Representations of the Joint Probability Distribution

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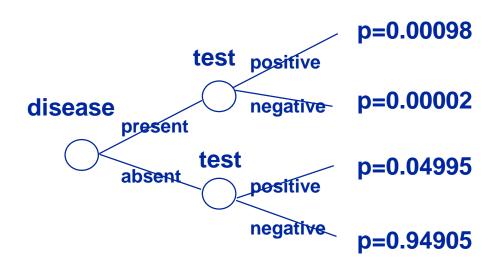
Probabilistic knowledge representations

- A probabilistic (Bayesian) model encodes the joint probability distribution over its variables.
- Knowledge of the joint probability distribution is sufficient to derive any marginal and conditional probability over the model's variables.



Probability trees

The simplest and quite natural graphical representation of a joint probability distribution over discrete variables

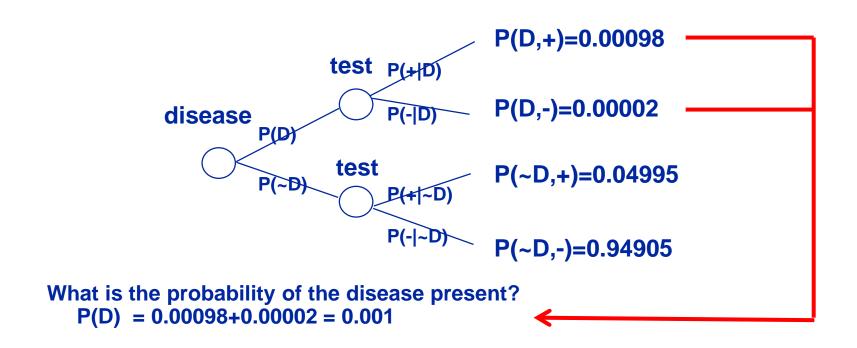


P(disease present
$$\land$$
 test positive) = P(D \cap +) = 0.00098
P(disease present \land test negative) = P(D \cap +) = 0.00002
P(disease absent \land test positive) = P(\sim D \cap +) = 0.04995
P(disease absent \land test negative) = P(\sim D \cap +) = 0.94905



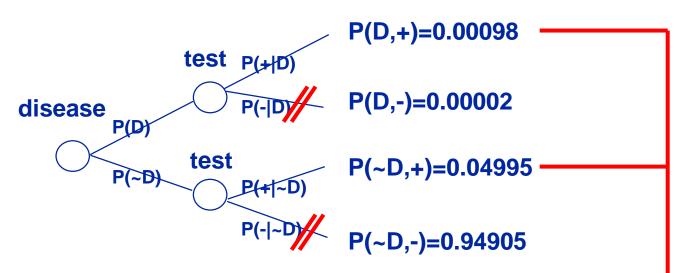
Computation in probability trees

We can calculate any marginal or conditional probability distribution from the joint probability distribution encoded in the tree.



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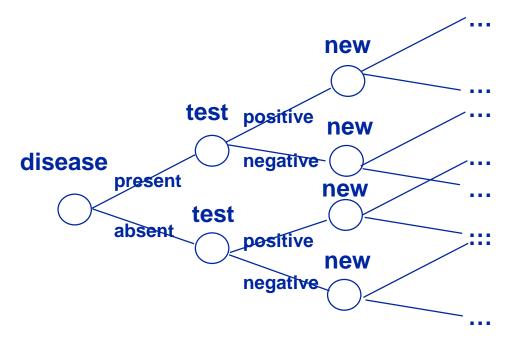
What is the probability of the disease present given a positive test result? Observation of a positive test result makes some of the branches of the tree impossible. What we need to do is just renormalize the remaining, possible (i.e., those that are compatible with the evidence) branches!

 $P(D|+) = 0.00098/(0.00098+0.04995) \approx 0.01924$



What is wrong with probability trees?

Trees grow exponentially with the number of variables



For n binary variables, we will have 2^n branches. When n=10, the total number of branches is 1,024 When n=11, it is 2,048

. . .

When n=20, it is 1,048,576 (which is a lot ⊕)



Great idea (only 30-40 years old)

Use independences among variables in the joint probability distribution to reduce the number of parameters in its representation!

