

PSG COLLEGE OF ARTS & SCIENCE
(AUTONOMOUS)

MSc DEGREE EXAMINATION MAY 2023
(Fourth Semester)

Branch – APPLIED MICROBIOLOGY

**DISCIPLINE SPECIFIC ELECTIVE – II: INTRODUCTION TO
BIOINFORMATICS**

Time: Three Hours

Maximum: 50 Marks

SECTION-A (5 Marks)

Answer ALL questions

ALL questions carry EQUAL marks

(5 x 1 = 5)

- 1 Each record in a database is called an-----.
(i) Entry (ii) File
(iii) Record (iv) Ticket
- 2 The alignment procedure that tries to align the entire sequence is-----.
(i) multiple sequence alignment (ii) pairwise alignment
(iii) Global alignment (iv) local alignment
- 3 The phylogenetic tree represents evolutionary relationship among species and also called as-----.
(i) Genetic tree (ii) Evolutionary tree
(iii) Ploycystric tree (iv) Polysaccharide tree
- 4 Which of the following is correct regarding gene ontology?
(i) need to standardize protein function (ii) limited molecular functions
(iii) Facilitate grouping of protein (iv) Biological processes not involved
- 5 The identification of drugs through the genomic study is called-----.
(i) Genomics (ii) Pharmacogenomics
(iii) Pharmacogenetics (iv) Cheminformatics

SECTION - B (15 Marks)

Answer ALL Questions

ALL Questions Carry EQUAL Marks

(5 x 3 = 15)

- 6 a Discuss in brief note on db-tables as a mode of data storage.
OR
b State out the importance of PDB with suitable examples.
- 7 a Evaluate the impacts of global sequence alignment with suitable explanation.
OR
b Briefly explain about Substitution matrices.
- 8 a Illustrate in brief about rooted phylogenetic tree.
OR
b Analyse the importance of Maximum parsimony.
- 9 a Distinguish wet and dry experiments with suitable examples.
OR
b Discuss in brief about significance of EST clusters in functional annotation.
- 10 a State out the importance of protein structure prediction.
OR
b Determine about metabolomics and add a note on its advantages.

Cont...

SECTION -C (30 Marks)

Answer ALL questions

ALL questions carry EQUAL Marks

(5 x 6 = 30)

- 11 a Analyze the importance of various mode of database search.
OR
b Give critical comment on file formats for DDBJ.
- 12 a Explain in brief note on suitable scoring method for sequence alignment.
OR
b Criticize the impacts of pairwise sequence alignment.
- 13 a State out Basic concepts of phylogenetic analysis.
OR
b Expand UPGMA and explain its advantages.
- 14 a Predict the advantages of predictions and simulations.
OR
b Recommend strategies for whole genome annotations.
- 15 a Determine in brief note on tertiary RNA predictions with suitable examples.
OR
b Distinguish a brief note on Genomics and transcriptomics.

Z-Z-Z

END