

2055
Bachelor of Science (FYUP) Second Semester
Bio-Informatics
Paper: Bioinformatics II

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. Give answer in a very short:-

- a) What is E-Value?
- b) Write two applications of BLAST.
- c) T-coffee
- d) Genome coverage.
- e) VISTA.
- f) What is the MSA?
- g) MEGA package.
- h) Give name tool used for Multiple Sequence Alignment.
- i) Give names of two Sequence Alignment Methods.
- j) Phylogenetic tree.
- k) What is the application of BLOSUM?
- l) SCOP.

(12x1)

UNIT - I

- II. a) Briefly describe the BLAST and its applications in bioinformatics.
- b) What are the differences between BLAST and FASTA?
- III. a) Write about the Amino acid substitution matrices.
- b) Describe in brief about the Clustal Omega.
- IV. a) Briefly explain Multiple Sequence Alignment and its importances.
- b) Write a short note on scoring function

(2x6)

(2x6)

(2x6)

UNIT - II

- V. a) Write in brief about phylogenetic analysis.
- b) Write a short note on UPGMA.

(2x6)

P.T.O.

(2)

Sub. Code: 11755

- VI. a) Explained in brief about the bootstrapping and its utility.
b) Describe briefly about one protein structural databases. (2x6)
- VII. a) What type of data is stored in the PDB (Protein Data Bank)?
b) How can MEGA help in estimating evolutionary distances? (2x6)

x-x-x