# Important Reminder! Learning Parameters using EM in the presence of incomplete data

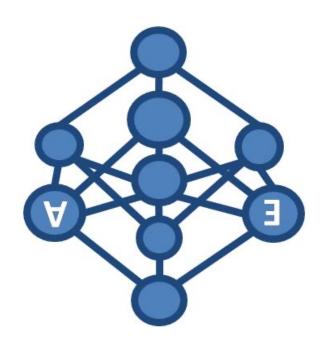
- Initialize parameters
- 2. Compute **pseudo counts** for each variable

$$heta_{k| exttt{pa}}^* = rac{\sum_{i=1}^m P(k, exttt{pa}|X_i)}{\sum_{i=1}^m P( exttt{pa}|X_i)}$$
 junction tree algorithm

- 3. Set parameters to the (completed) ML estimates
- 4. If not converged, iterate to 2

## Probabilistic Graphical Models\* Bayesian Networks - Learning





\*Thanks to Carlos Guestrin, Pedro Domingos and many others for making their slides publically available





#### What you need to know so far about learning

- Different Learning Settings
  - Fully vs. partially observable variables
  - Structure known vs. unknown
  - Latent variables vs. scientific discovery
- Maximum Likelihood and Decomposable Scores
- EM and Gradient-based ML parameter estimation
  - Update rules for binomial and multinomial vars



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#### What's next

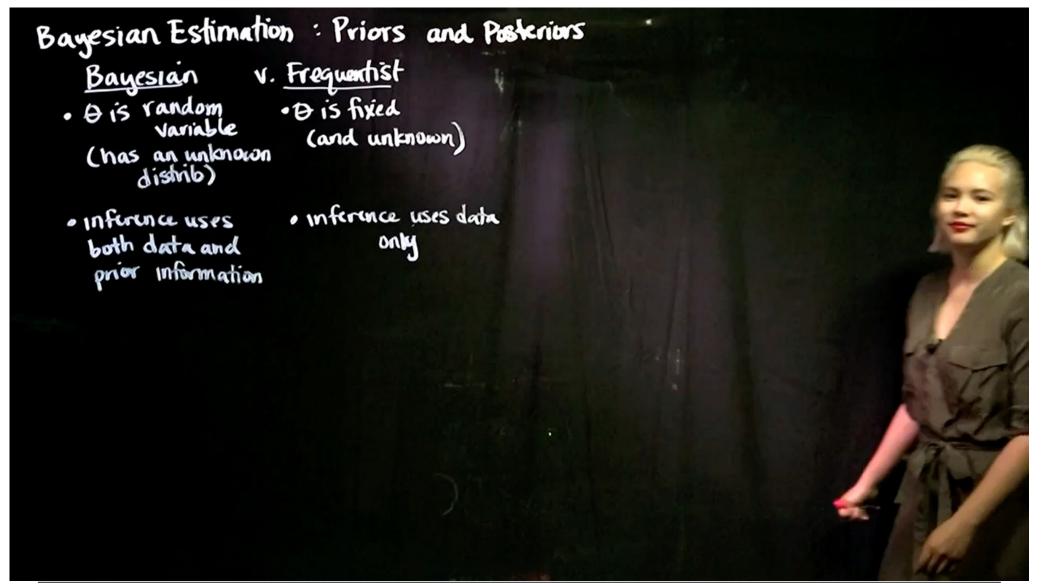
Bayesian Parameter Estimation



#### **Bayesian versus Frequentist Estimation**



https://www.youtube.com/watch?v=TUgqL9c1jik







#### **Bayesian Inference**

Recall, training data has the form:

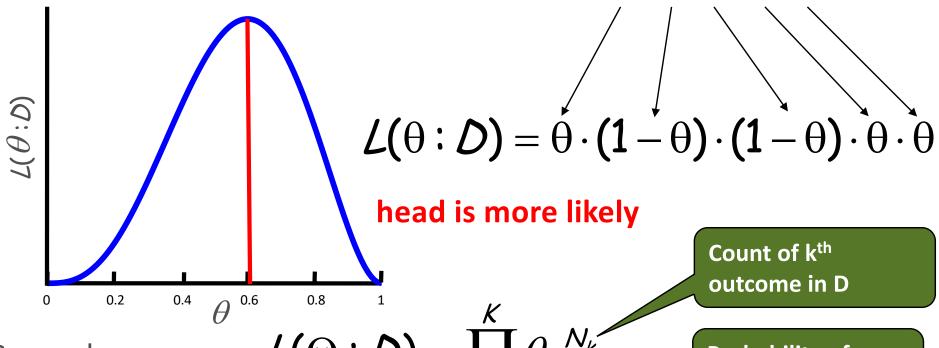
$$D = \begin{bmatrix} E[1] & B[1] & A[1] & C[1] \\ \vdots & \vdots & \ddots & \vdots \\ E[M] & B[M] & A[M] & C[M] \end{bmatrix}$$



#### Recall, Likelihood Function for Multinomials

$$L(\theta:D) = P(D \mid \theta) = \prod P(x[m] \mid \theta)$$

The likelihood for the sequence H, T, T, H, H is



General case:

$$L(\Theta:D) = \prod_{k=1}^{K} \theta_{k} e^{N_{k}}$$

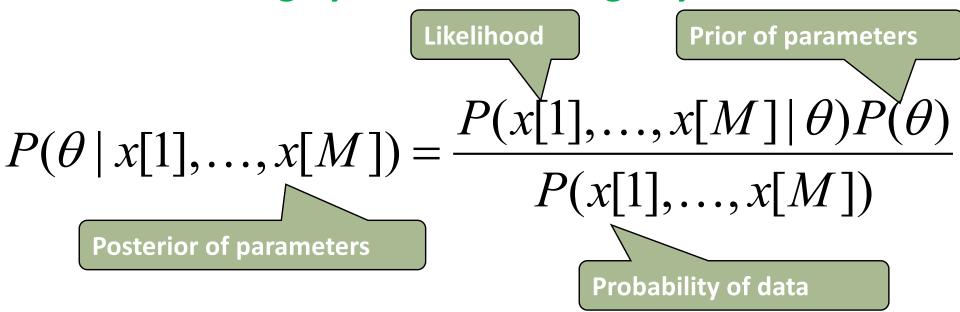
Probability of kth outcome

$$LL(\Theta:D) = \sum_{k=1}^{K} N_k \cdot \log \theta_k$$

#### Now, what is Bayesian Inference?



- In contrast to MLE, it represents uncertainty about parameters using a probability distribution over parameters and data (recall, "θ is a RV with an unknown distribution")
- It is "Learning by inference" using Bayes' rule





#### **Bayesian Estimation**



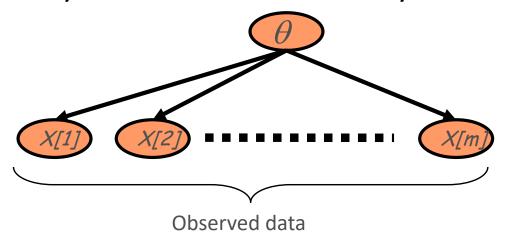






#### Bayesian Inference (for the Heads/Tails Example)

Represent Bayesian distribution as Bayesian net



• Thus, the values of X are independent given  $\theta$  (which we do not know though)

$$P(x[m] / \theta) = \theta$$
 (keep this in mind!)

Bayesian prediction is inference in this network



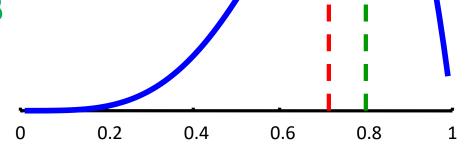


#### **Example: Binomial Data**

- Prior: uniform for  $\theta$  in [0,1]
  - $\Rightarrow P(\theta \mid D) \propto \text{the likelihood } L(\theta : D)$

$$P(\theta \mid x[1], ...x[M]) \propto P(x[1], ...x[M] \mid \theta) \cdot P(\theta)$$
  
 $(N_{H}, N_{T}) = (4,1), e.g., H, T, H, H, H$ 

- MLE for P(X = H) is 4/5 = 0.8
- Bayesian prediction is



$$P(x[M+1] = H \mid D) = \int \theta \cdot P(\theta \mid D) d\theta = \frac{5}{7} = 0.7142...$$

We do not know theta! So, we have to integrate over all values. Bayesian prediction = Inference in the <u>extended network</u>

### Why is this the case?



We start with

- $P(\theta)$  prior distribution about the values of  $\theta$
- $P(x_1, ..., x_n/\theta)$  likelihood of examples given a known value  $\theta$

Given examples  $X_1, ..., X_n$ , we can compute **posterior distribution** on  $\theta$ 

$$P(\theta \mid x_1, \dots x_n) = \frac{P(x_1, \dots x_n \mid \theta) P(\theta)}{P(x_1, \dots x_n)}$$

