CSE 549: Hidden Markov Models (in prep for ab initio gene finding)



All slides marked * are courtesy of Carl Kingsford

A Basic Probability Refresher

 Ω — The sample space (set of all possible outcomes)

e.g. all possible values for a roll of a die {1,2,3,4,5,6}, need not be finite

E — An event; a subset of the sample space

e.g. all even rolls of a die {2,4,6}

X — Random variable; measurable function from $\Omega \rightarrow E$

e.g. X = value on the upward face of the die

Pr(E) — Probability of the event E

e.g. Pr(X is even) = Pr(X ∈ {2,4,6}) = |{2,4,6}| / |{1,2,3,4,5,6}| = 0.5

In a discrete, finite, sample space, if all outcomes are equally likely, one can think of this as $|E| / |\Omega|$

Probabilities

Joint Probability



Probabilities



Probabilities

Conditional Probability



Independence

Independent Events

 $X \perp Y \iff Pr(X,Y) = Pr(X) Pr(Y)$

Conditionally Independent Events

 $X \perp Y \mid Z \Leftrightarrow Pr(X,Y \mid Z) = Pr(X \mid Z) Pr(Y \mid Z)$

Checking a Casino



How could we guess which coin was more likely?

Compute the Probability of the Observed Sequence

> Fair coin: Pr(Heads) = 0.5 Biased coin: Pr(Heads) = 0.75

 $X = \uparrow \qquad \uparrow \qquad \downarrow \qquad \downarrow \qquad \downarrow \qquad \uparrow \qquad \uparrow$

 $Pr(x | Fair) = 0.5 \times 0.5 = 0.5^7 = 0.0078125$

 $Pr(x \mid Biased) = 0.75 \times 0.75 \times 0.25 \times 0.25 \times 0.25 \times 0.25 \times 0.75 = 0.001647949$

The log-odds score:

$$\log_2 \frac{\Pr(x \mid Fair)}{\Pr(x \mid Biased)} = \log_2 \frac{0.0078}{0.0016} = 2.245 \quad \longleftarrow \quad > 0. \text{ Hence "Fair" is a better guess.}$$

(1st order) Markov Chain

What if the coin tosses weren't independent?

e.g. coin tended to have "runs" of the same value.

Discrete, random process where the *next state depends* only on the current state.

Markov Chain describing a "hot" coin



Total transition probability at each state is unity

(1st order) Markov Chain

What if the coin tosses weren't independent?

e.g. coin tended to have "runs" of the same value.

Discrete, random process where the *next state depends only on the current state*.

Factorization Always True

Factorization True if process is Markovian

 $Pr(x_1, x_2, ..., x_n) = Pr(x_n | x_{n-1}) Pr(x_{n-1} | x_{n-2}) ... Pr(x_2 | x_1) Pr(x_1)$



(1st order) Markov Chain

Markov Chain describing a "hot" coin



Can define the joint probability for a sequence of observations:

$$Pr(\mathbf{x}) = Pr(x_1, x_2, ..., x_n) = Pr(x_1) \prod_{t=2}^{n} Pr(x_t | x_{t-1})$$

e.g. above, if we were equally likely to start at H or T

 $Pr(\mathbf{x}) = 0.5 \times 0.2 \times 0.8 \times 0.8 \times 0.8 \times 0.2 \times 0.8 \times 0.8 \times 0.8 \times 0.2 \times 0.8 \times 0.2 \times 0.8 \times 0.2 \times 0.8 \times$

Markov Chain Detour

Mark V Shaney Developed by Bruce Ellis & Rob Pike in the 1980s

>From mvs Fri Nov 16 17:11 EST 1984 remote from alice

It looks like Reagan is going to say? Ummm... Oh yes, I was looking for. I'm so glad I remembered it. Yeah, what I have wondered if I had committed a crime. Don't eat with your assessment of Reagon and Mondale. Up your nose with a guy from a firm that specifically researches the teen-age market. As a friend of mine would say, "It really doesn't matter"... It looks like Reagan is holding back the arms of the American eating public have changed dramatically, and it got pretty boring after about 300 games.

People, having a much larger number of varieties, and are very different from what one can find in Chinatowns across the country (things like pork buns, steamed dumplings, etc.) They can be cheap, being sold for around 30 to 75 cents apiece (depending on size), are generally not greasy, can be adequately explained by stupidity. Singles have felt insecure since we came down from the Conservative world at large. But Chuqui is the way it happened and the prices are VERY reasonable.

