential (page 53)

addStructureListener(*whenNodeAdded=None*, *whenNodeDeleted=None*, *whenEdgeAdded=None*, *whenedgeDeleted=None*)

Add the listeners in parameters to the list of existing ones.

Parameters

- **whenNodeAdded** (*lambda expression*) – a function for when a node is added
- **whenNodeDeleted** (*lambda expression*) – a function for when a node is removed
- **whenEdgeAdded** (*lambda expression*) – a function for when an edge is added
- **whenEdgeDeleted** (*lambda expression*) – a function for when an edge is removed

addVariables(*listFastVariables*, *default_nbr_mod=2*)

Add a list of variable in the form of 'fast' syntax.

Parameters

- **listFastVariables** (*List[str]*) – the list of variables in 'fast' syntax.
- **default_nbr_mod** (*int*) – the number of modalities for the variable if not specified following *fast syntax* (page 281). Note that default_nbr_mod=1 is mandatory to create variables with only one modality (for utility for instance).

Returns

the list of created ids.

Return type

List[int]

beginTopologyTransformation()

Return type

None

changeVariableLabel(**args*)

change the label of the variable associated to nodeId to the new value.

Parameters

- **var** (*Union[int,str]*) – a variable's id (int) or name
- **old_label** (*str*) – the old label
- **new_label** (*str*) – the new label

Raises

pyAgrum.NotFound (page 291) – if id/name is not a variable or if old_label does not exist.

Return type

None

changeVariableName(**args*)

Changes a variable's name in the pyAgrum.MarkovNet.

This will change the "pyAgrum.DiscreteVariable" names in the pyAgrum.MarkovNet.

Parameters

- **car** (*Union[int,str]*) – a variable's id (int) or name
- **new_name** (*str*) – the new name of the variable

Raises

- *pyAgrum.DuplicateLabel* (page 289) – If new_name is already used in this MarkovNet.
- *pyAgrum.NotFound* (page 291) – If no variable matches id.

Return type

None

clear()

Clear the whole MarkovNet

Return type

None

completeInstantiation()

Return type
Instantiation (page 47)

connectedComponents()

connected components from a graph/BN

Compute the connected components of a pyAgrum's graph or Bayesian Network (more generally an object that has *nodes*, *children*/*parents* or *neighbours* methods)

The firstly visited node for each component is called a 'root' and is used as a key for the component. This root has been arbitrarily chosen during the algorithm.

Returns
dict of connected components (as set of nodeIds (int)) with a nodeId (root) of each component as key.

Return type
dict(int,Set[int])

dim()

Return type
int

edges()

Return type
object

empty()

Return type
bool

endTopologyTransformation()

Terminates a sequence of insertions/deletions of arcs by adjusting all CPTs dimensions. End Multiple Change for all CPTs.

Return type
pyAgrum.MarkovNet (page 218)

erase(**args*)

Remove a variable from the pyAgrum.MarkovNet.

Removes the corresponding variable from the pyAgrum.MarkovNet and from all of it's children pyAgrum.Potential.

If no variable matches the given id, then nothing is done.

Parameters
var (*Union[int,str,*pyAgrum.DiscreteVariable (page 25)*]*) – a variable's id (int) or name of variable or a reference of this variable to remove.

Return type
None

eraseFactor(**args*)

Return type
None

exists(*node*)

Parameters
node (int) –

Return type
bool

existsEdge(**args*)

Return type
bool

factor(**args*)

Returns the factor of a set of variables (if existing).

Parameters

vars (*Union[Set[int],Set[str]]*) – A set of ids or names of variable the pyAgrum.MarkovNet.

Returns

The factor of the set of nodes.

Return type

pyAgrum.Potential (page 53)

Raises

pyAgrum.NotFound (page 291) – If no variable's id matches varId.

factors()

Return type

List[Set[int]]

static fastPrototype(*dotlike*, *domainSize=2*)

Create a Markov network with a modified dot-like syntax which specifies:

- the structure `a-b-c;b-d-e;`. The substring `a-b-c` indicates a factor with the scope (a,b,c).
- the type of the variables with different syntax (cf documentation).

Examples

```
>>> import pyAgrum as gum
>>> bn=pyAgrum.MarkovNet.fastPrototype('A--B[1,3]-C{yes|No}--D[2,4]--
↪E[1,2.5,3.9]',6)
```

Parameters

- **dotlike** (*str*) – the string containing the specification
- **domainSize** (*int*) – the default domain size for variables

Returns

the resulting Markov network

Return type

pyAgrum.MarkovNet (page 218)

static fromBN(*bn*)

Parameters

bn (*BayesNet* (page 64)) –

Return type

MarkovNet (page 218)

generateFactor(*vars*)

Randomly generate factor parameters for a given factor in a given structure.

Parameters

- **node** (*Union[int,str]*) – a variable's id (int) or name
- **vars** (List[int]) –

Return type

None

generateFactors()

Randomly generates factors parameters for a given structure.

Return type

None

graph()

Return type

UndiGraph (page 12)

hasSameStructure(*other*)

idFromName(*name*)

Parameters
name (str) –
Return type
int

ids(*names*)

isIndependent(**args*)

Return type
bool

loadUAI(**args*)

Load an UAI file.

Parameters
- **name** (*str*) – the name's file
- **l** (*list*) – list of functions to execute

Raises
- *pyAgrum.IOError* (page 290) – If file not found
- *pyAgrum.FatalError* (page 289) – If file is not valid

Return type
str

log10DomainSize()

Return type
float

maxNonOneParam()

Return type
float

maxParam()

Return type
float

maxVarDomainSize()

Return type
int

minNonZeroParam()

Return type
float

minParam()

Return type
float

minimalCondSet(**args*)

Return type
object

names()

Returns
The names of the graph variables
Return type
List[str]

neighbours(*norid*)

Parameters
norid (object) –

Return type
object

nodeId(*var*)

Parameters
var (*DiscreteVariable* (page 25)) –
Return type
int

nodes()

Return type
object

nodeset(*names*)

Parameters
names (Vector_string) –
Return type
List[int]

saveUAI(*name*)

Save the MarkovNet in an UAI file.
Parameters
name (*str*) – the file's name
Return type
None

size()

Return type
int

sizeEdges()

Return type
int

smallestFactorFromNode(*node*)

Parameters
node (int) –
Return type
List[int]

property thisown

The membership flag

toDot()

Return type
str

toDotAsFactorGraph()

Return type
str

variable(**args*)

Return type
DiscreteVariable (page 25)

variableFromName(*name*)

Parameters
name (str) –
Return type
DiscreteVariable (page 25)

variableNodeMap()

1.7.2 Inference in Markov Networks

Inference is the process that consists in computing new probabilistc information from a Markov network and some evidence. aGrUM/pyAgrum mainly focus and the computation of (joint) posterior for some variables of the Markov networks given soft or hard evidence that are the form of likelihoods on some variables. Inference is a hard task (NP-complete). For now, aGrUM/pyAgrum implements only one exact inference for Markov Network.

Shafer Shenoy Inference in Markov Network

class pyAgrum.**ShaferShenoyMNInference**(*MN*, *use_binary_join_tree=True*)

Class used for Shafer-Shenoy inferences for Markov network.

ShaferShenoyInference(bn) -> ShaferShenoyInference

Parameters:

- **mn** (*pyAgrum.MarkovNet*) – a Markov network

Parameters

- **MN** (IMarkovNet) –
- **use_binary_join_tree** (bool) –

H(**args*)

Parameters
- **X** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
the computed Shanon's entropy of a node given the observation

Return type
float

I(*X*, *Y*)

Parameters
- **X** (*int or str*) – a node Id or a node name
- **Y** (*int or str*) – another node Id or node name

Returns
- ------- –
- **float** – the Mutual Information of X and Y given the observation

Return type
float

MN()

VI(*X*, *Y*)

Parameters
- **X** (*int or str*) – a node Id or a node name
- **Y** (*int or str*) – another node Id or node name

Returns
- ------- –
- **float** – variation of information between X and Y

Return type
float

addAllTargets()

Add all the nodes as targets.

Return type
None

addEvidence(*args)

Adds a new evidence on a node (might be soft or hard).

Parameters

- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** – (int) a node value
- **val** – (str) the label of the node value
- **vals** (*list*) – a list of values

Raises

- *pyAgrum.InvalidArgument* (page 290) – If the node already has an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type

None

addJointTarget(*targets*)

Add a list of nodes as a new joint target. As a collateral effect, every node is added as a marginal target.

Parameters

- **list** – a list of names of nodes
- **targets** (object) –

Raises

pyAgrum.UndefinedElement (page 293) – If some node(s) do not belong to the Bayesian network

Return type

None

addTarget(*args)

Add a marginal target to the list of targets.

Parameters

- **target** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Raises

pyAgrum.UndefinedElement (page 293) – If target is not a NodeId in the Bayes net

Return type

None

chgEvidence(*args)

Change the value of an already existing evidence on a node (might be soft or hard).

Parameters

- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name
- **val** (*intstr*) – a node value or the label of the node value
- **vals** (*List[float]*) – a list of values

Raises

- *pyAgrum.InvalidArgument* (page 290) – If the node does not already have an evidence
- *pyAgrum.InvalidArgument* (page 290) – If val is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of vals is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If vals is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If the node does not belong to the Bayesian network

Return type
None

eraseAllEvidence()

Removes all the evidence entered into the network.

Return type
None

eraseAllJointTargets()

Clear all previously defined joint targets.

Return type
None

eraseAllMarginalTargets()

Clear all the previously defined marginal targets.

Return type
None

eraseAllTargets()

Clear all previously defined targets (marginal and joint targets).

As a result, no posterior can be computed (since we can only compute the posteriors of the marginal or joint targets that have been added by the user).

Return type
None

eraseEvidence(**args*)

Remove the evidence, if any, corresponding to the node Id or name.

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

Return type
None

eraseJointTarget(*targets*)

Remove, if existing, the joint target.

Parameters
- **list** – a list of names or Ids of nodes
- **targets** (object) –

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

eraseTarget(**args*)

Remove, if existing, the marginal target.

Parameters
- **target** (*int*) – a node Id
- **nodeName** (*int*) – a node name

Raises
- **pyAgrum.IndexError** – If one of the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

Return type
None

evidenceImpact(*target*, *evs*)

Create a pyAgrum.Potential for P(target|evs) (for all instanciation of target and evs)

Parameters
- **target** (*set*) – a set of targets ids or names.
- **evs** (*set*) – a set of nodes ids or names.

> **Warning:** if some evs are d-separated, they are not included in the Potential.

Returns
a Potential for P(targets|evs)

Return type
pyAgrum.Potential (page 53)

evidenceJointImpact(**args*)

Create a pyAgrum.Potential for P(joint targets|evs) (for all instanciation of targets and evs)

Parameters
- **targets** (*List[intstr]*) – a list of node Ids or node names
- **evs** (*Set[intstr]*) – a set of nodes ids or names.

Returns
a Potential for P(target|evs)

Return type
pyAgrum.Potential (page 53)

Raises
pyAgrum.Exception – If some evidene entered into the Bayes net are incompatible (their joint proba = 0)

evidenceProbability()

Returns
the probability of evidence

Return type
float

getNumberOfThreads()

returns the number of threads used by LazyPropagation during inferences.

Returns
the number of threads used by LazyPropagation during inferences

Return type
int

hardEvidenceNodes()

Returns
the set of nodes with hard evidence

Return type
set

hasEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if some node(s) (or the one in parameters) have received evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasHardEvidence(*nodeName*)

Parameters
- **id** (*int*) – a node Id

- **nodeName** (*str*) – a node name

Returns
True if node has received a hard evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

hasSoftEvidence(**args*)

Parameters
- **id** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if node has received a soft evidence

Return type
bool

Raises
pyAgrum.IndexError – If the node does not belong to the Bayesian network

isGumNumberOfThreadsOverriden()

Indicates whether LazyPropagation currently overrides aGrUM's default number of threads (see method setNumberOfThreads).

Returns
A Boolean indicating whether LazyPropagation currently overrides aGrUM's default number of threads

Return type
bool

isJointTarget(*targets*)

Parameters
- **list** – a list of nodes ids or names.
- **targets** (object) –

Returns
True if target is a joint target.

Return type
bool

Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

isTarget(**args*)

Parameters
- **variable** (*int*) – a node Id
- **nodeName** (*str*) – a node name

Returns
True if variable is a (marginal) target

Return type
bool

Raises
- **pyAgrum.IndexError** – If the node does not belong to the Bayesian network
- *pyAgrum.UndefinedElement* (page 293) – If node Id is not in the Bayesian network

joinTree()

Returns
the current join tree used

Return type
pyAgrum.CliqueGraph (page 15)

jointMutualInformation(*targets*)

Parameters
targets (object) –
Return type
float

jointPosterior(*targets*)

Compute the joint posterior of a set of nodes.

Parameters
list – the list of nodes whose posterior joint probability is wanted

> **Warning:** The order of the variables given by the list here or when the jointTarget is declared can not be assumed to be used by the Potential.

Returns
a const ref to the posterior joint probability of the set of nodes.
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets
Parameters
targets (object) –

jointTargets()

Returns
the list of target sets
Return type
list

junctionTree()

Returns
the current junction tree
Return type
pyAgrum.CliqueGraph (page 15)

makeInference()

Perform the heavy computations needed to compute the targets' posteriors

In a Junction tree propagation scheme, for instance, the heavy computations are those of the messages sent in the JT. This is precisely what makeInference should compute. Later, the computations of the posteriors can be done 'lightly' by multiplying and projecting those messages.

Return type
None

nbrEvidence()

Returns
the number of evidence entered into the Bayesian network
Return type
int

nbrHardEvidence()

Returns
the number of hard evidence entered into the Bayesian network
Return type
int

nbrJointTargets()

Returns
the number of joint targets
Return type
int

`nbrSoftEvidence`()

Returns
the number of soft evidence entered into the Bayesian network
Return type
int

`nbrTargets`()

Returns
the number of marginal targets
Return type
int

`posterior`(**args*)

Computes and returns the posterior of a node.

Parameters
- **var** (*int*) – the node Id of the node for which we need a posterior probability
- **nodeName** (*str*) – the node name of the node for which we need a posterior probability

Returns
a const ref to the posterior probability of the node
Return type
pyAgrum.Potential (page 53)
Raises
pyAgrum.UndefinedElement (page 293) – If an element of nodes is not in targets

`setEvidence`(*evidces*)

Erase all the evidences and apply addEvidence(key,value) for every pairs in evidces.

Parameters
evidces (*dict*) – a dict of evidences
Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

`setMaxMemory`(*gigabytes*)

sets an upper bound on the memory consumption admissible

Parameters
gigabytes (*float*) – this upper bound in gigabytes.
Return type
None

`setNumberOfThreads`(*nb*)

If the argument nb is different from 0, this number of threads will be used during inferences, hence overriding aGrUM's default number of threads. If, on the contrary, nb is equal to 0, the parallelized inference engine will comply with aGrUM's default number of threads.

Parameters
nb (*int*) – the number of threads to be used by ShaferShenoyMNInference
Return type
None

setTargets(*targets*)

Remove all the targets and add the ones in parameter.

Parameters
targets (*set*) – a set of targets

Raises
pyAgrum.UndefinedElement (page 293) – If one target is not in the Bayes net

softEvidenceNodes()

Returns
the set of nodes with soft evidence

Return type
set

targets()

Returns
the list of marginal targets

Return type
list

property thisown

The membership flag

updateEvidence(*evidces*)

Apply chgEvidence(key,value) for every pairs in evidces (or addEvidence).

Parameters
evidces (*dict*) – a dict of evidences

Raises
- *pyAgrum.InvalidArgument* (page 290) – If one value is not a value for the node
- *pyAgrum.InvalidArgument* (page 290) – If the size of a value is different from the domain side of the node
- *pyAgrum.FatalError* (page 289) – If one value is a vector of 0s
- *pyAgrum.UndefinedElement* (page 293) – If one node does not belong to the Bayesian network

1.8 Probabilistic Relational Models

For now, pyAgrum only allows to explore Probabilistic Relational Models written with o3prm syntax (see O3PRM website (https:://o3prm.gitlab.io/)).

class pyAgrum.**PRMexplorer**

PRMexplorer helps navigate through probabilistic relational models.

PRMexplorer() -> PRMexplorer
default constructor

property aggType

min/max/count/exists/forall/or/and/amplitude/median

classAggregates(*class_name*)

Parameters
class_name (*str*) – a class name

Returns
the list of aggregates in the class

Return type
list

Raises
pyAgrum.IndexError – If the class is not in the PRM

classAttributes(*class_name*)

Parameters
class_name (*str*) – a class name
Returns
the list of attributes
Return type
list
Raises
pyAgrum.IndexError – If the class is not in the PRM

classDag(*class_name*)

Parameters
class_name (*str*) – a class name
Returns
a description of the DAG
Return type
tuple
Raises
pyAgrum.IndexError – If the class is not in the PRM

classImplements(*class_name*)

Parameters
class_name (*str*) – a class name
Returns
the list of interfaces implemented by the class
Return type
list

classParameters(*class_name*)

Parameters
class_name (*str*) – a class name
Returns
the list of parameters
Return type
list
Raises
pyAgrum.IndexError – If the class is not in the PRM

classReferences(*class_name*)

Parameters
class_name (*str*) – a class name
Returns
the list of references
Return type
list
Raises
pyAgrum.IndexError – If the class is not in the PRM

classSlotChains(*class_name*)

Parameters
class_name (*str*) – a class name
Returns
the list of class slot chains
Return type
list
Raises
pyAgrum.IndexError – if the class is not in the PRM

classes()

Returns
the list of classes
Return type
list

`cpf`(*class_name*, *attribute*)

Parameters
- **class_name** (*str*) – a class name
- **attribute** (*str*) – an attribute

Returns
the potential of the attribute
Return type
pyAgrum.Potential (page 53)
Raises
- ***pyAgrum.OperationNotAllowed*** (page 292) – If the class element doesn't have any pyAgrum.Potential (like a gum::PRMReferenceSlot).
- **pyAgrum.IndexError** – If the class is not in the PRM
- **pyAgrum.IndexError** – If the attribute in parameters does not exist

`getDirectSubClass`(*class_name*)

Parameters
class_name (*str*) – a class name
Returns
the list of direct subclasses
Return type
list
Raises
pyAgrum.IndexError – If the class is not in the PRM

`getDirectSubInterfaces`(*interface_name*)

Parameters
interface_name (*str*) – an interface name
Returns
the list of direct subinterfaces
Return type
list
Raises
pyAgrum.IndexError – If the interface is not in the PRM

`getDirectSubTypes`(*type_name*)

Parameters
type_name (*str*) – a type name
Returns
the list of direct subtypes
Return type
list
Raises
pyAgrum.IndexError – If the type is not in the PRM

`getImplementations`(*interface_name*)

Parameters
interface_name (*str*) – an interface name
Returns
the list of classes implementing the interface
Return type
str
Raises
pyAgrum.IndexError – If the interface is not in the PRM

`getLabelMap`(*type_name*)

Parameters
type_name (*str*) – a type name
Returns
a dict containing pairs of label and their values
Return type
dict
Raises
pyAgrum.IndexError – If the type is not in the PRM

getLabels(*type_name*)

Parameters
type_name (*str*) – a type name
Returns
the list of type labels
Return type
list
Raises
pyAgrum.IndexError – If the type is not in the PRM

getSuperClass(*class_name*)

Parameters
class_name (*str*) – a class name
Returns
the class extended by class_name
Return type
str
Raises
pyAgrum.IndexError – If the class is not in the PRM

getSuperInterface(*interface_name*)

Parameters
interface_name (*str*) – an interface name
Returns
the interace extended by interface_name
Return type
str
Raises
pyAgrum.IndexError – If the interface is not in the PRM

getSuperType(*type_name*)

Parameters
type_name (*str*) – a type name
Returns
the type extended by type_name
Return type
str
Raises
pyAgrum.IndexError – If the type is not in the PRM

getalltheSystems()

Returns
the list of all the systems and their components
Return type
list

interAttributes(*interface_name*, *allAttributes=False*)

Parameters
- **interface_name** (*str*) – an interface
- **allAttributes** (*bool*) – True if supertypes of a custom type should be indicated

Returns
the list of (<type>,<attribute_name>) for the given interface
Return type
list
Raises
pyAgrum.IndexError – If the type is not in the PRM

interReferences(*interface_name*)

Parameters
interface_name (*str*) – an interface
Returns
the list of (<reference_type>,<reference_name>,<True if the reference is an array>) for the given interface
Return type
list
Raises
pyAgrum.IndexError – If the type is not in the PRM

interfaces()

Returns
the list of interfaces in the PRM
Return type
list

isAttribute(*class_name*, *att_name*)

Parameters
- **class_name** (*str*) – a class name
- **att_name** (*str*) – the name of the attribute to be tested

Returns
True if att_name is an attribute of class_name
Return type
bool
Raises
- **pyAgrum.IndexError** – If the class is not in the PRM
- **pyAgrum.IndexError** – If att_name is not an element of class_name

isClass(*name*)

Parameters
name (*str*) – an element name
Returns
True if the parameter correspond to a class in the PRM
Return type
bool

isInterface(*name*)

Parameters
name (*str*) – an element name
Returns
True if the parameter correspond to an interface in the PRM
Return type
bool

isType(*name*)

Parameters
name (*str*) – an element name
Returns
True if the parameter correspond to a type in the PRM
Return type
bool

load(**args*)

Load a PRM into the explorer.

Parameters
- **filename** (*str*) – the name of the o3prm file
- **classpath** (*str*) – the classpath of the PRM

Raises
pyAgrum.FatalError (page 289) – If file not found

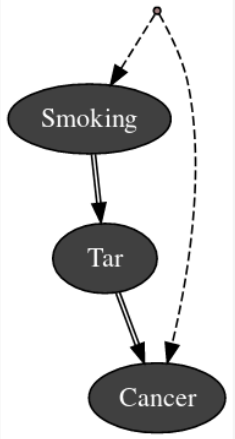
Return type
None

types()

Returns
the list of the custom types in the PRM

Return type
list

1.9 pyAgrum.causal documentation



$$P(Cancer \mid \hookrightarrow Smoking) = \sum_{Tar} P(Tar \mid Smoking) \cdot \left(\sum_{Smoking'} P(Cancer \mid Smoking', Tar) \cdot P(Smoking') \right)$$

Causality in pyAgrum mainly consists in the ability to build a causal model, i.e. a (observational) Bayesian network and a set of latent variables and their relation with observation variables and in the abilidy to compute using do-calculus the causal impact in such a model.

Causality is a set of pure python3 scripts based on pyAgrum's tools.

Note: As it can be seen in the figure above, *pyAgrum.causal* module uses a LaTeX special arrow (↪) to compactly represent an intervention. If you prefer the classical "do" notation, you can change this behavior by using:

```
gum.config["causal","latex_do_prefix"]="do("
gum.config["causal","latex_do_suffix"]=")"
```

Tutorials

- Notebooks on causality in pyAgrum.
- Some implemented examples (https://webia.lip6.fr/~phw/aGrUM/BookOfWhy/) from the book of Why (http://bayes.cs.ucla.edu/WHY/) from Judea Pearl and Dana Mackenzie.

Reference

1.9.1 Causal Model

class pyAgrum.causal.**CausalModel**(*bn*, *latentVarsDescriptor=None*, *keepArcs=False*)

From an observational BNs and the description of latent variables, this class represent a complet causal model obtained by adding the latent variables specified in `latentVarsDescriptor` to the Bayesian network bn.

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) – an observational Bayesian network
- **latentVarsDescriptor** (*List[(str,List[int])]*) – list of couples (<latent variable name>, <list of affected variables' ids>).
- **keepArcs** (*bool*) – By default, the arcs between variables affected by a common latent variable will be removed but this can be avoided by setting `keepArcs` to `True`

addCausalArc(*x*, *y*)

Add an arc x->y

Parameters
- **x** (*int|str*) – the nodeId or the name of the first node
- **y** (*int|str*) – the nodeId or the name of the second node

Return type
None

addLatentVariable(*name*, *lchild*, *keepArcs=False*)

Add a new latent variable with a name, a tuple of children and replacing (or not) correlations between children.

Parameters
- **name** (*str*) – the name of the latent variable
- **lchild** (*Tuple[str,str]*) – the tuple of (2) children
- **keepArcs** (*bool*) – do wee keep (or not) the arc between the children ?

Return type
None

arcs()

Return type
Set[Tuple[NewType()(NodeId, int), NewType()(NodeId, int)]]

Returns
the set of arcs

backDoor(*cause*, *effect*, *withNames=True*)

Check if a backdoor exists between *cause* and *effect*

Parameters
- **cause** (*int|str*) – the nodeId or the name of the cause
- **effect** (*int|str*) – the nodeId or the name of the effect
- **withNames** (*bool*) – wether we use ids (int) or names (str)

Returns
None if no found backdoor. Otherwise return the found backdoors as set of ids or set of names.

Return type
None|Set[str]|Set[int]

causalBN()

Return type
BayesNet (page 64)

Returns
the causal Bayesian network

Warning
do not infer any computations in this model. It is strictly a structural model

children(*x*)

From a NodeId, returns its children (as a set of NodeId)

Parameters
x (*int*) – the node

Returns
the set of children

Return type
Set[int]

eraseCausalArc(*x*, *y*)

Erase the arc x->y

Parameters
- **x** (*int|str*) – the nodeId or the name of the first node
- **y** (*int|str*) – the nodeId or the name of the second node

Return type
None

existsArc(*x*, *y*)

Does the arc x->y exist ?

Parameters
- **x** (*int|str*) – the nodeId or the name of the first node
- **y** (*int|str*) – the nodeId or the name of the second node

Returns
True if the arc exists.

Return type
bool

frontDoor(*cause*, *effect*, *withNames=True*)

Check if a frontdoor exists between cause and effet

Parameters
- **cause** (*int|str*) – the nodeId or the name of the cause
- **effect** (*int|str*) – the nodeId or the name of the effect
- **withNames** (*bool*) – wether we use ids (int) or names (str)

Returns
None if no found frontdoot. Otherwise return the found frontdoors as set of ids or set of names.

Return type
None|Set[str]|Set[int]

idFromName(*name*)

Parameters
name (*str*) – the name of the variable

Returns
the id of the variable

Return type
int

latentVariablesIds()

Returns
the set of ids of latent variables in the causal model

Return type
NodeSet

names()

Returns
the map NodeId,Name

Return type
Dict[int,str]

nodes()

Return type
Set[NewType()(NodeId, int)]
Returns
the set of nodes

observationalBN()

Return type
BayesNet (page 64)
Returns
the observational Bayesian network

parents(*x*)

From a NodeId, returns its parent (as a set of NodeId)
Parameters
x (*int*) – the node
Returns
the set of parents
Return type
Set[int]

toDot()

Create a dot representation of the causal model
Return type
str
Returns
the dot representation in a string

1.9.2 Causal Formula

CausalFormula is the class that represents a causal query in a causal model. Mainly it consits in

- a reference to the CausalModel
- Three sets of variables name that represent the 3 sets of variable in the query P(set1 | doing(set2),knowing(set3)).
- the AST for compute the query.

class pyAgrum.causal.**CausalFormula**(*cm*, *root*, *on*, *doing*, *knowing=None*)

Represents a causal query in a causal model. The query is encoded as an CausalFormula that can be evaluated in the causal model : $P(on|knowing, overhook (doing))$

Parameters

- **cm** (*CausalModel* (page 237)) – the causal model
- **root** (*ASTtree* (page 242)) – the syntax tree
- **on** (*str|Set[str]*) – the variable or the set of variables of interest
- **doing** (*str|Set[str]*) – the intervention variable(s)
- **knowing** (*None|str|Set[str]*) – the observation variable(s)

property cm: *CausalModel* (page 237)

Returns
the causal model
Return type
CausalModel (page 237)

`copy()`

Copy theAST. Note that the causal model is just referenced. The tree is copied.

Returns
the copu

Return type
CausalFormula (page 239)

`eval()`

Compute the Potential from the CausalFormula over vars using cond as value for others variables

Returns
The resulting distribution

Return type
pyAgrum.Potential (page 53)

`latexQuery(values=None)`

Returns a string representing the query compiled by this Formula. If values, the query is annotated with the values in the dictionary.

Parameters
values (*None|Dict[str,str]*) – the values to add in the query representation

Returns
the LaTeX representation of the causal query for this CausalFormula

Return type
str

`property root: ASTtree (page 242)`

Returns
the causalFormula as an ASTtree

Return type
ASTtree (page 242)

`toLatex()`

Returns
a LaTeX representation of the CausalFormula

Return type
str

1.9.3 Causal Inference

Obtaining and evaluating a CausalFormula is done using one these functions :

`pyAgrum.causal.causalImpact(cm, on, doing, knowing=None, values=None)`

Determines the causal impact of interventions.

Determines the causal impact of the interventions specified in `doing` on the single or list of variables `on` knowing the states of the variables in `knowing` (optional). These last parameters is dictionary <variable name>:<value>. The causal impact is determined in the causal DAG `cm`. This function returns a triplet with a latex format formula used to compute the causal impact, a potential representing the probability distribution of `on` given the interventions and observations as parameters, and an explanation of the method allowing the identification. If there is no impact, the joint probability of `on` is simply returned. If the impact is not identifiable the formula and the adjustment will be `None` but an explanation is still given.

Parameters

- **cm** (`CausalModel` (page 237)) – the causal model
- **on** (*str|NameSet*) – variable name or variable names set of interest
- **doing** (*str|NameSet*) – the interventions

- **knowing** (*str|NameSet*) – the observations
- **values** (*Dict[str,int] default=None*) – the values of interventions and observations

Returns
the CausalFormula, the computation, the explanation

Return type
Tuple[*CausalFormula* (page 239),*pyAgrum.Potential* (page 53),str]

pyAgrum.causal.**doCalculusWithObservation**(*cm*, *on*, *doing*, *knowing=None*)

Compute the CausalFormula for an impact analysis given the causal model, the observed variables and the variable on which there will be intervention.

Parameters

- **cm** (CausalModel (page 237)) – the causal model
- **on** (*Set[str]*) – the variables of interest
- **doing** (*Set[str]*) – the interventions
- **knowing** (*Set[str] default=None*) – the observations

Returns
if possible, returns the formula to compute this intervention

Return type
CausalFormula (page 239)

Raises
HedgeException (page 253), *UnidentifiableException* (page 253) – if this calculous is not possible

pyAgrum.causal.**identifyingIntervention**(*cm*, *Y*, *X*, *P=None*)

Following Shpitser, Ilya and Judea Pearl. 'Identification of Conditional Interventional Distributions.' UAI2006 and 'Complete Identification Methods for the Causal Hierarchy' JMLR 2008

Parameters

- **cm** (*CausalModel* (page 237)) – the causal model
- **Y** (Set[str]) – The variables of interest (named following the paper)
- **X** (Set[str]) – The variable of intervention (named following the paper)
- **P** (Optional[*ASTtree* (page 242)]) – The ASTtree representing the calculus in construction

Return type
ASTtree (page 242)

Returns
the ASTtree representing the calculus

1.9.4 Other functions

pyAgrum.causal.**backdoor_generator**(*bn*, *cause*, *effect*, *not_bd=None*)

Generates backdoor sets for the pair of nodes *(cause, effect)* in the graph *bn* excluding the nodes in the set *not_bd* (optional)

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) –
- **cause** (*int*) –

- **effect** (*int*) –
- **not_bd** (*Set[int] default=None*) –

Yields
List[int] – the different backdoors

pyAgrum.causal.**frontdoor_generator**(*bn*, *x*, *y*, *not_fd=None*)

Generates frontdoor sets for the pair of nodes *(x, y)* in the graph *bn* excluding the nodes in the set *not_fd* (optional)

Parameters

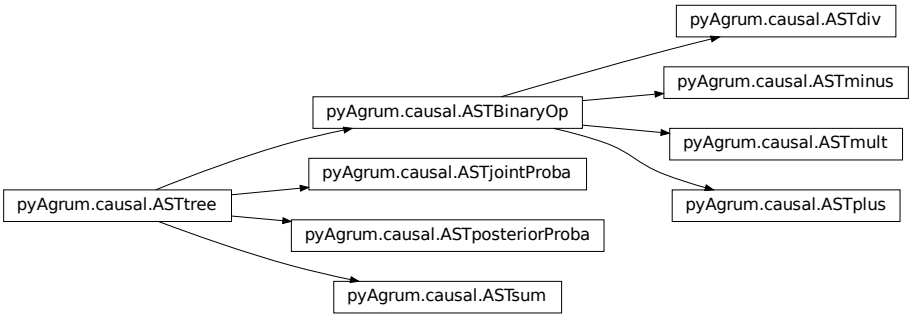
- **bn** (pyAgrum.BayesNet (page 64)) –
- **x** (*int*) –
- **y** (*int*) –
- **not_fd** (*Set[int] default=None*) –

Yields
List[int] – the different frontdoors

1.9.5 Abstract Syntax Tree for Do-Calculus

The pyCausal package compute every causal query into an Abstract Syntax Tree (CausalFormula) that represents the exact computations to be done in order to answer to the probabilistic causal query.

The different types of node in an CausalFormula are presented below and are organized as a hierarchy of classes from *pyAgrum.causal.ASTtree* (page 242).



Internal node structure

class pyAgrum.causal.**ASTtree**(*typ*, *verbose=False*)

Represents a generic node for the CausalFormula. The type of the node will be registered in a string.

Parameters

- **typ** (*str*) – the type of the node (will be specified in concrete children classes.
- **verbose** (*bool*) – if True, add some messages

copy()

Copy an CausalFormula tree

Returns
the new causal tree
Return type
ASTtree (page 242)

eval(*contextual_bn*)

Evaluation of a AST tree from inside a BN

Parameters
contextual_bn (pyAgrum.BayesNet (page 64)) – the observational Bayesian network in which will be done the computations
Returns
the resulting Potential
Return type
pyAgrum.Potential (page 53)

fastToLatex(*nameOccur*)

Internal virtual function to create a LaTeX representation of the ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable
Returns
LaTeX representation of the tree
Return type
str

protectToLatex(*nameOccur*)

Create a protected LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable
Returns
a protected version of LaTeX representation of the tree
Return type
str

toLatex(*nameOccur=None*)

Create a LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int] default=None*) – the number of occurrence for each variable
Returns
LaTeX representation of the tree
Return type
str

property type: str

Returns
the type of the node
Return type
str

class pyAgrum.causal.**ASTBinaryOp**(*typ*, *op1*, *op2*)

Represents a generic binary node for the CausalFormula. The op1 and op2 are the two operands of the class.

Parameters

- **typ** (*str*) – the type of the node (will be specified in concrete children classes
- **op1** (ASTtree (page 242)) – left operand
- **op2** (ASTtree (page 242)) – right operand

copy()

Copy an CausalFormula tree

Returns
the new causal tree

Return type
ASTtree (page 242)

eval(*contextual_bn*)

Evaluation of a AST tree from inside a BN

Parameters
contextual_bn (pyAgrum.BayesNet (page 64)) – the observational Bayesian network in which will be done the computations

Returns
the resulting Potential

Return type
pyAgrum.Potential (page 53)

fastToLatex(*nameOccur*)

Internal virtual function to create a LaTeX representation of the ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable

Returns
LaTeX representation of the tree

Return type
str

property op1: *ASTtree* (page 242)

Returns
the left operand

Return type
ASTtree (page 242)

property op2: *ASTtree* (page 242)

Returns
the right operand

Return type
ASTtree (page 242)

protectToLatex(*nameOccur*)

Create a protected LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable

Returns
a protected version of LaTeX representation of the tree

Return type
str

toLatex(*nameOccur=None*)

Create a LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int] default=None*) – the number of occurrence for each variable

Returns
LaTeX representation of the tree

Return type
str

property type: str

Returns
the type of the node

Return type
str

Basic Binary Operations

class pyAgrum.causal.**ASTplus**(*op1*, *op2*)

Represents the sum of 2 causal.ASTtree

Parameters

- **op1** (ASTtree (page 242)) – left operand
- **op2** (ASTtree (page 242)) – right operand

copy()

Copy an CausalFormula tree

Returns
the new causal tree
Return type
ASTtree (page 242)

eval(*contextual_bn*)

Evaluation of a AST tree from inside a BN

Parameters
contextual_bn (pyAgrum.BayesNet (page 64)) – the observational Bayesian network in which will be done the computations
Returns
the resulting Potential
Return type
pyAgrum.Potential (page 53)

fastToLatex(*nameOccur*)

Internal virtual function to create a LaTeX representation of the ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable
Returns
LaTeX representation of the tree
Return type
str

property op1: *ASTtree* (page 242)

Returns
the left operand
Return type
ASTtree (page 242)

property op2: *ASTtree* (page 242)

Returns
the right operand
Return type
ASTtree (page 242)

protectToLatex(*nameOccur*)

Create a protected LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable
Returns
a protected version of LaTeX representation of the tree
Return type
str

toLatex(*nameOccur=None*)

Create a LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int] default=None*) – the number of occurrence for each variable

Returns
LaTeX representation of the tree

Return type
str

property type: str

Returns
the type of the node

Return type
str

class pyAgrum.causal.**ASTminus**(*op1*, *op2*)

Represents the substraction of 2 causal.ASTtree

Parameters

- **op1** (ASTtree (page 242)) – left operand
- **op2** (ASTtree (page 242)) – right operand

copy()

Copy an CausalFormula tree

Returns
the new causal tree

Return type
ASTtree (page 242)

eval(*contextual_bn*)

Evaluation of a AST tree from inside a BN

Parameters
contextual_bn (pyAgrum.BayesNet (page 64)) – the observational Bayesian network in which will be done the computations

Returns
the resulting Potential

Return type
pyAgrum.Potential (page 53)

fastToLatex(*nameOccur*)

Internal virtual function to create a LaTeX representation of the ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable

Returns
LaTeX representation of the tree

Return type
str

property op1: *ASTtree* (page 242)

Returns
the left operand

Return type
ASTtree (page 242)

property op2: *ASTtree* (page 242)

Returns
the right operand

Return type
ASTtree (page 242)

protectToLatex(*nameOccur*)

Create a protected LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable
Returns
a protected version of LaTeX representation of the tree
Return type
str

toLatex(*nameOccur=None*)

Create a LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int] default=None*) – the number of occurrence for each variable
Returns
LaTeX representation of the tree
Return type
str

property type: str

Returns
the type of the node
Return type
str

class pyAgrum.causal.**ASTdiv**(*op1*, *op2*)

Represents the division of 2 causal.ASTtree

Parameters

- **op1** (ASTtree (page 242)) – left operand
- **op2** (ASTtree (page 242)) – right operand

copy()

Copy an CausalFormula tree

Returns
the new causal tree
Return type
ASTtree (page 242)

eval(*contextual_bn*)

Evaluation of a AST tree from inside a BN

Parameters
contextual_bn (pyAgrum.BayesNet (page 64)) – the observational Bayesian network in which will be done the computations
Returns
the resulting Potential
Return type
pyAgrum.Potential (page 53)

fastToLatex(*nameOccur*)

Internal virtual function to create a LaTeX representation of the ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable
Returns
LaTeX representation of the tree
Return type
str

property op1: *ASTtree* (page 242)

Returns
the left operand
Return type
ASTtree (page 242)

property op2: *ASTtree* (page 242)

Returns
the right operand
Return type
ASTtree (page 242)

protectToLatex(*nameOccur*)

Create a protected LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable
Returns
a protected version of LaTeX representation of the tree
Return type
str

toLatex(*nameOccur=None*)

Create a LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int] default=None*) – the number of occurrence for each variable
Returns
LaTeX representation of the tree
Return type
str

property type: str

Returns
the type of the node
Return type
str

class pyAgrum.causal.**ASTmult**(*op1*, *op2*)

Represents the multiplication of 2 causal.ASTtree

Parameters

- **op1** (ASTtree (page 242)) – left operand
- **op2** (ASTtree (page 242)) – right operand

copy()

Copy an CausalFormula tree

Returns
the new causal tree
Return type
ASTtree (page 242)

eval(*contextual_bn*)

Evaluation of a AST tree from inside a BN

Parameters
contextual_bn (pyAgrum.BayesNet (page 64)) – the observational Bayesian network in which will be done the computations
Returns
the resulting Potential

Return type
pyAgrum.Potential (page 53)

fastToLatex(*nameOccur*)

Internal virtual function to create a LaTeX representation of the ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable

Returns
LaTeX representation of the tree

Return type
str

property op1: *ASTtree* (page 242)

Returns
the left operand

Return type
ASTtree (page 242)

property op2: *ASTtree* (page 242)

Returns
the right operand

Return type
ASTtree (page 242)

protectToLatex(*nameOccur*)

Create a protected LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable

Returns
a protected version of LaTeX representation of the tree

Return type
str

toLatex(*nameOccur=None*)

Create a LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int] default=None*) – the number of occurrence for each variable

Returns
LaTeX representation of the tree

Return type
str

property type: str

Returns
the type of the node

Return type
str

Complex operations

class pyAgrum.causal.**ASTsum**(*var*, *term*)

Represents a sum over a variable of a causal.ASTtree.

Parameters

- **var** (*str*) – name of the variable on which to sum
- **term** (ASTtree (page 242)) – the tree to be evaluated

copy()

Copy an CausalFormula tree

Returns
the new causal tree

Return type
ASTtree (page 242)

eval(*contextual_bn*)

Evaluation of a AST tree from inside a BN

Parameters
contextual_bn (pyAgrum.BayesNet (page 64)) – the observational Bayesian network in which will be done the computations

Returns
the resulting Potential

Return type
pyAgrum.Potential (page 53)

fastToLatex(*nameOccur*)

Internal virtual function to create a LaTeX representation of the ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable

Returns
LaTeX representation of the tree

Return type
str

protectToLatex(*nameOccur*)

Create a protected LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable

Returns
a protected version of LaTeX representation of the tree

Return type
str

property term: *ASTtree* (page 242)

Returns
the term to sum

Return type
ASTtree (page 242)

toLatex(*nameOccur=None*)

Create a LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int] default=None*) – the number of occurrence for each variable

Returns
LaTeX representation of the tree

Return type
str

property type: str

Returns
the type of the node
Return type
str

class pyAgrum.causal.**ASTjointProba**(*varNames*)

Represent a joint probability in the base observational part of the causal.CausalModel

Parameters
varNames (*Set[str]*) – a set of variable names

copy()

Copy an CausalFormula tree
Returns
the new causal tree
Return type
ASTtree (page 242)

eval(*contextual_bn*)

Evaluation of a AST tree from inside a BN
Parameters
contextual_bn (pyAgrum.BayesNet (page 64)) – the observational Bayesian network in which will be done the computations
Returns
the resulting Potential
Return type
pyAgrum.Potential (page 53)

fastToLatex(*nameOccur*)

Internal virtual function to create a LaTeX representation of the ASTtree
Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable
Returns
LaTeX representation of the tree
Return type
str

protectToLatex(*nameOccur*)

Create a protected LaTeX representation of a ASTtree
Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable
Returns
a protected version of LaTeX representation of the tree
Return type
str

toLatex(*nameOccur=None*)

Create a LaTeX representation of a ASTtree
Parameters
nameOccur (*Dict[str,int] default=None*) – the number of occurrence for each variable
Returns
LaTeX representation of the tree
Return type
str

property type: str

Returns
the type of the node

Return type
str

property varNames: Set[str]

Returns
the set of names of var
Return type
Set[str]

class pyAgrum.causal.**ASTposteriorProba**(*bn*, *varset*, *knw*)

Represent a conditional probability $P_{bn}(vars|knw)$ that can be computed by an inference in a BN.

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) – the pyAgrum:pyAgrum.BayesNet
- **varset** (*Set[str]*) – a set of variable names (in the BN) conditioned in the posterior
- **knw** (*Set[str]*) – a set of variable names (in the BN) conditioning in the posterior

property bn: *BayesNet* (page 64)

Returns
the observationnal BayesNet in $P_{bn}(vars|knw)$
Return type
pyAgrum.BayesNet (page 64)

copy()

Copy an CausalFormula tree
Returns
the new causal tree
Return type
ASTtree (page 242)

eval(*contextual_bn*)

Evaluation of a AST tree from inside a BN
Parameters
contextual_bn (pyAgrum.BayesNet (page 64)) – the observational Bayesian network in which will be done the computations
Returns
the resulting Potential
Return type
pyAgrum.Potential (page 53)

fastToLatex(*nameOccur*)

Internal virtual function to create a LaTeX representation of the ASTtree
Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable
Returns
LaTeX representation of the tree
Return type
str

property knw: Set[str]

Returns
(Conditioning) knw in $P_{bn}(vars|knw)$
Return type
Set[str]

protectToLatex(*nameOccur*)

Create a protected LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int]*) – the number of occurrence for each variable

Returns
a protected version of LaTeX representation of the tree

Return type
str

toLatex(*nameOccur=None*)

Create a LaTeX representation of a ASTtree

Parameters
nameOccur (*Dict[str,int] default=None*) – the number of occurrence for each variable

Returns
LaTeX representation of the tree

Return type
str

property type: str

Returns
the type of the node

Return type
str

property vars: Set[str]

Returns
(Conditioned) vars in $P_{bn}(vars|knw)$

Return type
Set[str]

1.9.6 Exceptions

class pyAgrum.causal.**HedgeException**(*msg*, *observables*, *gs*)

Represents an hedge exception for a causal query

Parameters

- **msg** (*str*) –
- **observables** (*NameSet*) –
- **gs** –

args

class pyAgrum.causal.**UnidentifiableException**(*msg*)

Represents an unidentifiability for a causal query

Parameters
msg (*str*) –

args

1.9.7 Notebook's tools for causality

This file defines some helpers for handling causal concepts in notebooks

pyAgrum.causal.notebook.**getCausalImpact**(*model*, *on*, *doing*, *knowing=None*, *values=None*)

return a HTML representing of the three values defining a causal impact : formula, value, explanation

Parameters

- **model** (CausalModel (page 237)) – the causal model
- **on** (*str | Set[str]*) – the impacted variable(s)
- **doing** (*str | Set[str]*) – the interventions
- **knowing** (*str | Set[str]*) – the observations
- **values** (*Dict[str,int] default=None*) – value for certain variables

Return type
HTML

pyAgrum.causal.notebook.**getCausalModel**(*cm*, *size=None*)

return a HTML representing the causal model

Parameters

- **cm** (CausalModel (page 237)) – the causal model
- **size** (*int|str*) – the size of the rendered graph

Returns
the dot representation

Return type
pydot.Dot

pyAgrum.causal.notebook.**showCausalImpact**(*model*, *on*, *doing*, *knowing=None*, *values=None*)

display a HTML representing of the three values defining a causal impact : formula, value, explanation

Parameters

- **model** (CausalModel (page 237)) – the causal model
- **on** (*str | Set[str]*) – the impacted variable(s)
- **doing** (*str | Set[str]*) – the interventions
- **knowing** (*str | Set[str]*) – the observations
- **values** (*Dict[str,int] default=None*) – value for certain variables

pyAgrum.causal.notebook.**showCausalModel**(*cm*, *size=None*)

Shows a pydot svg representation of the causal DAG

Parameters

- **cm** (CausalModel (page 237)) – the causal model
- **size** (*int|str*) – the size of the rendered graph

1.10 pyAgrum.skbn documentation

Probabilistic classification in pyAgrum aims to propose a scikit-learn-like (binary and multi-class) classifier class that can be used in the same codes as scikit-learn classifiers. Moreover, even if the classifier wraps a full Bayesian network, skbn optimally encodes the classifier using the smallest set of needed features following the d-separation criterion (Markov Blanket).

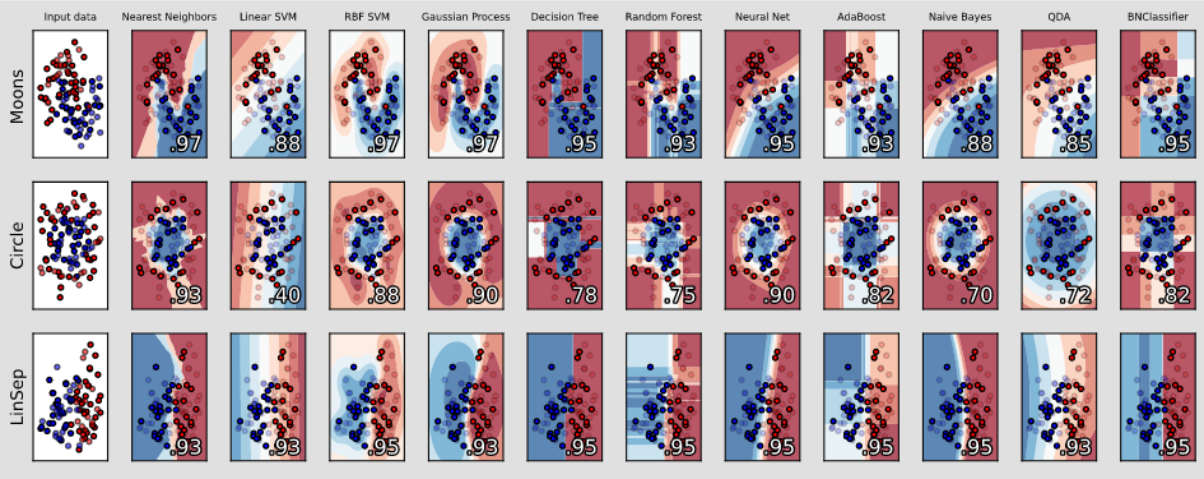


Fig. 1: An example from scikit-learn (https://scikit-learn.org/stable/auto_examples/classification/plot_classifier_comparison.html) where a last column with a BNClassifier has been added flawlessly (see this notebooks).

The module proposes to wrap the pyAgrum's learning algorithms and some others (naive Bayes, TAN, Chow-Liu tree) in the fit method of a classifier. In order to be used with continuous variable, the module proposes also some different discretization methods.

skbn is a set of pure python3 scripts based on pyAgrum's tools.

Tutorials

Notebooks on scikit-learn compliant classifiers in pyAgrum,

Reference

1.10.1 Classifier using Bayesian networks

class pyAgrum.skbn.**BNClassifier**(*learningMethod='GHC'*, *prior=None*, *scoringType='BIC'*, *constraints=None*, *priorWeight=1*, *possibleSkeleton=None*, *DirichletCsv=None*, *discretizationStrategy='quantile'*, *discretizationNbBins=5*, *discretizationThreshold=25*, *usePR=False*, *significant_digit=10*)

Represents a (scikit-learn compliant) classifier which uses a BN to classify. A BNClassifier is build using

- a Bayesian network,
- a database and a learning algorithm and parameters
- the use of BNDiscretizer to discretize with different algorithms some variables.

parameters:

learningMethod: str
A string designating which type of learning we want to use. Possible values are: Chow-Liu, NaiveBayes, TAN, MIIC + (MDL ou NML), GHC, 3off2 +

(MDL ou NML), Tabu. GHC designates Greedy Hill Climbing. MIIC designates Multivariate Information based Inductive Causation TAN designates Tree-augmented NaiveBayes Tabu designated Tabu list searching

prior: str
A string designating the type of a priorsmoothing we want to use. Possible values are Smoothing, BDeu, Dirichlet and NoPrior . Note: if using Dirichlet smoothing DirichletCsv cannot be set to none By default (when prior is None) : a smoothing(0.01) is applied.

scoringType: str
A string designating the type of scoring we want to use. Since scoring is used while constructing the network and not when learning its parameters, the scoring will be ignored if using a learning algorithm with a fixed network structure such as Chow-Liu, TAN or NaiveBayes. possible values are: AIC, BIC, BD, BDeu, K2, Log2 AIC means Akaike information criterion BIC means Bayesian Information criterion BD means Bayesian-Dirichlet scoring BDeu means Bayesian-Dirichlet equivalent uniform Log2 means log2 likelihood ratio test

constraints: dict()
A dictionary designating the constraints that we want to put on the structure of the Bayesian network. Ignored if using a learning algorithm where the structure is fixed such as TAN or NaiveBayes. the keys of the dictionary should be the strings "PossibleEdges" , "MandatoryArcs" and "ForbiddenArcs". The format of the values should be a tuple of strings (tail,head) which designates the string arc from tail to head. For example if we put the value ("x0"."y") in MandatoryArcs the network will surely have an arc going from x0 to y. Note: PossibleEdge allows between nodes x and y allows for either (x,y) or (y,x) (or none of them) to be added to the Bayesian network, while the others are not symmetric.

priorWeight: double
The weight used for a prior.

possibleSkeleton: pyAgrum.undigraph
An undirected graph that serves as a possible skeleton for the Bayesian network

DirichletCsv: str
the file name of the csv file we want to use for the dirichlet prior. Will be ignored if prior is not set to Dirichlet.

discretizationStrategy: str
sets the default method of discretization for this discretizer. This method will be used if the user has not specified another method for that specific variable using the setDiscretizationParameters method possible values are: 'quantile', 'uniform', 'kmeans', 'NML', 'CAIM' and 'MDLP'

defaultNumberOfBins: str or int
sets the number of bins if the method used is quantile, kmeans, uniform. In this case this parameter can also be set to the string 'elbowMethod' so that the best number of bins is found automatically. If the method used is NML, this parameter sets the maximum number of bins up to which the NML algorithm searches for the optimal number of bins. In this case this parameter must be an int If any other discretization method is used, this parameter is ignored.

discretizationThreshold: int or float
When using default parameters a variable will be treated as continuous only if it has more unique values than this number (if the number is an int greater than 1). If the number is a float between 0 and 1, we will test if the proportion of unique values is bigger than this number. For instance, if you have entered 0.95, the variable will be treated as continuous only if more than 95% of its values are unique.

usePR: bool
indicates if the threshold to choose is Prevision-Recall curve's threshold or ROC's threshold by default. ROC curves should be used when there are roughly equal numbers of observations for each class. Precision-Recall curves should be used when there is a moderate to large class imbalance especially for the target's class.

significant_digit:
number of significant digits when computing probabilities

`XYfromCSV`(*filename*, *with_labels=True*, *target=None*)

Reads the data from a csv file and separates it into an X matrix and a y column vector.

Parameters
- `filename` (*str*) – the name of the csv file
- `with_labels` (*bool*) – tells us whether the csv includes the labels themselves or their indexes.
- `target` (*str or None*) – The name of the column that will be put in the dataframe y. If target is None, we use the target that is already specified in the classifier

Returns
Matrix X containing the data,Column-vector containing the class for each data vector in X

Return type
Tuple(pandas.Dataframe,pandas.Dataframe)

`fit`(*X=None*, *y=None*, *data=None*, *targetName=None*, *filename=None*)

parameters:

X: {array-like, sparse matrix} of shape (n_samples, n_features)
training data. Warning: Raises ValueError if either filename or targetname is not None. Raises ValueError if y is None.

y: array-like of shape (n_samples)
Target values. Warning: Raises ValueError if either filename or targetname is not None. Raises ValueError if X is None

data: Union[str,pandas.DataFrame]
the source of training data : csv filename or pandas.DataFrame. targetName is mandatory to find the class in this source.

targetName: str
specifies the name of the targetVariable in the csv file. Warning: Raises ValueError if either X or y is not None. Raises ValueError if filename is None.

filename: str
(deprecated, use data instead) specifies the csv file where the training data and target values are located. Warning: Raises ValueError if either X or y is not None. Raises ValueError if targetName is None

returns:
void

Fits the model to the training data provided. The two possible uses of this function are *fit(X,y)* and *fit(data=..., targetName=...)*. Any other combination will raise a ValueError

`fromTrainedModel`(*bn*, *targetAttribute*, *targetModality=''*, *copy=False*, *threshold=0.5*, *variableList=None*)

parameters:

bn: pyagrum.BayesNet
The Bayesian network we want to use for this classifier

targetAttribute: str
the attribute that will be the target in this classifier

targetModality: str
If this is a binary classifier we have to specify which modality we are looking at if the target attribute has more than 2 possible values if !="", a binary classifier is created. if ==="", a classifier is created that can be non-binary depending on the number of

modalities for targetAttribute. If binary, the second one is taken as targetModality.

copy: bool
Indicates whether we want to put a copy of bn in the classifier, or bn itself.

threshold: double
The classification threshold. If the probability that the target modality is true is larger than this threshold we predict that modality

variableList: list(str)
A list of strings. variableList[i] is the name of the variable that has the index i. We use this information when calling predict to know which column corresponds to which variable. If this list is set to none, then we use the order in which the variables were added to the network.

returns:
void

Creates a BN classifier from an already trained pyAgrum Bayesian network

`get_params`(*deep=True*)

Get parameters for this estimator.

Parameters
deep (*bool, default=True*) – If True, will return the parameters for this estimator and contained subobjects that are estimators.

Returns
params – Parameter names mapped to their values.

Return type
dict

`predict`(*X*, *with_labels=True*)

parameters:

X: str,{array-like, sparse matrix} of shape (n_samples, n_features) or str
test data, can be either dataFrame, matrix or name of a csv file

with_labels: bool
tells us whether the csv includes the labels themselves or their indexes.

returns:

y: array-like of shape (n_samples,)
Predicted classes

Predicts the most likely class for each row of input data, with bn's Markov Blanket

`predict_proba`(*X*)

Predicts the probability of classes for each row of input data, with bn's Markov Blanket

Parameters
X (*str or {array-like, sparse matrix} of shape (n_samples, n_features) or str*) – test data, can be either dataFrame, matrix or name of a csv file

Returns
Predicted probability for each classes

Return type
array-like of shape (n_samples,)

`preparedData`(*X=None*, *y=None*, *data=None*, *filename=None*)

Given an X and a y (or a data source : filename or pandas.DataFrame), returns a pandas.Dataframe with the prepared (especially discretized) values of the base

Parameters

- **X** (*{array-like, sparse matrix} of shape (n_samples, n_features)*) – training data. Warning: Raises ValueError if either filename or targetname is not None. Raises ValueError if y is None.
- **y** (*array-like of shape (n_samples)*) – Target values. Warning: Raises ValueError if either filename or targetname is not None. Raises ValueError if X is None
- **data** (*Union[str,pandas.DataFrame]*) – specifies the csv file or the DataFrame where the data values are located. Warning: Raises ValueError

if either X or y is not None.
- **filename** (*str*) – (deprecated) specifies the csv file where the data are located. Warning: Raises ValueError if either X or y is not None.

Return type
pandas.Dataframe

score(*X*, *y*, *sample_weight=None*)

Return the mean accuracy on the given test data and labels.

In multi-label classification, this is the subset accuracy which is a harsh metric since you require for each sample that each label set be correctly predicted.

Parameters
- **X** (*array-like of shape (n_samples, n_features)*) – Test samples.
- **y** (*array-like of shape (n_samples,) or (n_samples, n_outputs)*) – True labels for *X*.
- **sample_weight** (*array-like of shape (n_samples,), default=None*) – Sample weights.

Returns
score – Mean accuracy of `self.predict(X)` wrt. *y*.

Return type
float

set_params(***params*)

Set the parameters of this estimator.

The method works on simple estimators as well as on nested objects (such as `Pipeline`). The latter have parameters of the form `<component>__<parameter>` so that it's possible to update each component of a nested object.

Parameters
****params** (*dict*) – Estimator parameters.

Returns
self – Estimator instance.

Return type
estimator instance

showROC_PR(*filename*, *save_fig=False*, *show_progress=False*)

Use the *pyAgrum.lib.bn2roc* tools to create ROC and Precision-Recall curve

Parameters
- **filename** (*str*) – a csv filename
- **save_fig** (*bool*) – whether the graph should be saved
- **show_progress** (*bool*) – indicates if the resulting curve must be printed

1.10.2 Discretizer for Bayesian networks

class pyAgrum.skbn.**BNDiscretizer**(*defaultDiscretizationMethod='quantile'*, *defaultNumberOfBins=10*, *discretizationThreshold=25*)

Represents a tool to discretize some variables in a database in order to obtain a way to learn a pyAgrum's (discrete) Bayesian networks.

parameters:

defaultDiscretizationMethod: str
sets the default method of discretization for this discretizer. Possible values are: 'quantile', 'uniform', 'kmeans', 'NML', 'CAIM' and 'MDLP'. This method will be used if the user has not specified another method for that specific variable using the setDiscretizationParameters method.

defaultNumberOfBins: str or int
sets the number of bins if the method used is quantile, kmeans, uniform. In this case this parameter can also be set to the string 'elbowMethod' so that the best number of bins is

found automatically. If the method used is NML, this parameter sets the the maximum number of bins up to which the NML algorithm searches for the optimal number of bins. In this case this parameter must be an int If any other discetization method is used, this parameter is ignored.

discretizationThreshold: int or float
When using default parameters a variable will be treated as continous only if it has more unique values than this number (if the number is an int greater than 1). If the number is a float between 0 and 1, we will test if the proportion of unique values is bigger than this number. For example if you have entered 0.95, the variable will be treated as continous only if more than 95% of its values are unique.

`audit`(*X*, *y=None*)

parameters:
X: {array-like, sparse matrix} of shape (n_samples, n_features)
training data
y: array-like of shape (n_samples,)
Target values
returns:
auditDict: dict()
Audits the passed values of X and y. Tells us which columns in X we think are already discrete and which need to be discretized, as well as the discretization algorithm that will be used to discretize them The parameters which are suggested will be used when creating the variables. To change this the user can manually set discretization parameters for each variable using the setDiscretizationParameters function.

`clear`(*clearDiscretizationParameters=False*)

parameters:
clearDiscretizationParamaters: bool
if True, this method also clears the parameters the user has set for each variable and resets them to the default.
returns:
void
Sets the number of continous variables and the total number of bins created by this discretizer to 0. If clearDiscretizationParameters is True, also clears the the parameters for discretization the user has set for each variable.

`createVariable`(*variableName*, *X*, *y=None*, *possibleValuesY=None*)

parameters:
variableName:
the name of the created variable
X: ndarray shape(n,1)
A column vector containing n samples of a feature. The column for which the variable will be created
y: ndarray shape(n,1)
A column vector containing the corresponding for each element in X.
possibleValuesX: onedimensional ndarray
An ndarray containing all the unique values of X
possibleValuesY: onedimensional ndarray
An ndarray containing all the unique values of y
returnModifiedX: bool
X could be modified by this function during
returns:
var: pyagrum.DiscreteVariable
the created variable
Creates a variable for the column passed in as a parameter and places it in the Bayesian network

`discretizationCAIM`(*x*, *y*, *possibleValuesX*, *possibleValuesY*)

parametres:

x: ndarray with shape (n,1) where n is the number of samples
Column-vector that contains all the data that needs to be discretized
y: ndarray with shape (n,1) where n is the number of samples
Column-vector that contains the class for each sample. This vector will not be discretized, but the class-value of each sample is needed to properly apply the algorithm
possibleValuesX: one dimensional ndarray
Contains all the possible values that x can take sorted in increasing order. There shouldn't be any doubles inside
possibleValuesY: one dimensional ndarray
Contains the possible values of y. There should be two possible values since this is a binary classifier

returns:
binEdges: a list of the edges of the bins that are chosen by this algorithm

Applies the CAIM algorithm to discretize the values of x

`discretizationElbowMethodRotation`(*discretizationStrategy*, *X*)

parameters:
discretizationStrategy: str
The method of discretization that will be used. Possible values are: 'quantile' , 'kmeans' and 'uniform'
X: one dimensional ndarray
Contains the data that should be discretized

returns:
binEdges: the edges of the bins the algorithm has chosen.

Calculates the sum of squared errors as a function of the number of clusters using the discretization strategy that is passed as a parameter. Returns the bins that are optimal for minimizing the variation and the number of bins at the same time. Uses the elbow method to find this optimal point. To find the "elbow" we rotate the curve and look for its minimum.

`discretizationMDLP`(*x*, *y*, *possibleValuesX*, *possibleValuesY*)

parametres:
x: ndarray with shape (n,1) where n is the number of samples
Column-vector that contains all the data that needs to be discretized
y: ndarray with shape (n,1) where n is the number of samples
Column-vector that contains the class for each sample. This vector will not be discretized, but the class-value of each sample is needed to properly apply the algorithm
possibleValuesX: one dimensional ndarray
Contains all the possible values that x can take sorted in increasing order. There shouldn't be any doubles inside
possibleValuesY: one dimensional ndarray
Contains the possible values of y. There should be two possible values since this is a binary classifier

returns:
binEdges: a list of the edges of the bins that are chosen by this algorithm

Uses the MDLP algorithm described in Fayyad, 1995 to discretize the values of x.

`discretizationNML`(*X*, *possibleValuesX*, *kMax=10*, *epsilon=None*)

parameters:
X: one dimensional ndarray
array that that contains all the data that needs to be discretized
possibleValuesX: one dimensional ndarray
Contains all the possible values that x can take sorted in increasing order. There shouldn't be any doubles inside.
kMax: int
the maximum number of bins before the algorithm stops itself.
epsilon: float or None
the value of epsilon used in the algorithm. Should be as small as possible. If None is passed the value is automatically calculated.

returns:

binEdges: a list of the edges of the bins that are chosen by this algorithm

Uses the disceretization algorithm described in “MDL Histogram Density Estimator”, Kontkaken and Myllymaki, 2007 to discretize.

setDiscretizationParameters(*variableName=None*, *method=None*, *numberOfBins=None*)

parameters:

variableName: str

the name of the variable you want to set the discretization paramaters of. Set to None to set the new default for this BNClassifier.

method: str

The method of discretization used for this variable. Type “NoDiscretization” if you do not want to discretize this variable. Possible values are: ‘NoDiscretization’, ‘quantile’, ‘uniform’, ‘kmeans’, ‘NML’, ‘CAIM’ and ‘MDLP’

numberOfBins:

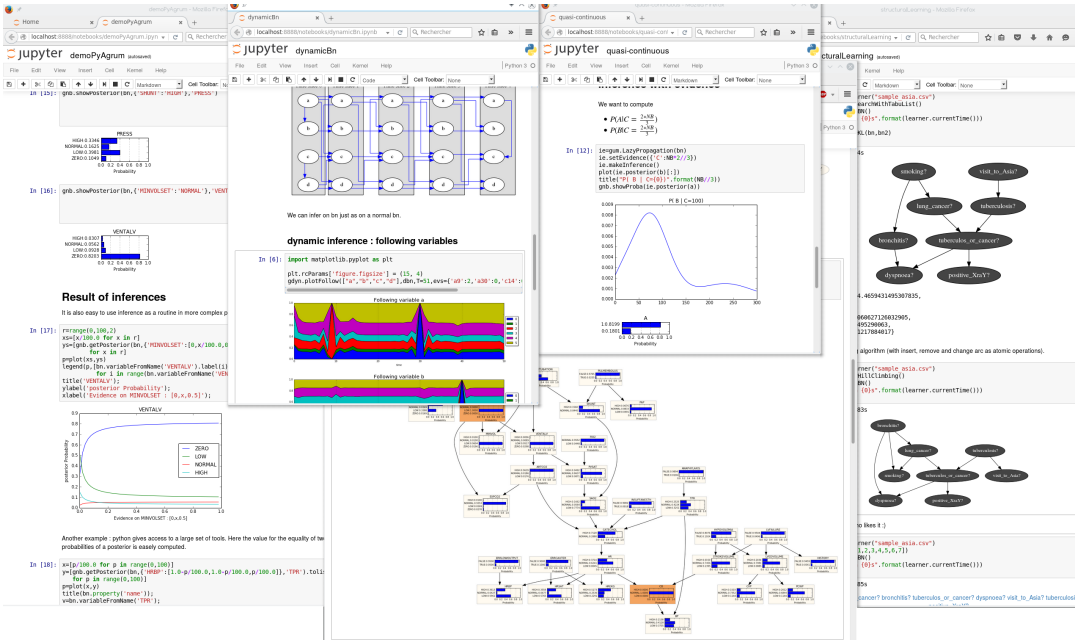
sets the number of bins if the method used is quantile, kmeans, uniform. In this case this parameter can also be set to the string ‘elbowMethod’ so that the best number of bins is found automatically. if the method used is NML, this parameter sets the the maximum number of bins up to which the NML algorithm searches for the optimal number of bins. In this case this parameter must be an int If any other discetization method is used, this parameter is ignored.

returns:

void

1.11 pyAgrum.lib.notebook

`pyAgrum.lib.notebook` aims to facilitate the use of pyAgrum with jupyter notebook (or lab).

