2055

B.Sc. (Hons.) Bio-Informatics (FYUP)

Second Semester

BIN-2002: Fundamentals of Bioinformatics - II

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 briefly:-

(a) Unrooted tree

(b) SCOP

(c) Cladogram

(d) Taxa

(e) Clade

(f) Monophyletic   (6x2)

UNIT - I

II.   a) How is sum of pairs used as a scoring function in MSA?

b) Discuss the applications of MSA.   (2x6)

III. Explain any one method based on the progressive method of multiple sequence alignment.   (12)

IV.   a) Which method is based on identifying conserved, ungapped regions in sequences for performing MSA? Explain.

b) Write a note on T-Coffee.   (2x6)

UNIT - II

V.   a) Discuss any one method used for phylogenetic tree evaluation.

b) Explain the advantages and disadvantages of using UPGMA for phylogenetic tree construction.   (2x6)

P.T.O.

VI. Write notes on:-

a) Phylip

b) PDB

(2x6)

VII. a) Describe the neighbor joining method for phylogenetic tree construction.

b) Write a short notes on the applications of phylogenetic analysis.

(8,4)

x-x-x