

Modèles Probabilistes Complexes

Models et Algorithms

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8 novembre 2011

DESIR



UPMC
SORBONNE UNIVERSITÉS

Variable elimination

Input : a set of CPTs \mathbf{P} and a set of variables \mathbf{X}

Output : $P(\mathbf{X})$

- 1 $\mathbf{W} \leftarrow$ all the variables of the CPTs of \mathbf{P} except \mathbf{X}
- 2 **while** $\mathbf{W} \neq \emptyset$ **do**
- 3 let X_j be a variable in \mathbf{W} ; remove X_j from \mathbf{W}
- 4 let \mathbf{Q} be the set of tables in \mathbf{P} containing X_j
- 5 compute table $q = \sum_{X_j} \prod_{f \in \mathbf{Q}} f$
- 6 $\mathbf{P} \leftarrow (\mathbf{P} \setminus \mathbf{Q}) \cup \{q\}$
- 7 **return** table $\prod_{f \in \mathbf{P}} f$

Dynamic Bayesian networks (dBNs)

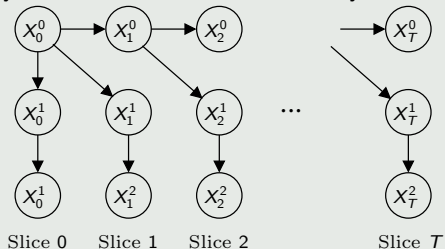
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Bayesian network that models a dynamic system (or a repetition of patterns) :

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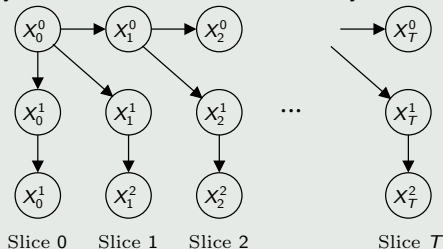
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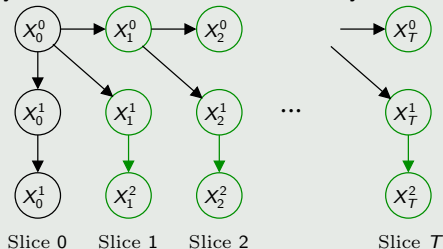
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$$p(\mathbf{X}_t | \mathbf{X}_{t-1}) = p(\mathbf{X}_1 | \mathbf{X}_0)$$
$$= \prod_{i=0}^{n-1} p(X_t^i | pa(X_t^i))$$

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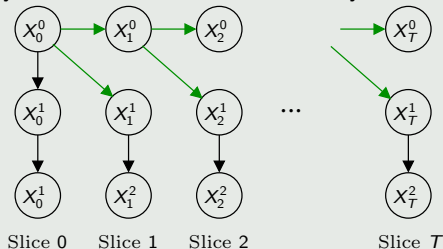
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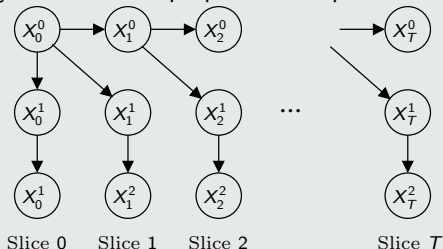
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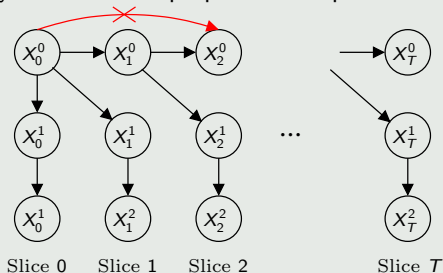
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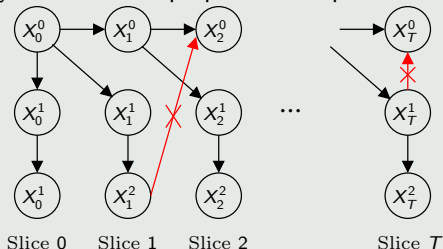
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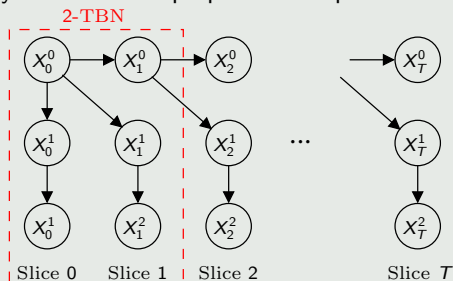
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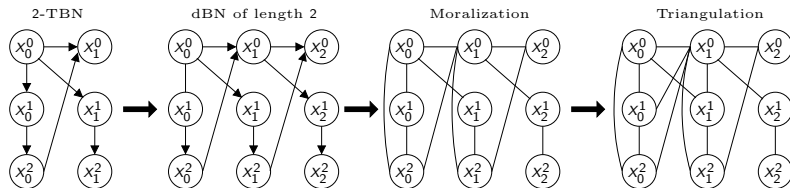
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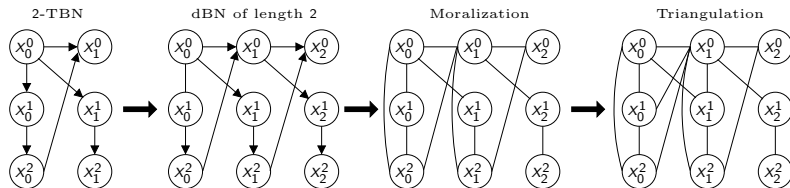


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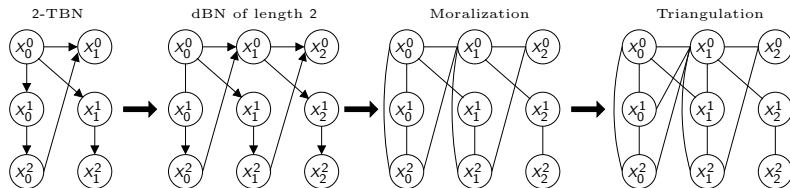
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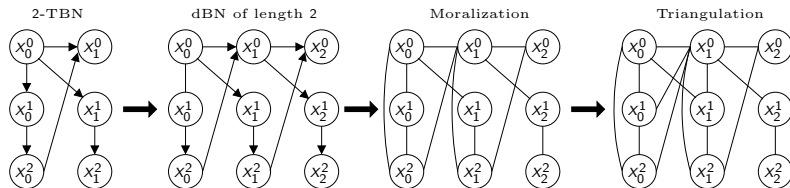
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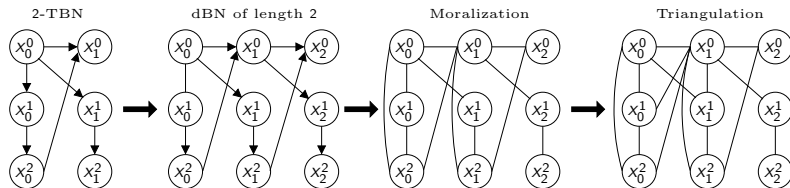
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- 3 The size of some cliques may be a function of T .

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Elimination order such that we enforce nodes to be eliminated with respect to a partial order.

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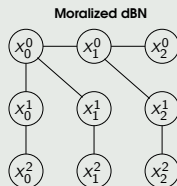
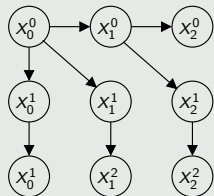
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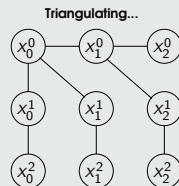
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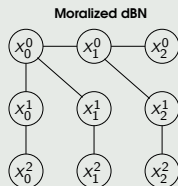
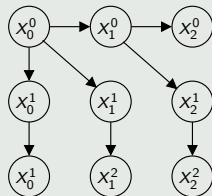
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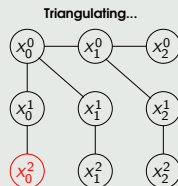
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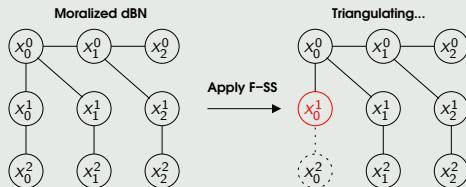
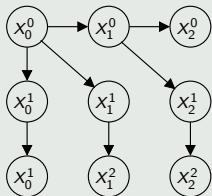
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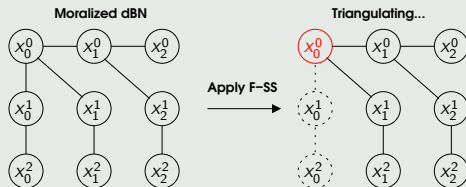
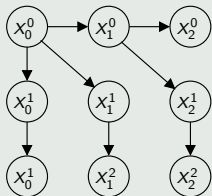
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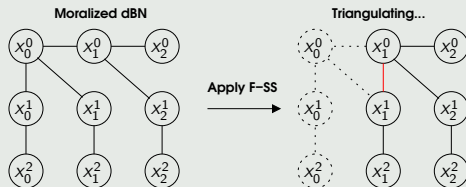
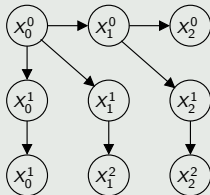
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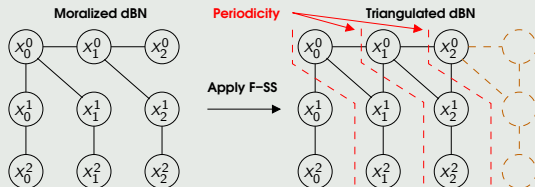
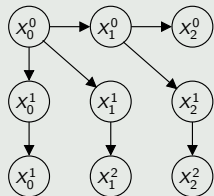
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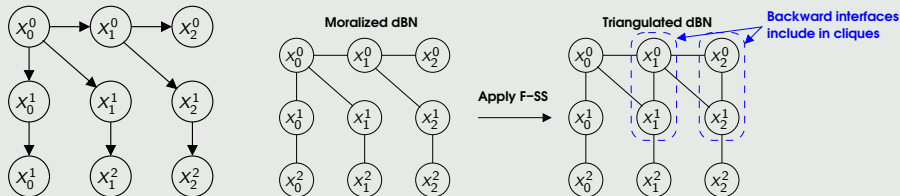
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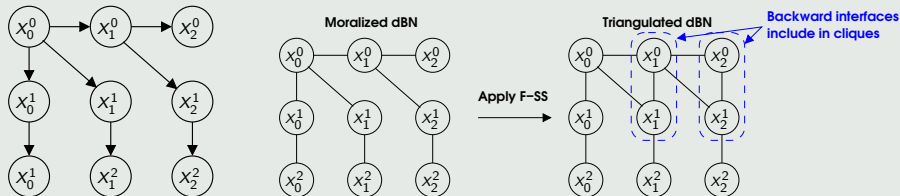
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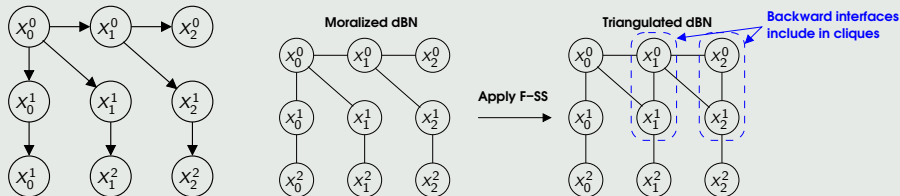
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\hookrightarrow *Backward interface* : nodes with parents or spouses in the previous slice.

