Sr. No. 7104

Exam. Code: 206602
Subject Code : 4597

M.Sc. Bio-informatics - 2nd Sem.

(2517)

Paper - BI-524: Computational Methods for Sequence Analysis

Time allowed: 3 hrs.   Max. Marks: 75

Section A   10X1.5=15

Explain the following in less than four sentences.

a) Global alignment   f) Molecular clock hypothesis

b) Dynamic programming   g) Markov model

c) PSSM   h) Promoter

d) PILEUP   i) Motif

e) Taxa   j) Epitopes

Section B   12X5=60

1) What are scoring matrices? Discuss different types of BLOSUM with its derivation.

OR

2) Align AGGTCGG and AGGTTCCGG using Dot matix method. Explain significance of gap penalty.

3) What is CLUSTALw? Explain its algorithm. Discuss its merit and demerit.

OR

4) What is PSI BLAST? Discuss algorithm of BLAST. When would you use tBLASTx and tBLASTn?

5) What is an evolutionary tree? Explain maximum parsimony method.

OR

6) Explain the algorithm of Neighbour joining method. How it is different than other distance based method?

7) Discuss tools used for promoter prediction in prokaryotic genome.

OR

8) Discuss how evaluation of gene prediction methods is done.

9) Explain an algorithm used for identification of B Cell Epitopes using protein sequences.   OR

10) What is secondary structure of protein? Discuss tools used for secondary structure of protein.

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