

Lecture Diary for MATH2307 (Bioinformatics and Biological Modelling)

1. Sequence similarity.
2. Dynamic programming: global alignment (the Needleman-Wunsch algorithm).
3. Dynamic programming: local alignment (the Smith-Waterman algorithm).
4. Alignment with affine gap model.
5. Heuristic alignment algorithms: FASTA and BLAST.
6. Significance of scores (introduction).
7. Multiple alignment: multi-dimensional dynamic programming, MSA, progressive alignment (star alignment).
8. Markov chains.
9. Hidden Markov models.
10. The Viterbi algorithm.
11. The forward algorithm.
12. The backward algorithm and posterior decoding.
13. Parameter estimation for HMMs.
14. HMMs with silent states.
15. Profile HMMs.
16. Multiple sequence alignment by profile HMMs.
17. Levels of protein structure.
18. Prediction by profile HMMs.
19. Threading.
20. Molecular modelling.
21. Lattice HP-models.
22. Phylogenetic trees.

23. Parsimony methods.
24. Distance methods: Neighbour-Joining, UPGMA, the least squares method.
25. Evolutionary models.
26. The Jukes-Cantor model.
27. The Kimura model.
28. The Felsenstein model.
29. The Hasegawa-Kishino-Yano model.
30. The maximum likelihood method, calculation of evolutionary distances.
31. Model comparison, hypothesis testing.