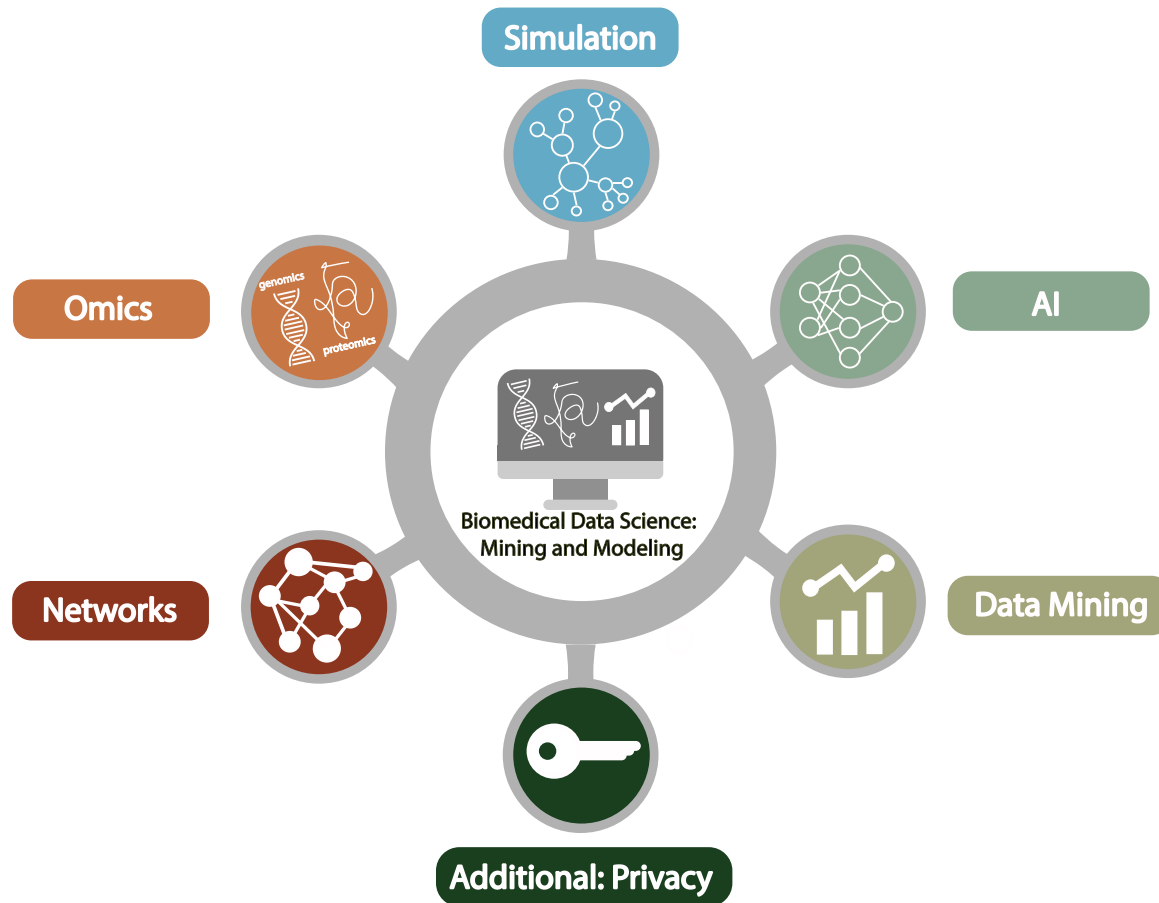
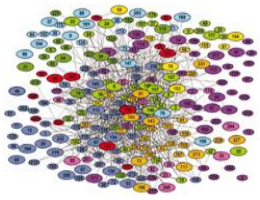


Biomedical Data Science (GersteinLab.org/courses/452)

Network Prediction (23m10e)

