

JAMIA HAMDARD
Department of Computer Science & Engineering
School of Engineering Sciences & Technology
New Delhi-110062
Odd Semester Examination 2024 M.Sc. (CSB)

Paper Name: NGS Data analysis – Microarray, RNA Seq, Single Cell sequencing

Paper Code: MCSB 301

Time: 2.5 Hours

Maximum Marks: 60

Section A (Attempt all question; 4x5 = 20 Marks)

Q. No.	Questions	Marks	CO	BL
1.	Describe the basic working principle of Sanger and Roche454 sequencing..	5	1	2
2.	What are the various library preparation steps in a typical NGS experiment?	5	2	2
3.	Choose the most appropriate experiment design and provide the explanation for the same: For Genome wide identification of gene expression and discovery of splice variants.	5	3	4
4.	How bridge PCR and emulsion PCR differ from one another?	5	4	3

P.T.O

Section B (Attempt any four; 10x4 = 40 Marks)

Q. No	Questions	Marks	CO	BL
1	What do you understand by sequencing coverage and sequencing depth? Provide formulation of mean coverage of reads. Highlight the reason behind variation in coverage across genome sequence.	10	1	2,3
2	Explain Single Cell RNA sequencing. How does it differ from bulk RNA sequencing? Explain various steps of single cell RNA sequencing in detail. Highlight some applications of single cell sequencing.	10	5	5
3	Explain the following: a) Strand displacement DNA synthesis and Circular consensus sequences. b) what is the need of PHRED + 33 and PHRED + 64 encoding?	10	3	4
4	Explain sequencing data formats of the followings: a) PacBio SMRT sequencing c) Roche 454 file format.	10	4	3
5	Explain the followings: a) ZMW (zero mode waveguide) b) What are homopolymeric stretches and how various sequencing technologies deal with it?	10	2	4
6	Explain any genome assembly and annotation pipeline/workflow with tools involved at every step of the process.	10	5	4