

Computational Genomics

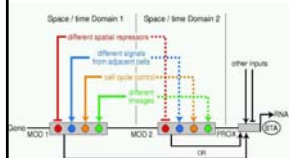
10-810/02-710, Spring 2009

Advanced models and algorithms for motif detection

Eric Xing

Lecture 9, February 11, 2009

Reading: Durbin Chap 9,
class assignment



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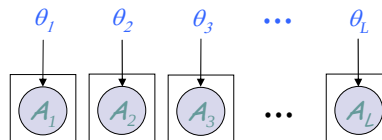
1

The product multinomial model

[Lawrence *et al.* Science 1993]

- Positional specific multinomial distribution:

$$\theta_l = [\theta_{lA}, \dots, \theta_{lC}]^T$$



AAAAGAGTCA
AAATGACTCA
AAGTGAGTCA
AAAAGAGTCA
GGATGCGTCA
AAATGAGTCA
GAATGAGTCA
AAAAGAGTCA

$\equiv A$

$$A \sim P_{PM}(A | \theta)$$

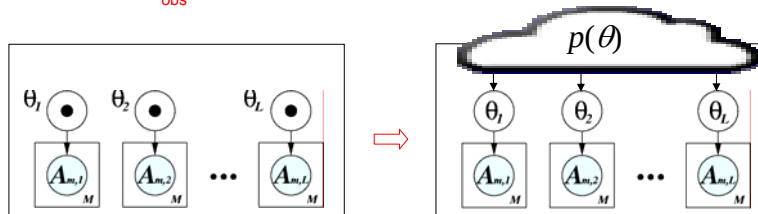
- Position weight matrix (PWM): θ
 - The nucleotide distributions at different positions are independent

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2

Bayesian approach

- For model $P(\mathbf{A}|\theta)$:
 - Treat parameters θ as unobserved random variable(s)
 - probabilistic statements of θ is conditioned on the values of the observed variables $\mathbf{A}_{\text{obs}}$



- Bayes' rule:

$$p(\theta | \mathbf{A}) \propto p(\mathbf{A} | \theta) p(\theta)$$

posterior likelihood prior
- Bayesian estimation:

$$\theta_{\text{Bayes}} = \int \theta p(\theta | \mathbf{A}) d\theta$$

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3

Bayesian missing data problem

- θ : parameter of interest
- $\mathbf{X} = \{x_1, \dots, x_n\}$: a set of complete i.i.d. **observations** from a density that depends upon θ : $p(\mathbf{X} | \theta)$

$$p(\theta | \mathbf{X}) = \prod_{i=1, \dots, n} p(x_i | \theta) p(\theta) / p(\mathbf{X})$$

- In **practical** situations, x_i may **not** be completely observed.
 - Assuming the **unobserved values** are missing completely at random,
 - let $\mathbf{X} = (\mathbf{Y}, \mathbf{Z})$, $x_i = (y_i, z_i)$, $i = 1, \dots, n$
 - y_i : observed part, z_i : missing part

$$p(\theta | \mathbf{Y}) = \int p(\theta | \mathbf{Y}, \mathbf{Z}) p(\mathbf{Z} | \mathbf{Y}) d\mathbf{Z}$$

- This integration is usually hard obtain in close-form → **Imputation**

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4

Example

```

5' - TCTCTCTCCACGGCTAATTAGGTGATCATGAAAAATGAAAAATTCATGAGAAAAGAGTCAGACATCGAAACATACAT ...HIS7
5' - ATGGCAGAATCACTTTAAACGTGGCCCCACCCGCTGCACCCGTGTCATTTTGTACGTTACTGCGAAATGACTCAACG ...AR04
5' - CACATCCAACGAATCACCTCACCGTTATCGTGACTCACTTTCTTCGCATCGCCGAAGTGCCATAAAAAATATTTTT ...ILV6
5' - TGCGAACAAAAGAGTCATTACAACGAGGAAATAGAAGAAAAATGAAAAATTTTCGACAAAATGTATAGTCATTTCTATC ...THR4
5' - ACAAGGTACCTTCCTGGCCAATCTCACAGATTTAATATAGTAAATTGTCATGCATATGACTCATCCGAAACATGAAA ...AR01
5' - ATTGATTGACTCATTTTCCTCTGACTACTACGAGTTCAAAATGTTAGAGAAAAATAGAAAAGCAGAAAAATAAATAA ...HOM2
5' - GGCGCCACAGTCCGCGTTTGTTATCCGGCTGACTCATTCTGACTCTTTTTTGGAAGTGTGGCATGTGCTTCACACA ...PRO3
  
```

Data Imputation

- Multiple values, $z^{(1)}, \dots, z^{(m)}$ are drawn from $p(Z | Y)$ to form m complete data sets.
- With these **imputed** data sets and the ergodicity theorem,

$$p(\theta | Y) \approx 1/m \cdot \{p(\theta | Y, z^{(1)}) + \dots + p(\theta | Y, z^{(m)})\}$$

- But in most applied problems it is **impossible to draw Z from $(Z | Y)$ directly.**