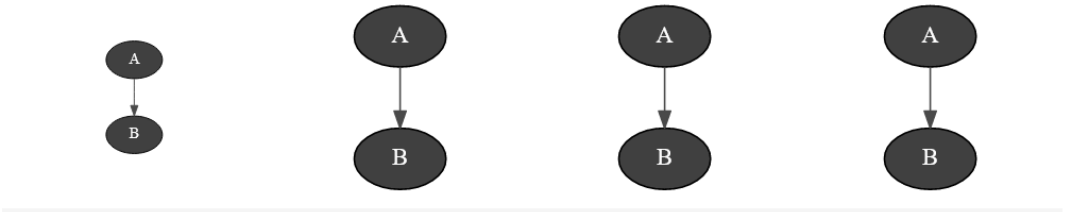


1.11.1 Visualization of graphical models

Important: For many graphical representations functions, the parameter *size* is directly transferred to *graphviz*. Hence, Its format is a string containing an int. However if *size* ends in an exclamation point "!" (such as *size="4!"*), then *size* is taken to be the desired minimum size. In this case, if both dimensions of the drawing are less than size, the drawing is scaled up uniformly until at least one dimension equals its dimension in size.

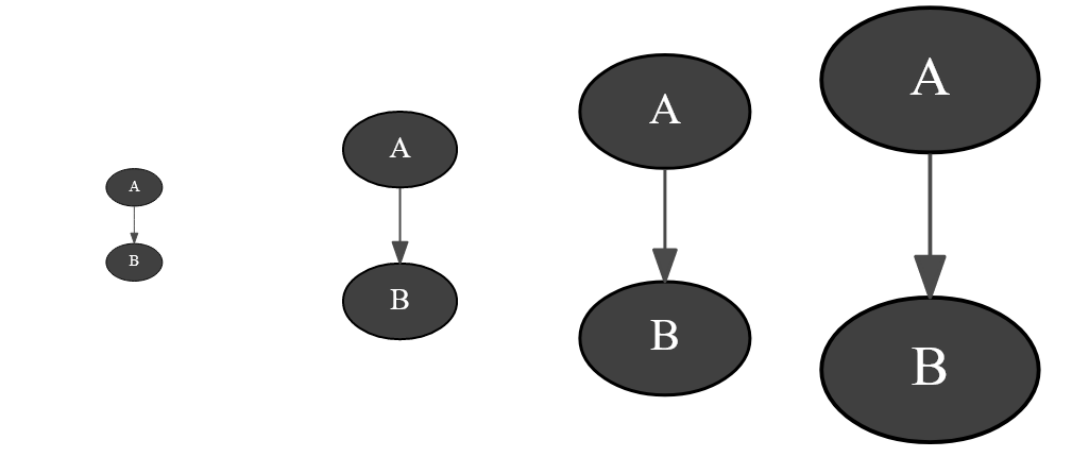
```
1 bn=gum.fastBN("A->B")
2 print("* withtout '!'")
3 gnb.sideBySide(*[gnb.getBN(bn,size=f"{i}") for i in range(1,5)],captions=[f'size="{i}"' for i in range(1,5)])
4
5 print("* witht '!'")
6 gnb.sideBySide(*[gnb.getBN(bn,size=f"{i}!") for i in range(1,5)],captions=[f'size="{i}!"' for i in range(1,5)])
```

```
* withtout '!'
```



size="1" size="2" size="3" size="4"

```
* witht '!'
```



size="1!" size="2!" size="3!" size="4!"

pyAgrum.lib.notebook.**showBN**(*bn*, *size=None*, *nodeColor=None*, *arcWidth=None*, *arcLabel=None*, *arcColor=None*, *cmap=None*, *cmapArc=None*)

show a Bayesian network

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) – the Bayesian network
- **size** (*str*) – size of the rendered graph
- **nodeColor** (*dict[Tuple(int,int),float]*) – a nodeMap of values to be shown as color nodes (with special color for 0 and 1)
- **arcWidth** (*dict[Tuple(int,int),float]*) – an arcMap of values to be shown as bold arcs
- **arcLabel** (*dict[Tuple(int,int),str]*) – an arcMap of labels to be shown next to arcs

- **arcColor** (*dict[Tuple(int,int),float]*) – an arcMap of values (between 0 and 1) to be shown as color of arcs
- **cmapNode** (*ColorMap*) – color map to show the vals of Nodes
- **cmapArc** (*ColorMap*) – color map to show the vals of Arcs
- **showMsg** (*dict*) – a nodeMap of values to be shown as tooltip

pyAgrum.lib.notebook.**getBN**(*bn*, *size=None*, *nodeColor=None*, *arcWidth=None*, *arcLabel=None*, *arcColor=None*, *cmap=None*, *cmapArc=None*)

get a HTML string for a Bayesian network

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) – the Bayesian network
- **size** (*str*) – size of the rendered graph
- **nodeColor** (*dict[Tuple(int,int),float]*) – a nodeMap of values to be shown as color nodes (with special color for 0 and 1)
- **arcWidth** (*dict[Tuple(int,int),float]*) – an arcMap of values to be shown as bold arcs
- **arcLabel** (*dict[Tuple(int,int),str]*) – an arcMap of labels to be shown next to arcs
- **arcColor** (*dict[Tuple(int,int),float]*) – an arcMap of values (between 0 and 1) to be shown as color of arcs
- **cmapNode** (*ColorMap*) – color map to show the vals of Nodes
- **cmapArc** (*ColorMap*) – color map to show the vals of Arcs
- **showMsg** (*dict*) – a nodeMap of values to be shown as tooltip

Returns
the desired representation of the Bayesian network

Return type
pydot.Dot

pyAgrum.lib.notebook.**showInfluenceDiagram**(*diag*, *size=None*)

show an influence diagram as a graph

Parameters

- **diag** – the influence diagram
- **size** – size of the rendered graph

Returns
the representation of the influence diagram

pyAgrum.lib.notebook.**getInfluenceDiagram**(*diag*, *size=None*)

get a HTML string for an influence diagram as a graph

Parameters

- **diag** – the influence diagram
- **size** – size of the rendered graph

Returns
the HTML representation of the influence diagram

pyAgrum.lib.notebook.**showMN**(*mn*, *view=None*, *size=None*, *nodeColor=None*, *factorColor=None*, *edgeWidth=None*, *edgeColor=None*, *cmap=None*, *cmapEdge=None*)

show a Markov network

Parameters

- **mn** – the markov network
- **view** – 'graph' | 'factorgraph' | None (default)
- **size** – size of the rendered graph
- **nodeColor** – a nodeMap of values (between 0 and 1) to be shown as color of nodes (with special colors for 0 and 1)
- **factorColor** – a function returning a value (beeween 0 and 1) to be shown as a color of factor. (used when view='factorgraph')
- **edgeWidth** – a edgeMap of values to be shown as width of edges (used when view='graph')
- **edgeColor** – a edgeMap of values (between 0 and 1) to be shown as color of edges (used when view='graph')
- **cmap** – color map to show the colors
- **cmapEdge** – color map to show the edge color if distinction is needed

Returns
the graph

pyAgrum.lib.notebook.**getMN**(*mn*, *view=None*, *size=None*, *nodeColor=None*, *factorColor=None*, *edgeWidth=None*, *edgeColor=None*, *cmap=None*, *cmapEdge=None*)

get an HTML string for a Markov network

Parameters

- **mn** – the markov network
- **view** – 'graph' | 'factorgraph' | None (default)
- **size** – size of the rendered graph
- **nodeColor** – a nodeMap of values (between 0 and 1) to be shown as color of nodes (with special colors for 0 and 1)
- **factorColor** – a function returning a value (beeween 0 and 1) to be shown as a color of factor. (used when view='factorgraph')
- **edgeWidth** – a edgeMap of values to be shown as width of edges (used when view='graph')
- **edgeColor** – a edgeMap of values (between 0 and 1) to be shown as color of edges (used when view='graph')
- **cmap** – color map to show the colors
- **cmapEdge** – color map to show the edge color if distinction is needed

Returns
the graph

pyAgrum.lib.notebook.**showCN**(*cn*, *size=None*, *nodeColor=None*, *arcWidth=None*, *arcLabel=None*, *arcColor=None*, *cmap=None*, *cmapArc=None*)

show a credal network

Parameters

- **cn** (pyAgrum.CredalNet (page 205)) – the Credal network
- **size** (*str*) – size of the rendered graph

- **nodeColor** (*dict[int,float]*) – a nodeMap of values to be shown as color nodes (with special color for 0 and 1)
- **arcWidth** (*dict[Tuple(int,int),float]*) – an arcMap of values to be shown as bold arcs
- **arcLabel** (*dict[Tuple(int,int),float]*) – an arcMap of labels to be shown next to arcs
- **arcColor** (*dict[Tuple(int,int),float]*) – an arcMap of values (between 0 and 1) to be shown as color of arcs
- **cmapNode** (*matplotlib.color.colormap*) – color map to show the vals of Nodes
- **cmapArc** (*matplotlib.color.colormap*) – color map to show the vals of Arcs
- **showMsg** (*dict[int,str]*) – a nodeMap of values to be shown as tooltip

Return type
the graph

pyAgrum.lib.notebook.**getCN**(*cn*, *size=None*, *nodeColor=None*, *arcWidth=None*, *arcLabel=None*, *arcColor=None*, *cmap=None*, *cmapArc=None*)

get a HTML string for a credal network

Parameters

- **cn** (pyAgrum.CredalNet (page 205)) – the Credal network
- **size** (*str*) – size of the rendered graph
- **nodeColor** (*dict[int,float]*) – a nodeMap of values to be shown as color nodes (with special color for 0 and 1)
- **arcWidth** (*dict[Tuple(int,int),float]*) – an arcMap of values to be shown as bold arcs
- **arcLabel** (*dict[Tuple(int,int),float]*) – an arcMap of labels to be shown next to arcs
- **arcColor** (*dict[Tuple(int,int),float]*) – an arcMap of values (between 0 and 1) to be shown as color of arcs
- **cmapNode** (*matplotlib.color.colormap*) – color map to show the vals of Nodes
- **cmapArc** (*matplotlib.color.colormap*) – color map to show the vals of Arcs
- **showMsg** (*dict[int,str]*) – a nodeMap of values to be shown as tooltip

Returns
the desired representation of the Credal Network

Return type
pydot.Dot

pyAgrum.lib.notebook.**showInference**(*model*, ***kwargs*)

show pydot graph for an inference in a notebook

Parameters

- **model** (*GraphicalModel*) – the model in which to infer (pyAgrum.BayesNet, pyAgrum.MarkovNet or pyAgrum.InfluenceDiagram)
- **engine** (*gum.Inference*) – inference algorithm used. If None, gum.LazyPropagation will be used for BayesNet, gum.ShaferShenoy

for gum.MarkovNet and gum.ShaferShenoyLIMIDInference for gum.InfluenceDiagram.

- **evs** (*dictionnary*) – map of evidence
- **targets** (*set*) – set of targets
- **size** (*string*) – size of the rendered graph
- **nodeColor** – a nodeMap of values (between 0 and 1) to be shown as color of nodes (with special colors for 0 and 1)
- **factorColor** – a nodeMap of values (between 0 and 1) to be shown as color of factors (in MarkovNet representation)
- **arcWidth** – a arcMap of values to be shown as width of arcs
- **arcColor** – a arcMap of values (between 0 and 1) to be shown as color of arcs
- **cmap** – color map to show the color of nodes and arcs
- **cmapArc** – color map to show the vals of Arcs.
- **graph** – only shows nodes that have their id in the graph (and not in the whole BN)
- **view** – graph | factorgraph | None (default) for Markov network

Returns
the desired representation of the inference

pyAgrum.lib.notebook.**getInference**(*model*, ***kwargs*)

get a HTML string for an inference in a notebook

Parameters

- **model** (*GraphicalModel*) – the model in which to infer (pyAgrum.BayesNet, pyAgrum.MarkovNet or pyAgrum.InfluenceDiagram)
- **engine** (*gum.Inference*) – inference algorithm used. If None, gum.LazyPropagation will be used for BayesNet, gum.ShaferShenoy for gum.MarkovNet and gum.ShaferShenoyLIMIDInference for gum.InfluenceDiagram.
- **evs** (*dictionnary*) – map of evidence
- **targets** (*set*) – set of targets
- **size** (*string*) – size of the rendered graph
- **nodeColor** – a nodeMap of values (between 0 and 1) to be shown as color of nodes (with special colors for 0 and 1)
- **factorColor** – a nodeMap of values (between 0 and 1) to be shown as color of factors (in MarkovNet representation)
- **arcWidth** – a arcMap of values to be shown as width of arcs
- **arcColor** – a arcMap of values (between 0 and 1) to be shown as color of arcs
- **cmap** – color map to show the color of nodes and arcs
- **cmapArc** – color map to show the vals of Arcs.
- **graph** – only shows nodes that have their id in the graph (and not in the whole BN)
- **view** – graph | factorgraph | None (default) for Markov network

Returns
the desired representation of the inference

pyAgrum.lib.notebook.**showJunctionTree**(*bn*, *withNames=True*, *size=None*)

Show a junction tree of a Bayesian network

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) – the model
- **withNames** (*bool*) – names or id in the graph (names can created very large nodes)
- **size** (*float|str*) – size of the rendered graph

pyAgrum.lib.notebook.**getJunctionTree**(*bn*, *withNames=True*, *size=None*)

get a HTML string for a junction tree (more specifically a join tree)

Parameters

- **bn** – the Bayesian network
- **withNames** (*boolean*) – display the variable names or the node id in the clique
- **size** – size of the rendered graph

Returns

the HTML representation of the graph

1.11.2 Visualization of Potentials

pyAgrum.lib.notebook.**showProba**(*p*, *scale=1.0*)

Show a mono-dim Potential (a marginal)

Parameters

- **p** (pyAgrum.Potential (page 53)) – the marginal to show
- **scale** (*float*) – the zoom factor

pyAgrum.lib.notebook.**getPosterior**(*bn*, *evs*, *target*)

shortcut for proba2histo(gum.getPosterior(bn,evs,target))

Parameters

- **bn** (*gum.BayesNet*) – the BayesNet
- **evs** (*dict(str->int)*) – map of evidence
- **target** (*str*) – name of target variable

Returns

the matplotlib graph

pyAgrum.lib.notebook.**showPosterior**(*bn*, *evs*, *target*)

shortcut for showProba(gum.getPosterior(bn,evs,target))

Parameters

- **bn** – the BayesNet
- **evs** – map of evidence
- **target** – name of target variable

pyAgrum.lib.notebook.**getPotential**(*pot*, *digits=None*, *withColors=None*, *varnames=None*)

return a HTML string of a gum.Potential as a HTML table. The first dimension is special (horizontal) due to the representation of conditional probability table

Parameters

- **pot** (*gum.Potential*) – the potential to show

- **digits** (*int*) – number of digits to show
- **withColors** (*bool*) – bgcolor for proba cells or not
- **varnames** (*List[str]*) – the aliases for variables name in the table

Returns
the html representation of the Potential (as a string)

Return type
str

pyAgrum.lib.notebook.**showPotential**(*pot*, *digits=None*, *withColors=None*, *varnames=None*)

show a gum.Potential as a HTML table. The first dimension is special (horizontal) due to the representation of conditional probability table

Parameters

- **pot** (*gum.Potential*) – the potential to show
- **digits** (*int*) – number of digits to show
- **withColors** (*bool*) – bgcolor for proba cells or not
- **varnames** (*List[str]*) – the aliases for variables name in the table

1.11.3 Visualization of graphs

pyAgrum.lib.notebook.**getDot**(*dotstring*, *size=None*)

get an HTML representation of a dot string

Parameters

- **dotstring** (*str*) – the dot string
- **size** (*float|str*) – size of the rendered graph

Return type
the HTML representation of the dot string

pyAgrum.lib.notebook.**showDot**(*dotstring*, *size=None*)

show a dot string as a graph

Parameters

- **dotstring** (*str*) – the dot string
- **size** (*float|str*) – size of the rendered graph

pyAgrum.lib.notebook.**getGraph**(*gr*, *size=None*)

get an HTML representation of a pydot graph

Parameters

- **gr** (*pydot.Dot*) – the graph
- **size** (*float|str*) – the size of the rendered graph

Return type
the HTML representation of the graph (as a string)

pyAgrum.lib.notebook.**showGraph**(*gr*, *size=None*)

show a pydot graph in a notebook

Parameters

- **gr** (*pydot.Dot*) – the graph
- **size** (*float|str*) – the size of the rendered graph

1.11.4 Visualization of approximation algorithm

pyAgrum.lib.notebook.**animApproximationScheme**(*apsc*, *scale=<ufunc 'log10'>*)

show an animated version of an approximation algorithm

Parameters

- **apsc** – the approximation algorithm
- **scale** – a function to apply to the figure

1.11.5 Helpers

pyAgrum.lib.notebook.**configuration**()

Display the collection of dependance and versions

pyAgrum.lib.notebook.**sideBySide**(**args*, ***kwargs*)

display side by side args as HMTL fragment (using string, _repr_html_() or str())

Parameters

- **args** – HMTL fragments as string arg, arg._repr_html_() or str(arg)
- **captions** – list of strings (captions)

1.12 pyAgrum.lib.image

pyAgrum.lib.image aims to graphically export models and inference using pydot (https://pypi.org/project/pydot/) (and then graphviz (https://graphviz.org/)).

For more details, see *this notebook* (page 486).

```
import pyAgrum as gum
from pyAgrum.lib.image as gumimage

bn = gum.fastBN("a->b->d;a->c->d[3]->e;f->b")
gumimage.export(bn,"out/test_export.png",
                nodeColor={'a': 1,
                           'b': 0.3,
                           'c': 0.4,
                           'd': 0.1,
                           'e': 0.2,
                           'f': 0.5},
                arcColor={(0, 1): 0.2,
                          (1, 2): 0.5},
                arcWidth={(0, 3): 0.4,
                          (3, 2): 0.5,
                          (2,4) :0.6})
```

1.12.1 Visualization of models and inference

pyAgrum.lib.image.**export**(*model*, *filename=None*, ***kwargs*)

export the graphical representation of the model in filename (png, pdf,etc.)

Parameters

- **model** (*pyAgrum.GraphicalModel*) – the model to show (pyAgrum.BayesNet, pyAgrum.MarkovNet, pyAgrum.InfluenceDiagram or pyAgrum.Potential)
- **filename** (*str*) – the name of the resulting file (suffix in ['pdf', 'png', 'fig', 'jpg', 'svg', 'ps']). If filename is None, the result is a np.array ready to be used with imshow().

Note: Model can also just possess a method *toDot()* or even be a simple string in dot syntax.

---

pyAgrum.lib.image.**exportInference**(*model*, *filename=None*, ***kwargs*)

the graphical representation of an inference in a notebook

Parameters

- **model** (*pyAgrum:GraphicalModel*) – the model in which to infer (pyAgrum.BayesNet, pyAgrum.MarkovNet or pyAgrum.InfluenceDiagram)
- **filename** (*str*) – the name of the resulting file (suffix in ['pdf', 'png', 'ps']). If filename is None, the result is a np.array ready to be used with imshow().
- **engine** (*pyAgrum.Inference*) – inference algorithm used. If None, gum.LazyPropagation will be used for BayesNet,gum.ShaferShenoy for gum.MarkovNet and gum.ShaferShenoyLIMIDInference for gum.InfluenceDiagram.
- **evs** (*Dict[str,str|int]*) – map of evidence
- **targets** (*Set[str|int]*) – set of targets
- **size** (*str*) – size of the rendered graph
- **nodeColor** (*Dict[int,float]*) – a nodeMap of values (between 0 and 1) to be shown as color of nodes (with special colors for 0 and 1)
- **factorColor** (*Dict[int,float]*) – a nodeMap of values (between 0 and 1) to be shown as color of factors (in MarkovNet representation)
- **arcWidth** (*Dict[(int,int),float]*) – a arcMap of values to be shown as width of arcs
- **arcColor** (*Dict[(int,int),float]*) – a arcMap of values (between 0 and 1) to be shown as color of arcs
- **cmap** (*matplotlib.colors.ColorMap*) – color map to show the color of nodes and arcs
- **cmapArc** (*matplotlib.colors.ColorMap*) – color map to show the vals of Arcs.
- **graph** (*pyAgrum.Graph*) – only shows nodes that have their id in the graph (and not in the whole BN)
- **view** (*str*) – graph | factorgraph | None (default) for Markov network

Returns
the desired representation of the inference

Return type
str|dot.Dot

1.13 pyAgrum.lib.explain

The purpose of `pyAgrum.lib.explain` is to give tools to explain and interpret the structure and parameters of a Bayesian network.

1.13.1 Dealing with independence

`pyAgrum.lib.explain.`**`independenceListForPairs`**(*bn*, *filename*, *target=None*, *plot=True*, *alphabetic=False*)

get the p-values of the chi2 test of a (as simple as possible) independence proposition for every non arc.

Parameters

- **bn** (*gum.BayesNet*) – the Bayesian network
- **filename** (*str*) – the name of the csv database
- **alphabetic** (*bool*) – if True, the list is alphabetically sorted else it is sorted by the p-value
- **target** (*(optional) str or int*) – the name or id of the target variable
- **plot** (*bool*) – if True, plot the result

Return type
the list

1.13.2 Dealing with mutual information and entropy

`pyAgrum.lib.explain.`**`getInformation`**(*bn*, *evs=None*, *size=None*, *cmap=<matplotlib.colors.LinearSegmentedColormap object>*)

get a HTML string for a bn annotated with results from inference : entropy and mutual information

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) – the model
- **evs** (*Dict[str|int,str|int|List[float]]*) – the observations
- **size** (*int|str*) – size of the rendered graph
- **cmap** (*matplotlib.colours.Colormap*) – the cmap

Returns
return the HTML string

Return type
str

`pyAgrum.lib.explain.`**`showInformation`**(*bn*, *evs=None*, *size=None*, *cmap=<matplotlib.colors.LinearSegmentedColormap object>*)

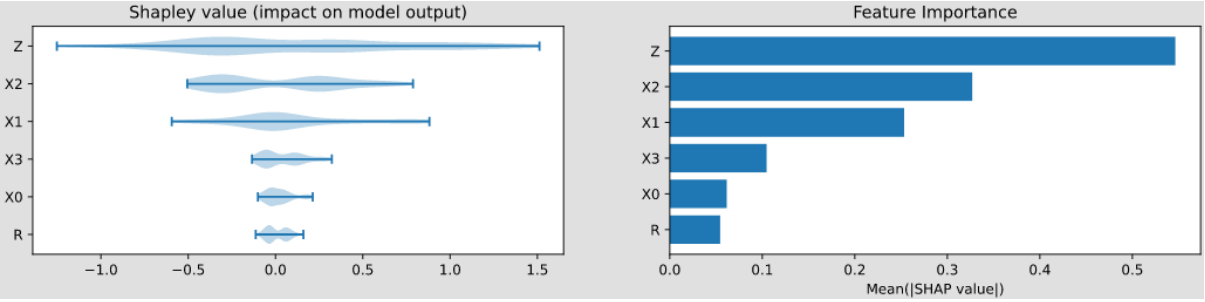
diplay a bn annotated with results from inference : entropy and mutual information

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) – the model
- **evs** (*Dict[str|int,str|int|List[float]]*) – the observations
- **size** (*int|str*) – size of the rendered graph

- **cmap** (*matplotlib.colours.Colormap*) – the cmap

1.13.3 Dealing with ShapValues



class pyAgrum.lib.explain.**ShapValues**(*bn*, *target*)

Bases: object

The ShapValue class implements the calculation of Shap values in Bayesian networks.

The main implementation is based on Conditional Shap values[3], but the Interventional calculation method proposed in[2] is also present. In addition, a new causal method, based on[1], is implemented which is well suited for Bayesian networks.

causal(*train*, *plot=False*, *plot_importance=False*, *percentage=False*)

Compute the causal Shap Values for each variables.

Parameters

- **train** (*pandas.DataFrame*) – the database
- **plot** (*bool*) – if True, plot the violin graph of the shap values
- **plot_importance** (*bool*) – if True, plot the importance plot
- **percentage** (*bool*) – if True, the importance plot is shown in percent.

Return type

a dictionary Dict[str,float]

conditional(*train*, *plot=False*, *plot_importance=False*, *percentage=False*)

Compute the conditional Shap Values for each variables.

Parameters

- **train** (*pandas.DataFrame*) – the database
- **plot** (*bool*) – if True, plot the violin graph of the shap values
- **plot_importance** (*bool*) – if True, plot the importance plot
- **percentage** (*bool*) – if True, the importance plot is shown in percent.

Return type

a dictionary Dict[str,float]

marginal(*train*, *sample_size=200*, *plot=False*, *plot_importance=False*, *percentage=False*)

Compute the marginal Shap Values for each variables.

Parameters

- **train** (*pandas.DataFrame*) – the database
- **sample_size** (*int*) – The computation of marginal ShapValue is very slow. The parameter allow to compute only on a fragment of the database.
- **plot** (*bool*) – if True, plot the violin graph of the shap values
- **plot_importance** (*bool*) – if True, plot the importance plot
- **percentage** (*bool*) – if True, the importance plot is shown in percent.

[3] Lundberg, S. M., & Su-In, L. (2017). A Unified Approach to Interpreting Model. 31st Conference on Neural Information Processing Systems. Long Beach, CA, USA.

[2] Janzing, D., Minorics, L., & Blöbaum, P. (2019). Feature relevance quantification in explainable AI: A causality problem. arXiv: Machine Learning. Retrieved 6 24, 2021, from https://arxiv.org/abs/1910.13413

[1] Heskes, T., Sijben, E., Bucur, I., & Claassen, T. (2020). Causal Shapley Values: Exploiting Causal Knowledge. 34th Conference on Neural Information Processing Systems. Vancouver, Canada.

Return type
a dictionary Dict[str,float]

showShapValues(*results*, *cmap='plasma'*)

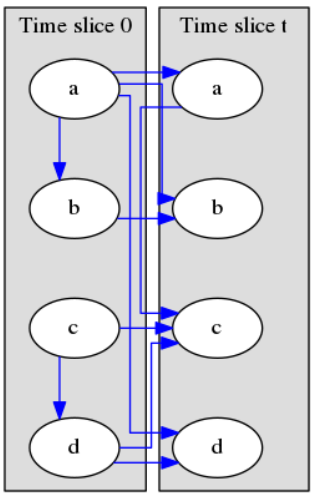
Parameters
- **results** (*dict[str,float]*) – The (Shap) values associates to each variable
- **cmap** (*Matplotlib.ColorMap*) – The colormap used for colouring the nodes

Return type
a pydot.graph

1.14 pyAgrum.lib.dynamicBN

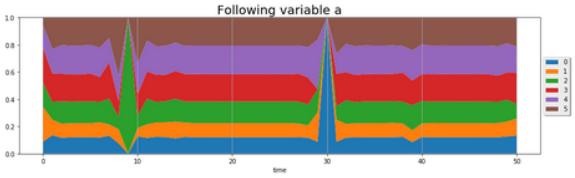
dynamic Bayesian Network are a special class of BNs where variables can be subscripted by a (discrete) time. See *this notebook* (page 369).

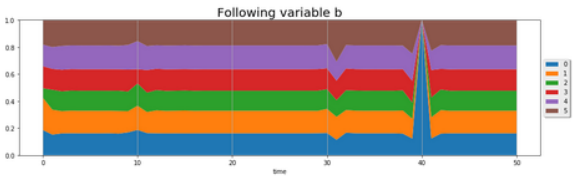
```
gdyn.showTimeSlices(dbn,format="png")
```

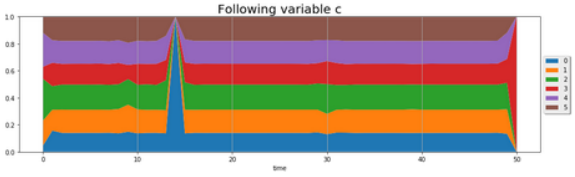


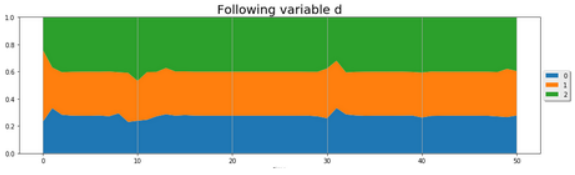

```
import matplotlib.pyplot as plt

plt.rcParams['figure.figsize'] = (15, 4)
gdyn.plotFollow(["a","b","c","d"],dbn,T=51,evs={'a9':2,'a30':0,'c14':0,'b40':0,'c50':3})
```



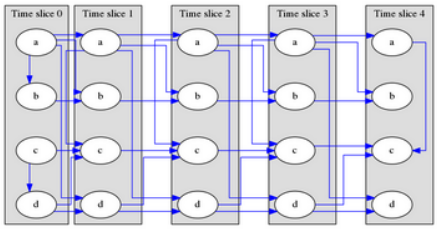







```
T=5

bn=gdyn.unroll2TBN(dbn,T)
gdyn.showTimeSlices(bn,size="10")
```



The purpose of this module is to provide basic tools for dealing with dynamic Bayesian Network (and inference) : modeling, visualisation, inference.

pyAgrum.lib.dynamicBN.**getTimeSlices**(*dbn*, *size=None*)

Try to correctly represent dBN and 2TBN as an HTML string

Parameters
- **dbn** (pyAgrum.BayesNet (page 64)) – a 2TBN or an unrolled BN
- **size** (*int or str*) – size of the fig

pyAgrum.lib.dynamicBN.**getTimeSlicesRange**(*dbn*)

get the range and (name,radical) of each variables

Parameters
dbn (*gum.BayesNet*) – a 2TBN or an unrolled BN

Returns
all the timeslice of a dbn : ['0','t'] for a classic 2TBN, range(T) for a classic unrolled BN

Return type
Dict[str,List[T[str,str]]]

pyAgrum.lib.dynamicBN.**is2TBN**(*bn*)

Check if bn is a 2 TimeSlice Bayesian network

Parameters
bn (pyAgrum.BayesNet (page 64)) – the Bayesian network

Returns
True if the BN is syntaxically correct to be a 2TBN

Return type
bool

pyAgrum.lib.dynamicBN.**plotFollow**(*lovars*, *twoTdbn*, *T*, *evs*)

plots modifications of variables in a 2TDN knowing the size of the time window (T) and the evidence on the sequence.

Parameters

- **lovars** – list of variables to follow
- **twoTdbn** – the two-timeslice dbn
- **T** – the time range
- **evs** – observations

pyAgrum.lib.dynamicBN.**plotFollowUnrolled**(*lovars*, *dbn*, *T*, *evs*, *vars_title=None*)

plot the dynamic evolution of a list of vars with a dBN

Parameters

- **lovars** – list of variables to follow
- **dbn** – the unrolled dbn
- **T** – the time range
- **evs** – observations
- **vars_title** – string for default or a dictionary with the variable name as key and the respective title as value.

pyAgrum.lib.dynamicBN.**realNameFrom2TBNname**(*name*, *ts*)

@return dynamic name from static name and timeslice (no check)

pyAgrum.lib.dynamicBN.**showTimeSlices**(*dbn*, *size=None*)

Try to correctly display dBN and 2TBN

Parameters

- **dbn** (pyAgrum.BayesNet (page 64)) – a 2TBN or an unrolled BN
- **size** (*int or str*) – size of the fig

pyAgrum.lib.dynamicBN.**unroll2TBN**(*dbn*, *nbr*)

unroll a 2TBN given the nbr of timeslices

Parameters

- **dbn** (pyAgrum.BayesNet (page 64)) – a 2TBN or an unrolled BN

- **nbr** (*int*) – the number of timeslice

Returns
unrolled BN from a 2TBN and the nbr of timeslices

Return type
pyAgrum.BayesNet (page 64)

1.15 other pyAgrum.lib modules

1.15.1 bn2roc

The purpose of this module is to provide tools for building ROC and PR from Bayesian Network.

pyAgrum.lib.bn2roc.**showPR**(*bn*, *csv_name*, *target*, *label*, *show_progress=True*, *show_fig=True*, *save_fig=False*, *with_labels=True*, *significant_digits=10*)

Compute the ROC curve and save the result in the folder of the csv file.

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) – a Bayesian network
- **csv_name** (*str*) – a csv filename
- **target** (*str*) – the target
- **label** (*str*) – the target label
- **show_progress** (*bool*) – indicates if the progress bar must be printed
- **save_fig** – save the result ?
- **show_fig** – plot the resuls ?
- **with_labels** – labels in csv ?
- **significant_digits** – number of significant digits when computing probabilities

pyAgrum.lib.bn2roc.**showROC**(*bn*, *csv_name*, *target*, *label*, *show_progress=True*, *show_fig=True*, *save_fig=False*, *with_labels=True*, *significant_digits=10*)

Compute the ROC curve and save the result in the folder of the csv file.

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) – a Bayesian network
- **csv_name** (*str*) – a csv filename
- **target** (*str*) – the target
- **label** (*str*) – the target label
- **show_progress** (*bool*) – indicates if the progress bar must be printed
- **save_fig** – save the result
- **show_fig** – plot the resuls
- **with_labels** – labels in csv
- **significant_digits** – number of significant digits when computing probabilities

pyAgrum.lib.bn2roc.**showROC_PR**(*bn*, *csv_name*, *target*, *label*, *show_progress=True*, *show_fig=True*, *save_fig=False*, *with_labels=True*, *show_ROC=True*, *show_PR=True*, *significant_digits=10*)

Compute the ROC curve and save the result in the folder of the csv file.

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) – a Bayesian network
- **csv_name** (*str*) – a csv filename
- **target** (*str*) – the target
- **label** (*str*) – the target label
- **show_progress** (*bool*) – indicates if the progress bar must be printed
- **save_fig** – save the result
- **show_fig** – plot the resuls
- **with_labels** – labels in csv
- **show_ROC** (*bool*) – whether we show the ROC figure
- **show_PR** (*bool*) – whether we show the PR figure
- **significant_digits** – number of significant digits when computing probabilitie

Returns
(pointsROC, thresholdROC, pointsPR, thresholdPR)

Return type
tuple

1.15.2 bn2scores

The purpose of this module is to provide tools for computing different scores from a BN.

pyAgrum.lib.bn2scores.**checkCompatibility**(*bn*, *fields*, *csv_name*)

check if the variables of the bn are in the fields

Parameters

- **bn** (*gum.BayesNet*) – the model
- **fields** (*Dict[str,int]*) – Dict of name,position in the file
- **csv_name** (*str*) – name of the csv file

Raises
gum.DatabaseError – if a BN variable is not in fields

Returns
return a dictionary of position for BN variables in fields

Return type
Dict[int,str]

pyAgrum.lib.bn2scores.**computeScores**(*bn_name*, *csv_name*, *visible=False*)

Compute scores (likelihood, aic, bic, mdl, etc.) from a bn w.r.t to a csv

Parameters

- **bn_name** (pyAgrum.BayesNet (page 64) | *str*) – a gum.BayesianNetwork or a filename for a BN
- **csv_name** (*str*) – a filename for the CSV database

- **visible** (*bool*) – do we show the progress

Returns
percentDatabaseUsed,scores

Return type
Tuple[float,Dict[str,float]]

pyAgrum.lib.bn2scores.**lines_count**(*filename*)

count lines in a file

1.15.3 bn_vs_bn

The purpose of this module is to provide tools for comaring different BNs.

class pyAgrum.lib.bn_vs_bn.**GraphicalBNComparator**(*name1*, *name2*, *delta=1e-06*)

Bases: object

BNGraphicalComparator allows to compare in multiple way 2 BNs...The smallest assumption is that the names of the variables are the same in the 2 BNs. But some comparisons will have also to check the type and domainSize of the variables. The bns have not exactly the same role : _bn1 is rather the referent model for the comparison whereas _bn2 is the compared one to the referent model.

Parameters

- **name1** (*str or* pyAgrum.BayesNet (page 64)) – a BN or a filename for reference
- **name2** (*str or* pyAgrum.BayesNet (page 64)) – another BN or antoher filename for comparison

dotDiff()

Return a pydot graph that compares the arcs of _bn1 (reference) with those of self._bn2. full black line: the arc is common for both full red line: the arc is common but inverted in _bn2 dotted black line: the arc is added in _bn2 dotted red line: the arc is removed in _bn2

> **Warning:** if pydot is not installed, this function just returns None

Returns
the result dot graph or None if pydot can not be imported

Return type
pydot.Dot

equivalentBNs()

Check if the 2 BNs are equivalent :

- same variables
- same graphical structure
- same parameters

Returns
"OK" if bn are the same, a description of the error otherwise

Return type
str

hamming()

Compute hamming and structural hamming distance

Hamming distance is the difference of edges comparing the 2 skeletons, and Structural Hamming difference is the difference comparing the cpdags, including the arcs' orientation.

Returns
A dictionnary containing 'hamming','structural hamming'

Return type
dict[double,double]

`scores()`

Compute Precision, Recall, F-score for self._bn2 compared to self._bn1

precision and recall are computed considering BN1 as the reference

Fscor is 2*(recall* precision)/(recall+precision) and is the weighted average of Precision and Recall.

dist2opt=square root of (1-precision)^2+(1-recall)^2 and represents the euclidian distance to the ideal point (precision=1, recall=1)

Returns
A dictionnary containing 'precision', 'recall', 'fscore', 'dist2opt' and so on.

Return type
dict[str,double]

`skeletonScores()`

Compute Precision, Recall, F-score for skeletons of self._bn2 compared to self._bn1

precision and recall are computed considering BN1 as the reference

Fscor is 2*(recall* precision)/(recall+precision) and is the weighted average of Precision and Recall.

dist2opt=square root of (1-precision)^2+(1-recall)^2 and represents the euclidian distance to the ideal point (precision=1, recall=1)

Returns
A dictionnary containing 'precision', 'recall', 'fscore', 'dist2opt' and so on.

Return type
dict[str,double]

`pyAgrum.lib.bn_vs_bn.graphDiff(`*bnref*, *bncmp*, *noStyle=False*`)`

Return a pydot graph that compares the arcs of bnref to bncmp. graphDiff allows bncmp to have less nodes than bnref. (this is not the case in GraphicalBNComparator.dotDiff())

if noStyle is False use 4 styles (fixed in pyAgrum.config) :

- the arc is common for both
- the arc is common but inverted in _bn2
- the arc is added in _bn2
- the arc is removed in _bn2

See graphDiffLegend() to add a legend to the graph. .. warning:: if pydot is not installed, this function just returns None

Returns
the result dot graph or None if pydot can not be imported

Return type
pydot.Dot

`pyAgrum.lib.bn_vs_bn.graphDiffLegend()`

1.16 Functions from pyAgrum

1.16.1 Useful functions in pyAgrum

pyAgrum.**about**()

about() for pyAgrum

pyAgrum.**getPosterior**(*model*, *evs*, *target*)

Compute the posterior of a single target (variable) in a BN given evidence

getPosterior uses a VariableElimination inference. If more than one target is needed with the same set of evidence or if the same target is needed with more than one set of evidence, this function is not relevant since it creates a new inference engine every time it is called.

Parameters

- **bn** (pyAgrum.BayesNet (page 64) *or* pyAgrum.MarkovNet (page 218)) – The probabilistic Graphical Model
- **evs** (*dictionaryDict*) – {name|id:val, name|id : [val1, val2], ... }
- **target** (*string or int*) – variable name or id

Return type
posterior (*pyAgrum.Potential* (page 53) or other)

pyAgrum.**generateSample**(*bn*, *n=1*, *name_out=None*, *show_progress=False*, *with_labels=True*, *random_order=True*)

generate a CSV file of samples from a bn.

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) – the Bayes Net from which the sample is generated
- **n** (*int*) – the number of samples
- **name_out** (*str*) – the name for the output csv filename. If name_out is None, a pandas.DataFrame is generated
- **show_progress** (*bool*) – if True, show a progress bar. Default is False
- **with_labels** (*bool*) – if True, use the labels of the modalities of variables in the csv. If False, use their ids. Default is True
- **random_order** (*bool*) – if True, the columns in the csv are randomized sorted. Default is True

Returns
the log2-likelihood of the generated base or if name_out is None, the couple (generated pandas.DataFrame,log2-likelihood)

Return type
float|Tuple[pandas.DataFrame,float]

pyAgrum.**generateCSV**(*bn*, *name_out*, *n=1*, *show_progress=False*, *with_labels=False*, *random_order=True*)

Deprecated. Please use *pyAgrum.generateSample* instead.

1.16.2 Quick specification of (randomly parameterized) graphical models

aGrUM/pyAgrum offers a so-called "fact" syntax that allows to quickly and compactly specify prototypes of graphical models. These *fastPrototype* aGrUM's methods have also been wrapped in functions of pyAgrum.

```
gum.fastBN("A[10]->B<-C{top|middle|bottom};B->D")
```

The type of the random variables can be specifiy with different syntaxes:

- by default, a variable is a *pyAgrum.RangeVariable* (page 39) using the default domain size (second argument of the functions).
- with `a[10]`, the variable is a *pyAgrum.RangeVariable* (page 39) using 10 as domain size (from 0 to 9)
- with `a[3,7]`, the variable is a *pyAgrum.RangeVariable* (page 39) using a domainSize from 3 to 7
- with `a[1,3.14,5,6.2]`, the variable is a *pyAgrum.DiscretizedVariable* (page 31) using the given ticks (at least 3 values)
- with `a{top|middle|bottom}`, the variable is a *pyAgrum.LabelizedVariable* (page 27) using the given labels (here : 'top', 'middle' and 'bottom').
- with `a{-1|5|0|3}`, the variable is a *pyAgrum.IntegerVariable* (page 35) using the sorted given values.
- with 'a{-0.5|5.01|0|3.1415}', the variable is a *pyAgrum.NumericalDiscreteVariable* (page 42) using the sorted given values.

Note:

- If the dot-like string contains such a specification more than once for a variable, the first specification will be used.
- the CPTs are randomly generated.

---

pyAgrum.**fastBN**(*structure*, *domain_size=2*)

Create a Bayesian network with a dot-like syntax which specifies:

- the structure 'a->b->c;b->d<-e;',
- the type of the variables with different syntax (cf documentation).

Examples

```
>>> import pyAgrum as gum
>>> bn=gum.fastBN('A->B[1,3]<-C{yes|No}->D[2,4]<-E[1,2.5,3.9]',6)
```

Parameters

- **structure** (*str*) – the string containing the specification
- **domain_size** (*int*) – the default domain size for variables

Returns
the resulting bayesian network

Return type
pyAgrum.BayesNet (page 64)

pyAgrum.**fastMN**(*structure*, *domain_size=2*)

Create a Markov network with a modified dot-like syntax which specifies:

- the structure 'a-b-c;b-d;c-e;' where each chain 'a-b-c' specifies a factor,
- the type of the variables with different syntax (cf documentation).

Examples

```
>>> import pyAgrum as gum
>>> bn=gum.fastMN('A--B[1,3]--C{yes|No};C--D[2,4]--E[1,2.5,3.9]',6)
```

Parameters

- **structure** (*str*) – the string containing the specification
- **domain_size** (*int*) – the default domain size for variables

Returns
the resulting Markov network

Return type
pyAgrum.MarkovNet (page 218)

pyAgrum.**fastID**(*structure*, *domain_size=2*)

Create an Influence Diagram with a modified dot-like syntax which specifies:

- the structure and the type of the variables following *fast syntax* (page 281),
- a prefix for the type of node (chance/decision/utiliy nodes):
  - `a` : a chance node named 'a' (by default)
  - `$a` : a utility node named 'a'
  - `*a` : a decision node named 'a'

Examples

```
>>> import pyAgrum as gum
>>> bn=gum.fastID('A->B[1,3]<-*C{yes|No}->$D<-E[1,2.5,3.9]',6)
```

Parameters

- **structure** (*str*) – the string containing the specification
- **domain_size** (*int*) – the default domain size for variables

Returns
the resulting Influence Diagram

Return type
pyAgrum.InfluenceDiagram (page 191)

1.16.3 Input/Output for Bayesian networks

pyAgrum.**availableBNExts**()

Give the list of all formats known by pyAgrum to save a Bayesian network.

Returns
a string which lists all suffixes for supported BN file formats.

pyAgrum.**loadBN**(*filename*, *listeners=None*, *verbose=False*, ***opts*)

load a BN from a file with optional listeners and arguments

Parameters

- **filename** (*str*) – the name of the input file
- **listeners** (*List[object]*) – list of functions to execute when listening
- **verbose** (*bool*) – whether to print or not warning messages
- **system** (*str*) – (for O3PRM) name of the system to flatten in a BN
- **classpath** (*List[str]*) – (for O3PRM) list of folders containing classes

Returns
a BN from a file using one of the availableBNExts() suffixes.

Return type
pyAgrum.BayesNet (page 64)

Notes

Listeners could be added in order to monitor its loading.

Examples

```
>>> import pyAgrum as gum
>>>
>>> # creating listeners
>>> def foo_listener(progress):
>>>     if progress==200:
>>>         print(' BN loaded ')
>>>         return
>>>     elif progress==100:
>>>         car='%'
>>>     elif progress%10==0:
>>>         car='#'
>>>     else:
>>>         car='.'
>>>     print(car,end='',flush=True)
>>>
>>> def bar_listener(progress):
>>>     if progress==50:
>>>         print('50%')
>>>
>>> # loadBN with list of listeners
>>> gum.loadBN('./bn.bif',listeners=[foo_listener,bar_listener])
>>> # .........#.........#.........#.........#..50%
>>> # .......#.........#.........#.........#.........#.........% | bn␣
↪loaded
```

pyAgrum.**saveBN**(*bn*, *filename*, *allowModificationWhenSaving=None*)

save a BN into a file using the format corresponding to one of the availableWriteBNExts() suffixes.

Parameters

- **bn** (pyAgrum.BayesNet (page 64)) – the BN to save
- **filename** (*str*) – the name of the output file
- **allowModificationWhenSaving** (*bool*) – whether syntax errors in the BN should throw a FatalError or can be corrected. Also controlled by *pyAgrum.config["BN","allow_modification_when_saving"]*.

1.16.4 Input/Output for Markov networks

pyAgrum.**availableMNExts**()

Give the list of all formats known by pyAgrum to save a Markov network.

Returns

a string which lists all suffixes for supported MN file formats.

Return type

str

pyAgrum.**loadMN**(*filename*, *listeners=None*, *verbose=False*)

load a MN from a file with optional listeners and arguments

Parameters

- **filename** (*str*) – the name of the input file
- **listeners** (*List[Object]*) – list of functions to execute
- **verbose** (*bool*) – whether to print or not warning messages

Returns

- *pyAgrum.MarkovNet* – a MN from a file using one of the availableMNExts() suffixes.
- *Listeners could be added in order to monitor its loading.*

Examples

```
>>> import pyAgrum as gum
>>>
>>> # creating listeners
>>> def foo_listener(progress):
>>>     if progress==200:
>>>         print(' BN loaded ')
>>>         return
>>>     elif progress==100:
>>>         car='%'
>>>     elif progress%10==0:
>>>         car='#'
>>>     else:
>>>         car='.'
>>>     print(car,end='',flush=True)
>>>
>>> def bar_listener(progress):
>>>     if progress==50:
```

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```
>>>         print('50%')
>>>
>>> # loadBN with list of listeners
>>> gum.loadMN('./bn.uai',listeners=[foo_listener,bar_listener])
>>> # .........#.........#.........#.........#..50%
>>> # .......#.........#.........#.........#.........#.........% | bn␣
↪loaded
```

pyAgrum.**saveMN**(*mn*, *filename*)

save a MN into a file using the format corresponding to one of the availableWriteMNExts() suffixes.

Parameters

- **mn** (pyAgrum.MarkovNet (page 218)) – the MN to save
- **filename** (*str*) – the name of the output file

1.16.5 Input for influence diagram

pyAgrum.**availableIDExts**()

Give the list of all formats known by pyAgrum to save a influence diagram.

Returns
a string which lists all suffixes for supported ID file formats.

Return type
str

pyAgrum.**loadID**(*filename*)

read a gum.InfluenceDiagram from a ID file

Parameters
filename (*str*) – the name of the input file

Returns
the InfluenceDiagram

Return type
pyAgrum.InfluenceDiagram (page 191)

pyAgrum.**saveID**(*infdiag*, *filename*)

save an ID into a file using the format corresponding to one of the availableWriteIDExts() suffixes.

Parameters

- **infdiag** (pyAgrum.InfluenceDiagram (page 191)) – the Influence Diagram to save
- **filename** (*str*) – the name of the output file

1.17 Other functions from aGrUM

1.17.1 Listeners

aGrUM includes a mechanism for listening to actions (close to QT signal/slot). Some of them have been ported to pyAgrum :

LoadListener

Listeners could be added in order to monitor the progress when loading a pyAgrum.BayesNet

```
>>> import pyAgrum as gum
>>>
>>> # creating a new liseners
>>> def foo(progress):
>>>     if progress==200:
>>>         print(' BN loaded ')
>>>         return
>>>     elif progress==100:
>>>         car='%'
>>>     elif progress%10==0:
>>>         car='#'
>>>     else:
>>>         car='.'
>>>     print(car,end='',flush=True)
>>>
>>> def bar(progress):
>>>     if progress==50:
>>>         print('50%')
>>>
>>>
>>> gum.loadBN('./bn.bif',listeners=[foo,bar])
>>> # .........#.........#.........#.........#..50%
>>> # .......#.........#.........#.........#.........#.........% | bn loaded
```

StructuralListener

Listeners could also be added when structural modification are made in a pyAgrum.BayesNet:

```
>>> import pyAgrum as gum
>>>
>>> ## creating a BayesNet
>>> bn=gum.BayesNet()
>>>
>>> ## adding structural listeners
>>> bn.addStructureListener(whenNodeAdded=lambda n,s:print(f'adding {n}:{s}
↪'),
>>>                         whenArcAdded=lambda i,j: print(f'adding {i}->{j}
↪'),
>>>                         whenNodeDeleted=lambda n:print(f'deleting {n}'),
>>>                         whenArcDeleted=lambda i,j: print(f'deleting {i}-
↪>{j}'))
>>>
>>> ## adding another listener for when a node is deleted
>>> bn.addStructureListener(whenNodeDeleted=lambda n: print('yes, really␣
```

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```
↪deleting '+str(n)))
>>>
>>> ## adding nodes to the BN
>>> l=[bn.add(item,3) for item in 'ABCDE']
>>> # adding 0:A
>>> # adding 1:B
>>> # adding 2:C
>>> # adding 3:D
>>> # adding 4:E
>>>
>>> ## adding arc to the BN
>>> bn.addArc(1,3)
>>> # adding 1->3
>>>
>>> ## removing a node from the BN
>>> bn.erase('C')
>>> # deleting 2
>>> # yes, really deleting 2
```

ApproximationSchemeListener

DatabaseGenerationListener

1.17.2 Random functions

pyAgrum.**initRandom**(*seed=0*)

Initialize random generator seed.

Parameters
seed (*int*) – the seed used to initialize the random generator

Return type
None

pyAgrum.**randomProba**()

Returns
a random number between 0 and 1 included (i.e. a proba).

Return type
float

pyAgrum.**randomDistribution**(*n*)

Parameters
n (*int*) – The number of modalities for the ditribution.

Return type
a random discrete distribution.

1.17.3 OMP functions

pyAgrum.**isOMP**()

Returns
True if OMP has been set at compilation, False otherwise

Return type
bool

pyAgrum.**setNumberOfThreads**(*number*)

To aNone spare cycles (less then 100% CPU occupied), use more threads than logical processors (x2 is a good all-around value).

Returns
number – the number of threads to be used

Return type
int

Parameters
number (int) –

pyAgrum.**getNumberOfLogicalProcessors**()

Return type
int

pyAgrum.**getNumberOfThreads**()

Return type
int

1.18 Exceptions from aGrUM

exception pyAgrum.**GumException**(**args*)

args

errorCallStack()

Returns
the error call stack
Return type
str

errorContent()

Returns
the error content
Return type
str

errorType()

Returns
the error type
Return type
str

what()

Return type
str

with_traceback()

Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

All the exception classes inherit pyAgrum.GumException's functions errorType, errorCallStack and errorContent.

exception pyAgrum.DefaultInLabel(*args)

args

property thisown

The membership flag

exception pyAgrum.DuplicateElement(*args)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.DuplicateLabel(*args)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.FatalError(*args)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.FormatNotFound(*args)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.GraphError(*args)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.**IOError**(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.**InvalidArc**(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.**InvalidArgument**(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.**InvalidArgumentsNumber**(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.**InvalidDirectedCycle**(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.**InvalidEdge**(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.InvalidNode(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.NoChild(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.NoNeighbour(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.NoParent(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.NotFound(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.NullElement(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.OperationNotAllowed(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.OutOfBounds(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.ArgumentError(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.SizeError(**args*)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.SyntaxError(**args*)

args

col()

Returns
the indice of the colonne of the error
Return type
int

filename()

Return type
str

line()

Returns
the indice of the line of the error
Return type
int

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.UndefinedElement(*args)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.UndefinedIteratorKey(*args)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.UndefinedIteratorValue(*args)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.UnknownLabelInDatabase(*args)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.DatabaseError(*args)

args

property thisown

The membership flag

what()

Return type
str

exception pyAgrum.**CPTError**(**args*)

args

property thisown

The membership flag

what()

Return type
str

1.19 Configuration for pyAgrum

Configuration for pyAgrum is centralized in an object `gum.config`, singleton of the class `PyAgrumConfiguration`.

class pyAgrum.**PyAgrumConfiguration**(**args*, ***kwargs*)

PyAgrumConfiguration is a the pyAgrum configuration singleton. The configuration is build as a classical ConfigParser with read-only structure. Then a value is adressable using a double key: `[section,key]`.

See this notebook (https://lip6.fr/Pierre-Henri.Wuillemin/aGrUM/docs/last/notebooks/configForPyAgrum.ipynb.html).

Examples

```
>>> gum.config['dynamicBN','default_graph_size']=10
>>> gum.config['dynamicBN','default_graph_size']
"10"
```

class CastAsBool(*container*)

class CastAsFloat(*container*)

class CastAsInt(*container*)

class Casterization(*container*)

add_hook(*fn*)

check_bool(*s*)

check_bool_false(*s*)

check_bool_true(*s*)

check_float(*s*)

check_int(*s*)

diff()

print the diff between actual configuration and the defaults. This is what is saved in the file `pyagrum.ini` by the method *PyAgrumConfiguration.save()*

get(*section*, *option*)

Give the value associated to section.option. Preferably use `__getitem__` and `__setitem__`.

Examples

```
>>> gum.config['dynamicBN','default_graph_size']=10
>>> gum.config['dynamicBN','default_graph_size']
"10"
```

Arguments:
section {str} – the section option {str} – the property

Returns:
str – the value (as string)

grep(*search*)

grep in the configuration any section or properties matching the argument. If a section match the argume, all the section is displayed.

Arguments:
search {str} – the string to find

load()

load pyagrum.ini in the current directory, and change the properties if needed

Raises:
FileNotFoundError: if there is no pyagrum.ini in the current directory

reset()

back to defaults

run_hooks()

save()

Save the diff with the defaults in `pyagrum.ini` in the current directory

set(*section*, *option*, *value*, *no_hook=False*)

set a property in a section. Preferably use `__getitem__` and `__setitem__`.

Examples

```
>>> gum.config['dynamicBN','default_graph_size']=10
>>> gum.config['dynamicBN','default_graph_size']
"10"
```

Arguments:
section {str} – the section name (has to exist in defaults) option {str} – the option/property name (has to exist in defaults) value {str} – the value (will be store as string) no_hook {bool} – (optional) should this call trigger the hooks ?

Raises:
SyntaxError: if the secion name or the property name does not exist

1.20 Tutorials on pyAgrum

1.20.1 Tutorial pyAgrum

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
from pylab import *
import matplotlib.pyplot as plt
import os
```

Creating your first Bayesian network with pyAgrum

(This example is based on an OpenBayes [closed] website tutorial)

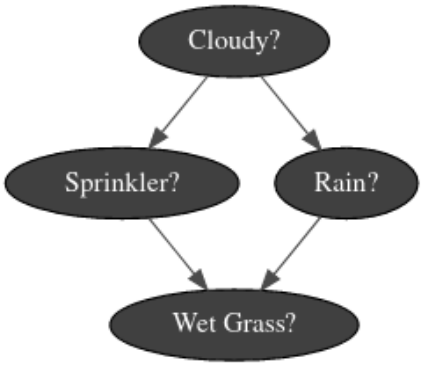
A Bayesian network (BN) is composed of random variables (nodes) and their conditional dependencies (arcs) which, together, form a directed acyclic graph (DAG). A conditional probability table (CPT) is associated with each node. It contains the conditional probability distribution of the node given its parents in the DAG:

Cloudy?
0	1
$\frac{1}{2}$	$\frac{1}{2}$

$P(Cloudy)$

	Sprinkler?	
Cloudy?	0	1
0	$\frac{1}{2}$	$\frac{1}{2}$
1	$\frac{9}{10}$	$\frac{1}{10}$

$P(Sprinkler|Cloudy)$



	Rain?	
Cloudy?	0	1
0	$\frac{4}{5}$	$\frac{1}{5}$
1	$\frac{1}{5}$	$\frac{4}{5}$

$P(WetGrass|Sprinkler, Rain)$

		Wet Grass?	
Rain?	Sprinkler?	0	1
0	0	$\frac{1}{1}$	$\frac{0}{1}$
	1	$\frac{1}{10}$	$\frac{9}{10}$
1	0	$\frac{1}{10}$	$\frac{9}{10}$
	1	$\frac{1}{100}$	$\frac{99}{100}$

$P(WetGrass|Sprinkler, Rain)$

Such a BN allows to manipulate the joint probability $P(C, S, R, W)$ using this decomposition :

$$P(C, S, R, W) = \prod_X P(X|Parents_X) = P(C) \cdot P(S|C) \cdot P(R|C) \cdot P(W|S, R)$$

Imagine you want to create your first Bayesian network, say for example the 'Water Sprinkler' network. This is an easy example. All the nodes are Boolean (only 2 possible values). You can proceed as follows.

Import the pyAgrum package

In [2]:
```
import pyAgrum as gum
```

Create the network topology

Create the BN

The next line creates an empty BN network with a 'name' property.

In [3]:
```
bn=gum.BayesNet('WaterSprinkler')
print(bn)
```

```
BN{nodes: 0, arcs: 0, domainSize: 1, dim: 0}
```

Create the variables

pyAgrum(aGrUM) provides 4 types of variables :

- LabelizedVariable
- RangeVariable
- IntegerVariable
- DiscretizedVariable

In this tutorial, we will use LabelizedVariable, which is a variable whose domain is a finite set of labels. The next line will create a variable named 'c', with 2 values and described as 'cloudy?', and it will add it to the BN. The value returned is the id of the node in the graphical structure (the DAG). pyAgrum actually distinguishes the random variable (here the labelizedVariable) from its node in the DAG: the latter is identified through a numeric id. Of course, pyAgrum provides functions to get the id of a node given the corresponding variable and conversely.

In [4]:
```
c=bn.add(gum.LabelizedVariable('c','cloudy ?',2))
print(c)
```

```
0
```

You can go on adding nodes in the network this way. Let us use python to compact a little bit the code:

In [5]:
```
s, r, w = [ bn.add(name, 2) for name in "srw" ] #bn.add(name, 2) === bn.add(gum.
↪LabelizedVariable(name, name, 2))
print (s,r,w)
print (bn)
```

```
1 2 3
BN{nodes: 4, arcs: 0, domainSize: 16, dim: 8}
```

Create the arcs

Now we have to connect nodes, i.e., to add arcs linking the nodes. Remember that c and s are ids for nodes:

In [6]:
```
bn.addArc(c,s)
```

Once again, python can help us :

In [7]:
```
for link in [(c,r),(s,w),(r,w)]:
    bn.addArc(*link)
print(bn)
```

```
BN{nodes: 4, arcs: 4, domainSize: 16, dim: 18}
```

pyAgrum provides tools to display bn in more user-frendly fashions. Notably, pyAgrum.lib is a set of tools written in pyAgrum to help using aGrUM in python. pyAgrum.lib.notebook adds dedicated functions for iPython notebook.

In [8]:
```
import pyAgrum.lib.notebook as gnb
bn
```

Out[8]:
```
(pyAgrum.BayesNet<double>@000002A6F47562B0) BN{nodes: 4, arcs: 4, domainSize: 16, dim:
↪ 18}
```

Shorcuts with fastBN

The functions `fast[model]` encode the structure of the graphical model and the type of the variables in a concise language somehow derived from the `dot` language for graphs (see the doc for the underlying method : fastPrototype (https://pyagrum.readthedocs.io/en/latest/BNModel.html?highlight=fastPrototype#pyAgrum.BayesNet.fastPrototype)).

In [9]:
```
bn=gum.fastBN("c->r->w<-s<-c")
bn
```

Out[9]:
```
(pyAgrum.BayesNet<double>@000002A6F4755810) BN{nodes: 4, arcs: 4, domainSize: 16, dim:
↪ 18}
```

Create the probability tables

Once the network topology is constructed, we must initialize the conditional probability tables (CPT) distributions. Each CPT is considered as a Potential object in pyAgrum. There are several ways to fill such an object.

To get the CPT of a variable, use the cpt method of your BayesNet instance with the variable's id as parameter.

Now we are ready to fill in the parameters of each node in our network. There are several ways to add these parameters.

Low-level way

In [10]:
```
bn.cpt(c).fillWith([0.4,0.6]) # remember : c=  0
```

Out[10]:
```
(pyAgrum.Potential<double>@000002A6D51B8CF0)
  c                 |
0         |1        |
----------|---------|
 0.4000   | 0.6000  |
```

Most of the methods using a node id will also work with name of the random variable.

In [11]:
```
bn.cpt("c").fillWith([0.5,0.5])
```

Out[11]:
```
(pyAgrum.Potential<double>@000002A6D51B8CF0)
  c                 |
0         |1        |
----------|---------|
 0.5000   | 0.5000  |
```

Using the order of variables

In [12]:
```
bn.cpt("s").names
```

Out[12]:
```
('s', 'c')
```

In [13]:
```
bn.cpt("s")[:]=[ [0.5,0.5],[0.9,0.1]]
```

Then $P(S|C=0)=[0.5,0.5]$ and $P(S|C=1)=[0.9,0.1]$.

In [14]:
```
print(bn.cpt("s")[1])
```

```
[0.9 0.1]
```

The same process can be performed in several steps:

In [15]:
```
bn.cpt("s")[0,:]=0.5 # equivalent to [0.5,0.5]
bn.cpt("s")[1,:]=[0.9,0.1]
```

In [16]:
```
print(bn.cpt("w").names)
bn.cpt("w")
```

```
('w', 'r', 's')
```

Out[16]:
```
(pyAgrum.Potential<double>@000002A6D51B8E30)
              ||  w                 |
r     |s      ||0         |1         |
------|-------||----------|----------|
0     |0      || 0.1595   | 0.8405   |
1     |0      || 0.5073   | 0.4927   |
0     |1      || 0.4252   | 0.5748   |
1     |1      || 0.1210   | 0.8790   |
```

In [17]:
```
bn.cpt("w")[0,0,:] = [1, 0] # r=0,s=0
bn.cpt("w")[0,1,:] = [0.1, 0.9] # r=0,s=1
bn.cpt("w")[1,0,:] = [0.1, 0.9] # r=1,s=0
bn.cpt("w")[1,1,:] = [0.01, 0.99] # r=1,s=1
```

Using a dictionnary

This is probably the most convenient way:

In [18]:
```
bn.cpt("w")[{'r': 0, 's': 0}] = [1, 0]
bn.cpt("w")[{'r': 0, 's': 1}] = [0.1, 0.9]
bn.cpt("w")[{'r': 1, 's': 0}] = [0.1, 0.9]
bn.cpt("w")[{'r': 1, 's': 1}] = [0.01, 0.99]
bn.cpt("w")
```

Out[18]:
```
(pyAgrum.Potential<double>@000002A6D51B8E30)
              ||  w                 |
r     |s     ||0         |1         |
------|------||----------|----------|
0     |0     || 1.0000   | 0.0000   |
1     |0     || 0.1000   | 0.9000   |
0     |1     || 0.1000   | 0.9000   |
1     |1     || 0.0100   | 0.9900   |
```

The use of dictionaries is a feature borrowed from OpenBayes. It facilitates the use and avoid common errors that happen when introducing data into the wrong places.

In [19]:
```
bn.cpt("r")[{'c':0}]=[0.8,0.2]
bn.cpt("r")[{'c':1}]=[0.2,0.8]
```

Input/output

Now our BN is complete. It can be saved in different format :

In [20]:
```
print(gum.availableBNExts())
```

```
bif|dsl|net|bifxml|o3prm|uai
```

We can save a BN using BIF format

In [21]:
```
gum.saveBN(bn,"out/WaterSprinkler.bif")
```

In [22]:
```
with open("out/WaterSprinkler.bif","r") as out:
    print(out.read())
```

```
network "unnamedBN" {
// written by aGrUM 1.1.0.9
}

variable c {
   type discrete[2] {0, 1};
}

variable r {
   type discrete[2] {0, 1};
}

variable w {
   type discrete[2] {0, 1};
}

variable s {
   type discrete[2] {0, 1};
}

probability (c) {
   default 0.5 0.5;
}
probability (r | c) {
   (0) 0.8 0.2;
   (1) 0.2 0.8;
}
```

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```
probability (w | r, s) {
   (0, 0) 1 0;
   (1, 0) 0.1 0.9;
   (0, 1) 0.1 0.9;
   (1, 1) 0.01 0.99;
}
probability (s | c) {
   (0) 0.5 0.5;
   (1) 0.9 0.1;
}
```

In [23]:
```
bn2=gum.loadBN("out/WaterSprinkler.bif")
```

We can also save and load it in other formats

In [24]:
```
gum.saveBN(bn,"out/WaterSprinkler.net")
with open("out/WaterSprinkler.net","r") as out:
    print(out.read())
bn3=gum.loadBN("out/WaterSprinkler.net")
```

```

net {
  name = unnamedBN;
  software = "aGrUM 1.1.0.9";
  node_size = (50 50);
}

node c {
   states = (0 1 );
   label = "c";
   ID = "c";
}

node r {
   states = (0 1 );
   label = "r";
   ID = "r";
}

node w {
   states = (0 1 );
   label = "w";
   ID = "w";
}

node s {
   states = (0 1 );
   label = "s";
   ID = "s";
}

potential (c) {
   data = (  0.5 0.5);
}
```

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```
potential ( r | c   ) {
   data =
   ((   0.8   0.2)   % c=0
   (   0.2   0.8));   % c=1
}

potential ( w | r   s   ) {
   data =
   (((   1   0)   % s=0   r=0
   (   0.1   0.9))   % s=1   r=0
   ((   0.1   0.9)   % s=0   r=1
   (   0.01   0.99)));   % s=1   r=1
}

potential ( s | c   ) {
   data =
   ((   0.5   0.5)   % c=0
   (   0.9   0.1));   % c=1
}
```

Inference in Bayesian networks

We have to choose an inference engine to perform calculations for us. Many inference engines are currently available in pyAgrum:

- **Exact inference**, particularly :
  - `gum.LazyPropagation` : an exact inference method that transforms the Bayesian network into a hypergraph called a join tree or a junction tree. This tree is constructed in order to optimize inference computations.
  - others: `gum.VariableElimination`, `gum.ShaferShenoy`, ...
- **Samplig Inference** : approximate inference engine using sampling algorithms to generate a sequence of samples from the joint probability distribution (`gum.GibbSSampling`, etc.)
- **Loopy Belief Propagation** : approximate inference engine using inference algorithm exact for trees but not for DAG

In [25]:
```
ie=gum.LazyPropagation(bn)
```

Inference without evidence

In [26]:
```
ie.makeInference()
print (ie.posterior("w"))
```

```
  w                |
0        |1        |
---------|---------|
 0.3529  | 0.6471  |
```

In [27]:
```
from IPython.core.display import HTML
HTML(f"In our BN, $P(W)=${ie.posterior('w')[:]}")
```

Out[27]:
```
<IPython.core.display.HTML object>
```

With notebooks, it can be viewed as an HTML table

In [28]:
```
ie.posterior("w")[:]
```

Out[28]:
```
array([0.3529, 0.6471])
```

Inference with evidence

Suppose now that you know that the sprinkler is on and that it is not cloudy, and you wonder what Is the probability of the grass being wet, i.e., you are interested in distribution $P(W|S=1,C=0)$. The new knowledge you have (sprinkler is on and it is not cloudy) is called evidence. Evidence is entered using a dictionary. When you know precisely the value taken by a random variable, the evidence is called a hard evidence. This is the case, for instance, when I know for sure that the sprinkler is on. In this case, the knowledge is entered in the dictionary as 'variable name':label

In [29]:
```
ie.setEvidence({'s':0, 'c': 0})
ie.makeInference()
ie.posterior("w")
```

Out[29]:
```
(pyAgrum.Potential<double>@000002A6D52EC110)
  w                 |
0         |1        |
----------|---------|
 0.8200   | 0.1800  |
```

When you have incomplete knowledge about the value of a random variable, this is called a soft evidence. In this case, this evidence is entered as the belief you have over the possible values that the random variable can take, in other words, as P(evidence|true value of the variable). Imagine for instance that you think that if the sprinkler is off, you have only 50% chances of knowing it, but if it is on, you are sure to know it. Then, your belief about the state of the sprinkler is [0.5, 1] and you should enter this knowledge as shown below. Of course, hard evidence are special cases of soft evidence in which the beliefs over all the values of the random variable but one are equal to 0.

In [30]:
```
ie.setEvidence({'s': [0.5, 1], 'c': [1, 0]})
ie.makeInference()
ie.posterior("w") # using gnb's feature
```

Out[30]:
```
(pyAgrum.Potential<double>@000002A6D52EC370)
  w                 |
0         |1        |
----------|---------|
 0.3280   | 0.6720  |
```

the pyAgrum.lib.notebook utility proposes certain functions to graphically show distributions.

In [31]:
```
gnb.showProba(ie.posterior("w"))
```

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In [32]:
```
gnb.showPosterior(bn,{'s':1,'c':0},'w')
```

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inference in the whole Bayes net

In [33]:
```
gnb.showInference(bn,evs={})
```
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inference with hard evidence

In [34]:
```
gnb.showInference(bn,evs={'s':1,'c':0})
```
nbsphinx-code-borderwhite

inference with soft and hard evidence

In [35]:
```
gnb.showInference(bn,evs={'s':1,'c':[0.3,0.9]})
```
nbsphinx-code-borderwhite

inference with partial targets

In [36]:
```
gnb.showInference(bn,evs={'c':[0.3,0.9]},targets={'c','w'})
```
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Testing independence in Bayesian networks

One of the strength of the Bayesian networks is to form a model that allows to read qualitative knwoledge directly from the grap : the conditional independence. aGrUM/pyAgrum comes with a set of tools to query this qualitative knowledge.

In [37]:
```
# fast create a BN (random paramaters are chosen for the CPTs)
bn=gum.fastBN("A->B<-C->D->E<-F<-A;C->G<-H<-I->J")
bn
```

Out[37]:
```
(pyAgrum.BayesNet<double>@000002A6F4756800) BN{nodes: 10, arcs: 10, domainSize: 1024,␣
↪dim: 46}
```

Conditional Independence

Directly

First, one can directly test independence

In [38]:
```
def testIndep(bn,x,y,knowing):
    res="" if bn.isIndependent(x,y,knowing) else " NOT"
    giv="." if len(knowing)==0 else f" given {knowing}."
    print(f"{x} and {y} are{res} independent{giv}")

testIndep(bn,"A","C",[])
testIndep(bn,"A","C",["E"])
print()
testIndep(bn,"E","C",[])
testIndep(bn,"E","C",["D"])
print()
testIndep(bn,"A","I",[])
```

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```
testIndep(bn,"A","I",["E"])
testIndep(bn,"A","I",["G"])
testIndep(bn,"A","I",["E","G"])
```

```
A and C are independent.
A and C are NOT independent given ['E'].

E and C are NOT independent.
E and C are independent given ['D'].

A and I are independent.
A and I are independent given ['E'].
A and I are independent given ['G'].
A and I are NOT independent given ['E', 'G'].
```

Markov Blanket

Second, one can investigate the Markov Blanket of a node. The Markov blanket of a node X is the set of nodes $MB(X)$ such that X is independent from the rest of the nodes given $MB(X)$.

