Paper Code: BT-23

M.Tech. (SEM II) EVEN SEMESTER EXAMINATION, 2015-16 BIOINFORMATICS

[Time: 3 hrs.] [Max. Ma	rks: 100]
Note: Attempt ANY FIVE questions only.	
1. (a) Write the applications of bioinformatics in various industries.	[10]
(b) What is biological database? Describe in detail.	[10]
2. (a) Discuss the steps involved in BLAST.	[10]
(b) Align the following sequences using Smith-Waterman algorithm	[10]
Seq1- VALLAR	
Seq2- PAMMAR	
Let: Match= +2; Mismatch= -1; Gap= -1	
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	[10]
C 4 4 0 is a distance matrix for three species A, B and C.	
How many rooted and unrooted trees are possible for these sequences? Draw a	
phylogram for the same using UPGMA method.	
(b) Write about the importance of structural biology in drug discovery.	[10]
4. (a) Discuss the steps of Computer Aided Drug Design (CADD).	[10]
(b) What is gene prediction? Briefly explain the various methods of gene prediction.	[10]
5. (a) What is QSAR? Differentiate the 2D and 3D QSAR. Give the name of any two QSAR tools.	[10]
(b) Define the DNA microarray. Discuss the applications of microarray technique.	[10]
6. Write short notes on ANY FOUR.	[5x4=20]
 (a) Open Reading Frame (b) PHI Blast (c) Neighbor Joining method (d) PAM Matrix (e) Vaccine (f) High-scoring Segment Pairs 	