

RAMAKRISHNA MISSION VIDYAMANDIRA
(Residential Autonomous College affiliated to University of Calcutta)

B.A./B.Sc. SIXTH SEMESTER EXAMINATION, MAY 2025
THIRD YEAR [BATCH 2022-25]

MICROBIOLOGY (HONOURS)

Date : 10/05/2025

Time : 11 am – 1 pm

PAPER : DSE 3

Full Marks : 50

1. Answer **any ten** questions : [10×2]

- a) Name one enzyme involved in the microbial degradation of xenobiotics. Mention the function of oxygenases in xenobiotic degradation.
- b) How do biofuels differ from fossil fuels in terms of environmental impact?
- c) Define: Landfarming and composting.
- d) What is Insitu and Exsitu Bioremediation?
- e) What is “Biocatalysis”? Mention one of its industrial application.
- f) How do first-generation and second-generation biofuels differ?
- g) Why is Prof. Ananda Mohan Chakraborty so famous?
- h) How cladogram differs from phylogram?
- i) What do you mean by multifurcating node of a phylogenetic tree?
- j) Differentiate between local alignment and global alignment.
- k) Differentiate between gene phylogeny and species phylogeny.
- l) What is UPGMA method?
- m) What is a scoring matrix in sequence alignment? Give example.
- n) What are Orthologs and Paralogs?
- o) Define the term extension gap penalty.

Answer **any three** questions: [3×10]

2. a) What are the most common bioremediation techniques? Briefly describe ‘biostimulation’ and ‘bioaugmentation’.
b) Discuss the role of microorganisms in bioethanol production.
c) How is bioremediation used to address oil spills in marine environments? [(1+4)+2+3]
3. a) Write the differences between slurry phase and solid phase bioremediation.
b) Discuss the various techniques for cultivating algae for biodiesel production.
c) What is ‘biogas’? Briefly mention the role of microorganisms in biogas production. [3+3+4]
4. a) Write the significance of motif discovery in gene prediction. Name two software used to construct phylogenetic tree.
b) Find out the proper alignment from the given two sequence by FASTA with *ktups* method :
AMPSDGL
GPSDNAT
c) What do you mean by parametric and nonparametric bootstrapping method? [(2+1)+5+2]
5. a) Define the term ‘data mining’.
b) How sequence alignment plays a major role in evolutionary studies?
c) Mention the basic steps involved in homology modeling of a protein. Define “Bootstrap value” in context to phylogenetic tree.
d) Differentiate between PAM and BLOSUM matrix. [2+2+(3+1)+2]
6. a) Mention the various significances of E value in BLAST algorithm.
b) What is the function of ribosomal RNA in sequence analysis?
c) List out the various interpretation of dot matrix analysis with a suitable diagram. [3+2+5]