Readings: K&F 19.2, 19.3

# EM Algorithm & Learning Problems in Real Applications

Lecture 13 – May 9, 2011

CSE 515, Statistical Methods, Spring 2011

Instructor: Su-In Lee

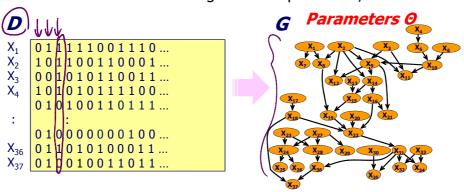
University of Washington, Seattle

#### **Outline**

- Expectation Maximization (EM)
  - Parameter estimation with missing data
- Structural EM
  - Structure learning with missing data
- Learning problems in real world applications
  - Computational biology, natural language processing, robotics, collaborative filtering, etc
  - Student presenters: Nathan, John, Kris
- Mid-quarter review (1-1:20pm)
  - Jim Borgford-Parnell, Center for Engineering Learning and Teaching (CELT)



Recall that when learning from complete data,

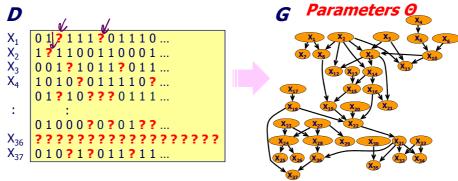


- We would first collect sufficient statistics for each CPD.
- We can estimate parameters that maximize the likelihood with respect to these statistics.

For table CPDs:  $heta_{
m v}^{ extit{MLE}}$ 

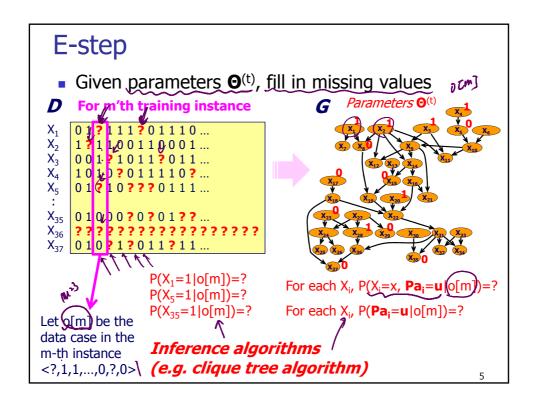
#### **Expectation Maximization (EM)**

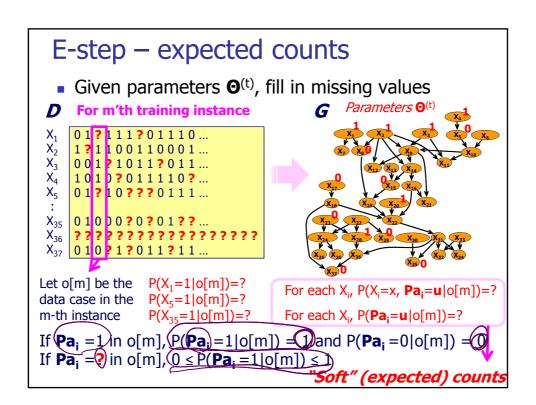
Parameter estimation when D has missing data



- Set initial set of parameters  $\Theta^{(1)} = \Theta_n$
- Iterate E-step and M-step until convergence
  - In the t-th iteration,
  - E-step: Given  $\Theta^{(t)}$ , fill in missing values

    M-step: Given complete
    - M-step: Given complete data, learn parameters O(t+1)





#### E-step cont. & M-step

- Compute sufficient statistics:
- If D is complete data,

$$M[X_i = \emptyset, \mathbf{Pa}_i = \mathbf{u}] = \sum_{\mathbf{u}} \mathbf{1}(X_i = x, \mathbf{Pa}_i = \mathbf{u} \mid o[m])$$

