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

III B.Tech II Semester Examinations,December 2010
COMPUTIONAL 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) Insertional Mutagenesis
   (b) Gene Silencing by Disrupting RNA. [8+8]
2. Write in detail about sequence- structure alignment and protein threading. [16]
3. What do you need for distance based methods? Why is percent of change often not a good measure of distance? [16]
4. Briefly explain how one may determine a plausible root for an unrooted evolutionary tree obtained from a phylogenetic tree inference algorithm, such as neighbor joining. [16]
5. Explain gene prediction in microbial genomes. [16]
6. Write short notes on the following
   (a) In Silico Protein Design
   (b) Bioinformatics Approaches in Genome-Based Target Selection. [8+8]
7. Write about the significance of alignments in Secondary Structure. [16]
8. Explain construction of Carbohydrate Microarrays. [16]

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

III B.Tech II Semester Examinations,December 2010
COMPUTIONAL 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) UPGMA
   (b) Neighbor joining . [8+8]
2. Explain Secondary structure prediction from protein sequences? [16]
3. What are the methods we looked at for creating an initial phylogenetic tree? Describe UPGMA. [16]
4. Discuss in detail about ADME and molecular descriptors. [16]
5. Write short notes on the following
   (a) Analysis of prokarotic genomes (b) Gene content of eukaryotic chromosomes. [8+8]
6. Explain in detail about peptide-based Microarrays. [16]
7. How can gene prediction in eukaryotes can be done? Explain. [16]
8. What is the relationship between Structure and Specificity? Explain. [16]

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

III B.Tech II Semester Examinations,December 2010
COMPUTIONAL 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) The Early Prediction Methods
   (b) Modern Methods. [8+8]
2. Write short notes on the following
   (a) Cladistics
   (b) Phylogenetic tree [8+8]
3. Write short notes on the following
   (a) Maximum parsimony method
   (b) Neighbor joining method. [8+8]
4. Write an account of lead discovery and optimization. [16]
5. Discuss about detection of Proteases and other Hydrolytic Enzymes by using microarray technology. [16]
6. Explain the strategy for the application of target prediction to functional genomics. [16]
7. Explain procedure for Reverse Gene Finding and Locating Exons in cDNA. [16]
8. Write short notes on the following
   (a) Reverse genetics approaches
   (b) Role of Bioinformatics in Taxonomy. [8+8]

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

III B.Tech II Semester Examinations,December 2010
COMPUTIONAL 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 about exploring secondary structure-specific amino acid exchanges in structure prediction . [16]
2. Describe the structure and values found in a typical scoring matrix for sequence alignment for DNA sequences. [16]
3. Write short notes on the following
   (a) Microarray Analysis in Drug Discovery
   (b) PROTEIN-DOCKING [8+8]
4. Write short notes on the following
   (a) Membrane Microarrays
   (b) Hydrogel Microarrays. [8+8]
5. Describe about distance methods to produce Phylogenetic trees of the group? [16]
6. (a) How do probabilistic methods work?
   (b) How do distance based methods work? [8+8]
7. What can be done to improve the utilization of data from structural genomic programs by the research community at large? Explain. [16]
8. How is the reliability of gene predictions assessed? Explain. [16]

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