CSCE 970 Lecture 2: Markov Chains and Hidden Markov Models

Stephen D. Scott

Introduction

- When classifying sequence data, need to model the influence that one part of the sequence has on other ("downstream") parts
  - E.g. natural language understanding, speech recognition, genomic sequences
- For each class of sequences (e.g. set of related DNA sequences, set of similar phoneme sequences), want to build a probabilistic model
- This Markov model is a sequence generator
  - We classify a new sequence by measuring how likely it is generated by the model

Outline

- Markov chains
- Hidden Markov models (HMMs)
  - Formal definition
  - Finding most probable state path (Viterbi algorithm)
  - Forward and backward algorithms
- Specifying an HMM

An Example from Computational Biology
CpG Islands

- Genomic sequences are one-dimensional series of letters from $\{A,C,G,T\}$, frequently many thousands of letters (bases, nucleotides, residues) long
- The sequence "CG" (written "CpG") tends to appear more frequently in some places than in others
- Such CpG islands are usually 10^2–10^3 letters long
- Questions:
  1. Given a short segment, is it from a CpG island?
  2. Given a long segment, where are its islands?

Modeling CpG Islands

- Model will be a CpG generator
- Want probability of next symbol to depend on current symbol
- Will use a standard (non-hidden) Markov model
  - Probabilistic state machine
  - Each state emits a symbol

Modeling CpG Islands
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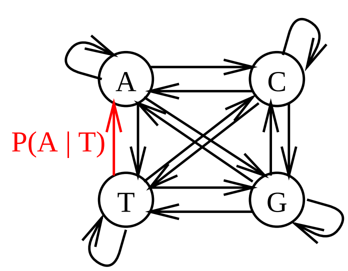


The Markov Property

- A first-order Markov model (what we study) has the property that observing symbol x_i while in state π_i depends only on the previous state π_{i-1} (which generated x_{i-1})

- Standard model has 1-1 correspondence between symbols and states, thus

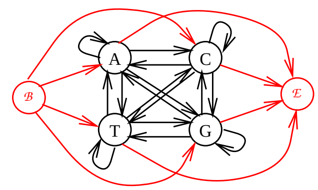
$$P(\mathrm{x}_i \mid \mathrm{x}_{i-1}, \ldots, \mathrm{x}_1) = P(\mathrm{x}_i \mid \mathrm{x}_{i-1})$$

and

$$P(\mathrm{x}_1, \ldots, \mathrm{x}_L) = P(\mathrm{x}_1) \prod_{i=2}^{L} P(\mathrm{x}_i \mid \mathrm{x}_{i-1})$$

Begin and End States

- For convenience, can add special "begin" ($\mathcal{B}$) and "end" ($\mathcal{E}$) states to clarify equations and define a distribution over sequence lengths
- Emit empty (null) symbols x_0 and x_{L+1} to mark ends of sequence



$$P(\mathrm{x}_1, \ldots, \mathrm{x}_L) = \prod_{i=1}^{L+1} P(\mathrm{x}_i \mid \mathrm{x}_{i-1})$$

- Will represent both with single state named 0

Markov Chains for Discrimination

- How do we use this to differentiate islands from non-islands?
- Define two Markov models: islands ("$+$") and non-islands ("$-$")
  - Each model gets 4 states (A, C, G, T)
  - Take training set of known islands and non-islands
  - Let c_{st}^{+} = number of times symbol t followed symbol s in an island:

$$\hat{P}^{+}(t \mid s) = \frac{c_{st}^{+}}{\sum_{t'} c_{st'}^{+}}$$

- Example probabilities in [Durbin et al., p. 50]
- Now score a sequence $X = \langle \mathrm{x}_1, \ldots, \mathrm{x}_L \rangle$ by summing the log-odds ratios:

$$\log\left(\frac{\hat{P}(X \mid +)}{\hat{P}(X \mid -)}\right) = \sum_{i=1}^{L+1} \log\left(\frac{\hat{P}^{+}(\mathrm{x}_i \mid \mathrm{x}_{i-1})}{\hat{P}^{-}(\mathrm{x}_i \mid \mathrm{x}_{i-1})}\right)$$

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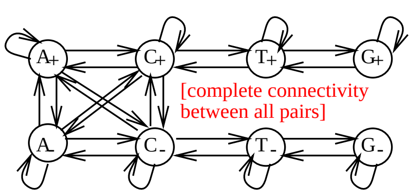
Hidden Markov Models

- Second CpG question: Given a long sequence, where are its islands?
  - Could use tools just presented by passing a fixed-width window over the sequence and computing scores
  - Trouble if islands' lengths vary
  - Prefer single, unified model for islands vs. non-islands

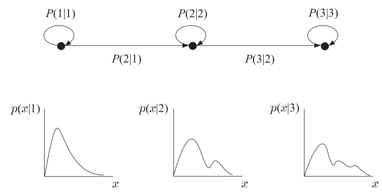


  - Within the $+$ group, transition probabilities similar to those for the separate $+$ model, but there is a small chance of switching to a state in the $-$ group

What's Hidden in an HMM?

