Logic and Bayesian Networks

Part 5: Applications

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NICTA and ANU

Applications

- Medical diagnosis
- Genetic linkage analysis
- Probabilistic planning

Constructing Bayesian Networks

- Define network variables & their domains
  - Query & evidence variables, usually from problem statement
  - Intermediary variables, harder to determine
- Define network structure (edges)
  - What variables are *direct causes* of X?
- Define network CPTs
  - Determined objectively from problem statement
  - Reflection of subjective beliefs
  - Estimated from data

Medical Diagnosis

- Flu characterized by fever and body aches, can be associated with chilling and sore throat
- Cold associcated with chilling, can cause sore throat
- Tonsillitis (inflammation of tonsils) causes sore throat, can be associated with fever

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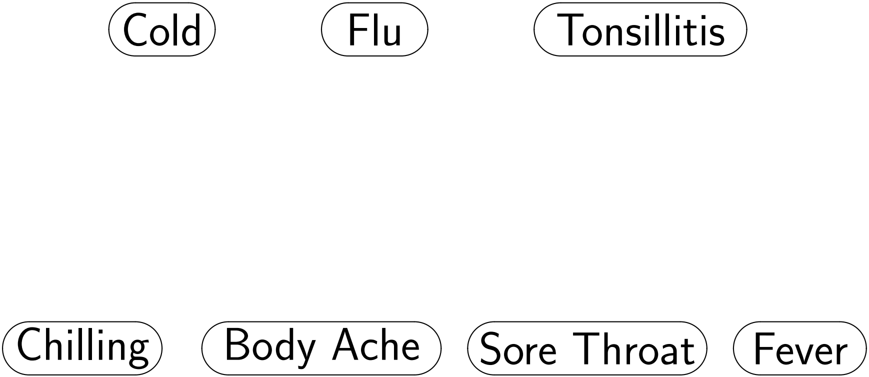
- Query, evidence, intermediary variables?
- Flu, cold, tonsillitis; chilling, body ache, sore throat, fever

Medical Diagnosis: Network Structure



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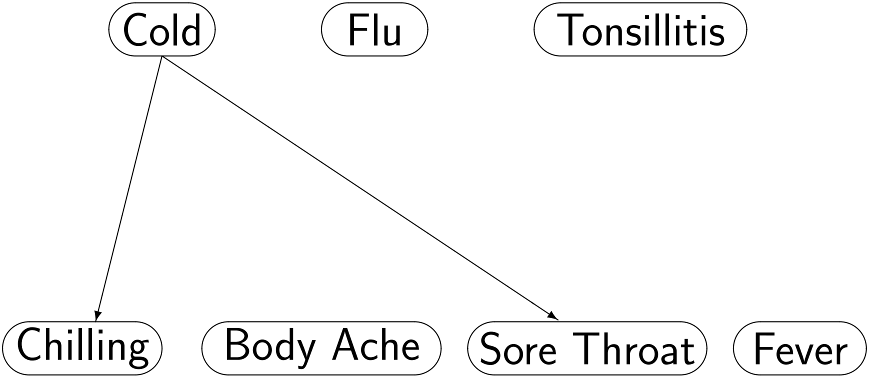

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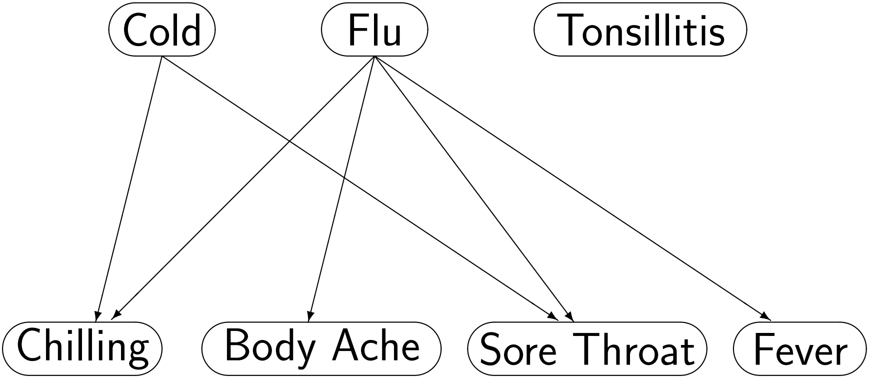