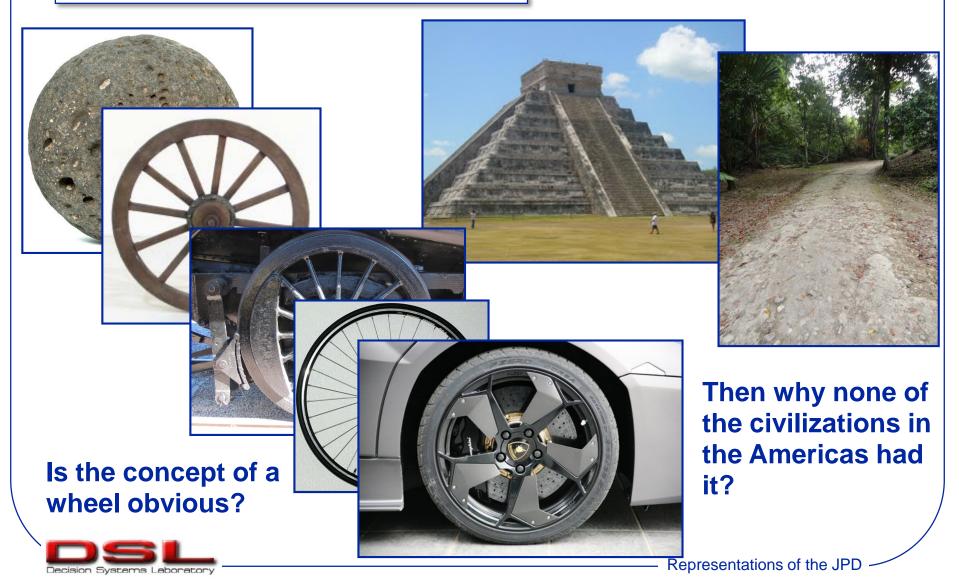
Due to seminal work on probabilistic independence by A. Philip Dawid and Judea Pearl







All brilliant ideas are obvious (once we have them ③)



Factorability of the joint probability distribution

Every joint probability distribution can be factorized, i.e., rewritten as a product of prior and conditional probability distributions of each of the model's variables

$$f(X_1, X_2, ..., X_n) = f(X_1 \mid X_2, X_3, ..., X_n) f(X_2 \mid X_3, ..., X_n) ...$$
$$f(X_{n-2} \mid X_{n-1}, X_n) f(X_{n-1} \mid X_n) f(X_n)$$

e.g., four variables (a, b, c, d), we have:

P(A,B,C,D)=P(A|B,C,D) P(B|C,D) P(C|D) P(D)
P(A,B,C,D)=P(A|B,C,D) P(B|C,D) P(D|C) P(C)
...
P(A,B,C,D)=P(B|A,C,D) P(D|A,C) P(A|C) P(C)

There are n! different directed graphs corresponding to various ways of factorizing a joint probability distribution over n variables.

For n=4, we have 4!=24 different factorizations.



Factorability of the joint probability distribution

- Any factorization can be simplified if we consider independencies among variables.
- Those factorizations that become the simplest are better than others in terms of efficiency of representation.

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e.g., suppose we know that B\(\perp D\), D\(\perp A\), and A\(\perp C\)

We can simplify

P(A,B,C,D)=P(B|A,C,D) P(D|A,C) P(A|C) P(C)

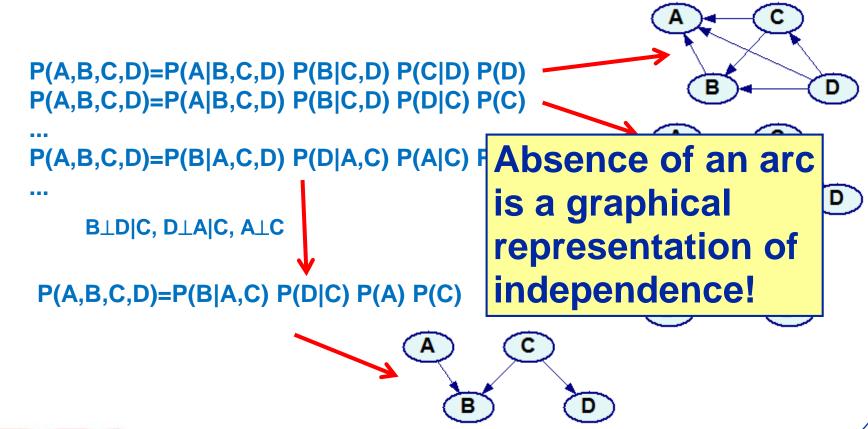
into

P(A,B,C,D)=P(B|A,C) P(D|C) P(A) P(C)
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Bayesian networks

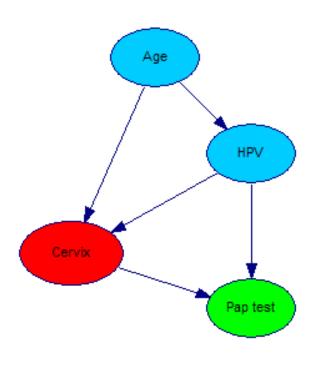
- This underlies the very idea of Bayesian networks.
- We draw a directed graph with arc from the conditioning variables to the variables in the factorization.





