Computational Complexity of Bayesian Networks

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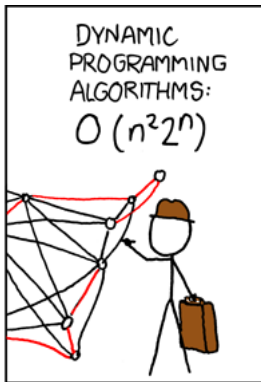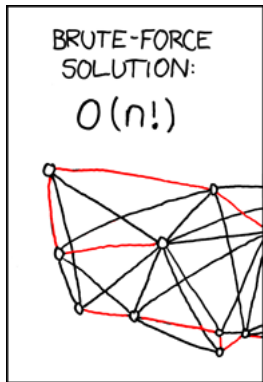
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Bayesian network inference is hard

- Are there (sub-)cases which are tractable?

- Are these cases (if any exists) interesting?

- If inference is hard, then approximation is an option. Can we approximate well?

- Where do lie the real-world problems?

Where do lie the real-world problems

Bayesian network moralization

*Marry any nodes with common children, then drop arc directions*
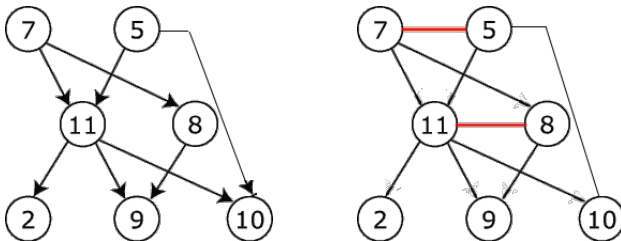
Adapted from wikipedia

Bayesian network triangularization/chordalization

- Bayesian network already moralized.
- Include edges in order to eliminate any cycle of length 4 (or more) without a chord (that is, a shortcut between nodes in the cycle).
- There are multiple ways to do that!

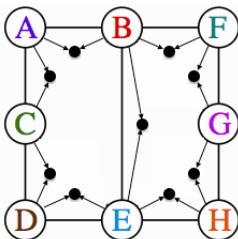# Bayesian network triangularization (I)

Let us work with this example:
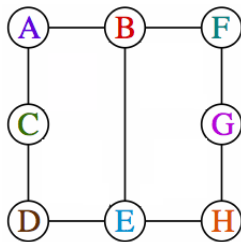
Adapted from wikipedia (while this is a valid graph, it cannot be obtained from a BN moralization – why?)

Bayesian network triangularization (II)
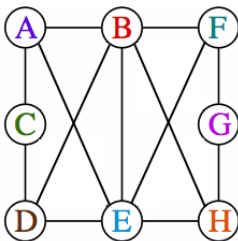
We could have obtained it from this moralization:

and then removed the black nodes as for the triangularization, as they are *simplicial*.

Bayesian network triangularization (III)

We may try to include some edges, but still not enough (check e.g. (A,C,D,E))...

Bayesian network triangularization (IV)

So we can keep trying to break those cycles (still not there, see (A,C,D,B))...

Bayesian network triangularization (V)
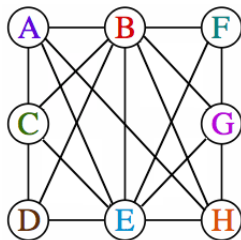
And eventually we did it! The *width* of a triangularization is the size of its largest clique minus one.

Perhaps not optimally: (A,B,E,H) is a 4-clique, could we have done with at most 3-cliques?

Bayesian network triangularization (VI)
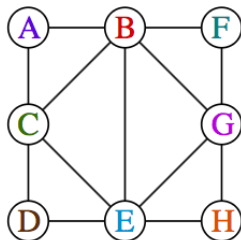
Yes, we can!

Theewidth of a BN is the minimum width over all possible triangularizations of its moral graph.

Bayesian network tree-decomposition (aka junction tree)
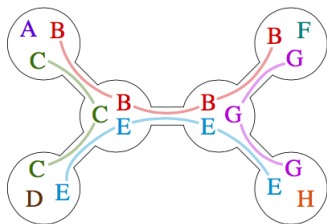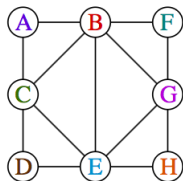
Source: wikipedia

"Easy" problems

EXACT INFERENCE and THRESHOLD INFERENCE are in P for bounded treewidth Bayesian networks.

