

Code No: 07A72302

R07

Set No. 2

IV B.Tech I Semester Examinations November 2010

BIOINFORMATICS

Bio-Technology

Time: 3 hours

Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks

1. What search engines are available at EMBL website? Discuss briefly the search criteria. [16]
2. Describe the Russel Wallace Contribution to Evolutionary Theory? [16]
3. Describe in brief about the Metabolic databases. [16]
4. Describe the Basic Local Alignment Search Tool (BLAST) algorithm? [16]
5. What is Bioinformatics? Describe its scope in modern biology? [16]
6. Explain how secondary databases in bioinformatics are different in organization and management from primary databases. [16]
7. How would you trace out mutations in proteins using multiple sequence alignments. Illustrate with one example. [16]
8. Write short notes on: **[16]**
 - (a) Cytogenetic map.
 - (b) RFLP's.

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Set No. 4

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BIOINFORMATICS

Bio-Technology

Time: 3 hours

Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks

1. Write short notes on:
 - (a) Clone-based sequencing.
 - (b) Shot-gun method. [8+8]
2. Overview of methods of sequence alignment. [16]
3. Explain briefly about Hidden Markov Models? Explain how they are useful in performing Multiple Sequence Alignments. [16]
4. Explain in brief about the biological databases with their URL (website) addresses? [16]
5. Explain about any standard process that is used in homology modelling. [16]
6. Discuss the search parameter criteria in Swissprot with one example. [16]
7. List out the elementary commands for working with files and Directories. [16]
8. Describe in brief the tools and software available in KEGG databases. Explain them with suitable examples. [16]

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Set No. 1

IV B.Tech I Semester Examinations November 2010

BIOINFORMATICS

Bio-Technology

Time: 3 hours

Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks

1. Describe the following:
 - (a) Physical mapping of DNA
 - (b) Genetic mapping of DNA. [8+8]
2. Write short notes on the following:
 - (a) Domain and Domain name
 - (b) Modem. [8+8]
3. What are conserved sequences? Explain significance of them in homology with an example. [16]
4. Discuss the relative merits of Pair-wise and Multiple sequence alignment methods? [16]
5. Describe in brief about the tools to find out secondary and tertiary structures of proteins at EXPASY. [16]
6. Discuss the secondary databases of bioinformatics and state their applications in research with suitable examples. [16]
7. What is a database ? How do you organize and manage biological databases? [16]
8. Explain how would you trace out ancestors using multiple sequence alignments and phylogenetic trees? [16]

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R07**Set No. 3****IV B.Tech I Semester Examinations November 2010****BIOINFORMATICS****Bio-Technology****Time: 3 hours****Max Marks: 80**

Answer any FIVE Questions
All Questions carry equal marks

1. What is the difference between pair-wise and multiple alignments? Explain. [16]
2. What is a database? Give some examples biological databases and their organization? [16]
3. Write a note on contributions of:
 - (a) Sir Richard Owen
 - (b) Willie Henning. [8+8]
4. Discuss briefly the search and analysis tools available in PIR. [16]
5. Describe in brief about BRENDA and how it is useful in research. [16]
6. How is computing changing Biology? What are the advantages of using computers in biology. [16]
7. Explain the different methods used in Genome Sequencing? [16]
8. Write short notes on:
 - (a) DNA substitution matrices.
 - (b) Gap scores. [8+8]