Data Augmentation



- Tanner and Wong's data augmentation (DA)
 - apply Gibbs Sampler to draw multiples of θ 's and multiples of Z 's jointly from $p(\theta, Z | Y)$
- DA algorithm
 - Notice that: $p(Z | Y) = \int p(\theta, Z | Y) d\theta = \int p(Z | \theta, Y) p(\theta | Y) d\theta$
 $\approx 1/m \cdot \{p(Z | \theta^{(1)}, Y) + \dots + p(Z | \theta^{(m)}, Y)\}$
 - I-step $z^{(m)} \sim p(Z | \theta^{(m)}, Y)$
 - Recall that: $p(\theta | Y) \approx 1/m \cdot \{p(\theta | Y, z^{(1)}) + \dots + p(\theta | Y, z^{(m)})\}$
 - P-step $\theta^{(m)} \sim p(\theta | Y, z^{(m)})$
- By iterating between drawing θ from $p(\theta | Y, Z)$ and drawing Z from $p(Z | \theta, Y)$, DA constructs a Markov chain whose equilibrium distribution is $p(\theta, Z | Y)$

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7

Collapsed Gibbs Sampler (J. Liu)



- Consider Sampling from $p(\theta | D)$, $\theta = (\theta_1, \theta_2, \theta_3)$
 - Original Gibbs Sampler
 - (i) $\theta_1 \sim p(\theta_1 | \theta_2, \theta_3, D)$
 - (ii) $\theta_2 \sim p(\theta_2 | \theta_1, \theta_3, D)$
 - (iii) $\theta_3 \sim p(\theta_3 | \theta_1, \theta_2, D)$
 - Collapsed Gibbs Sampler (J. Liu):
 - (i) $(\theta_1, \theta_2) \sim p(\theta_1, \theta_2 | D)$
 - (ii) $\theta_3 \sim p(\theta_3 | \theta_1, \theta_2, D)$

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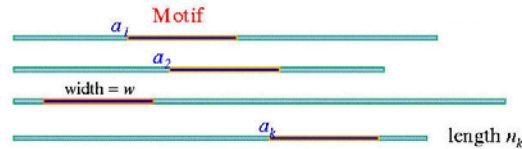
8

Back to *de novo* Motif Detection

— Bayesian missing data problem



- The oops model (one occurrence per sequence)



- Parameter of Interest

$$\theta_{4 \times W} = \begin{pmatrix} \theta_{1A} & \theta_{2A} & \cdots & \theta_{WA} \\ \theta_{1T} & \theta_{2T} & \cdots & \theta_{WT} \\ \theta_{1G} & \theta_{2G} & \cdots & \theta_{WG} \\ \theta_{1C} & \theta_{2C} & \cdots & \theta_{WC} \end{pmatrix} \quad \theta_{0, 4 \times 1} = \begin{pmatrix} \theta_{0A} \\ \theta_{0T} \\ \theta_{0G} \\ \theta_{0C} \end{pmatrix}$$

- Missing Data $A = \{a_1, a_2, \dots, a_k\}$
- Observed Data $Y = \text{Given Sequences}$

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9

The Gibbs Motif Sampler



- Standard Gibbs Sampler (Iterative sampling):** $p(\theta|A, Y); p(A|\theta, Y)$
 - ❖ Draw from $[\theta | A, \text{Data}]$, then draw from $[A | \theta, \text{Data}]$
- Collapsed Gibbs Sampler (Predictive Updating):** $A \sim p(A | Y)$
 - ❖ pretend that $K-1$ motif instances have been found. We stochastically predict for the K -th instance!!
- Step0. choose an arbitrary starting point

$$\mathbf{A}^{(0)} = (a_1^{(0)}, a_2^{(0)}, \dots, a_K^{(0)});$$
- Step1. Generate $\mathbf{A}^{(t+1)} = (a_1^{(t+1)}, a_2^{(t+1)}, \dots, a_K^{(t+1)})$ as follows:
 - Generate $a_1^{(t+1)} \sim p(a_1 | a_2^{(t)}, \dots, a_K^{(t)}, Y)$;
 - Generate $a_2^{(t+1)} \sim p(a_2 | a_1^{(t+1)}, a_3^{(t)}, \dots, a_K^{(t)}, Y)$;
 - ...
 - Generate $a_K^{(t+1)} \sim p(a_K | a_1^{(t+1)}, a_2^{(t+1)}, \dots, a_{K-1}^{(t+1)}, Y)$;
 - Generate $\theta^{(t+1)} \sim p(\theta | a_1^{(t+1)}, a_2^{(t+1)}, \dots, a_K^{(t+1)}, Y)$;
- Step2. Set $t=t+1$, and go to step 1

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10

The Predictive Update Version

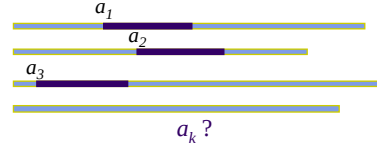


- Initialized by choosing random starting positions

$$a_1^{(0)}, a_2^{(0)}, \dots, a_K^{(0)}$$

- Iterate the following steps many times:

- Randomly or systematically choose a sequence, say, **sequence k**, to exclude.



- Carry out the **predictive-updating** step to update a_k
(no need to sample $\theta^{(t)}$ at each t, we can compute it in close-form, see next slide)

- Notations:

$$\mathcal{A}_{[-k]} \equiv \{a_1, \dots, a_{k-1}, a_{k+1}, \dots, a_K\} \Rightarrow c_{l,j,[-k]}, l=1 \dots W, j=A, T, G, C$$

$$a_k \Rightarrow c_{l,j}(a_k)$$

- Stop when not much change observed, or some criterion met.

