

The class site is at

<http://www.stats.ox.ac.uk/~evans/gms/>

You'll find

- lecture notes;
- slides;
- problem sheets;
- data sets.

There will be four problem sheets and four associated classes.

Details will be available on the website.

SC6/SM9 Graphical Models

Michaelmas Term, 2021

Robin Evans

evans@stats.ox.ac.uk
Department of Statistics
University of Oxford

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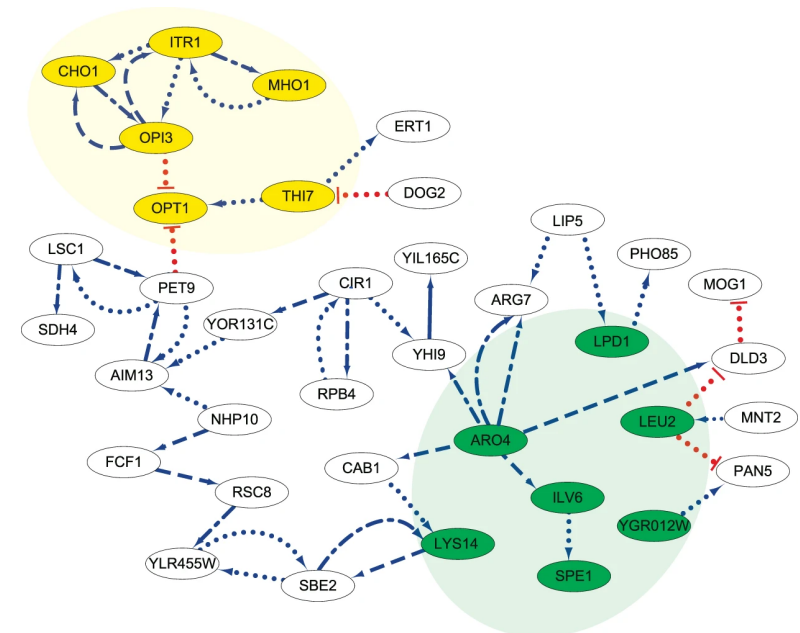
Books

These books might be useful.

- Lauritzen (1996). *Graphical Models*, OUP.
- Wainwright and Jordan (2008). *Graphical Models, Exponential Families, and Variational Inference*. (Available online).
- Pearl (2009). *Causality*, (3rd edition), Cambridge.
- Koller and Friedman (2009), *Probabilistic Graphical Models: Principles and Techniques*, MIT Press.
- Agresti (2002). *Categorical Data Analysis*, (2nd edition), John Wiley & Sons.

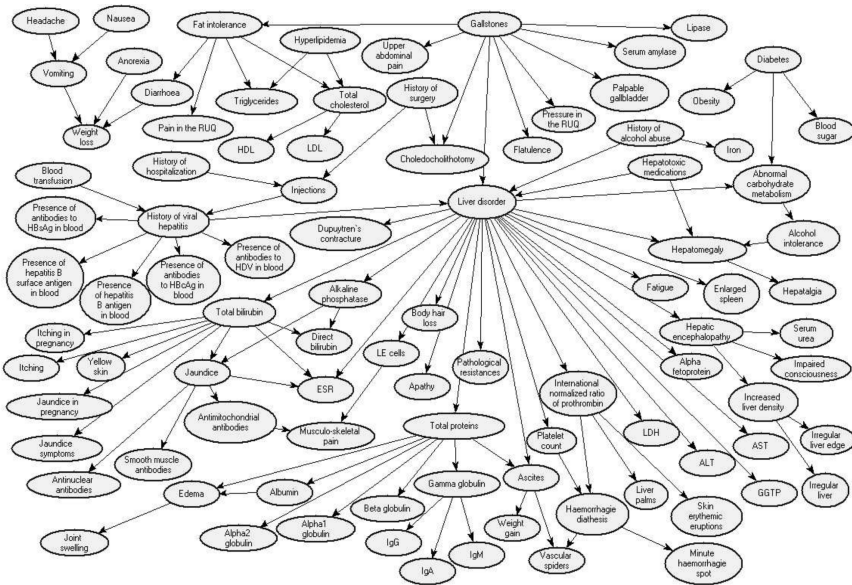
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Gene Regulatory Networks



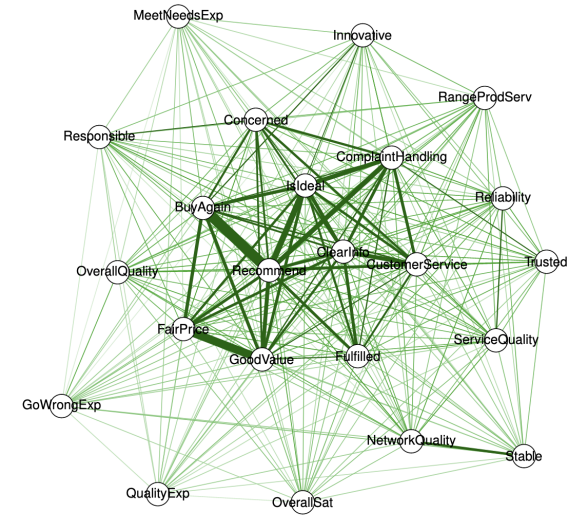
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Medical Diagnosis



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Customer Satisfaction



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Main Issues

There are two main problems with large data sets that we will consider in this course:

- statistical;
 - we need to predict outcomes from scenarios that have never been observed (i.e., we need a model).
- computational:
 - we can't store probabilities for all combinations of variables;
 - even if we could, we can't sum/integrate them to find a marginal or conditional probability:

$$P(X = x) = \sum_{\mathbf{y}} P(X = x, \mathbf{Y} = \mathbf{y}).$$

Our solution will be to impose nonparametric structure, in the form of **conditional independences**.

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Conditional Independence

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Simpson's Paradox

Death Penalty?	Defendant's Race	
	White	Black
Yes	53	15
No	430	176

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Simpson's Paradox

Victim's Race	Death Penalty?	Defendant's Race	
		White	Black
White	Yes	53	11
	No	414	37
Black	Yes	0	4
	No	16	139

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Morals

Let:

- D be an indicator that the death penalty was imposed;
- V be an indicator for the race of the victim;
- R be an indicator for the race of the defendant.

By changing the numbers only very slightly, it is easy to obtain either:

$$D \perp R \quad \text{and} \quad D \not\perp R | V,$$

or

$$D \not\perp R \quad \text{and} \quad D \perp R | V.$$

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Exponential Families

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Contingency Tables: Some Notation

We will consider multivariate systems of vectors $X_V \equiv (X_v : v \in V)$ for some set $V = \{1, \dots, p\}$.

Write $X_A \equiv (X_v : v \in A)$ for any $A \subseteq V$.

We assume that each $X_v \in \{1, \dots, d_v\}$ (usually $d_v = 2$).

If we have n i.i.d. observations write

$$X_V^{(i)} \equiv (X_1^{(i)}, \dots, X_p^{(i)})^T, \quad i = 1, \dots, n.$$

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Marginal Table

Victim's Race	Death Penalty?	Defendant's Race	
		White	Black
White	Yes	53	11
	No	414	37
Black	Yes	0	4
	No	16	139

If we sum out the Victim's race...

Death Penalty?	Defendant's Race	
	White	Black
Yes	53	15
No	430	176

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Contingency Tables: Some Notation

We typically summarize categorical data by counts:

	heart attack	
	Y	N
Y	Y	N
N	N	N
N	N	N
Y	N	N
⋮	⋮	⋮

	heart attack	
	Y	N
no aspirin	28	656
aspirin	18	658

Write

$$n(x_V) = \sum_{i=1}^n \mathbb{1}\{X_1^{(i)} = x_1, \dots, X_p^{(i)} = x_p\}$$

A **marginal table** only counts some of the variables.

$$n(x_A) = \sum_{i=1}^n \mathbb{1}\{X_a^{(i)} = x_a : a \in A\} = \sum_{x_{V \setminus A}} n(x_A, x_{V \setminus A}).$$

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Contingency Tables

The death penalty data is on the class website.

```
> getwd()
[1] "/Users/robinevans/Dropbox/Teaching/Graphical Models"
> deathpen <- read.table("deathpen.txt", header=TRUE)
> deathpen

  DeathPen Defendant Victim freq
1      Yes      White  White   53
2      No      White  White  414
3      Yes      Black  White   11
4      No      Black  White   37
5      Yes      White  Black    0
6      No      White  Black   16
7      Yes      Black  Black    4
8      No      Black  Black  139
```

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Contingency Tables

We can fit models on it in R:

```
> summary(glm(freq ~ Victim*Defendant + Victim*DeathPen,
+             family=poisson, data=deathpen))
```

Coefficients:

	Estimate	Std. Error
(Intercept)	4.93737	0.08459
VictimWhite	-1.19886	0.16812
DefendantWhite	-2.19026	0.26362
DeathPenYes	-3.65713	0.50641
VictimWhite:DefendantWhite	4.46538	0.30408
VictimWhite:DeathPenYes	1.70455	0.52373

Residual deviance: 5.394 on 2 degrees of freedom

(So $p \approx 0.07$ in hypothesis test of model fit.)

