

## Recap of Basic Prob. Concepts

- Joint probability dist. on multiple variables:

$$
\begin{aligned}
& P\left(X_{1}, X_{2}, X_{3}, X_{4}, X_{5}, X_{6}\right) \\
= & P\left(X_{1}\right) P\left(X_{2} \mid X_{1}\right) P\left(X_{3} \mid X_{1}, X_{2}\right) P\left(X_{4} \mid X_{1}, X_{2}, X_{3}\right) P\left(X_{5} \mid X_{1}, X_{2}, X_{3}, X_{4}\right) P\left(X_{6} \mid X_{1}, X_{2}, X_{3}, X_{4}, X_{5}\right)
\end{aligned}
$$

- If $X_{i}$ 's are independent: $\left(P\left(X_{i} \mid \cdot\right)=P\left(X_{i}\right)\right)$
$P\left(X_{1}, X_{2}, X_{3}, X_{4}, X_{5}, X_{6}\right)$
$=P\left(X_{1}\right) P\left(X_{2}\right) P\left(X_{3}\right) P\left(X_{4}\right) P\left(X_{5}\right) P\left(X_{6}\right)=\prod P\left(X_{i}\right)$
- If $X_{i}$ 's are conditionally independent (as described by a GM), the joint can be factored to simpler products, e.g.,


$$
\begin{aligned}
& P\left(X_{1}, X_{2}, X_{3}, X_{4}, X_{5}, X_{6}\right) \\
= & P\left(X_{1}\right) P\left(X_{2}\right) P\left(X_{3} \mid X_{1}, X_{2}\right) P\left(X_{4} \mid X_{3}\right) P\left(X_{5} \mid X_{3}\right) P\left(X_{6} \mid X_{4}, X_{5}\right)
\end{aligned}
$$

## Inference and Learning

- We now have compact representations of probability distributions: Graphical Models
- A GM $M$ describes a unique probability distribution $P$
- Typical tasks:
- Task 1: How do we answer queries about $P$ ?
- We use inference as a name for the process of computing answers to such queries
- Task 2: How do we estimate a plausible model $M$ from data $D$ ?
i. We use learning as a name for the process of obtaining point estimate of $M$.
ii. But for Bayesian, they seek $p(M \mid D)$, which is actually an inference problem.
iii. When not all variables are observable, even computing point estimate of $M$ need to do inference to impute the missing data.


## Inferential Query 1: Likelihood

- Most of the queries one may ask involve evidence
- Evidence $\mathbf{x}_{\mathrm{v}}$ is an assignment of values to a set $\mathbf{X}_{\mathrm{v}}$ of nodes in the GM over varialbe set $\mathbf{X}=\left\{X_{1}, X_{2}, \ldots, X_{\mathrm{n}}\right\}$
- Without loss of generality $\mathbf{X}_{\mathrm{v}}=\left\{X_{k+1}, \ldots, X_{\mathrm{n}}\right\}$,
- Write $\mathbf{X}_{\mathbf{H}}=\mathbf{X} \backslash \mathbf{X}_{\mathrm{v}}$ as the set of hidden variables, $\mathbf{X}_{\mathbf{H}}$ can be $\varnothing$ or $\mathbf{X}$
- Simplest query: compute probability of evidence

$$
P\left(\mathbf{x}_{\mathbf{v}}\right)=\sum_{\mathbf{x}_{\mathbf{H}}} P\left(\mathbf{X}_{\mathbf{H}},, \mathbf{X}_{\mathbf{v}}\right)=\sum_{x_{1}} \ldots \sum_{x_{k}} P\left(x_{1}, \ldots, x_{k}, \mathbf{X}_{\mathbf{v}}\right)
$$

- this is often referred to as computing the likelihood of $\mathrm{x}_{\mathrm{v}}$


## Inferential Query 2: Conditional Probability

- Often we are interested in the conditional probability distribution of a variable given the evidence

$$
P\left(\mathbf{X}_{\mathrm{H}} \mid \mathbf{X}_{\mathrm{V}}=\mathbf{x}_{\mathrm{V}}\right)=\frac{P\left(\mathbf{X}_{\mathrm{H}}, \mathbf{x}_{\mathrm{V}}\right)}{P\left(\mathbf{x}_{\mathrm{V}}\right)}=\frac{P\left(\mathbf{X}_{\mathrm{H}}, \mathbf{x}_{\mathrm{V}}\right)}{\sum_{\mathrm{x}_{\mathrm{H}}} P\left(\mathbf{X}_{\mathrm{H}}=\mathbf{x}_{\mathrm{H}}, \mathbf{x}_{\mathrm{V}}\right)}
$$

- this is the a posteriori belief in $X_{H}$, given evidence $\mathbf{x}_{\mathrm{v}}$
- We usually query a subset $\mathbf{Y}$ of all hidden variables $\mathbf{X}_{\mathbf{H}}=\{\mathbf{Y}, \mathbf{Z}\}$ and "don't care" about the remaining, $\mathbf{Z}$ :

$$
P\left(\mathbf{Y} \mid \mathbf{x}_{\mathbf{v}}\right)=\sum_{\mathbf{z}} P\left(\mathbf{Y}, \mathbf{Z}=\mathbf{z} \mid \mathbf{x}_{\mathbf{v}}\right)
$$

- the process of summing out the "don't care" variables $z$ is called marginalization, and the resulting $P\left(\mathbf{Y} \mid \mathbf{x}_{v}\right)$ is called a marginal prob.