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11

Predictive Distribution



- The predictive distribution for a_k :

$$p(a_k = i | \mathcal{A}_{[-k]}, \mathcal{Y}) \approx \text{Const} \cdot \prod_{l=1}^W \prod_j \left(\frac{\hat{\theta}_{l,j,[-k]}}{\hat{\theta}_{0,j,[-k]}} \right)^{c_{l,j}(i)} \quad (*)$$

- Predictive update:

$$\hat{\theta}_{l,j,[-k]} = \frac{c_{l,j,[-k]} + \beta_{l,j}}{K-1 + \sum_j \beta_{l,j}}, \quad \hat{\theta}_{0,j,[-k]} \text{ similarly}$$

assuming: $\theta_0 \sim \text{Dirichlet}(\alpha)$, $\theta \sim \text{Product Dirichlet}(B)$, $B = (\beta_{l,j})$, $a \sim \text{Uniform}$

- Sampling: every segment of width W in Y_k has probability (*). Choose one at random according to these probabilities, and this becomes the new a_k .

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12

Derivation



$$p(a_k | a_1, \dots, a_{k-1}, a_{k+1}, \dots, a_K, Y) = \frac{p(Y | a_k, A_{-k}) p(A)}{\sum_i p(Y | a_k = i, A_{-k}) p(A)} = \frac{p(Y | a_k, A_{-k})}{\sum_i p(Y | a_k = i, A_{-k})} \quad (1)$$

$$p(Y | A) = \int p(Y | \theta, \theta_0, A) p(\theta) p(\theta_0) d\theta d\theta_0 \quad (2)$$

$$\begin{aligned} p(Y | \theta, \theta_0, A) p(\theta | \beta) p(\theta_0 | \beta) &= \left(\prod_j \theta_{0,j}^{c_{0,j}(A)} \times \prod_{l,j} \theta_{l,j}^{c_{l,j}(A)} \right) \times \left(\frac{\Gamma(\beta_0)}{\prod_j \Gamma(\beta_{0,j})} \prod_j \theta_{0,j}^{\beta_{0,j}-1} \times \prod_l \frac{\Gamma(\beta_l)}{\prod_j \Gamma(\beta_{l,j})} \prod_j \theta_{l,j}^{\beta_{l,j}-1} \right) \\ &= \frac{\Gamma(\beta)}{\prod_j \Gamma(\beta_j)} \prod_j \theta_{0,j}^{c_{0,j}(A)+\beta_{0,j}-1} \times \prod_l \frac{\Gamma(\beta_l)}{\prod_j \Gamma(\beta_{l,j})} \prod_j \theta_{l,j}^{c_{l,j}(A)+\beta_{l,j}-1} \end{aligned} \quad (3)$$

$$\begin{aligned} p(Y | A) &= \int p(Y | \theta, \theta_0, A) p(\theta) p(\theta_0) d\theta d\theta_0 \\ &= \left(\frac{\Gamma(\sum_j \beta_{0,j})}{\prod_j \Gamma(\beta_{0,j})} \times \frac{\Gamma(\sum_j \beta_j + c_{0,j}(A))}{\Gamma(\sum_j \beta_{0,j} + c_{0,j}(A))} \right) \times \left(\prod_l \frac{\Gamma(\sum_j \beta_{l,j})}{\prod_j \Gamma(\beta_{l,j})} \times \frac{\Gamma(\sum_j \beta_{l,j} + c_{l,j}(A))}{\Gamma(\sum_j \beta_{l,j} + c_{l,j}(A))} \right) \\ &= \left(\frac{\Gamma(\sum_j \beta_{0,j})}{\prod_j \Gamma(\beta_{0,j})} \times \frac{\Gamma(\sum_j \beta_j + c_{0,j}(A_{-k}) + c_{0,j}(a_k))}{\Gamma(\sum_j \beta_{0,j} + c_{0,j}(A_{-k}) + c_{0,j}(a_k))} \right) \times \left(\prod_l \frac{\Gamma(\sum_j \beta_{l,j})}{\prod_j \Gamma(\beta_{l,j})} \times \frac{\Gamma(\sum_j \beta_{l,j} + c_{l,j}(A_{-k}) + \delta(c_{l,j}(a_k)))}{\Gamma(\sum_j \beta_{l,j} + c_{l,j}(A_{-k}))} \right) \end{aligned} \quad (4)$$

...

$$p(a_k | a_1, \dots, a_{k-1}, a_{k+1}, \dots, a_K, Y) = \frac{p(Y | a_k, A_{-k})}{\sum_i p(Y | a_k = i, A_{-k})} \approx \prod_l \left(\frac{\beta_{l,j} + c_{l,j}(A_{-k})}{\sum_j \beta_{l,j} + c_{l,j}(A_{-k})} \right)^{c_{l,j}(a_k)} = \prod_l \left(\frac{\hat{\theta}_{l,j}}{\hat{\theta}_{0,j}} \right)^{c_{l,j}(a_k)} \quad (5)$$