Can anyone think of myself as a third sex. Yes, I am expected to have. People often get used to me knowing these things and then a cover is placed over all of them. Along the side of the \$\$ are spent by (or at least for) the girls. You can't settle the issue. It seems I've forgotten what it is, but I don't. I know about violence against women, and I really doubt they will ever join together into a large number of jokes. It showed Adam, just after being created. He has a modem and an autodial routine. He calls my number 1440 times a day. So I will conclude by saying that I can well understand that she might soon have the time, it makes sense, again, to get the gist of my argument, I was in that (though it's a Republican administration).

--Mark

- "I spent an interesting evening recently with a grain of salt."
- "I hope that there are sour apples in every bushel."

One appealing property of Markov Chains is that they are **generative** models

Walk the model and take transitions proportional to their probabilities — you get a stochastic output that is consistent with your model!

Back to the casino: What if the casino can switch coins?



Looks like a Markov chain, but different. The "state" (i.e. "fair" or "biased") is not observed. **However**, we do observe output that depends, probabilistically, on the states (e.g. heads or tails). This is a **Hidden Markov Model** (HMM).

Typically, we're interested in questions involving these hidden states

Fair coin: Pr(Heads) = 0.5 Biased coin: Pr(Heads) = 0.75 Probability of switching coins = 0.1



How can we compute the probability of the entire sequence?

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

How can we compute the probability of the entire sequence?

Fair coin: Pr(Heads) = 0.5 Biased coin: Pr(Heads) = 0.75 Probability of switching coins = 0.1



If we knew the set of hidden states, computing this would be easy!

How can we compute the probability of the entire sequence?



How can we compute the probability of the entire sequence?









But, remember, we don't observe π in practice

How can we compute the probability of the entire sequence?



What does this have to do with biology?

Before:

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?





Prokaryotic (bacterial) genes look like this:

Eukaryotic genes usually look like this:

ATG



TAG

Eukaryotic Genes & Exon Splicing

Given this

Recover this



Under what sequence of "states" (exon, intron, start codon etc.) is the observed sequence of nucleotides maximized?

Hidden Markov Model (Think of this picture)



 $p = \{p_1, p_2, ..., p_n\}$ is a sequence of *states* (AKA a *path*). Each p_i takes a value from set Q. We **do not** observe p.

 $x = \{x_1, x_2, ..., x_n\}$ is a sequence of *emissions*. Each x_i takes a value from set Σ . We **do** observe x.

Hidden Markov Model



Like for Markov chains, edges capture conditional independence:

 X_2 is conditionally independent of everything else given p_2

 p_4 is conditionally independent of everything else given p_3

Probability of being in a particular state at step *i* is known once we know what state we were in at step *i*-1. Probability of seeing a particular emission at step *i* is known once we know what state we were in at step *i*.

Formal Definition of a HMM

- Σ = alphabet of symbols.
- Q = set of states.

A = an $|Q| \times |Q|$ matrix where entry (k,l) is the probability of moving from state k to state l.

 $E = a |Q| \times |\Sigma|$ matrix, where entry (k,b) is the probability of emitting b when in state k.



Constraints on A and E



Sum of the # in each row must be 1.

The Decoding Problem

Given x and π , we can compute:

- $Pr(x \mid \pi)$: product of $Pr(x_i \mid \pi_i)$
- $Pr(\pi)$: product of $Pr(\pi_i \rightarrow \pi_{i+1})$
- $Pr(x, \pi)$: product of all the $Pr(x_i \mid \pi_i)$ and $Pr(\pi_i \rightarrow \pi_{i+1})$

$$\Pr(x,\pi) = \Pr(\pi_0 \to \pi_1) \prod_{i=1}^n \Pr(x_i \mid \pi_i) \Pr(\pi_i \to \pi_{i+1})$$

But they are "hidden" Markov models because π is unknown.

Decoding Problem: Given a sequence $x_{1,x_{2,x_{3,...,x_n}}$ generated by an HMM (\sum , Q, A, E), find a path π that maximizes Pr(x, π).

The Viterbi Algorithm to Find Best Path

A[a, k] := the probability of the **best** path for $x_1...x_k$ that ends at state a.



A[a, k] = the probability of the best path for $x_1...x_{k-1}$ that goes to some state *b* times probability of a transition from b to a, and then the probability to output x_k from state a.





Which Cells Do We Depend On?



*

Order to Fill in the Matrix:



Where's the answer?



Trellis Graph



The trellis graph "unfolds" the states of the HMM over (discrete) time.

Trellis Graph



Finding the maximum probability path through the trellis graph can be accomplished efficiently with the Viterbi algorithm — think back to lecture 3

DAG View of Dynamic Programming

The formulation of a DP as traversal of a DAG is a very powerful framework for thinking about and implementing different DPs.

