B.Tech. DEGREE EXAMINATION, MAY 2023
Fifth Semester

18GEO104T – COMPUTATIONAL GENOMICS
(For the candidates admitted from the academic year 2018-2019 to 2021-2022)

Note:
(i) **Part - A** should be answered in OMR sheet within first 40 minutes and OMR sheet should be handed over to hall invigilator at the end of 40th minute.
(ii) **Part - B & Part - C** should be answered in answer booklet.

Time: 3 hours

Max. Marks: 100

PART – A (20 × 1 = 20 Marks)
Answer ALL Questions

	Marks	BL	CO

1. Which of the following is not present in DNA? — 1, 1, 1
   - (A) Adenine
   - (B) Guanine
   - (C) Cytosine
   - (D) Uracil

2. Which of the following is not a part of central dogma of molecular biology? — 1, 1, 1
   - (A) RNA
   - (B) Protein
   - (C) Virus
   - (D) DNA

3. Study of total gene expression of a cell is called as — 1, 1, 1
   - (A) Lipidomics
   - (B) Proteomics
   - (C) Transcriptomics
   - (D) Genomics

4. Which of the following is a stop codon? — 1, 1, 1
   - (A) AUG
   - (B) UAG
   - (C) CGG
   - (D) GGC

5. Which of the following is not a nucleotide sequence database? — 1, 1, 2
   - (A) Genbank
   - (B) EMBL
   - (C) DDBJ
   - (D) Uniprot

6. Which of the following is not a sequence file format related to genomic data? — 1, 1, 2
   - (A) PDB
   - (B) BAM
   - (C) Fastq
   - (D) Genbank

7. Which of the following is not a part of level Gene Ontology studies? — 1, 1, 2
   - (A) Biological Process
   - (B) Cellular Component
   - (C) Molecular Function
   - (D) Enzyme Action

8. Which of the following is not related to homology? — 1, 1, 2
   - (A) Orthology
   - (B) Paralogy
   - (C) Xenology
   - (D) Parasitology

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9. The data stored in the R data frame cannot be a _____ type.   1   1   3
   (A) numeric   (B) factor
   (C) character   (D) special function

10. Which of the following is not a built-in datatype in python under the numeric category?   1   1   3
   (A) int   (B) float
   (C) complex   (D) bytes

11. Which of the following is used in python to concatenate two elements?   1   1   3
   (A) concat ( )   (B) paste ( )
   (C) hash   (D) addition

12. Dataframes can be converted into a matrix by calling the following function data _____   1   1   3
   (A) matr()   (B) matrix()
   (C) matrixf()   (D) matrixfunc()

13. The content of a package is only available when a package is loaded using _____   1   1   4
   (A) install()   (B) library()
   (C) update()   (D) search ()

14. Differential gene expression analysis can NOT be done using _____   1   1   4
   (A) RSEM   (B) edgeR
   (C) DESeq   (D) limma

15. _____ are built in R so that you get HTML.   1   1   4
   (A) Vignettes   (B) Vighnaants
   (C) Bignats   (D) Viddnets

16. _____ consists of commands to create complex plots from data in a data frame.   1   1   4
   (A) ggplot2   (B) ABSSeq
   (C) clusterProfiler   (D) splots

17. How many open reading frames are there?   1   2   5
   (A) 1   (B) 3
   (C) 5   (D) 6

18. Bio.Alphabet.IUPAC provides definitions for DNA, RNA and proteins, but _____.   1   2   5
   (A) IUPACProtein   (B) IUPACUnambiguousDNA
   (C) IUPACUnambiguousRNA (D) IUPACDNA

19. The Seq object is _____   1   2   5
   (A) writable   (B) readable
   (C) executable   (D) revokable

20. The SeqRecord (Sequence Record) class is defined in the _____ module.   1   2   5
   (A) Bio.SeqRecord   (B) Bio_SeqRecord
   (C) BioSeqRecord   (D) SeqRecord

PART – B (5 × 4 = 20 Marks)
Answer ANY FIVE Questions

	Marks	BL	CO
21. Compare Intron and Exon.	4	2	1
22. Comment about different types of RNA.	4	2	1
23. Summarize the important features of FastQ file format.	4	2	2
24. Write short notes on vectors in R.	4	2	3
25. Write the importance of classes and objects in Python.	4	2	3
26. Define GViz package.	4	1	4
27. Define FastA file format.	4	1	5

PART – C (5 × 12 = 60 Marks)
Answer ALL Questions

	Marks	BL	CO
28. a. Write in detail about the structure and components of a gene with a neat sketch.	12	3	1
(OR)			
b. Explain in detail the significance and scope of bioinformatics in biological research.	12	3	1
29. a. Explain in details the importance of Phred Score, its different levels and how it is related to the quality of the sequencing data.	12	4	2
(OR)			
b. Explain in detail the Genbank file format with an example.	12	4	2
30. a. Demonstrate the syntax for R- data-frames and matrices. Explain how different are these two to each other.	12	4	3
(OR)			
b. Explain in detail about datatypes in Python with suitable examples.	12	4	3
31. a. Explain in detail basic interval operations for GRanges object.	12	4	4
(OR)			
b. Explain in detail about the IRanges package and demonstrate any five of them.	12	4	4
32. a. Explain MutableSeq objects.	12	4	5
(OR)			
b. Illustrate the use of Biopython module to perform translation.	12	4	5

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