## Applications of a posteriori Belief

- Prediction: what is the probability of an outcome given the starting condition

- the query node is a descendent of the evidence
- Diagnosis: what is the probability of disease/fault given symptoms

- the query node an ancestor of the evidence
- Learning under partial observation
- fill in the unobserved values under an "EM" setting (more later)
- The directionality of information flow between variables is not restricted by the directionality of the edges in a GM
- probabilistic inference can combine evidence form all parts of the network


## Inferential Query 3: Most Probable Assignment

- In this query we want to find the most probable joint assignment (MPA) for some variables of interest
- Such reasoning is usually performed under some given evidence $\mathbf{x}_{\mathbf{v}}$, and ignoring (the values of) other variables $\mathbf{Z}$ :

$$
\mathbf{Y}^{*} \mid \mathbf{x}_{\mathrm{v}}=\arg \max _{\mathrm{y}} P\left(\mathbf{Y} \mid \mathbf{x}_{\mathrm{v}}\right)=\arg _{\max }^{\mathrm{y}_{\mathrm{z}}} \sum_{\mathrm{z}} P\left(\mathbf{Y}, \mathbf{Z}=\mathbf{z} \mid \mathbf{x}_{\mathrm{v}}\right)
$$

- this is the maximum a posteriori configuration of $\mathbf{Y}$.


## Applications of MPA

- Classification
- find most likely label, given the evidence
- Explanation
- what is the most likely scenario, given the evidence

Cautionary note:

- The MPA of a variable depends on its "context"---the set of variables been jointly queried
- Example:
- MPA of $X$ ?
- MPA of $(X, Y)$ ?

| $x$ | $y$ | $P(x, y)$ |
| ---: | ---: | ---: |
| 0 | 0 | 0.35 |
| 0 | 1 | 0.05 |
| 1 | 0 | 0.3 |
| 1 | 1 | 0.3 |

## Complexity of Inference

Thm:
Computing $P\left(\mathbf{X}_{\mathbf{H}}=\mathbf{x}_{\mathbf{H}} \mid \mathbf{x}_{\mathbf{v}}\right)$ in an arbitrary GM is NP-hard

- Hardness does not mean we cannot solve inference
- It implies that we cannot find a general procedure that works efficiently for arbitrary GMs
- For particular families of GMs, we can have provably efficient procedures


## Approaches to inference

- Exact inference algorithms
- The sum-product algorithm
- The junction tree algorithm $\sqrt{ }$
- Approximate inference techniques
- Stochastic simulation / sampling methods
- Markov chain Monte Carlo methods
- Variational algorithms (later lectures)


## The Junction Tree Algorithm

- There are several inference algorithms; some of which operate directly on (special) directed graph
- Forward-backward algorithm for HMM (we will see it later)
- Pealing algorithm for trees and phylogenies
- The junction tree algorithm is the most popular and general inference algorithm, it operates on an undirected graph
- To understand the JT-algorithm, we need to understand how to compile a directed graph into an undirected graph


## Moral Graph

- Note that for both directed GMs and undirected GMs, the joint probability is in a product form:

$$
\mathrm{BN}: P(\mathbf{X})=\prod_{i=1: d} P\left(X_{i} \mid \mathbf{X}_{\pi_{i}}\right) \quad \text { MRF: } P(\mathbf{X})=\frac{1}{Z} \prod_{c \in C} \psi_{c}\left(\mathbf{X}_{c}\right)
$$

- So let's convert local conditional probabilities into potentials; then the second expression will be generic, but how does this operation affect the directed graph?
- We can think of a conditional probability, e.g,. $P(C \mid A, B)$ as a function of the three variables $A, B$, and $C$ (we get a real number of each configuration):


- Problem: But a node and its parent are not generally in the same clique in a BN
- Solution: Marry the parents to obtain the "moral graph"


## Moral Graph (cont.)

- Define the potential on a clique as the product over all conditional probabilities contained within the clique
- Now the product of potentials gives the right answer:


$$
\begin{aligned}
& P\left(X_{1}, X_{2}, X_{3}, X_{4}, X_{5}, X_{6}\right) \\
= & P\left(X_{1}\right) P\left(X_{2}\right) P\left(X_{3} \mid X_{1}, X_{2}\right) P\left(X_{4} \mid X_{3}\right) P\left(X_{5} \mid X_{3}\right) P\left(X_{6} \mid X_{4}, X_{5}\right) \\
= & \psi\left(X_{1}, X_{2}, X_{3}\right) \psi\left(X_{3}, X_{4}, X_{5}\right) \psi\left(X_{4}, X_{5}, X_{6}\right)
\end{aligned}
$$

where
$\psi\left(X_{1}, X_{2}, X_{3}\right)=P\left(X_{1}\right) P\left(X_{2}\right) P\left(X_{3} \mid X_{1}, X_{2}\right)$
$\psi\left(X_{3}, X_{4}, X_{5}\right)=P\left(X_{4} \mid X_{3}\right) P\left(X_{5} \mid X_{3}\right)$
$\psi\left(X_{4}, X_{5}, X_{6}\right)=P\left(X_{6} \mid X_{4}, X_{5}\right)$

Note that here the interpretation of potential is ambivalent: it can be either marginals or conditionals

## Clique trees

- A clique tree is an (undirected) tree of cliques

- Consider cases in which two neighboring cliques $V$ and $W$ have an overlap $S$ (e.g., ( $X_{1}, X_{2}, X_{3}$ ) overlaps with ( $X_{3}, X_{4}, X_{5}$ ) ),

- Now we have an alternative representation of the joint in terms of the potentials:


## Clique trees

- A clique tree is an (undirected) tree of cliques


- The alternative representation of the joint in terms of the potentials:

$$
\begin{aligned}
& P\left(X_{1}, X_{2}, X_{3}, X_{4}, X_{5}, X_{6}\right) \\
= & P\left(X_{1}\right) P\left(X_{2}\right) P\left(X_{3} \mid X_{1}, X_{2}\right) P\left(X_{4} \mid X_{3}\right) P\left(X_{5} \mid X_{3}\right) P\left(X_{6} \mid X_{4}, X_{5}\right) \\
= & P\left(X_{1}, X_{2}, X_{3}\right) \frac{P\left(X_{3}, X_{4}, X_{5}\right)}{P\left(X_{3}\right)} \frac{P\left(X_{4}, X_{5}, X_{6}\right)}{P\left(X_{4}, X_{5}\right)} \\
= & \psi\left(X_{1}, X_{2}, X_{3}\right) \frac{\psi\left(X_{3}, X_{4}, X_{5}\right)}{\phi\left(X_{3}\right)} \frac{\psi\left(X_{4}, X_{5}, X_{6}\right)}{\phi\left(X_{4}, X_{5}\right)} \\
& \begin{array}{l}
\text { Now each potential is } \\
\text { isomorphic to the cluster } \\
\text { marginal of the attendant } \\
\text { set of variables }
\end{array} \\
P(\mathbf{X})=\frac{\prod_{C} \psi_{C}\left(\mathbf{X}_{C}\right)}{\prod_{S} \phi_{S}\left(\mathbf{X}_{S}\right)} &
\end{aligned}
$$

- Generally:


## Why this is useful?

- Propagation of probabilities
- Now suppose that some evidence has been "absorbed" (i.e., certain values of some nodes have been observed). How do we propagate this effect to the rest of the graph?