Where the marginal likelihood is

$$P(x_1,...x_n) = \int P(x_1,...x_n \mid \theta) P(\theta) d\theta$$



# Let us illustrate this using the Binomial Distribution. This leads to Laplace Estimates

- Assuming a Binomial, the unknown parameter is  $\theta = P(H)$
- Simplest **prior** (density)  $P(\theta) = 1$  for  $0 < \theta < 1$
- Likelihood  $P(x_1,...x_n \mid \theta) = \theta^k (1-\theta)^{n-k}$  where k is number of heads in the sequence
- Marginal Likelihood:

$$P(x_1,...x_n) = \int_0^1 \theta^k (1-\theta)^{n-k} d\theta$$

Now, we use integration by parts

#### **Recap: Integration by parts**



First, start with the Product Rule for differentiation.

$$\frac{\mathrm{d}}{\mathrm{dx}}(\mathrm{uv}) = \mathrm{u}\,\frac{\mathrm{dv}}{\mathrm{dx}} + \mathrm{v}\,\frac{\mathrm{du}}{\mathrm{dx}}$$

Integrate both sides of the equation to obtain:

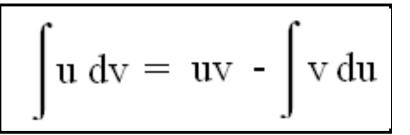
$$\int \frac{d}{dx} (uv) dx = \int u \frac{dv}{dx} dx + \int v \frac{du}{dx} dx$$

$$uv = \int u dv + \int v du$$

and by manipulating the equation we get ... (see next page)

The Fundamental Theorem of Calculus tells us that if we take the derivative of the integral, then we are left with the original function.

The derivative and the integral "cancel" each other out.





#### This is the formula for Integration by Parts.

Just as the Substitution Method could be thought of as the Chain Rule for integration, Integration by Parts could also be thought of as the Product Rule for integration.

When using this formula, we need to choose which part of the integrand (what we are taking the integral of) is u, and which part of it is dv.

When choosing u and dv, we want to find a u that will be simplified after we take its derivative, and a dv that won't be too complex after integrating it.

#### **Marginal Likelihood**

Using integration by parts we have:

$$P(x_1, ..., x_n) = \int_0^1 \frac{\theta^k (1-\theta)^{n-k} d\theta}{\text{dv u}}$$

$$= \frac{1}{k+1} \frac{\theta^{k+1} (1-\theta)^{n-k}}{\theta^{k+1}} \frac{\theta^{k+1} (1-\theta)^{n-k-1} d\theta}{\theta^{k+1}}$$

$$= \frac{n-k}{k+1} \int_0^1 \theta^{k+1} (1-\theta)^{n-k-1} d\theta$$

$$= \frac{n-k}{k+1} \int_0^1 \theta^{k+1} (1-\theta)^{n-k-1} d\theta$$

Multiply both side by n choose k, we have

$$\binom{n}{k}\int_{0}^{1}\theta^{k}(1-\theta)^{n-k}d\theta = \binom{n}{k+1}\int_{0}^{1}\theta^{k+1}(1-\theta)^{n-k-1}d\theta$$



 $u \, dv = uv - v \, du$ 

+ insteat of – because of the

### **Marginal Likelihood - Cont**

Cavalieri's quadrature formula



$$\int_0^u x^n dx = rac{1}{n+1} a^{n+1} \qquad n \geq 0,$$

• The recursion terminates when (the initial) k = n

$$\binom{n}{n}\int_{0}^{1}\theta^{n}(1-\theta)^{n-n}d\theta=\int_{0}^{1}\theta^{n}d\theta=\frac{1}{n+1}$$

Thus 
$$P(x_1,...x_n) = \int_{0}^{1} \theta^k (1-\theta)^{n-k} d\theta = \frac{1}{n+1} \binom{n}{k}^{-1}$$

We left multiplied by n chooses k, so we have to get rid of it again, i.e., defide by it!

We conclude (just plug in all terms and recall that **P(theta)=1**) that the **posterior** is

$$P(\theta \mid x_1, ... x_n) = \frac{P(x_1, ... x_n \mid \theta) P(\theta)}{P(x_1, ... x_n)} = (n+1) \binom{n}{k} \theta^k (1-\theta)^{n-k} \cdot 1$$

$$P(\theta \mid x_1, \dots x_n) = \frac{P(x_1, \dots x_n \mid \theta) P(\theta)}{P(x_1, \dots x_n)}$$

#### **Bayesian Prediction**

- So, we have a posterior over the parameters. But how do we predict a probability using this posterior?
- We can think of this as computing the probability of the next element in the sequence

$$P(x_{n+1} \mid x_1, ..., x_n) = \int P(x_{n+1}, \theta \mid x_1, ..., x_n) d\theta$$

$$= \int P(x_{n+1} \mid \theta, x_1, ..., x_n) P(\theta \mid x_1, ..., x_n) d\theta$$

$$= \int P(x_{n+1} \mid \theta) P(\theta \mid x_1, ..., x_n) d\theta$$

• Assumption: if we know  $\theta$ , the probability of  $X_{n+1}$  is independent of  $X_1, ..., X_n$ 

$$P(X_{n+1} \mid \theta, X_1, \dots, X_n) = P(X_{n+1} \mid \theta)$$



#### **Bayesian Prediction**

Thus, we conclude that

$$P(x_{n+1} = H \mid x_1, ..., x_n) = \int P(x_{n+1} \mid \theta) P(\theta \mid x_1, ..., x_n) d\theta$$

$$= \int \theta P(\theta \mid x_1, ..., x_n) d\theta$$
Plug-in formula for the posterior and move everything out of the intergal that does not depend on theta
$$= (n+1) \binom{n}{k} \int \theta^{k+1} (1-\theta)^{n-k} d\theta$$
Same type of derivation as before
$$= (n+1) \binom{n}{k} \frac{1}{n+2} \binom{n+1}{k+1}^{-1} = \frac{k+1}{n+2}$$

Plugging in the counts from our example (k=4 and n=5) we get the result seen already earlier

$$P(x[M+1] = H \mid D) = \int \theta \cdot P(\theta \mid D) d\theta = \frac{5}{7} = 0.7142...$$





#### How do we choose the prior?

- Many possible answers...
- Pragmatic approach:
  - Want computationally "simple" (and still flexible) prior: conjugate priors



#### **Conjugate Prior**



A conjugate prior is an algebraic convenience, giving a closed-form expression for the posterior; otherwise, numerical integration may be necessary.

- Consider parametric families of prior distributions:
  - $P(\theta) = f(\theta; \alpha)$
  - $\bullet$   $\alpha$  is called "hyperparameters" of prior
- A prior  $P(\theta) = f(\theta; \alpha)$  is called **conjugate** for a likelihood function  $P(D \mid \theta)$  if  $P(\theta \mid D) = f(\theta; \alpha')$ 
  - Posterior has same parametric form
  - Hyperparameters are updated based on data D

#### Wikipedia

In Bayesian probability theory, if the posterior distribution  $p(\theta \mid x)$  is in the same probability distribution family as the prior probability distribution  $p(\theta)$ , the prior and posterior are then called **conjugate distributions**, and the prior is called a **conjugate prior** for the likelihood function  $p(x \mid \theta)$ .

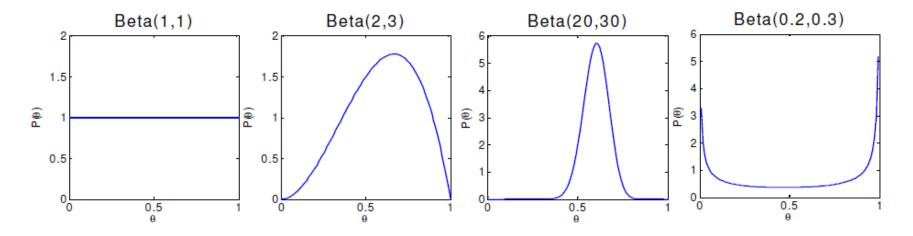




#### **Conjugate for Binomial**

Beta distribution

$$Beta(\theta; \alpha_H, \alpha_T) = \frac{\theta^{\alpha_H - 1} (1 - \theta)^{\alpha_T - 1}}{B(\alpha_H, \alpha_T)}$$
Mondization constant







#### **Posterior for Binomial**

Beta distribution

$$P(\theta) = \text{Beta}(\theta; \alpha_H, \alpha_T) = \frac{\theta^{\alpha_H - 1} (1 - \theta)^{\alpha_T - 1}}{B(\alpha_H, \alpha_T)}$$

Likelihood:

$$P(\mathcal{D} \mid \theta) = \theta^{m_H} (1 - \theta)^{m_T}$$

Posterior:





#### **Bayesian Prediction**

- Prior  $P(\theta) = Beta(\alpha_H, \alpha_T)$
- Suppose we observe D= {m<sub>H</sub> heads, and m<sub>T</sub> tails}
- What's P(X=H | D), i.e., prob. that next flip is heads?





