(FOR THE CANDIDATES ADMITTED IN DURING THE ACADEMIC YEARS 2024 ONLY)

(NO. OF PAGES: 1)

24UBY4N2

REG No

N.G.M.COLLEGE (AUTONOMOUS) : POLLACHI
END-OF-SEMESTER EXAMINATIONS : APRIL-2026
B.Sc.-BOTANY **MAXIMUM MARKS: 50**
SEMESTER IV **TIME : 2 HOURS**

PART - IV
BIOINFORMATICS

SECTION –A (10X1=10 MARKS)

ANSWER THE FOLLOWING QUESTIONS. **K1**

MULTIPLE CHOICE QUESTIONS.

1. Genetic code is ----------
   a) singlet b) doublet c) triplet d) quadrat

2. EXPASY is a ----------
   a) proteomic server b) genome database c) nucleotide server d) sequencing tool

3. Pairwise sequence alignment can be done using ----------
   a) CLUSTAL X b) BLAST c) RASMOL d) GENMARK

4. Prediction of secondary structure of proteins reveal the----------
   a) molecular weight b) atomic number c) coils and strands d) aminoacid composition

5. Each leaf of a phylogenetic tree denotes a ----------
   a) species b) family c)group d) ancestor

ANSWER THE FOLLOWING IN ONE OR TWO SENTENCES. **K2**

6. What are biomolecules?
7. What are specialised databases?
8. Define FASTA format.
9. Name any two biomolecular visualization tool.
10. What is homology?

SECTION –B (5X8=40 MARKS)

ANSWER EITHER (a) OR (b) IN EACH OF THE FOLLOWING QUESTIONS. K4 & K5

11.(a) Describe the structure of DNA.

(OR)

(b) Write an essay on biological databases.

12. (a) Differentiate generalised and specialised databases.

(OR)

(b) Give an account of Virtual library.

13. (a) Explain pairwise sequence alignment using BLAST.

(OR)

(b) Discuss in detail on gene finding techniques.

14. (a) Explain multiple sequence alignment.

(OR)

(b) Write an essay on drug designing.

15. (a) Briefly explain the steps involved in the construction of a phylogenetic tree.

(OR)

(b) Write in detail on biomolecular visualization.

****