

Study Guide for Nov. 13 Exam in Bioinformatics I

1. Write a brief essay on computer methods for analyzing a genomic DNA sequence. What specific tools would you recommend? Include brief definitions of the important features that can be found by the methods you discuss.
2. What are the differences among blastn, blastp and psi-blast? Under what conditions can one expect psi-blast to do a better job than blastp? Briefly explain how psi-blast works.
3. Describe how “log odds” approaches can be used to determine amino-acid substitution scores that are appropriate for, say, blastp. Sketch the approaches taken for the PAM and BLOSUM matrices.
4. What is the “dynamic programming method” for aligning two sequences? Be able to apply it by hand to two short sequences.
5. What are “weight matrices” for identifying, say, transcription factor binding sites, and how can they be determined from experimental data?
6. What is a “hidden Markov model”? What is meant by “the probable state-path for generating a given observable sequence”?
7. Write an essay on the inner workings of GenScan.
8. Be able to read and interpret dotplots, PIPs and MultiPIPs.
9. Contrast the approaches used for building phylogenetic trees using any TWO of the following: Parsimony, Weighted parsimony, Neighbor joining, and Maximum likelihood. What are the limitations of using any of these programs for reconstructing evolutionary history?
10. Contrast the meaning of the terms ”ortholog” and ”paralog.” Be able to identify putative orthologs and paralogs on a gene tree.
11. The eukaryotic cell is sometimes called a “chimera” of genes from different sources. How do the histories of mitochondrial, chloroplast, and nuclear genes illustrate this point?
12. Given a phylogenetic tree and a dataset of sequences, apply ACCTRAN analysis to use parsimony to infer the evolutionary history of one or more of the bases.
13. What is the basis of hyp. testing using likelihood analysis? How might you construct a likelihood test of the hypothesis that some members of a gene family are evolving at a different rate than other lineages?