

Bioinformatics – Lecture Notes

Announcements

Class 14 – February 19, 2002 -

1. Evolutionary Problems

- i) Markov Processes (text p 140-144) Finish determination of substitution matrix for nucleotides.
- ii) Clustering Methods – How do we determine the best fit phylogenetic data?

Cannot determine the minimum number of mutations for all possible tree topologies having n leaves since the number of binary trees is exponential. Instead we will use some concepts from graph theory

- a) ultrametric trees
- b) additive metric
- c) estimating branch lengths