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13

Phase-shift and fragmentation



- Sometimes get stuck in a local shift optimum



- How to "escape" from this local optimum?
 - Simultaneous move: $A \rightarrow A + \delta$, $A + \delta = \{a_1 + \delta, \dots, a_K + \delta\}$
 - Use a Metropolis step: accept the move with prob= p ,

$$r = \min \left\{ 1, \frac{p(A + \delta | Y)}{p(A | Y)} \right\}$$

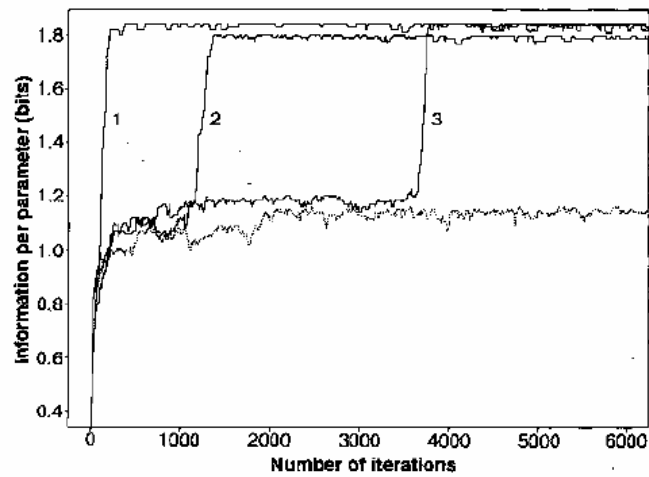


Compare entropies between new columns and left-out ones.

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14

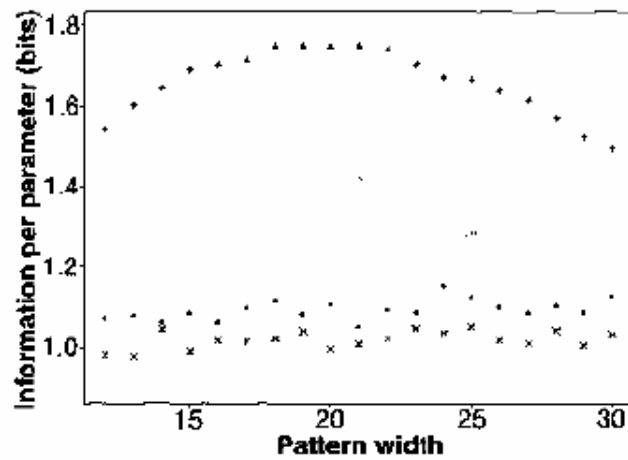
Convergence



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15

Model Selection



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16

Natural Extensions to Basic Model I



- Multiple Pattern Occurances in the same sequences:

Liu, J., "The collapsed Gibbs sampler with applications to a gene regulation problem," *Journal of the American Statistical Association* 89 958-966.

- Prior:** any position i has a small probability ε to start a binding site:

$$A=(a_1, \dots, a_k) \quad P(A) \approx \varepsilon^k (1-\varepsilon)^{N-k} \quad (\text{with nonoverlapping constraints})$$



- Recall**

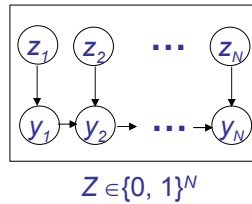
$$p(a_k | a_1, \dots, a_{k-1}, a_{k+1}, \dots, a_L, Y) = \frac{p(Y | a_k, A_{-k}) p(A)}{\sum_i p(Y | a_k = i, A_{-k}) p(A)}$$

- augmented proposal distribution for the Gibbs motif sampler

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17

Back to the binary indicator model



Although sampling $\mathbf{z}$ directly is prohibitive, a very simple form of the conditional distribution of any z_n given all the rest $\mathbf{z}_{[-n]}$ is available

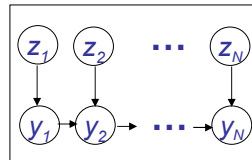
$$\frac{p(z_n = 1 | \mathbf{z}_{[-n]}, \mathbf{y})}{p(z_n = 0 | \mathbf{z}_{[-n]}, \mathbf{y})} = \frac{\hat{\varepsilon}}{1 - \hat{\varepsilon}} \prod_{l=1}^L \prod_{j=1}^4 \left(\frac{\hat{\theta}_{l,j}}{\hat{\theta}_{0,j}} \right)^{\delta(y_{n+l-1}, j)}$$

where $\hat{\varepsilon}$ and $\hat{\theta}$ are estimated from $\mathbf{y}$ and $\mathbf{z}_{[-n]}$.

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18

Any problem with the model?



$$Z \in \{0, 1\}^N$$

- How about multiple types of motifs?
This model can be easily extended to solving K different types motif simultaneously by letting $Z \in \{0, \dots, K\}^{NT}$
- Can motif overlap?
A Markov chain for Z .
- Are motif sites independent?
See next ...

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19

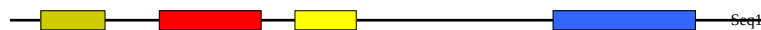
Natural Extensions to Basic Model II

- **Composite Patterns:**

BioOptimizer: the Bayesian Scoring Function Approach to Motif Discovery *Bioinformatics*



- Multiply the motif p -values



$$\begin{aligned} \text{Combined } p\text{-value} &= 0.00001 * 0.0035 * 0.007 * 0.00000005 \\ &= 1.225 * 10^{-17} \end{aligned}$$

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20

The product of p -values



- Theorem: The probability $F_n(p)$ that the product of n independent, uniform $[0, 1]$ random variables

$$Z_n = \prod_{i=1}^n p_i$$

- has an observed value less than or equal to p , is given by

$$F_n(p) = p \sum_{i=0}^{n-1} \frac{(-\ln p)^i}{i!}$$

- for $0 < p \leq 1$, and is zero when p is zero.

