BIRLA INSTITUTE OF TECHNOLOGY, MESRA, RANCHI
(END SEMESTER EXAMINATION)

CLASS: MSc **SEMESTER : III**
BRANCH: BIOENGINEERING & BIOTECHNOLOGY **SESSION : MO/2025**

SUBJECT: BI303 NGS DATA ANALYSIS

TIME: 3 Hours **FULL MARKS: 50**

INSTRUCTIONS:
1. The question paper contains 5 questions each of 10 marks and total 50 marks.
2. Attempt all questions.
3. The missing data, if any, may be assumed suitably.
***4*. Before attempting the question paper, be sure that you have got the correct question paper.**
5. Tables/Data hand book/Graph paper etc. to be supplied to the candidates in the examination hall.

			CO	BL
Q.1(a)	List the major applications of NGS technology.	[5]	1	1
Q.1(b)	Describe the working principle of Oxford Nanopore sequencing platform.	[5]	2	2
Q.2(a)	Discuss the role of GC content analysis in ensuring reliable RNA-Seq results and explain situations where abnormal GC bias may occur.	[5]	2	4
Q.2(b)	Find the Burrows-Wheeler Transform (BWT) of sequence “ATCGATGC” and map read “ATG” onto the reference sequence using the BWT approach.	[5]	2	3
Q.3(a)	List the best practice guidelines for generating high-quality RNA-Seq data.	[5]	3	3
Q.3(b)	Compare the different methods of data normalization with suitable examples and discuss why TPM is a better option?	[5]	2	4
Q.4(a)	Describe in detail the various types of genomic variations.	[5]	2	2
Q.4(b)	What is a Variant Call Format (VCF) file? Discuss its structure, key fields and the interpretation of VCF results for variant analysis.	[5]	4	4
Q.5(a)	What is the Shortest Common Superstring (SCS)? Discuss the algorithm with a suitable example and list the challenges.	[5]	2	5
Q.5(b)	Explain how a De Bruijn graph can be constructed from short nucleotide reads and how it helps in reconstructing the original DNA sequence.	[5]	3	2

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