# Hidden Markov Models 

Slides by Carl Kingsford

Based on Chapter II of Jones \& Pevzner, An Introduction to Bioinformatics Algorithms

## Eukaryotic Genes \& Exon Splicing

Prokaryotic (bacterial) genes look like this:

Eukaryotic genes usually look like this:


This spliced RNA is what is translated into a protein.

## Checking a Casino



Fair coin:
$\operatorname{Pr}($ Heads $)=0.5$


Biased coin: $\operatorname{Pr}($ Heads $)=0.75$

Suppose either a fair or biased coin was used to generate a sequence of heads \& tails. But we don't know which type of coin was actual used.

Heads/Zals: $\uparrow \uparrow \downarrow \downarrow \downarrow \downarrow \uparrow \uparrow \uparrow \uparrow \downarrow \uparrow \downarrow \uparrow \downarrow \uparrow \downarrow \uparrow$

## Checking a Casino



HeadssTails: $\uparrow \uparrow \downarrow \downarrow \downarrow \downarrow \uparrow \uparrow \uparrow \uparrow \downarrow \uparrow \downarrow \uparrow \downarrow \uparrow \downarrow \uparrow$

## Checking a Casino



How could we guess which coin was more likely?

## Compute the Probability of the <br> Observed Sequence

Fair coin: $\operatorname{Pr}($ Heads $)=0.5$
Biased coin: $\operatorname{Pr}($ Heads $)=0.75$
$x=\uparrow \uparrow \downarrow \downarrow \downarrow \downarrow \downarrow$
$\operatorname{Pr}(x \mid$ Fair $)=\begin{array}{lllllll}0.5 & 0.5 & 0.5 & 0.5 & 0.5 & 0.5 & 0.5\end{array}$
$\operatorname{Pr}(\mathrm{x} \mid$ Biased $)=0.750 .75 \quad 0.25 \quad 0.25 \quad 0.25 \quad 0.25 \quad 0.75$

## Compute the Probability of the Observed Sequence

Fair coin: $\operatorname{Pr}($ Heads $)=0.5$
Biased coin: $\operatorname{Pr}($ Heads $)=0.75$

$$
x=\uparrow \quad \uparrow \quad \downarrow \quad \downarrow \quad \downarrow \quad \downarrow \quad \uparrow
$$

$$
\operatorname{Pr}(x \mid \text { Fair })=0.5 \times 0.5 \times 0.5 \times 0.5 \times 0.5 \times 0.5 \times 0.5 \quad=0.5=0.0078125
$$

$$
\operatorname{Pr}(x \mid \text { Biased })=0.75 \times 0.75 \times 0.25 \times 0.25 \times 0.25 \times 0.25 \times 0.75=0.001647949
$$

## Compute the Probability of the Observed Sequence

Fair coin: $\operatorname{Pr}($ Heads $)=0.5$
Biased coin: $\operatorname{Pr}($ Heads $)=0.75$
$\operatorname{Pr}(\times \mid$ Fair $)=0.5 \times 0.5 \times 0.5 \times 0.5 \times 0.5 \times 0.5 \times 0.5=0.5^{7}=0.0078125$
$\operatorname{Pr}(\times \mid$ Biased $)=0.75 \times 0.75 \times 0.25 \times 0.25 \times 0.25 \times 0.25 \times 0.75=0.001647949$

The log-odds score:

$$
\log _{2} \frac{\operatorname{Pr}(x \mid \text { Fair })}{\operatorname{Pr}(x \mid \text { Biased })}=\log _{2} \frac{0.0078}{0.0016}=2.245 \longleftarrow>0 . \text { Hence "Fair" is a }
$$

## What if the casino switches coins?

> | Fair coin: $\operatorname{Pr}($ Heads $)=0.5$ |
| :--- |
| Biased coin: $\operatorname{Pr}($ Heads $)=0.75$ |
| Probability of switching coins $=0.1$ |



## What if the casino switches coins?

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How can we compute the probability of the entire sequence?