Given "soft" counts (expected sufficient statistics) ESS),

$$\underbrace{\overline{M}_{\theta^{(t)}}[X_i = x, \mathbf{Pa}_i = \mathbf{u}]}_{\theta^{(t)}} = \underbrace{\sum_{m} P(X_i = x, \mathbf{Pa}_i = \mathbf{u} \mid o[m], \theta^{(t)})}_{P(\mathbf{Pa}_i = \mathbf{u} \mid o[m], \theta^{(t)})}$$

 M-step: Treat the ESS as those from complete data, and set the parameters to the MLE with respect to the ESS

$$\underbrace{\left( \underbrace{\boldsymbol{\theta}_{X_{i}=X_{i}^{\mathbf{P}}\mathbf{a}_{i}=\mathbf{u}}^{(t+1)} = \frac{\overline{M}_{\boldsymbol{\theta}^{(t)}}[X_{i}=x,\mathbf{Pa}_{i}=\mathbf{u}]}_{\overline{M}_{\boldsymbol{\theta}^{(t)}}[\mathbf{Pa}_{i}=\mathbf{u}]} \right)}^{\mathbf{Pa}_{i}=\mathbf{u}}$$

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## **Expectation Maximization (EM)**

Formal Guarantees:

 $L(D: \Theta^{(t+1)}) \ge L(D: \Theta^{(t)})$ 

- Each iteration improves the likelihood (read Andrew Ng's lecture note on EM)
- If  $\Theta^{(t+1)} = \Theta^{(t)}$ , then  $\Theta^{(t)}$  is a stationary point of  $L(D:\Theta)$ 
  - Usually, this means a local maximum
- Main cost:
  - Computations of expected counts in E-Step
  - Requires inference for each instance in training set
    - ullet Exactly the same as in gradient ascent!  $^{ullet}$

#### **EM – Practical Considerations**

- Initial parameters
  - Highly sensitive to starting parameters Θ<sub>0</sub>
  - Choose randomly ←
  - Choose by guessing from another source ←
- Stopping criteria
  - Small change in data likelihood
  - Small change in parameters



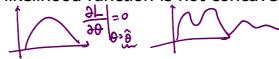
- Avoiding bad local maxima

  - Early pruning of unpromising starting points

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#### Partially Observed Data: Parameter Estimation

Log-likelihood function is not concave



- Methods for learning: EM and Gradient Ascent
  - Exploit inference for learning
- Challenges
  - Exploration of a complex likelihood/posterior
    - More missing data ⇒ many more local maxima
  - Inference <
    - Main computational bottleneck for learning
    - Learning large networks ⇒ exact inference is infeasible
       ⇒ resort to approximate inference

## Structure Learning w. Missing Data

- Distinguish two learning problems
  - Learning structure for a given set of random variables
  - Introduce new hidden variables (K&F 19.5)
    - How do we recognize the need for a new variable?
    - Where do we introduce a newly added hidden variable within G?
    - Open ended and less understood...

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#### Structure Learning w. Missing Data

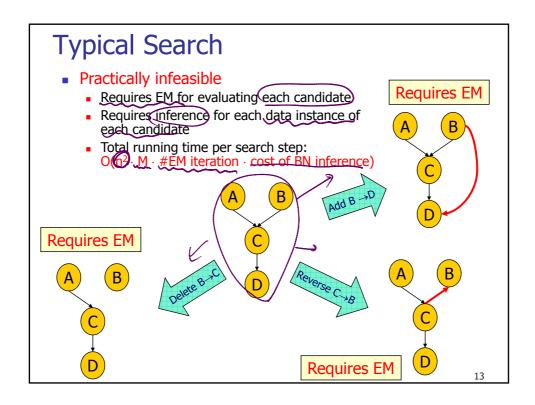
- Theoretically, there is no problem
  - Define score, and search for structure that maximizes it



Likelihood term will require gradient ascent or EM



- Practically infeasible
  - Typically we have Q(n²) candidates at each search step



#### Structural EM

- Basic idea: use expected sufficient statistics to learn structure, not just parameters

  - Use current network to complete the data using EM D\*
     Treat the completed data as "real" to score candidate structures
  - Pick the candidate network with the best score
  - Use the previous completed counts to evaluate networks in the next step
  - After several steps, compute a new data completion from the current network

