Code :R7322301 1

III B.Tech II Semester(R07) Regular & Supplementary Examinations, April/May 2011
COMPUTATIONAL MOLECULAR BIOLOGY
(Biotechnology)

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

Answer any FIVE questions
All questions carry equal marks

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1. Outline the steps in BLAST algorithm.
2. Discuss homology identification in biological sequence alignment.
3. Describe the process of developing spotted arrays.
4. What do you mean by protein function prediction? Explain with a suitable example.
5. What is artificial neural network? Discuss the applications of fed forward back propagation method in protein structure prediction.
6. (a) Explain the methods of determining phylogenetic relationships among species.
   (b) What are the strengths and weakness of phenetic classification versus phylogenetic classification (or cladistics)? Define and describe how each proceeds, and explain.
7. Comment on the evolution of PDB? What are its classifications?
8. How can computational molecular biology help in novel drug design?

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Code :R7322301 2

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COMPUTATIONAL MOLECULAR BIOLOGY
(Biotechnology)

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

Answer any FIVE questions
All questions carry equal marks

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1. Explain why every genome is different.
2. What do you understand by gene regulatory network? Explain with a suitable example.
3. Discuss the procedure of microarray data analysis and various software tools used for the purpose.
4. Define any one computational method for 3-D protein structure modeling.
5. What are the difficulties faced from ab- initio protein structure prediction. How can we solve it?
6. What are the advantages of phylogenetic analysis?
7. Protein structures are more highly conserved than sequences- explain?
8. Discuss recent trends in computational drug designing?

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Code :R7322301 **3**

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COMPUTATIONAL MOLECULAR BIOLOGY
(Biotechnology)

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

Answer any FIVE questions
All questions carry equal marks

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1. (a) Write about the significance of substitution scores and gap penalties in sequence alignment?
   (b) Explain FASTA database similarity searching program.
2. Discuss the current methods for genome sequencing and importance of genome sequence annotation.
3. Describe the advantages of clustering techniques in computational molecular biology (microarray data analysis).
4. How can you predict protein structure using Ramachandran's plot?
5. (a) What do you mean by protein design?
   (b) What are the goals of protein design?
6. Write short notes on:
   (a) Rooted and un rooted trees.
   (b) Genes Vs species trees.
7. What methods would you use to visually estimate the number of clusters in a gene expression data?
8. Trans membrane proteins are important in drug discovery. What are their properties and how can we generate their 3D structures?

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Code :R7322301 4

III B.Tech II Semester(R07) Regular & Supplementary Examinations, April/May 2011
COMPUTATIONAL MOLECULAR BIOLOGY
(Biotechnology)

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

Answer any FIVE questions
All questions carry equal marks

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1. Write shorts notes on:
   (a) Gapped - BLAST
   (b) Double - filtration algorithm.
2. What are the different methods used for detecting SNPs and give its applications?
3. Discuss the application of microarray technology.
4. Comment on the nature of information provided by structure classification of databases.
5. What is artificial neural network? Discuss the applications of fed forward back propagation method in protein structure prediction.
6. Describe the following:
   (a) Various tree building methods.
   (b) Concept of evolutionary trees.
7. Protein structures are more highly conserved than sequences- explain.
8. Explain the importance of protein designing in the field of drug designing.

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