Register No: ....

M. TECH DEGREE EXAMINATIONS: JUNE 2011

Second Semester

BIOTECHNOLOGY

BTY508: Computational Biology

Time: Three Hours **Maximum Marks: 100**

Answer ALL questions:-

PARTA (10 x 2 = 20 Marks)

1. How computational biology differs from bioinformatics?
2. What is a protocol?
3. Name any two protein structural databases.
4. What are edit operators?
5. Define the term phylogenetics.
6. Differentiate between rooted and unrooted tree.
7. What is the use of neural networks?
8. What are decision trees?
9. List out various data types.
10. What is systems biology?

PART B (5 x 16 = 80 Marks)

11. a) (i) Compare Computational Biology and Bioinformatics. (8)

(ii) What is the role of hardwares in networking? (8)

(OR)

b) Explain in detail about TCP/IP and Topology.

12. a) Discuss in detail about Biological Databases and their uses.

(OR)

b) Explain the steps involved in Smith-Waterman algorithm for pair wise comparison of the nucleotide sequences.

13. a) Expand and Explain the UPGMA tree and construct UPGMA tree for the following distance matrix.

	I	**II**	**III**	**IV**	**V**
I	2	4	6	6	8
II		4	6	6	8
III			6	6	8
IV				4	8
V					8

(OR)

b) (i) Explain the steps involved in multiple sequence alignment using CLUSTAL W. (8)

(ii) Write short notes on bootstrapping technique (8)

14. a) How is the protein secondary structure, predicted by different computational techniques?

(OR)

b) Explain the following

(i) Gene finding programs

(ii) Short gun DNA assembly

15. a) Write in detail about basic UNIX commands.

(OR)

b) (i) How is microarray fabricated using cDNA? (12)

(ii) List out few microarray data analysis soft wares. (4)

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