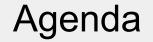
## Genome 540 discussion

#### March 4th, 2025 Joe Min







#### Homework 8

#### Homework 8 overview

Part 1:

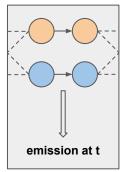
- Make a 2-state HMM with given initial parameters Part 2:
- Use the Baum-Welch method to find improved parameters for the HMM

#### Homework 8: part 1

### Making the initial HMM: definitions

- $\pi_i$ : initial probability of state i
- a:: transition probability from state i to state j
- bi(N): emission probability of nucleotide N
  from state i
- t: the position of emission for the given node

notation borrowed from the <u>Shen tutorial</u> (also on website)



### Making the initial HMM

State 1 is AT-rich

State 2 is GC-rich

#### Emission probabilities

	Α	С	G	Т
State 1	<b>b</b> <sub>1</sub> ( <b>A</b> ) = 0.3	<b>b</b> <sub>1</sub> ( <b>C</b> ) = 0.2	<b>b</b> <sub>1</sub> ( <b>G</b> ) = 0.2	<b>b</b> <sub>1</sub> ( <b>T</b> ) = 0.3
State 2	<b>b</b> <sub>2</sub> ( <b>A</b> ) = 0.15	<b>b</b> <sub>2</sub> ( <b>C</b> ) = 0.35	<b>b₂(G) =</b> 0.35	<b>b₂(T)</b> = 0.15

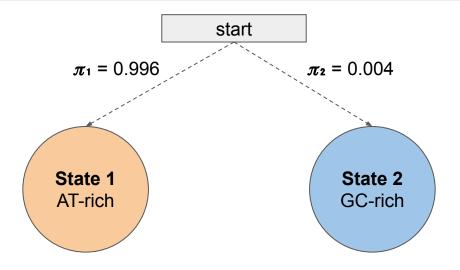
#### Initiation probabilities Transition probabilities

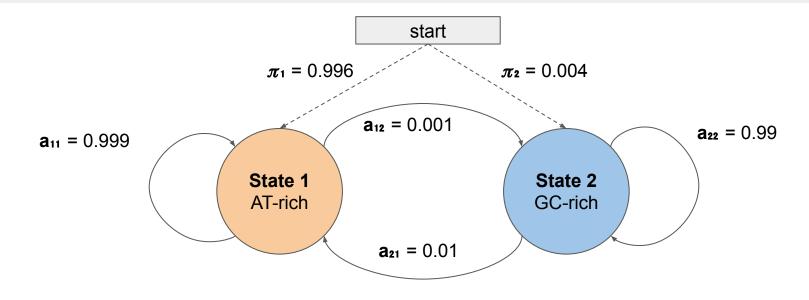
- **π**<sub>1</sub>: 0.996
- $\pi_2$ : 0.004

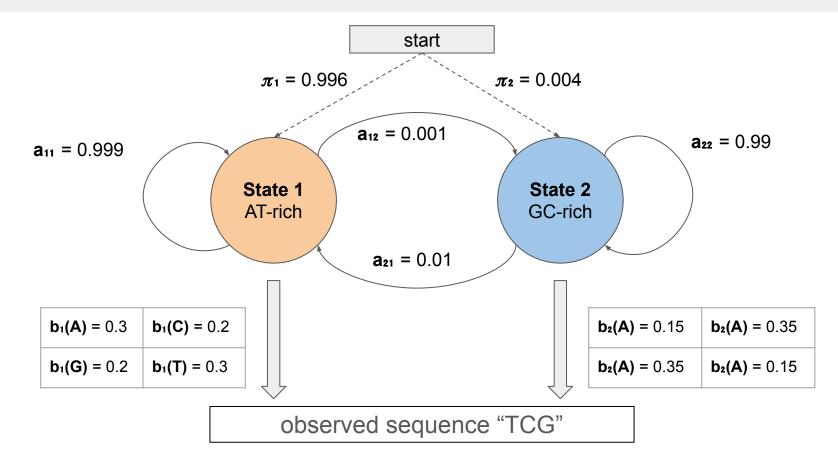
	to State 1	to State 2
From State 1	<b>a</b> <sub>11</sub> = 0.999	<b>a</b> <sub>12</sub> = 0.001
From State 2	<b>a</b> <sub>21</sub> = 0.01	<b>a</b> <sub>22</sub> = 0.99