Bayesian networks

A Bayesian network [Pearl 1988] is an acyclic directed graph consisting of:



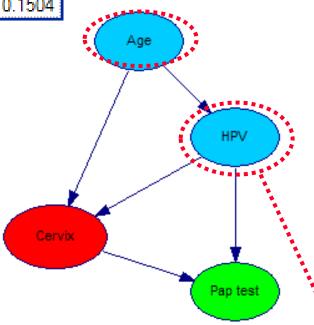
- The qualitative part, encoding a domain's variables (nodes) and the probabilistic (usually causal) influences among them (arcs).
- The quantitative part, encoding the joint probability distribution over these variables.



Bayesian networks: Numerical parameters

þ	a1_below_20	0.0416
	a2_20_29	0.2012
	a3_29_45	0.3079
	a4_45_60	0.2989
	a5_60_up	0.1504

Prior probability distribution tables for nodes without predecessors (Age)



Please note that each absence of an arc (i.e., each independence modeled) is means one less dimension in the corresponding conditional probability table!

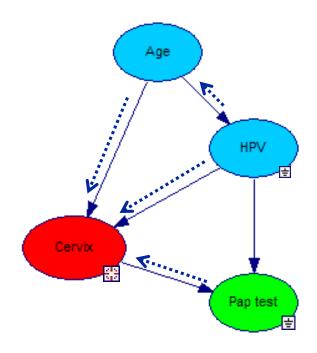
Conditional probability distributions tables for nodes with predecessors (HPV, Pap test, Cervix)

Age		a1_below_20	a2_20_29	a3_29_45	a4_45_60	a5_60_up
	NA	0.8652	0.8387	0.7904	0.8055	0.8851
	Negative	0.069	0.0901	0.1782	0.1765	0.1012
▶	Positive	0.0613	0.0667	0.0282	0.0142	0.0082
	Qns	0.0045	0.0045	0.0032	0.0038	0.0055



Reasoning in Bayesian networks

The most important type of reasoning in Bayesian networks is updating the probability of a hypothesis (e.g., a diagnosis) given new evidence (e.g., medical findings, test results).



P(CxCa | HPV=positive, HSIL=yes)

Example:

What is the probability of invasive cervical cancer in a (female) patient with high grade dysplasia with a history of HPV infection?

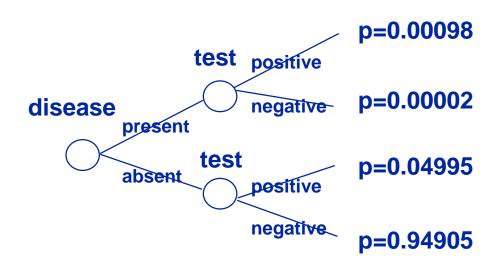
Generally, the more sparse the structure of your network, the fewer parameters, the faster inference in the Bayesian network.

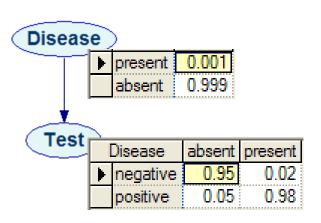


Probability trees and Bayesian networks

probability tree

Bayesian network





The two representations are equivalent But, when there are independences in the domain, Bayesian networks are much, much more efficient!