In [39]:
```
print(gum.MarkovBlanket(bn,"C").toDot())
gum.MarkovBlanket(bn,"C")
```

```
digraph "no_name" {
node [shape = ellipse];
  0[label="A"];
  1[label="B"];
  2[label="C", color=red];
  3[label="D"];
  6[label="G"];
  7[label="H"];

  0 -> 1;
  2 -> 3;
  2 -> 1;
  2 -> 6;
  7 -> 6;

}
```

Out[39]:
```
<pyAgrum.pyAgrum.MarkovBlanket; proxy of <Swig Object of type 'gum::MarkovBlanket *'␣
↪at 0x000002A6F8AF50E0> >
```

In [40]:
```
gum.MarkovBlanket(bn,"J")
```

Out[40]:
```
<pyAgrum.pyAgrum.MarkovBlanket; proxy of <Swig Object of type 'gum::MarkovBlanket *'␣
↪at 0x000002A6F8A644B0> >
```

Minimal conditioning set and evidence Impact using probabilistic inference

For a variable and a list of variables, one can find the sublist that effectively impacts the variable if the list of variables was observed.

In [41]:
```
[bn.variable(i).name() for i in bn.minimalCondSet("B",["A","H","J"])]
```

Out[41]:
```
['A']
```

In [42]:
```
[bn.variable(i).name() for i in bn.minimalCondSet("B",["A","G","H","J"])]
```

Out[42]:
```
['A', 'G', 'H']
```

This can be also viewed when using `gum.LazyPropagation.evidenceImpact(target,evidence)` which computes $P(target|evidence)$ but reduces as much as possible the set of needed evidence for the result :

In [43]:
```
ie=gum.LazyPropagation(bn)
ie.evidenceImpact("B",["A","C","H","G"]) # H,G will be removed w.r.t the␣
↪minimalCondSet above
```

Out[43]:
```
(pyAgrum.Potential<double>@000002A6D52EC310)
             ||  B                |
A     |C     ||0        |1        |
------|------||---------|---------|
0     |0     || 0.6883  | 0.3117  |
1     |0     || 0.2372  | 0.7628  |
0     |1     || 0.3500  | 0.6500  |
1     |1     || 0.5294  | 0.4706  |
```

In [44]:
```
ie.evidenceImpact("B",["A","G","H","J"]) # "J" is not necessary to compute the impact␣
↪of the evidence
```

Out[44]:
```
(pyAgrum.Potential<double>@000002A6D52EC1B0)
                    ||  B                |
G     |H     |A     ||0        |1        |
------|------|------||---------|---------|
0     |0     |0     || 0.4486  | 0.5514  |
1     |0     |0     || 0.4965  | 0.5035  |
0     |1     |0     || 0.5267  | 0.4733  |
1     |1     |0     || 0.3516  | 0.6484  |
0     |0     |1     || 0.4442  | 0.5558  |
1     |0     |1     || 0.4029  | 0.5971  |
0     |1     |1     || 0.3768  | 0.6232  |
1     |1     |1     || 0.5280  | 0.4720  |
```

PS- the complete code to create the first image

In [45]:
```
bn=gum.fastBN("Cloudy?->Sprinkler?->Wet Grass?<-Rain?<-Cloudy?")

bn.cpt("Cloudy?").fillWith([0.5,0.5])

bn.cpt("Sprinkler?")[:]=[[0.5,0.5],
                         [0.9,0.1]]

bn.cpt("Rain?")[{'Cloudy?':0}]=[0.8,0.2]
bn.cpt("Rain?")[{'Cloudy?':1}]=[0.2,0.8]
```

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```
bn.cpt("Wet Grass?")[{'Rain?': 0, 'Sprinkler?': 0}] = [1, 0]
bn.cpt("Wet Grass?")[{'Rain?': 0, 'Sprinkler?': 1}] = [0.1, 0.9]
bn.cpt("Wet Grass?")[{'Rain?': 1, 'Sprinkler?': 0}] = [0.1, 0.9]
bn.cpt("Wet Grass?")[{'Rain?': 1, 'Sprinkler?': 1}] = [0.01, 0.99]

# the next line control the number of visible digits
gum.config['notebook','potential_visible_digits']=2
gnb.sideBySide(bn.cpt("Cloudy?"),captions=['$P(Cloudy)$'])
gnb.sideBySide(bn.cpt("Sprinkler?"),gnb.getBN(bn,size="3!"),bn.cpt("Rain?"),
               captions=['$P(Sprinkler|Cloudy)$',"",'$P(WetGrass|Sprinkler,Rain)$'])
gnb.sideBySide(bn.cpt("Wet Grass?"),captions=['$P(WetGrass|Sprinkler,Rain)$'])
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

PS2- a second glimpse of `gum.config`

(for more, see the notebook : config for pyAgrum)

In [46]:
```
bn=gum.fastBN("Cloudy?->Sprinkler?->Wet Grass?<-Rain?<-Cloudy?")

bn.cpt("Cloudy?").fillWith([0.5,0.5])

bn.cpt("Sprinkler?")[:]=[[0.5,0.5],
                         [0.9,0.1]]

bn.cpt("Rain?")[{'Cloudy?':0}]=[0.8,0.2]
bn.cpt("Rain?")[{'Cloudy?':1}]=[0.2,0.8]

bn.cpt("Wet Grass?")[{'Rain?': 0, 'Sprinkler?': 0}] = [1, 0]
bn.cpt("Wet Grass?")[{'Rain?': 0, 'Sprinkler?': 1}] = [0.1, 0.9]
bn.cpt("Wet Grass?")[{'Rain?': 1, 'Sprinkler?': 0}] = [0.1, 0.9]
bn.cpt("Wet Grass?")[{'Rain?': 1, 'Sprinkler?': 1}] = [0.01, 0.99]

# the next lines control the visualisation of proba as fraction
gum.config['notebook','potential_with_fraction']=True
gum.config['notebook', 'potential_fraction_with_latex']=True
gum.config['notebook', 'potential_fraction_limit']=100

gnb.sideBySide(bn.cpt("Cloudy?"),captions=['$P(Cloudy)$'])
gnb.sideBySide(bn.cpt("Sprinkler?"),gnb.getBN(bn,size="3!"),bn.cpt("Rain?"),
               captions=['$P(Sprinkler|Cloudy)$',"",'$P(WetGrass|Sprinkler,Rain)$'])
gnb.sideBySide(bn.cpt("Wet Grass?"),captions=['$P(WetGrass|Sprinkler,Rain)$'])
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

1.20.2 Using pyAgrum

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt

import os
```

Initialisation

- importing pyAgrum
- importing pyAgrum.lib tools
- loading a BN

In [2]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
gnb.configuration()
```

```
<IPython.core.display.HTML object>
```

In [3]:
```
bn=gum.loadBN("res/alarm.dsl")
gnb.showBN(bn,size='9')
```

nbsphinx-code-borderwhite

Visualisation and inspection

In [4]:
```
print(bn.variableFromName('SHUNT'))
```

```
SHUNT:Labelized({NORMAL|HIGH})
```

In [5]:
```
print(bn.cpt(bn.idFromName('SHUNT')))
```

```
              ||  SHUNT             |
PULMEM|INTUBA||NORMAL   |HIGH      |
------|------||---------|---------|
TRUE  |NORMAL|| 0.1000  | 0.9000  |
FALSE |NORMAL|| 0.9500  | 0.0500  |
TRUE  |ESOPHA|| 0.1000  | 0.9000  |
FALSE |ESOPHA|| 0.9500  | 0.0500  |
TRUE  |ONESID|| 0.0100  | 0.9900  |
FALSE |ONESID|| 0.0500  | 0.9500  |
```

In [6]:
```
gnb.showPotential(bn.cpt(bn.idFromName('SHUNT')),digits=3)
```

```
<IPython.core.display.HTML object>
```

Results of inference

It is easy to look at result of inference

In [7]:
```
gnb.showPosterior(bn,{'SHUNT':'HIGH'},'PRESS')
```

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In [8]:
```
gnb.showPosterior(bn,{'MINVOLSET':'NORMAL'},'VENTALV')
```

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Overall results

In [9]:
```
gnb.showInference(bn,size="10")
```

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What is the impact of observed variables (SHUNT and VENTALV for instance) on another on (PRESS) ?

In [10]:
```
ie=gum.LazyPropagation(bn)
ie.evidenceImpact('PRESS',['SHUNT','VENTALV'])
```

Out[10]:
```
(pyAgrum.Potential<double>@000001B0648303F0)
              ||  PRESS                                |
VENTAL|SHUNT ||ZERO     |LOW      |NORMAL   |HIGH     |
------|------||---------|---------|---------|---------|
ZERO  |NORMAL|| 0.0569  | 0.2669  | 0.2005  | 0.4757  |
LOW   |NORMAL|| 0.0208  | 0.2515  | 0.0553  | 0.6724  |
NORMAL|NORMAL|| 0.0769  | 0.3267  | 0.1772  | 0.4192  |
HIGH  |NORMAL|| 0.0501  | 0.1633  | 0.2796  | 0.5071  |
ZERO  |HIGH  || 0.0589  | 0.2726  | 0.1997  | 0.4688  |
LOW   |HIGH  || 0.0318  | 0.2237  | 0.0521  | 0.6924  |
NORMAL|HIGH  || 0.1735  | 0.5839  | 0.1402  | 0.1024  |
HIGH  |HIGH  || 0.0711  | 0.2347  | 0.2533  | 0.4410  |
```

Using inference as a function

It is also easy to use inference as a routine in more complex procedures.

In [11]:
```
import time
r=range(0,100,2)
xs=[x/100.0 for x in r]

tf=time.time()
ys=[gum.getPosterior(bn,{'MINVOLSET':[0,x/100.0,0.5]},'VENTALV').tolist()
        for x in r]
delta=time.time()-tf

p=plot(xs,ys)
legend(p,[bn.variableFromName('VENTALV').label(i)
          for i in range(bn.variableFromName('VENTALV').domainSize())],loc=7);
title('VENTALV (100 inferences in %d ms)'%delta);
ylabel('posterior Probability');
xlabel('Evidence on MINVOLSET : [0,x,0.5]')
plt.show()
```

nbsphinx-code-borderwhite

Another example : python gives access to a large set of tools. Here the value for the equality of two probabilities of a posterior is easely computed.

In [12]:
```
x=[p/100.0 for p in range(0,100)]

tf=time.time()
y=[gum.getPosterior(bn,{'HRBP':[1.0-p/100.0,1.0-p/100.0,p/100.0]},'TPR').tolist()
   for p in range(0,100)]
delta=time.time()-tf

p=plot(x,y)
title('HRBP (100 inferences in %d ms)'%delta);
v=bn.variableFromName('TPR');
legend([v.label(i) for i in range(v.domainSize())],loc='best');
np1=(transpose(y)[0]>transpose(y)[2]).argmin()
text(x[np1]-0.05,y[np1][0]+0.005,str(x[np1]),bbox=dict(facecolor='red', alpha=0.1))
plt.show()
```

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BN as a classifier

Generation of databases

Using the CSV format for the database:

In [13]:
```
gum.generateSample(bn,1000,"out/test.csv",with_labels=True)
```

Out[13]:
```
-14917.511725169048
```

In [14]:
```
with open("out/test.csv","r") as src:
    for _ in range(10):
        print(src.readline(),end="")
```

```
HYPOVOLEMIA,STROKEVOLUME,EXPCO2,CATECHOL,PULMEMBOLUS,VENTTUBE,BP,HRSAT,CO,ANAPHYLAXIS,
↪VENTALV,VENTMACH,HR,PAP,ERRLOWOUTPUT,VENTLUNG,ARTCO2,PCWP,SHUNT,LVEDVOLUME,SAO2,CVP,
↪DISCONNECT,KINKEDTUBE,ERRCAUTER,HISTORY,INSUFFANESTH,MINVOLSET,TPR,HREKG,PRESS,
↪PVSAT,FIO2,INTUBATION,HRBP,MINVOL,LVFAILURE
FALSE,NORMAL,LOW,HIGH,FALSE,LOW,HIGH,HIGH,HIGH,FALSE,NORMAL,NORMAL,HIGH,NORMAL,FALSE,
↪ZERO,NORMAL,NORMAL,HIGH,NORMAL,LOW,NORMAL,FALSE,FALSE,FALSE,FALSE,FALSE,NORMAL,
↪NORMAL,HIGH,ZERO,LOW,NORMAL,ONESIDED,HIGH,LOW,FALSE
FALSE,NORMAL,ZERO,HIGH,FALSE,LOW,HIGH,HIGH,HIGH,FALSE,ZERO,NORMAL,HIGH,NORMAL,TRUE,
↪ZERO,LOW,NORMAL,NORMAL,NORMAL,LOW,NORMAL,FALSE,FALSE,FALSE,FALSE,FALSE,NORMAL,
↪NORMAL,HIGH,HIGH,LOW,NORMAL,NORMAL,NORMAL,HIGH,FALSE
FALSE,LOW,NORMAL,HIGH,FALSE,NORMAL,LOW,HIGH,LOW,FALSE,HIGH,HIGH,HIGH,NORMAL,FALSE,
↪NORMAL,LOW,NORMAL,NORMAL,NORMAL,NORMAL,NORMAL,TRUE,FALSE,FALSE,FALSE,FALSE,HIGH,
↪HIGH,HIGH,NORMAL,HIGH,NORMAL,NORMAL,HIGH,LOW,FALSE
TRUE,LOW,NORMAL,HIGH,FALSE,HIGH,LOW,HIGH,LOW,FALSE,LOW,HIGH,HIGH,NORMAL,FALSE,LOW,
↪HIGH,HIGH,NORMAL,HIGH,LOW,HIGH,FALSE,FALSE,FALSE,FALSE,FALSE,NORMAL,HIGH,HIGH,HIGH,
↪NORMAL,NORMAL,NORMAL,HIGH,NORMAL,FALSE
FALSE,NORMAL,LOW,HIGH,FALSE,ZERO,HIGH,HIGH,HIGH,FALSE,ZERO,NORMAL,HIGH,NORMAL,FALSE,
↪ZERO,HIGH,LOW,NORMAL,LOW,LOW,LOW,TRUE,FALSE,FALSE,FALSE,FALSE,NORMAL,NORMAL,HIGH,
↪LOW,LOW,NORMAL,NORMAL,HIGH,ZERO,FALSE
FALSE,NORMAL,LOW,HIGH,FALSE,LOW,HIGH,HIGH,HIGH,FALSE,ZERO,NORMAL,HIGH,NORMAL,FALSE,
↪ZERO,HIGH,NORMAL,NORMAL,NORMAL,LOW,NORMAL,FALSE,FALSE,FALSE,FALSE,FALSE,NORMAL,
↪NORMAL,HIGH,HIGH,LOW,NORMAL,NORMAL,HIGH,ZERO,FALSE
```

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```
TRUE,LOW,LOW,HIGH,FALSE,LOW,NORMAL,HIGH,NORMAL,FALSE,ZERO,NORMAL,HIGH,NORMAL,FALSE,
↪ZERO,HIGH,HIGH,NORMAL,HIGH,LOW,HIGH,FALSE,FALSE,FALSE,FALSE,TRUE,NORMAL,NORMAL,HIGH,
↪HIGH,LOW,NORMAL,NORMAL,HIGH,ZERO,FALSE
FALSE,NORMAL,LOW,HIGH,FALSE,LOW,LOW,LOW,LOW,FALSE,ZERO,NORMAL,NORMAL,NORMAL,FALSE,
↪ZERO,HIGH,NORMAL,NORMAL,NORMAL,LOW,NORMAL,FALSE,FALSE,FALSE,FALSE,FALSE,NORMAL,HIGH,
↪LOW,HIGH,LOW,NORMAL,NORMAL,LOW,ZERO,FALSE
FALSE,NORMAL,LOW,HIGH,FALSE,LOW,HIGH,HIGH,HIGH,FALSE,ZERO,NORMAL,HIGH,NORMAL,FALSE,
↪ZERO,HIGH,NORMAL,NORMAL,NORMAL,LOW,NORMAL,FALSE,FALSE,FALSE,FALSE,FALSE,NORMAL,
↪NORMAL,HIGH,NORMAL,LOW,NORMAL,NORMAL,HIGH,ZERO,FALSE
```

probabilistic classifier using BN

(because of the use of from-bn-generated csv files, quite good ROC curves are expected)

In [15]:
```
from pyAgrum.lib.bn2roc import showROC_PR

showROC_PR(bn,"out/test.csv",
        target='CATECHOL',label='HIGH',  # class and label
        show_progress=True,show_fig=True,with_labels=True)
```

```
out/test.csv: 100%||
```

nbsphinx-code-borderwhite

Out[15]:
```
(0.9525796038953934, 0.9300899828, 0.9980437992339163, 0.34813415895)
```

Using another class variable

In [16]:
```
showROC_PR(bn,"out/test.csv",'SAO2','HIGH',show_progress=True)
```

```
out/test.csv: 100%||
```

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Out[16]:
```
(0.9629093016516952, 0.048531175, 0.7758007513206207, 0.5385017134)
```

Fast prototyping for BNs

In [17]:
```
bn1=gum.fastBN("a->b;a->c;b->c;c->d",3)

gnb.sideBySide(*[gnb.getInference(bn1,evs={'c':val},targets={'a','c','d'}) for val in␣
↪range(3)],
               captions=[f"Inference given that $c={val}$" for val in range(3)])
```

```
<IPython.core.display.HTML object>
```

In [18]:
```
print(gum.getPosterior(bn1,evs={'c':0},target='c'))
print(gum.getPosterior(bn1,evs={'c':0},target='d'))

# using pyagrum.lib.notebook's helpers
gnb.flow.row(gum.getPosterior(bn1,evs={'c':0},target='c'),gum.getPosterior(bn1,evs={'c
↪':0},target='d'))
```

```
  c                          |
0        |1        |2        |
---------|---------|---------|
 1.0000  | 0.0000  | 0.0000  |
```

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```
  d                          |
0        |1        |2        |
---------|---------|---------|
 0.6638  | 0.1259  | 0.2103  |
```

```
<IPython.core.display.HTML object>
```

Joint posterior, impact of multiple evidence

In [19]:
```
bn=gum.fastBN("a->b->c->d;b->e->d->f;g->c")
gnb.sideBySide(bn,gnb.getInference(bn))
```

```
<IPython.core.display.HTML object>
```

In [20]:
```
ie=gum.LazyPropagation(bn)
ie.addJointTarget({"e","f","g"})
ie.makeInference()
gnb.sideBySide(ie.jointPosterior({"e","f","g"}),ie.jointPosterior({"e","g"}),
               captions=["Joint posterior $P(e,f,g)$","Joint posterior $P(e,f)$"])
```

```
<IPython.core.display.HTML object>
```

In [21]:
```
gnb.sideBySide(ie.evidenceImpact("a",["e","f"]),ie.evidenceImpact("a",["d","e","f"]),
               captions=["$\\forall e,f, P(a|e,f)$",
                         "$\\forall d,e,f, P(a|d,e,f)=P(a|d,e)$ using d-separation"]
                         )
```

```
<IPython.core.display.HTML object>
```

In [22]:
```
gnb.sideBySide(ie.evidenceJointImpact(["a","b"],["e","f"]),ie.evidenceJointImpact(["a
↪","b"],["d","e","f"]),
               captions=["$\\forall e,f, P(a,b|e,f)$",
                         "$\\forall d,e,f, P(a,b|d,e,f)=P(a,b|d,e)$ using d-separation
↪"]
                         )
```

```
<IPython.core.display.HTML object>
```

In [ ]:
```

```

1.21 Inference in Bayesian networks

1.21.1 Probablistic Inference with pyAgrum

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In this notebook, we will show different basic features for probabilistic inference on Bayesian networks using pyAgrum.

First we need some external modules:

In [1]:
```
import os

%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt
```

Basic inference and display

Then we import pyAgrum and the pyAgrum's notebook module, that offers very usefull methods when writting a notebook.

This first example shows how you can load a BayesNet and show it as graph. Note that pyAgrum handles serveral BayesNet file format such as DSL, BIF and UAI.

In [2]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
bn=gum.loadBN("res/alarm.dsl")
gnb.showBN(bn,size="9")
```

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From there, it is easy to get a posterior using an inference engine :

In [3]:
```
ie=gum.LazyPropagation(bn)
ie.makeInference()
print(ie.posterior(bn.idFromName("CATECHOL")))
```

```
  CATECHOL          |
NORMAL    |HIGH     |
----------|---------|
 0.0512   | 0.9488  |
```

But since we are in notebook, why not use pyAgrum notebook's methods ?

In [4]:
```
gnb.showPosterior(bn,evs={},target='CATECHOL')
```

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You may also want to see the graph with some posteriors

In [5]:
```
# due to matplotlib, format is forced to png.
gnb.showInference(bn,evs={},targets={"VENTALV","CATECHOL","HR","MINVOLSET"},size="11")
```

nbsphinx-code-borderwhite

In [6]:
```
gnb.showInference(bn,
                  evs={"CO":1,"VENTLUNG":1},
                  targets={"VENTALV",
                           "CATECHOL",
                           "HR",
                           "MINVOLSET",
                           "ANAPHYLAXIS",
                           "STROKEVOLUME",
                           "ERRLOWOUTPUT",
                           "HBR",
```

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```
                           "PULMEMBOLUS",
                           "HISTORY",
                           "BP",
                           "PRESS",
                           "CO"},
                  size="10")
```

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You can even compute all posteriors by leaving the `targets` parameter empty (which is its default value).

In [7]:
```
gnb.showInference(bn,evs={"CO":1,"VENTLUNG":1},size="14")
```

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Showing the information graph

To have a global view of the knowledge brought by the inference, you can also draw the entropy of all nodes

In [8]:
```
import pyAgrum.lib.explain as explain
explain.showInformation(bn,{},size="14")
```

```
<IPython.core.display.HTML object>
```

... and then observe the impact of an evidence on the whole bayes network :

In [9]:
```
explain.showInformation(bn,{"CO":0},size="9")
```

```
<IPython.core.display.HTML object>
```

Exploring the junction tree

Lazy Propagation, like several other inference algorithms, uses a junction tree to propagate information.

You can show the junction tree used by Lazy Propagation with pyAgrum:

In [10]:
```
jt=ie.junctionTree()
gnb.showJunctionTree(bn,size="12")
```

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In [11]:
```
# another representation of the junction, more convenient for investigating the flow␣
↪of data in the jt
# the size/width of cliques and separators are proportionnal to the number of nodes␣
↪in the factor.
jt.map()
```

Out[11]:
```
<pydot.Dot at 0x20f932ea560>
```

Introspection in junction trees

One can easily walk through the junction tree.

In [12]:
```
for n in jt.nodes():
    print([bn.variable(n).name() for n in jt.clique(n)])
```

```
['CVP', 'LVEDVOLUME']
['FIO2', 'VENTALV', 'PVSAT']
['ARTCO2', 'EXPCO2', 'VENTLUNG']
```

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```
['VENTMACH', 'MINVOLSET']
['VENTMACH', 'DISCONNECT', 'VENTTUBE']
['PRESS', 'KINKEDTUBE', 'INTUBATION', 'VENTTUBE']
['ANAPHYLAXIS', 'TPR']
['HRBP', 'ERRLOWOUTPUT', 'HR']
['LVFAILURE', 'HISTORY']
['HREKG', 'HR', 'ERRCAUTER']
['PCWP', 'LVEDVOLUME']
['PAP', 'PULMEMBOLUS']
['SHUNT', 'INTUBATION', 'PULMEMBOLUS']
['HRSAT', 'HR', 'ERRCAUTER']
['LVFAILURE', 'HYPOVOLEMIA', 'LVEDVOLUME']
['HYPOVOLEMIA', 'STROKEVOLUME', 'LVFAILURE']
['CO', 'BP', 'TPR']
['INTUBATION', 'VENTLUNG', 'MINVOL']
['KINKEDTUBE', 'INTUBATION', 'VENTTUBE', 'VENTLUNG']
['INSUFFANESTH', 'TPR', 'ARTCO2', 'SAO2', 'CATECHOL']
['CO', 'STROKEVOLUME', 'HR']
['CO', 'CATECHOL', 'HR']
['CO', 'TPR', 'CATECHOL']
['INTUBATION', 'SHUNT', 'PVSAT', 'SAO2']
['INTUBATION', 'ARTCO2', 'PVSAT', 'SAO2']
['ARTCO2', 'VENTALV', 'INTUBATION', 'PVSAT']
['VENTALV', 'INTUBATION', 'ARTCO2', 'VENTLUNG']
```

In [13]:
```
for e in jt.edges():
    print(f"Separator for {e} : {jt.clique(e[0]).intersection(jt.clique(e[1]))}")
```

```
Separator for (13, 30) : {18, 2}
Separator for (2, 33) : {26, 22}
Separator for (3, 4) : {16}
Separator for (26, 27) : {34, 30}
Separator for (7, 26) : {31}
Separator for (12, 13) : {4}
Separator for (31, 32) : {27, 26, 2}
Separator for (23, 31) : {26, 28}
Separator for (5, 22) : {0, 2, 20}
Separator for (17, 24) : {13}
Separator for (19, 27) : {34, 14}
Separator for (24, 26) : {34, 31}
Separator for (32, 33) : {25, 2, 26}
Separator for (6, 23) : {14}
Separator for (23, 27) : {14, 30}
Separator for (11, 16) : {15}
Separator for (10, 14) : {7, 31}
Separator for (8, 17) : {9}
Separator for (0, 16) : {15}
Separator for (1, 32) : {25, 27}
Separator for (20, 33) : {2, 22}
Separator for (4, 22) : {20}
Separator for (14, 26) : {31}
Separator for (22, 33) : {2, 22}
Separator for (30, 31) : {2, 27, 28}
Separator for (16, 17) : {1, 9}
```

In [14]:
```
jt.hasRunningIntersection()
```

Out[14]:
```
True
```

Introspecting junction trees and friends

The junction tree created by a LazyPropagation is optimized for the query (see `RelevanceReasonning` notebook). But you can also introspect a junction tree directly from a BN or a graph using the `JunctionTreeGenerator`'s class.

In [15]:
```
bn=gum.fastBN("0->1->2<-3->4->5->6<-2->7")
jtg=gum.JunctionTreeGenerator()
gnb.sideBySide(bn,jtg.junctionTree(bn),jtg.eliminationOrder(bn),jtg.
↪binaryJoinTree(bn),
               captions=["A Bayesien network",
                         "a junction tree for this BN",
                         "its elimination order",
                         "an (optimized) binary join tree"])
```

```
<IPython.core.display.HTML object>
```

junction tree from graphs (using uniform domainSize)

In [16]:
```
#creating a dag slightly different
dag=bn.dag()
dag.addArc(0,3)
dag.addArc(0,7)
gnb.sideBySide(dag,dag.moralGraph(),jtg.junctionTree(dag),jtg.eliminationOrder(dag),
↪jtg.binaryJoinTree(dag),
               captions=["A DAG","its moral graph",
                         "a junction tree for this dag (with partial order)",
                         "its elimination order (with partial order)",
                         "an (optipmized) binary jointree (with partial order)"])
```

```
<IPython.core.display.HTML object>
```

In [17]:
```
#creating an undigraph slightly different
ug=bn.dag().moralGraph()
ug.addEdge(0,7)
gnb.sideBySide(ug,jtg.junctionTree(ug),jtg.eliminationOrder(ug),jtg.
↪binaryJoinTree(ug),
               captions=["A undigraph",
                         "a junction tree for this undigraph",
                         "its elimination order",
                         "an (optipmized) binary jointree"])
```

```
<IPython.core.display.HTML object>
```

Using partial order to specify the elimination order

In [18]:
```
#adding a partial order for the elimination order
po=[[1,2,3],[0,4,7],[5,6]]
gnb.sideBySide(bn,jtg.junctionTree(bn,po),jtg.eliminationOrder(bn,po),jtg.
↪binaryJoinTree(bn),
               captions=["A Bayesien network",
                         "a junction tree for this BN using partial order",
                         "its elimination order following partial order",
                         "an (optimized) binary join tree"])
```

```
<IPython.core.display.HTML object>
```

In [19]:
```
#adding a partial order for the elimination order also for the graphs
po=[[0,4,7],[1,3],[5,6,2]]

#creating a dag slightly different
dag=bn.dag()
dag.addArc(0,3)
dag.addArc(0,7)

gnb.sideBySide(dag,dag.moralGraph(),jtg.junctionTree(dag,po),jtg.eliminationOrder(dag,
↪po),jtg.binaryJoinTree(dag,po),
               captions=["A DAG","its moral graph",
                         "a junction tree for this dag (with partial order)",
                         "its elimination order (with partial order)",
                         "an (optipmized) binary jointree (with partial order)"])
```

```
<IPython.core.display.HTML object>
```

In [ ]:
```
```

1.21.2 Relevance Reasoning with pyAgrum

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

Relevance reasoning is the analysis of the influence of evidence on a Bayesian network.

In this notebook we will explain what is relevance reasoning and how to do it using pyAgrum.

In [1]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb

import time
import os
%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt
```

Multiple inference

In the well known 'alarm' BN, how to analyze the influence on 'VENTALV' of a soft evidence on 'MINVOLSET' ?

In [2]:
```
bn=gum.loadBN("res/alarm.dsl")
gnb.showBN(bn,size="6")
```

nbsphinx-code-borderwhite

We propose to draw the plot of the posterior of 'VENTALV' for the evidence :

$$\forall x \in [0,1], e_{MINVOLSET} = [0, x, 0.5]$$

To do so, we perform a large number of inference and plot the posteriors.

In [3]:
```
K=1000
r=range(0,K)
xs=[x/K for x in r]

def getPlot(xs,ys,K,duration):
    p=plot(xs,ys)
    legend(p,[bn.variableFromName('VENTALV').label(i)
              for i in range(bn.variableFromName('VENTALV').domainSize())],loc=7);
    title('VENTALV ({} inferences in {:5.3} s)'.format(K,duration));
    ylabel('posterior Probability');
    xlabel('Evidence on MINVOLSET : [0,x,0.5]');
```

First try : classical lazy propagation

In [4]:
```
tf=time.time()
ys=[]
for x in r:
    ie=gum.LazyPropagation(bn)
    ie.setNumberOfThreads(1) # to be fair, we avoid multithreaded inference
    ie.addEvidence('MINVOLSET',[0,x/K,0.5])
    ie.makeInference()
    ys.append(ie.posterior('VENTALV').tolist())
delta1=time.time()-tf
getPlot(xs,ys,K,delta1)
```

nbsphinx-code-borderwhite

The title of the figure above gives the time for those 1000 inference.

Second try : classical variable elimination

One can note that we just need one posterior. This is a case where VariableElimination should give better results.

In [5]:
```
tf=time.time()
ys=[]
for x in r:
    ie=gum.VariableElimination(bn)
    ie.addEvidence('MINVOLSET',[0,x/K,0.5])
    ie.makeInference()
    ys.append(ie.posterior('VENTALV').tolist())
delta2=time.time()-tf
getPlot(xs,ys,K,delta2)
```

nbsphinx-code-borderwhite

pyAgrum give us a function `gum.getPosterior` to do this same job more easily.

In [6]:
```
tf=time.time()
ys=[gum.getPosterior(bn,{'MINVOLSET':[0,x/K,0.5]},'VENTALV').tolist()
        for x in r]
getPlot(xs,ys,K,time.time()-tf)
```

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Last try : optimized Lazy propagation with relevance reasoning and incremental inference

Optimized inference in aGrUM can use the targets and the evidence to optimize the computations. This is called **relevance reasonning**.

Moreover, if the values of the evidence change but not the structure of the query (same nodes as target, same nodes as hard evidence, same nodes as soft evidence), inference in aGrUM may re-use some of the computations from a query to another. This is called **incremental inference**.

In [7]:
```
tf=time.time()
ie=gum.LazyPropagation(bn)
ie.setNumberOfThreads(1) # to be fair, we avoid multithreaded inference
ie.addEvidence('MINVOLSET',[1,1,1])
ie.addTarget('VENTALV')
ys=[]
for x in r:
    ie.chgEvidence('MINVOLSET',[0,x/K,0.5])
    ie.makeInference()
    ys.append(ie.posterior('VENTALV').tolist())
delta3=time.time()-tf
getPlot(xs,ys,K,delta3)
```

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In [8]:
```
print("Mean duration of a lazy propagation           : {:5.3f}ms".format(1000*delta1/
↪K))
print("Mean duration of a variable elimination       : {:5.3f}ms".format(1000*delta2/
↪K))
print("Mean duration of an optimized lazy propagation : {:5.3f}ms".format(1000*delta3/
↪K))
```

```
Mean duration of a lazy propagation           : 4.837ms
Mean duration of a variable elimination       : 0.589ms
Mean duration of an optimized lazy propagation : 0.420ms
```

How it works

In [9]:
```
bn=gum.fastBN("Y->X->T1;Z2->X;Z1->X;Z1->T1;Z1->Z3->T2")
ie=gum.LazyPropagation(bn)

gnb.flow.row(bn,bn.cpt("X"),gnb.getJunctionTree(bn),gnb.getJunctionTreeMap(bn,size="3!
↪"),
             captions=["BN","potential","Junction Tree","The map"])
```

```
<IPython.core.display.HTML object>
```

aGrUM/pyAgrum uses as much as possible techniques of relevance reasonning to reduce the complexity of the inference.

In [10]:
```
ie.setEvidence({"X":0})
gnb.sideBySide(ie,gnb.getDot(ie.joinTree().toDotWithNames(bn)),ie.joinTree().map(),
               captions=["","Join tree optimized for hard evidence on X","the map"])
```

```
<IPython.core.display.HTML object>
```

In [11]:
```
ie.updateEvidence({"X":[0.1,0.9]})
gnb.sideBySide(ie,gnb.getDot(ie.joinTree().toDotWithNames(bn)),ie.joinTree().map(),
               captions=["","Join tree optimized for soft evidence on X","the map"])
```

```
<IPython.core.display.HTML object>
```

In [12]:
```
ie.updateEvidence({"Y":0,"X":0,3:[0.1,0.9],"Z1":[0.4,0.6]})
gnb.sideBySide(ie,gnb.getDot(ie.joinTree().toDotWithNames(bn)),ie.joinTree().map(),
               captions=["","Join tree optimized for hard evidence on X and Y, soft␣
↪on Z2 and Z1","the map"])
```

```
<IPython.core.display.HTML object>
```

In [13]:
```
ie.setEvidence({"X":0})
ie.setTargets({"T1","Z1"})
gnb.sideBySide(ie,gnb.getDot(ie.joinTree().toDotWithNames(bn)),ie.joinTree().map(),
               captions=["","Join tree optimized for hard evidence on X and targets␣
↪T1,Z1","the map"])
```

```
<IPython.core.display.HTML object>
```

In [14]:
```
ie.updateEvidence({"Y":0,"X":0,3:[0.1,0.9],"Z1":[0.4,0.6]})
ie.addJointTarget({"Z2","Z1","T1"})

gnb.sideBySide(ie,
               gnb.getDot(ie.joinTree().toDotWithNames(bn)),ie.joinTree().map(),
               captions=["","Join tree optimized for hard evidence on X and targets␣
↪T1,Z1","the map"])
```

```
<IPython.core.display.HTML object>
```

In [15]:
```
ie.makeInference()
ie.jointPosterior({"Z2","Z1","T1"})
```

Out[15]:
```
(pyAgrum.Potential<double>@000002BF59732F60)
              ||  Z1                |
T1    |Z2    ||0         |1         |
------|------||----------|----------|
0     |0     || 0.0218   | 0.0111   |
1     |0     || 0.0125   | 0.0356   |
0     |1     || 0.0342   | 0.2052   |
1     |1     || 0.0196   | 0.6599   |
```

In [16]:
```
ie.jointPosterior({"Z2","Z1"})
```

Out[16]:
```
(pyAgrum.Potential<double>@000002BF59732F80)
      ||  Z1                |
Z2    ||0         |1         |
------||----------|----------|
0     || 0.0343   | 0.0467   |
1     || 0.0538   | 0.8651   |
```

In [17]:
```
# this will not work
try:
    ie.jointPosterior({"Z3","Z1"})
except gum.UndefinedElement:
    print("Indeed, there is no joint target which contains {4,5} !")
```

```
Indeed, there is no joint target which contains {4,5} !
```

In [18]:
```
ie.addJointTarget({"Z2","Z1"})
gnb.sideBySide(ie,
               gnb.getDot(ie.joinTree().toDotWithNames(bn)),
              captions=['','JoinTree'])
```

```
<IPython.core.display.HTML object>
```

In [ ]:
```
```

1.21.3 Some other features in Bayesian inference

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

Lazy Propagation uses a secondary structure called the “Junction Tree” to perform the inference.

In [1]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb

bn=gum.loadBN("res/alarm.dsl")
gnb.showJunctionTreeMap(bn);
```

nbsphinx-code-borderwhite

But this junction tree can be transformed to build different probabilistic queries.

In [2]:
```
bn=gum.fastBN("A->B->C->D;A->E->D;F->B;C->H")
ie=gum.LazyPropagation(bn)
bn
```

Out[2]:
```
(pyAgrum.BayesNet<double>@00000129E82E9A10) BN{nodes: 7, arcs: 7, domainSize: 128,␣
↪dim: 32}
```

Evidence impact

Evidence Impact allows the user to analyze the effect of any variables on any other variables

In [3]:
```
ie.evidenceImpact("B",["A","H"])
```

Out[3]:
```
(pyAgrum.Potential<double>@00000129E86B3E30)
              ||  B                |
H     |A     ||0         |1        |
------|------||---------|---------|
0     |0     || 0.4631  | 0.5369  |
1     |0     || 0.5761  | 0.4239  |
0     |1     || 0.3879  | 0.6121  |
1     |1     || 0.4996  | 0.5004  |
```

Evidence impact is able to find the minimum set of variables which effectively conditions the analyzed variable

In [4]:
```
ie.evidenceImpact("E",["A","F","B","D"]) # {A,D,B} d-separates E and F
```

Out[4]:
```
(pyAgrum.Potential<double>@00000129E86B3BF0)
                     ||  E                |
D     |B     |A     ||0         |1        |
------|------|------||---------|---------|
0     |0     |0     || 0.1907  | 0.8093  |
1     |0     |0     || 0.3157  | 0.6843  |
0     |1     |0     || 0.1025  | 0.8975  |
1     |1     |0     || 0.4230  | 0.5770  |
0     |0     |1     || 0.2897  | 0.7103  |
1     |0     |1     || 0.4440  | 0.5560  |
0     |1     |1     || 0.1651  | 0.8349  |
1     |1     |1     || 0.5592  | 0.4408  |
```

In [5]:
```
ie.evidenceImpact("E",["A","B","C","D","F"]) # {A,C,D} d-separates E and {B,F}
```

Out[5]:
```
(pyAgrum.Potential<double>@00000129E86B3AB0)
                     ||  E                |
D     |A     |C     ||0         |1        |
------|------|------||---------|---------|
0     |0     |0     || 0.3251  | 0.6749  |
1     |0     |0     || 0.0133  | 0.9867  |
0     |1     |0     || 0.4546  | 0.5454  |
1     |1     |0     || 0.0229  | 0.9771  |
0     |0     |1     || 0.0633  | 0.9367  |
1     |0     |1     || 0.4591  | 0.5409  |
0     |1     |1     || 0.1047  | 0.8953  |
1     |1     |1     || 0.5950  | 0.4050  |
```

Evidence Joint Imapct

In [6]:
```
ie.evidenceJointImpact(["A","F"],["B","C","D","E","H"]) # {B,E} d-separates [A,F] and
↪[C,D,H]
```

Out[6]:
```
(pyAgrum.Potential<double>@00000129E86B3DB0)
                     ||  A                |
F     |B     |E     ||0         |1        |
------|------|------||---------|---------|
0     |0     |0     || 0.0977  | 0.3931  |
1     |0     |0     || 0.0170  | 0.4922  |
```

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```
0     |1     |0     || 0.0173  | 0.5420  |
1     |1     |0     || 0.0696  | 0.3711  |
0     |0     |1     || 0.1561  | 0.3627  |
1     |0     |1     || 0.0272  | 0.4541  |
0     |1     |1     || 0.0282  | 0.5096  |
1     |1     |1     || 0.1133  | 0.3489  |
```

In [ ]:

1.21.4 Approximate inference in aGrUM (pyAgrum)

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

There are several approximate inference for BN in aGrUM (pyAgrum). They share the same API than exact inference. - Loopy Belief Propagation : LBP is an approximate inference that uses exact calculous methods (when the BN os a tree) even if the BN is not a tree. LBP is a special case of inference : the algorithm may not converge and even if it converges, it may converge to anything (but the exact posterior). LBP however is fast and usually gives not so bad results. - Sampling inference : Sampling inference use sampling to compute the posterior. The sampling may be (very) slow but those algorithms converge to the exac distribution. aGrUM implements : - Montecarlo sampling, - Weighted sampling, - Importance sampling, - Gibbs sampling. - Finally, aGrUM propose the so-called 'loopy version' of the sampling algorithms : the idea is to use LBP as a Dirichlet prior for the sampling algorithm. A loopy version of each sampling algorithm is proposed.

In [1]:
```
import os

%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt

def unsharpen(bn):
  """
  Force the parameters of the BN not to be a bit more far from 0 or 1
  """
  for nod in bn.nodes():
    bn.cpt(nod).translate(bn.maxParam() / 10).normalizeAsCPT()

def compareInference(ie,ie2,ax=None):
    """
    compare 2 inference by plotting all the points from (posterior(ie),posterior(ie2))
    """
    exact=[]
    appro=[]
    errmax=0
    for node in bn.nodes():
        # potentials as list
        exact+=ie.posterior(node).tolist()
```

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```
        appro+=ie2.posterior(node).tolist()
        errmax=max(errmax,
                   (ie.posterior(node)-ie2.posterior(node)).abs().max())

    if errmax<1e-10: errmax=0
    if ax==None:
        ax=plt.gca() # default axis for plt

    ax.plot(exact,appro,'ro')
    ax.set_title("{} vs {}\n {}\nMax error {:2.4} in {:2.4} seconds".format(
        str(type(ie)).split(".")[2].split("_")[0][0:-2], # name of first inference
        str(type(ie2)).split(".")[2].split("_")[0][0:-2], # name of second inference
        ie2.messageApproximationScheme(),
        errmax,
        ie2.currentTime())
                )
```

In [2]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
bn=gum.loadBN("res/alarm.dsl")
unsharpen(bn)

ie=gum.LazyPropagation(bn)
ie.makeInference()
```

In [3]:
```
gnb.showBN(bn,size='8')
```

nbsphinx-code-borderwhite

First, an exact inference.

In [4]:
```
gnb.sideBySide(gnb.getJunctionTreeMap(bn),gnb.getInference(bn,size="8")) # using␣
↪LazyPropagation by default
print(ie.posterior("KINKEDTUBE"))
```

```
<IPython.core.display.HTML object>
```

```
  KINKEDTUBE       |
TRUE     |FALSE    |
---------|---------|
 0.1167  | 0.8833  |
```

Gibbs Inference

Gibbs inference with default parameters

Gibbs inference iterations can be stopped : - by the value of error (epsilon) - by the rate of change of epsilon (MinEpsilonRate) - by the number of iteration (MaxIteration) - by the duration of the algorithm (MaxTime)

In [5]:
```
ie2=gum.GibbsSampling(bn)
ie2.setEpsilon(1e-2)
gnb.showInference(bn,engine=ie2,size="8")
print(ie2.posterior("KINKEDTUBE"))
print(ie2.messageApproximationScheme())
compareInference(ie,ie2)
```

nbsphinx-code-borderwhite

```
  KINKEDTUBE       |
TRUE     |FALSE    |
---------|---------|
 0.1156  | 0.8844  |

stopped with rate=0.00673795
```

nbsphinx-code-borderwhite

With default parameters, this inference has been stopped by a low value of rate.

Changing parameters

In [6]:
```
ie2=gum.GibbsSampling(bn)
ie2.setMaxIter(1000)
ie2.setEpsilon(5e-3)
ie2.makeInference()

print(ie2.posterior(2))
print(ie2.messageApproximationScheme())
```

```
  INTUBATION                  |
NORMAL   |ESOPHAGEA|ONESIDED  |
---------|---------|---------|
 0.8264  | 0.1136  | 0.0600  |

stopped with max iteration=1000
```

In [7]:
```
compareInference(ie,ie2)
```

nbsphinx-code-borderwhite

In [8]:
```
ie2=gum.GibbsSampling(bn)
ie2.setMaxTime(3)
ie2.makeInference()

print(ie2.posterior(2))
print(ie2.messageApproximationScheme())
compareInference(ie,ie2)
```

```
  INTUBATION                  |
NORMAL   |ESOPHAGEA|ONESIDED  |
```

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```
---------|---------|---------|
 0.9700  | 0.0033  | 0.0267  |

stopped with epsilon=0.201897
```

nbsphinx-code-borderwhite

Looking at the convergence

In [9]:
```
ie2=gum.GibbsSampling(bn)
ie2.setEpsilon(10**-1.8)
ie2.setBurnIn(300)
ie2.setPeriodSize(300)
ie2.setDrawnAtRandom(True)
gnb.animApproximationScheme(ie2)
ie2.makeInference()
```

nbsphinx-code-borderwhite

In [10]:
```
compareInference(ie,ie2)
```

nbsphinx-code-borderwhite

Importance Sampling

In [11]:
```
ie4=gum.ImportanceSampling(bn)
ie4.setEpsilon(10**-1.8)
ie4.setMaxTime(10) #10 seconds for inference
ie4.setPeriodSize(300)
ie4.makeInference()
compareInference(ie,ie4)
```

nbsphinx-code-borderwhite

Loopy Gibbs Sampling

Every sampling inference has a 'hybrid' version which consists in using a first loopy belief inference as a prior for the probability estimations by sampling.

In [12]:
```
ie3=gum.LoopyGibbsSampling(bn)

ie3.setEpsilon(10**-1.8)
ie3.setMaxTime(10) #10 seconds for inference
ie3.setPeriodSize(300)
ie3.makeInference()
compareInference(ie,ie3)
```

nbsphinx-code-borderwhite

Comparison of approximate inference

These computations may be a bit long

In [13]:
```
def compareAllInference(bn,evs={},epsilon=10**-1.6,epsilonRate=1e-8,maxTime=20):
    ies=[gum.LazyPropagation(bn),
         gum.LoopyBeliefPropagation(bn),
         gum.GibbsSampling(bn),
         gum.LoopyGibbsSampling(bn),
         gum.WeightedSampling(bn),
         gum.LoopyWeightedSampling(bn),
         gum.ImportanceSampling(bn),
         gum.LoopyImportanceSampling(bn)]

    # burn in for Gibbs samplings
    for i in [2,3]:
        ies[i].setBurnIn(300)
        ies[i].setDrawnAtRandom(True)

    for i in range(2,len(ies)):
        ies[i].setEpsilon(epsilon)
        ies[i].setMinEpsilonRate(epsilonRate)
        ies[i].setPeriodSize(300)
        ies[i].setMaxTime(maxTime)

    for i in range(len(ies)):
        ies[i].setEvidence(evs)
        ies[i].makeInference()

    fig, axes = plt.subplots(1,len(ies)-1,figsize=(35, 3),num='gpplot')
    for i in range(len(ies)-1):
        compareInference(ies[0],ies[i+1],axes[i])
```

Inference stopped by epsilon

In [14]:
```
compareAllInference(bn,epsilon=1e-1)
```
nbsphinx-code-borderwhite

In [15]:
```
compareAllInference(bn,epsilon=1e-2)
```
nbsphinx-code-borderwhite

inference stopped by time

In [16]:
```
compareAllInference(bn,maxTime=1,epsilon=1e-8)
```
nbsphinx-code-borderwhite

In [17]:
```
compareAllInference(bn,maxTime=2,epsilon=1e-8)
```
nbsphinx-code-borderwhite

Inference with Evidence

In [18]:
```
funny={'BP':1,'PCWP':2,'EXPCO2':0,'HISTORY':0}
compareAllInference(bn,maxTime=1,evs=funny,epsilon=1e-8)
```

nbsphinx-code-borderwhite

In [19]:
```
compareAllInference(bn,maxTime=4,evs=funny,epsilon=1e-8)
```

nbsphinx-code-borderwhite

In [20]:
```
compareAllInference(bn,maxTime=10,evs=funny,epsilon=1e-8)
```

nbsphinx-code-borderwhite

In [ ]:

1.21.5 Different sampling inference

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import os

%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt
```

In [2]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb

bn=gum.loadBN("res/Diabetes.bif")
#gnb.showBN(bn,size='8')
print(bn)
```

```
BN{nodes: 413, arcs: 602, domainSize: 10^406.108, dim: 461069}
```

First, some helpers

In [3]:
```
import timeit

class Timer:
    def __enter__(self):
        self.start =  timeit.default_timer()
        return self

    def __exit__(self, *args):
        self.end = timeit.default_timer()
        self.duration = self.end - self.start
```

In [4]:
```
def execute(ie):
    with Timer() as t:
        ie.makeInference()
        for i in bn.nodes():
            a=ie.posterior(i)
    return "duration : {:3.3f}s".format(t.duration)

def vals(bn,ie):
    exact=[]
    appro=[]
    for node in bn.nodes():
        # potentials as numpy array
        exact+=ie.posterior(node).tolist()

    return exact
```

Exact inference.

In [5]:
```
import matplotlib_inline
matplotlib_inline.backend_inline.set_matplotlib_formats('png')

plt.rcParams["figure.figsize"] = [30,3]

def compareIE(bn,maxtime,epsilon,evs=None):
    ie=gum.LazyPropagation(bn)
    if evs is not None:
        ie.setEvidence(evs)
    x=vals(bn,ie)

    ie2=gum.GibbsSampling(bn)
    if evs is not None:
        ie2.setEvidence(evs)
    ie2.setMaxTime(maxtime)
    ie2.setEpsilon(epsilon)
    txt="Gibbs : "+execute(ie2)+"\n"+ie2.messageApproximationScheme()
    y=vals(bn,ie2)
    plt.subplot(181)
    plt.plot(x,y,'ro')
    plt.title(txt)

    ie3=gum.MonteCarloSampling(bn)
    if evs is not None:
        ie3.setEvidence(evs)
    ie3.setMaxTime(maxtime)
    ie3.setEpsilon(epsilon)
    txt="MonteCarlo : "+execute(ie3)+"\n"+ie3.messageApproximationScheme()
    y=vals(bn,ie3)
    plt.subplot(182)
    plt.plot(x,y,'ro')
    plt.title(txt)

    ie4=gum.WeightedSampling(bn)
    if evs is not None:
        ie4.setEvidence(evs)
    ie4.setMaxTime(maxtime)
```

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```
    ie4.setEpsilon(epsilon)
    txt="Weighted : "+execute(ie4)+"\n"+ie4.messageApproximationScheme()
    y=vals(bn,ie4)
    plt.subplot(183)
    plt.plot(x,y,'ro')
    plt.title(txt)

    ie5=gum.ImportanceSampling(bn)
    if evs is not None:
        ie5.setEvidence(evs)
    ie5.setMaxTime(maxtime)
    ie5.setEpsilon(epsilon)
    txt="Importance: "+execute(ie5)+"\n"+ie5.messageApproximationScheme()
    y=vals(bn,ie5)
    plt.subplot(184)
    plt.plot(x,y,'ro')
    plt.title(txt)

    ie6=gum.LoopyBeliefPropagation(bn)
    if evs is not None:
        ie6.setEvidence(evs)
    ie6.setMaxTime(maxtime)
    ie6.setEpsilon(epsilon)
    txt="LBP: "+execute(ie6)+"\n"+ie6.messageApproximationScheme()
    y=vals(bn,ie6)
    plt.subplot(185)
    plt.plot(x,y,'ro')
    plt.title(txt)

    ie7=gum.LoopyWeightedSampling(bn)
    if evs is not None:
        ie7.setEvidence(evs)
    ie7.setMaxTime(maxtime)
    ie7.setEpsilon(epsilon)
    txt="LoopyWeighted: "+execute(ie7)+"\n"+ie7.messageApproximationScheme()
    y=vals(bn,ie7)
    plt.subplot(186)
    plt.plot(x,y,'ro')
    plt.title(txt)

    ie8=gum.LoopyGibbsSampling(bn)
    if evs is not None:
        ie8.setEvidence(evs)
    ie8.setMaxTime(maxtime)
    ie8.setEpsilon(epsilon)
    txt="LoopyGibbs: "+execute(ie8)+"\n"+ie8.messageApproximationScheme()
    y=vals(bn,ie8)
    plt.subplot(187)
    plt.plot(x,y,'ro')
    plt.title(txt)

    ie9=gum.LoopyImportanceSampling(bn)
    if evs is not None:
        ie9.setEvidence(evs)
    ie9.setMaxTime(maxtime)
    ie9.setEpsilon(epsilon)
```

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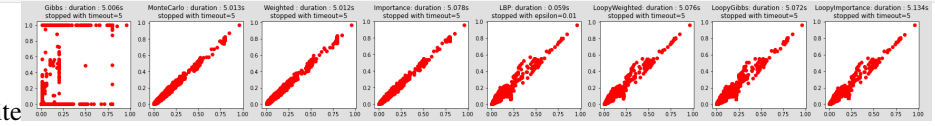
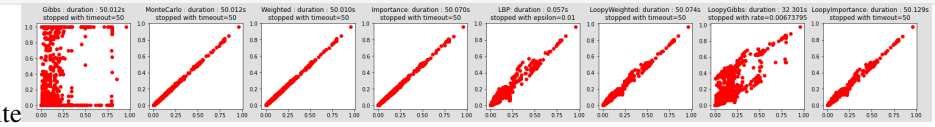
```
    txt="LoopyImportance: "+execute(ie9)+"\n"+ie9.messageApproximationScheme()
    y=vals(bn,ie9)
    plt.subplot(188)
    plt.plot(x,y,'ro')
    plt.title(txt)

    plt.show()
```

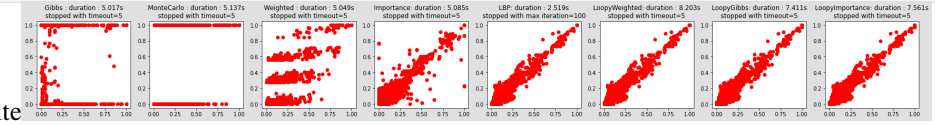
In [6]:
```
compareIE(bn,5,1e-2)
```

nbsphinx-code-borderwhite 

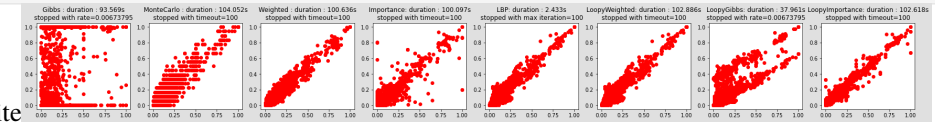
In [7]:
```
compareIE(bn,50,1e-2)
```

nbsphinx-code-borderwhite 

In [8]:
```
compareIE(bn,5,1e-2,evs={'bg_24':0,'ins_indep_util_23':1,'renal_cl_14':1})
```

nbsphinx-code-borderwhite 

In [9]:
```
compareIE(bn,100,1e-2,evs={'bg_24':0,'ins_indep_util_23':1,'renal_cl_14':1})
```

nbsphinx-code-borderwhite 

In [ ]:
```
```

1.22 Learning Bayesian networks

1.22.1 Learning the structure of a Bayesian network

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt
```

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```
import os
```

In [2]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
import pyAgrum.lib.explain as explain
import pyAgrum.lib.bn_vs_bn as bnvsbn

gum.about()
gnb.configuration()
```

```
pyAgrum 1.1.0.9
(c) 2015-2022 Pierre-Henri Wuillemin, Christophe Gonzales

    This is free software; see the source code for copying conditions.
    There is ABSOLUTELY NO WARRANTY; not even for MERCHANTABILITY or
    FITNESS FOR A PARTICULAR PURPOSE.  For details, see 'pyAgrum.warranty'.
```

```
<IPython.core.display.HTML object>
```

Generating the database from a BN

In [3]:
```
bn=gum.loadBN("res/asia.bif")
bn
```

Out[3]:
```
(pyAgrum.BayesNet<double>@0000022A4F0FBFD0) BN{nodes: 8, arcs: 8, domainSize: 256, dim: 36}
```

In [4]:
```
gum.generateSample(bn,500000,"out/sample_asia.csv",True);
```

```
out/sample_asia.csv: 100%||
```

```
Log2-Likelihood : -1613285.0339585799
```

In [5]:
```
with open("out/sample_asia.csv","r") as src:
    for _ in range(10):
        print(src.readline(),end="")
```

```
tuberculosis,smoking,tuberculos_or_cancer,visit_to_Asia,positive_XraY,bronchitis,lung_cancer,dyspnoea
1,0,1,1,1,1,1,0
1,0,1,1,1,0,1,1
1,1,1,1,1,1,1,1
1,1,1,1,1,1,1,1
1,1,1,1,1,1,1,1
1,0,0,1,0,1,0,0
1,0,1,1,1,1,1,0
1,1,1,1,1,0,1,0
1,1,1,1,1,0,1,0
```

In [6]:
```
learner=gum.BNLearner("out/sample_asia.csv",bn) #using bn as template for variables
print(learner)
```

```
Filename       : out/sample_asia.csv
Size           : (500000,8)
Variables      : visit_to_Asia[2], tuberculosis[2], tuberculos_or_cancer[2], positive_
↪XraY[2], lung_cancer[2], smoking[2], bronchitis[2], dyspnoea[2]
Induced types  : False
Missing values : False
Algorithm      : Greedy Hill Climbing
Score          : BDeu
Prior          : -
```

In [7]:
```
print(f"Row of visit_to_Asia : {learner.idFromName('visit_to_Asia')}") # first row is␣
↪0
```

```
Row of visit_to_Asia : 0
```

In [8]:
```
print(f"Variable in row 4 : {learner.nameFromId(4)}")
```

```
Variable in row 4 : lung_cancer
```

The BNLearner is capable of recognizing missing values in databases. For this purpose, just indicate as a last argument the list of the strings that represent missing values.

In [9]:
```
# it is possible to add as a last argument a list of the symbols that represent␣
↪missing values:
# whenever a cell of the database is equal to one of these strings, it is considered␣
↪as a
# missing value
learner=gum.BNLearner("res/asia_missing.csv",bn, ['?', 'N/A'] )
print(f"Are there missing values in the database ? {learner.state()['Missing values
↪'][0]}")
```

```
Are there missing values in the database ? True
```

type induction

When reading a csv file, BNLearner can try to find the correct type for discrete variable. Especially for numeric values.

