

Biological Sequence Analysis

Monday 11. February at Noon in C221

NOTE: The lecture on February 11th will be at the usual time at 2 p.m.

1. 4.1 from Durbin (page 86)
2. 4.2 from Durbin (page 86)
3. Describe the structure of a pair-HMM that corresponds to the gap model with *linear* gap penalties.
4. One wants to list (global) pairwise alignments of two sequences in descending order of the score of the alignment, starting from the highest scoring alignment. How can you do this? Sketch an algorithm. NOTE: You are expected to list only K best alignments.
5. Try the HMMER tool (<http://hmmmer.janelia.org/>). Produce a profile-HMM from the alignment given in Figure 5.3 of Durbin. Is the resulting HMM any good? (More guidance of using HMMER available <http://www.cs.helsinki.fi/u/prastas/hmmmer.html>.)
6. Estimate for the HMM in Fig 5.4. the transition probabilities from state M3 to state I3 and from state M3 to state D4 using the alignment of Fig 5.3.