



Machine learning: lecture 19

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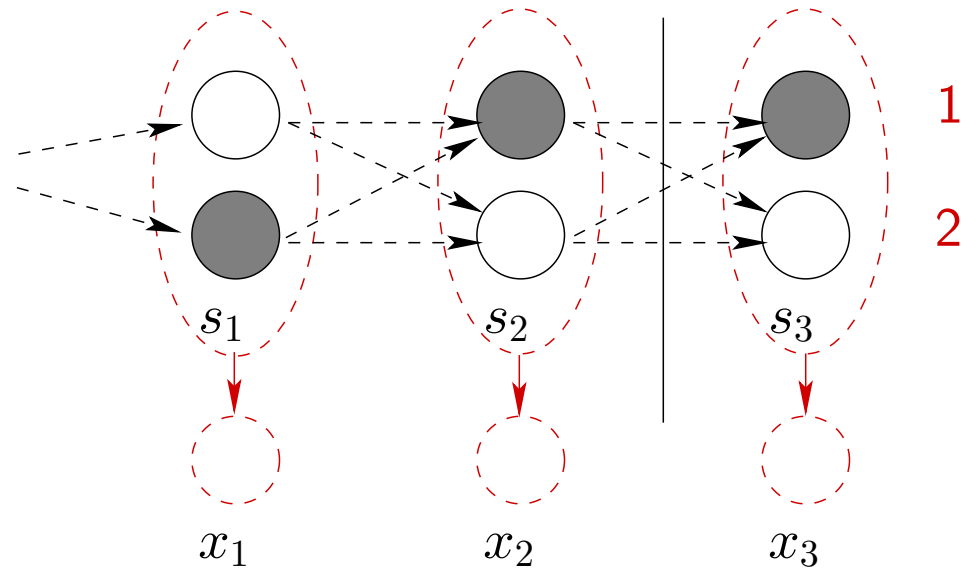
Topics

- Hidden markov models
 - Viterbi algorithm, examples
 - alignment
- Graphical models
 - representation
 - examples

HMM problems

- There are several problems we have to solve
 1. How do we evaluate the probability of an observation sequence $\{\mathbf{x}_1, \dots, \mathbf{x}_n\}$?
 - forward-backward algorithm
 2. How do we adapt the parameters of the HMM to better account for the observations?
 - the EM-algorithm
 3. How do we uncover the most likely hidden state sequence corresponding to the observations?
 - dynamic programming (Viterbi algorithm)

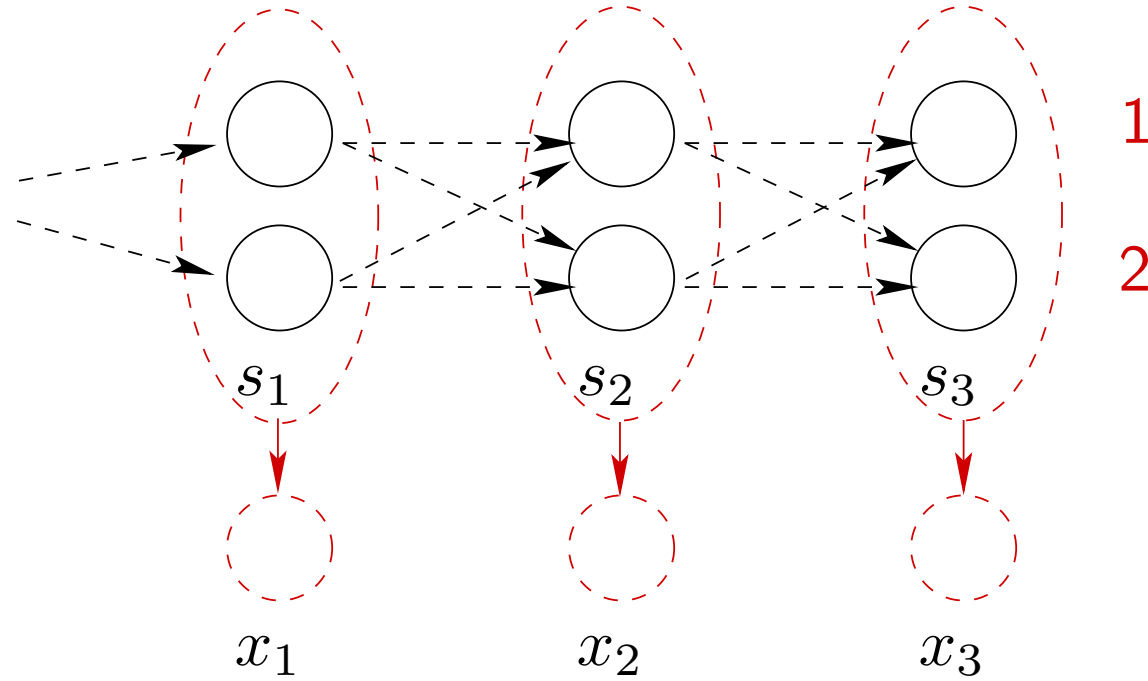
Max-probabilities



- We can recover the most likely hidden state sequence corresponding to a sequence of observations by evaluating the following max-probabilities:

$$\delta_t(i) = \max_{s_1, \dots, s_{t-1}} P(\mathbf{x}_1, \dots, \mathbf{x}_t, s_1, \dots, s_{t-1}, s_t = i)$$

