Learning Sequence Motif Models Using Gibbs Sampling

BMI/CS 776
www.biostat.wisc.edu/bmi776/
Spring 2012
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Goals for Lecture

the key concepts to understand are the following
• Markov Chain Monte Carlo (MCMC) and Gibbs sampling
• Gibbs sampling applied to the motif-finding task
• parameter tying
• incorporating prior knowledge using Dirichlets and Dirichlet mixtures
Gibbs Sampling: An Alternative to EM

- EM can get trapped in local minima
- one approach to alleviate this limitation: try different (perhaps random) initial parameters
- Gibbs sampling exploits randomized search to a much greater degree
- can view it as a stochastic analog of EM for this task
- in theory, Gibbs sampling is less susceptible to local minima than EM
- [Lawrence et al., Science 1993]
Gibbs Sampling Approach

• in the EM approach we maintained a distribution $Z_i^{(t)}$ over the possible motif starting points for each sequence at iteration $t$

• in the Gibbs sampling approach, we’ll maintain a specific starting point for each sequence $a_i$, but we’ll keep randomly resampling these
Gibbs Sampling Algorithm for Motif Finding

given: length parameter $W$, training set of sequences
choose random positions for $a$
do
  pick a sequence $X_i$
estimate $p$ given current motif positions $a$
    (using all sequences but $X_i$) (predictive update step)
sample a new motif position $a_i$ for $X_i$ (sampling step)
until convergence
return: $p, a$
Markov Chain Monte Carlo (MCMC)

- Consider a Markov chain in which, on each time step, a grasshopper randomly chooses to stay in its current state, jump one state left or jump one state right.

Let $P^{(t)}(u)$ represent the probability of being in state $u$ at time $t$ in the random walk.

\[
\begin{align*}
P^{(0)}(0) &= 1 & P^{(0)}(+1) &= 0 & P^{(0)}(+2) &= 0 \\
P^{(1)}(0) &= 0.5 & P^{(1)}(+1) &= 0.25 & P^{(1)}(+2) &= 0 \\
P^{(2)}(0) &= 0.375 & P^{(2)}(+1) &= 0.25 & P^{(2)}(+2) &= 0.0625 \\
\vdots & \vdots & \vdots & \vdots & \vdots \\
P^{(100)}(0) &\approx 0.11 & P^{(100)}(+1) &\approx 0.11 & P^{(100)}(+2) &\approx 0.11
\end{align*}
\]
The Stationary Distribution

- let $P(u)$ represent the probability of being in state $u$ at any given time in a random walk on the chain

$$P^{(t)}(u) \approx P^{(t+1)}(u)$$

$$P^{(t+1)}(u) = \sum_v P^{(t)}(v) \tau(u \mid v)$$

- the stationary distribution is the set of such probabilities for all states
Markov Chain Monte Carlo (MCMC)

- we can view the motif finding approach in terms of a Markov chain
- each state represents a configuration of the starting positions ($a_i$ values for a set of random variables $A_1 \ldots A_n$)
- transitions correspond to changing selected starting positions (and hence moving to a new state)

\[
\begin{align*}
\text{state } u & \quad \text{state } v \\
ACATCCG & \quad ACATCCG \\
CGACTAC & \quad CGACTAC \\
ATTGAGC & \quad ATTGAGC \\
CGTTGAC & \quad CGTTGAC \\
GAGTGTAT & \quad GAGTGTAT \\
TCGTTGG & \quad TCGTTGG \\
ACAGGAT & \quad ACAGGAT \\
TAGCTAT & \quad TAGCTAT \\
GCTACCG & \quad GCTACCG \\
GGCCTCA & \quad GGCCTCA \\
\end{align*}
\]
Markov Chain Monte Carlo

• for the motif-finding task, the number of states is enormous
• key idea: construct Markov chain with stationary distribution equal to distribution of interest; use sampling to find most probable states
• detailed balance:

\[ P(u)\tau(v \mid u) = P(v)\tau(u \mid v) \]

- probability of state \( u \)
- probability of transition \( u \rightarrow v \)

• when detailed balance holds:

\[ \frac{1}{N} \lim_{N \to \infty} \text{count}(u) = P(u) \]
Gibbs sampling is a special case of MCMC in which
• Markov chain transitions involve changing one variable at a time

• transition probability is conditional probability of the changed variable given all others