1. topological sort

2. visit each vertex in the topological ordering and do updates

The pseudo-code of the Viterbi algorithm is presented in Algorithm 1.

Al	Algorithm 1 Viterbi Algorithm.				
1:	procedure VITERBI (G, w, s)				
2:	topologically sort the vertices of G				
3:	INITIALIZE (G, s)				
4:	for each vertex v in topological order do				
5:	for each edge $e = (u, v)$ in $BS(v)$ do				
6:	$d(v)\oplus=d(u)\otimes w(e)$				

Semiring	Set	⊕	8	ō	1	intuition/application
Boolean	$\{0, 1\}$	V	\wedge	0	1	logical deduction, recognition
Viterbi	[0, 1]	max	×	0	1	prob. of the best derivation
Inside	$\mathbb{R}^+ \cup \{+\infty\}$	+	×	0	1	prob. of a string
Real	$\mathbb{R} \cup \{+\infty\}$	min	+	$+\infty$	0	shortest-distance
Tropical	$\mathbb{R}^+ \cup \{+\infty\}$	min	+	$+\infty$	0	with non-negative weights
Counting	N	+	×	0	1	number of paths

Table 1: Examples of semirings

Huang, Liang. "Dynamic programming algorithms in semiring and hypergraph frameworks." Qualification Exam Report (2006): 1-19.
Trellis Graph

When we want to compute the prob. of the best path ending here, we already have the prob. of the best path at all predecessors, as well as the conditional prob. of each incoming edge n R R R R S F F **X** =



















































































































In this case, transitions to the end state (emitting no symbol), won't matter





We can "trace back" our path to determine the hidden states taken on when traversing the optimal path.





In this case, the path was simple — implying a biased coin the entire time.





Note that in practice, esp. with long sequences, the absolute prob. of the best path may be **very** small.

Running Time

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

Using Logs

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

$$\log(A[a,k]) = \max_{b \in Q} \{ \log(A[b,k-1] \times \Pr(b \to a) \times \Pr(x_k \mid \pi_k = a)) \}$$
$$= \max \{ \log(A[b,k-1]) + \log(\Pr(b \to a)) + \log(\Pr(x_k \mid \pi_k = a)) \}$$

$$= \max_{b \in Q} \{ \log(A[b, k-1]) + \log(\Pr(b \to a)) + \log(\Pr(x_k \mid \pi_k = a)) \}$$

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

Why do we want to avoid multiplying lots of terms?

Multiplying leads to very small numbers: 0.1 x 0.1 x 0.1 x 0.1 x 0.1 = 0.00001 This can lead to underflow. Taking logs and adding keeps numbers bigger.

Estimating HMM Parameters

$$(\mathbf{x}^{(1)}, \pi^{(1)}) = \begin{cases} x_1^{(1)} x_2^{(1)} x_3^{(1)} x_4^{(1)} x_5^{(1)} \dots x_n^{(1)} \\ \pi_1^{(1)} \pi_2^{(1)} \pi_3^{(1)} \pi_4^{(1)} \pi_5^{(1)} \dots \pi_n^{(1)} \\ \pi_1^{(1)} \pi_2^{(2)} x_3^{(2)} x_4^{(2)} x_5^{(2)} \dots x_n^{(2)} \\ \pi_1^{(2)} \pi_2^{(2)} \pi_3^{(2)} \pi_4^{(2)} \pi_5^{(2)} \dots \pi_n^{(2)} \end{cases} \end{cases}$$

$$Training examples where outputs and paths are known.$$

of times x was observed to be output from state a.

of times transition

$$a \rightarrow b$$
 is observed.
 $Pr(a \rightarrow b) = \frac{A_{ab}}{\sum_{q \in Q} A_{aq}}$

 $\Pr(x \mid a) = \frac{E_{xa}}{\sum_{x' \in \Sigma} E_{x'a}}$
$$\begin{array}{l} \text{Pseudocounts} \\ \text{# of times transition} \\ a \rightarrow b \text{ is observed.} \\ \Pr(a \rightarrow b) = \frac{A_{ab}}{\sum_{q \in Q} A_{aq}} \\ \end{array} \quad \Pr(x \mid a) = \frac{\bigoplus_{\substack{t \in \Sigma E_{xq}}} E_{xq}}{\sum_{x \in \Sigma} E_{xq}} \end{array}$$

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 $A_{ab} = (\#times a \rightarrow b \text{ was observed}) + I \longleftarrow "pseudocount" Similarly for <math>E_{xa}$.

Viterbi Training

• **Problem**: typically, in the real would we only have examples of the output x, and we don't know the paths π.