## What if the casino switches coins?

$$
\begin{aligned}
& \text { Fair coin: } \operatorname{Pr}(\text { Heads })=0.5 \\
& \text { Biased coin: } \operatorname{Pr}(\text { Heads })=0.75 \\
& \text { Probability of switching coins }=0.1 \\
& \hline
\end{aligned}
$$



How can we compute the probability of the entire sequence?

How could we guess which coin was more likely at each position?

## What does this have to do with biology?

atg gat ggg agc aga tca gat cag atc agg gac gat aga cga tag tga

## What does this have to do with

Before:

## biology?

How likely is it that this sequence was generated by a fair coin? Which parts were generated by a biased coin?
atg gat ggg agc aga tca gat cag atc agg gac gat aga cga tag tga

## What does this have to do with

Before:

## biology?

How likely is it that this sequence was generated by a fair coin? Which parts were generated by a biased coin?

Now:
How likely is it that this is a gene?
Which parts are the start, middle and end?
atg gat ggg agc aga tca gat cag atc agg gac gat aga cga tag tga

## What does this have to do with

Before:

## biology?

How likely is it that this sequence was generated by a fair coin? Which parts were generated by a biased coin?

Now:
How likely is it that this is a gene?
Which parts are the start, middle and end?


## Hidden Markov Model (HMM)

Fair coin: $\operatorname{Pr}($ Heads $)=0.5$<br>Biased coin: $\operatorname{Pr}($ Heads $)=0.75$<br>Probability of switching coins $=0.1$



Fair

| 0.5 | 0.5 |
| :---: | :---: |
| H | T |


| Biased | 0.75 | 0.25 |
| :---: | :---: | :---: |
| H T |  |  |

## Formal Definition of a HMM

$\Sigma=$ alphabet of symbols.
$\mathrm{Q}=$ set of states.
$\mathrm{A}=\mathrm{an}|\mathrm{Q}| \times|\mathrm{Q}|$ matrix where entry $(\mathrm{k}, \mathrm{l})$ is the probability of moving from state k to state l .
$\mathrm{E}=\mathrm{a}|\mathrm{Q}| \times|\Sigma|$ matrix, where entry $(\mathrm{k}, \mathrm{b})$ is the probability of emitting b when in state $k$.



## Constraints on $A$ and $E$



## Sum of the \# in each row must be I.

## Computing Probabilities Given Path


$x=\downarrow \uparrow \downarrow \uparrow \uparrow \uparrow \downarrow$
$\pi=\quad F \quad F \quad F \quad B \quad B \quad B \quad B \quad F \quad F \quad F$
$\operatorname{Pr}\left(\mathrm{x}_{\mathrm{i}} \mid \Pi_{\mathrm{i}}\right)=\begin{array}{llllllllll}0.5 & 0.5 & 0.5 & 0.75 & 0.75 & 0.75 & 0.25 & 0.5 & 0.5 & 0.5\end{array}$
$\operatorname{Pr}\left(\Pi_{\mathrm{i}} \rightarrow \pi_{i+1}\right)=0.1 \quad 0.9 \quad 0.9 \quad 0.1 \quad 0.9 \quad 0.9 \quad 0.9 \quad 0.1 \quad 0.1 \quad 0.1$

## The Decoding Problem

Given $x$ and $\pi$, we can compute:

- $\operatorname{Pr}(x \mid \pi)$ : product of $\operatorname{Pr}\left(\mathbf{x}_{\mathbf{i}} \mid \pi_{\mathbf{i}}\right)$
- $\operatorname{Pr}(\pi)$ : product of $\operatorname{Pr}\left(\pi_{i} \rightarrow \pi_{i+1}\right)$
- $\operatorname{Pr}(\mathbf{x}, \pi)$ : product of all the $\operatorname{Pr}\left(\mathrm{x}_{\mathrm{i}} \mid \pi_{\mathrm{i}}\right)$ and $\operatorname{Pr}\left(\pi_{\mathrm{i}} \rightarrow \pi_{\mathrm{i}+1}\right)$

$$
\operatorname{Pr}(x, \pi)=\operatorname{Pr}\left(\pi_{0} \rightarrow \pi_{1}\right) \prod_{i=1}^{n} \operatorname{Pr}\left(x_{i} \mid \pi_{i}\right) \operatorname{Pr}\left(\pi_{i} \rightarrow \pi_{i+1}\right)
$$

