Biological Sequence Analysis

Monday 18. February at Noon in C221

1. What is the value given to S1 when the MAP model construction algorithm is applied on the alignment of Fig. 5.7?

2. Exercise 6.1 from Durbin et.al. (page 142). Additional question: How many more sequences could be aligned with a million times faster computer for which pairwise comparison takes 1/1 000 0000 seconds?

3. Explain how the MSA algorithm works (Durbin pp. 142-143)

4. Explain how simulated annealing can be used with the BW-algorithm (Durbin pp. 155-156)

5. Try CLUSTAL program for constructing multiple alignments (more guidance `http://www.cs.helsinki.fi/u/prastas/clustal.html`)

6. T-Coffee is a recent multiple alignment software. Explain the main principles of T-Coffee. How does it differ from CLUSTAL? (Hint: Find answers from the WWW). Try T-Coffee (a server is here: `http://www.tcoffee.org/`)