

B. TECH.**THEORY EXAMINATION (SEM-VI) 2016-17
BIOINFORMATICS****Time : 3 Hours****Max. Marks : 100****Note : Be precise in your answer. In case of numerical problem assume data wherever not provided.****SECTION-A****1 Explain the following :****(10×2=20)**

- a) What is bioinformatics?
- b) Expand NCBI, EMBJ, DDBJ, and PIR.
- c) Write a short note on interfaces?
- d) What is informative site?
- e) What is the role of microarray in bioinformatics?
- f) Mention the various data mining tools, their description and classification.
- g) Give examples of macromolecular structure data and point out the information present in it.
- h) What are the three methods by which you can align a pair of sequence?
- i) Define genetic distance and state two distances based phylogenetic tree prediction methods.
- j) What type of information is obtained in a cluster analysis of microarray data? Explain with a suitable example.

SECTION-B**2 Attempt any five of the following:****(10×5=50)**

- a) Classify and explain major databases in bioinformatics giving examples of each database.
- b) Explain central dogma of molecular biology with neat diagram. Explain how it is an information science.
- c) State and explain various data retrieval tools in bioinformatics. Explain the steps for data mining and knowledge discovery of biological databases.
- d) What is structure visualization? Explain the various rendering tools in structure visualization.
- e) Explain microarray spotting process flow in detail. How is microarray result analysis done?
- f) Explain in detail the various methods of data mining for extracting patterns from data
- g) Differentiate between clustering and classification. Explain hierarchical and k-means clustering in brief.
- h) What is text mining? Explain NLP approach of text mining in detail, giving significance of each stage.

SECTION-C**Attempt any two of the following:****(15×2=30)**

- 3 Define bioinformatics. Explain bioinformatics applications related to the following areas :
 - a) Phylogenetic Analysis.
 - b) Genome Annotation.
 - c) Proteomics.
 - d) Drug Discovery.
- 4 Explain the basic machine learning process with neat diagram. Describe following machine learning processes in brief.
 - a) Neural networks.
 - b) Decision Trees.
- 5 Draw the collaboration – communication model. Explain collaboration and communication hierarchy in detail with neat diagram and appropriate examples.