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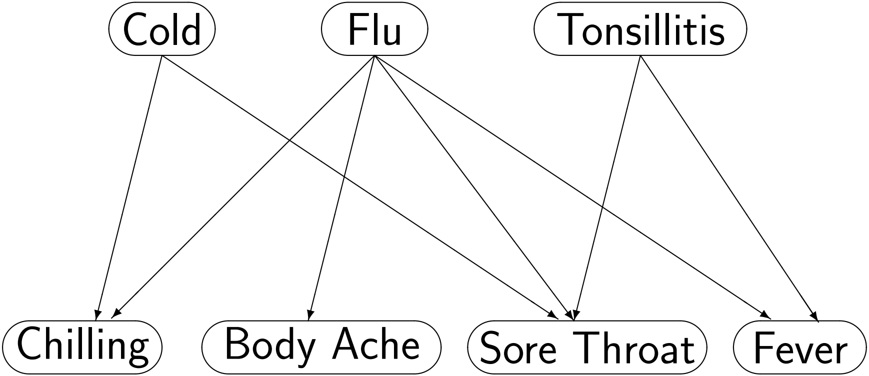
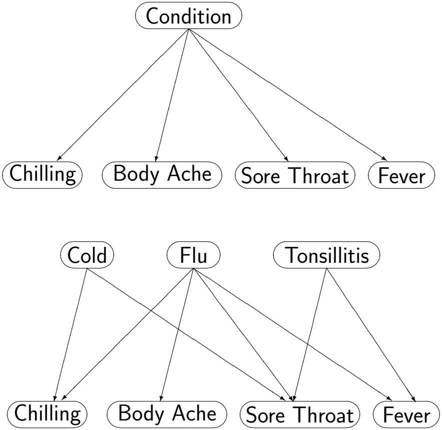


Medical Diagnosis: Naive Bayes



Condition: normal, cold, flu, tonsillitis

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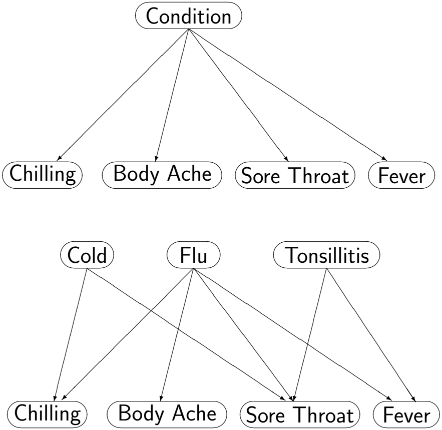

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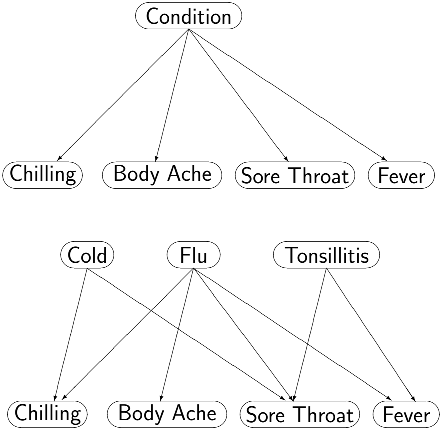

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- Cold ⇒ Fever & Sore Throat independent