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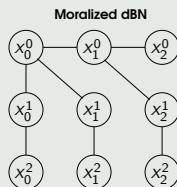
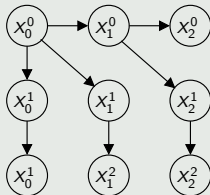
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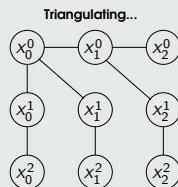
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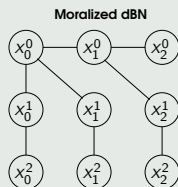
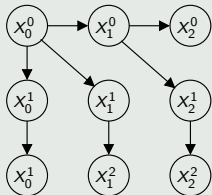
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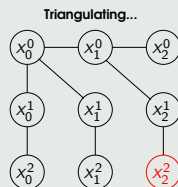
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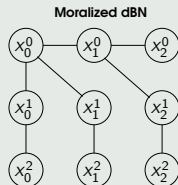
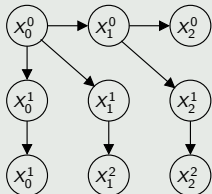
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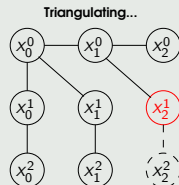
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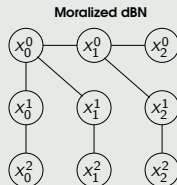
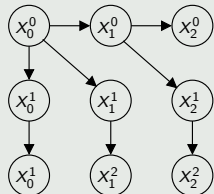
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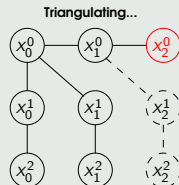
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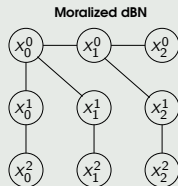
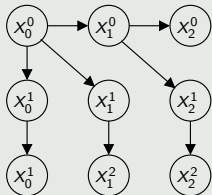
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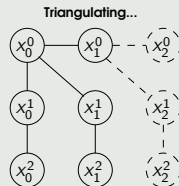
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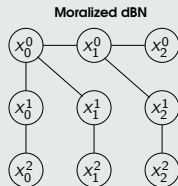
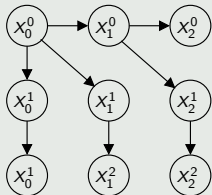
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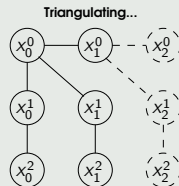
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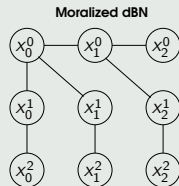
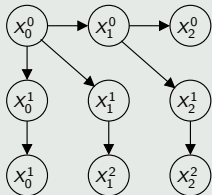
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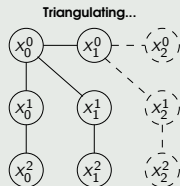
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The backward slice-by-slice elimination (B-SS) [darwiche, 2001]

Consists in eliminating a slice after an other from the future to the past :

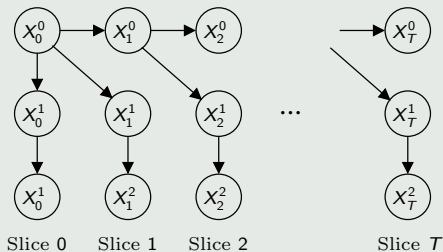


Apply F-SS



↪ *Forward interface* : nodes with children in the next slice.

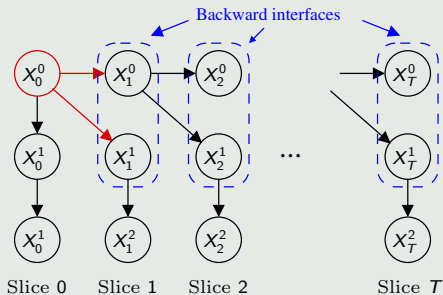
General interface



- *Transition model* :
$$p(\mathbf{X}_t | \mathbf{X}_{t-1}) = p(\mathbf{X}_1 | \mathbf{X}_0)$$
$$= \prod_{i=0}^{n-1} p(X_1^i | pa(X_1^i))$$

- *Prior distribution* :
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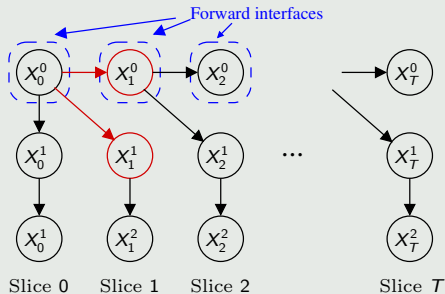
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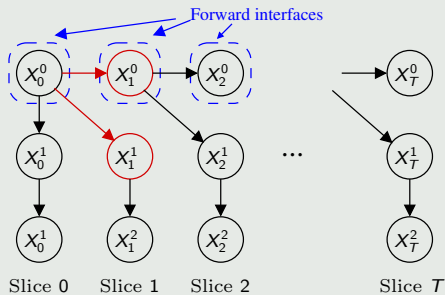
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Interface

Subset of nodes such that if they were removed they will disconnect the past from the future in the moral graph of a dBN.

Complexity for interface based ceo

Interface based Constrained elimination order (ceo)

Elimination order such that we enforce nodes to be eliminated with respect to a partial order given by an interface.

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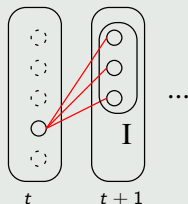
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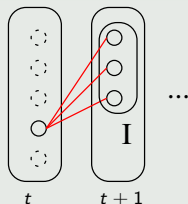
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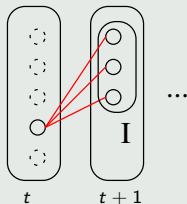
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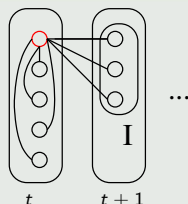
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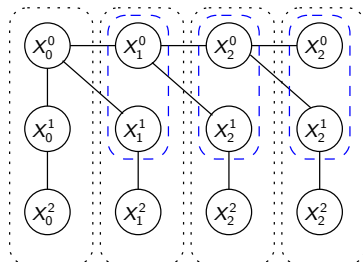
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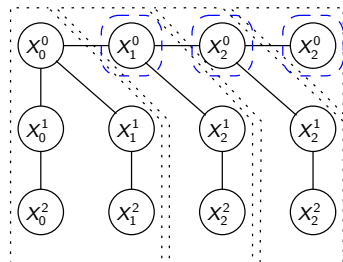


Worst case : clique of size $|I| + S$
(S : # nodes in a slice)

How to improve the bounds?

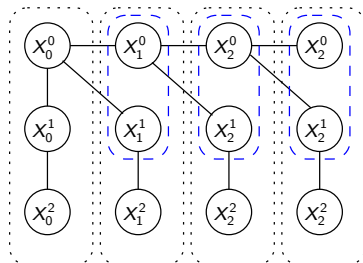


$$|I| + 1 = 3 \leq \omega = 3 \leq |I| + N = 5$$

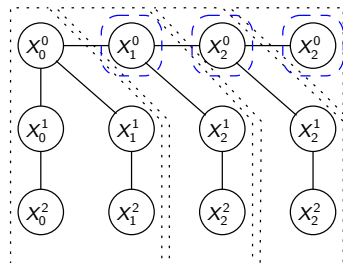


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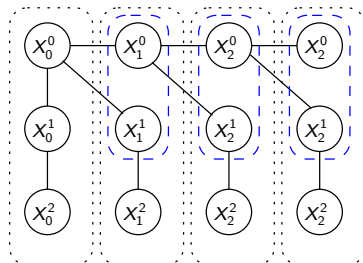
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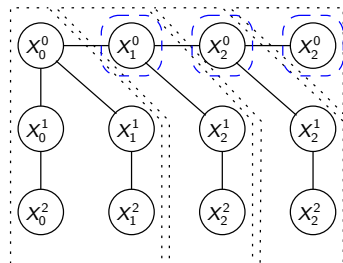
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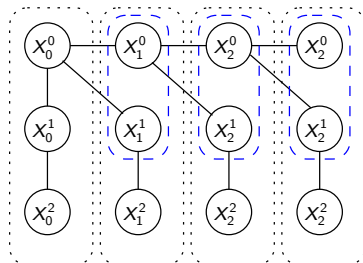