#### Structural EM

- Set the initial parameters  $\Theta^{(1)} = \Theta_0$ , structure  $G^{(1)} = G_0$
- Iterate:



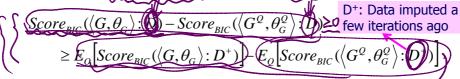
Given the complete data D\*, learn structure G(t+1)

Given the complete data D<sup>\*</sup> and structure G<sup>(t+1)</sup>, learn parameters Θ<sup>(t+1)</sup>

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#### Structural EM Benefits

- Many fewer EM rung
- Score relative to completed data is decomposable!
  - Utilize same benefits as structure learning w. complete data
  - Each candidate network requires fewer re-computations
  - Here savings is large since each sufficient statistics computation requires inference
- As in EM, we optimize a simpler score
- Can show improvements and convergence



An SEM step that improves in D+ space, improves real score

Week	Dates	Topics and Lecture Notes	Readings		
I. Proba	abilistic (	Graphical Models Representation			
1	3/28	Introduction to the class	2.1, 2.2, 2.3	1. Probabilistic model	
	3/30	Bayesian network representation	3.1, 3.2, 3.3		
2	4/4	Local probability models	3.4, 5	representation	
	4/6	Undirected graphical models I	4.1, 4.2, 4.3		
3	4/11	Undirected graphical models II + P-DAGs	4.4, 4.5, 4.6		
II. Exac	t Inferen	ce		<del>-</del>	
	4/13	Inference: exact inference	9.1, 9.2, 9.3	A PART IN DA	
4	4/18	Exact inference in BNs	9.4, 9.5, 9.6	2 Exact inference in BN	
	4/20	Exact inference: Clique Trees	10.1, 10.2, 10.3, 10.4	*(P( <b>X</b> =x  <b>E</b> =e)=?)	
III. Lea	rning				
5	4/25	Learning: parameter estimation	17	(3) Longing	
	4/27	Parameter learning in BNs	17	3 Learning	
6	5/2	Structure learning in BNs	18	parameters/structure	
	5/4	Partially observed data (learning with missing data)	19	- Learning CPDs,	
7	5/9	More on learning (TBD)		structure from data	
IV. App	roximate	Inference		<del></del>	
	5/11	Approximate inference: particle-based I	12	4. Approximate inferen	
8	5/16	Approximate inference: particle-based II	12		
	5/18	Global approximate inference l	11	-(P( <b>X</b> =x  <b>E</b> =e)	
9	5/23	Global approximate inference II	11		
V. Spec	ial Topic	cs & Applications		_	
	5/25	Markov Decision Processes		5. Applications 🗸	
		(Instructor: Mausam)			
10	5/30	(memorial day)		- Decision making,	
	6/1	Temporal models (DBNs, HMMs)		temporal processes	
		Final examination @		17	

# LEARNING PROBLEMS IN REAL APPLICATIONS

CSE 515 – Statistical Methods – Spring 2011

### Learning Problems in Real Applications

- Robotics, AI, Natural Language Processing, Computational <sup>n</sup> Biology, Computer Vision...
- Robotic mapping
- Collaborative filtering
- Part-of-speech tagging
  - Presented by Nathan Imse
- Peptide identification in MSMS
  - Presented by John Halloran
- Finding tumor-specific mutations
  - Presented by Kris Weber
- Text classification
  - Collective classification of web pages
- Computer vision
  - Image segmentation and de-noising

#### **Background**

- Robotic mapping: acquiring a spatial model of a robot's environment. (Sebastian Thrun, 2002)
  - Maps are commonly used for robot navigation (e.g. localization).
  - Robots must posses sensors (sonar, laser, radar, GPS, etc) to be able to perceive the outside world.
  - All sensors are subject to errors, often referred to as measurement noise.

