B. Tech.
(SEM. VIII) EXAMINATION, 2006-07
BIOINFORMATICS

Time : 3 Hours] 
[Total Marks : 100

Note : Attempt all questions

1 Attempt any two parts of the following : 2x10
   (a) Discuss Smith and Waterman algorithm with suitable example.
   (b) Explain the Needleman and Wunch algorithm for Pairwise sequence alignment with scoring method, gap penalties, substitution matrices and tool name.
   (c) Define BLAST. Explain the various types of BLAST with flow chart demonstration.

2 Attempt any two parts of the following : 2x10
   (a) What is HMM ? Discuss the application of profile hmm in bioinformatics.
   (b) Discuss the applications of Chau-fosman algorithm with a suitable example.
   (c) Briefly explain parametric test, cross validation and empirical significance testing.

VB-9528] 1 [Contd...
3 Attempt any two parts of the following: 2x10

(a) Explain different types of biological sequence databases with examples. Define Primary, Secondary and Structural databases of protein sequences with example.

(b) What do you understand by comparative protein modeling? Discuss with suitable examples.

(c) Discuss the methods for protein fold recognition.

4 Attempt any two parts of the following: 2x10

(a) Explain how molecular modeling is facilitating the new drug discovery process.

(b) What is lead generation? Explain how leads are identified in drug designing process.

(c) How leads are optimized? Explain with suitable examples and also give the name of one software tool.

5 Attempt any two parts of the following: 2x10

(a) What do you mean by putative genes? Explain how they are identified.

(b) Where regulatory genes are located on the genomic sequence? How are they identified?

(c) What do you mean by comparative genomics? Discuss the recent trends of insilico genomics.