Code No: 2421206

Set No. 1

IV B.Tech II Semester Regular Examinations, April/May 2009
BIO-INFORMATICS
(Information Technology)

Time: 3 hours　　　　　　　　　　　　　　　　　　　　Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks
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1. What is Hypertext Transfer Protocol (HTTP)? Describe different commands used in HTTP? [16]

2. Describe the following:

   (a) Sequence Homology

   (b) Differences between orthologs and paralogs. [8+8]

3. What is genome sequencing? Describe its application? [16]

4. Explain the various methods that can be adapted in sequence similarity searching. Discuss their relative merits and demerits? [16]

5. What are the search engines available at NCBI website? Discuss briefly the search criteria. [16]

6. What is a secondary database? Discuss the bioinformatics databases available on Internet. [16]

7. What tools and search criteria is used to search protein profiles in Expasy. Give suitable examples. [16]

8. What is dynamic programming method. Explain with an example. [16]

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Code No: 2421206

Set No. 2

IV B.Tech II Semester Regular Examinations, April/May 2009
BIO-INFORMATICS
(Information Technology)

Time: 3 hours

Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks

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1. What is Bioinformatics? Describe its scope in modern biology? [16]

2. Describe the Richard Owen's Contribution to Evolutionary Theory? [16]

3. Describe the following:

   (a) Physical mapping of DNA
   (b) Genetic mapping of DNA. [8+8]

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

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

6. Discuss the search criteria in the tools of Swissprot with suitable examples. [16]

7. Describe in brief about Enzymatic databases and state its applications in bioinformatics. [16]

8. What is multiple sequence alignment. Explain with an example. [16]

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Code No: 2421206

Set No. 3

IV B.Tech II Semester Regular Examinations, April/May 2009
BIO-INFORMATICS
(Information Technology)

Time: 3 hours

Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks
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1. Describe the following:

   (a) Uniform Resource Locator (URL)

   (b) Role of Internet in Bioinformatics. [8+8]

2. What is homology and how this homology is helpful for evolutionary theories. [16]

3. Describe in detail about the Shot gun large sequencing method? [16]

4. Write a detailed notes on Dynamic Programming Algorithm (DPA)? [16]

5. What are biological databases? What are the parameters are used in management of these biological databases? [16]

6. What is KEGG? Discuss the types of bioinformatics tools available and state their applications. [16]

7. Describe the search parameter criteria in BRENDA. [16]

8. Explain how you will trace out different types of mutations using multiple sequence alignments. [16]

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Code No: 2421206

$\boxed{\textbf{Set No. } 4}$

IV B.Tech II Semester Regular Examinations, April/May 2009
BIO-INFORMATICS
(Information Technology)

Time: 3 hours

Max Marks: 80

Answer any FIVE Questions
All Questions carry equal marks

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1. What is File Transfer Protocol (FTP)? Describe different types of FTP's? [16]

2. Describe the Richard Owen's Contribution to Evolutionary Theory? [16]

3. Describe the following:

   (a) Physical mapping of DNA
   (b) Genetic mapping of DNA. [8+8]

4. Discuss the relative merits of Pair-wise and Multiple sequence alignment methods? [16]

5. Discuss about the molecular modeling databases and their applications in bioinformatics. [16]

6. Discuss the secondary databases of bioinformatics and state their applications in research with suitable examples. [16]

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

8. How would you construct phylogenetic trees using clustal programs. [16]

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