

III B.Tech II Semester Regular Examinations, Apr/May 2006

BIO-INFORMATICS

(Bio-Technology)

Time: 3 hours

Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks

1. What is Bioinformatics? Describe its scope in modern biology? [16]
2. Write short notes on:
 - (a) Dot plot
 - (b) Local alignment [16]
3. Write short notes on:
 - (a) Relationship of Multiple sequence alignment to Phylogenetic Analysis
 - (b) Uses of Multiple sequence alignment [16]
4. Explain in detail about Structural databases? [16]
5. What is Block Substitution Matrices (BLOSUM)? Describe them in detail? [16]
6. Describe the following:
 - (a) Perfect phylogeny
 - (b) The relationship of Phylogenetic analysis and sequence alignment. [16]
7. Discuss in detail about the steps involved in sequence assembly? [16]
8. Write brief account on any two of the following:
 - (a) Codon usage
 - (b) Introns and Exons
 - (c) Regulatory sequences and their role. [16]

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1. Explain the steps involved in protein prediction and modeling by using Bioinformatics? [16]
2. Explain in detail about Dynamic: Programming method for sequence alignment? [16]
3. Give the general account on different common multiple sequence alignment methods? [16]
4. Explain about BLAST sequence Database search? [16]
5. What is Block Substitution Matrices (BLOSUM)? Describe them in detail? [16]
6. Describe the following:
 - (a) Perfect phylogeny
 - (b) The relationship of Phylogenetic analysis and sequence alignment. [16]
7. Define Genome? Outline the structure and composition of prokaryotic and Eukaryotic genomes? [16]
8. Write short notes on:
 - (a) GRAIL II
 - (b) ORF [16]

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1. What is Bioinformatics? Describe its scope in modern biology? [16]
2. Explain about computational method for aligning DNA and Protein sequences? [16]
3. What is multiple sequence alignment? Describe the applications of multiple sequence alignments? [16]
4. Describe the following:
 - (a) Structural classifications of proteins
 - (b) The CATH (Class, Architecture, Topology, Homology) databases [16]
5. What is Block Substitution Matrices (BLOSUM)? Describe them in detail? [16]
6. Define Parsimony? Write in detail how Parsimony is used to infer Phylogenetic relationships? [16]
7. Write short note son:
 - (a) Clone mapping
 - (b) STS mapping [16]
8. Write short notes on:
 - (a) GRAIL II
 - (b) ORF [16]

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1. What are the main objectives of Bioinformatics and what does Bioinformatics comprises of? [16]
2. Explain about word or k-tuple methods such as used by programs FAASTA &BLAST? [16]
3. What is a multiple alignment and why we do it? [16]
4. Write short notes on:
 - (a) Swiss-Prot
 - (b) PIR [16]
5. Name the Database search algorithm employed in alignment of sequences and explain in detail about any one of it? [16]
6. Describe about Phylogenetic tree construction by using UPGMA method? [16]
7. Define Genome? Outline the structure and composition of prokaryotic and Eukaryotic genomes? [16]
8. Write short notes on:
 - (a) GRAIL II
 - (b) ORF [16]