In [10]:
```
%%writefile out/testTypeInduction.csv
A,B,C,D
1,2,0,hot
0,3,-2,cold
0,1,2,hot
1,2,2,warm
```

```
Overwriting out/testTypeInduction.csv
```

In [11]:
```
print("* by default, type induction is on (True) :")
learner=gum.BNLearner("out/testTypeInduction.csv")
bn3=learner.learnBN()
for v in sorted(bn3.names()):
    print(f"  - {bn3.variable(v)}")

print("")
print("* but you can disable it :")
learner=gum.BNLearner("out/testTypeInduction.csv",["?"],False)
```

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```
bn3=learner.learnBN()
for v in sorted(bn3.names()):
    print(f"  - {bn3.variable(v)}")

print("")
print("Note that when a Labelized variable is found, the labesl are alphabetically␣
↪sorted.")
```

```
* by default, type induction is on (True) :
  - A:Range([0,1])
  - B:Range([1,3])
  - C:Integer({-2|0|2})
  - D:Labelized({cold|hot|warm})

* but you can disable it :
  - A:Labelized({0|1})
  - B:Labelized({1|2|3})
  - C:Labelized({-2|0|2})
  - D:Labelized({cold|hot|warm})

Note that when a Labelized variable is found, the labesl are alphabetically sorted.
```

Parameters learning from the database

We give the bn as a parameter for the learner in order to have the variables and the order of the labels for each variables. Please try to remove the argument bn in the first line below to see the difference ...

In [12]:
```
learner=gum.BNLearner("out/sample_asia.csv",bn) #using bn as template for variables␣
↪and labels
bn2=learner.learnParameters(bn.dag())
gnb.showBN(bn2)
```

nbsphinx-code-borderwhite

In [13]:
```
from IPython.display import HTML

gnb.sideBySide("<H3>Original BN</H3>","<H3>Learned NB</H3>",
               bn.cpt ('visit_to_Asia'),bn2.cpt ('visit_to_Asia'),
               bn.cpt ('tuberculosis'),bn2.cpt ('tuberculosis'),
               ncols=2)
```

```
<IPython.core.display.HTML object>
```

Structural learning a BN from the database

Note that, currently, the BNLearner is not yet able to learn in the presence of missing values. This is the reason why, when it discovers that there exist such values, it raises a gum.MissingValueInDatabase exception.

In [14]:
```
with open("res/asia_missing.csv","r") as asiafile:
    for _ in range(10):
        print(asiafile.readline(),end="")
try:
    learner=gum.BNLearner("res/asia_missing.csv",bn, ['?', 'N/A'] )
    bn2=learner.learnBN()
except gum.MissingValueInDatabase:
    print ( "exception raised: there are missing values in the database" )
```

```
smoking,lung_cancer,bronchitis,visit_to_Asia,tuberculosis,tuberculos_or_cancer,
↪dyspnoea,positive_XraY
0,0,0,1,1,0,0,0
1,1,0,1,1,1,0,1
1,1,1,1,1,1,1,1
1,1,0,1,1,1,0,N/A
0,1,0,1,1,1,1,1
1,1,1,1,1,1,1,1
1,1,1,1,1,1,0,1
1,1,0,1,1,1,0,1
1,1,1,1,1,1,1,1
exception raised: there are missing values in the database
```

Different learning algorithms

For now, there are three algorithms that are wrapped in pyAgrum : LocalSearchWithTabuList,

In [15]:
```
learner=gum.BNLearner("out/sample_asia.csv",bn) #using bn as template for variables
learner.useLocalSearchWithTabuList()
print(learner)
bn2=learner.learnBN()
print("Learned in {0}ms".format(1000*learner.currentTime()))
gnb.flow.row(bn,bn2,explain.getInformation(bn2),captions=["Original BN","Learned BN",
↪"information"])
```

```
Filename       : out/sample_asia.csv
Size           : (500000,8)
Variables      : visit_to_Asia[2], tuberculosis[2], tuberculos_or_cancer[2], positive_
↪XraY[2], lung_cancer[2], smoking[2], bronchitis[2], dyspnoea[2]
Induced types  : False
Missing values : False
Algorithm      : Local Search with Tabu List
Tabu list size : 2
Score          : BDeu
Prior          : -

Learned in 131.2133ms
```

```
<IPython.core.display.HTML object>
```

To apprehend the distance between the original and the learned BN, we have several tools : - Compute the KL divergence (and other distance) between original and learned joint distribution

In [16]:
```
kl=gum.ExactBNdistance(bn,bn2)
kl.compute()
```

Out[16]:
```
{'klPQ': 2.111734327848637e-05,
 'errorPQ': 0,
 'klQP': 1.8016224314088024e-05,
 'errorQP': 128,
 'hellinger': 0.0027903639478247424,
 'bhattacharya': 3.887431170729849e-06,
 'jensen-shannon': 5.392839278947e-06}
```

- Compute some scores on the BNs (as binary classifiers) abd show the graphical diff between the two graphs

In [17]:
```
gcmp=bnvsbn.GraphicalBNComparator(bn,bn2)
gnb.flow.add(bnvsbn.graphDiff(bn,bn2))
gnb.flow.add(bnvsbn.graphDiffLegend())
gnb.flow.new_line()
gnb.flow.add_html("<br/>".join([f"{k} : {v:.2f}" for k,v in gcmp.skeletonScores().
↪items() if k!='count']),"Skeleton scores")
gnb.flow.add_html("<br/>".join([f"{k} : {v:.2f}" for k,v in gcmp.scores().items() if␣
↪k!='count']),"Scores")

gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

A greedy Hill Climbing algorithm (with insert, remove and change arc as atomic operations).

In [18]:
```
learner=gum.BNLearner("out/sample_asia.csv",bn) #using bn as template for variables
learner.useGreedyHillClimbing()
print(learner)
bn2=learner.learnBN()
print("Learned in {0}ms".format(1000*learner.currentTime()))
gnb.sideBySide(bn,bn2,gnb.getBNDiff(bn,bn2),explain.getInformation(bn2),captions=[
↪"Original BN","Learned BN","Graphical diff","information"])
```

```
Filename       : out/sample_asia.csv
Size           : (500000,8)
Variables      : visit_to_Asia[2], tuberculosis[2], tuberculos_or_cancer[2], positive_
↪XraY[2], lung_cancer[2], smoking[2], bronchitis[2], dyspnoea[2]
Induced types  : False
Missing values : False
Algorithm      : Greedy Hill Climbing
Score          : BDeu
Prior          : -

Learned in 108.212ms
```

```
<IPython.core.display.HTML object>
```

And a K2 for those who likes it :)

In [19]:
```
learner=gum.BNLearner("out/sample_asia.csv",bn) #using bn as template for variables
learner.useK2([0,1,2,3,4,5,6,7])
print(learner)
bn2=learner.learnBN()
print("Learned in {0}ms".format(1000*learner.currentTime()))
gnb.sideBySide(bn,bn2,gnb.getBNDiff(bn,bn2),explain.getInformation(bn2),captions=[
↪"Original BN","Learned BN","Graphical diff","information"])
```

```
Filename       : out/sample_asia.csv
Size           : (500000,8)
Variables      : visit_to_Asia[2], tuberculosis[2], tuberculos_or_cancer[2], positive_
↪XraY[2], lung_cancer[2], smoking[2], bronchitis[2], dyspnoea[2]
Induced types  : False
Missing values : False
Algorithm      : K2
K2 order       : visit_to_Asia, tuberculosis, tuberculos_or_cancer, positive_XraY,␣
↪lung_cancer, smoking, bronchitis, dyspnoea
Score          : BDeu
Prior          : -

Learned in 51.1976ms
```

```
<IPython.core.display.HTML object>
```

K2 can be very good if the order is the good one (a topological order of nodes in the reference)

In [20]:
```
learner=gum.BNLearner("out/sample_asia.csv",bn) #using bn as template for variables
learner.useK2([7,6,5,4,3,2,1,0])
print(learner)
bn2=learner.learnBN()
print("Learned in {0}s".format(learner.currentTime()))
gnb.sideBySide(bn,bn2,gnb.getBNDiff(bn,bn2),explain.getInformation(bn2),captions=[
↪"Original BN","Learned BN","Graphical diff","information"])
```

```
Filename       : out/sample_asia.csv
Size           : (500000,8)
Variables      : visit_to_Asia[2], tuberculosis[2], tuberculos_or_cancer[2], positive_
↪XraY[2], lung_cancer[2], smoking[2], bronchitis[2], dyspnoea[2]
Induced types  : False
Missing values : False
Algorithm      : K2
K2 order       : dyspnoea, bronchitis, smoking, lung_cancer, positive_XraY,␣
↪tuberculos_or_cancer, tuberculosis, visit_to_Asia
Score          : BDeu
Prior          : -

Learned in 0.065218s
```

```
<IPython.core.display.HTML object>
```

Following the learning curve

In [21]:
```
import numpy as np
%matplotlib inline

learner=gum.BNLearner("out/sample_asia.csv",bn) #using bn as template for variables
learner.useLocalSearchWithTabuList()

# we could prefere a log2likelihood score
# learner.useScoreLog2Likelihood()
learner.setMaxTime(10)

# representation of the error as a pseudo log (negative values really represents␣
↪negative epsilon
@np.vectorize
def pseudolog(x):
    res=np.log(x)#np.log(y)

    return res if x>0 else -res

# in order to control the complexity, we limit the number of parents
learner.setMaxIndegree(7) # no more than 3 parent by node
learner.setEpsilon(1e-10)
gnb.animApproximationScheme(learner,
                            scale=pseudolog) # scale by default is np.log10

bn2=learner.learnBN()
```

nbsphinx-code-borderwhite

Customizing the learning algorithms

1. Learn a tree ?

In [22]:
```
learner=gum.BNLearner("out/sample_asia.csv",bn) #using bn as template for variables
learner.useGreedyHillClimbing()

learner.setMaxIndegree(1) # no more than 1 parent by node
print(learner)
bntree=learner.learnBN()
gnb.sideBySide(bn,bntree,gnb.getBNDiff(bn,bntree),explain.getInformation(bntree),
↪captions=["Original BN","Learned BN","Graphical diff","information"])
```

```
Filename                : out/sample_asia.csv
Size                    : (500000,8)
Variables               : visit_to_Asia[2], tuberculosis[2], tuberculos_or_cancer[2],␣
↪positive_XraY[2], lung_cancer[2], smoking[2], bronchitis[2], dyspnoea[2]
Induced types           : False
Missing values          : False
Algorithm               : Greedy Hill Climbing
Score                   : BDeu
Prior                   : -
Constraint Max InDegree : 1  (Used only for score-based algorithms.)
```

```
<IPython.core.display.HTML object>
```

2. with prior structural knowledge

In [23]:
```
learner=gum.BNLearner("out/sample_asia.csv",bn) #using bn as template for variables
learner.useGreedyHillClimbing()

# I know that smoking causes cancer
learner.addMandatoryArc("smoking","lung_cancer") # smoking->lung_cancer
# I know that visit to Asia may change the risk of tuberculosis
learner.addMandatoryArc("visit_to_Asia","tuberculosis") # visit_to_Asia->tuberculosis
print(learner)
bn2=learner.learnBN()
gnb.sideBySide(bn,bn2,gnb.getBNDiff(bn,bn2),explain.getInformation(bn2),captions=[
↪"Original BN","Learned BN","Graphical diff","information"])
```

```
Filename                : out/sample_asia.csv
Size                    : (500000,8)
Variables               : visit_to_Asia[2], tuberculosis[2], tuberculos_or_
↪cancer[2], positive_XraY[2], lung_cancer[2], smoking[2], bronchitis[2], dyspnoea[2]
Induced types           : False
Missing values          : False
Algorithm               : Greedy Hill Climbing
Score                   : BDeu
Prior                   : -
Constraint Mandatory Arcs : {visit_to_Asia->tuberculosis, smoking->lung_cancer}
```

```
<IPython.core.display.HTML object>
```

3. changing the scores

By default, a BDEU score is used. But it can be changed.

In [24]:
```
learner=gum.BNLearner("out/sample_asia.csv",bn) #using bn as template for variables
learner.useGreedyHillClimbing()

# I know that smoking causes cancer
learner.addMandatoryArc(0,1)

# we prefere a log2likelihood score
learner.useScoreLog2Likelihood()

# in order to control the complexity, we limit the number of parents
learner.setMaxIndegree(1) # no more than 1 parent by node
print(learner)
bn2=learner.learnBN()
kl=gum.ExactBNdistance(bn,bn2)
gnb.sideBySide(bn,bn2,gnb.getBNDiff(bn,bn2),
               "<br/>".join(["<b>"+k+"</b> :"+str(v) for k,v in kl.compute().
↪items()]),
               captions=["original","learned BN","diff","distances"])
```

```
Filename                  : out/sample_asia.csv
Size                      : (500000,8)
Variables                 : visit_to_Asia[2], tuberculosis[2], tuberculos_or_
↪cancer[2], positive_XraY[2], lung_cancer[2], smoking[2], bronchitis[2], dyspnoea[2]
Induced types             : False
Missing values            : False
Algorithm                 : Greedy Hill Climbing
Score                     : Log2Likelihood
Prior                     : -
Constraint Max InDegree   : 1  (Used only for score-based algorithms.)
Constraint Mandatory Arcs : {visit_to_Asia->tuberculosis}
```

```
<IPython.core.display.HTML object>
```

4. comparing BNs

There are multiple ways to compare Bayes net...

In [25]:
```
help(gnb.getBNDiff)
```

```
Help on function getBNDiff in module pyAgrum.lib.notebook:

getBNDiff(bn1, bn2, size=None, noStyle=False)
    get a HTML string representation of a graphical diff between the arcs of _bn1␣
↪(reference) with those of _bn2.

    if `noStyle` is False use 4 styles (fixed in pyAgrum.config) :
      - the arc is common for both
      - the arc is common but inverted in `bn2`
      - the arc is added in `bn2`
```

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```
    - the arc is removed in `bn2`

  Parameters
  ----------
  bn1: pyAgrum.BayesNet
    the reference
  bn2: pyAgrum.BayesNet
    the compared one
  size: float|str
    size of the rendered graph
  noStyle: bool
    with style or not.

  Returns
  -------
    the HTML representation of the comparison
```

In [26]:
```
gnb.showBNDiff(bn,bn2)
```

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In [27]:
```
import pyAgrum.lib.bn_vs_bn as gbnbn
help(gbnbn.graphDiff)
```

```
Help on function graphDiff in module pyAgrum.lib.bn_vs_bn:

graphDiff(bnref, bncmp, noStyle=False)
    Return a pydot graph that compares the arcs of bnref to bncmp.
    graphDiff allows bncmp to have less nodes than bnref. (this is not the case in␣
↪GraphicalBNComparator.dotDiff())

    if noStyle is False use 4 styles (fixed in pyAgrum.config) :
      - the arc is common for both
      - the arc is common but inverted in _bn2
      - the arc is added in _bn2
      - the arc is removed in _bn2

    See graphDiffLegend() to add a legend to the graph.
    Warning
    -------
    if pydot is not installed, this function just returns None

    Returns
    -------
    pydot.Dot
      the result dot graph or None if pydot can not be imported
```

In [28]:
```
gbnbn.GraphicalBNComparator?
```

```
Init signature: gbnbn.GraphicalBNComparator(name1, name2, delta=1e-06)
Docstring:
BNGraphicalComparator allows to compare in multiple way 2 BNs...The smallest␣
↪assumption is that the names of the variables are the same in the 2 BNs. But some␣
↪comparisons will have also to check the type and domainSize of the variables. The␣
↪bns have not exactly the  same role : _bn1 is rather the referent model for the␣
↪comparison whereas _bn2 is the compared one to the referent model.
```

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```
Parameters
----------
name1 : str or pyAgrum.BayesNet
  a BN or a filename for reference
name2 : str or pyAgrum.BayesNet
  another BN or antoher filename for comparison
File:           c:\users\phw\scoop\apps\python\current\lib\site-packages\pyagrum\lib\
↪bn_vs_bn.py
Type:           type
Subclasses:
```

In [29]:
```
gcmp=gbnbn.GraphicalBNComparator(bn,bn2)
gnb.sideBySide(bn,bn2,gcmp.dotDiff(),gbnbn.graphDiffLegend(),
               bn2,bn,gbnbn.graphDiff(bn2,bn),gbnbn.graphDiffLegend(),
               ncols=4)
```

```
<IPython.core.display.HTML object>
```

In [30]:
```
print("But also gives access to different scores :")
print(gcmp.scores())
print(gcmp.skeletonScores())
print(gcmp.hamming())
```

```
But also gives access to different scores :
{'count': {'tp': 4, 'tn': 45, 'fp': 3, 'fn': 4}, 'recall': 0.5, 'precision': 0.
↪5714285714285714, 'fscore': 0.5333333333333333, 'dist2opt': 0.6585388898066349}
{'count': {'tp': 6, 'tn': 19, 'fp': 1, 'fn': 2}, 'recall': 0.75, 'precision': 0.
↪8571428571428571, 'fscore': 0.7999999999999999, 'dist2opt': 0.2879377767249482}
{'hamming': 3, 'structural hamming': 7}
```

In [31]:
```
print("KL divergence can be computed")
kl=gum.ExactBNdistance (bn,bn2)
kl.compute()
```

```
KL divergence can be computed
```

Out[31]:
```
{'klPQ': 0.12241870078655698,
 'errorPQ': 0,
 'klQP': 0.03312237743290082,
 'errorQP': 64,
 'hellinger': 0.20546805471860538,
 'bhattacharya': 0.02133452626980637,
 'jensen-shannon': 0.024300742692194646}
```

5. Mixing algorithms

First we learn a structure with HillClimbing (faster ?)

In [32]:
```
learner=gum.BNLearner("out/sample_asia.csv",bn) #using bn as template for variables
learner.useGreedyHillClimbing()
learner.addMandatoryArc(0,1)
bn2=learner.learnBN()
kl=gum.ExactBNdistance(bn,bn2)
gnb.sideBySide(bn,bn2,gnb.getBNDiff(bn,bn2),
```

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```
                "<br/>".join(["<b>"+k+"</b> :"+str(v) for k,v in kl.compute().
↪items()]),
                captions=["original","learned BN","diff","distances"])
```

```
<IPython.core.display.HTML object>
```

And then we refine with tabuList

In [33]:
```
learner=gum.BNLearner("out/sample_asia.csv",bn) #using bn as template for variables
learner.useLocalSearchWithTabuList()

learner.setInitialDAG(bn2.dag())
print(learner)
bn3=learner.learnBN()
kl=gum.ExactBNdistance(bn,bn3)
gnb.sideBySide(bn,bn2,gnb.getBNDiff(bn,bn2),
                "<br/>".join(["<b>"+k+"</b> :"+str(v) for k,v in kl.compute().
↪items()]),
                captions=["original","learned BN","diff","distances"])
```

```
Filename       : out/sample_asia.csv
Size           : (500000,8)
Variables      : visit_to_Asia[2], tuberculosis[2], tuberculos_or_cancer[2], positive_
↪XraY[2], lung_cancer[2], smoking[2], bronchitis[2], dyspnoea[2]
Induced types  : False
Missing values : False
Algorithm      : Local Search with Tabu List
Tabu list size : 2
Score          : BDeu
Prior          : -
Initial DAG    : True  (digraph {
     0;
     1;
     2;
     3;
     4;
     5;
     6;
     7;

     1 -> 7;
     0 -> 1;
     6 -> 5;
     2 -> 1;
     4 -> 1;
     4 -> 5;
     4 -> 2;
     2 -> 6;
     0 -> 2;
     4 -> 6;
     2 -> 3;
     2 -> 7;
     7 -> 6;
}

)
```

```
<IPython.core.display.HTML object>
```

Impact of the size of the database for the learning

In [34]:
```
import IPython.display
rows=3
sizes=[400,500,700,1000,2000,5000,
       10000,50000,75000,
       100000,150000,175000,
       200000,300000,500000]

def extract_asia(n):
    """
    extract n line from asia.csv to extract.csv
    """
    with open("out/sample_asia.csv","r") as src:
        with open("out/extract_asia.csv","w") as dst:
            for _ in range(n+1):
                print(src.readline(),end="",file=dst)
```

In [35]:
```
gnb.flow.clear()
nbr=0
l=[]
for i in sizes:
    extract_asia(i)
    learner=gum.BNLearner("out/extract_asia.csv",bn) # using bn as template for␣
↪variables
    learner.useGreedyHillClimbing()
    print(learner.state()["Size"][0])
    bn2=learner.learnBN()

    kl=gum.ExactBNdistance(bn,bn2)
    r=kl.compute()
    l.append(r['klPQ'])

    gnb.flow.add(gnb.getBNDiff(bn,bn2,size='3!'),f"size={i}")

gnb.flow.display()
plot(sizes,l)
print(l[-1])
```

```
(400,8)
(500,8)
(700,8)
(1000,8)
(2000,8)
(5000,8)
(10000,8)
(50000,8)
(75000,8)
(100000,8)
(150000,8)
(175000,8)
(200000,8)
```

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```
(300000,8)
(500000,8)
```

```
<IPython.core.display.HTML object>
```

```
1.7210567024329108e-05
```

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In [36]:
```
gnb.flow.clear()
nbr=0
l=[]
for i in sizes:
    extract_asia(i)
    learner=gum.BNLearner("out/extract_asia.csv",bn) #using bn as template for␣
↪variables
    learner.useLocalSearchWithTabuList()
    print(learner.state()["Size"][0])
    bn2=learner.learnBN()

    kl=gum.ExactBNdistance(bn,bn2)
    r=kl.compute()
    l.append(r['klPQ'])

    gnb.flow.add(gnb.getBNDiff(bn,bn2,size='3!'),f"size={i}")

gnb.flow.display()
plot(sizes,l)
print(l[-1])
```

```
(400,8)
(500,8)
(700,8)
(1000,8)
(2000,8)
(5000,8)
(10000,8)
(50000,8)
(75000,8)
(100000,8)
(150000,8)
(175000,8)
(200000,8)
(300000,8)
(500000,8)
```

```
<IPython.core.display.HTML object>
```

```
2.111734327848637e-05
```

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In [ ]:
```
```

1.22.2 Learning BN as probabilistic classifier

Learning a Bayesian network can be used to obtain a classifier for one of the nodes of the model. For more about classifier, see `pyAgrum.skbn`.

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import sys
import os

import numpy as np

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb

%matplotlib inline
from pyAgrum.lib.bn2roc import showROC
from pyAgrum.lib.bn2roc import showPR
from pyAgrum.lib.bn2roc import showROC_PR

SIZE_LEARN=10000
SIZE_VALID=2000
```

In [2]:
```
bn=gum.loadBN("res/alarm.dsl")
bn
```

Out[2]:
```
(pyAgrum.BayesNet<double>@0000026D683B2B20) BN{nodes: 37, arcs: 46, domainSize: 10^16.
↪2389, dim: 752}
```

In [3]:
```
gum.generateSample(bn,SIZE_LEARN,"out/learn.csv",show_progress=True,with_labels=True)
gum.generateSample(bn,SIZE_VALID,"out/train.csv",show_progress=True,with_labels=True)
```

```
out/learn.csv: 100%||
Log2-Likelihood : -151324.2303803304
out/train.csv: 100%||
Log2-Likelihood : -30435.043192561592
```

Out[3]:
```
-30435.043192561592
```

Learning a BN from learn.csv

In [4]:
```
# Learning a BN from the database
learner=gum.BNLearner("out/train.csv")

bn2=learner.useMIIC().learnBN()
currentTime=learner.currentTime()
```

In [5]:
```
gnb.flow.add(gnb.getBN(bn2,size="9"),f"Learned with {SIZE_LEARN} lines in
↪{currentTime:.3f}s")
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

In [6]:
```
import pyAgrum.lib.bn_vs_bn as bnvsbn
gnb.flow.add(gnb.getBNDiff(bn,bn2,size="8!"),"Diff with MIIC")
gnb.flow.add(bnvsbn.graphDiffLegend())
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

In [7]:
```
bn3=learner.useGreedyHillClimbing().useNMLCorrection().useScoreBDeu().learnBN()
gnb.flow.add(gnb.getBNDiff(bn,bn3,size="8!"),"Diff with GHC/NMD/BDEU")
gnb.flow.add(bnvsbn.graphDiffLegend())
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

In [8]:
```
bn4=learner.useGreedyHillClimbing().useNMLCorrection().useScoreBDeu().
↪setInitialDAG(bn2.dag()).learnBN()
gnb.flow.add(gnb.getBNDiff(bn,bn4,size="8!"),"Diff with GHC/NMD/BDEU with intial DAG␣
↪from MIIC")
gnb.flow.add(bnvsbn.graphDiffLegend())
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

In [9]:
```
print(bn2.names())
```

```
{'INSUFFANESTH', 'ERRCAUTER', 'SAO2', 'LVEDVOLUME', 'PAP', 'HREKG', 'BP', 'HISTORY',
↪'HR', 'PCWP', 'CO', 'ERRLOWOUTPUT', 'TPR', 'VENTMACH', 'ARTCO2', 'KINKEDTUBE',
↪'MINVOL', 'HRBP', 'CATECHOL', 'STROKEVOLUME', 'SHUNT', 'VENTLUNG', 'INTUBATION',
↪'ANAPHYLAXIS', 'PVSAT', 'LVFAILURE', 'VENTTUBE', 'MINVOLSET', 'HRSAT', 'PULMEMBOLUS
↪', 'EXPCO2', 'PRESS', 'VENTALV', 'CVP', 'DISCONNECT', 'HYPOVOLEMIA', 'FIO2'}
```

In [10]:
```
gnb.showInference(bn2,evs={},size="14")
```

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Two classifiers from the learned BN

In [11]:
```
print(bn2.variableFromName("HRSAT"))
print(bn2.variableFromName("INTUBATION"))
```

```
HRSAT:Labelized({HIGH|LOW|NORMAL})
INTUBATION:Labelized({ESOPHAGEAL|NORMAL|ONESIDED})
```

In [12]:
```
showROC(bn2,"out/train.csv",'HRSAT','LOW',show_progress=False)
showROC(bn2,"out/train.csv",'HRSAT','NORMAL',show_progress=False)
showROC(bn2,"out/train.csv",'HRSAT','HIGH',show_progress=False);
```

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nbsphinx-code-borderwhite
nbsphinx-code-borderwhite

In [13]:
```
showROC(bn2,"out/train.csv",'INTUBATION',"ESOPHAGEAL",show_progress=False);
```

nbsphinx-code-borderwhite

In [14]:
```
showPR(bn2,"out/train.csv",'HRSAT','LOW',show_progress=False);
```

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In [15]:
```
showPR(bn2,"out/train.csv",'INTUBATION',"ESOPHAGEAL",show_progress=False);
```

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In [16]:
```
showROC_PR(bn2,"out/train.csv",'HRSAT','LOW',show_progress=False);
```

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In [17]:
```
showROC_PR(bn2,"out/train.csv",'INTUBATION',"ESOPHAGEAL",show_progress=False);
```

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In [ ]:
```
```

1.22.3 Learning essential graphs

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt

import os

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
```

Compare learning algorithms

Essentially MIIC and 3off2 computes the essential graph (CPDAG) from data. Essential graphs are mixed graphs.

In [2]:
```
learner=gum.BNLearner("out/sample_asia.csv")
learner.use3off2()
learner.useNMLCorrection()
print(learner)
ge3off2=learner.learnEssentialGraph()
```

```
Filename       : out/sample_asia.csv
Size           : (500000,8)
Variables      : tuberculosis[2], smoking[2], tuberculos_or_cancer[2], visit_to_
↪Asia[2], positive_XraY[2], bronchitis[2], lung_cancer[2], dyspnoea[2]
Induced types  : True
Missing values : False
Algorithm      : 3off2
Correction     : NML
Prior          : -
```

In [3]:
```
gnb.showDot(ge3off2.toDot());
```

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In [4]:
```
learner=gum.BNLearner("out/sample_asia.csv")
learner.useMIIC()
learner.useNMLCorrection()
print(learner)
gemiic=learner.learnEssentialGraph()
gemiic
```

```
Filename       : out/sample_asia.csv
Size           : (500000,8)
Variables      : tuberculosis[2], smoking[2], tuberculos_or_cancer[2], visit_to_
↪Asia[2], positive_XraY[2], bronchitis[2], lung_cancer[2], dyspnoea[2]
Induced types  : True
Missing values : False
Algorithm      : MIIC
Correction     : NML
Prior          : -
```

Out[4]:
```
<pyAgrum.pyAgrum.EssentialGraph; proxy of <Swig Object of type 'gum::EssentialGraph *
↪' at 0x000001E06A662FD0> >
```

For the others methods, it is possible to obtain the essential graph from the learned BN.

In [5]:
```
learner=gum.BNLearner("out/sample_asia.csv")
learner.useGreedyHillClimbing()
bnHC=learner.learnBN()
print(learner)
geHC=gum.EssentialGraph(bnHC)
geHC
gnb.sideBySide(bnHC,geHC)
```

```
Filename       : out/sample_asia.csv
Size           : (500000,8)
Variables      : tuberculosis[2], smoking[2], tuberculos_or_cancer[2], visit_to_
↪Asia[2], positive_XraY[2], bronchitis[2], lung_cancer[2], dyspnoea[2]
```

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```
Induced types  : True
Missing values : False
Algorithm      : Greedy Hill Climbing
Score          : BDeu
Prior          : -
```

```
<IPython.core.display.HTML object>
```

In [6]:
```
learner=gum.BNLearner("out/sample_asia.csv")
learner.useLocalSearchWithTabuList()
print(learner)
bnTL=learner.learnBN()
geTL=gum.EssentialGraph(bnTL)
geTL
gnb.sideBySide(bnTL,geTL)
```

```
Filename       : out/sample_asia.csv
Size           : (500000,8)
Variables      : tuberculosis[2], smoking[2], tuberculos_or_cancer[2], visit_to_
↪Asia[2], positive_XraY[2], bronchitis[2], lung_cancer[2], dyspnoea[2]
Induced types  : True
Missing values : False
Algorithm      : Local Search with Tabu List
Tabu list size : 2
Score          : BDeu
Prior          : -
```

```
<IPython.core.display.HTML object>
```

Hence we can compare the 4 algorithms.

In [7]:
```
(
  gnb.flow.clear()
  .add(ge3off2,"Essential graph from 3off2")
  .add(gemiic,"Essential graph from miic")
  .add(bnHC,"BayesNet from GHC")
  .add(geHC,"Essential graph from GHC")
  .add(bnTL,"BayesNet from TabuList")
  .add(geTL,"Essential graph from TabuList")
  .display()
)
```

```
<IPython.core.display.HTML object>
```

In [ ]:
```
```

1.22.4 Dirichlet prior

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

Dirichlet prior as database

BNLearner gives access of many priors for the parameters and structural learning. One of them is the Dirichlet prior which needs a a prior for every possible parameter in a BN. aGrUM/pyAgrum allows to use a database as a source of Dirichlet prior.

In [1]:
```
%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt

import os

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
import pyAgrum.lib.explain as explain

sizePrior=30000
sizeData=20000

import os
#the bases will be saved in "out/dirichlet_database.csv" and "out/observaition_
↪database.csv"
dirichletDatabase="out/dirichlet_database.csv"
obsDatabase="out/observation_database.csv"
```

Generating databases for Dirichlet prior and for the learning

In [2]:
```
bnPrior = gum.fastBN("A->B;C;D")
bnData = gum.fastBN("A->B->C->D")
bnData.cpt("B").fillWith([0.99,0.01,
                          0.01,0.99])
bnData.cpt("C").fillWith([0.9,0.1,
                          0.1,0.9])
bnData.cpt("D").fillWith([0.9,0.1,
                          0.1,0.9])
bnPrior.cpt("B").fillWith(bnData.cpt("B"))

gum.generateSample(bnPrior, sizePrior, dirichletDatabase, with_labels=True,random_
↪order=True)

gum.generateSample(bnData, sizeData, obsDatabase, with_labels=True,random_order=False)
```

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```
gnb.sideBySide(bnData,bnPrior,
               captions=[f"Database ({sizeData} cases)",f"Prior ({sizePrior} cases)"])
```

```
<IPython.core.display.HTML object>
```

Learning databases

In [3]:
```
# bnPrior is used to give the variables and their domains
learnerData = gum.BNLearner(obsDatabase)
learnerPrior = gum.BNLearner(dirichletDatabase)
learnerData.useScoreBIC()
learnerPrior.useScoreBIC()
gnb.sideBySide(learnerData.learnBN(),learnerPrior.learnBN(),
               captions=["Learning from Data","Learning from Prior"])
```

```
<IPython.core.display.HTML object>
```

Learning with Dirichlet prior

Now we use the Dirichlet prior. In order to have an idea of the influence of the priori, we change the weights of Data and Prior from [0,1] to [1,0] using a $ratio \in [0,1]$. The weight of a database is considered equal to the sum of the weights of each row. It is therefore in fact an equivalent sample size that is given.

In [4]:
```
learner = gum.BNLearner(obsDatabase, bnPrior)
print(learner)
```

```
Filename       : out/observation_database.csv
Size           : (20000,4)
Variables      : A[2], B[2], C[2], D[2]
Induced types  : False
Missing values : False
Algorithm      : Greedy Hill Climbing
Score          : BDeu
Prior          : -
```

In [5]:
```
def learnWithRatio(ratio):
    # bnPrior is used to give the variables and their domains

    learner = gum.BNLearner(obsDatabase, bnPrior)
    learner.useDirichletPrior(dirichletDatabase,ratio*sizeData)
    learner.setDatabaseWeight((1-ratio)*sizeData)
    learner.useScoreBIC() # or another score with no included prior
    return learner.learnBN()

ratios=[0.0,0.01,0.05,0.2,0.5,0.8,0.9,0.95,0.99,1.0]
bns=[learnWithRatio(r) for r in ratios]
gnb.sideBySide(*bns,
               captions=[*[f"with ratio {r}<br/> [datasize : {(int(r*sizeData),int((1-
↪r)*sizeData))}]" for r in ratios]],
               valign="bottom")
```

```
<IPython.core.display.HTML object>
```

The BNs learned when mixing the 2 data sources look much more complex than the data and the Dirichlet structures (with $ratio \in [0.01, 0.99]$). It may seem odd. However, if one looks at the mutual information,

In [6]:
```
gnb.sideBySide(*[explain.getInformation(bn) for bn in bns],
               captions=[*[f"with ratio {r}<br/> [datasize : {r*sizePrior+(1-
↪r)*sizeData}]" for r in ratios]],
               valign="bottom")
```

```
<IPython.core.display.HTML object>
```

It is obvious that these arcs represent weak and spurious correlations due to mixing probabilities (see Wellman et Peacock (99)) that become weaker when the weight of the prior increases.

Another way to look at the mixing is to plot the Kullback-Leibler divergence between the learned BNs and the 2 templates ($bnData$ and $bnPrior$)

In [7]:
```
def kls(i):
    kl=gum.ExactBNdistance(bnPrior,bns[i])
    y1=kl.compute()
    kl=gum.ExactBNdistance(bnData,bns[i])
    y2=kl.compute()
    return y1['klPQ'],y2['klPQ'],y1['klQP'],y2['klQP']


fig=figure(figsize=(10,6))
ax  = fig.add_subplot(1, 1, 1)

x=ratios
y1,y2,y3,y4=zip(*[kls(i) for i in range(len(ratios))])
ax.plot(x,y1,label="M-projection with bnPrior")
ax.plot(x,y3,label="I-projection with bnPrior")
ax.plot(x,y2,label="M-projection with bnData")
ax.plot(x,y4,label="I-projection with bnData")
ax.set_xticks(ratios)
ax.tick_params(rotation=90)
ax.set_xlabel("weight ratio between data and prior")
ax.set_ylabel("KL")
ax.legend(bbox_to_anchor=(0.15, 0.88, 0.7, .102), loc=3,ncol=2, mode="expand",␣
↪borderaxespad=0.)
t=ax.set_title("Weight ratio's Impact on KLs")
plt.show()
```

nbsphinx-code-borderwhite

We can use other divergences (or distances)

In [8]:
```
def distances(i):
    kl=gum.ExactBNdistance(bnPrior,bns[i])
    y1=kl.compute()
    kl=gum.ExactBNdistance(bnData,bns[i])
    y2=kl.compute()
    return y1['hellinger'],y2['hellinger'],y1['bhattacharya'],y2['bhattacharya'],y1[
↪'jensen-shannon'],y2['jensen-shannon']


fig=figure(figsize=(10,6))
ax  = fig.add_subplot(1, 1, 1)

x=ratios
y1,y2,y3,y4,y5,y6=zip(*[distances(i) for i in range(len(ratios))])
```

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```
ax.plot(x,y1,label="Hellinger with bnPrior")
ax.plot(x,y3,label="Bhattacharya with bnPrior")
ax.plot(x,y5,label="Jensen-Shannon with bnPrior")
ax.plot(x,y2,label="Hellinger with bnData")
ax.plot(x,y4,label="Bhattacharya with bnData")
ax.plot(x,y6,label="Jensen-Shannon with bnData")
ax.set_xticks(ratios)
ax.tick_params(rotation=90)
ax.set_xlabel("weight ratio between data and prior")
ax.set_ylabel("distances")
ax.legend(bbox_to_anchor=(0.15, 0.85, 0.7, .102), loc=3,ncol=2, mode="expand",␣
↪borderaxespad=0.)
t=ax.set_title("Weight ratio's Impact on distances")
plt.show()
```

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Less informative but still possible, we can trace the scores (precision, etc.) from a `pyAgrum.lib.bn_vs_bn.GraphicalBNComparator` (see `07-ComparingBN` for more)

In [9]:
```
import pyAgrum.lib.bn_vs_bn as gcm

def scores(i):
    cmp=gcm.GraphicalBNComparator(bnPrior,bns[i])
    y1=cmp.scores()
    cmp=gcm.GraphicalBNComparator(bnData,bns[i])
    y2=cmp.scores()
    return y1['recall']   ,y2['recall'],y1['precision'],y2['precision'],y1['fscore'],
↪y2['fscore'],y1['dist2opt'] ,y2['dist2opt']


fig=figure(figsize=(20,6))
ax1  = fig.add_subplot(1, 2, 1)
ax2  = fig.add_subplot(1, 2, 2)

x=ratios
y1,y2,y3,y4,y5,y6,y7,y8=zip(*[scores(i) for i in range(len(ratios))])
ax1.plot(x,y1,label="recall with bnPrior")
ax1.plot(x,y3,label="precision with bnPrior")
ax1.plot(x,y5,label="fscore with bnPrior")
ax1.plot(x,y7,label="dist2opt with bnPrior")

ax2.plot(x,y2,label="recall with bnData")
ax2.plot(x,y4,label="precision with bnData")
ax2.plot(x,y6,label="fscore with bnData")
ax2.plot(x,y8,label="dist2opt with bnData")

ax1.set_xticks(ratios)
ax1.tick_params(rotation=90)
ax1.set_xlabel("weight ratio between data and prior")
ax1.set_ylabel("KL")
ax1.legend(bbox_to_anchor=(0.15, 0.88, 0.7, .102), loc=3,ncol=2, mode="expand",␣
↪borderaxespad=0.)
ax1.set_title("Weight ratio's Impact on scores")

ax2.set_xticks(ratios)
ax2.tick_params(rotation=90)
ax2.set_xlabel("weight ratio between data and prior")
```

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```
ax2.set_ylabel("KL")
ax2.legend(bbox_to_anchor=(0.15, 0.88, 0.7, .102), loc=3,ncol=2, mode="expand",␣
↪borderaxespad=0.)
ax2.set_title("Weight ratio's Impact on scores")

plt.show()
```

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Weighted database and records

Database can be weighted as done above. But you can also fix the weight record by record in the database. Note that the weight of database is the sum of all weights for each record. And then

```
learner.setDatabaseWeight(2.5)
```

is equivalent to

```
siz=learner.nbRows()
for i in range(siz):
    learner.setRecordWeight(i,2.5/siz)
```

In [10]:
```
bn=gum.fastBN("X->Y")

#the base will be saved in basefile="out/dataW.csv"
basefile="out/dataW.csv"
```

In the 2 next cells, we compute the parameters of bn using 2 bases : in the next cell, the base contains 8 rows of weight 1. In the next one, the base contains only 4 rows but two of them have different weights. The sum of the weights in this second base is 8 as well ...

So the parameters are exactly the same.

In [11]:
```
%%writefile 'out/dataW.csv'
X,Y
1,0
0,1
0,1
0,0
1,0
0,1
1,1
0,1
```

```
Overwriting out/dataW.csv
```

In [12]:
```
learner=gum.BNLearner(basefile)
bn1=learner.learnParameters(bn.dag())
gnb.flow.row(bn1.cpt("X"),bn1.cpt("Y"))
```

```
<IPython.core.display.HTML object>
```

In [13]:
```
%%writefile 'out/dataW.csv'
X,Y
0,0
1,0
0,1
1,1
```

```
Overwriting out/dataW.csv
```

In [14]:
```
learner.setRecordWeight(1,2.0)
learner.setRecordWeight(2,4.0)

bn2=learner.learnParameters(bn.dag())
gnb.flow.row(bn2.cpt("X"),bn2.cpt("Y"))
```

```
<IPython.core.display.HTML object>
```

In [ ]:
```
```

1.22.5 Parametric EM (missing data)

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb

import os
#the bases will be saved in "out/*.csv"
EMnomissing="out/EM_nomissing.csv"
EMmissing="out/EM_missing.csv"
```

Generating data with missing values (at random)

In [2]:
```
src=gum.fastBN("A->B<-C->D->E<-B;D->F")
gum.generateSample(src,5000,EMnomissing,random_order=False)
src
```

Out[2]:
```
(pyAgrum.BayesNet<double>@0000021FF6B63560) BN{nodes: 6, arcs: 6, domainSize: 64, dim:
↪ 28}
```

In [3]:
```
import pandas as pd
import numpy as np

def add_missing(src,dst,proba):
  df=pd.read_csv(src)
  mask=np.random.choice([True, False], size=df.shape,p=[proba,1-proba])
  df.mask(mask).to_csv(dst,na_rep='?',index=False,float_format='%.0f')

gum.generateSample(src,5000,EMnomissing,random_order=False)
add_missing(EMnomissing,EMmissing,proba=0.1)
```

In [4]:
```
print("No missing")
with open(EMnomissing,"r") as srcfile:
    for _ in range(10):
        print(srcfile.readline(),end="")
print("Missing")
with open(EMmissing,"r") as srcfile:
    for _ in range(10):
        print(srcfile.readline(),end="")
```

```
No missing
A,B,C,D,E,F
1,1,1,0,0,1
1,1,0,1,1,1
0,1,1,0,0,0
1,1,0,0,1,1
1,1,1,0,1,0
0,1,1,0,1,1
1,1,1,0,0,1
1,0,0,1,0,0
1,0,1,0,1,1
Missing
A,B,C,D,E,F
1,1,?,0,?,1
1,1,0,1,1,1
?,?,1,0,?,0
?,1,?,0,1,1
1,1,1,0,1,0
0,1,1,0,1,1
1,1,1,0,0,1
1,0,0,1,0,?
1,0,?,0,1,1
```

Learning with missing data

In [5]:
```
learner = gum.BNLearner(EMmissing,src, ["?"])
print(f"Missing values in {EMmissing} : {learner.hasMissingValues()}")
```

```
Missing values in out/EM_missing.csv : True
```

In [6]:
```
try:
  learner.learnParameters(src.dag())
except gum.MissingValueInDatabase:
  print("Learning is not possible without EM if there are some missing values.")
```

```
Learning is not possible without EM if there are some missing values.
```

In [7]:
```
learner.useEM(1e-3)
learner.useSmoothingPrior()
print(learner)
bn=learner.learnParameters(src.dag())
print(f"# iterations : {learner.nbrIterations()}")
gnb.flow.row(gnb.getInference(src),gnb.getInference(bn))
```

```
Filename       : out/EM_missing.csv
Size           : (5000,6)
Variables      : A[2], B[2], C[2], D[2], E[2], F[2]
Induced types  : False
```

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```
Missing values : True
Algorithm      : Greedy Hill Climbing
Score          : BDeu
Prior          : Smoothing  (The BDeu score already contains a different 'implicit'␣
↪prior. Therefore, the learning will probably be biased.)
Prior weight   : 1.000000
EM             : True
EM epsilon     : 0.001000

# iterations : 6
```

```
<IPython.core.display.HTML object>
```

Learning with smaller error (and no smoothing)

In [8]:
```
learner = gum.BNLearner(EMmissing,src, ["?"])
learner.setVerbosity(True)
learner.useEM(1e-8)
bn2=learner.learnParameters(src.dag())
gnb.flow.row(gnb.getInference(src),gnb.getInference(bn2),captions=["Source",f
↪"Estimation EM en {learner.nbrIterations()} iteration(s)"])
```

```
<IPython.core.display.HTML object>
```

In [9]:
```
import matplotlib.pyplot as plt
import numpy as np
plt.plot(np.arange(1,1+learner.nbrIterations()),learner.history())
plt.xticks(np.arange(1, 1+learner.nbrIterations(), step=2))
plt.title("Error during EM iterations");
```

nbsphinx-code-borderwhite

In [ ]:
```
```

1.22.6 Scores, Chi2, etc. with BNLearner

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import os

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
```

Generating the database for scoring

In [2]:
```
bn=gum.loadBN("res/asia.bif")
bn
```

Out[2]:
```
(pyAgrum.BayesNet<double>@000001C4B7746690) BN{nodes: 8, arcs: 8, domainSize: 256,␣
↪dim: 36}
```

In [3]:
```
# we create a quite large database
gum.generateSample(bn,500000,"out/sample_score.csv",False)
```

Out[3]:
```
-1615826.0306111004
```

Testing d-separations using chi2 in the database

In [4]:
```
# do not forget that the generation process above is random : from time to time, the␣
↪tests my not be correct...
def isIndep(pvalue):
    return pvalue>=0.05

def testIndepFromChi2(learner,var1,var2,kno=[]):
    """
    Just prints the resultat of the chi2
    """
    stat,pvalue=learner.chi2(var1,var2,kno)
    if len(kno)==0:
        print("From Chi2 tests, is '{}' indep from '{}' ==> {}".format(var1,var2,
↪isIndep(pvalue)))
    else:
        print("From Chi2 tests, is '{}' indep from '{}' given {} : {}".format(var1,
↪var2,kno,isIndep(pvalue)))

learner=gum.BNLearner("out/sample_score.csv")

testIndepFromChi2(learner,"visit_to_Asia","smoking")
testIndepFromChi2(learner,"visit_to_Asia","smoking",['tuberculos_or_cancer'])
testIndepFromChi2(learner,"visit_to_Asia","smoking",['positive_XraY'])
testIndepFromChi2(learner,"dyspnoea","smoking")
testIndepFromChi2(learner,"dyspnoea","smoking",["lung_cancer","bronchitis"])
```

```
From Chi2 tests, is 'visit_to_Asia' indep from 'smoking' ==> True
From Chi2 tests, is 'visit_to_Asia' indep from 'smoking' given ['tuberculos_or_cancer
↪'] : False
From Chi2 tests, is 'visit_to_Asia' indep from 'smoking' given ['positive_XraY'] :␣
↪False
From Chi2 tests, is 'dyspnoea' indep from 'smoking' ==> False
From Chi2 tests, is 'dyspnoea' indep from 'smoking' given ['lung_cancer', 'bronchitis
↪'] : True
```

Evolution of chi2 p-values w.r.t the size of the database (in Asia)

In [5]:
```
def consolidationIndepFromChi2(bn,size,lindep,nbr=20):
    """
    Using $nbr$ generated databases of size $size$ from the bn $bn$,
    consolidate the p-value for a list $lindep$ of conditional independence to test.

    return the list of consolidated pValues
    """
    pvalue_cumul=[0.0]*len(lindep)
    for i in range(nbr):
        gum.generateSample(bn,size,"out/sample_score.csv",False)
        learner=gum.BNLearner("out/sample_score.csv")
        for i,(var1,var2,kno) in enumerate(lindep):
            stat,pvalue=learner.chi2(var1,var2,kno)
            pvalue_cumul[i]+=pvalue
    return [p/nbr for p in pvalue_cumul]

sizes=[50,100,500,1000,2000,5000,10000,20000,50000,100000,200000]
pvalues1,pvalues2,pvalues3,pvalues4,pvalues5,
↪pvalues6=zip(*[consolidationIndepFromChi2(bn,siz,
                                    [("visit_to_Asia","smoking",['tuberculos_or_
↪cancer']),
                                     ("visit_to_Asia","smoking",[]),
                                     ("dyspnoea","smoking",[]),
                                     ("dyspnoea","smoking",["lung_cancer","bronchitis
↪"]),
                                     ("tuberculosis","bronchitis",[]),
                                     ("tuberculosis","bronchitis",["dyspnoea"])])
                                         for siz in sizes])
```

In [6]:
```
%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt
import matplotlib.patches as patches

fig=figure(figsize=(10,6))
ax  = fig.add_subplot(1, 1, 1)

ax.plot(sizes,pvalues1,label="NOT(A indep S given TorC)", linestyle='dashed')
ax.plot(sizes,pvalues2,label="A indep S")
ax.plot(sizes,pvalues3,label="NOT(D indep S)", linestyle='dashed')
ax.plot(sizes,pvalues4,label="D indep S given L,B")
ax.plot(sizes,pvalues5,label="T indep B")
ax.plot(sizes,pvalues6,label="NOT(T indep B given D)", linestyle='dashed')

ax.tick_params(rotation=90)
ax.set_xlabel("data size")
ax.set_ylabel("pValue")
ax.legend(bbox_to_anchor=(0.15, 0.88, 0.7, .102), loc=3,ncol=3, mode="expand",␣
↪borderaxespad=0.)

rect = patches.Rectangle((0,0),max(sizes),0.05,linewidth=1,edgecolor='#FF8888',
↪facecolor='#FF8888')
ax.add_patch(rect)
ax.annotate("Critical region",xytext=(190000,0.2),xy=(190000,0.05),
```

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```
            ha="right", va="center",
            arrowprops=dict(arrowstyle="->",
                            connectionstyle="arc3,rad=-0.15"
                           ),
            bbox=dict(boxstyle="square", fc="w"))

ax.set_title("Chi2 pvalue=f(datasize)")
gnb.flow.add(fig)
gnb.flow.add(gnb.getBN(gum.fastBN("A->T->TorC->X;S->C->TorC->D<-B<-S")))
gnb.flow.new_line()

fig
```

nbsphinx-code-bordercolor

Testing d-separations using G2 in the database

In [7]:
```
def testIndepFromG2(learner,var1,var2,kno=[]):
    """
    Just prints the resultat of the G2
    """
    stat,pvalue=learner.G2(var1,var2,kno)
    if len(kno)==0:
        print("From G2 tests, is '{}' indep from '{}' ==> {}".format(var1,var2,
↪isIndep(pvalue)))
    else:
        print("From G2 tests, is '{}' indep from '{}' given {} : {}".format(var1,var2,
↪kno,isIndep(pvalue)))

learner=gum.BNLearner("out/sample_score.csv")

testIndepFromG2(learner,"visit_to_Asia","smoking")
testIndepFromG2(learner,"visit_to_Asia","smoking",['tuberculos_or_cancer'])
testIndepFromG2(learner,"visit_to_Asia","smoking",['positive_XraY'])
testIndepFromG2(learner,"dyspnoea","smoking")
testIndepFromG2(learner,"dyspnoea","smoking",["lung_cancer","bronchitis"])
```

```
From G2 tests, is 'visit_to_Asia' indep from 'smoking' ==> True
From G2 tests, is 'visit_to_Asia' indep from 'smoking' given ['tuberculos_or_cancer']␣
↪: False
From G2 tests, is 'visit_to_Asia' indep from 'smoking' given ['positive_XraY'] : True
From G2 tests, is 'dyspnoea' indep from 'smoking' ==> False
From G2 tests, is 'dyspnoea' indep from 'smoking' given ['lung_cancer', 'bronchitis']␣
↪: True
```

Evolution of G2 p-values w.r.t the size of the database (in Asia)

In [8]:
```
def consolidationIndepFromG2(bn,size,lindep,nbr=20):
    """
    Using $nbr$ generated databases of size $size$ from the bn $bn$,
    consolidate the p-value for a list $lindep$ of conditional independence to test.

    return the list of consolidated pValues
    """
    pvalue_cumul=[0.0]*len(lindep)
    for i in range(nbr):
        gum.generateSample(bn,size,"out/sample_chi2.csv",False)
        learner=gum.BNLearner("out/sample_chi2.csv")
        for i,(var1,var2,kno) in enumerate(lindep):
            stat,pvalue=learner.G2(var1,var2,kno)
            pvalue_cumul[i]+=pvalue
    return [p/nbr for p in pvalue_cumul]

sizes=[50,100,500,1000,2000,5000,10000,20000,50000,100000,200000]
pvalues1,pvalues2,pvalues3,pvalues4,pvalues5,
↪pvalues6=zip(*[consolidationIndepFromG2(bn,siz,
                                                                                    ␣
↪[("visit_to_Asia","smoking",['tuberculos_or_cancer']),
                                                                                     ␣
↪("visit_to_Asia","smoking",[]),
                                                                                     ␣
↪("dyspnoea","smoking",[]),
                                                                                     ␣
↪("dyspnoea","smoking",["lung_cancer","bronchitis"]),
                                                                                     ␣
↪("tuberculosis","bronchitis",[]),
                                                                                     ␣
↪("tuberculosis","bronchitis",["dyspnoea"])])
                                                        for siz in sizes])
```

In [9]:
```
fig=figure(figsize=(10,6))
ax  = fig.add_subplot(1, 1, 1)

ax.plot(sizes,pvalues1,label="NOT(A indep S given TorC)", linestyle='dashed')
ax.plot(sizes,pvalues2,label="A indep S")
ax.plot(sizes,pvalues3,label="NOT(D indep S)", linestyle='dashed')
ax.plot(sizes,pvalues4,label="D indep S given L,B")
ax.plot(sizes,pvalues5,label="T indep B")
ax.plot(sizes,pvalues6,label="NOT(T indep B given D)", linestyle='dashed')

ax.tick_params(rotation=90)
ax.set_xlabel("data size")
ax.set_ylabel("pValue")
ax.legend(bbox_to_anchor=(0.15, 0.83, 0.7, .102), loc=3,ncol=2, mode="expand",␣
↪borderaxespad=0.)

rect = patches.Rectangle((0,0),max(sizes),0.05,linewidth=1,edgecolor='#FF8888',
↪facecolor='#FF8888')
ax.add_patch(rect)
ax.annotate("Critical region",xytext=(190000,0.2),xy=(190000,0.05),
            ha="right", va="center",
            arrowprops=dict(arrowstyle="->",
```

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```
                              connectionstyle="arc3,rad=-0.15"
                             ),
            bbox=dict(boxstyle="square", fc="w"))

ax.set_title("G2 pvalue=f(datasize)")
gnb.flow.add(fig)
gnb.flow.add(gnb.getBN(gum.fastBN("A->T->TorC->X;S->C->TorC->D<-B<-S")))
gnb.flow.new_line()
```

nbsphinx-code-border Out[9]:

Conditional joint log-likelihood

With BNLearner, you can also check the joint (condtional) log-likelihood in the base

In [10]:
```
bn
```

Out[10]:
```
(pyAgrum.BayesNet<double>@000001C4B7746690) BN{nodes: 8, arcs: 8, domainSize: 256,␣
↪dim: 36}
```

In [11]:
```
siz=10000
gum.generateSample(bn,siz,"out/sample_score.csv",False)
learner=gum.BNLearner("out/sample_score.csv")

def affLL(learner,s1,s2=[]):
    if len(s2)==0:
        print("{} : {}".format(s1,learner.logLikelihood(s1)))
    else:
        print("{}|{} : {}".format(s1,s2,learner.logLikelihood(s1,s2)))

def dsepByLL(learner,x,y,z): # is X indep of Y given Z ?
    lxy_z=learner.logLikelihood([x,y],[z])
    lx_z=learner.logLikelihood([x],[z])
    ly_z=learner.logLikelihood([y],[z])
    print("{} indep {} given {} : {}".format(x,y,z,lxy_z-lx_z-ly_z))

print("Condional Joint LogLikelihood")
affLL(learner,["lung_cancer","bronchitis","smoking"])
affLL(learner,["smoking"])
affLL(learner,["lung_cancer","bronchitis"],["smoking"])

print("--------------")
print("LL indep test")
dsepByLL(learner,"lung_cancer","bronchitis","smoking")
dsepByLL(learner,"tuberculos_or_cancer","bronchitis","dyspnoea")
```

```
Condional Joint LogLikelihood
['lung_cancer', 'bronchitis', 'smoking'] : -22142.063042301077
['smoking'] : -9995.844639313984
['lung_cancer', 'bronchitis']|['smoking'] : -12146.218402987093
--------------
LL indep test
lung_cancer indep bronchitis given smoking : 0.4046632959161798
tuberculos_or_cancer indep bronchitis given dyspnoea : 160.49141588867315
```

Evolution of conditional log-likelihood w.r.t the size of the database (in Asia)

In [12]:
```
def consolidationIndepFromLL(bn,size,lindep,nbr=20):
    """
    Using $nbr$ generated databases of size $size$ from the bn $bn$,
    consolidate the logLikelihoos for a list $lindep$ of conditional independence to␣
↪test.

    return the list of consolidated pValues
    """
    LL_cumul=[0.0]*len(lindep)
    for i in range(nbr):
        gum.generateSample(bn,size,"out/sample_score.csv",False)
        learner=gum.BNLearner("out/sample_score.csv")
        for i,(var1,var2,kno) in enumerate(lindep):
            LL12=learner.logLikelihood([var1,var2],kno)
            LL1=learner.logLikelihood([var1],kno)
            LL2=learner.logLikelihood([var2],kno)
            LL_cumul[i]+=(LL12-LL1-LL2)/size
    return [p/nbr for p in LL_cumul]

sizes=[50,100,500,1000,2000,5000,10000,20000,50000,100000,200000]
LL1,LL2,LL3,LL4,LL5,LL6=zip(*[consolidationIndepFromLL(bn,siz,
                                    [("visit_to_Asia","smoking",['tuberculos_or_
↪cancer']),
                                     ("visit_to_Asia","smoking",[]),
                                     ("dyspnoea","smoking",[]),
                                     ("dyspnoea","smoking",["lung_cancer","bronchitis
↪"]),
                                     ("tuberculosis","bronchitis",[]),
                                     ("tuberculosis","bronchitis",["dyspnoea"])])
                                         for siz in sizes])
```

In [13]:
```
%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt
import matplotlib.patches as patches

fig=figure(figsize=(10,6))
ax  = fig.add_subplot(1, 1, 1)

ax.plot(sizes,LL1,label="NOT(A indep S given TorC)", linestyle='dashed')
ax.plot(sizes,LL2,label="A indep S")
ax.plot(sizes,LL3,label="NOT(D indep S)", linestyle='dashed')
ax.plot(sizes,LL4,label="D indep S given C,B")
ax.plot(sizes,LL5,label="T indep B")
ax.plot(sizes,LL6,label="NOT(T indep B given D)", linestyle='dashed')
ax.tick_params(rotation=90)
ax.set_xlabel("data size")
ax.set_ylabel("LL/size")
ax.semilogy()
ax.legend(bbox_to_anchor=(0.15, 0.8, 0.8, .102), loc=3,ncol=3, mode="expand",␣
↪borderaxespad=0.)
```

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```
ax.set_title("logLikelihood=f(datasize)")
gnb.flow.add(fig)
gnb.flow.add(gnb.getBN(gum.fastBN("A->T->TorC->X;S->C->TorC->D<-B<-S")))
gnb.flow.new_line();
```

Comparing the scores

In [14]:
```
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

In [ ]:
```
```

1.23 Different Graphical Models

1.23.1 Influence diagram

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import os

%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt
from IPython.display import display,HTML

import math
```

In [2]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
```

Build a influencediagram

fast build with string

In [3]:
```
gum.fastID("A->*B->$C<-D<-*E->*G->H->*I<-D")
```

Out[3]:
```
(pyAgrum.InfluenceDiagram<double>@0000021388516920) Influence Diagram{
  chance: 3,
  utility: 1,
  decision: 4,
  arcs: 8,
```

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```
  domainSize: 128
}
```

bifxml format file

In [4]:
```
diag=gum.loadID("res/diag.bifxml")
gnb.showInfluenceDiagram(diag)
```

nbsphinx-code-borderwhite

In [5]:
```
diag
```

Out[5]:
```
(pyAgrum.InfluenceDiagram<double>@0000021388516F30) Influence Diagram{
  chance: 5,
  utility: 2,
  decision: 4,
  arcs: 12,
  domainSize: 512
}
```

the hard way :-)

In [6]:
```
F=diag.addChanceNode(gum.LabelizedVariable("F","F",2))
diag.addArc(diag.idFromName("decisionVar1"),F)

U=diag.addUtilityNode(gum.LabelizedVariable("U","U",1))
diag.addArc(diag.idFromName("decisionVar3"),U)
diag.addArc(diag.idFromName("F"),U)
gnb.showInfluenceDiagram(diag)
```

nbsphinx-code-borderwhite

In [7]:
```
diag.cpt(F)[{'decisionVar1':0}]=[0.9,0.1]
diag.cpt(F)[{'decisionVar1':1}]=[0.3,0.7]

diag.utility(U)[{'F':0,'decisionVar3':0}]=2
diag.utility(U)[{'F':0,'decisionVar3':1}]=4
diag.utility(U)[{'F':1}]=[[0],[5]]
```

Optimization in an influence diagram (actually LIMID)

In [8]:
```
oil=gum.loadID("res/OilWildcatter.bifxml")
gnb.flow.row(oil,gnb.getInference(oil))
```

```
<IPython.core.display.HTML object>
```

In [9]:
```
# a function to show results on decision nodes T and D
def show_decisions(ie):
    gnb.flow.row(ie.optimalDecision("Testing"),
                 ie.optimalDecision("Drilling"),
                 f"$${ie.MEU()['mean']:5.3f}\\ (stdev : {math.sqrt(ie.MEU()[
↪'variance']):5.3f})$$",
                 captions=["Strategy for T",
                           "Strategy for D",
```

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```
                              "MEU and its standard deviation>"])
    gnb.flow.row(ie.posterior("Testing"),ie.posteriorUtility("Testing"),
                 ie.posterior("Drilling"),ie.posteriorUtility("Drilling"),
                captions=["Final decision for Testing","Final reward for Testing",
                          "Final decision for Drilling","Final reward for Drilling
↪"])

ie=gum.ShaferShenoyLIMIDInference(oil)

display(HTML("<h2>Inference in the LIMID optimizing the decisions nodes</h2>"))
ie.makeInference()
show_decisions(ie)
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

Graphical inference with evidence and targets (developped nodes)

In [10]:
```
gnb.sideBySide(oil,
               gnb.getInference(oil,evs={'TestResult':'closed'}),
               gnb.getInference(oil,evs={'TestResult':'open'}),
               gnb.getInference(oil,evs={'TestResult':'diffuse'}),
               oil,
               gnb.getInference(oil,evs={'OilContents':'Dry'}),
               gnb.getInference(oil,evs={'OilContents':'Wet'}),
               gnb.getInference(oil,evs={'OilContents':'Soaking'}),
               ncols=4)
```

```
<IPython.core.display.HTML object>
```

Soft evidence on chance node

In [11]:
```
gnb.showInference(oil,evs={'OilContents':[0.7,0.5,0.8]})
```

nbsphinx-code-borderwhite

Forced decision

In [12]:
```
gnb.showInference(oil,evs={'Drilling':'Yes'})
```

nbsphinx-code-borderwhite

LIMID versus Influence Diagram

The default inference for influence diagram actually an inference for LIMIDs. In order to use it for classical (and solvable) influence diagram, do not forget to add the sequence of decision nodes using `addNoForgettingAssumption`.

In [13]:
```
infdiag=gum.fastID("Chance->*Decision1->Chance2->$Utility<-Chance3<-*Decision2<-
↪Chance->Utility")
infdiag
```

Out[13]:
```
(pyAgrum.InfluenceDiagram<double>@0000021388517540) Influence Diagram{
  chance: 3,
  utility: 1,
  decision: 2,
  arcs: 7,
  domainSize: 32
}
```

In [14]:
```
ie=gum.ShaferShenoyLIMIDInference(infdiag)
try:
    ie.makeInference()
except gum.GumException as e:
    print(e)
```

```
[pyAgrum] Fatal error: This LIMID/Influence Diagram is not solvable.
```

In [15]:
```
ie.addNoForgettingAssumption(["Decision1","Decision2"])
gnb.sideBySide(ie.reducedLIMID(),ie.junctionTree(),gnb.getInference(infdiag,
↪engine=ie))
```

```
<IPython.core.display.HTML object>
```

Customizing visualization of the results

Using `pyAgrum.config`, it is possible to adapt the graphical representations for Influence Diagram (see 99-Tools_configForPyAgrum.ipynb).

In [16]:
```
gum.config.reset()
gnb.showInference(infdiag,engine=ie,size="7!")
```

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Many visual options can be changed when displaing an inference (especially for influence diagrams)

In [17]:
```
# do not show inference time
gum.config["notebook","show_inference_time"]=False
# more digits for probabilities
gum.config["notebook","histogram_horizontal_visible_digits"]=3

gnb.showInference(infdiag,engine=ie,size="7!")
```

nbsphinx-code-borderwhite

In [18]:
```
# specificic for influence diagram :
# more digits for utilities
gum.config["influenceDiagram","utility_visible_digits"]=5
# disabling stdev for utility and MEU
gum.config["influenceDiagram","utility_show_stdev"]=False
# showing loss (=-utility) and mEL (minimum Expected Loss) instead of MEU
gum.config["influenceDiagram","utility_show_loss"]=True

gnb.showInference(infdiag,engine=ie,size="7!")
```

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In [19]:
```
# more visual changes for influence diagram and inference
gum.config.reset()

#shape (https://graphviz.org/doc/info/shapes.html)
gum.config["influenceDiagram","chance_shape"] = "cylinder"
```

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```
gum.config["influenceDiagram","utility_shape"] = "star"
gum.config["influenceDiagram","decision_shape"] = "box3d"

#colors
gum.config["influenceDiagram","default_chance_bgcolor"] = "green"
gum.config["influenceDiagram","default_utility_bgcolor"] = "MediumVioletRed"
gum.config["influenceDiagram","default_decision_bgcolor"] = "DarkSalmon"

gum.config["influenceDiagram","utility_show_stdev"]=False

gnb.sideBySide(infdiag,gnb.getInference(infdiag,engine=ie,targets=["Decision1",
↪"Chance3"]))
```

```
<IPython.core.display.HTML object>
```

In [ ]:

1.23.2 dynamic Bayesian networks

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In [1]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
import pyAgrum.lib.dynamicBN as gdyn
```

Building a 2TBN

Note the naming convention for a 2TBN : a variable with a name A is present at t=0 with the name $A0$ and at time t as At.

In [2]:
```
#twodbn=gum.BayesNet()
#a0,b0,c0,at,bt,ct=[twodbn.add(gum.LabelizedVariable(s,s,6))
#                   for s in ["a0","b0","c0","at","bt","ct"]]
#d0,dt=[twodbn.add(gum.LabelizedVariable(s,s,3))
#       for s in ["d0","dt"]]

#twodbn.addArc(a0,b0)

#twodbn.addArc(c0,d0)
#twodbn.addArc(c0,at)

#twodbn.addArc(a0,at)
#twodbn.addArc(a0,bt)
#twodbn.addArc(a0,dt)
#twodbn.addArc(b0,bt)
```

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```
#twodbn.addArc(c0,ct)
#twodbn.addArc(d0,ct)
#twodbn.addArc(d0,dt)

#twodbn.addArc(at,ct)
#twodbn.generateCPTs()
twodbn=gum.fastBN("d0[3]->ct<-at<-a0->b0->bt<-a0->dt[3]<-d0<-c0->ct;c0->at",6)
twodbn
```

Out[2]:
```
(pyAgrum.BayesNet<double>@0x564c823db630) BN{nodes: 8, arcs: 11, domainSize: 419904,␣
↪dim: 1200}
```

2TBN

The dbn above actually is a 2TBN and is not correctly shown as a BN. Using the naming convention, it can be shown as a 2TBN.

In [3]:
```
gdyn.showTimeSlices(twodbn)
```

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unrolling 2TBN

A dBN is 'unrolled' using the 2TBN and the time period size. For a couple a_0,a_t in the 2TBN, the unrolled dBN will include $a_0, a_1, \cdots, a_{T-1}$

In [4]:
```
T=5

dbn=gdyn.unroll2TBN(twodbn,T)
gdyn.showTimeSlices(dbn,size="10")
```

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We can infer on bn just as on a normal bn. Following the naming convention in 2TBN, the variables in a dbN are named using the convention a_i where i is the number of their time slice.

In [5]:
```
gnb.flow.clear()
for i in range(T):
    gnb.flow.add_html(gnb.getPosterior(dbn,target="d{}".format(i),evs={}),"$P(d{})$".
↪format(i))
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

dynamic inference : following variables

`gdyn.plotFollow` directly ask for the 2TBN, unroll it and add evidence `evs`. Then it shows the dynamic of variable a for instance by plotting $a_0, a_1, \cdots, a_{T-1}$.