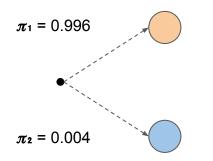
start

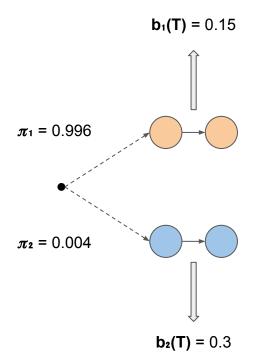


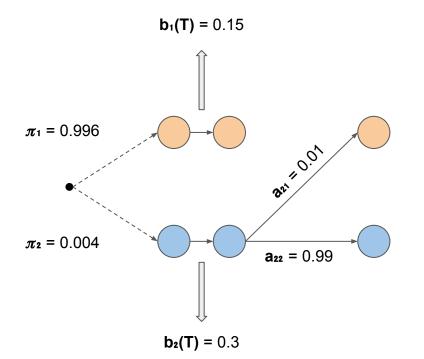


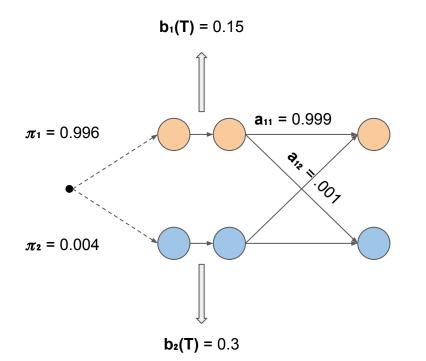


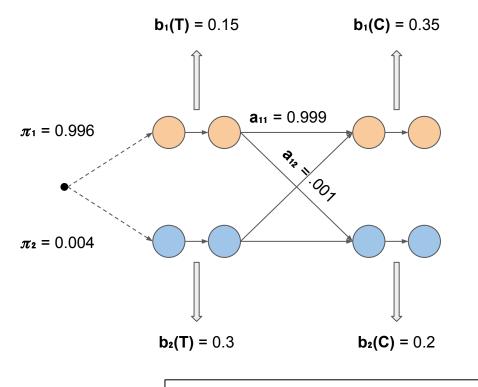


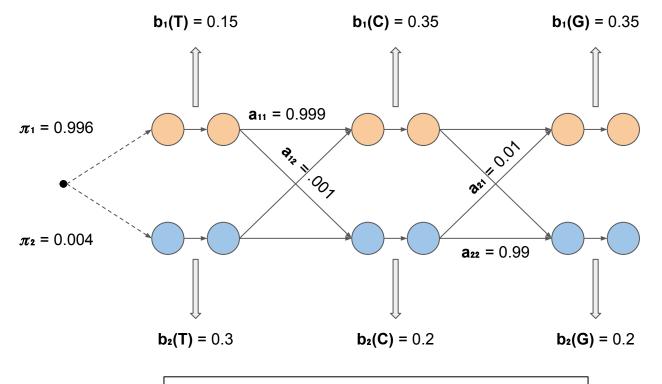


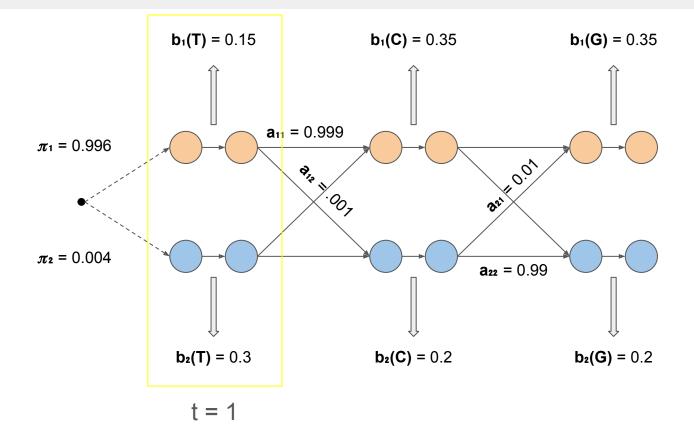


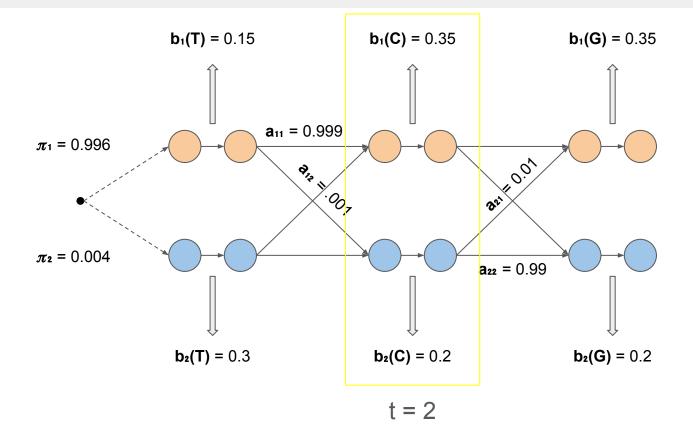


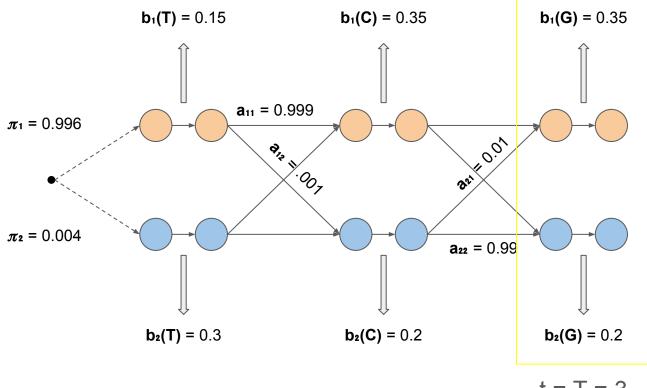












t = T = 3

#### Baum-Welch example

Baum-Welch will iteratively adjust parameters of the HMM to maximize the likelihood of the observed sequence

- First, calculate forward and backward variables using the forward/backward algorithm
- Using these values, update the HMM's:
  - Emission probabilities
  - Transition probabilities

#### The forward part

Calculating forward values for all nodes is what we're used to! But with a twist:

- Use dynamic programming to find highest weight parent and weight of highest-weight path ending at each node
- <u>The twist</u>! For downstream reasons, keep things in the normal probability space (how??)

t: the observation position for a given node

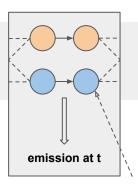
