Register Number: ……..

M.TECH DEGREE EXAMINATIONS: JUNE 2013

Second Semester

BIOTECHNOLOGY

BTY508: Computational Biology

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

Answer all the Questions:-

PART A (10 x 2 = 20 Marks)

1. Recite the definition for *in silico* analysis.
2. Expand and explain what is HTTP?
3. Define composite database with example.
4. Write notes on FASTA format.
5. List out the gene prediction tools and its importance.
6. What is sequence alignment?
7. Comment on neural network.
8. Define a primary database with an example.
9. What are microarray analysis tools?
10. Comment on metabolic pathway.

PART B (5 x 16 = 80 Marks)

11. a) (i) Write the aim, scope of computational biology in detail. (8)

(ii) Provide notes on search engines and its role in *in silico* research. (8)

(OR)

b) (i) What is a network? Explain the OSI Reference Model for networking? (8)

(ii) Give an account on various components of computer. (8)

12. a) (i) Explain the importance of substitution matrices. (8)

(ii) Give a detailed account on PAM matrices. (8)

(OR)

b) (i) Explain in detail the classification of biological databases. (10)

(ii) Write brief note on derived and structural databases. (6)

13. a) (i) What are the various method of multiple sequence alignment? What are the most important examples of these types? (10)

(ii) Elaborate the steps involved in CLUSTAL W programme to do msa. (6)

(OR)

b) (i) Compare maximum likelihood and maximum parsimony and distance methods of phylogeny construction principles. (6)

(ii) Discuss the steps involved in phylogenetic tree building and their tools with examples. (10)

14. a) (i) Write short notes on the following UNIX operations:

(a) Viewing and Editing files (6)

(b) Transformations and filters (10)

(OR)

b) Explain the three methods of gene prediction and give examples of programs in each methods.

15. a) (i) What is DNA microarray technology? Gene expression data can be analyzed by hierarchial cluster method Describe the process.

(OR)

b)) How does system biology has its impact in Bio Informatics? Describe in detail the various factors and issues pertaining to it.

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