In fact, assuming that any exact algorithm for SAT takes time $\Omega(c^n)$ for some constant $c > 0$, then any exact algorithm for THRESHOLD INFERENCE (and hence for EXACT INFERENCE) takes time at least exponential in the treewidth (except for a log factor).

Complexity of problems under some restrictions

THRESHOLD INFERENCE is:

- ▶ Bayesian network has bounded treewidth: EASY (in P)
- ▶ Bayesian network is a polytree/tree: EASY (in P)
- ▶ There is no evidence (no observed nodes): PP-complete
- ▶ Variables have bounded cardinality: PP-complete
- ▶ Nodes are binary and evidence is restricted to be positive (TRUE): PP-complete
- ▶ Nodes are binary and parameters satisfy the following condition:
  - ▶ Root nodes are associated to marginal distributions;
  - ▶ Non-root nodes are associated to Boolean operators ($\land$, $\lor$, $\lnot$): PP-complete (even if only $\land$ or only $\lor$ are allowed)

THRESHOLD INFERENCE is PP-hard in very restricted nets

THRESHOLD INFERENCE in bipartite two-layer binary Bayesian networks with no evidence and nodes defined either as marginal uniform distributions or as the disjunction $\vee$ operator is PP-hard (using only the conjunction $\wedge$ also gets there).

We reduce MAJ-2MONSAT, which is PP-complete [Roth 1996], to THRESHOLD INFERENCE:

Input: A 2-CNF formula $\phi(X_1, \ldots, X_n)$ with m clauses where all literals are positive.
Question: Does the majority of the assignments to $X_1, \ldots, X_n$ satisfy ϕ?

The transformation is as follows. For each Boolean variable X_i, build a root node such that $\Pr(X_i = \text{TRUE}) = 1/2$. For each clause C_j with literals x_a and x_b (note that literals are always positive), build a disjunction node Y_{ab} with parents X_a and X_b, that is, $Y_{ab} \Leftrightarrow X_a \vee X_b$. Now set all non-root nodes to be queried at their true state, that is, $\mathbf{h} = \{Y_{ab} = \text{TRUE}\}_{\forall ab}$.
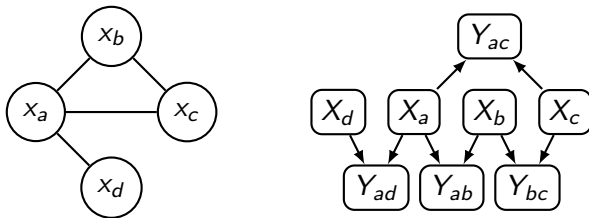

Figure: A Bayesian network (on the right) and the clauses as edges (on the left): $(x_a \vee x_b), (x_a \vee x_c), (x_a \vee x_d), (x_b \vee x_c)$.
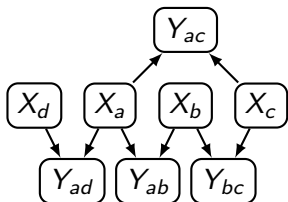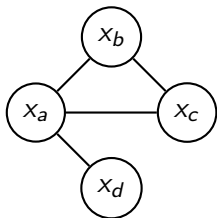
So with this specification for **h** fixed to TRUE, at least one of the parents of each of them must be set to TRUE too. These are exactly the satisfying assignments of the propositional formula, so $\Pr(\mathbf{H} = \mathbf{h} \mid \mathbf{E} = \mathbf{e})$ for empty **E** is exactly the percentage of satisfying assignments, with $\mathbf{H} = \mathbf{Y}$ and $\mathbf{h} = $ TRUE.

$\Pr(\mathbf{H} = \mathbf{h}) = \sum_{\mathbf{x}} \Pr(\mathbf{Y} = \text{TRUE} \mid \mathbf{x}) \Pr(\mathbf{x}) = \frac{1}{2^n} \sum_{\mathbf{x}} \Pr(\mathbf{Y} = \text{TRUE} \mid \mathbf{x}) > 1/2$ if and only if the majority of the assignments satisfy the formula.

