

**III B.Tech II Semester Supplementary Examinations,
November/December 2005
BIO-INFORMATICS
(Bio-Technology)**

Time: 3 hours

Max Marks: 80

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

1. What is HTTP? Explain about operation of HTTP? [16]
2. Explain about computational method for aligning DNA and Protein sequences? [16]
3. Define Multiple Alignment? Describe in detail about methods employed for Multiple sequence alignment? [16]
4. What is meant by Database Similarity searches? Explain different ways of Database similarity searching? [16]
5. Explain about Percent Accepted Mutation? [16]
6. Describe the following:
 - (a) Perfect phylogeny
 - (b) The relationship of Phylogenetic analysis and sequence alignment. [16]
7. Define Genome? Outline the structure and composition of prokaryotic and Eukaryotic genomes? [16]
8. What is a gene? Write the fine structure of the gene and compare the structural differences of gene between prokaryotes and eukaryotes? [16]

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1. Explain the steps involved in protein prediction and modeling by using Bioinformatics? [16]
2. Give an account of BLAST programs and how are they useful? [16]
3. Explain about Localized alignments in sequences? [16]
4. Describe the different databases available for the storage of protein information resources? [16]
5. Explain about Percent Accepted Mutation? [16]
6. Discuss about Concept of Trees in phylogenetic Analysis? [16]
7. Define Genome? Outline the structure and composition of prokaryotic and Eukaryotic genomes? [16]
8. Write short notes on:
 - (a) GRAIL II
 - (b) ORF [16]

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1. Describe the following:
 - (a) Uniform Resource Locator (URL)
 - (b) Role of Internet in Bioinformatics [16]
2. Define Multiple sequence alignment? Describe in detail about methods employed in Multiple sequence alignment? [16]
3. Describe any one progressive method of multiple sequence alignment? [16]
4. How can you classify sequence databases? Describe about Nucleotide sequence databases? [16]
5. Explain about Pairwise database searching. [16]
6. Discuss about relationships of Phylogenetic analysis to sequence alignment? [16]
7. Write an essay on sequence assembly and Gene Identification? [16]
8. Write short notes on:
 - (a) GRAIL II
 - (b) ORF [16]

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1. What is Bioinformatics? Describe its scope in modern biology? [16]
2. What type of scoring matrix is used by BLAST? Explain about different substitution matrices? [16]
3. What is multiple sequence alignment? Describe the applications of multiple sequence alignments? [16]
4. Write in detail about DNA versus Protein searches? [16]
5. Write short notes on:
 - (a) BLOSUM
 - (b) Differentiate between PAM & BLOSUM [16]
6. Discuss about relationships of Phylogenetic analysis to sequence alignment? [16]
7. What is DNA mapping? Describe its applications? [16]
8. Explain in detail about Feature based approaches to Gene Prediction? [16]