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Contingency Tables

If we fit the marginal table over the races of Victim and Defendant, the parameters involving 'Defendant' are the same.

```
> summary(glm(freq ~ Victim*Defendant,
+             family=poisson, data=deathpen))
```

Coefficients:

	Estimate	Std. Error
(Intercept)	4.26970	0.08362
VictimWhite	-1.09164	0.16681
DefendantWhite	-2.19026	0.26360
VictimWhite:DefendantWhite	4.46538	0.30407

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Contingency Tables

We can also check that the subsets of $S = \{\text{Victim}\}$ are given by the other condition we had:

$$\lambda_W = \lambda_W^{AS} + \lambda_W^{BS} - \lambda_W^S.$$

```
> out1 <- glm(freq ~ Victim*Defendant, family=poisson,
+             data=deathpen)$coef[1:2]
> out2 <- glm(freq ~ Victim*DeathPen, family=poisson,
+             data=deathpen)$coef[1:2]
> out <- glm(freq ~ Victim, family=poisson,
+            data=deathpen)$coef[1:2]
>
> out1 + out2 - out
```

```
(Intercept) VictimWhite
 4.937366   -1.198864
```

Indeed these match the coefficients from the larger model.

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Poisson-Multinomial Equivalence

The following distributions are equivalent.

1. Independent Poisson random variables:

$$X_i \sim \text{Poisson}(\mu_i) \quad \text{for } i = 1, \dots, k.$$

2. One Poisson random variable $N \sim \text{Poisson}(\mu)$ where $\mu = \sum_i \mu_i$; and a multinomial

$$(X_1, \dots, X_k)^T | \{N = n\} \sim \text{Multinom}(n, (\pi_1, \dots, \pi_k)^T),$$

where $\pi_i = \mu_i / \mu$.

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Poisson-Multinomial Equivalence

We can see this by comparing the likelihoods.

The Poisson likelihood is

$$\begin{aligned} L(\mu_1, \dots, \mu_k; x_1, \dots, x_k) &= \prod_{i=1}^k e^{-\mu_i} \mu_i^{x_i} = \prod_{i=1}^k e^{-\mu \pi_i} \mu^{x_i} \pi_i^{x_i} \\ &= \mu^{\sum_i x_i} e^{-\mu \sum_i \pi_i} \prod_{i=1}^k \pi_i^{x_i} \\ &= \mu^n e^{-\mu} \prod_{i=1}^k \pi_i^{x_i} \\ &= L(\mu; n) \cdot L(\pi_1, \dots, \pi_k; x_1, \dots, x_k \mid n). \end{aligned}$$

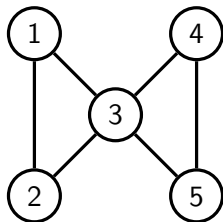
Hence the distributions are equivalent.

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Undirected Graphical Models

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Undirected Graphs

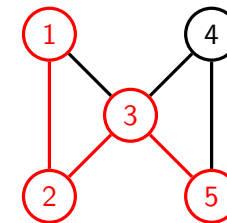


$$V = \{1, 2, 3, 4, 5\}$$

$$E = \{\{1, 2\}, \{1, 3\}, \{2, 3\}, \{3, 4\}, \{3, 5\}, \{4, 5\}\}.$$

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Paths



Paths:

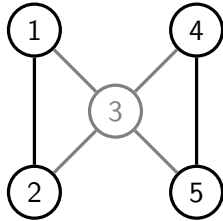
$$\pi_1 : 1 - 2 - 3 - 5$$

$$\pi_2 : 3$$

Note that paths may consist of one vertex and no edges.

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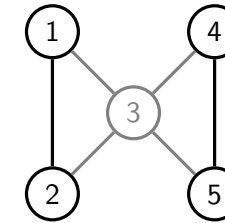
Induced Subgraph



The **induced subgraph** $\mathcal{G}_{\{1,2,4,5\}}$ drops any edges that involve $\{3\}$.

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Separation

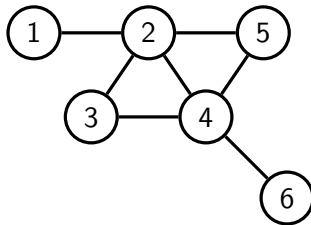


All paths between $\{1, 2\}$ and $\{4, 5\}$ pass through $\{3\}$.

Hence $\{1, 2\}$ and $\{4, 5\}$ are **separated** by $\{3\}$.

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Cliques and Running Intersection



Cliques:

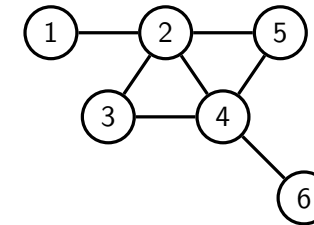
$\{1, 2\}$ $\{2, 3, 4\}$ $\{2, 4, 5\}$ $\{4, 6\}$.

Separator sets:

\emptyset $\{2\}$ $\{2, 4\}$ $\{4\}$.

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Cliques and Running Intersection



A different ordering of the cliques:

$\{2, 3, 4\}$ $\{2, 4, 5\}$ $\{4, 6\}$ $\{1, 2\}$.

Separator sets:

\emptyset $\{2, 4\}$ $\{4\}$ $\{2\}$.

Any ordering works in this case as long $\{1, 2\}$ and $\{4, 6\}$ aren't the first two entries.

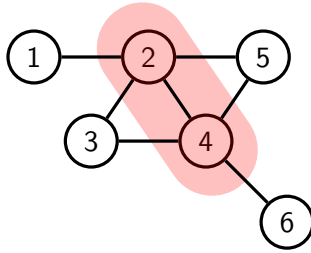
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Estimation

Given a decomposition of the graph, we have an associated conditional independence: e.g. $(\{1, 3\}, \{2, 4\}, \{5, 6\})$ suggests

$$X_1, X_3 \perp\!\!\!\perp X_5, X_6 \mid X_2, X_4$$

$$p(x_{123456}) \cdot p(x_{24}) = p(x_{1234}) \cdot p(x_{2456}).$$



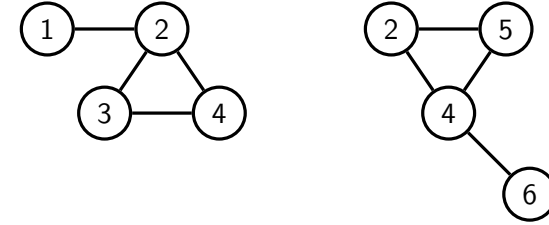
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Estimation

Given a decomposition of the graph, we have an associated conditional independence: e.g. $(\{1, 3\}, \{2, 4\}, \{5, 6\})$ suggests

$$X_1, X_3 \perp\!\!\!\perp X_5, X_6 \mid X_2, X_4$$

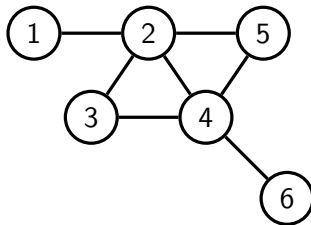
$$p(x_{123456}) \cdot p(x_{24}) = p(x_{1234}) \cdot p(x_{2456}).$$



And $p(x_{1234})$ and $p(x_{2456})$ are Markov with respect to \mathcal{G}_{1234} and \mathcal{G}_{2456} respectively.

