

Code: 9A23701

R09

B.Tech IV Year I Semester (R09) Regular & Supplementary Examinations December 2015

BIOINFORMATICS

(Biotechnology)

Time: 3 hours

Max. Marks: 70

Answer any FIVE questions

All questions carry equal marks

- 1 (a) What is homology and analogy?
(b) Define the terms homologs, paralogs, orthologs and xenologs.
(c) The word 'Dinosauria' was coined by a famous English botanist. Briefly comment on the contributions to evolutionary theory and his opposition to Darwin's theory of natural selection.
- 2 Give an mRNA sequence SQPT and the original sequence ELSQPTQ from the organism genome. We are interested in finding mRNA corresponding location in the organism genome.
(a) Which alignment should be performed?
(b) Use the appropriate algorithm for this alignment. Fill in the DP matrix and calculate the optimal alignment score. Obtain the optimal alignment by trace back the matrix.
- 3 (a) Compare and contrast the three major methods of phylogenetic analysis. Give an elaborate note on the pros and cons of each method.
(b) Define sum of pairs.
(c) Define quasi and affine gap penalty with examples.
- 4 (a) How DNA sequences of organisms are collected in the laboratory? Explain the two main methods of large scale sequencing.
(b) What is map alignment? Briefly explain in two points how it is useful in sequencing genomes.
- 5 (a) What is FTP protocol? Explain with a neat flow chart how TCP/IP protocol works.
(b) Explain how information theory is used in bio-informatics.
- 6 (a) What are relational and hierarchical databases? Highlight their differences using a representative sketch.
(b) List two sequence and structure databases.
(c) You are given with an unknown DNA sequence. Develop and explain a strategy to find the function and structure of the unknown sequences using the databases you know.
- 7 (a) What are primary and secondary databases? Compare and contrast with an example highlighting the organization and management of the databases.
(b) What information you will get from Swiss-prot, PIR and KEGG?
- 8 (a) KEGG is a database resource for understanding high level functions. What are the different entry point and analysis tools available in KEGG that you can use to identify biological functions?
(b) For a given unknown DNA sequence, how EXPASY is useful to identify the biological function?