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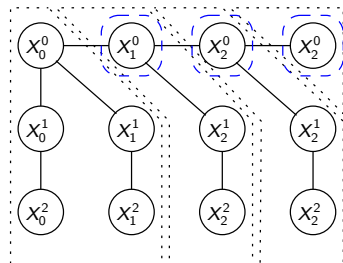
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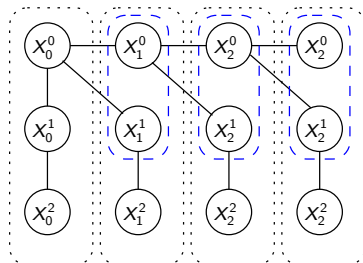
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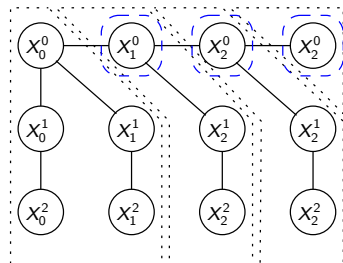
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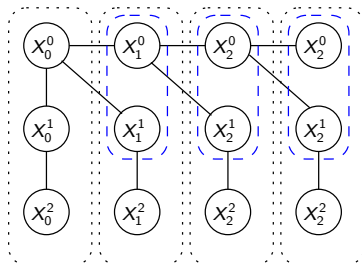
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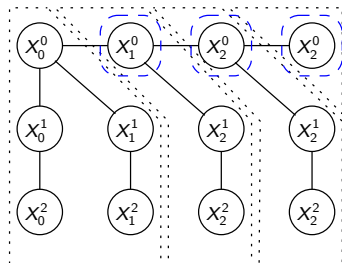
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Relation to the MINIMUM $s-t$ CUT problem

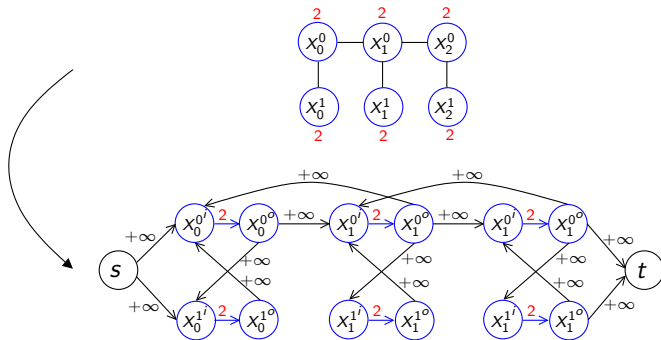
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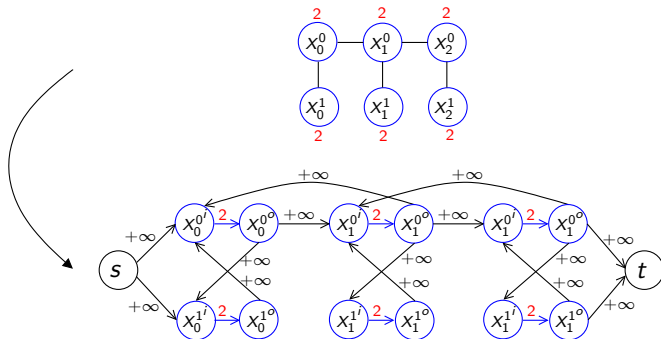
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\Rightarrow Polynomial time algorithm to find the minimum interface in a dBN of length T

Building the optimal elimination order

For wich value of T do we have the minimum interface?

Building the optimal elimination order

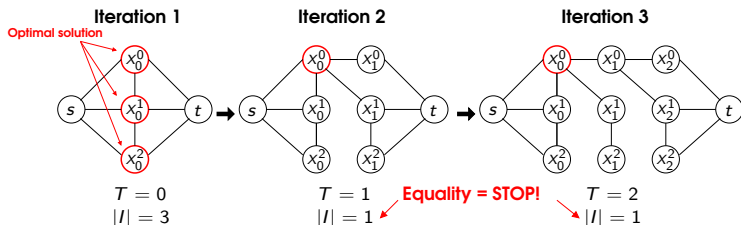
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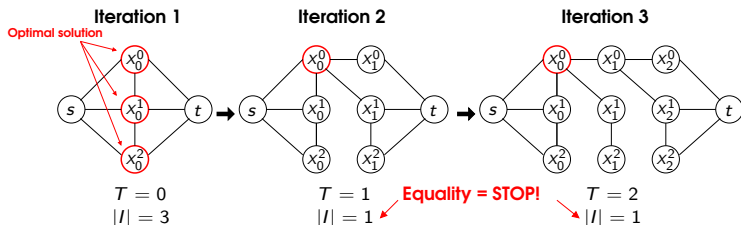
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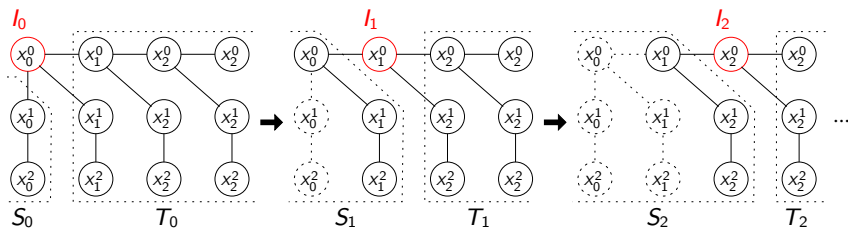
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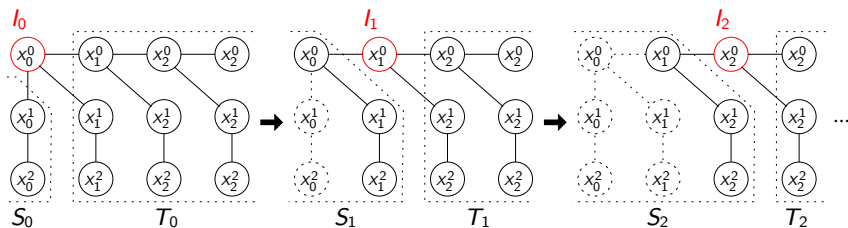
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At most $O(h)$ iterations where h is the number of nodes in a slice.

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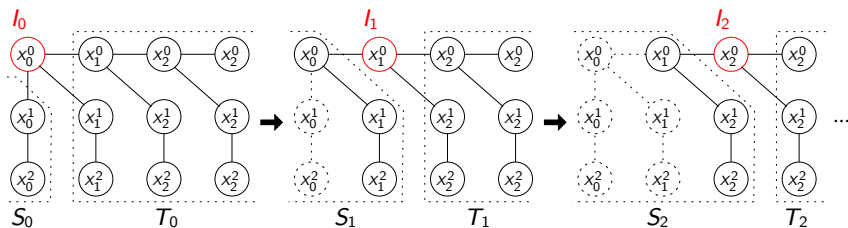


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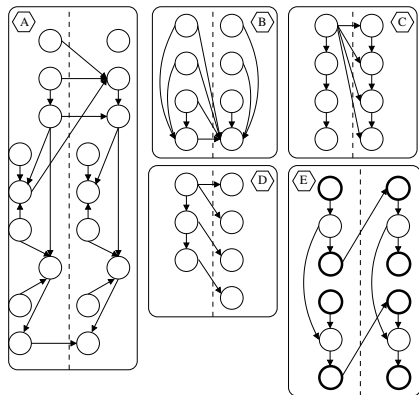
Better lower bound

Best case : clique of size $|I^*| + 1$

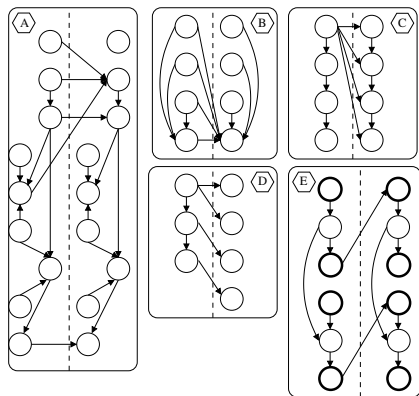
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Experimental results – Classical dBNs



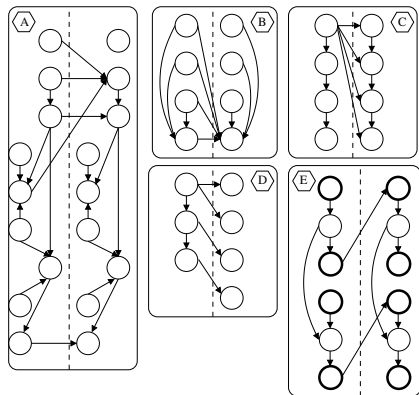
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Maximum clique size :

Fig.	B-SS	F-SS	MIN-ELIM
C	3.16	3.03	3.03
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D	1.38	3.00	1.38
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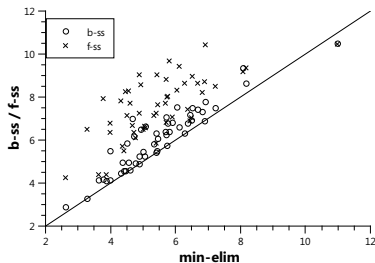
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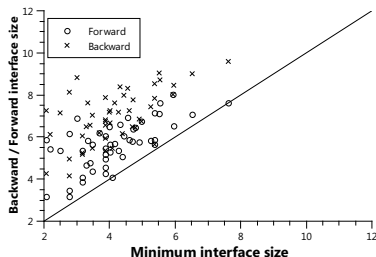
Results on randomly generated dBNs

- 1 5 variables per slices
- 2 Cardinalities chosen uniformly between 2 and 8
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Mean clique size



Interface size

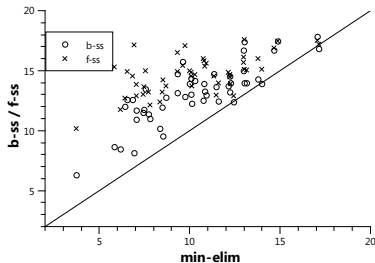


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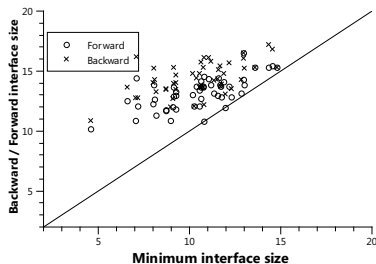
Results on randomly generated dBNs