- What do we mean by propagate?

Can we adjust all the potentials $\{\psi\}$, $\{\phi\}$ so that they still represent the correct cluster marginals (or unnormalized equivalents) of their respective attendant variables?

- Utility?

$$
\begin{gathered}
P\left(X_{1} \mid X_{6}=x_{6}\right)=\sum_{X_{2}, X_{3}} \psi\left(X_{1}, X_{2}, X_{3}\right) \\
P\left(X_{3} \mid X_{6}=x_{6}\right)=\phi\left(X_{3}\right)
\end{gathered}
$$



Local operations!

Eric Xing

$$
P\left(X_{6}\right)=\sum_{X_{4}, X_{5}} \psi\left(X_{4}, X_{5}, x_{6}\right)
$$

## Local Consistency

- We have two ways of obtaining $p(S)$

$$
P(S)=\sum_{V \backslash S} \psi(V) \quad P(S)=\sum_{W \backslash S} \psi(W)
$$


and they must be the same

- The following update-rule ensures this:
- Forward update: $\phi_{S}^{*}=\sum_{V \backslash S} \psi_{V} \quad \psi_{W}^{*}=\frac{\phi_{S}^{*}}{\phi_{S}} \psi_{W}$
- Backward update $\phi_{S}^{* *}=\sum_{W \backslash S} \psi_{W}^{*} \psi_{V}^{* *}=\frac{\phi_{S}}{\phi_{S}^{*}} \psi_{V}^{*}$
- Two important identities can be proven

$$
\begin{gathered}
\sum_{V \backslash S} \psi_{V}^{* *}=\sum_{W \backslash S} \psi_{W}^{*}=\phi_{S}^{* *} \\
\text { Local Consistency }
\end{gathered}
$$

$\frac{\psi_{V}^{*} \psi_{W}^{*}}{\phi_{S}^{*}}=\frac{\psi_{V}^{* *} \psi_{W}^{* *}}{\phi_{S}^{* *}}=\frac{\psi_{V} \psi_{W}}{\phi_{S}}$
Invariant Joint

## Message Passing Algorithm



$$
\begin{array}{ll}
\phi_{S}^{*}=\sum_{V \backslash S} \psi_{V} & \psi_{W}^{*}=\frac{\phi_{S}^{*}}{\phi_{S}} \psi_{W} \\
\phi_{S}^{* *}=\sum_{W \backslash S} \psi_{W}^{*} & \psi_{V}^{* *}=\frac{\phi_{S}^{* *}}{\phi_{S}^{*}} \psi_{V}^{*}
\end{array}
$$

- This simple local message-passing algorithn on a clique tree defines the general probability propagation algorithm for directed graphs!
- Many interesting algorithms are special cases:
- Forward-backward algorithm for hidden Markov models,
- Kalman filter updates
- Pealing algorithms for probabilistic trees
- The algorithm seems reasonable. Is it correct?


## A problem

- Consider the following graph and a corresponding clique tree

- Note that C appears in two non-neighboring cliques
- Question: with the previous message passage, can we ensure that the probability associated with C in these two (nonneighboring) cliques consistent?
- Answer: No. It is not true that in general local consistency implies global consistency
- What else do we need to get such a guarantee?


## Triangulation

- A triangulated graph is one in which no cycles with four or more nodes exist in which there is no chord

- We triangulate a graph by adding chords:
- Now we no longer have our global inconsistency problem.

- A clique tree for a triangulated graph has the running intersection property: If a node appears in two cliques, it appears everywhere on the path between the cliques
- Thus local consistency implies global consistency



## Junction trees

- A clique tree for a triangulated graph is referred to as a junction tree
- In junction trees, local consistency implies global consistency. Thus the local message-passing algorithms is (provably) correct
- It is also possible to show that only triangulated graphs have the property that their clique trees are junctions. Thus if we want local algorithms, we must triangulate
- Are we now all set?
- How to triangulate?
- The complexity of building a

JT depends on how we triangulate!!

- Consider this network:
it turns out that we will need to pay an $\mathrm{O}\left(2^{4}\right)$
or $\mathrm{O}\left(2^{6}\right)$ cost depending on how we triangulate!
Eric Xing



## How to triangulate

- A graph elimination algorithm

- Intermediate terms correspond to the cliques resulted from elimination
- "good" elimination orderings lead to small cliques and hence reduce complexity (what will happen if we eliminate "e" first in the above graph?)
- finding the optimum ordering is NP-hard, but for many graph optimum or near-optimum can often be heuristically found


## From Elimination to Message Passing

- Our algorithm so far answers only one query (e.g., on one node), do we need to do a complete elimination for every such query?
- Elimination $\equiv$ message passing on a clique tree




## From Elimination to Message Passing

- Our algorithm so far answers only one query (e.g., on one node), do we need to do a complete elimination for every such query?
- Elimination $\equiv$ message passing on a clique tree
- Another query ...

