R4543

Sub. Code
25MBI2C1

M.Sc. DEGREE EXAMINATION, APRIL – 2026

Second Semester

Bioinformatics

GENOMICS AND PROTEOMICS

(CBCS – 2025 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

Answer **all** the following objective questions by choosing the correct option.

1. The complete protein complement of a cell is called ___________. (CO2, K1)

   (a) Genome (b) Transcriptome

   (c) Proteome (d) Metabolome

2. Genomics primarily deals with the study of_______. (CO2, K2)

   (a) Proteins (b) Genes and DNA

   (c) Metabolites (d) Lipids

3. Which technique is widely used for large-scale gene expression analysis? (CO3, K2)

   (a) Western blot (b) Southern blot

   (c) ELISA (d) DNA microarray

4. Transcriptomics focuses on the study of___________ (CO2, K1)

   (a) RNA transcripts (b) DNA mutations

   (c) Protein folding (d) Metabolites

5. SDS-PAGE separates proteins based on ____ (CO3, K1)

(a) Charge (b) Hydrophobicity

(c) Size (d) Isoelectric point

6. Mass spectrometry is mainly used for __________ (CO2, K2)

(a) Protein identification

(b) DNA amplification

(c) Cell imaging

(d) Gene cloning

7. GenBank is a database of __________ (CO3, K1)

(a) Protein structures

(b) Protein interactions

(c) Nucleotide sequences

(d) Metabolic pathways

8. STRING database is used for __________ (CO4, K1)

(a) SNP detection

(b) Protein-protein interaction analysis

(c) Gene cloning

(d) RNA sequencing

9. SNP stands for _______ (CO2, K1)

(a) Single Nucleotide Polymorphism

(b) Short Nucleotide Primer

(c) Structural Nucleotide Protein

(d) Sequence Network Pattern

10. Personalized medicine mainly relies on ____ (CO2, K1)
(a) Classical genetics
(b) Genomics data
(c) Histology
(d) Cytology

Part B

(5 × 5 = 25)

Answer **all** questions not more than 500 words each.

11. (a) Explain the scope and significance of genomics. (CO3, K3)

Or

(b) Differentiate between genomics and proteomics. (CO2, K2)

12. (a) Describe the principle of DNA microarray technology. (CO2, K3)

Or

(b) Explain the role of transcriptomics in functional genomics. (CO3, K2)

13. (a) Describe the principle of SDS-PAGE. (CO4, K3)

Or

(b) Explain the role of mass spectrometry in proteomics. (CO3, K2)

14. (a) Discuss the importance of biological databases in genomics. (CO5, K3)

Or

(b) Explain protein—protein interaction analysis. (CO5, K3)

15. (a) Explain the role of genomics in disease diagnosis. (CO2, K4)

Or

(b) Discuss applications of proteomics in biomarker discovery. (CO3, K5)

Part C (5 × 8 = 40)

Answer **all** questions not more than 1000 words each.

16. (a) Analyze the importance of genomics and proteomics in modern biology. (CO4, K5)

Or

(b) Evaluate the challenges involved in proteome analysis. (CO3, K5)

17. (a) Assess the applications of next-generation sequencing in genomics. (CO4, K4)

Or

(b) Critically analyze the role of transcriptomics in disease studies. (CO2, K4)

18. (a) Compare different protein separation techniques used in proteomics. (CO3, K4)

Or

(b) Design a proteomics workflow for protein identification. (CO3, K5)

19. (a) Evaluate the role of bioinformatics tools in genomics and proteomics research. (CO5, K5)

Or

(b) Analyze the significance of protein interaction networks. (CO4, K4)

20. (a) Critically evaluate the role of genomics in personalized medicine. (CO5, K5)

Or

(b) Propose a genomics—proteomics approach for disease biomarker identification. (CO5, K6)

R4544

Sub. Code
25MBI2C2

M.Sc. DEGREE EXAMINATION, APRIL – 2026

Second Semester

Bioinformatics

MOLECULAR MODELLING AND DRUG DESIGN

(CBCS – 2025 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

Answer **all** the following questions by
choosing the correct options.