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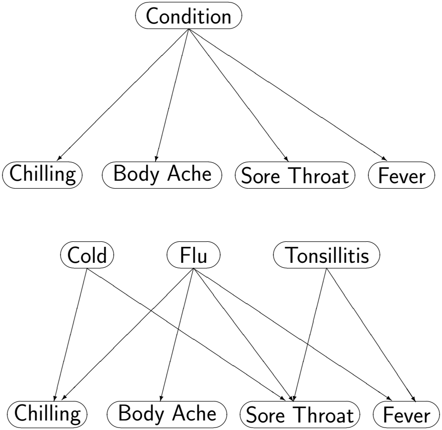

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- Cold $\Rightarrow$ Fever & Sore Throat independent
- Body Ache $\Rightarrow$ Flu $\uparrow$ $\Rightarrow$ Cold & Tonsillitis $\downarrow$

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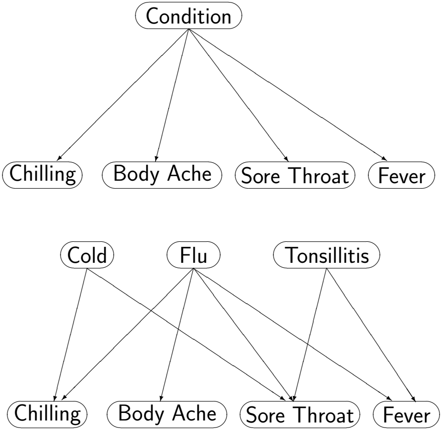

Condition: normal, cold, flu, tonsillitis

Model inaccuracy: *single fault* assumption

- Cold $\Rightarrow$ Fever & Sore Throat independent
- Body Ache $\Rightarrow$ Flu $\uparrow$ $\Rightarrow$ Cold & Tonsillitis $\downarrow$
- No Fever $\Rightarrow$ Cold $\uparrow$

Medical Diagnosis: CPTs

From medical experts, based on known stats or subjective beliefs

- CPTs for conditions (roots of graph): $\Pr(\mathit{condition})$ without knowledge of symptoms
- CPTs for symptoms: $\Pr(\mathit{Chilling}|\mathit{Cold}, \mathit{Flu})$ etc

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Estimated directly from medical records

Case	Cold	Flu	Tonsillitis	Chilling	Body Ache	Sore Throat	Fever
1	T	F	?	T	F	F	F
2	F	T	F	T	T	F	T
3	?	?	T	F	?	T	F
...	...						

Maximize $$\prod_{i=1}^{N} \Pr(\mathbf{d}_i)$$

Medical Diagnosis: Queries

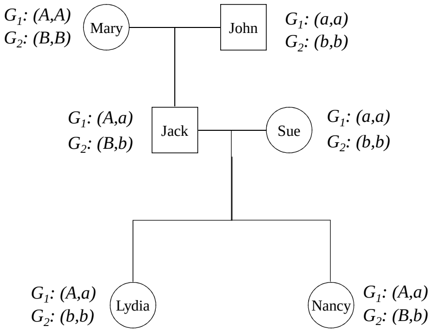
Given symptoms (chilling, body ache, sore throat, fever), pose MAP query on Cold, Flu, & Tonsillitis

Reduces to MPE if evidence covers all four symptoms

Genetic Linkage Analysis

- Goal: map genes onto chromosome (i.e., determine location of genes on chromosome)
- Useful for detecting and predicting diseases
- Input: pedigree, observed genotype/phenotype

Pedigree



- Genes: G_1, G_2
- Gene has *alleles* (states): $G_1(A, a)$, $G_2(B, b)$
- Individual carries two alleles per gene, from father & mother
- *Genotype*: collection of alleles of individual, composed of two *haplotypes*
- *Phenotype*: observable traits of individual

Genotype and Phenotype

Genotype	Phenotype
A/A	blood type A
A/B	blood type AB
A/O	blood type A
B/B	blood type B
B/O	blood type B
O/O	blood type O

- Deterministic
- However, not in reverse direction: Blood type A $\Rightarrow$ A/A or A/O

