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BRAINWARE UNIVERSITY

Term End Examination 2024-2025

Programme – M.Sc.(MB)-2024

Course Name – Bioinformatics and Metagenomics

Course Code - MMB20205

(Semester II)

Full Marks : 60

Time : 2:30 Hours

[The figure in the margin indicates full marks. Candidates are required to give their answers in their own words as far as practicable.]

Group-A

(Multiple Choice Type Question)

1 x 15=15

1. Choose the correct alternative from the following :

- (i) Select which factor contributes most to microbial genome annotation.
 - a) Gene prediction algorithms
 - b) Optical microscopy
 - c) Mass spectrometry
 - d) Chromatography
- (ii) Select the different types of protein structure databases.
 - a) UniProt, PDB, SCOP
 - b) GenBank, ENA, DDBJ
 - c) BLAST, ClustalW, MEGA
 - d) AutoDock, SwissDock, PatchDock
- (iii) Select a method for studying evolutionary relationships among microbes.
 - a) Phylogenetic analysis
 - b) Mass spectrometry
 - c) NMR spectroscopy
 - d) Western blotting
- (iv) Decide which tool is best for visualizing protein-protein interactions.
 - a) STRING
 - b) BLAST
 - c) ClustalW
 - d) MEGA
- (v) Decide which component is essential for adapter ligation in Illumina sequencing.
 - a) DNA ligase
 - b) RNA polymerase
 - c) Reverse transcriptase
 - d) DNA helicase
- (vi) Classify the different applications of metagenomics.
 - a) Environmental microbiome studies, human gut microbiome analysis, pathogen detection
 - b) PCR, protein blotting, hybridization, spectrometry
 - c) ELISA, chromatography, immunoassay, microscopy
 - d) Gel electrophoresis, X-ray crystallography, mass spectrometry
- (vii) Recommend a tool for mapping short sequencing reads to a reference genome.

- a) BWA
c) ClustalW
(viii) Identify the category that viral metagenomics falls under.
a) Bacterial genome analysis
c) 16S rRNA sequencing
(ix) Indicate the classification of metagenomic sequencing techniques.
a) Whole-genome, targeted, functional
c) Amplicon, shotgun, hybrid
(x) Classify the advantages of long-read sequencing over short-read sequencing.
a) Higher accuracy, lower cost
c) Less computational demand, higher throughput
(xi) Decide which metagenomic approach provides the best functional annotation.
a) 16S rRNA sequencing
c) Shotgun metagenomics
(xii) Write which global biodiversity law regulates access to genetic resources.
a) The Nagoya Protocol
c) The Geneva Convention
(xiii) Recommend a database for functional annotation in metagenomics.
a) KEGG
c) UniRef
(xiv) Recommend a tool for taxonomic profiling in metagenomic studies.
a) HUMAnN
c) BLAST
(xv) Recommend an ideal method for studying microbial metabolic pathways.
a) KEGG analysis
c) Western blot
- b) BLAST
d) MEGA
b) Whole-genome sequencing of viruses
d) Protein structure analysis
b) Next-generation, third-generation, hybrid
d) Culture-based, PCR-based, sequencing-based
b) Better genome completeness, fewer gaps
d) More errors, lower resolution
b) Whole-genome sequencing
d) PCR amplification
b) The Kyoto Protocol
d) None
b) MetaCyc
d) All
b) MetaPhlAn
d) FastQC
b) MetaPhlAn
d) PCR

Group-B

(Short Answer Type Questions)

3 x 5=15

2. Describe the impact of metagenomics in microbial ecology. (3)
3. Illustrate the significance of metagenomics in microbiome research and its impact on understanding microbial diversity. (3)
4. Classify the different types of genetic variations and their impact. (3)
5. Summarize the role of metagenomics in detecting antibiotic resistance genes. (3)
6. Summarize the challenges faced in functional metagenomics and potential solutions. (3)

OR

Illustrate how functional annotation is performed in metagenomics and its significance. (3)

Group-C

(Long Answer Type Questions)

5 x 6=30

7. Illustrate the importance of multiple sequence alignment in bioinformatics. (5)
8. Classify different visualization techniques used in microbiome studies. (5)
9. Construct how functional annotation is performed in metagenomics and its significance. (5)
10. Create a comparative analysis of de novo and reference-guided genome assembly. (5)

11. Analyze the role of structural variation detection in understanding genetic disorders. (5)
12. Summarize the importance of metagenomic assembly evaluation and the metrics used. (5)

OR

Summarize the role of hybrid assembly in improving metagenomic analysis. (5)

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