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Mean clique size



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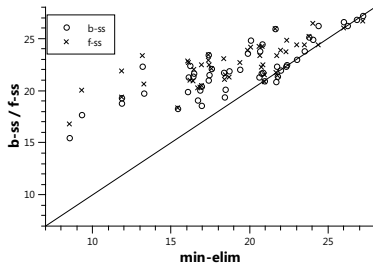


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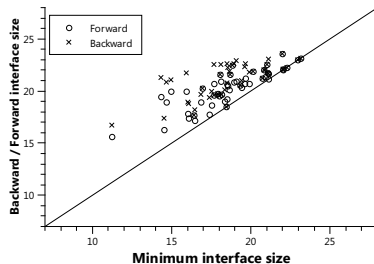
Results on randomly generated dBNs

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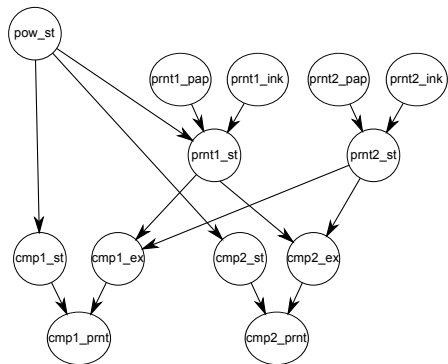
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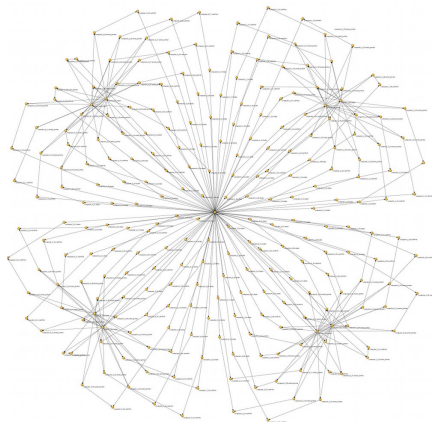
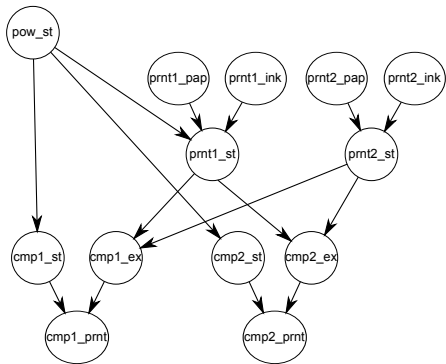
Interface size



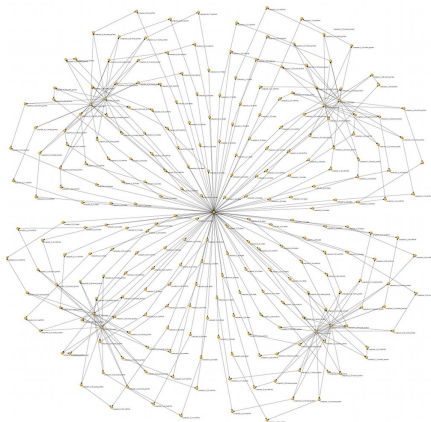
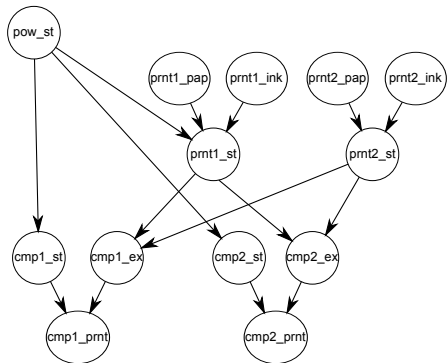
Motivation



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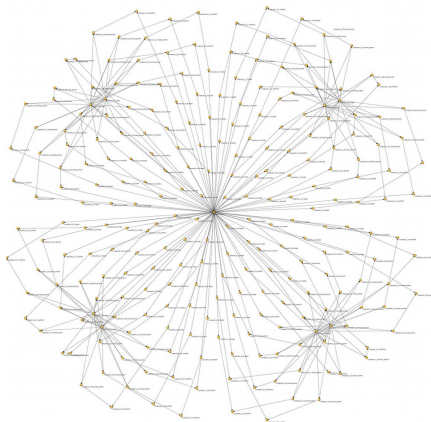
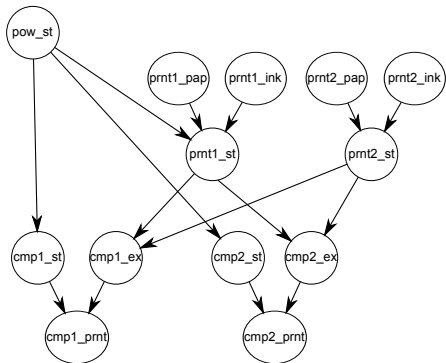


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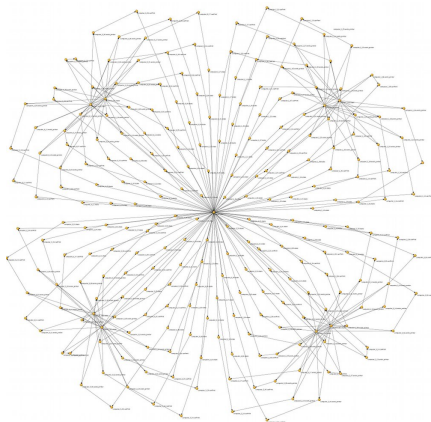
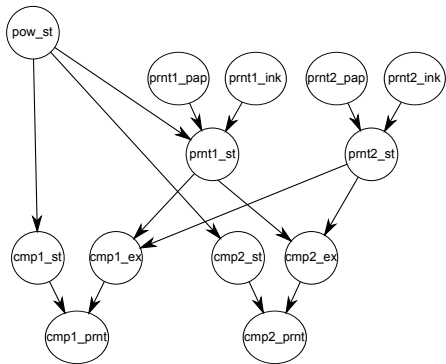
- Large-scale Bayesian networks “undesirable” features :

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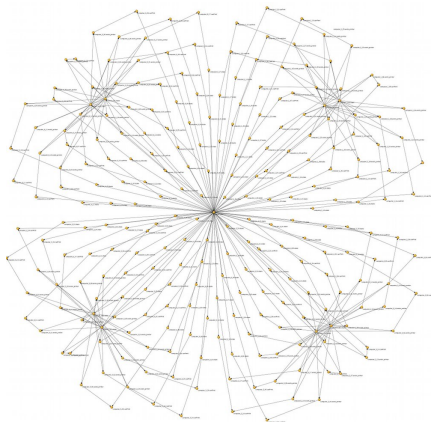
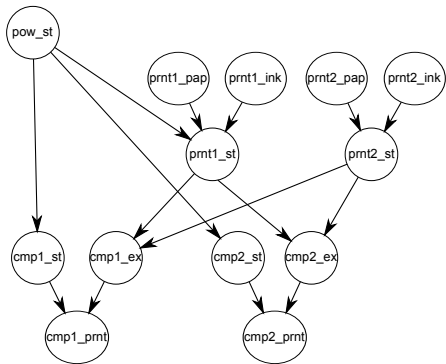
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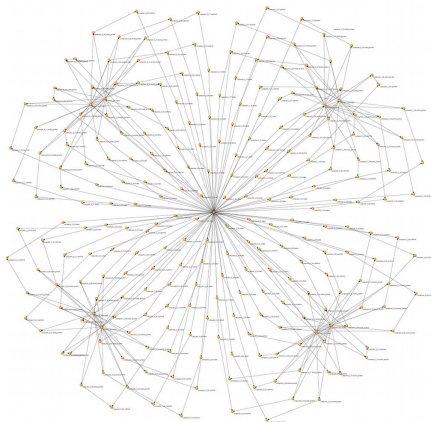
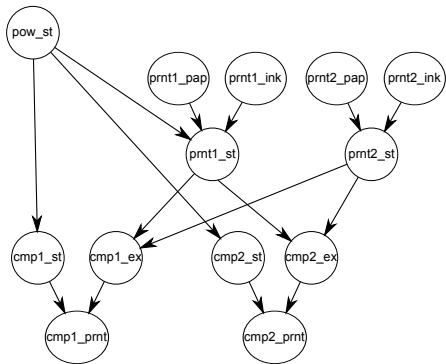
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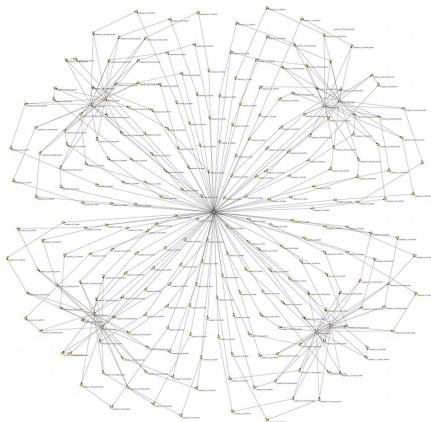
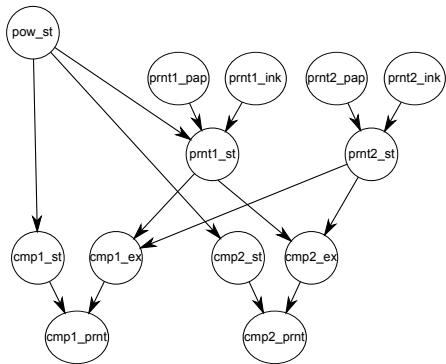
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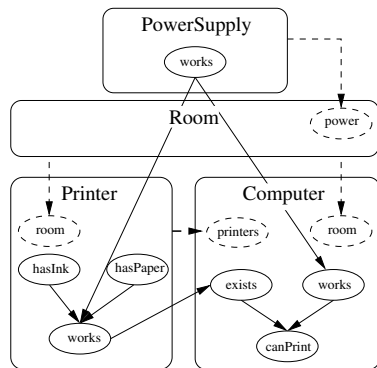
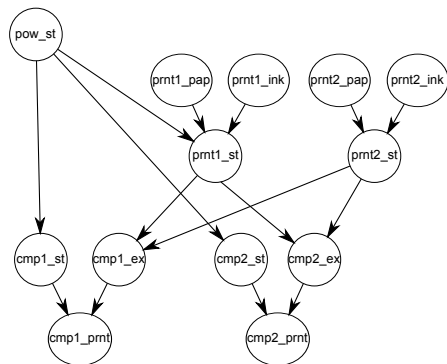
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our goal : design complex PGM **and** speed-up inference in PRMs

Probabilistic Relational Models (Pfeffer, 2000)

PRMs are an extension of object-oriented Bayesian Networks (Pfeffer & Koller, 1997) and (Bangsø & Willemin, 2000).

