CBCS Scheme

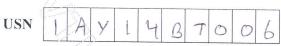USN `1 A Y 1 4 B T 0 0 6`   **15BT54**

Fifth Semester B.E. Degree Examination, Dec.2017/Jan.2018
Bioinformatics

Time: 3 hrs.   Max. Marks: 80

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

Module-1

1   a. Substantiate the need and important of KEGG database in bioinformatics projects. **(04 Marks)**
    b. Discuss the structure of a PDB flat file. Highlight the importance of PDB as a knowledge database for bioinformatics exercise. **(06 Marks)**
    c. Justify the need for PHI – BLAST and PSI – BLAST variants in sequence search operations. **(06 Marks)**

OR

2   a. What is optimum Alignment? Discuss the parameters that are used to achieve the same, with an example. **(06 Marks)**
    b. What are PAM and BLOSUM matrices? Discuss their signification in sequence alignment methods. **(06 Marks)**
    c. Highlight the relevance of SCOP and Pfam database in bioinformatics exercise. **(04 Marks)**

Module-2

3   a. Comparatively describe the merits of distance based and character based methods for deriving phylogentic trees. **(08 Marks)**
    b. Comparatively discuss the utilities of CLUSTALWZ and PHYLIP tools towards phylogenetic analysis of molecular sequences. **(08 Marks)**

OR

4   a. Schematically discuss the structure of an Eukaryotic genome and describe the popular tools GENSCAN to decipher the presence of exons in them. Explain its output features. **(08 Marks)**
    b. Substantiate the importance of popular predictive methods towards analyzing the probable folds in new protein sequences. Comment on the tools STRIDE and NNPREDICT. **(08 Marks)**

Module-3

5   a. Explain Sanger's dideoxy chain termination method of DNA sequencing. **(06 Marks)**
    b. Discuss the popular tools employed in aiding genome sequencing projects. **(06 Marks)**
    c. Highlight the utility of EST database in sequencing approaches. **(04 Marks)**

OR

6   a. What is a micro-array? Explain the need for relevant tools towards micro-array data analysis, for diverse applications. **(08 Marks)**
    b. Highlight the importance of suitable tools for comparative genomics, for specific applications. **(08 Marks)**

Module-4

7 a. Discuss the steps involved in comparative modeling. Highlight the utilities of various tools and techniques towards validation exercises of modeled 3D structures. **(08 Marks)**

  b. Substantiate the utilities of molecular visualization tools in bioinformatics exercises, with appropriate examples. **(08 Marks)**

OR

8 a. What is a force – field? Comment on the various energy minimization techniques adopted towards achieving the minimum energy conformation. **(08 Marks)**

  b. Discuss the importance of structure alignment and molecular superposition tools and techniques in bioinformatics exercise, with relevant software. **(08 Marks)**

Module-5

9 a. Substantiate the need for design of primers via in silico methods. Discuss the parameters considered for design of primers, via relevant tools and software. **(08 Marks)**

  b. What are restriction Maps? Highlight their importance. Mention the utilities of databases and web –based tools towards generation of restriction maps. **(08 Marks)**

OR

10 a. What is 3D QSAR? Explain its relevance in computational drug design strategies. **(04 Marks)**

  b. What is Molecular Docking? Discuss the protocol with reference to Ligand receptor docking exercise in drug discovery process. **(08 Marks)**

  c. What is a Pharmacophore ? Discuss the methods towards deriving the patterns in the context of computational drug design. **(04 Marks)**

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