KUMARAGURU
college of technology
character is life

Register Number: ……..

B.TECH DEGREE EXAMINATIONS: MAY 2015

(Regulation 2009)

Seventh Semester

BIOTECHNOLOGY

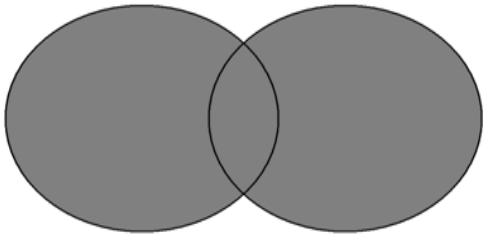
BTY12: Bioinformatics

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

Answer all the Questions:-

PART A (10 x 1 = 10 Marks)

1. Carefully observe the given below Venn diagram and identify the correct Boolean operator:



a) AND b) OR

c) NOT d) IF

2. Identify the best physical medium (cable) for the transmission of the information in a network

a) Twisted pair b) Coaxial

c) Fiber optic d) Microwave

3. What does a negative value in a dynamic program denotes?

a) The substitution mutation is lethal b) The substitution mutation is neutral

c) There is NO substitution mutation d) A transversion mutation occurs

4. OWL is an example of ---------- database

a) Protein structure b) Protein sequence

c) Nucleotide sequence d) Nucleotide structure

5. Select the correct complexity number of the given below nucleotide string:

“ACCTTATATTA”

a) 11 b) 7

c) 3 d) 4

6. An example of a convergent matrix is----------

a) PAM 120 b) BLOSUM 45

c) SOPMA d) MODELLER

7. When the character change is uniformly proportional to time across the tree, it is termed as ---------

a) Ultrametric b) Phylogram

c) Cladogram d) Phenogram

8. Assume, a strong similarity has been revealed in a set of multiple sequences (k =7) by the CLUSTAL OMEGA program. Which program will you select for the phylogenetic tree prediction?

a) Maximum Likelihood (ML) b) UPGMA method

c) Maximum parsimony (MP) d) NJ method

9. In the microarray analysis, the expression of a down regulated gene is denoted by a value of -------

a) Zero b) Negative

c) Positive d) High positive

10. Which of the following amino acid favors the formation of a "TURN" in a protein?

a) Methionine b) Isoleucine

c) Aspartate d) Phenylalanine

PART B (10 x 2 = 20 Marks)

11. List out the layers present in an OSI model
12. Draw the structure of a token ring network model
13. Write the full form of the following databases:

i) TrEMBL; ii) CATH; iii) SIB; iv) PDB

14. Calculate the edit distance of the following string pair with the provided base conditions:

Ma = +2; Ms = 0; Gap = -2

A	**-**	**T**	**Y**	**-**	**R**	**S**
-	**Y**	**S**	**G**	**S**	**K**	**T**

15. What does the condition **"d (i, j-1, k)"** of a particular position in a **"msa"** reveal?
16. List the BLAST family programs
17. Draw an unrooted tree and indicate its OTU
18. Using Fitch-Margoliasch algorithm calculate the branch length(s) of the protein strings from the given below distance table:

	X	**Y**	**Z**
X	**-**	**12**	**57**

Y	**-**	**-**	**36**

19. Define the normalization process of microarray analysis

20. What is systems biology?

PART C (5 x 14 = 70 Marks)

21. a) Explain in detail the architecture of OSI model with appropriate sketch

(OR)

b) i) Describe in detail the various star, bus and ring network topologies with suitable diagrams (10)

ii) List out few UNIX commands (4)

22. a) Align the two peptide strings using Smith - Waterman algorithm with the following base conditions: gap penalty of **-1,** match as **+1** and mismatch as **-1**.
DIRTEYY and **DITEYSS**

(OR)

b) Classify the biological databases with suitable examples

23. a) Discuss in brief the construction of a substitution matrix with an appropriate calculation and brief its significance

(OR)

b) i) Give a detailed account on the algorithm of FASTA (10)

ii) Write the significance of Hidden Markov Model (HMM) in Bioinformatics (4)

24. a) Discuss in detail the UPGMA algorithm with a suitable example

(OR)

b) Explain the Neighbour Joining (NJ) algorithm with an apt example

25. a) i) Explain the working modality of the microarray analysis with the necessary steps (10)

ii) Give the significance of computer aided drug discovery (CADD) (4)

(OR)

b) Describe the algorithm proposed by Chou and Fasman for the prediction of secondary structure of protein

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