AN INTRODUCTION TO GRAPHICAL MODELS

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Acknowledgments:

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GRAPHICAL MODELS

- Graphical models are a marriage between graph theory and probability theory
- They clarify the relationship between neural networks and related network-based models such as HMMs, MRFs, and Kalman filters
- Indeed, they can be used to give a fully probabilistic interpretation to many neural network architectures
- Some advantages of the graphical model point of view
  - inference and learning are treated together
  - supervised and unsupervised learning are merged seamlessly
  - missing data handled nicely
  - a focus on conditional independence and computational issues
  - interpretability (if desired)

Graphical models (cont.)

- There are two kinds of graphical models; those based on *undirected* graphs and those based on *directed* graphs. Our main focus will be directed graphs.

- Alternative names for graphical models: *belief networks, Bayesian networks, probabilistic independence networks, Markov random fields, loglinear models, influence diagrams*

- A few myths about graphical models:
  - they require a localist semantics for the nodes
  - they require a causal semantics for the edges
  - they are necessarily Bayesian
  - they are intractable

Learning and inference

- A key insight from the graphical model point of view:

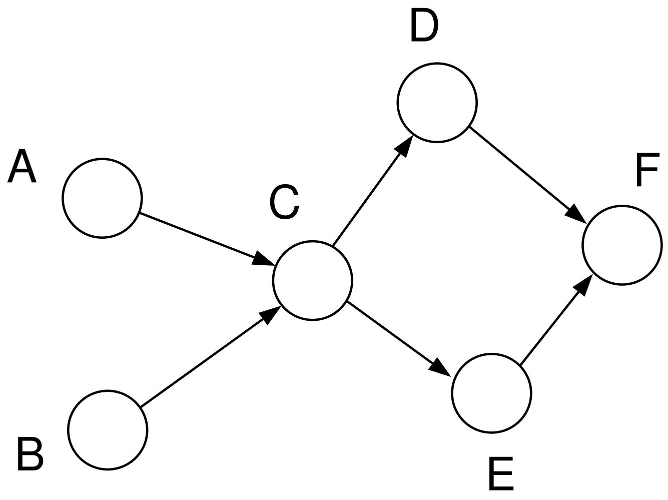
  It is not necessary to learn that which can be inferred

- The weights in a network make local assertions about the relationships between neighboring nodes
- Inference algorithms turn these local assertions into global assertions about the relationships between nodes
  - e.g., correlations between hidden units conditional on an input-output pair
  - e.g., the probability of an input vector given an output vector

- This is achieved by associating a joint probability distribution with the network

Directed graphical models—basics

- Consider an arbitrary directed (acyclic) graph, where each node in the graph corresponds to a random variable (scalar or vector):



- There is no a priori need to designate units as "inputs," "outputs" or "hidden"

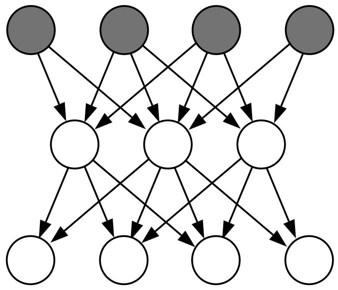
- We want to associate a probability distribution $P(A, B, C, D, E, F)$ with this graph, and we want all of our calculations to respect this distribution

e.g.,

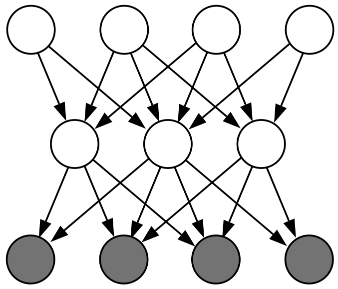
$$P(F|A,B) = \frac{\Sigma_C \Sigma_D \Sigma_E P(A,B,C,D,E,F)}{\Sigma_C \Sigma_D \Sigma_E \Sigma_F P(A,B,C,D,E,F)}$$

Some ways to use a graphical model

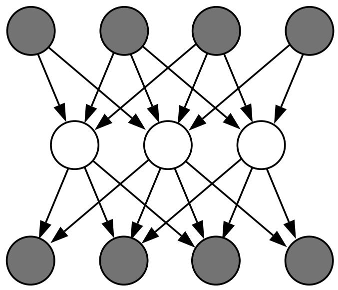
Prediction:



Diagnosis, control, optimization:



Supervised learning:



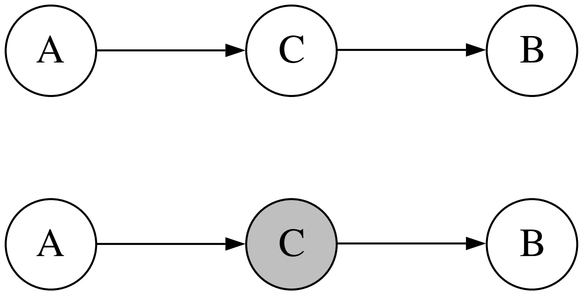
- we want to marginalize over the unshaded nodes in each case (i.e., integrate them out from the joint probability)
- "unsupervised learning" is the general case

Specification of a graphical model

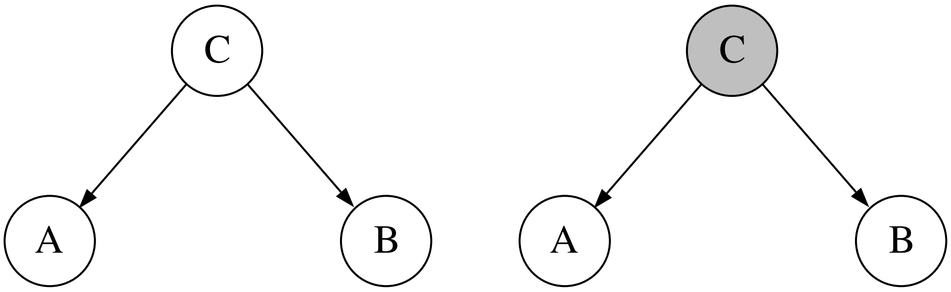
- There are two components to any graphical model:
  - the *qualitative* specification
  - the *quantitative* specification

- Where does the qualitative specification come from?
  - prior knowledge of causal relationships
  - prior knowledge of modular relationships
  - assessment from experts
  - learning from data
  - we simply like a certain architecture (e.g., a layered graph)

Qualitative specification of graphical models

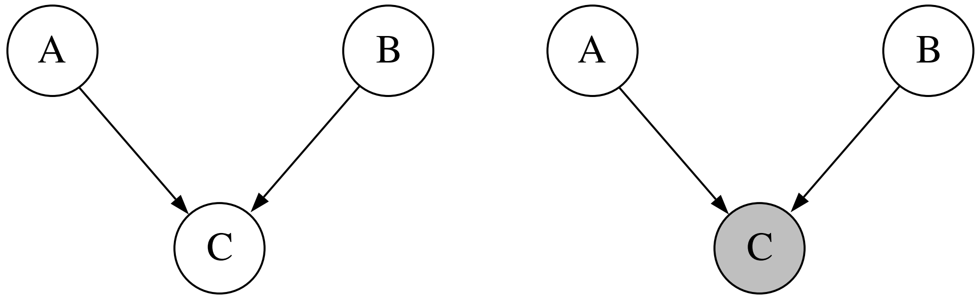


- A and B are marginally *dependent*
- A and B are conditionally *independent*



- A and B are marginally *dependent*
- A and B are conditionally *independent*

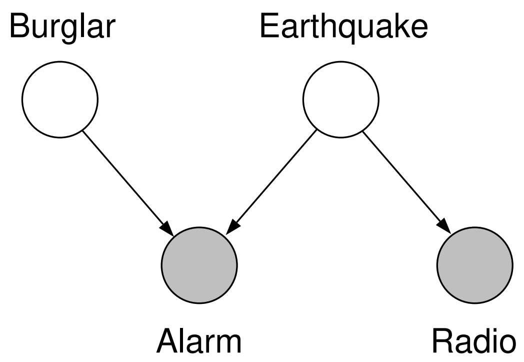
Semantics of graphical models (cont)



- A and B are marginally *independent*
- A and B are conditionally *dependent*

- This is the interesting case...

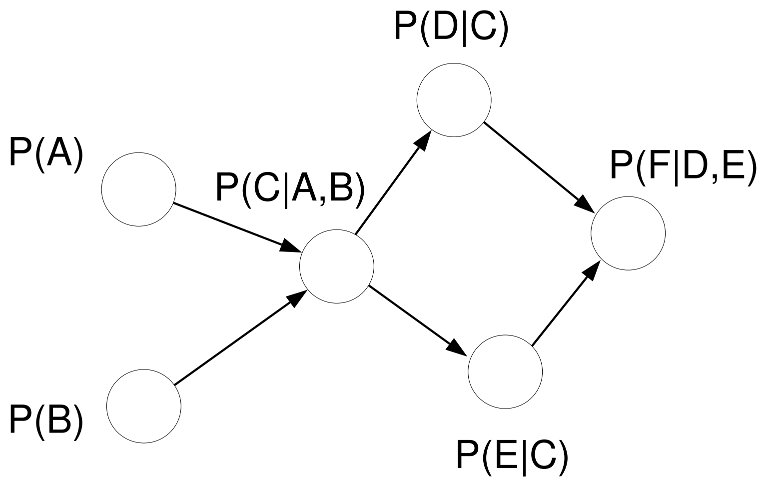
"Explaining away"



- All connections (in both directions) are "excitatory"
- But an increase in "activation" of Earthquake leads to a decrease in "activation" of Burglar
- Where does the "inhibition" come from?

Quantitative specification of directed models

- *Question*: how do we specify a joint distribution over the nodes in the graph?
- *Answer*: associate a conditional probability with each node:



and take the product of the *local* probabilities to yield the *global* probabilities

Justification

- In general, let $\{S\}$ represent the set of random variables corresponding to the N nodes of the graph

- For any node S_i, let $\mathrm{pa}(S_i)$ represent the set of parents of node S_i

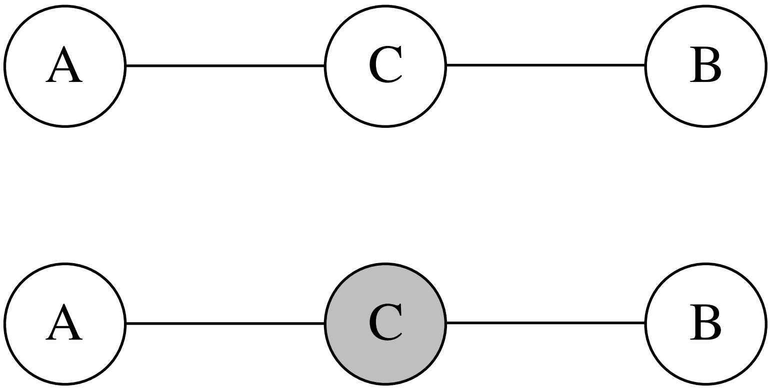
- Then

$$\begin{aligned} P(S) &= P(S_1)P(S_2|S_1)\cdots P(S_N|S_{N-1},\ldots,S_1) \\ &= \prod_i P(S_i|S_{i-1},\ldots,S_1) \\ &= \prod_i P(S_i|\mathrm{pa}(S_i)) \end{aligned}$$

  where the last line is by assumption

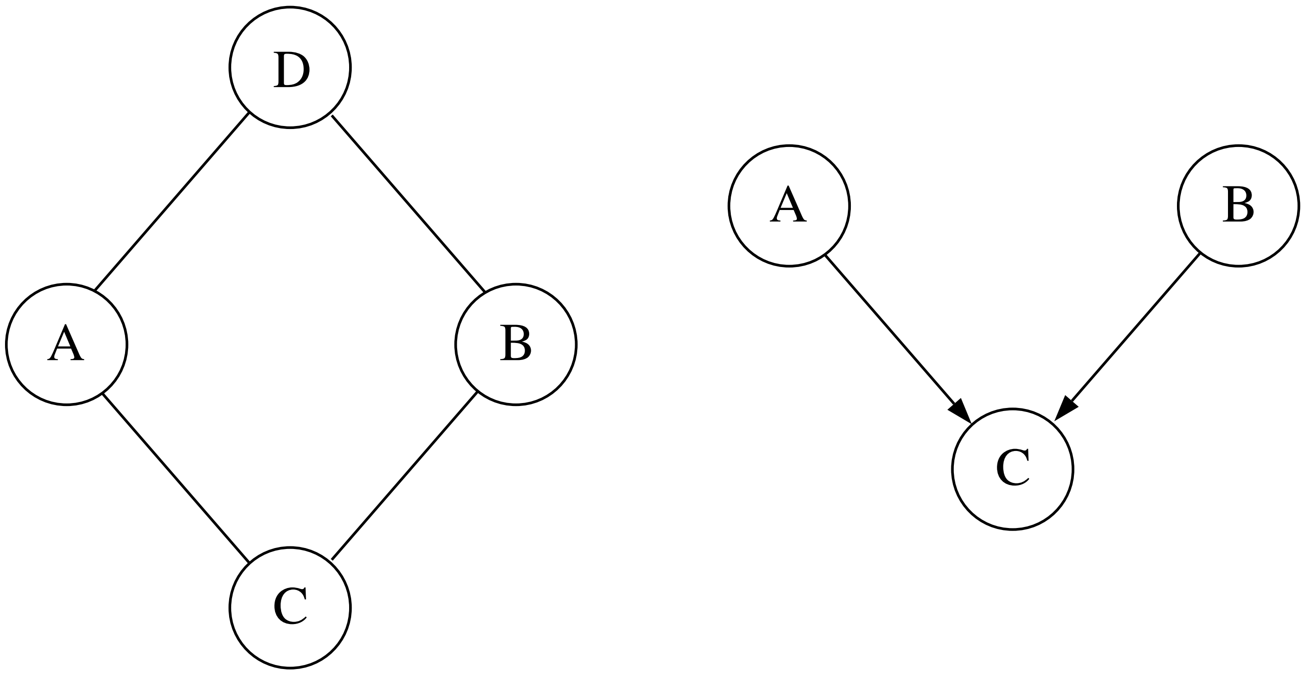
- *It is possible to prove a theorem that states that if arbitrary probability distributions are utilized for $P(S_i|\mathrm{pa}(S_i))$ in the formula above, then the family of probability distributions obtained is exactly that set which respects the qualitative specification (the conditional independence relations) described earlier*

Semantics of undirected graphs



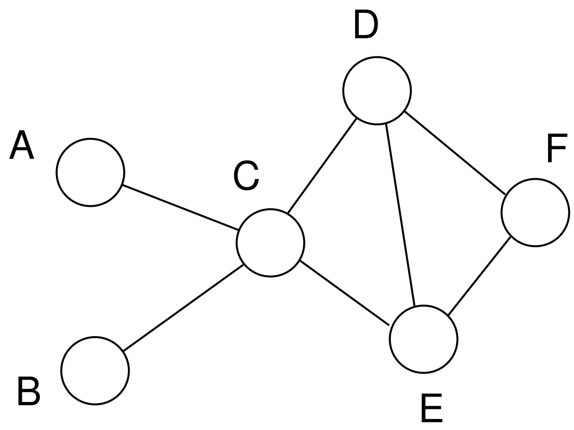
- A and B are marginally *dependent*
- A and B are conditionally *independent*

Comparative semantics

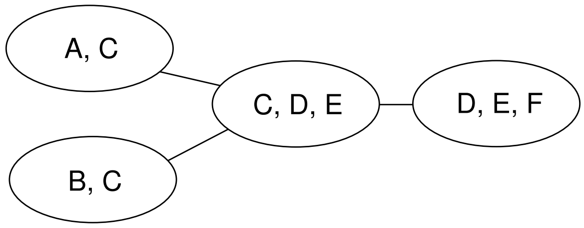


- The graph on the left yields conditional independencies that a directed graph can't represent
- The graph on the right yields marginal independencies that an undirected graph can't represent

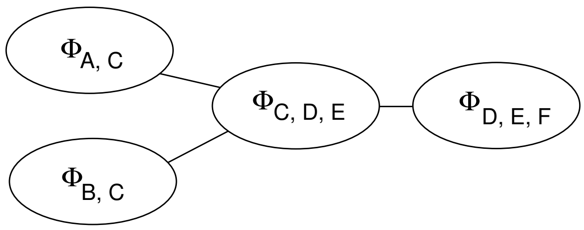
Quantitative specification of undirected models



- identify the *cliques* in the graph:



- define a *configuration* of a clique as a specification of values for each node in the clique
- define a *potential* of a clique as a function that associates a real number with each configuration of the clique



Quantitative specification (cont.)