1. Which phase of drug discovery involves validation of biological targets? (CO4, K1)

   (a) Lead optimization

   (b) Target identification and validation

   (c) Clinical trials

   (d) Drug marketing

2. Pharmacoinformatics is mainly applied in ________. (CO2, K1)

   (a) Drug storage

   (b) Drug marketing

   (c) Drug design and discovery

   (d) Drug regulation

3. Molecular dynamics simulation primarily studies of _________ (CO1, K1)

   (a) Static molecular structures

   (b) Molecular motion over time

   (c) Chemical synthesis

   (d) Drug toxicity

4. Which ensemble maintains constant temperature, volume, and number of particles? (CO2, K2)

   (a) NVT (b) NPT

   (c) NVE (d) Grand canonical

5. Bond stretching energy is best described by _______. (CO2, K2)

   (a) Coulomb's law

   (b) Lennard—Jones potential

   (c) Harmonic oscillator model

   (d) van der Waals equation

6. Hydrogen bonds are classified as ________ (CO1, K1)

   (a) Covalent bonds

   (b) Ionic bonds

   (c) Non - covalent interactions

   (d) Metallic bonds

7. Phamucophore modeling is used to ______________. (CO4, K2)

   (a) Predict toxicity

   (b) Perform chemical synthesis

   (c) Study metabolism

   (d) Identify essential molecular features

8. Virtual screening is mainly employed for ________. (CO2, K1)

(a) Optimize ADMET properties

(b) Identify lead compounds

(c) Validate targets

(d) Perform clinical testing

9. Phase I drug metabolism mainly involves in ________. (CO2, K1)

(a) Oxidation, reduction, hydrolysis

(b) Conjugation reactions

(c) Drug excretion

(d) Target binding

10. ADMET prediction primarily evaluating the _______. (CO3, K2)

(a) Drug solubility only

(b) Drug—target interaction

(c) Absorption, distribution, metabolism, excretion, toxicity

(d) Chemical synthesis

Part B (5 × 5 = 25)

Answer **all** the questions not more than 500 words each

11. (a) Explain the major phases involved in drug discovery with suitable examples. (CO2, K3)

Or

(b) Illustrate the role of AI and machine learning in modern drug design. (CO3, K4)

12. (a) Describe the basic steps involved in molecular dynamics simulation. (CO4, K4)

Or

(b) Compare molecular mechanics and molecular dynamics approaches. (CO2, K3)

13. (a) Explain different types of molecular interactions involved in ligand binding. (CO2, K3)

Or

(b) Analyze the importance of force fields in molecular modeling. (CO3, K4)

14. (a) Discuss the steps involved in structure-based drug design. (CO5, K4)

Or

(b) Explain the significance of QSAR in drug discovery. (CO3, K3)

15. (a) Describe different receptor theories explaining drug action. (CO2, K4)

Or

(b) Analyze the importance of ADMET profiling in drug development. (CO4, K4)

Part C (5 × 8 = 40)

Answer **all** the questions not more than 1000 words each

16. (a) Critically analyze the role of molecular modeling in target identification and lead optimization. (CO4, K5)

Or

(b) Evaluate the impact of GPU computing and cloud platforms in accelerating drug discovery. (CO4, K5)

17. (a) Elaborate on molecular dynamics simulations and their applications in studying biomolecular systems. (CO3, K5)

Or

(b) Assess the role of simulation parameters and boundary conditions in molecular modeling studies. (CO4, K4)

18. (a) Examine the contribution of different bonding and non-bonding interactions in protein— ligand stability. (CO2, K4)

Or

(b) Evaluate how AI-assisted structural prediction improves drug design accuracy. (CO3, K4)

19. (a) Compare structure-based and ligand-based drug design approaches with suitable examples. (CO2, K4)

Or

(b) Critically discuss the role of virtual screening and HTVS in modern drug discovery pipelines. (CO4, K5)

20. (a) Analyze the mechanisms of enzyme inhibition and inactivation with relevant examples. (CO2, K4)

Or

(b) Design a workflow integrating AI/ML tools for ADMET and PK/PD prediction of drug-like molecules. (CO4, K5)

R4545

Sub. Code
25MBI2C3

M.Sc. DEGREE EXAMINATION, APRIL – 2026

Second Semester

Bioinformatics

STRUCTURAL BIOLOGY

(CBCS – 2025 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

Answer **all** the following questions by
choosing the correct options.