In [6]:
```
import matplotlib.pyplot as plt

plt.rcParams['figure.figsize'] = (10, 2)
gdyn.plotFollow(["a","b","c","d"],twodbn,T=51,evs={'a9':2,'a30':0,'c14':0,'b40':0,'c50
↪':3})
```

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nsDBN (Non-Stationnary Dynamic Bayesian network)

In [7]:
```
T=15

dbn=gdyn.unroll2TBN(twodbn,T)
gdyn.showTimeSlices(dbn)
```

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Non-stationnaty DBN allows to express that the dBN do not follow the same 2TBN during all steps. A `unrolled` dbn is a classical BayesNet and then can be changed as you want after unrolling.

In [8]:
```
# new P(ct|c0)
pot=gum.Potential().add(twodbn.variableFromName("ct")).add(twodbn.variableFromName("c0
↪"))
pot.fillWith([1,0,0,0.1]*9).normalizeAsCPT() # 36 valeurs normalized as CPT
```

Out[8]:
```
(pyAgrum.Potential<double>@0x564c84150e70)
      ||  ct                                                  |
c0    ||0        |1        |2        |3        |4        |5        |
------||---------|---------|---------|---------|---------|---------|
0     || 0.4762  | 0.0000  | 0.0000  | 0.0476  | 0.4762  | 0.0000  |
1     || 0.0000  | 0.0833  | 0.8333  | 0.0000  | 0.0000  | 0.0833  |
2     || 0.4762  | 0.0000  | 0.0000  | 0.0476  | 0.4762  | 0.0000  |
3     || 0.0000  | 0.0833  | 0.8333  | 0.0000  | 0.0000  | 0.0833  |
4     || 0.4762  | 0.0000  | 0.0000  | 0.0476  | 0.4762  | 0.0000  |
5     || 0.0000  | 0.0833  | 0.8333  | 0.0000  | 0.0000  | 0.0833  |
```

In [9]:
```
# from steps 5 to 10, $C_t$ only depends on $C_{t-1}$ and follows this new CPT
for i in range(5,11):
    dbn.eraseArc(f"d{i-1}",f"c{i}")
    dbn.eraseArc(f"a{i}",f"c{i}")
    dbn.cpt(f"c{i}").fillWith(pot,["ct","c0"]) # ct in pot <- first var of cpt, c0 in␣
↪pot<-second var in cpt

gdyn.showTimeSlices(dbn,size="14")
```

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In [10]:
```
plt.rcParams['figure.figsize'] = (10, 2)
gdyn.plotFollowUnrolled(["a","b","c","d"],dbn,T=15,evs={'a9':2,'c14':0})
```

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In [ ]:
```

```

1.23.3 Markov networks

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In [1]:
```
%load_ext autoreload
%autoreload 2

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
import pyAgrum.lib.mn2graph as m2g
```

building a Markov Network

In [2]:
```
gum.config.reset() # back to default
mn=gum.fastMN("A--B--C;C--D;B--E--F;F--D--G;H--J;E--A;J")
mn
```

Out[2]:
```
(pyAgrum.MarkovNet<double>@00000269F09E9870) MN{nodes: 9, edges: 12, domainSize: 512,␣
↪dim: 38}
```

Using `pyAgrum.config`, it is possible to adapt the graphical representations for Markov Network (see 99-Tools_configForPyAgrum.ipynb).

In [3]:
```
gum.config.reset() # back to default
gum.config['factorgraph','edge_length']='0.4'
gnb.showMN(mn)
```

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In [4]:
```
gum.config.reset() # back to default
print("Default view for Markov network: "+gum.config['notebook','default_
↪markovnetwork_view'])
gum.config['notebook','default_markovnetwork_view']='graph'
print("modified to: "+gum.config['notebook','default_markovnetwork_view'])
mn
```

```
Default view for Markov network: factorgraph
modified to: graph
```

Out[4]:
```
(pyAgrum.MarkovNet<double>@00000269F09E9870) MN{nodes: 9, edges: 12, domainSize: 512,␣
↪dim: 38}
```

In [5]:
```
gnb.sideBySide(gnb.getMN(mn,view="graph",size="5"),
               gnb.getMN(mn,view="factorgraph",size="5"))
```

```
<IPython.core.display.HTML object>
```

In [6]:
```
gnb.showMN(mn)
print(mn)
```

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```
MN{nodes: 9, edges: 12, domainSize: 512, dim: 38}
```

Accessors for Markov Networks

In [7]:
```
print(f"nodes       : {mn.nodes()}")
print(f"node names  : {mn.names()}")
print(f"edges       : {mn.edges()}")
print(f"components  : {mn.connectedComponents()}")
print(f"factors     : {mn.factors()}")
print(f"factor(C,D) : {mn.factor({2,3})}")
print(f"factor(C,D) : {mn.factor({'C','D'})}")
print(f"factor(C,D) : {mn.factor({'D','C'})}")
```

```
nodes       : {0, 1, 2, 3, 4, 5, 6, 7, 8}
node names  : {'B', 'J', 'D', 'G', 'C', 'A', 'F', 'E', 'H'}
edges       : {(0, 1), (1, 2), (0, 4), (1, 5), (1, 4), (2, 3), (4, 5), (0, 2), (5, 6),
↪ (7, 8), (3, 6), (3, 5)}
components  : {0: {0, 1, 2, 3, 4, 5, 6}, 7: {8, 7}}
factors     : [{0, 1, 2}, {2, 3}, {8, 7}, {1, 4, 5}, {3, 5, 6}, {0, 4}, {8}]
factor(C,D) :
      ||  C                |
D     ||0        |1        |
------||---------|---------|
0     || 0.9965  | 0.9677  |
1     || 0.7258  | 0.9811  |

factor(C,D) :
      ||  C                |
D     ||0        |1        |
------||---------|---------|
0     || 0.9965  | 0.9677  |
1     || 0.7258  | 0.9811  |

factor(C,D) :
      ||  C                |
D     ||0        |1        |
------||---------|---------|
0     || 0.9965  | 0.9677  |
1     || 0.7258  | 0.9811  |
```

In [8]:
```
try:
    mn.factor({0,1})
except gum.GumException as e:
    print(e)
try:
    mn.factor({"A","B"})
except gum.GumException as e:
    print(e)
```

```
[pyAgrum] Object not found: No element with the key <{1,0}>
[pyAgrum] Object not found: No element with the key <{1,0}>
```

Manipulating factors

In [9]:
```
mn.factor({'A','B','C'})
```

Out[9]:
```
(pyAgrum.Potential<double>@00000269CD3AAAE0)
              ||  A                 |
B     |C      ||0         |1         |
------|-------||----------|----------|
0     |0      || 0.1355   | 0.8350   |
1     |0      || 0.9689   | 0.2210   |
0     |1      || 0.3082   | 0.5472   |
1     |1      || 0.1884   | 0.9929   |
```

In [10]:
```
mn.factor({'A','B','C'})[{'B':0}]
```

Out[10]:
```
array([[0.135477  , 0.83500859],
       [0.30816705, 0.5472206 ]])
```

In [11]:
```
mn.factor({'A','B','C'})[{'B':0}]=[[1,2],[3,4]]
mn.factor({'A','B','C'})
```

Out[11]:
```
(pyAgrum.Potential<double>@00000269CD3AAAE0)
              ||  A                 |
B     |C      ||0         |1         |
------|-------||----------|----------|
0     |0      || 1.0000   | 2.0000   |
1     |0      || 0.9689   | 0.2210   |
0     |1      || 3.0000   | 4.0000   |
1     |1      || 0.1884   | 0.9929   |
```

Customizing graphical representation

In [12]:
```
gum.config.reset() # back to default
gum.config['factorgraph','edge_length']='0.5'

maxnei=max([len(mn.neighbours(n)) for n in mn.nodes()])
nodemap={n:len(mn.neighbours(mn.idFromName(n)))/maxnei for n in mn.names()}

facmax=max([len(f) for f in mn.factors()])
fgma=lambda factor: (1+len(factor)**2)/(1+facmax*facmax)

gnb.flow.row(gnb.getGraph(m2g.MN2UGdot(mn)),
             gnb.getGraph(m2g.MN2UGdot(mn,nodeColor=nodemap)),
             gnb.getGraph(m2g.MN2FactorGraphdot(mn)),
             gnb.getGraph(m2g.MN2FactorGraphdot(mn,factorColor=fgma,
↪nodeColor=nodemap)),
             captions=['Markov network',
                       'MarkovNet with colored node w.r.t number of neighbours',
                       'Markovnet as factor graph',
                       'MN with colored factor w.r.t to the size of scope'])
```

```
<IPython.core.display.HTML object>
```

from BayesNet to MarkovNet

In [13]:
```
bn=gum.fastBN("A->B<-C->D->E->F<-B<-G;A->H->I;C->J<-K<-L")
mn=gum.MarkovNet.fromBN(bn)
gnb.flow.row(bn,
             gnb.getGraph(m2g.MN2UGdot(mn)),
             captions=['a Bayesian network',
                       'the corresponding Markov Network'])
```

```
<IPython.core.display.HTML object>
```

In [14]:
```
# The corresponding factor graph
m2g.MN2FactorGraphdot(mn)
```

Out[14]:
```
<pydot.Dot at 0x269f2cc5ea0>
```

Inference in Markov network

In [15]:
```
bn=gum.fastBN("A->B<-C->D->E->F<-B<-G;A->H->I;C->J<-K<-L")
iebn=gum.LazyPropagation(bn)

mn=gum.MarkovNet.fromBN(bn)
iemn=gum.ShaferShenoyMNInference(mn)
iemn.setEvidence({"A":1,"F":[0.4,0.8]})
iemn.makeInference()
iemn.posterior("B")
```

Out[15]:
```
(pyAgrum.Potential<double>@00000269F0EFA580)
  B                 |
0         |1        |
----------|---------|
 0.6152   | 0.3848  |
```

In [16]:
```
def affAGC(evs):
    gnb.sideBySide(gnb.getSideBySide(gum.getPosterior(bn,target="A",evs=evs),
                                     gum.getPosterior(bn,target="G",evs=evs),
                                     gum.getPosterior(bn,target="C",evs=evs)),
                   gnb.getSideBySide(gum.getPosterior(mn,target="A",evs=evs),
                                     gum.getPosterior(mn,target="G",evs=evs),
                                     gum.getPosterior(mn,target="C",evs=evs)),
                   captions=["Inference in the Bayesian network bn with evidence
↪"+str(evs),
                             "Inference in the markov network mn with evidence
↪"+str(evs)]
                  )

print("Inference for both the corresponding models in BayesNet and MarkovNet worlds␣
↪when the MN comes from a BN")
affAGC({})
print("C has no impact on A and G")
affAGC({'C':1})

print("But if B is observed")
affAGC({'B':1})
print("C has an impact on A and G")
affAGC({'B':1,'C':0})
```

```
Inference for both the corresponding models in BayesNet and MarkovNet worlds when the MN comes from a BN
<IPython.core.display.HTML object>
C has no impact on A and G
<IPython.core.display.HTML object>
But if B is observed
<IPython.core.display.HTML object>
C has an impact on A and G
<IPython.core.display.HTML object>
```

In [17]:
```
mn.generateFactors()
print("But with more general factors")
affAGC({})
print("C has impact on A and G even without knowing B")
affAGC({'C':1})
```

```
But with more general factors
<IPython.core.display.HTML object>
C has impact on A and G even without knowing B
<IPython.core.display.HTML object>
```

Graphical inference in markov network

In [18]:
```
bn=gum.fastBN("A->B<-C->D->E->F<-B<-G;A->H->I;C->J<-K<-L")
mn=gum.MarkovNet.fromBN(bn)

gnb.sideBySide(gnb.getJunctionTree(bn),gnb.getJunctionTree(mn),captions=["Junction tree for the BN","Junction tree for the induced MN"])
gnb.sideBySide(gnb.getJunctionTreeMap(bn,size="3!"),gnb.getJunctionTreeMap(mn,size="3!"),captions=["Map of the junction tree for the BN","Map of the junction tree for the induced MN"])
```

```
<IPython.core.display.HTML object>
<IPython.core.display.HTML object>
```

In [19]:
```
gnb.showInference(bn,evs={"D":1,"H":0})
```

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In [20]:
```
gum.config.reset()
gnb.showInference(mn,size="8",evs={"D":1,"H":0})
```

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In [21]:
```
gum.config['factorgraph','edge_length_inference']='1.1'
gnb.showInference(mn,size="11",evs={"D":1,"H":0})
```

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In [22]:
```
gum.config['notebook','default_markovnetwork_view']='graph'
gnb.showInference(mn,size="8",evs={"D":1,"H":0})
```

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In [ ]:

1.23.4 Credal Networks

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In [1]:
```
import os

%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt
```

In [2]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
gnb.configuration()
```

```
<IPython.core.display.HTML object>
```

Credal Net from BN

In [3]:
```
bn=gum.fastBN("A->B[3]->C<-D<-A->E->F")
bn_min=gum.BayesNet(bn)
bn_max=gum.BayesNet(bn)
for n in bn.nodes():
  x=0.4*min(bn.cpt(n).min(),1-bn.cpt(n).max())
  bn_min.cpt(n).translate(-x)
  bn_max.cpt(n).translate(x)

cn=gum.CredalNet(bn_min,bn_max)
cn.intervalToCredal()

gnb.flow.row(bn,bn.cpt("B"),cn,bn_min.cpt("B"),bn_max.cpt("B"),captions=["Bayes Net",
↪"CPT","Credal Net","CPTmin","CPTmax"])
```

```
<IPython.core.display.HTML object>
```

We can use LBP on CN (L2U) only for binary credal networks (here B is not binary). We then propose the classical binarization (but warn the user that this leads to approximation in the inference)

In [4]:
```
cn2=gum.CredalNet(bn_min,bn_max)
cn2.intervalToCredal()
cn2.approximatedBinarization()
cn2.computeBinaryCPTMinMax()

gnb.flow.row(cn,cn2,captions=["Credal net","Binarized credal net"])
```

```
<IPython.core.display.HTML object>
```

Here, B becomes - B-b:math:i : the i-th bit of B - instrumental B-v:math:k : the indicator variable for each modality k of B

In [5]:
```
ie_mc=gum.CNMonteCarloSampling(cn)
ie2_lbp=gum.CNLoopyPropagation(cn2)
ie2_mc=gum.CNMonteCarloSampling(cn2)
```

In [6]:
```
gnb.sideBySide(gnb.getInference(cn,engine=ie_mc),
               gnb.getInference(cn2,engine=ie2_mc),
               gnb.getInference(cn2,engine=ie2_lbp))
```

```
<IPython.core.display.HTML object>
```

In [7]:
```
gnb.sideBySide(ie_mc.CN(),ie_mc.marginalMin("F"),ie_mc.marginalMax("F"),
               ie_mc.CN(),ie2_lbp.marginalMin("F"),ie2_lbp.marginalMax("F"),
              ncols=3)
print(cn)
```

```
<IPython.core.display.HTML object>


A:Range([0,1])
<> : [[0.0837589 , 0.916241] , [0.195435 , 0.804565]]

B:Range([0,2])
<A:0> : [[0.60315 , 0.147547 , 0.249304] , [0.60315 , 0.19114 , 0.20571] , [0.646745 ,
↪ 0.19114 , 0.162115] , [0.690339 , 0.147547 , 0.162115] , [0.646744 , 0.103952 , 0.
↪249304] , [0.690339 , 0.103952 , 0.20571]]
<A:1> : [[0.272995 , 0.108987 , 0.618018] , [0.272995 , 0.152582 , 0.574423] , [0.
↪316589 , 0.152582 , 0.530829] , [0.360184 , 0.108987 , 0.530829] , [0.31659 , 0.
↪0653924 , 0.618018] , [0.360184 , 0.0653924 , 0.574424]]

C:Range([0,1])
<B:0|D:0> : [[0.500982 , 0.499018] , [0.513663 , 0.486337]]
<B:1|D:0> : [[0.418886 , 0.581114] , [0.431566 , 0.568434]]
<B:2|D:0> : [[0.114657 , 0.885343] , [0.127336 , 0.872664]]
<B:0|D:1> : [[0.977811 , 0.0221893] , [0.990491 , 0.00950872]]
<B:1|D:1> : [[0.143169 , 0.856831] , [0.155849 , 0.844151]]
<B:2|D:1> : [[0.62924 , 0.37076] , [0.641919 , 0.358081]]

D:Range([0,1])
<A:0> : [[0.593434 , 0.406566] , [0.783228 , 0.216772]]
<A:1> : [[0.142344 , 0.857656] , [0.332139 , 0.667861]]

E:Range([0,1])
```

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```
<A:0> : [[0.209976 , 0.790024] , [0.489943 , 0.510057]]
<A:1> : [[0.389381 , 0.610619] , [0.669348 , 0.330652]]

F:Range([0,1])
<E:0> : [[0.251754 , 0.748246] , [0.479112 , 0.520888]]
<E:1> : [[0.602119 , 0.397881] , [0.82948 , 0.17052]]
```

Credal Net from bif files

In [8]:
```
cn=gum.CredalNet("res/cn/2Umin.bif","res/cn/2Umax.bif")
cn.intervalToCredal()
```

In [9]:
```
gnb.showCN(cn,"2")
```

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In [10]:
```
ie=gum.CNMonteCarloSampling(cn)
ie.insertEvidenceFile("res/cn/L2U.evi")
```

In [11]:
```
ie.setRepetitiveInd(False)
ie.setMaxTime(1)
ie.setMaxIter(1000)

ie.makeInference()
```

In [12]:
```
cn
```

Out[12]:
```
(pyAgrum.CredalNet<double>@0x5647983253f0)
A:Labelized({0|1})
<> : [[0.6 , 0.4] , [0.7 , 0.3]]

B:Labelized({0|1})
<> : [[0.6 , 0.4] , [0.8 , 0.2]]

C:Labelized({0|1})
<> : [[0 , 1] , [0.1 , 0.9]]

D:Labelized({0|1})
<> : [[0.1 , 0.9] , [0.5 , 0.5]]

E:Labelized({0|1})
<A:0|B:0> : [[0.3 , 0.7] , [0.4 , 0.6]]
<A:1|B:0> : [[0.8 , 0.2] , [1 , 0]]
<A:0|B:1> : [[0.7 , 0.3] , [0.9 , 0.1]]
<A:1|B:1> : [[0.5 , 0.5] , [0.7 , 0.3]]

F:Labelized({0|1})
<C:0|D:0> : [[0.1 , 0.9] , [0.2 , 0.8]]
<C:1|D:0> : [[0.5 , 0.5]]
<C:0|D:1> : [[0.3 , 0.7] , [0.5 , 0.5]]
<C:1|D:1> : [[0.6 , 0.4] , [0.9 , 0.1]]

G:Labelized({0|1})
```

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```
<D:0> : [[0.6 , 0.4] , [0.8 , 0.2]]
<D:1> : [[0.2 , 0.8] , [0.3 , 0.7]]

H:Labelized({0|1})
<E:0|F:0> : [[0 , 1] , [0.1 , 0.9]]
<E:1|F:0> : [[0.6 , 0.4] , [0.8 , 0.2]]
<E:0|F:1> : [[0.2 , 0.8] , [0.4 , 0.6]]
<E:1|F:1> : [[0.8 , 0.2] , [0.9 , 0.1]]

L:Labelized({0|1})
<H:0> : [[0.8 , 0.2] , [1 , 0]]
<H:1> : [[0.5 , 0.5] , [0.6 , 0.4]]
```

In [13]:
```
gnb.showInference(cn,targets={"A","H","L","D"},engine=ie,evs={"L":[0,1],"G":[1,0]})
```

nbsphinx-code-borderwhite

Comparing inference in credal networks

In [14]:
```
import pyAgrum as gum

def showDiffInference(model,mc,lbp):
    for i in model.current_bn().nodes():
        a,b=mc.marginalMin(i)[:]
        c,d=mc.marginalMax(i)[:]

        e,f=lbp.marginalMin(i)[:]
        g,h=lbp.marginalMax(i)[:]

        plt.scatter([a,b,c,d],[e,f,g,h])


cn=gum.CredalNet("res/cn/2Umin.bif","res/cn/2Umax.bif")
cn.intervalToCredal()
```

The two inference give quite the same result

In [15]:
```
ie_mc=gum.CNMonteCarloSampling(cn)
ie_mc.makeInference()

cn.computeBinaryCPTMinMax()
ie_lbp=gum.CNLoopyPropagation(cn)
ie_lbp.makeInference()

showDiffInference(cn,ie_mc,ie_lbp)
```

nbsphinx-code-borderwhite

but not when evidence are inserted

In [16]:
```
ie_mc=gum.CNMonteCarloSampling(cn)
ie_mc.insertEvidenceFile("res/cn/L2U.evi")
ie_mc.makeInference()

ie_lbp=gum.CNLoopyPropagation(cn)
ie_lbp.insertEvidenceFile("res/cn/L2U.evi")
ie_lbp.makeInference()

showDiffInference(cn,ie_mc,ie_lbp)
```

nbsphinx-code-borderwhite

Dynamical Credal Net

In [17]:
```
cn=gum.CredalNet("res/cn/bn_c_8.bif","res/cn/den_c_8.bif")
cn.bnToCredal(0.8,False)
```

In [18]:
```
ie=gum.CNMonteCarloSampling(cn)
ie.insertModalsFile("res/cn/modalities.modal")

ie.setRepetitiveInd(True)
ie.setMaxTime(5)
ie.setMaxIter(1000)

ie.makeInference()
```

In [19]:
```
print(ie.dynamicExpMax("temp"))
```

```
(14.203404647522472, 11.669951317919612, 12.10019505553209, 11.99476087981647, 11.
↪964516312727358, 11.941414476248845, 11.94838537443891, 11.945414782442136, 11.
↪946445491630861)
```

In [20]:
```
fig=figure()
ax=fig.add_subplot(111)
ax.fill_between(range(9),ie.dynamicExpMax("temp"),ie.dynamicExpMin("temp"))
```

Out[20]:
```
<matplotlib.collections.PolyCollection at 0x7fe6a7429000>
```

nbsphinx-code-borderwhite

In [21]:
```
ie=gum.CNMonteCarloSampling(cn)
ie.insertModalsFile("res/cn/modalities.modal")

ie.setRepetitiveInd(False)
ie.setMaxTime(5)
ie.setMaxIter(1000)

ie.makeInference()
print(ie.messageApproximationScheme())
```

```
stopped with epsilon=0
```

In [22]:
```
fig=figure()
ax=fig.add_subplot(111)
ax.fill_between(range(9),ie.dynamicExpMax("temp"),ie.dynamicExpMin("temp"))
```

Out[22]:
```
<matplotlib.collections.PolyCollection at 0x7fe6a728bbe0>
```
nbsphinx-code-borderwhite

In [23]:
```
ie=gum.CNMonteCarloSampling(cn)
ie.insertModalsFile("res/cn/modalities.modal")

ie.setRepetitiveInd(False)
ie.setMaxTime(5)
ie.setMaxIter(5000)

gnb.animApproximationScheme(ie)
ie.makeInference()
```
nbsphinx-code-borderwhite

In [24]:
```
fig=figure()
ax=fig.add_subplot(111)
ax.fill_between(range(9),ie.dynamicExpMax("temp"),ie.dynamicExpMin("temp"));
```
nbsphinx-code-borderwhite

In [ ]:

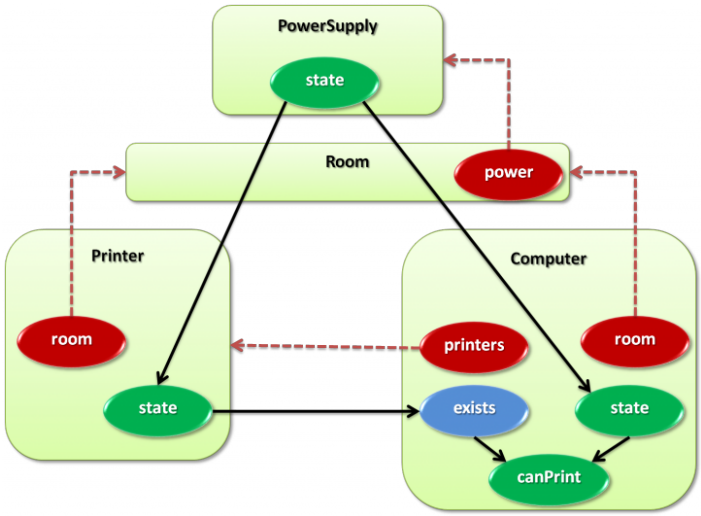
1.23.5 Object-Oriented Probabilistic Relational Model

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import os
os.chdir("res")

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
```

O3PRM is inspired by relational language, directly based on the BN and improved by object oriented paradigms, where the focus is set on classes of objects and by defining relations among these objects (see http://o3prm.gitlab.io/ for more details)



O3PRM syntax

In [2]:
```
with open('./Asia.o3prm','r') as prm:
  for line in prm.readlines():
    print(line,end="")
```

```
class Asia {

    boolean visitToAsia {
        [ 0.99,  // False
          0.01 ] // True
    };

    boolean tuberculosis dependson visitToAsia {
        // False | True
        [    0.99, 0.95,  // False
             0.01, 0.05 ] // True
    };

    boolean smoking {
        [ 0.50,  // False
          0.50 ] // True
    };

    boolean lungCancer dependson smoking {
        // False | True => smoking
        [    0.99, 0.90,  // False
             0.01, 0.10 ] // True
    };

    boolean bronchitis dependson smoking {
        // False | True => smoking
        [    0.70, 0.40,  // False
             0.30, 0.60 ] // True
    };

    boolean tubOrCancer dependson tuberculosis, lungCancer {
        //      False    ||     True      => tuberculosis
        //  False | True || False | True  => lungCancer
        [     1.00, 0.00,     0.00, 0.00,  // False
```

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```
              0.00, 1.00,     1.00, 1.00 ] // True
    };

    boolean positiveXRay dependson tubOrCancer {
        // False | True => tubOrCancer
        [ 0.95, 0.02,  // False
          0.05, 0.98 ] // True
    };

    boolean dyspnea dependson tubOrCancer, bronchitis {
        //      False    ||     True      => tubOrCancer
        //  False | True || False | True  => bronchitis
        [     0.90, 0.20,     0.30, 0.10,  // False
              0.10, 0.80,     0.70, 0.90 ] // True
    };
}
```

Using o3prm syntax for creating BayesNet

In [3]:
```
bn=gum.loadBN("./Asia.o3prm",verbose=False)
bn
```

Out[3]:
```
(pyAgrum.BayesNet<double>@000001C0FD7C9590) BN{nodes: 8, arcs: 8, domainSize: 256,␣
↪dim: 36}
```

In [4]:
```
bn=gum.loadBN("./aSys.o3prm")
bn
```

Out[4]:
```
(pyAgrum.BayesNet<double>@000001C0FD7CB020) BN{nodes: 10, arcs: 9, domainSize: 1024,␣
↪dim: 38}
```

In [5]:
```
classpath="./ComplexPrinters"
filename="./ComplexPrinters/fr/lip6/printers/system.o3prm"

system="Work"
bn=gum.loadBN(filename,system=system,classpath=classpath)
```

In [6]:
```
# the inference will take place in a rather large junction tree
gnb.showJunctionTreeMap(bn,scaleClique=0.1,scaleSep=0.05,lenEdge=1.0,size="8!")
```

nbsphinx-code-borderwhite

In [7]:
```
gnb.showInference(bn,size="25!")
```

nbsphinx-code-borderwhite

In [8]:
```
# if cairosvg is installed, one can export a graph (or inference) as a pdf
# gnb.exportInference(bn,filename="../out/ComplexPrinters.pdf")
```

In [9]:
```
bn=gum.loadBN("./aSys.o3prm")
gnb.sideBySide(
        gnb.getBN(bn,size='5'),
        gnb.getInference(bn,size='5')
        )
```

```
<IPython.core.display.HTML object>
```

Exploring Probabilistic Relational Model

In [10]:
```
classpath="./ComplexPrinters"
filename="./ComplexPrinters/complexprinters_system.o3prm"
explor=gum.PRMexplorer()
explor.load(filename)
```

In [11]:
```
for cl in explor.classes():
    print("Class : "+cl)
    print("  - Super class : "+ ("None" if explor.getSuperClass(cl)==None else explor.
↪getSuperClass(cl)) )
    print("  - Implemented interface : ")
    for inter in explor.classImplements(cl):
        print("      "+inter)
    print("  - Direct sub-types : ")
    for ext in explor.getDirectSubClass(cl):
        print("      "+ext)
    print("  - Attributes : ")
    for (t,n, depensons) in explor.classAttributes(cl):
        s = ""
        for depenson in depensons:
            s = s + depenson + " "
        print("      "+t+" "+n+" ("+s+")")
    print("  - References : ")
    for (t, n, isArray) in explor.classReferences(cl):
        print("      "+t+("[]" if isArray else "")+" "+n)
    print("  - Aggragates : ")
    for (t, n, g, l, slots) in explor.classAggregates(cl):
        s = ""
        for slot in slots:
            s = s + slot + " "
        print("      "+t+" "+n+" "+g+" "+("NoLabel" if l==None else l)+ " (" +s+")")
    print("  - SlotChains : ")
    for (t, n, isMultiple) in explor.classSlotChains(cl):
        print("      "+t+" "+n+" "+("[]" if isMultiple else ""))
    print("  - Parameters : ")
    for param in explor.classParameters(cl):
        print("      "+param)
    #print("  - Dag : ")
    #(dic, dotString) = explor.classDag(cl)
    #print(dic)
    #print(dotString)

    print()
```

```
Class : Room
  - Super class : None
  - Implemented interface :
  - Direct sub-types :
  - Attributes :
  - References :
      PowerSupply power
  - Aggragates :
  - SlotChains :
  - Parameters :

Class : Computer
```

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```
  - Super class : None
  - Implemented interface :
      Equipment
  - Direct sub-types :
  - Attributes :
      t_degraded equipState (room.power.state )
      boolean can_print (equipState working_printer )
  - References :
      Printer[] printers
      Room room
  - Aggragates :
      boolean functional_printer exists OK (printers.equipState )
      boolean working_printer exists true (degraded_printer functional_printer )
      boolean degraded_printer exists Degraded (printers.equipState )
      mycount count_printers count true (degraded_printer functional_printer )
  - SlotChains :
      t_degraded printers.equipState []
      t_state room.power.state
  - Parameters :

Class : SafeComputer
  - Super class : None
  - Implemented interface :
      Equipment
  - Direct sub-types :
  - Attributes :
      t_degraded equipState (room.power.(t_state)state )
      boolean can_print (working_printer equipState )
  - References :
      Room room
      Printer[] printers
  - Aggragates :
      boolean functional_printer exists OK (printers.(t_state)equipState )
      boolean degraded_printer exists Degraded (printers.(t_degraded)equipState )
      boolean working_printer exists true (functional_printer degraded_printer )
  - SlotChains :
      t_state printers.(t_state)equipState []
      t_degraded printers.(t_degraded)equipState []
      t_state room.power.(t_state)state
  - Parameters :

Class : ParamClass
  - Super class : None
  - Implemented interface :
  - Direct sub-types :
      ParamClass<lambda=0.001,t=4>
      ParamClass<lambda=0.4,t=4>
  - Attributes :
      t_degraded equipState (room.power.state hasInk hasPaper )
      t_ink hasInk ()
      t_paper hasPaper ()
  - References :
      Room room
  - Aggragates :
  - SlotChains :
      t_state room.power.state
```

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```
  - Parameters :
      lambda
      t

Class : ParamClass<lambda=0.001,t=4>
  - Super class : ParamClass
  - Implemented interface :
  - Direct sub-types :
  - Attributes :
      t_degraded equipState (room.power.state hasInk hasPaper )
      t_paper hasPaper ()
      t_ink hasInk ()
  - References :
      Room room
  - Aggragates :
  - SlotChains :
      t_state room.power.state
  - Parameters :
      lambda
      t

Class : PowerSupply
  - Super class : None
  - Implemented interface :
  - Direct sub-types :
  - Attributes :
      t_state state ()
  - References :
  - Aggragates :
  - SlotChains :
  - Parameters :

Class : BWPrinter
  - Super class : None
  - Implemented interface :
      Printer
  - Direct sub-types :
  - Attributes :
      t_ink hasInk ()
      t_paper hasPaper ()
      t_degraded equipState (room.power.state hasPaper hasInk )
  - References :
      Room room
  - Aggragates :
  - SlotChains :
      t_state room.power.state
  - Parameters :

Class : ColorPrinter
  - Super class : None
  - Implemented interface :
      Printer
  - Direct sub-types :
  - Attributes :
      t_ink yellow ()
      t_ink magenta ()
```

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```
      t_paper hasPaper ()
      t_degraded equipState (room.power.state hasPaper hasInk black )
      t_ink cyan ()
      t_ink black ()
  - References :
      Room room
  - Aggragates :
      boolean hasInk forall NotEmpty (yellow cyan black magenta )
  - SlotChains :
      t_state room.power.state
  - Parameters :

Class : ParamClass<lambda=0.4,t=4>
  - Super class : ParamClass
  - Implemented interface :
  - Direct sub-types :
  - Attributes :
      t_ink hasInk ()
      t_degraded equipState (room.power.state hasInk hasPaper )
      t_paper hasPaper ()
  - References :
      Room room
  - Aggragates :
  - SlotChains :
      t_state room.power.state
  - Parameters :
      t
      lambda
```

In [12]:
```
print("The following lists the systems of the prm:\n")
systems=explor.getalltheSystems()
sys1=systems[0]
print("Name of the system: "+sys1[0]+"\n")
print("Nodes : dict(id: [name,type])")
print(sys1[1])
print("\n")
print("Arcs : List[(tail, head),(tail, head)...]")
print(sys1[2])
```

```
The following lists the systems of the prm:

Name of the system: aSys

Nodes : dict(id: [name,type])
{0: ('pow', 'PowerSupply'), 1: ('r', 'Room'), 2: ('bw_printers[0]', 'BWPrinter'), 3: (
↪'bw_printers[1]', 'BWPrinter'), 4: ('bw_printers[2]', 'BWPrinter'), 5: ('bw_
↪printers[3]', 'BWPrinter'), 6: ('bw_printers[4]', 'BWPrinter'), 7: ('bw_printers[5]
↪', 'BWPrinter'), 8: ('bw_printers[6]', 'BWPrinter'), 9: ('bw_printers[7]',
↪'BWPrinter'), 10: ('bw_printers[8]', 'BWPrinter'), 11: ('bw_printers[9]', 'BWPrinter
↪'), 12: ('color_printers[0]', 'ColorPrinter'), 13: ('color_printers[1]',
↪'ColorPrinter'), 14: ('c1', 'Computer'), 15: ('c2', 'Computer'), 16: ('p',
↪'ParamClass<lambda=0.4,t=4>'), 17: ('paramBis', 'ParamClass<lambda=0.001,t=4>')}


Arcs : List[(tail, head),(tail, head)...]
[]
```

In [13]:
```
gnb.showPotential(explor.cpf('Computer','equipState'))
```

```
<IPython.core.display.HTML object>
```

In [14]:
```
for cl in explor.types():
    print("Type : "+cl)
    print("  - Super type : "+ ("None" if explor.getSuperType(cl)==None else explor.
↪getSuperType(cl)) )
    print("  - Direct sub-types : ")
    for name in explor.getDirectSubTypes(cl):
        print("      "+name)
    print("  - Labels : ")
    for t in explor.getLabels(cl):
        print("      "+t)
    print("  - Labels mapping : ")
    for key,val in dict().items() if explor.getLabelMap(cl)==None else explor.
↪getLabelMap(cl).items():
        print("      "+key+ ' -> '+val)
    print()
```

```
Type : t_ink
  - Super type : t_state-000001C0888DA180
  - Direct sub-types :
  - Labels :
      NotEmpty
      Empty
  - Labels mapping :
      NotEmpty -> OK
      Empty -> NOK

Type : boolean
  - Super type : None
  - Direct sub-types :
      t_state
  - Labels :
      false
      true
  - Labels mapping :

Type : t_degraded
  - Super type : t_state-000001C0888DA180
  - Direct sub-types :
  - Labels :
      OK
      Dysfunctional
      Degraded
  - Labels mapping :
      OK -> OK
      Dysfunctional -> NOK
      Degraded -> NOK

Type : t_state
  - Super type : boolean-000001C0888D95A0
  - Direct sub-types :
      t_ink
      t_degraded
```

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```
      t_paper
  - Labels :
      OK
      NOK
  - Labels mapping :
      OK -> true
      NOK -> false

Type : t_paper
  - Super type : t_state-000001C0888DA180
  - Direct sub-types :
  - Labels :
      Ready
      Jammed
      Empty
  - Labels mapping :
      Ready -> OK
      Jammed -> NOK
      Empty -> NOK

Type : mycount
  - Super type : None
  - Direct sub-types :
  - Labels :
      0
      1
      2
      3
      4
      5
  - Labels mapping :
```

In [15]:
```
for cl in explor.interfaces():
    print("Interface : "+cl)
    print("  - Super interface : "+ ("None" if explor.getSuperInterface(cl)==None␣
↪else explor.getSuperInterface(cl)) )
    print("  - Direct sub-interfaces : ")
    for name in explor.getDirectSubInterfaces(cl):
        print("      "+name)
    print("  - Implementations : ")
    for impl in explor.getImplementations(cl):
        print("      "+impl)
    print("  - Attributes : ")
    for (t,n) in explor.interAttributes(cl, allAttributes=True):
        print("      "+t+" "+n)
    print("  - References : ")
    for (t, n, isArray) in explor.interReferences(cl):
        print("      "+t+("[]" if isArray else "")+" "+n)
    print()
```

```
Interface : Printer
  - Super interface : Equipment
  - Direct sub-interfaces :
  - Implementations :
      BWPrinter
```

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```
      ColorPrinter
  - Attributes :
      t_degraded equipState
      boolean hasPaper
      boolean hasInk
      boolean equipState
      t_state equipState
  - References :
      Room room

Interface : Equipment
  - Super interface : None
  - Direct sub-interfaces :
      Printer
  - Implementations :
      Computer
      SafeComputer
  - Attributes :
      t_degraded equipState
      t_state equipState
      boolean equipState
  - References :
      Room room
```

In [16]:
```
print(explor.isType("fr.lip6.printers.base.Printer"))
print(explor.isClass("fr.lip6.printers.base.Printer"))
print(explor.isInterface("fr.lip6.printers.base.Printer"))
```

```
False
False
False
```

In [ ]:
```
```

1.24 Bayesian networks as scikit-learn compliant classifiers

1.24.1 Learning classifiers

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import pyAgrum.skbn as skbn
import pyAgrum.lib.notebook as gnb
```

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```
import os
import pandas
```

skbn is a pyAgrum's module that allows to use bayesian networks as classifier in the scikit-learn environment. ## Initialization of parameters

First, we initialize the parameters to indicate properties we want our classifier to have.

In [2]:
```
BNTest= skbn.BNClassifier(learningMethod = 'Chow-Liu', prior= 'Smoothing',␣
↪priorWeight = 0.5,
                          discretizationStrategy = 'quantile', usePR = True,␣
↪significant_digit = 13)
```

Then, we train the classifier thanks to two types of objects.

Learn from csv file

In [3]:
```
BNTest.fit(filename = 'res/creditCardTest.csv', targetName = 'Class')
```

```
**pyAgrum** : 'filename' is deprecated since 1.1.1. Please use 'data' instead.
```

In [4]:
```
for i in BNTest.bn.nodes():
    print(BNTest.bn.variable(i))
```

```
Class:Labelized({0.0|1.0})
Time:Discretized(<(0;1578[,[1578;3733[,[3733;6982[,[6982;11033[,[11033;170348)>)
V1:Discretized(<(-30.5524;-1.33295[,[-1.33295;-0.654664[,[-0.654664;0.305375[,[0.
↪305375;1.18346[,[1.18346;2.13239)>)
V2:Discretized(<(-25.6405;-0.362408[,[-0.362408;0.104022[,[0.104022;0.582468[,[0.
↪582468;1.12626[,[1.12626;22.0577)>)
V3:Discretized(<(-31.1037;0.107723[,[0.107723;0.675277[,[0.675277;1.14525[,[1.14525;1.
↪73106[,[1.73106;4.10172)>)
V4:Discretized(<(-4.65755;-0.835683[,[-0.835683;0.0334235[,[0.0334235;0.648386[,[0.
↪648386;1.44563[,[1.44563;12.1147)>)
V5:Discretized(<(-22.1055;-0.813666[,[-0.813666;-0.355923[,[-0.355923;0.0329468[,[0.
↪0329468;0.534605[,[0.534605;11.9743)>)
V6:Discretized(<(-7.5748;-0.789778[,[-0.789778;-0.370597[,[-0.370597;0.0353554[,[0.
↪0353554;0.711815[,[0.711815;10.0339)>)
V7:Discretized(<(-43.5572;-0.691953[,[-0.691953;-0.264738[,[-0.264738;0.111993[,[0.
↪111993;0.57616[,[0.57616;12.2192)>)
V8:Discretized(<(-41.0443;-0.248778[,[-0.248778;-0.0618973[,[-0.0618973;0.101159[,[0.
↪101159;0.417327[,[0.417327;20.0072)>)
V9:Discretized(<(-13.4341;-0.258886[,[-0.258886;0.432783[,[0.432783;1.00315[,[1.00315;
↪1.60675[,[1.60675;10.3929)>)
V10:Discretized(<(-24.5883;-0.887242[,[-0.887242;-0.486914[,[-0.486914;-0.17427[,[-0.
↪17427;0.281998[,[0.281998;12.2599)>)
V11:Discretized(<(-2.59533;-0.21685[,[-0.21685;0.467606[,[0.467606;1.06928[,[1.06928;
↪1.89436[,[1.89436;12.0189)>)
V12:Discretized(<(-18.6837;-2.60336[,[-2.60336;-1.98917[,[-1.98917;-1.01028[,[-1.
↪01028;0.297745[,[0.297745;3.77484)>)
V13:Discretized(<(-3.38951;-0.277526[,[-0.277526;0.487335[,[0.487335;1.192[,[1.192;1.
↪87168[,[1.87168;4.46541)>)
V14:Discretized(<(-19.2143;-0.198436[,[-0.198436;0.39438[,[0.39438;1.12921[,[1.12921;
↪1.5604[,[1.5604;5.74873)>)
V15:Discretized(<(-4.49894;-0.898218[,[-0.898218;-0.252119[,[-0.252119;0.228109[,[0.
↪228109;0.673846[,[0.673846;2.53366)>)
```

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```
V16:Discretized(<(-14.1299;-0.73753[,[-0.73753;-0.191439[,[-0.191439;0.226074[,[0.
↪226074;0.649708[,[0.649708;3.93088)>)
V17:Discretized(<(-25.1628;-0.37327[,[-0.37327;0.0631357[,[0.0631357;0.445363[,[0.
↪445363;0.906548[,[0.906548;7.89339)>)
V18:Discretized(<(-9.49875;-0.642528[,[-0.642528;-0.179343[,[-0.179343;0.16627[,[0.
↪16627;0.556347[,[0.556347;4.11556)>)
V19:Discretized(<(-4.93273;-0.673233[,[-0.673233;-0.228783[,[-0.228783;0.150301[,[0.
↪150301;0.636972[,[0.636972;5.22834)>)
V20:Discretized(<(-13.276;-0.183662[,[-0.183662;-0.0677703[,[-0.0677703;0.0444333[,[0.
↪0444333;0.232763[,[0.232763;11.059)>)
V21:Discretized(<(-22.7976;-0.298193[,[-0.298193;-0.179497[,[-0.179497;-0.0548622[,[-
↪0.0548622;0.105119[,[0.105119;27.2028)>)
V22:Discretized(<(-8.88702;-0.649014[,[-0.649014;-0.291808[,[-0.291808;0.00962799[,[0.
↪00962799;0.351258[,[0.351258;8.36199)>)
V23:Discretized(<(-19.2543;-0.215265[,[-0.215265;-0.0924607[,[-0.0924607;-1.53e-05[,[-
↪1.53e-05;0.122579[,[0.122579;13.8762)>)
V24:Discretized(<(-2.51238;-0.441547[,[-0.441547;-0.0137249[,[-0.0137249;0.248364[,[0.
↪248364;0.468669[,[0.468669;3.2002)>)
V25:Discretized(<(-4.78161;-0.238382[,[-0.238382;0.024469[,[0.024469;0.212094[,[0.
↪212094;0.411607[,[0.411607;5.52509)>)
V26:Discretized(<(-1.33856;-0.390763[,[-0.390763;-0.124995[,[-0.124995;0.128837[,[0.
↪128837;0.66481[,[0.66481;3.51735)>)
V27:Discretized(<(-7.9761;-0.0970824[,[-0.0970824;-0.0255692[,[-0.0255692;0.0347242[,
↪[0.0347242;0.216123[,[0.216123;4.17339)>)
V28:Discretized(<(-3.05408;-0.0430296[,[-0.0430296;0.00633497[,[0.00633497;0.0299365[,
↪[0.0299365;0.111331[,[0.111331;4.86077)>)
Amount:Discretized(<(0;2.78[,[2.78;11.66[,[11.66;25.52[,[25.52;73.5[,[73.5;4002.88)>)
```

In [5]:
```
gnb.showBN(BNTest.bn)
```
nbsphinx-code-borderwhite

In [6]:
```
gnb.showBN(BNTest.MarkovBlanket)
```
nbsphinx-code-borderwhite

Learn from array-likes

We use a method to transform the csv file in two array-likes in order to train from the same database.

In [7]:
```
#we use now another method to learn the BN (MIIC)
BNTest= skbn.BNClassifier(learningMethod = 'MIIC', prior= 'Smoothing', priorWeight =␣
↪0.5,
                          discretizationStrategy = 'quantile', usePR = True,␣
↪significant_digit = 13)

xTrain, yTrain = BNTest.XYfromCSV(filename = 'res/creditCardTest.csv', target = 'Class
↪')
```

In [8]:
```
BNTest.fit(xTrain, yTrain)
```

In [9]:
```
gnb.showBN(BNTest.bn)
```
nbsphinx-code-borderwhite

In [10]:
```
gnb.showBN(BNTest.MarkovBlanket)
```
nbsphinx-code-borderwhite

Create a classifier from a Bayesian network

If we already have a Bayesian network with learned parameters, we can create a classifier that uses it. In this case we do not have to train the classifier on data since it the Bayesian network is already trained.

In [11]:
```
ClassfromBN = skbn.BNClassifier(significant_digit = 7)
```

In [12]:
```
ClassfromBN.fromTrainedModel(bn = BNTest.bn, targetAttribute = 'Class',␣
↪targetModality = '1.0',
                             threshold = BNTest.threshold, variableList = xTrain.
↪columns.tolist())
```

In [13]:
```
gnb.showBN(ClassfromBN.bn)
```
nbsphinx-code-borderwhite

In [14]:
```
gnb.showBN(ClassfromBN.MarkovBlanket)
```
nbsphinx-code-borderwhite

Then, we work with functions from scikit-learn like score. We can also call it with a csv file or two array-likes.

In [15]:
```
xTest, yTest = ClassfromBN.XYfromCSV(filename = 'res/creditCardTest.csv', target =
↪'Class')
```

Prediction for classifier

Prediction with csv file

In [16]:
```
scoreCSV1 = BNTest.score('res/creditCardTest.csv', y = yTest)
print("{0:.2f}% good predictions".format(100*scoreCSV1))
```
```
99.77% good predictions
```

In [17]:
```
scoreCSV2 = ClassfromBN.score('res/creditCardTest.csv', y = yTest)
print("{0:.2f}% good predictions".format(100*scoreCSV2))
```
```
99.77% good predictions
```

Prediction with array-like

In [18]:
```
scoreAR1 = BNTest.score(xTest, yTest)
print("{0:.2f}% good predictions".format(100*scoreAR1))
```
```
99.77% good predictions
```

In [19]:
```
scoreAR2 = ClassfromBN.score(xTest, yTest)
print("{0:.2f}% good predictions".format(100*scoreAR2))
```
```
99.77% good predictions
```

ROC and Precision-Recall curves with all methods

In addition (and of course), we can work with functions from pyAgrum (from `pyAgrum.lib.bn2roc`).

In [20]:
```
BNTest.showROC_PR('res/creditCardTest.csv')
```

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In [ ]:
```
```

1.24.2 The BNDiscretizer Class

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

Most of the functionality of pyAgrum works only on discrete data. However data in the real world can be often continous. This class can be used to create dizcretized variables from continous data. Since this class was made for the purposes of the class BNClassifier, this class accepts data in the form of ndarrays. To transform data from a csv file to an ndarray we can use the function in BNClassifier XYfromCSV.

Creation of an instance and setting parameters

To create an instance of this class we need to specify the default parameters (the discretization method and the number of bins) for discretizing data. We create a discretizer which uses the EWD (Equal Width Discretization) method with 5 bins. The threshold is used for determining if a variable is already discretized. In this case, if a variable has more than 10 unique values we treat it as continous. we can use the setDiscretizationParameters method to set the discretization parameters for a specific variable

In [1]:
```
import pyAgrum.skbn as skbn

discretizer=skbn.BNDiscretizer(defaultDiscretizationMethod='uniform',
↪defaultNumberOfBins=5,discretizationThreshold=10)

discretizer.setDiscretizationParameters('var4','quantile',10)
discretizer.setDiscretizationParameters('var5','NoDiscretization',None)
```

Auditing data

To see how certain data will be treated by the discretizer we can use the audit method.

In [2]:
```
import pandas
X = pandas.DataFrame.from_dict({
  'var1': [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 1, 2, 3],
  'var2': ['a', 'b', 'c', 'd', 'e', 'f', 'g', 'h', 'i', 'j', 'k', 'l', 'm', 'n'],
  'var3': [1, 2, 5, 1, 2, 5, 1, 2, 5, 1, 2, 5, 1, 2],
  'var4': [1.11, 2.213, 3.33, 4.23, 5.42, 6.6, 7.5, 8.9, 9.19, 10.11, 11.12, 12.21,␣
↪13.3, 14.5],
```

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```
  'var5': [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 1]
})

print(X)

auditDict=discretizer.audit(X)

print()
print("** audit **")
for var in auditDict:
    print(f"- {var} : ")
    for k,v in auditDict[var].items():
        print(f"    + {k} : {v}")
```

```
    var1 var2  var3    var4  var5
0      1    a     1   1.110     1
1      2    b     2   2.213     2
2      3    c     5   3.330     3
3      4    d     1   4.230     4
4      5    e     2   5.420     5
5      6    f     5   6.600     6
6      7    g     1   7.500     7
7      8    h     2   8.900     8
8      9    i     5   9.190     9
9     10    j     1  10.110    10
10    11    k     2  11.120    11
11     1    l     5  12.210    12
12     2    m     1  13.300    13
13     3    n     2  14.500     1

** audit **
- var1 :
    + k : 5
    + methode : uniform
    + type : Continuous
- var2 :
    + methode : NoDiscretization
    + k : 14
    + type : Discrete
- var3 :
    + methode : NoDiscretization
    + k : 3
    + type : Discrete
- var4 :
    + k : 10
    + methode : quantile
    + type : Continuous
- var5 :
    + k : None
    + methode : NoDiscretization
    + type : Discrete
```

We can see that even though var2 has more unique values than var1 it is treated as a discrete variable. This is because the values of var2 are strings and therefore cannot be discretized.

Creating variables from data

To create variables from data we can use the createVariable method for each column in our data matrix. This will use the parameters that we have already set to create discrete (or discretized) variables from our data.

In [3]:
```
var1=discretizer.createVariable('var1',X['var1'])
var2=discretizer.createVariable('var2',X['var2'])
var3=discretizer.createVariable('var3',X['var3'])
var4=discretizer.createVariable('var4',X['var4'])
var5=discretizer.createVariable('var5',X['var5'])

print(var1)
print(var2)
print(var3)
print(var4)
print(var5)
```

```
var1:Discretized(<(1;3[,[3;5[,[5;7[,[7;9[,[9;11)>)
var2:Labelized({a|b|c|d|e|f|g|h|i|j|k|l|m|n})
var3:Integer({1|2|5})
var4:Discretized(<(1.11;2.5481[,[2.5481;3.87[,[3.87;5.301[,[5.301;6.78[,[6.78;8.2[,[8.
↪2;9.132[,[9.132;10.211[,[10.211;11.556[,[11.556;12.973[,[12.973;14.5)>)
var5:Range([1,13])
```

For supervised discretization algorithms (MDLP and CAIM) the list of class labels for each datapoint is also needed.

In [4]:
```
y=[True,False,False,True,False,False,True,True,False,False,True,True,False,True]

discretizer.setDiscretizationParameters('var4','CAIM')
var4=discretizer.createVariable('var4',X['var4'],y)
print(var4)
discretizer.setDiscretizationParameters('var4','MDLP')
var4=discretizer.createVariable('var4',X['var4'],y)
print(var4)
```

```
var4:Discretized(<(1.11;10.615[,[10.615;14.5)>)
var4:Discretized(<(1.11;1.6615[,[1.6615;14.5)>)
```

The discretizer keeps track of the number of discretized variables created by it and the number of bins used to discretize them. To reset these two numbers to 0 we can use the clear method. We can also use it to clear the specific parameteres we have set for each variable.

In [5]:
```
print(f"numberOfContinuous : {discretizer.numberOfContinous}")
print(f"totalNumberOfBins : {discretizer.totalNumberOfBins}")

discretizer.clear()
print("\n")

print(f"numberOfContinuous : {discretizer.numberOfContinous}")
print(f"totalNumberOfBins : {discretizer.totalNumberOfBins}")

discretizer.audit(X)
```

```
numberOfContinuous : 4
totalNumberOfBins : 19


numberOfContinuous : 0
totalNumberOfBins : 0
```

Out[5]:
```
{'var1': {'k': 5, 'methode': 'uniform', 'type': 'Continuous'},
 'var2': {'methode': 'NoDiscretization', 'k': 14, 'type': 'Discrete'},
 'var3': {'methode': 'NoDiscretization', 'k': 3, 'type': 'Discrete'},
 'var4': {'k': 10, 'methode': 'MDLP', 'type': 'Continuous'},
 'var5': {'k': None, 'methode': 'NoDiscretization', 'type': 'Discrete'}}
```

In [6]:
```
discretizer.clear(True)
discretizer.audit(X)
```

Out[6]:
```
{'var1': {'k': 5, 'methode': 'uniform', 'type': 'Continuous'},
 'var2': {'methode': 'NoDiscretization', 'k': 14, 'type': 'Discrete'},
 'var3': {'methode': 'NoDiscretization', 'k': 3, 'type': 'Discrete'},
 'var4': {'k': 5, 'methode': 'uniform', 'type': 'Continuous'},
 'var5': {'k': 5, 'methode': 'uniform', 'type': 'Continuous'}}
```

Using Discretizer with BNLearner

In [7]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb

import pyAgrum.skbn as skbn
import pandas as pd

file_name = 'res/discretizable.csv'
data = pd.read_csv(file_name)

discretizer = skbn.BNDiscretizer(defaultDiscretizationMethod='uniform',
                                 defaultNumberOfBins=5,
                                 discretizationThreshold=25)
```

In [8]:
```
template = gum.BayesNet()
for name in data:
    template.add(discretizer.createVariable(name, data[name]))
```

In [9]:
```
learner = gum.BNLearner(file_name, template)
learner.useMIIC()
learner.useNMLCorrection()

bn = learner.learnBN()
gnb.show(bn,size="10!")
```

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In [ ]:
```
```

1.24.3 Comparing classifiers (including Bayesian networks) with scikit-learn

In this notebook, we use the skbn module to insert bayesian networks into some examples from the scikit-learn documentation (that we refer).

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
from pyAgrum.skbn import BNClassifier
```

Binary classifiers

In [2]:
```
# From https://scikit-learn.org/stable/auto_examples/classification/plot_classifier_
↪comparison.html)
# Code source: Gael Varoquaux
#              Andreas Muller
# Modified for documentation by Jaques Grobler
# License: BSD 3 clause
```

In [3]:
```
import numpy as np

import matplotlib.pyplot as plt
import matplotlib.patheffects as pe

from matplotlib.colors import ListedColormap
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.datasets import make_moons, make_circles, make_classification
from sklearn.neural_network import MLPClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.gaussian_process import GaussianProcessClassifier
from sklearn.gaussian_process.kernels import RBF
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier, AdaBoostClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.discriminant_analysis import QuadraticDiscriminantAnalysis
```

In [4]:
```
# the data
X, y = make_classification(n_features=2, n_redundant=0, n_informative=2,
                           random_state=1, n_clusters_per_class=1)
rng = np.random.RandomState(2)
X += 2 * rng.uniform(size=X.shape)
linearly_separable = (X, y)

datasets = [make_moons(noise=0.3, random_state=0),
            make_circles(noise=0.2, factor=0.5, random_state=1),
            linearly_separable
            ]
datasets_name=['Moons ',
```

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```
              'Circle',
              'LinSep']
```

In [5]:
```
def showComparison(names,classifiers,datasets,datasets_name):# the results
    bnres=[None]*len(datasets_name)
    h = .02  # step size in the mesh
    fs=6

    figure = plt.figure(figsize=(10, 4))
    i = 1
    # iterate over datasets
    for ds_cnt, ds in enumerate(datasets):
        print(datasets_name[ds_cnt]+' : ',end='')
        # preprocess dataset, split into training and test part
        X, y = ds
        X = StandardScaler().fit_transform(X)
        X_train, X_test, y_train, y_test = \
            train_test_split(X, y, test_size=.4, random_state=42)

        x_min, x_max = X[:, 0].min() - .5, X[:, 0].max() + .5
        y_min, y_max = X[:, 1].min() - .5, X[:, 1].max() + .5
        xx, yy = np.meshgrid(np.arange(x_min, x_max, h),
                             np.arange(y_min, y_max, h))

        # just plot the dataset first
        cm = plt.cm.RdBu
        cm_bright = ListedColormap(['#FF0000', '#0000FF'])
        ax = plt.subplot(len(datasets), len(classifiers) + 1, i)
        if ds_cnt == 0:
            ax.set_title("Input data",fontsize=fs)
        ax.set_ylabel(datasets_name[ds_cnt])

        # Plot the training points
        ax.scatter(X_train[:, 0], X_train[:, 1], c=y_train, cmap=cm_bright,
                   edgecolors='k',marker=".")
        # Plot the testing points
        ax.scatter(X_test[:, 0], X_test[:, 1], c=y_test, cmap=cm_bright, alpha=0.6,
                   edgecolors='k',marker=".")
        ax.set_xlim(xx.min(), xx.max())
        ax.set_ylim(yy.min(), yy.max())
        ax.set_xticks(())
        ax.set_yticks(())
        i += 1

        # iterate over classifiers
        for name, clf in zip(names, classifiers):
            print(".",end="",flush=True)
            ax = plt.subplot(len(datasets), len(classifiers) + 1, i)
            clf.fit(X_train, y_train)
            score = clf.score(X_test, y_test)

            # Plot the decision boundary. For that, we will assign a color to each
            # point in the mesh [x_min, x_max]x[y_min, y_max].
            if hasattr(clf, "decision_function"):
                Z = clf.decision_function(np.c_[xx.ravel(), yy.ravel()])
            else:
```

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```
                Z = clf.predict_proba(np.c_[xx.ravel(), yy.ravel()])[:, 1]

            # Put the result into a color plot
            Z = Z.reshape(xx.shape)
            ax.contourf(xx, yy, Z, cmap=cm, alpha=.7)

            # Plot the training points
            #ax.scatter(X_train[:, 0], X_train[:, 1], c=y_train, cmap=cm_bright,
            #           edgecolors='k', alpha=0.2,marker='.')
            # Plot the testing points
            ax.scatter(X_test[:, 0], X_test[:, 1], c=y_test, cmap=cm_bright,
                       edgecolors='k',marker='.')

            ax.set_xlim(xx.min(), xx.max())
            ax.set_ylim(yy.min(), yy.max())
            ax.set_xticks(())
            ax.set_yticks(())
            if ds_cnt == 0:
                ax.set_title(name,fontsize=fs)
            ax.text(xx.max() - .3, yy.min() + .3, ('%.2f' % score).lstrip('0'),
                    size=12, horizontalalignment='right',color="white",
                    path_effects=[pe.withStroke(linewidth=2, foreground="black")])
            i += 1
        bnres[ds_cnt]=gum.BayesNet(classifiers[-1].bn)
        print()

    plt.tight_layout()
    plt.show()

    return bnres
```

In [6]:
```
# the classifiers
names = ["Nearest Neighbors", "Linear SVM", "RBF SVM", "Gaussian Process",
         "Decision Tree", "Random Forest", "Neural Net", "AdaBoost",
         "Naive Bayes", "QDA","BNClassifier"
        ]

classifiers = [
  KNeighborsClassifier(3),
  SVC(kernel="linear", C=0.025),
  SVC(gamma=2, C=1),
  GaussianProcessClassifier(1.0 * RBF(1.0)),
  DecisionTreeClassifier(max_depth=5),
  RandomForestClassifier(max_depth=5, n_estimators=10, max_features=1),
  MLPClassifier(alpha=1, max_iter=1000),
  AdaBoostClassifier(),
  GaussianNB(),
  QuadraticDiscriminantAnalysis(),
  BNClassifier(learningMethod='MIIC', prior='Smoothing', priorWeight=1,␣
↪discretizationNbBins=5,discretizationStrategy="uniform",usePR=False)
]

bnres=showComparison(names,classifiers,datasets,datasets_name)
```

```
Moons  : ...
Circle : ...
LinSep : ...
```

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The three BNs learned for each task:

In [7]:
```
gnb.sideBySide(*bnres,captions=datasets_name)
```

```
<IPython.core.display.HTML object>
```

Note that, for LinSep, the BNClassifier has correctly learned that $x1$ and y are independent (no need of $x1$ to predict y). $x1$ is not a relevant feature for this classification.

A zoom of one of this BN classifiers

In [8]:
```
h=0.2
ds=make_moons(noise=0.3, random_state=0)
X, y = ds
X = StandardScaler().fit_transform(X)
X_train, X_test, y_train, y_test =train_test_split(X, y, test_size=.4, random_
↪state=42)
x_min, x_max = X[:, 0].min() - .5, X[:, 0].max() + .5
y_min, y_max = X[:, 1].min() - .5, X[:, 1].max() + .5
xx, yy = np.meshgrid(np.arange(x_min, x_max, h),
                     np.arange(y_min, y_max, h))
clf=BNClassifier(learningMethod='MIIC', prior='Smoothing', priorWeight=1,␣
↪discretizationNbBins=5,discretizationStrategy="uniform",usePR=False)

clf.fit(X_train,y_train)
score = clf.score(X_test, y_test)

Z = clf.predict_proba(np.c_[xx.ravel(), yy.ravel()])[:, 1]
clf.bn

Z = Z.reshape(xx.shape)


ax = plt.subplot(1, 1,1)

ax.set_xlim(xx.min(), xx.max())
ax.set_ylim(yy.min(), yy.max())
ax.set_xticks(())
ax.set_yticks(())

ax.scatter(X_test[:, 0], X_test[:, 1], c=y_test,  alpha=0.6,edgecolors='k',marker=".")
ax.contourf(xx, yy, Z,  alpha=.7)

ax.text(xx.max() - .3, yy.min() + .3, ('%.2f' % score).lstrip('0'),
        size=12, horizontalalignment='right',color="white",
        path_effects=[pe.withStroke(linewidth=2, foreground="black")]);
```

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n-ary classifiers on IRIS dataset

In [9]:
```
# From https://scikit-learn.org/stable/auto_examples/classification/plot_
↪classification_probability.html#sphx-glr-auto-examples-classification-plot-
↪classification-probability-py
# Author: Alexandre Gramfort <alexandre.gramfort@inria.fr>
# License: BSD 3 clause
```

In [10]:
```
import matplotlib.pyplot as plt
import numpy as np

from sklearn.metrics import accuracy_score
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.gaussian_process import GaussianProcessClassifier
from sklearn.gaussian_process.kernels import RBF
from sklearn import datasets

iris = datasets.load_iris()
X = iris.data[:, 0:2]  # we only take the first two features for visualization
y = iris.target

n_features = X.shape[1]

C = 10
kernel = 1.0 * RBF([1.0, 1.0])  # for GPC

# Create different classifiers.
classifiers = {
    'L1 logistic': LogisticRegression(C=C, penalty='l1',
                                      solver='saga',
                                      multi_class='multinomial',
                                      max_iter=10000),
    'L2 logistic (Multinomial)': LogisticRegression(C=C, penalty='l2',
                                                    solver='saga',
                                                    multi_class='multinomial',
                                                    max_iter=10000),
    'L2 logistic (OvR)': LogisticRegression(C=C, penalty='l2',
                                            solver='saga',
                                            multi_class='ovr',
                                           max_iter=10000),
    'Linear SVC': SVC(kernel='linear', C=C, probability=True,
                      random_state=0),
    'GPC': GaussianProcessClassifier(kernel),
    'BN' : BNClassifier(learningMethod='MIIC',
                        prior='Smoothing', priorWeight=1,
                        discretizationNbBins=6,
                        discretizationStrategy="kmeans",
                        discretizationThreshold=10)
}

n_classifiers = len(classifiers)

plt.figure(figsize=(3 * 2, n_classifiers * 2))
plt.subplots_adjust(bottom=.2, top=.95)

xx = np.linspace(3, 9, 100)
```

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```
yy = np.linspace(1, 5, 100).T
xx, yy = np.meshgrid(xx, yy)
Xfull = np.c_[xx.ravel(), yy.ravel()]

for index, (name, classifier) in enumerate(classifiers.items()):
    classifier.fit(X, y)

    y_pred = classifier.predict(X)
    accuracy = accuracy_score(y, y_pred)
    print("Accuracy (train) for %s: %0.1f%% " % (name, accuracy * 100))

    # View probabilities:
    probas = classifier.predict_proba(Xfull)
    n_classes = np.unique(y_pred).size
    for k in range(n_classes):
        plt.subplot(n_classifiers, n_classes, index * n_classes + k + 1)
        plt.title("Class %d" % k)
        if k == 0:
            plt.ylabel(name)
        imshow_handle = plt.imshow(probas[:, k].reshape((100, 100)),
                                   extent=(3, 9, 1, 5), origin='lower')
        plt.xticks(())
        plt.yticks(())
        idx = (y_pred == k)
        if idx.any():
            plt.scatter(X[idx, 0], X[idx, 1], marker='o', c='w', edgecolor='k')

ax = plt.axes([0.15, 0.04, 0.7, 0.05])
plt.title("Probability")
plt.colorbar(imshow_handle, cax=ax, orientation='horizontal')

plt.show()
```

```
Accuracy (train) for L1 logistic: 82.7%
Accuracy (train) for L2 logistic (Multinomial): 82.7%
Accuracy (train) for L2 logistic (OvR): 79.3%
Accuracy (train) for Linear SVC: 82.0%
Accuracy (train) for GPC: 82.7%
Accuracy (train) for BN: 83.3%
```

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So the BNClassifier gives the 'best' accuracy (even if discretized). Moreover, once again, it propose a structural representation of the classification mechanism.