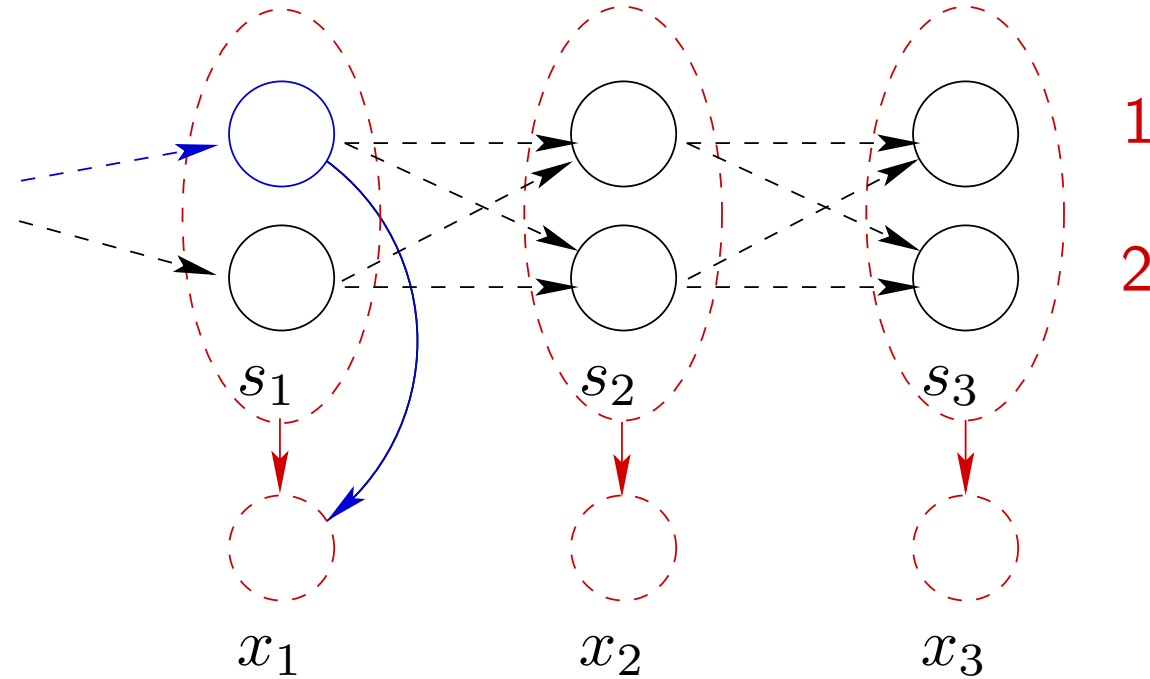
Viterbi algorithm



$$\delta_1(1) = P(x_1, s_1 = 1)$$

$$\delta_1(2) = P(x_1, s_1 = 2)$$

Viterbi algorithm

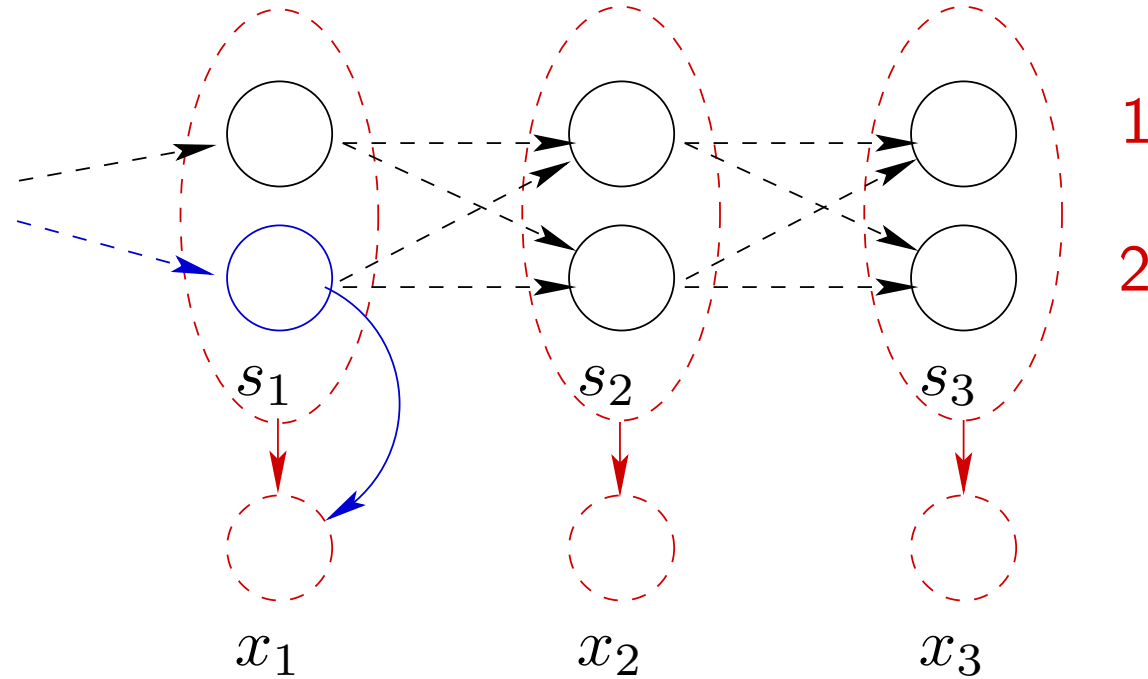


$$\delta_1(1) = P(x_1, s_1 = 1)$$

$$\delta_1(2) = P(x_1, s_1 = 2)$$

$$\delta_1(1) = P(1)P_x(\mathbf{x}_1|1)$$

Viterbi algorithm



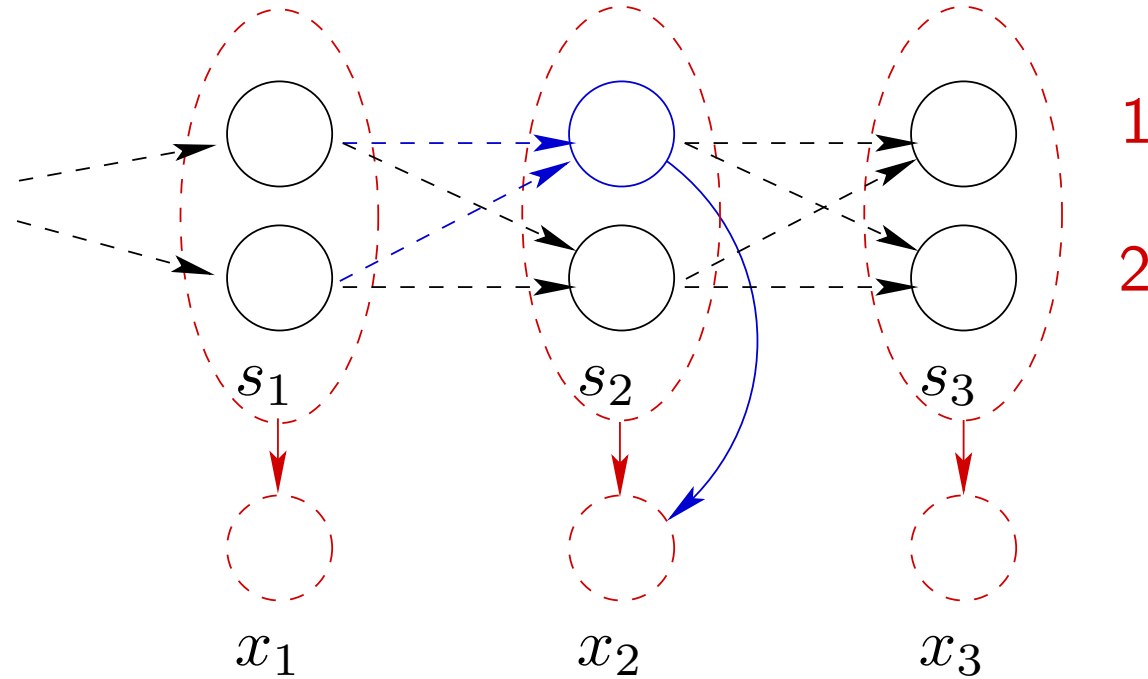
$$\delta_1(1) = P(x_1, s_1 = 1)$$

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$$\delta_1(1) = P(1)P_x(\mathbf{x}_1|1)$$