- No longer have one-to-one correspondence between states and emitted characters
  - E.g. was C emitted by C_{+} or C_{-}?
- Must differentiate the symbol sequence X from the state sequence $\pi = \langle \pi_1, \ldots, \pi_L \rangle$
  - State transition probabilities same as before: $P(\pi_i = \ell \mid \pi_{i-1} = j)$ (i.e. $P(\ell \mid j)$)
  - Now each state has a prob. of emitting any value: $P(\mathrm{x}_i = \mathrm{x} \mid \pi_i = j)$ (i.e. $P(\mathrm{x} \mid j)$)

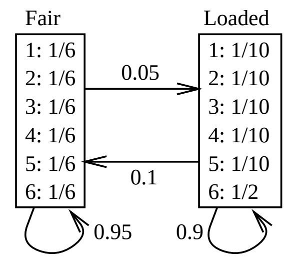
What's Hidden in an HMM?
(cont'd)



[In CpG HMM, emission probs discrete and $= 0$ or 1]

Example: The Occasionally Dishonest Casino

- Assume that a casino is typically fair, but with probability 0.05 it switches to a loaded die, and switches back with probability 0.1



- Given a sequence of rolls, what's hidden?

The Viterbi Algorithm

- Probability of seeing symbol sequence X and state sequence π is

$$P(X,\pi) = P(\pi_1 \mid 0) \prod_{i=1}^{L} P(\mathbf{x}_i \mid \pi_i)\, P(\pi_{i+1} \mid \pi_i)$$

- Can use this to find most likely path:

$$\pi^* = \operatorname*{argmax}_{\pi} P(X,\pi)$$

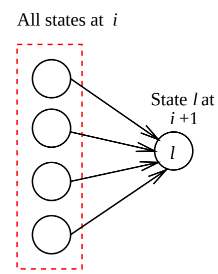
  and trace it to identify islands (paths through $+$ states)

- There are an exponential number of paths through chain, so how do we find the most likely one?

The Viterbi Algorithm
(cont'd)

- Assume that we know (for all k) $v_k(i) =$ probability of most likely path ending in state k with observation $\mathbf{x}_i$
- Then

$$v_\ell(i+1) = P(\mathbf{x}_{i+1} \mid \ell)\ \max_k \{v_k(i)\, P(\ell \mid k)\}$$



The Viterbi Algorithm
(cont'd)

- Given the formula, can fill in table with dynamic programming:
  - $v_0(0) = 1$, $v_k(0) = 0$ for $k > 0$
  - For $i = 1$ to L; for $\ell = 1$ to M (# states)
    - $v_\ell(i) = P(\mathbf{x}_i \mid \ell)\, \max_k\{v_k(i-1)P(\ell \mid k)\}$
    - $\text{ptr}_i(\ell) = \text{argmax}_k\{v_k(i-1)P(\ell \mid k)\}$
  - $P(X,\pi^*) = \max_k\{v_k(L)P(0 \mid k)\}$
  - $\pi_L^* = \text{argmax}_k\{v_k(L)P(0 \mid k)\}$
  - For $i = L$ to 1
    - $\pi_{i-1}^* = \text{ptr}_i(\pi_i^*)$
- To avoid underflow, use $\log(v_\ell(i))$ and add

The Forward Algorithm

- Given a sequence X, find $P(X) = \sum_\pi P(X,\pi)$
- Use dynamic programming like Viterbi, replacing max with sum, and $v_k(i)$ with $f_k(i) = P(\mathbf{x}_1, \ldots, \mathbf{x}_i, \pi_i = k)$ (= prob. of observed sequence through $\mathbf{x}_i$, stopping in state k)
  - $f_0(0) = 1$, $f_k(0) = 0$ for $k > 0$
  - For $i = 1$ to L; for $\ell = 1$ to M (# states)
    - $f_\ell(i) = P(\mathbf{x}_i \mid \ell) \sum_k f_k(i-1)P(\ell \mid k)$
  - $P(X) = \sum_k f_k(L)P(0 \mid k)$
- To avoid underflow, can again use logs, though exactness of results compromised (Section 3.6)

The Backward Algorithm

- Given a sequence X, find the probability that $\mathbf{x}_i$ was emitted by state k, i.e.

$$P(\pi_i = k \mid X) = \frac{P(\pi_i = k, X)}{P(X)}$$
$$= \frac{\overbrace{P(\mathbf{x}_1, \ldots, \mathbf{x}_i, \pi_i = k)}^{f_k(i)} \; \overbrace{P(\mathbf{x}_{i+1}, \ldots, \mathbf{x}_L \mid \pi_i = k)}^{b_k(i)}}{\underbrace{P(X)}_{\text{computed by forward alg}}}$$

