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22BCP315AN

PSG COLLEGE OF ARTS & SCIENCE
(AUTONOMOUS)

MSc DEGREE EXAMINATION DECEMBER 2025
(Third Semester)

Branch - **BIOCHEMISTRY**

MAJOR ELECTIVE COURSE – I : BIOINFORMATICS

Time: Three Hours

Maximum: 75 Marks

SECTION-A (10 Marks)

Answer **ALL** questions

ALL questions carry **EQUAL** marks (10 × 1 = 10)

Module No.	Question No.	Question	K Level	CO
1	1	Which Linux Command is used to remove files? a) remove b) rm c) delete d) del	K1	CO1
	2	When a string is used for numeral computations perl converts it into _____ a) Character b) Floating point number c) Number d) Boolean value	K2	CO1
2	3	Label the information retrieval tool of NCBI GenBank a) Entrez b) STAG c) Seqln d) Text search	K1	CO2
	4	Give the typical example of Sequence data a) Large scale data b) Very small data c) medium size data d) Unstructured data	K2	CO2
3	5	Which of the following is an example of homology and similarity tool? a) BLAST b) RasMoL c) EMBOSS d) PROSPECT	K1	CO3
	6	Which of the following tools is used for the identification of motifs? a) BLAST b) COPIA c) PROSPECT d) Pattern hunter	K2	CO3
4	7	What is the process of finding the relative location of genes on a chromosome a) Gene tracking b) Genome walking c) Genome mapping d) Chromosome walking	K1	CO4
	8	Infer the database used to search specific metabolic pathway a) Array express b) OMIA c) KEGG d) Gene	K2	CO4
5	9	Which bioinformatics technique predicts the 3-D structure of proteins? a) Homology modeling b) Phylogenetic analysis c) Sequence alignment d) PCR	K1	CO4
	10	Visualize the features provided by NMR spectrometer in determining the structure of soluble chemical compounds. a) Accurate, destructive b) accurate, non-destructive c) inaccurate, destructive d) inaccurate, non- destructive	K2	CO4

Cont...

SECTION - B (35 Marks)

Answer **ALL** questions
ALL questions carry **EQUAL** Marks (5 × 7 = 35)

Module No.	Question No.	Question	K Level	CO
1	11.a.	How EMBOSS software is used in sequence analysis?	K2	CO1
		(OR)		
	11.b.	Compare the characteristics of HTML and XML.		
2	12.a.	Classify the biological databases.	K3	CO2
		(OR)		
	12.b.	Discuss the retrieval of information through Pubmed.		
3	13.a.	Discuss motif analysis tools.	K3	CO3
		(OR)		
	13.b.	Compare BLAST and FASTA.		
4	14.a.	Examine KEGG mapping tools.	K4	CO4
		(OR)		
	14.b.	How would you design a metabolomics experiment?		
5	15.a.	Discuss the NMR spectroscopic technique with the help of appropriate diagram.	K4	CO4
		(OR)		
	15.b.	Explain the principle and applications of Monte Carlo simulations.		

SECTION -C (30 Marks)

Answer **ANY THREE** questions
ALL questions carry **EQUAL** Marks (3 × 10 = 30)

Module No.	Question No.	Question	K Level	CO
1	16	Describe the applications of Perl in Bioinformatics.	K4	CO1
2	17	Discuss the specialized databases designed to serve research of interest.	K5	CO2
3	18	Illustrate the types of bioinformatics tools used for sequence alignment.	K4	CO3
4	19	Analyze the computer tools used in gene mapping.	K4	CO3
5	20	Explain the principle and working of in silico 2D protein structure prediction.	K5	CO4

Z-Z-Z END