$$\delta_1(2) = P(2)P_x(\mathbf{x}_1|2)$$

Viterbi algorithm

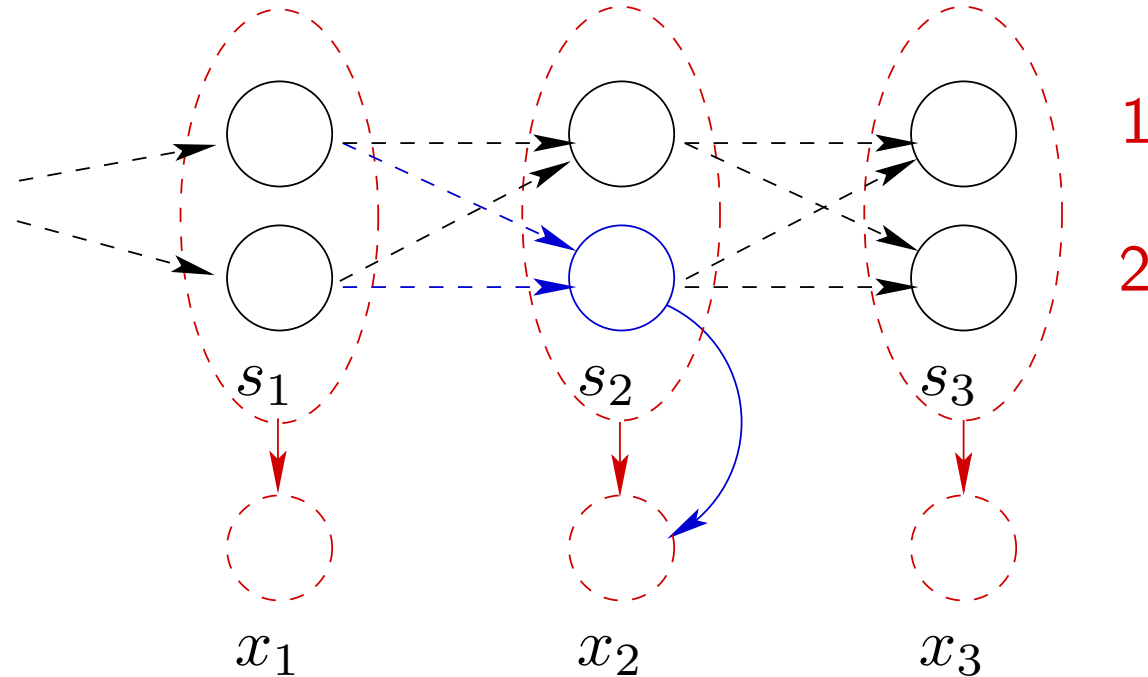


$$\delta_2(1) = \max_{s_1} P(x_1, x_2, s_1, s_2 = 1)$$

$$\delta_2(2) = \max_{s_1} P(x_1, x_2, s_1, s_2 = 2)$$

$$\delta_2(1) = \max \{ \delta_1(1)P_1(1|1), \delta_1(2)P_1(1|2) \} P_x(\mathbf{x}_2|1)$$

Viterbi algorithm



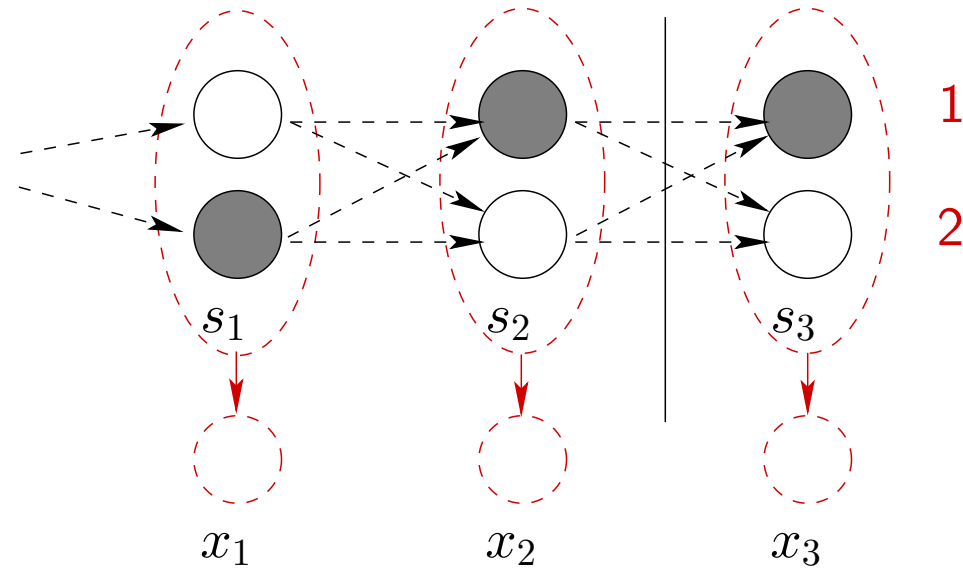
$$\delta_2(1) = \max_{s_1} P(x_1, x_2, s_1, s_2 = 1)$$

$$\delta_2(2) = \max_{s_1} P(x_1, x_2, s_1, s_2 = 2)$$

$$\delta_2(1) = \max \{ \delta_1(1)P_1(1|1), \delta_1(2)P_1(1|2) \} P_x(\mathbf{x}_2|1)$$

$$\delta_2(2) = \max \{ \delta_1(1)P_1(2|1), \delta_1(2)P_1(2|2) \} P_x(\mathbf{x}_2|2)$$