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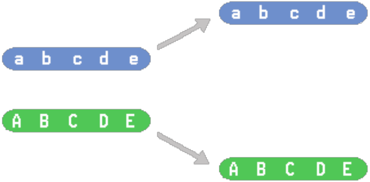
Genotype	Phenotype
H/H	healthy
H/D	healthy
D/D	ill with probability .9

- Not deterministic
- *Penetrance*: Pr(phenotype | genotype)

Recombination



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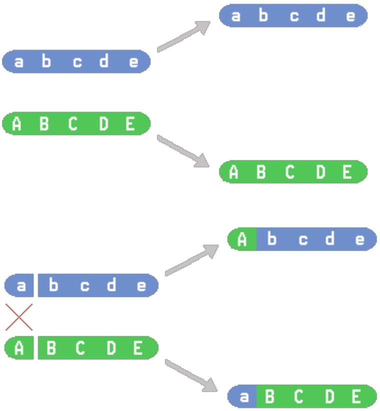

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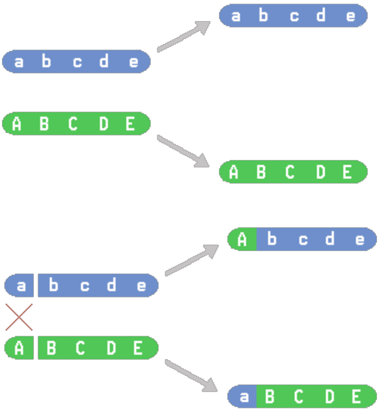
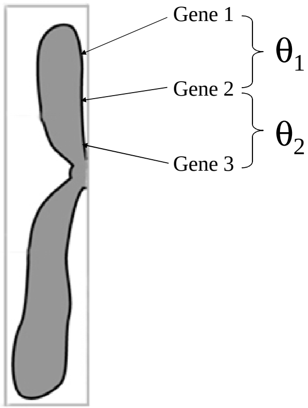
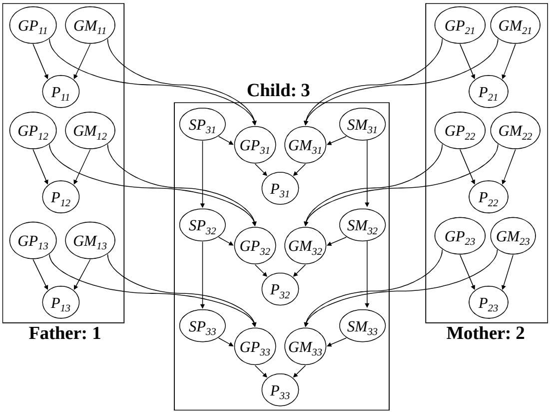


- Independent genes: *recombination frequency* $\theta = 1/2$
- *Linked* genes: $\theta < 1/2$
- Closer on chromosome $\approx$ more linked
- Genetic linkage analysis: Estimate distances between, and hence locations of, genes on chromosome based on data containing recombination information

Recombination Frequencies

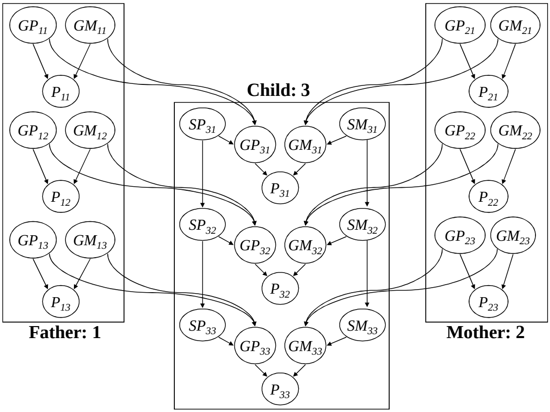


Pedigree as Bayesian Network



- 3 genes: GP_{i1}/GM_{i1}, GP_{i2}/GM_{i2}, GP_{i3}/GM_{i3}
- Phenotype: P_{i1}, P_{i2}, P_{i3}
- Selectors: SP_{31}/SM_{31}, SP_{32}/SM_{32}, SP_{33}/SM_{33}

