

Name:

CAP 5991: Bioinformatics
FINAL EXAM; Fall 2003

1. In what situation is a **local sequence alignment** more useful than a **global sequence alignment**?
2. Explain the purpose of BLOSUM matrices.
3. **True or False?** PAM substitution matrix is preferred over BLOSUM for aligning longer protein sequences?
4. Given a nucleotide sequence, which version of **BLAST** would one use to find the protein sequence that best matches it? Why?
5. Explain what is **codon bias**.
6. What is **cDNA**?
7. Explain the difference between the **tertiary** and **quaternary** structure of a protein?
8. Explain the concept of a “kernel” in SVMs.
9. What is the difference between **genomics** and **proteomics**?
10. What are **single nucleotide polymorphisms** (SNPs)?
11. How can the use of an **outgroup** improve the methods used for phylogenetic tree construction?
12. What is a **restriction enzyme**?