

U.G. 4th Semester Examination - 2021
Molecular Biology and Biotechnology
[HONOURS]
Course Code : MBBT-H-403-T-CCR-10
(Bioinformatics)

Full Marks : 20 Time : 1 Hour

The figures in the right-hand margin indicate marks.
Candidates are required to give their answers in
their own words as far as practicable.

1. Answer any **five** questions: $1 \times 5 = 5$
- a) Name one nucleotide database and one protein sequence database.
 - b) Write the URL of UNIGENE and PIR.
 - c) Define Homology.
 - d) Name a software used for Restriction enzymes digestion and a gene expression data repository. What is the use of Primer-BLAST?
 - e) When do we use PAM 250 and BLOSSUM 62 substitution matrix?
 - f) What record does ATOM and TER provide in PDB?

- g) What is the signature of FASTA format?
 - h) Define Cladogram.
2. Answer any **one** question: $5 \times 1 = 5$
- a) State the difference between Global and Local alignment. What is Gap Opening Penalty? $4 + 1$
 - b) Define Rooted tree. What is OTU? Define Ortholog. $2 + 1 + 2$
 - c) What is Genome Annotation? Define Structural annotation. $3 + 2$
3. Answer any **one** question: $10 \times 1 = 10$
- a) What is meant by Optimal Alignment? Align the following two sequences using Dynamic Programming Algorithm.
Seq 1: A T G Seq 2: A G
Match=1, Mismatch=0, Gap=0 $2 + 8$
 - b) When do we use Maximum Parsimony Method? What is meant by Informative site in Maximum Parsimony?
Find out the informative sites in the following sequences:
 $1 \ 2 \ 3 \ 4 \ 5 \ 6 \ 7 \ 8 \ 9 \ 10$
Species 1 - A G G G T A A C T G

Species 2 - A C G A T T A T T A

Species 3 - A T A A T T G T C T

Species 4 - A A T G T T G T C G

Mention two disadvantages of Maximum Parsimony. Name one Tree Constructing Programs. 2+2+3+2+1

- c) Why do we need Multiple Sequence Alignment? Name one Multiple sequence alignment program. Distinguish between Paraphyletic and Polyphyletic group. Define Multifurcating tree. 4+1+4+1
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