Sequence comparison

BLAST (Basic Local Alignment Search Tool)

1. What is the purpose of this tool?

2. What is a gap penalty and why is it necessary to use it in assigning a score to a local match?

3. What is an "E value"?

Protein sequence alignment

4. How do BLASTX and TBLASTX differ?

5. What is a "protein substitution matrix"? Why is it important for scoring protein sequence matches?

6. Which do you think diverge more rapidly, a DNA or a protein match? Which type of search would find matches between sequences more distant from each other in time?