- Consider the example of a graph with binary nodes
- A “potential” is a table with entries for each combination of nodes in a clique

		B = 0	B = 1
A	0	1.5	.4
	1	.7	1.2

- “Marginalizing” over a potential table simply means collapsing (summing) the table along one or more dimensions

  - marginalizing over B

A	0	1.9
	1	1.9

  - marginalizing over A

	B = 0	B = 1
	2.2	1.6

Quantitative specification (cont.)

- finally, define the probability of a *global* configuration of the nodes as the product of the *local* potentials on the cliques:

$$P(A, B, C, D, E, F) = \phi_{(A,B)}\phi_{(B,C)}\phi_{(C,D,E)}\phi_{(D,E,F)}$$

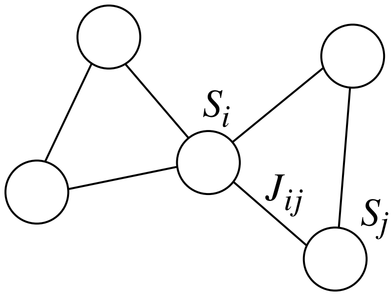
  where, without loss of generality, we assume that the normalization constant (if any) has been absorbed into one of the potentials

- *It is then possible to prove a theorem that states that if arbitrary potentials are utilized in the product formula for probabilities, then the family of probability distributions obtained is exactly that set which respects the qualitative specification (the conditional independence relations) described earlier*

  (This theorem is known as the Hammersley-Clifford theorem)

Boltzmann machine

- The Boltzmann machine is a special case of an undirected graphical model
- For a Boltzmann machine all of the potentials are formed by taking products of factors of the form $\exp\{J_{ij}S_iS_j\}$



- Setting J_{ij} equal to zero for non-neighboring nodes guarantees that we respect the clique boundaries
- But we don't get the full conditional probability semantics with the Boltzmann machine parameterization
  - i.e., the family of distributions parameterized by a Boltzmann machine on a graph is a proper subset of the family characterized by the conditional independencies

Evidence and Inference

- "Absorbing evidence" means observing the values of certain of the nodes
- Absorbing evidence divides the units of the network into two groups:

visible units $\{V\}$	those for which we have instantiated values ("evidence nodes").
hidden units $\{H\}$	those for which we do not have instantiated values.

- "Inference" means calculating the *conditional distribution*

$$P(H|V) = \frac{P(H,V)}{\Sigma_{\{H\}} P(H,V)}$$

  - *prediction* and *diagnosis* are special cases

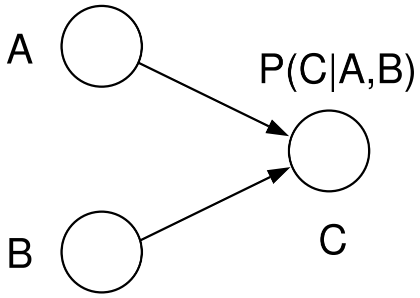
Inference algorithms for directed graphs

- There are several inference algorithms; some of which operate directly on the directed graph
- The most popular inference algorithm, known as the *junction tree* algorithm (which we'll discuss here), operates on an undirected graph
- It also has the advantage of clarifying some of the relationships between the various algorithms

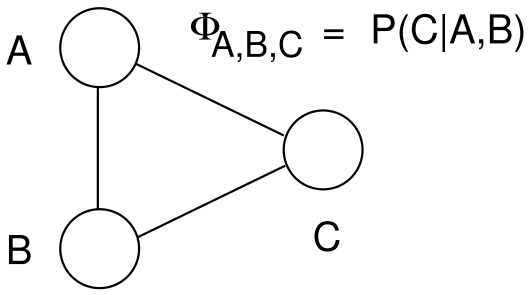
To understand the junction tree algorithm, we need to understand how to "compile" a directed graph into an undirected graph

Moral graphs

- Note that for both directed graphs and undirected graphs, the joint probability is in a product form
- So let's convert local conditional probabilities into potentials; then the products of potentials will give the right answer
- Indeed we can think of a conditional probability, e.g., $P(C|A,B)$ as a function of the three variables A, B, and C (we get a real number for each configuration):



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



Moral graphs (cont.)

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

$$\begin{aligned} &P(A,B,C,D,E,F) \\ &= P(A)P(B)P(C|A,B)P(D|C)P(E|C)P(F|D,E) \\ &= \phi_{(A,B,C)}\phi_{(C,D,E)}\phi_{(D,E,F)} \end{aligned}$$

where

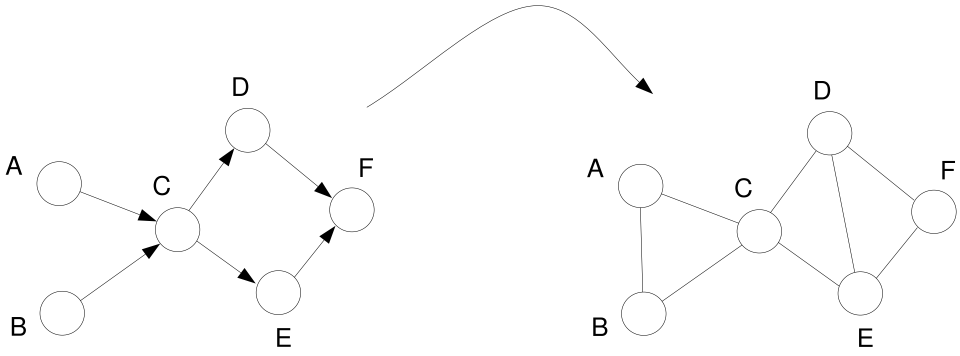
$$\phi_{(A,B,C)} = P(A)P(B)P(C|A,B)$$

and

$$\phi_{(C,D,E)} = P(D|C)P(E|C)$$

and

$$\phi_{(D,E,F)} = P(F|D,E)$$

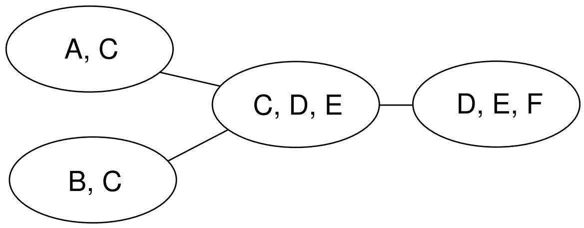


Propagation of probabilities

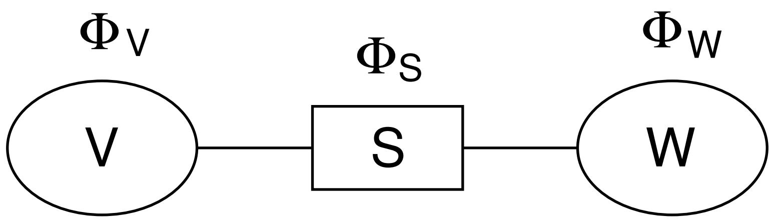
- Now suppose that some evidence has been absorbed. How do we propagate this effect to the rest of the graph?

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., (A, C) overlaps with (C, D, E)).



  - the cliques need to "agree" on the probability of nodes in the overlap; this is achieved by *marginalizing* and *rescaling*:

$$\phi_S^* = \sum_{V \setminus S} \phi_V$$

$$\phi_W^* = \phi_W \frac{\phi_S^*}{\phi_S}$$

  - this occurs in parallel, distributed fashion throughout the clique tree

Clique trees (cont.)

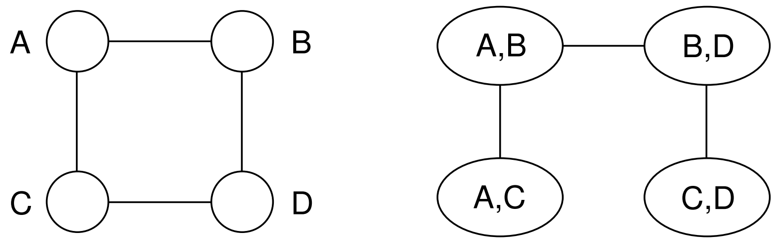
- This simple local message-passing algorithm on a clique tree defines the general probability propagation algorithm for directed graphs!

- Many interesting algorithms are special cases:
  - calculation of posterior probabilities in mixture models
  - Baum-Welch algorithm for hidden Markov models
  - posterior propagation for probabilistic decision trees
  - Kalman filter updates

- 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.

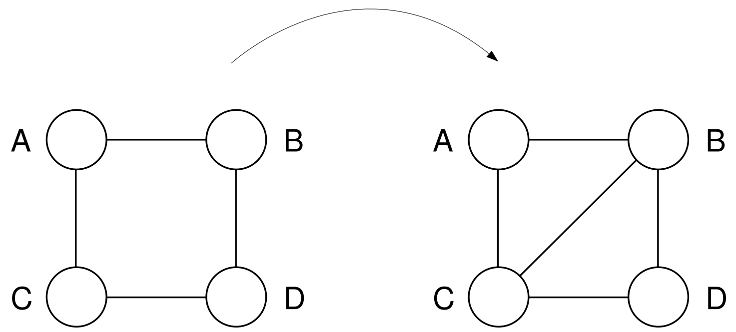
- *Question*: What guarantee do we have that the probability associated with C in these two cliques will be the same?

- *Answer*: Nothing. In fact this is a problem with the algorithm as described so far. It is not true that in general *local* consistency implies *global* consistency.

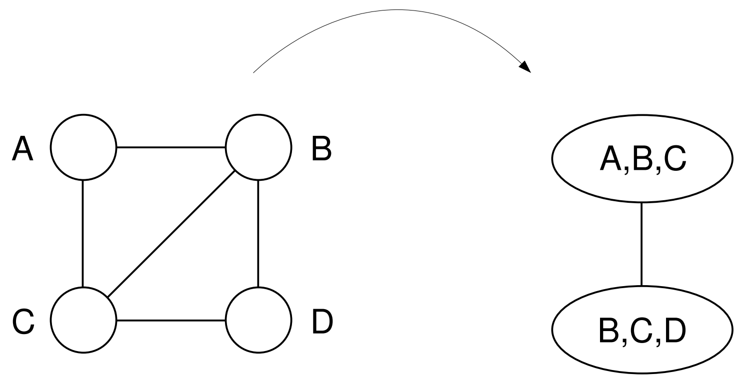
- What else do we need to get such a guarantee?

Triangulation (last idea, hang in there)

- 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 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* for such clique trees

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 algorithm is (provably) correct.

- It's also possible to show that *only* triangulated graphs have the property that their clique trees are junction trees. Thus, if we want local algorithms, we *must* triangulate.

Summary of the junction tree algorithm

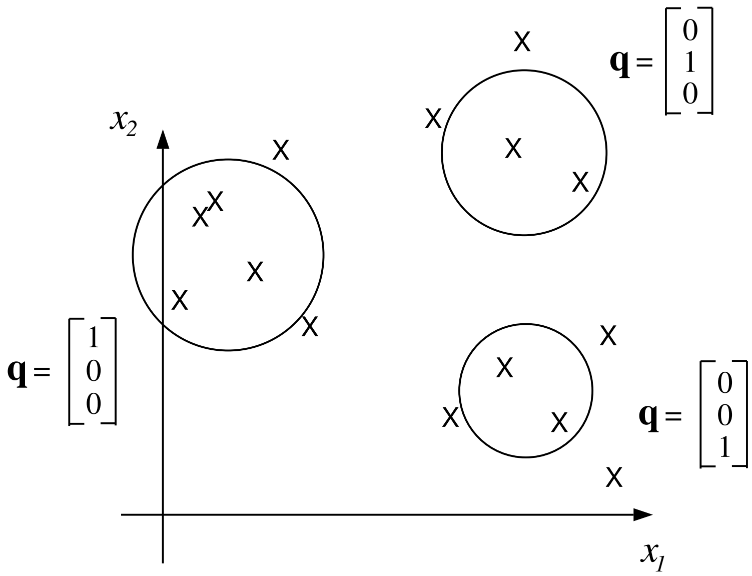
---

1. *Moralize* the graph
2. *Triangulate* the graph
3. *Propagate* by local message-passing in the junction tree

- Note that the first two steps are "off-line"
- Note also that these steps provide a bound of the complexity of the propagation step

Example: Gaussian mixture models

- A Gaussian mixture model is a popular clustering model



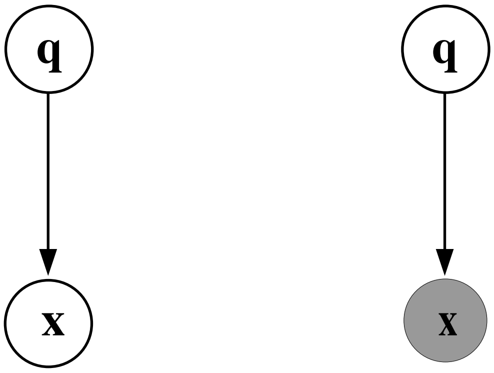
- hidden state $\mathbf{q}$ is a multinomial RV
- output $\mathbf{x}$ is a Gaussian RV
- prior probabilities on hidden states:

$$\pi_i = P(q_i = 1)$$

- class-conditional probabilities:

$$P(\mathbf{x}|q_i = 1) = \frac{1}{(2\pi)^{d/2}|\Sigma_i|^{1/2}} \exp\{-\frac{1}{2}(\mathbf{x} - \mu_i)^T \Sigma_i^{-1} (\mathbf{x} - \mu_i)\}$$