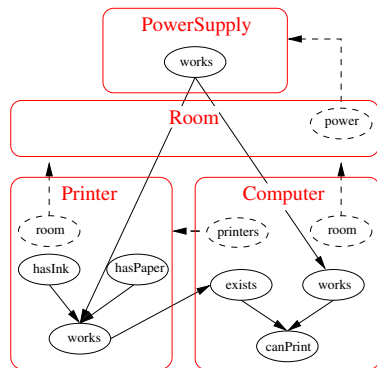


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PRMs in 4 definitions

- Classes are BNs fragments.

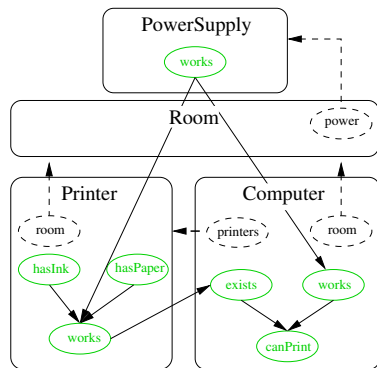


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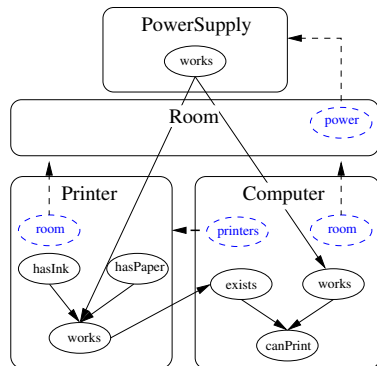


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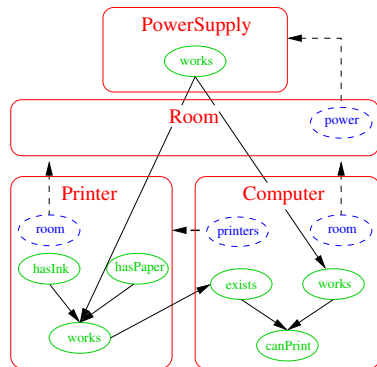


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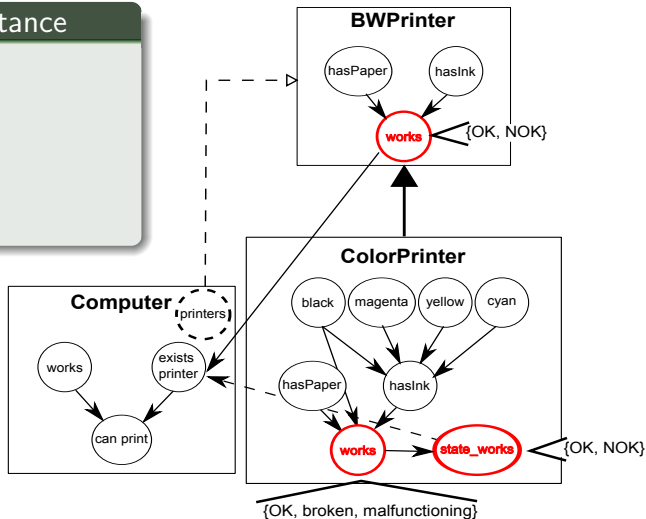
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(1) Reinforcing the object-oriented aspect of PRMs ([ANR SKOOR, Wullemir, Tort], 07-10)

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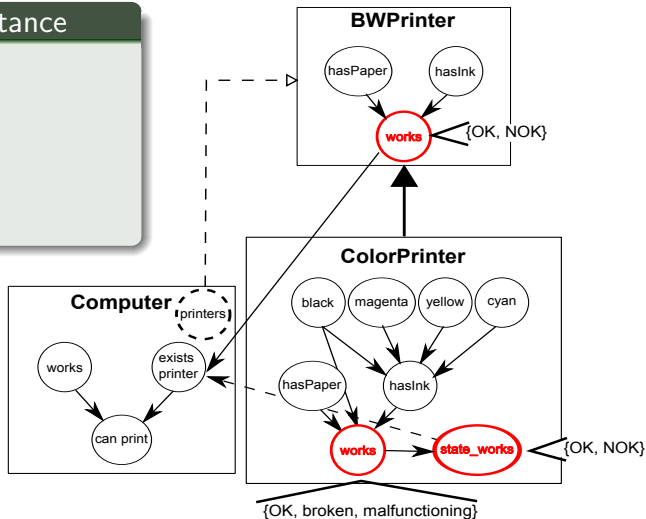


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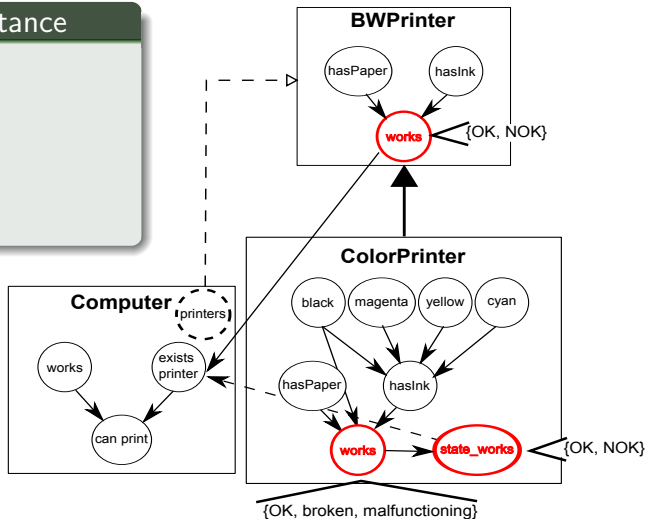


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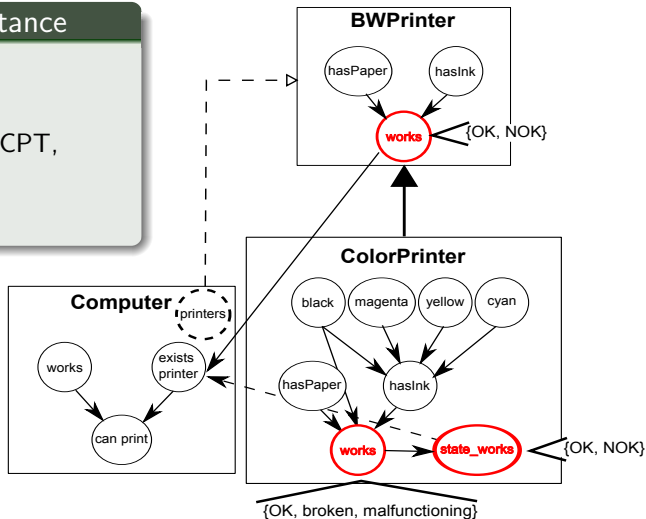


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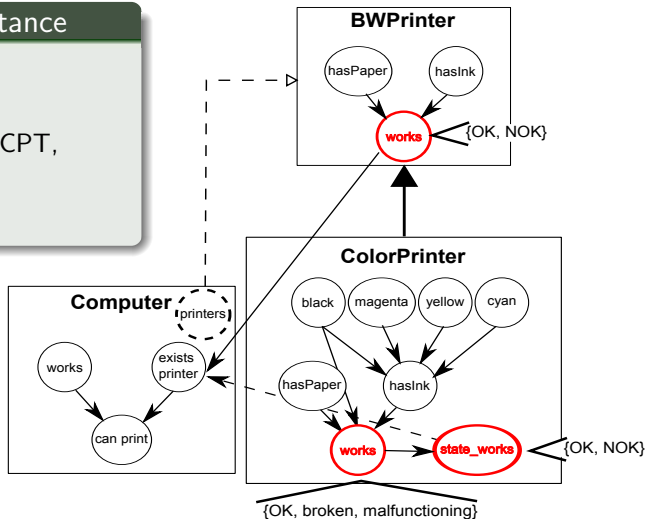


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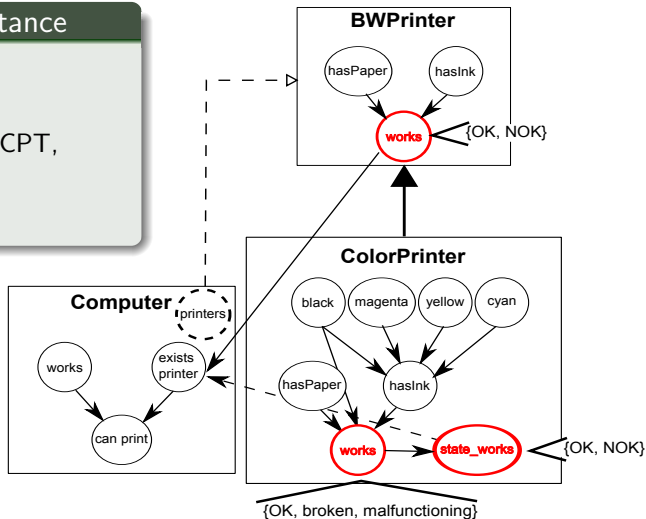