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Estimation



Repeating this process on each subgraph we obtain:

$$p(x_{123456}) \cdot p(x_{24}) \cdot p(x_2) \cdot p(x_4) = p(x_{12}) \cdot p(x_{234}) \cdot p(x_{245}) \cdot p(x_{46}).$$

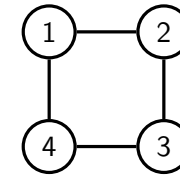
i.e.

$$p(x_{123456}) = \frac{p(x_{12}) \cdot p(x_{234}) \cdot p(x_{245}) \cdot p(x_{46})}{p(x_{24}) \cdot p(x_2) \cdot p(x_4)}.$$

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Non-Decomposable Graphs

But can't we do this for any factorization?



No! Although

$$p(x_{1234}) = \psi_{12}(x_{12}) \cdot \psi_{23}(x_{23}) \cdot \psi_{34}(x_{34}) \cdot \psi_{14}(x_{14}),$$

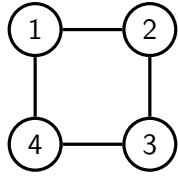
the ψ s are constrained by the requirement that

$$\sum_{x_{1234}} p(x_{1234}) = 1.$$

There is no nice representation of the ψ_C s in terms of p .

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Non-Decomposable Graphs



If we 'decompose' without a complete separator set then we introduce constraints between the factors:

$$p(x_{1234}) = p(x_1 | x_2, x_4) \cdot p(x_3 | x_2, x_4),$$

but how to ensure that $X_2 \perp\!\!\!\perp X_4 | X_1, X_3$?

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Iterative Proportional Fitting

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The Iterative Proportional Fitting Algorithm

```

function IPF(collection of margins  $q(x_{C_i})$ )
  set  $p(x_V)$  to uniform distribution;
  while  $\max_i \max_{x_{C_i}} |p(x_{C_i}) - q(x_{C_i})| > \text{tol}$  do
    for  $i$  in  $1, \dots, k$  do
      update  $p(x_V)$  to  $p(x_{V \setminus C_i} | x_{C_i}) \cdot q(x_{C_i})$ ;
    end for
  end while
  return distribution  $p$  with margins  $p(x_{C_i}) \approx q(x_{C_i})$ .
end function
  
```

If any distribution satisfying $p(x_{C_i}) = q(x_{C_i})$ for each $i = 1, \dots, k$ exists, then the algorithm converges to the **unique distribution** with those margins and which is Markov with respect to the graph with cliques C_1, \dots, C_k .

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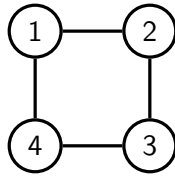
Some Data

		$X_2 = 0$		$X_2 = 1$	
		$X_1 = 0$	1	0	1
$X_4 = 0$	$X_3 = 0$	9	9	0	8
	1	6	4	4	3
$X_4 = 1$	0	22	0	2	6
	1	5	3	10	5

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Margins

Suppose we want to fit the 4-cycle model:



The relevant margins are:

$n(x_{12})$	$X_2 = 0$	1
$X_1 = 0$	42	16
1	16	22

$n(x_{23})$	$X_3 = 0$	1
$X_2 = 0$	40	18
1	16	22

$n(x_{34})$	$X_4 = 0$	1
$X_3 = 0$	26	30
1	17	23

$n(x_{14})$	$X_4 = 0$	1
$X_1 = 0$	19	39
1	24	14

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Start with a Uniform Table

		$X_2 = 0$		$X_2 = 1$	
		$X_1 = 0$	1	0	1
$X_4 = 0$	$X_3 = 0$	6	6	6	6
	1	6	6	6	6
$X_4 = 1$	0	6	6	6	6
	1	6	6	6	6

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Set Margin X_1, X_2 to Correct Value

		$X_2 = 0$		$X_2 = 1$	
		$X_1 = 0$	1	0	1
$X_4 = 0$	$X_3 = 0$	10.5	4	4	5.5
	1	10.5	4	4	5.5
$X_4 = 1$	0	10.5	4	4	5.5
	1	10.5	4	4	5.5

Replace

$$p^{(i+1)}(x_1, x_2, x_3, x_4) = p^{(i)}(x_1, x_2, x_3, x_4) \cdot \frac{n(x_1, x_2)}{p^{(i)}(x_1, x_2)}$$

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Set Margin X_2, X_3 to Correct Value

		$X_2 = 0$		$X_2 = 1$	
		$X_1 = 0$	1	0	1
$X_4 = 0$	$X_3 = 0$	14.48	5.52	3.37	4.63
	1	6.52	2.48	4.63	6.37
$X_4 = 1$	0	14.48	5.52	3.37	4.63
	1	6.52	2.48	4.63	6.37

Replace

$$p^{(i+1)}(x_1, x_2, x_3, x_4) = p^{(i)}(x_1, x_2, x_3, x_4) \cdot \frac{n(x_2, x_3)}{p^{(i)}(x_2, x_3)}$$

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Set Margin X_3, X_4 to Correct Value

		$X_2 = 0$		$X_2 = 1$	
		$X_1 = 0$	1	0	1
$X_4 = 0$	$X_3 = 0$	13.45	5.12	3.13	4.3
	1	5.54	2.11	3.94	5.41
$X_4 = 1$	0	15.52	5.91	3.61	4.96
	1	7.49	2.86	5.33	7.32

Replace

$$p^{(i+1)}(x_1, x_2, x_3, x_4) = p^{(i)}(x_1, x_2, x_3, x_4) \cdot \frac{n(x_3, x_4)}{p^{(i)}(x_3, x_4)}$$

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Set Margin X_1, X_2 to Correct Value

		$X_2 = 0$		$X_2 = 1$	
		$X_1 = 0$	1	0	1
$X_4 = 0$	$X_3 = 0$	9.82	7.27	2.28	6.1
	1	4.02	2.97	2.86	7.63
$X_4 = 1$	0	18.87	3.92	4.39	3.29
	1	9.18	1.91	6.52	4.89

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Set Margin X_1, X_4 to Correct Value

		$X_2 = 0$		$X_2 = 1$	
		$X_1 = 0$	1	0	1
$X_4 = 0$	$X_3 = 0$	9.81	7.26	2.28	6.09
	1	4.04	2.99	2.87	7.67
$X_4 = 1$	0	18.94	3.93	4.41	3.3
	1	9.15	1.9	6.5	4.87

Replace

$$p^{(i+1)}(x_1, x_2, x_3, x_4) = p^{(i)}(x_1, x_2, x_3, x_4) \cdot \frac{n(x_1, x_4)}{p^{(i)}(x_1, x_4)}$$

Notice that sum of first column is now 41.94.

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Eventually:

Waiting for this process to converge leads to the MLE:

		$X_2 = 0$		$X_2 = 1$	
		$X_1 = 0$	1	0	1
$X_4 = 0$	$X_3 = 0$	10.07	7.41	2.29	6.23
	1	3.87	2.85	2.77	7.51
$X_4 = 1$	0	18.7	3.83	4.26	3.22
	1	9.36	1.91	6.68	5.04

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Gaussian Graphical Models

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Multivariate Data

```
> library(ggm)
> data(marks)
> dim(marks)

[1] 88 5

> head(marks, 8)

  mechanics vectors algebra analysis statistics
1         77      82     67         67         81
2         63      78     80         70         81
3         75      73     71         66         81
4         55      72     63         70         68
5         63      63     65         70         63
6         53      61     72         64         73
7         51      67     65         65         68
8         59      70     68         62         56
```

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Multivariate Data

```
> sapply(marks, mean)

 mechanics   vectors   algebra   analysis statistics
      39.0       50.6       50.6       46.7       42.3

> cor(marks)

      mechanics vectors algebra analysis statistics
mechanics  1.000  0.553  0.547  0.409  0.389
vectors    0.553  1.000  0.610  0.485  0.436
algebra     0.547  0.610  1.000  0.711  0.665
analysis    0.409  0.485  0.711  1.000  0.607
statistics  0.389  0.436  0.665  0.607  1.000
```

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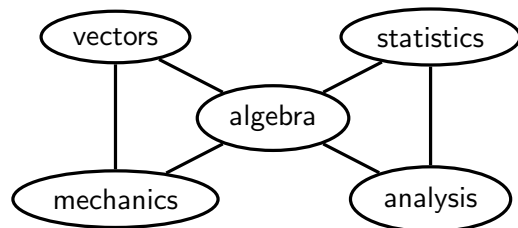
Multivariate Data

```
> conc <- solve(cov(marks)) # concentration matrix
> round(1000*conc, 2)

      mechanics vectors algebra analysis statistics
mechanics    5.24  -2.44  -2.74    0.01   -0.14
vectors     -2.44  10.43  -4.71   -0.79   -0.17
algebra     -2.74  -4.71  26.95   -7.05   -4.70
analysis     0.01  -0.79  -7.05    9.88   -2.02
statistics  -0.14  -0.17  -4.70   -2.02    6.45
```