Gaussian mixture models as a graphical model



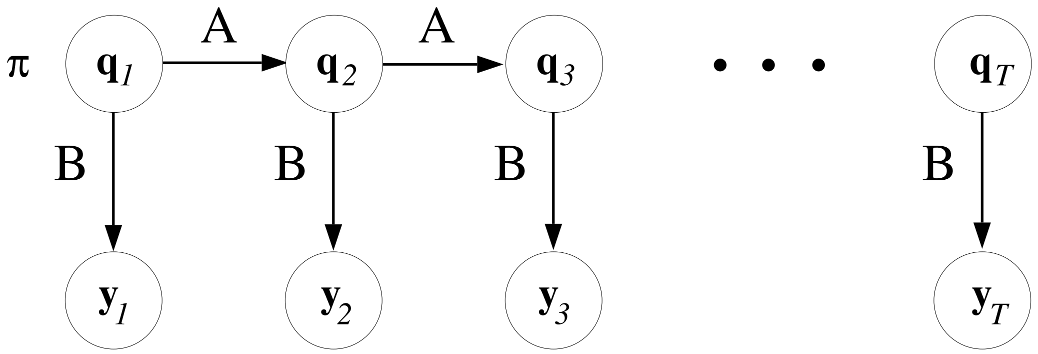
- The inference problem is to calculate the posterior probabilities:

$$
\begin{aligned}
P(q_i = 1|\mathbf{x}) &= \frac{P(\mathbf{x}|q_i = 1)P(q_i = 1)}{P(\mathbf{x})} \\
&= \frac{\frac{\pi_{\mathrm{i}}}{|\Sigma_{\mathrm{i}}|^{1=2}} \exp\{-\frac{1}{2}(\mathbf{x}-\mu_i)^T \Sigma_i^{-1}(\mathbf{x}-\mu_i)\}}{\sum_j \frac{\pi_{\mathrm{j}}}{|\Sigma_{\mathrm{j}}|^{1=2}} \exp\{-\frac{1}{2}(\mathbf{x}-\mu_j)^T \Sigma_j^{-1}(\mathbf{x}-\mu_j)\}}
\end{aligned}
$$

- This is a (trivial) example of the rescaling operation on a clique potential

Example: Hidden Markov models

- A hidden Markov model is a popular time series model
- It is a "mixture model with dynamics"



- T time steps
- M states ($\mathbf{q}_t$ is a multinomial RV)
- N outputs ($\mathbf{y}_t$ is a multinomial RV)
- state transition probability matrix A:

$$A = P(\mathbf{q}_{t+1}|\mathbf{q}_t)$$

- emission matrix B:

$$B = P(\mathbf{y}_t|\mathbf{q}_t)$$

- initial state probabilities π:

$$\pi = P(\mathbf{q}_1)$$

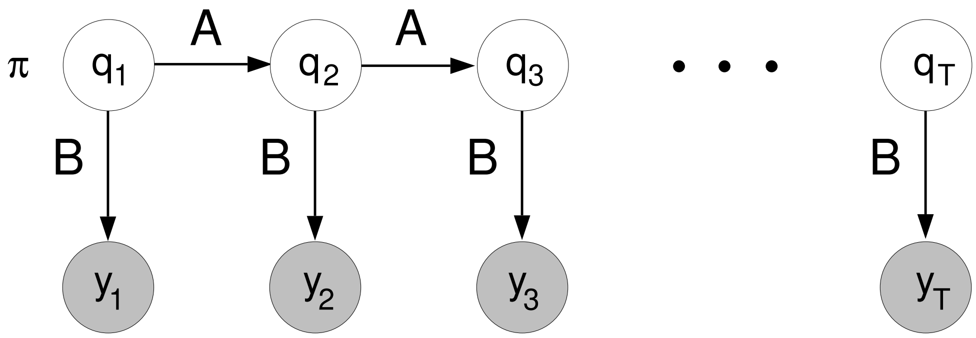
HMM as a graphical model

- Each node has a probability distribution associated with it.
- The graph of the HMM makes conditional independence statements.
- For example,

$$P(\mathbf{q}_{t+1}|\mathbf{q}_t, \mathbf{q}_{t-1}) = P(\mathbf{q}_{t+1}|\mathbf{q}_t)$$

can be read off the graph as a separation property.

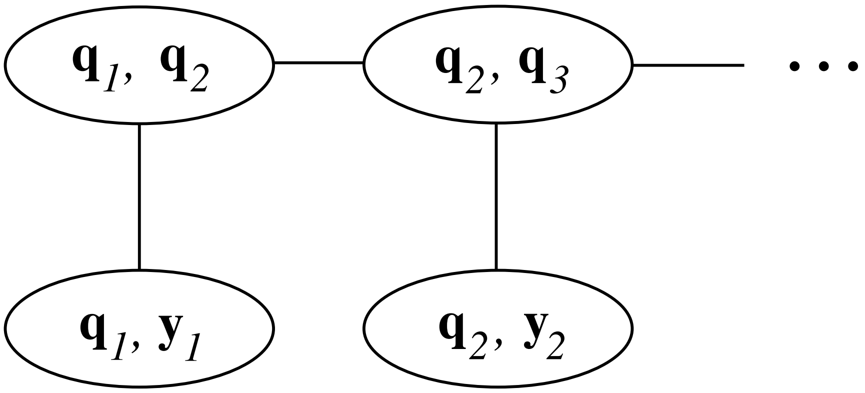
HMM probability calculations



- The time series of $\mathbf{y}_t$ values is the *evidence*
- The *inference* calculation involves calculating the probabilities of the hidden states $\mathbf{q}_t$ given the evidence
- The classical algorithm for doing this calculation is the *forward-backward* algorithm
- The forward-backward algorithm involves:
  - multiplication (conditioning)
  - summation (marginalization) in the lattice.
- It is a special case of the junction tree algorithm (cf. Smyth, et al., 1997)

Is the algorithm efficient?

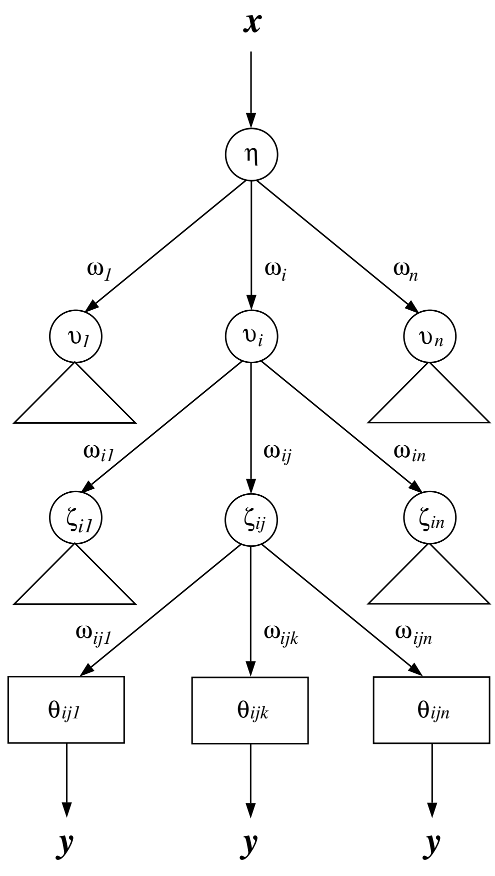
- To answer this question, let's consider the junction tree
- Note that the moralization and triangulation steps are trivial, and we obtain the following junction tree:



- The cliques are no bigger than N^2, thus the marginalization and rescaling required by the junction tree algorithm runs in time $O(N^2)$ per clique
- There are T such cliques, thus the algorithm is $O(N^2T)$ overall

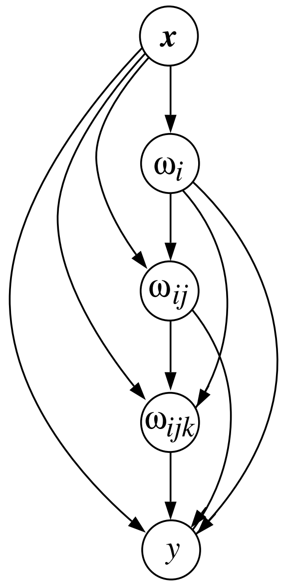
Hierarchical mixture of experts

- The HME is a "soft" decision tree
- The input vector **x** drops through a tree of "gating networks," each of which computes a probability for the branches below it

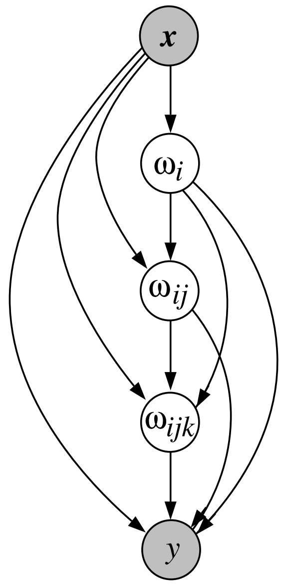


- At the leaves, the "experts" compute a probability for the output **y**
- The overall probability model is a conditional mixture model

Representation as a graphical model



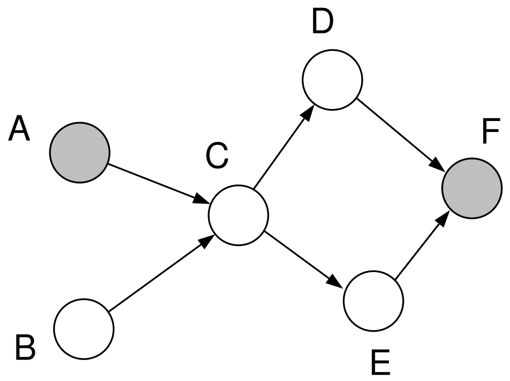
- For learning and inference, the nodes for **x** and **y** are observed (shaded)



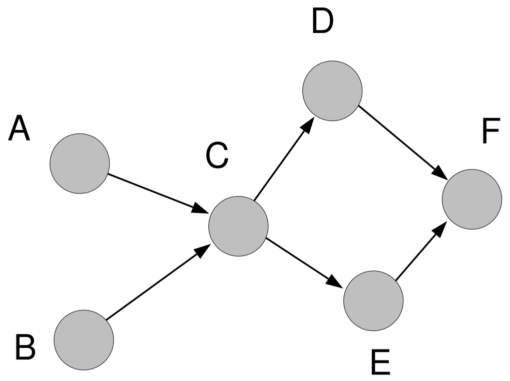
- We need to calculate probabilities of unshaded nodes (E step of EM)

Learning (parameter estimation)

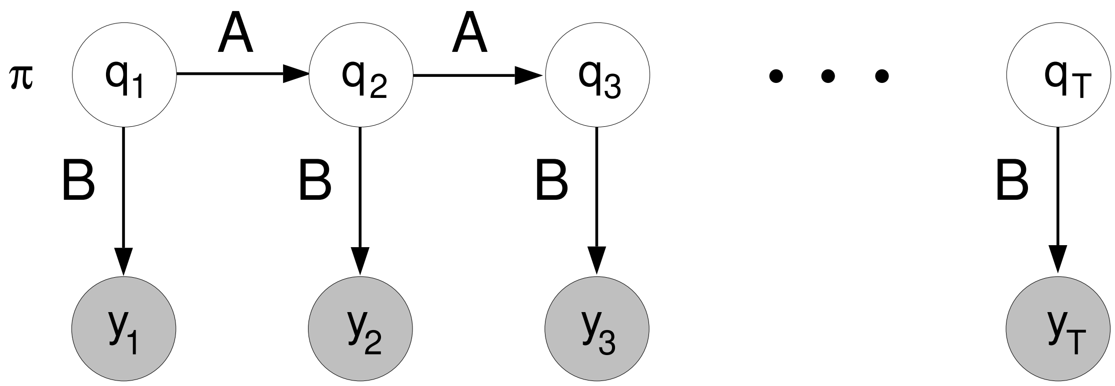
- The EM algorithm is natural for graphical models
- The E step of the EM algorithm involves calculating the probabilities of hidden variables given visible variables
  - this is exactly the inference problem



- The M step involves parameter estimation for a fully observed graph
  - this is generally straightforward



Example—Hidden Markov models



Problem: Given a sequence of outputs

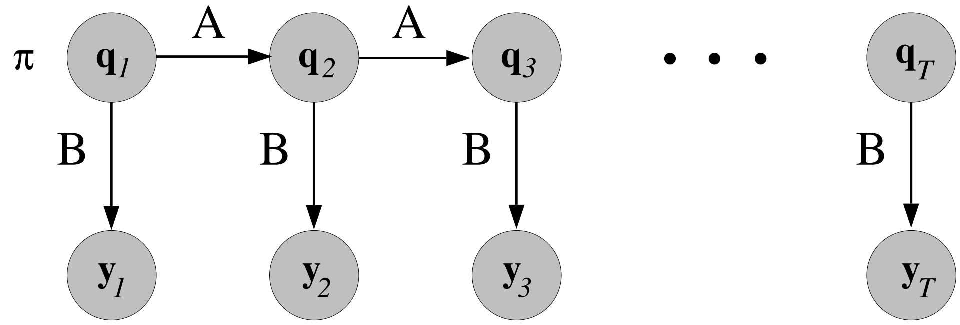
$$\mathbf{y}_{\overline{1,T}} = \{\mathbf{y}_1, \mathbf{y}_2, \ldots, \mathbf{y}_T\}$$

infer the parameters A, B and π.

- To see how to solve this problem, let's consider a simpler problem

Fully observed Markov models

- Suppose that at each moment in time we know what state the system is in:



- Parameter estimation is *easy* in this case:
  - to estimate the state transition matrix elements, simply keep a running count of the number n_{ij} of times the chain jumps from state i to state j. Then estimate a_{ij} as:
  $$\hat{a}_{ij} = \frac{n_{ij}}{\Sigma_j \, n_{ij}}$$
  - to estimate the Gaussian output probabilities, simply record which data points occurred in which states and compute sample means and covariances
  - as for the initial state probabilities, we need multiple output sequences (which we usually have in practice)

HMM parameter estimation

- When the hidden states are not in fact observed (the case we're interested in), we first *estimate* the probabilities of the hidden states
  - this is a straightforward application of the junction tree algorithm (i.e., the forward-backward algorithm)
- We then use the probability estimates instead of the counts in the parameter estimation formulas to get *update* formulas
- This gives us a better model, so we run the junction tree algorithm again to get *better estimates* of the hidden state probabilities
- And we *iterate* this procedure

CONCLUSIONS (PART I)

- Graphical models provide a general formalism for putting together graphs and probabilities
  - most so-called "unsupervised neural networks" are special cases
  - Boltzmann machines are special cases
  - mixtures of experts and related mixture-based models are special cases
  - some supervised neural networks can be treated as special cases
- The graphical model framework allows us to treat inference and learning as two sides of the same coin

INTRACTABLE GRAPHICAL MODELS

- There are a number of examples of graphical models in which exact inference is efficient:
  - chain-like graphs
  - tree-like graphs
- However, there are also a number of examples of graphical models in which exact inference can be (hopelessly) inefficient:
  - dense graphs
  - layered graphs
  - coupled graphs
- A variety of methods are available for *approximate* inference in such situations:
  - Markov chain Monte Carlo (stochastic)
  - variational methods (deterministic)

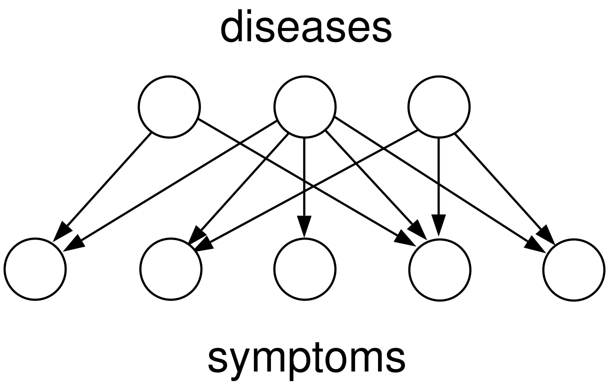
Computational complexity of exact computation

- passing messages requires marginalizing and scaling the clique potentials
- thus the time required is exponential in the number of variables in the largest clique
- good triangulations yield small cliques
  - but the problem of finding an optimal triangulation is hard (#P in fact)
- in any case, the triangulation is “off-line”; our concern is generally with the “on-line” problem of message propagation

Quick Medical Reference (QMR)

(University of Pittsburgh)

- 600 diseases, 4000 symptoms
- arranged as a bipartite graph

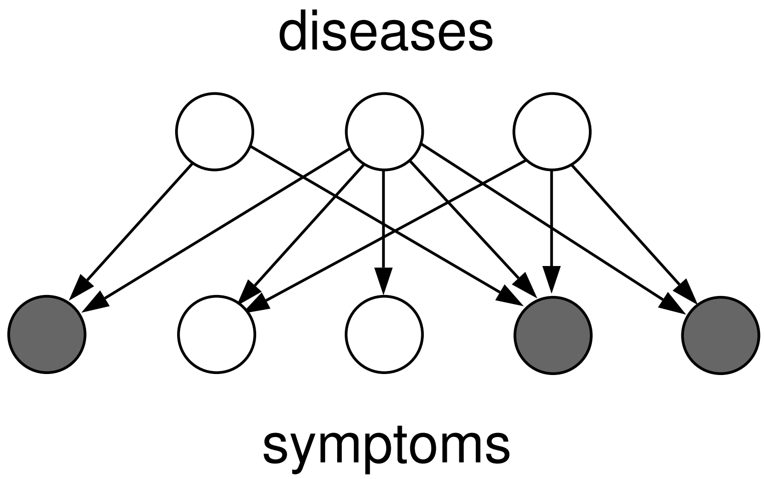


- Node probabilities $P(symptom_i|diseases)$ were obtained from an expert, under a noisy-OR model
- Want to do diagnostic calculations:

$$P(diseases|findings)$$

- Current methods (exact and Monte Carlo) are infeasible

QMR (cont.)