Timothy L. Bailey and Michael Gribskov, "Combining evidence using p-values: application to sequence homology searches," *Bioinformatics*, 14:48-54, 1998.

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21

Natural Extensions to Basic Model III



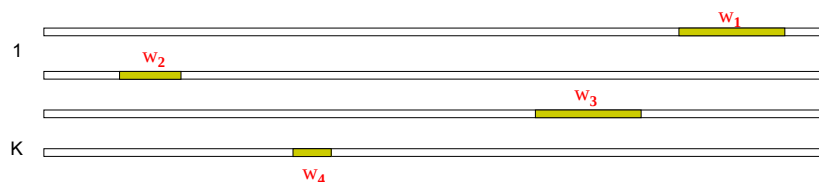
- Correlated in Nucleotide Occurrence in Motif:**

Modeling within-motif dependence for transcription factor binding site predictions. *Bioinformatics*, 6, 909-916.



- Insertion-Deletion**

BALSA: Bayesian algorithm for local sequence alignment *Nucl. Acids Res.*, 30 1268-77.

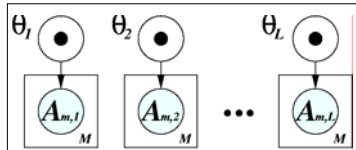


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22

Recall the PM Model

- The PM parameter, $\theta_l = [\theta_{lA}, \dots, \theta_{lC}]^T$, corresponds exactly to the PWM of a motif



The nucleotide distributions at different sites are independent !

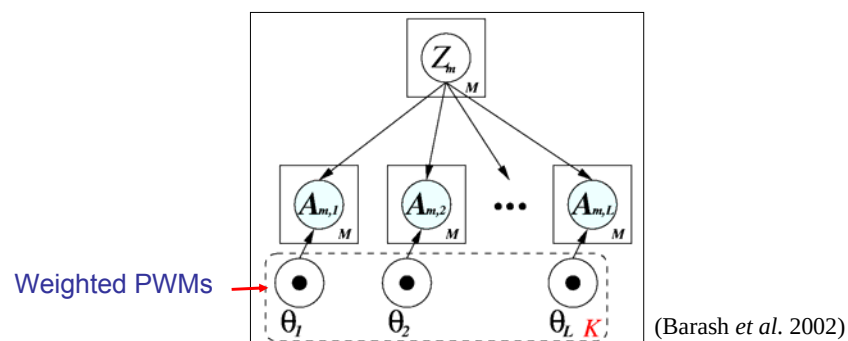
- The **score** (likelihood-ratio) of a candidate substring: **AAAAGAGTCA**

$$R = \frac{p(x = \{\text{AAAAGAGTCA}\} | \text{PWM})}{p(x = \{\text{AAAAGAGTCA}\} | \text{bk})} = \prod_{l=1}^{10} \frac{p(y_l | \text{PWM})}{p(y_l | \text{bk})} = \prod_{l=1}^{10} \frac{\theta_{l,y_l}}{\theta_{0,y_l}}$$

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23

Mixture of PM models



The nt-distributions at different sites are conditionally independent but marginally dependent !

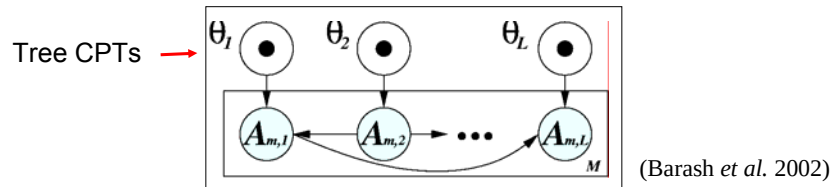
The **likelihood** of a candidate substring: **AAAAGAGTCA**

$$P(x = \{\text{AAAAGAGTCA}\}) = \pi_1 p(\cdot | \text{PWM}_1) + \pi_2 p(\cdot | \text{PWM}_2)$$

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24

Tree models



The nt-distributions at different sites are pairwise dependent !

The **likelihood** of a candidate substring: **AAAAGAGTCA**

$$P(x = \{\text{AAAAGAGTCA}\}) = \prod_i p(x_i | \text{pi}(x_i)) = p(x_1 | x_2) p(x_1 | x_2) \cdots p(x_m | x_1)$$

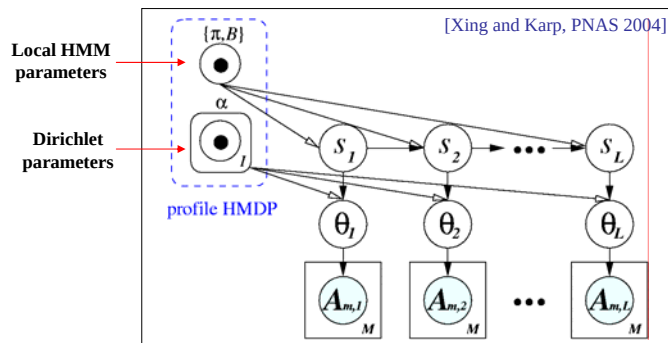
Mixture of trees

...

