Code No: 07A81204 | **R07** | | **Set No. 2** |

IV B.Tech II Semester Examinations,April/May 2012
BIO-INFORMATICS
Information Technology

Time: 3 hours   Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks
⋆ ⋆ ⋆ ⋆ ⋆

1. Write short notes on:

    (a) Shot gun Sequencing.
    (b) Direct Shot gun assembly.   [8+8]

2. Discuss in briefly about NCBI and discuss its importance in biological research.
                                                                           [16]

3. Explain the applications of multiple sequence alignments with examples.   [16]

4. How is a secondary database organized? Discuss about the major secondary databases
   you have studied.   [16]

5. Explain about Darwin's evolutionary thoery.   [16]

6. Describe the search parameter criteria in BRENDA with one example.   [16]

7. List out the elementary commands for working with files and Directories. [16]

8. What are PAM matrices? Describe the general steps in deriving the matrices? [16]

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Code No: 07A81204 | R07 | | Set No. 4 |

IV B.Tech II Semester Examinations,April/May 2012
BIO-INFORMATICS
Information Technology

Time: 3 hours   Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks
⋆ ⋆ ⋆ ⋆ ⋆

1. Define Gene? Discuss about important features of Prokaryotic and Eukaryotic gene structure. [16]

2. Write short notes on:

   (a) PAM matrices.

   (b) PAM and Blosum comparision. [8+8]

3. Describe the file format in EMBL and describe its parameters? [16]

4. Describe in brief about the tools to find out secondary and tertiary structures of proteins at EXPASY. [16]

5. What does Informatics mean to Biologists? What is the role of bioinformatics in biotechnolosy? [16]

6. Discuss the search parameter criteria in Swissprot with one example. [16]

7. What is the difference between pair-wise and multiple alignments illustrate with suitable examples. [16]

8. How does the theory of Charles Darwin can be related to homology modelling. [16]

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Code No: 07A81204   **R07**   **Set No. 1**

IV B.Tech II Semester Examinations,April/May 2012
BIO-INFORMATICS
Information Technology

Time: 3 hours   **Max Marks: 80**

Answer any FIVE Questions
All Questions carry equal marks
⋆ ⋆ ⋆ ⋆ ⋆

1. Write short notes on:

   (a) Maxam-Gilbert Chemical Sequencing

   (b) Sanger dideoxy DNA Sequencing.   [8+8]

2. Write short notes on:

   (a) Telnet.

   (b) WWW.   [8+8]

3. Explain how you can build a homology model. What are the methods that can be implemented in building homology models?   [16]

4. Describe the Basic Local Alignment Search Tool (BLAST) algorithm?   [16]

5. What tools and search criteria is used to search protein profiles in Expasy.   [16]

6. Discuss the bioinformatics analysis tools available in KEGG.   [16]

7. Explain briefly about CLUSTALX & CLUSTALW programs in construction of protein profiles and motifs.   [16]

8. What is a database ? How do you organize and manage biological databases? [16]

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3

Code No: 07A81204   **R07**   **Set No. 3**

IV B.Tech II Semester Examinations,April/May 2012
BIO-INFORMATICS
Information Technology

Time: 3 hours   Max Marks: 80
Answer any FIVE Questions
All Questions carry equal marks
⋆ ⋆ ⋆ ⋆ ⋆

1. Discuss about the concept of Homology searches.   [16]

2. What is KEGG? Discuss the bioinformatics tools available in it.   [16]

3. What is the central dogma of molecular Biology? How can molecular biology be considered as an information science.   [16]

4. How can you search and retrieve information of unknown gene from World Wide Web. Explain thesteps involved with one example.   [16]

5. Explain about the methods employed for sequencing an entire Genome.   [16]

6. Describe in brief about KEGG and state how it is useful in research.   [16]

7. By choosing two sequences when do you say that both sequences are significantly similar. Explain with neat flow chart.   [16]

8. Explain the types of trees available for phylogenetic analysis and their applications.
[16]

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