- "noisy-OR" parameterization:

$$P(f_i = 0|d) = (1 - q_{i0}) \prod_{j \in pa_i} (1 - q_{ij})^{d_j}$$

- rewrite in an exponential form:

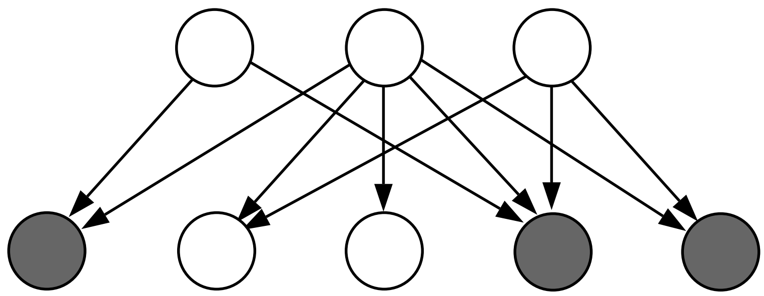
$$P(f_i = 0|d) = e^{-\theta_{i0} - \sum_{j \in pa_i} \theta_{ij} d_j}$$

where $\theta_{ij} \equiv -\log(1 - q_{ij})$

- probability of positive finding:

$$P(f_i = 1|d) = 1 - e^{-\theta_{i0} - \sum_{j \in pa_i} \theta_{ij} d_j}$$

QMR (cont.)



- Joint probability:

$$
\begin{aligned}
P(f,d) &= P(f|d)P(d) \\
&= \left[\prod_i P(f_i|d)\right]\left[\prod_j P(d_j)\right] \\
&= \left[\left(1-e^{-\theta_{10}-\sum_{j\in pa_1}\theta_{1j}d_j}\right)\left(1-e^{-\theta_{20}-\sum_{j\in pa_2}\theta_{2j}d_j}\right)\right. \\
&\quad \left.\cdots\left(1-e^{-\theta_{k0}-\sum_{j\in pa_k}\theta_{kj}d_j}\right)\right]\left[\prod_j P(d_j)\right]
\end{aligned}
$$

- Positive findings couple the disease nodes
- Median size of maximal clique is 151 nodes

Multilayer neural networks as graphical models

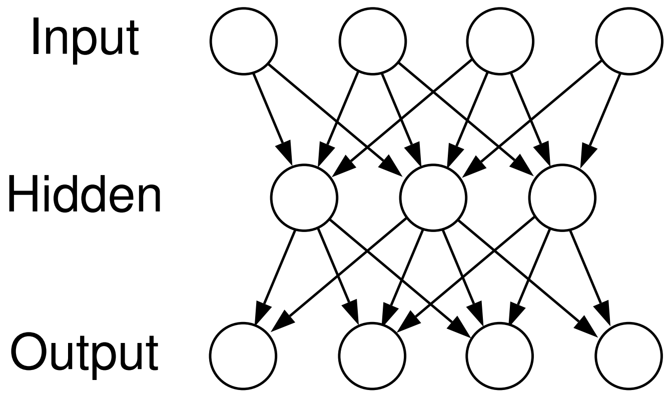
(cf. Neal, 1992; Saul, Jaakkola, & Jordan, 1996)

- Associate with node i a latent binary variable whose conditional probability is given by:

$$P(S_i = 1|S_{pa_i}) = \frac{1}{1 + e^{-\sum_{j \in pa_i} \theta_{ij} S_j - \theta_{i0}}}$$

where pa_i indexes the parents of node i

- A multilayer neural network with logistic hidden units:

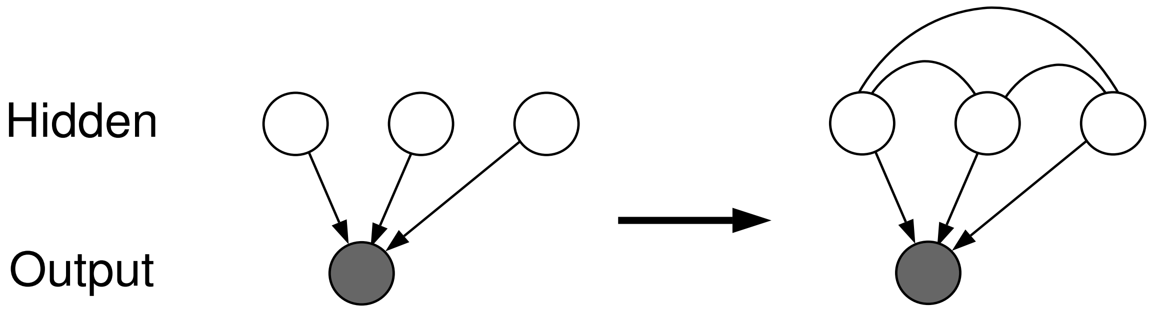


- has a joint distribution that is a product of logistic functions:

$$P(S) = \prod_i \left[\frac{e^{\left(\sum_{j \in pa_i} \theta_{ij} S_j + \theta_{i0}\right) S_i}}{1 + e^{\sum_{j \in pa_i} \theta_{ij} S_j + \theta_{i0}}} . \right]$$

Complexity of neural network inference

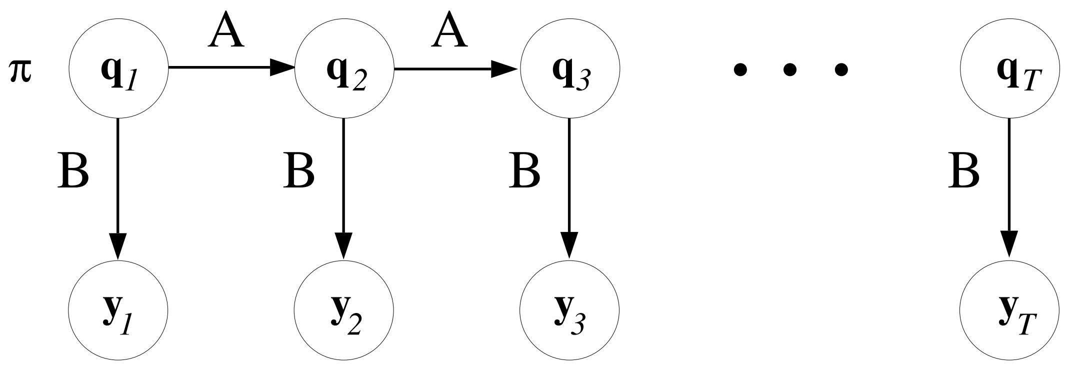
- When an output node is known (as it is during learning), moralization links the hidden units:



- So inference scales at least as badly as $O(2^N)$
- And triangulation adds even more links

Hidden Markov models

- Recall the hidden Markov model:



- T time steps
- M states ($\mathbf{q}_t$ is a multinomial RV)
- N outputs ($\mathbf{y}_t$ is a multinomial RV)
- state transition probability matrix A:

$$A = P(\mathbf{q}_{t+1}|\mathbf{q}_t)$$

- emission matrix B:

$$B = P(\mathbf{y}_t|\mathbf{q}_t)$$

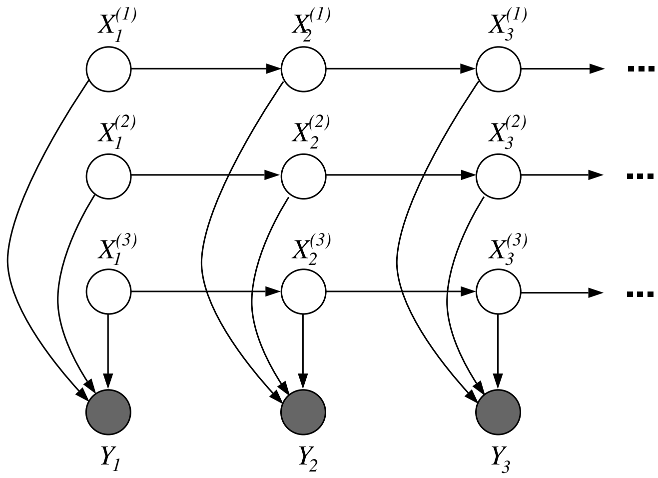
- initial state probabilities π:

$$\pi = P(\mathbf{q}_1)$$

Factorial hidden Markov models

(cf. Williams & Hinton, 1991; Ghahramani & Jordan, 1997)

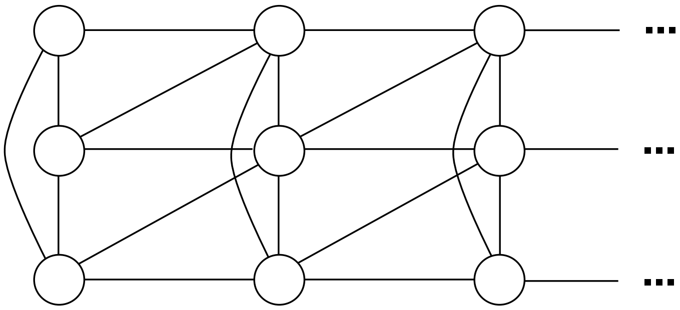
- Imagine that a time series is created from a set of M loosely-coupled underlying mechanisms
- Each of these mechanisms may have their own particular dynamic laws, and we want to avoid merging them into a single "meta-state," with a single transition matrix
  - avoid choosing a single time scale
  - avoid over-parameterization
- Here is the graphical model that we would like to use:



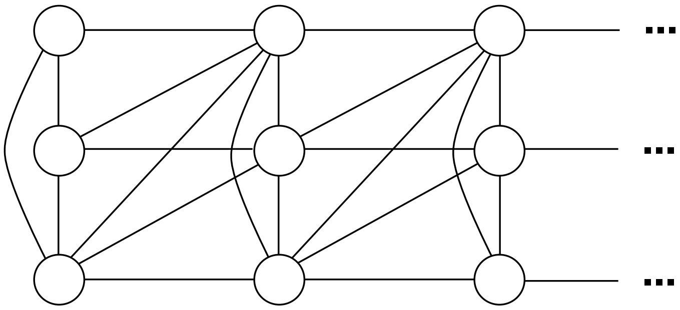
- When we triangulate do we get an efficient structure?

Triangulation?

- Unfortunately, the following graph is not triangulated:



- Here is a triangulation:

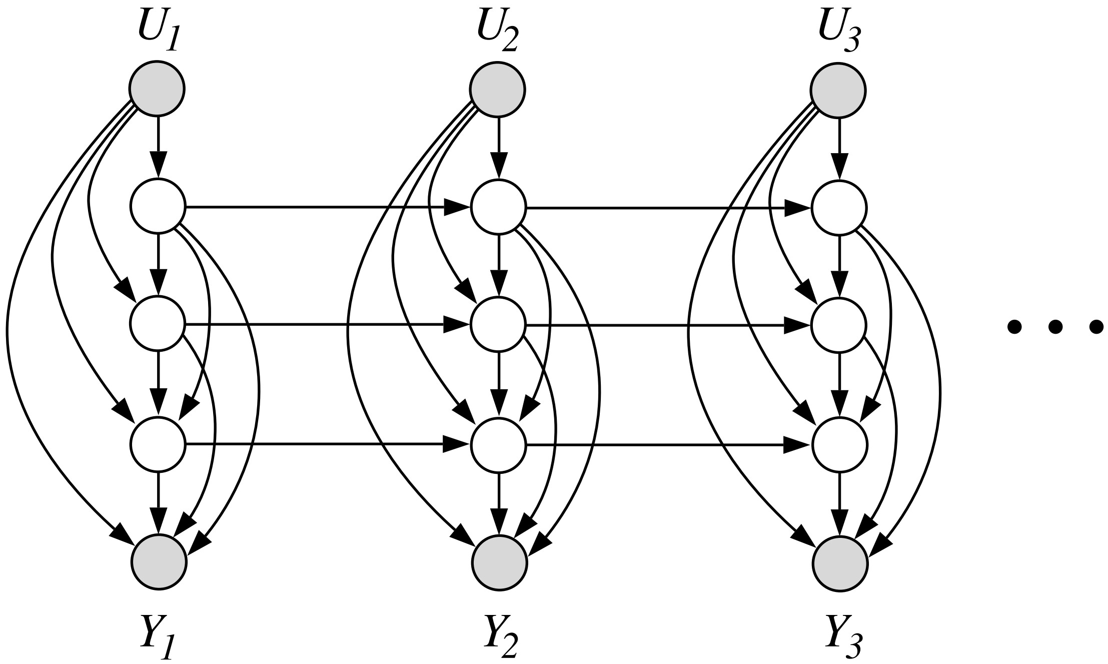


- We have created cliques of size N^4. The junction tree algorithm is not efficient for factorial HMMs.

Hidden Markov decision trees

(Jordan, Ghahramani, & Saul, 1997)

- We can combine decision trees with factorial HMMs
- This gives a "command structure" to the factorial representation



- Appropriate for multiresolution time series
- Again, the exact calculation is intractable and we must use variational methods

Markov chain Monte Carlo (MCMC)

- Consider a set of variables $S = \{S_1, S_2, \ldots, S_N\}$
- Consider a joint probability density $P(S)$
- We would like to calculate statistics associated with $P(S)$:
  - marginal probabilities, e.g., $P(S_i)$, or $P(S_i, S_j)$
  - conditional probabilities, e.g., $P(H|V)$
  - likelihoods, i.e., $P(V)$
- One way to do this is to generate samples from $P(S)$ and compute empirical statistics
  - but generally it is hard to see how to sample from $P(S)$
- We set up a simple Markov chain whose *equilibrium distribution* is $P(S)$

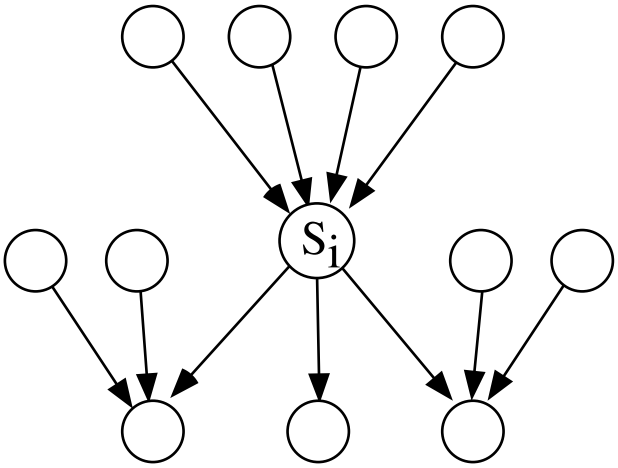
Gibbs sampling

- Gibbs sampling is a widely-used MCMC method
- Recall that we have a set of variables $S = \{S_1, S_2, \ldots, S_N\}$
- We set up a Markov chain as follows:
  - initialize the S_i to arbitrary values
  - choose i randomly
  - sample from $P(S_i|S \backslash S_i)$
  - iterate
- It is easy to prove that this scheme has $P(S)$ as its equilibrium distribution

- How to do Gibbs sampling in graphical models?