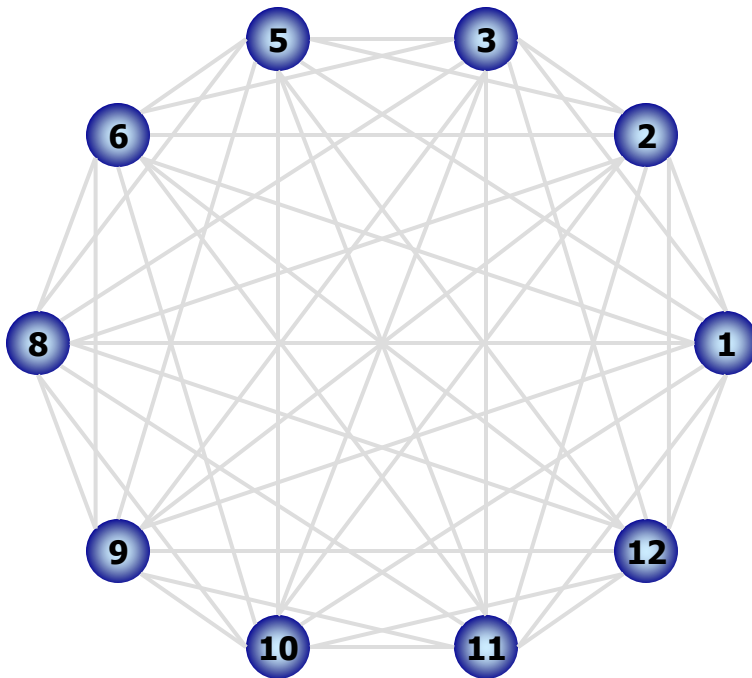


Predicting Networks via Bayesian Integration: Problem Motivation



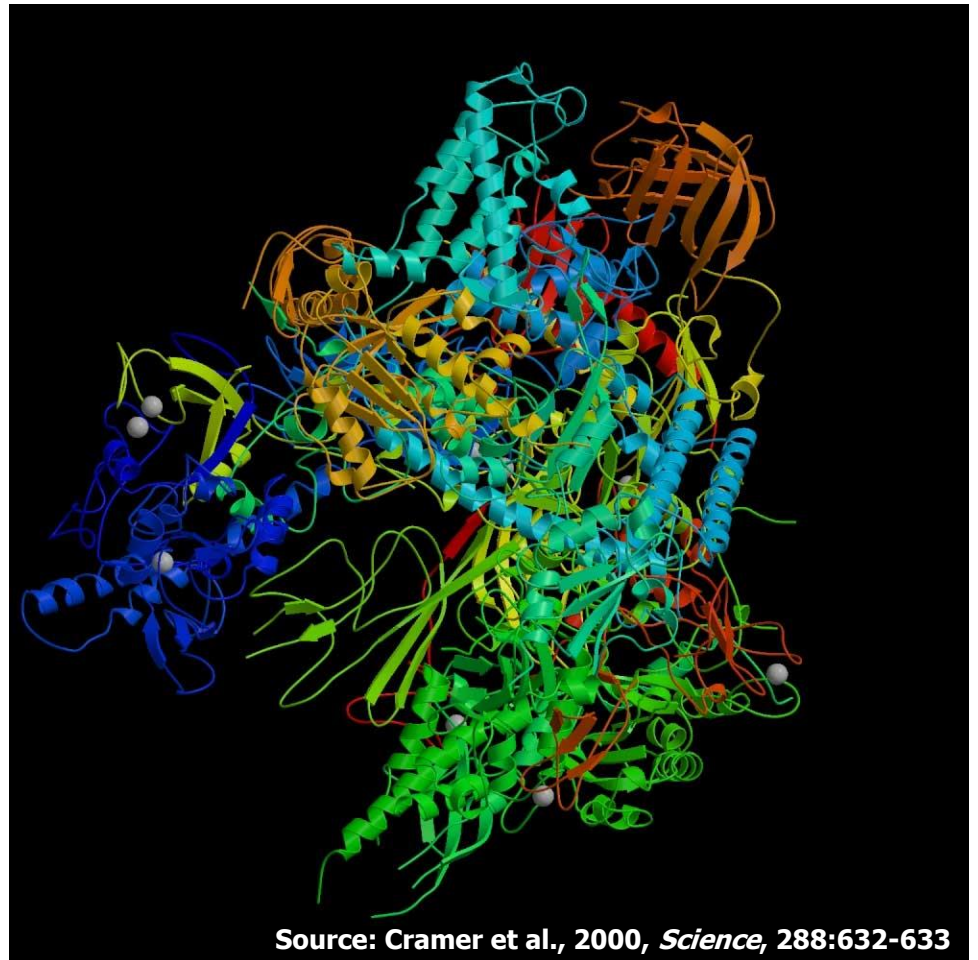
RNA polymerase II: Structure

Which subunits interact?
Based on Binding
experiments

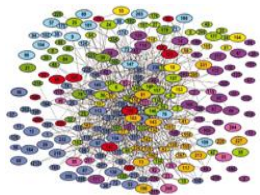


Source: Edwards et al., 2002, *Trends in Genetics*

Compare with Gold Std. Structure



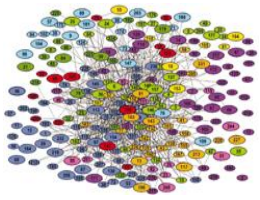
Source: Cramer et al., 2000, *Science*, 288:632-633