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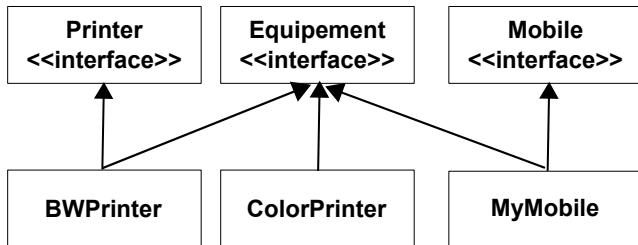
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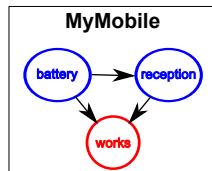
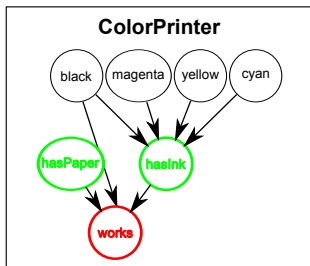
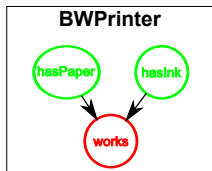
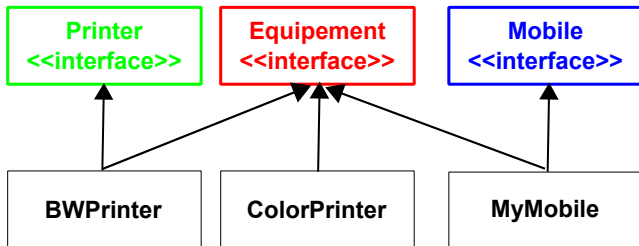
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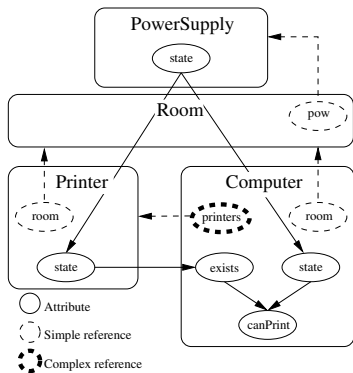


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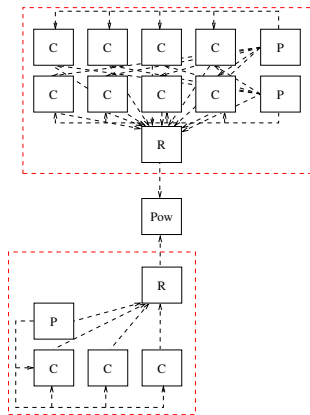


System : the printer example

A Class Dependency Graph.



A Relational Skeleton.



The SKOOB ANR project

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- **The models we created required the modification of the PRM framework presented here.**

Inference in PRM

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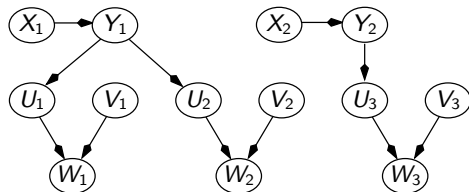
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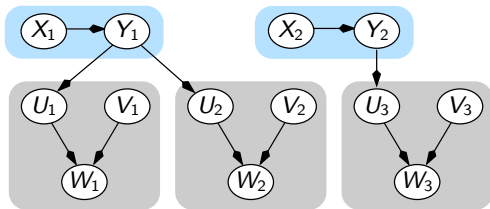
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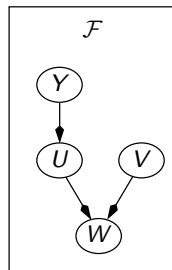
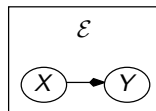
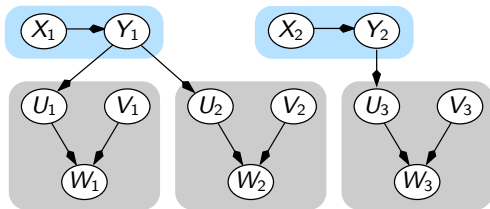
Overview of PRMs



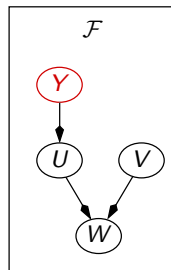
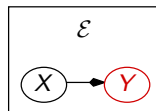
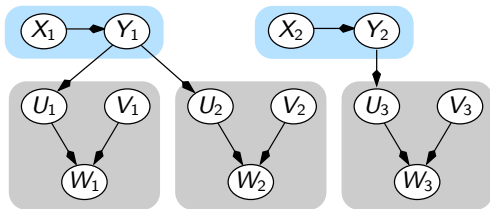
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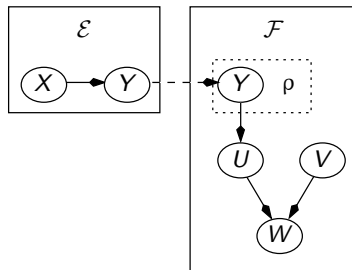
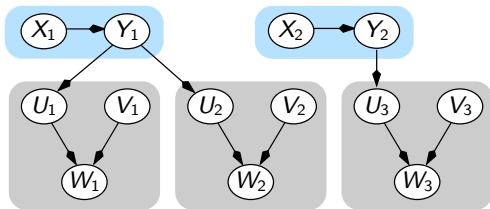
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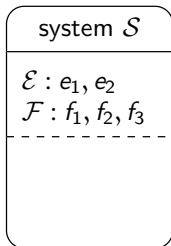
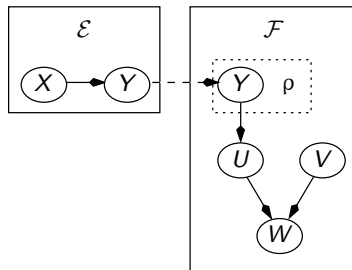
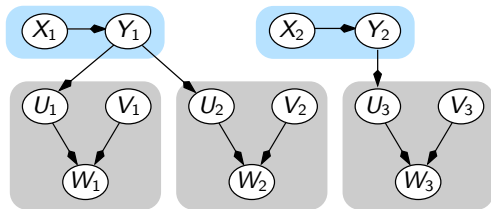
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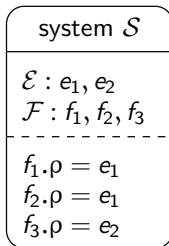
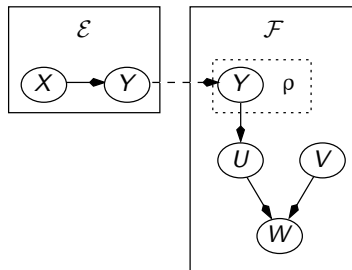
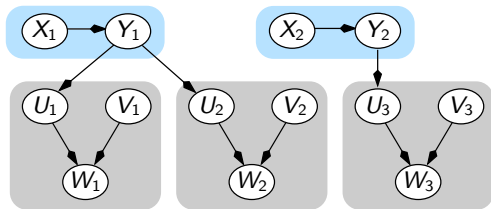
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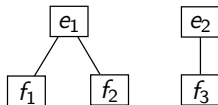
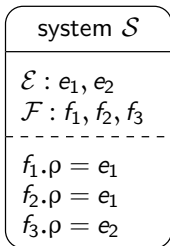
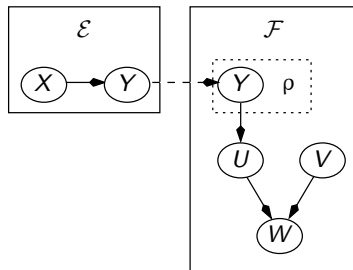
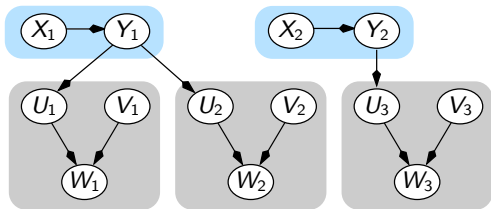
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Relational skeleton

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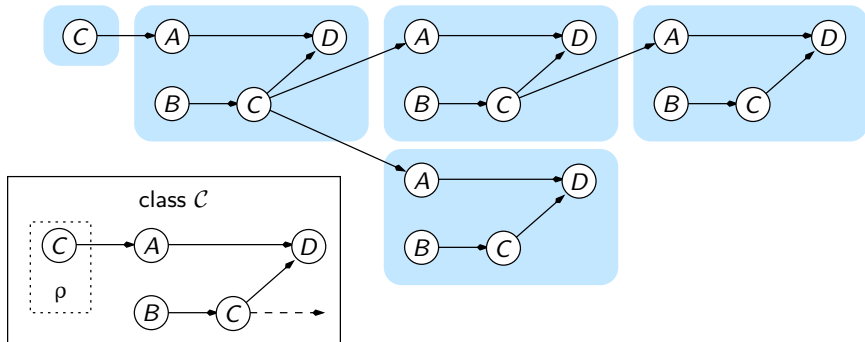
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Once inner attributes are eliminated, SVE proceeds with a **bottom-up** elimination of each instance.

