



Reg. No. :

Name :

Fourth Semester M.Sc. Degree Examination, July 2018

Branch : BOTANY

**BO 241 : Bioinformatics
(2013 Admission Onwards)**

Time : 3 Hours

Max. Marks : 75

I. Write short notes on the following :

- 1) Local Alignment algorithms.
- 2) Muscle.
- 3) Gen bank.
- 4) PDB.
- 5) Metabolomics.
- 6) Phylogram.
- 7) Sequin.
- 8) Tree View.
- 9) Homology modeling.
- 10) Swiss-Prot.

(10×1=10 Marks)

II. Answer the following in **not** more than **50** words.

- 11) a) Compare and contrast global and local sequence alignment.

OR

- b) What are the different sequence databases ?

- 12) a) Write a brief note on BLAST and its variants.

OR

- b) Briefly explain the algorithm of FASTA.

- 13) a) Briefly explain the steps involved in searching Nucleotide database through ENTREZ taking human papillomavirus 13 as an example.

OR

- b) Briefly explain the common format of sequence data input files of FASTA, NEXUS and MEGA.

P.T.O.



- 14) a) What are the main constraints encountered in Multiple sequence Alignments ?

OR

- b) How do you test the node reliability of a phylogenetic tree ?

- 15) a) What are microarrays ? How do they help in functional genomics ?

OR

- b) What are paralogous and orthologs ?

(5×2=10 Marks)

III. Answer the following questions in **not** more than **150** words.

- 16) a) What are the different Docking Tools ?

OR

- b) What are the advantages and disadvantages involved in computer aided drug design ?

- 17) a) What is meant by a gene tree ? How does it differ from a species tree ? Explain the tree building softwares MEGA, PAuP* and Rax ML briefly.

OR

- b) What are the constraints, advantages, disadvantages and applications of molecular phylogeny in comparison with traditional taxonomy ?

- 18) a) What are the different types of repetitive sequences found in eukaryotic genome ?

OR

- b) What are somatic hybrids ? How do they aid in functional genomics ?
What are DNA microarrays ?

- 19) a) What are the different techniques for a tertiary structure prediction ?

OR

- b) How do protein databases help in proteomics and comparative genomics ?

- 20) a) What are secondary databases ?

OR

- b) What are the applications of computational biology ?



21) a) What are the different tools for searching a databases ?

OR

b) Briefly explain Ras Mol.

22) a) What are the applications of Linux in bioinformatics ?

OR

b) What are the applications of Bio-Perl in Bioinformatics ? (7×5=35 Marks)

IV. Answer the following questions in **not** more than **250** words.

23) a) Briefly explain the applications of Bioinformatics.

OR

b) What are the different DNA sequence evolution models for phylogeny ?

24) a) What are the applications of proteomics ?

OR

b) Briefly explain the significance of HGP on the growth of Bioinformatics.

(2×10=20 Marks)

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