Viterbi algorithm



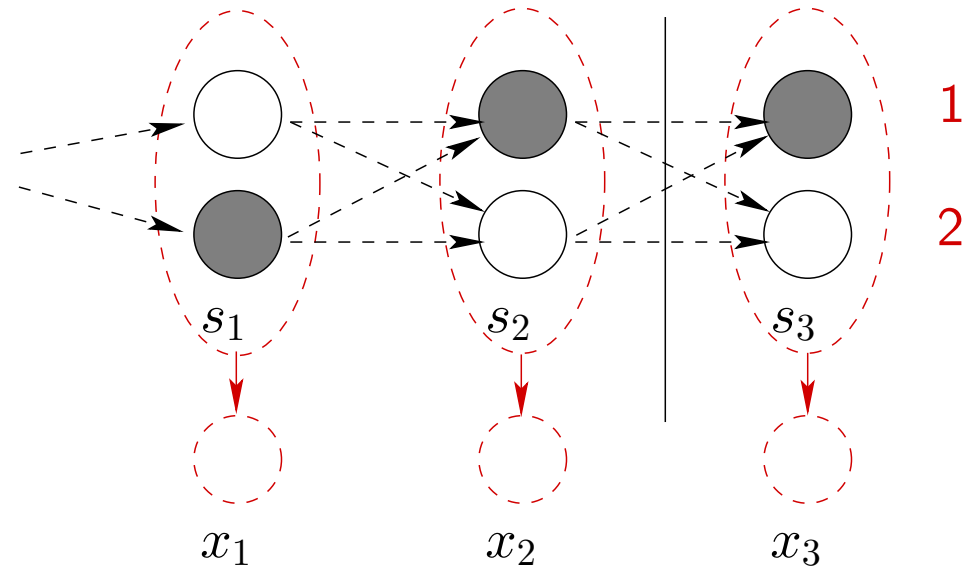
$$\delta_t(i) = \max_{s_1, \dots, s_{t-1}} P(\mathbf{x}_1, \dots, \mathbf{x}_t, s_1, \dots, s_{t-1}, s_t = i)$$

- We get the following recursive equation for calculating the max probabilities:

$$\delta_1(i) = P(i)P_x(\mathbf{x}_1|i)$$

$$\delta_t(i) = \max_j \{ \delta_{t-1}(j)P_1(i|j) \} P_x(\mathbf{x}_t|i)$$

Viterbi algorithm: back-tracking

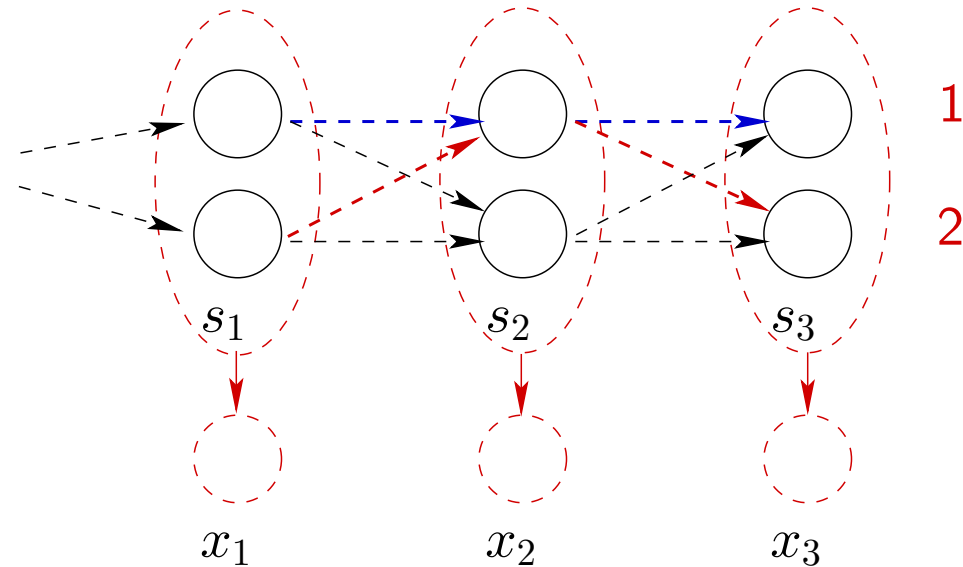


- We can recover the most likely state sequence by working backwards:

$$s_n^* = \operatorname{argmax}_i \delta_n(i)$$

$$s_t^* = \operatorname{argmax}_j \{ \delta_t(j) P_1(s_{t+1}^* | j) \}$$

Viterbi algorithm: properties

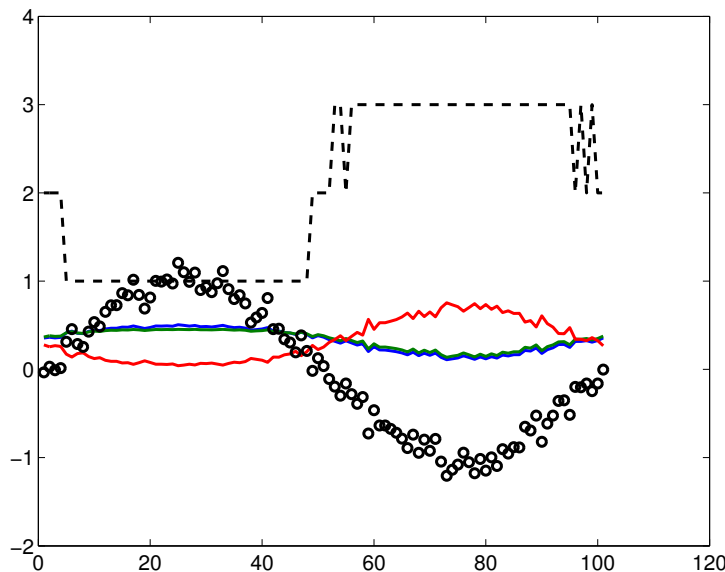


- The most likely path has the property that any partial path is also optimal:

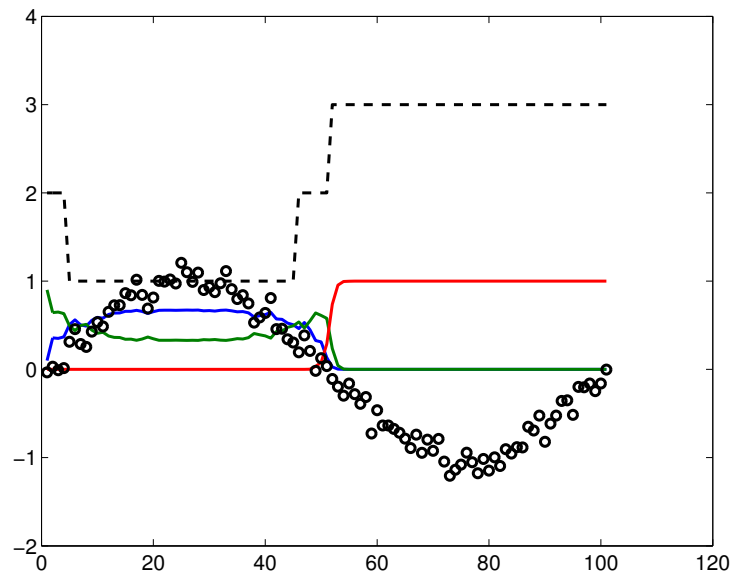
If $s_t^* = i$ then $\{s_1^*, \dots, s_t^*\}$ is also the most likely state sequence forced to end up in $s_t = i$ at time t given only $\mathbf{X}_1, \dots, \mathbf{X}_t$.

Viterbi algorithm: example

- Same example as in the EM case (3 states, Gaussian outputs)



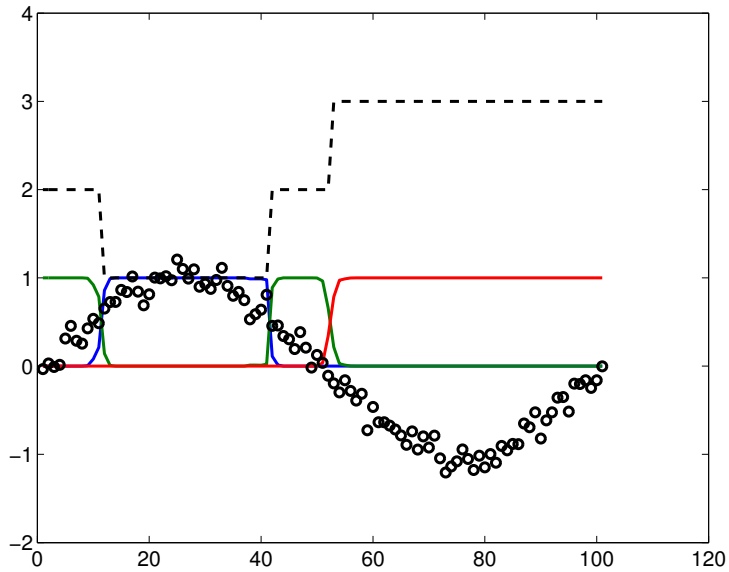
after 0 iterations



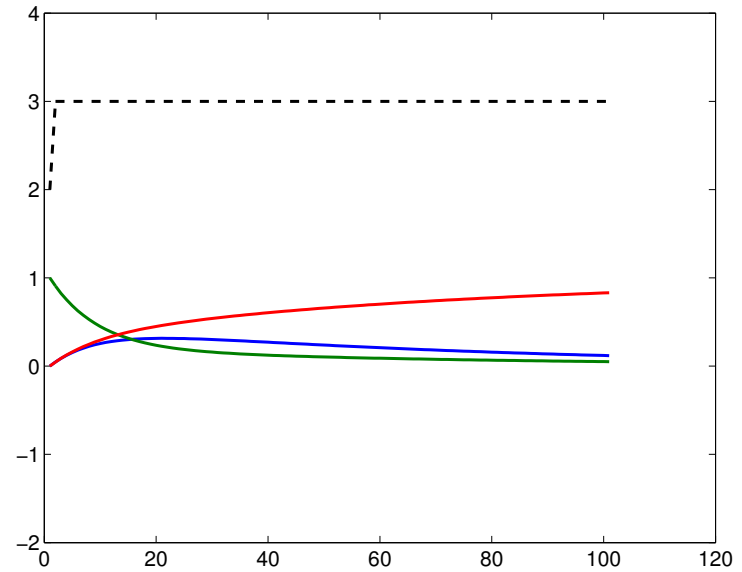
after 7 iterations

- The most likely hidden state sequence $\{s_0^*, \dots, s_n^*\}$ need not agree with the most likely states derived from the posterior marginals $\gamma_t(i)$