#### **Robotic Mapping**



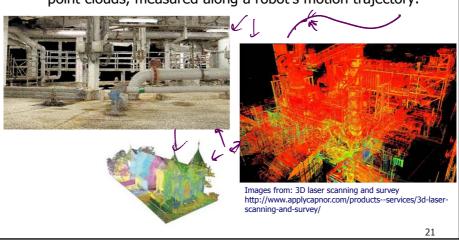
Howard et al. Towards 3D mapping in large urban environments, Intelligent

- Object maps
  - A family mapping algorithms addresses the problem of building maps composed of basic geometric shapes or objects, such as lines, walls and so on.
  - Let's focus on one by Thrun et al. (2004) that explicitly tries to use the probabilistic model to capture the structure in the environment.

#### **Training Data**

#### **Robotic Mapping**

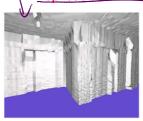
- Data: A point cloud representation of an indoor environment.
  - The point cloud can be obtained by collecting a sequence of point clouds, measured along a robot's motion trajectory.

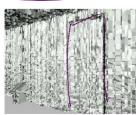


#### **Problem Statement**

#### **Robotic Mapping**

- Goal: Take the points obtained over the trajectory and fit the points using polygons, to derive a 3D map of the surfaces in the robot's environment.
  - However, the noise in the laser measurements, combined with the errors in localization, leads adjacent polygons to have slightly different surface normals, giving rise to a very jagged representation of the environment.





Polygonal map generated from raw data. The display without texture shows the level of noise involved. In particular, it illustrates the difficulty of separating the door from the nearby wall. Thrun et al. (2004)

 Probabilistic model: Fit a more compact representation of the environment to the data, reducing the noise and providing a smoother, more realistic output.

#### Modeling

#### **Robotic Mapping**

- The model consists of a set of 3D planes  $p_1, \dots, p_K$ , each characterized by two parameters  $(\alpha_k, \beta_k)$ 
  - $\alpha_k$ : a unit-length vector in  $\mathbf{R}^3$  that encodes the plane's sürface normal vectors
  - $\bullet$ ( $\beta_k$ ): a scalar that denotes its distance to the origin of the global coordinate system.

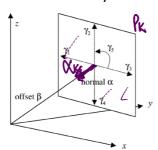


Illustration of the parameters in the planar surface model Thrun et al. (2004)

 The distance of any point x to the plane is  $(d(\mathbf{x}, p)) = |\alpha_{\nu}\mathbf{x} - \beta_{\nu}|$ 

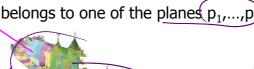
23

observed

#### **Probabilistic Model**

#### **Robotic Mapping**

Each point(x<sub>m</sub>) belongs to one of the planes p<sub>1</sub>,...,p<sub>n</sub>



- This assignment can be modeled via a set of correspondence variables (Cm
  - Cm k if the measurement point xm was generated by the k-th plane p.
  - is not observed (hidden variable)
- Define \( \frac{\partial P}{\text{X}} \)  $= k!: \theta_{i}$ ) to be  $\propto N$ 
  - Allow an additional value C<sub>m</sub>=0 that encodes points that are not generated by any of the planes
- Data: each point  $(x_m)$  is a training instance, e.g.  $x_m = (1,1,1)$

#### Learning

#### **Robotic Mapping**

#### **Probabilistic model**

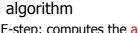
- Define  $P(\mathbf{X}_m \mid C_m = k : \theta_k)$  to be  $\propto N(d(\mathbf{x}, p_k) : 0, \sigma^2)$ 
  - Allow an additional value C<sub>m</sub>=0 that encodes points that are not generated by any of the planes



■ Goal: the assignment of points to planes (C<sub>m</sub>) for all m's), the parameters  $(\alpha_k, \beta_k)$  that characterize the planes.



EM algorithm



- E-step: computes the <u>assignment to the correspondence variables</u> C<sub>m</sub>'s by assigning the weight of each point proportionately to its distance to each of them.
- M-step: recomputes the parame f each plane to fit the points assigned to it.