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Undirected Graphs



	mech	vecs	alg	anlys	stats
mechanics	5.24	-2.43	-2.72	0.01	-0.15
vectors	-2.43	10.42	-4.72	-0.79	-0.16
algebra	-2.72	-4.72	26.94	-7.05	-4.70
analysis	0.01	-0.79	-7.05	9.88	-2.02
statistics	-0.15	-0.16	-4.70	-2.02	6.45

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The Multivariate Gaussian Distribution

Let $X_V \sim N_p(0, \Sigma)$, where $\Sigma \in \mathbb{R}^{p \times p}$ is a symmetric positive definite matrix.

$$\log p(x_V; \Sigma) = -\frac{1}{2} \log |\Sigma| - \frac{1}{2} x_V^T \Sigma^{-1} x_V + \text{const.}$$

The log-likelihood for Σ is

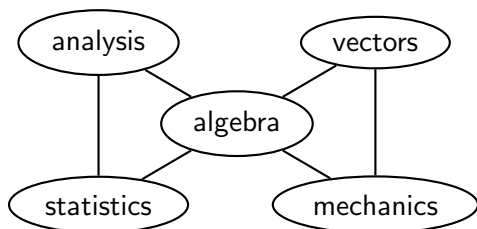
$$l(\Sigma) = -\frac{n}{2} \log |\Sigma| - \frac{n}{2} \text{tr}(S \Sigma^{-1})$$

where S is the sample covariance matrix, and this is maximized by choosing $\hat{\Sigma} = S$.

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Gaussian Graphical Models

We have $X_a \perp\!\!\!\perp X_b \mid X_{V \setminus \{a,b\}}$ if and only if $k_{ab} = 0$.



	mechanics	vectors	algebra	analysis	statistics
mechanics	k_{11}	k_{12}	k_{13}	0	0
vectors		k_{22}	k_{23}	0	0
algebra			k_{33}	k_{34}	k_{35}
analysis				k_{44}	k_{45}
statistics					k_{55}

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Likelihood

From Lemma 4.23, we have

$$\log p(x_V) + \log p(x_S) = \log p(x_A, x_S) + \log p(x_B, x_S).$$

This becomes

$$x_V^T \Sigma^{-1} x_V + x_S^T (\Sigma_{SS})^{-1} x_S - x_{AS}^T (\Sigma_{AS,AS})^{-1} x_{AS} - x_{SB}^T (\Sigma_{SB,SB})^{-1} x_{SB} = 0$$

But can rewrite each term in the form $x_V^T M x_V$, e.g.:

$$x_{AS}^T (\Sigma_{AS,AS})^{-1} x_{AS} = x_V^T \begin{pmatrix} (\Sigma_{AS,AS})^{-1} & 0 \\ 0 & 0 & 0 \end{pmatrix} x_V$$

Equating terms gives:

$$\Sigma^{-1} = \begin{pmatrix} (\Sigma_{AS,AS})^{-1} & 0 \\ 0 & 0 & 0 \end{pmatrix} + \begin{pmatrix} 0 & 0 & 0 \\ 0 & (\Sigma_{SB,SB})^{-1} \end{pmatrix} - \begin{pmatrix} 0 & 0 & 0 \\ 0 & (\Sigma_{SS})^{-1} & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

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Maximum Likelihood Estimation

Iterating this process with a decomposable graph shows that:

$$\Sigma^{-1} = \sum_{i=1}^k \{(\Sigma_{C_i, C_i})^{-1}\}_{C_i, C_i} - \sum_{i=1}^k \{(\Sigma_{S_i, S_i})^{-1}\}_{S_i, S_i}.$$

For maximum likelihood estimation, using Theorem 4.24 we have

$$\begin{aligned} \hat{\Sigma}^{-1} &= \sum_{i=1}^k \{(\hat{\Sigma}_{C_i, C_i})^{-1}\}_{C_i, C_i} - \sum_{i=1}^k \{(\hat{\Sigma}_{S_i, S_i})^{-1}\}_{S_i, S_i} \\ &= \sum_{i=1}^k \{(W_{C_i, C_i})^{-1}\}_{C_i, C_i} - \sum_{i=1}^k \{(W_{S_i, S_i})^{-1}\}_{S_i, S_i} \end{aligned}$$

where $W_{CC} = \frac{1}{n} \sum_i X_C^{(i)} X_C^{(i)T}$ is the sample covariance matrix.

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Example

```
> true_inv      # true concentration matrix
      [,1] [,2] [,3] [,4]
[1,]  1.0  0.3  0.2  0.0
[2,]  0.3  1.0 -0.1  0.0
[3,]  0.2 -0.1  1.0  0.3
[4,]  0.0  0.0  0.3  1.0

> solve(true_inv) # Sigma
      [,1] [,2] [,3] [,4]
[1,]  1.17 -0.382 -0.30  0.090
[2,] -0.38  1.136  0.21 -0.063
[3,] -0.30  0.209  1.19 -0.356
[4,]  0.09 -0.063 -0.36  1.107

> # rmvnorm is in the mvtnorm package
> dat <- rmvnorm(1000, mean=rep(0,4), sigma = solve(true_inv))
> W <- cov(dat)      # sample covariance
```

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Example

```
> round(W, 3)      # sample covariance
      [,1] [,2] [,3] [,4]
[1,]  1.158 -0.374 -0.242  0.036
[2,] -0.374  1.099  0.227 -0.065
[3,] -0.242  0.227  1.169 -0.378
[4,]  0.036 -0.065 -0.378  1.085

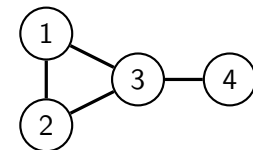
> round(solve(W), 3) # sample concentration
      [,1] [,2] [,3] [,4]
[1,]  0.995  0.308  0.160  0.040
[2,]  0.308  1.044 -0.138  0.004
[3,]  0.160 -0.138  1.026  0.344
[4,]  0.040  0.004  0.344  1.040
```

Note that these are fairly close to the true values.

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Example

Fit the model with decomposition $(\{1, 2\}, \{3\}, \{4\})$:



```
> K_hat = matrix(0, 4, 4)
> K_hat[1:3, 1:3] = solve(W[1:3, 1:3])
> K_hat[3:4, 3:4] = K_hat[3:4, 3:4] + solve(W[3:4, 3:4])
> K_hat[3, 3] = K_hat[3, 3] - 1/W[3, 3]
> K_hat
      [,1] [,2] [,3] [,4]
[1,]  0.993  0.308  0.146  0.000
[2,]  0.308  1.044 -0.139  0.000
[3,]  0.146 -0.139  1.021  0.336
[4,]  0.000  0.000  0.336  1.038
```

Note this is close to the true concentration matrix.

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The graphs considered so far are all **undirected**. Directed graphs give each edge an orientation.

A **directed graph** \mathcal{G} is a pair (V, D) , where

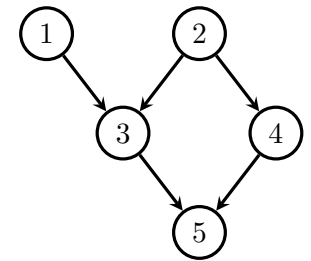
- V is a set of vertices;
- D is a set of ordered pairs (i, j) with $i, j \in V$ and $i \neq j$.

If $(i, j) \in D$ we write $i \rightarrow j$.

$$V = \{1, 2, 3, 4, 5\}$$

$$D = \{(1, 3), (2, 3), (2, 4), (3, 5), (4, 5)\}.$$

If $i \rightarrow j$ or $i \leftarrow j$ we say i and j are **adjacent** and write $i \sim j$.



Directed Graphical Models

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Acyclicity

Paths are sequences of adjacent vertices, without repetition:

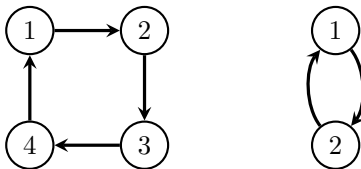
$$1 \rightarrow 3 \leftarrow 2 \rightarrow 4 \rightarrow 5$$

$$1 \rightarrow 3 \rightarrow 5.$$

The path is **directed** if all the arrows point away from the start.

