

CSE182 Lecture 7 questions

Vineet Bafna

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The questions are open ended, but should help you understand lectures better. Do these questions make sense? Are they helpful in following the lecture? Constructive feedback is appreciated.

1. Consider a profile P of length m . For any position i , residue a , $P_i[a]$ is the score (not the frequency) of aligning residue a to the i -th position of the profile. Describe an algorithm that finds the highest scoring local alignment of a sequence $s[1..n]$ allowing for gaps and with an indel score δ .
2. Consider the question posed in L7, slide 6. Suppose your friend uses a 'loaded' coin in which the probability of Tails is 1. Assume also that he will switch the two coins with probability 0.3.
 - (a) Describe an HMM that models the string of coin tosses
 - (b) Suppose you see the following sequence $HTHTHTTTTTHTTHTHTH$. Compute the maximum likelihood probability of number of times he cheated.
3. See L7, Slide 10. Construct an HMM for the 3 sequences in the family using the red ovals as match states. Compute the probability that ALIL is a member of the family using both the forward and the viterbi algorithm. (You can make up numbers for transition probabilities).
4. What is an EST? What is a 5' EST? What is a 3' EST? If you wanted to search for possible function using protein sequence analysis, would you prefer 5' ESTs, or 3'ESTs? Why? If you wanted to cluster ESTs, would you prefer 5'ESTs, or 3'ESTs?