#### **Prior = Smoothing**

$$\mathbb{E}[\theta] = \frac{m_H + \alpha_H}{m_H + m_T + \alpha_H + \alpha_T} = \frac{m_H + \gamma m'}{m_H + m'}$$

- Where m' =  $\alpha_H$  +  $\alpha_T$ , and  $\gamma$  =  $\alpha_H$  / m'
- m' is called "equivalent sample size"
  - → "hallucinated" coin flips

$$E[\theta] = \frac{m}{m+m} \frac{m_{H}}{m} + \frac{m_{I}}{m+m_{I}} \gamma$$

$$m \Rightarrow \infty \quad E[\theta] \Rightarrow MLE \quad Farget prior$$

$$m = 0 \quad prior$$

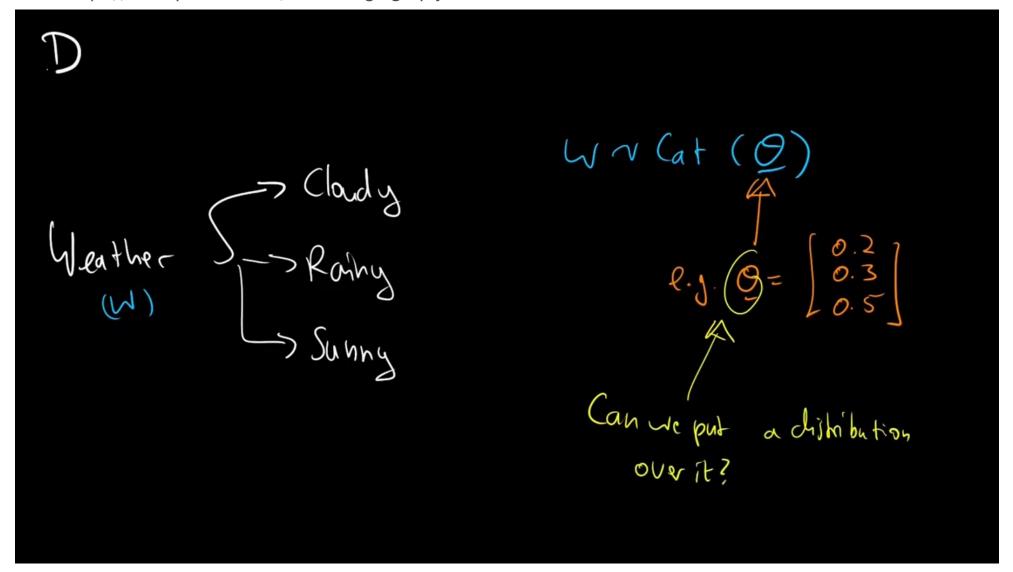
→ Interpolate between MLE and prior mean



#### **Conjuagte for Multinomial**



https://www.youtube.com/watch?v=gWgsKyEjclw







#### **Conjuagte for Multinomial**

- If X∈{1,...,k} has k states:
- Multinomial likelihood

$$P(\mathcal{D} \mid \theta) = \theta_1^{m_1} \theta_2^{m_2} \dots \theta_k^{m_k}$$

where 
$$\sum_{i} \theta_{i} = 1$$
,  $\theta_{i} \geq 0$ 

Conjugate prior: Dirichlet distribution

$$P(\theta) = \text{Dir}(\theta; \alpha_1, \dots, \alpha_k) = \frac{1}{Z} \prod_i \theta_i^{\alpha_i - 1}$$

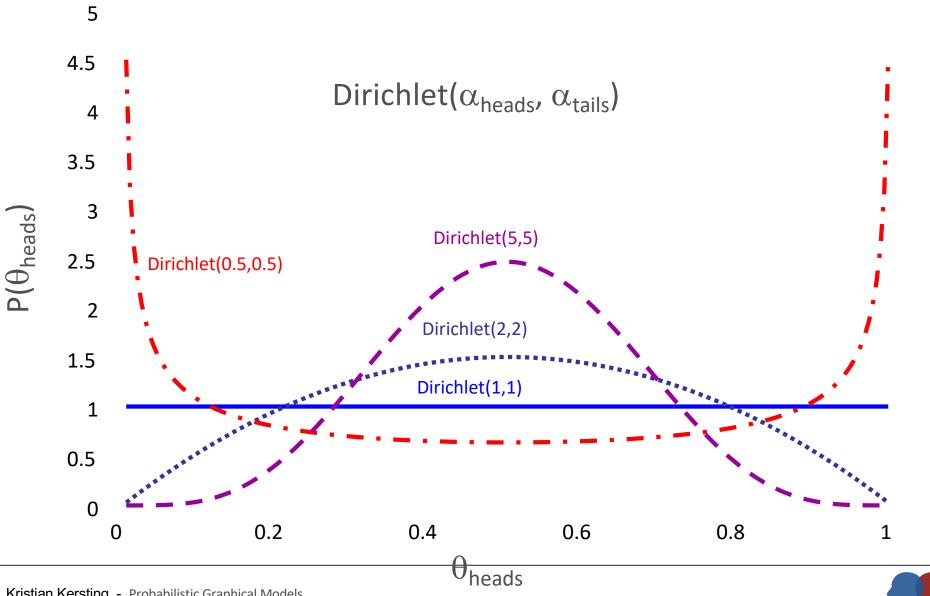
If observe D={m<sub>1</sub> 1s, m<sub>2</sub> 2s, ... m<sub>k</sub> ks}, then

$$P(\theta \mid \mathcal{D}) = \text{Dir}(\theta; \alpha_1 + m_1, \dots, \alpha_k + m_k)$$





### **Dirichlet Priors - Example**



#### Dirichlet visualization

https://www.youtube.com/watch?v=CEVELIz4WXM&t=425s



#### Dirichlet distribution

 The Dirichlet distribution is a generalization of the Beta distribution for multiple random variables

The Dirichlet distribution is over <u>vectors</u> whose values are all in the interval [0, 1] and the sum of values in the vector is 1.

In other words, the vectors in the sample space of the Dirichlet have the same properties as probability distributions.

The Dirichlet distribution can be thought of as a "distribution over distributions".

The PDF for a K-dimensional Dirichlet distribution has a vector parameters denoted α, given by:

$$f(\mathbf{x}) = \frac{\prod_{k=1}^{K} \Gamma(\alpha_k)}{\Gamma(\sum_{k=1}^{K} \alpha_i)} \prod_{k=1}^{K} x_k^{\alpha_k - 1}$$

Data Science: Jordan Boyd-Graber | UMI

Continuous Distributions





#### **Dirichlet Priors (cont.)**

• If  $P(\Theta)$  is Dirichlet with hyperparameters  $\alpha_1, ..., \alpha_K$ 

$$P(X[1] = k) = \int \theta_k \cdot P(\Theta) d\Theta = \frac{\alpha_k}{\sum_{\ell} \alpha_{\ell}}$$

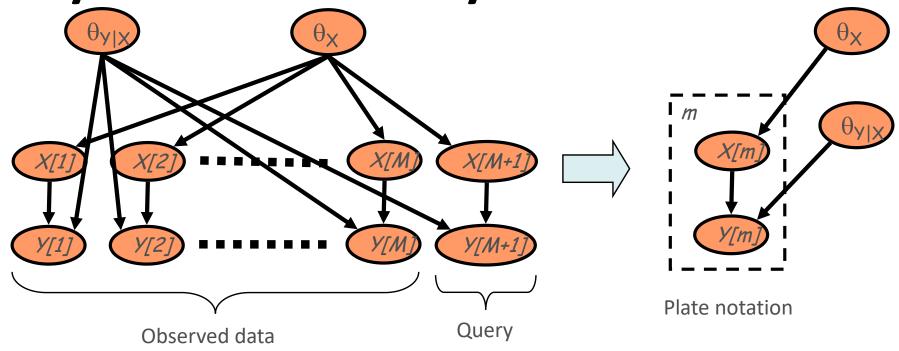
Since the posterior is also Dirichlet, we get

$$P(X[M+1]=k \mid D) = \int \theta_k \cdot P(\Theta \mid D) d\Theta = \frac{\alpha_k + N_k}{\sum_{\ell} (\alpha_\ell + N_\ell)}$$





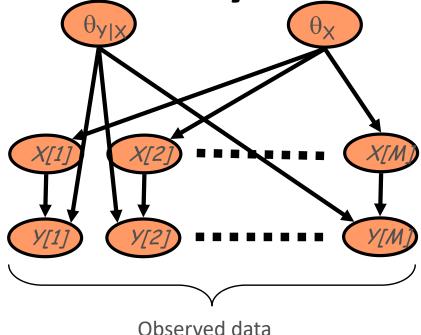
**Bayesian Nets & Bayesian Prediction** 



- Priors for each parameter group are independent
- Data instances are independent given the unknown parameters (so to say the "Bayesian iid")



**Bayesian Nets & Bayesian Prediction** 



We can also "read" from the network:

Complete data ⇒ posteriors on parameters are independent

Can compute posterior over parameters separately!