(A path of length 0 is just a single vertex.)

A **directed cycle** is a directed path from i to $j \neq i$, together with $j \rightarrow i$.



Graphs that contain no directed cycles are called **acyclic**. or more specifically, **directed acyclic graphs** (DAGs).

All the directed graphs we consider are acyclic.

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Happy Families

$$i \rightarrow j \quad \begin{cases} i \in \text{pa}_{\mathcal{G}}(j) & i \text{ is a parent of } j \\ j \in \text{ch}_{\mathcal{G}}(i) & j \text{ is a child of } i \end{cases}$$

$$a \rightarrow \dots \rightarrow b \quad \begin{cases} a \in \text{ang}(b) & a \text{ is an ancestor of } b \\ \text{or } a = b & b \in \text{deg}(a) & b \text{ is a descendant of } a \end{cases}$$

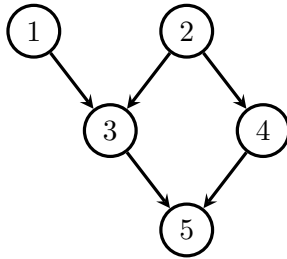
If $w \notin \text{deg}(v)$ then w is a **non-descendant** of v :

$$\text{nd}_{\mathcal{G}}(v) = V \setminus \text{deg}(v).$$

(Notice that no v is a non-descendant of itself).

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Examples



$$\text{pa}_G(3) = \{1, 2\}$$

$$\text{ch}_G(5) = \emptyset$$

$$\text{an}_G(4) = \{2, 4\}$$

$$\text{de}_G(1) = \{1, 3, 5\}$$

$$\text{nd}_G(1) = \{2, 4\}.$$

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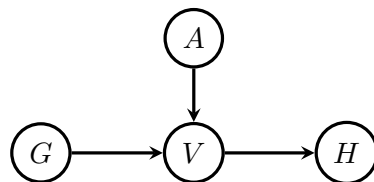
Parameter Estimation

G : group assigned to patient;

A : patient's age in years;

V : whether patient received flu vaccine;

H : patient hospitalized with respiratory problems;



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Topological Orderings

If the graph is acyclic, we can find a **topological ordering**: i.e. one in which no vertex comes before any of its parents. (Proof: induction)

Topological orderings:

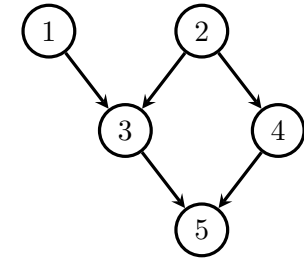
1, 2, 3, 4, 5

1, 2, 4, 3, 5

2, 1, 3, 4, 5

2, 1, 4, 3, 5

2, 4, 1, 3, 5



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Parameter Estimation

We can model the data (G_i, A_i, V_i, H_i) as

group : $G_i \sim \text{Bernoulli}(p)$;

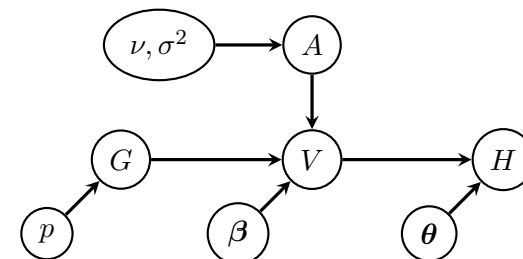
age : $A_i \sim N(\nu, \sigma^2)$;

vaccine : $V_i \mid A_i, G_i \sim \text{Bernoulli}(\mu_i)$ where

$$\text{logit } \mu_i = \beta_0 + \beta_1 A_i + \beta_2 G_i.$$

hospital : $H_i \mid V_i \sim \text{Bernoulli}(\text{expit}(\theta_0 + \theta_1 V_i))$.

Assuming independent priors:



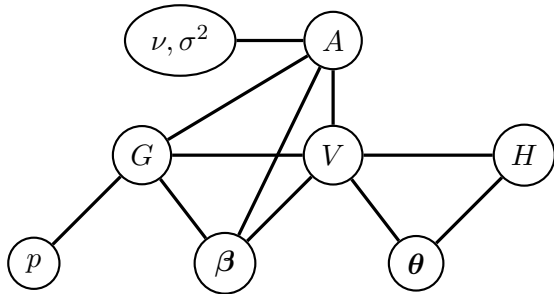
63

Bayesian Inference

From our argument, we have

$$\begin{aligned} \pi(\beta | G, A, V, H) &= \pi(\beta | G, A, V) \\ &\propto p(V | A, G, \beta) \cdot \pi(\beta). \end{aligned}$$

Looking at the moral graph we see



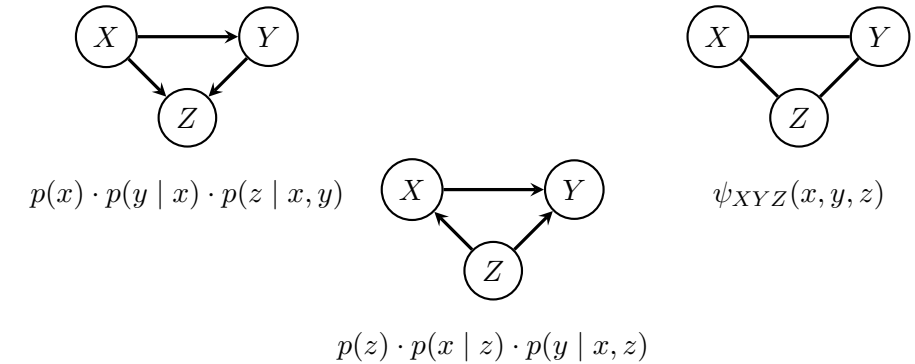
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Markov Equivalence

All undirected graphs induce distinct models.

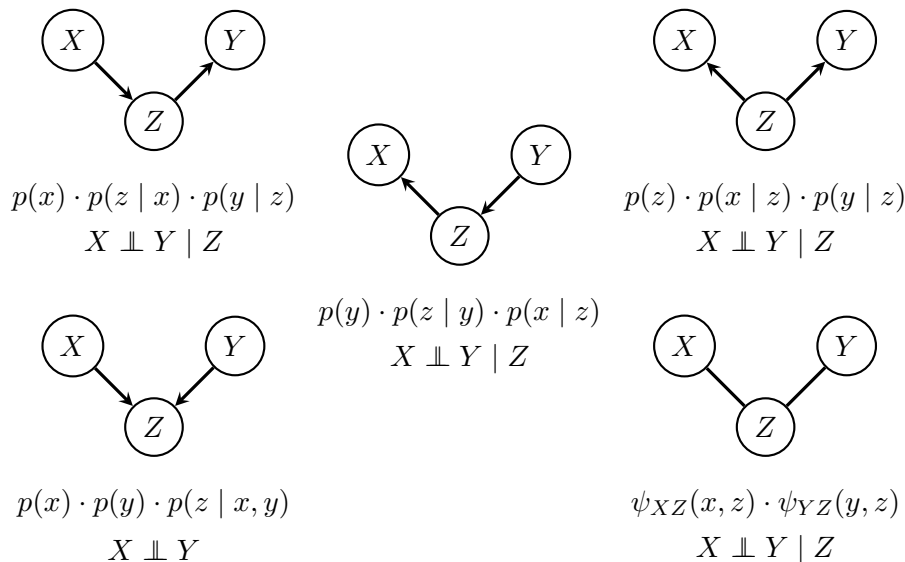
$$v \not\perp w \iff X_v \perp X_w | X_{V \setminus \{v,w\}} \text{ implied}$$

The same is not true for directed graphs:



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Markov Equivalence

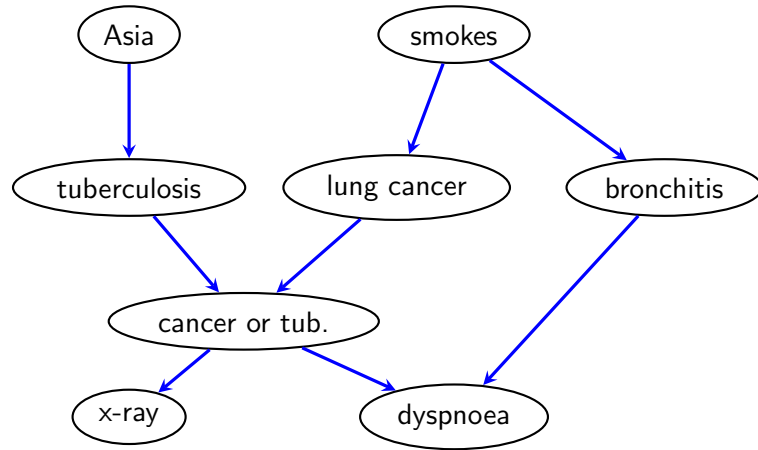


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Expert Systems

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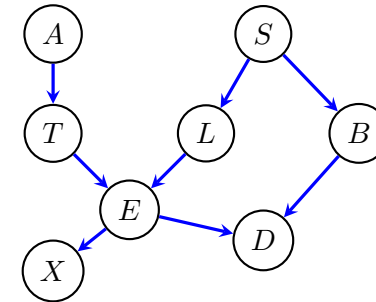
Expert Systems



The 'Chest Clinic' network, a fictitious diagnostic model.