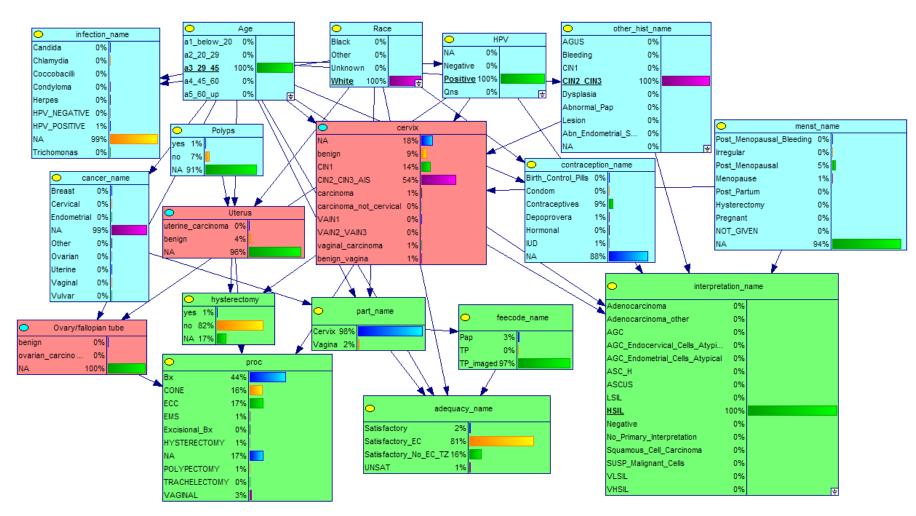


HEPAR II Model History of Gallstones Amylase Surgery in Choledocholithotomy Hepatotoxic Diabetes Sex hospitalization the past medications Flatulence Fat intolerance Upper Age abdominal pain Obesity Injections in History of History of the past transfusion Pressure in right History of viral alcohol abuse upper quadrant hepatitis Reactive hepatitis Toxic hepatitis Hepatic steatosis Hepatic fibrosis present 2% present 4% Carcinoma absent 98% present 10% present 4% absent 96% present 6% absent 90% absent 96% absent 94% Functional hyperbilir. Chronic hepatitis Cirrhosis Total PBC active 13% present 7% decompensate 5% triglycerides present 38% persistent 5% absent 93% Anorexia compensate Presence of absent 62% 82% antibodies to absent HBcAg in blood Presence of ALT Pain in right Nausea GGTP hepatitis B upper quadrant Total ESR AST Presence of antigen in blood cholesterol antibodies to Platelet Hepatomegaly HCV in blood count Antimytochondrial Alcohol Alkaline Fatigue antibodies intolerance phosphatase Enlarged Hepatalgia Presence of A TIPE spleen Joints hepatitis B surface swelling Total bilirubin antigen in blood proteins Hepatic Haemorrhagie Edema LE cells encephalopathy diathesis Vascular Musculo-skeletal pain spiders Presence of antibodies to Irregular Increased Liver palms Yellowing of HBsAg in blood Itching liver edge liver density Blood urea the skin Irregular liver Jaundice Impaired Ascites Albumin consciousness

70 variables; 2,139 numerical parameters (instead of over 2⁷⁰≈ 10²¹!)



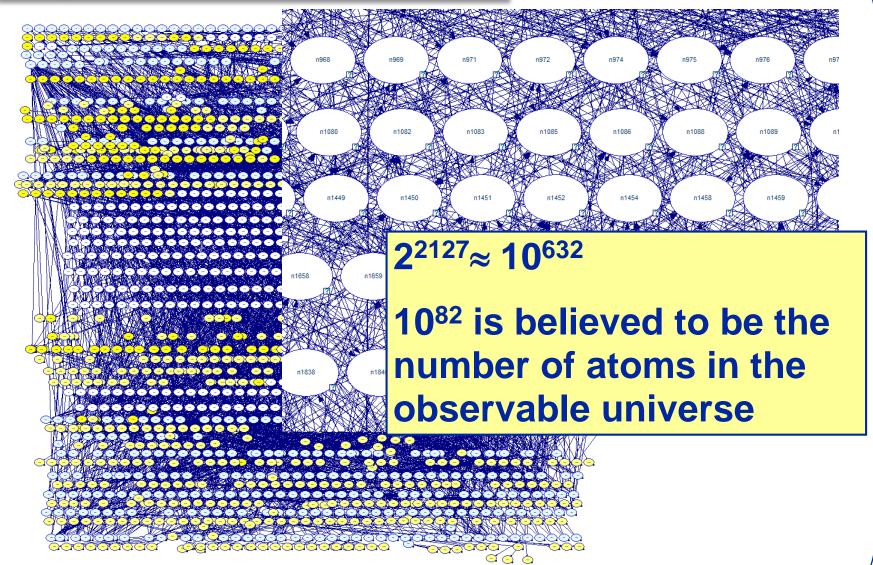
Pittsburgh Cervical Cancer Screening Model



[Oniśko et al.] 18 variables; 295,163 numerical parameters (instead of over 10¹³!)



Diagnosis of Diesel locomotives



[Przytula et al.] 2,127 variables; 12,351 numerical parameters (instead of 2²¹²⁷!)



