

(ii) List out FEW UNIX commands (4)

(OR)

b) (i) Write a short note on search engines (4)

(ii) Describe in brief the star and bus topology with their advantages and limitations (10)

22. a) Classify and explain in detail the different biological databases with suitable examples

(OR)

b) Using a gap penalty of **-1**, match as **+1** and mismatch as **0**, find the best alignment of two sequences, **AKRST** and **ARS** using Needleman-Wunsch dynamic programming approach

23. a) Describe in detail the algorithm of BLAST in the pairwise alignment of protein / polynucleotide sequences and add a note on its families

(OR)

b) (i) Write a short note on BLOSUM matrix (4)

(ii) Explain in brief the algorithm of CLUSTAL W for msa of protein / polynucleotide sequences (10)

24. a) Discuss in detail the algorithm of maximum likelihood method in the prediction of phylogenetic tree. Compare and contrast maximum parsimony with maximum likelihood method

(OR)

b) Elaborate in detail the algorithm of UPGMA method for the prediction of a phylogenetic tree

25. a) Briefly explain the different types of microarrays and their applications

(OR)

b) (i) Discuss in detail the algorithm proposed by Chou-Fasman for the prediction of secondary structure of proteins (10)

(ii) Write a short note on systems biology (4)
