

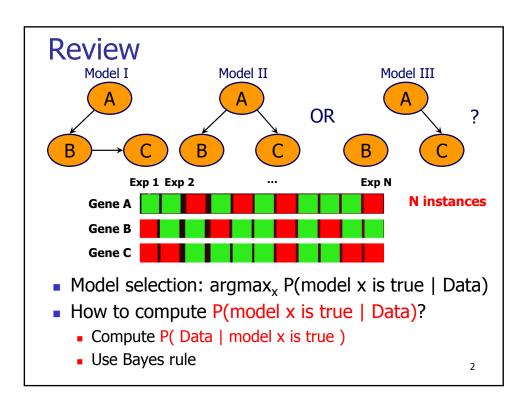
Maximum Likelihood Estimation & Expectation Maximization

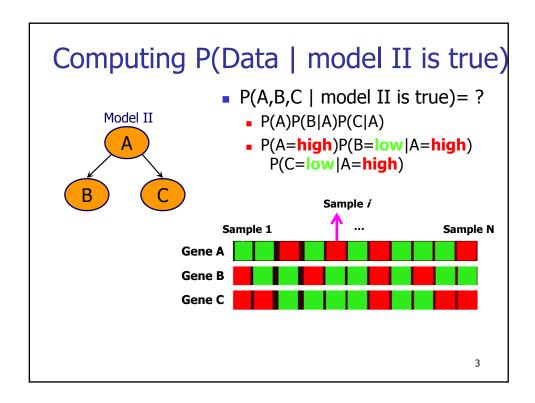
Lectures 3 – Oct 5, 2011 CSE 527 Computational Biology, Fall 2011

Instructor: Su-In Lee TA: Christopher Miles

Monday & Wednesday 12:00-1:20

Johnson Hall (JHN) 022

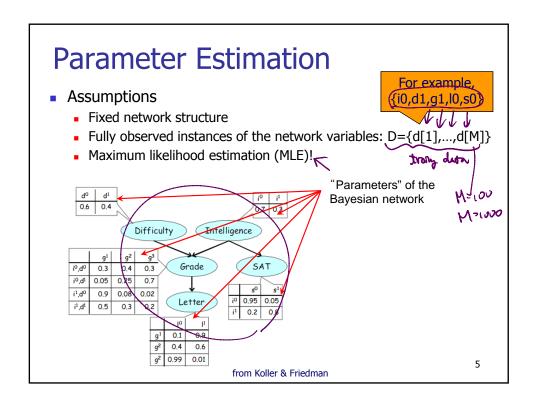


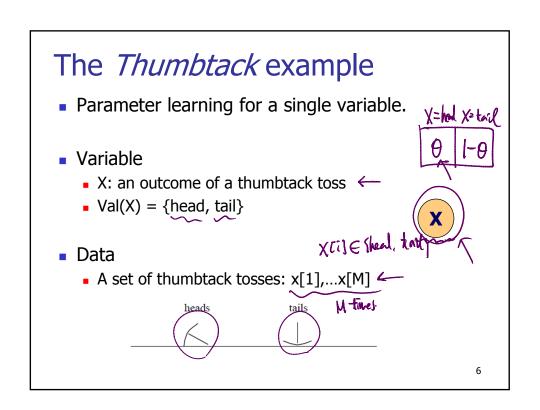


Outline

- Probabilistic models in biology
 - Model selection problem
- Mathematical foundations
- Bayesian networks
- Learning from data
 - Maximum likelihood estimation
 - Maximum a posteriori (MAP)
 - Expectation and maximization







Maximum likelihood estimation

- Say that $P(x=head) = \Theta$, $P(x=tail) = 1-\Theta$
 - P(HHTTHHH...< M_h heads, M_t tails>; Θ) = $\theta \theta ((-\theta))$ = $\theta^{Mh} ((-\theta))^{Mh}$
- Definition: The likelihood function
 - -(L(Θ:D)) = P(D(Θ)) = Θ^{Mn}(1-0)^{Mt}

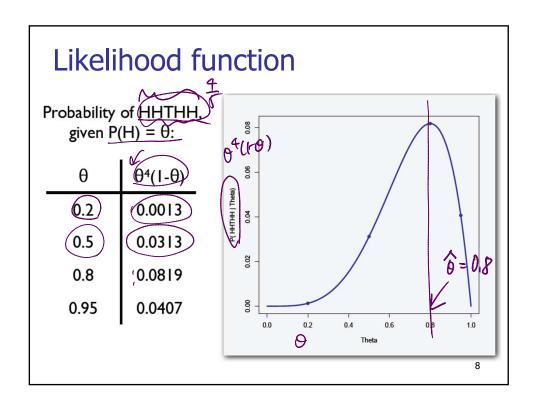
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- Maximum likelihood estimation (MLE)
 - Given data D=HHTTHHH...
 M_h heads, M_t tails>, find Θ that maximizes the (likelihood function L(Θ : D).