MPE and MAP
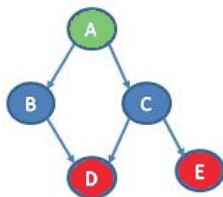
- ▶ THRESHOLD MAP: Given observation $A = a$, threshold q and explanation set $\{D, E\}$ Decide whether exists d, e such that $\Pr(D = d, E = e \mid A = a) > q$.
- ▶ THRESHOLD MPE: Each variable B and C must appear either as query or as observation (no intermediate nodes).

MPE and MAP

Threshold MAP (DMAP)

Instance: A Bayesian network $\mathcal{B} = (\mathbf{G}_{\mathcal{B}}, \Pr)$, where $\mathbf{V}$ is partitioned into a set of evidence nodes $\mathbf{E}$ with a joint value assignment $\mathbf{e}$, a set of intermediate nodes $\mathbf{I}$, and an explanation set $\mathbf{H}$. Let $0 \leq q < 1$.

Question: Is there $\mathbf{h}$ such that $\Pr(\mathbf{H} = \mathbf{h}, \mathbf{E} = \mathbf{e}) > q$?

Threshold MPE (DMPE)

Instance: A Bayesian network $\mathcal{B} = (\mathbf{G}_{\mathcal{B}}, \Pr)$, where $\mathbf{V}$ is partitioned into a set of evidence nodes $\mathbf{E}$ with a joint value assignment $\mathbf{e}$ and an explanation set $\mathbf{H}$. Let $0 \leq q < 1$.

Question: Is there $\mathbf{h}$ such that $\Pr(\mathbf{H} = \mathbf{h}, \mathbf{E} = \mathbf{e}) > q$?

DMAP is NP^{PP}-hard [Park 2002]

$\phi = \neg(x_1 \vee x_2) \vee \neg x_3$
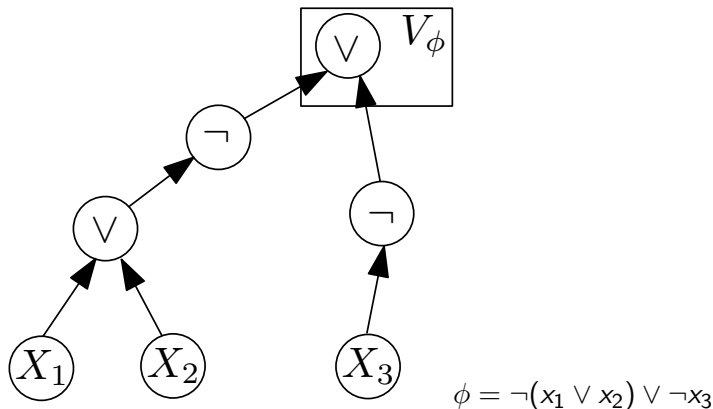
Reduction comes from an NP^{PP}-hard problem: given $\phi(X_1, \ldots, X_n)$, integer k and rational q, is there an assignment to $X_1, \ldots, X_k$ such that the majority of the assignments to $X_{k+1}, \ldots, X_n$ satisfy ϕ?

DMAP is NP$^{\mathrm{PP}}$-hard

- Similar construction as done to prove hardness of INFERENCE, but variables **X** are partitioned into explanation $(X_1, \ldots, X_k)$ and intermediate ones $(X_{k+1}, \ldots, X_n)$.
- Marginal probabilities $\Pr(X_i = \text{TRUE}) = 1/2$ are defined as before, but $X_1, \ldots, X_k$ are to be explained during DMAP.
- As before, for an arbitrary truth assignment **x** to the set of all propositional variables **X** in the formula ϕ we have that $\Pr(V_\phi = \text{TRUE} \mid \mathbf{X} = \mathbf{x})$ equals 1 if **x** satisfies ϕ, and 0 if **x** does not satisfy ϕ.

$$\Pr(\mathbf{X}_{1:k} = \mathbf{x}_{1:k}, V_\phi = \text{TRUE}) =$$
$$\Pr(V_\phi = \text{TRUE} \mid \mathbf{X}_{1:k} = \mathbf{x}_{1:k})\Pr(\mathbf{X}_{1:k} = \mathbf{x}_{1:k}) =$$
$$\frac{1}{2^k}\Pr(V_\phi = \text{TRUE} \mid \mathbf{X}_{1:k} = \mathbf{x}_{1:k}) > \frac{1}{2^{k+1}}$$

if and only if there is $\mathbf{X}_{1:k} = \mathbf{x}_{1:k}$ such that the majority of truth assignments of $\mathbf{X}_{(k+1):n}$ satisfy ϕ.

