

M.A / M. Sc. DEGREE EXAMINATION, APRIL 2022  
SECOND SEMESTER

COURSE : ELECTIVE  
PAPER : INTRODUCTION TO BIOINFORMATICS  
TIME : 3 HOURS

MAX. MARKS: 100

SECTION – A

ANSWER ALL QUESTIONS

(20 X 1=20)

Choose the correct answer:

- The term Bioinformatics was coined by
  - J.D.Watson
  - Pauline Hogeweg
  - Margaret Dayhoff
  - Frederic Sanger
- Which one of the following is a command based offline tool for molecular structural visualization?
  - Swiss-PDB viewer
  - RasMol
  - Qmol
  - PyMol
- Which of the following is incorrect about bootstrapping?
  - It is a statistical technique that tests the sampling errors of a phylogenetic tree
  - It does the tests by repeatedly sampling trees through slightly perturbed datasets
  - A newly constructed tree is not biased at all
  - The robustness of the original tree can be assessed here
- With respect to microsatellite DNA which of the following is correct?
  - Tandem repeats
  - Dinucleotide repeats
  - 100bp units
  - Inaccurate duplicating
- Which of the following is/are true about the stacking gel?
  - The stacking gel solution contains acrylamide
  - It is on the top of the separating gel.
  - It is used to dilute the protein sample before it enters the main separating gel
  - It is into this gel that the wells are formed and the proteins loaded
  - i, ii and iii only
  - ii, iii, and iv only
  - i, ii and iv only
  - All of them

Fill in the Blanks:

- \_\_\_\_\_ is the sequence retrieval system used in NCBI
- \_\_\_\_\_ is the database used to access the protein structure information
- \_\_\_\_\_ tree diagram indicates the hypothetical common ancestor, or ancestral lineage
- \_\_\_\_\_ and \_\_\_\_\_ are the two gene finding methods.
- \_\_\_\_\_ and \_\_\_\_\_ are the secondary structures of protein molecule.

Define in single line:

- Mention the single letter code for the aminoacids: ARG, TYR, PHE.
- List the variants of BLAST.
- What is the purpose of phylogenetic tree?
- Name any two gene prediction tools.
- What is the use of SDS in protein separation?

Say True or False:

- The databases GenBank, EMBL, DDBJ are updated daily.
- BLASTX uses protein sequences as queries to search against a protein sequence database.

18. Building phylogenetic tree involves bifurcation and multifurcation.
19. Repeated DNA can be referred to as junk DNA.
20. Type IV restriction enzymes cleave only methylated DNA and show weak sequence specificity.

### SECTION – B

**ANSWER ANY FOUR QUESTIONS. EACH ANSWER SHOULD NOT EXCEED 500 WORDS. ALL QUESTIONS CARRY EQUAL MARKS. (4 x 10 = 40 )**

21. Comment on Entrez retrieval system.
22. Elaborate the steps involved in BLAST analysis.
23. How the PDB database can be accessed and their uses in protein analysis.
24. Highlight the strategies in phylogenetic tree construction.
25. Classify the repeat sequences based on their size, location and its uses.
26. Describe the protein structure architecture with diagrams.
27. Discuss the types of restriction enzymes and mapping technologies.

### SECTION – C

**ANSWER ANY TWO QUESTIONS. EACH ANSWER SHOULD NOT EXCEED 1200 WORDS. ALL QUESTIONS CARRY EQUAL MARKS. (2 x 20 = 40 )**

28. Illustrate the important applications of bioinformatics in detail.
29. Brief about Cladistic and Phenetic methods of evolutionary analysis
30. Elaborate the gene finding methods in detail.
31. Comment on SDS-PAGE protein separation technique in detail with diagram.

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