Markov blankets

- The *Markov blanket* of node S_i is the minimal set of nodes that renders S_i conditionally independent of all other nodes
- For undirected graphs, the Markov blanket is just the set of neighbors
- For directed graphs, the Markov blanket is the set of parents, children and co-parents:



- The conditional $P(S_i|S \backslash S_i)$ needed for Gibbs sampling is formed from the product of the conditional probabilities associated with S_i and each of its children
- This implies that the conditioning set needed to form $P(S_i|S \backslash S_i)$ is the Markov blanket of S_i (which is usually much smaller than $S \backslash S_i$)

Issues in Gibbs sampling

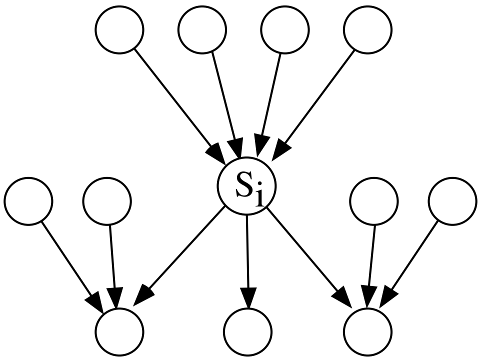
- Gibbs sampling is generally applicable
- It can be very slow
  - i.e., the time to converge can be long
- Moreover it can be hard to diagnose convergence
  - but reasonable heuristics are available
- It is often possible to combine Gibbs sampling with exact methods

Variational methods

- Variational methods are deterministic approximation methods
  - perhaps unique among deterministic methods in that they tend to work best for *dense* graphs
- They have some advantages compared to MCMC methods
  - they can be much faster
  - they yield upper and lower bounds on probabilities
- And they have several disadvantages
  - they are not as simple and widely applicable as MCMC methods
  - they require more art (thought on the part of the user) than MCMC methods
- But both variational approaches and MCMC approaches are evolving rapidly
- Note also that they can be combined (and can be combined with exact methods)

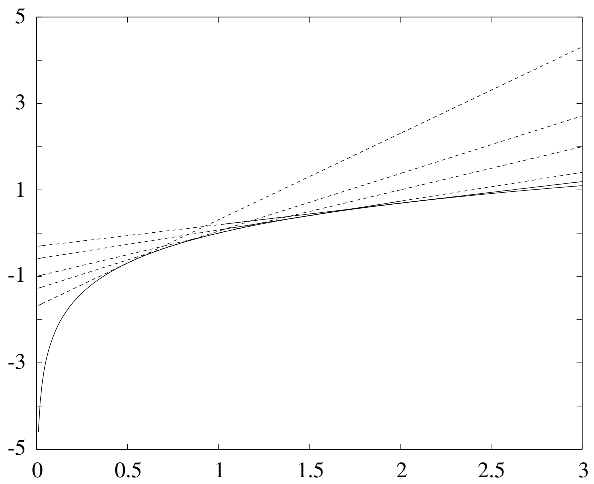
Introduction to variational methods

- Intuition—in a dense graph, each node is subject to many stochastic influences from nodes in its Markov blanket
  - laws of large numbers
  - coupled, nonlinear interactions between averages



- We want to exploit such averaging where applicable and where needed, while using exact inference algorithms on tractable "backbones"

Example of a variational transformation

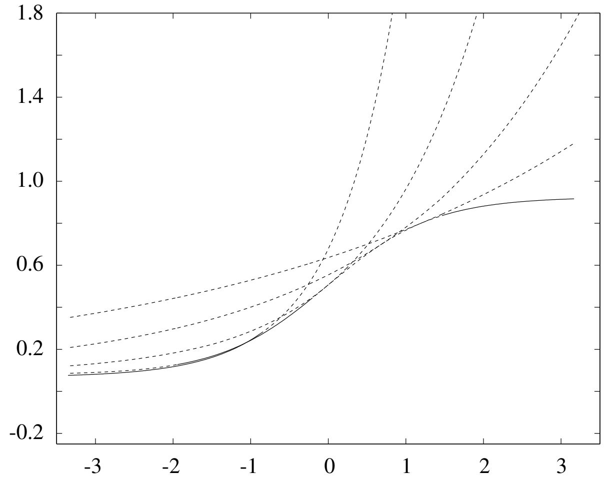


- $$\log(x) = \min_{\lambda}\{\lambda x - \log\lambda - 1\}$$
  $$\leq \lambda x - \log\lambda - 1$$

  – λ is a *variational parameter*

  – transforms a nonlinearity into a linearity

Example of a variational transformation



- $$g(x) = \frac{1}{1+e^{-x}} \; = \; \min_{\lambda}\{e^{\lambda x - H(\lambda)}\}$$
  $$\leq \; e^{\lambda x - H(\lambda)}$$

  – where $H(\cdot)$ is the binary entropy

  – a nonlinear function now a simple exponential

  – cf. "tilted distributions"

Convex duality approach

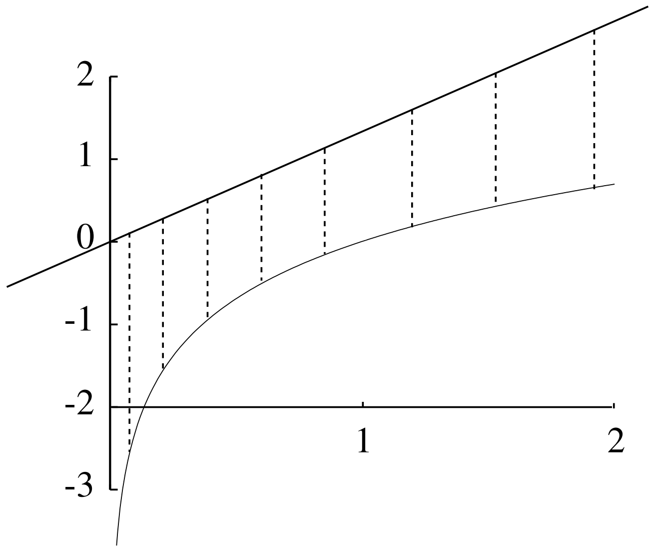
(Jaakkola & Jordan, NIPS '97)

- for concave $f(x)$:

$$\begin{aligned} f(x) &= \min_{\lambda} \left\{ \lambda^T x - f^*(\lambda) \right\} \\ f^*(\lambda) &= \min_{x} \left\{ \lambda^T x - f(x) \right\} \end{aligned}$$

- yields bounds:

$$\begin{aligned} f(x) &\leq \lambda^T x - f^*(\lambda) \\ f^*(\lambda) &\leq \lambda^T x - f(x) \end{aligned}$$



- (lower bounds obtained from convex $f(x)$)

Variational transformations and inference

- Two basic approaches—*sequential* and *block*
  - we discuss the sequential approach first and return to the block approach later

- In the *sequential* approach, we introduce variational transformations sequentially, node by node
  - this yields a sequence of increasingly simple graphical models
  - every transformation introduces a new variational parameter, which we (lazily) put off evaluating until the end
  - eventually we obtain a model that can be handled by exact techniques, at which point we stop introducing transformations

Variational QMR

(Jaakkola & Jordan, 1997)

- Recall the noisy-OR probability of a positive finding:

$$P(f_i = 1|d) = 1 - e^{-\theta_{i0} - \Sigma_{j \in pa_i} \theta_{ij} d_j}$$

- The logarithm of this function is concave, thus we can utilize convex duality
  - evaluating the conjugate function, we obtain:

$$f^*(\lambda) = -\lambda \ln \lambda + (\lambda + 1) \ln(\lambda + 1)$$

- Thus we upper bound the probability of a positive finding:

$$\begin{aligned} P(f_i = 1|d) &\leq e^{\lambda_i (\theta_{i0} + \Sigma_{j \in pa_i} \theta_{ij} d_j) - f^*(\lambda_i)} \\ &= e^{\lambda_i \theta_{i0} - f^*(\lambda_i)} \prod_{j \in pa_i} \left[e^{\lambda_i \theta_{ij}} \right]^{d_j} \end{aligned}$$

- This is a factorized form; it effectively changes the "priors" $P(d_j)$ by multiplying them by $e^{\lambda_i \theta_{ij}}$ and delinking the i^{th} node from the graph

Variational QMR (cont.)

- Recall the joint distribution:

$$P(f,d) = \left[\left(1 - e^{-\theta_{10} - \Sigma_{j\in pa_1}\theta_{1j}d_j}\right)\left(1 - e^{-\theta_{20} - \Sigma_{j\in pa_2}\theta_{2j}d_j}\right) \cdots \left(1 - e^{-\theta_{k0} - \Sigma_{j\in pa_k}\theta_{kj}d_j}\right)\right]\left[\prod_j P(d_j)\right]$$

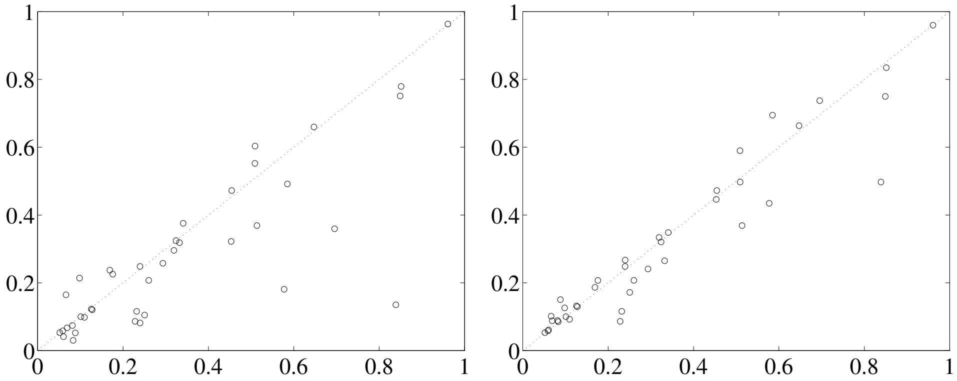
- After a variational transformation:

$$P(f,d) \leq \left[\left(1 - e^{-\theta_{10} - \Sigma_{j\in pa_1}\theta_{1j}d_j}\right)\left(1 - e^{-\theta_{20} - \Sigma_{j\in pa_2}\theta_{2j}d_j}\right) \cdots \left(e^{\lambda_k\theta_{k0} - f^*(\lambda_k)} \prod_{j\in pa_k}\left[e^{\lambda_k\theta_{kj}}\right]^{d_j}\right)\right]\left[\prod_j P(d_j)\right]$$

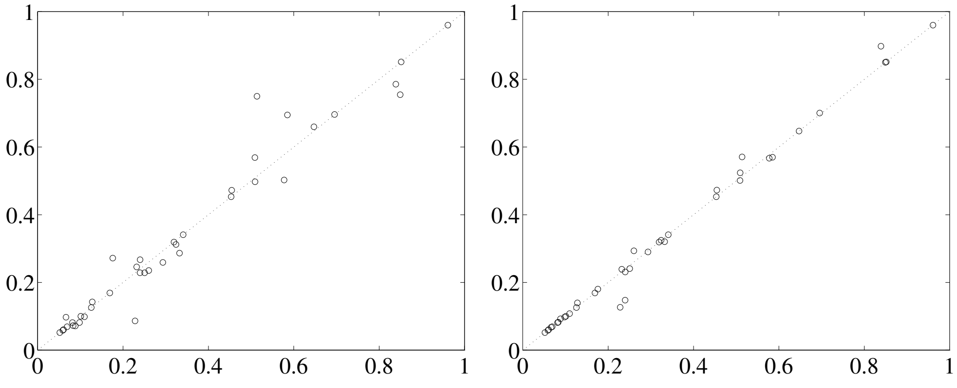
- Use a greedy method to introduce the variational transformations
  - choose the node that is estimated to yield the most accurate transformed posterior
- Optimize across the variational parameters λ_i
  - this turns out to be a convex optimization problem

QMR results

- We studied 48 clinicopathologic (CPC) cases
- 4 of these CPC cases had less than 20 positive findings; for these we calculated the disease posteriors exactly
- Scatterplots of exact vs. variational posteriors for (a) 4 positive findings treated exactly, (b) 8 positive findings treated exactly:

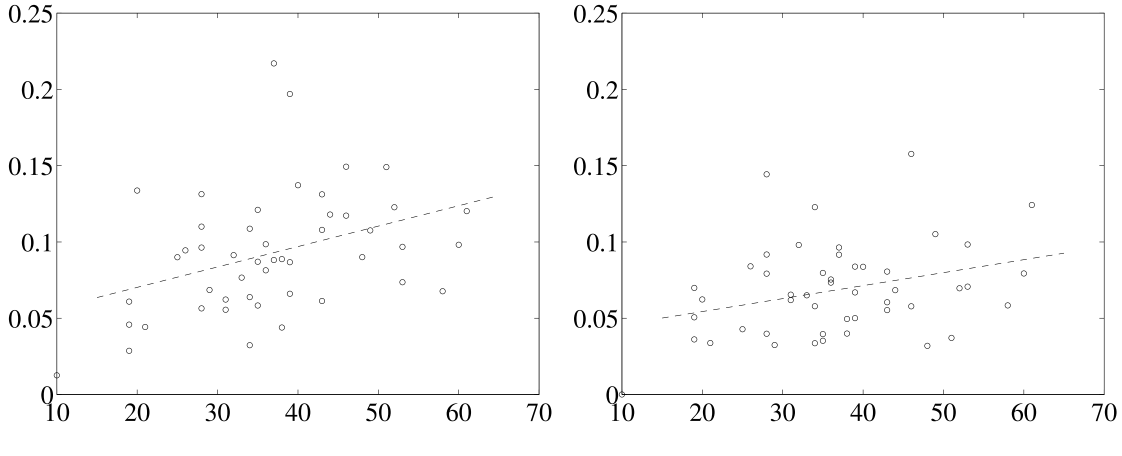


- Scatterplots of exact vs. variational posteriors for (a) 12 positive findings treated exactly, (b) 16 positive findings treated exactly:



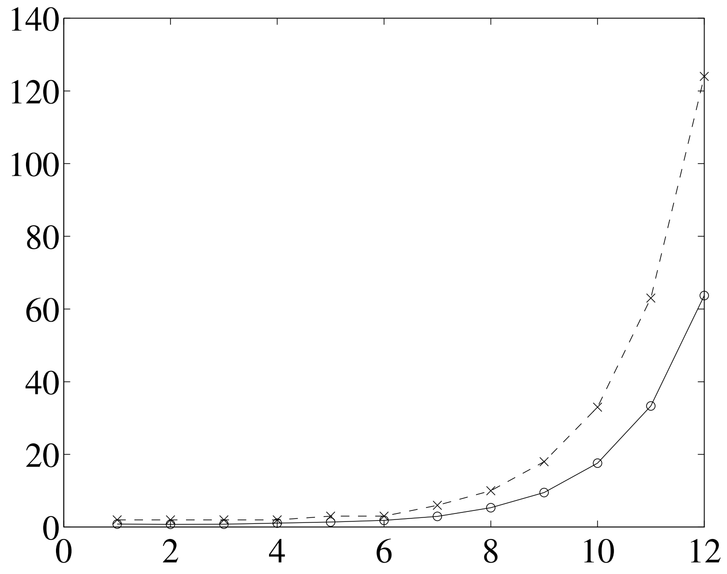
QMR results (cont.)

