

QP CODE: 24001175



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# B.Sc DEGREE (CBCS) REGULAR / REAPPEARANCE EXAMINATIONS, MARCH 2024 Sixth Semester

B.Sc Botany and Biotechnology Model III Double Main

## **CORE COURSE - BO6CRT23 - BIOINFORMATICS**

Common for B.Sc Botany Model I, B.Sc Botany Model II Food Microbiology, B.Sc Botany Model II Environmental Monitoring And Management, B.Sc Botany Model II Horticulture and Nursery Management & B.Sc Botany Model II Plant Biotechnology

2017 Admission Onwards

# F45FFCD9

Time: 3 Hours Max. Marks : 60

### Part A

Answer any **ten** questions.

Each question carries **1** mark.

- 1. What is Shotgun Sequencing?
- 2. Define bibliographic database.
- 3. Enumerate on biological databases.
- 4. Write two tool used in Prosite.
- Expand mmCIF.
- 6. List out the names of DNA microarray databases.
- 7. What is sequence alignment?
- 8. Define local sequence alignment.
- 9. Write any two use of FASTA.
- 10. Give the name of method of producing direct multiple alignment.
- 11. What is protein threading?
- 12. What is meant by comparative modelling?

 $(10 \times 1 = 10)$ 

### Part B

Answer any six questions.

Each question carries 5 marks.

13. Differentiate between Epigenomics and Metagenomics.



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- 14. Write on EMBL database.
- 15. Comment on Entrez genome database.
- 16. Comment on Stanford microarray database.
- 17. What is sequence alignment? Comment on its 2 types.
- 18. Comment on the Needle-Wunsch algorithm.
- 19. What is PHYLIP and how it is used in Bioinformatics?
- 20. Briefly explain homology based method of protein function prediction.
- 21. Write a note on the application of scoring functions on molecular docking.

 $(6 \times 5 = 30)$ 

#### Part C

Answer any two questions.

Each question carries 10 marks.

- 22. Discuss on NCBI.
- 23. Write on 2D gel electrophoresis data bases.
- 24. Elaborate phenetic and cladistics methods of phylogenetic tree building.
- 25. Comment on different levels of protein conformation.

 $(2 \times 10 = 20)$ 