 $\alpha_{t}(i)$ : the highest probability of the partial observed sequence (i.e., observations from t=1 to t=t) for the post-emission node for **state i** at **time t** (unscaled)

 $\boldsymbol{c}_t$ : the scaling factor at time t

 $\alpha^{*}(i)$ : the scaled  $\alpha(i)$ 



 $\hat{a}_{t}(i) = \alpha^{*}_{t}(i) \leftarrow \text{no "alpha hat" in slides, so}$ use  $\alpha^{*}$  instead



post-emission node

#### The forward part: scaling

- $\boldsymbol{c}_t$ : the scaling factor at time t
- Note: independent of state! Because:

$$\mathbf{c}_{t} = \frac{1}{\sum_{i} \alpha_{t}(i)}$$

That is,  $c_t$  is the inverse of the sum of the  $\alpha_t$  values across all states at **time t** 

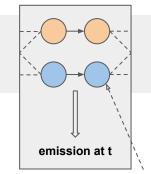
t: the observation position for a given node

 $\alpha_t$ (i): the highest probability of the partial observed sequence (i.e., observations from t=1 to t=t) for the post-emission node for **state i** at **time t** (unscaled)

 $\boldsymbol{c}_t$  : the scaling factor at time  $\boldsymbol{t}$ 

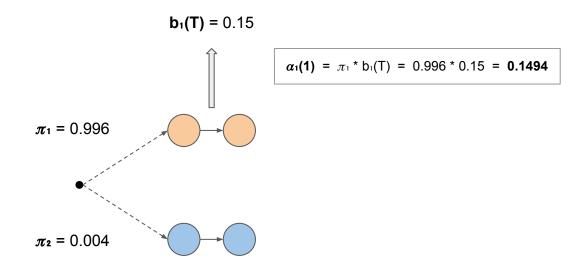
α\*t(i): Ctαt(i) (scaled probability)