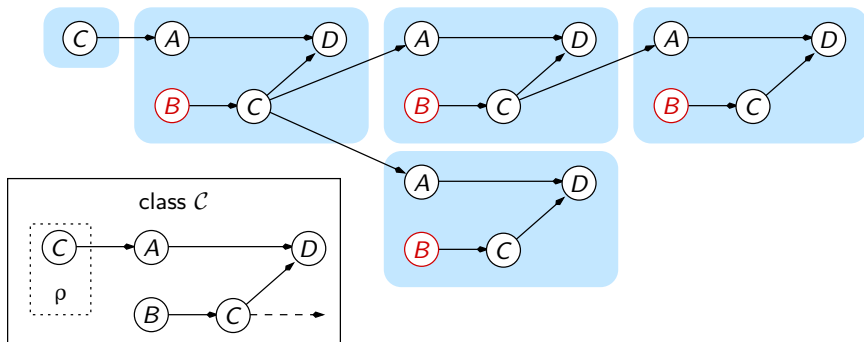
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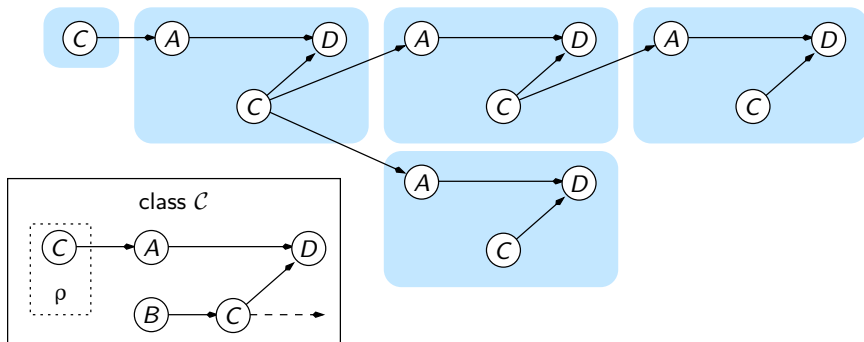
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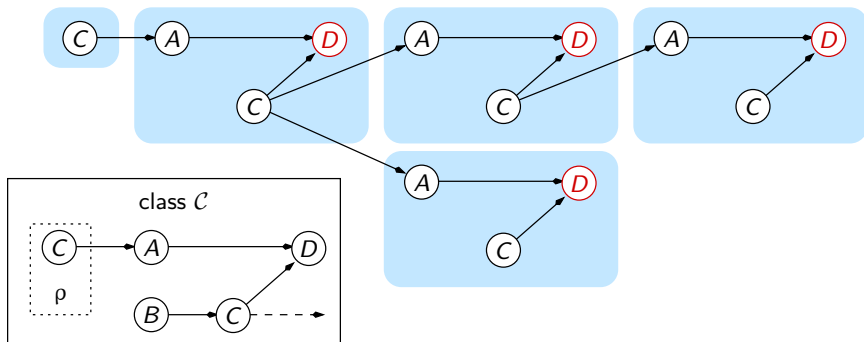
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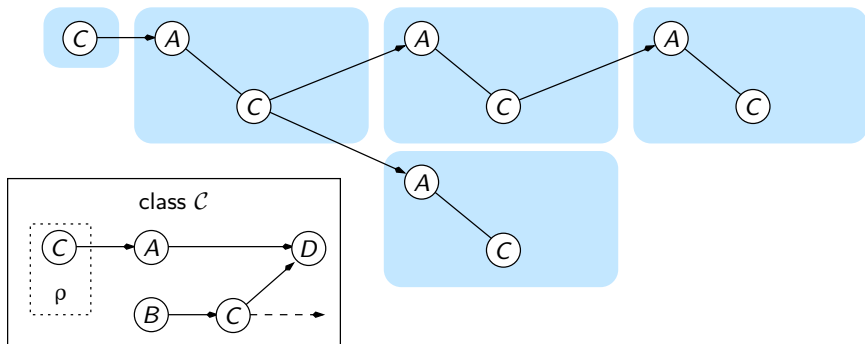
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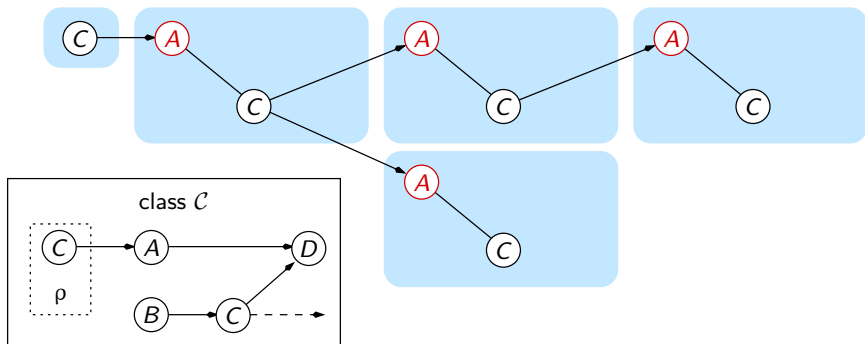
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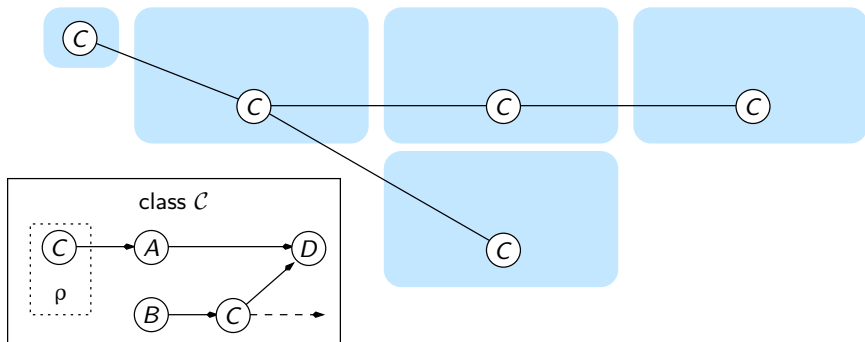
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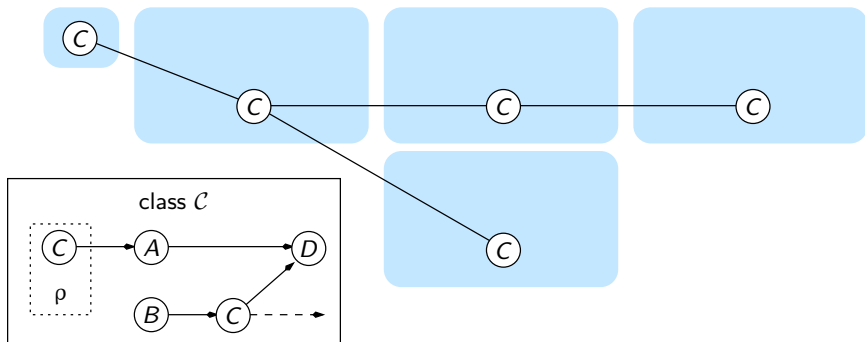
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Elimination at class level : performed only once !



It works only if the inner attributes are not observed.
Only internal variables can be eliminated at class level !

D-Separation in PRMs ([Tortì and Willemin, 2010])

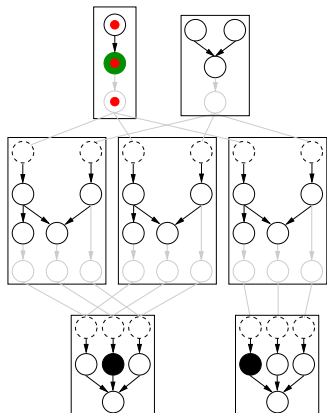


FIGURE: Different configurations due to evidence.

Integrating D-Separation in SVE

Following SVE bottom-up elimination order :

- 1 Recursive calls are made on each reverse slot chain.
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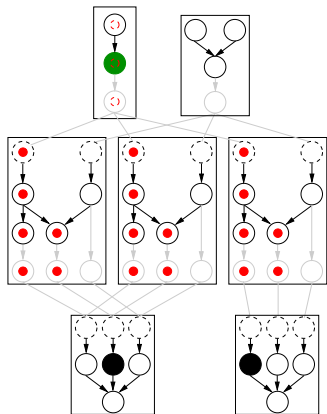


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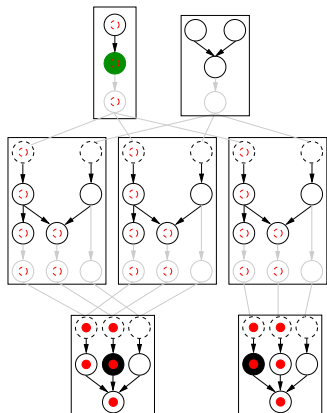


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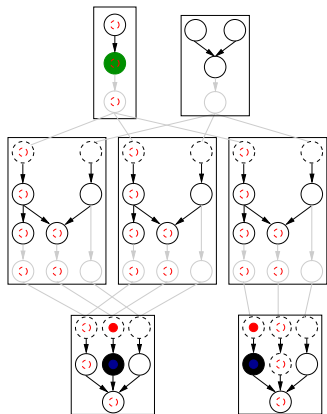


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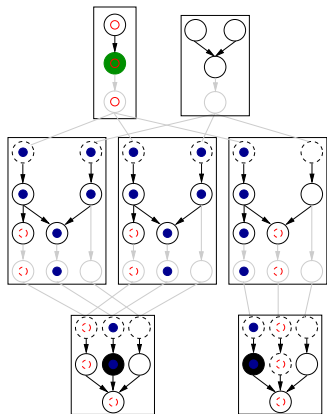


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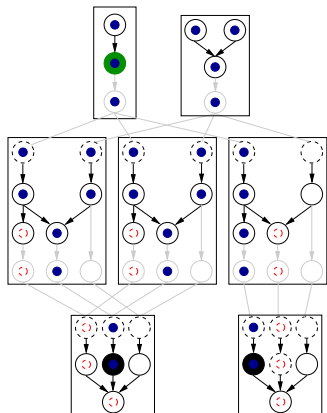


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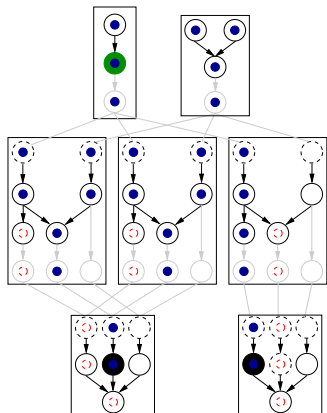