- Messages $m_{f}$ and $m_{h}$ are reused, others need to be recomputed


## Message-passing algorithms


collect

distribute

- Message update
- The Hugin update

$$
\phi_{S}^{*}=\sum_{V \backslash S} \psi_{V} \quad \psi_{W}^{*}=\frac{\phi_{S}^{*}}{\phi_{S}} \psi_{W}
$$

- The Shafer-Shenoy update

$$
m_{i \rightarrow j}\left(S_{i j}\right)=\sum_{C_{i} \backslash S_{i j}} \psi_{C_{i}} \prod_{k \neq j} m_{k \rightarrow i}\left(S_{k i}\right)
$$

## A Sketch of the Junction Tree Algorithm

- The algorithm

1. Moralize the graph (trivial)
2. Triangulate the graph (good heuristic exist, but actually NP hard)
3. Build a clique tree (e.g., using a maximum spanning tree algorithm
4. Propagation of probabilities --- a local message-passing protocol

- Results in marginal probabilities of all cliques --- solves all queries in a single run
- A generic exact inference algorithm for any GM
- Complexity: exponential in the size of the maximal clique --- a good elimination order often leads to small maximal clique, and hence a good (i.e., thin) JT


## Case study:

## Recall definition of HMM

 $0 \cdot 0$ 000 000 - 0- Transition probabilities between any two states

$$
p\left(y_{t}^{j}=1 \mid y_{t-1}^{i}=1\right)=a_{i, j},
$$


or $p\left(y_{t} \mid y_{t-1}^{i}=1\right) \sim \operatorname{Multinomial}\left(a_{i, 1}, a_{i, 2}, \ldots, a_{i, M}\right), \forall i \in \mathbb{I}$.

- Start probabilities

$$
p\left(y_{1}\right) \sim \operatorname{Multinomial}\left(\pi_{1}, \pi_{2}, \ldots, \pi_{M}\right) .
$$

- Emission probabilities associated with each state

$$
p\left(x_{t} \mid y_{t}^{i}=1\right) \sim \operatorname{Multinomial}\left(b_{i, 1}, b_{i, 2}, \ldots, b_{i, K}\right), \forall i \in \mathbb{I} .
$$

or in general:

$$
p\left(x_{t} \mid y_{t}^{i}=1\right) \sim \mathrm{f}\left(\cdot \mid \theta_{i}\right), \forall i \in \mathbb{I} .
$$

## Probability of a parse

- Given a sequence $\mathbf{x}=x_{1} \ldots \ldots x_{T}$ and a parse $y=y_{1}, \ldots \ldots, y_{\mathrm{T}}$,
- To find how likely is the parse: (given our HMM and the sequence)

$$
\begin{aligned}
p(\mathbf{x}, \mathbf{y}) & =p\left(x_{1} \ldots \ldots x_{\mathrm{T}}, y_{1}, \ldots \ldots, y_{\mathrm{T}}\right) \quad \text { (Joint probability) } \\
& =p\left(y_{1}\right) p\left(x_{1} \mid y_{1}\right) p\left(y_{2} \mid y_{1}\right) p\left(x_{2} \mid y_{2}\right) \ldots p\left(y_{\mathrm{T}} \mid y_{\mathrm{T}-1}\right) p\left(x_{\mathrm{T}} \mid y_{\mathrm{T}}\right) \\
& =p\left(y_{1}\right) \mathrm{P}\left(y_{2} \mid y_{1}\right) \ldots p\left(y_{\mathrm{T}} \mid y_{\mathrm{T}-1}\right) \times p\left(x_{1} \mid y_{1}\right) p\left(x_{2} \mid y_{2}\right) \ldots p\left(x_{\mathrm{T}} \mid y_{\mathrm{T}}\right) \\
& =p\left(y_{1}, \ldots \ldots, y_{\mathrm{T}}\right) p\left(x_{1} \ldots \ldots x_{\mathrm{T}} \mid y_{1}, \ldots \ldots, y_{\mathrm{T}}\right)
\end{aligned} \quad \begin{aligned}
& \text { Let } \pi_{y_{1}} \stackrel{\text { def }}{=} \prod_{i=1}^{M}\left[\pi_{i}\right]^{y_{1}^{\prime}}, \quad a_{y_{t}, y_{t+1}} \stackrel{\text { def }}{=} \prod_{i, j=1}^{M}\left[a_{i j}\right]^{y_{1}^{\prime}+y_{t+1}^{\prime}}, \quad \text { and } b_{y_{t}, x_{t}} \stackrel{\text { def }}{=} \prod_{i=1}^{M} \prod_{k=1}^{K}\left[b_{i k}\right]^{y_{t}^{\prime} x_{t}^{k}}, \\
&=\pi_{y_{1}} a_{y_{1}, y_{2}} \cdots a_{y_{T-1}, y_{T}} \quad b_{y_{1}, x_{1}} \cdots b_{y_{T}, x_{T}} \\
& \bullet \quad \text { Marginal probability: } \quad p(\mathbf{x})=\sum_{\mathbf{y}} p(\mathbf{x}, \mathbf{y})=\sum_{y_{1}} \sum_{y_{2}} \ldots \sum_{y_{N}} \pi_{y_{1}} \prod_{t=2}^{T} a_{y_{t_{t-1}, y_{t}}} \prod_{t=1}^{T} p\left(x_{t} \mid y_{t}\right)
\end{aligned}
$$

## Three main questions on HMMs

1. Evaluation

| GIVEN | an $H M M \boldsymbol{M}$, |
| :--- | :--- |
| FIND | Prob $(\mathbf{x} \mid \boldsymbol{M})$ |
| ALGO. | Forward |

2. Decoding

GIVEN an HMM $\boldsymbol{M}$, and a sequence $\mathbf{x}$,
FIND the sequence $\mathbf{y}$ of states that maximizes, e.g., $\mathrm{P}(\mathbf{y} \mid \mathbf{x}, \boldsymbol{M})$, or the most probable subsequence of states
ALGO. Viterbi, Forward-backward
3. Learning (next lecture)