• i.e. we sample the joint distribution of a set of random variables \( P(A_1 \ldots A_n) \) by iteratively sampling from

\[
P(A_i \mid A_1 \ldots A_{i-1}, A_{i+1} \ldots A_n)
\]
Gibbs Sampling Approach

- possible state transitions when first sequence is selected
Gibbs Sampling Approach

• How do we get the transition probabilities when we don’t know what the motif looks like?
Gibbs Sampling Approach

- the probability of a state is given by

\[
P(u) \propto \prod_{c} \prod_{j=1}^{W} \left( \frac{p_{c,j}}{p_{c,0}} \right)^{n_{c,j}(u)}
\]

- count of \( c \) in motif position \( j \)
- background probability for character \( c \)
- probability of \( c \) in motif position \( j \)

<table>
<thead>
<tr>
<th>( u )</th>
<th>( n(u) )</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACATCCG</td>
<td>1 2 3</td>
</tr>
<tr>
<td>CGACTAC</td>
<td></td>
</tr>
<tr>
<td>ATTGAGC</td>
<td></td>
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<td>CGTTGAC</td>
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<td>GAGTGAT</td>
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<tr>
<td>GGCCTCA</td>
<td></td>
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</tbody>
</table>

\( n_{c,j}(u) \) is the count of \( c \) in motif position \( j \) for state \( u \).
Sampling New Motif Positions

- for each possible starting position, $A_i = j$, compute the likelihood ratio (leaving sequence $i$ out of estimates of $p$)

$$LR(j) = \frac{\prod_{k=j}^{j+W-1} p_{c_k, k-j+1}}{\prod_{k=j}^{j+W-1} \prod_{k=j} p_{c_k, 0}}$$

- randomly select a new starting position $A_i = j$ with probability

$$\frac{LR(j)}{\sum_{k \in \{\text{starting positions}\}} LR(k)}$$
The Phase Shift Problem

- Gibbs sampler can get stuck in a local maximum that corresponds to the correct solution shifted by a few bases.

- Solution: add a special step to shift the $a$ values by the same amount for all sequences. Try different shift amounts and pick one in proportion to its probability score.
Convergence of Gibbs
Using Background Knowledge to Bias the Parameters

let’s consider two ways in which background knowledge can be exploited in the motif finding process

1. accounting for palindromes that are common in DNA binding sites
2. using Dirichlet mixture priors to account for biochemical similarity of amino acids
Using Background Knowledge to Bias the Parameters

- Many DNA motifs have a palindromic pattern because they are bound by a protein *homodimer*: a complex consisting of two identical proteins.
Representing Palindromes

• parameters in probabilistic models can be “tied” or “shared”

\[
\begin{bmatrix}
p_{a,0} & p_{a,1} & \cdots & p_{a,W} \\
p_{c,0} & p_{c,1} & \cdots & p_{c,W} \\
p_{g,0} & p_{g,1} & \cdots & p_{g,W} \\
p_{t,0} & p_{t,1} & \cdots & p_{t,W}
\end{bmatrix}
\]

• during motif search, try tying parameters according to palindromic constraint; accept if it increases likelihood test (half as many parameters)
Updating Tied Parameters

\[
\begin{bmatrix}
p_{a,0} & p_{a,1} & \cdots & p_{a,W} \\
p_{c,0} & p_{c,1} & \cdots & p_{c,W} \\
p_{g,0} & p_{g,1} & \cdots & p_{g,W} \\
p_{t,0} & p_{t,1} & \cdots & p_{t,W}
\end{bmatrix}
\]

\[
p_{a,1} \equiv p_{t,W} = \frac{n_{a,1} + n_{t,W} + d_{a,1} + d_{t,W}}{\sum_{b} (n_{b,1} + d_{b,1}) + \sum_{b} (n_{b,W} + d_{b,W})}
\]
• recall that the EM/Gibbs update the parameters by:

\[ p_{c,k} = \frac{n_{c,k} + d_{c,k}}{\sum_b (n_{b,k} + d_{b,k})} \]

• Can we use background knowledge to guide our choice of pseudocounts \( d_{c,k} \)?