But they are "hidden" Markov models because $\pi$ is unknown.
Decoding Problem: Given a sequence $x_{1} x_{2} x_{3} \ldots x_{n}$ generated by an HMM $(\Sigma, Q, A, E)$, find a path $\pi$ that maximizes $\operatorname{Pr}(x, \pi)$.

## The Viterbi Algorithm to Find Best Path

$\mathrm{A}[\mathrm{a}, \mathrm{k}]:=$ the probability of the best path for $\mathrm{x}_{\mathrm{I}} . . . \mathrm{x}_{\mathrm{k}}$ that ends at state a .

$A[a, k]=$ the path for $x_{\mid \ldots} . . x_{k-1}$ that goes to some state $b$ times cost of $a$ transition from b to i , and then to output $\mathrm{x}_{\mathrm{k}}$ from state a .


## Viterbi DP Recurrence

Q


Base case:

$$
A[a, 1]=\underbrace{\operatorname{Pr}\left(\pi_{1}=a\right)}_{\begin{array}{c}
\text { Probability } \\
\text { that the first } \\
\text { state is } a
\end{array}} \times \underbrace{\operatorname{Pr}\left(x_{1} \mid \pi_{1}=a\right)}_{\begin{array}{c}
\text { Probability of } \\
\text { emitting } x_{1} \\
\text { given the first } \\
\text { state is } a .
\end{array}}
$$

Which Cells Do We Depend On?


## Order to Fill in the Matrix:



## Where's the answer?



## Graph View of Viterbi



## Running Time

- \# of subproblems $=O(n|Q|)$, where n is the length of the sequence.
- Time to solve a subproblem $=\mathrm{O}(|\mathrm{Q}|)$
- Total running time: $\mathrm{O}\left(\mathrm{n}|\mathrm{Q}|^{2}\right)$


## Using Logs

Typically, we take the log of the probabilities to avoid multiplying a lot of terms:

$$
\begin{aligned}
\log (A[a, k]) & =\max _{b \in Q}\left\{\log \left(A[b, k-1] \times \operatorname{Pr}(b \rightarrow a) \times \operatorname{Pr}\left(x_{k} \mid \pi_{k}=a\right)\right)\right\} \\
& =\max _{b \in Q}\left\{\log (A[b, k-1])+\log (\operatorname{Pr}(b \rightarrow a))+\log \left(\operatorname{Pr}\left(x_{k} \mid \pi_{k}=a\right)\right)\right\}
\end{aligned}
$$

Remember: $\log (a b)=\log (a)+\log (b)$

Why do we want to avoid multiplying lots of terms?

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\end{aligned}
$$

Remember: $\log (a b)=\log (a)+\log (b)$

Why do we want to avoid multiplying lots of terms?
Multiplying leads to very small numbers:

$$
0.1 \times 0.1 \times 0.1 \times 0.1 \times 0.1=0.00001
$$

This can lead to underflow.
Taking logs and adding keeps numbers bigger.