#### **Learning Parameters: Summary**

- Estimation relies on sufficient statistics
  - For multinomials: counts  $N(x_i, pa_i)$
  - Parameter estimation

$$\hat{\theta}_{x_i|pa_i} = \frac{N(x_i, pa_i)}{N(pa_i)} \qquad \qquad \tilde{\theta}_{x_i|pa_i} = \frac{\alpha(x_i, pa_i) + N(x_i, pa_i)}{\alpha(pa_i) + N(pa_i)}$$

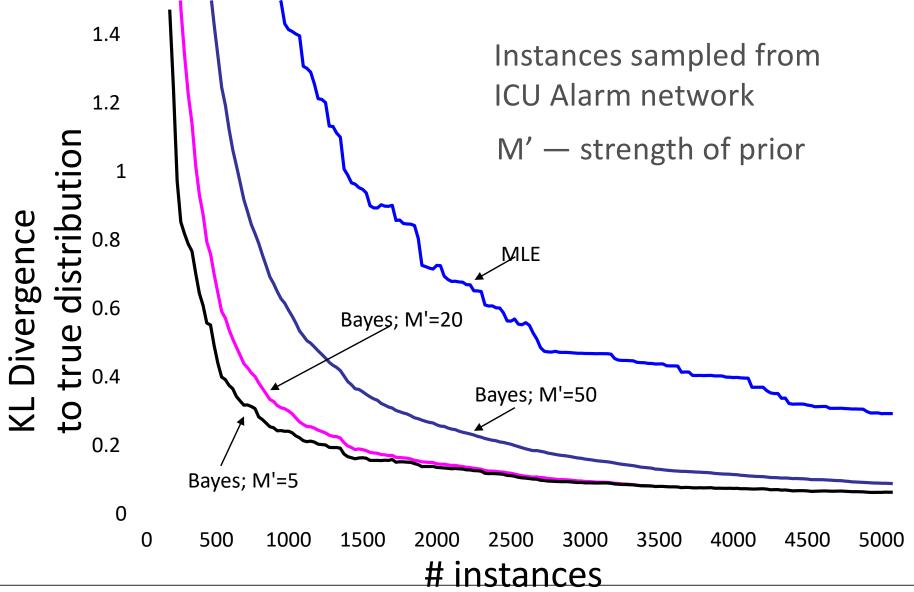
MLE Bayesian (Dirichlet)

Both are asymptotically equivalent and consistent



### **Learning Parameters: Case Study**







#### So far

- Where do the numbers come frome?
  - Expectation-Maximization (EM)
  - Gradient
  - Bayesian learning





#### What's next

- Structure Learning/Model Selection
  - Constrained-based
  - Score-based

- But first
  - I-equivalence, perfect maps etc.





# Recap: Building BNs from independence properties

- From d-separation we learned:
  - Start from local Markov assumptions, obtain all independence assumptions encoded by graph
  - For most P's that factorize over G, I(G) = I(P)
  - All of this discussion was for a given G that is an I-map for P



## **Recap: I-Map to Factorization**



## G is I-map of P obtain

#### P factorizes according to G

- Start with a topological ordering, wlog  $X_1,...,X_n$
- Apply chain rule

$$P(X_1,...,X_n) = P(X_1)P(X_2 | X_1)...P(X_n | X_1,...,X_{n-1})$$

- Consider  $P(X_i | X_1,...,X_{i-1})$
- We know that  $Pa(X_i) \subseteq \{X_1,...,X_{i-1}\}$ , i.e., there are no descendants of Xi in X1,...Xi-1
- Hence, due to local Markov assumption

$$P(X_i | X_1,...,X_{i-1}) = P(X_i | Pa(X_i))$$



## Recap:

## **D-Separation**

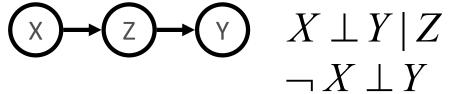
Local Markov Assumption: A variable X is independent of ist non-descendants given its parents and only ist parents:

(Xi  $\perp$  NonDescendants<sub>Xi</sub> | Pa<sub>Xi</sub>)

same distribution

Represent all

#### Indirect causal effect:

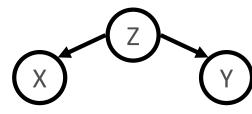


Indirect evidential effect:



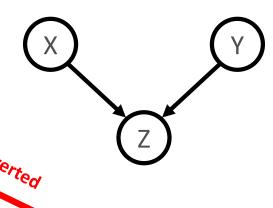
$$X \perp Y \mid Z$$

Common cause:



$$X \perp Y \mid Z$$
  
 $\neg X \perp Y$ 

(v-structure)
Common effect:



$$X \perp Y$$
  
 $\neg X \perp Y \mid Z$ 

# Recap: Building BNs from independence properties



- From d-separation we learned:
  - Start from local Markov assumptions, obtain all independence assumptions encoded by graph
  - For most P's that factorize over G, I(G) = I(P)
  - All of this discussion was for a given G that is an I-map for P
- Now, given a P, how can I get a G?
  - i.e., give me the independence assertions entailed by P
  - However, many Gs are "equivalent".
  - How do we represent this?
  - Most of this discussion is not about practical algorithms, but useful concepts that are used by practical algorithms





#### **Minimal I-maps**

- Given the independence assertions that are true for P,
   find G
- One option:
  - G is an I-map for P,  $I_I(G) \subseteq I(P)$
  - G is as simple as possible
- But what do we mean by "simple"? G is a minimal I-map for P if deleting any edges from G makes it no longer an I-map
- Is this a good idea?

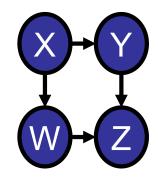




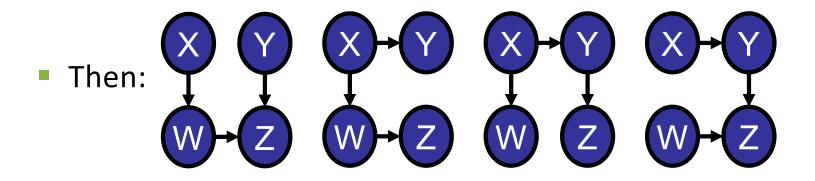
## **Obtaining Minimal I-maps**

Example:

if



is an minimal I-map



are not minimal-maps

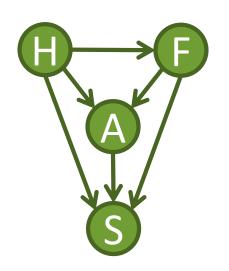


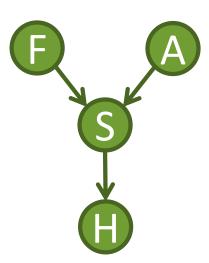


#### **Obtaining Minimal I-maps**

Flu, Allergy, SinusInfection, Headache

Flu, Allergy, SinusInfection, Headache





Both are minimal I-maps (if we remove an edge, they are not I-maps anymore) but the left-hand side BN is much more complicated!





## Perfect maps (P-maps)

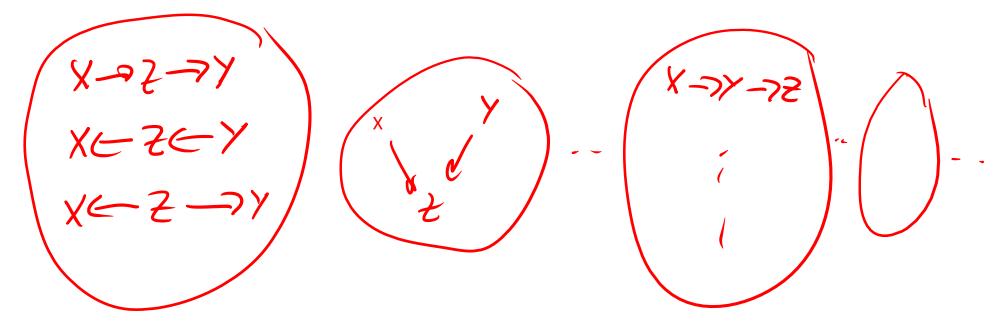
- I-maps are not unique and often not simple enough
- Define "simplest" G differently
  - A BN structure G is a <u>perfect map</u> for P if I(P) = I(G)
- Our new goal is now:
  - Find a perfect map!
  - Must address equivalent BNs





#### **I-Equivalence**

- Two graphs G<sub>1</sub> and G<sub>2</sub> are I-equivalent if I(G<sub>1</sub>) = I(G<sub>2</sub>)
- However, p-maps are not unique
- Equivalence class of BN structures
  - Mutually-exclusive and exhaustive partition of graphs

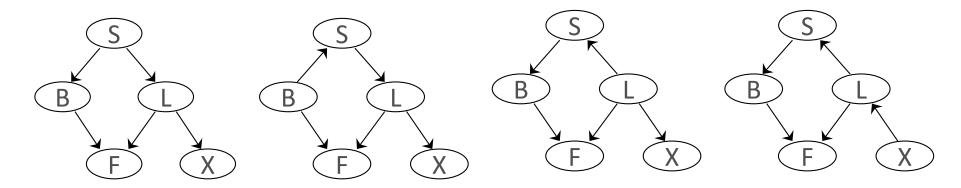


How do we characterize these equivalence classes?