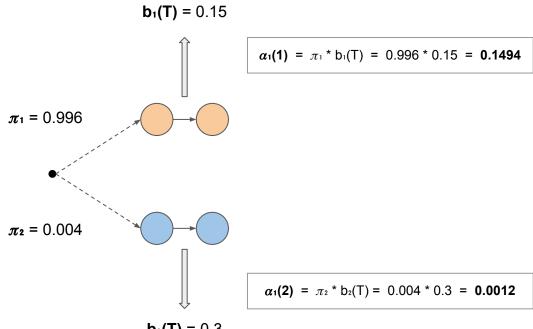




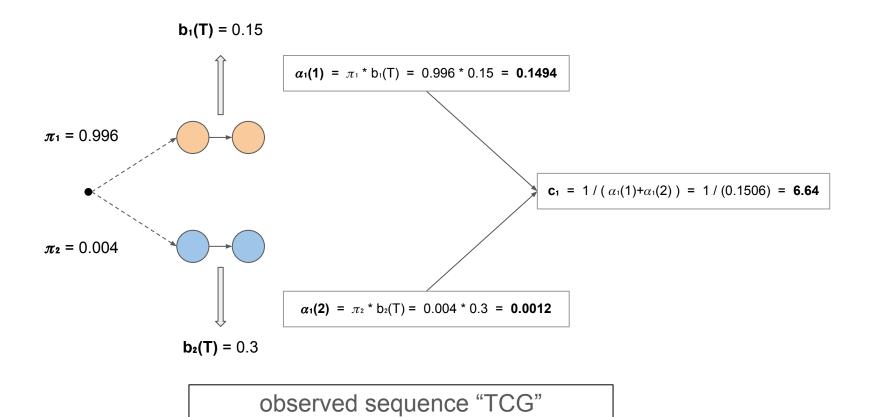
Notation discrepancies with the tutorial:

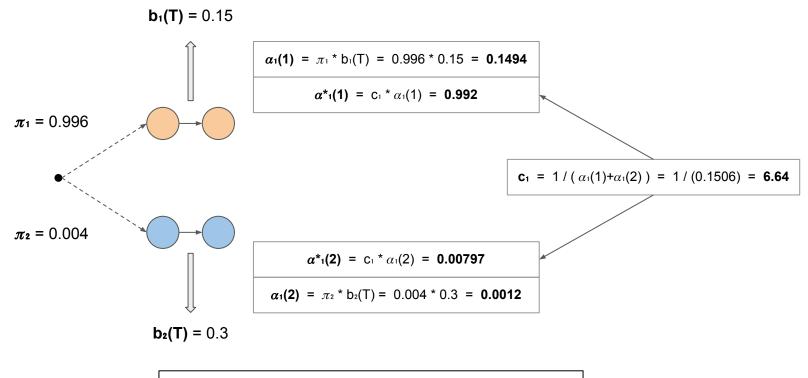
$$\hat{a}_{t}(i) = \alpha^{*}_{t}(i) \leftarrow \text{no "alpha hat" in slides, so}$$
  