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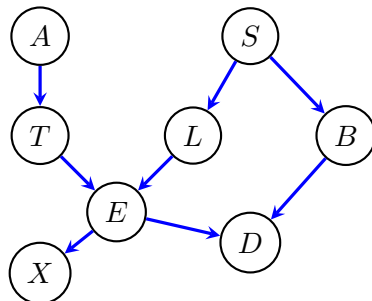
Variables



- A has the patient recently visited southern Asia?
- S does the patient smoke?
- T,L,B tuberculosis, lung cancer, bronchitis.
- E logical: tuberculosis OR lung cancer.
- X shadow on chest X-ray?
- D does the patient have dyspnoea?

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Conditional Probability Tables



We have our factorization:

$$p(a, s, t, \ell, b, e, x, d) = p(a) \cdot p(s) \cdot p(t | a) \cdot p(\ell | s) \cdot p(b | s) \cdot p(e | t, \ell) \cdot p(x | e) \cdot p(d | e, b).$$

Assume that we are given each of these factors. How could we calculate $p(\ell | x, d, a, s)$?

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Probabilities

$$p(a) = \begin{array}{c|cc} & \text{yes} & \text{no} \\ \hline & 0.01 & 0.99 \end{array}$$

$$p(s) = \begin{array}{c|cc} & \text{yes} & \text{no} \\ \hline & 0.5 & 0.5 \end{array}$$

$$p(t | a) = \begin{array}{c|cc} A & \text{yes} & \text{no} \\ \hline \text{yes} & 0.05 & 0.95 \\ \text{no} & 0.01 & 0.99 \end{array}$$

$$p(\ell | s) = \begin{array}{c|cc} S & \text{yes} & \text{no} \\ \hline \text{yes} & 0.1 & 0.9 \\ \text{no} & 0.01 & 0.99 \end{array}$$

$$p(b | s) = \begin{array}{c|cc} S & \text{yes} & \text{no} \\ \hline \text{yes} & 0.6 & 0.4 \\ \text{no} & 0.3 & 0.7 \end{array}$$

$$p(x | e) = \begin{array}{c|cc} E & \text{yes} & \text{no} \\ \hline \text{yes} & 0.98 & 0.02 \\ \text{no} & 0.05 & 0.95 \end{array}$$

$$p(d | b, e) = \begin{array}{cc|cc} B & E & \text{yes} & \text{no} \\ \hline \text{yes} & \text{yes} & 0.9 & 0.1 \\ & \text{no} & 0.8 & 0.2 \\ \text{no} & \text{yes} & 0.7 & 0.3 \\ & \text{no} & 0.1 & 0.9 \end{array}$$

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$$p(\ell | x, d, a, s) = \frac{p(\ell, x, d | a, s)}{\sum_{\ell'} p(\ell', x, d | a, s)}$$

From the graph $p(\ell, x, d | a, s)$ is

$$\sum_{t,e,b} p(t | a) \cdot p(\ell | s) \cdot p(b | s) \cdot p(e | t, \ell) \cdot p(x | e) \cdot p(d | e, b).$$

By this method there are up to 5×256 multiplications and $256 - 32 = 224$ additions.

This amounts to a complexity of around 1504 arithmetic operations.

Junction Trees

But this is the same as:

$$p(\ell | s) \sum_e p(x | e) \left(\sum_b p(b | s) \cdot p(d | e, b) \right) \left(\sum_t p(t | a) \cdot p(e | t, \ell) \right).$$

Each large bracket requires 16 multiplications and 8 additions, and gives a vector of length 8.

Then the outer sum has 64 entries, so at most 128 multiplications and 32 additions.

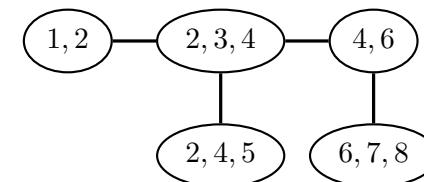
This totals 208 arithmetic operations.

Junction Trees

A **junction tree**:

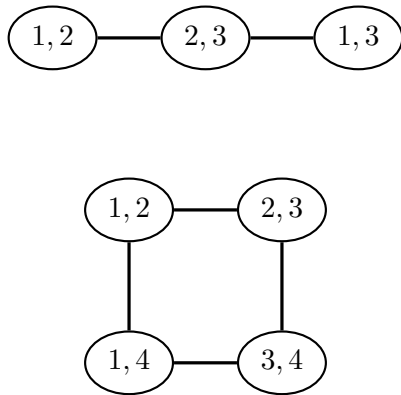
- is a (connected) undirected graph without cycles (a tree);
- has vertices C_i that consist of **subsets** of a set V ;
- satisfies the property that if $C_i \cap C_j = S$ then every vertex on the (unique) path from C_i to C_j contains S .

Example.



Junction Trees

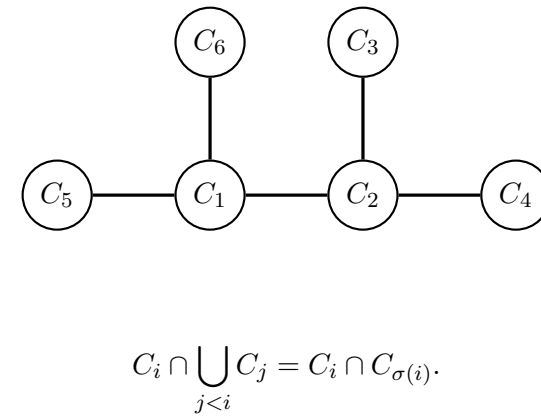
The following graphs are **not** junction trees:



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Junction Trees

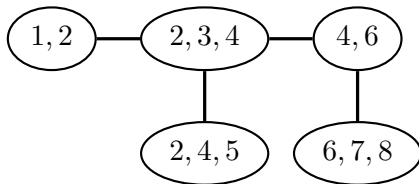
Junction trees can be constructed directly from sets of cliques satisfying running intersection.



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Example: Junction Trees and RIP

Given sets $\{1, 2\}$, $\{2, 3, 4\}$, $\{2, 4, 5\}$, $\{4, 6\}$, $\{6, 7, 8\}$, we can build this tree:

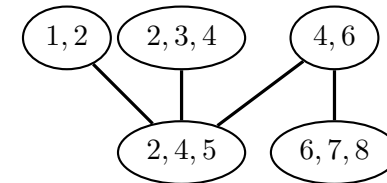


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Example: Junction Trees and RIP

Equally, we could use a different ordering:

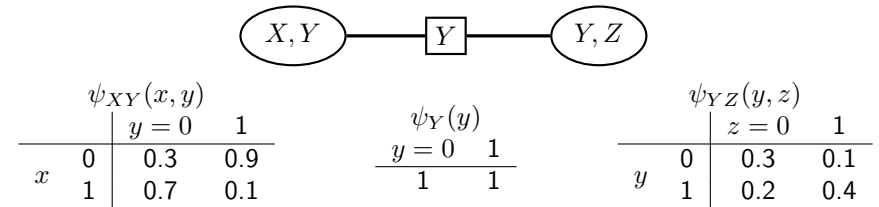
$\{6, 7, 8\}$, $\{4, 6\}$, $\{2, 4, 5\}$, $\{1, 2\}$, $\{2, 3, 4\}$.