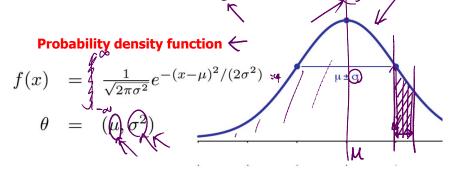


MLE for the *Thumbtack* problem

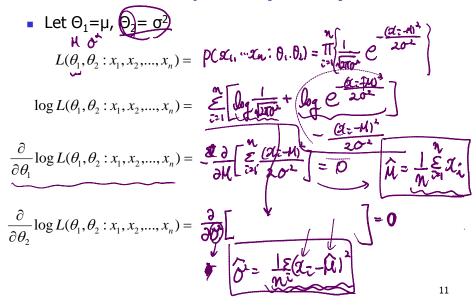
- Given data D=HHTTHHH...<M_h heads, M_t tails>,
 - MLE solution $\widehat{\Theta}^{?} = M_h / (M_h + M_t)$.
- Proof: $L(\theta;D) = P(D;\theta)$ $= \frac{\partial H}{\partial t} (1-\theta) + \frac{\partial H}{\partial t}$ $\Rightarrow \frac{\partial I}{\partial t} (1-\theta) + \frac{\partial I}{\partial t} (1-\theta)$ $= \frac{\partial I}{\partial t} (1-\theta) + \frac{\partial I}{\partial t} (1-\theta)$ $= \frac{\partial I}{\partial t} (1-\theta) + \frac{\partial I}{\partial t} (1-\theta)$ $= \frac{\partial I}{\partial t} (1-\theta) + \frac{\partial I}{\partial t} (1-\theta)$

Continuous Space

- Assuming sample $x_1, x_2, ..., x_n$ is from a parametric distribution $f(x|\Theta)$, estimate Θ .
- Say that the n samples are from a normal distribution with mean μ and variance σ?.



Continuous Space (cont.)



Any Drawback?

■ Is it biased?

• Is it? Yes. As an extreme, when n = 1, $(\hat{\theta}_2)$

• The MLE $\hat{\theta}_2$ systematically underestimates θ_2 . Why? A bit harder to see, but think about n=2. Then θ_I is exactly between the two sample points, the position that exactly minimizes the expression for $\hat{\theta}_2$. Any other choices for (θ_I, θ_2) make the likelihood of the observed data slightly lower. But it's actually pretty unlikely that two sample points would be chosen exactly equidistant, and on opposite sides of the mean, so the MLE $\hat{\theta}_2$ systematically underestimates θ_2 .

Maximum A Posteriori

0-> 0.5



• Incorporating priors. How?

MLE: PCD(0) Jog PCD(0)

MAP: $p(O|D) = \frac{p(D|O)p(O)}{p(D)}$



MLE vs MAP estimation

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MLE for General Problems

- Learning problem setting ¼ · 🏵
 - A set of random variables X from unknown distribution P*
 - Training data D = M instances of X: {d[1],...,d[M]}
- A parametric model P(X; Θ) (a 'legal' distribution)
- Define the likelihood function:

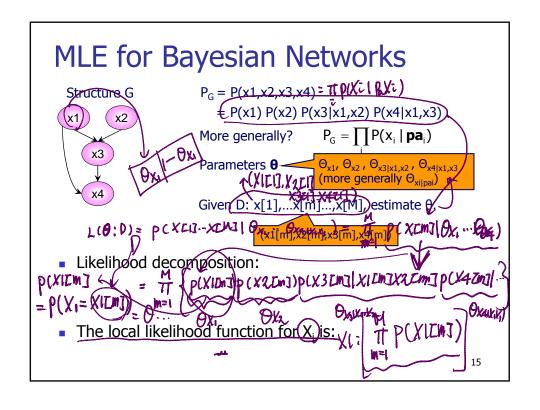
• $L(\Theta : D) = PCD : \theta$

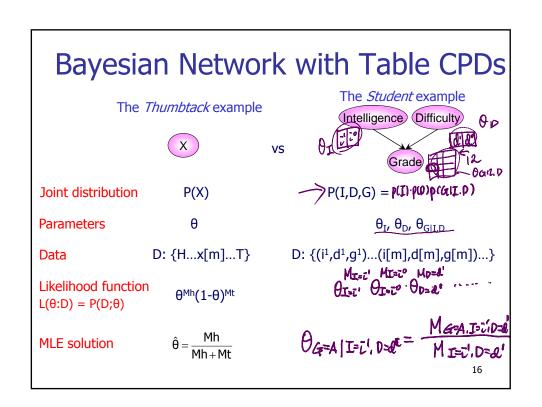
6 = argunant P(D:0)

Maximum likelihood estimation

• Choose parameters of that satisfy:







Maximum Likelihood Estimation Review

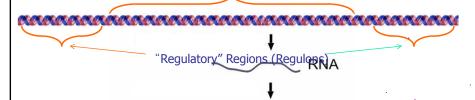
- General approach, as long as tractable likelihood function exists
- Can use all available information <

