Code No: 07A62301 **R07** **Set No. 2**

III B.Tech II Semester Examinations,APRIL 2011
COMPUTATIONAL MOLECULAR BIOLOGY
Bio-Technology

Time: 3 hours **Max Marks: 80**

Answer any FIVE Questions
All Questions carry equal marks

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1. How does the progress in genomics and bioinformatics change our view on biology and medicine? Explain. [16]
2. What do you mean by biochipnology? Discuss. [16]
3. Discuss in detail on genome sequencing and DNA sequencing methods. [16]
4. Draw a species tree that contains gene trees to illustrate how lineage sorting can occur. [16]
5. Write short notes on the following
   (a) Reverse genetics approaches
   (b) Role of Bioinformatics in Taxonomy. [8+8]
6. Discuss about the criteria to determine tertiary structure of an unknown protein by profile threading. [16]
7. How is protein structure described and what are the goals for protein structure prediction? [16]
8. Explain the computational methods used for phylogenic analysis. [16]

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Code No: 07A62301 **R07** **Set No. 4**

III B.Tech II Semester Examinations,APRIL 2011
COMPUTATIONAL MOLECULAR BIOLOGY
Bio-Technology

Time: 3 hours **Max Marks: 80**

Answer any FIVE Questions
All Questions carry equal marks

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1. Write short notes on the following
   (a) Rooted phylogenetic tree
   (b) Unrooted phylogenetic tree [8+8]
2. Write short notes on the following
   (a) Microfluidics
   (b) On-Chip Assays. [8+8]
3. What are the various CATH data formats and main classification levels of CATH? [16]
4. Show all steps of the UPGMA algorithm as applied to the following five sequences, where the distance between two sequences is defined as the number of base positions in which they differ.
   - CGGGGCUGAUGAGGC
   - CGGAAGGCUGAAGGC
   - AUGCUUGAUGGCAGA
   - CUAUGCGCGAUUGCA
   - CCUGCGUUGUUUACC

   [16]
5. Write short notes on the following
   (a) ROSETTA
   (b) Protein Threading [8+8]
6. Write short notes on the following
   (a) High-Throughput Screening
   (b) Pharmacogenomics and Toxicogenomics [8+8]
7. Write short notes on the following
   (a) Model refinement
   (b) Annotation of Genes in Eukaryotes. [8+8]
8. Explain procedure for Reverse Gene Finding and Locating Exons in cDNA. [16]

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Code No: 07A62301 **R07** **Set No. 1**

III B.Tech II Semester Examinations,APRIL 2011
COMPUTATIONAL MOLECULAR BIOLOGY
Bio-Technology

Time: 3 hours **Max Marks: 80**

Answer any FIVE Questions
All Questions carry equal marks

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1. Write short notes on the following
   (a) Properties of phylogenetic trees.
   (b) Tree Roots. [8+8]
2. Define Parsimony? Write in detail how Parsimony is used to infer Phylogenetic relationships? [16]
3. Write short notes on the following
   (a) Chou-Fasman method
   (b) GOR method. [8+8]
4. Explain Computational Analysis of Gene Rearrangements. [16]
5. Write short notes on the following
   (a) Automated Web-Based Homology Modeling
   (b) Databases of Structures from Homology [8+8]
6. Write short notes on the following
   (a) New Strategies in Drug Discovery
   (b) Target Validation [8+8]
7. Write short notes on the following
   (a) Spotting Microarray Approach
   (b) Applications of Peptide-Based Microarray. [8+8]
8. What is Biological Information and Where Does It Come From? How DNA Sequences Code for Information? Explain. [16]

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Code No: 07A62301 **R07** **Set No. 3**

III B.Tech II Semester Examinations,APRIL 2011
COMPUTATIONAL MOLECULAR BIOLOGY
Bio-Technology

Time: 3 hours **Max Marks: 80**

Answer any FIVE Questions
All Questions carry equal marks

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1. What are the methods we looked at for creating an initial phylogenetic tree? Describe UPGMA. [16]
2. Outline the steps in homology modeling process. [16]
3. Describe about methodology of In situ Synthesis of Oligonucleotide Probes on Microarrays. [16]
4. Explain the following
   (a) methods of determining phylogenetic relationships among species
   (b) What are the strengths and weaknesses of phenetic classification versus phylogenetic classification (or cladistics)? Define & describe how each proceeds. [8+8]
5. Discuss about experimental protein structure determination methods. [16]
6. How can gene prediction in eukaryotes can be done? Explain. [16]
7. Write short notes on the following
   (a) In Silico Protein Design
   (b) Bioinformatics Approaches in Genome-Based Target Selection. [8+8]
8. If you had the resources and facilities to sequence the entire genome of five individuals, which would you select? Why? Describe how you would approach the data analysis. [16]

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