GIVEN an HMM $\boldsymbol{M}$, with unspecified transition/emission probs., and a sequence $\mathbf{x}$,
FIND parameters $\theta=\left(\pi_{\mathrm{i}}, a_{\mathrm{ij}}, \eta_{\mathrm{ik}}\right)$ that maximize $\mathrm{P}(\mathbf{x} \mid \theta)$
ALGO. Baum-Welch (EM)

## The Forward Algorithm

- We want to calculate $P(x)$, the likelihood of x , given the HMM
- Sum over all possible ways of generating x:

$$
p(\mathbf{x})=\sum_{\mathbf{y}} p(\mathbf{x}, \mathbf{y})=\sum_{y_{1}} \sum_{y_{2}} \cdots \sum_{y_{N}} \pi_{y_{1}} \prod_{t=2}^{T} a_{y_{t-1}, y_{t}} \prod_{t=1}^{T} p\left(x_{t} \mid y_{t}\right)
$$

- To avoid summing over an exponential number of paths $\mathbf{y}$, define

$$
\alpha\left(y_{t}^{k}=1\right)=\alpha_{t}^{k} \stackrel{\text { def }}{=} P\left(x_{1}, \ldots, x_{t}, y_{t}^{k}=1\right) \quad \text { (the forward probability) }
$$

- The recursion:

$$
\begin{aligned}
\alpha_{t}^{k} & =p\left(x_{t} \mid y_{t}^{k}=1\right) \sum_{i} \alpha_{t-1}^{i} a_{i, k} \\
P(\mathbf{x}) & =\sum_{k} \alpha_{T}^{k}
\end{aligned}
$$

## The Backward Algorithm

- We want to compute $P\left(y_{t}^{k}=1 \mid \mathbf{x}\right)$, the posterior probability distribution on the $t{ }^{\text {th }}$ position, given $\mathbf{x}$

- We start by computing

$$
\begin{aligned}
P\left(y_{t}^{k}=1, \mathbf{x}\right)= & P\left(x_{1}, \ldots, x_{t}, y_{t}^{k}=1, x_{t+1}, \ldots, x_{T}\right) \\
& =P\left(x_{1}, \ldots, x_{t}, y_{t}^{k}=1\right) P\left(x_{t+1}, \ldots, x_{T} \mid x_{1}, \ldots, x_{t}, y_{t}^{k}=1\right) \\
& =P\left(x_{1} \ldots x_{t}, y_{t}^{k}=1\right) P\left(x_{t+1} \ldots x_{T} \mid y_{t}^{k}=1\right)
\end{aligned}
$$

Forward, $\alpha_{t}^{k}$ Backward, $\quad \beta_{t}^{k}=P\left(x_{t+1}, \ldots, x_{T} \mid y_{t}^{k}=1\right)$

- The recursion:

$$
\beta_{t}^{k}=\sum_{i} a_{k, i} p\left(x_{t+1} \mid y_{t+1}^{i}=1\right) \beta_{t+1}^{i}
$$

## Shafer Shenoy for HMMs

- Recap: Shafer-Shenoy algorithm

(a)

(b)
- Message from clique $i$ to clique $j$ :

$$
\mu_{i \rightarrow j}=\sum_{C_{i} \backslash S_{i j}} \psi_{C_{i}} \prod_{k \neq j} \mu_{k \rightarrow i}\left(S_{k i}\right)
$$

- Clique marginal

$$
p\left(C_{i}\right) \propto \psi_{C_{i}} \prod_{k} \mu_{k \rightarrow i}\left(S_{k i}\right)
$$

## Shafer Shenoy for HMMs (cont.)

- A junction tree for the HMM



- Rightward pass

- Leftward pass ...

$$
\begin{aligned}
& \mu_{t-1 \leftarrow t}\left(y_{t}\right)=\sum_{y_{t+1}} \psi\left(y_{t}, y_{t+1}\right) \mu_{t \leftarrow t+1}\left(y_{t+1}\right) \mu_{t \uparrow}\left(y_{t+1}\right) \\
&=\sum_{Y_{t+1}} p\left(y_{t+1} \mid y_{t}\right) \mu_{t \leftarrow t+1}\left(y_{t+1}\right) p\left(x_{t+1} \mid y_{t+1}\right) \\
& \text { This is exactly the backward algorithm! }
\end{aligned}
$$



## Approaches to inference

- Exact inference algorithms
- The elimination algorithm
- The junction tree algorithms $\sqrt{ }$
- 
- Approximate inference techniques
- Stochastic simulation / sampling methods
- Markov chain Monte Carlo methods
- Variational algorithms (later lectures)


## The motif detection problem

Biological background: the transcriptional regulatory machinery


## In silico motif detection

5' - TCTCTCTCCACGGCTAATTAGGTGATCATGAAAAAATGAAAAATTCATGAGAAAAGAGTCAGACATCGAAACATACAT... $\overrightarrow{H I S 7}$
5' - ATGGCAGAATCACTTTAAAACGTGGCCCCACCCGCTGCACCCTGTGCATTTTGTACGTTACTGCGAAATGACTCAACG $\quad . .$.
$5^{\prime}$ - CACATCCAACGAATCACCTCACCGTTATCGTGACTCACTTTCTTTCGCATCGCCGAAGTGCCATAAAAAATATTTTTT ...ILV6
$5^{\prime}$ - TGCGAACAAAAGAGTCATTACAACGAGGAAATAGAAGAAAATGAAAAATTTTCGACAAAATGTATAGTCATTTCTATC ... $\xrightarrow[H R 4]{\longrightarrow}$
$5^{\prime}$ - ACAAAGGTACCTTCCTGGCCAATCTCACAGATTTAATATAGTAAATTGTCATGCATATGACTCATCCCGAACATGAAA ....
$5^{\prime}$ - ATTGATTGACTCATTTTCCTCTGACTACTACCAGTTCAAAATGTTAGAGAAAAATAGAAAAGCAGAAAAAATAAATAA ....HOM2
$5^{\prime}$ - GGCGCCACAGTCCGCGTTTGGTTATCCGGCTGACTCATTCTGACTCTTTTTTGGAAAGTGTGGCATGTGCTTCACACA $\ldots \longrightarrow$...PRO3