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Message Passing

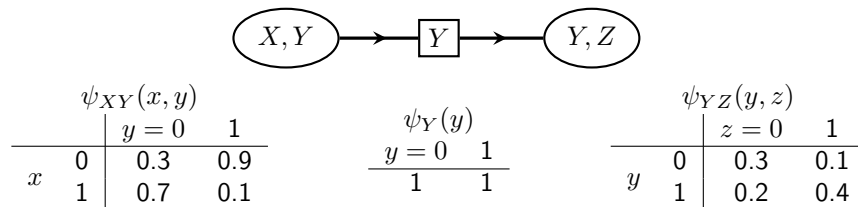
Suppose we have two vertices and one separator set.



Initialize with

$$\psi_{XY}(x, y) = p(x | y) \quad \psi_{YZ}(y, z) = p(z | y) \cdot p(y) \quad \psi_Y(y) = 1.$$

Suppose we have two vertices and one separator set.



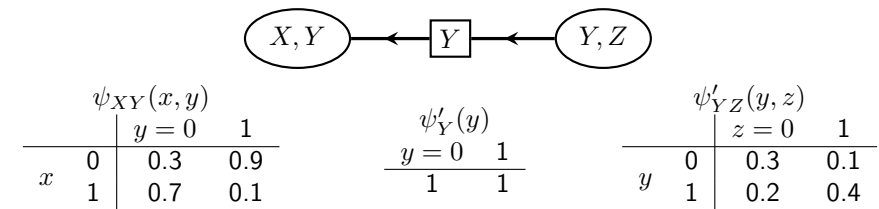
Pass message from X, Y to Y, Z . We set

$$\psi'_Y(y) = \sum_x \psi_{XY}(x, y) = (1, 1);$$

$$\psi'_{YZ}(y, z) = \frac{\psi'_Y(y)}{\psi_Y(y)} \psi_{YZ}(y, z) = \psi_{YZ}(y, z).$$

So in this case nothing changes.

Suppose we have two vertices and one separator set.



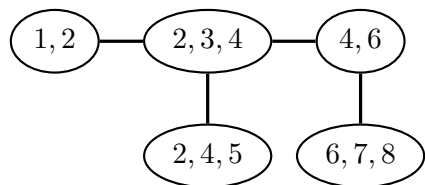
Pass message from Y, Z to X, Y . We set

$$\psi''_Y(y) = \sum_x \psi_{YZ}(y, z) = (0.4, 0.6);$$

$$\psi'_{XY}(x, y) = \frac{\psi''_Y(y)}{\psi'_Y(y)} \psi_{XY}(x, y) = \begin{matrix} 0.12 & 0.54 \\ 0.28 & 0.06 \end{matrix}.$$

And now we note that $\psi'_{XY}(x, y) = p(x, y)$ as intended.

Rooting



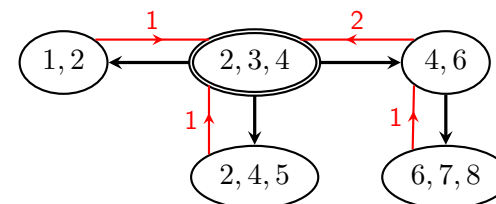
Given a tree, we can pick any vertex as a 'root', and direct all edges away from it.

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Collection and Distribution

```

function COLLECT(rooted tree  $\mathcal{T}$ , potentials  $\psi_t$ )
  let  $1 < \dots < k$  be a topological ordering of  $\mathcal{T}$ 
  for  $t$  in  $k, \dots, 2$  do
    send message from  $\psi_t$  to  $\psi_{\sigma(t)}$ ;
  end for
  return updated potentials  $\psi_t$ 
end function
    
```

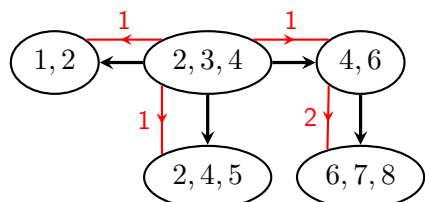


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Collection and Distribution

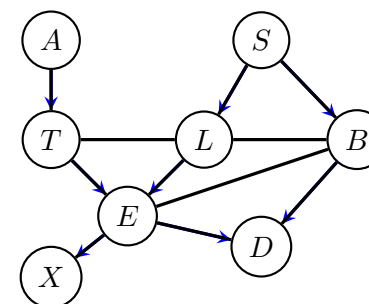
```

function DISTRIBUTE(rooted tree  $\mathcal{T}$ , potentials  $\psi_t$ )
  let  $1 < \dots < k$  be a topological ordering of  $\mathcal{T}$ 
  for  $t$  in  $2, \dots, k$  do
    send message from  $\psi_{\sigma(t)}$  to  $\psi_t$ ;
  end for
  return updated potentials  $\psi_t$ 
end function
    
```



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Forming A Junction Tree



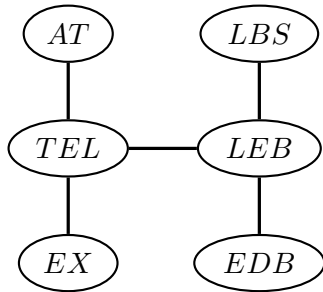
Steps to Forming a Junction Tree:

- Moralize
- Drop directions
- Triangulate (add edges to get a decomposable graph)

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Forming A Junction Tree

Finally, form the tree of cliques.



Initialization

$$p(a) = \begin{array}{c|cc} & \text{yes} & \text{no} \\ \hline & 0.01 & 0.99 \end{array}$$

$$p(s) = \begin{array}{c|cc} & \text{yes} & \text{no} \\ \hline & 0.5 & 0.5 \end{array}$$

$$p(t | a) = \begin{array}{c|cc} A & \text{yes} & \text{no} \\ \hline \text{yes} & 0.05 & 0.95 \\ \text{no} & 0.01 & 0.99 \end{array}$$

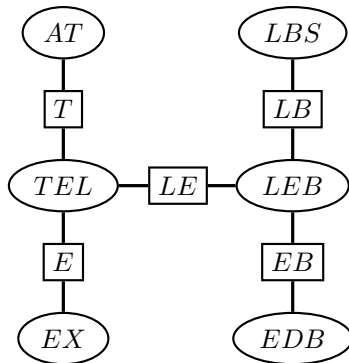
$$p(\ell | s) = \begin{array}{c|cc} S & \text{yes} & \text{no} \\ \hline \text{yes} & 0.1 & 0.9 \\ \text{no} & 0.01 & 0.99 \end{array}$$

$$p(b | s) = \begin{array}{c|cc} S & \text{yes} & \text{no} \\ \hline \text{yes} & 0.6 & 0.4 \\ \text{no} & 0.3 & 0.7 \end{array}$$

$$p(x | e) = \begin{array}{c|cc} E & \text{yes} & \text{no} \\ \hline \text{yes} & 0.98 & 0.02 \\ \text{no} & 0.05 & 0.95 \end{array}$$

$$p(d | b, e) = \begin{array}{cc|cc} B & E & \text{yes} & \text{no} \\ \hline \text{yes} & \text{yes} & 0.9 & 0.1 \\ & \text{no} & 0.8 & 0.2 \\ \text{no} & \text{yes} & 0.7 & 0.3 \\ & \text{no} & 0.1 & 0.9 \end{array}$$

Initialization

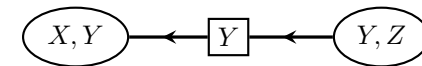


Can set, for example:

$$\begin{aligned} \psi_{AT}(a, t) &= p(a) \cdot p(t | a) & \psi_{LBS}(\ell, b, s) &= p(s) \cdot p(\ell | s) \cdot p(b | s) \\ \psi_{TEL}(t, e, \ell) &= p(e | t, \ell) & \psi_{ELB}(e, \ell, b) &= 1 \\ \psi_{EX}(e, x) &= p(x | e) & \psi_{EDB}(e, d, b) &= p(d | e, b). \end{aligned}$$

Evidence

Now, suppose we want to calculate $p(x | z = 0)$.



		$\psi_{XY}(x, y)$	
		$y = 0$	1
x	0	0.12	0.54
	1	0.28	0.06

		$\psi_Y(y)$	
		$y = 0$	1
y	0	0.4	0.6
	1	0.4	0

		$\psi_{YZ}(y, z)$	
		$z = 0$	1
y	0	0.6	0
	1	0.4	0

Replace $\psi_{YZ}(y, z)$ with $p(y | z = 0)$.