DMPE is NP-complete

Pertinence in NP is immediate, as given **h** (the so-called certificate), we can check whether $\Pr(\mathbf{H} = \mathbf{h}, \mathbf{E} = \mathbf{e}) > q$ in polynomial time.

(Question to think about: if DMPE were defined with conditional probability $\Pr(\mathbf{H} = \mathbf{h}|\mathbf{E} = \mathbf{e}) > q$, then would it still be in NP?)

Hardness: Reduction comes from an NP-hard problem: given 3-CNF propositional $\phi(X_1, \ldots, X_n)$, is there an assignment to **X** that satisfies ϕ?

DMPE is NP-complete

The transformation is as follows. For each Boolean variable X_i, build a root node such that $\Pr(X_i = \text{TRUE}) = 1/2$. For each clause C_j with literals x_a, x_b, x_c (note that literals might be positive or negative), build a disjunction node Y_{abc} with parents X_a, X_b and X_c, that is, the probability function is defined such that $Y_{abc} \Leftrightarrow X_a \vee X_b \vee X_c$. Now set all non-root nodes to be observed at their true state, that is, $\mathbf{e} = \{Y_{abc} = \text{TRUE}\}_{\forall abc}$.
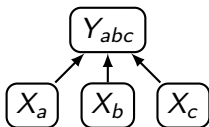

Figure: Building block representing a 3-CNF clause $(x_a \vee x_b \vee x_c)$.

Define all root nodes as **H** and ask whether there is **h** such that $\Pr(\mathbf{H} = \mathbf{h}, \mathbf{E} = \mathbf{e}) > 0$, which is true if and only if there is a satisfying assignment for the propositional formula.

Source: xkcd

MPE and MAP

What about MPE and MAP under these restrictions?

- ▶ Bayesian network has bounded treewidth.
- ▶ Bayesian network is a polytree/tree.
- ▶ There is no evidence (no observed nodes).
- ▶ Variables have bounded cardinality.
- ▶ Nodes are binary and evidence is restricted to be positive (TRUE).
- ▶ Nodes are binary and parameters satisfy the following condition:
    - ▶ Root nodes are associated to marginal distributions;
    - ▶ Non-root nodes are associated to Boolean operators ($\land$, $\lor$, $\neg$).

Complexity of problems under some restrictions

Notation: $\mathrm{DMPE}^?\text{-}c\text{-}tw(\mathsf{L})$ and $\mathrm{DMAP}^?\text{-}c\text{-}tw(\mathsf{L})$, where:

- ? is either 0 (meaning no evidence) or $+$ (positive evidence only). If omitted, then both positive and negative are allowed.
- tw is the bound on the treewidth.
- c is the maximum cardinality of any variable.
- L defines the propositional logic operators that are allowed for the non-root nodes.

Complexity of problems under some restrictions

Notation: $\mathrm{DMPE}^?\text{-}c\text{-}tw(\mathsf{L})$ and $\mathrm{DMAP}^?\text{-}c\text{-}tw(\mathsf{L})$, where:

- ? is either 0 (meaning no evidence) or $+$ (positive evidence only). If omitted, then both positive and negative are allowed.
- tw is the bound on the treewidth.
- c is the maximum cardinality of any variable.
- L defines the propositional logic operators that are allowed for the non-root nodes.

We could also talk about THRESHOLD INFERENCE, but the only restriction that is known to make a great difference is treewidth. We also refrain from discussing DMPE of bounded treewidth, as this is known to be in P (by using junction tree or variable elimination algorithms – *result is not practical unless a good tree decomposition is given*).

Problems under some restrictions: In general, bad news

- DMPE-2-∞(Prop($\wedge$)) is NP-complete.
- DMPE$^+$-2-∞(Prop($\vee$)) is NP-complete.
- DMAP$^+$-2-∞(Prop($\vee$)) is NP^{PP}-complete.
- DMAP-2-∞(Prop($\wedge$)) is NP^{PP}-complete.
- DMAP-2-2 and DMAP-3-1 are NP-complete.
- DMAP-∞-1 with naive-like structure and DMAP-5-1 with HMM structure (and single observation) are NP-complete.