1: AAAAGAGTCA
2: AAATGACTCA
AAGTGAGTCA

. AAATGAGTCA
GAATGAGTCA
M: AAAAGAGTCA

## A Generative Scheme <br> - 00

## The LOGOS motif model

[Xing, Wu, Jordan and Karp, JBCB 2004]

An integrated LOcal and GlObal motif Sequence model

- The occurrences of motifs in DNA sequences are governed by a global motif syntax model $p_{\mathrm{g}}(X)$
- All instances of a specific motif admit a local motif prior model $p_{1}(\mathbf{A}, \theta \mid X)$
- Non-motif sequences are modeled by a background model $p_{\mathrm{b}}(Y-\mathbf{A} \mid X)$


## The global hidden Markov model (HMM)

1st order Markov grammar


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## The background model

$k$-th order Markov background


## The local prior model

Hidden Markov Dicichlet-multinomial (HMDM)
[Xing, Jordan, Karp and Russell, NIPS 2002]


## A modular Bayesian model for motif detection



Joint posterior:

$$
p(X, S, \theta \mid \mathbf{y})=p(X \mid \theta, \mathbf{y}) p(\theta, S)
$$

## Inference in LOGOS model

- Joint posterior: $p(X, S, \theta \mid \mathbf{y})=p(X \mid \theta, \mathbf{y}) p(\theta, S)$
- inference on motif locations

$$
p\left(x_{t} \mid \mathbf{y}\right)=\int_{\theta} \sum_{s} \sum_{\forall x_{t} \neq t} p(\mathbf{x} \mid \theta, \mathbf{y}) p(\theta, s)
$$

- state space to be summed (and integrated) over

$$
\mathfrak{R}^{4 \times \sum L_{k}} \times\left|\Omega_{s}\right|^{\sum L_{k}} \times\left|\Omega_{x}\right|^{T}
$$

$\sim \mathfrak{R}^{120} \times 10^{1200}$ for a 1000 bpsequencewith twomotif patternsof length15bp

- Approximate inference
- Stochastic approximation: Gibbs sampling
- Deterministic approximation: Variational inference $\sqrt{ }$


## Variational Methods

- For a distribution $p(\mathrm{X} \mid \theta)$ associated with a complex graph, computing the marginal (or conditional) probability of arbitrary random variable(s) is intractable
- Variational methods
- formulating probabilistic inference as an optimization problem:

$$
\begin{array}{ll}
\text { e.g. } & \quad f^{*}=\arg \max _{f \in S}\{F(f)\} \\
f: & \begin{array}{l}
\text { a (tractable) probability distribution } \\
\text { or, solutions to certain probabilistic queries }
\end{array}
\end{array}
$$

Exponential Family

- Exponential representation of graphical models:

$$
P(\mathbf{X})=\frac{1}{Z} \prod_{c \in C} \psi_{c}\left(\mathbf{X}_{c}\right) \quad \Rightarrow \quad p(\mathbf{X} \mid \theta)=\exp \left\{\sum_{\alpha} \theta_{\alpha} \phi_{\alpha}\left(\mathbf{X}_{D_{\alpha}}\right)-A(\boldsymbol{\theta})\right\}
$$

- Includes discrete models, Gaussian, Poisson, exponential, and many others

$$
\begin{aligned}
& E(\mathbf{X})=-\sum_{\alpha} \theta_{\alpha} \phi_{\alpha}\left(\mathbf{X}_{D_{\alpha}}\right) \text { is referred to as the energy of state } \mathbf{X} \\
& \Rightarrow \quad \begin{aligned}
p(\mathbf{X} \mid \boldsymbol{\theta}) & =\exp \{-E(\mathbf{X})-A(\boldsymbol{\theta})\} \\
& =\exp \left\{-E\left(\mathbf{X}_{H}, \mathbf{x}_{E}\right)-A\left(\boldsymbol{\theta}, \mathbf{x}_{E}\right)\right\}
\end{aligned}
\end{aligned}
$$

## Example: the Boltzmann distribution on atomic lattice



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## Lower bounds of exponential functions



## Lower bounding likelihood

Representing $q\left(\mathbf{X}_{H}\right)$ by $\exp \left\{-E^{\prime}\left(\mathbf{X}_{H}\right)\right\}$ :

Lemma: Every marginal distribution $q\left(\mathrm{X}_{H}\right)$ defines a lower bound of likelihood:

$$
\begin{aligned}
p\left(\mathbf{x}_{E}\right) \geq & \int d \mathbf{x}_{H} \exp \left\{-E^{\prime}\left(\mathbf{x}_{H}\right)\right\} \\
& \left(1-A\left(\mathbf{x}_{E}\right)-\left(E\left(\mathbf{x}_{H}, \mathbf{x}_{E}\right)-E^{\prime}\left(\mathbf{x}_{H}\right)\right)\right),
\end{aligned}
$$

where $\mathrm{x}_{E}$ denotes observed variables (evidence).

Upgradeable to higher order bound [Leisink and Kappen, 2000]


Representing $q\left(\mathbf{X}_{H}\right)$ by $\exp \left\{-E^{\prime}\left(\mathbf{X}_{H}\right)\right\}$ :

Lemma: Every marginal distribution $q\left(\mathrm{X}_{H}\right)$ defines a lower bound of likelihood:

$$
\begin{aligned}
p\left(\mathbf{x}_{E}\right) & \geq C-\left\langle E\left(\mathbf{X}_{H}, \mathbf{x}_{E}\right)\right\rangle_{q\left(\mathbf{x}_{H}\right)}+\int d \mathbf{x}_{H} q\left(\mathbf{x}_{H}\right) \log q\left(\mathbf{x}_{H}\right) \\
& =C-\langle E\rangle_{q}-H_{q},
\end{aligned}
$$

where $\mathrm{x}_{E}$ denotes observed variables (evidence).
$\langle E\rangle_{q}$ : expected energy $\quad\langle E\rangle_{q}+H_{q}$ : Gibbs free energy
$H_{q}$ : entropy

