

Code No: 56077

**JAWAHARLAL NEHRU TECHNOLOGICAL UNIVERSITY HYDERABAD****B. Tech III Year II Semester Examinations, December - 2017****BIOINFORMATICS****(Bio-Technology)****Time: 3 hours****Max. Marks: 75****Answer any five questions  
All questions carry equal marks**

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1. Explain how Bioinformatics is helpful in dealing with biomolecules. [15]
2. Write in detail about Shotgun and Sanger method for DNA sequencing. [15]
3. Explain
  - a) Needleman-Wunsch Algorithm.
  - b) Smith-Waterman Algorithm. [7+8]
- 4.a) Write a note on structure databases.
  - b) Discuss about NCBL, EMBL as primary data bases. [7+8]
- 5.a) Give an overview of secondary databases.
  - b) Explain the salient features of SWISS PROT protein data base. [7+8]
- 6.a) Give a detailed description of a phylogentic tree.
  - b) Discuss the tools available for multiple sequence alignment. [7+8]
7. Discuss the salient features of KEGG and ERGO database along with the differences between them and their applications. [15]
- 8.a) Explain the protein structural hierarchy.
  - b) Discuss how Cn3D, RasMol and SPDv are useful for protein structure visualization. [7+8]

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