DMPE^+-2-∞(Prop($\vee$)) is NP-hard

To prove hardness, we use a reduction from VERTEX COVER:

Input: A graph $G = (V, A)$ and an integer k.
Question: Is there a set $C \subseteq V$ of cardinality at most k such that each edge in A is incident to at least one node in C?

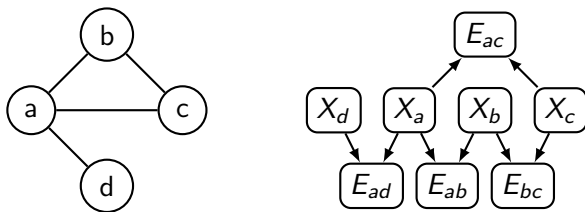# DMPE^+-2-∞(Prop($\vee$)) is NP-hard

Figure: A Bayesian network (on the right) that solves VERTEX COVER with the graph on the left.

▶ Construct a Bayesian network containing nodes X_v, $v \in V$, associated with the probabilistic assessment $\Pr(X_v = \mathrm{TRUE}) = 1/4$ and nodes $E_{uv}, (u, v) \in A$, associated with the logical equivalence $E_{uv} \Leftrightarrow X_u \vee X_v$. By forcing observations $E_{uv} = \mathrm{TRUE}$ for every edge (u, v), we guarantee that such edge will be covered (at least one of the parents must be TRUE).

DMPE^{+}-2-∞(Prop($\vee$)) is NP-hard
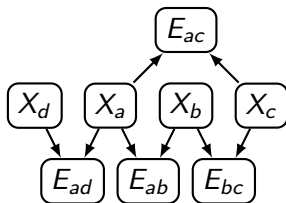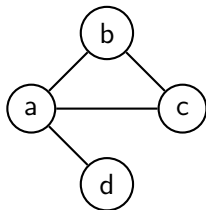
- Let $C(\mathbf{v}) = \{v : X_v = \text{TRUE}\}$. Then $\mathrm{Pr}(\mathbf{X} = \mathbf{v}, \mathbf{E} = \text{TRUE}) =$

$$= \prod_{v \in C(\mathbf{v})} \mathrm{Pr}(X_v = \text{TRUE}) \prod_{v \notin C(\mathbf{v})} (1 - \mathrm{Pr}(X_v = \text{TRUE})) = \frac{3^{n-|C|}}{4^n}$$

  which is greater than or equal to $3^{n-k}/4^n$ if and only if $C(\mathbf{v})$ is a vertex cover of cardinality at most k.

Some easy cases

Theorem
DMPE$^+$-2-∞(Prop($\oplus$)) *is in P.*

Proof.
The operation XOR $\oplus$ is supermodular, hence the logarithm of the joint probability is also supermodular and the MPE problem can be solved efficiently [Nemhauser et al. 1978]. $\qquad\square$

Some easy cases

Theorem
DMPE$^+$-2-∞(Prop($\wedge$)) and DMPE^0-2-∞(Prop($\vee$)) are in P.

Proof.
For solving DMPE$^+$-2-∞(Prop($\wedge$)), propagate the evidence up the network by making all ancestors of evidence nodes take on value true, which is the only configuration assigning positive probability. Now, for both MPE$_d^+$-2-∞(Prop($\wedge$)) and MPE$_d^0$-2-∞(Prop($\vee$)), the procedure is as follows. Assign values of the remaining root nodes as to maximize their marginal probability independently (i.e., for every non-determined root node X select $X = \text{TRUE}$ if and only if $\Pr(X = \text{TRUE}) \geq 1/2$). Assign the remaining internal nodes the single value which makes their probability non-zero. This can be done in polynomial time and achieves the maximum probability. $\qquad\square$

Some DMAP^0-2-∞ might be easier than $\mathrm{NP}^{\mathrm{PP}}$

Theorem
DMAP^0-*2*-$\infty(\mathrm{Prop}(\wedge))$ *and* DMAP^0-*2*-$\infty(\mathrm{Prop}(\vee))$ *are PP-hard.*

We reduce MAJ-$2\mathrm{MONSAT}$, which is PP-hard [Roth 1996], to DMAP^0_d-2-$\infty(\mathrm{Prop}(\vee))$:

Input: *A 2-CNF formula* $\phi(X_1, \ldots, X_n)$ *with m clauses where all literals are positive.*
Question: *Does the majority of the assignments to* $X_1, \ldots, X_n$ *satisfy* ϕ*?*

