PSG COLLEGE OF ARTS & SCIENCE
(AUTONOMOUS)

MSc DEGREE EXAMINATION MAY 2019
(Second Semester)

Branch - BIOTECHNOLOGY

<u>INTRODUCTION TO BIOINFORMATICS / BIOINFORMATICS</u>

Time: Three Hours   Maximum: 75 Marks
<u>SECTION-A (10 Marks!</u>
Answer ALL questions
ALL questions carry EQUAL marks   (10 x 1 = 10)

Networking of databases uses a markup language   that allow database program to embed images and objects into rendered page.
(i)   COBOL   (ii) QML
(iii) Perl   (iv) HTML

The Research collaboratory for structural bioinformatics manages the_____ website.
(i)   PDB   (ii) OMIM
(iii) EBI   (iv) NCB1

In BLOSOM matrices the sequence pattern called_____ are ungapped alignment of less than 60 amino acids residue in length.
(i)   blocks   (ii) substitutions
(iii) PAM unit   (iv) deletions

DIALIGN 2 performs block based multiple sequence alignment to detect local conserved sequence domains and motifs by calculation of,____ .
(i)   iterative score   (ii) progressive score
(iii) high scoring pairs   (iv) global score

_____is a web based program used for gene prediction that is based on neural networking.
(i)   BLAST   (ii) GRAIL
(iii) Coli   (iv) Gibbs

Primers should be stickier at   by high a/c content to prevent annealing at multiple sites.
(i)   5' end   (ii) 3'end
(iii) both 3'and 5'   (iv) between 3' and 5'

The   __is a protein structure classifying database that is entirely based on manual comparison by human experts.
(i) SCOP   (ii) MMCIF
(iii) CATH   (iv) MMDB

Ab initio protein structure prediction is a method to determine the_____ structure of protein.
(i)   Primary   (ii) Tertiary
(iii) Secondary   (iv) Quartinary

_____spectroscopy is the tool of choice for metabolite detection and identification in metabolomics.
(i) UV   (ii) ESR
(iii) NMR   (iv) MS

10   The integrative approach to model pathways and networks at cellular level is called
      _____biology.
      (i)   syntheny   (ii) system
      (iii) Transition   (iv) True

SECTION - B (25 Marks)
Answer ALL questions
ALL questions carry EQUAL Marks (5 x 5 = 25)

11 a   Discuss databases and data resources for EST and STS.
                                    OR
   b   Explain the retrieval method for DNA and protein sequences.

12 a   Prepare a matrix to demonstrate substitution matrices PAM and BLOSOM.
                                    OR
   b   Illustrate PSH and PHI BLAST and list its significances.

13 a   Choose the different tools for restriction mapping and PCR primer design. State
        their advantages.
                                    OR
   b   Justify the role of promoters, splice site and termination signals as signals for ORF
        and gene prediction.

14 a   Recommend the use of secondary databases SCOP, CATH and FSSP for
        determining secondary structures.
                                    OR
   b   Formulate OSAR and ADMET modeling for drug designing.

15 a   Explain OMIM mutation database and give their significances.
                                    OR
   b   Determine the various web based neuro bioinformatics programs.

SECTION -C (40 Marks')
Answer ALL questions
ALL questions carry EQUAL Marks (5 x 8 = 40)

16 a   Enumerate the various features of RDBMS and give its role in design of various
        biological databases.
                                    OR
   b   Assess the various tools for determining. Write the significance of markup
        languages and scripting languages.

17 a   Evaluate BLAST and FASTA - sequence analysis tool and determine significance
        of scoring word and filters.
                                    OR
   b   Formulate the programs for multiple sequence analysis to perform phylogenetic
        analysis using UPGMA, neighbour going method and phylip.

18 a   Interpret the sequence analysis for identification of disease gene.
                                    OR
   b   Analysis of high through put micro array data for transcriptome analysis. Justify.

19 a   Classify the levels of protein structure and give their role in creation of structure
        databases.
                                    OR
   b   Justify the use of RasMol and Chime for homology modeling, threading and ab
        initio prediction of protein structure.

20 a   Evaluate the role of target identification validation, ligands and docking for
        structure based drug designing.
                                    OR
   b   Formulate genome databases of model organisms, E.coli, S.cerevisiae and C.elegans.

Z-Z-Z   END