In [11]:
```
classifiers['BN'].bn
```

Out[11]:
```
(pyAgrum.BayesNet<double>@00000201020A7680) BN{nodes: 3, arcs: 2, domainSize: 108,␣
↪dim: 120}
```

Recognizing hand-written digits with Bayesian Networks

In [12]:
```
#From https://scikit-learn.org/stable/auto_examples/classification/plot_digits_
↪classification.html#sphx-glr-auto-examples-classification-plot-digits-
↪classification-py
# Author: Gael Varoquaux <gael dot varoquaux at normalesup dot org>
# License: BSD 3 clause
```

In [13]:
```
# Standard scientific Python imports
import matplotlib.pyplot as plt

# Import datasets, classifiers and performance metrics
from sklearn import datasets, metrics
from sklearn.model_selection import train_test_split

digits = datasets.load_digits()

_, axes = plt.subplots(nrows=1, ncols=4, figsize=(10, 3))
for ax, image, label in zip(axes, digits.images, digits.target):
    ax.set_axis_off()
    ax.imshow(image, cmap=plt.cm.gray_r, interpolation='nearest')
    ax.set_title('Training: %i' % label)
```

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In [14]:
```
# flatten the images
n_samples = len(digits.images)
data = digits.images.reshape((n_samples, -1)).astype(int)

# Create a classifier: a support vector classifier
#clf = svm.SVC(gamma=0.001)
clf = BNClassifier(learningMethod='MIIC', prior='Smoothing', priorWeight=1,
                   discretizationNbBins=3,discretizationStrategy="kmeans",
↪discretizationThreshold=10)

# Split data into 50% train and 50% test subsets
X_train, X_test, y_train, y_test = train_test_split(
    data, digits.target, test_size=0.5, shuffle=False)

# Learn the digits on the train subset
clf.fit(X_train, y_train)

# Predict the value of the digit on the test subset
predicted = clf.predict(X_test)

_, axes = plt.subplots(nrows=1, ncols=4, figsize=(10, 3))
for ax, image, prediction in zip(axes, X_test, predicted):
    ax.set_axis_off()
    image = image.reshape(8, 8)
    ax.imshow(image, cmap=plt.cm.gray_r, interpolation='nearest')
    ax.set_title(f'Prediction: {prediction}')

cm = metrics.confusion_matrix(y_test, predicted)
disp = metrics.ConfusionMatrixDisplay(confusion_matrix=cm)
disp.plot()

plt.show()
```

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```
print(f"Classification report for classifier {clf}:\n"
      f"{metrics.classification_report(y_test, predicted)}\n")
```

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nbsphinx-code-borderwhite

```
Classification report for classifier BNClassifier(prior='Smoothing',␣
↪discretizationNbBins=3,
             discretizationStrategy='kmeans', discretizationThreshold=10,
             learningMethod='MIIC'):
              precision    recall  f1-score   support

           0       0.98      0.95      0.97        88
           1       0.86      0.80      0.83        91
           2       0.91      0.85      0.88        86
           3       0.84      0.80      0.82        91
           4       0.99      0.91      0.95        92
           5       0.79      0.82      0.81        91
           6       0.95      0.95      0.95        91
           7       0.89      0.90      0.89        89
           8       0.79      0.76      0.77        88
           9       0.72      0.90      0.80        92

    accuracy                           0.87       899
   macro avg       0.87      0.87      0.87       899
weighted avg       0.87      0.87      0.87       899
```

Focus on the pixels needed for the classification

As always, using BNClassifier make us learn a bit more about the structure of the problem.

In [15]:
```
gnb.show(clf.bn,size="13!")
```

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Then, once again, the Markov Blanket gives us the relevant features (here the pixels)

In [16]:
```
print("Markov blanket of the classifier:")
gnb.show(clf.MarkovBlanket,size="14!")
print(f"Number of pixels used for classification : {clf.MarkovBlanket.size()-1}/64")
```

```
Markov blanket of the classifier:
```

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```
Number of pixels used for classification : 33/64
```

It appears that many pixels are not relevant for this classification.

In [17]:
```
#Visualization of the pixels of the Markov Blanket

fig, ax = plt.subplots()
ax.set_axis_off()
relevant_pixels = set([int(x[1:]) for x in clf.MarkovBlanket.names() if x!='y'])
ax.imshow(np.array([1 if i in relevant_pixels else 0 for i in range(64)]).reshape(8,
↪8),
          cmap=plt.cm.gray_r)
plt.show()
```

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In [ ]:

1.24.4 Using sklearn to cross-validate bayesian network classifier

The purpose of this notebook is to show the possible integration of the pyAgrum's classifier in the scikit-learn's ecosystem. Thus, it is possible to use the tools provided by scikit-learn for crossfolding for pyAgrum's Bayesian network.

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
from pyAgrum.skbn import BNClassifier
```

In [2]:
```
from sklearn.model_selection import cross_validate
from sklearn import datasets
# get iris data
iris = datasets.load_iris()
X = iris.data
y = iris.target
```

In [3]:
```
model = BNClassifier(learningMethod='MIIC', prior='Smoothing', priorWeight=1,
                     discretizationNbBins=3,discretizationStrategy="kmeans",
 ↪discretizationThreshold=10)
```

In [4]:
```
cv = cross_validate(model, X, y, cv=30)
print(f"scores with cross-folding : {cv['test_score']}")
print()

print(f"mean score : {cv['test_score'].mean()}")
```

```
scores with cross-folding : [1.  1.  1.  1.  1.  1.  1.  1.  1.  1.  0.8 1.  1.  1. ␣
 ↪0.8 1.  1.  0.8
 1.  1.  1.  0.8 1.  1.  1.  1.  1.  1.  1.  1. ]

mean score : 0.9733333333333333
```

In [5]:
```
cv = cross_validate(model, X, y, cv=50)
print(f"scores with cross-folding : {cv['test_score']}")
print()

print(f"mean score : {cv['test_score'].mean()}")
```

```
scores with cross-folding : [1.         1.         1.         1.         1.         1.
 1.         1.         1.         1.         1.         1.
```

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```
 1.         1.         1.         1.         1.         1.
 1.         1.         0.66666667 1.         1.         1.
 1.         1.         1.         0.66666667 1.         1.
 1.         1.         1.         0.66666667 1.         1.
 1.         1.         1.         1.         1.         1.
 1.         1.         1.         1.         1.         1.
 1.         1.        ]

mean score : 0.98
```

In [ ]:

1.24.5 From a Bayesian network to a Classifier

This notebook shows how to build a classifier from an Bayesian network (and not from a database).

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import pyAgrum as gum
import pyAgrum.skbn as skbn
import pyAgrum.lib.notebook as gnb
```

In [2]:
```
bn=gum.loadBN("res/alarm.dsl")
gnb.showBN(bn,size="10")
print(bn.variable("HR"))
```

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```
HR:Labelized({LOW|NORMAL|HIGH})
```

Let's say that you would like to use this Bayesian network to learn a classifier for the class HR (3 classes)

In [3]:
```
#generating the base of 10 values for testing purpose
print(f"LL(alarm-10)={gum.generateSample(bn,100,'out/alarm-10.csv')}")
```

```
LL(alarm-10)=-1523.1404258054915
```

In [4]:
```
bnc=skbn.BNClassifier()
bnc.fromTrainedModel(bn,targetAttribute="HR")
print(f"Binary classifier : {bnc.isBinaryClassifier}")
gnb.showBN(bnc.MarkovBlanket)

xTrain, yTrain = bnc.XYfromCSV(filename ='out/alarm-10.csv' )
print(f"predicted : {list(bnc.predict(xTrain))}")
print(f"in base   : {yTrain.to_list()}")
```

```
Binary classifier : False
```

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```
predicted : ['NORMAL', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪ 'HIGH', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'NORMAL', 'HIGH',
↪'HIGH', 'NORMAL', 'NORMAL', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH
↪', 'HIGH', 'LOW', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'NORMAL
↪', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'LOW', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'HIGH', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH']
in base   : ['NORMAL', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪ 'HIGH', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'NORMAL', 'HIGH',
↪'HIGH', 'NORMAL', 'NORMAL', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH
↪', 'HIGH', 'LOW', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'LOW',
↪'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'LOW', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'HIGH', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH']
```

In [5]:
```
print(list(bnc.predict(X ='out/alarm-10.csv')))
```

```
['NORMAL', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'NORMAL', 'HIGH', 'HIGH',
↪'NORMAL', 'NORMAL', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH
↪', 'LOW', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'HIGH
↪', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'LOW', 'HIGH', 'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'HIGH',
↪'HIGH', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'NORMAL', 'HIGH', 'HIGH', 'HIGH', 'HIGH']
```

In [6]:
```
scoreCSV1 = bnc.score('out/alarm-10.csv', y = yTrain)
print("{0:.2f}% good predictions".format(100*scoreCSV1))
```

```
99.00% good predictions
```

From a Bayesian network to a Binary classifier

By targetting a specific label, one can create a binary classifier to predict this very target.

In [7]:
```
bnc=skbn.BNClassifier()
bnc.fromTrainedModel(bn,targetAttribute="HR",targetModality="LOW")
print(f"Binary classifier : {bnc.isBinaryClassifier}")
gnb.showBN(bnc.MarkovBlanket)

xTrain, yTrain = bnc.XYfromCSV(filename ='out/alarm-10.csv' )
print(f"predicted : {list(bnc.predict(xTrain))}")
print(f"in base   : {yTrain.to_list()}")
```

```
Binary classifier : True
```

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```
predicted : [False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, True, False, False, False]
in base   : [False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪True, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, True, False, False, False]
```

In [8]:
```
print(list(bnc.predict(X ='out/alarm-10.csv')))
```

```
[False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪False, False, False, False, False, False, False, False, False, False, False, False,␣
↪True, False, False, False]
```

In [9]:
```
scoreCSV1 = bnc.score('out/alarm-10.csv', y = yTrain)
print("{0:.2f}% good predictions".format(100*scoreCSV1))
```

```
99.00% good predictions
```

In [10]:
```
print(f"LL(alarm-1000)={gum.generateSample(bn,1000,'out/alarm-1000.csv',with_
↪labels=True)}")
bnc.showROC_PR('out/alarm-1000.csv')
```

```
LL(alarm-1000)=-14788.400035254197
```

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In [ ]:
```

```

1.25 Causal Bayesian Networks

1.25.1 Smoking, Cancer and causality

This notebook follows the famous example from *Causality* (Pearl, 2009).

A correlation has been observed between Smoking and Cancer, represented by this Bayesian network :

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
from IPython.display import display, Math, Latex,HTML

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
import pyAgrum.causal as csl
import pyAgrum.causal.notebook as cslnb



obs1 = gum.fastBN("Smoking->Cancer")

obs1.cpt("Smoking")[:]=[0.6,0.4]
obs1.cpt("Cancer")[{"Smoking":0}]=[0.9,0.1]
obs1.cpt("Cancer")[{"Smoking":1}]=[0.7,0.3]

gnb.flow.row(obs1,obs1.cpt("Smoking")*obs1.cpt("Cancer"),obs1.cpt("Smoking"),obs1.cpt(
↪"Cancer"),
             captions=["the BN","the joint distribution","the marginal for $smoking$
↪","the CPT for $cancer$"])
```

```
<IPython.core.display.HTML object>
```

Direct causality between Smoking and Cancer

The very strong observed correlation between smoking and lung cancer suggests a causal relationship as the Surgeon General asserts in 1964, then, the proposed model is as follows :

In [2]:
```
# the Bayesian network is causal
modele1=csl.CausalModel(obs1)

cslnb.showCausalImpact(modele1,"Cancer", "Smoking", values={"Smoking":1})
```

```
<IPython.core.display.HTML object>
```

Latent confounder between Smoking and Cancer

This model is highly contested by the tobacco industry which answers by proposing a different model in which Smoking and Cancer are simultaneously provoked by a common factor, the Genotype (or other latent variable) :

In [3]:
```
# a latent varible exists between Smoking and Cancer in the causal model
modele2 = csl.CausalModel(obs1, [("Genotype", ["Smoking","Cancer"])])

cslnb.showCausalImpact(modele2, "Cancer", "Smoking",values={"Smoking":1})
```

```
<IPython.core.display.HTML object>
```

In [4]:
```
# just check P(Cancer) in the bn `obs1`
(obs1.cpt("Smoking")*obs1.cpt("Cancer")).margSumIn(["Cancer"])
```

Out[4]:
```
(pyAgrum.Potential<double>@0000029C313077C0)
  Cancer           |
0         |1        |
----------|---------|
 0.8200   | 0.1800  |
```

Confounder and direct causality

In a diplomatic effort, both parts agree that there must be some truth in both models :

In [5]:
```
# a latent variable exists between Smoking and Cancer but the direct causal relation␣
↪exists also
modele3 = csl.CausalModel(obs1, [("Genotype", ["Smoking","Cancer"])], True)

cslnb.showCausalImpact(modele3, "Cancer", "Smoking",values={"Smoking":1})
```

```
<IPython.core.display.HTML object>
```

Smoking's causal effect on Cancer becomes uncomputable in such a model because we can't distinguish both causes' impact from the observations.

A intermediary observed variable

We introduce an auxilary factor between Smoking and Cancer, tobacco causes cancer because of the tar deposits in the lungs.

In [6]:
```
obs2 = gum.fastBN("Smoking->Tar->Cancer;Smoking->Cancer")

obs2.cpt("Smoking")[:] = [0.6, 0.4]
obs2.cpt("Tar")[{"Smoking": 0}] = [0.9, 0.1]
obs2.cpt("Tar")[{"Smoking": 1}] = [0.7, 0.3]
obs2.cpt("Cancer")[{"Tar": 0, "Smoking": 0}] = [0.9, 0.1]
obs2.cpt("Cancer")[{"Tar": 1, "Smoking": 0}] = [0.8, 0.2]
obs2.cpt("Cancer")[{"Tar": 0, "Smoking": 1}] = [0.7, 0.3]
obs2.cpt("Cancer")[{"Tar": 1, "Smoking": 1}] = [0.6, 0.4]

gnb.flow.row(obs2,obs2.cpt("Smoking"),obs2.cpt("Tar"),obs2.cpt("Cancer"),
             captions=["","$P(Smoking)$","$P(Tar|Smoking)$","$P(Cancer|Tar,Smoking)$
↪"])
```

```
<IPython.core.display.HTML object>
```

In [7]:
```
modele4 = csl.CausalModel(obs2, [("Genotype", ["Smoking","Cancer"])])
cslnb.showCausalModel(modele4)
```

nbsphinx-code-borderwhite

In [8]:
```
cslnb.showCausalImpact(modele4, "Cancer", "Smoking",values={"Smoking":1})
```

```
<IPython.core.display.HTML object>
```

In this model, we are, again, able to calculate the causal impact of Smoking on Cancer thanks to the verification of the Frontdoor criterion by the Tar relatively to the couple (Smoking, Cancer)

In [9]:
```
# just check P(Cancer|do(smoking)) in the bn `obs2`
((obs2.cpt("Cancer")*obs2.cpt("Smoking")).margSumOut(["Smoking"])*obs2.cpt("Tar")).
↪margSumOut(['Tar']).putFirst("Cancer")
```

Out[9]:
```
(pyAgrum.Potential<double>@0000029C31307400)
      ||  Cancer           |
Smokin||0         |1         |
------||---------|---------|
0     || 0.8100  | 0.1900  |
1     || 0.7900  | 0.2100  |
```

Other causal impacts for this last model

In [10]:
```
cslnb.showCausalImpact(modele4, "Smoking", doing="Cancer",knowing={"Tar"}, values={
↪"Cancer":1,"Tar":1})
```

```
<IPython.core.display.HTML object>
```

In [11]:
```
cslnb.showCausalImpact(modele4, "Smoking", doing="Cancer",values={"Cancer":1})
```

```
<IPython.core.display.HTML object>
```

In [12]:
```
cslnb.showCausalImpact(modele4, "Smoking", doing={"Cancer","Tar"},values={"Cancer":1,
↪"Tar":1})
```

```
<IPython.core.display.HTML object>
```

In [13]:
```
cslnb.showCausalImpact(modele4, "Tar", doing={"Cancer","Smoking"},values={"Cancer":1,
↪"Smoking":1})
```

```
<IPython.core.display.HTML object>
```

1.25.2 Simpson's Paradox

This notebook follows the famous example from *Causality* (Pearl, 2009).

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
from IPython.display import display, Math, Latex

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
import pyAgrum.causal as csl
import pyAgrum.causal.notebook as cslnb
```

In a statistical study about a drug, we try to evaluate the latter's efficiency among a population of men and women. Let's note: - $Drug$: drug taking - $Patient$: cured patient - $Gender$: patient's gender

The model from the observed date is as follow :

In [2]:
```
m1 = gum.fastBN("Gender{F|M}->Drug{Without|With}->Patient{Sick|Healed}<-Gender")

m1.cpt("Gender")[:]=[0.5,0.5]
m1.cpt("Drug")[:]=[[0.25,0.75],  #Gender=F
                   [0.75,0.25]]  #Gender=M

m1.cpt("Patient")[{'Drug':'Without','Gender':'F'}]=[0.2,0.8] #No Drug, Male -> healed␣
↪in 0.8 of cases
m1.cpt("Patient")[{'Drug':'Without','Gender':'M'}]=[0.6,0.4] #No Drug, Female ->␣
↪healed in 0.4 of cases
m1.cpt("Patient")[{'Drug':'With','Gender':'F'}]=[0.3,0.7] #Drug, Male -> healed 0.7␣
↪of cases
m1.cpt("Patient")[{'Drug':'With','Gender':'M'}]=[0.8,0.2] #Drug, Female -> healed in␣
↪0.2 of cases
gnb.flow.row(m1,m1.cpt("Gender"),m1.cpt("Drug"),m1.cpt("Patient"))
```

```
<IPython.core.display.HTML object>
```

In [3]:
```
def getCuredObservedProba(m1,evs):
    evs0=dict(evs)
    evs1=dict(evs)
    evs0["Drug"]='Without'
    evs1["Drug"]='With'

    return gum.Potential().add(m1.variableFromName("Drug")).fillWith([
            gum.getPosterior(m1,target="Patient",evs=evs0)[1],
            gum.getPosterior(m1,target="Patient",evs=evs1)[1]
        ])

gnb.sideBySide(getCuredObservedProba(m1,{}),
```

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```
                getCuredObservedProba(m1,{'Gender':'F'}),
                getCuredObservedProba(m1,{'Gender':'M'}),
                captions=["$P(Patient = Healed \mid Drug )$<br/>Taking $Drug$ is␣
↪observed as efficient to cure",
                          "$P(Patient = Healed \mid Gender=F,Drug)$<br/>except if the
↪$gender$ of the patient is female",
                          "$P(Patient = Healed \mid Gender=M,Drug)$<br/>... or male."])
```

```
<IPython.core.display.HTML object>
```

Those results form a paradox called Simpson paradox :

$$P(C \mid \neg D) = 0.5 < P(C \mid D) = 0.575$$

$$P(C \mid \neg D, G = Male) = 0.8 > P(C \mid D, G = Male) = 0.7$$

$$P(C \mid \neg D, G = Female) = 0.4 > P(C \mid D, G = Female) = 0.2$$

Actuallay, giving a drug is not an observation in our model but rather an intervention. What if we use intervention instead of observation ?

How to compute causal impacts on the patient's health ?

We propose this causal model.

In [4]:
```
d1 = csl.CausalModel(m1)
cslnb.showCausalModel(d1)
```

nbsphinx-code-borderwhite

Computing $P(Patient = Healed \mid\hookrightarrow Drug = Without)$

In [5]:
```
cslnb.showCausalImpact(d1, "Patient", doing="Drug",values={"Drug" : "Without"})
```

```
<IPython.core.display.HTML object>
```

We have, $P(Patient = Healed \mid\hookrightarrow Drug = without) = 0.6$

Computing $P(Patient = Healed \mid\hookrightarrow Drug = With)$

In [6]:
```
d1 = csl.CausalModel(m1)
cslnb.showCausalImpact(d1, "Patient", "Drug",values={"Drug" : "With"})
```

```
<IPython.core.display.HTML object>
```

And then : $P(Patient = Healed \mid \text{`} : nbsphinx-math : hookrightarrow \text{`} Drug = With) = 0.45$

Therefore : $P(Patient = Healed:nbsphinx-math:*mid* \text{`}:nbsphinx-math:hookrightarrow *Drug = Without)* = 0.6 > *P(Patient = Healed:nbsphinx-math:*mid *:nbsphinx-math:*hookrightarrow \text{`}Drug = With) = 0.45 $

Which means that taking this drug would not enhance the patient's healing process, and it is better not to prescribe this drug for treatment.

Simpson paradox solved by interventions

So to summarize, the paradox appears when wrongly dealing with observations on $Drug$:

In [7]:
```
gnb.sideBySide(getCuredObservedProba(m1,{}),
               getCuredObservedProba(m1,{'Gender':'F'}),
               getCuredObservedProba(m1,{'Gender':'M'}),
               captions=["$P(Patient = Healed \mid Drug )$<br/>Taking $Drug$ is␣
↪observed as efficient to cure",
                         "$P(Patient = Healed \mid Gender=F,Drug)$<br/>except if the
↪$gender$ of the patient is female",
                         "$P(Patient = Healed \mid Gender=M,Drug)$<br/>... or male."])
```

```
<IPython.core.display.HTML object>
```

... and disappears when dealing with intervention on $Drug$:

In [8]:
```
gnb.sideBySide(csl.causalImpact(d1,on="Patient",doing="Drug",values={"Patient":"Healed
↪"})[1],
               csl.causalImpact(d1,on="Patient",doing="Drug",knowing={"Gender"},
↪values={"Patient":"Healed","Gender":"F"})[1],
               csl.causalImpact(d1,on="Patient",doing="Drug",knowing={"Gender"},
↪values={"Patient":"Healed","Gender":"M"})[1],
               captions=["$P(Patient = 1 \mid \hookrightarrow Drug )$<br/>Effectively
↪$Drug$ taking is not efficient to cure",
                         "$P(Patient = 1 \mid \hookrightarrow Drug, gender=F )$<br/>,␣
↪the $gender$ of the patient being female",
                         "$P(Patient = 1 \mid \hookrightarrow Drug, gender=M )$<br/>,␣
↪... or male."])
```

```
<IPython.core.display.HTML object>
```

In [ ]:
```
```

1.25.3 Multinomial Simpson Paradox

this notebook shows a model for a multinomial Simpson paradox.

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import matplotlib.pyplot as plt
import random

import pandas as pd
import numpy as np

import pyAgrum as gum
```

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```
import pyAgrum.lib.notebook as gnb

import pyAgrum.causal as csl
import pyAgrum.causal.notebook as cslnb
```

Building the models

In [2]:
```
# building a model including a Simpson's paradox
def fillWithUniform(p,fmin=None,fmax=None):
  if fmin is None:
    vmin=0
  if fmax is None:
    vmax=p.variable(0).domainSize()-1

  mi=int(p.variable(0).numerical(0))
  ma=int(p.variable(0).numerical(p.variable(0).domainSize()-1))

  p.fillWith(0)

  I=gum.Instantiation(p)

  I.setFirst()
  while not I.end():
    vars={p.variable(i).name():p.variable(i).numerical(I.val(i)) for i in range(1,p.
↪nbrDim())}
    if fmin is not None:
      vmin=int(eval(fmin,None,vars))
    if fmax is not None:
      vmax=int(eval(fmax,None,vars))
    if vmin<mi:
      vmin=mi
    if vmin>ma:
      vmin=ma
    if vmax<mi:
      vmax=mi
    if vmax>ma:
      vmax=ma

    for pos in range(vmin,vmax+1):
      I.chgVal(0,pos)
      p.set(I,1)
    I.incNotVar(p.variable(0))
  p.normalizeAsCPT()

size=70
sizeZ=5
bn=gum.fastBN(f"A[0,{size-1}]->B[0,{size-1}]<-C[0,{sizeZ-1}]->A")

bn.cpt("C").fillWith(1).normalize()
fillWithUniform(bn.cpt("A"),fmin="C*12",fmax="C*12+30")
bn.cpt("B").fillWithFunction("5+C*4-int(A/8)",[0.05,0.2,0.5,0.2,0.05]);
```

In [3]:
```
#  generating a CSV, taking this model as the causal one.
gum.generateSample(bn,400,"out/sample.csv")
```

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```
df=pd.read_csv("out/sample.csv")
df.plot.scatter(x='A', y='B', c='C',colormap="tab20");
```

nbsphinx-code-borderwhite

In [4]:
```
cm=csl.CausalModel(bn)
_,p,_=csl.causalImpact(cm,on="B",doing="A")
```

In [5]:
```
# building an Markov-equivalent model, generating a CSV, taking this model as the␣
↪causal one.
bn2=gum.BayesNet(bn)
bn2.reverseArc("C","A")

gum.generateSample(bn2,400,"out/sample2.csv")
df2=pd.read_csv("out/sample2.csv")

cm2=csl.CausalModel(bn2)
_,p2,_=csl.causalImpact(cm2,on="B",doing="A")
```

The observationnal model and its paradoxal structure (exactly the same with the second Markov-equivalent model)

In [6]:
```
gnb.flow.row(gnb.getBN(bn),
             df.plot.scatter(x='A', y='B'),
             df.plot.scatter(x='A', y='B', c='C',colormap="tab20"),
             captions=["the observationnal model","the trend is increasing","the␣
↪trend is decreasing for any value for C !"])
gnb.flow.row(gnb.getBN(bn2),
             df2.plot.scatter(x='A', y='B'),
             df2.plot.scatter(x='A', y='B', c='C',colormap="tab20"),
             captions=["the Markov-equivalent model","the trend is increasing","the␣
↪trend is decreasing for any value for C !"])
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

The paradox is revealed in the trend of the inferred means : the means are increasing with the value of A except for any value of :math:`C` ...

In [7]:
```
for v in [10,20,30]:
  gnb.flow.add_html(gnb.getPosterior(bn,target="B",evs={"A":v}),f"$P(B|A={v})$")
gnb.flow.new_line()
for v in [10,20,30]:
  gnb.flow.add_html(gnb.getPosterior(bn,target="B",evs={"A":v,"C":0}),f"P(B | $A={v},
↪C=0)$")
gnb.flow.new_line()
for v in [10,20,30]:
  gnb.flow.add_html(gnb.getPosterior(bn,target="B",evs={"A":v,"C":2}),f"P(B | $A={v},
↪C=2$)")
gnb.flow.new_line()
for v in [10,20,30]:
  gnb.flow.add_html(gnb.getPosterior(bn,target="B",evs={"A":v,"C":4}),f"P(B | $A={v},
↪C=4$)")
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

Now that the paradoxal structure is understood and the paradox is revealed, will we choose to observe C (or not) before deciding to increase or decrease A (with the goal to maximize B) ?

Of course, it depends on the causal structure of the problem !

In [8]:
```
gnb.flow.add_html(cslnb.getCausalModel(cm),"the first causal model")
for v in [10,20,30]:
  gnb.flow.add_html(gnb.getProba(p.extract({'A':v})),f"Doing $A={v}$")
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

If C is cause for A, observing C really gives a new information about B.

In [9]:
```
gnb.flow.add_html(cslnb.getCausalModel(cm2),"the second causal model")
for v in [10,20,30]:
  gnb.flow.add_html(gnb.getProba(p2.extract({'A':v})),f"Doing $A={v}$")
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

if A is cause for C, observing C may lead to misinterpretations about the causal role of A.

In [ ]:
```
```

1.25.4 Some examples of do-calculus

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
from IPython.display import display, Math, Latex, HTML

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
import pyAgrum.causal as csl
import pyAgrum.causal.notebook as cslnb
```

S. Tikka and J. Karvanen, 2016 [CRAN]

In [2]:
```
bn = gum.fastBN("w->x->z->y;w->z")

bn.cpt("w")[:] = [0.7,0.3]

bn.cpt("x")[:] = [[0.4,0.6],[0.3,0.7]]

bn.cpt("z")[{'w':0,'x':0}]=[0.2,0.8]
bn.cpt("z")[{'w':0,'x':1}]=[0.1,0.9]
bn.cpt("z")[{'w':1,'x':0}]=[0.9,0.1]
bn.cpt("z")[{'w':1,'x':1}]=[0.5,0.5]

bn.cpt("y")[:] = [[0.1,0.9],[0.8,0.2]]


d = csl.CausalModel(bn, [("lat1", ["x","y"])])
#csl.causalImpact(d,"y",{"x":0})
cslnb.showCausalImpact(d,"y","x",values={"x":0})
cslnb.showCausalImpact(d,"y","x",values={"x":1})
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

Since we have the formula, let us compute by hand this intervention :

In [3]:
```
(((bn.cpt("x") * bn.cpt("y")).margSumOut(["x"]) * bn.cpt("w") * bn.cpt("z")).
↪margSumOut(["z", "w"])).putFirst("y")
```

Out[3]:
```
(pyAgrum.Potential<double>@0000019F24E70C80)
      ||  y                |
x     ||0        |1        |
------||---------|---------|
0     || 0.5130  | 0.4870  |
1     || 0.6460  | 0.3540  |
```

In [4]:
```
bn = gum.fastBN("Z1->X->Z2->Y")
d=csl.CausalModel(bn,[("L1",["Z1","X"]),
                      ("L2",["Z1","Z2"]),
                      ("L3",["Z1","Y"]),
                      ("L4",["Y","X"])],
                  True)
cslnb.showCausalImpact(d,"Y","X",values={"X":1})
```

```
<IPython.core.display.HTML object>
```

Front door

In [5]:
```
modele4 = gum.BayesNet()
modele4.add(gum.LabelizedVariable("Smoking"))
modele4.add(gum.LabelizedVariable("Cancer"))
modele4.add(gum.LabelizedVariable("Tar"))

modele4.addArc(0,2)
modele4.addArc(2,1)
modele4.addArc(0,1)

#Smoking
modele4.cpt(0)[:]=[0.5, 0.5]

#Tar
modele4.cpt(2)[{"Smoking":0}] = [0.4, 0.6]
modele4.cpt(2)[{"Smoking":1}] = [0.3, 0.6]

#Cancer
modele4.cpt(1)[{'Smoking':0,'Tar':0}]=[0.1,0.9] #No Drug, Male -> healed in 0.8 of␣
↪cases
modele4.cpt(1)[{'Smoking':0,'Tar':1}]=[0.15,0.85] #No Drug, Female -> healed in 0.4␣
↪of cases
modele4.cpt(1)[{'Smoking':1,'Tar':0}]=[0.2,0.8] #Drug, Male -> healed 0.7 of cases
modele4.cpt(1)[{'Smoking':1,'Tar':1}]=[0.25,0.75]

d4 = csl.CausalModel(modele4, [("Genotype", ["Smoking","Cancer"])],False)
cslnb.showCausalModel(d4)
```

nbsphinx-code-borderwhite

In [6]:
```
try:
    a = csl.doCalculusWithObservation (d4,"Cancer", {"Smoking"})
except csl.HedgeException as h:
    print (h.message)
```

In [7]:
```
display(Math(a.toLatex()))
```

$$P(Cancer \mid \hookrightarrow Smoking) = \sum_{Tar} P(Tar \mid Smoking) \cdot \left(\sum_{Smoking'} P(Smoking') \cdot P(Cancer \mid Smoking', Tar) \right)$$

nbsphinx-code-borderwhite

In [8]:
```
try:
    adjj = a.eval()
except csl.UnidentifiableException as u:
    print (u.message)

print (adjj)
```

```
      ||  Cancer           |
Smokin||0         |1        |
------||---------|---------|
0     || 0.1774   | 0.8226  |
1     || 0.1626   | 0.7374  |
```

In [9]:
```
formula, adj, exp = csl.causalImpact(d4, "Cancer", "Smoking",values={"Smoking":0})
```

In [10]:
```
display(Math(formula.toLatex()))
adj
```

$$P(Cancer \mid\hookrightarrow Smoking) = \sum_{Tar} P\left(Tar \mid Smoking\right) \cdot \left(\sum_{Smoking'} P\left(Cancer \mid Smoking', Tar\right) \cdot P\left(Smoking'\right) \right)$$

nbsphinx-code-borderwhite

Out[10]:
```
(pyAgrum.Potential<double>@0000019F24E6FF40)
  Cancer           |
0        |1        |
---------|---------|
 0.1774  | 0.8226  |
```

Last example from R

In [11]:
```
m = gum.fastBN("z2->x->z1->y;z2->z1;z2->z3->y")

m.cpt("z2") [:] = [0.5, 0.5]
m.cpt("x") [:] = [[0.4,0.6], #z2=0
                  [0.4,0.6]] #z2=1
m.cpt("z3") [:] = [[0.3,0.7], #z2=0
                   [0.3,0.7]] #z2=1
m.cpt("z1")[{"z2":0, "x":0}]= [0.2, 0.8]
m.cpt("z1")[{"z2":0, "x":1}]= [0.25, 0.75]
m.cpt("z1")[{"z2":1, "x":0}]= [0.1, 0.9]
m.cpt("z1")[{"z2":1, "x":1}]= [0.15, 0.85]

m.cpt("y")[{"z1":0,"z3":0}]= [0.5,0.5]
m.cpt("y")[{"z1":0,"z3":1}]= [0.45,0.55]
m.cpt("y")[{"z1":1,"z3":0}]= [0.4,0.6]
m.cpt("y")[{"z1":1,"z3":1}]= [0.35,0.65]


d = csl.CausalModel(m, [("X-Z2",["x","z2"]),
                        ("X-Z3",["x","z3"]),
                        ("X-Y",["x","y"]),
                        ("Y-Z2",["y","z2"])],
                    True)

cslnb.showCausalModel(d)
```

nbsphinx-code-borderwhite

In [12]:
```
try:
    formula,result,msg = csl.causalImpact(d,on={"y","z2","z1","z3"},doing={"x"})
except csl.HedgeException as h:
    print (h.message)

print(msg)
display(Math(formula.toLatex()))
```

```
Do-calculus computations
```

$$P(z1, y, z3, z2 \mid\hookrightarrow x) = P\left(z3 \mid z2\right) \cdot P\left(z1 \mid x, z2\right) \cdot \frac{\sum_{x'} P\left(y \mid x', z1, z2, z3\right) \cdot P\left(x' \mid z2\right) \cdot P\left(z3 \mid x', z2\right) \cdot P\left(z2\right)}{\sum_{x', y'} P\left(y' \mid x', z1, z2, z3\right) \cdot P\left(x' \mid z2\right) \cdot P\left(z3 \mid x', z2\right) \cdot P\left(z2\right)} \cdot P\left(z2\right)$$

nbsphinx-code-borderwhite

In [13]:
```
# computation for this formula directly in pyAgrum
f1=m.cpt("x")*m.cpt("z2")*m.cpt("z3")*m.cpt("y")
f2=f1.margSumOut(["x"])
f3=f1.margSumOut(["x","y"])
f4=f2/f3
pyResult=m.cpt("z3")*m.cpt("z1")*m.cpt("z2")*f4
```

In [14]:
```
# computation for this formula directly by creating the causal AST
a = csl.ASTposteriorProba(m,{"z1"},{"x","z2"})
b= csl.ASTposteriorProba(m,{"y","z3"},{"x","z1","z2"})
c = csl.ASTjointProba(["x","z2"])
correct = csl.ASTmult(a,csl.ASTsum(["x"],csl.ASTmult(b,c)))

print("According to [ref], the result should be :")
display(Math(correct.toLatex()))
```

```
According to [ref], the result should be :
```

nbsphinx-code-borderwhite

$$P\left(z1 \mid x, z2\right) \cdot \left(\sum_{x} P\left(y, z3 \mid z1, z2\right) \cdot P\left(x, z2\right)\right)$$

In [15]:
```
# computation for that formula
ie=gum.LazyPropagation(m)
refResult=(ie.evidenceJointImpact(["y","z3"],["x","z1","z2"])*
     ie.evidenceJointImpact(["x","z2"],[])
    ).margSumOut(["x"])* m.cpt("z1")
```

In [16]:
```
print("Maximum error between these 3 versions : {}".format(max((refResult-pyResult).
↪abs().max(),
                                                               (refResult-result).
↪abs().max(),
                                                               (pyResult-result).new_
↪abs().max())))
```

```
Maximum error between these 3 versions : 5.551115123125783e-17
```

Unidentifiabilty

In [17]:
```
m1 = gum.fastBN("z1->x->z2->y")

cdg = csl.CausalModel(m1, [("Z1X",["z1","x"]),
                           ("Z1-Y",["z1","y"]),
                           ("Z1-Z1",["z1","z2"]),
                           ("XY",["x","y"])
                          ], True )
cslnb.showCausalModel(cdg)
```

nbsphinx-code-borderwhite

In [18]:
```
err = cslnb.showCausalImpact(cdg,"y","x",values={"x":0})
```

```
<IPython.core.display.HTML object>
```

another one

In [19]:
```
# EXEMPLE PAGE 17 : http://ftp.cs.ucla.edu/pub/stat_ser/r350.pdf


m1 = gum.BayesNet()
m1.add(gum.LabelizedVariable("x"))
m1.add(gum.LabelizedVariable("y"))
m1.add(gum.LabelizedVariable("z1"))
m1.add(gum.LabelizedVariable("z2"))
m1.add(gum.LabelizedVariable("z3"))

m1.addArc(2,4)
m1.addArc(2,0)
m1.addArc(3,4)
m1.addArc(3,1)
m1.addArc(4,1)
m1.addArc(4,0)
m1.addArc(0,1)

gnb.showBN(m1)
d = csl.CausalModel(m1)
```

nbsphinx-code-borderwhite

In [20]:
```
display(Math(csl.identifyingIntervention (d,{"z1","z2","z3","y"}, {"x"}).toLatex()))
```

nbsphinx-code-borderwhite$$P\left(z3 \mid z1, z2\right) \cdot P\left(z2\right) \cdot P\left(z1\right) \cdot P\left(y \mid x, z2, z3\right)$$

In [21]:
```
display(Math(csl.identifyingIntervention(d,{"y"}, {"x"}).toLatex()))
```

nbsphinx-code-borderwhite$$\sum_{z1,z2,z3} P\left(z3 \mid z1, z2\right) \cdot P\left(z2\right) \cdot P\left(z1\right) \cdot P\left(y \mid x, z2, z3\right)$$

In [22]:
```
display(Math(csl.identifyingIntervention(d,{"z1","z3","y"}, {"x","z2"}).toLatex()))
```

nbsphinx-code-borderwhite$$P\left(z3 \mid z1, z2\right) \cdot P\left(z1\right) \cdot P\left(y \mid x, z2, z3\right)$$

In [23]:
```
display(Math(csl.identifyingIntervention(d,{"y"}, {"x","z2"}).toLatex()))
```

nbsphinx-code-borderwhite$$\sum_{z1,z3} P\left(z3 \mid z1, z2\right) \cdot P\left(z1\right) \cdot P\left(y \mid x, z2, z3\right)$$

Other example

In [24]:
```
#http://www.stats.ox.ac.uk/~lienart/gml15_causalinference.html

m1 = gum.BayesNet()
m1.add(gum.LabelizedVariable("a"))
m1.add(gum.LabelizedVariable("p"))
m1.add(gum.LabelizedVariable("b"))
m1.add(gum.LabelizedVariable("y"))

m1.addArc(0,1)
m1.addArc(1,2)
m1.addArc(0,3)
m1.addArc(1,3)
m1.addArc(2,3)
gnb.showBN(m1)
d = csl.CausalModel(m1)
```

nbsphinx-code-borderwhite

In [25]:
```
display(Math(csl.identifyingIntervention(d,{"y"}, {"a","b"}).toLatex()))
```

$$\sum_p P(y \mid a,b,p) \cdot P(p \mid a)$$

nbsphinx-code-borderwhite

example f

In [26]:
```
#https://cse.sc.edu/~mgv/talks/AIM2010.ppt , example (f)

m1 = gum.BayesNet()
m1.add(gum.LabelizedVariable("X"))
m1.add(gum.LabelizedVariable("Y"))
m1.add(gum.LabelizedVariable("Z1"))
m1.add(gum.LabelizedVariable("Z2"))

m1.addArc(0,1)
m1.addArc(0,2)
m1.addArc(2,3)
m1.addArc(3,1)
m1.addArc(2,1)
d = csl.CausalModel(m1, [("l1",["X","Z1"]) ,("l2",["Y","Z1"])],True)
cslnb.showCausalModel(d)
```

nbsphinx-code-borderwhite

In [27]:
```
try:
    display(Math(csl.identifyingIntervention (d,{"Y"}, {"X"}).toLatex()))
except csl.HedgeException as e:
    print("Hedge exception : {}".format(e))
```

```
Hedge exception : Hedge Error: G={'Y', 'Z1', 'X'}, G[S]={'Z1', 'Y'}
```

Example [Pearl,2009] Causality, p66

In [28]:
```
bn = gum.fastBN("Z1->Z2->Z3->Y<-X->Z2;Z2->Y;Z1->X->Z3<-Z1")
gnb.showBN(bn)
```

nbsphinx-code-borderwhite

In [29]:
```
c = csl.CausalModel(bn, [("Z0", ("X", "Z1", "Z3"))], False)
cslnb.showCausalModel(c)
```

nbsphinx-code-borderwhite

In [30]:
```
formula, impact, explanation = csl.causalImpact(c, "Y", "X")
cslnb.showCausalImpact(c,"Y","X")
```

```
<IPython.core.display.HTML object>
```

In [ ]:
```

```

1.25.5 Counterfactual : the Effect of Education and Experience on Salary

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

This notebook follows the example from “The Book Of Why” (Pearl, 2018) chapter 8 page 251.

Counterfactuals

In [1]:
```
from IPython.display import display, Math, Latex,HTML

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
import pyAgrum.causal as csl
import pyAgrum.causal.notebook as cslnb
import os
import math
import numpy as np
import scipy.stats
```

In this example we are interested in the effect of experience and education on the salary of an employee, we are in possession of the following data:

```
<tr>
    <th>Employé</th> <th>EX(u)</th> <th>ED(u)</th> <th> $S_{0}(u)$</th> <th> $S_{1}(u)
↪$</th> <th>$S_{2}(u)$</th>
</tr>
<tr>
    <td>Alice</td> <td>8</td> <td>0</td> <td>86,000</td> <td>?</td> <td>?</td>
</tr>
<tr>
    <td>Bert</td> <td>9</td> <td>1</td> <td>?</td> <td>92,500</td> <td>?</td>
</tr>
<tr>
    <td>Caroline</td> <td>9</td> <td>2</td> <td>?</td> <td>?</td> <td>97,000</td>
</tr>
<tr>
    <td>David</td> <td>8</td> <td>1</td> <td>?</td> <td>91,000</td> <td>?</td>
</tr>
<tr>
    <td>Ernest</td> <td>12</td> <td>1</td> <td>?</td> <td>100,000</td> <td>?</td>
</tr>
<tr>
    <td>Frances</td> <td>13</td> <td>0</td> <td>97,000</td> <td>?</td> <td>?</td>
</tr>
<tr>
```

(continues on next page)

(continued from previous page)

```
    <td>etc</td> <td> </td> <td> </td> <td> </td> <td> </td> <td> </td> <td> </td>
</tr>
```

- $EX(u)$: years of experience of employee u. [0,20]
- $ED(u)$: Level of education of employee u (0:high school degree (low), 1:college degree (medium), 2:graduate degree (high)) [0,2]
- $S_i(u)$ [65k,150k] :
- salary (observable) of employee u if $i = ED(u)$,
- Potential outcome (unobservable) if $i \neq ED(u)$, salary of employee u if he had a level of education of i.

We are left with the previous data and we want to answer the counterfactual question What would Alice's salary be if she attended college ? (i.e. $S_1(Alice)$)

We create the causal diagram

In this model it is assumed that an employee's salary is determined by his level of education and his experience. Years of experience are also affected by the level of education. Having a higher level of education means spending more time studying hence less experience.

In [2]:
```
edex = gum.fastBN("Ux[-2,10]->experience[0,20]<-education{low|medium|high}->salary[65,
↪150];"
                  "experience->salary<-Us[0,25]")
edex
```

Out[2]:
```
(pyAgrum.BayesNet<double>@000001EA84D50440) BN{nodes: 5, arcs: 5, domainSize: 10^6.
↪26276, dim: 141729}
```

However counterfactual queries are specific to one datapoint (in our case Alice), we need to add additional variables to our model to allow for individual variations: * Us : unobserved variables that affect salary.[0,25k] * Ux : unobserved variables that affect experience.[-2,10]

In [3]:
```
# no prior information about the individual (datapoint)
edex.cpt("Us").fillWith(1).normalize()
edex.cpt("Ux").fillWith(1).normalize()
# education level(supposed)
edex.cpt("education")[:] = [0.4, 0.4, 0.2]
```

In [4]:
```
# To have probabilistic results, we add a perturbation. (Gaussian around the exact␣
↪values)
# we calculate a gaussian distribution
x_min = 0.0
x_max = 4.0

mean = 2.0
std = 0.65

x = np.linspace(x_min, x_max, 5)

y = scipy.stats.norm.pdf(x,mean,std)
print("We'll use the following distribution \n",y)
```

```
We'll use the following distribution
 [0.00539715 0.18794845 0.61375735 0.18794845 0.00539715]
```

Experience listens to Education and Ux :

$$Ex = 10 - 4 \times Ed + Ux$$

In [5]:
```
edex.cpt("experience").fillWithFunction("10-4*education+Ux",noise=list(y))
edex.cpt("experience")
```

Out[5]:
```
(pyAgrum.Potential<double>@000001EA84CF94A0)
             ||  experience                                                  ␣
↪                                                                            ␣
↪                                                  |
Ux    |educat||0        |1        |2        |3        |4        |5        |6       ␣
↪|7        |8        |9        |10       |11       |12       |13       |14       |15␣
↪      |16       |17       |18       |19       |20       |
------|------||---------|---------|---------|---------|---------|---------|---------|-
↪--------|---------|---------|---------|---------|---------|---------|---------|-----
↪----|---------|---------|---------|---------|---------|
-2    |low   || 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0054  |␣
↪0.1879  | 0.6135  | 0.1879  | 0.0054  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
-1    |low   || 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |␣
↪0.0054  | 0.1879  | 0.6135  | 0.1879  | 0.0054  | 0.0000  | 0.0000  | 0.0000  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
0     |low   || 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |␣
↪0.0000  | 0.0054  | 0.1879  | 0.6135  | 0.1879  | 0.0054  | 0.0000  | 0.0000  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
1     |low   || 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |␣
↪0.0000  | 0.0000  | 0.0054  | 0.1879  | 0.6135  | 0.1879  | 0.0054  | 0.0000  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
2     |low   || 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |␣
↪0.0000  | 0.0000  | 0.0000  | 0.0054  | 0.1879  | 0.6135  | 0.1879  | 0.0054  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
3     |low   || 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |␣
↪0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0054  | 0.1879  | 0.6135  | 0.1879  | 0.
↪0054  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
[...27 more line(s) ...]
5     |high  || 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0054  | 0.1879  |␣
↪0.6135  | 0.1879  | 0.0054  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
6     |high  || 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0054  |␣
↪0.1879  | 0.6135  | 0.1879  | 0.0054  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
7     |high  || 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |␣
↪0.0054  | 0.1879  | 0.6135  | 0.1879  | 0.0054  | 0.0000  | 0.0000  | 0.0000  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
8     |high  || 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |␣
↪0.0000  | 0.0054  | 0.1879  | 0.6135  | 0.1879  | 0.0054  | 0.0000  | 0.0000  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
9     |high  || 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |␣
↪0.0000  | 0.0000  | 0.0054  | 0.1879  | 0.6135  | 0.1879  | 0.0054  | 0.0000  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
10    |high  || 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |␣
↪0.0000  | 0.0000  | 0.0000  | 0.0054  | 0.1879  | 0.6135  | 0.1879  | 0.0054  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
```

Salary listens to Education, Experience and Us :

$$S = 65 + 2.5 \times Ex + 5 \times Ed + Us$$

In [6]:
```
edex.cpt("salary").fillWithFunction("round(65+2.51*experience+5*education+Us)",
↪noise=list(y))
gnb.showInference(edex)
```

nbsphinx-code-borderwhite

To answer this counterfactual question we will follow the three steps algorithm from "The Book Of Why" (Pearl 2018) chapter 8 page 253 :

Step 1 : Abduction

Use the data to retrieve all the information that characterizes Alice

From the data we can retrieve Alice's profile : * $Ed(Alice)$: 0 * $Ex(Alice)$: 8 * $S_0(Alice)$: 86k

We will use Alice's profile to get U_s and U_x, which tell Alice apart from the rest of the data.

In [7]:
```
ie=gum.LazyPropagation(edex)
ie.setEvidence({'experience':8, 'education': 'low', 'salary' : "86"})
ie.makeInference()
newUs = ie.posterior("Us")
newUs
```

Out[7]:
```
(pyAgrum.Potential<double>@000001EAA5565340)
  Us
↪                                                                              ␣
↪                                                                              ␣
↪                                                                              ␣
↪     |
0        |1        |2        |3        |4        |5        |6        |7        |8     ␣
↪   |9        |10       |11       |12       |13       |14       |15       |16      ␣
↪|17       |18       |19       |20       |21       |22       |23       |24       |25␣
↪      |
---------|---------|---------|---------|---------|---------|---------|---------|------
↪---|---------|---------|---------|---------|---------|---------|---------|---------
↪|---------|---------|---------|---------|---------|---------|---------|---------|---
↪------|
 0.1889  | 0.6168  | 0.1889  | 0.0054  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.
↪0000  | 0.0000  |
```

In [8]:
```
ie=gum.LazyPropagation(edex)
ie.setEvidence({'experience':8, 'education': 'low', 'salary' : "86"})
ie.makeInference()
newUx = ie.posterior("Ux")
newUx
```

Out[8]:
```
(pyAgrum.Potential<double>@000001EAA55648E0)
  Ux
↪                                                                              ␣
↪                                        |
-2       |-1       |0        |1        |2        |3        |4        |5        |6     ␣
↪   |7        |8        |9        |10       |
---------|---------|---------|---------|---------|---------|---------|---------|------
↪---|---------|---------|---------|---------|
 0.7604  | 0.2329  | 0.0067  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  | 0.
↪0000  | 0.0000  | 0.0000  | 0.0000  | 0.0000  |
```

In [9]:
```
gnb.showInference(edex,evs={'experience':8, 'education': "low", 'salary' : "86"},
↪targets={'Ux','Us'})
```
nbsphinx-code-borderwhite

Step 2 & 3 : Action And Prediction

Change the model to match the hypothesis implied by the query (if she had attended university) and then use the data that characterizes Alice to calculate her salary.

We create a counterfactual world with Alice's idiosyncratic factors, and we operate the intervention:

In [10]:
```
# the counterfactual world
edexCounterfactual = gum.BayesNet(edex)
```

In [11]:
```
# we replace the prior probabilities of idiosynatric factors with potentials␣
↪calculated earlier
edexCounterfactual.cpt("Ux").fillWith(newUx)
edexCounterfactual.cpt("Us").fillWith(newUs)
gnb.showInference(edexCounterfactual,size="10")
print("counterfactual world created")
```
nbsphinx-code-borderwhite
```
counterfactual world created
```

In [12]:
```
# We operate the intervention
edexModele = csl.CausalModel(edexCounterfactual)
cslnb.showCausalImpact(edexModele,"salary",doing="education",values={"education":
↪"medium"})
```
```
<IPython.core.display.HTML object>
```

> Since education has no parents in our model (no graph surgery, no causes to emancipate it from), an intervention is equivalent to an observation, the only thing we need to do is to set the value of education:

In [13]:
```
gnb.showInference(edexCounterfactual,targets={"salary",'experience'},evs={'education':
↪"medium"},size="10")
```
nbsphinx-code-borderwhite

The result (salary if she had attended college) is given by the formaula:

$$\sum_{salary} salary \times P(salary^* \mid RealSalary = 86k, education = 0, experience = 8, education^* = 1)$$

$$Where variables marked with an asterisk are inobservable.$$

In [14]:
```
formula, adj, exp = csl.causalImpact(edexModele,"salary",doing="education",values={
↪"education":"medium"})
gnb.showProba(adj)
```
nbsphinx-code-borderwhite

In [15]:
```
i = gum.Instantiation(adj)
i.setFirst()
mean = 0
while (not i.end()):
    v = i.val(0)
    mean = mean + (v+65)*adj.get(i)
    i.inc()
print(mean)
```

```
81.84325639929716
```

$$S_1(Alice) = 81k$$

Alice's salary would be $81.843 if she had attended college !

pyAgrum.causal.counterfactual

We can now use a function that answers counterfactual queries using the previous algorithm.

In [16]:
```
help(csl.counterfactual)
```

```
Help on function counterfactual in module pyAgrum.causal._causalImpact:

counterfactual(cm: pyAgrum.causal._CausalModel.CausalModel, profile:␣
↪Optional[Dict[str, int]], on: Union[str, Set[str]], whatif: Union[str, Set[str]],␣
↪values: Optional[Dict[str, int]] = None) -> 'pyAgrum.Potential'
    Determines the estimation of a counterfactual query following the the three steps␣
↪algorithm from "The Book Of Why"
    (Pearl 2018) chapter 8 page 253.

    Determines the estimation of the counterfactual query: Given the "profile"␣
↪(dictionary <variable name>:<value>),what
    would variables in "on" (single or list of variables) be if variables in "whatif"␣
↪(single or list of variables) had
    been as specified in "values" (dictionary <variable name>:<value>)(optional).

    This is done according to the following algorithm:
        -Step 1-2: compute the twin causal model
        -Step 3 : determine the causal impact of the interventions specified in
↪"whatif" on the single or list of
        variables "on" in the causal model.

    This function returns the potential calculated in step 3, representing the␣
↪probability distribution of  "on" given
    the interventions  "whatif", if it had been as specified in "values" (if "values"␣
↪is omitted, every possible value of
    "whatif")

    Parameters
    ----------
    cm: CausalModel
    profile: Dict[str,int] default=None
      evidence
    on: variable name or variable names set
     the variable(s) of interest
    whatif: str|Set[str]
      idiosyncratic nodes
    values: Dict[str,int]
      values for certain variables in whatif.

    Returns
    -------
    pyAgrum.Potential
```

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```
      the computed counterfactual impact
```

Let's try with the previous query :

In [17]:
```
cm_edex= csl.CausalModel(edex)
pot=csl.counterfactual(cm =cm_edex,
                       profile = {'experience':8, 'education': "low", 'salary' : "86"}
↪,
                       whatif={"education"},
                       on={"salary"},
                       values = {"education" : "medium"})
```

In [18]:
```
gnb.showProba(pot)
```

nbsphinx-code-borderwhite

We get the same result !

If we omit values:

We get every potential outcome :

In [19]:
```
pot=csl.counterfactual(cm =cm_edex,
                       profile = {'experience':8, 'education': 'low', 'salary' : '86'}
↪,
                       whatif={"education"},
                       on={"salary"})
```

In [20]:
```
gnb.showPotential(pot)
```

```
<IPython.core.display.HTML object>
```

What would Alice's salary be if she had attended college and had 8 years of experience ?

In [21]:
```
pot=csl.counterfactual(cm =cm_edex,
                       profile = {'experience':8, 'education': 'low', 'salary' : '86'}
↪,
                       whatif={"education", "experience"},
                       on={"salary"},
                       values = {"education" : 'medium', "experience" : 8})
```

In [22]:
```
gnb.showProba(pot)
```

nbsphinx-code-borderwhite

if she attended college and had 8 years of experience Alice's salary would be 91k !

In the previous query, Alice's salary if she attended college was lower than her actual salary, that's because in the counterfactual world where she attended college she had less time to work hence her diminished salary.

In this query, Alice's counterfactual salary was higher than her actual salary (+5k corresponding to one level of education), that's because in the counterfactual world Alice attended college and still had time to work 8 years, so her salary went up.

if she had more experience :

of course, her salary goes up.

In [23]:
```
pot=csl.counterfactual(cm =cm_edex,
                       profile = {'experience':8, 'education': 'low', 'salary' : '86'}
↪,
                       whatif={"education", "experience"},
                       on={"salary"},
                       values = {"education" : 'medium', "experience" : 10})
gnb.showProba(pot)
```

nbsphinx-code-borderwhite

In [24]:
```
twin=csl.counterfactualModel(cm = csl.CausalModel(edex),
                       profile = {'experience':8, 'education': 'low', 'salary' : '86'}
↪,
                       whatif={"experience"})
gnb.showInference(twin.observationalBN(),size="10")
```

nbsphinx-code-borderwhite

In [25]:
```
edexModeleWithout = csl.CausalModel(edex) #(<latent variable name>, <list of affected␣
↪variables' ids>).
edexModeleWithout
```

Out[25]:
```
<pyAgrum.causal._CausalModel.CausalModel at 0x1eaa631f820>
```

Let's try with the previous queries :

In [26]:
```
pot = csl.counterfactual(cm = edexModeleWithout,
                         profile = {'experience':8, 'education': "low", 'salary' : "86
↪"},
                         whatif={"education"},
                         on={"salary"},
                         values = {"education" : "medium"})
gnb.showProba(pot)
```

nbsphinx-code-borderwhite

In [27]:
```
pot=csl.counterfactual(cm = edexModeleWithout,
                       profile = {'experience':8, 'education': 'low', 'salary' : '86'}
↪,
                       whatif={"education", "experience"},
                       on={"salary"},
                       values = {"education" : 'medium', "experience" : 8})
gnb.showProba(pot)
```

nbsphinx-code-borderwhite

We get the same results.

Latent variable between U_x and $experience$:

In [28]:
```
edexModeleWithOne = csl.CausalModel(edex,[("u1", ["Ux","experience"])],False) #(
↪<latent variable name>, <list of affected variables' ids>).
edexModeleWithOne
```

Out[28]:
```
<pyAgrum.causal._CausalModel.CausalModel at 0x1eaa51ed390>
```

In [29]:
```
pot = csl.counterfactual(cm = edexModeleWithOne,
                         profile = {'experience':8, 'education': "low", 'salary' : "86
↪"},
                         whatif={"education"},
                         on={"salary"},
                         values = {"education" : "medium"})
gnb.showProba(pot)
```

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With one latent variable between U_x and $experience$, we get $96k corresponding to one education level (we don't need to worry about experience any more.)

In [30]:
```
pot = csl.counterfactual(cm = edexModeleWithOne,
                         profile = {'experience':8, 'education': "low", 'salary' : "86
↪"},
                         whatif={"education"},
                         on={"salary"},
                         values = {"education" : "high"})
gnb.showProba(pot)
```

nbsphinx-code-borderwhite

In [ ]:
```
```

1.26 Examples

1.26.1 Asthma

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import matplotlib.pyplot as plt

# import the computation tools of aGrUM
import pyAgrum as gum
```

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```
# import the graphical display functions
import pyAgrum.lib.notebook as gnb
```

The model

In [2]:
```
# load the "asthma" Bayesian network
bn=gum.loadBN('res/asthma.bif')
```

In [3]:
```
# display the Bayesian network
gnb.showBN(bn,nodeColor={n:0.9 for n in bn.names()},cmap=plt.get_cmap('Blues'))
```

nbsphinx-code-borderwhite

In [12]:
```
# display the conditional probability table of asthme given pollution
gnb.showPotential(bn.cpt(bn.idFromName('asthma')),digits=4)
```

```
<IPython.core.display.HTML object>
```

Some inference

In [5]:
```
# display the probability distribution of Variable "trafic"
gnb.showPosterior (bn, {}, "traffic" )
```

nbsphinx-code-borderwhite

In [6]:
```
# display the probability distribution of Variable "pollution"
gnb.showPosterior ( bn, {}, "pollution")
```

nbsphinx-code-borderwhite

In [7]:
```
# display the distribution somewhat differently
gum.getPosterior ( bn, {}, "pollution")
```

Out[7]:
```
(pyAgrum.Potential<double>@0x55fd6fe5a300)
  pollution                                                                  ␣
↪              |
1        |2        |3        |4        |5        |6        |7        |8        |9    ␣
↪    |10       |
---------|---------|---------|---------|---------|---------|---------|---------|------
↪---|---------|
 0.0000  | 0.0355  | 0.4233  | 0.2788  | 0.1475  | 0.0629  | 0.0164  | 0.0219  | 0.
↪0082  | 0.0055  |
```

In [8]:
```
# more interesting: display the posterior distribution of "asthme"
# given that we observed that time is 8:00 and weather is cloudy
gnb.showPosterior (bn, {'hour' : 8, 'weather' : 'cloudy'}, "asthma" )
```

nbsphinx-code-borderwhite

In [9]:
```
# show the complete model on morning (from 8 to 12)
gnb.showInference(bn,evs={'hour' : [0]*8+[1]*5+[0]*11})
```

nbsphinx-code-borderwhite

In [10]:
```
# show the posterior distributions of all the variables given that
# we observed that heure=8 and meteo=nuageux.
# the tables in beige represent the observations
gnb.flow.row(gnb.getInference(bn,size="9",evs={'hour' : 8, 'weather' : 'cloudy'}),
```

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```
                gnb.getInference(bn,size="9",evs={'hour': 7, 'accident' : 'yes'}),
               captions=["When time is 8:00 and weatcher is cloudy","When time is 7:00␣
↪and there hase been an accident"])
```

```
<IPython.core.display.HTML object>
```

1.26.2 Kaggle Titanic

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import pandas
import os
import math
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
from pyAgrum.lib.bn2roc import showROC_PR

from sklearn.metrics import accuracy_score, roc_auc_score, confusion_matrix
import pandas as pd
```

Titanic: Machine Learning from Disaster

This notebook is an introduction to the Kaggle titanic challenge (https://www.kaggle.com/c/titanic). The goal here is not to produce the best possible classifier, at least not yet, but to show how pyAgrum and Bayesian networks can be used to easily and quickly explore and understand data.

To undestand this notebook, basic knowledge of Bayesian networks is required. If you are looking for an introduction to pyAgrum, check this notebook (http://www-desir.lip6.fr/~phw/aGrUM/docs/last/notebooks/Tutorial.ipynb.html).

This notebook present three different Bayesien Networks techniques to answer the Kaggle Titanic challenge. The first approach we will answer the challenge without using the training set and we will only use our prior knowledge about shipwrecks. In the second approach we will only use the training set with pyAgrum's machine learning algorithms. Finally, in the third approach we will use both prior knowledge about shipwrecks and machine learning.

Before we start, some disclaimers about aGrUM and pyAgrum.

aGrUM is a C++ library designed for easily building applications using graphical models such as Bayesian networks, influence diagrams, decision trees or Markov decision processes.

pyAgrum is a Python wrapper for the C++ aGrUM library. It provides a high-level interface to the part of aGrUM allowing to create, handle and make computations into Bayesian networks. The module mainly is an application of the SWIG (http://www.swig.org/) interface generator. Custom-written code is added to simplify and extend the aGrUM API.

Both projects are open source (https://gitlab.com/agrumery/aGrUM/blob/master/LICENSE) and can be freely downloaded from aGrUM's gitlab repository (https://gitlab.com/agrumery/aGrUM) or installed using pip or anaconda (http://agrum.gitlab.io/pages/pyagrum.html).

If you have questions, remarks or suggestions, feel free to ask us on info@agrum.org.

Pretreatment

We will be using pandas (http://pandas.pydata.org/) to setup the learning data to fit with pyAgrum requirements.

In [2]:
```
traindf=pandas.read_csv('res/titanic/train.csv')

testdf=pandas.merge(pandas.read_csv('res/titanic/test.csv'),
                    pandas.read_csv('res/titanic/gender_submission.csv'),
                    on="PassengerId")
```

This merges both the test base with the fact that a passager has survived or not.

In [3]:
```
for k in traindf.keys():
    print('{0}: {1}'.format(k, len(traindf[k].unique())))
```

```
PassengerId: 891
Survived: 2
Pclass: 3
Name: 891
Sex: 2
Age: 89
SibSp: 7
Parch: 7
Ticket: 681
Fare: 248
Cabin: 148
Embarked: 4
```

Looking at the number of unique values for each variable is necessary since Bayesian networks are discrete models. We will want to reduce the domain size of some discrete varaibles (like age) and discretize continuous variables (like Fare).

For starters you can filter out variables with a large number of values. Choosing a large number will have an impact on performances, which boils down to how much CPU and RAM you have at your disposal. Here, we choose to filter out any variable with more than 10 different outcomes.

In [4]:
```
for k in traindf.keys():
    if len(traindf[k].unique())<=15:
        print(k)
```

```
Survived
Pclass
Sex
SibSp
Parch
Embarked
```

This leaves us with 6 variables, not much but still enough to learn a Bayesian network. Will just add one more variable by reducing the cardinality of the Age variable.

In [5]:
```
testdf=pandas.merge(pandas.read_csv('res/titanic/test.csv'),
                    pandas.read_csv('res/titanic/gender_submission.csv'),
                    on="PassengerId")


def forAge(row):
    try:
        age = float(row['Age'])
        if age < 1:
```

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```
            #return '[0;1['
            return 'baby'
        elif age < 6:
            #return '[1;6['
            return 'toddler'
        elif age < 12:
            #return '[6;12['
            return 'kid'
        elif age < 21:
            #return '[12;21['
            return 'teen'
        elif age < 80:
            #return '[21;80['
            return 'adult'
        else:
            #return '[80;200]'
            return 'old'
    except ValueError:
        return np.nan

def forBoolean(row, col):
    try:
        val = int(row[col])
        if row[col] >= 1:
            return "True"
        else:
            return "False"
    except ValueError:
        return "False"

def forGender(row):
    if row['Sex'] == "male":
        return "Male"
    else:
        return "Female"


testdf
```

