

CSE 527

Lecture 7

Relative entropy
Convergence of EM
Weight matrix motif models

Talk Today

COMBI Seminar Today:

Dr. David Baker
"Progress in High-Resolution Modeling
of Protein Structure and Interactions"

Today, October 19, 2005
1:30-2:30
HSB K-069

Relative Entropy

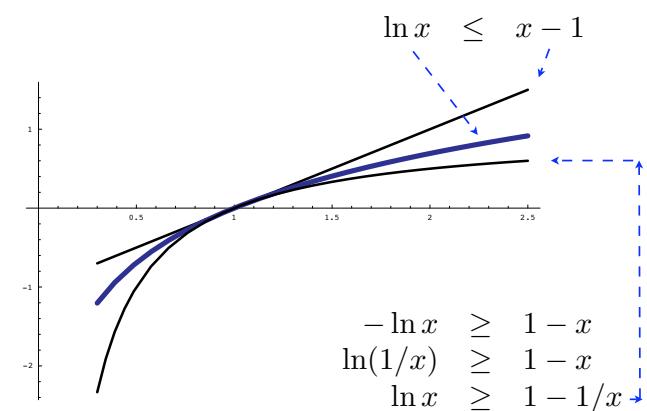
- AKA Kullback-Liebler Distance/Divergence,
AKA Information Content
- Given distributions P, Q

$$H(P||Q) = \sum_{x \in \Omega} P(x) \log \frac{P(x)}{Q(x)}$$

Notes:

Let $P(x) \log \frac{P(x)}{Q(x)} = 0$ if $P(x) = 0$ [since $\lim_{y \rightarrow 0} y \log y = 0$]

Undefined if $0 = Q(x) < P(x)$



Theorem: $H(P||Q) \geq 0$

$$\begin{aligned}
 H(P||Q) &= \sum_x P(x) \log \frac{P(x)}{Q(x)} \\
 &\geq \sum_x P(x) \left(1 - \frac{Q(x)}{P(x)}\right) \\
 &= \sum_x (P(x) - Q(x)) \\
 &= \sum_x P(x) - \sum_x Q(x) \\
 &= 1 - 1 \\
 &= 0
 \end{aligned}$$

Furthermore: $H(P||Q) = 0$ if and only if $P = Q$

EM Convergence

Visible x
hidden y
parameters θ

Goal: Maximum likelihood estimate of θ
i.e. Find θ maximizing $\Pr(x|\theta)$ (or $\log \Pr(x|\theta)$)

$$P(y|x) = P(x,y)/P(x) \text{ so } P(x) = P(x,y)/P(y|x)$$

By:

$$\log \Pr(x|\theta) = \log \Pr(x,y|\theta) - \log \Pr(y|x,\theta)$$

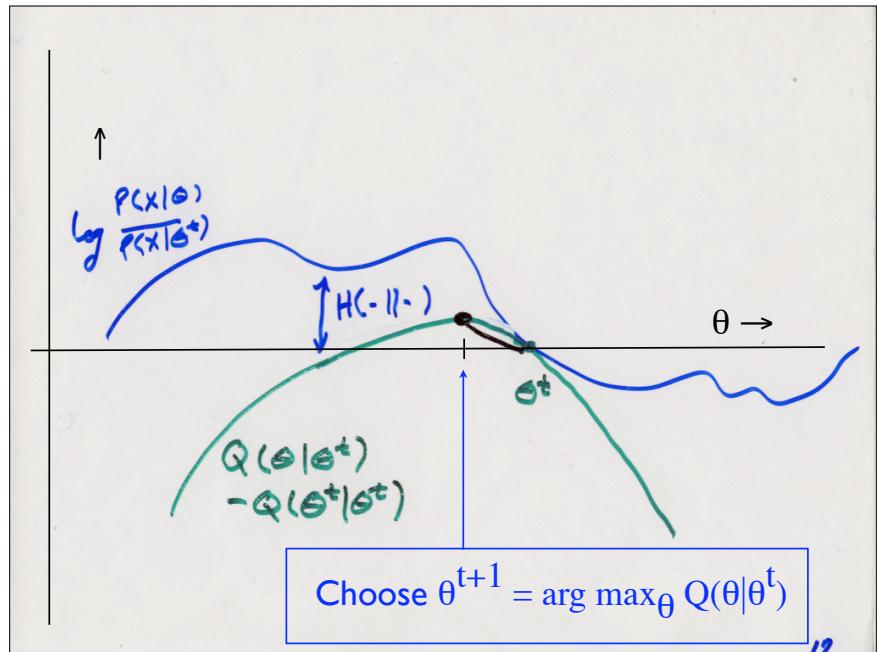
$$\begin{aligned}
 \log \Pr(x|\theta) &= \\
 &\underbrace{\sum_y P(y|x,\theta^t) \cdot \log P(x,y|\theta)}_{Q(\theta|\theta^t)} - \underbrace{\sum_y P(y|x,\theta^t) \cdot \log \Pr(y|x,\theta)}_{H(P(y|x,\theta^t) || \Pr(y|x,\theta))} \\
 &\geq 0
 \end{aligned}$$