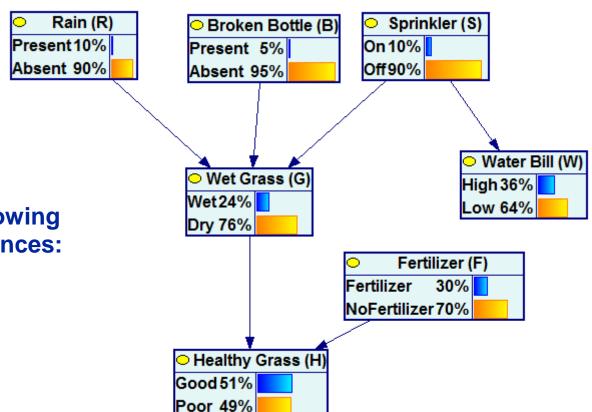
Independences: Markov condition

- Allows to read back dependences and independences from the graph.
- Informally speaking, it is an assumption that ties directed probabilistic graphs with probability, specifying how a directed graphs represents independence.
- A node is independent of its non-descendants given its predecessors.



Markov condition: Example

P(H,G,W,R,B,S,F)=P(H|G,F) P(G|R,B,S) P(W|S) P(R) P(B) P(S) P(F)



This graph implies the following (conditional) independences:

RIB, RIS, BIS, RIF, BIF, SIF RIW, BIW, WIF, GIF RIH|G, BIH|G, SIH|G, WIH|G WI*|S RIW|G,S, BIW|G,S



Equation-based systems and graphical models

classsize = (nstud * cload) / (nfac * tload) **Core equations** facsal = (oinc + tuition * nstud) / (nfac * (1 + overh)) ← stratio = nstud / nfac cload = 15tload = 6**Equations for exogenous variables**

nstud = 22102

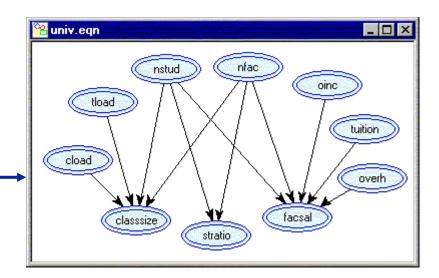
nfac = 3006

oinc = 30000000

tuition = 12000

overh = 0.48

Together they determine the structure of the model





Equation-based systems: Reversibility of causal ordering

```
classsize = (nstud * cload) / (nfac * tload)
facsal = (oinc + tuition * nstud) / (nfac * (1 + overh))
stratio = nstud / nfac
cload = 15
tload = 6
nstud = 22102
                     stratio = 10
```

Setting *stratio* to be exogenous at the expense of *nfac*

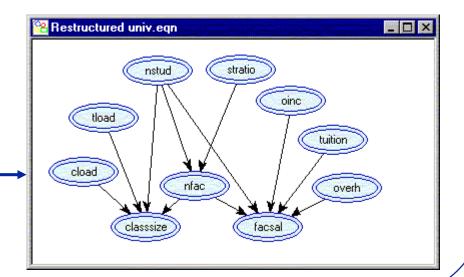
oinc = 30000000

tuition = 12000

overh = 0.48

The new model structure

Explication of the asymmetries due to Herb Simon (early 1950s)





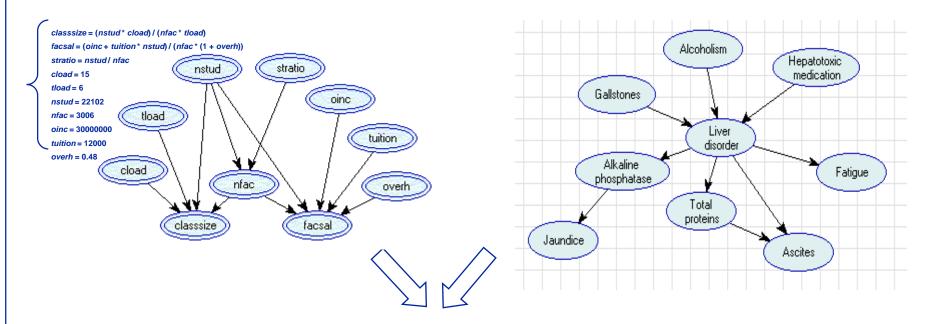
Advantages of directed graphs

- May be built to reflect the causal structure of a model (helps with obtaining <u>insight</u> into the problem)
- Can accommodate representation of uncertainty
- Can be reconfigured as needed
- Have sound theoretical foundations: We are dealing here with probability theory and decision theory
- We can talk (almost) the same language with statisticians, philosophers, and scientists



Family of directed graphs (a bigger picture)

(a.k.a. "influence nets," "causal diagrams," etc.)



Both, systems of equations and joint probability distributions can be pictured by acyclic directed graphs.