Binding Experiments on Subunit Pairs

Subunits	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	3	3	3	3	3	3	5	5	5	5	5	5	6	6	6	6	6	8	8	8	8	9	9	9	9	10	10	12			
Subunits	2	3	5	6	8	9	10	11	12	3	5	6	8	9	10	11	12	5	6	8	9	10	11	12	6	8	9	10	11	12	8	9	10	11	12	9	10	11	12	10	11	12	11	11	12			
Pull-down 1	1	1	0	1	0	1	0			1	1	0	1	0	1	0		1	1	1	0	1	1		1	1	0	1	0		0	0	0	0		0	1	0		0	0		0					
Pull-down 2	1	1	1	1	0	1	0			1	1	0	1	0	1	0		1	1	1	0	1	1		0	1	0	1	0		0	0	0	0		0	0	0		0	0		0	0		0		
Pull-down 3	1									1								1	0	1	0	0	1	0																								
Cross-linking	1	1	1	1	1		0	1	1	1	1	1	0		1	1	1			1	1		1	0				1																				
Far Western 1	1	1								1	1							1	0	0		0	0	0	0	1		0	0	0																		
Far Western 2			1	1		1	1	1		1	1		1	1	1			0	0		0	1	0	0	0		0	0	0	0		0	0	0	0		0	0	0		0	0	0		0	0	0	
Far Western 3																		1	0	0		0	1	0																								

Interaction experiments
before structure was known

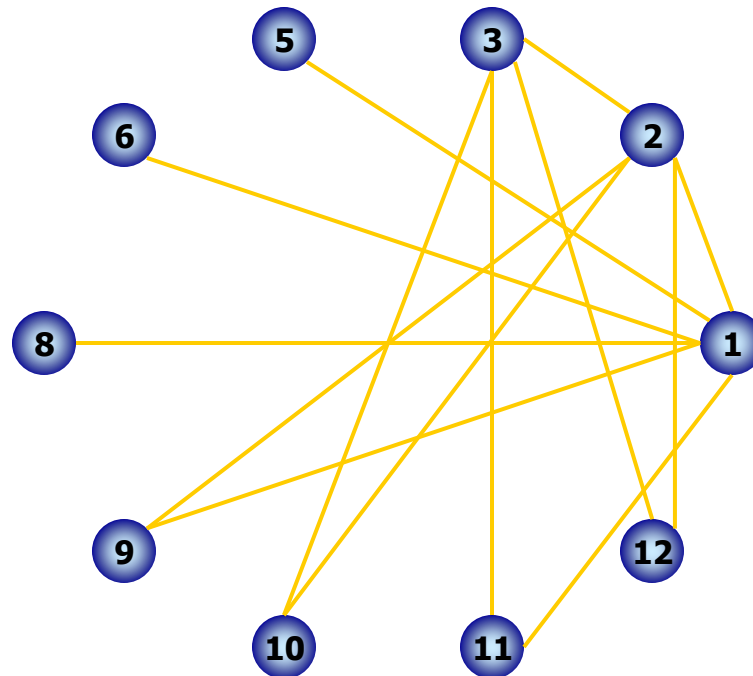


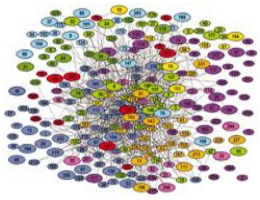
Gold-Standard Positives

Subunits
Subunits

1	1	1	1	1	1	1	1	2	2	2	2	2	2	3	3	3	3	3	3	5	5	5	5	5	5	6	6	6	6	6	8	8	8	8	9	9	9	9	10	10	12			
2	3	5	6	8	9	10	11	12	3	5	6	8	9	10	11	12	5	6	8	9	10	11	12	6	8	9	10	11	12	8	9	10	11	12	9	10	11	12	10	11	12	11	11	12

