

Reg. No. :

Name :

Ph.D. ENTRANCE EXAMINATION 2023

FACULTY OF APPLIED SCIENCES AND TECHNOLOGY

COMPUTATIONAL BIOLOGY AND BIOINFORMATICS

Time : 3 Hours

Max. Marks : 100

Instructions :

- 1) Answer **any ten** questions each from Section **A** and Section **B**.
- 2) Each question carries **5** marks.
- 3) No additional Answer sheets will be provided.
- 4) Candidates should clearly indicate the section, Question number in the answer booklet.

Section – A

Research Methodology

Answer any **ten** questions. Each question carries **5** marks.

1. Discuss the different stages of research process.
2. Briefly discuss what plagiarism is and how you will take care to ensure its avoidance.
3. Explain the relevance of information literacy in cyber age.
4. Briefly explain RSS feeds, TOC alerts and DB alerts.
5. Compare Open access and traditional publishing
6. What are the ways available for a researcher to effectively use web resources for benefiting research? Discuss any five points.

7. Compare patenting and publishing.
8. Discuss ethical issues in modern science, related to life science-based research.
9. Give an example of reference citing in IMARD format.
10. Discuss any five ways to improve the logical thinking.
11. Briefly contrast the following
 - (a) creativity and craft
 - (b) innovation and creativity
 - (c) copyrights and patents
12. Discuss the scientific method based on a selected experiment that you have conducted or are familiar with
13. Explain the relevance of information literacy in cyber age.
14. Compare and contrast between h index i10 index.
15. Explain pros and cons of open Access publishing.

(10 × 5 = 50 Marks)

Section – B

Computational Biology

Answer any **ten** questions. Each question carries **5** marks.

1. Bioinformatics is the application of computational technology to handle the rapidly growing repository of information related to molecular biology”. Give a brief insight based on your knowledge on this definition of bioinformatics
2. Align AGCTCAG with AGGTCA by using a suitable scoring scheme.
3. Differentiate between Pairwise and Multiple sequence alignment.
4. Briefly explain the big data challenges in the field of Bioinformatics.
5. Distinguish between Bowtie and BWA.

6. What is a contig? What is a scaffold? Describe de novo assembly. Name a software used for de novo assembly.
7. An online educational platform offers three courses: Programming Courses, Robotics Courses and Academic Writing Courses: The vendor gives a discount of 10% on orders for programming-based courses if the order is for more than Rs. 1,000. On orders of more than Rs. 750 for Robotics Courses, a discount of 5% is given, and a discount of 10% is given on orders for academic writing courses of value more than Rs. 500. Assume that the numeric codes 1,2 and 3 are used for Programming, Robotics and Academic Writing Courses respectively. Write a python program that reads the product code and the order amount and prints out the net amount that the learner is required to pay after the discount.
8. Briefly explain the public sequence databases which support Next generation sequencing data and the various data formats being supported.
9. Perform the following string manipulation using perl script
 - (a) Apply String*repetition operator on "ATC"
 - (b) Find Length of the DNA sequence "cgtgggggttttt"
 - (c) Convert the above sequence into upper case
10. Explain various intermolecular interactions of proteins. What is their role in structural stability of protein?
11. Write short notes on X ray crystallography and NMR spectroscopy.
12. Briefly explain the various steps in homology modelling.
13. What are mutations? Discuss briefly the various types of mutations and the consequences of mutation.
14. Briefly explain the steps involved in rDNA technology.
15. Discuss the DNA repair mechanisms briefly.

(10 × 5 = 50 Marks)