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 a 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. (basically EM for HMM training)

Some probabilities in which we are interested

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

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

What is the probability of observing x using a path where the ith state is a?

$$\Pr(x, \pi_i = a) = \sum_{\pi:\pi_i = a} \Pr(x, \pi)$$

What is the probability that the ith state is a?

$$\Pr(\pi_i = a | x) = \frac{\Pr(x, \pi_i = a)}{\Pr(x)}$$

How do we compute this:

$$\Pr(x, \pi_k = a) = \Pr(x_1, \dots, x_i, \pi_i = a) \Pr(x_{i+1}, \dots, x_n \mid \pi_i = a)$$

Recall the recurrence to compute **best** path for $x_1...x_k$ that ends at state a:

$$A[a,k] = \max_{b \in Q} \{A[b,k-1] \times \Pr(b \to a) \times \Pr(x_k \mid \pi_k = a)\}$$

We can compute the probability of emitting $x_1, ..., x_k$ using **any** path that ends in *a*:

$$F[a,k] = \sum_{b \in Q} F[b,k-1] \times \Pr(b \to a) \times \Pr(x_k \mid \pi_k = a)$$

The Forward Algorithm

We can compute the probability of emitting $x_1,...,x_k$ using **any** path that ends in *a*:

$$F[a,k] = \sum_{b \in Q} F[b,k-1] \times \Pr(b \to a) \times \Pr(x_k \mid \pi_k = a)$$

The forward algorithm also allows us to solve the "Evaluation Problem".

Evaluation Problem:

Given an HMM $\lambda = (\Sigma, Q, A, E)$ and an observation **x**

Find $Pr(\mathbf{x} \mid \lambda)$ — the prob. of the observations under the model

The Forward Algorithm



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 $x_{k+1},...,x_n$ starting from state b"

$$B[a,k] = \sum_{b \in Q} \underbrace{B[b,k+1]}_{\substack{b \in Q}} \times \underbrace{\Pr(a \to b)}_{\substack{b \in Q}} \times \underbrace{\Pr(x_{k+1} \mid \pi_{k+1} = b)}_{\substack{b \in Q} \times \underbrace{\Pr(x_{k$$

The Forward-Backward Algorithm

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



The Forward-Backward Algorithm





This works because F[a,i] is independent of B[a,i], given that we are in state **a** at time **i** (the Markovian assumption).

Alternative Training (Baum-Welch)

 $\theta = (A, E, \pi)$ Initialize transition, emission and initial state distribution "randomly" Y Training data such that Y_t represents the vector of observations at step t

While not converged:

Run the forward algorithm

Run the backward algorithm

Compute γ , the probability of being in each hidden state at each time:

$$\gamma_{i}(t) = \Pr\left(X_{t} = i \mid Y, \theta\right) = \frac{F\left[i, t\right] \cdot B\left[i, t\right]}{\sum_{j=1}^{|Q|} F\left[j, t\right] \cdot B\left[j, t\right]}$$

Compute ξ , the prob of being in state i at step t, j at t+1 and producing the observed output at t+1

$$\xi_{ij}(t) = \Pr\left(X_t = i, X_{t+1} = j \mid Y, \theta\right) = \frac{F[i, t] \cdot A[i, j] \cdot B[j, t+1] \cdot E[j, y_{t+1}]}{\sum_{i=1}^{|Q|} \sum_{j=1}^{|Q|} F[i, t] \cdot A[i, j] \cdot B[j, t+1] \cdot E[j, y_{t+1}]}$$

update parameters

 $\pi_{i}^{*}=\gamma_{i}\left(1\right)$

$$A^{*}[i,j] = \frac{\sum_{t=1}^{T-1} \xi_{ij}(t)}{\sum_{t=1}^{T-1} \gamma_{i}(t)}$$

Use these updated parameter estimates in the next iteration of the algo.

$$E^{*}[i, v_{k}] = \frac{\sum_{t=1}^{T} 1_{y_{t}=v_{k}} \gamma_{i}(t)}{\sum_{t=1}^{T} \gamma_{i}(t)}$$

notation inspired by: <u>https://en.wikipedia.org/wiki/Baum%E2%80%93Welch_algorithm</u>

Baum-Welch

Tries to find the maximum likelihood parameters given observations

Application of the EM algorithm (which we'll see again in RNA-seq quantification) to training of HMMs

Not guaranteed to find a global maximum

Can overfit the data i.e., possible that $P(Y | \theta^*) > P(Y | \theta^{real})$

However, it is an effective and widely-used algorithm for HMM training. It often works very well in practice (given sufficient, unbiased, training data)

Recap

- Hidden Markov Model (HMM) model the generation of sequences of symbols.
- They are governed by a symbol alphabet (∑), a set of states (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 sequence (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.