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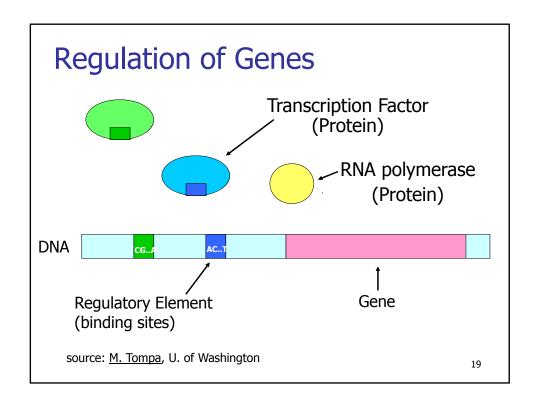
Example – Gene Expression

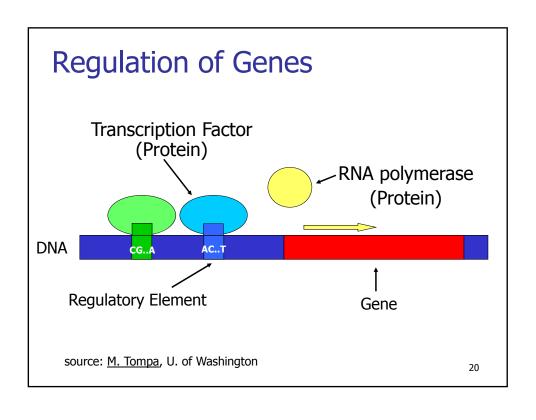
- Instruction for making the proteins
- Instruction for when and where to make them

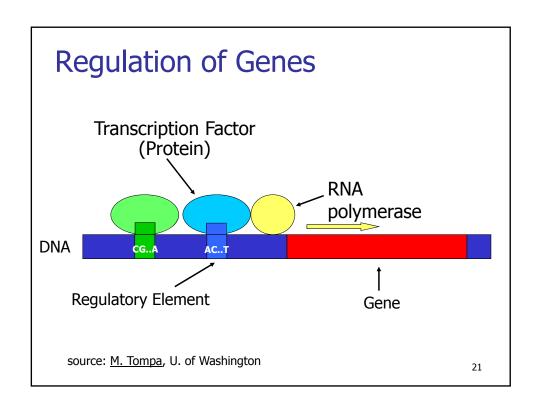
"Coding" Regions

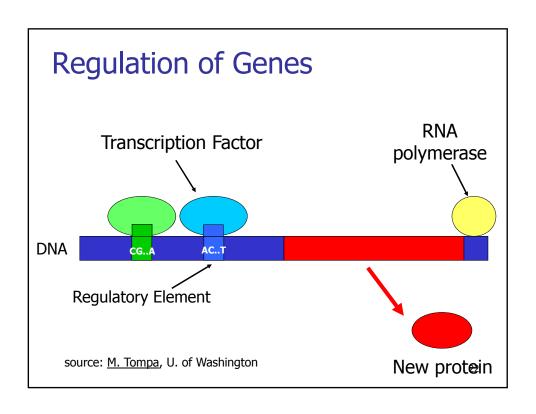


- Regulatory regions contain "binding sites" (6-20 bp).
- "Binding sites" attract a special class of proteins, known as "transcription factors".
- Bound transcription factors can initiate transcription (making RNA).
- Proteins that inhibit transcription can also be bound to their binding sites.









The Gene regulation example What determines the expression level of a gene? What are observed and hidden variables? e.G, e.TF's: observed; Process.G: hidden variables ⇒ want to infer! **Expression level** of TF e.TF₂ e.TF₃ e.TF₄ $e.TF_N$ Biological process the gene is involved in Process.G **Expression level** of a gene 23

Not All Data Are Perfect

- Most MLE problems are simple to solve with complete data.
- Available data are "incomplete" in some way.

Outline

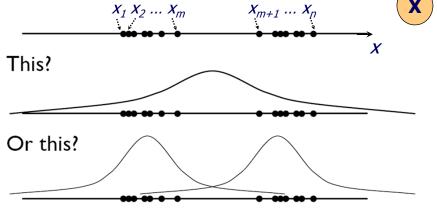
- Learning from data
 - Maximum likelihood estimation (MLE)
 - Maximum a posteriori (MAP)
 - Expectation-maximization (EM) algorithm



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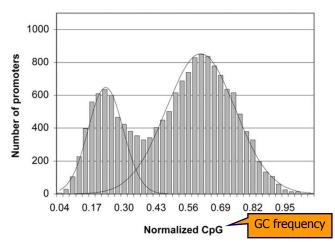
Continuous Space Revisited...

 Assuming sample x₁, x₂,..., x_n is from a mixture of parametric distributions,





CpG content of human gene promoters



"A genome-wide analysis of CpG dinucleotides in the human genome distinguishes two 27 distinct classes of promoters" Saxonov, Berg, and Brutlag, PNAS 2006;103:1412-1417

Acknowledgement

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