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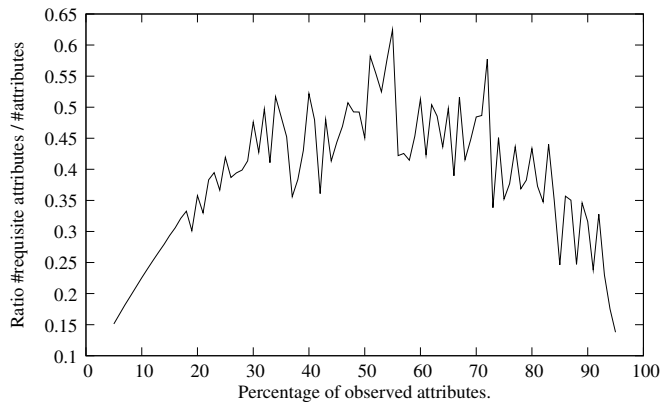
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Generalized BayesBall rule

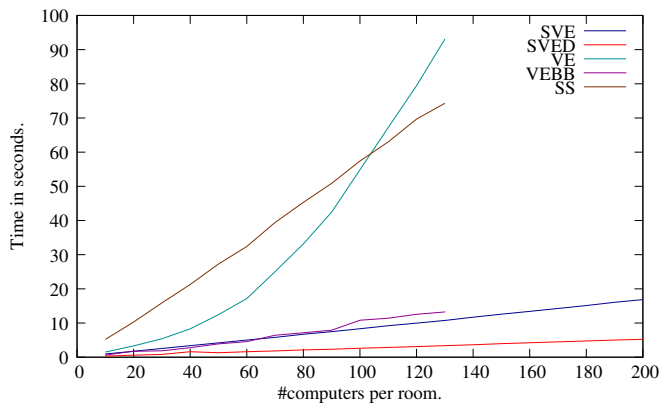
The example used for our experimentations

- We used the printer example with the following parameters :
 - different number of computers per room ;
 - different number of printers per room ;
 - different number of evidences.
- The examples we used have a 1400 to 24000 attributes.

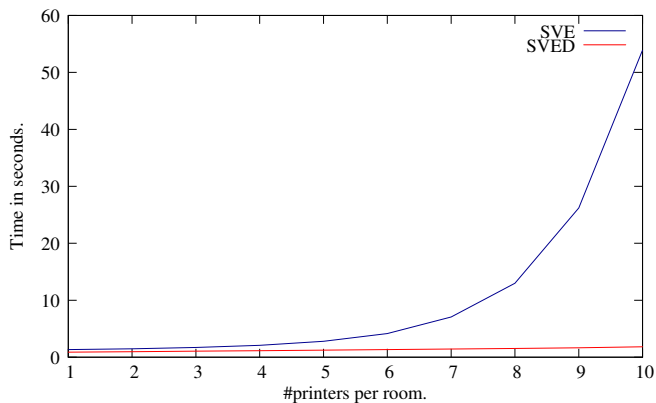
Efficiency of D-Separation



Increasing the number of computers



Increasing the number of printers



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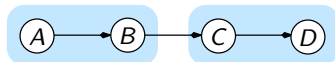
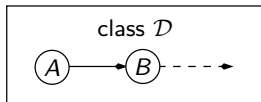
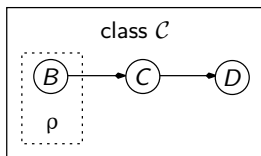
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\implies For instance : in genealogy, relations only between parents and children.

Only internal variables can be eliminated at class level

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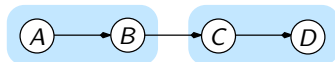
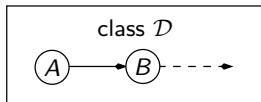
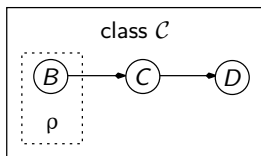
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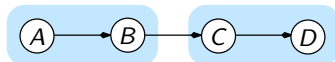
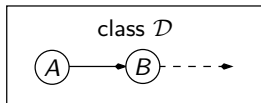
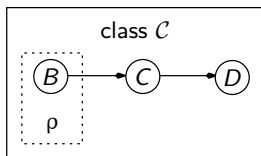
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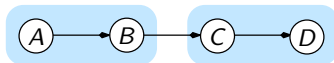
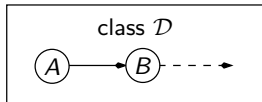
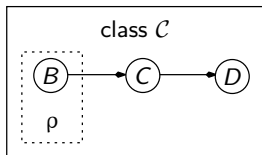


● Solution : create compound classes : **dynamic classes**

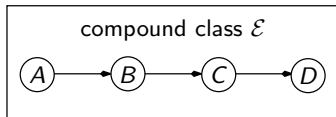
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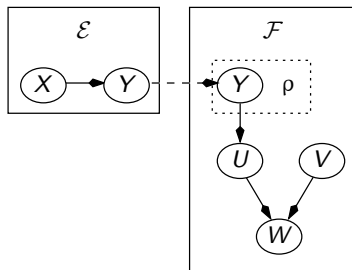
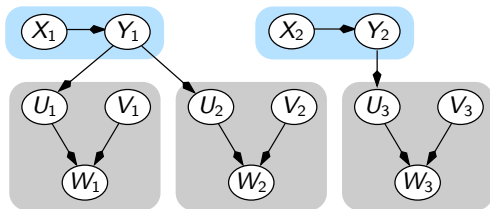
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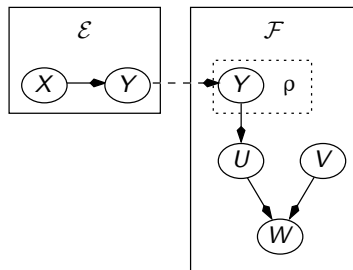
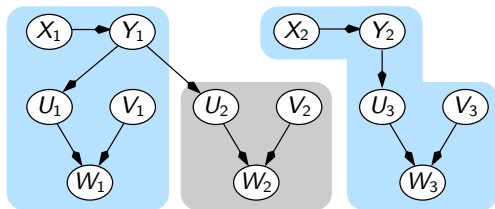
Substitution rule



Rule

One random variable can only belong to **one** instance.

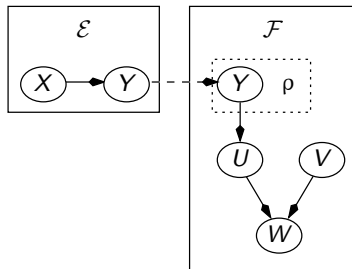
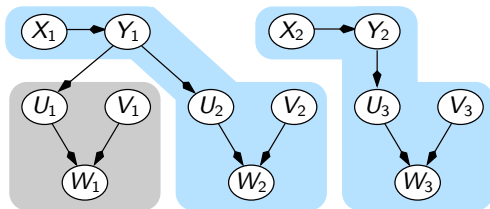
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Proposition

The following problem is NP-hard :

Instance : a PRM, an integer $K \geq 0$

Question : does there exist a set of dynamic classes / substitutions s.t. the number of operations performed by structured inference is $\leq K$?

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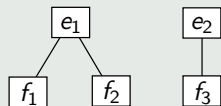
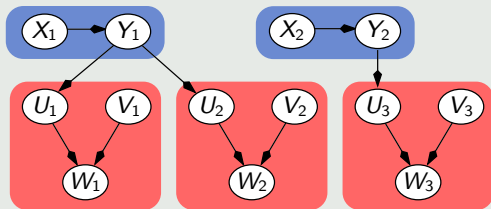
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remains NP-hard even when classical inference is polynomial

Approximate algorithm

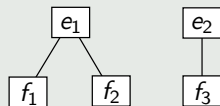
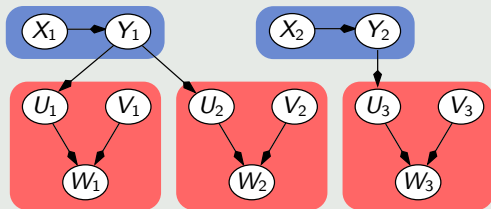
Boundary graph



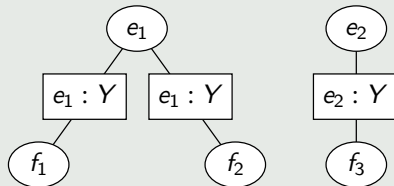
Relational skeleton

Approximate algorithm

Boundary graph



Relational skeleton



Boundary graph

\Rightarrow find frequent patterns in the boundary graph

- Mining frequent subgraphs

[Inokuchi et al, 05], [Kuramochi and Karypis, 01], [Yan and Han, 02]

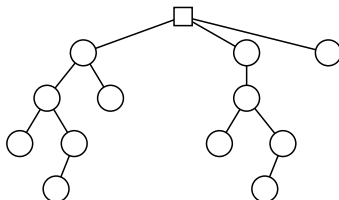
Search tree

- Mining frequent subgraphs

[Inokuchi et al, 05], [Kuramochi and Karypis, 01], [Yan and Han, 02]

- Variant of the gSpan algorithm :

1 edge
2 edges
3 edges
4 edges



- Node = (dynamic class, set of instances)

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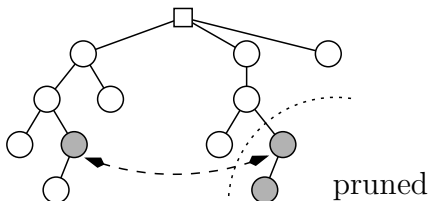
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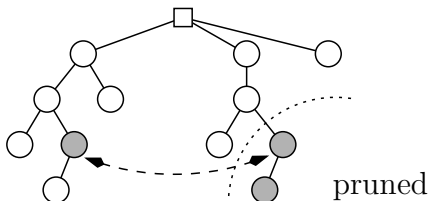
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- Node = (dynamic class, set of instances)

- Possible substitutions (Rule 1) : Max Independence Set

Another pruning rule

Efficiency Pruning Rule

Prune nodes/classes whose substitutions do not speed-up inference.

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Prune nodes/classes whose substitutions do not speed-up inference.

- Gain estimation by dynamic programming

$\implies \alpha\text{-value} : \alpha > 0 \iff \text{class unattractive}$



search tree not monotonically α -decreasing!

- Rule applied : prune subtree whenever $\alpha > 0$

Experiments

