



Uva Wellassa University, Sri Lanka
Faculty of Science and Technology
Science and Technology Degree program
2nd Semester Examination – September/ October 2013
SCT.411-1 Bioinformatics



Number of questions: Four (04)

Answer all questions

Time allocation: One (01) hour

Total marks allocated: 100

1.
 - a. Explain what a 'Multiple Sequence Alignment' is.
 - b. Name a bioinformatic tool that can be used for Multiple Sequence Alignment
 - c. Briefly explain how a Multiple Sequence Alignment can be done
 - d. Describe two uses/applications of Multiple Sequence Alignment.

2.
 - a. Explain what is meant by 'correct reading frame'.
 - b. Name a bioinformatic tool that can be used to find the correct reading frame
 - c. Explain the procedure you would follow to find the correct reading frame
 - d. What is the main purpose of finding correct reading frame?

3.
 - a. What is BLASTX?
 - b. Explain how exactly you would carry out a BLASTX search
 - c. Explain the purpose of carrying out a BLASTX search
 - d. Suppose you want to find whether the 3D structure of a protein of your interest is already stored in a database. Give the specific BLAST tool and the database you would search to carry out this task.

4.
 - a. What is 'SWISS PROT'?
 - b. Explain the statement, 'SWISS PROT is a very popular and a reliable source of data'
 - c. Explain why the number of entries in a protein 3D structure database is very low, compared to the number of entries in a protein sequence data base.