Pedigree as Bayesian Network

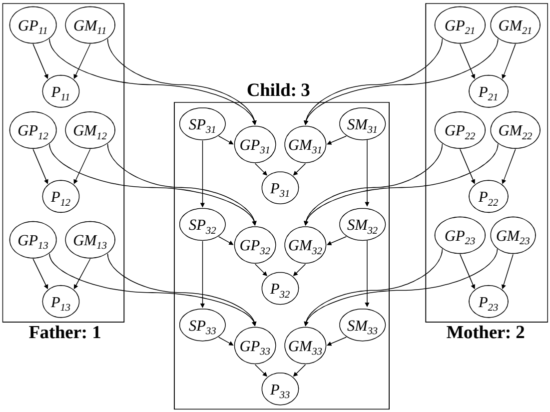


Encoding recombination frequencies

SP_{31}	SP_{32}	$\theta_{sp_{32} \mid sp_{31}}$
p	p	$1-\theta_{12}$
p	m	θ_{12}
m	p	θ_{12}
m	m	$1-\theta_{12}$

Priors on GP/GM of *founders* obtained from population stats

Pedigree as Bayesian Network



Given $\mathbf{e}$ on subset of genotype (GP, GM) and phenotype (P), $\Pr(\mathbf{e})$ indicates likelihood of $\hat{\theta}$ (recombination frequencies)

Can compute preferred $\hat{\theta}$, or search for most likely $\hat{\theta}$

Given $\hat{\theta}$ and relative order of genes, determine their locations on chromosome

Probabilistic Planning

- Planning: Find plan (sequence of actions) to go from initial to goal state
- Probabilistic planning: In uncertain domains, find plan to reach goal with high probability

Slippery Griper

Goal: Block painted and held, gripper clean

Probabilistic initial state

- Block not painted, not held
- Gripper clean, but dry with probability 0.7

Probabilistic action effects

- Paint: Paints block w/p 1; makes gripper dirty w/p 1 if it holds block, w/p 0.1 if not
- Pick-up: Succeeds w/p 0.5 if gripper wet, 0.95 if gripper dry
- Dry: Dries wet gripper w/p 0.8; doesn't affect dry gripper

Conformant Probabilistic Planning

- Probabilistic initial state and action effects
- Conformant: Action effects not observable (can't decide next action by observing environment)
- Need straight-line plan with max probability of success, for given horizon (number of steps)
- Example 2-step plan: [paint, pickup] (succeeds with probability 0.7335)

Brute-force Approach

- Compute success probability for all plans of length one
- Given success probabilities of plans of length i, compute probability of success for plans of length $i + 1$
- Iterate to planning horizon n
- Pick n-step plan with max success probability
- Exponential in planning horizon

Planning Domain as Bayesian Network

- Suppose *action variable* A_i represents action taken at step i
- Planning $\Leftrightarrow \max \Pr(\text{goal}|A_1, \ldots, A_n)$
  $\Leftrightarrow \max \Pr(\text{goal}, A_1, \ldots, A_n)$

Planning Domain as Bayesian Network

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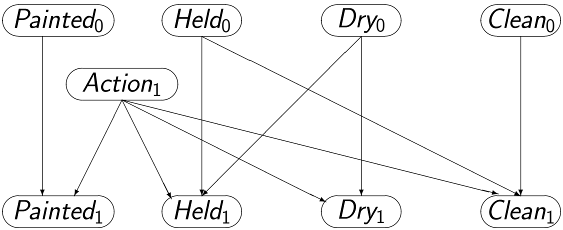
- Planning $\Leftrightarrow \max \Pr(\text{goal}|A_1, \ldots, A_n)$
  $\Leftrightarrow \max \Pr(\text{goal}, A_1, \ldots, A_n)$
- How to define Bayesian network?

