Exam.Code:0041
Sub. Code: 1002

1127

B.Sc. (Hons.) Bio-Informatics
Third Semester
BIN-3002: Computational Methods in Bio-molicular 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. Attempt the following:-

a) What is a profile?

b) Differentiate between the types of Pfams.

c) Give full forms of CDD and PSSM.

d) Differentiate between motif and patterns.

e) What is Occam's razor and its applications in phylogenetic analysis?

f) What is the importance of a phylogenetic tree? (6x2)

UNIT – I

II. a) Discuss profile based database searching using PSI-BLAST?

b) What is a regular expression w.r.t. motifs. Give suitable example? (8,4)

III. Write notes on the following:-
a) InterPro
b) SMART
c) PROSITE. (3x4)

IV. a) What are sequence logos and their importance?

b) Write a note on BLOCKS. (2x6)

UNIT – II

V. a) Discuss phylogenetic analysis using UPGMA method.

b) How many rooted and unrooted trees are possible for 4 taxas? (8,4)

VI. a) Compare and contrast bootstrapping and jackknifing.

b) Discuss Maximum Likelihood method of phylogenetic analysis. (2x6)

VII. Write notes-on the following:-
a) Phylogram and Cladogram
b) MEGA package
c) Molecular clock and its importance in phylogenetic analysis (3x4)

x-x-x