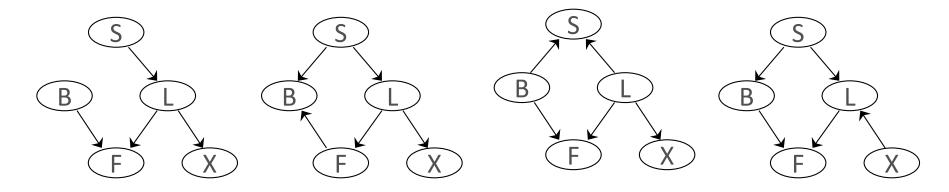


#### **Examples of I-Equivalence**

The following four DAGs are Markov equivalent and are said to form a Markov equivalence class.



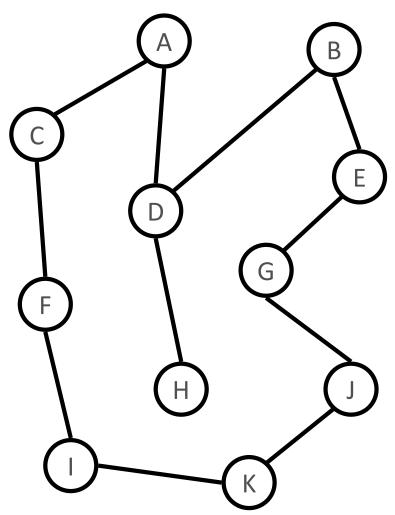
The following four DAGs are not Markov equivalent to those given above:





#### Skeleton of a BN

- Skeleton of a BN structure G is an undirected graph over the same variables that has an edge X-Y for every X->Y or Y->X in G (as we used it already for trails)
- (Little) Lemma: Two I-equivalent
   BN structures must have the same skeleton
- Proof via trials

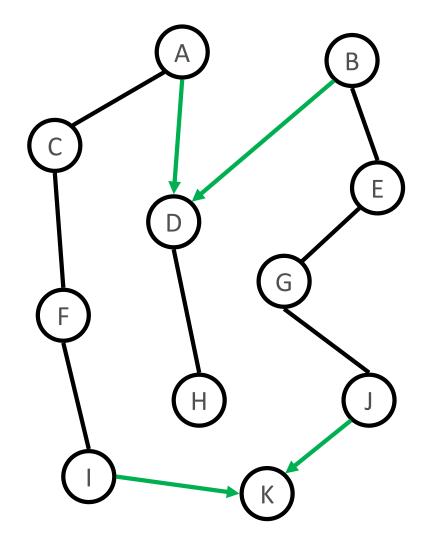


What about the other "direction"?



#### What about V-structures?

- V-structures are key property of BN structure (as used for dseparation)
- Theorem: If G<sub>1</sub> and G<sub>2</sub> have the same skeleton and V-structures, then G<sub>1</sub> and G<sub>2</sub> are I-equivalent
- Proof via trials and rules of dseparation

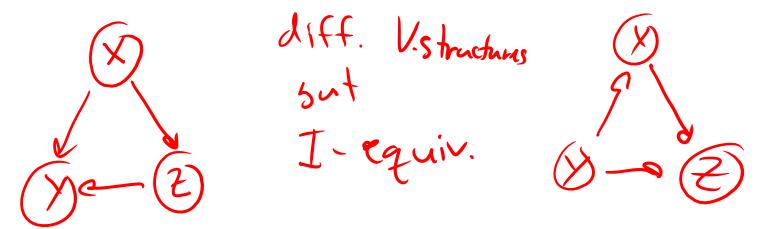




## Same V-structures not necessary

■ **Theorem:** If  $G_1$  and  $G_2$  have the same skeleton and V-structures, then  $G_1$  and  $G_2$  are I-equivalent

Though sufficient, same V-structures not necessary, i.e., no iff



Actually, for the "none-necessity", any complete graph can be considered. They are I-equivalent but they do not have the same V-structures





## **Immoralities & I-Equivalence**

- Key concept is not V-structure, but "immoralities" (unmarried parents <a>></a>)
  - X -> Z <- Y, with no arrow between X and Y</p>
- Important pattern: X and Y independent (given their parents), but not given Z
- (If edge exists between X and Y (moralized), we have covered the V-structure)
- Theorem:

 $G_1$  and  $G_2$  have the same skeleton and immoralities if and only if  $G_1$  and  $G_2$  are lequivalent



#### **Obtaining a P-map**

- Step 1: Given the independence assertions that are true for P
  - Obtain skeleton
  - Obtain immoralities
- We have found the right equivalence class
- Step 2: From skeleton and immoralities, obtain every (and any) BN structure from the equivalence class





#### **Obtaining a P-map**

https://www.youtube.com/watch?v=o2A61bJ0UCw

#### Independence-Based Causal Discovery

Assumptions

Markov Equivalence and Main Theorem

The PC Algorithm

Can We Do Better?

#### Semi-Parametric Causal Discovery

No Identifiability Without Parametric Assumptions

Linear Non-Gaussian Setting

Nonlinear Additive Noise Setting

Brady Neal The PC Algorithm 19 / 45





## Identifying the skeleton

- When is there an edge between X and Y?
  - Difficult to answer

- When is there no edge between X and Y?
  - Local Markov Assumption
  - Exists  $\mathbf{U} \subseteq \mathbf{X} \{X,Y\}$ ,  $|\mathbf{U}| \leq d$ , such that  $(X \perp Y \mid \mathbf{U})$
  - d maximal number of parents





## Identifying the skeleton

- Assume d<=(n-1) is max number of parents</p>
- For each X<sub>i</sub> and X<sub>j</sub>
  - $E_{ij} \leftarrow true$
  - For each  $U \subseteq X \{X_i, X_j\}$ ,  $|U| \le d$ 
    - Is  $(X_i \perp X_j \mid \mathbf{U})$ ? // note that we "assume " to know this
      - $E_{ij} \leftarrow false$
      - break
  - If E<sub>ij</sub> is true
    - Add edge X Y to skeleton
- For measuring independence, there are several ways. One considers the mutual information (you will see this later)





#### Identifying the skeleton

https://www.youtube.com/watch?v=o2A61bJ0UCw

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### **Identifying immoralities**

- Consider X –Z–Y in skeleton, when should it be an immorality X->Z<-Y, i.e., we add the directions X->Z and Y->Z? Essentially when X  $\perp$  Y holds
- Must be X -> Z <- Y (immorality):</p>
  - When X and Y are never independent given U, if Z in U
    - Proof: Assume no Z exists but X—Z—Y is not an immorality
    - Then, either  $X \rightarrow Z \rightarrow Y$  or  $X \leftarrow Z \leftarrow Y$  or  $X \leftarrow Z \rightarrow Y$  exists
    - But then, we can block X–Z–Y by Z
    - Then, since X and Y are not connected, can find U that includes Z such that Ind(X;Y | W)
    - Contradiction
- Must not be X -> Z <- Y (not immorality):</p>
  - When there exists U with Z in U, such that X and Y are independent given U





#### **Identifying immoralities**

https://www.youtube.com/watch?v=o2A61bJ0UCw

#### **Independence-Based Causal Discovery**

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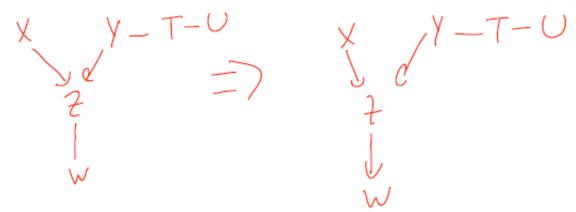
Nonlinear Additive Noise Setting

Brady Neal The PC Algorithm 19 / 45



## From immoralities and skeleton to BN structures

- Representing BN equivalence class as a partiallydirected acyclic graph (PDAG)
- Immoralities force direction on other BN edges



Otherwise we would get another immoral v-structure, which was ruled out by the algorithm

Full (polynomial-time) procedure exists





## **Discovering more directions**

https://www.youtube.com/watch?v=o2A61bJ0UCw

#### **Independence-Based Causal Discovery**

Assumptions

Markov Equivalence and Main Theorem

The PC Algorithm

Can We Do Better?

