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18BT63

Sixth Semester B.E. Degree Examination, July/August 2022 Bioinformatics

Time: 3 hrs.

Max. Marks: 100

Note: Answer any FIVE full questions, choosing ONE full question from each module.

Module-1

- 1 a. Detail the classification of Biological databases, with appropriate examples. Highlight the relevance of OMIM and KEGG databases in Bioinformatics exercise. (10 Marks)
- b. Distinguish between the application of Eutrez and ExPASy tools towards structural Bioinformatics projects. (10 Marks)

OR

- 2 a. Substantiate the statement that RCSB (PDB) database is a knowledge database for structural Bioinformatics work with relevant examples. (10 Marks)
- b. Compare the utilities of dbSNP and dbEST in the context of Genome analysis. (10 Marks)

Module-2

- 3 a. What are PAM and BLOSUM metrics? Highlighting their relevance, substantiate as to why BLOSUM62 is preferred over PAM250 in sequence analysis. (10 Marks)
- b. Compare the merits of PSI-BLAST, PHI-BLAST and RPS-BLAST tools, with a case study. (10 Marks)

OR

- 4 a. Elaborate the steps involved in the homology search via VISTA Mummer tools towards genome analysis. (10 Marks)
- b. With suitable examples, compare the algorithm of 'pair - wise' and 'Multiple - Sequence' Alignment tools. (10 Marks)

Module-3

- 5 a. Write in detail the method of detecting Codon bias and functional sites in the DNA. (10 Marks)
- b. Prediction of protein folds and secondary structures are important in structural Bioinformatics projects. Justify your answer with an example and relevant tools. (10 Marks)

OR

- 6 a. Compare the merits of GENSCAN and GRAIL towards elucidation of functional sites in a Eukaryotic genome. (10 Marks)
- b. Describe prediction of secondary and folding classes based on physical properties. (10 Marks)

Module-4

- 7 a. Elaborate the steps involved in comparative modeling of target protein via appropriate tools, with an example. (10 Marks)
- b. Justify the importance of molecular visualization tools in the context of structural bioinformatics projects. Comment on the merits of VMD and C_n3D towards the same. (10 Marks)

OR

- 8 a. Substantiate that “Energy minimization and structure refinement” are critical aspects towards elucidating the active conformations of bimolecular with a relevant case study. (10 Marks)
- b. Justify the need for molecules superposition and 3D alignment techniques, in the context of computational drug design. Comment on suitable tools towards the same. (10 Marks)

Module-5

- 9 a. What are Restriction maps? Justify the utilities of tools like OMIGA and Mapper towards the same. (10 Marks)
- b. What is a Pharmacophore? Describe the method pharmacophore based drug design, highlighting the utilities of relevant tools. (10 Marks)

OR

- 10 a. Comparatively discuss the protocol with reference to Ligand – receptor and Receptor – Receptor docking exercises via appropriate tools. (10 Marks)
- b. Evaluate the important of parameters involved in computational design of primers for molecular biology projects, highlighting suitable tools. (10 Marks)