use  $\alpha^{*}$  instead





**b<sub>2</sub>(T) =** 0.3

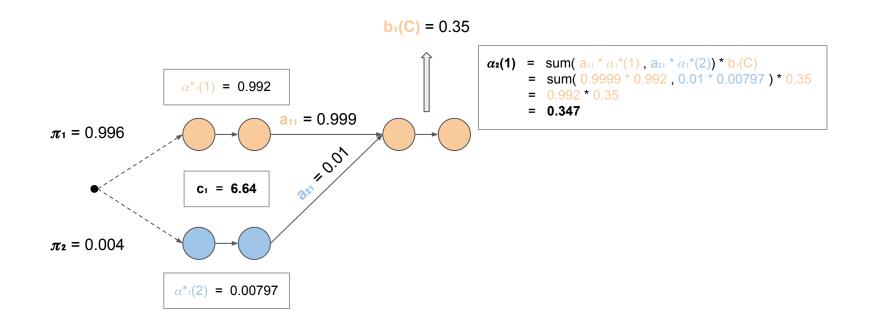


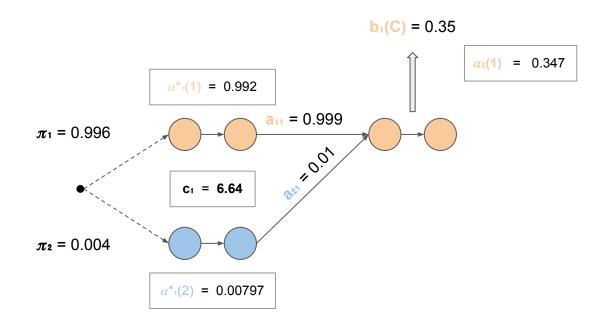


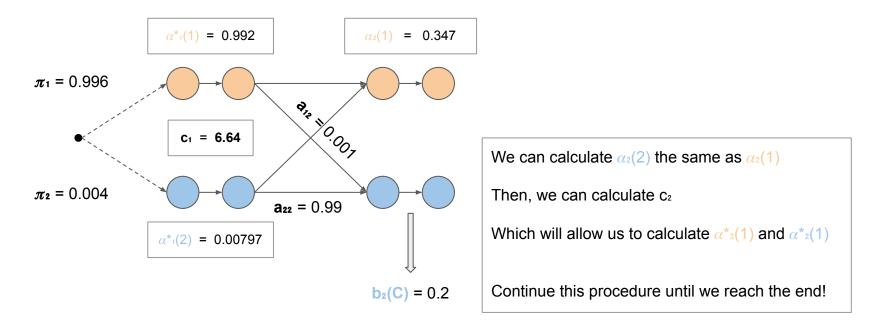
# Past t=1, we have to perform a sum to generate new values for $\alpha_t(i)$ :

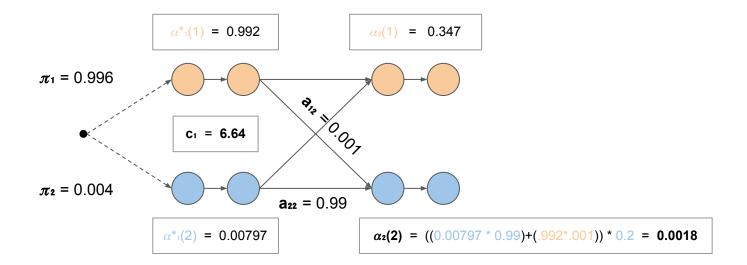
$$\alpha_{t+1}(j) = [\sum_{i} \alpha_{t}(i)^{*}a_{ij}]^{*} b_{j}(N_{+1})$$

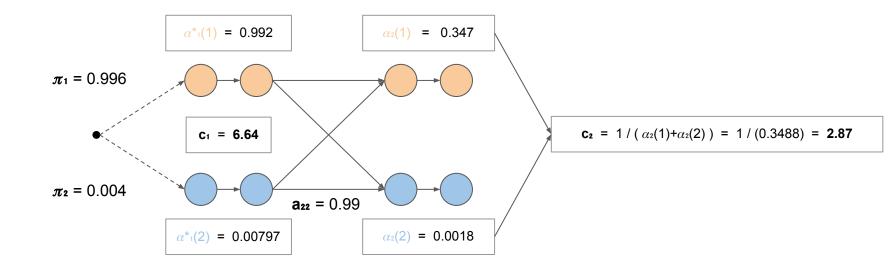
This is the cumulative probability of all paths ending at **state j** at **time t+1** given the set of observed nucleotides

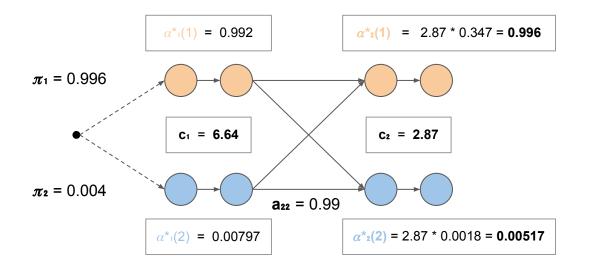




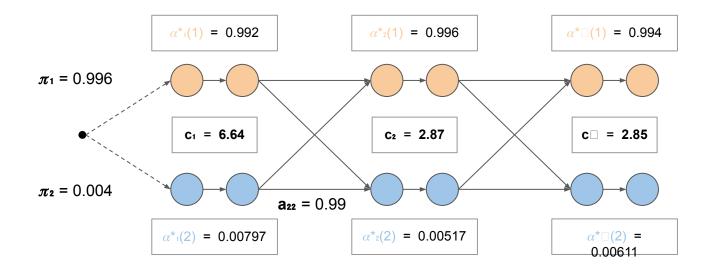








# The forward part: t>1



observed sequence "TCG"

