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(FOR THE CANDIDATES ADMITTED DURING THE ACADEMIC YEAR 2024 ONLY)

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REG.NO. :

N.G.M. COLLEGE (AUTONOMOUS), POLLACHI
END-OF-SEMESTER EXAMINATIONS: MAY - 2026

M.Sc.-BOTANY **MAXIMUM MARKS: 75**
SEMESTER: IV **TIME : 3 HOURS**

BIOINFORMATICS AND CYBER SECUTIRY

SECTION – A (10 X 1 = 10 MARKS)

ANSWER THE FOLLOWING QUESTIONS.
MULTIPLE CHOICE QUESTIONS. K1

1. What does BLAST stand for?
   a) Basic Local Alignment Search Tool b) Building Large Alignment Search Tools
   c) Biological Linkage Analysis Software Tool d) Bayesian Linked Algorithm Search Tool

2. Which of the following describes the ab initio approach to gene prediction?
   a) It predicts genes based on similarity to known sequences in databases
   b) It relies solely on the given sequence's signals and statistical content
   c) It requires relative homology data from multiple organisms
   d) It uses experimental mRNA evidence only

3. What does CADD stand for?
   a) Computational Analysis of Drug Design b) Chemical Application in Drug Development
   c) Computer-Aided Drug Design d) Clinical Assessment of Drug Development

4. What are the features of Cyber Security?
   a) Provides security against malware b) provides security against cyber-terrorists
   c) protects a system from cyberattacks d) All of the above

5. What are the three primary requirements for an invention to be patentable?
   a) Originality, Fixation, and Utility b) Distinctiveness, Usefulness, and Fame
   c) Beauty, Rarity, and Complexity d) Novelty, Inventive Step, and Industrial Application

ANSWER THE FOLLOWING IN ONE (OR) TWO SENTENCES. K2

6. What is GenBank?
7. List the gene prediction methods.
8. Define proteomics.
9. What do you mean by rootkit?
10. Differentiate between patent and trade secret.

SECTION – B (5 X 5 = 25 MARKS)

ANSWER EITHER (a) OR (b) IN EACH OF THE FOLLOWING QUESTIONS. K3

11. a) What is a biological database? Discuss the primary and secondary databases with suitable Examples.

(OR)

b) Explain the working of BLAST based on your knowledge of sequence alignment.

12. a) What are the fundamental differences between PAM and BLOSUM matrices? Explain.

(OR)

b) Discuss the concept of molecular phylogeny.

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13.a) Describe how proteomics can be useful in protein structure prediction.

(OR)

b) Interpret the role of molecular visualization tools in proteomics.

14.a) Discuss why passwords remain the most widely used authentication method.

(OR)

b) Discuss the role of cryptography in securing modern communication systems.

15.a) Explain the difference between threat, vulnerability and risk in network security.

(OR)

b) Analyze the role of authentication and authorization in preventing unauthorized access.

SECTION – C (5 X 8 = 40 MARKS)

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

16. a) Elaborate the importance and scope of bioinformatics.

(OR)

b) Interpret the importance of DDBJ and NCBI.

17. a) Critically analyze the two major categories of gene prediction methods.

(OR)

b) What is the primary goal of sequence alignment? Differentiate between pairwise and multiple sequence alignment?

18. a) Evaluate the use of structure prediction in de novo protein design.

(OR)

b) Explain the relationship between SWISS-PROT and PDB with suitable examples.

19. a) Evaluate the effectiveness of different types of cybersecurity tools, from antivirus software to advanced detection models.

(OR)

b) Describe how the memory errors like buffer overflows and integer overflows can be exploited to compromise a system.

20. a) Is cybercrime a fundamentally new type of crime or an evolution of offenses? Discuss.

(OR)

b) Elucidate the importance of following intellectual property with suitable examples.
(i) Patents, (ii) Copyrights, (iii) Trade secrets

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