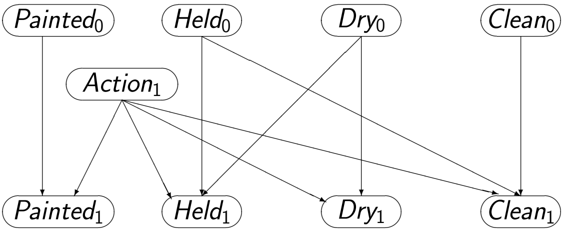
Planning Domain as Bayesian Network



Paint: Paints block with probability 1

$Painted_0$	$Action_1$	$Painted_1$	Pr(.)
F	paint	T	1
T	$*$	T	1
...	...	...	...

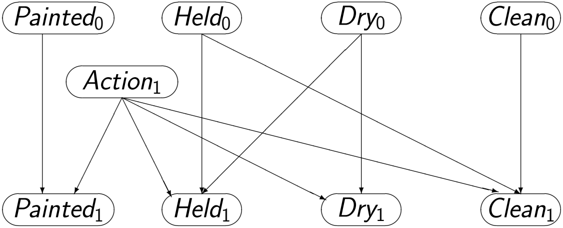
Planning Domain as Bayesian Network



Paint: Makes gripper dirty w/p 1 if it holds block, w/p 0.1 if not

$Clean_0$	$Held_0$	$Action_1$	$Clean_1$	Pr(.)
T	T	paint	F	1
T	F	paint	F	.1
F	$*$	$*$	F	1
...	...	...	...	...

Planning Domain as Bayesian Network

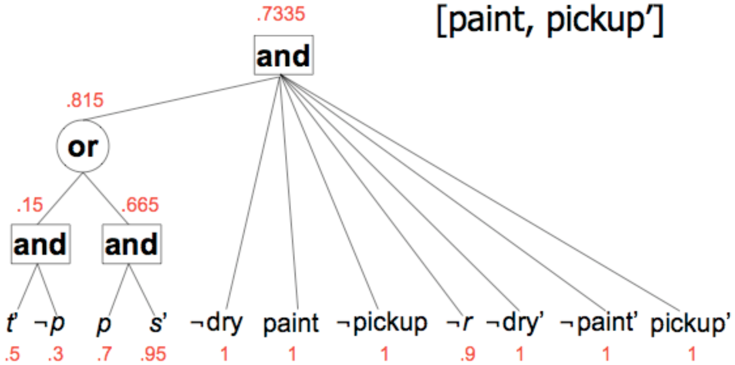


Add one layer per time step

Initial state $\rightarrow$ priors on $Painted_0, Held_0, Dry_0, Clean_0$
Goal state $\rightarrow$ evidence $\mathbf{e}$ on $Painted_n, Held_n, Dry_n, Clean_n$
Optimal plan $\rightarrow$ $\operatorname{argmax} \Pr(\mathbf{e}, A_1, \ldots, A_n)$

