Ref. No. : Ex/PG/BME/T/1210B/2024

Name of the Examinations: MASTER OF BIO-MEDICAL ENGINEERING FIRST YEAR SECOND SEMESTER - 2024

Subject : BIO-INFORMATICS **Time :** **Full Marks :100**

Instructions: Answer any ten questions

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1. Define primary, composite and structural database with example. What are identifier and accession code present in biological database. 2X3+2X2
2. Describe different types of databases. Write down the advantages of relational databases. 6+4
3. What are overlapping and alternative genes? Differentiate the structural features between prokaryotic and eukaryotic genome. Define C-value paradox? 2X2+4+2
4. Write down the significance of genome mapping. Describe the two types of genome maps. Name two genome resources on the web. Define transposable elements. 2+2X2+2+2
5. Define following terms: RFLPs, STS, EST, chromosome walking, chromosome jumping 2X5
6. Explain the term genome sequencing. Name two different methods of DNA sequencing methodologies. How would you identify genes in contigs? Write a short note on human genome project. 2+2+3+3
7. Describe the following terms in relation to sequence similarity: homologous, analogous, orthologous, paralogous, xenologous. What are five major variants of biosequence alignment problems? 5+5
8. Describe different methods of sequence alignments. Define scoring matrices. Define the terms: PAM, BLOSUM 4+2+2X2
9. What is BLAST? Describe the significance of pairwise sequence alignment. Describe two methods for multiple sequence alignments. Name two progressive alignment programs. 2+2+2X2+2
10. Define molecular phylogenetic tree. What are the terms which are used in phylogenetic tree? Describe the methods of phylogenetic analysis. Name different tools for phylogenetic analysis. 2+2+4+2
11. What is FASTA algorithm? Write down its implementation and output. Define the terms: PSI-BLAST, Gapped-BLAST 2+2+2+2X2
12. Describe the methods for gene finding by i) ORF prediction and ii) homology-based approaches. What are the features present in secondary structure of RNA. Name two principal approaches for RNA structure prediction. 2X2+4+2
13. Describe the protein structure prediction by i) Nearest Neighbour methods and ii) Hidden Markov models. What ae the differences between homology modeling and Ab Initio approach for protein prediction? Explain the protein structure validation by Ramachandran plot. 2X2+3+3
14. Write down the steps of drug discovery and design. Explain the terms: virtual screening and QSAR analysis in computer-aided drug design. Differentiate between the terms ligand based and structure based drug design. 3+2x2+3