4. Write short notes on : ***(any four)*** 7×4=28

(i) SwissProt

(ii) Needleman-Wunsch method of alignments of sequences

(iii) NCBI

(iv) Application of Bioinformatics in biology

(v) Use of 2D gels in proteomics

(vi) Maximum likelihood method of molecular phylogeny

5. Answer the following questions : 12×2=24

(a) What do you mean by sequence analysis? Discuss the sequence analysis tool BLAST and FASTA and their application in bioinformatics. 2+10=12

(b) Discuss different types of phylogenetic trees and their application in evolutionary studies.

Total number of printed pages–4

44 (2) BCA–HG–2026

2024

INTRODUCTION TO BIOINFORMATICS

Paper : BCA–HG–2026

Full Marks : 80

Time : Three hours

The figures in the margin indicate full marks for the questions.

1. Choose the correct answer : 2×8=16

(i) Which of the following is not a type of Phylogenetic tree?

(a) Rooted tree
(b) Unrooted tree
(c) Decision tree
(d) Rooted bifurcating tree

(ii) In which year did the SWISSPROT protein sequence database begin?

(a) 1980
(b) 1985
(c) 1987
(d) 1984

Contd.

(iii) Who is the founder of NCBI ?

(a) Pauline Hogeweg

(b) Claude Pepper

(c) Sanger

(d) J. W. Watson

(iv) Which is the largest DNA database in the world ?

(a) UK National DNA database

(b) GenBank

(c) DDBJ

(d) CODIS

(v) Which alignment is useful to detect the highly similar sequences ?

(a) Local

(b) Global

(c) Multiple sequence

(d) Pairwise sequence

(vi) BLAST programme is used for :

(a) Translate amino acid sequence

(b) Translate input sequence

(c) Translate DNA sequence

(d) Translate RNA sequence

(vii) Which of the following is not a sequence alignment tool ?

(a) BLAST

(b) FASTA

(c) Rasmol

(d) ClustalW

(viii) Which of the following is a multiple sequence alignment tool ?

(a) Chime

(b) PDB

(c) ClustalW

(d) BLAST

2. Distinguish between : 4×2=8

(a) Protein and Nucleic acid sequence

(b) Primary and Secondary database

3. Write the full form of the following abbreviation : ***(any four)*** 1×4=4

(i) UPGMA

(ii) NCBI

(iii) PDB

(iv) MEGA

(v) EMBL

(vi) FASTA