Name: **Enrolment No:**	UPES UNIVERSITY OF TOMORROW

UPES

End Semester Examination, May 2025

Course: Microbiome and Omics — **Semester: II**

Program: M.Sc. Microbiology — **Time: 03 hrs.**

Course Code: HSMB7039P — **Max. Marks: 100**

Instructions: Attempt all the questions

S. No.	Section A Short answer questions/ MCQ/T&F (20Qx1.5M= 30 Marks)	Marks	COs
Q 1	The following statement best describes a microbiome a) A single isolated microbial strain b) A microbial metabolite c) A community of microorganisms and their genetic material d) Only the DNA from environmental samples	**1.5**	**CO1**
Q 2	In BioPython, which module is primarily used for working with DNA sequences? a) Bio.Align b) Bio.SeqIO c) Bio.Seq d) Bio.Data	**1.5**	**CO1**
Q 3	The main advantage of shotgun metagenomics over 16S rRNA sequencing is a) Faster processing time b) Higher PCR sensitivity c) Functional gene prediction d) Cost-effectiveness	**1.5**	**CO1**
Q 4	Tool which is used to generate Operational Taxonomic Unit (OTU) tables is a) RAxML b) MEGA c) QIIME d) Cytoscape	**1.5**	**CO1**
Q 5	Visual method which is commonly used to represent microbial community composition differences across samples is a) Venn diagram b) PCA plot c) Heat map d) All of the above	**1.5**	**CO1**

Q 6	A heat map is a common visual representation of what type of data?	**1.5**	**CO2**
Q 7	Name the technique used to separate proteins based on charge and size.	**1.5**	**CO2**
Q 8	Give the full form of MALDI in proteomics?	**1.5**	**CO2**
Q 9	Name the omics field which studies metabolic products?	**1.5**	**CO2**
Q 10	Name the technology used to analyze protein masses?	**1.5**	**CO2**
Q 11	The technique which is used to study differential gene expression in microbial communities is a) 16S sequencing b) Mass spectrometry c) RNA-Seq d) ChIP-Seq	**1.5**	**CO3**
Q 12	ICAT-MS is primarily used for: a) Protein quantification b) Gene editing c) Sequence alignment d) RNA splicing	**1.5**	**CO3**
Q 13	Predicting microbial functions based on omics data is called: a) Taxonomy assignment b) Functional annotation c) Host profiling d) Sequence assembly	**1.5**	**CO3**
Q 14	The most commonly used marker gene for assessing microbial diversity is a) ITS b) 18S rRNA c) 16S rRNA d) COX1	**1.5**	**CO3**
Q 15	Host-microbiome interaction is mainly studied using: a) Proteomics b) Transcriptomics c) Multi-omics integration d) Only metagenomics	**1.5**	**CO3**
Q 16	Precision medicine aims to: a) Provide a single treatment for all diseases b) Personalize treatment based on genetic and microbial data c) Replace antibiotics d) Enhance agricultural yields only	**1.5**	**CO4**
Q 17	In diagnostics, microbiome analysis helps by: a) Estimating antibiotic cost b) Monitoring microbial biomarkers of disease c) Isolating pathogens for culture d) Determining WBC count	**1.5**	**CO4**

Q 18	Name the tool used for pathway analysis of gene/protein expression data?	**1.5**	**CO4**
Q 19	Give the gene acting as a marker for fungal diversity?	**1.5**	**CO4**
Q 20	Name the major host system influenced by the gut microbiome?	**1.5**	**CO4**
	Section B **(4Qx5M=20 Marks)**		
Q 1	Explain how alpha and beta diversity metrics together provide a comprehensive understanding of microbial communities?	**5**	**CO1**
Q 2	Mention two tools used for functional profiling of microbial communities.	**5**	**CO2**
Q 3	Justify the reason for quality control as a critical step in microbiome sequencing analysis? Name any two bioinformatics tools used.	**5**	**CO3**
Q 4	Explain the significance of omics technologies to monitor and mitigate the impact of agricultural practices on environmental microbiomes.	**5**	**CO4**
	Section C **(2Qx15M=30 Marks)**		
Q 1	A biotech company is trying to develop a biofertilizer by isolating beneficial microbes from the rhizosphere of legume plants. They use 16S rRNA amplicon sequencing and metaproteomics to characterize microbial composition and protein expression under drought and non-drought conditions. They find that drought-resistant plants harbor bacteria with enhanced nitrogen fixation and osmoprotectant pathways. Based on this case study, answer the following questions: 1. Compare the use of 16S rRNA sequencing and metaproteomics in this context. (3 marks) 2. Explain the role of rhizosphere microbiome in plant stress tolerance? (3 marks) 3. Justify how metaproteomics data can help identify functionally active pathways under stress? (3 marks) 4. Explain how this data could guide the formulation of a biofertilizer. (3 marks) 5. List the potential environmental benefits of using such engineered microbial formulations in agriculture? (3 marks)	**15**	**CO3**
Q 2	A hospital experiences an outbreak of a multi-drug resistant infection. Researchers collect surface swabs, air samples, and patient microbiomes for shotgun metagenomic sequencing. They identify a previously uncharacterized microbial strain carrying	**15**	**CO4**

	resistance genes and trace its source to the hospital's air-conditioning ducts. BioPython tools were used for initial data parsing and statistical analysis. Based on this case study, answer the following questions: 1. Explain how shotgun metagenomics is more suitable than 16S rRNA in this outbreak scenario? (4 marks) 2. BioPython be used to process and visualize large-scale metagenomic data. Justify the statement. (3 marks) 3. Describe the bioinformatics tools would you use to identify resistance genes from this data? (4 marks) 4. Suggest a workflow (with tools) for comparing microbial communities across different hospital zones. (4 marks)		
Section D **(2Qx10M=20 Marks)**			
Q 1	A) Describe the data analysis pipeline for 16S rRNA gene amplicon sequencing, including taxonomy assignment, OTU clustering, and diversity analysis. B) Discuss the limitations of this sequencing method and how they are addressed using newer approaches.	**6+4**	**CO1**
Q 2	A) Compare and contrast the analysis workflows of metatranscriptomics and metaproteomics, highlighting the steps from sample preparation to data interpretation. B) Mention the specific bioinformatics tools used or data processing, quantification, and functional annotation. How do these tools aid in understanding microbial community function and dynamics?	**5+5**	**CO2**