The transformation is as follows. For each Boolean variable X_i, build a root node such that $\Pr(X_i = 1) = 1/2$. For each clause C_j with literals x_a and x_b (note that literals are always positive), build a disjunction node Y_{ab} with parents X_a and X_b, that is, $Y_{ab} \Leftrightarrow X_a \vee X_b$. Now set all non-root nodes to be MAP nodes, that is, $\mathbf{M} = \{Y_{ab}\}_{\forall ab}$.
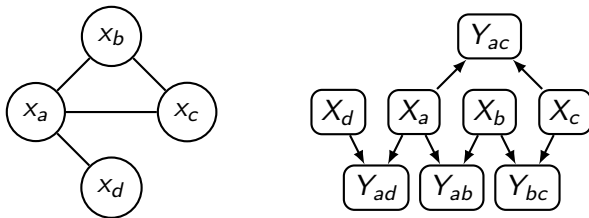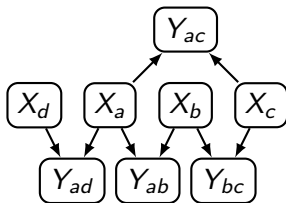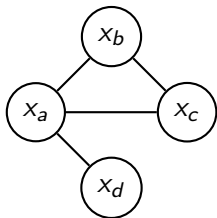

Figure: A Bayesian network (on the right) and the clauses as edges (on the left).

Suppose that variables in **M** are chosen to be **m** where at least one of them is set to state FALSE. This implies that both parents of this conjunction node must be set to state FALSE too, and thus the joint probability $\Pr(\mathbf{m}) \leq \frac{1}{2} \cdot \frac{1}{2} = \frac{1}{4} < \frac{1}{2}$ (and the answer will be *NO*). So with MAP variables fixed to TRUE, at least one of the parents of them must be set to TRUE too. These are exactly the satisfying assignments, so the problem becomes that of counting the number of satisfying assignments, which will answer *YES* if and only if the majority of assignments satisfy the formula.

DMAP-2-2 is NP-complete

Pertinence is immediate, as a certificate (assignment to the explanation variables) can be verified in polynomial time (network has treewidth bounded).

Hardness is shown using a reduction from PARTITION, which is NP-hard and can be stated as follows: *given a set of m positive integers $s_1, \ldots, s_m$, is there a set $I \subset A = \{1, \ldots, m\}$ such that $\sum_{i \in I} s_i = \sum_{i \in A \setminus I} s_i$?* All the input is encoded using $b > 0$ bits. Denote $S = \frac{1}{2} \sum_{i \in A} s_i$ and call *even partition* a subset $I \subset A$ that achieves $\sum_{i \in I} s_i = S$. To solve PARTITION, one may consider the rescaled problem (dividing every element by S), so as $v_i = \frac{s_i}{S} \leq 2$ are the elements and the goal is a partition I with sum equals to 1.

DMAP-2-2 is NP-complete
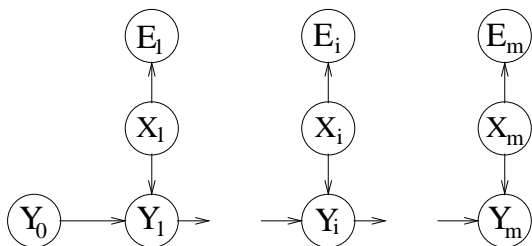
- $X_i \in \mathbf{X}$ has uniform distribution.
- $\Pr(E_i = \text{TRUE} \mid X_i = \text{FALSE}) = 1$ and
  $\Pr(E_i = \text{TRUE} \mid X_i = \text{TRUE}) = 2^{-v_i}$ for every E_i.
- Y_0 has $\Pr(Y_0 = \text{TRUE}) = 1$. For $Y_i \in \mathbf{Y}$:
  $\Pr(Y_i = \text{TRUE} \mid Y_{i-1} = \text{TRUE}, X_i = \text{TRUE}) = 2^{-v_i}$,
  $\Pr(Y_i = \text{TRUE} \mid Y_{i-1} = \text{TRUE}, X_i = \text{FALSE}) = 1$,
  $\Pr(Y_i = \text{TRUE} \mid Y_{i-1} = \text{FALSE}, X_i) = 0$.