## Estimating HMM Parameters

$$
\begin{gathered}
\left.\left(\mathbf{x}^{(1)}, \boldsymbol{\Pi}^{(1)}\right)=\begin{array}{c}
x_{1}^{(1)} x_{2}^{(1)} x_{3}^{(1)} x_{4}^{(1)} x_{5}^{(1)} \ldots x_{n}^{(1)} \\
\pi_{1}^{(1)} \pi_{2}^{(1)} \pi_{3}^{(1)} \pi_{4}^{(1)} \pi_{5}^{(1)} \ldots \pi_{n}^{(1)} \\
\left(\mathbf{x}^{(2)}, \boldsymbol{\pi}^{(2)}\right)= \\
x_{1}^{(2)} x_{2}^{(2)} x_{3}^{(2)} x_{4}^{(2)} x_{5}^{(2)} \ldots x_{n}^{(2)} \\
\pi_{1}^{(2)} \pi_{2}^{(2)} \pi_{3}^{(2)} \pi_{4}^{(2)} \pi_{5}^{(2)} \ldots \pi_{n}^{(2)}
\end{array}\right\} \begin{array}{l}
\text { Training examples } \\
\text { where outputs and } \\
\text { paths are known. }
\end{array}
\end{gathered}
$$

$$
\begin{gathered}
\begin{array}{c}
\# \text { of times transition } \\
a \rightarrow b \text { is observed. }
\end{array} \\
\operatorname{Pr}(a \rightarrow b)=\frac{A_{a b}}{\sum_{q \in Q} A_{a q}}
\end{gathered}
$$

\# of times $x$ was observed to be output from state $a$.
$\operatorname{Pr}(x \mid a)=\frac{\stackrel{\downarrow}{E_{x a}}}{\sum_{x \in \Sigma} E_{x q}}$

$$
\begin{array}{cc}
\text { Pseudocounts } \\
\operatorname{Pr}(a \rightarrow b \text { of times transition } \\
a \rightarrow b \text { is observed. }
\end{array} \sum_{\substack{\# \text { of times } x \text { was } \\
\text { observed to be } \\
\text { output from state }}}^{\sum_{a b} A_{a q}} \quad \operatorname{Pr}(x \mid a)=\frac{E_{x a}^{\downarrow}}{\sum_{x \in \Sigma} E_{x q}}
$$

What if a transition or emission is never observed in the training data?
$\Rightarrow 0$ probability

Meaning that if we observe an example with that transition or emission in the real world, we will give it 0 probability.

But it's unlikely that our training set will be large enough to observe every possible transition.

Hence: we take $\mathrm{A}_{\mathrm{ab}}=$ (\#times $\mathrm{a} \rightarrow \mathrm{b}$ was observed) $+\mathrm{I} \longleftarrow$ "pseudocount" Similarly for $\mathrm{E}_{\mathrm{xa}}$.

## Viterbi Training

- Problem: typically, in the real would we only have examples of the output $x$, and we don't know the paths $\pi$.


## Viterbi Training Algorithm:

I. Choose a random set of parameters.
2. Repeat:
I. Find the best paths.
2. Use those paths to estimate new parameters.

This is an local search algorithm.
It's also an example of a "Gibbs sampling" style algorithm.
The Baum-Welch algorithm is similar, but doesn't commit to a single best path for each example.

## Some probabilities in which we are interested

What is the probability of observing a string $x$ under the assumed HMM?

$$
\operatorname{Pr}(x)=\sum_{\pi} \operatorname{Pr}(x, \pi)
$$

What is the probability of observing $x$ using a path where the $\mathrm{i}^{\text {th }}$ state is $a$ ?

$$
\operatorname{Pr}\left(x, \pi_{i}=a\right)=\sum_{\pi: \pi_{i}=a} \operatorname{Pr}(x, \pi)
$$

What is the probability that the $\mathrm{i}^{\text {th }}$ state is $a$ ?

$$
\operatorname{Pr}\left(\pi_{i}=a \mid x\right)=\frac{\operatorname{Pr}\left(x, \pi_{i}=a\right)}{\operatorname{Pr}(x)}
$$

## The Forward Algorithm

How do we compute this:

$$
\operatorname{Pr}\left(x, \pi_{k}=a\right)=\operatorname{Pr}\left(x_{1}, \ldots, x_{i}, \pi_{i}=a\right) \operatorname{Pr}\left(x_{i+1}, \ldots, x_{n} \mid \pi_{i}=a\right)
$$

