

PSG COLLEGE OF ARTS & SCIENCE
(AUTONOMOUS)

MSc DEGREE EXAMINATION MAY 2022
(Fourth Semester)

Branch – APPLIED MICROBIOLOGY

DISCIPLINE SPECIFIC ELECTIVE –II
INTRODUCTION TO BIOINFORMATICS

Time: Three Hours

Maximum: 75 Marks

SECTION-A (10 Marks)

Answer ALL questions

ALL questions carry EQUAL marks (10 x 1 = 10)

1. NCBI hosts -----
(i) DDBJ (ii) Genbank (iii) EMBL (iv) all.
2. Three-dimensional structural data of proteins are obtained by
(i) taxography (ii) autoradiography
(iii) radiography (iv) X-ray crystallography
3. The program Clustal Omega is for ----- sequence alignment.
(i) single (ii) pairwise (iii) triple (iv) multiple
4. BLAST finds regions of ----- similarity.
(i) local (ii) foreign (iii) external (iv) alien
5. A phylogenetic tree is also referred as
(i) cladogram (ii) photogram (iii) clade (iv) dendrogram
6. Neighbor joining approach of phylogenetic tree construction is
(i) moderate; analyses no data (ii) slower; analyses least data.
(iii) faster; analyses large data (iv) slower
7. Protein coding genes also known as
(i) exons (ii) introns (iii) operons (iv) splison
8. Systems biology emerged as a new field of science from ----- onwards
(i) 1990 (ii) 2000 (iii) 2010 (iv) 2020
9. If structure of a protein is known, it often allows ----- prediction also.
(i) functional (ii) efficacy
(iii) composition (iv) molecular weight
10. Pharmacogenomics analyzes between the genetic makeup of an individual and its response to -----
(i) living ecosystem (ii) water (iii) drugs (iv) food

SECTION - B (25 Marks)

Answer ALL questions

ALL questions carry EQUAL Marks (5 x 5 = 25)

11 a. What is a flat-file database? Explain.

(OR)

b. Comment on PDB.

12. a. Briefly explain a conserved genomic sequence.

(OR)

b. What is local sequence alignment? Write in brief.

13. a. Describe briefly a phylogeny.

(OR)

b. State the concept of phylogenetic tree.

Cont...

14. a. Give a note on a whole- genome sequence.
(OR)
b. What is known as an annotated sequence?
- 15.a. Write an account on metabolomics.
(OR)
b. Bring out the need for synthetic biology.

SECTION -C (40 Marks)

Answer ALL questions

ALL questions carry EQUAL Marks (5 x 8 = 40)

16. a. Summarize the features of biological databases.
(OR)
b. Give a detailed account on EMBL flat file.
17. a. Elaborate multiple sequence alignment with examples.
(OR)
b. Describe global sequence alignment. Add a note on its uniqueness.
18. a. Exemplify Neighbour joining method of phylogenetic tree construction.
(OR)
b. Explain a rooted phylogenetic tree.
19. a. List out and explain the features of genome annotation.
(OR)
b. Write about the reductionist approach of systems biology.
20. a. With suitable examples, explain the methods of predicting RNA secondary structure.
(OR)
b. Discuss the basic approaches of predicting protein structures.

Z-Z-Z

END