Out[5]:

```
     PassengerId  Pclass                                          Name  \
0            892       3                              Kelly, Mr. James
1            893       3              Wilkes, Mrs. James (Ellen Needs)
2            894       2                     Myles, Mr. Thomas Francis
3            895       3                             Wirz, Mr. Albert
4            896       3  Hirvonen, Mrs. Alexander (Helga E Lindqvist)
..           ...     ...                                           ...
413         1305       3                           Spector, Mr. Woolf
414         1306       1                 Oliva y Ocana, Dona. Fermina
415         1307       3                 Saether, Mr. Simon Sivertsen
416         1308       3                          Ware, Mr. Frederick
417         1309       3                     Peter, Master. Michael J

        Sex   Age  SibSp  Parch              Ticket      Fare Cabin Embarked  \
0      male  34.5      0      0              330911    7.8292   NaN        Q
1    female  47.0      1      0              363272    7.0000   NaN        S
2      male  62.0      0      0              240276    9.6875   NaN        Q
3      male  27.0      0      0              315154    8.6625   NaN        S
```

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```
4    female  22.0      1      1              3101298   12.2875   NaN        S
..      ...   ...    ...    ...                  ...       ...   ...      ...
413    male   NaN      0      0           A.5. 3236    8.0500   NaN        S
414  female  39.0      0      0            PC 17758  108.9000  C105        C
415    male  38.5      0      0  SOTON/O.Q. 3101262    7.2500   NaN        S
416    male   NaN      0      0              359309    8.0500   NaN        S
417    male   NaN      1      1                2668   22.3583   NaN        C

     Survived
0           0
1           1
2           0
3           0
4           1
..        ...
413         0
414         1
415         0
416         0
417         0

[418 rows x 12 columns]
```

When pretreating data, you will want to wrap your changes inside a function, this will help you keep track of your changes and easily compare them.

In [6]:
```
def pretreat(df):
    if 'Survived' in df.columns:
        df['Survived'] = df.apply(lambda row: forBoolean(row, 'Survived'), axis=1)
    df['Age'] = df.apply(forAge, axis=1)
    df['SibSp'] = df.apply(lambda row: forBoolean(row, 'SibSp'), axis=1)
    df['Parch'] = df.apply(lambda row: forBoolean(row, 'Parch'), axis=1)
    df['Sex'] = df.apply(forGender, axis=1)
    droped_cols = [col for col in ['PassengerId', 'Name', 'Ticket', 'Fare', 'Cabin']␣
↪if col in df.columns]
    df = df.drop(droped_cols, axis=1)
    df = df.rename(index=str, columns={'Sex': 'Gender', 'SibSp': 'Siblings', 'Parch':
↪'Parents'})
    df.dropna(inplace=True)
    return df

traindf = pandas.read_csv('res/titanic/train.csv')
testdf  = pandas.merge(pandas.read_csv('res/titanic/test.csv'),
                       pandas.read_csv('res/titanic/gender_submission.csv'),
                       on="PassengerId")

traindf = pretreat(traindf)
testdf = pretreat(testdf)
```

We will need to save this intermediate learning database, since pyAgrum accepts only files as inputs. As a rule of thumb, save your CSV using comma as separators and do not quote values when you plan to use them with pyAgrum.

In [7]:
```
import csv
traindf.to_csv('res/titanic/post_train.csv', index=False)
testdf.to_csv('res/titanic/post_test.csv', index=False)
```

Modeling withtout learning

In some cases, we might not have any data to learn from. In such cases, we can rely on experts to provide correlation between variables and conditional probabilities.

It can be simpler to start with a simple topography, leaving room to add more complexe correlations as the model is confonted aginst data. Here, we will use three hypothesis: - All variables are independent conditionnaly to each other given the fact that a passenger has survive or not. - Women and children are more likelly to survive. - The more sibling or parents abord, the less likelly the passenger will survive.

The first assumption results in the following DAG for our Bayesian network:

In [8]:
```
bn = gum.BayesNet("Surviving Titanic")
bn =gum.fastBN("Age{baby|toddler|kid|teen|adult|old}<-Survived{False|True}->Gender
↪{Female|Male};Siblings{False|True}<-Survived->Parents{False|True}")
print(bn.variable("Survived"))
print(bn.variable("Age"))
print(bn.variable("Gender"))
print(bn.variable("Siblings"))
print(bn.variable("Parents"))

bn
```

```
Survived:Labelized({False|True})
Age:Labelized({baby|toddler|kid|teen|adult|old})
Gender:Labelized({Female|Male})
Siblings:Labelized({False|True})
Parents:Labelized({False|True})
```

Out[8]:
```
(pyAgrum.BayesNet<double>@0000015731AFF180) BN{nodes: 5, arcs: 4, domainSize: 96, dim:
↪ 26}
```

Hypothesis two and three can help us define the parameters for this Bayesian network. Remember that we assume that we do not have any data to learn from. So we will use simple definition such as “a women is 10 times more likeliy to survive than a man”. We can then normalize the values to obtain a proper conditional probability distribution.

This technique may not be the most precise or scientifically sounded, it however has the advantage to be easy to use.

In [9]:
```
bn.cpt('Survived')[:] = [100, 1]
bn.cpt('Survived').normalizeAsCPT()
bn.cpt('Survived')
```

Out[9]:
```
(pyAgrum.Potential<double>@0000015731815A20)
  Survived         |
False    |True     |
---------|---------|
 0.9901  | 0.0099  |
```

In [10]:
```
bn.cpt('Age')[{'Survived':0}] = [ 1, 1, 1, 10, 10, 1]
bn.cpt('Age')[{'Survived':1}] = [ 10, 10, 10, 1, 1, 10]
bn.cpt('Age').normalizeAsCPT()
bn.cpt('Age')
```

Out[10]:
```
(pyAgrum.Potential<double>@0000015731815B00)
      ||  Age                                                  |
Surviv||baby     |toddler  |kid      |teen     |adult    |old      |
------||---------|---------|---------|---------|---------|---------|
False || 0.0417  | 0.0417  | 0.0417  | 0.4167  | 0.4167  | 0.0417  |
True  || 0.2381  | 0.2381  | 0.2381  | 0.0238  | 0.0238  | 0.2381  |
```

In [11]:
```
bn.cpt('Gender')[{'Survived':0}] = [ 1, 1]
bn.cpt('Gender')[{'Survived':1}] = [ 10, 1]
bn.cpt('Gender').normalizeAsCPT()
bn.cpt('Gender')
```

Out[11]:
```
(pyAgrum.Potential<double>@0000015731815A00)
      ||  Gender           |
Surviv||Female   |Male     |
------||---------|---------|
False || 0.5000  | 0.5000  |
True  || 0.9091  | 0.0909  |
```

In [12]:
```
bn.cpt('Siblings')[{'Survived':0}] = [ 1, 10]
bn.cpt('Siblings')[{'Survived':1}] = [ 10, 1]
bn.cpt('Siblings').normalizeAsCPT()
bn.cpt('Siblings')
```

Out[12]:
```
(pyAgrum.Potential<double>@00000157318159C0)
      ||  Siblings         |
Surviv||False    |True     |
------||---------|---------|
False || 0.0909  | 0.9091  |
True  || 0.9091  | 0.0909  |
```

In [13]:
```
bn.cpt('Parents')[{'Survived':0}] = [ 1, 10]
bn.cpt('Parents')[{'Survived':1}] = [ 10, 1]
bn.cpt('Parents').normalizeAsCPT()
bn.cpt('Parents')
```

Out[13]:
```
(pyAgrum.Potential<double>@0000015731815740)
      ||  Parents          |
Surviv||False    |True     |
------||---------|---------|
False || 0.0909  | 0.9091  |
True  || 0.9091  | 0.0909  |
```

Now we can start using the Bayesian network and check that our hypothesis hold.

In [14]:
```
gnb.showInference(bn,size="10")
```

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We can see here that most passengers (99% of them) will not survive and that we have almost as much women (50.4%) as men (49.6%). The majority of passengers are either teenagers or adults. Finally, most passenger had siblings or parents aboard.

Recall that we have not use any data to learn the Bayesian Netork's parameters and our expert did not have any knowledge about the passengers aboard the Titanic.

In [15]:
```
gnb.showInference(bn,size="10", evs={'Survived':'False'})
gnb.showInference(bn,size="10", evs={'Survived':'True'})
```

nbsphinx-code-borderwhite
nbsphinx-code-borderwhite

Here, we can see that our second and third hypothesis hold since when we enter envidence that a passenger survived, it is more likely to be a woman with no siblings or parents. On the contrary, if we observe that a passenger did not survive we can see that it is more likely to be a man with siblings or parents.

In [16]:
```
gnb.showInference(bn,size="10", evs={'Survived':'True', 'Gender':'Male'})
gnb.showInference(bn,size="10", evs={'Gender':'Male'})
```

nbsphinx-code-borderwhite
nbsphinx-code-borderwhite

This validates our first hypothesis: if we know that a passenger survived or not, then evidence about that passenger does not changes our belief about other variables. On the contrary, if we do not know if a passenger survived, then evidence about the passenger will change our belief about other variables, including the fact that he or she survived or not.

In [17]:
```
ie=gum.LazyPropagation(bn)

def init_belief(engine):
    # Initialize evidence
    for var in engine.BN().names():
        if var != 'Survived':
            engine.addEvidence(var, 0)

def update_beliefs(engine, bayesNet, row):
    # Update beliefs from a given row less the Survived variable
    for var in bayesNet.names():
        if var == "Survived":
            continue
        try:
            label = str(row.to_dict()[var])
            idx = bayesNet.variable(var).index(str(row.to_dict()[var]))
            engine.chgEvidence(var, idx)
        except gum.NotFound:
            # this can happend when value is missing is the test base.
            pass
    engine.makeInference()

def is_well_predicted(engine, bayesNet, auc, row):
    update_beliefs(engine, bayesNet, row)
    marginal = engine.posterior('Survived')
    outcome = row.to_dict()['Survived']
    if outcome == "False": # Did not survived
        if marginal.toarray()[1] < auc:
            return "True Positive"
        else:
            return "False Negative"
    else: # Survived
        if marginal.toarray()[1] >= auc:
            return "True Negative"
        else:
            return "False Positive"

init_belief(ie)
ie.addTarget('Survived')
result = testdf.apply(lambda x: is_well_predicted(ie, bn, 0.5, x), axis=1)
result.value_counts(True)
```

Out[17]:
```
True Positive     0.516746
False Positive    0.322967
False Negative    0.119617
True Negative     0.040670
dtype: float64
```

In [18]:
```
positives = sum(result.map(lambda x: 1 if x.startswith("True") else 0 ))
total = result.count()
```

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```
print("{0:.2f}% good predictions".format(positives/total*100))
```

```
55.74% good predictions
```

This first model achieve a 55.74% of good predictions, not a good result but we have plenty of room to improve it.

Pre-learning

We will now learn a Bayesian network from the training set without any prior knowledge about shipwreks.

Before learning a Bayesian network, we first need to create a template. This is not mandatory, however it is sometimes usefull since not all varaibles values are present in the learning base (in this example the number of relatives).

If during the learning step, the algorithm encounters an unknown value it will raise an error. This would be an issue if we wanted to automitize our classifier but, we will directly use values working with the test and learning base. This is not ideal but the objective here it to explore the data fast, not thoroughly.

To help creating de the template Bayesian network that we will use to learn our classifier, let us firt recall all the variables wa have at our disposal.

In [19]:
```
df = pandas.read_csv('res/titanic/post_train.csv')
for k in traindf.keys():
    print('{0}: {1}'.format(k, len(traindf[k].unique())))
```

```
Survived: 2
Pclass: 3
Gender: 2
Age: 6
Siblings: 2
Parents: 2
Embarked: 3
```

From here, creating the BayesNet is straitforward: for each variable we either use the `RangeVariable` class or the `LabelizedVariable`.

The `RangeVariable` class creates a discrete random variable over a range. With the `LabelizedVariable` you will need to add each label ony by one. Note however that you can pass an argument to create as much labels starting from `0`.

In [20]:
```
template=gum.BayesNet()
template.add(gum.LabelizedVariable("Survived", "Survived", ['False', 'True']))
template.add(gum.RangeVariable("Pclass", "Pclass",1,3))
template.add(gum.LabelizedVariable("Gender", "The passenger's gender",['Female', 'Male
↪'']))
template.add(gum.LabelizedVariable("Siblings", "Siblings",['False', 'True']))
template.add(gum.LabelizedVariable("Parents", "Parents",['False', 'True']))
template.add(gum.LabelizedVariable("Embarked", "Embarked", ['', 'C', 'Q', 'S']))
template.add(gum.LabelizedVariable("Age", "The passenger's age category", ["baby",
↪"toddler", "kid", "teen", "adult", "old"]))
gnb.showBN(template)
```

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You can also let the learning algorithm create the BayesNet random variables. However please be aware that the algorithm will no be able to handle values absent from the learning database.

Learning a probabilistic model

We can now learn our first Bayesian network. As you will see, this is really easy.

In [21]:
```
learner = gum.BNLearner(df, template)
bn = learner.learnBN()
bn
```

Out[21]:
```
(pyAgrum.BayesNet<double>@0000015731AFE190) BN{nodes: 7, arcs: 9, domainSize: 1152,␣
↪dim: 78}
```

In a notebook, a Bayesian network will automatically be shown graphically, you can also use the helper function `gnb.showBN(bn)`.

Exploring the data

Now that we have a BayesNet, we can start looking how the variables corelate with each other. pyAgum offer the perfect tool for that: the information graph.

In [22]:
```
import pyAgrum.lib.explain as explain
explain.showInformation(bn,{},size="20")
```

```
<IPython.core.display.HTML object>
```

To read this graph, you must understand what the entropy of a variable means: the hightest the value the more uncertain the variable marginal probability distrubition is (maximum entropy beging the equiprobable law). The lowest the value is, the more /certain/ the law is.

A consequence of how entropy is calculated, is that entropy tends to get bigger if the random varaible has many modalities.

What the information graph tells us is that the `decade` variable has a hight entropy. Thus, we can conclude that the passengers `decade` is distributed between all of its modalities.

What it also tells us, it that high modality variables with low entropy, such as `Parch` or `SibSp`, are not evenly distributed.

Let us look at he variables marginal probability by using the `showInference()` function.

In [23]:
```
gnb.showInference(bn)
```

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The `showInference()` is really usefull as it shows the marginal probability distribution for each random variable of a BayesNet.

We can now confirm what the entropy learned us: `Parch` and `SibSp` are unevenly distributed and `decade` is more evenly distributed.

Lets focus on the Kaggle challenge now, and look at the `Survived` variable. We show a single posterior using the `showPosterior()` function.

In [24]:
```
gnb.showPosterior(bn,evs={},target='Survived')
```

nbsphinx-code-borderwhite

So more than 40% of the passenger in our learning database survived.

So how can we use this BayesNet as a classifier ? Given a set of evidence, we can infer an update posterio distribution of the target variable `Survived`.

Lets look at the odds of surviving as a man in his thirties.

In [25]:
```
gnb.showPosterior(bn,evs={"Gender": "Male", "Age": 'adult'},target='Survived')
```

nbsphinx-code-borderwhite

And now the odds of an old lady to survive.

In [26]:
```
gnb.showPosterior(bn,evs={"Gender": "Female", "Age": 'old'},target='Survived')
```

nbsphinx-code-borderwhite

Well, children and ladies first, that's right ?

One last information we will need is which variables are required to predict the `Survived` variable. To do, we will use the markov blanket of `Survived`.

In [27]:
```
gnb.flow.row(bn, gum.MarkovBlanket(bn, 'Survived'),
             captions=["Learned Bayesian network", "Markov blanket of 'Survived'"])
```

```
<IPython.core.display.HTML object>
```

The Markov Blanket of the `Survived` variable tells us that we only need to observe `Sex` and `Pclass` in order to predict `Survived`. Not really usefull here but on larger Bayesian networks it can save you a lot of time and CPU.

So how to use this BayesNet we have learned as a classifier ? We simply infer the posterior the `Survive` variable given the set of evidence we are given, and if the passanger odds of survival are above some value he will be taged as a survivor.

To compute the best value given the BayesNet and our training database, we can use the `showROC()` function.

In [28]:
```
showROC_PR(bn, 'res/titanic/post_train.csv', 'Survived', 'True', False, True);
```

nbsphinx-code-borderwhite

In [29]:
```
ie=gum.LazyPropagation(bn)
init_belief(ie)
ie.addTarget('Survived')
result = testdf.apply(lambda x: is_well_predicted(ie, bn, 0.157935, x), axis=1)
result.value_counts(True)
```

Out[29]:
```
True Negative     0.363636
True Positive     0.349282
False Negative    0.287081
dtype: float64
```

In [30]:
```
positives = sum(result.map(lambda x: 1 if x.startswith("True") else 0 ))
total = result.count()
print("{0:.2f}% good predictions".format(positives/total*100))
```

```
71.29% good predictions
```

With 71% of good prediction, this model performs better than the first one.

Using BNClassifier

'BNClassifier' is a BN-wrapping object that you can use as a classifier directly. It is inspired and compatible with scikitlearn methods.

In [31]:
```
import pyAgrum.skbn as skbn
```

In [32]:
```
post_train_df = pandas.read_csv('res/titanic/post_train.csv').dropna().astype(str)
post_test_df = pandas.read_csv('res/titanic/post_test.csv').dropna().astype(str)
```

In [33]:
```
targetColumn = 'Survived'

x_train_df = post_train_df.drop(targetColumn, axis=1)
y_train_df = post_train_df[targetColumn]
x_test_df = post_test_df.drop(targetColumn, axis=1)
y_test_df = post_test_df[targetColumn]
```

You create the object. Then you fit the classifier to your training dataset. The fitted classifier can now predict the class for the testing dataset.

In [34]:
```
bn = skbn.BNClassifier(prior="NoPrior")
bn.fit(x_train_df, y_train_df)
y_test_pred = bn.predict(x_test_df)

print("{0:.2f}% good predictions".format(accuracy_score(y_test_df, y_test_pred)*100))
```

```
86.36% good predictions
```

You can try different parameters and use the same procedure. For example, with a a-priori-smoothing :

In [35]:
```
bn_prior = skbn.BNClassifier(prior='Smoothing',priorWeight=1)
bn_prior.fit(x_train_df, y_train_df)
y_test_pred_prior = bn_prior.predict(x_test_df)

print("{0:.2f}% good predictions".format(accuracy_score(y_test_df, y_test_pred_
↪prior)*100))
```

```
86.36% good predictions
```

Making a BN without learning data

In this last part we will combine both methods: we will force the BayesNet DAG and learn its parameters. We will assume the naive bayes hypothesis, which states that all random variables are independant conditionally to the target variable (here the variable Survived).

This results in the following (already seen) above topology.

In [36]:
```
bn = gum.BayesNet("Surviving Titanic")
bn =gum.fastBN("Age{baby|toddler|kid|teen|adult|old}<-Survived{False|True}->Gender
↪{Female|Male};Siblings{False|True}<-Survived->Parents{False|True}")
print(bn.variable("Survived"))
print(bn.variable("Age"))
print(bn.variable("Gender"))
print(bn.variable("Siblings"))
print(bn.variable("Parents"))

bn
```

```
Survived:Labelized({False|True})
Age:Labelized({baby|toddler|kid|teen|adult|old})
Gender:Labelized({Female|Male})
Siblings:Labelized({False|True})
Parents:Labelized({False|True})
```

Out[36]:
```
(pyAgrum.BayesNet<double>@0000015731AFF6D0) BN{nodes: 5, arcs: 4, domainSize: 96, dim:
↪ 26}
```

The next step is to learn the parameters, this can easily be done using the `learnParameters` method.

In [37]:
```
learner = gum.BNLearner("res/titanic/post_train.csv", bn)
bn = learner.learnParameters(bn.dag())
gnb.showInference(bn, size="10")
```

nbsphinx-code-borderwhite

If we compare the CPTs obtained here with those defined by our expert in the first example we can see that they differ. They ressemble those obtained in the second example. This result is expected since we have learn the parameters from the training data, the learned probabilities distribution should match the data.

The final steps consists of confronting this model agains our test dataset.

In [38]:
```
showROC_PR(bn, "res/titanic/post_train.csv", 'Survived', "True", True, True)
showROC_PR(bn, "res/titanic/post_test.csv", 'Survived', "True", True, True)
```

```
res/titanic/post_train.csv: 100%||
```

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```
res/titanic/post_test.csv: 100%||
```

nbsphinx-code-borderwhite

Out[38]:
```
(0.9879550850811238,
 0.47050241859999997,
 0.922493887637304,
 0.47050241859999997)
```

In [39]:
```
ie = gum.LazyPropagation(bn)
init_belief(ie)
ie.addTarget('Survived')
result = testdf.apply(lambda x: is_well_predicted(ie, bn, 0.4705, x), axis=1)
result.value_counts(True)
```

Out[39]:
```
True Positive     0.624402
True Negative     0.363636
False Negative    0.011962
dtype: float64
```

In [40]:
```
positives = sum(result.map(lambda x: 1 if x.startswith("True") else 0 ))
total = result.count()
print("{0:.2f}% good predictions".format(positives/total*100))
```

```
98.80% good predictions
```

Naive Bayes perform well when used for classification tasks, as shown by the 95% of good predictions achieved by our third model.

Conclusion

We have demonstradted with different classification techniques using Bayesian networks. In the first approach, we mangaged to model a classifier without using any training set and relying solely on prior knowledge. In the second approach we used only machine learning techniques. Finally, in the third example we assumed the naive bayes hypothesis and obtained a model combinede

In [ ]:
```
```

1.26.3 Naive modeling of credit defaults using a Markov Random Field

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

This notebook is the adaptation to pyAgrum of the model proposed by Gautier Marti (https://marti.ai/quant/2022/01/30/default-distribution-mrf.html) which is itself inspired by the paper Graphical Models for Correlated Defaults (https://arxiv.org/pdf/0809.1393.pdf) (adaptation by **Marvin Lasserre** and Pierre-Henri Wuillemin).

In [1]:
```
import numpy as np
import matplotlib.pyplot as plt

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
import pyAgrum.lib.mn2graph as m2g
```

Constructing the model

Three sectors co-dependent in their stress state are modelled: (`Finance`, `Energy`, `Retail`). For each of these sectors, we consider a universe of three issuers.

Within *Finance*	Within *Energy*	Within *Retail*
Deutsche Bank	EDF	New Look
Metro Bank	Petrobras	Matalan
Barclays	EnQuest	Marks & Spencer

The probability of default of these issuers is partly idiosyncratic and partly depending on the stress within their respective sectors. Some distressed names such as New Look can have a high marginal probability of default, so high that the state of their sector (normal or stressed) does not matter much. Some other high-yield risky names such as Petrobras may strongly depend on how the whole energy sector is doing. On the other hand, a company such as EDF should be quite robust, and would require a very acute and persistent sector stress to move its default probability significantly higher.

We can encode this basic knowledge in terms of potentials:

	Finance	
Energy	**no stress**	**under stress**
no stress	90.0000	70.0000
under stress	60.0000	10.0000

Conventions:

Sector variables can be either in the state `no stress` or in the state `under stress` while issuer variables can be either in the state `no default` or in the state `default`.

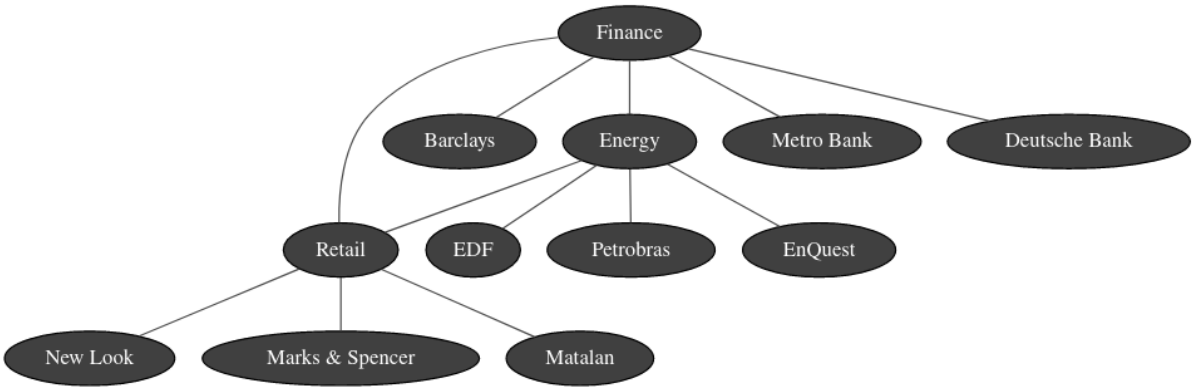
The choice of these potentials is not an easy task; It can be driven by historical fundamental or statistical relationships or forward-looking views.

Given a network structure, and a set of potentials, one can mechanically do inference using the pyAgrum library.

We will show how to obtain a distribution of the number of defaults (and the expected number of defaults), a distribution of the losses (and the expected loss). From the joint probability table, we could also extract the default correlation

tl;dr We use here the library pyAgrum (https://agrum.org) to illustrate, on a toy example, how one can use a Markov Random Field (MRF) for modelling the distribution of defaults and losses in a credit portfolio.

Building accurate PGM/MRF models require expert knowledge for considering a relevant graph structure, and attributing useful potentials. For this toy model, we use the following structure:



The first step consists in creating the model. For that, we use the pyAgrum class `MarkovNet`.

In [2]:
```
# building nodes (with types)
mn = gum.MarkovNet('Credit default modeling')

# Adding sector variables
sectors = ['Finance', 'Energy', 'Retail']
finance, energy, retail = [mn.add(gum.LabelizedVariable(name, '', ['no stress',
↪'under stress']))
                           for name in sectors]

# Adding issuer variables
edf, petro, eq = [mn.add(gum.LabelizedVariable(name, '', ['no default', 'default']))
              for name in ['EDF','Petrobras','EnQuest']]

mb, db, ba = [mn.add(gum.LabelizedVariable(name, '', ['no default', 'default']))
              for name in ['Metro Bank', 'Deutsche Bank', 'Barclays']]

nl, matalan, ms = [mn.add(gum.LabelizedVariable(name, '', ['no default', 'default']))
              for name in ['New Look', 'Matalan', 'Marks & Spencer']]
```

In [3]:
```
# Adding and filling factors between sectors
mn.addFactor([finance, energy])[:] = [[90, 70],
                                      [60, 10]]
mn.addFactor([finance, retail])[:] = [[80, 10],
                                      [30, 80]]
mn.addFactor([energy, retail])[:]  = [[60,  5],
                                      [70, 95]]

# Adding factors between sector and issuer
mn.addFactor([db, finance])[:] = [[90, 30],
                                  [10, 60]]
mn.addFactor([mb, finance])[:] = [[80, 40],
                                  [ 5, 60]]
```

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```
mn.addFactor([ba, finance])[:] = [[90, 20],
                                  [20, 50]]

mn.addFactor([edf, energy])[:]   = [[90, 5],
                                    [80, 40]]
mn.addFactor([petro, energy])[:] = [[60, 50],
                                    [ 5, 60]]
mn.addFactor([eq, energy])[:]    = [[80, 20],
                                    [10, 50]]


mn.addFactor([nl, retail])[:]      = [[ 5, 60],
                                      [ 2, 90]]
mn.addFactor([matalan, retail])[:] = [[40, 30],
                                      [20, 70]]
mn.addFactor([ms, retail])[:]       = [[80, 10],
                                      [30, 50]]
```

In [4]:
```
nodetypes={n:0.1 if n in sectors else
             0.2 for n in mn.names()}

gnb.sideBySide(gnb.getMN(mn,view='graph',nodeColor=nodetypes),
               gnb.getMN(mn,view='factorgraph',nodeColor=nodetypes),
              captions=['The model as a Markov Network','The model as a factor graph
↪'])

gnb.sideBySide(mn.factor({'Energy', 'Finance'}),
               mn.factor({'Finance', 'Retail'}),
               mn.factor({'Energy', 'Retail'}),
               mn.factor({'Deutsche Bank', 'Finance'}),
               mn.factor({'Metro Bank', 'Finance'}),
               mn.factor({'Barclays', 'Finance'}),
               mn.factor({'EDF', 'Energy'}),
               mn.factor({'Petrobras', 'Energy'}),
               mn.factor({'EnQuest', 'Energy'}),
               mn.factor({'New Look', 'Retail'}),
               mn.factor({'Matalan', 'Retail'}),
               mn.factor({'Marks & Spencer', 'Retail'}),
              ncols=3)
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

Making inferences

Example 1 & 2

The first two examples consists in finding the chance of `EDF` to default with no evidence and knowing that the energy sector is not under stress. For that, we can use the `getPosterior` method:

In [5]:
```
gnb.sideBySide(gum.getPosterior(mn, target='EDF', evs={}),
               gum.getPosterior(mn, target='EDF', evs={'Energy':'no stress'}),
               captions=['$P(EDF)$','$P(EDF|Energy=$under stress$)$'])
```

```
<IPython.core.display.HTML object>
```

Hence, if we cannot observe the state of the energy sector, then EDF has a higher chance of defaulting (9%) as it is possible that the energy sector is under stress.

Example 3 & 4

Given that Marks & Spencer (a much safer name) has defaulted, New Look has now an increased chance of defaulting: 97%.

Even if the retail sector is doing ok, New Look is a distressed name with a high probability of default (92%).

In [6]:
```
gnb.sideBySide(gum.getPosterior(mn, target='New Look', evs={'Marks & Spencer':
↪'default'}),
               gum.getPosterior(mn, target='New Look', evs={'Retail':'no stress'}),
               captions=['P(New Look|Marks & Spencer=default)',
                         'P(New Look | Retail = no stress)'])
```

```
<IPython.core.display.HTML object>
```

pyAgrum offers the option to vizualise the marginal probability of each variable using `showInference`.

In [7]:
```
#gum.config['factorgraph','edge_length_inference']=1.
gnb.showInference(mn, size='7!',nodeColor=nodetypes)
```

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Impact of defaults on a credit portfolio and the distribution of losses

Amongst the 9 available issuers, let's consider the following portfolio containing bonds from these 6 issuers:

In [8]:
```
portfolio_names = ['EDF', 'Petrobras', 'EnQuest', 'Matalan', 'Barclays']
portfolio_exposures = [2e6, 400e3, 300e3, 600e3, 3e6]
LGD = 0.9
losses = {portfolio_names[i]:(portfolio_exposures[i]*LGD) for i in␣
↪range(len(portfolio_names))}

print('** Total notional: USD {} MM'.format(sum(portfolio_exposures)/1e6))
```

```
** Total notional: USD 6.3 MM
```

We have a USD 6.3MM total exposure to these names (notional).

We assume that in case of default, we recover only 10% (LGD = 90%).

Let's start using the model:

In [9]:
```
ie = gum.ShaferShenoyMNInference(mn)
ie.makeInference()
p=ie.jointPosterior(set(sectors))

print(f'** There is {100*p[{"Retail":0,"Energy":0,"Finance":0}]:.2f}% chance that no␣
↪sector in under stress.')
print()
p
```

```
** There is 42.38% chance that no sector in under stress.
```

Out[9]:
```
(pyAgrum.Potential<double>@0000021CD885C120)
             ||  Finance          |
Energy|Retail||no stress|under str|
------|------||---------|---------|
```

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```
no str|no str|| 0.4238  | 0.0083  |
under |no str|| 0.0105  | 0.0000  |
no str|under || 0.2999  | 0.1251  |
under |under || 0.1215  | 0.0109  |
```

If we observe that the finance sector is doing ok, and that Marks & Spencer is still doing business as usual, then this is the current joint probabilities associated to the potential defaults in the portfolio:

In [10]:
```
ie = gum.ShaferShenoyMNInference(mn)
ie.addJointTarget(set(portfolio_names))
ie.setEvidence({'Finance': 'no stress', 'Marks & Spencer': 'no default'})
ie.makeInference()
portfolio_posterior = ie.jointPosterior(set(portfolio_names))
```

Note that the line `ie.addJointTarget(set(portfolio_names))` is important here because adding hard evidences removes the corresponding nodes in the graph and then no factor containing the variables in `portfolio_names` can be found. The method addJointTarget ensure that such a factor exists.

In [11]:
```
portfolio_posterior
```

Out[11]:
```
(pyAgrum.Potential<double>@0000021CD885BE00)
                          ||  Barclays         |
Matala|Petrob|EnQues|EDF   ||no defaul|default  |
------|------|------|------||---------|---------|
no def|no def|no def|no def|| 0.1495  | 0.0332  |
defaul|no def|no def|no def|| 0.1552  | 0.0345  |
no def|defaul|no def|no def|| 0.1268  | 0.0282  |
defaul|defaul|no def|no def|| 0.1350  | 0.0300  |
no def|no def|defaul|no def|| 0.0383  | 0.0085  |
defaul|no def|defaul|no def|| 0.0412  | 0.0092  |
[...4 more line(s) ...]
no def|defaul|no def|defaul|| 0.0081  | 0.0018  |
defaul|defaul|no def|defaul|| 0.0102  | 0.0023  |
no def|no def|defaul|defaul|| 0.0026  | 0.0006  |
defaul|no def|defaul|defaul|| 0.0034  | 0.0008  |
no def|defaul|defaul|defaul|| 0.0077  | 0.0017  |
defaul|defaul|defaul|defaul|| 0.0170  | 0.0038  |
```

We now want to compute the distribution of the number of defaults. For that, we create a new Markov network containing an additional node `Number of defaults` connected to each issuers:

In [12]:
```
mn2 = gum.MarkovNet(mn)

mn2.add(gum.RangeVariable('Number of defaults', '', 0, len(portfolio_names)))
factor = mn2.addFactor(['Number of defaults',*portfolio_names]).fillWithFunction('+'.
↪join(portfolio_names))
```

In [13]:
```
gum.config['factorgraph','edge_length']=1.1
nodetypes={n:0.1 if n in sectors else
             0.3 if "Number of defaults"==n else
             0.2 for n in mn2.names()}
gnb.flow.add(gnb.getMN(mn2, view="graph",size='7!',nodeColor=nodetypes))
gnb.flow.add(gnb.getMN(mn2, view="factorgraph",size='7!',nodeColor=nodetypes))
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

Once this new network is created, we can obtain the distribution of `Number of defaults` using `getPosterior`

:

In [14]:
```
ndefault_posterior = gum.getPosterior(mn2, target='Number of defaults',
                                      evs={'Finance': 'no stress', 'Marks &␣
↪Spencer': 'no default'})
ndefault_posterior
```

Out[14]:
```
(pyAgrum.Potential<double>@0000021CD885CFC0)
  Number of defaults                                    |
0         |1         |2         |3         |4         |5         |
----------|----------|----------|----------|----------|----------|
 0.1495   | 0.3620   | 0.3119   | 0.1371   | 0.0357   | 0.0038   |
```

In [15]:
```
fig, ax = plt.subplots()
l = ndefault_posterior.tolist()
ax.bar(range(len(l)), l)
ax.set_xlabel('Number of defaults')
ax.set_title('Distribution of the number of defaults in the portfolio')
plt.show()
```

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In [16]:
```
q=gum.Potential(ndefault_posterior).fillWith(range(ndefault_posterior.domainSize()))
print(f'Expected number of defaults in the portfolio: {(q*ndefault_posterior).sum():.
↪1f}')
```

```
Expected number of defaults in the portfolio: 1.6
```

Besides the expected number of defaults, the distribution of losses is even more informative:

In [17]:
```
pot_losses = gum.Potential(portfolio_posterior)
for i in pot_losses.loopIn():
    pot_losses[i] = sum([losses[key]*i.val(key) for key in losses])
print("Table of losses")
pot_losses
```

```
Table of losses
```

Out[17]:
```
(pyAgrum.Potential<double>@0000021CD87AD8F0)
                          ||  Barclays         |
Matala|Petrob|EnQues|EDF   ||no defaul|default  |
------|------|------|------||---------|---------|
no def|no def|no def|no def|| 0.0000  | 2700000.0000|
defaul|no def|no def|no def|| 540000.0000| 3240000.0000|
no def|defaul|no def|no def|| 360000.0000| 3060000.0000|
defaul|defaul|no def|no def|| 900000.0000| 3600000.0000|
no def|no def|defaul|no def|| 270000.0000| 2970000.0000|
defaul|no def|defaul|no def|| 810000.0000| 3510000.0000|
[...4 more line(s) ...]
no def|defaul|no def|defaul|| 2160000.0000| 4860000.0000|
defaul|defaul|no def|defaul|| 2700000.0000| 5400000.0000|
no def|no def|defaul|defaul|| 2070000.0000| 4770000.0000|
defaul|no def|defaul|defaul|| 2610000.0000| 5310000.0000|
no def|defaul|defaul|defaul|| 2430000.0000| 5130000.0000|
defaul|defaul|defaul|defaul|| 2970000.0000| 5670000.0000|
```

In [18]:
```
expected_loss = (portfolio_posterior * pot_losses ).sum()

print(f'Expected loss with respect to a par value of USD {sum(portfolio_exposures)/
↪1e6:.1f} MM is USD {expected_loss / 1e6:.1f} MM.')
```

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```
print(f'Expected loss: {100 * expected_loss / sum(portfolio_exposures):2.1f}% of the␣
↪notional.')
```

```
Expected loss with respect to a par value of USD 6.3 MM is USD 1.2 MM.
Expected loss: 18.6% of the notional.
```

In [19]:
```
cuts=list(np.percentile([pot_losses[i] for i in pot_losses.loopIn()],range(0,101,10)))
cuts[0] = cuts[0] - 0.001

loss_bucket_distribution = []
d = gum.Potential(pot_losses)
for j in range(len(cuts) - 1):
    for i in pot_losses.loopIn():
        d[i] = 1 if cuts[j]<pot_losses[i]<=cuts[j+1] else 0
    loss_bucket_distribution.append(((portfolio_posterior*d).sum()))
```

In [20]:
```
buckets = [f'({cuts[i]:10.0f}, {cuts[i+1]:10.0f}]' for i in range(len(cuts)-1)]

fig, ax = plt.subplots()
ax.bar(range(10), height=loss_bucket_distribution)
ax.set_xticks(range(10), labels=buckets, rotation=90)
ax.set_title('Distribution of losses with respect to par value')
ax.set_xlabel('Loss buckets')
plt.show()
```

nbsphinx-code-borderwhite

In [21]:
```
cumsum = 0.
for i in range(len(loss_bucket_distribution)):
    cumsum += loss_bucket_distribution[i]
    print('{:24} | {:0.6f}'.format(buckets[i], cumsum))
```

```
(        -0,      549000] | 0.469960
(    549000,      954000] | 0.689263
(    954000,     2097000] | 0.762897
(   2097000,     2502000] | 0.787553
(   2502000,     2835000] | 0.834408
(   2835000,     3168000] | 0.888119
(   3168000,     3573000] | 0.941345
(   3573000,     4716000] | 0.987143
(   4716000,     5121000] | 0.991483
(   5121000,     5670000] | 1.000000
```

Impact of a belief of stress on a sector for the number of defaults in the portfolio

Belief from $[1, 0]$ (no stress) to $[1, 1]$ (no specific belief) to $[0, 1]$ (stress in a sector).

In [22]:
```
def show_expected_number_of_defaults(sector,q,enod_nobelief):
  v1=[]
  for i in range(101):
     posterior=gum.getPosterior(mn2, target='Number of defaults',evs={sector:[100-i,
↪i]})
     v1.append((posterior*q).sum())

  fig, ax = plt.subplots()
  ax.set_title(f"Expected number of defaults w.r.t stress in {sector}")
```

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```
  ax.plot(np.arange(0,1.01,0.01),v1)
  ax.plot(0.5,enod_nobelief,'x',color="red")
  ax.text(0.5, enod_nobelief-0.05, ' No specific belief')
  return fig

enod_nobelief=(gum.getPosterior(mn2, target='Number of defaults',evs={})*q).sum()

gnb.flow.add(show_expected_number_of_defaults('Retail',q,enod_nobelief))
gnb.flow.add(show_expected_number_of_defaults('Finance',q,enod_nobelief))
gnb.flow.add(show_expected_number_of_defaults('Energy',q,enod_nobelief))
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

In [ ]:

1.26.4 Learning and causality

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
```

Model

Let's assume a process $X_1 \rightarrow Y_1$ with a control on X_1 by C_a and a parameter P_b on Y_1.

In [2]:
```
bn=gum.fastBN("Ca->X1->Y1<-Pb")
bn.cpt("Ca").fillWith([0.8,0.2])
bn.cpt("Pb").fillWith([0.3,0.7])

bn.cpt("X1")[:]=[[0.9,0.1],[0.1,0.9]]

bn.cpt("Y1")[{"X1":0,"Pb":0}]=[0.8,0.2]
bn.cpt("Y1")[{"X1":1,"Pb":0}]=[0.2,0.8]
bn.cpt("Y1")[{"X1":0,"Pb":1}]=[0.6,0.4]
bn.cpt("Y1")[{"X1":1,"Pb":1}]=[0.4,0.6]

gnb.flow.row(bn,*[bn.cpt(x) for x in bn.nodes()])
```

```
<IPython.core.display.HTML object>
```

Actually the process is duplicated in the system but the control C_a and the parameter P_b are shared.

In [3]:
```
bn.add("X2",2)
bn.add("Y2",2)
```

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```
bn.addArc("X2","Y2")
bn.addArc("Ca","X2")
bn.addArc("Pb","Y2")

bn.cpt("X2").fillWith(bn.cpt("X1"),["X1","Ca"]) # copy cpt(X1) with the translation X2
↪<-X1,Ca<-Ca
bn.cpt("Y2").fillWith(bn.cpt("Y1"),["Y1","X1","Pb"]) # copy cpt(Y1) with translation␣
↪Y2<-Y1,X2<-X1,Pb<-Pb

gnb.flow.row(bn,bn.cpt("X2"),bn.cpt("Y2"))
```

```
<IPython.core.display.HTML object>
```

Simulation of the data

The process is partially observed : the control has been taken into account. However the parameter has not been identified and therefore is not collected.

In [4]:
```
#the base will be saved in completeData="out/complete_data.csv", observedData="out/
↪observed_data.csv"
import os
completeData="out/complete_data.csv"
observedData="out/observed_data.csv"
fixedObsData="res/fixed_observed_data.csv"

# generating complete date with pyAgrum
size=35000
#gum.generateSample(bn,5000,"data.csv",random_order=True)
generator=gum.BNDatabaseGenerator(bn)
generator.setRandomVarOrder()
generator.drawSamples(size)
generator.toCSV(completeData)
```

In [5]:
```
# selecting some variables using pandas
import pandas as pd
f=pd.read_csv(completeData)
keep_col = ["X1","Y1","X2","Y2","Ca"] # Pb is removed
new_f = f[keep_col]
new_f.to_csv(observedData, index=False)
```

In order to have fixed results, we will use now a database fixed_observed_data.csv generated with the process above.

statistical learning

Using a classical statistical learning method, one can approximate a model from the observed data.

In [6]:
```
learner=gum.BNLearner(fixedObsData)
learner.useGreedyHillClimbing()
bn2=learner.learnBN()
```

Evaluating the impact of $X2$ on $Y1$

Using the database, a question for the user is to evaluate the impact of the value of $X2$ on $Y1$.

In [7]:
```
target="Y1"
evs="X2"
ie=gum.LazyPropagation(bn)
ie2=gum.LazyPropagation(bn2)
p1=ie.evidenceImpact(target,[evs])
p2=gum.Potential(p1).fillWith(ie2.evidenceImpact(target,[evs]),[target,evs])
errs=((p1-p2)/p1).scale(100)
quaderr=(errs*errs).sum()
gnb.flow.row(p1,p2,errs,f"$${quaderr:3.5f}$$",
             captions=['in original model','in learned model','relative errors',
↪'quadratic error'])
```

```
<IPython.core.display.HTML object>
```

Evaluating the causal impact of $X2$ on $Y1$ with the learned model

The statistician notes that the change wanted by the user to apply on X_2 is not an observation but rather an intervention.

In [8]:
```
import pyAgrum.causal as csl
import pyAgrum.causal.notebook as cslnb

model=csl.CausalModel(bn)
model2=csl.CausalModel(bn2)
```

In [9]:
```
cslnb.showCausalModel(model)
```

nbsphinx-code-borderwhite

In [10]:
```
gum.config['notebook','graph_format']='svg'
cslnb.showCausalImpact(model,on=target, doing={evs})
cslnb.showCausalImpact(model2,on=target, doing={evs})
```

```
sum on Ca for
| *
| | P(Y1|Ca)
| | joint P(Ca)
```

```
---------------------------------------------------------------------------
TypeError                                 Traceback (most recent call last)
Cell In [10], line 2
      1 gum.config['notebook','graph_format']='svg'
----> 2 cslnb.showCausalImpact(model,on=target, doing={evs})
      3 cslnb.showCausalImpact(model2,on=target, doing={evs})

File ~/.virtualenvs/devAgrum/lib/python3.10/site-packages/pyAgrum/causal/notebook.py:
↪129, in showCausalImpact(model, on, doing, knowing, values)
    111 def showCausalImpact(model: csl.CausalModel, on: Union[str, NameSet], doing:␣
↪Union[str, NameSet],
    112                     knowing: Optional[NameSet] = None, values:␣
↪Optional[Dict[str, int]] = None):
    113   """
    114   display a HTML representing of the three values defining a causal impact : ␣
↪formula, value, explanation
```

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```
    115
   (...)
    127     value for certain variables
    128   """
--> 129   html = getCausalImpact(model, on, doing, knowing, values)
    130   IPython.display.display(html)

File ~/.virtualenvs/devAgrum/lib/python3.10/site-packages/pyAgrum/causal/notebook.py:
↪104, in getCausalImpact(model, on, doing, knowing, values)
    102   gnb.flow.add(explanation,caption="Impossible")
    103 else:
--> 104   gnb.flow.add('$$\\begin{equation*}' + formula.toLatex() + '\\end{equation*}$
↪$',caption="Explanation : "+explanation )
    106 gnb.flow.add("No result" if formula is None else impact,caption="Impact") # :
↪$" + ("?" if formula is None else formula.latexQuery(values)) + "$")
    108 return gnb.flow.html()

File ~/.virtualenvs/devAgrum/lib/python3.10/site-packages/pyAgrum/causal/_
↪CausalFormula.py:182, in CausalFormula.toLatex(self)
    180 for n in self._doing:
    181   occur[n] = 1
--> 182 for n in self._knowing:
    183   occur[n] = 1
    184 for n in self._on:

TypeError: 'NoneType' object is not iterable
```

Unfortunately, due to the fact that P_a is not learned, the computation of the causal impact still is imprecise.

In [ ]:
```
_, impact1, _ = csl.causalImpact(model, on=target, doing={evs})
_, impact2orig, _ = csl.causalImpact(model2, on=target, doing={evs})

impact2=gum.Potential(p2).fillWith(impact2orig,['Y1','X2'])
errs=((impact1-impact2)/impact1).scale(100)
quaderr=(errs*errs).sum()
gnb.flow.row(impact1,impact2,errs,f"$${quaderr:3.5f}$$",
             captions=['$P( Y_1 \mid \hookrightarrow X_2)$ <br/>in original model',
                       '$P( Y_1 \mid \hookrightarrow X_2)$  <br/>in learned model','
↪<br/>relative errors',' <br/>quadratic error'])
```

Just to be certain, we can verify that in the original model, $P(Y_1 \mid\hookrightarrow X_2) = P(Y_1)$

In [ ]:
```
gnb.flow.row(impact1,ie.evidenceImpact(target,[]),
             captions=["$P( Y_1 \mid \hookrightarrow X_2)$ <br/>in the original␣
↪model","$P(Y_1)$ <br/>in the original model"])
```

Causal learning and causal impact

Some learning algorthims such as MIIC (Verny et al., 2017) aim to find the trace of latent variables in the data

In [ ]:
```
learner=gum.BNLearner(fixedObsData)
learner.useMIIC()
bn3=learner.learnBN()
```

In [ ]:
```
gnb.flow.row(bn,bn3,f"$${[(bn3.variable(i).name(),bn3.variable(j).name()) for (i,j)␣
↪in learner.latentVariables()]}$$",
             captions=['original model','learned model','Latent variables found'])
```

Then we can build a causal model taking into account this latent variable found by MIIC.

In [ ]:
```
model3=csl.CausalModel(bn2,[("L1",("Y1","Y2"))])
cslnb.showCausalImpact(model3,target, {evs})
```

Then at least, the statistician can say that X_2 has no impact on Y_1 from the data. The error is just due to the approximation of the parameters in the database.

In [ ]:
```
_, impact1, _ = csl.causalImpact(model, on=target, doing={evs})
_, impact3orig, _ = csl.causalImpact(model3, on=target, doing={evs})

impact3=gum.Potential(impact1).fillWith(impact3orig,['Y1'])
errs=((impact1-impact3)/impact1).scale(100)
quaderr=(errs*errs).sum()
gnb.flow.row(impact1,impact3,errs,f"$${quaderr:3.5f}$$",
             captions=['in original model','in learned model','relative errors',
↪'quadratic error'])
```

In [ ]:
```
```

1.26.5 Sensitivity analysis for Bayesian networks using credal networks

(https://agrum.org)

(https://agrum.gitlab.io/extra/agrum_at_binder.html)

There are several sensitivity analysis frameworks for Bayesian networks. A fairly efficient method is certainly to use credal networks to do this analysis.

Creating a Bayesian network

In [1]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
```

In [2]:
```
bn=gum.fastBN("A->B->C<-D->E->F<-B")
gnb.flow.row(bn,gnb.getInference(bn))
```

```
<IPython.core.display.HTML object>
```

Building a credal network from a BN

It is easy to build a credal network from a Bayesian network by indicating the 'noise' on each parameter.

In [3]:
```
cr=gum.CredalNet(bn,bn)
gnb.show(cr)
```

nbsphinx-code-borderwhite

In [4]:
```
cr.bnToCredal(beta=1e-10,oneNet=False)
cr.computeBinaryCPTMinMax()
print(cr)
```

```
A:Range([0,1])
<> : [[0.182055 , 0.817945] , [0.132709 , 0.867291]]

B:Range([0,1])
<A:0> : [[0.814242 , 0.185758] , [0.814241 , 0.185759]]
<A:1> : [[0.360802 , 0.639198] , [0.359964 , 0.640036]]

C:Range([0,1])
<B:0|D:0> : [[0.187328 , 0.812672] , [0.15419 , 0.84581]]
<B:1|D:0> : [[0.507362 , 0.492638] , [0.507283 , 0.492717]]
<B:0|D:1> : [[0.425391 , 0.574609] , [0.425104 , 0.574896]]
<B:1|D:1> : [[0.184355 , 0.815645] , [0.112276 , 0.887724]]

D:Range([0,1])
<> : [[0.984151 , 0.0158492]]

E:Range([0,1])
<D:0> : [[0.18389 , 0.81611] , [0.143465 , 0.856535]]
<D:1> : [[0.635584 , 0.364416] , [0.635572 , 0.364428]]

F:Range([0,1])
<E:0|B:0> : [[0.688333 , 0.311667] , [0.688327 , 0.311673]]
<E:1|B:0> : [[0.242911 , 0.757089] , [0.235478 , 0.764522]]
<E:0|B:1> : [[0.350608 , 0.649392] , [0.34961 , 0.65039]]
<E:1|B:1> : [[0.529391 , 0.470609] , [0.529335 , 0.470665]]
```

Testing difference hypothesis about the global precision on the parameters

We can therefore easily conduct a sensitivity analysis based on an assumption of error on all the parameters of the network.

In [5]:
```
def showNoisy(bn,beta):
  cr=gum.CredalNet(bn,bn)
  cr.bnToCredal(beta=beta,oneNet=False)
  cr.computeBinaryCPTMinMax()
  ielbp=gum.CNLoopyPropagation(cr)
  return gnb.getInference(cr,engine=ielbp)
```

In [6]:
```
for eps in [1,1e-3,1e-5,1e-8,1e-10]:
  gnb.flow.add(showNoisy(bn,eps),caption=f"noise={eps}")
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

In [ ]:
```
```

1.26.6 Quasi-continuous BN

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
from pylab import *
import matplotlib.pyplot as plt
```

aGrUM cannot (currently) deal with with continuous variables. However, a discrete variable with a large enough domain size is an approximation of such variables.

In [2]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb

#nbr of states for quasi continuous variables. You can change the value
#but be careful of the quadratic behavior of both memory and time complexity
#in this example.
minB,maxB=-3,3
minC,maxC=4,14
NB=300
```

In [3]:
```
bn=gum.BayesNet("Quasi-Continuous")
bn.add(gum.LabelizedVariable("A","A binary variable",2))
bn.add(gum.NumericalDiscreteVariable("B","A range variable",minB,maxB,NB))
bn.addArc("A","B")
print(bn)
gnb.showBN(bn)
```

```
BN{nodes: 2, arcs: 1, domainSize: 600, dim: 602}
```

nbsphinx-code-borderwhite

In [4]:
```
bn.cpt("A")[:]=[0.4, 0.6]
gnb.showProba(bn.cpt("A"))
```

nbsphinx-code-borderwhite

CPT for quasi-continuous variables (with parents)

Using python (and scipy), it is easy to find pdf for continuous variable

In [5]:
```
# we truncate a pdf, so we need to normalize
def normalize(rv,vmin,vmax,size):
    pdf=rv.pdf(linspace(vmin,vmax,size))
    return (pdf/sum(pdf))

from scipy.stats import norm,genhyperbolic
p, a, b = 0.5, 1.5, -0.7
bn.cpt("B")[{'A':0}]=normalize(norm(2.41),minB,maxB,NB)
bn.cpt("B")[{'A':1}]=normalize(genhyperbolic(p,a,b),minB,maxB,NB)
gnb.flow.clear()
gnb.flow.add(gnb.getProba(bn.cpt("B").extract({"A":0})),caption="P(B|A=0)")
gnb.flow.add(gnb.getProba(bn.cpt("B").extract({"A":1})),caption="P(B|A=1)")
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

Quasi-continuous inference (with no evidence)

In [6]:
```
gnb.showPosterior(bn,target="B",evs={})
```

nbsphinx-code-borderwhite

Quasi-continuous variable with quasi-continuous parent

In [7]:
```
bn.add(gum.NumericalDiscreteVariable("C","Another quasi continuous variable",minC,
↪maxC,NB))
bn.addArc("B","C")
gnb.showBN(bn) # B and C are quasi-continouous
```

nbsphinx-code-borderwhite

Even if this BN is quite small (and linear), the size of nodes B et C are rather big and creates a complex model (NBxNB parameters in $P(C|B)$).

In [8]:
```
print("nombre de paramètres du bn : {0}".format(bn.dim()))
print("domaine du bn : 10^{0}".format(bn.log10DomainSize()))
```

```
nombre de paramètres du bn : 90299
domaine du bn : 10^5.2552725051033065
```

In [9]:
```
help(gnb.flow.add)
```

```
Help on method add in module pyAgrum.lib.notebook:

add(obj, caption=None, title=None) method of pyAgrum.lib.notebook.FlowLayout instance
    add an element in the row by trying to treat it as plot or html if possible.
```

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```
    (title is an obsolete parameter)
```

In [10]:
```
from scipy.stats import gamma
# cpt("C") is NB x NB matrix !
l=[]
for i in range(NB):
    k=(i*10.0)/NB
    l.append(normalize(gamma(k+1),4,14,NB))

bn.cpt("C")[:]=l

def showB(n:int):
    gnb.flow.add(gnb.getProba(bn.cpt("C").extract({"B":n})),
                 caption=f"P(C|B={bn.variable('B').label(n)})")

gnb.flow.clear()
showB(0)
showB(NB//4)
showB(NB*2//3)
showB(NB-1)
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

Inference in quasi-continuous BN

In [11]:
```
import time

ts = time.time()
ie=gum.LazyPropagation(bn)
ie.makeInference()
q=ie.posterior("C")
te=time.time()
gnb.flow.add(gnb.getPosterior(bn,target="C",evs={}),caption=f"P(C) computed in {te-ts:
↪2.5f} sec for a model with {bn.dim()} paramters")
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

Changing prior

In [12]:
```
bn.cpt("A")[:]=[0.9,0.1]

gnb.flow.add(gnb.getPosterior(bn,target="C",evs={}),caption="P(C) with P(A)=[0.9,0.1]
↪")
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

inference with evidence in quasi-continuous BN

We want to compute

$P(A|C=9)$

$P(B|C=9)$

In [13]:
```
ie=gum.LazyPropagation(bn)
ie.setEvidence({'C':bn.variable("C").toNumericalDiscreteVar().closestLabel(9)})
ie.makeInference()
plot(linspace(minB,maxB,NB),ie.posterior("B")[:])
title("P( B | C={0})".format(bn.variable("C").toNumericalDiscreteVar().
↪closestLabel(9)));
```
nbsphinx-code-borderwhite

In [14]:
```
gnb.showPosterior(bn,target="B",evs={"C":bn.variable("C").toNumericalDiscreteVar().
↪closestLabel(9)})
```
nbsphinx-code-borderwhite

In [15]:
```
gnb.showProba(ie.posterior("A"))
```
nbsphinx-code-borderwhite

Multiple inference : MAP DECISION between Gaussian and generalized hyperbolic distributions

What is the behaviour of $P(A|C=i)$ when i varies ? I.e. we perform a MAP decision between the two models ($A=0$ for the Gaussian distribution and $A=1$ for the generalized hyperbolic distribution).

In [16]:
```
bn.cpt("A")[:]=[0.1, 0.9]
ie=gum.LazyPropagation(bn)
p0=[]
p1=[]
for i in bn.variable("C").labels():
    ie.setEvidence({'C':i})
    ie.makeInference()
    p0.append(ie.posterior("A")[0])
    p1.append(ie.posterior("A")[1])

x=[float(v) for v in bn.variable("C").labels()]
plot(x,p0)
plot(x,p1)
title("P( A | C=i) with prior p(A)=[0.1,0.9]")
legend(["A=0","A=1"],loc='best')
inters=(transpose(p0)<transpose(p1)).argmin()

text(x[inters]-0.2,p0[inters],
     "{0},{1:5.4f}  ".format(x[inters],p0[inters]),
     bbox=dict(facecolor='red', alpha=0.1),ha='right');
```
nbsphinx-code-borderwhite

i.e. if $C < 13.2308$ then $A=1$ else $A=0$

Changing the prior $P(A)$

In [17]:
```
bn.cpt("A").fillWith([0.4, 0.6])
ie=gum.LazyPropagation(bn)
p0=[]
p1=[]
for i in range(300):
    ie.setEvidence({'C':i})
    ie.makeInference()
    p0.append(ie.posterior("A")[0])
    p1.append(ie.posterior("A")[1])
x=[float(v) for v in bn.variable("C").labels()]
plot(x,p0)
plot(x,p1)
title("P( A | C=i) with prior p(A)=[0.1,0.9]")
legend(["A=0","A=1"],loc='best')
inters=(transpose(p0)<transpose(p1)).argmin()

text(x[inters]+0.2,p0[inters],
     "{0},{1:5.4f}  ".format(x[inters],p0[inters]),
     bbox=dict(facecolor='red', alpha=0.1),ha='left');
```

nbsphinx-code-borderwhite

ie. with $p(A) = [0.4, 0.6]$, if $C < 7.8462$ then $A = 1$ else $A = 0$.

In [ ]:
```
```

1.26.7 Parameter learning with Pandas

This notebook uses pandas to learn the parameters. However **the simplest way to learn parameters is to use ``BNLearner`` :-)**. Moreover, you will be able to add priors, etc (see learning BN).

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt

import os
```

Importing pyAgrum

In [2]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
```

Loading two BNs

In [3]:
```
bn=gum.loadBN("res/asia.bif")
bn2=gum.loadBN("res/asia.bif")

gnb.sideBySide(bn,bn2,
               captions=['First bn','Second bn'])
```

```
<IPython.core.display.HTML object>
```

Randomizing the parameters

In [4]:
```
bn.generateCPTs()
bn2.generateCPTs()
```

Direct comparison of parameters

In [5]:
```
from IPython.display import HTML

gnb.sideBySide(bn.cpt(3),
               bn2.cpt(3),
               captions=['<h3>cpt of node 3 in first bn</h3>','<h3>same cpt in second␣
↪bn</h3>'])
```

```
<IPython.core.display.HTML object>
```

Exact KL-divergence

Since the BN is not too big, BruteForceKL can be computed ...

In [6]:
```
g1=gum.ExactBNdistance(bn,bn2)
before_learning=g1.compute()
print(before_learning['klPQ'])
```

```
5.0030971388003485
```

Just to be sure that the distance between a BN and itself is 0 :

In [7]:
```
g0=gum.ExactBNdistance(bn,bn)
print(g0.compute()['klPQ'])
```

```
0.0
```

Generate a database from the original BN

In [8]:
```
gum.generateSample(bn,10000,"out/test.csv",True)
```

```
out/test.csv: 100%||

Log2-Likelihood : -62895.748932625655

```

Out[8]:
```
-62895.748932625655
```

Using pandas for _counting

As an exercise, we will use pandas to learn the parameters.