Example cont'd



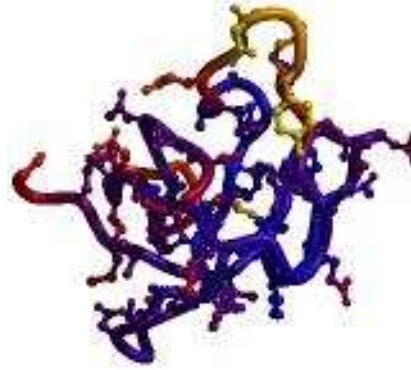
final



ML model, no observations

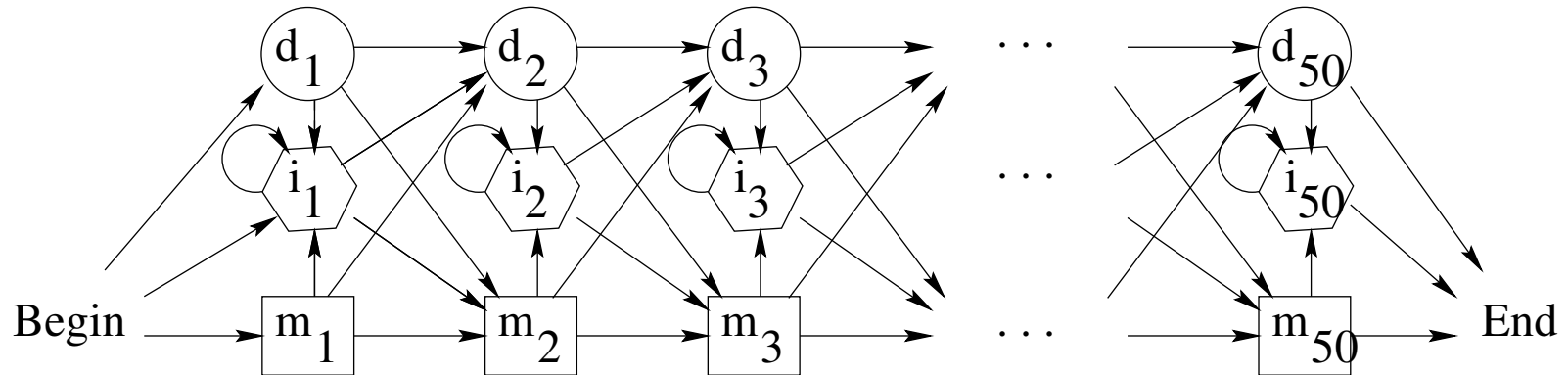
Linear HMMs, alignment

- Proteins



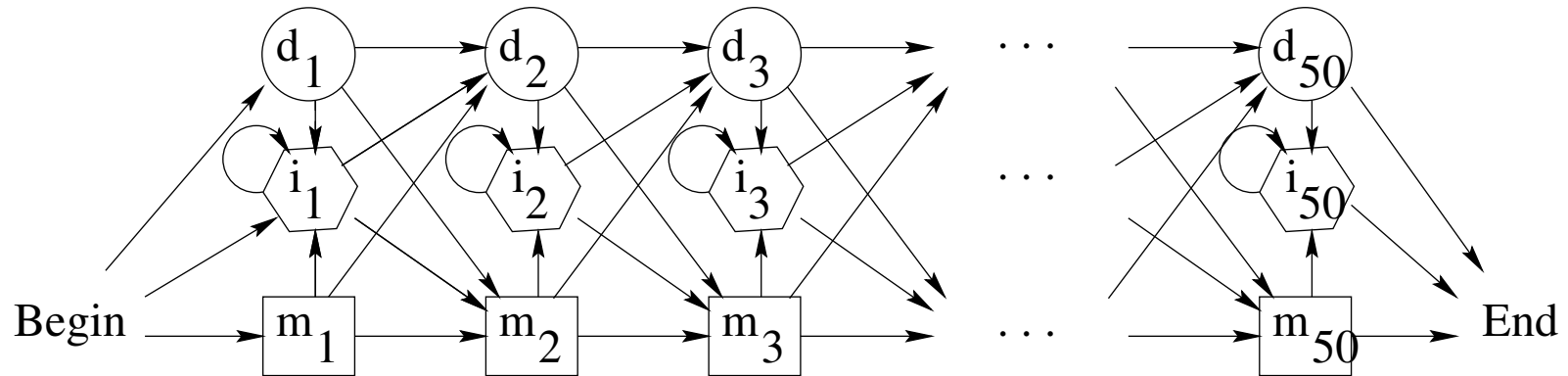
GVAALGAKVLAQIGVAVSHLGDEGKMVAQMKA VGRHKG YGNKH IKAQYFEPLGASLLSAMEHRIG

- A Linear HMM model for protein sequences



GVAALGAKVLAQIGVAVSHLGD~~egk~~MVAQMKA VGRHKG~~gyg~~NK-HIKAQYFEPLGASLLSAMEHRIG

Linear HMMs, multiple alignment



-VKGHGKKVADALTNVAHVDDMPNALSALSDLHA . . .HKLRVDPV.NFKLLSHCLLVTLAAHLP
 KVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHC . . .DKLHVDPE.NFRL LGNVLCVLAHHFG
 DLKKHGVTVLTALGAILKKKGHHEAELKPLAQSHA . . .TK-HKIPikYLEFISEAIIHVLHSRHP
 PFETHANRIVGFFSKIIGELPNIEADVNTFVASHK . . .PR-GVTHD.QLNNFRAGFVSYMKAH--
 DVRWHAERIINAVNDAVASMDDtek . .MSMKLRDL SGKHA . . .KSFQVDPQ.YFKVLA AVIADTVAA---
 ELQAHAGKVFKLVYEAAIQLQVtgvvvTDATLKNLGSVHV . . .SK-GVADA.HFPVVKEAILKTIKEVVG
 GVAALGAKVLAQIGVAVSHLGDegk . .MVAQMKA VGVVRHKgygNK-HIKAQ.YFEPLGASLLSAMEHRIG



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 - representation
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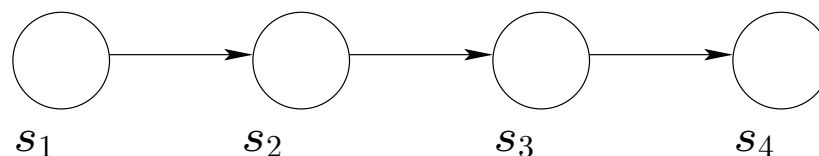


What is a good representation?

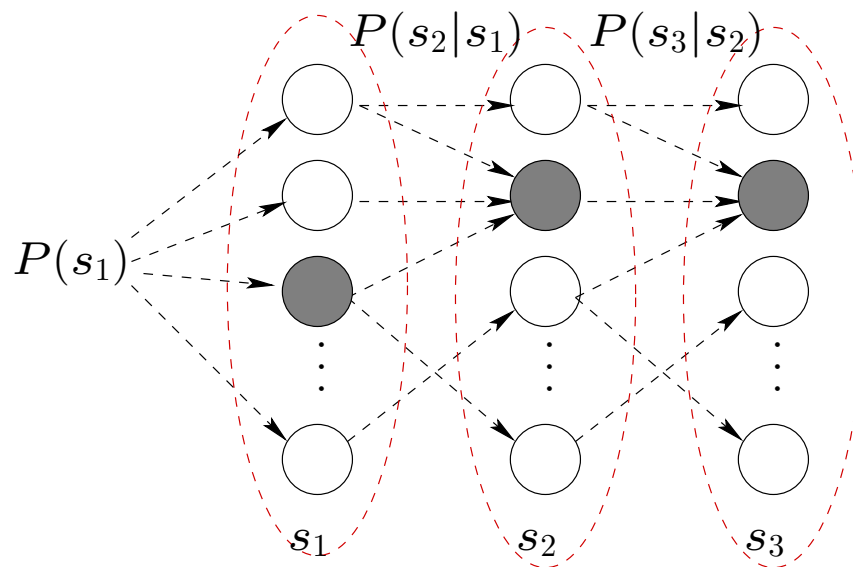
- Properties of good representations
 1. Explicit
 2. Modular
 3. Permits efficient computation
 4. etc.