#### The forward part: summary from tutorial

Initialization

$$egin{array}{rcl} \ddot{lpha}_{1}(i) &=& lpha_{1}(i) \ c_{1} &=& rac{1}{\sum_{i=1}^{N} \ddot{lpha}_{1}(i)} \ \hat{lpha}_{1}(i) &=& c_{1} \ddot{lpha}_{1}(i) \end{array}$$

Notation discrepancies with the tutorial:

- $\ddot{a}_t(i) = \alpha_t(i) \quad \leftarrow \text{ redefinition from tutorial (eq10)}$
- â<sub>t</sub>(i) = α<sup>\*</sup>t(i) ← no "alpha hat" in slides, so use α<sup>\*</sup> instead

(10)

(11)

•

#### Induction

$$egin{array}{rcl} \ddot{lpha}_t(i)&=&\sum_{j=1}^N \hat{lpha}_{t-1}(j) a_{ji} b_i(O_t)\ c_t&=&rac{1}{\sum_{i=1}^N \ddot{lpha}_t(i)}\ \hat{lpha}_t(i)&=&c_t \ddot{lpha}_t(i) \end{array}$$

### The forward part: summary from tutorial

also note we can prove that:

$$\hat{\alpha}_t(i) = \left(\prod_{\tau=1}^t c_\tau\right) \alpha_t(i).$$

(12)

Notation discrepancies with the tutorial:

- ä<sub>t</sub>(i) = α<sub>t</sub>(i) ← redefinition from tutorial (eq10)
- â<sub>t</sub>(i) = α<sup>\*</sup>t(i) ← no "alpha hat" in slides, so use α<sup>\*</sup> instead

# The backward part

Similar to the forward part, but slightly different because of the ordering of the edges

Also, we get to reuse our forward-computed **c**<sup>t</sup> values!

Additionally, initial probabilities are  $\pi_1 = \pi_2 = 1$  because from post-emission nodes where **t**=T (the end), the only possible edge is to the end node

# The backward part: more definitions

β(i): the highest probability of the partial
observed sequence (this time, observations
from t=t to t=T) for the post-emission node for
state i at time t (unscaled)

 $\beta^{*}(i)$ : the scaled version of  $\beta_{t}(i)$ 

Defined as: c<sub>t</sub>\*β<sub>t</sub>(i)

Notation discrepancies with the tutorial:

•  $B^{t}(i) = \beta^{t}(i) \leftarrow$  no "beta hat" in slides, so use  $\beta^{t}$  instead

emission at t

post-emission

node

# The backward part: calculating $\beta^* \Box(i)$

- For t = T:
- β<sub>τ</sub>(i) = 1
- $\beta^*_{\tau}(i) = c_{\tau}^*\beta_{\tau}(i) = c_{\tau}$
- For t < T,  $\beta_t(i)$ :
- $\beta_t(i) = \sum (a_{ij})(b_j)(\beta^*_{t+1}(j))$ •  $\beta^*_t(i) = c_t^*\beta_t(i)$

Initialization

$$\ddot{\beta}_T(i) = 1 \hat{\beta}_T(i) = c_T \ddot{\beta}_T(i)$$
(15)

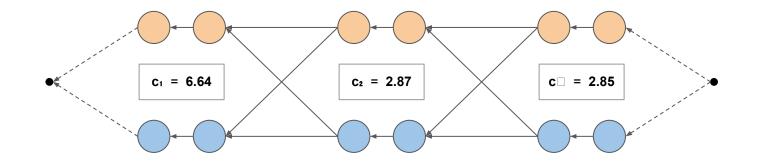
Induction

$$\ddot{\beta}_{t}(i) = \sum_{j=1}^{N} a_{ij} b_{j}(O_{t+1}) \hat{\beta}_{t+1}(j)$$
$$\hat{\beta}_{t}(i) = c_{t} \ddot{\beta}_{t}(i)$$
(16)