## KL and variational (Gibbs) free energy

- Kullback-Leibler Distance:

$$
K L(q \| p) \equiv \sum_{z} q(z) \ln \frac{q(z)}{p(z)}
$$

- "Boltzmann's Law" (definition of "energy"):

$$
\begin{gathered}
p(z)=\frac{1}{C} \exp [-E(z)] \\
K L(q \| p) \underbrace{\sum_{z} q(z) E(z)+\sum_{z} q(z) \ln q(z)}_{\begin{array}{c}
\text { Gibbs Free Energy } G(q) ; \\
\text { minimized when } q(Z)=p(Z)
\end{array}}+\ln C
\end{gathered}
$$

## KL and Log Likelihood

- Jensen's inequality
$\ell(\theta ; x)=\log p(x \mid \theta)$
$=\log \sum_{z} p(x, z \mid \theta)$

$$
\begin{aligned}
& =\log \sum_{z} q(z \mid x) \frac{p(x, z \mid \theta)}{q(z \mid x)} \\
& \geq \sum_{z} q(z \mid x) \log \frac{p(x, z \mid \theta)}{q(z \mid x)}
\end{aligned}
$$



- KL and Lower bound of likelihood
$\ell(\theta ; x)=\log p(x \mid \theta)=\log \frac{p(x, z \mid \theta)}{p(z \mid x, \theta)}=\sum_{z} q(z) \log \frac{p(x, z \mid \theta)}{p(z \mid x, \theta)}$
$=\sum_{z} q(z) \log \frac{p(x, z \mid \theta)}{q(z)} \frac{q(z)}{p(z \mid x, \theta)}$
$=\sum_{z} q(z) \log \frac{p(x, z \mid \theta)}{q(z)}+\sum_{z} q(z) \log \frac{q(z)}{p(z \mid x, \theta)}$

$\Rightarrow \quad \ell(\theta ; x)=\mathcal{L}(q)+K L(q \| p)$
- Setting $q()=p(z \mid x)$ closes the gap (c.f. EM)


## A variational representation of probability distributions

$$
\begin{aligned}
q & =\arg \max _{q \in Q}\left\{-\langle E\rangle_{q}-H_{q}\right\} \\
& =\arg \min _{q \in Q}\left\{\langle E\rangle_{q}+H_{q}\right\}
\end{aligned}
$$

where $Q$ is the equivalent sets of realizable distributions, e.g., all valid parameterizations of exponential family distributions, marginal polytopes [winright et al. 2003].

Difficulty: $\quad H_{q}$ is intractable for general $q$
"solution": approximate $H_{q}$ and/or,
relax or tighten $Q$

## Mean field methods

- Optimize $q\left(\mathbf{X}_{H}\right)$ in the space of tractable families
- i.e., subgraph of $G_{p}$ over which exact computation of $H_{q}$ is feasible
- Tightening the optimization space
- exact objective:

$$
H_{q}
$$

- tightened feasible set:

$$
Q \rightarrow \mathcal{T} \quad(\mathcal{T} \subseteq Q)
$$

$$
q^{*}=\arg \min _{q \in \mathcal{T}}\langle E\rangle_{q}+H_{q}
$$

## Belief Propagation

- Do not optimize $q\left(\mathbf{X}_{H}\right)$ explicitly, but focus on the set of beliefs
- e.g., $b=\left\{b_{i, j}=\tau\left(X_{i}, x_{j}\right), \quad b_{i}=\tau\left(X_{i}\right)\right\}$
- Relax the optimization problem
- approximate objective: $H_{\text {Betha }}=H\left(b_{i, j}, b_{i}\right)$
- relaxed feasible set: $\quad \mathscr{M}_{o}=\left\{\tau \geq 0 \mid \sum_{x_{i}} \tau\left(X_{i}\right)=1, \sum_{x_{i}} \tau\left(X_{i}, X_{j}\right)=\tau\left(X_{j}\right)\right\}$

$$
b^{*}=\arg \min _{b \in \mathcal{M}_{o}}\left\{\langle E\rangle_{b}+F(b)\right\}
$$

- The loopy BP algorithm:
- a fixed point iteration procedure that tries to solve $b^{*}$



## Mean Field Approximation

## Cluster-based approx. to the Gibbs free energy

## Exact: $\quad G[q(X)] \quad$ (intractable)

Clusters: $G\left[\left\{q_{c}\left(X_{c}\right)\right\}\right]$


## Mean field approx. to Gibbs free energy

- Given a disjoint clustering, $\left\{\mathrm{C}_{1}, \ldots, \mathrm{C}_{\mid}\right\}$, of all variables
- Let

$$
q(\mathbf{X})=\prod_{i} q_{i}\left(\mathbf{X}_{C_{i}}\right),
$$

- Mean-field free energy

$$
\begin{aligned}
& G_{\mathrm{MF}}=\sum_{i} \sum_{\mathbf{x}_{C_{i}}} \prod_{i} q_{i}\left(\mathbf{x}_{C_{i}}\right) E(\mathbf{x})+\sum_{i} \sum_{\mathbf{x}_{C_{i}}} q_{i}\left(\mathbf{x}_{C_{i}}\right) \ln q_{i}\left(\mathbf{x}_{C_{i}}\right) \\
& \text { e.g., } \quad G_{\mathrm{MF}}=\sum_{i<i} \sum_{x_{x}, i} q\left(x_{i}\right) q\left(x_{i}\right) \phi\left(x_{i} x_{j}\right)+\sum_{i} \sum_{x_{i}} q\left(x_{i}\right) \phi\left(x_{i}\right)+\sum_{i} \sum_{x_{i}} q\left(x_{i}\right) \ln q\left(x_{i}\right)
\end{aligned}
$$

- Will never equal to the exact Gibbs free energy no matter what clustering is used, but it does always define a lower bound of the likelihood
- Optimize each $q_{i}\left(x_{c}\right)$ 's.
- Variational calculus ..
- Do inference in each $q_{i}\left(x_{c}\right)$ using any tractable algorithm


## The Generalized Mean Field theorem

Theorem: The optimum GMF approximation to the cluster marginal is isomorphic to the cluster posterior of the original distribution given internal evidence and its generalized mean fields:

$$
q_{i}^{*}\left(\mathbf{X}_{H, C_{i}}\right)=p\left(\mathbf{X}_{H, C_{i}} \mid \mathbf{x}_{E, C_{i}},\left\langle\mathbf{X}_{H, M B_{i}}\right\rangle_{q_{j \neq i}}\right)
$$

GMF algorithm: Iterate over each $q_{i}$

A generalized mean field


## A generalized mean field algorithm



Theorem: The GMF algorithm is guaranteed to converge to a local optimum, and provides a lower bound for the likelihood of evidence (or partition function) the model.