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Brady Neal The PC Algorithm 19 / 45





#### What you need to know

- Minimal I-map
  - every P has one, but usually many
- Perfect map
  - better choice for BN structure
  - not every P has one
  - can find one (if it exists) by considering Iequivalence
  - Two structures are I-equivalent if they have same skeleton and immoralities



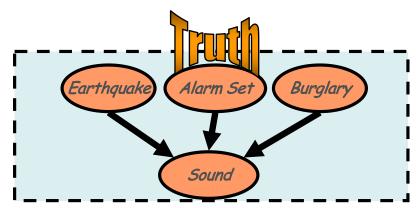
## **Learning With Bayesian Networks**



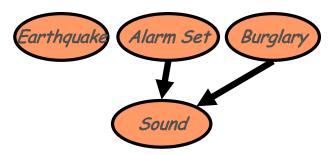
		Fixed structure $A \longrightarrow B$	Fixed variables  A ? B	Hidden variables  A?B?H
obs	fully	Easiest problem counting	Selection of arcs New domain with no domain expert Data mining	
observed	Partially	Numerical, nonlinear optimization, Multiple calls to BNs, Difficult for large networks	Encompasses to difficult subproblem, "Only" Structural EM is known	Scientific discouvery
		Parameter Estimation	Stucture learing	



#### Why Struggle for Accurate Structure?

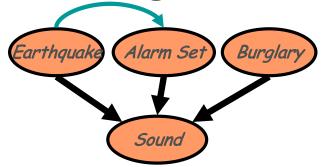


#### Missing an arc



- Cannot be compensated for by fitting parameters
- Wrong assumptions about domain structure

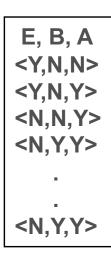
#### Adding an arc



- Increases the number of parameters to be estimated
- Wrong assumptions about domain structure

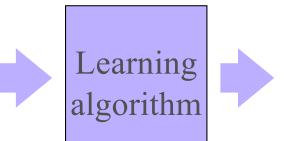


## Unknown Structure, (In)complete Data



- Network structure is not specified
  - Learnerr needs to select arcs & estimate parameters
- Data does not contain missing values

E	В	P(A	/ E,B)	
e	Ь	?	?	
е	Ь	?	?	
e	Ь	?	?	
е	Ь	?	?	

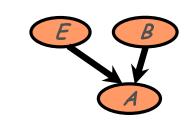






<?,Y,Y>

- Network structure is not specified
- Data contains missing values
  - Need to consider assignments to missing values



| E | В | P(A | / E,B) |
|---|---|-----|--------|
| е | Ь | .9  | .1     |
| е | Ь | .7  | .3     |
| e | Ь | .8  | .2     |
| e | Ь | .99 | .01    |





## **Structure Learning**

Two main approaches

- 1. Constrained-based
- 2. Score-based





#### **Constraint-Based Learning**

- Remember: Optaining a P-Map?
  - Given the independence assertions that are true for P
    - Obtain skeleton and then obtain immoralities
  - From skeleton and immoralities, obtain every (and any)
     BN structure from the equivalence class
- Only now, we do not have I(X,Y|Z) statements
- Basic task:
  - Determine whether two variables are independent
  - Well studied question in statistics





#### **Testing Independence**

- Null hypothesis H0 is
  - Data was sampled from P(X,Y)=P(X)\*P(Y)
- Need a procedure that will Accept or Reject H0
- Use  $\chi^2$  -test
  - χ² (X,Y) ~ I(X,Y)\* N \* In(4) where I(X,Y) is the mutual information
- Or directly mutual information

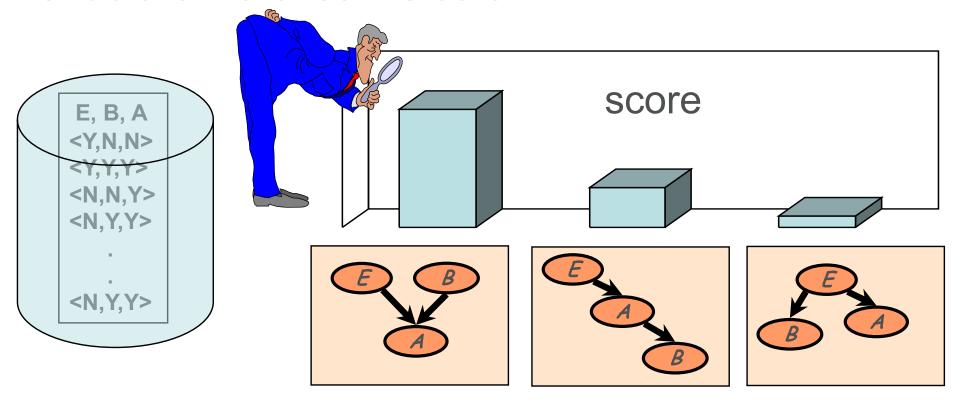
$$\widehat{P}(x_i, x_j) = \frac{\mathsf{Count}(x_i, x_j)}{m} \qquad \qquad \widehat{I}(X_i, X_j) = \sum_{x_i, x_j} \widehat{P}(x_i, x_j) \log \frac{\widehat{P}(x_i, x_j)}{\widehat{P}(x_i) \widehat{P}(x_j)}$$



## **Score-based Learning**



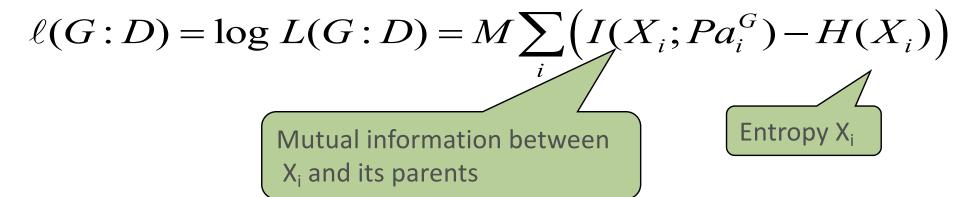
Define scoring function that evaluates how well a structure matches the data



Search for a structure that maximizes the score



#### **Likelihood Score for Structure**



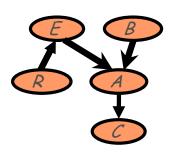
- Larger dependence of  $X_i$  on  $Pa_i \Rightarrow$  higher score
- Adding arcs always helps
  - $I(X; Y) \leq I(X; \{Y,Z\})$
  - Max score attained by fully connected network
  - Overfitting: A bad idea...





P(G|D)

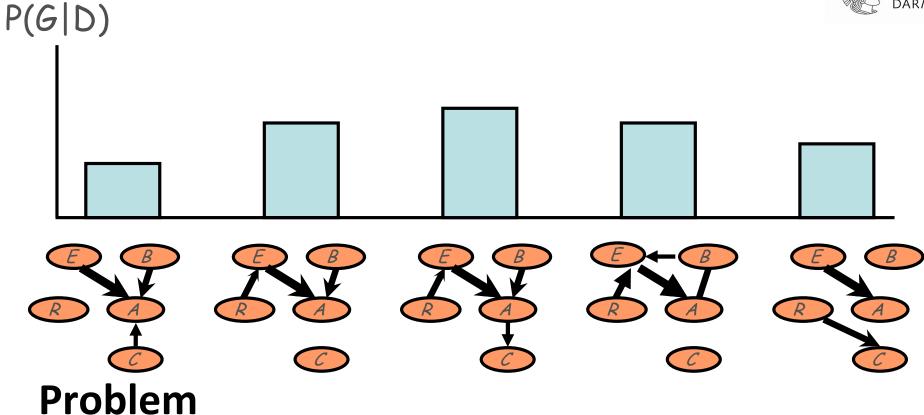
Picking a single best model can be misleading



- Current practice: model selection
  - Pick a single high-scoring model
  - Use that model to infer domain structure







- Small sample size ⇒ many high scoring models
- Answer based on one model often useless





Likelihood score:

$$L(G:D) = P(D \mid G, \hat{\theta}_G)$$

Max likelihood params

#### **Bayesian approach:**

Deal with uncertainty by assigning probability to all possibilities

$$P(G \mid D) = \frac{P(D \mid G)P(G)}{P(D)}$$





- Bayesian has difficult integrals
- For Dirichlet prior, can use simple Bayes information criterion (BIC) approximation

Theorem: for Dirichlet prior, and a BN with Dim(G) independent parameters, as m→∞:

$$\log P(D \mid G) = \log(D \mid G, \theta) - \frac{\log M}{2} \dim(G) + O(1)$$

## **Bayesian Information Criterion (BIC)**

$$\log P(D | G) = \ell(G : D) - \frac{\log M}{2} \dim(G) + O(1)$$

$$= M \sum_{i} \left( I(X_i; Pa_i^G) - H(X_i) \right) - \frac{\log M}{2} \dim(G) + O(1)$$