In [9]:
```
# using bn as a template for the specification of variables in test.csv
learner=gum.BNLearner("out/test.csv",bn)
bn3=learner.learnParameters(bn.dag())

#the same but we add a Laplace adjustment (smoothing) as a Prior
learner=gum.BNLearner("out/test.csv",bn)
learner.useSmoothingPrior(1000) # a count C is replaced by C+1000
bn4=learner.learnParameters(bn.dag())

after_pyAgrum_learning=gum.ExactBNdistance(bn,bn3).compute()
after_pyAgrum_learning_with_smoothing=gum.ExactBNdistance(bn,bn4).compute()
print("without prior:{}".format(after_pyAgrum_learning['klPQ']))
print("with prior smooting(1000):{}".format(after_pyAgrum_learning_with_smoothing[
↪'klPQ']))
```

```
without prior:0.0018130896108582272
with prior smooting(1000):0.23166819139971712
```

Now, let's try to learn the parameters with pandas

In [10]:
```
import pandas
```

In [11]:
```
# We directly generate samples in a DataFrame
df,_=gum.generateSample(bn,10000,None,True)
```

```
100%||

Log2-Likelihood : -62901.86568237794

```

In [12]:
```
df.head()
```

Out[12]:

	bronchitis	smoking	tuberculosis	visit_to_Asia	positive_XraY	lung_cancer	tuberculos_or_cancer	dyspnoea
0	0	1	0	0	1	0	1	0
1	1	1	1	1	1	1		
2	1	1	1	1	0	0		
3	1	1	1	1	1	0		
4	1	1	0	1	0	0		

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```
1                    1        1
2                    0        1
3                    1        0
4                    1        1
```

We use the crosstab function in pandas

In [13]:
```
c=pandas.crosstab(df['dyspnoea'],[df['tuberculos_or_cancer'],df['bronchitis']])
c
```

Out[13]:
```
tuberculos_or_cancer     0           1
bronchitis               0     1     0     1
dyspnoea
0                      563  1484  2348  1889
1                     1000   247   927  1542
```

Playing with numpy reshaping, we retrieve the good form for the CPT from the pandas cross-table

In [14]:
```
gnb.sideBySide('<pre>'+str(np.array((c/c.sum().apply(np.float32)).transpose()).
↪reshape(2,2,2))+'</pre>',
               bn.cpt(bn.idFromName('dyspnoea')),
               captions=["<h3>Learned parameters in crosstab","<h3>Original␣
↪parameters in bn</h3>"])
```

```
<IPython.core.display.HTML object>
```

A global method for estimating Bayesian network parameters from CSV file using PANDAS

In [15]:
```
def computeCPTfromDF(bn,df,name):
    """
    Compute the CPT of variable "name" in the BN bn from the database df
    """
    id=bn.idFromName(name)
    parents=list(reversed(bn.cpt(id).names))
    domains=[bn.variableFromName(name).domainSize()
             for name in parents]
    parents.pop()

    if (len(parents)>0):
        c=pandas.crosstab(df[name],[df[parent] for parent in parents])
        s=c/c.sum().apply(np.float32)
    else:
        s=df[name].value_counts(normalize=True)

    bn.cpt(id)[:]=np.array((s).transpose()).reshape(*domains)

def ParametersLearning(bn,df):
    """
    Compute the CPTs of every varaible in the BN bn from the database df
    """
    for name in bn.names():
        computeCPTfromDF(bn,df,name)
```

In [16]:
```
ParametersLearning(bn2,df)
```

KL has decreased a lot (if everything's OK)

In [17]:
```
g1=gum.ExactBNdistance(bn,bn2)
print("BEFORE LEARNING")
print(before_learning['klPQ'])
print
print("AFTER LEARNING")
print(g1.compute()['klPQ'])
```

```
BEFORE LEARNING
5.0030971388003485
AFTER LEARNING
2.7808990516850507
```

And CPTs should be close

In [18]:
```
gnb.sideBySide(bn.cpt(3),
               bn2.cpt(3),
               captions=["<h3>Original BN","<h3>learned BN</h3>"])
```

```
<IPython.core.display.HTML object>
```

Influence of the size of the database on the quality of learned parameters

What is the effect of increasing the size of the database on the KL ? We expect that the KL decreases to 0.

In [19]:
```
res=[]
for i in range(200,10001,50):
    ParametersLearning(bn2,df[:i])
    g1=gum.ExactBNdistance(bn,bn2)
    res.append(g1.compute()['klPQ'])
fig=figure(figsize=(10,6))
ax  = fig.add_subplot(1, 1, 1)
ax.plot(range(200,10001,50),res)
ax.set_xlabel("size of the database")
ax.set_ylabel("KL")
ax.set_title("klPQ(bn,learnedBN(x))");
```

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In [ ]:
```
```

1.26.8 Bayesian Beta Distributed Coin Inference

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

build a fully bayesian beta distributed coin inference

This notebook is based on examples from Benjamin Datko (https://gist.github.com/bdatko).

The basic idea of this notebook is to show you could assess the probability for a coin, knowing a sequence of heads/tails.

In [1]:
```
import itertools
import time

from pylab import *
import matplotlib.pyplot as plt
import numpy as np
import scipy.stats

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
```

In [2]:
```
gum.config["notebook","default_graph_size"]="12!"
gum.config["notebook","default_graph_inference_size"]="12!"
```

1.26.9 Fill Beta parameters with a re-parameterization

- https://en.wikipedia.org/wiki/Beta_distribution

Alternative parameterizations [edit]

Two parameters [edit]

Mean and sample size [edit]

The beta distribution may also be reparameterized in terms of its mean μ ($0 < \mu < 1$) and the sum of the two shape parameters $\nu = \alpha + \beta > 0$([5] p. 83). Denoting by αPosterior and βPosterior the shape parameters of the posterior beta distribution resulting from applying Bayes theorem to a binomial likelihood function and a prior probability, the interpretation of the addition of both shape parameters to be sample size = $\nu = \alpha$Posterior + βPosterior is only correct for the Haldane prior probability Beta(0,0). Specifically, for the Bayes (uniform) prior Beta(1,1) the correct interpretation would be sample size = α Posterior + β Posterior − 2, or ν = (sample size) + 2. For sample size much larger than 2, the difference between these two priors becomes negligible. (See section Bayesian inference for further details.) ν = α + β is referred to as the "sample size" of a Beta distribution, but one should remember that it is, strictly speaking, the "sample size" of a binomial likelihood function only when using a Haldane Beta(0,0) prior in Bayes theorem.

This parametrization may be useful in Bayesian parameter estimation. For example, one may administer a test to a number of individuals. If it is assumed that each person's score ($0 \le \theta \le 1$) is drawn from a population-level Beta distribution, then an important statistic is the mean of this population-level distribution. The mean and sample size parameters are related to the shape parameters α and β via[9]

$\alpha = \mu\nu, \beta = (1 - \mu)\nu$

Under this parametrization, one may place an uninformative prior probability over the mean, and a vague prior probability (such as an exponential or gamma distribution) over the positive reals for the sample size, if they are independent, and prior data and/or beliefs justify it.

We propose a model where : mu and nu are the parameters of a beta which gives the distribution for the coins.

- below are some useful definitions

$$\alpha = \mu\nu$$

$$\beta = (1-\mu)\nu$$

$$\mu = \frac{\alpha}{\alpha+\beta}$$

- like in Wikipedia article, we will have a uniform prior on and an expoential prior on

In [3]:
```
# the sequence of COINS
serie=[1,0,0,0,1,0,1,1,0,1,0,0,1,0,0,1]
```

In [4]:
```
def fillvect_(rv,vmin,vmax,size, **pdf_kwargs):
    x = linspace(vmin,vmax,size)
    pdf=rv.pdf(x, **pdf_kwargs)
    return x,pdf

def normalize_(rv,vmin,vmax,size, **pdf_kwargs):
    x = linspace(vmin,vmax,size)
    pdf=rv.pdf(x, **pdf_kwargs)
    return x,(pdf/sum(pdf))
```

In [5]:
```
NB_ = 300
vmin, vmax = 0.001, 0.999
pmin_mu, pmax_mu = 0.001, 0.999
pmin_nu, pmax_nu = 1,50
size_ = 16
```

In [6]:
```
bn=gum.BayesNet("SEQUENCE OF COINS MODEL")
mu = bn.add(gum.NumericalDiscreteVariable("mu","mean of the Beta distribution",0,1,NB_
↪))
nu = bn.add(gum.NumericalDiscreteVariable("nu","'sample size' of the Beta where nu =␣
↪a + b > 0",0,50,NB_))
bias=bn.add(gum.NumericalDiscreteVariable("bias","The bias of the coin",0,1,NB_))
hs=[bn.add(gum.LabelizedVariable(f"H{i}","The hallucinations of coin flips",2)) for i␣
↪in range(size_)]

bn.addArc(mu,bias)
bn.addArc(nu,bias)
for h in hs:
    bn.addArc(bias,h)
print(bn)
bn
```

```
BN{nodes: 19, arcs: 18, domainSize: 10^12.2478, dim: 27010200}
```

Out[6]:
```
(pyAgrum.BayesNet<double>@0000017F2FEDD2A0) BN{nodes: 19, arcs: 18, domainSize: 10^12.
↪2478, dim: 27010200}
```

In [7]:
```
loc_, scale_ = 2, 5
x_nu, y_nu = normalize_(scipy.stats.expon,pmin_nu,pmax_nu,NB_,loc=loc_, scale=scale_)
x_mu, y_mu = normalize_(scipy.stats.uniform,pmin_mu,pmax_mu,NB_,)

bn.cpt(mu)[:] = y_mu # uniform prior for hyperparameter
bn.cpt(nu)[:] = y_nu # expoential prior for hyperparameter

gnb.flow.clear()
gnb.flow.add(gnb.getProba(bn.cpt(nu)),caption="Distribution for nu")
gnb.flow.add(gnb.getProba(bn.cpt(mu)),caption="Distribution for mu")
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

In [8]:
```
# https://scicomp.stackexchange.com/a/10800
al_ = (x_mu[:,newaxis] * x_nu[newaxis,:])
be_ = (1 - x_mu)[:,newaxis] * x_nu[newaxis,:]

t_start = time.time()
pdf = scipy.stats.beta(al_,be_).pdf(linspace(vmin, vmax,NB_)[:,newaxis, newaxis])
bn.cpt("bias").fillWith(np.swapaxes(pdf, 0, -1).flatten())
bn.cpt("bias").normalizeAsCPT()
end_time = time.time() - t_start
print(f"Filling {NB_}^3 parameters in {end_time:5.3f}s")
```

```
Filling 300^3 parameters in 7.695s
```

In [9]:
```
x_bias = linspace(vmin, vmax, NB_)
x_hs = np.array([1 - x_bias, x_bias]).T
for h in hs:
    bn.cpt(h).fillWith(x_hs.flatten()).normalizeAsCPT()
```

Evidence without evidence

In [10]:
```
gnb.showInference(bn)
```
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Evidence with the sequence

In [11]:
```
coin_evidence={f"H{i}":serie[i] for i in range(len(serie))}

gnb.showInference(bn,evs=coin_evidence)
```
nbsphinx-code-borderwhite

In [12]:
```
ie=gum.LazyPropagation(bn)
ie.setEvidence(coin_evidence)
ie.makeInference()
```

In [13]:
```
from scipy.ndimage import center_of_mass

idx, _ = ie.posterior('bias').argmax()
map_bias = x_bias[idx[0]["bias"]]
idx, _ = ie.posterior('mu').argmax()
map_mu = x_mu[idx[0]["mu"]]
com = center_of_mass(ie.posterior('nu').toarray())[0]

print(f"MAP for mu : {map_mu}")
print(f"center of mass for nu : {com}")
print(f"MAP for bias : {map_bias}")
```
```
MAP for mu : 0.4449264214046823
center of mass for nu : 39.753046030402764
MAP for bias : 0.4382508361204014
```

In [ ]:
```
```

1.27 pyAgrum's specific features

1.27.1 Potentials : named tensors

In *pyAgrum*, Potentials represent multi-dimensionnal arrays with (discrete) random variables attached to each dimension. This mathematical object have tensorial operators w.r.t. to the variables attached.

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
```

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```
a,b,c=[gum.LabelizedVariable(s,s,2) for s in "abc"]
```

potential algebra

In [2]:
```
p1=gum.Potential().add(a).add(b).fillWith([1,2,3,4]).normalize()
p2=gum.Potential().add(b).add(c).fillWith([4,5,2,3]).normalize()
```

In [3]:
```
gnb.flow.row(p1,p2,p1+p2,
             captions=['p1','p2','p1+p2'])
```

```
<IPython.core.display.HTML object>
```

In [4]:
```
p3=p1+p2
gnb.showPotential(p3/p3.margSumOut(["b"]))
```

```
<IPython.core.display.HTML object>
```

In [5]:
```
p4=gum.Potential()+p3
gnb.flow.row(p3,p4,
             captions=['p3','p4'])
```

```
<IPython.core.display.HTML object>
```

Bayes' theorem

In [6]:
```
bn=gum.fastBN("a->c;b->c",3)
bn
```

Out[6]:
```
(pyAgrum.BayesNet<double>@0000029D371A81A0) BN{nodes: 3, arcs: 2, domainSize: 27, dim:
↪ 33}
```

In such a small bayes net, we can directly manipulate $P(a,b,c)$. For instance :

$$P(b|c) = \frac{\sum_a P(a,b,c)}{\sum_{a,b} P(a,b,c)}$$

In [7]:
```
pABC=bn.cpt("a")*bn.cpt("b")*bn.cpt("c")
pBgivenC=(pABC.margSumOut(["a"])/pABC.margSumOut(["a","b"]))

pBgivenC.putFirst("b") # in order to have b horizontally in the table
```

Out[7]:
```
(pyAgrum.Potential<double>@0000029D371494D0)
      ||  b                         |
c     ||0        |1        |2        |
------||---------|---------|---------|
0     || 0.3267  | 0.1174  | 0.5559  |
1     || 0.4532  | 0.1154  | 0.4314  |
2     || 0.4143  | 0.2231  | 0.3626  |
```

Joint, marginal probability, likelihood

Let's compute the joint probability $P(A,B)$ from $P(A,B,C)$

In [8]:
```
pAC=pABC.margSumOut(["b"])
print("pAC really is a probability : it sums to {}".format(pAC.sum()))
pAC
```

```
pAC really is a probability : it sums to 1.0000000000000002
```

Out[8]:
```
(pyAgrum.Potential<double>@0000029D371497B0)
      ||  a                          |
c     ||0         |1         |2         |
------||----------|----------|----------|
0     || 0.0156   | 0.0621   | 0.2078   |
1     || 0.0206   | 0.1758   | 0.1153   |
2     || 0.0337   | 0.1927   | 0.1765   |
```

Computing $p(A)$

In [9]:
```
pAC.margSumOut(["c"])
```

Out[9]:
```
(pyAgrum.Potential<double>@0000029D37149610)
  a                          |
0         |1         |2         |
----------|----------|----------|
 0.0699   | 0.4306   | 0.4996   |
```

Computing $p(A|C=1)$

It is easy to compute $p(A,C=1)$

In [10]:
```
pAC.extract({"c":1})
```

Out[10]:
```
(pyAgrum.Potential<double>@0000029D37149830)
  a                          |
0         |1         |2         |
----------|----------|----------|
 0.0206   | 0.1758   | 0.1153   |
```

Moreover, we know that $P(C=1)=\sum_A P(A,C=1)$

In [11]:
```
pAC.extract({"c":1}).sum()
```

Out[11]:
```
0.3116561031542595
```

Now we can compute $p(A|C=1)=\frac{P(A,C=1)}{p(C=1)}$

In [12]:
```
pAC.extract({"c":1}).normalize()
```

Out[12]:
```
(pyAgrum.Potential<double>@0000029D37149570)
  a                          |
0         |1         |2         |
----------|----------|----------|
 0.0660   | 0.5640   | 0.3700   |
```

Computing $P(A|C)$

$P(A|C)$ is represented by a matrix that verifies $p(A|C) = \frac{P(A,C)}{P(C}$

In [13]:
```
pAgivenC=(pAC/pAC.margSumIn("c")).putFirst("a")
# putFirst("a") : to correctly show a cpt, the first variable have to bethe␣
↪conditionned one
gnb.flow.row(pAgivenC,pAgivenC.extract({'c':1}),
             captions=["$P(A|C)$","$P(A|C=1)$"])
```

```
<IPython.core.display.HTML object>
```

Likelihood $P(A = 2|C)$

A likelihood can also be found in this matrix.

In [14]:
```
pAgivenC.extract({'a':2})
```

Out[14]:
```
(pyAgrum.Potential<double>@0000029D37149630)
  c                         |
0        |1        |2        |
---------|---------|---------|
 0.7278  | 0.3700  | 0.4381  |
```

A likelihood does not have to sum to 1. It is not relevant to normalize it.

In [15]:
```
pAgivenC.margSumIn(["a"])
```

Out[15]:
```
(pyAgrum.Potential<double>@0000029D371497F0)
  a                         |
0        |1        |2        |
---------|---------|---------|
 0.2043  | 1.2598  | 1.5359  |
```

entropy of potential

In [16]:
```
%matplotlib inline
from pylab import *
import matplotlib.pyplot as plt
import numpy as np
```

In [17]:
```
p1=gum.Potential().add(a)
x = np.linspace(0, 1, 100)
plt.plot(x,[p1.fillWith([p,1-p]).entropy() for p in x])
plt.show()
```

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In [18]:
```
t=gum.LabelizedVariable('t','t',3)
p1=gum.Potential().add(t)

def entrop(bc):
    """
    bc is a list [a,b,c] close to a distribution
    (normalized just to be sure)
    """
    return p1.fillWith(bc).normalize().entropy()
```

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```
import matplotlib.tri as tri

corners = np.array([[0, 0], [1, 0], [0.5, 0.75**0.5]])
triangle = tri.Triangulation(corners[:, 0], corners[:, 1])

# Mid-points of triangle sides opposite of each corner
midpoints = [(corners[(i + 1) % 3] + corners[(i + 2) % 3]) / 2.0 \
             for i in range(3)]
def xy2bc(xy, tol=1.e-3):
    """
    From 2D Cartesian coordinates to barycentric.
    """
    s = [(corners[i] - midpoints[i]).dot(xy - midpoints[i]) / 0.75 \
         for i in range(3)]
    return np.clip(s, tol, 1.0 - tol)

def draw_entropy(nlevels=200, subdiv=6, **kwargs):
    import math

    refiner = tri.UniformTriRefiner(triangle)
    trimesh = refiner.refine_triangulation(subdiv=subdiv)
    pvals = [entrop(xy2bc(xy)) for xy in zip(trimesh.x, trimesh.y)]

    plt.tricontourf(trimesh, pvals, nlevels, **kwargs)
    plt.axis('equal')
    plt.xlim(0, 1)
    plt.ylim(0, 0.75**0.5)
    plt.axis('off')

draw_entropy()
plt.show()
```

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In [ ]:

1.27.2 Aggregators

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Aggregators are special type of nodes that includes a generic CPT for any numbers of parents.

pyAgrum proposes a list of such aggregators. Some of then are used below.

In [1]:
```
import numpy as np

import pyAgrum as gum
```

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```
import pyAgrum.lib.notebook as gnb
```

In [2]:
```
min_x=0
max_x=15

bn=gum.BayesNet()
l=[bn.add(gum.RangeVariable(item,item,min_x,max_x)) for item in ["a","b","c","d","e",
↪"f"]]

gum.config['notebook','histogram_line_threshold']=15
```

In [3]:
```
nmax=bn.addMAX(gum.RangeVariable("MAX","MAX",min_x,max_x))
bn.addArc(l[0],nmax)
bn.addArc(l[1],nmax)
bn.addArc(l[2],nmax)

nmin=bn.addMIN(gum.RangeVariable("MIN","MIN",min_x,max_x))
bn.addArc(l[3],nmin)
bn.addArc(l[4],nmin)
bn.addArc(l[5],nmin)

nampl=bn.addAMPLITUDE(gum.RangeVariable("DELTA","DELTA",0,max_x-min_x))
bn.addArc(nmax,nampl)
bn.addArc(nmin,nampl)

nmedian=bn.addMEDIAN(gum.RangeVariable("MEDIAN","MEDIAN",min_x,max_x))
for n in [l[0],l[1],l[2],l[3]]:
    bn.addArc(n,nmedian)
#potential for median has a size : 16^5=2^20 double !

nexists=bn.addEXISTS(gum.LabelizedVariable("EXISTS_0","EXISTS"),0)
bn.addArc(l[0],nexists)
bn.addArc(l[1],nexists)
bn.addArc(l[2],nexists)

nforall=bn.addFORALL(gum.LabelizedVariable("FORALL_1","FORALL"),1)
bn.addArc(l[3],nforall)
bn.addArc(l[4],nforall)
bn.addArc(l[5],nforall)

ncount=bn.addCOUNT(gum.RangeVariable("COUNT_1","COUNT_1,",0,3),1)
bn.addArc(l[0],ncount)
bn.addArc(l[1],ncount)
bn.addArc(l[2],ncount)
```

In [4]:
```
for nod in l:
    bn.cpt(nod).fillWith(1).normalize()
gnb.showInference(bn,size="13")
```

nbsphinx-code-borderwhite

In [5]:
```
gnb.showInference(bn,size="13",evs={'MEDIAN':[0,0,0,0,0,0,0,0,1,1,1,1,1,1,0,0]})
```

nbsphinx-code-borderwhite

In [6]:
```
# if the roots do not have uniform but random distribution
```

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```
for nod in l:
    bn.generateCPT(nod)

gnb.showInference(bn,size="13")
```

nbsphinx-code-borderwhite

In [7]:
```
gnb.showInference(bn,size="13",evs={'MEDIAN':[0,0,0,0,0,0,0,0,1,1,1,1,1,1,0,0]})
```

nbsphinx-code-borderwhite

In [ ]:
```
```

1.27.3 Explaining a model

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import time

from pyAgrum.lib.bn2graph import BN2dot
import numpy as np
import pandas as pd

import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
import pyAgrum.lib.explain as expl

import matplotlib.pyplot as plt
```

Building the model

We build a simple graph for the example

In [2]:
```
template=gum.fastBN("X1->X2->Y;X3->Z->Y;X0->Z;X1->Z;X2->R[5];Z->R;X1->Y")
data_path = "res/shap/Data_6var_direct_indirect.csv"

#gum.generateSample(template,1000,data_path)

learner = gum.BNLearner(data_path,template)
bn = learner.learnParameters(template.dag())
bn
```

Out[2]:
```
(pyAgrum.BayesNet<double>@00000236AF7DC340) BN{nodes: 7, arcs: 9, domainSize: 320,␣
↪dim: 62}
```

1-independence list (w.r.t. the class Y)

Given a model, it may be interesting to investigate the conditional independences of the class Y created by this very model.

In [3]:
```
# this function explores all the CI between 2 variables and computes the p-values w.r.
↪t to a csv file.
expl.independenceListForPairs(bn,data_path)
```

Out[3]:
```
{('R', 'X0', ('X1', 'Z')): 0.7083382647903902,
 ('R', 'X1', ('X2', 'Z')): 0.46938486254099493,
 ('R', 'X3', ('X1', 'Z')): 0.4128522974536623,
 ('R', 'Y', ('X2', 'Z')): 0.8684231094674686,
 ('X0', 'X1', ()): 0.723302358657366,
 ('X0', 'X2', ()): 0.9801394906304377,
 ('X0', 'X3', ()): 0.7676868597218647,
 ('X0', 'Y', ('X1', 'Z')): 0.5816487109659612,
 ('X1', 'X3', ()): 0.5216508257424717,
 ('X2', 'X3', ()): 0.9837021981131505,
 ('X2', 'Z', ('X1',)): 0.6638491605436834,
 ('X3', 'Y', ('X1', 'Z')): 0.8774081450472304}
```

nbsphinx-code-borderwhite

... with respect to a specific target.

In [4]:
```
expl.independenceListForPairs(bn,data_path,target="Y")
```

Out[4]:
```
{('Y', 'R', ('X2', 'Z')): 0.8684231094674686,
 ('Y', 'X0', ('X1', 'Z')): 0.5816487109659612,
 ('Y', 'X3', ('X1', 'Z')): 0.8774081450472304}
```

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2-ShapValues

In [5]:
```
print(expl.ShapValues.__doc__)
```

```
  The ShapValue class implements the calculation of Shap values in Bayesian networks.

  The main implementation is based on Conditional Shap values [3]_, but the␣
↪Interventional calculation method proposed in [2]_ is also present. In addition, a␣
↪new causal method, based on [1]_, is implemented which is well suited for Bayesian␣
↪networks.

.. [1] Heskes, T., Sijben, E., Bucur, I., & Claassen, T. (2020). Causal Shapley␣
↪Values: Exploiting Causal Knowledge. 34th Conference on Neural Information␣
↪Processing Systems. Vancouver, Canada.

.. [2] Janzing, D., Minorics, L., & Blöbaum, P. (2019). Feature relevance␣
↪quantification in explainable AI: A causality problem. arXiv: Machine Learning.␣
↪Retrieved 6 24, 2021, from https://arxiv.org/abs/1910.13413

.. [3] Lundberg, S. M., & Su-In, L. (2017). A Unified Approach to Interpreting Model.␣
↪31st Conference on Neural Information Processing Systems. Long Beach, CA, USA.
```

The ShapValue class implements the calculation of Shap values in Bayesian networks. It is necessary to specify a target and to provide a Bayesian network whose parameters are known and will be used later in the different calculation methods.

In [6]:
```
gumshap = expl.ShapValues(bn, 'Y')
```

Compute Conditionnal in Bayesian Network

A dataset (as a `pandas.dataframe`) must be provided so that the Bayesian network can learn its parameters and then predict.

The method `conditional` computes the conditonal shap values using the Bayesian Networks. It returns 2 graphs and a dictionary. The first one shows the distribution of the shap values for each of the variables, the second one classifies the variables by their importance.

In [7]:
```
train = pd.read_csv(data_path).sample(frac=1.)
```

In [8]:
```
t_start = time.time()
resultat = gumshap.conditional(train, plot=True,plot_importance=True,percentage=False)
print(f'Run Time : {time.time()-t_start} sec')
```

```
Run Time : 6.830995082855225 sec
```

nbsphinx-code-borderwhite

In [9]:
```
t_start = time.time()
resultat = gumshap.conditional(train, plot=False,plot_importance=True,
↪percentage=False)
print(f'Run Time : {time.time()-t_start} sec')
```

```
Run Time : 6.594994783401489 sec
```

nbsphinx-code-borderwhite

In [10]:
```
resultat = gumshap.conditional(train, plot=True,plot_importance=False,
↪percentage=False)
```

nbsphinx-code-borderwhite

The result is returned as a dictionary, the keys are the names of the features and the associated value is the absolute value of the average of the calculated shap.

In [11]:
```
t_start = time.time()
resultat = gumshap.conditional(train, plot=False,plot_importance=False,
↪percentage=False)
print(f'Run Time : {time.time()-t_start} sec')
resultat
```

```
Run Time : 6.998995780944824 sec
```

Out[11]:
```
{'Z': 0.5464180054433385,
 'X2': 0.3271606443752007,
 'X1': 0.2533375405370652,
 'X0': 0.061767122000001715,
 'X3': 0.10465402104047901,
 'R': 0.05445633444152401 4}
```

Causal Shap Values

This method is similar to the previous one, except the formula of computation. It computes the causal shap value as described in the paper of Heskes *Causal Shapley Values: Exploiting Causal Knowledge to Explain Individual Predictions of Complex Models* .

In [12]:
```
t_start = time.time()
causal = gumshap.causal(train, plot=True, plot_importance=True, percentage=False)
print(f'Run Time : {time.time()-t_start} sec')
```

```
Run Time : 7.8449952602386475 sec
```

nbsphinx-code-borderwhite

As you can see, since R is not among the 'causes' of Y, its causal importance is null.

Marginal Shap Values

Similarly, one can also compute marginal Shap Value.

In [13]:
```
t_start = time.time()
marginal = gumshap.marginal(train, sample_size=10, plot=True,plot_importance=True,
↪percentage=False)
print(f'Run Time : {time.time()-t_start} sec')
print(marginal)
```

```
Run Time : 42.12499499320984 sec
{'Z': 0.7937690075288257, 'X2': 0.36899838317867956, 'X1': 0.3507606787561853, 'X0':␣
↪0.0, 'X3': 0.0, 'R': 0.0}
```

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As you can see, since R, $X0$ and $X3$ are no in the Markov Blanket of Y, their marginal importances are null.

Visualizing shapvalues directly on a BN

This method returns a coloured graph that makes it easier to understand which variable is important and where it is located in the graph.

In [14]:
```
import pyAgrum.lib.notebook as gnb

g = gumshap.showShapValues(causal)
gnb.showGraph(g)
```

nbsphinx-code-borderwhite

Visualizing information

In [15]:
```
expl.showInformation(bn)
```

```
<IPython.core.display.HTML object>
```

In [ ]:
```

```

1.27.4 Kullback-Leibler for Bayesian networks

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import os

%matplotlib inline

from pylab import *
import matplotlib.pyplot as plt
```

Initialisation

- importing pyAgrum
- importing pyAgrum.lib tools
- loading a BN

In [2]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
```

Create a first BN : bn

In [3]:
```
bn=gum.loadBN("res/asia.bif")
# randomly re-generate parameters for every Conditional Probability Table
bn.generateCPTs()
bn
```

Out[3]:
```
(pyAgrum.BayesNet<double>@000001FE27031DE0) BN{nodes: 8, arcs: 8, domainSize: 256,␣
↪dim: 36}
```

Create a second BN : bn2

In [4]:
```
bn2=gum.loadBN("res/asia.bif")
bn2.generateCPTs()
bn2
```

Out[4]:
```
(pyAgrum.BayesNet<double>@000001FE27035300) BN{nodes: 8, arcs: 8, domainSize: 256,␣
↪dim: 36}
```

bn vs bn2 : different parameters

In [5]:
```
gnb.flow.row(bn.cpt(3),bn2.cpt(3),
             captions=["a CPT in bn","same CPT in bn2 (with different parameters)"])
```

```
<IPython.core.display.HTML object>
```

Exact and (Gibbs) approximated KL-divergence

In order to compute KL-divergence, we just need to be sure that the 2 distributions are defined on the same domain (same variables, etc.)

Exact KL

In [6]:
```
g1=gum.ExactBNdistance(bn,bn2)
print(g1.compute())
```

```
{'klPQ': 5.0030971388003485, 'errorPQ': 0, 'klQP': 3.527314407069579, 'errorQP': 0,
↪'hellinger': 1.037499761443752, 'bhattacharya': 0.7726296131290553, 'jensen-shannon
↪': 0.6385791723188207}
```

If the models are not on the same domain :

In [7]:
```
bn_different_domain=gum.loadBN("res/alarm.dsl")

# g=gum.BruteForceKL(bn,bn_different_domain) # a KL-divergence between asia and alarm␣
↪... :(
#
# would cause
#---------------------------------------------------------------------------
#OperationNotAllowed                       Traceback (most recent call last)
#
#OperationNotAllowed: this operation is not allowed : KL : the 2 BNs are not␣
↪compatible (not the same vars : visit_to_Asia?)
```

Gibbs-approximated KL

In [8]:
```
g=gum.GibbsBNdistance(bn,bn2)
g.setVerbosity(True)
g.setMaxTime(120)
g.setBurnIn(5000)
g.setEpsilon(1e-7)
g.setPeriodSize(500)
```

In [9]:
```
print(g.compute())
print("Computed in {0} s".format(g.currentTime()))
```

```
{'klPQ': 4.999350547660979, 'errorPQ': 0, 'klQP': 3.309147414499417, 'errorQP': 0,
↪'hellinger': 1.0241904644545237, 'bhattacharya': 0.7786179301380848, 'jensen-shannon
↪': 0.6228385613041574}
Computed in 1.9164245 s
```

In [10]:
```
print("--")

print(g.messageApproximationScheme())
print("--")
```

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```
print("Temps de calcul : {0}".format(g.currentTime()))
print("Nombre d'itérations : {0}".format(g.nbrIterations()))
```

```
--
stopped with epsilon=1e-07
--
Temps de calcul : 1.9164245
Nombre d'itérations : 176500
```

In [11]:
```
p=plot(g.history(), 'g')
```

nbsphinx-code-borderwhite

Animation of Gibbs KL

Since it may be difficult to know what happens during approximation algorithm, pyAgrum allows to follow the iteration using animated matplotlib figure

In [12]:
```
g=gum.GibbsBNdistance(bn,bn2)
g.setMaxTime(60)
g.setBurnIn(500)
g.setEpsilon(1e-7)
g.setPeriodSize(5000)
```

In [13]:
```
gnb.animApproximationScheme(g) # logarithmique scale for Y
g.compute()
```

Out[13]:
```
{'klPQ': 5.016855829234866,
 'errorPQ': 0,
 'klQP': 3.3839420489270537,
 'errorQP': 0,
 'hellinger': 1.0291151959143872,
 'bhattacharya': 0.7805282966474169,
 'jensen-shannon': 0.6282516385879086}
```

nbsphinx-code-borderwhite

In [ ]:
```

```

1.27.5 Comparing BNs

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
def dict2html(di1,di2=None):
    res= "<br/>".join([f"<b>{k:15}</b>:{v}" for k,v in di1.items()])
    if di2 is not None:
        res+="<br/><br/>"
```

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```
        res+= "<br/>".join([f"<b>{k:15}</b>:{v}" for k,v in di2.items()])
    return res
```

In [2]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
import pyAgrum.lib.bn_vs_bn as gcm
```

How to compare two BNs

PyAgrum allows you to compare BNs in several ways. This notebook show you some of them: - a graphical diff between the 2 BNs - some scores form recal and precision - distance measures (for more, see notebook `26-klForBNs` for more)

Between two different structures

In [3]:
```
bn1=gum.fastBN("A->B->C->D->E<-A->F")
bn2=gum.fastBN("A->B<-C->D->E<-A;F->E")
cmp=gcm.GraphicalBNComparator(bn1,bn2)
kl=gum.ExactBNdistance(bn1,bn2) # bruteForce is possible car the BNs are small
gnb.sideBySide(bn1,bn2,gnb.getBNDiff(bn1,bn2),dict2html(cmp.scores(),cmp.hamming()),
↪cmp.equivalentBNs(),dict2html(kl.compute()),
               captions=['bn1','bn2','graphical diff','Scores','equivalent ?',
↪'distances'],valign="bottom")
```

```
<IPython.core.display.HTML object>
```

The logic for the arcs of the graphical diff is the following. When comparaing bn1 with bn2 (in that order) : - full black line: the arc is common for both - full red line: the arc is common but inverted in bn2 - dotted black line: the arc is added in bn2 - dotted red line: the arc is removed in bn2

For the scores : - precision and recall are computed considering BN1 as the reference - $Fscore = \frac{2 \cdot recall \cdot precision}{recall + precision}$ is the weighted average of Precision and Recall. - $dist2opt = \sqrt{(1-precision)^2 + (1-recall)^2}$ represents the euclidian distance to the ideal(precision=1,recall=1)

`EquivalentBN` return "OK" if equivalent or a reason for non equivalence

Finally, `BruteForceKL` compute in the same time several distances : I-projection, M-projection, Hellinger and Bhattacharya. For more complex BNs, there exists a `GibbsKL` to approximate those distances. Of course, the computation are much slower.

Same structure, different parameters

In [4]:
```
bn1=gum.fastBN("A->B->C->D->E<-A->F")
bn2=gum.fastBN("A->B->C->D->E<-A->F")
cmp=gcm.GraphicalBNComparator(bn1,bn2)
kl=gum.ExactBNdistance(bn1,bn2) # bruteForce is possible car the BNs are small
gnb.sideBySide(bn1,bn2,gnb.getBNDiff(bn1,bn2),dict2html(cmp.scores(),cmp.hamming()),
↪cmp.equivalentBNs(),dict2html(kl.compute()),
               captions=['bn1','bn2','graphical diff','Scores','equivalent ?',
↪'distances'],valign="bottom")
```

```
<IPython.core.display.HTML object>
```

identical BNs

In [5]:
```
bn1=gum.fastBN("A->B->C->D->E<-A->F")
bn2=bn1
cmp=gcm.GraphicalBNComparator(bn1,bn2)
kl=gum.ExactBNdistance(bn1,bn2) # bruteForce is possible car the BNs are small
gnb.sideBySide(bn1,bn2,gnb.getBNDiff(bn1,bn2),dict2html(cmp.scores(),cmp.hamming()),
↪cmp.equivalentBNs(),dict2html(kl.compute()),
               captions=['bn1','bn2','graphical diff','Scores','equivalent ?',
↪'distances'],valign="bottom")
```

```
<IPython.core.display.HTML object>
```

In the notebook `Learning_DirichletPriorAndWeightedDatabase`, you can find an interresting discussion on how can change those scores and distance.

In [ ]:

In [ ]:

1.27.6 Coloring and exporting graphical models as image (pdf, png)

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
from pylab import *
import matplotlib.pyplot as plt
```

In [2]:
```
import pyAgrum as gum
import pyAgrum.lib.notebook as gnb
```

In [3]:
```
bn=gum.fastBN("a->b->c->d;b->e->d->f;g->c")
gnb.flow.row(bn,gnb.getInference(bn))
```

```
<IPython.core.display.HTML object>
```

customizing colours and width for model and inference

In [9]:
```
def nodevalue(n):
    return 0.5 if n in "aeiou" else 0.7
def arcvalue(a):
    return (10-a[0])*a[1]
def arcvalue2(a):
    return (a[0]+a[1]+5)/22
gnb.showBN(bn,
```

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```
            nodeColor={n:nodevalue(n) for n in bn.names()},
            arcWidth={a:arcvalue(a) for a in bn.arcs()},
            arcLabel={a:f"v={arcvalue(a):02d}" for a in bn.arcs()},
            arcColor={a:arcvalue2(a) for a in bn.arcs()})
```

nbsphinx-code-borderwhite

In [10]:
```
gnb.showInference(bn,
            targets={"a","g","f","b"},
            evs={'e':0},
            nodeColor={n:nodevalue(n) for n in bn.names()},
            arcWidth={a:arcvalue(a) for a in bn.arcs()})
```

nbsphinx-code-borderwhite

In [11]:
```
gnb.flow.row(gnb.getBN(bn,
                       nodeColor={n:nodevalue(n) for n in bn.names()},
                       arcWidth={a:arcvalue(a) for a in bn.arcs()}),
             gnb.getInference(bn,
                              nodeColor={n:nodevalue(n) for n in bn.names()},
                              arcWidth={a:arcvalue(a) for a in bn.arcs()})
            )
```

```
<IPython.core.display.HTML object>
```

In [12]:
```
import matplotlib.pyplot as plt
mycmap=plt.get_cmap('Reds')
formyarcs=plt.get_cmap('winter')
gnb.flow.row(gnb.getBN(bn,
                       nodeColor={n:nodevalue(n) for n in bn.names()},
                       arcColor={a:arcvalue2(a) for a in bn.arcs()},
                       cmap=mycmap,
                       cmapArc=formyarcs),
             gnb.getInference(bn,
                              nodeColor={n:nodevalue(n) for n in bn.names()},
                              arcColor={a:arcvalue2(a) for a in bn.arcs()},
                              arcWidth={a:arcvalue(a) for a in bn.arcs()},
                              cmap=mycmap,
                              cmapArc=formyarcs)
              )
```

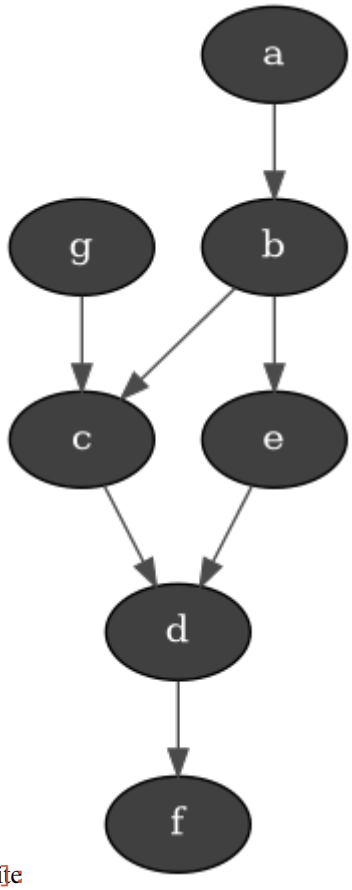
```
<IPython.core.display.HTML object>
```

Exporting model and inference as image

Exporting as image (pdf, png, etc.) has been gathered in 2 functions : `pyAgrum.lib.image.export()` and `pyAgrum.lib.image.exportInference()`. The argument are the same as for `pyAgrum.notebook.show{Model}` and `pyAgrum.notebook.show{Inference}`.

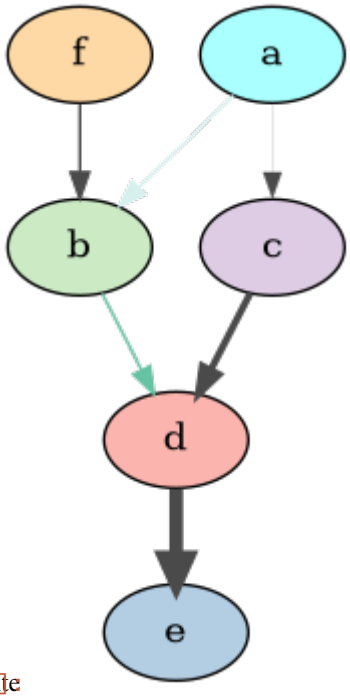
In [13]:
```
import pyAgrum.lib.image as gumimage
from IPython.display import Image # to display the exported images
```

In [14]:
```
gumimage.export(bn,"out/test_export.png")

Image(filename='out/test_export.png')
```



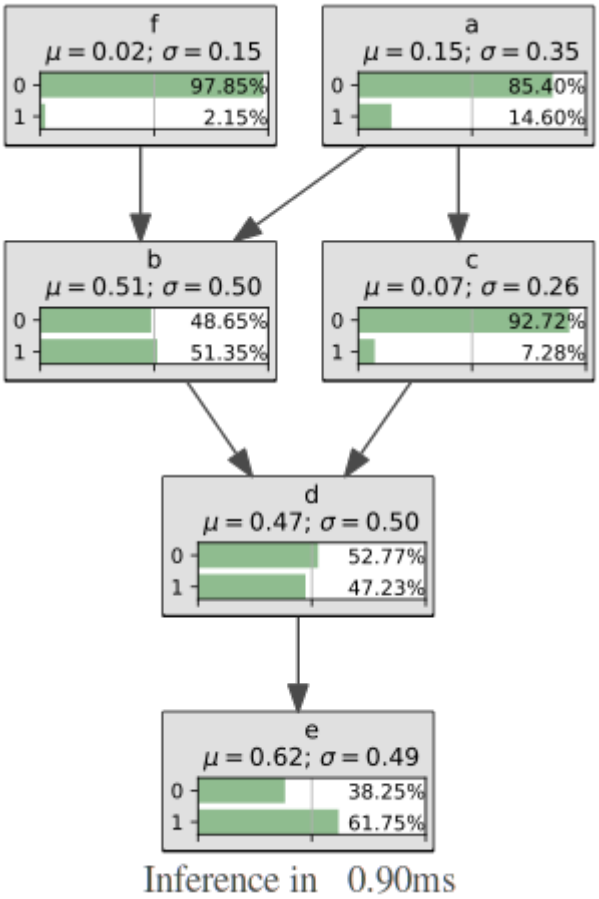
nbsphinx-code-border-white Out[14]:

In [15]:
```
bn = gum.fastBN("a->b->d;a->c->d[3]->e;f->b")
gumimage.export(bn,"out/test_export.png",
                nodeColor={'a': 1,
                           'b': 0.3,
                           'c': 0.4,
                           'd': 0.1,
                           'e': 0.2,
                           'f': 0.5},
                arcColor={(0, 1): 0.2,
                          (1, 2): 0.5},
                arcWidth={(0, 3): 0.4,
                          (3, 2): 0.5,
                          (2,4) :0.6})

Image(filename='out/test_export.png')
```



nbsphinx-code-border-white Out[15]:

In [16]:
```
gumimage.exportInference(bn,"out/test_export.png")

Image(filename='out/test_export.png')
```



nbsphinx-code-border-white Out[16]:

In [17]:
```
gumimage.export(bn,"out/test_export.pdf")
```

Link to out/test_export.pdf

exporting inference with evidence

In [18]:
```
bn=gum.loadBN("res/alarm.dsl")
gumimage.exportInference(bn,"out/test_export.pdf",
                         evs={"CO":1,"VENTLUNG":1},
                         targets={"VENTALV",
                                  "CATECHOL",
                                  "HR",
                                  "MINVOLSET",
                                  "ANAPHYLAXIS",
                                  "STROKEVOLUME",
                                  "ERRLOWOUTPUT",
                                  "HBR",
                                  "PULMEMBOLUS",
                                  "HISTORY",
                                  "BP",
                                  "PRESS",
                                  "CO"},
                         size="15!")
```

Link to out/test_export.pdf

Other models

Other models can also use these functions.

In [19]:
```
infdiag=gum.loadID("res/OilWildcatter.bifxml")
gumimage.export(infdiag,"out/test_export.pdf")
```

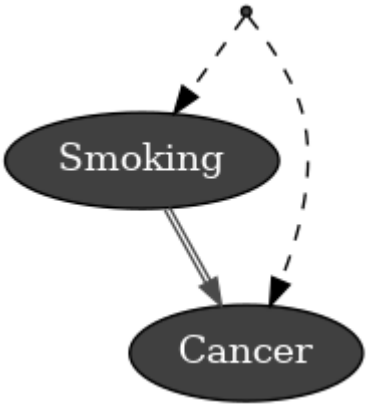
Link to out/test_export.pdf

In [20]:
```
gumimage.exportInference(infdiag,"out/test_export.pdf")
```

Link to out/test_export.pdf

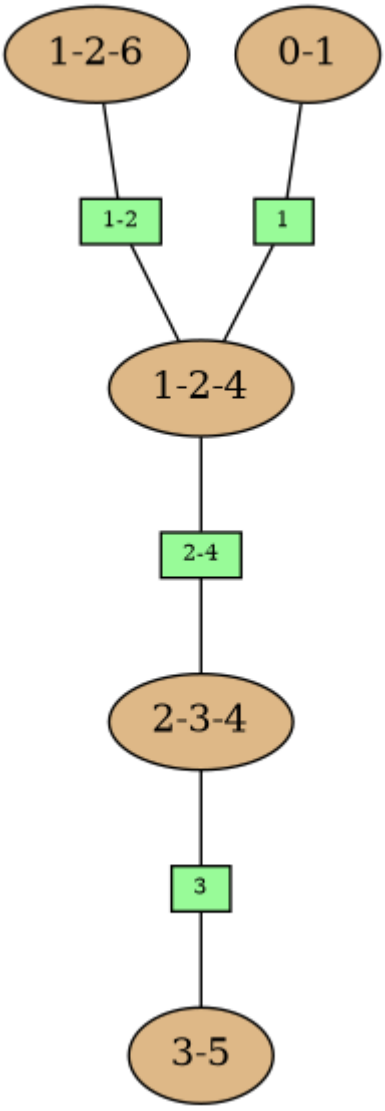
Exporting any object with `toDot()` method

In [21]:
```
import pyAgrum.causal as csl
obs1 = gum.fastBN("Smoking->Cancer")
modele3 = csl.CausalModel(obs1, [("Genotype", ["Smoking","Cancer"])], True)
gumimage.export(modele3,"out/test_export.png") # a causal model has a toDot method.
Image(filename='out/test_export.png')
```



nbsphinx-code-border-w[21]

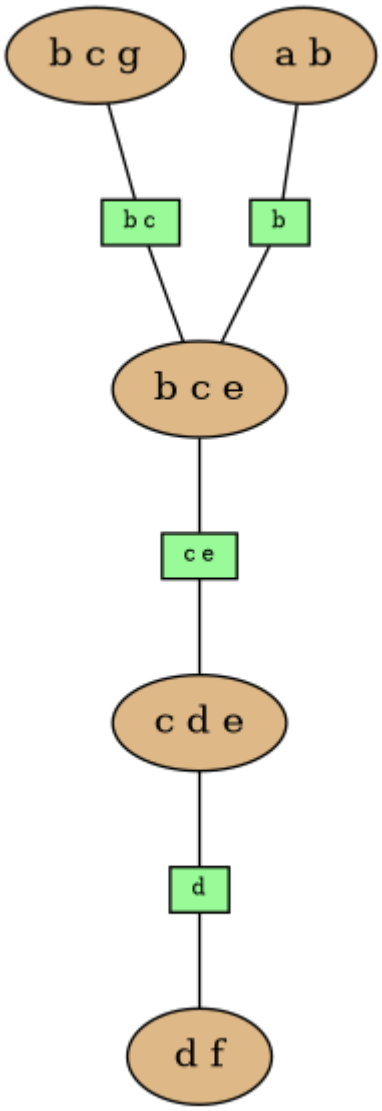
In [22]:
```
bn=gum.fastBN("a->b->c->d;b->e->d->f;g->c")
ie=gum.LazyPropagation(bn)
jt=ie.junctionTree()
gumimage.export(jt,"out/test_export.png") # a JunctionTree has a method jt.toDot()
Image(filename='out/test_export.png')
```



nbsphinx-code-border-w[22]

... or even a string in dot syntax

In [23]:
```
gumimage.export(jt.toDotWithNames(bn),"out/test_export.png") # jt.toDotWithNames(bn)␣
↪creates a dot-string for a junction tree with names of variables
Image(filename='out/test_export.png')
```



nbsphinx-code-border-width

Exporting to pyplot

In [24]:
```
import matplotlib.pyplot as plt

bn=gum.fastBN("A->B->C<-D")

plt.imshow(gumimage.export(bn))
plt.show()

plt.imshow(gumimage.exportInference(bn,size="15!"))
plt.show()

plt.figure(figsize = (10,10))
plt.imshow(gumimage.exportInference(bn,size="15!"))
```

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```
plt.show()
```

nbsphinx-code-borderwhite
nbsphinx-code-borderwhite
nbsphinx-code-borderwhite

In [ ]:

1.27.7 `gum.config` :the configuration object for pyAgrum

 (http://creativecommons.org/licenses/by-nc/4.0/)	 (https://agrum.org)	(https://agrum.gitlab.io/extra/agrum_at_binder.html)

In [1]:
```
import pyAgrum as gum
print("="*35)
print(gum.config)
print("="*35)
```

```
===================================
[core]
  default_maxnumberofthreads = 24
[notebook]
  potential_visible_digits = 4
  potential_with_colors = True
  potential_color_0 = #FF7F64
  potential_color_1 = #7FFF64
  potential_with_fraction = False
  potential_fraction_limit = 50
  potential_fraction_round_error = 1e-6
  potential_fraction_with_latex = True
  histogram_horizontal_visible_digits = 2
  histogram_vertical_visible_digits = 2
  histogram_horizontal_threshold = 8
  histogram_line_threshold = 40
  histogram_color = darkseagreen
  histogram_use_percent = True
  histogram_mode = compact
  potential_parent_values = merge
  figure_facecolor = #E0E0E0
  graph_format = svg
  show_inference_time = True
  default_graph_size = 5
  default_graph_inference_size = 8
  default_arc_color = #4A4A4A
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  evidence_bgcolor = sandybrown
  evidence_fgcolor = black
  default_node_cmap = Pastel1
```

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```
  default_arc_cmap = BuGn
  default_edge_cmap = BuGn
  default_markovnetwork_view = factorgraph
  junctiontree_graph_size = 10
  junctiontree_with_names = True
  junctiontree_separator_bgcolor = palegreen
  junctiontree_separator_fgcolor = black
  junctiontree_separator_fontsize = 8
  junctiontree_clique_bgcolor = burlywood
  junctiontree_clique_fgcolor = black
  junctiontree_clique_fontsize = 10
  junctiontree_map_cliquescale = 0.3
  junctiontree_map_sepscale = 0.1
  junctiontree_map_edgelen = 1
  graphdiff_missing_style = dashed
  graphdiff_missing_color = red
  graphdiff_overflow_style = dashed
  graphdiff_overflow_color = purple
  graphdiff_reversed_style = solid
  graphdiff_reversed_color = purple
  graphdiff_correct_style = solid
  graphdiff_correct_color = grey
[BN]
  allow_modification_when_saving = False
[factorgraph]
  default_node_bgcolor = coral
  default_node_fgcolor = black
  default_factor_bgcolor = burlywood
  edge_length = 0.7
  edge_length_inference = 0.9
[dynamicBN]
  default_graph_size = 6
[influenceDiagram]
  default_graph_size = 6
  default_chance_bgcolor = #808080
  default_chance_fgcolor = white
  default_utility_bgcolor = #50508A
  default_utility_fgcolor = white
  default_decision_bgcolor = #9A5050
  default_decision_fgcolor = white
  chance_shape = ellipse
  utility_shape = hexagon
  decision_shape = box
  decision_arc_style = tapered, bold, dotted
  utility_arc_style = dashed
  default_id_size = 6
  default_id_inference_size = 6
  utility_visible_digits = 2
  utility_show_stdev = True
  utility_show_loss = False
[credalnet]
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  histo_max_color = #BBFFAA
[causal]
  show_latent_names = False
```

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```
  latex_do_prefix = \hookrightarrow\mkern-6.5mu
  latex_do_suffix =
  default_graph_size = 2.5
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  default_latent_bgcolor = #A08080
  default_latent_fgcolor = black
[ROC]
  draw_color = #008800
  fill_color = #AAEEAA
====================================
```

gum.config as singleton

As far as it can be done with Python, `gum.config` is a singleton

In [2]:
```
cfg2=gum.PyAgrumConfiguration()
print(id(cfg2))
print(id(gum.config))
```

```
140365302311008
140365302311008
```

pyagrum.ini

The configuration is a mix between the defaults (which exactly define the possible `section` and `property`) and a file `pyagrum.ini` (if present in the current folder) that contains only the changed properties.

`section` and `key` are case insensitive.

config constantly keeps track of the differences between defaults and actual values :

In [3]:
```
gum.config['dynamicBN','default_graph_size']=10

print("Configuration only for the current session")
print('-'*40)
gum.config.diff()
```

```
Configuration only for the current session
----------------------------------------
[dynamicBN]
  default_graph_size = 10
```

In [4]:
```
# if there is a local modification, __repr__ shows only the diff other wise it show␣
↪all properties
gum.config
```

Out[4]:
```
[dynamicBN]
  default_graph_size = 10
```

In [12]:
```
# __str__ shows all the properties
print(gum.config)
```

```
[core]
  default_maxnumberofthreads = 24
[notebook]
  potential_visible_digits = 4
  potential_with_colors = True
  potential_color_0 = #FF7F64
  potential_color_1 = #7FFF64
  potential_with_fraction = False
  potential_fraction_limit = 50
  potential_fraction_round_error = 1e-6
  potential_fraction_with_latex = True
  histogram_horizontal_visible_digits = 2
  histogram_vertical_visible_digits = 2
  histogram_horizontal_threshold = 8
  histogram_line_threshold = 40
  histogram_color = darkseagreen
  histogram_use_percent = True
  histogram_mode = compact
  potential_parent_values = merge
  figure_facecolor = #E0E0E0
  graph_format = svg
  show_inference_time = True
  default_graph_size = 5
  default_graph_inference_size = 8
  default_arc_color = #4A4A4A
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  evidence_bgcolor = papayawhip
  evidence_fgcolor = black
  default_node_cmap = Pastel1
  default_arc_cmap = BuGn
  default_edge_cmap = BuGn
  default_markovnetwork_view = factorgraph
  junctiontree_graph_size = 10
  junctiontree_with_names = True
  junctiontree_separator_bgcolor = palegreen
  junctiontree_separator_fgcolor = black
  junctiontree_separator_fontsize = 8
  junctiontree_clique_bgcolor = burlywood
  junctiontree_clique_fgcolor = black
  junctiontree_clique_fontsize = 10
  junctiontree_map_cliquescale = 0.3
  junctiontree_map_sepscale = 0.1
  junctiontree_map_edgelen = 1
  graphdiff_missing_style = dashed
  graphdiff_missing_color = red
  graphdiff_overflow_style = dashed
  graphdiff_overflow_color = purple
  graphdiff_reversed_style = solid
  graphdiff_reversed_color = purple
  graphdiff_correct_style = solid
  graphdiff_correct_color = grey
[BN]
  allow_modification_when_saving = False
[factorgraph]
  default_node_bgcolor = coral
  default_node_fgcolor = black
```

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```
  default_factor_bgcolor = burlywood
  edge_length = 0.7
  edge_length_inference = 0.9
[dynamicBN]
  default_graph_size = 10
[influenceDiagram]
  default_graph_size = 6
  default_chance_bgcolor = #808080
  default_chance_fgcolor = white
  default_utility_bgcolor = #50508A
  default_utility_fgcolor = white
  default_decision_bgcolor = #9A5050
  default_decision_fgcolor = white
  chance_shape = ellipse
  utility_shape = hexagon
  decision_shape = box
  decision_arc_style = tapered, bold, dotted
  utility_arc_style = dashed
  default_id_size = 6
  default_id_inference_size = 6
  utility_visible_digits = 2
  utility_show_stdev = True
  utility_show_loss = False
[credalnet]
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  histo_max_color = #BBFFAA
[causal]
  show_latent_names = False
  latex_do_prefix = \hookrightarrow\mkern-6.5mu
  latex_do_suffix =
  default_graph_size = 1.9
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  default_latent_bgcolor = #A08080
  default_latent_fgcolor = black
[ROC]
  draw_color = #008800
  fill_color = #AAEEAA
```

Accessors

Getter

In [6]:
```
print(gum.config["notebook","evidence_bgcolor"])
print(gum.config.get("notebook","evidence_bgcolor"))
```

```
sandybrown
sandybrown
```

Setter

In [7]:
```
gum.config["notebook","evidence_bgcolor"]="papayawhip"
gum.config["causal","default_graph_size"]=1.9
```

In [8]:
```
gum.config # once again, only the diff with defaults
```

Out[8]:
```
[notebook]
  evidence_bgcolor = papayawhip
[dynamicBN]
  default_graph_size = 10
[causal]
  default_graph_size = 1.9
```

constant structure, mutable content

The structure `section.key` is fixed by default and readonly : one can only change the value of an existing property

In [9]:
```
try:
    gum.config["AAA","OOO"]=1
except SyntaxError as e:
    print("Syntax error : {}".format(e.msg))
```

```
Syntax error : You can not add section 'AAA' in pyAgrum configuration
```

In [10]:
```
try:
    gum.config["causal","OOO"]=1
except SyntaxError as e:
    print("Syntax error : {}".format(e.msg))
```

```
Syntax error : You can not add option 'causal,OOO' in pyAgrum configuration
```

properties as string

All the properties are stored as string !

In [11]:
```
gum.config["notebook","default_graph_size"]
```

Out[11]:
```
'5'
```

In [12]:
```
gum.config["notebook","default_graph_size"]=10
gum.config["notebook","default_graph_size"]
```

Out[12]:
```
'10'
```

... but can be typed using asInt, asFloat, asBool

In [14]:
```
gum.config['dynamicBN','default_graph_size']
```

Out[14]:
```
'10'
```

In [15]:
```
gum.config.asInt['dynamicBN','default_graph_size']
```

Out[15]:
```
10
```

In [16]:
```
print(type(gum.config['dynamicBN','default_graph_size']))
print(type(gum.config.asInt['dynamicBN','default_graph_size']))
```

```
<class 'str'>
<class 'int'>
```

In [17]:
```
if gum.config["causal","show_latent_names"]=="False":
    print("not very convenient test")
if not gum.config.asBool["causal","show_latent_names"]:
    print("better test")
```

```
not very convenient test
better test
```

Reset, reload, save

The configuration can be saved in the current folder (`gum.config.save()`).

The configuration can be restored from the default (reset) or the current saved state (reload).

In [13]:
```
gum.config.reset() # back to defaults
gum.config # no diff => shows all the properties
```

Out[13]:
```
# no customized property
[core]
  default_maxnumberofthreads = 24
[notebook]
  potential_visible_digits = 4
  potential_with_colors = True
  potential_color_0 = #FF7F64
  potential_color_1 = #7FFF64
  potential_with_fraction = False
  potential_fraction_limit = 50
  potential_fraction_round_error = 1e-6
  potential_fraction_with_latex = True
  histogram_horizontal_visible_digits = 2
  histogram_vertical_visible_digits = 2
  histogram_horizontal_threshold = 8
  histogram_line_threshold = 40
  histogram_color = darkseagreen
  histogram_use_percent = True
  histogram_mode = compact
  potential_parent_values = merge
  figure_facecolor = #E0E0E0
  graph_format = svg
  show_inference_time = True
  default_graph_size = 5
  default_graph_inference_size = 8
  default_arc_color = #4A4A4A
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  evidence_bgcolor = sandybrown
  evidence_fgcolor = black
  default_node_cmap = Pastel1
  default_arc_cmap = BuGn
  default_edge_cmap = BuGn
  default_markovnetwork_view = factorgraph
```

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```
  junctiontree_graph_size = 10
  junctiontree_with_names = True
  junctiontree_separator_bgcolor = palegreen
  junctiontree_separator_fgcolor = black
  junctiontree_separator_fontsize = 8
  junctiontree_clique_bgcolor = burlywood
  junctiontree_clique_fgcolor = black
  junctiontree_clique_fontsize = 10
  junctiontree_map_cliquescale = 0.3
  junctiontree_map_sepscale = 0.1
  junctiontree_map_edgelen = 1
  graphdiff_missing_style = dashed
  graphdiff_missing_color = red
  graphdiff_overflow_style = dashed
  graphdiff_overflow_color = purple
  graphdiff_reversed_style = solid
  graphdiff_reversed_color = purple
  graphdiff_correct_style = solid
  graphdiff_correct_color = grey
[factorgraph]
  default_node_bgcolor = coral
  default_node_fgcolor = black
  default_factor_bgcolor = burlywood
  edge_length = 0.7
  edge_length_inference = 0.9
[dynamicBN]
  default_graph_size = 6
[influenceDiagram]
  default_graph_size = 6
  default_chance_bgcolor = #808080
  default_chance_fgcolor = white
  default_utility_bgcolor = #50508A
  default_utility_fgcolor = white
  default_decision_bgcolor = #9A5050
  default_decision_fgcolor = white
  chance_shape = ellipse
  utility_shape = hexagon
  decision_shape = box
  decision_arc_style = tapered, bold, dotted
  utility_arc_style = dashed
  default_id_size = 6
  default_id_inference_size = 6
  utility_visible_digits = 2
  utility_show_stdev = True
  utility_show_loss = False
[credalnet]
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  histo_max_color = #BBFFAA
[causal]
  show_latent_names = False
  latex_do_prefix = \hookrightarrow\mkern-6.5mu
  latex_do_suffix =
  default_graph_size = 2.5
  default_node_bgcolor = #404040
  default_node_fgcolor = white
```

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```
  default_latent_bgcolor = #A08080
  default_latent_fgcolor = black
[ROC]
  draw_color = #008800
  fill_color = #AAEEAA
```

In [14]:
```
try:
    gum.config.load() # reload pyagrum.ini
except FileNotFoundError:
    pass # no pyagrum.ini in the folder
gum.config
```

Out[14]:
```
# no customized property
[core]
  default_maxnumberofthreads = 24
[notebook]
  potential_visible_digits = 4
  potential_with_colors = True
  potential_color_0 = #FF7F64
  potential_color_1 = #7FFF64
  potential_with_fraction = False
  potential_fraction_limit = 50
  potential_fraction_round_error = 1e-6
  potential_fraction_with_latex = True
  histogram_horizontal_visible_digits = 2
  histogram_vertical_visible_digits = 2
  histogram_horizontal_threshold = 8
  histogram_line_threshold = 40
  histogram_color = darkseagreen
  histogram_use_percent = True
  histogram_mode = compact
  potential_parent_values = merge
  figure_facecolor = #E0E0E0
  graph_format = svg
  show_inference_time = True
  default_graph_size = 5
  default_graph_inference_size = 8
  default_arc_color = #4A4A4A
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  evidence_bgcolor = sandybrown
  evidence_fgcolor = black
  default_node_cmap = Pastel1
  default_arc_cmap = BuGn
  default_edge_cmap = BuGn
  default_markovnetwork_view = factorgraph
  junctiontree_graph_size = 10
  junctiontree_with_names = True
  junctiontree_separator_bgcolor = palegreen
  junctiontree_separator_fgcolor = black
  junctiontree_separator_fontsize = 8
  junctiontree_clique_bgcolor = burlywood
  junctiontree_clique_fgcolor = black
  junctiontree_clique_fontsize = 10
  junctiontree_map_cliquescale = 0.3
  junctiontree_map_sepscale = 0.1
```

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```
  junctiontree_map_edgelen = 1
  graphdiff_missing_style = dashed
  graphdiff_missing_color = red
  graphdiff_overflow_style = dashed
  graphdiff_overflow_color = purple
  graphdiff_reversed_style = solid
  graphdiff_reversed_color = purple
  graphdiff_correct_style = solid
  graphdiff_correct_color = grey
[factorgraph]
  default_node_bgcolor = coral
  default_node_fgcolor = black
  default_factor_bgcolor = burlywood
  edge_length = 0.7
  edge_length_inference = 0.9
[dynamicBN]
  default_graph_size = 6
[influenceDiagram]
  default_graph_size = 6
  default_chance_bgcolor = #808080
  default_chance_fgcolor = white
  default_utility_bgcolor = #50508A
  default_utility_fgcolor = white
  default_decision_bgcolor = #9A5050
  default_decision_fgcolor = white
  chance_shape = ellipse
  utility_shape = hexagon
  decision_shape = box
  decision_arc_style = tapered, bold, dotted
  utility_arc_style = dashed
  default_id_size = 6
  default_id_inference_size = 6
  utility_visible_digits = 2
  utility_show_stdev = True
  utility_show_loss = False
[credalnet]
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  histo_max_color = #BBFFAA
[causal]
  show_latent_names = False
  latex_do_prefix = \hookrightarrow\mkern-6.5mu
  latex_do_suffix =
  default_graph_size = 2.5
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  default_latent_bgcolor = #A08080
  default_latent_fgcolor = black
[ROC]
  draw_color = #008800
  fill_color = #AAEEAA
```

Using configuration

In [15]:
```
import pyAgrum.lib.notebook as gnb

bn=gum.fastBN("D->C<-A->B[4];A->E")
bn.cpt("B")
```

Out[15]:
```
(pyAgrum.Potential<double>@000001695C982BD0)
      ||  B                                   |
A     ||0        |1        |2        |3        |
------||---------|---------|---------|---------|
0     || 0.0908  | 0.6597  | 0.2455  | 0.0040  |
1     || 0.0527  | 0.2998  | 0.4116  | 0.2360  |
```

In [16]:
```
gum.config["notebook","potential_visible_digits"]=1
bn.cpt("B")
```

Out[16]:
```
(pyAgrum.Potential<double>@000001695C982BD0)
      ||  B                                   |
A     ||0        |1        |2        |3        |
------||---------|---------|---------|---------|
0     || 0.0908  | 0.6597  | 0.2455  | 0.0040  |
1     || 0.0527  | 0.2998  | 0.4116  | 0.2360  |
```

In [17]:
```
gum.config['notebook', 'potential_color_0']="#AA00AA"
gum.config['notebook', 'potential_color_1']="#00FFAA"
bn.cpt("B")
```

Out[17]:
```
(pyAgrum.Potential<double>@000001695C982BD0)
      ||  B                                   |
A     ||0        |1        |2        |3        |
------||---------|---------|---------|---------|
0     || 0.0908  | 0.6597  | 0.2455  | 0.0040  |
1     || 0.0527  | 0.2998  | 0.4116  | 0.2360  |
```

In [18]:
```
gum.config["notebook","potential_visible_digits"]=4
gnb.flow.add(bn.cpt("B"),"Ugly float")

gum.config["notebook","potential_visible_digits"]=1
gnb.flow.add(bn.cpt("B"),"Ugly 1digit-float")

gum.config['notebook', 'potential_with_fraction']=True
gum.config['notebook', 'potential_fraction_with_latex']=False
gum.config['notebook', 'potential_fraction_limit']=2000
gnb.flow.add(bn.cpt("B"),"Simple fraction")

gum.config['notebook', 'potential_fraction_with_latex']=True
gnb.flow.add(bn.cpt("B"),"Sophisticated fraction with LaTeX")
gnb.flow.display()
```

```
<IPython.core.display.HTML object>
```

In [19]:
```
gnb.sideBySide(bn,gnb.getInference(bn,evs={"A":1},targets={"B"}))
```

```
<IPython.core.display.HTML object>
```

In [20]:
```
gum.config["notebook","evidence_bgcolor"]="green"
gum.config["notebook","default_node_bgcolor"]="yellow"
```

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```
gum.config["notebook","default_node_fgcolor"]="red"
gnb.sideBySide(bn,gnb.getInference(bn,evs={"A":1},targets={"B"}))
```

```
<IPython.core.display.HTML object>
```

In [21]:
```
gum.config["notebook","default_graph_size"]=1
gnb.sideBySide(bn,gnb.getInference(bn,evs={"A":1},targets={"B"}))
```

```
<IPython.core.display.HTML object>
```

In [22]:
```
gum.config["notebook","default_graph_inference_size"]="1"
gnb.sideBySide(bn,gnb.getInference(bn,evs={"A":1},targets={"B"}))
```

```
<IPython.core.display.HTML object>
```

Finding a specific property

In [23]:
```
#find anything containing arc
gum.config.grep("arc")
```

```
[notebook]
  default_arc_color = #4A4A4A
  default_arc_cmap = BuGn
[influenceDiagram]
  decision_arc_style = tapered, bold, dotted
  utility_arc_style = dashed
```

In [24]:
```
#find anything containing default
gum.config.grep("default")
```

```
[core]
  default_maxnumberofthreads = 24
[notebook]
  default_graph_size = 1
  default_graph_inference_size = 1
  default_arc_color = #4A4A4A
  default_node_bgcolor = yellow
  default_node_fgcolor = red
  default_node_cmap = Pastel1
  default_arc_cmap = BuGn
  default_edge_cmap = BuGn
  default_markovnetwork_view = factorgraph
[factorgraph]
  default_node_bgcolor = coral
  default_node_fgcolor = black
  default_factor_bgcolor = burlywood
[dynamicBN]
  default_graph_size = 6
[influenceDiagram]
  default_graph_size = 6
  default_chance_bgcolor = #808080
  default_chance_fgcolor = white
  default_utility_bgcolor = #50508A
  default_utility_fgcolor = white
  default_decision_bgcolor = #9A5050
  default_decision_fgcolor = white
```

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```
  default_id_size = 6
  default_id_inference_size = 6
[credalnet]
  default_node_bgcolor = #404040
  default_node_fgcolor = white
[causal]
  default_graph_size = 2.5
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  default_latent_bgcolor = #A08080
  default_latent_fgcolor = black
```

In [25]:
```
# if a section contains the search, all its properties are shown
gum.config.grep("caus")
```

```
[causal]
  show_latent_names = False
  latex_do_prefix = \hookrightarrow\mkern-6.5mu
  latex_do_suffix =
  default_graph_size = 2.5
  default_node_bgcolor = #404040
  default_node_fgcolor = white
  default_latent_bgcolor = #A08080
  default_latent_fgcolor = black
```

Saving current configuration in `pyagrum.ini`

In [26]:
```
gum.config.reset() # back to defaults
gum.config['notebook','default_arc_color'] = "#AAAAAA"
gum.config['notebook','evidence_bgcolor'] = "green"
gum.config.save() # store curent changes
```

In [27]:
```
gum.config.reset() # back to defaults
gum.config.save() # store defaults back
```

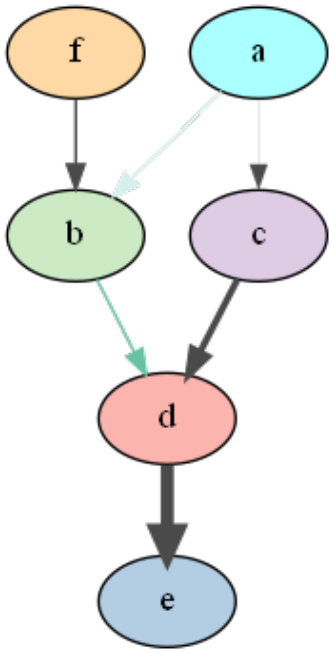
From PyAgrumConfiguration to ConfigParser

In [28]:
```
from configparser import ConfigParser
c=ConfigParser()

gum.config['notebook','default_arc_color'] = "#AAAAAA"
gum.config['notebook','evidence_bgcolor'] = "green"
c.read_string(gum.config.__repr__())
print(c.sections())
```

```
['notebook']
```

In [ ]:
```
```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