

**LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034****M.Sc. DEGREE EXAMINATION – BIOTECHNOLOGY****SECOND SEMESTER – APRIL 2023****PBT2MC03 – BIOINFORMATICS AND COMPUTATIONAL BIOLOGY**

Date: 06-05-2023

Dept. No. 

Max. : 100 Marks

Time: 01:00 PM - 04:00 PM

**SECTION A – K1 (CO1)****Answer ALL the questions****(5 x 1 = 5)****1. Choose the best option**

a) Database that has putative protein sequence

- i) TrEMBL      ii) SWISS – PROT      iii) PIR – PSD      iv) None of the above

b) Multiple sequence alignment has a unique advantage because

- i) It reveals more biological information than pairwise alignment  
 ii) It reveals less biological information than pairwise alignment  
 iii) It reveals less biological information  
 iv) It reveals only conserved sequences

c) Which of the following is based on MolView

- i) Raswin      ii) RasMol      iii) QMol      iv) Moldraw

d) Python code is

- i) both compiled and interpreted      ii) neither compiled nor interpreted  
 iii) only compiled      iv) only interpreted

e) The largest gene in human is

- i) insulin      ii) Keratin      iii) Dystrophin      iv) Titin

**SECTION A – K2 (CO1)****Answer ALL the questions****(5 x 1 = 5)****2. Answer in one or two sentences**

a) Differentiate: Structural genomics and functional genomics.

b) Define Global alignment with examples.

c) Examine the secondary structure prediction.

d) Paraphrase on regex with examples.

e) What is Entrez?

**SECTION B – K3 (CO2)****Answer any THREE of the following****(3 x 10 = 30)**

3. Identify the type of following database and write its significance: Flybase, Wormbase, Gobase, Omniome, GPCRDB, HUGE, ClusTr, PROSITE, BLOCKS, PRINTS.
4. Compare and contrast: PAM and BLOSUM matrix.
5. Explain how the Rasmol tool is used in creating protein structure.
6. Examine the module functions and explain about syntax and regex.
7. Identify the data models of Seq-Ids, BIOSEQ-SETs and SEQ-ANNOT.

**SECTION C – K4 (CO3)****Answer any TWO of the following****(2 x 12.5 = 25)**

8. Illustrate and expand key codes in a SWISS – PROT record.
9.
  - a) Explain any one method of constructing phylogenetic tree in detail.
  - b) Prioritize the method used to check the validity of protein structure.
10. Determine the importance of Biopython used in the construction of various applications in bioinformatics.
11. Explain how to submit the sequence to Genbank.

**SECTION D – K5 (CO4)****Answer any ONE of the following****(1 x 15 = 15)**

12. Explain different applications of bioinformatics in-detail.
13. Enumerate the various types of multiple sequence alignment. Give the programmes under each category and mention the drawbacks of progressive alignment.

**SECTION E – K6 (CO5)****Answer any ONE of the following****(1 x 20 = 20)**

14. Summarize the following :
  - (i) Abinitio and comparative gene predictions.
  - (ii) Prediction of Cis's acting elements and ORF findings.
15. Discuss the International HapMap project with ethical issues and explain about SNPs, alleles and genotypes.

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