

Code No: 07A72302

R07

Set No. 2

IV B.Tech I Semester Examinations, MAY 2011
BIOINFORMATICS
Bio-Technology

Time: 3 hours

Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks

1. Describe the Charles Darwin Contribution to Evolutionary Theory? [16]
2. Discuss the applications of bioinformatics tools available with Swissprot. [16]
3. Explain about Shannon's Primer on Information theory. [16]
4. (a) What are the goals of sequence analysis.
(b) Importance of C-DNA libraries. [8+8]
5. How can you search and retrieve information of unknown gene from World Wide Web. Explain the steps involved with one example. [16]
6. Describe about the Needleman-Wunch algorithm for sequence alignment. [16]
7. Describe in brief about the tools to find out secondary and tertiary structures of proteins at EXPASY with suitable examples. [16]
8. Explain briefly the method of Neighborhood Joining method in construction of a Phylogenetic Tree. [16]

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Set No. 4

IV B.Tech I Semester Examinations, MAY 2011
BIOINFORMATICS
Bio-Technology

Time: 3 hours

Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks

1. Write short notes on:
 - (a) PAM matrices.
 - (b) PAM and Blosum comparison. [8+8]
2. "Bioinformatics has emerged as a distinct discipline that straddles the interface between traditional biological sciences and computer sciences and advanced computational methodologies". justify the statement. [16]
3. Describe in brief about the Metabolic databases and applications. [16]
4. Write short notes on:
 - (a) Xenologus
 - (b) Paralogs. [8+8]
5. Write short notes on:
 - (a) Physical map of genome.
 - (b) Physical mapping using hybridization. [8+8]
6. Write the steps involved in construction of phylogenetic trees? Explain. [16]
7. How can you search and retrieve information of unknown gene from NCBI? Explain steps involved with one example you have studied? [16]
8. What is Swissprot? Discuss bioinformatics tools available in it and their applications. [16]

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Set No. 1

IV B.Tech I Semester Examinations, MAY 2011
BIOINFORMATICS
Bio-Technology

Time: 3 hours

Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks

1. Discuss the secondary databases of bioinformatics and discuss their applications in biological research. [16]
2. Describe the Willie Contribution to Evolutionary Theory? [16]
3. Discuss in briefly about NCBI and discuss its importance in biological research. [16]
4. Explain about the methods employed for sequencing an entire Genome. [16]
5. Discuss the relative merits of Pair-wise and Multiple sequence alignment methods? [16]
6. Why do we store the biological data and how this stored information helpful for future scientists. [16]
7. Describe in brief about BRENDA and how it is useful in biology research. Explain with one example. [16]
8. Explain briefly about Hidden Markov Models. Explain how they are useful in performing Multiple Sequence Alignments. [16]

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Set No. 3

IV B.Tech I Semester Examinations, MAY 2011
BIOINFORMATICS
Bio-Technology

Time: 3 hours

Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks

1. Discuss in briefly about DDBJ and discuss its importance in biological research. [16]
2. Overview of methods of sequence alignment. [16]
3. What is the central dogma of molecular Biology? How can molecular biology be considered as an information science. [16]
4. Explain about Darwin's evolutionary thoery. [16]
5. Write short notes on:
 - (a) Shot gun approach.
 - (b) Clone contig approach. [8+8]
6. How would you construct phylogenetic trees using clustal programs? Explain. [16]
7. Describe in brief about KEGG and describe any one metabolic pathway with respect to enzyme you have studied. [16]
8. What is PIR? Discuss the tools available in it and their applications. [16]