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25

MotifPrototyper: A Bayesian Markovian model



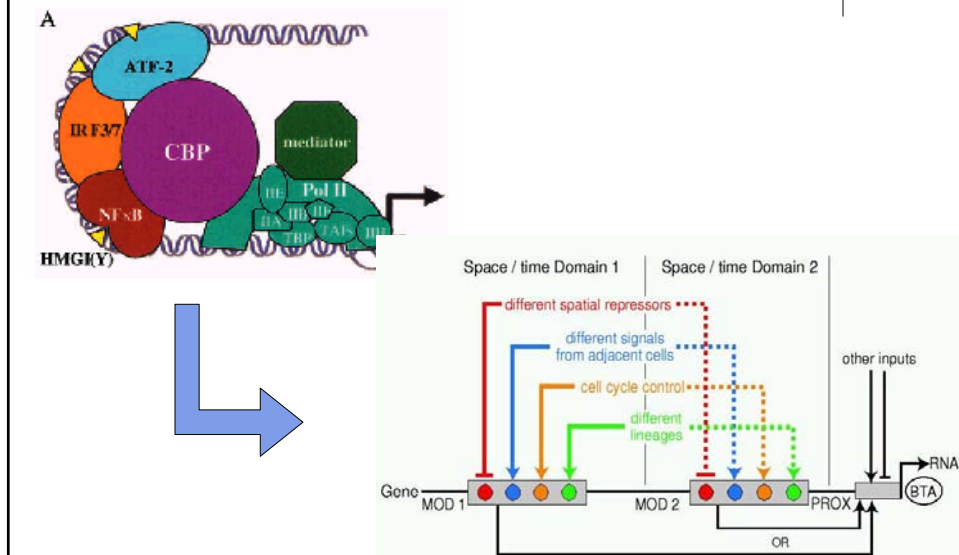
Learning: empirical Bayes estimation:

a family of training motifs $\{A\}_k \Rightarrow$ hyperparameters $\{\alpha, \pi, B\}_k$

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26

Enhanceosome: Cis-Regulatory Modules



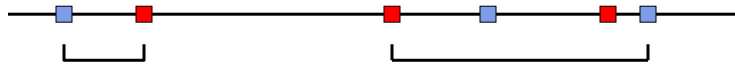
Cluster Finding Methods



- Poisson model
 - A. Wagner
- Cister (CIS-element clusTER finder)
 - M. Frith *et al.*
- Comet (Cluster Of Motifs E-value Tool)
 - M. Frith *et al.*
- cis-regulatory module finder
 - Gupta M, Liu JS.
- LOGOS
 - Xing *et al.*

Finding Motif Clusters

- Poisson Method



Exponential distribution:

$$pdf(x) = ae^{-ax}$$

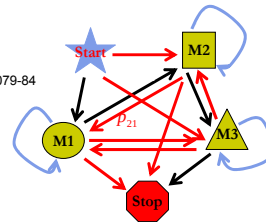
“Pearson type III distribution”:

$$pdf(x) = \frac{a}{(k-2)!} (ax)^{k-2} e^{-ax}$$

- Regulatory Modules:

Cister & Comet

De novo cis-regulatory module elicitation for eukaryotic genomes. *Proc Natl Acad Sci USA*, 102, 7079-84
LOGOS



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29

Cister & Comet: Introduction

DNA sequence

segment



$$\text{score}(\text{segment}) = \ln \left[\frac{\text{Prob}(\text{segment} | \text{cluster model})}{\text{Prob}(\text{segment} | \text{random model})} \right]$$

Cluster model:

