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BT-303

(Following Paper ID and Roll No. to be filled in your Answer Book)

PAPER ID : 154303

Roll No.

B. Tech.

(SEM. III) (ODD SEM.) THEORY EXAMINATION, 2014-15

INTRODUCTION TO BIOINFORMATICS

Time : **3** Hours] [Total Marks : **100**

Note : 1) Attempt all questions.
2) All questions carry equal marks.

1 Attempt any **four** parts of the following : **(5×4=20)**

a) Briefly describe the Smith-Waterman algorithm for local sequence alignment.

b) What is the basic concept of scoring matrix ?

c) What is CLUSTAL W ? Also write its application.

d) Differentiate between distance and similarity matrix.

e) Mention the tools used for secondary structure prediction.

2 Attempt any **two** parts of the following : **(10×2=20)**

a) Describe briefly the steps of comparative modeling of protein three dimensional structures.

b) What is secondary database ? Discuss the applications of Pfam and PROSITE.

c) Discuss about the sequence based database searches.

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3 Attempt any **four** parts : **(5×4=20)**

a) Write note on PSI-BLAST.

b) Differentiate between PAM and BLOSUM matrices.

c) What do you understand by structure visualization ? Explain visualization of data by using RASMOL.

d) Describe phylogenetic trees and also discuss about various types of phylogenetic trees.

e) Briefly discuss the primary sequence databases of nucleic acid and protein.

4 Attempt any **two** parts : **(10×2=20)**

a) What do you understand by protein structure classification ? Discuss SCOP classification with suitable example.

b) Discuss the application of bioinformatics in drug discovery and drug designing.

c) What is MSA ? Discuss the need for MSA and various approaches for MSA.

5 Attempt any **two** parts : **(10×2=20)**

a) Discuss various steps in detail of chemical chain termination method of DNA sequencing.

b) Briefly discuss the Sanger method for DNA sequencing.

c) What do you mean by De-novo docking and how it is different from structure based drug designing ?