Fit dependencies in empirical distribution

Complexity penalty

- As M (amount of data) grows,
  - Increasing pressure to fit dependencies in distribution
  - Complexity term avoids fitting noise
- Asymptotic equivalence to MDL score
- Bayesian score/BIC is consistent
  - Observed data eventually overrides prior





## **Structure Search as Optimization**

#### Input:

- Training data
- Scoring function (MDL, BIC, ...)
- Set of possible structures

#### **Output:**

A network that maximizes the score





## **Learning Trees (complete data)**

https://www.youtube.com/watch?v=8N0HsrBY7WI&t=3629s Vibhav Gogate, UT Dallas

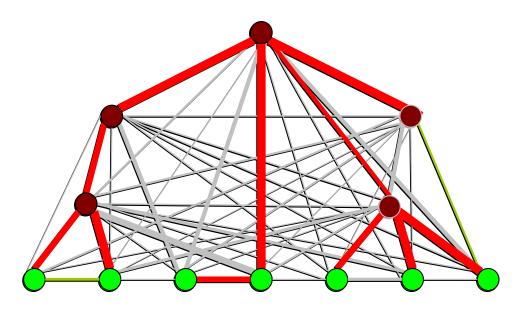
#### Learning Bounded Treewidth Models

- Good news: Models with treewidth 1 can be learned optimally in polynomial time! Recall that such Bayesian networks are called Singly-connected Bayesian networks and their primal graph is a tree.
- Bad news: Models having treewidth > 1 are NP-hard to learn.





## **Learning Trees (complete data)**



- Can find optimal tree structure in O(n² log n) time: just find the max-weight spanning tree
- If some of the variables are hidden, problem becomes hard again, but can use EM to fit mixtures of trees



## **Heuristic Search**



- Define a search space:
  - search states are possible structures
  - operators make small changes to structure
- Traverse space looking for high-scoring structures
- Search techniques:
  - Greedy hill-climbing
  - Best first search
  - Simulated Annealing

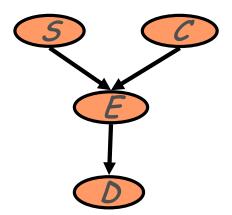
Theorem: Finding maximal scoring structure with at most k parents per node is NP-hard for k > 1

• • • •





- Start with a given network
  - empty network, best tree, a random network
- At each iteration
  - Evaluate all possible changes
  - Apply change based on score
- Stop when no modification improves score





Start with a given network

empty network, best tree , a random network

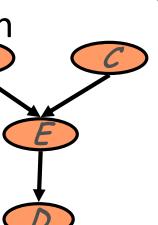
At each iteration

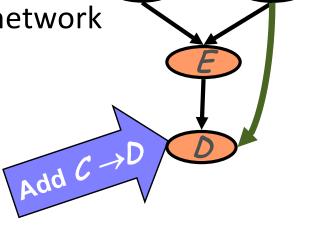
Evaluate all possible changes

Apply change based on score

Stop when no modification

improves score







Start with a given network

empty network, best tree , a random network

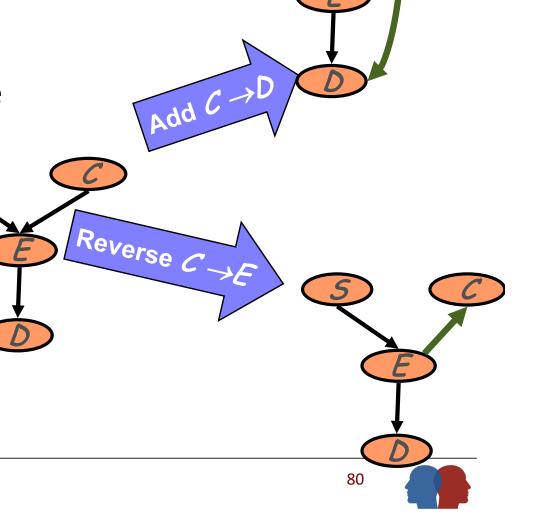
At each iteration

Evaluate all possible changes

Apply change based on score

Stop when no modification

improves score





Start with a given network

empty network, best tree , a random network

At each iteration

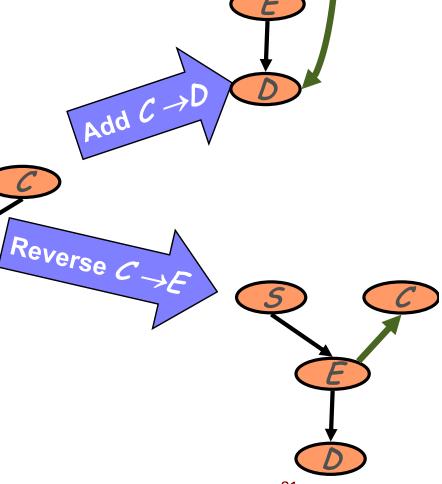
Evaluate all possible changes

Apply change based on score

Delete C

Stop when no modification

improves score



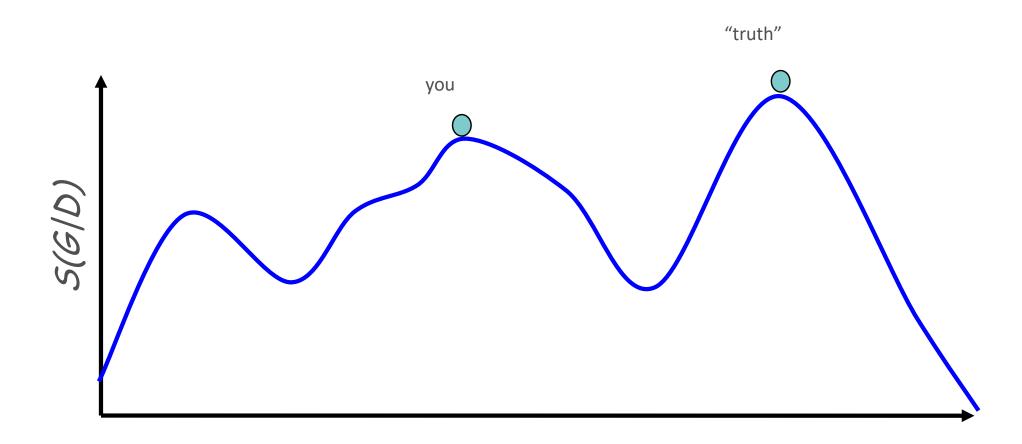


If data is **complete:** To update score after local change, only re-score (counting) families that changed Add  $C \rightarrow D$ Reverse C→E Delete C If data is **incomplete:** To update score after local change,

reran parameter estimation algorithm

#### Other Problem with local search





Easy to get stuck in local optima



#### **Local Search in Practice**



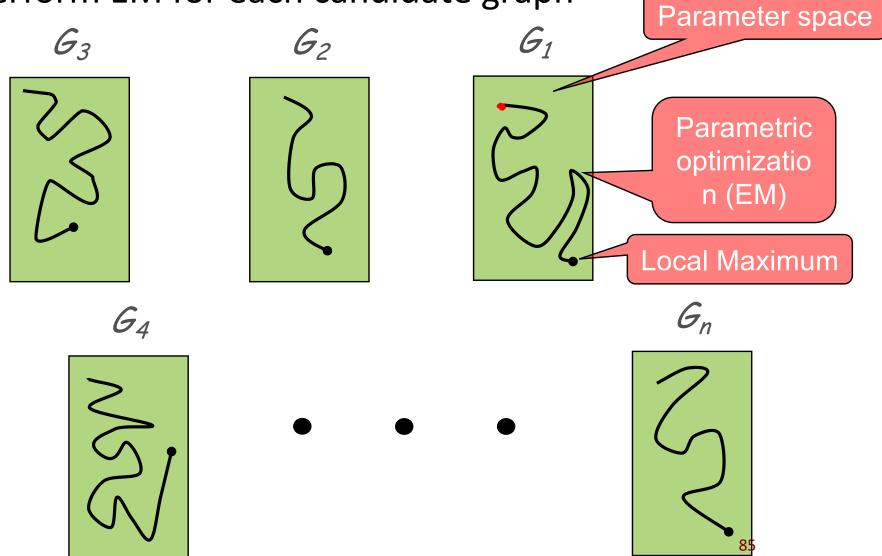
- Local search can get stuck in:
  - Local Maxima:
    - All one-edge changes reduce the score
  - Plateaux:
    - Some one-edge changes leave the score unchanged
- So, standard heuristics can escape both
  - Random restarts
  - TABU search
  - Simulated annealing