- For the remaining 44 CPC cases, we had no way to calculate the gold standard
- Thus we assessed the variational accuracy via a sensitivity estimate
  - we calculated the squared difference in posteriors when a particular node was treated exactly or variationally transformed, and averaged across nodes
  - a small value of this average suggests that we have the correct posteriors
  - (we validated this surrogate on the 4 cases for which we could do the exact calculation)
- Sensitivity estimates vs. number of positive findings when (a) 8 positive findings treated exactly, (b) 12 positive findings treated exactly:



QMR results (cont.)

- Timing results in seconds (Sparc 10) as a function of the number of positive findings treated exactly (solid line—average across CPC cases; dashed line—maximum across CPC cases):

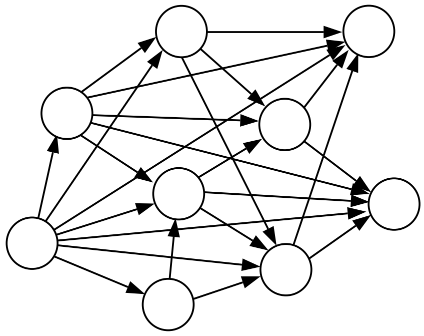


A cautionary note

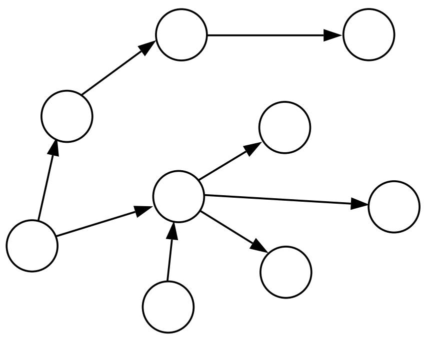
- these disease marginals are based on the upper variational distribution, which appears tight
- this distribution is guaranteed to upper bound the *likelihood*
- to obtain direct upper and lower bounds on the disease *marginals*, which are conditional probabilities, we need upper *and* lower bounds on the likelihood
- the lower bounds we obtain in our current implementation, however, are not tight enough
- thus, although the marginals we report appear to yield good approximations empirically, we cannot guarantee that they bound the true marginals

Variational transformations and inference

- Two basic approaches—*sequential* and *block*
- The block approach treats the approximation problem as a global optimization problem
- Consider a dense graph characterized by a joint distribution $P(H, V|\theta)$



- We remove links to obtain a simpler graph characterized by a conditional distribution $Q(H|V, \theta, \mu)$



- (Examples will be provided below...)

Variational inference (cont.)

(Dayan, et al., 1995; Hinton, et al., 1995; Saul & Jordan, 1996)

- $Q(H|V, \theta, \mu)$ has extra degrees of freedom, given by *variational parameters* μ_i
  - we can think of these as being obtained by a sequence of variational transformations applied to the nodes
  - but we now want to take a more global view
- Choose μ_i so as to minimize

$$KL(Q\|P) = \sum_{H} Q(H|V, \theta, \mu) \log \frac{Q(H|V, \theta, \mu)}{P(H|V, \theta)}$$

- We will show that this yields a lower bound on the probability of the evidence (the likelihood)
- Minimizing the KL divergence requires us to compute averages under the Q distribution; we must choose Q so that this is possible
  - i.e., we choose our simplified graph so that it is amenable to exact methods

Variational inference (cont.)

- The fact that this is a lower bound follows from Jensen's inequality

$$\begin{aligned}
\log P(V) &= \log \Sigma_H P(H,V) \\
&= \log \Sigma_H Q(H|V) \cdot \frac{P(H,V)}{Q(H|V)} \\
&\geq \Sigma_H Q(H|V) \log \left[\frac{P(H,V)}{Q(H|V)}\right]
\end{aligned}$$

- The difference between the left and right hand side is the KL divergence:

$$KL(Q||P) = \Sigma_H Q(H|V) \log \left[\frac{Q(H|V)}{P(H|V)}\right]$$

which is positive; thus we have a lower bound

Linking the two approaches

(Jaakkola, 1997)

- The block approach can be derived within the convex duality framework

$$f(x) \geq \lambda^T x - f^*(\lambda)$$

  - treat the distribution $Q(H|V, \theta, \mu)$ as λ; a vector-valued variational parameter (one value for each configuration H)
  - the argument x becomes $\log P(H, V|\theta)$; also a vector-valued variable (one value for each configuration H)
  - the function $f(x)$ becomes $\log P(V|\theta)$
  - it turns out that the conjugate function $f^*(x)$ is the negative entropy function

- Thus convex duality yields:

$$\log P(V) \geq \sum_H Q(H|V) \log P(H, V) - \sum_H Q(H|V) \log Q(H|V)$$

which is the bound derived earlier from Jensen's inequality

Learning via variational methods

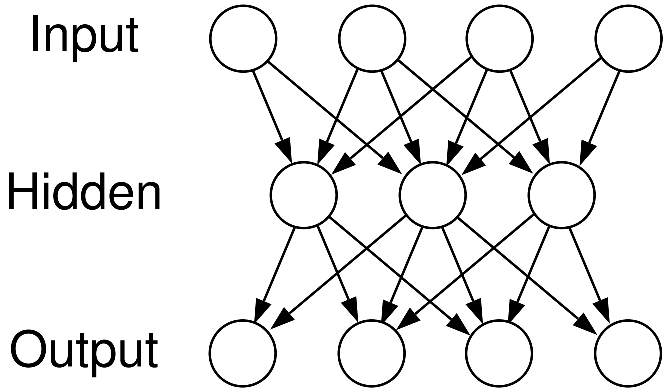
(Neal & Hinton, in press)

- MAP parameter estimation for graphical models:
  - the EM algorithm is a general method for MAP estimation
  - "inference" is the E step of EM for graphical models (calculate $P(H|V)$ to "fill in" the hidden values)
  - variational methods provide an approximate E step
  - more specifically we increase the lower bound on the likelihood at each iteration

Neural networks and variational approximations

(Saul, Jaakkola, & Jordan, 1996)

- A multilayer neural network with logistic hidden units:



has a joint distribution that is a product of logistic functions:

$$P(H,V|\theta) = \prod_i \left[\frac{e^{\left(\sum_{j \in pa_i} \theta_{ij} S_j + \theta_{i0}\right) S_i}}{1 + e^{\sum_{j \in pa_i} \theta_{ij} S_j + \theta_{i0}}} . \right]$$

- The simplest variational approximation, which we will refer to as a *mean field* approximation considers the factorized approximation:

$$Q(H|V,\mu) = \Pi_{i \in H} \ \mu_i^{S_i} (1 - \mu_i)^{1 - S_i}.$$

Division of labor

- The KL bound has two basic components:

$$\begin{pmatrix} \textit{variational} \\ \textit{entropy} \end{pmatrix} = -\Sigma_H \; Q(H|V) \log Q(H|V)$$

$$\begin{pmatrix} \textit{variational} \\ \textit{energy} \end{pmatrix} = -\Sigma_H \; Q(H|V) \log P(H,V)$$

- What we need is the difference:

$$\log P(V|\theta) \geq \begin{pmatrix} \textit{variational} \\ \textit{entropy} \end{pmatrix} - \begin{pmatrix} \textit{variational} \\ \textit{energy} \end{pmatrix}$$

Maximizing the lower bound

- We find the best approximation by varying $\{\mu_i\}$ to minimize $KL(Q||P)$.

- This amounts to maximizing the lower bound:

$$\log P(V|\theta) \geq \begin{pmatrix} \mathit{variational} \\ \mathit{entropy} \end{pmatrix} - \begin{pmatrix} \mathit{variational} \\ \mathit{energy} \end{pmatrix}.$$

- Abuse of notation: we define *clamped* values (0 or 1) for the instantiated nodes,

$$\mu_i = S_i \text{ for } i \in V.$$

Variational entropy

- The variational entropy is:

$$-\Sigma_H \; Q(H|V) \log Q(H|V)$$

- Our *factorized approximation* is:

$$Q(H|V) = \Pi_i \; \mu_i^{S_i}(1-\mu_i)^{1-S_i},$$

- The *joint entropy* is the sum of the individual unit entropies:

$$-\Sigma_i \; \left[\mu_i \log \mu_i + (1-\mu_i)\log(1-\mu_i)\right].$$

Variational energy

- The variational energy is:

$$-\Sigma_H \; Q(H|V) \log P(H, V)$$

- In sigmoid networks:

$$\begin{aligned}\log P(H, V) \;=\; & -\sum_{ij} \theta_{ij} S_i S_j \\ & + \sum_{i} \log \left[1 + e^{\Sigma_j \theta_{ij} S_j}\right].\end{aligned}$$

- The first term are common to undirected networks. *The last term is not.*

- Averaging over $Q(H|V)$ gives:

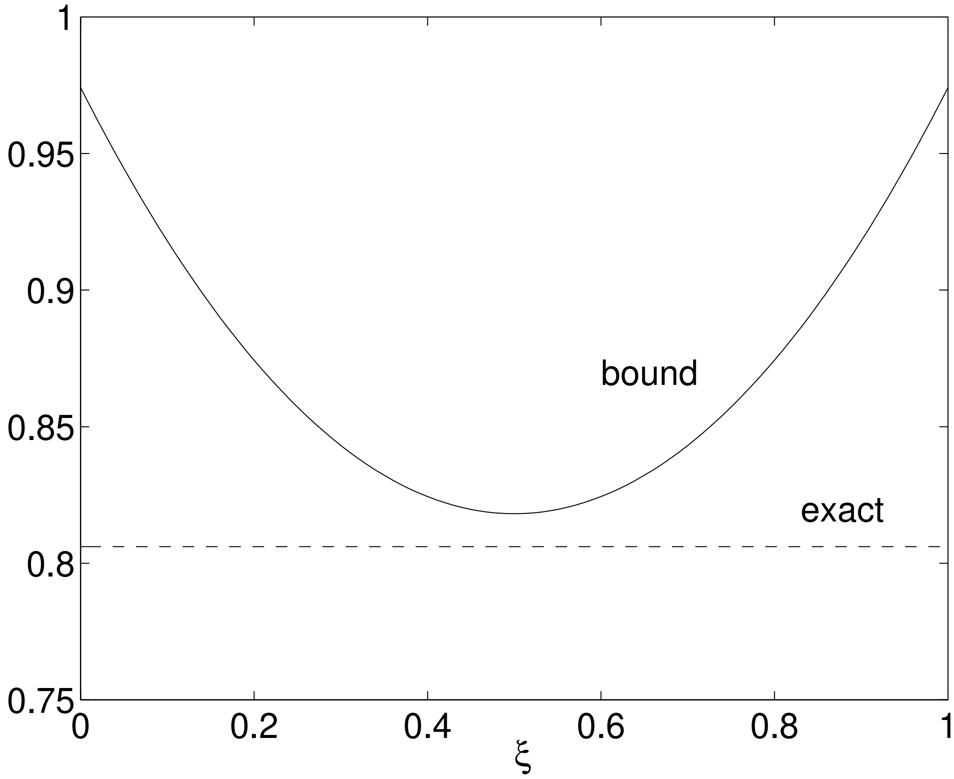
$$-\sum_{ij} \theta_{ij} \mu_i \mu_j \sum_{i} \left\langle \log \left[1 + e^{\Sigma_j \theta_{ij} S_j}\right]\right\rangle$$

- The last term is intractable, so (again) we use Jensen's inequality to obtain an upper bound…

- **Lemma** (Seung): for any random variable z, and any real number ξ:

$$\langle \log[1+e^z] \rangle \leq \xi \langle z \rangle + \log \left\langle e^{-\xi z} + e^{(1-\xi)z} \right\rangle .$$

- **Ex**: z is Gaussian with zero mean and unit variance.



- **Ex**: z is the sum of weighted inputs to S_i;

$$z = \sum_j \theta_{ij} S_j + h_i.$$

The lemma provides an upper bound on the intractable terms in the variational energy:

$$\sum_i \left\langle \log \left[1 + e^{\sum_j \theta_{ij} S_j} \right] \right\rangle$$

Variational (mean field) equations

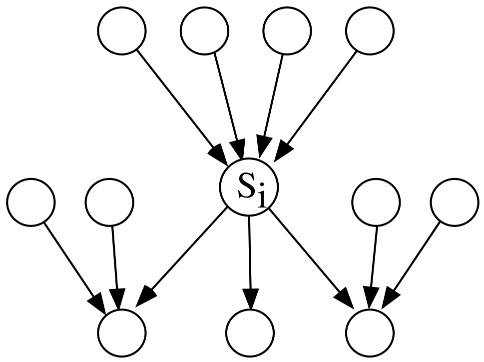
- The bound on the log-likelihood,

$$\log P(V|\theta) \geq \begin{pmatrix} \textit{variational} \\ \textit{entropy} \end{pmatrix} - \begin{pmatrix} \textit{variational} \\ \textit{energy} \end{pmatrix},$$

  is valid for any setting of the variational parameters, $\{\mu_i\}$

- The optimal $\{\mu_i\}$ are found by solving the variational equations:

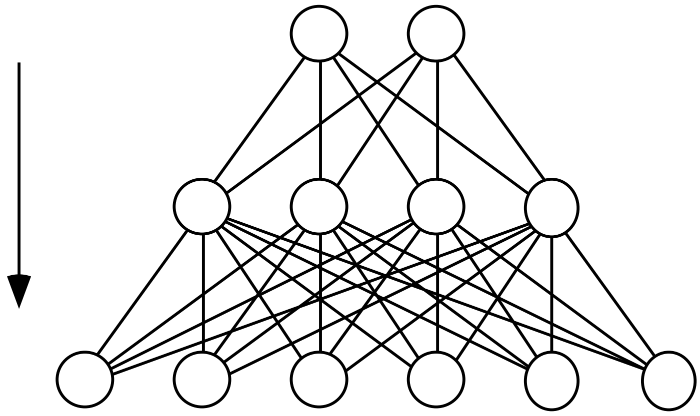
$$\mu_i = \sigma\left(\sum_j \left[\theta_{ij}\mu_j + \theta_{ji}(\mu_j - \xi_j) - K_{ji}\right]\right)$$



- The effective input to S_i is composed of terms from its *Markov blanket*

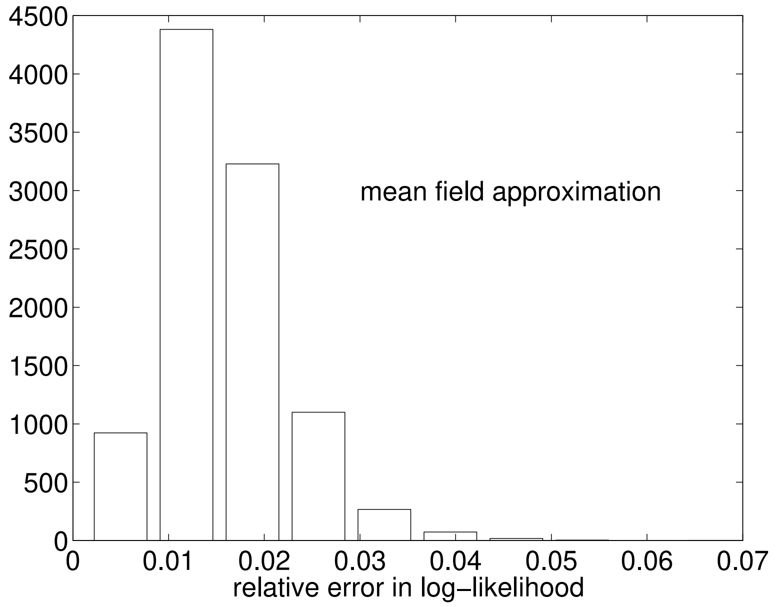
Numerical experiments

- For small networks, the variational bound can be compared to the true likelihood obtained by exact enumeration.