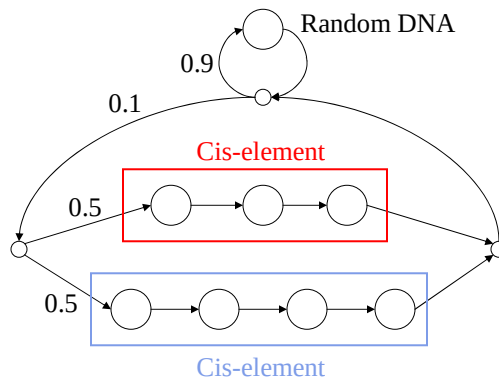


Poisson-distributed cis-elements, embedded in random DNA

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30

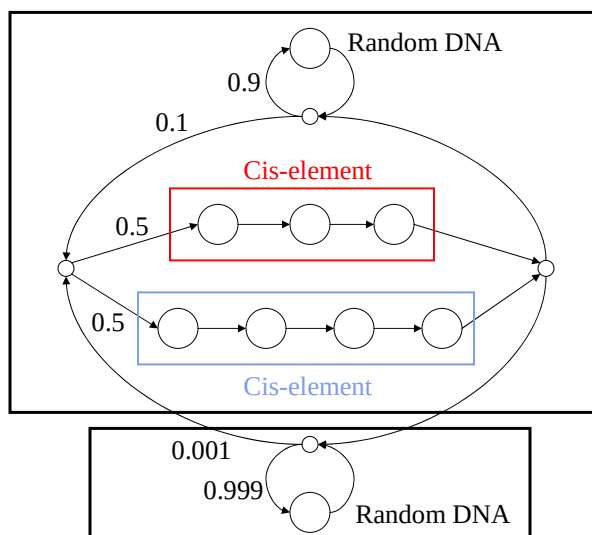
Hidden Markov Model



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31

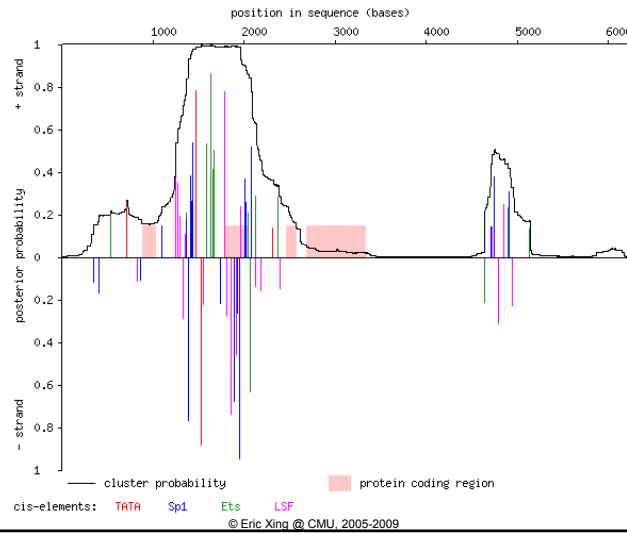
Cister



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32

Cister applied to Human c-fos



33

Comet

DNA sequence

segment

$$\text{score}(\text{segment}) = \ln \left[\frac{\text{Prob}(\text{segment} \wedge \text{optimal parse} \mid \text{cluster model})}{\text{Prob}(\text{segment} \mid \text{random model})} \right]$$

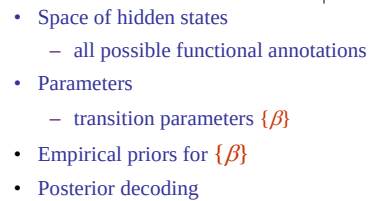
Parse:



One particular arrangement of cis-elements in the segment

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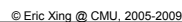
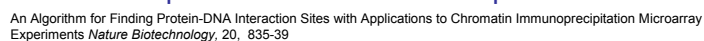
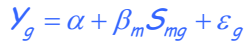
34



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35

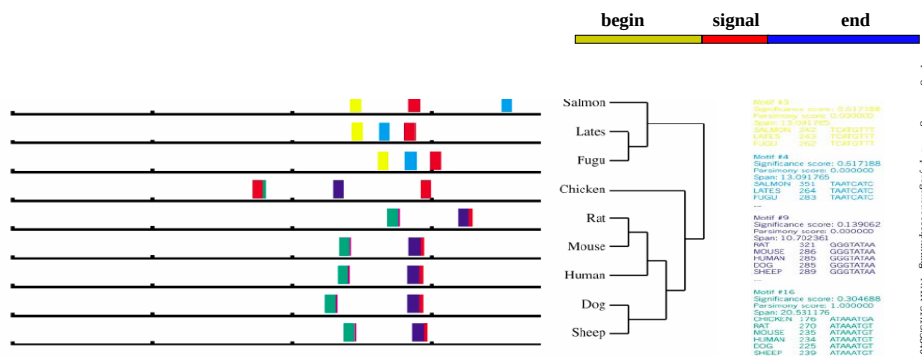
- Integrating Motif Discovery and Expression Analysis Proc.Natl.Acad.Sci. 100.3339-44



36

Phylogenetic Footprinting (homologous detection)

- Term originated in 1988 in Tagle et al. **Blanchette et al.:** For unaligned sequences related by phylogenetic tree, find all segments of length k with a history costing less than d . Motif loss an option.



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37

Discussion

- Model versus algorithm:
 - Model: e.g., oops, zoops, HMM,
 - Algorithms: EM, Gibbs, heuristics ...
- Different algorithms can be used for solving the same model!
 - Need to be clear whether improvement/loss is due to model or algorithm (many paper/author got confused with these two aspects, and discuss results in convolved way!)
 - Fix one, and analyze the other, one at a time!!