• suppose we’re modeling protein sequences…
Amino Acids

- Can we encode prior knowledge about amino acid properties into the motif finding process?
- There are classes of amino acids that share similar properties.
Using Dirichlet Mixture Priors

• since we’re estimating multinomial distributions (frequencies of amino acids at each motif position), a natural way to encode prior knowledge is using Dirichlet distributions

• let’s consider
  • the Beta distribution
  • the Dirichlet distribution
  • mixtures of Dirichlets
The Beta Distribution

- suppose we’re taking a Bayesian approach to estimating the parameter $\theta$ of a weighted coin
- the Beta distribution provides an appropriate prior

$$P(\theta) = \frac{\Gamma(\alpha_h + \alpha_t)}{\Gamma(\alpha_h)\Gamma(\alpha_t)} \theta^{\alpha_h-1} (1-\theta)^{\alpha_t-1}$$

where

$\alpha_h$ # of “imaginary” heads we have seen already

$\alpha_t$ # of “imaginary” tails we have seen already

$\Gamma$ continuous generalization of factorial function

0 Beta(1,1) 1 Beta(2,2) Beta(3,2) Beta(19,39)
The Beta Distribution

• suppose now we’re given a data set $D$ in which we observe $D_h$ heads and $D_t$ tails

$$P(\theta \mid D) = \frac{\Gamma(\alpha + D_h + D_t)}{\Gamma(\alpha_h + D_h)\Gamma(\alpha_t + D_t)} \theta^{\alpha_h + D_h - 1}(1 - \theta)^{\alpha_t + D_t - 1}$$

$$= \text{Beta}(\alpha_h + D_h, \alpha_t + D_t)$$

• the posterior distribution is also Beta: we say that the set of Beta distributions is a conjugate family for binomial sampling
The Dirichlet Distribution

- for discrete variables with more than two possible values, we can use Dirichlet priors

- Dirichlet priors are a conjugate family for multinomial data

\[ P(\theta) = \frac{\Gamma\left(\sum_{i=1}^{K} \alpha_i\right)}{\prod_{i=1}^{K} \Gamma(\alpha_i)} \prod_{i=1}^{K} \theta_i^{\alpha_i-1} \]

- if \( P(\theta) \) is Dirichlet(\( \alpha_1, \ldots, \alpha_K \)), then \( P(\theta|D) \) is Dirichlet(\( \alpha_1+D_1, \ldots, \alpha_K+D_K \)), where \( D_i \) is the # occurrences of the \( i^{th} \) value
Dirichlet Distributions

probability density (shown on a simplex) of Dirichlet distributions for $K=3$ and various parameter vectors $\alpha$

$\alpha = (6, 2, 2)$

$\alpha = (3, 7, 5)$

$\alpha = (2, 3, 4)$

$\alpha = (6, 2, 6)$
Mixture of Dirichlets

• we’d like to have Dirichlet distributions characterizing amino acids that tend to be used in certain “roles”

• Brown et al. [*ISMB ‘95*] induced a set of Dirichlets from “trusted” protein alignments
  – “large, charged and polar”
  – “polar and mostly negatively charged”
  – “hydrophobic, uncharged, nonpolar”
  – etc.
Trusted Protein Alignments

- a trusted protein alignment is one in which known protein structures are used to determine which parts of the given set of sequences should be aligned.
Using Dirichlet Mixture Priors

• recall that the EM/Gibbs update the parameters by:

\[ p_{c, k} = \frac{n_{c, k} + d_{c, k}}{\sum_b (n_{b, k} + d_{b, k})} \]

• we can set the pseudocounts using a mixture of Dirichlets:

\[ d_{c, k} = \sum_j P(\alpha^{(j)} | n_k) \alpha^{(j)}_c \]

• where \( \alpha^{(j)} \) is the \( j \)th Dirichlet component
Using Dirichlet Mixture Priors

\[ d_{c,k} = \sum_j P(\alpha^{(j)} | n_k) \alpha^{(j)}_c \]

- we don’t have to know which Dirichlet to pick
- instead, we’ll hedge our bets, using the observed counts to decide how much to weight each Dirichlet
Motif Finding: EM and Gibbs

- these methods compute local, multiple alignments
- both methods try to optimize the likelihood of the sequences
- EM converges to a local maximum
- Gibbs will “converge” to a global maximum, in the limit; in a reasonable amount of time, probably not
- can take advantage of background knowledge by
  - tying parameters
  - Dirichlet priors

- there are many other methods for motif finding
- in practice, motif finders often fail
  - motif “signal” may be weak
  - large search space, many local minima