## The naive mean field approximation

- Approximate $p(\mathbf{X})$ by fully factorized $q(\mathbf{X})=\mathrm{P}_{i} q_{i}\left(X_{i}\right)$
- For Boltzmann distribution $p(X)=\exp \left\{\sum_{i<j} q_{i j} X_{i} X_{j}+q_{i o} X_{i}\right\} / Z$ :
mean field equation:

$$
\begin{aligned}
q_{i}\left(X_{i}\right) & =\exp \left\{\theta_{i 0} X_{i}+\sum_{j \in \mathcal{N}_{i}} \theta_{i j} X_{i}\left\langle X_{j}\right\rangle_{q_{j}}+A_{i}\right\} \\
& =p\left(X_{i} \mid\left\{\left\langle X_{j}\right\rangle_{q_{j}}: j \in \mathcal{N}_{i}\right\}\right)
\end{aligned}
$$

- $\left\langle X_{j}\right\rangle_{q_{j}}$ resembles a "message" sent from node $j$ to $i$
- $\left\{\left\langle X_{j}\right\rangle_{q_{j}}: j \in \mathcal{N}_{i}\right\}$ forms the "mean field" applied to $X_{i}$ from its neighborhood


## Generalized MF approximation to Ising models



Cluster marginal of a square block $C_{k}$ :

$$
q\left(X_{C_{k}}\right) \propto \exp \left\{\sum_{i, j \in C_{k}} \theta_{i j} X_{i} X_{j}+\sum_{i \in C_{k}} \theta_{i 0} X_{i}+\sum_{\substack{i \in C_{k}, j \in M B_{k}, k^{\prime} \in M B C_{k}}} \theta_{i j} X_{i}\left\langle X_{j}\right\rangle_{q\left(X_{C_{k^{\prime}}}\right)}\right\}
$$

Virtually a reparameterized Ising model of small size.


## Cluster-based MF (e.g., GMF)

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- a general, iterative message passing algorithm
- clustering completely defines approximation
- preserves dependencies
- flexible performance/cost trade-off
- clustering automatable
- recovers model-specific structured VI algorithms, including:
- fHMM, LDA
- variational Bayesian learning algorithms
- easily provides new structured VI approximations to complex models


## Example 1: Latent Dirichlet Allocation

- Blei, Jordan and Ng (2003)
- Generative model of documents (but broadly applicable e.g. collaborative filtering, image retrieval, bioinformatics)
- Generative model:



## Latent Dirichlet Allocation

 000- Variational approximation

$$
\begin{aligned}
q(\theta, \boldsymbol{z})= & q_{\theta}(\theta) q_{z}(\boldsymbol{z}) \\
= & \operatorname{Dir}(\theta \mid \gamma=f(\alpha,\langle\boldsymbol{z}\rangle)) \times \\
& \operatorname{Multi}\left(\boldsymbol{z} \mid \phi=f\left(\beta_{w},\langle\ln \theta\rangle\right)\right)
\end{aligned}
$$

$$
\gamma_{i}=\alpha_{i}+\sum_{n=1}^{N} \phi_{n i} .
$$

- Data set:
- 15,000 documents
- 90,000 terms
- 2.1 million words
- Model:
- 100 factors
- 9 million parameters
- MCMC could be totally infeasible for this problem


## Example 2: Sigmoid belief network



10000
000000
0000000000




## Example 3: Factorial HMM





## Example 4: GMF approximation to LOGOS



- Approximate $p(X, S, \theta \mid y)$ with a tractable distribution $q(X, S, \theta)$
- Variable partition:

$$
\{X, S, \theta\}=\{X\} \quad+\quad\{S, \theta\}
$$



- Let

$$
q(X, S, \theta)=q_{1}(X) q_{2}(\theta, S)
$$

## GMF for DNA motif prediction

- GMF approximations:

$$
q(X, S, \theta) \propto q_{1}(X) q_{2}(\theta, S)
$$

$$
q_{1}^{*}(X)=p(X \mid y, \tilde{\theta})
$$

$$
q_{2}^{*}(\theta, S)=p(S) p\left(\theta \mid S, \tilde{\mathbf{A}}_{Y \mid X}\right)
$$

- GMF algorithm


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## Traces of GMF iterations

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A single round of FP-iteration


Sequentialized multiple random restarts

## GMF vs. Gibbs sampler on motif detection




## GMF vs. Gibbs sampler on motif detection

## Performance:



Sampling time of Gibbs $=10 \times$ the time for GMF

## Open Problem

- Idea:
- $\mathrm{A}(\theta)$ is convex
- Epigraph of $A(\theta)$ can be represented as a pointwise supremum of all affine functions that are global under-estimators of $A(\theta)$
- Variationally, compute $\mathrm{A}(\theta)$ using the following convex optimization:

$$
A(\theta)=\sup _{\mu \in \mathbb{R}^{d}}\left\{\langle\theta, \mu\rangle-A^{*}(\mu)\right\}
$$

- Investigate the form of the dual function $\mathrm{A}^{*}(\mu)$
- Important consequence

Solution also yields the marginal probabilities!
Martin Wainwright and Michael Jordan IEEE Transactions on Signal Processing, 2006