#### Results I

Notice that the map in (b) is smoother and appears to be visually more accurate than the one in (a)



Thrun et al. A Real-time EM Algorithm for Acquiring Multi-Planar Maps of Indoor Environments with Mobile Robots. IEEE Transactions on Robotics and Automation, 2004.

# Results II Maps generated in real-time, of office environments Notice that the map in (b) is smoother and appears to be visually more accurate than the one in (a) Thrun et al. A Real-time EM Algorithm for Acquiring Multi-Planar Maps of Indook Environments with Mobile Robots. IEEE Transactions on Robotics and Automation, 2004. (a) Raw data map (using a high-accuracy range finder)

#### Learning Problems in Real Applications

- Robotics, AI, Natural Language Processing, Computational Biology, Computer Vision...
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# Hidden Markov Models for Part of Speech Tagging

Nathan Imse njimse@uw.edu

## What Is Part of Speech Tagging?

- Labeling words based on their function
  - Nouns: person, place, thing
  - Verb: action
  - Adjective: describes a noun
- Tagsets often have anywhere from 10-90 tags

	Nouns	Verbs	Adjectives
\	Cat, dog, ball, car, zoo,	Book, chase, is, cook, live,	human, short,
	human, book	sleep, sing	cold, smelly

#### Why Tag the Part of Speech?

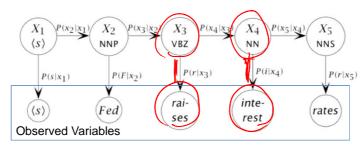
- Named Entity Recognition
  - Extract names of people, companies, and cities from text
- Word Sense Disambiguation
  - Differentiate between different meanings of the same word (e.g. bank, run, book)
- Parsing
  - Build a structure of the sentence with a much simpler grammar (<90 tags vs. 200,000+ words)</li>

# HMM Representation: Hidden Variables

• Hidden variables are Part of Speech (POS) tags

# HMM Representation: Observed Variables

- Observed variables are words, numbers, punctuation, etc...
- Observed variables are leaves in the network
  - No outgoing edges
- Edge from hidden variable to observed variable is the probability of that observation given that hidden variable



#### Training and Testing

- Training data consists of annotated text, either in parse trees or in flat text
  - Pierre NNP Vinken/NNP ,/, 61/CD years/NNS old/JJ ,/, will/MD join/VB the/DT board/NN ....
- Testing data does not have tags
  - "Fed raises interest rates"
  - Tags are considered "hidden"

## Decoding/Inference

- Viterbi Algorithm is common
  - Dynamic programming
  - Optimal global sequence, with probability
- Implemented for a course last fall

- Trained on ~1900 sentences from the Wall Street  $\,$ 

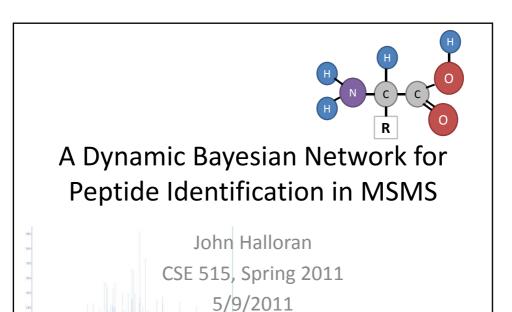
Journal

88% accuracy (with smoothing)

	Bigram	Trigram
States	47	2162
Observations	~7900	~7900
Transitions	~890	~99500
Emissions	~8700	~400800

#### Credit

The diagram of the HMM network as a Bayesian Network on slides 4 & 5 are the work of Andrew McCallum from Umass, Amherst



#### **Problem Statement**

- Tandem mass spectrometry
  - Spectrum of measured m/z intensities generated from sample proteins (peptides)
- Given MSMS spectrum, identify peptide which generated spectra
- Typically look up peptides in database of the mapped organism

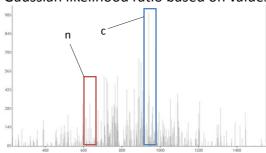
#### Model

- Normalize spectra, quantize into B bins
- Model fragmentation event:
  - Candidate Peptide: IEQFMEEMYQDK

