

Time : Three Hours



Max. Marks : 80

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**

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|-----------|----|--|----------|
| <b>2.</b> | a) | Discuss the application and challenges in bio-informatics.   | <b>7</b> |
|           | b) | Name the database search algorithm employed in align sequence and explain in detail about any one of them. | <b>6</b> |
| <b>3.</b> | a) | Explain the central dogma of molecular biology with neat diagram. Explain how it is a information science. | <b>7</b> |
|           | b) | What is multiple sequence alignment? Describe the applications of multiple sequence alignment?             | <b>6</b> |

**OR**

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|-----------|----|---|----------|
| <b>4.</b> | a) | Describe the CATH (Class, Architecture, Topology, Homology) databases.  | <b>6</b> |
|           | b) | Introduce important application of bio-informatics.   | <b>7</b> |
| <b>5.</b> | a) | Describe Tertiary and quaternary structure of proteins.   | <b>7</b> |
|           | b) | What are the different methods available for predicting protein structures? Write a note on tools for protein secondary structure prediction. | <b>7</b> |

**OR**

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|-----------|----|---|----------|
| <b>6.</b> | a) | Write a note on methods available for detecting functional sites in the DNA. Discuss about Genscan. | <b>7</b> |
|           | b) | Name and explain the various steps evolved in recombinant DNA technology.                           | <b>7</b> |

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. 10  
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
- 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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