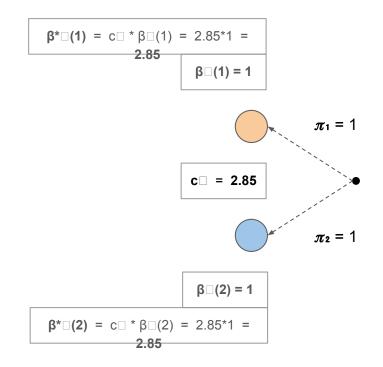
Notation discrepancies with the tutorial:

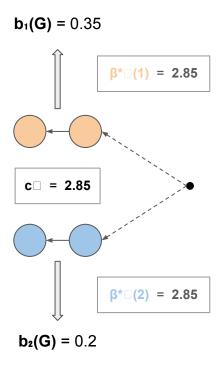
# The backward part

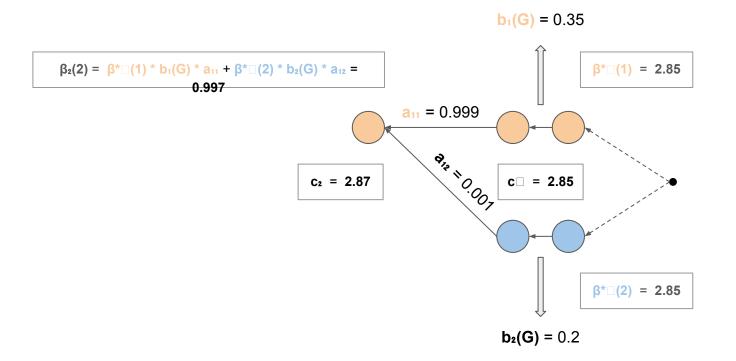
First, reverse the graph:

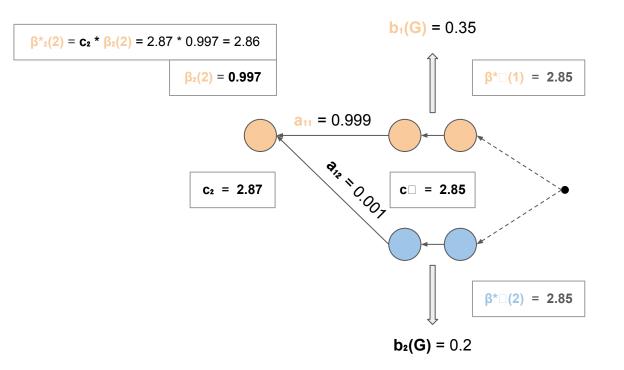


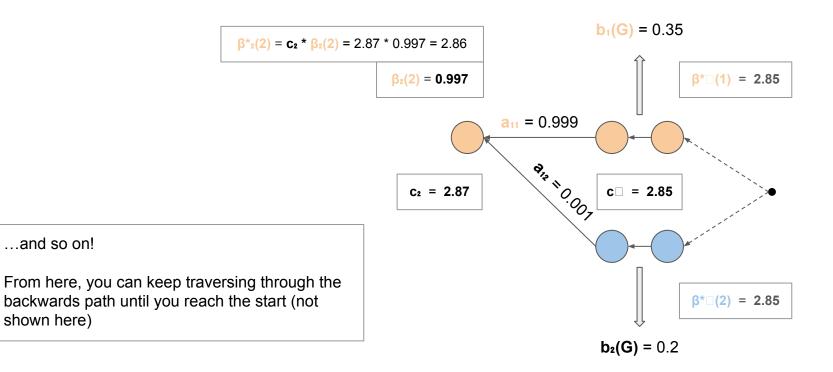
same direction of increasing t  $\rightarrow$ 











#### Homework 8: part 2

### More variable definitions: unscaled

 $P(O \mid \lambda)$ : Total probability of the **observed sequence O** given the **model**  $\lambda$ 

$$P(O|\lambda) = \sum_{i=1}^{N} \alpha_T(i)$$

$$P(O|\lambda) = \sum_{i=1}^{N} \pi_i \beta_1(i) b_i(O_1)$$

#### More variable definitions: unscaled

 $\gamma_t(i)$ : the probability of being in state i at time t given the observed sequence O and the model  $\lambda$ 

$$\gamma_t(i) = P(q_t = S_i | O, \lambda) = \frac{\alpha_t(i)\beta_t(i)}{P(O|\lambda)}$$
(6)