- Algorithm:
  - $b_k(L) = P(0 \mid k)$ for all k
  - For $i = L - 1$ to 1; for $k = 1$ to M (# states)
    - $b_k(i) = \sum_\ell P(\ell \mid k)\, P(\mathbf{x}_{i+1} \mid \ell)\, b_\ell(i+1)$

Example Use of Forward/Backward Algorithm

- Define $g(k) = 1$ if $k \in \{\mathrm{A}_+, \mathrm{C}_+, \mathrm{G}_+, \mathrm{T}_+\}$ and 0 otherwise
- Then $G(i \mid X) = \sum_k P(\pi_i = k \mid X)\, g(k)$ = probability that $\mathbf{x}_i$ is in an island
- For each state k, compute $P(\pi_i = k \mid X)$ with forward/backward algorithm
- Technique applicable to any HMM where set of states is partitioned into classes
  - Use to label individual parts of a sequence

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Specifying an HMM

- Two problems: defining structure (set of states) and parameters (transition and emission probabilities)
- Start with latter problem, i.e. given a training set $X_1, \ldots, X_N$ of independently generated sequences, learn a good set of parameters θ
- Goal is to maximize the (log) likelihood of seeing the training set given that θ is the set of parameters for the HMM generating them:

$$\sum_{j=1}^{N} \log(P(X_j; \theta))$$

When State Sequence Known

- Estimating parameters when e.g. islands already identified in training set
- Let $A_{k\ell}$ = number of $k \rightarrow \ell$ transitions and $E_k(b)$ = number of emissions of b in state k

$$P(\ell \mid k) = A_{k\ell} \Big/ \left(\sum_{\ell'} A_{k\ell'} \right)$$

$$P(b \mid k) = E_k(b) \Big/ \left(\sum_{b'} E_k(b') \right)$$

When State Sequence Known (cont'd)

- Be careful if little training data available
  - E.g. an unused state k will have undefined parameters
  - Workaround: Add pseudocounts $r_{k\ell}$ to $A_{k\ell}$ and $r_k(b)$ to $E_k(b)$ that reflect prior biases about parobabilities
  - Increased training data decreases prior's influence
  - [Sjölander et al. 96]

The Baum-Welch Algorithm

- Used for estimating parameters when state sequence unknown
- Special case of the expectation maximization (EM) algorithm
- Start with arbitrary $P(\ell \mid k)$ and $P(b \mid k)$, and use to estimate $A_{k\ell}$ and $E_k(b)$ as expected number of occurrences given the training set*:

$$A_{k\ell} = \sum_{j=1}^{N} \frac{1}{P(X_j)} \sum_{i=1}^{L} f_k^j(i) P(\ell \mid k) P(\mathbf{x}_{i+1}^j \mid \ell) b_\ell^j(i+1)$$

$$E_k(b) = \sum_{j=1}^{N} \sum_{i:\mathbf{x}_i^j = b} P(\pi_i = k \mid X_j) = \sum_{j=1}^{N} \frac{1}{P(X_j)} \sum_{i:\mathbf{x}_i^j = b} f_k^j(i) b_k^j(i)$$

- Use these (& pseudocounts) to recompute $P(\ell \mid k)$ and $P(b \mid k)$
- After each iteration, compute log likelihood and halt if no improvement

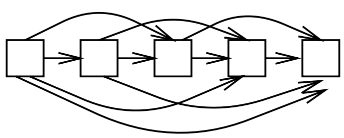
*Superscript j corresponds to jth train example

HMM Structure

- How to specify HMM states and connections?
- States come from background knowledge on problem, e.g. size-4 alphabet, $+/-$, $\Rightarrow$ 8 states
- Connections:
  - Tempting to specify complete connectivity and let Baum-Welch sort it out
  - Problem: Huge number of parameters could lead to local max
  - Better to use background knowledge to invalidate some connections by initializing $P(\ell \mid k) = 0$
    - Baum-Welch will respect this

Silent States

- May want to allow model to generate sequences with certain parts deleted
  - E.g. when aligning DNA or protein sequences against a fixed model or matching a sequence of spoken words against a fixed model, some parts of the input might be omitted



- Problem: Huge number of connections, slow training, local maxima

Silent States
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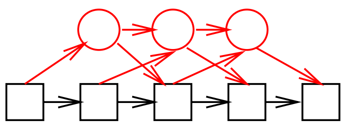
- Silent states (like begin and end states) don't emit symbols, so they can "bypass" a regular state



- If there are no purely silent loops, can update Viterbi, forward, and backward algorithms to work with silent states [Durbin et al., p. 71]
- Used extensively in profile HMMs for modeling sequences of protein families (aka multiple alignments)