B.E. Seventh Semester (Information Technology) (C.B.S.)

Elective - I : Bio-Informatics

P. Pages : 2 **NKT/KS/17/7503**

Time : Three Hours * 0 1 6 0 * 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.
9. Assume suitable data whenever necessary.

1. a) Classify and explain major data bases in bio-informatics giving example of each database. **7**

b) What is bio-informatics? Describe its scope in modern biology. **6**

OR

2. a) Discuss the application and challenges in bio-informatics. **7**

b) Name the database search algorithm employed in align sequence and explain in detail about any one of them. **6**

3. a) Explain the central dogma of molecular biology with neat diagram. Explain how it is a information science. **7**

b) What is multiple sequence alignment? Describe the applications of multiple sequence alignment? **6**

OR

4. a) Describe the CATH (Class, Architecture, Topology, Homology) databases. **6**

b) Introduce important application of bio-informatics. **7**

5. a) Describe Tertiary and quaternary structure of proteins. **7**

b) What are the different methods available for predicting protein structures? Write a note on tools for protein secondary structure prediction. **7**

OR

6. a) Write a note on methods available for detecting functional sites in the DNA. Discuss about Genscan. **7**

b) Name and explain the various steps evolved in recombinant DNA technology. **7**

7.	a)	Discuss the similarities and differences of FASTA and BLAST tools for sequence alignment.	**6**
	b)	What are the computational skill required for bioinformation? Write elementary commands in Linux operating system.	**7**

OR

8	a)	Why pert is suitable for bio-informatics. Give any five characteristics.	**6**
	b)	Explain how CDRBA is used in bio statistics.	**7**
9.	a)	For the following pair of sequence calculate the total score and align them locally and globally. Assume match score=5, mismatch score=–3, gap penalty = –4, Seq 1: A T T G C T A Seq 2: A T T G C A	**10**
	b)	Define Genome outline structure and composition of any one genome.	**4**

OR

10	a)	What are primary databases? Explain with example and add a note on Gen bank flat file.	**7**
	b)	Write a short note on biological data warehouses.	**7**
11.	a)	What are data types need in representing biological data? Explain in brief.	**7**
	b)	Explain the use of regular expression for representation of pattern and relationship.	**6**

OR

12	a)	How biological data is different than other statistical data? What are species requirements for solving biological data?	**7**
	b)	Explain major steps in pattern recognition and discovery process.	**6**

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