Gold-Standard Positive (GSTD+): 13



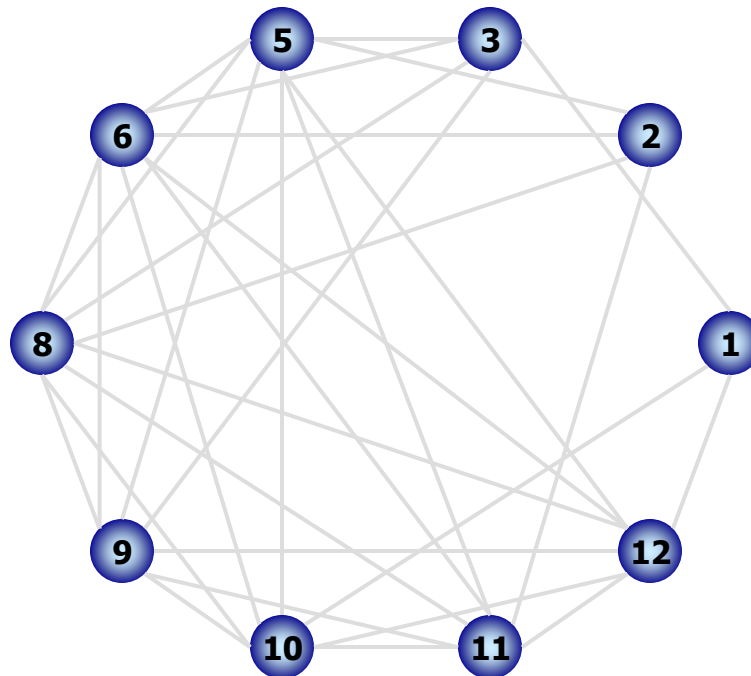


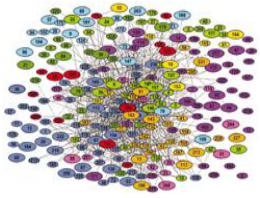
Gold-Standard Negatives

Subunits
Subunits

1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 5 5 5 5 5 5 6 6 6 6 6 8 8 8 8 9 9 9 10 10 12
2 3 5 6 8 9 10 11 12 3 5 6 8 9 10 11 12 5 6 8 9 10 11 12 6 8 9 10 11 12 8 9 10 11 12 9 10 11 12 10 11 12 11 11 12

Gold-Standard Negative (GSTD-): 32





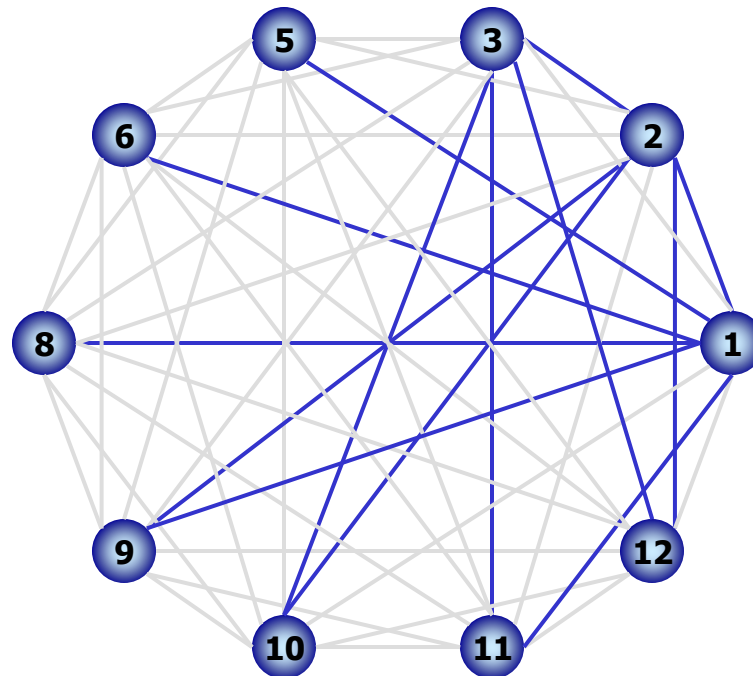
RNA Polymerase II: Gold-Standards

Subunits
Subunits

1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	3	3	3	3	3	3	3	5	5	5	5	5	5	6	6	6	6	6	8	8	8	8	9	9	9	9	10	10	12
2	3	5	6	8	9	10	11	12	3	5	6	8	9	10	11	12	5	6	8	9	10	11	12	6	8	9	10	11	12	8	9	10	11	12	9	10	11	12	10	11	12	11	11	12	

Gold-Standard Positive (GSTD+): 13

Gold-Standard Negative (GSTD-): 32



Weighted Voting: the Likelihood Ratio

structural contact

1 0 1 1 1 1 0 1 0 1 0 0 0 1 1 0 1 0 0 1 1 1 0 0 0 0

Far western

1 1 1 1 1 1 1 0 0 0 0 0 1 0

Far western (dup)

1 1 1 1 1 1 1 0 0 0 0 0 1 0

Cross-linking

1 1 1 1 1 0 1 1 1 1 1 0 1 1 1 1 1 1 0

Far western

1 1 1 1 1 1 1 1 1 1 1 0 0 1 0 0 0 0 0

Pull-down

1 1 0 1 0 1 0 1 1 0 1 0 1 0 1 0 1 1 0 1

Pull-down

1 1 1 1 0 1 0 1 1 0 1 0 1 0 1 0 1 0 1 1

Pull-down

1 0 0 0 1 0

Far western

0 0 1 0

Combined

0 1 1 1 1 0 0 0 1 1 1 0 0 0 1 0 1 0 0 0 0 1 0 0 0 0

Maj. Vote: 0 = round(avg(0 + 0 + 0 + 1 + 1 + 0 + 0))

With weights: likelihood ratio L = L₁ + L₂ + L₃ ...