DMAP-2-2 is NP-complete

- $X_i \in \mathbf{X}$ has uniform distribution.
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  $\Pr(E_i = \text{TRUE} \mid X_i = \text{TRUE}) = 2^{-v_i}$ for every E_i.
- Y_0 has $\Pr(Y_0 = \text{TRUE}) = 1$. For $Y_i \in \mathbf{Y}$:
  $\Pr(Y_i = \text{TRUE} \mid Y_{i-1} = \text{TRUE}, X_i = \text{TRUE}) = 2^{-v_i}$,
  $\Pr(Y_i = \text{TRUE} \mid Y_{i-1} = \text{TRUE}, X_i = \text{FALSE}) = 1$,
  $\Pr(Y_i = \text{TRUE} \mid Y_{i-1} = \text{FALSE}, X_i) = 0$.

- By construction, for any given $\mathbf{x}$:

$$\Pr(Y_m = \text{TRUE} \mid \mathbf{x}) = \Pr(\mathbf{E} = \mathbf{e} \mid \mathbf{x}) = \prod_{i \in I} 2^{-v_i},$$

where $\mathbf{e}$ are all TRUE, and $I \subseteq A$ is the set of indices of the elements such that X_i is at the state TRUE.

DMAP-2-2 is NP-complete

- Denote $\mathbf{t} = \prod_{i \in I} 2^{-v_i}$. Then

$$\begin{aligned} \Pr(\mathbf{x}, \mathbf{e}, Y_m = \textsc{false}) &= \Pr(Y_m = \textsc{false} \mid \mathbf{x})\Pr(\mathbf{x}, \mathbf{e}) \\ &= \Pr(\mathbf{x})\Pr(\mathbf{e} \mid \mathbf{x})\left(1 - \Pr(Y_m = \textsc{false} \mid \mathbf{x})\right) \\ &= \frac{1}{2^m}\mathbf{t}(1 - \mathbf{t}) \end{aligned}$$

- $\Pr(\mathbf{x}, \mathbf{e}, Y_m = \textsc{false}) = \frac{1}{2^m}\mathbf{t}(1 - \mathbf{t})$ is a concave quadratic function on $0 \leq \mathbf{t} \leq 1$ (while $\mathbf{t}$ is a function of $\mathbf{x}$) with maximum at 2^{-1} such that $\mathbf{t}(1 - \mathbf{t})$ monotonically increases when $\mathbf{t}$ approaches one half (from both sides).

$$\frac{1}{2^m}\mathbf{t}(1 - \mathbf{t}) = \frac{1}{2^m}2^{-\sum_{i \in I} v_i}\left(1 - 2^{-\sum_{i \in I} v_i}\right),$$

which achieves the maximum of $\frac{1}{2^m}2^{-1}(1 - 2^{-1}) = \frac{1}{2^{m+2}}$ if and only if $\sum_{i \in I} v_i = 1$, that is, if there is an even partition.

DMAP-2-2 is NP-complete

So the reduction is:

- Build a Bayesian network with that graph and the following parameters:
  - $X_i \in \mathbf{X}$ has uniform distribution.
  - $\Pr(E_i = \text{TRUE} \mid X_i = \text{FALSE}) = 1$ and
    $\Pr(E_i = \text{TRUE} \mid X_i = \text{TRUE}) = 2^{-s_i/S}$ for every E_i.
  - Y_0 has $\Pr(Y_0 = \text{TRUE}) = 1$. For $Y_i \in \mathbf{Y}$:
    $\Pr(Y_i = \text{TRUE} \mid Y_{i-1} = \text{TRUE}, X_i = \text{TRUE}) = 2^{-s_i/S}$,
    $\Pr(Y_i = \text{TRUE} \mid Y_{i-1} = \text{TRUE}, X_i = \text{FALSE}) = 1$,
    $\Pr(Y_i = \text{TRUE} \mid Y_{i-1} = \text{FALSE}, X_i) = 0$.