Pass message from Y, Z to X, Y. We set

$$\begin{aligned} \psi_Y(y) &= \sum_x \psi_{YZ}(y, z) = (0.6, 0.4); \\ \psi'_{XY}(x, y) &= \frac{\psi''_Y(y)}{\psi'_Y(y)} \psi_{XY}(x, y) = \begin{bmatrix} 0.18 & 0.36 \\ 0.42 & 0.04 \end{bmatrix}. \end{aligned}$$

And now calculate $\sum_y \psi_{XY}(x, y) = (0.54, 0.46)$.

Marginal Probability Tables:

$E \setminus X$	yes	no
yes	0.06	0
no	0.05	0.89

$A \setminus T$	yes	no
yes	0	0.01
no	0.01	0.98

$L \setminus S$	B		E	
	yes	no	yes	no
yes	0.03	0	0.02	0
no	0.27	0.15	0.18	0.35

$L \setminus B$	E		A	
	yes	no	yes	no
yes	0.03	0.02	0	0
no	0	0.01	0.41	0.52

$T \setminus L$	E		B	
	yes	no	yes	no
yes	0	0	0.01	0
no	0.05	0	0	0.94

$B \setminus D$	E		L	
	yes	no	yes	no
yes	0.03	0	0.02	0.01
no	0.33	0.08	0.05	0.47

Suppose now that we have a shadow on the chest X-ray:

$E \setminus X$	yes	no
yes	0.58	-
no	0.42	-

$A \setminus T$	yes	no
yes	0	0.01
no	0.09	0.9

$L \setminus S$	B		E	
	yes	no	yes	no
yes	0.27	0.01	0.18	0.03
no	0.15	0.08	0.1	0.19

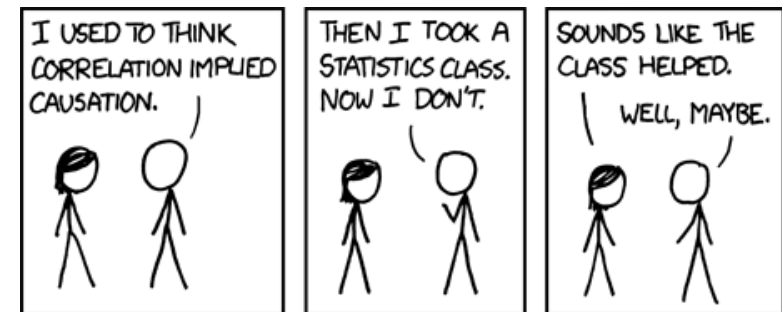
$L \setminus B$	E		A	
	yes	no	yes	no
yes	0.28	0.21	0	0
no	0.04	0.05	0.19	0.24

$T \setminus L$	E		B	
	yes	no	yes	no
yes	0.01	0	0.09	0
no	0.48	0	0	0.42

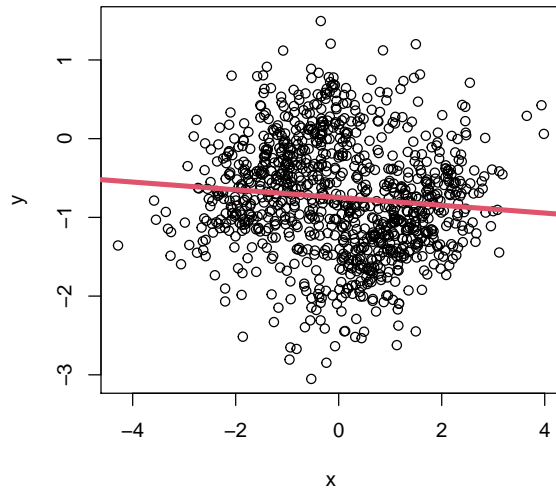
$B \setminus D$	E		L	
	yes	no	yes	no
yes	0.29	0.03	0.18	0.08
no	0.15	0.04	0.02	0.21

Correlation

Causal Inference

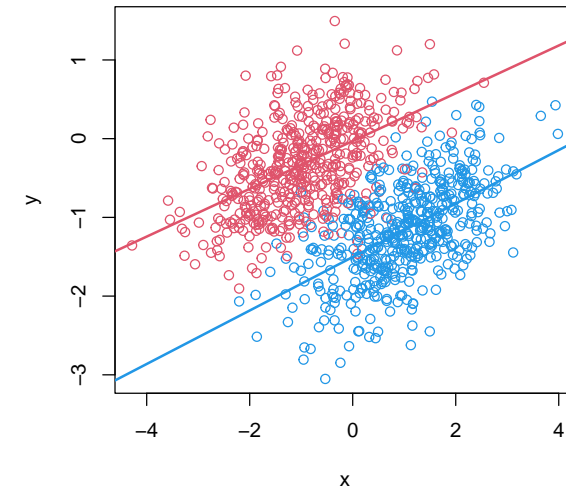


Controlling for Covariates



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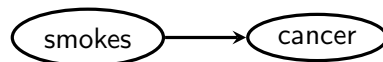
Controlling for Covariates



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Causation

Example. Smoking is strongly predictive of lung cancer. So maybe smoking causes lung cancer to develop.



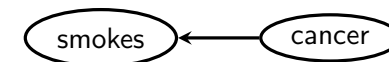
BUT: how do we know that this is a causal relationship? And what do we mean by that?

The central question is: “if we stop people from smoking, will they be less likely to get lung cancer?”

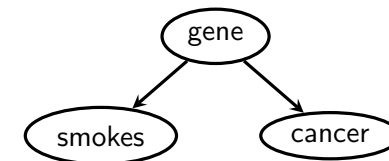
That is: does this ‘intervention’ on one variable change the distribution of another variable?

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Alternative Explanations



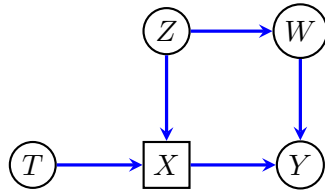
Reverse Causation. Lung cancer causes smoking: people with (undiagnosed) lung cancer smoke to soothe irritation in the lungs.



Confounding / Common Cause. There is a gene that makes people likely to smoke, and also more likely to get lung cancer.

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A DAG model can also encode causal information:



If we intervene to experiment on X , just delete incoming edges.

In distribution, just delete factor corresponding to X :

$$p(t, z, w, x, y) = p(t) \cdot p(z) \cdot p(w | z) \cdot p(x | t, z) \cdot p(y | w, x).$$

$$p(t, z, w, y | do(x)) = p(t) \cdot p(z) \cdot p(w | z) \quad \times \quad p(y | w, x).$$

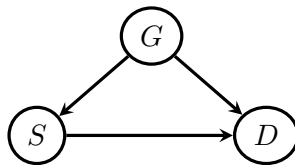
All other factors are preserved.

Note that (generally) $p(y | do(x)) \neq p(y | x)$ and $p(y | do(x)) \neq p(y)$.
It is **neither** a conditional **nor** an ordinary marginal distribution.

Causal Discovery is hard!

Determining which of the three explanations is correct is generally very hard, though methods do exist for distinguishing between such models.

Consider the following causal model, which we will assume is correct:



Here G is gender, S is smoking, and D is an indicator of lung damage.

Example

Suppose we take 32 men and 32 women, ask them whether they smoke and check for lung damage.

	women		men	
	not smoke	smoke	not smoke	smoke
no damage	21	6	6	6
damage	3	2	2	18

Marginally, there is clearly a strong relationship between smoking and damage

	not smoke	smoke
no damage	27	12
damage	5	20

$$P(D = 1 | S = 1) = \frac{5}{8} \quad P(D = 1 | S = 0) = \frac{5}{32}.$$

Example

This might suggest that if we had prevented them all from smoking, only $\frac{5}{32} \times 64 = 10$ would have had damage, whereas if we had made them all smoke, $\frac{5}{8} \times 64 = 40$ would have had damage.

But: both smoking and damage are also correlated with gender, so this estimate may be inaccurate. If we repeat this separately for men and women:

no-one smoking:

$$\frac{3}{21+3} \times 32 + \frac{2}{6+2} \times 32 = 12$$

everyone smoking

$$\frac{2}{6+2} \times 32 + \frac{18}{18+6} \times 32 = 32.$$

Compare these to 10 and 40.

'do' notation

In this example there is a difference between predicting damage when we 'observe' that someone smokes ...

$$P(D = 1 \mid S = 1) = \frac{5}{8},$$

... and predicting damage when we intervene to make someone smoke:

$$P(D = 1 \mid do(S = 1)) = \frac{32}{64} = \frac{1}{2}.$$