Somewhat intuitively, summing this term over all **t** is the expected number of times we are ever in **state i** 

### More variable definitions: unscaled

ξ<sub>t</sub>(i, j): the probability of being in state i at time t and state j at time t+1 given the observed sequence O and the model λ

$$\xi_t(i,j) = P(q_t = S_i, q_{t+1} = S_j | O, \lambda) = \frac{\alpha_t(i)a_{ij}b_j(O_{t+1})\beta_{t+1}(j)}{P(O|\lambda)}$$
(7)

Summing this term over all **t** (except T) is the expected number of times we transition from **state i** to **state j** 

#### Baum-Welch parameter updates: unscaled

To calculate new parameters, you simply follow:

$$\bar{\pi}_{i} = \gamma_{1}(i);$$
  
$$\bar{a}_{ij} = \sum_{t=1}^{T-1} \xi_{t}(i,j) / \sum_{t=1}^{T-1} \gamma_{t}(i);$$
  
$$\bar{b}_{j}(k) = \sum_{t=1,O_{t}=v_{k}}^{T} \gamma_{t}(j) / \sum_{t=1}^{T} \gamma_{t}(j)$$

You can just keep alternating between this and the forward/backward calculations until the parameters converge!

The equations on the following slides basically just plug in the definitions we've seen for forward and backward variables, allowing us to use our newly computed scaled variables for the parameter update step

### Baum-Welch **SCALED**

Log likelihood:

$$\log[P(O|\lambda)] = -\sum_{t=1}^{T} \log c_t.$$

 $\overline{a}_{ij}$ 

Parameter updates:

$$\pi_i'=rac{\hatlpha_1(i)\hateta_1(i)}{\sum_j \hatlpha_1(j)\hateta_1(j)}$$

$$\bar{b}_{j}(k) = \frac{\sum_{t=1,O_{t}=v_{k}}^{T} \gamma_{t}(j)}{\sum_{t=1}^{T} \gamma_{t}(j)} \\ = \frac{\sum_{t=1,O_{t}=v_{k}}^{T} \hat{\alpha}_{t}(j) \cdot \hat{\beta}_{t}(j)/c_{t}}{\sum_{t=1}^{T} \hat{\alpha}_{t}(j) \cdot \hat{\beta}_{t}(j)/c_{t}}.$$

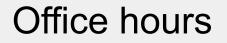
$$= \frac{\sum_{t=1}^{T-1} \xi_t(i,j)}{\sum_{t=1}^{T-1} \gamma_t(i)}$$

$$= \frac{\sum_{t=1}^{T-1} \alpha_t(i) a_{ij} b_j(O_{t+1}) \beta_{t+1}(j)}{\sum_{t=1}^{T-1} \alpha_t(i) \beta_t(i)}$$

$$= \frac{\sum_{t=1}^{T-1} \hat{\alpha}_t(i) / \mathbf{C}_t \cdot a_{ij} b_j(O_{t+1}) \cdot \hat{\beta}_{t+1}(j) / \mathbf{D}_{t+1}}{\sum_{t=1}^{T-1} \hat{\alpha}_t(i) / \mathbf{C}_t \cdot \hat{\beta}_t(i) / \mathbf{D}_t}$$

$$= \frac{\left(\sum_{t=1}^{T-1} \hat{\alpha}_t(i) \cdot a_{ij} b_j(O_{t+1}) \cdot \hat{\beta}_{t+1}(j)\right) / \mathbf{C}_T}{\left(\sum_{t=1}^{T-1} \hat{\alpha}_t(i) \cdot \hat{\beta}_t(i) / c_t\right) / \mathbf{C}_T}$$

$$= \frac{\sum_{t=1}^{T-1} \hat{\alpha}_t(i) \cdot a_{ij} b_j(O_{t+1}) \cdot \hat{\beta}_{t+1}(j)}{\sum_{t=1}^{T-1} \hat{\alpha}_t(i) \cdot \hat{\beta}_t(i) / c_t}.$$



Reminder:

Homework 8 is due Sunday, March 9th at 11:59pm!

Also remember:

Don't round decimal values until the very end! This will affect all your calculations, especially here when dealing with a lot of decimal products