- Then DMAP-2-2 is

$$\Pr(\mathbf{x}, \mathbf{e}, Y_m = \text{FALSE}) \geq \frac{1}{2^{m+2}}$$

if and only if $\sum_{i \in I} \frac{s_i}{S} = 1 = \sum_{i \notin I} \frac{s_i}{S}$, that is, if there is an even partition.
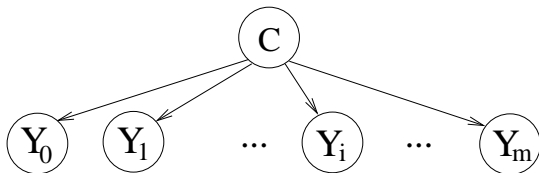
DMAP-2-2 is NP-complete

So the reduction is:

- Build a Bayesian network with that graph and the following parameters:
  - $X_i \in \mathbf{X}$ has uniform distribution.
  - $\Pr(E_i = \text{TRUE} \mid X_i = \text{FALSE}) = 1$ and $\Pr(E_i = \text{TRUE} \mid X_i = \text{TRUE}) = 2^{-s_i/S}$ for every E_i.
  - Y_0 has $\Pr(Y_0 = \text{TRUE}) = 1$. For $Y_i \in \mathbf{Y}$:
    $\Pr(Y_i = \text{TRUE} \mid Y_{i-1} = \text{TRUE}, X_i = \text{TRUE}) = 2^{-s_i/S}$,
    $\Pr(Y_i = \text{TRUE} \mid Y_{i-1} = \text{TRUE}, X_i = \text{FALSE}) = 1$,
    $\Pr(Y_i = \text{TRUE} \mid Y_{i-1} = \text{FALSE}, X_i) = 0$.

- Then DMAP-2-2 is

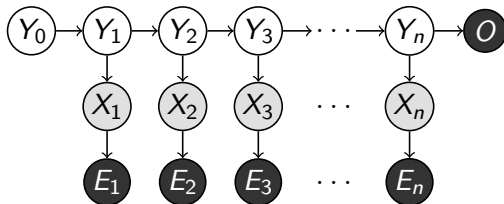$$\Pr(\mathbf{x}, \mathbf{e}, Y_m = \text{FALSE}) \geq \frac{1}{2^{m+2}}$$

if and only if $\sum_{i \in I} \frac{s_i}{S} = 1 = \sum_{i \notin I} \frac{s_i}{S}$, that is, if there is an even partition.

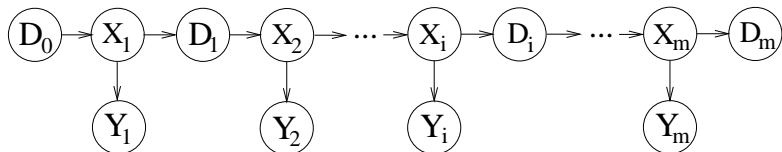- **What is wrong with this proof?** (It can be fixed, we won't)

DMAP-∞-1 is NP-complete

DMAP-3-1 (and multiple observations) is NP-complete

DMAP-5-1 (and single observation) is NP-complete

Markov Random Fields

Results in general can be translated to MRFs:

- **Hardness of problems in MRFs**: take the moralized Bayesian network as starting point of the proofs and the conditional probability functions as MRF's potentials.

- **Easiness of problems in MRFs:** build a Bayesian network creating an additional binary node for each potential (this node is the child of all nodes involved in the potential) and set the probability function for the true state of the new node as the potential of the MRF. Set evidence in these nodes to true, accordingly.

Open questions

There are many, some related to these slides:

- DMAP^0-2-∞(Prop($\wedge$)) and DMAP^0-2-∞(Prop($\vee$)) (known to be PP-hard)

- DMAP-2-1 (known to be in NP; interestingly, $\text{D}(\text{MIN})\text{AP}$-2-1 can be shown to be NP-complete)

- DMAP^0-c-1 for some $c < n$ (known to be in NP)

Some known results for the optimization version

- MAP-∞-*tw* is also shown not to be in Poly-APX [Park & Darwiche 2004]. (Unless P=NP) It is shown that there is no polynomial time approximation that can achieve a 2^{b^ε}-factor approximation, for $0 < \varepsilon < 1$, b is the length of the input.

- It is NP-hard to approximate MAP-∞-1 to any factor 2^{b^ε}.

- There is a *Fully Polynomial Time Approximation Scheme* (FPTAS) for MAP-*c*-*tw* (both *tw* and *c* do not depend on the input).

- MPE also cannot be approximable to any factor (that is, it is not even in Exp-APX), unless one assumes that $\Pr(\mathbf{E} = \mathbf{e}) > 0$.

Thanks

Thank you for your attention. Further questions:
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