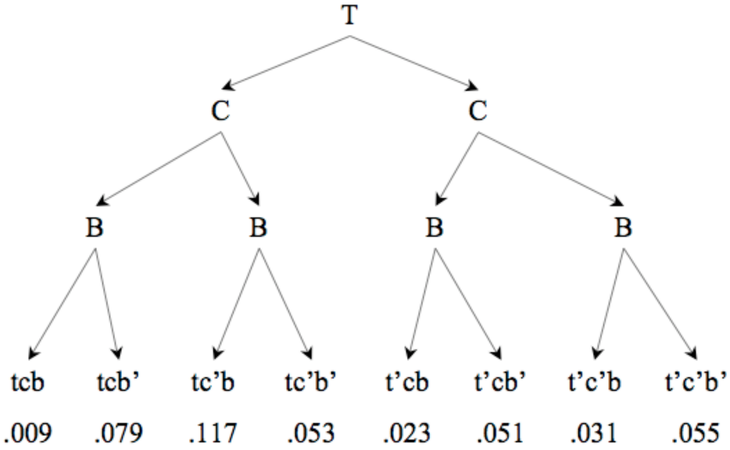
Priors on $Action_i$ irrelevant

Plan Assessment

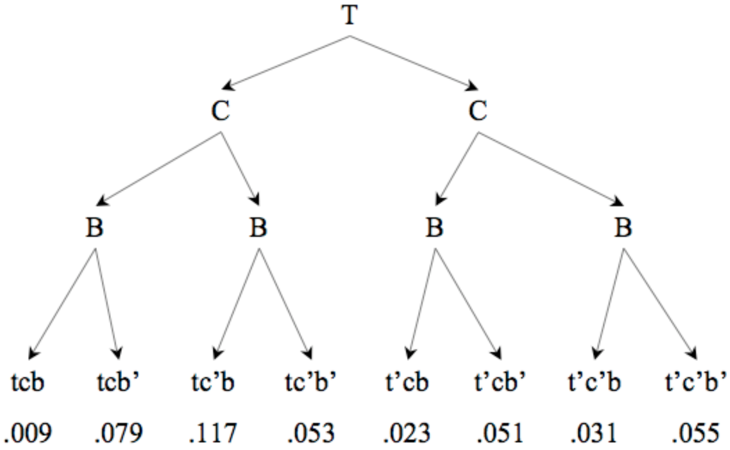


$\Pr(\mathbf{e}, A_1, \ldots, A_n)$

Plan Search

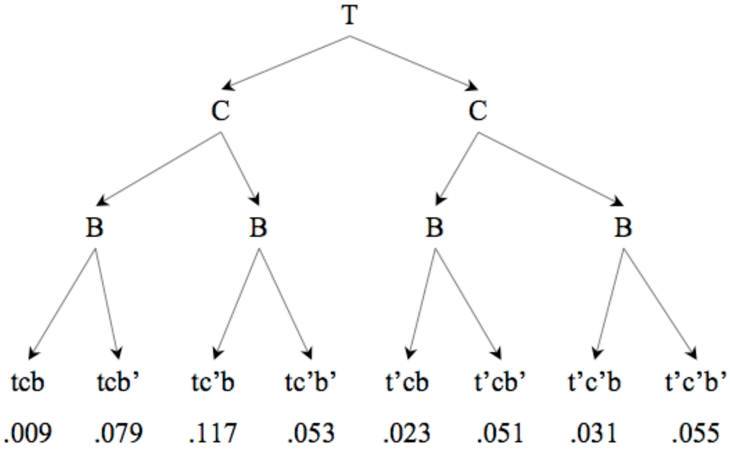

T
C
C
B
B
B
B
tcb
tcb'
tc'b
tc'b'
t'cb
t'cb'
t'c'b
t'c'b'
.009
.079
.117
.053
.023
.051
.031
.055

Plan Search



$$\max_{C,B} \Pr(\mathbf{e}, t', C, B) \leq$$

Plan Search



$$\max_{C,B} \Pr(\mathbf{e}, t', C, B) \leq .101$$

Upper Bounds

$$\max_{A_{k+1},\ldots,A_n} \Pr(\mathbf{e}, a_1, \ldots, a_k, A_{k+1}, \ldots, A_n)$$

Upper Bounds

$$\max_{A_{k+1},\ldots,A_n} \Pr(\mathbf{e}, a_1, \ldots, a_k, A_{k+1}, \ldots, A_n)$$

Some OR-nodes are decision nodes on $A_{k+1}, \ldots, A_n$

Turn these into max (instead of $+$)

Root of arithmetic circuit gives upper bound

Summary of the Course

- Bayesian networks as compact representations of probability distributions
- Inference by logical encoding and compilation to arithmetic circuits
- Inference by variable elimination
- Applications