

2046
NEP U.G. Common-Inter Disciplinary Course
Second Semester
Bioinformatics
Paper: Introduction to Bioinformatics - II

Time allowed: 3 Hours

Max. Marks: 40

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) Clustal X
- b) PDB
- c) Bootstrapping
- d) MEGA package (4x2)

UNIT - I

- II. a) Explain the block-based methods of Multiple Sequence Alignment.
b) Discuss the applications of MSA in bioinformatics. (2x4)
- III. a) Compare the tools Clustal Omega and PILEUP in terms of methodology and output.
b) Explain the principle of Iterative method of MSA. (5,3)
- IV. a) Explain the Sum of Pairs measure to determine scoring function.
b) Explain how visualization in Clustal-X helps in interpreting alignment results. (2x4)

UNIT - II

- V. a) Explain the concept of phylogenetic tree topologies with examples.
b) Discuss the importance of maximum parsimony in character-based methods. (2x4)
- VI. a) Describe the maximum likelihood method of phylogenetic tree construction.
b) Explain the jackknifing method for tree evaluation. (2x4)
- VII. a) Write short notes on SCOP databases.
b) Explain how the CATH database classifies protein structures. (2x4)

x-x-x