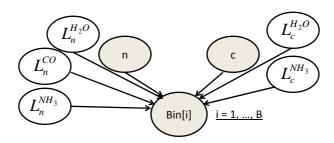
Fragment Ions
IEQFM+

EEMYQDK+-

 Check n=mass(IEQFM+), c=mass(EEMYQDK+) bins values, calculate Gaussian likelihood ratio based on values



#### Model



- •n, c, Bin[i] values are observed
- •Loss of CO, NH<sub>3</sub>, H<sub>2</sub>O(?) Losses are hidden variables (Bernoulli)
- •Peptide length N, N-1 such events: concatenate to form DBN

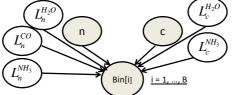
#### **Training**

- Learned parameters:
  - Gaussian variances, neutral loss probabilities
- Training Data:
  - 1208 high quality E-coli matches
  - Matches generated combining 7 peptideidentification algorithms
- Parameters trained using EM

#### Inference

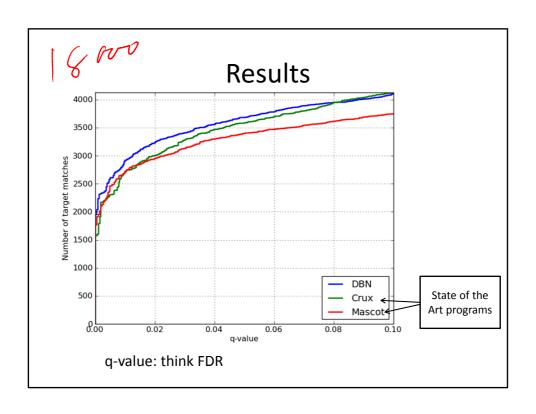
 Candidate peptide C and B bins assigned score of log(P(bins,C)), where:

$$P(bins, C) = \prod_{i}^{n-1} \sum_{losses} p(loss) \prod_{j}^{B} p_{I}(b_{j}) \frac{p_{A}(b_{n})}{p_{I}(b_{n})} \frac{p_{A}(b_{c})}{p_{I}(b_{c})}$$
Likelihood ratios



#### Results

- Testing performed using decoy database:
  - Permute target database values
  - Good algorithm should score targets high, decoys low
  - Performance metric: false discovery rates (FDR)



# Questions?

 Model implemented using GMTK (Graphical Models Toolkit) developed by Dr. Jeff Bilmes

# Cancer Genomics Problem: Finding tumor-specific mutations

#### **Problem Statement:**

#### Given:

- a human cancer patient
- sample from tumor tissue
- sample from normal tissue
- DNA sequence of both samples

Identify the mutations present in the tumor tissue that are not present in the normal tissue

#### Background: DNA, Genotypes, Mutations

TAACGCGGTCCCG...

 At the simplest level, we can think of DNA as a sequence of letters from the alphabet, {A,C,G,T}



Genotype AA

Genotype CT

- Humans have 2 copies of each chromosome.
- 10 possible "genotypes" at each position