Representation: explicit

- Representation in terms of variables and dependencies (a graphical model):



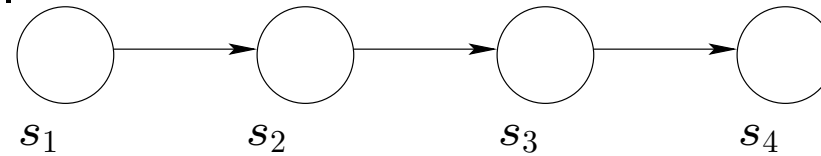
- Representation in terms of state transitions (transition diagram)



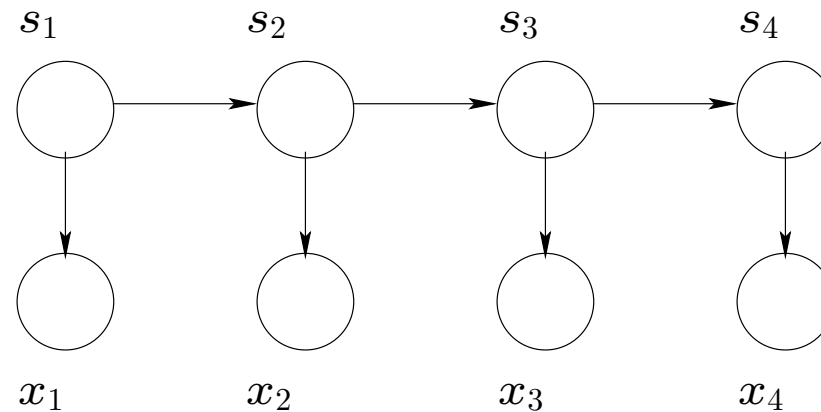
Representation: modular

- We can easily add/remove components of the model

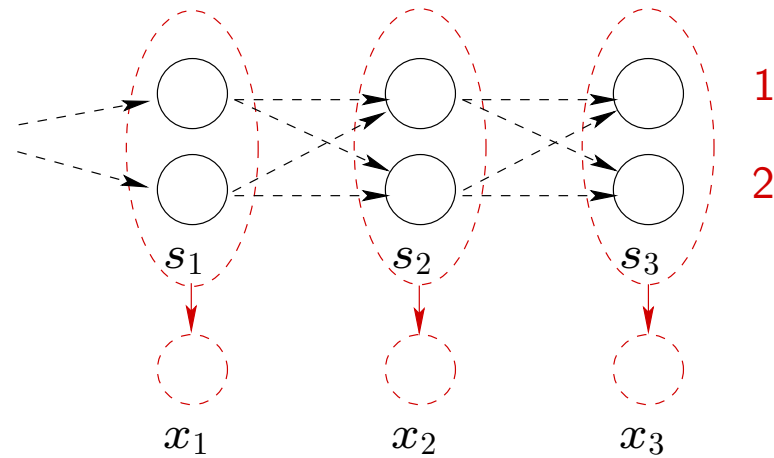
Markov model



Hidden Markov model



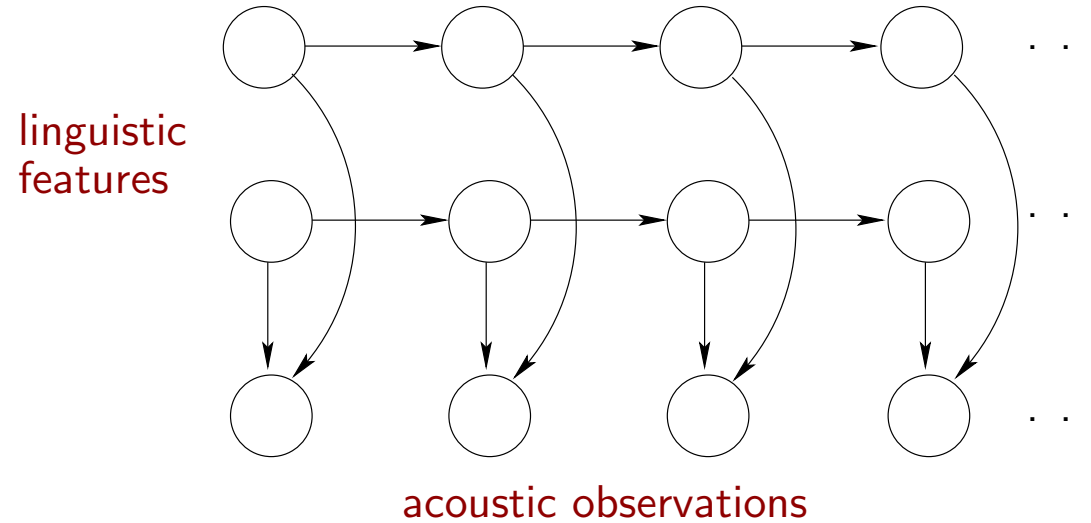
Representation: efficient computation



- Forward-backward probabilities
- EM algorithm
- Max-probabilities (viterbi)

Graphical models: examples

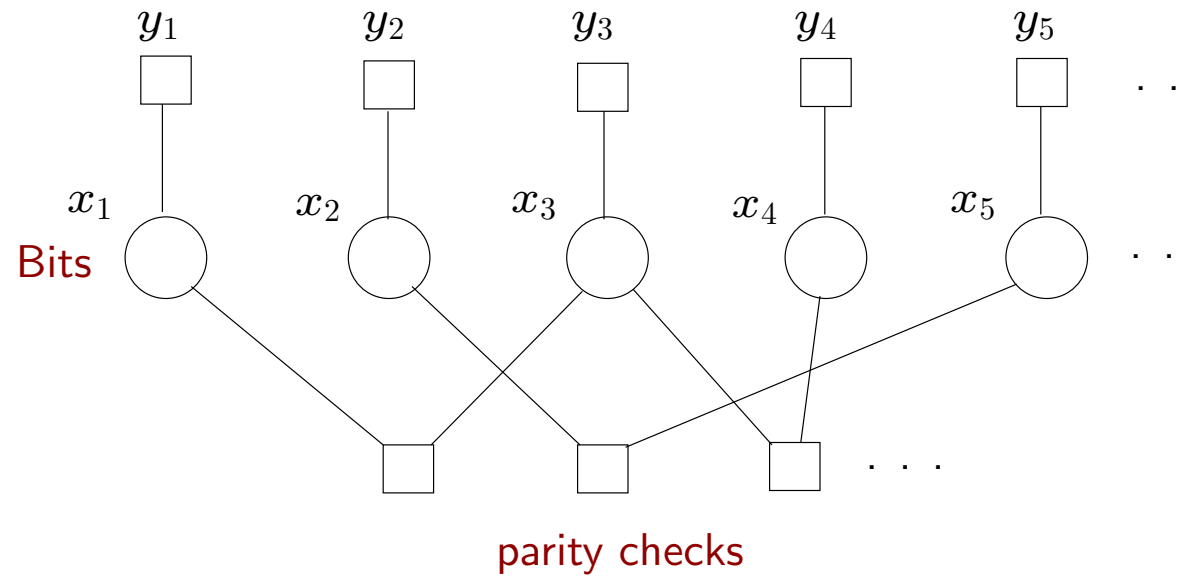
- (Factorial) Hidden Markov models



(a.k.a. directed graphs, Bayesian networks)