#### **Local Search in Practice**

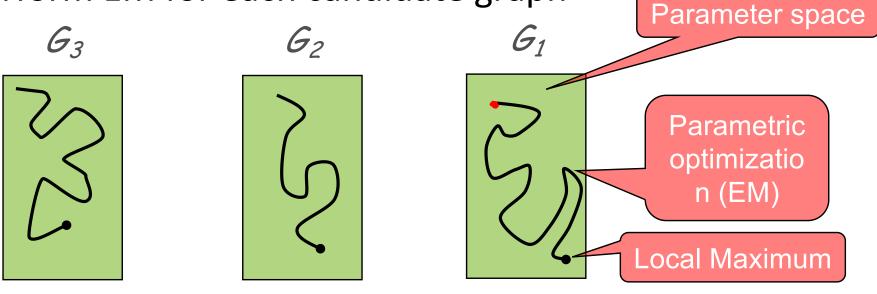
Perform EM for each candidate graph





#### **Local Search in Practice**

Perform EM for each candidate graph



- Computationally expensive:
  - Parameter optimization via EM non-trivial
  - Need to perform EM for all candidate structures
  - Spend time even on poor candidates
- ⇒ In practice, considers only a few candidates

#### Structural EM



[Friedman et al. 98]

## Recall, in complete data we had

■ Decomposition ⇒ efficient search

#### Idea:

- Instead of optimizing the real score...
- Find decomposable alternative score
- Such that maximizing new score
  - ⇒ improvement in real score



#### Structural EM



[Friedman et al. 98]

#### Idea:

Use current model to help evaluate new structures

#### **Outline:**

- Perform search in (Structure, Parameters) space
- At each iteration, use current model for finding
  - Better scoring parameters: "parametric" EM step

#### or

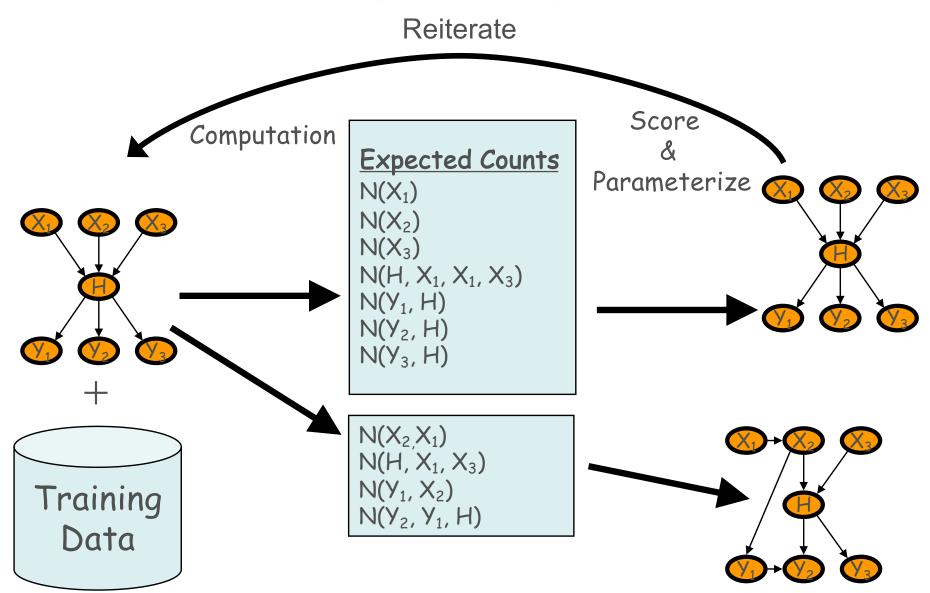
Better scoring structure: "structural" EM step



## Structural EM

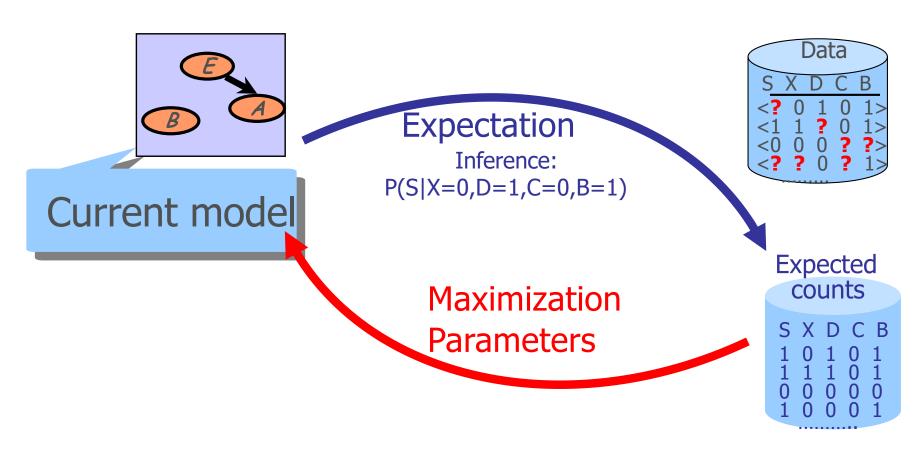


[Friedman et al. 98]





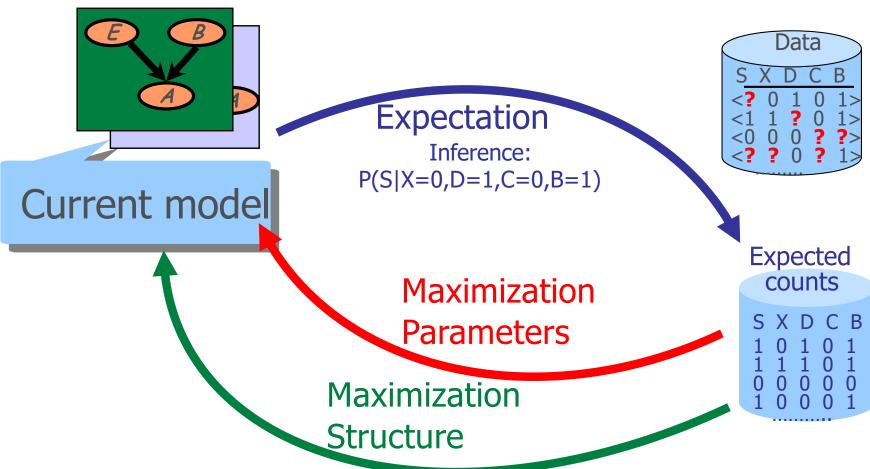
## Structure Learning: incomplete data



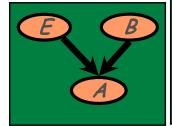
**EM**-algorithm: iterate until convergence

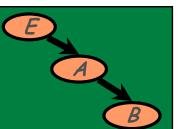


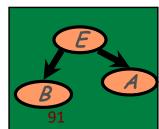
## Structure Learning: incomplete data



**SEM**-algorithm: iterate until convergence







## **Structure Learning: Summary**



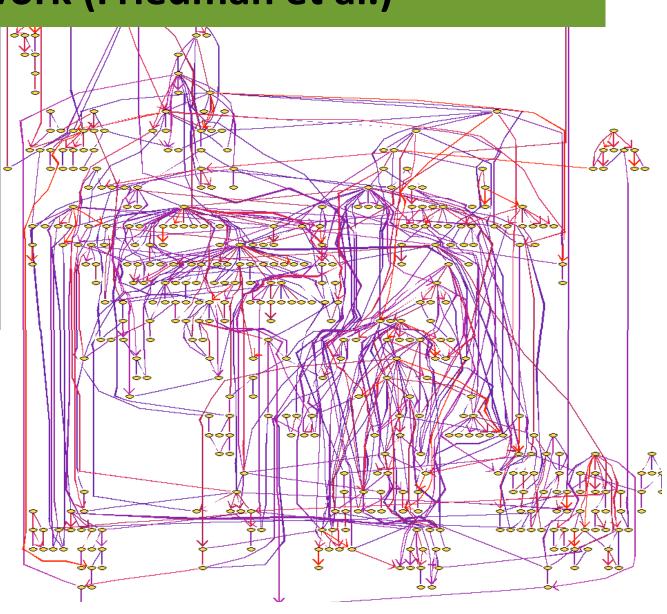
- Expert knowledge + learning from data
- Structure learning involves parameter estimation (e.g. EM)
- Optimization w/ score functions
  - likelihood + complexity penality = MDL
- Local traversing of space of possible structures:
  - add, reverse, delete (single) arcs
- Speed-up: Structural EM
  - Score candidates w.r.t. current best model



# Structure learning success stories: gene regulation network (Friedman et al.)

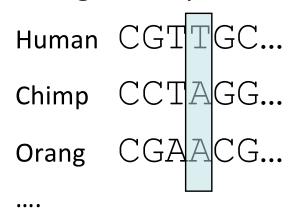
Yeast data [Hughes et al 2000]

- 600 genes
- 300 experiments



## Structure learning success stories II: Phylogenetic Tree Reconstruction (Friedman et al.)

**Input:** Biological sequences



Uses structural EM, with max-spanning-tree in the inner loop

Output: a phylogeny