Recall the recurrence to compute best path for $\mathrm{x}_{\mathrm{l}} \ldots \mathrm{x}_{\mathrm{k}}$ that ends at state a :

$$
A[a, k]=\max _{b \in Q}\left\{A[b, k-1] \times \operatorname{Pr}(b \rightarrow a) \times \operatorname{Pr}\left(x_{k} \mid \pi_{k}=a\right)\right\}
$$

We can compute the probability of emitting $\mathrm{x}_{\mathrm{l}}, \ldots, \mathrm{x}_{\mathrm{k}}$ using some path that ends in $a$ :

$$
F[a, k]=\sum_{b \in Q} F[b, k-1] \times \operatorname{Pr}(b \rightarrow a) \times \operatorname{Pr}\left(x_{k} \mid \pi_{k}=a\right)
$$

## The Forward Algorithm

How do we compute this:

$$
\operatorname{Pr}\left(x, \pi_{k}=a\right)=\operatorname{Pr}\left(x_{1}, \ldots, x_{i}, \pi_{i}=a\right) \operatorname{Pr}\left(x_{i+1}, \ldots, x_{n} \mid \pi_{i}=a\right)
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$$

We can comput the probability of emitting $x_{l}, \ldots, x_{k}$ using some path that ends in $a$ :

$$
F[a, k]=\sum_{b \in Q} \operatorname{H}[b, k-1] \times \operatorname{Pr}(b \rightarrow a) \times \operatorname{Pr}\left(x_{k} \mid \pi_{k}=a\right)
$$

## The Forward Algorithm

Computes the total probability of all the paths of length $k$ ending in state $a$.

$\mathrm{F}[\mathrm{a}, 4]$

## The Forward Algorithm

Computes the total probability of all the paths of length $k$ ending in state $a$.

Still need to compute the probability of paths leaving $a$ and going to the end.

$\mathrm{F}[\mathrm{a}, 4]$

## The Backward Algorithm

The same idea as the forward algorithm, we just start from the end of the input string and work towards the beginning:
$B[a, k]=$ "the probability of generating string $x_{k+1}, \ldots, x_{n}$ starting from state $b$ "

$$
B[a, k]=\sum_{b \in Q} \underbrace{B[b, k+1]}_{\begin{array}{c}
\text { Prob for } \\
x_{k+1} . . x_{n} \\
\text { starting in } \\
\text { state } b
\end{array}} \times \underbrace{\operatorname{Pr}(a \rightarrow b)}_{\begin{array}{c}
\text { Probability } \\
\text { going from } \\
\text { state } a \text { to } b
\end{array}} \times \underbrace{\operatorname{Pr}\left(x_{k+1} \mid \pi_{k+1}=b\right)}_{\begin{array}{c}
\text { Probability of emitting } \\
x_{k+1} \text { given that the next } \\
\text { state is } b .
\end{array}}
$$

## The Forward-Backward Algorithm

$$
\operatorname{Pr}\left(\pi_{i}=a \mid x\right)=\frac{\operatorname{Pr}\left(x, \pi_{i}=k\right)}{\operatorname{Pr}(x)}=\frac{F[a, i] \cdot B[a, i]}{\operatorname{Pr}(x)}
$$

F[a,i]
$B[a, i]$


## Recap

- Hidden Markov Model (HMM) model the generation of strings.
- They are governed by a string alphabet $(\Sigma)$, a set of states $(\mathrm{Q})$, a set of transition probabilities A , and a set of emission probabilities for each state (E).
- Given a string and an HMM, we can compute:

The most probable path the HMM took to generate the string (Viterbi).
The probability that the HMM was in a particular state at a given step (forwardbackward algorithm).

- Algorithms are based on dynamic programming.
- Finding good parameters is a much harder problem.

The Baum-Welch algorithm is an oft-used heuristic algorithm.