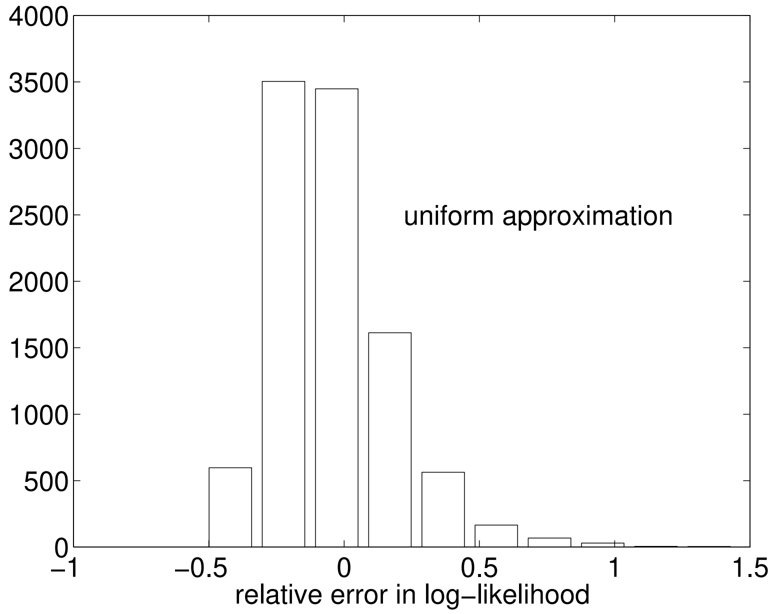


- We considered the event that all the units in the bottom layer were inactive.
- This was done for 10000 random networks whose weights and biases were uniformly distributed between -1 and 1.

- *Mean field approximation*:

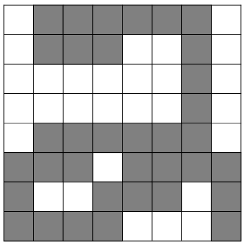


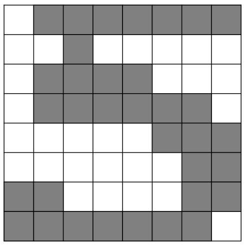
- *Uniform approximation*:



Digit recognition

- Images:





- Confusion matrix:

	0	1	2	3	4	5	6	7	8	9
0	388	2	2	0	1	3	0	0	4	0
1	0	393	0	0	0	1	0	0	6	0
2	1	2	376	1	3	0	4	0	13	0
3	0	2	4	373	0	12	0	0	6	3
4	0	0	2	0	383	0	1	2	2	10
5	0	2	1	13	0	377	2	0	4	1
6	1	4	2	0	1	6	386	0	0	0
7	0	1	0	0	0	0	0	388	3	8
8	1	9	1	7	0	7	1	1	369	4
9	0	4	0	0	0	0	0	8	5	383

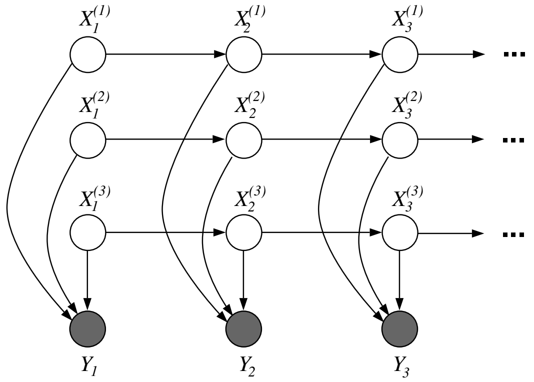
- Comparative results:

algorithm	test error
nearest neighbor	6.7
back propagation	5.6
Helmholtz machine	4.8
variational	4.6

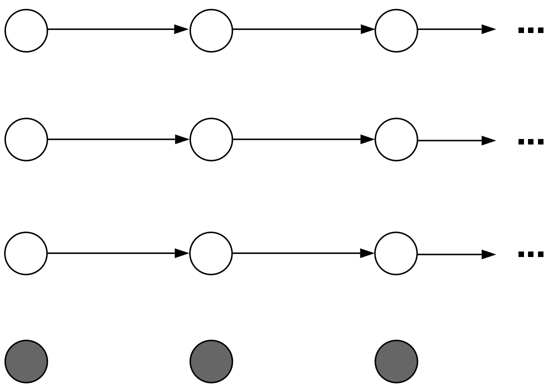
Example—Factorial HMM

(Ghahramani & Jordan, 1997)

- Recall the factorial hidden Markov model, which yielded intractably large cliques when triangulated:

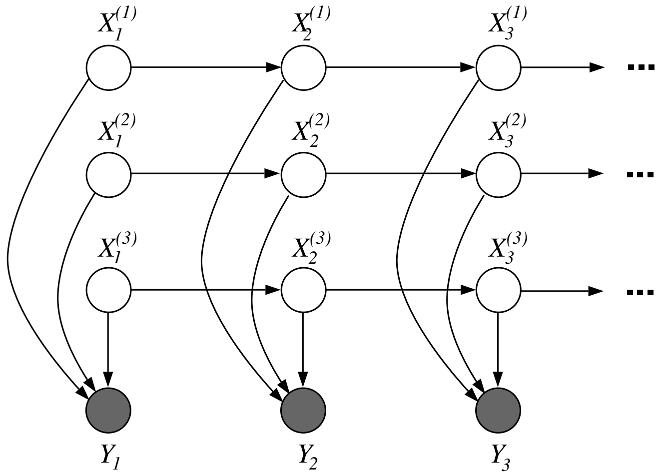


- We can variationally transform this model into:



where we see that we have to solve separate simple HMM problems on each iteration. The variational parameters couple the chains.

Example—Factorial HMM (cont.)



- M independent Markov chains given the observations

$$Q(\{X_t\}|\theta) = \prod_{m=1}^{M} Q(X_1^{(m)}|\theta) \prod_{t=2}^{T} Q(X_t^{(m)}|X_{t-1}^{(m)}, \theta),$$

  where

$$\begin{aligned} Q(X_1^{(m)}|\theta) &= \pi^{(m)} h_1^{(m)} \\ Q(X_t^{(m)}|X_{t-1}^{(m)}, \theta) &= P^{(m)} h_t^{(m)}. \end{aligned}$$

- The parameters of this approximation are the $h_t^{(m)}$, which play the role of observation log probabilities for the HMMs.

Example—Factorial HMM (cont.)

- Minimizing the KL divergence results in the following fixed point equation:

$$h_t^{(m)} \propto \exp\{W^{(m)\prime}C^{-1}\left(Y_t - \hat{Y}_t\right) \;+\; W^{(m)\prime}C^{-1}W^{(m)}\langle X_t^{(m)}\rangle \\ -\; \frac{1}{2}\Delta^{(m)}\},$$

  where

$$\hat{Y}^t = \sum_{\ell=1}^{M} W^{(\ell)}\langle X_t^{(\ell)}\rangle,$$

  and $\Delta^{(m)}$ is the vector of diagonal elements of $W^{(m)\prime}C^{-1}W^{(m)}$.

- Repeat until convergence of $KL(Q\|P)$:
  1. Compute $h_t^{(m)}$ using fixed-point equation, which depends on $\langle X_t^{(m)}\rangle$
  2. Compute $\langle X_t^{(m)}\rangle$ using forward-backward algorithm on HMMs with observation log probabilities given by $h_t^{(m)}$

Results

- Fitting the FHMM to the Bach Chorale dataset: (Ghahramani & Jordan, 1997):

Modeling J. S. Bach's chorales

Discrete event sequences:

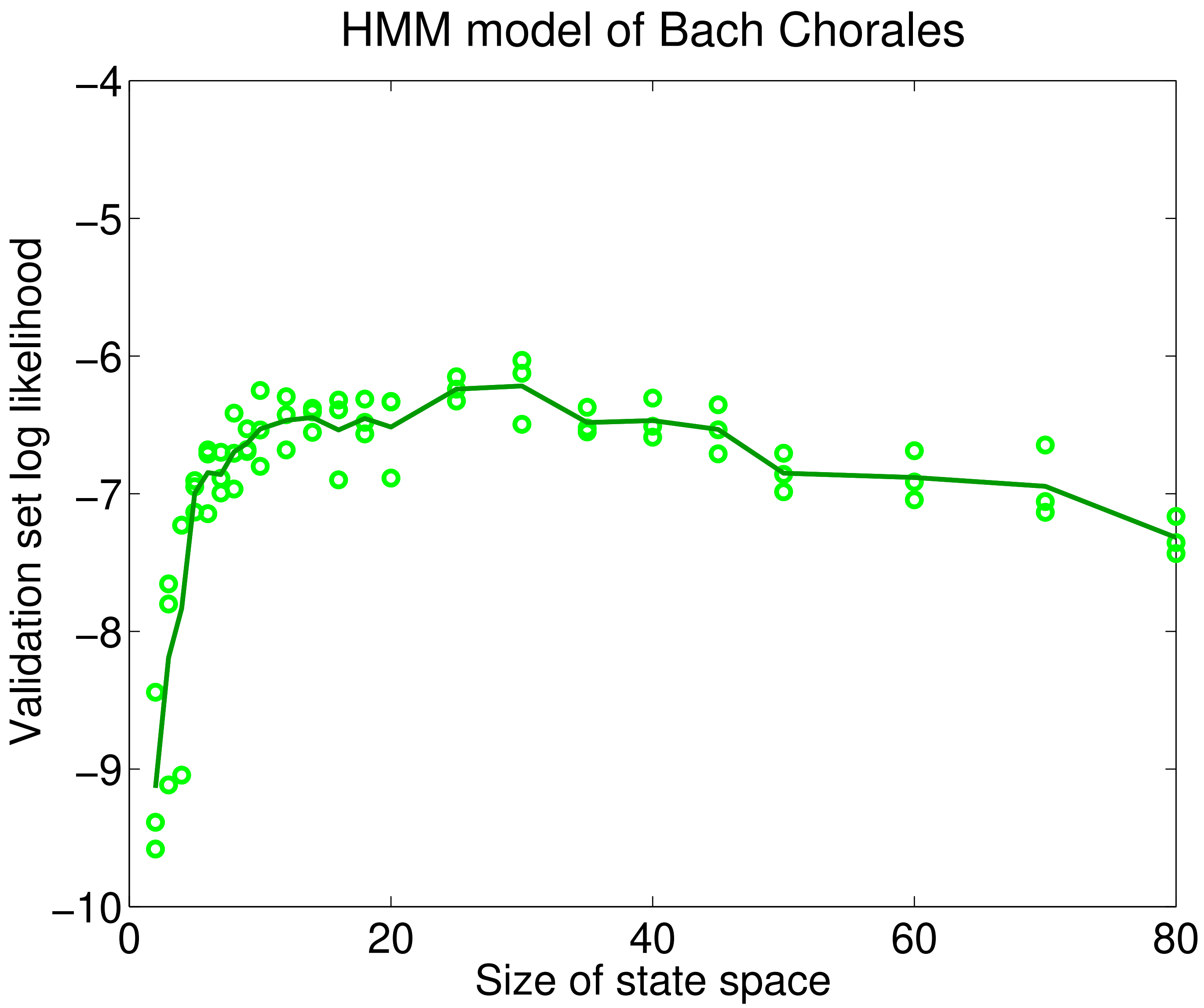
Attribute	Description	Representation
pitch	pitch of the event	int $[0, 127]$
keysig	key signature of the chorale (num of sharps and flats)	int $[7, 7]$
timesig	time signature of the chorale	int (1/16 notes)
fermata	event under fermata?	binary
st	start time of event	int (1/16 notes)
dur	duration of event	int (1/16 notes)

First 40 events of 66 chorale melodies:

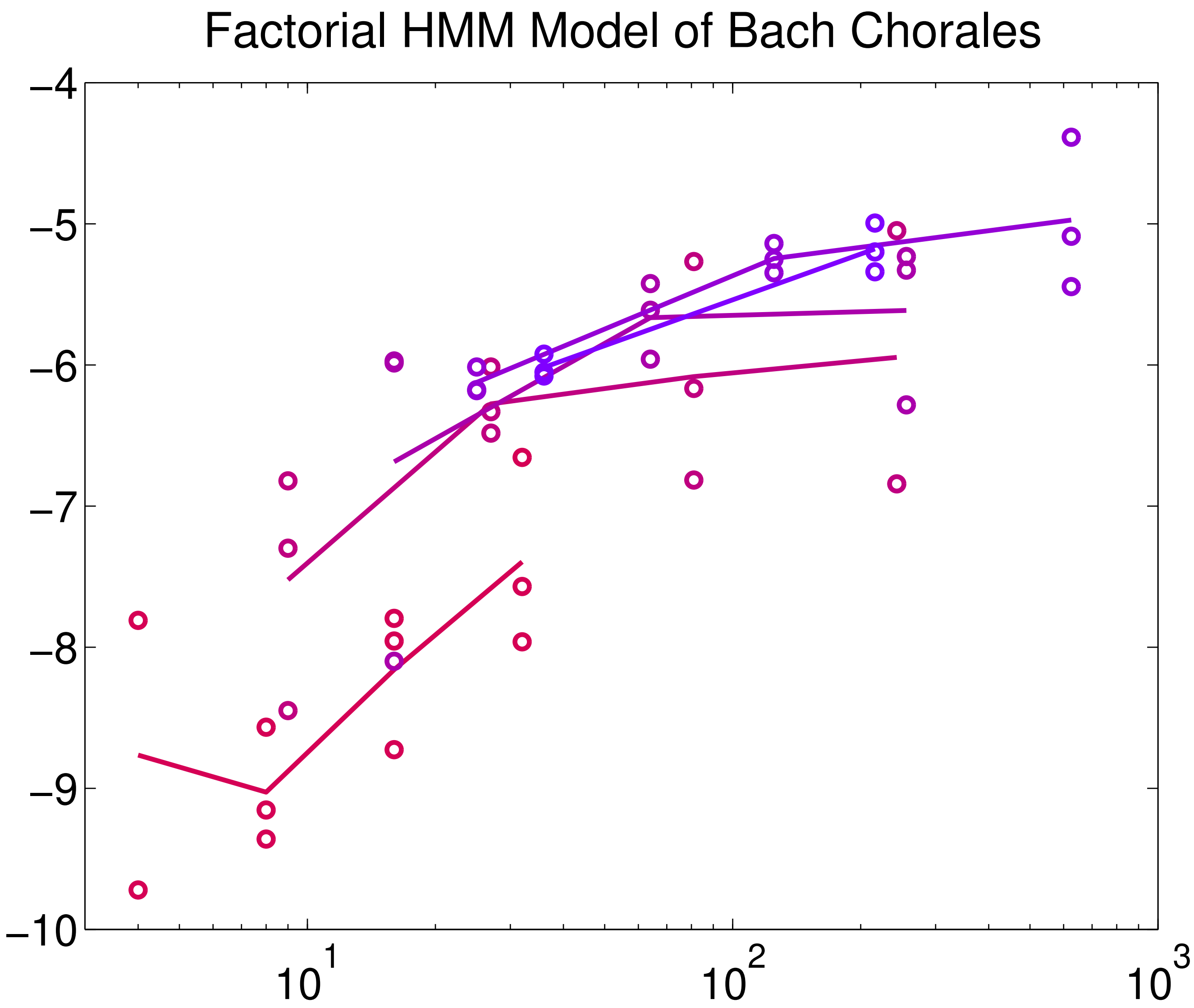
- training: 30 melodies
- test: 36 melodies

See Conklin and Witten (1995).