Genotype AT

Genotype CT

 We are trying to find single base mutations in the tumor DNA

#### Problem: Call Genotypes from Data

- Our data: lots of overlapping short reads.
- At each position, we count the number of reads for each base...

```
Read 1 ATGGTGGGAACCACCCACCTCCTTTGCG

Read 2 GGGAACCACCCACCCCCC

Read 3 ATGGTGGGAACCACCCACCCCC

Read 4 TGGGGAACCACCCACCTCCTTTGCG

Read 5 ATGGTGGGAACCACCCACCTCC

Read 6 GGTGGGAACCACCCACCTCC

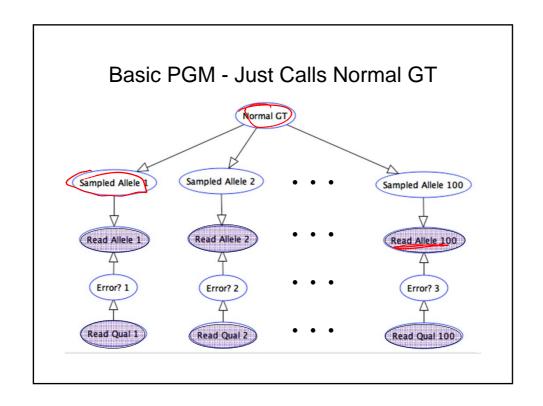
Read 7 ATGGTGGGAACCACCCACCTCC

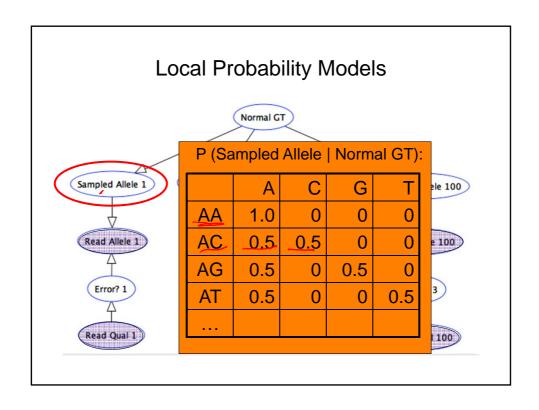
Read 8 ATGGTGGGAACCACCCACCTCC

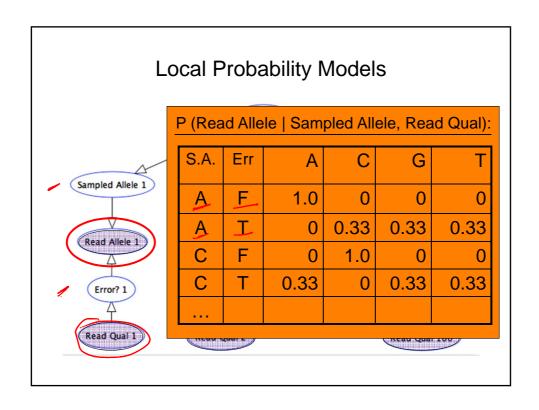
Read 9 GG 3C, 3T → CT
```

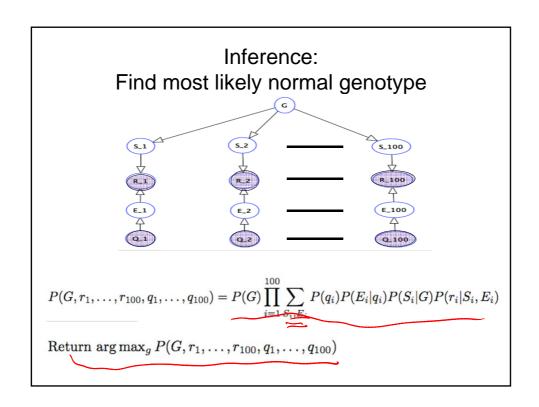
• But the data is noisy:

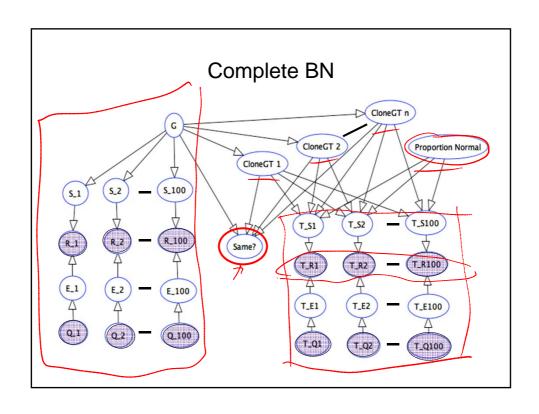
**1C, 9G** → CG? or GG?











## Example Results

A list of possible somatic mutations, ranked by probability:

Chrom	Position	Normal Genotype	Mutated Genotype	Probability
9	53,246,683	AA	AT	.9998
3	4,327,802	СТ	TT	.9992
1	10,234,906	GG	AG	.9934
9	52,132,888	GG	CG	.9897