Exam.Code:0041
Sub. Code: 18001

2124
B.Sc. (Hons.) Bio-Informatics
Third Semester

BIN-3002: Computational Methods in Bio-molecular Sequence and Phylogenetic Analysis

Time allowed: 3 Hours

Max. Marks: 60

NOTE: *Attempt five questions in all, including Question No. I which is compulsory and selecting two questions from each Unit.*

x-x-x

I. Answer the following:-

a) Give full form of BLAST.

b) Briefly explain sequence logos.

c) Name any two domain databases.

d) Differentiate between cladogram and phylograom.

e) What is phylip?

f) Briefly explain Occam's Razor and its application in phylogenetic analysis. (6x2)

UNIT - I

II. a) What is a domain and how are they detected using bioinformatics tools.

b) How is PSI-BLAST used for performing alignments? (2x6)

III. Write notes on the following:-

a) PRATT

b) Motif

c) PSSM (3x4)

IV. Differentiate between the following:-

a) Pfam A and B

b) ProDam and SMART

c) Regular expression and sequence profile (3x4)

UNIT - II

V. a) Discuss phylogenetic analysis using neighbour joining method.

b) Compare and contrast rooted and unrooted trees. (8,4)

VI. a) Explain any one character based method for phylogenetic analysis.

b) Write a note on MEGA package. (8,4)

VII. a) Differentiate between bootstrapping and jackknifing.

b) How many rooted and unrooted trees are possible for 3 taxas? (2x6)

x-x-x