

**PSG COLLEGE OF ARTS & SCIENCE
(AUTONOMOUS)**

**MSc DEGREE EXAMINATION DECEMBER 2022
(Second Semester)**

Branch – BIOTECHNOLOGY

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. The classification results from both systems, _____ are quite dissimilar.

(i) SCAPE and CAT	(ii) SCAPE
(iii) CAT	(iv) SCOP and CATH
2. PAUP is a _____ program with a user-friendly graphical interface.

(i) Macintosh	(ii) Windows
(iii) LINUX	(iv) NCBI
3. _____ refers to the inactivation of Insertional inactivation.

(i) HOST	(ii) Gene of host
(iii) Gene of vector	(iv) Gene of Host
4. In dot matrix in ab initio methods, the diagonals _____ to the main diagonal represent regions that can self hybridize.

(i) parallel	(ii) cutting randomly
(iii) perpendicular	(iv) adjacent parallel
5. _____ software is used for Phylogenetic analysis.

(i) LUDI	(ii) MEGA
(iii) CHEM3D	(iv) CoMFA

SECTION - B (15 Marks)

Answer ALL Questions

ALL Questions Carry EQUAL Marks (5 x 3 = 15)

6. a. Illustrate the retrieval method for DNA and Protein database.
(or)
b. Recommend the use of markup and script language in bioinformatics.
7. a. State the functions of PAM and Blosum.
(or)
b. Show the difference between PSI and Phi Blast.
8. a. Analyze the principle for PCR primer Design.
(or)
b. Determine the methods used to identify diseased gene.
9. a. Recommend the homology modelling as a functional genomic tool.
(or)
b. Discuss the protein sequence analysis.
- 10.a. Support the principles of neuro-bioinformatics as next generation tool in personalized medicine.
(or)
b. Explain SNPs.

Cont...

SECTION -C (30 Marks)

Answer ALL questions

ALL questions carry EQUAL Marks (5 x 6 = 30)

11. a. Assess the use of RDBMS for genome and protein related informations.
(or)
b. Evaluate the significance of EST and STS in data resource queries.
12. a. Compare the BLAST and FASTA technique for the retrieval of the sequence Information.
(or)
b. Construct a phylogeny for species of your own example to explain sequence homology.
13. a. Appraise the utility of microarray in genome mapping database.
(or)
b. Criticize the genomic tool usage for gene annotation methods.
14. a. Develop the protocol for the protein structure prediction using the informations from the secondary databases with suitable examples.
(or)
b. Elucidate the functions of molecular visualizing tools in detail.
15. a. Interpret the applications of QSAR in systems Biology.
(or)
b. Predict the application of metabolomics in medical informatics.

Z-Z-Z

END