

III B.Tech. II Semester Regular Examinations, April/May -2005

BIO-INFORMATICS

(Bio-Technology)

Time: 3 hours

Max Marks: 80

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

1. What is Bioinformatics? Describe its scope in modern biology?
2. Write short notes on:
 - (a) Dot plot
 - (b) Local alignment
3. Define Multiple Alignment? Describe in detail about methods employed for Multiple sequence alignment?
4. Explain in detail about DNA sequence databases?
5. Who created BLAST and explain the type of scoring matrix used by BLAST?
6. Describe the following:
 - (a) Perfect phylogeny
 - (b) The relationship of Phylogenetic analysis and sequence alignment.
7. Explain in detail about DNA sequence methodologies?
8. What are Neural Networks? How they are useful in predicting a gene structure?

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1. What is Bioinformatics? Describe its scope in modern biology?
2. Write short notes on:
 - (a) Dot plot
 - (b) Local alignment
3. How to multiply Aligned sequences and assessing quality of alignment?
4. How can you classify sequence databases? Describe about Nucleotide sequence databases?
5. Who created BLAST and explain the type of scoring matrix used by BLAST?
6. Describe the following:
 - (a) Perfect phylogeny
 - (b) The relationship of Phylogenetic analysis and sequence alignment.
7. Discuss in detail about the steps involved in sequence assembly?
8. Write short notes on:
 - (a) GRAIL II
 - (b) ORF

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1. Describe the following:
 - (a) Uniform Resource Locator (URL)
 - (b) Role of Internet in Bioinformatics
2. Describe the use of Scoring matrices and Gap penalties in Sequence alignment?
3. Describe about Progressive methods for Multiple sequence alignment?
4. Write an essay on different genome (DNA) information resources?
5. Explain Database searching with Smith-waterman Dynamic programming method?
6. Describe the following:
 - (a) Perfect phylogeny
 - (b) The relationship of Phylogenetic analysis and sequence alignment.
7. Explain in detail about DNA sequence methodologies?
8. Write short notes on:
 - (a) GRAIL II
 - (b) ORF

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1. Write short notes on:
 - (a) Structure of Internet
 - (b) URL general format
2. What type of scoring matrix is used by BLAST? Explain about different substitution matrices?
3. Explain about Dynamic Programming method for Multiple sequence alignment.
4. Write short notes on:
 - (a) Tr-EMBL
 - (b) P-fam
5. Explain Database searching with Smith-waterman Dynamic programming method?
6. Explain the significance of Phylogenetic analysis in inferring the relationship between distantly related sequences?
7. Explain in detail about DNA sequence methodologies?
8. Write short notes on:
 - (a) GRAIL II
 - (b) ORF
