B.E. (Computer Technology) Eighth Semester (C.B.S.)

Elective - III : Bioinformatics

P. Pages : 2 **TKN/KS/16/7685**

Time : Three Hours * 0 7 2 6 * Max. Marks : 80

Notes :
1. All questions carry marks as indicated.
2. Solve Question 1 OR Questions No. 2.
3. Solve Question 3 OR Questions No. 4.
4. Solve Question 5 OR Questions No. 6.
5. Solve Question 7 OR Questions No. 8.
6. Solve Question 9 OR Questions No. 10.
7. Solve Question 11 OR Questions No. 12.
8. Due credit will be given to neatness and adequate dimensions.
9. Assume suitable data whenever necessary.
10. Illustrate your answers whenever necessary with the help of neat sketches.

1. a) Define Bioinformatics. Explain Bioinformatic applications related to the following areas. **8**
i) Phylogenetic Analysis
ii) Drug Discovery

b) Give the importance of programming language Perl in bioinformatics. **5**

OR

2. a) Explain the central dogma of molecular biology with neat diagram. **7**

b) What is bioinformatics ? Explain the challenges in information processing. **6**

3. a) Give the HMM approach to gene prediction. **7**

b) What are gene prediction tools. **6**

OR

4. a) Describe the regulation of gene expression in prokaryotes. **7**

b) Give various applications of genetic engineering with suitable example. **6**

5. a) Compute the gobal alignment and the best side of the following sequences. **6**
CGTGAA, GACTTAC with the following parameters Match score = +5,
mismatch score = -3, gap penalty = -4.

b) Explain any one method of sequence alignment and its application. **7**

OR

6. a) What is multiple sequence alignment? Describe the applications of multiple sequence alignment? **7**

b) Determine the optimal alignment for the below two DNA sequence. **6**

i) GGGATATCC ii) GATTC

Using the score table provided below: Comment on final score.

S.N.	Parameter	Score
1	Identity	+10
2	Mismatch	-9
3	Gap Creation	-50
4	Terminal Gap all Mismatch	0

7. a) What is PAM matrices ? Discuss significance of PAM1, PAM120 and PAM250 matrices during sequences comparison. **7**

b) Explain various methods of aligning sequence ? Add a note on BLAST programe. **7**

OR

8. a) What are local and global alignments ? Explain the role of Dot Matrix method in sequence analysis with an example. **7**

b) Explain BLOSUM in brief. **7**

9. a) What are different methods, available for predicting protein structure, write a note on tools for protein secondary structure prediction. **7**

b) Write a note on fold classes of protein. **7**

OR

10. a) Define secondary databases. Give an overview of secondary databases. **5**

b) Name the database search algorithm employed in alignment of sequence and explain in brief about anyone of it. **9**

11. What are different databases available for genes and gnome. Explain various features of KEGG. **13**

OR

12. Write detail note on BRENDA. **13**

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