

Printed Pages : 2



BT-303

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

**PAPER ID : 154303**

Roll No.

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**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.

- 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 ?
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