Fitting a single HMM to the Bach chorale data



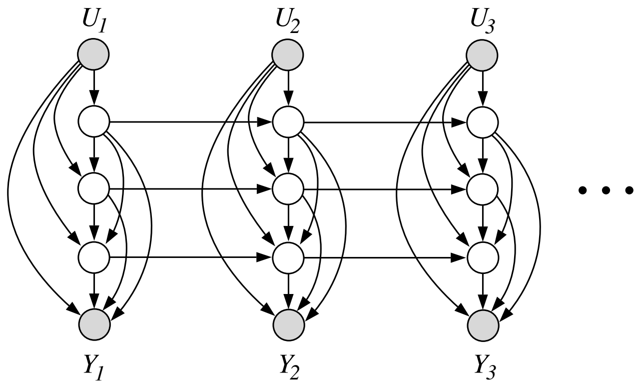
Fitting a factorial HMM to the Bach chorale data



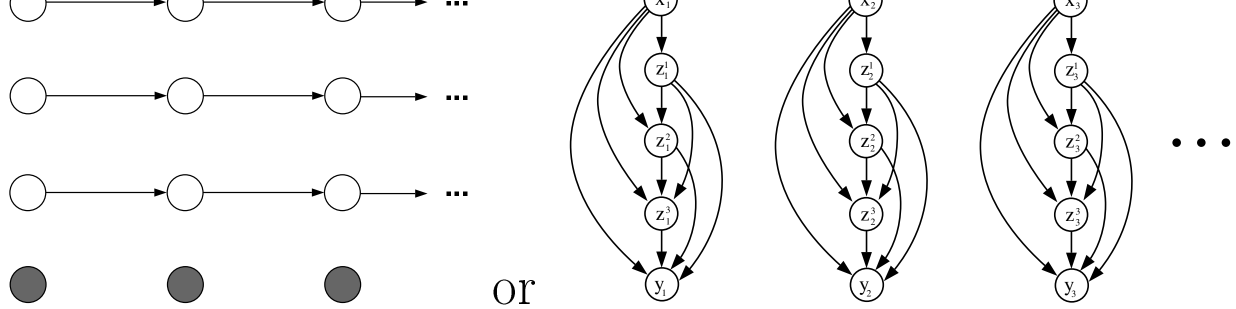
Example—hidden Markov decision tree

(Jordan, Ghahramani, & Saul, 1997)

- Recall the hidden Markov decision tree, which also yielded intractably large cliques when triangulated:

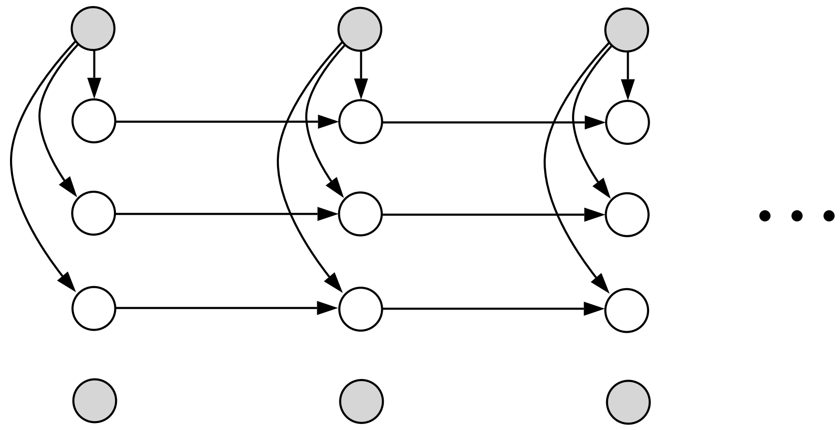


- We can variationally transform this model into one of two simplified models:



Forest of chains approximation

- Eliminating the vertical links that couple the states yields an approximating graph that is a forest of chains:



- The Q distribution is given by:

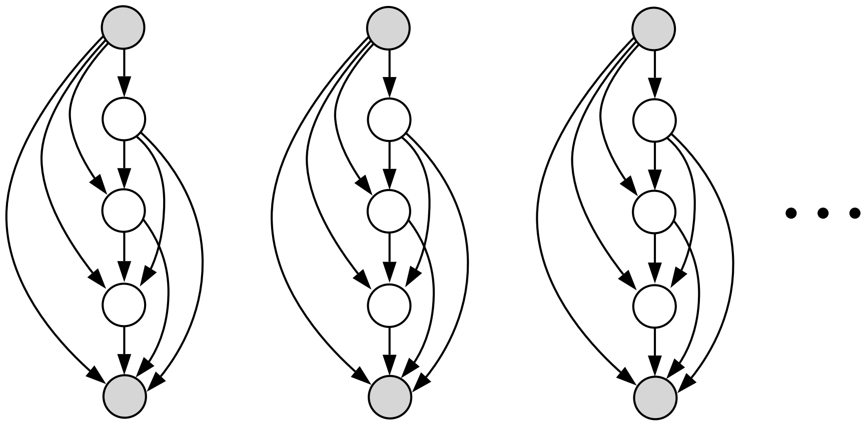
$$
\begin{aligned}
&Q(\{\mathbf{z}_t^1, \mathbf{z}_t^2, \mathbf{z}_t^3\} \mid \{\mathbf{y}_t\}, \{\mathbf{x}_t\}) = \\
&\quad \frac{1}{Z_Q} \prod_{t=2}^{T} \tilde{a}_t^1(\mathbf{z}_t^1|\mathbf{z}_{t-1}^1)\tilde{a}_t^2(\mathbf{z}_t^2|\mathbf{z}_{t-1}^2)\tilde{a}_t^3(\mathbf{z}_t^3|\mathbf{z}_{t-1}^3) \\
&\quad \prod_{t=1}^{T} \tilde{q}_t^1(\mathbf{z}_t^1)\tilde{q}_t^2(\mathbf{z}_t^2)\tilde{q}_t^3(\mathbf{z}_t^3)
\end{aligned}
$$

  where $\tilde{a}_t^i(\mathbf{z}_t^i|\mathbf{z}_{t-1}^i)$ and $\tilde{q}_t^i(\mathbf{z}_t^i)$ are potentials that provide the variational parameterization

- The resulting algorithm is efficient because we know an efficient subroutine for single chains (the forward-backward algorithm)

Forest of trees approximation

- Eliminating the horizontal links that couple the states yields an approximating graph that is a forest of trees:



- The Q distribution is given by:

$$Q(\{\mathbf{z}_t^1, \mathbf{z}_t^2, \mathbf{z}_t^3\} \mid \{\mathbf{y}_t\}, \{\mathbf{x}_t\}) = \\ \prod_{t=1}^{T} \tilde{r}_t^1(\mathbf{z}_1^1) \tilde{r}_t^2(\mathbf{z}_1^2 | \mathbf{z}_1^1) \tilde{r}_t^3(\mathbf{z}_1^3 | \mathbf{z}_1^1, \mathbf{z}_1^2)$$

- The resulting algorithm is efficient because we know an efficient subroutine for decision trees (the upward recursion from Jordan and Jacobs)

A Viterbi-like approximation

- We can develop a Viterbi-like algorithm by utilizing an approximation Q that assigns probability one to a single path $\{\bar{\mathbf{z}}_t^1, \bar{\mathbf{z}}_t^2, \bar{\mathbf{z}}_t^3\}$:

$$Q(\{\mathbf{z}_t^1, \mathbf{z}_t^2, \mathbf{z}_t^3\} \mid \{\mathbf{y}_t\}, \{\mathbf{x}_t\}) = \begin{cases} 1 \text{ if } \mathbf{z}_t^i = \bar{\mathbf{z}}_t^i, & \forall t, i \\ 0 \text{ otherwise} \end{cases}$$

- Note that the entropy $Q \ln Q$ is zero
- The evaluation of the energy $Q \ln P$ reduces to substituting $\bar{\mathbf{z}}_t^i$ for $\mathbf{z}_t^i$ in P
- The resulting algorithm involves a subroutine in which a standard Viterbi algorithm is run on a single chain, with the other (fixed) chains providing field terms

Mixture-based variational approximation

(Jaakkola & Jordan, 1997)

- Naive mean field approximations are unimodal
- Exact methods running as subroutines provide a way to capture multimodality
- But we would like a method that allows multimodality in the approximation itself

- This can be done by letting the Q distribution be a mixture:

$$Q_{mix}(H|V) = \sum_m \alpha_m Q_{mf}(H|V, m)$$

where each component $Q_{mix}(H|V)$ is a factorized model

Mixture-based approximation (cont.)

- The bound on the likelihood takes the following form:

$$\mathcal{F}(Q_{mix}) = \sum_m \alpha_m \mathcal{F}(Q_{mf}|m) + I(m;H)$$

  where $I(m;H)$ is the mutual information between the mixture components

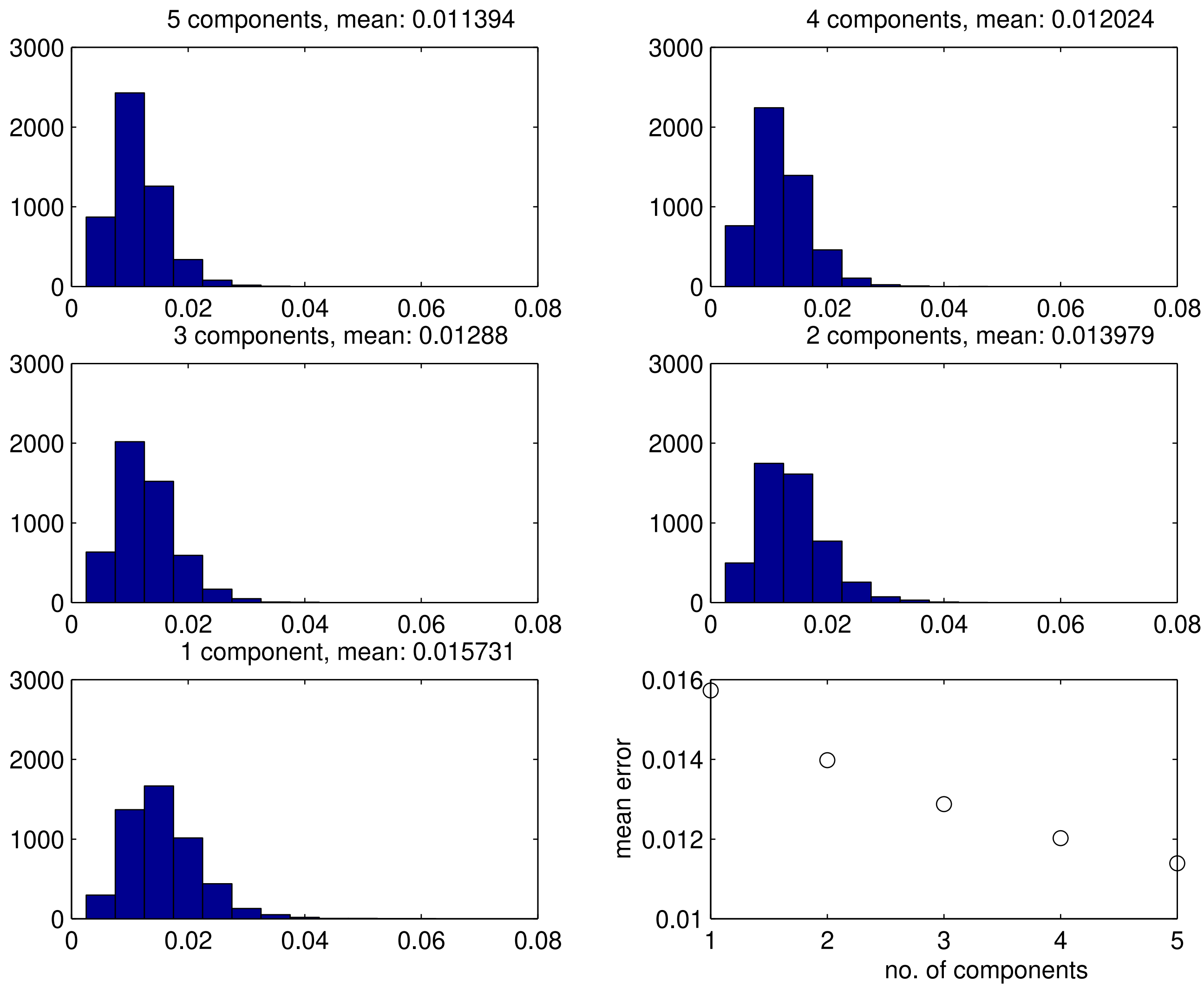
- (Derivation):

$$\begin{aligned}
\mathcal{F}(Q_{mix}) &= \sum_H Q_{mix}(H) \log \frac{P(H,V)}{Q_{mix}(H)} \\
&= \sum_{m,H} \alpha_m \left[Q_{mf}(H|m) \log \frac{P(H,V)}{Q_{mix}(H)} \right] \\
&= \sum_{m,H} \alpha_m \left[Q_{mf}(H|m) \log \frac{P(H,V)}{Q_{mf}(H|m)} + Q_{mf}(H|m) \log \frac{Q_{mf}(}{Q_{mi}} \right. \\
&= \sum_m \alpha_m \mathcal{F}(Q_{mf}|m) + \sum_{m,H} \alpha_m Q_{mf}(H|m) \log \frac{Q_{mf}(H|m)}{Q_{mix}(H)} \\
&= \sum_m \alpha_m \mathcal{F}(Q_{mf}|m) + I(m;H)
\end{aligned}$$

- We see that the bound can be improved vis-a-vis naive mean field via the mutual information term

Mixture-based variational approximation

(Bishop, et al., 1997)



CONCLUSIONS (PART II)

- General frameworks for probabilistic computation in graphical models:
  - exact computation
  - deterministic approximation
  - stochastic approximation
- Variational methods are deterministic approximation methods
  - they aim to take advantage of law-of-large-numbers phenomena in dense networks
  - they yield upper and lower bounds on desired probabilities
- The techniques can be combined to yield hybrid techniques which may well turn out to be better than any single technique

ADDITIONAL TOPICS

- There are many other topics that we have not covered, including:
  - learning structure (see Heckerman tutorial)
  - causality (see UAI homepage)
  - qualitative graphical models (see UAI homepage)
  - relationships to planning (see UAI homepage)
  - influence diagrams (see UAI homepage)
  - relationships to error control coding (see Frey thesis)

- The Uncertainty in Artificial Intelligence (UAI) homepage:

  `http://www.auai.org`

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