

Reg. No. :

Name :

Ph.D. ENTRANCE EXAMINATION, NOVEMBER 2022
FACULTY OF APPLIED SCIENCE AND TECHNOLOGY
COMPUTATIONAL BIOLOGY AND BIOINFORMATICS

Time : 3 Hours

Max. Marks : 100

Instructions :

- 1) Answer **any ten** questions each from Section **A** and **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

- I. Answer any **ten** questions. All questions carry equal marks.
 1. Pure research may, in course of time transform to applied research- Briefly discuss.
 2. Briefly discuss what plagiarism is and how you will take care to ensure its avoidance.
 3. Single blind and double blind peer-review are traditionally common. In recent times, open peer-review has come into popularity. Briefly compare these.
 4. Open source software and Copy-left licenses (such as creative commons) are argued to be ethically superior alternatives. What is your opinion? Briefly discuss with examples.

5. In 2005 patent amendment in India made drug molecules patentable. Earlier only the production process was patentable. How do you see this? Argue for and against this.
6. The abstract, introduction and conclusion part of a research paper is sometimes found to be overlapping. Explain the contrast between the three sections.
7. Briefly explain and give one example of each: (a) Pure Research (b) Innovative Research (c) Applied Research
8. (a) What is impact Factor? How is it calculated? (b) Give impact Factors of two Bioinformatics journals. (c) Compare Open access and traditional publishing
9. What is ethics? Discuss ethical issues in modern science, related to life science based research.
10. "Research is a systematic process to generate new knowledge through the scientific method" -- critically analyze this definition of research and briefly explain on scientific methods.
11. Compare copyright and patents.
12. Explain IMRAD model for writing research paper.
13. Explain the idea of IPR and how this help in research.
14. Logical thinking is an essential skill for a critical thinker, but logical fallacies can be found easily in public discourses. Discuss at least 3 logical fallacies with examples.
15. Discuss your idea about making a powerful multimedia presentation in a research seminar.

(10 × 5 = 50 Marks)

Section – B

Computational Biology and Bioinformatics

- II. Answer any **ten** questions. All questions carry equal marks.
1. Write a note on the principle and applications of PCR.
2. Discuss the importance of Nucleotide databases in Bioinformatics.

3. Briefly describe the mechanism of transcription.
4. Write short notes on the different types of RNAs with the help of diagram.
5. Briefly explain the principle and applications of chromatography.
6. What is Human Genome project? Discuss briefly.
7. Explain different steps in constructing a phylogenetic tree, explaining the assumptions/ choices of decisions in each step with illustrative examples.
8. What are the different intermolecular interactions involved in protein structure?
9. Consider an array, @array=('bioinformatics', 'cadd', 'biocomputing', 'computing', 'machinelearning', '2023') (i) describe the effect of the following regular expression modifiers on pattern matching.
 - (a) `foreach $i(@array) { if ($i= ~ /b/) {print "$i\n" ;}}`
 - (b) `foreach $i(@array) { if ($i= ~ /^bi/) {print "$i\n" ;}}`
 - (c) `foreach $i(@array) { if ($i= ~ /7?/) {print "$i\n" ;}}`
 - (d) `foreach $i(@array) { if ($i= ~ /d$/) {print "$i\n" ;}}`
 (ii) Write a bio-Perl program to translate a DNA sequence.
10. How do you submit biological data to a public database? List the major submission tools in NCBI.
11. (i) Align AGCTCAG with AGGTCA by using a suitable scoring scheme
 (ii) Differentiate between Pairwise and Multiple sequence alignment.
12. Write a simple python program for (i) checking whether a triangle is isosceles or scalene or right triangle , given sides as 6,8,10 (ii) illustrating to print the following pattern:


```

1
2 3
3 4 5
4 5 6 7

```

13. Explain Needleman-Wunch algorithm for optimal global alignment of the nucleotide sequence using the example of aligning ATTCGT and ATCCGT with match score +1, mismatch score 0 and gap penalty -1.
14. Briefly explain the structural organisation of DNA and protein.
15. Briefly explain the drug discovery pipeline.

_____ (10 × 5 = 50 Marks)