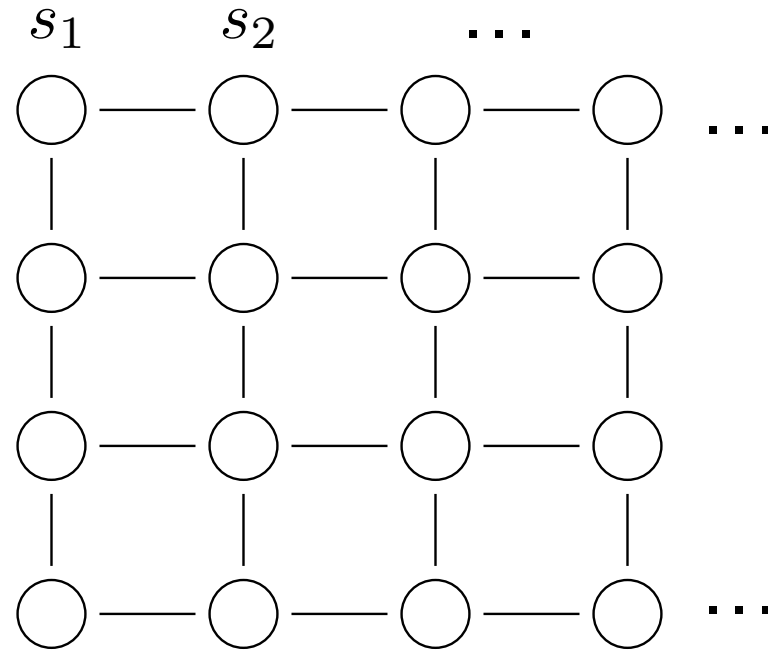
Graphical models: examples

- Factor graphs and codes (information theory)



Graphical models: examples

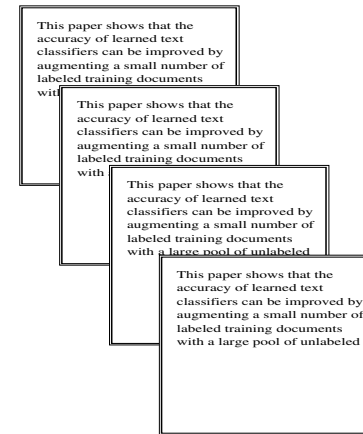
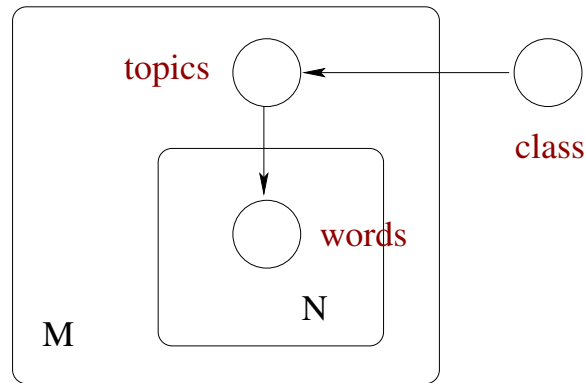
- Lattice models, Ising model (physics)



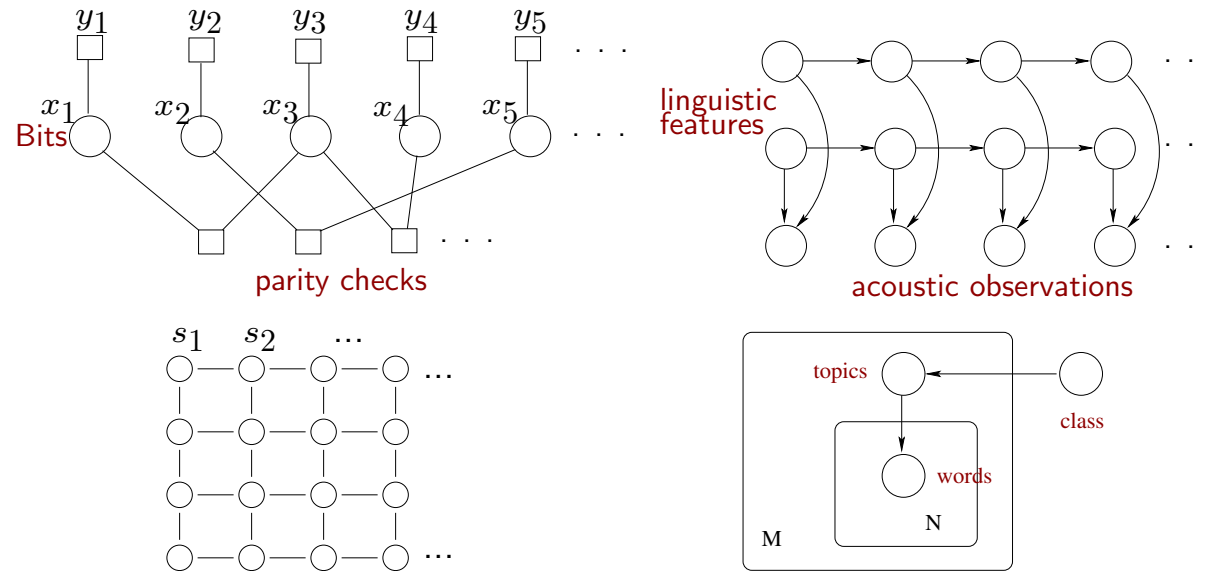
(a.k.a Markov random field)

Graphical models: examples

- Plates and relations (information retrieval, biology, etc.)



Graphical models



- Graph semantics:
 - graph \Rightarrow separation properties \Rightarrow independence
- Association with probability distributions:
 - independence \Rightarrow family of distributions
- Inference and estimation:
 - graph structure \Rightarrow efficient computation