Predicting Networks via Bayesian Integration: Intuition & Formalism

Derived from
"perceptron model"
 $R = \langle w, f \rangle + b$

Supervised Classification by Weighted Voting

Simple Vote: $R = f_1 + f_2 + f_3 + \dots + f_n$ With $f = 1$ or -1

If $\begin{cases} R > 0; & I \text{ Interact} \\ R < 0; & \sim I \text{ No interaction} \end{cases}$

Modify with feature weight:

$$R = w_1 f_1 + w_2 f_2 + w_3 f_3 + \dots + w_n f_n = \vec{w} \cdot \vec{f}$$

If has prior knowledge w_0

$$R = \vec{w} \cdot \vec{f} + w_0$$

Classification by Voting

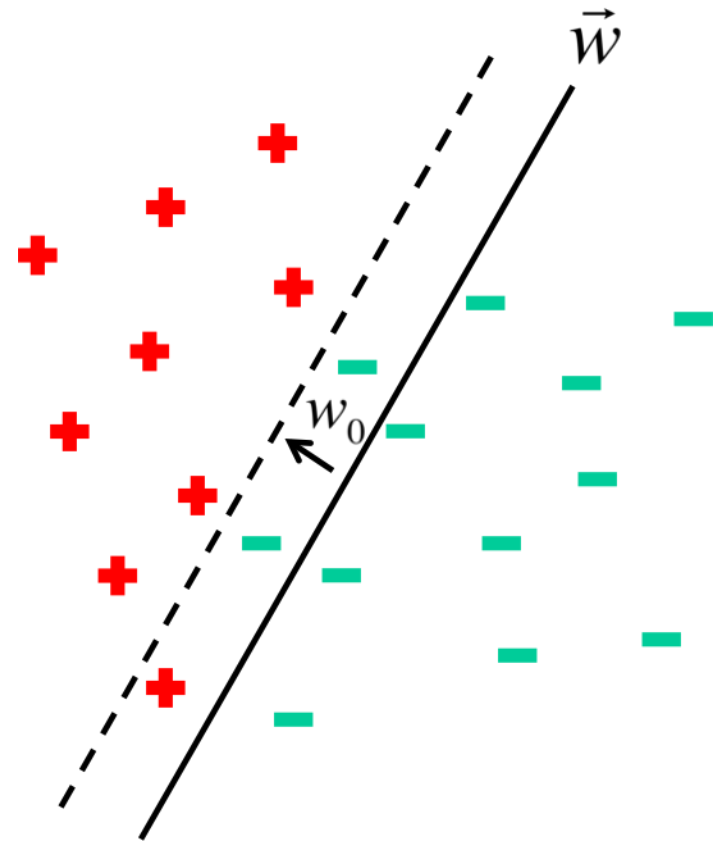
$$R = \vec{w} \cdot \vec{f} + w_0$$

$$w_1 = \log \frac{P(f_1 = 1 | I)}{P(f_1 = 1 | \sim I)}$$

$$= \log \frac{TP / P}{FR / N}$$

$$w_0 = \log \frac{P}{N} \quad (\text{Estimated from Golden Standard})$$

On Training Set



Bayes Rule

$$P(Y|X) = \frac{P(X|Y)P(Y)}{P(X)}$$

Which is shorthand for:

$$P(Y = y_i|X = x_j) = \frac{P(X = x_j|Y = y_i)P(Y = y_i)}{P(X = x_j)}$$

Thus

$$P(I \mid f_1, f_2, f_3, \dots) = \frac{P(f_1, f_2, f_3, \dots \mid I)P(I)}{P(f_1, f_2, f_3, \dots)}$$