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38

Databases

TRANSFAC: <http://www.gene-regulation.com/pub/databases.html#transfac>



TRANSFAC FACTOR TABLE, Release 7.0 - public - 2005-09-30, (C) Biobase G

```

AC T00302
XX
ID T00302
XX
DT 15.10.1992 (created); ewl.
DT 26.09.2002 (updated); hom.
CO Copyright (C), Biobase GmbH.
XX
FA GAL4
XX
SY GAL4; YPL248C.
XX
OS yeast, Saccharomyces cerevisiae
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
XX
SQ MKLLSIEQACDICRLKLLKCKEKPCKACLENNWECRYSPKTRSPTRAHLTEVER
SQ LERLEQLFLIFFPREDLEMIKMDSLQDIALLTGLFVQNVNNDVATORLASVETDML
SQ TLRQHRIGATSSSEESNKGQGLTVSIOAAHNDSTIFLQFMFRAHGFWEEDCM
SQ SDGLSPFKTDPNNNGFFDGGSLICLRLSICGKPNVTHSNVRLPTMTDRYTLASRSTT
SQ SRLQSYNNFRPYCPIVHSPILMMLYNNQIEIASKDQWQLFNCILAIGAWCIEGSTD
SQ IDVFYQNAKSHLTQKVFESGSIILVIALHLLSRYTQWRQNTSYNHFHSIRMAISLG
SQ LMRDLSPSSDSSILEQRRRIWBSVYSWEIQLSLYGRSILQSONTISFFSVDDVQRTT
SQ TQPTIVSGHIIETARLLQVPTIYELEKTVYAKSPICAKSLMICNIEIEVWQAAPFLQ
SQ MDISTALTNLKHPWLSFTFELKWKQLSLIIVYLDFFNTFTQKKSQLEQDQNDHQS
SQ YEVKRCSIMLSDAQAQRTVMNSVSYMDNHNVTPTFAWNCYFFFAVLVPIKILLNSKSN
SQ AENNETACLOOINTVIMLLKRLATFKIQTCEYIOVLEEVCAFFLLSOCAIPLFHSYN
XX
MX M00049 FSGAL4_01.
MX M00198 FSGAL4_C.
XX
ES R00501 ASFGAL4_01; Quality: 1.
ES R04203 ASFGAL4_02; Quality: 6.

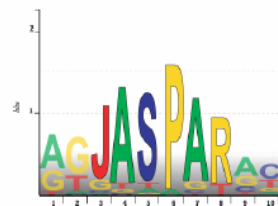
```

Binding Sites

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39

More Databases



The high-quality transcription factor binding profile database

BROWSE profiles by ID Name Species Class Taxonomic group [help](#)

SEARCH by Name Name Name

combine searches with AND AND AND [help](#)

Species-specific:

- SCPD (yeast) <http://rulai.cshl.edu/SCPD/>
- DPInteract (e. coli) <http://arep.med.harvard.edu/dpinteract/>
- Drosophila DNase I Footprint Database (v2.0) <http://www.flyreg.org/>

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40

Logos: <http://weblogo.berkeley.edu/>



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41

Gibbs Motif Sampler

<http://bayesweb.wadsworth.org/gibbs/gibbs.html>



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42

MEME

<http://meme.sdsc.edu/meme/website/meme.html>



File Edit View Favorites Tools Help

Back Forward Stop Search Favorites

Address <http://meme.sdsc.edu/meme/meme.html> Go Links David BBC CNN Yahoo Mail

MEME Version 3.5.0 Hosted by NCBIR

Data Submission Form

Use this form to submit DNA or protein sequences to MEME. MEME will analyze your sequences for similarities among them and produce a description (motif) for each pattern it discovers. Your results will be sent to you by e-mail.

Your e-mail address:

Re-enter e-mail address:

Please enter the sequences which you believe share one or more motifs. The sequences may contain no more than 60,000 characters total in any of a large number of formats.

[Optional] Description of your sequences:

• Enter the name of a file containing sequences here:

or the actual sequences here (Sample Input Sequences):

```
>TBR010C 176 433 649
TTGGTAAAGTAGAGGGGTAATTTTCCCTTTATTTGTCATACATT
CTTAAATTGCTTTGCTCTGCTTTTGGAAAGCTATAGTTGGAGCACTG
TTGAGGGAAGGCTGATTAGATATATTTCTGCTATTCTTCTTAAGCCAA
TATTAAGGGAAGGCTCCAAAAGGCTCGGCAACTGTTGACCTGAT
```

How do you think the occurrences of a single motif are distributed among the sequences?

☒ One per sequence

☐ Zero or one per sequence

[Optional] MEME will find the optimum number of sites for each motif within the limits you specify here: Minimum sites (>= 2)

MEME will find the optimum width of each motif within the limits you specify here: Minimum width (>= 2)

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 - Bulyk (2003), *Genome Biology* 5:201
- Logos
 - Schneider & Stephens (1990), *Nucleic Acids Res.* 18:6097-6100
- Probabilistic
 - GMS: Lawrence *et al.* (1993), *Science*, 262:208-214
 - MEME: Bailey & Elkan (1995), *Machine Learning*, 21:51-80
 - Bayesian models for multiple local sequence alignment and Gibbs sampling strategies. J. S. Liu, A. F. Neuwald, and C. E. Lawrence. *Journal of the American Statistical Association*, 90, 1156-1170, 1995.

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 - Modeling dependencies in protein-dna binding sites, Y. Barash et al. *ISMB* 2003
 - MotifPrototyper: a profile Bayesian model for motif family. E.P. Xing and R. M. Karp, *Proc. Natl. Acad. Sci. vol. 101, no. 29, 10523-10528, 2004.*
 - Kechris et al. (2004), *Genome Biology*, 5(7):R50.
- Regulatory models
 - Frith MC, Hansen U, Weng Z (2001) *Bioinformatics* 17(10): 878-889
 - Frith MC, Spouge JL, Hansen U, Weng Z (2002) *Nucleic Acids Research* (in press)
 - LOGOS: A modular Bayesian model for *de novo* motif detection. E.P. Xing, et al., *Journal of Bioinformatics and Computational biology* 2004, 2(1), 127-154.
 - CisModule: *De novo* discovery of *cis*-regulatory modules by hierarchical mixture modeling. *Proc. Natl. Acad. Sci. USA*, 101: 12114-12119.
 - *De novo* cis-regulatory module elicitation for eukaryotic genomes M. Gupta and J. Liu, *PNAS*, vol. 101, 7079-7084