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$$\begin{aligned}
 \log \Pr(x|\theta) &= Q(\theta|\theta^t) - \sum_y P(y|x,\theta^t) \cdot \log \Pr(y|x,\theta) \\
 \text{A key trick: } Q &\text{ is easier to optimize than whole thing} \\
 \textcircled{1} \quad \log \Pr(x|\theta) - \log \Pr(x|\theta^t) &= \\
 \textcircled{2} \quad Q(\theta|\theta^t) - Q(\theta^t|\theta^t) &+ \sum_y P(y|x,\theta^t) \cdot \log \frac{P(y|x,\theta^t)}{P(y|x,\theta)} \\
 &\geq 0
 \end{aligned}$$

$\therefore \textcircled{1} \geq 0$ if $\textcircled{2} \geq 0$

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Sequence Motifs

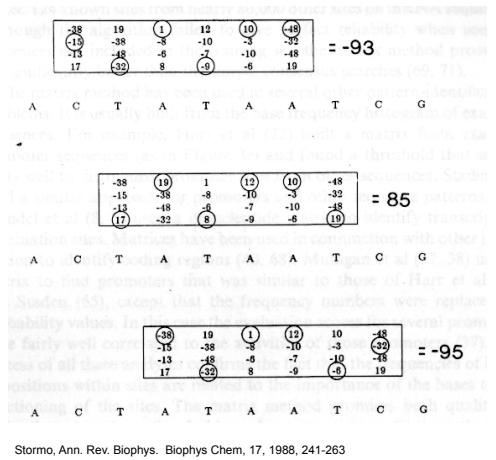
E. coli Promoters

- “TATA Box” - consensus TATAAT ~ 10bp upstream of transcription start
- Not exact: of 168 studied
 - nearly all had 2/3 of TAxyzT
 - 80-90% had all 3
 - 50% agreed in each of x,y,z
 - no perfect match
- Other common features at -35, etc.

TATA Box Frequencies

pos base	1	2	3	4	5	6
A	2	95	26	59	51	1
C	9	2	14	13	20	3
G	10	1	16	15	13	0
T	79	3	44	13	17	96

Scanning for TATA



Weight Matrices: Statistics

- Assume:

$$f_{b,i} = \text{frequency of base } b \text{ in position } i$$

$$f_b = \text{frequency of base } b \text{ in all sequences}$$

- Log likelihood ratio, given $S = B_1 B_2 \dots B_6$:

$$\log \left(\frac{P(S | \text{"promoter"})}{P(S | \text{"nonpromoter"})} \right) = \log \left(\frac{\prod_{i=1}^6 f_{B_i, i}}{\prod_{i=1}^6 f_{B_i}} \right) = \sum_{i=1}^6 \log \left(\frac{f_{B_i, i}}{f_{B_i}} \right)$$

Weight Matrices: Chemistry

- Experiments show ~80% correlation of log likelihood weight matrix scores to measured binding energy of RNA polymerase to variations on TATAAT consensus [Stormo & Fields]