Assume Naïve Bayes (independent) =
$$\frac{P(f_1 \mid I)P(f_2 \mid I)P(f_3 \mid I)\dots P(I)}{P(f_1, f_2, f_3, \dots)}$$

$$\begin{aligned} P(\sim I \mid f_1, f_2, f_3, \dots) &= \frac{P(f_1, f_2, f_3, \dots \mid \sim I)P(\sim I)}{P(f_1, f_2, f_3, \dots)} \\ &= \frac{P(f_1 \mid \sim I)P(f_2 \mid \sim I)P(f_3 \mid \sim I)\dots P(\sim I)}{P(f_1, f_2, f_3, \dots)} \end{aligned}$$

$$\begin{aligned} \log\left(\frac{P(I \mid f_1, f_2, f_3, \dots)}{P(\sim I \mid f_1, f_2, f_3, \dots)}\right) &= \log\left(\frac{P(f_1 \mid I)}{P(f_1 \mid \sim I)} \frac{P(f_2 \mid I)}{P(f_2 \mid \sim I)} \frac{P(f_3 \mid I)}{P(f_3 \mid \sim I)} \dots \frac{P(I)}{P(\sim I)}\right) \\ &= \log \frac{TPR_1}{FPR_1} + \log \frac{TPR_2}{FPR_2} + \log \frac{TPR_3}{FPR_3} + \dots + \log \frac{P}{N} \end{aligned}$$

More Bayes
Rule

$$\log\left(\frac{P(I \mid f_1, f_2, f_3, \dots)}{P(\sim I \mid f_1, f_2, f_3, \dots)}\right) = \log \frac{TPR_1}{FPR_1} + \log \frac{TPR_2}{FPR_2} + \log \frac{TPR_3}{FPR_3} + \dots + \log \frac{P}{N}$$

\uparrow
 w_1

\uparrow
 w_2

\uparrow
 w_3

\uparrow
 w_0

More Bayes Rule

Estimating Probabilities

- We have so far estimated $P(X=x | Y=y)$ by the fraction $n_{x|y}/n_y$, where n_y is the number of instances for which $Y=y$ and $n_{x|y}$ is the number of these for which $X=x$
- This is a problem when n_x is small
 - ◇ E.g., assume $P(X=x | Y=y)=0.05$ and the training set is s.t. that $n_y=5$. Then it is highly probable that $n_{x|y}=0$
 - ◇ The fraction is thus an underestimate of the actual probability
 - ◇ It will dominate the Bayes classifier for all new queries with $X=x$

$$\frac{\text{\# count with feature } i \text{ in GS+}}{\text{\# count with feature } i \text{ in GS-}} = \frac{TPR_i}{FPR_i}$$



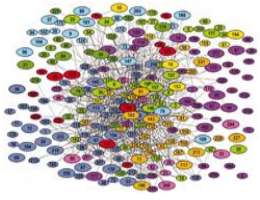
m -estimate

- Replace $n_{x|y}/n_y$ by:

$$\frac{n_{x|y} + mp}{n_y + m} \leftarrow \text{Dummy Counts}$$

- Where p is our prior estimate of the probability we wish to determine and m is a constant
 - ◇ Typically, $p = 1/k$ (where k is the number of possible values of X)
 - ◇ m acts as a weight (similar to adding m virtual instances distributed according to p)

Predicting Networks via Bayesian Integration: Worked Examples



Calculating Likelihood Ratios

Subunits
Subunits

1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	3	3	3	3	3	3	3	5	5	5	5	5	5	6	6	6	6	6	8	8	8	8	9	9	9	9	10	10	12
2	3	5	6	8	9	10	11	12	3	5	6	8	9	10	11	12	5	6	8	9	10	11	12	6	8	9	10	11	12	8	9	10	11	12	9	10	11	12	10	11	12	11	11	12

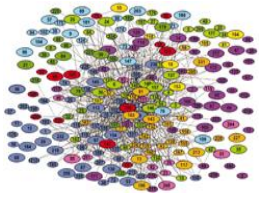
Pull-down 1

1	0	1	0	0	1	0	1	1	1
---	---	---	---	---	---	---	---	---	---

$$L_1 = \frac{p(x_1 | GSTD+)}{p(x_1 | GSTD-)} = \frac{6}{13}$$

$$L_0 = \frac{p(x_0 | GSTD+)}{p(x_0 | GSTD-)} = \frac{4}{13}$$

█ GSTD+
█ GSTD-
█ True
█ False



Calculating Likelihood Ratios

Subunits
Subunits

1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	3	3	3	3	3	3	3	5	5	5	5	5	5	6	6	6	6	6	8	8	8	8	8	9	9	9	9	10	10	10	12
2	3	5	6	8	9	10	11	12	3	5	6	8	9	10	11	12	5	6	8	9	10	11	12	6	8	9	10	11	12	8	9	10	11	12	9	10	11	12	10	11	12	11	11	12		

