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MTBT-301

Roll No. | | | | | | | | | | |

B. Tech. - M. Tech. (DUAL) (BIOTECHNOLOGY)

NINTH SEMESTER EXAMINATION, 2010-11

BIOINFORMATICS, GENOMICS & PROTEOMICS

Time : **3 Hours** Total Marks : **100**

Note : **(i)** Attempt any **FIVE** questions.
(ii) Marks are indicated against each question.

1. **(a)** What is NCBI? Enumerate few important resources available at NCBI. **5**

(b) What are data retrieval tools? Explain any one tool with suitable applications. **5**

(c) What is homalogy modeling, explain it by giving different steps involve in it? **10**

2. **(a)** Write short notes on any **Two** of the following : **10**

(i) ESTs

(ii) Biological Databases

(iii) Gene Sequencing Tags (GSTs)

(iv) PubMed

(b) Define BLAST. Discuss several variants of BLAST. How is it different from FASTA? **10**

3. Attempt any **Four** parts of following : **5 x 4 = 20**

(a) Expand the following terms :

EMBL, SWISS-PROT, PROSITE and CATH

(b) Differentiate between local and global sequence alignment.

(c) How is gene structure predicted using bioinformatics tools?

(d) What is multiple sequence alignment (MSA)? Mention its significance.

(e) Discuss the general software requirement specifications (srs) for developing a software tool for ORF finding.

4. Attempt any **Four** parts of following : **5 x 4 = 20**

(a) What is SAGE? How it helps to study gene expression?

(b) Write a brief account on Dideoxy method of DNA sequencing.

(c) Discuss the importance of genetic map of chromosomes.

(d) Discuss clone conting approach for genome sequencing.

(e) What are microarrays? Discuss applications of microarray analysis.

5. Attempt any **Two** parts of following : **10 x 2 = 20**

(a) How is a new drug designed? Discuss important steps of drug designing.

(b) What is Phylogenetic analysis? Discuss tools for phylogenetic analysis.

(c) Give a brief account on human genome project (HGP).

6. Attempt any **Two** parts of following : **10 x 2 = 20**

(a) Signal peptide bank

(b) OMIM database

(c) Smith waterman algorithm

(d) Shot gun sequencing

7. Attempt any **Two** parts of following : **10 x 2 = 20**

(a) Discuss the importance of protein-protein interaction studies.

(b) Discuss a suitable method for prediction of secondary structure of a protein.

(c) Differentiate between structural genomics and functional genomics.

(d) What is chromosome walking? How is it different from clone contig approach?