

Exam.Code:0041
Sub. Code: 18001

2125
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. 1 which is compulsory and selecting two questions from each Unit.

x-x-x

I. Answer the following:-

- a) Give full form of PSSM & UPGMA.
- b) Differentiate between domain and motif giving suitable examples.
- c) What information is available in interpro and give its applications?
- d) Differentiate between cladogram and phylogram.
- e) Briefly discuss phylip.
- f) What is molecular clock w.r.t. phylogenetics? (6x2)

UNIT - I

II. a) Define sequence patterns and profiles and give their applications.

b) Write a note on domain databases. (2x6)

III. a) What is PSSM and its applications.

b) Discuss types of pattern representation. (2x6)

IV. Write short notes on the following:-

a) PSI - BLAST

b) Pfam A and Pfam B (8,4)

UNIT - II

V. a) Discuss NJ method of phylogenetic analysis.

b) Calculate the number of rooted and unrooted trees for 3 taxas. (6,6)

VI. a) Compare and contrast bootstrapping and jackknifing.

b) Write a note on MEGA package. (6,6)

VII. a) Define molecular phylogenetics and give the major assumptions for using molecular data for constructing evolutionary history.

b) Compare and contrast Jukes-Cantor and Kimura model of nucleotide substitution. (2x6)

x-x-x