Pull-down 1

1	1	0	1	0	1	0	1	0	1	1	0	1	0	1	0	1	1	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

$$L_1 = \frac{p(x_1 | GSTD+)}{p(x_1 | GSTD-)} = \frac{6/13}{11/32} = 1.34$$

$$L_0 = \frac{p(x_0 | GSTD+)}{p(x_0 | GSTD-)} = \frac{4/13}{14/32} = 0.70$$

	GSTD+
	GSTD-
	True
	False

Predicting Networks via Bayesian Integration: Features Correlation

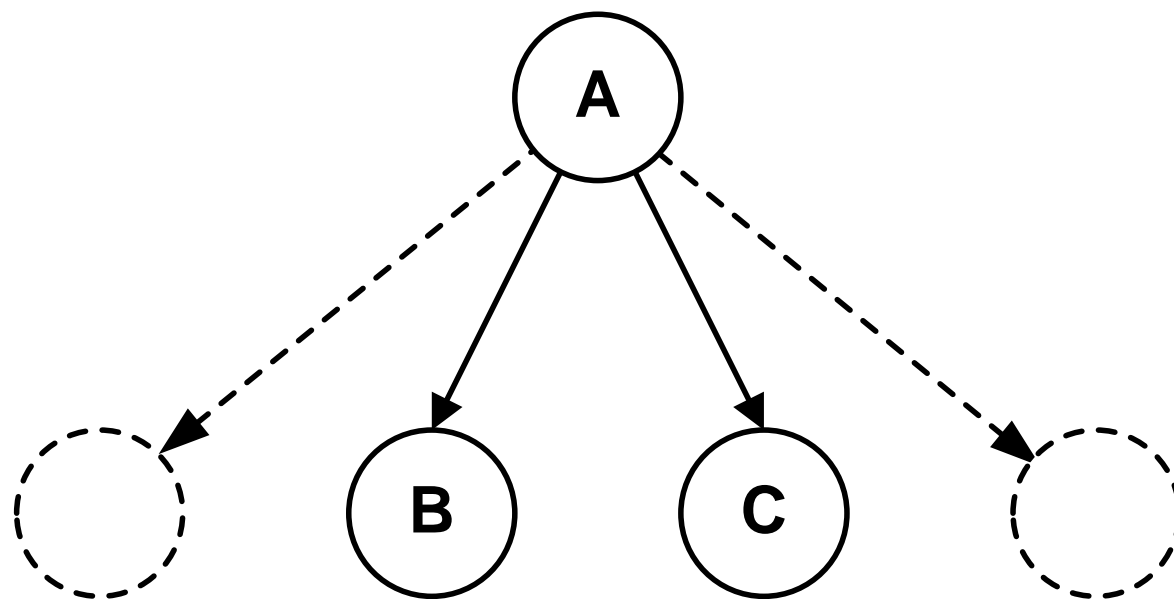
GS	1	0	0	1	1	1	...
F1	1	0	0	1	0	0	...
F2	1	0	0	1	0	0	...
F3	0	0	1	0	1	0	...
F4	0	1	0	0	1	0	...
F5	0	1	0	0	1	0	...
F6	1	0	1	1	0	0	...

Feature
Correlation
and Fully
Connected
Bayes

$$w_{4,5} = \log \frac{P(f_4 = 1, f_5 = 1 | I)}{P(f_4 = 1, f_5 = 1 | \sim I)}$$

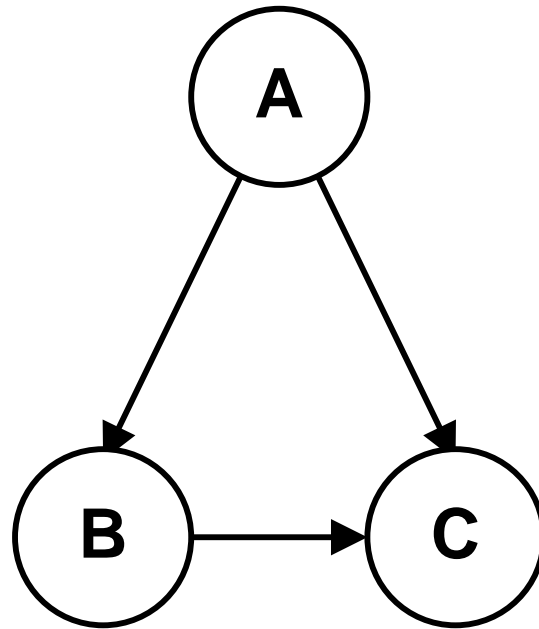
Naive Bayes

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

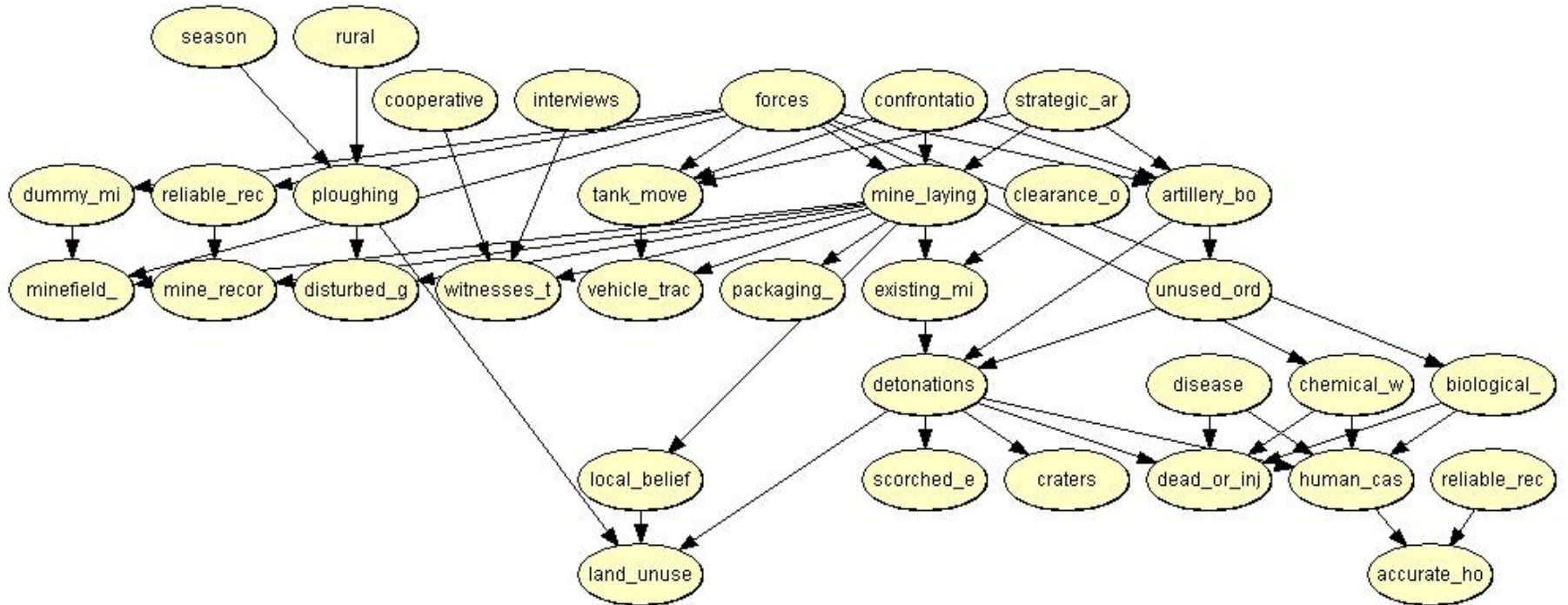


A 'correct' factorisation

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



A Typical BBN



Predicting Networks via
Bayesian Integration:
Real Thing
but with a few features

Papers on Predicting Protein Interactions

- A Enright et al. (**1999**) "Protein interaction maps for complete genomes based on gene fusion events." *Nature*. 402(6757):86-90.
- E Marcotte et al. (1999) "A Combined Algorithm for Genome-Wide Prediction of Protein Function." *Nature* 402, 83-86 (1999).
- E Marcotte et al. (1999) "Detecting Protein Function & Protein-Protein Interactions from Genome Sequences." *Science* 285, 751-753
- M Pellegrini et al. (1999) "Assigning protein functions by comparative genome analysis: protein phylogenetic profiles." *Proc.Natl. Acad. Sci.* 96, 4285-4288.
- R Jansen et al. (2003). "A Bayesian networks approach for predicting protein-protein interactions from genomic data." *Science* 302: 449-53.
- **I Lee et al. (2004) "A Probabilistic Functional Network of Yeast Genes". *Science* 206: 1555-1558**
- H Yu et al. (2004) "Annotation transfer between genomes: protein-protein interologs and protein-DNA regulogs." *Genome Res* 14: 1107-18.
- **L Lu et al. (2005) "Assessing the limits of genomic data integration for predicting protein networks." *Genome Res* 15: 945-53.**
- A Ramani et al. (2005) "Consolidating the set of known human protein-protein interactions in preparation for large-scale mapping of the human interactome." *Genome Biology* 6:r40.
- Xia et al. (**2006**) "Integrated prediction of the helical membrane protein interactome in yeast." *J Mol Biol.* 357:339-49