1. On what factor does the atomic scattering factor primarily depend? (CO1, K1)

   (a) Electron density (b) Temperature

   (c) pH (d) Solvent

2. What do the Laue equations explain in crystallography? (CO2, K2)

   (a) Crystal growth (b) Electron microscopy

   (c) Phase refinement (d) Diffraction condition

3. Why does chemical shift arise in NMR spectroscopy? (CO4, K1)

   (a) Proton spin

   (b) Magnetic field strength

   (c) Electronic environment

   (d) Temperature

4. What is small—angle X-ray scattering (SAXS) mainly used to study? (CO2, K2)

(a) Atomic resolution structures

(b) Overall shape of macromolecules

(c) Crystal defects

(d) Phase angles

5. Powder diffraction is mainly useful for ________ (CO3, K2)

(a) Non-crystalline solids

(b) Proteins

(c) Single crystals

(d) Viruses

6. What do space groups describe in crystallography? (CO2, K1)

(a) Atomic weight (b) Symmetry operations

(c) Electron density (d) Molecular flexibility

7. Data reduction in crystallography involves ________ (CO3, K1)

(a) Crystallization

(b) Protein expression

(c) Indexing and scaling

(d) Sample preparation

8. Co-crystallization is used to studying of ________ (CO2, K2)

(a) Protein folding (b) Diffraction errors

(c) Gene regulation (d) Protein—ligand complexes

9. B-factors indicates ________ (CO4, K2)

(a) Atomic mass (b) Charge density

(c) Thermal motion (d) Bond angles

10. What is the primary contribution of disulfide bonds in proteins? (CO3, K1)

(a) Flexibility (b) Structural stability

(c) Catalysis (d) Expression

Part B (5 × 5 = 25)

Answer **all** the questions not more than 500 words each

11. (a) Explain stereographic projection and its applications. (CO1, K3)

Or

(b) Analyze crystal defects and their impact on diffraction. (CO1, K4)

12. (a) Apply COSY and NOESY techniques in protein analysis. (CO2, K4)

Or

(b) Evaluate the role of synchrotron radiation in time-resolved studies. (CO2, K3)

13. (a) Explain the process of indexing reflections in small molecule crystallography. (CO3, K4)

Or

(b) Analyze challenges in structure solution of small molecules. (CO3, K4)

14. (a) Describe heavy atom methods used in protein crystallography. (CO4, K3)

Or

(b) Evaluate structure refinement strategies. (CO4, K4)

15. (a) Explain molecular geometry parameters in protein structures. (CO4, K4)

Or

(b) Evaluate X-ray crystallography applications in drug design. (CO5, K3)

Part C (5 × 8 = 40)

Answer **all** the questions not more than 1000 words each

16. (a) Analyze crystal symmetry and space groups with suitable examples. (CO4, K5)

Or

(b) Evaluate electron density calculation methods. (CO1, K4)

17. (a) Analyze NMR relaxation mechanisms in biomolecular studies. (CO2, K4)

Or

(b) Design a combined NMR—SAXS strategy for structure determination. (CO2, K5)

18. (a) Analyze the role of diffraction data quality in structure accuracy. (CO3, K4)

Or

(b) Evaluate advantages of small molecule crystallography in drug discovery. (CO3, K4)

19. (a) Analyze the steps involved in protein structure validation. (CO4, K4)

Or

(b) Evaluate the role of AI/ML in modern protein crystallography. (CO4, K5)

20. (a) Analyze intermolecular interactions stabilizing protein crystals. (CO3, K5)

Or

(b) Design a structure-based inhibitor using crystallographic data. (CO5, K6)

R4546

Sub. Code
25MBI2S1

M.Sc. DEGREE EXAMINATION, APRIL – 2026

Second Semester

Bioinformatics

CONCEPT OF CHEMOINFORMATICS

(CBCS – 2025 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

Answer **all** the following objective questions by choosing the correct options.

1. Chemoinformatics primarily deals with which of the following _____. (CO2, K1)
   (a) Large-scale chemical synthesis
   (b) Storage and analysis of chemical data
   (c) Wet lab experiments
   (d) Toxicological testing

2. Computational chemistry is mainly used for __________ purpose. (CO1, K1)
   (a) Chemical purification
   (b) Drug marketing
   (c) Molecular modelling and simulations
   (d) Sample collection

3. In graph theory, how is a molecule represented? (CO1, K2)
   (a) Only atoms
   (b) Only bonds
   (c) Atoms as nodes and bonds as edges
   (d) Molecular weight

4. Which notation represents chemical structures in a linear textual format? (CO2, K1)

(a) MOL file (b) SMILES

(c) PDB (d) CIF

5. Which database primarily focuses on toxicological chemical data? (CO1, K1)

(a) PubChem (b) ChEMBL

(c) PDB (d) DSSTox

6. SureChEMBL is mainly used for ___________ purpose? (CO2, K2)

(a) Patent chemical information

(b) Protein structures

(c) Drug metabolism

(d) Clinical trials

7. Substructure search is in chemoinformatics useful to ________________ (CO3, K1)

(a) Find identical molecules

(b) Locate molecules containing a specific fragment

(c) Predict toxicity

(d) Calculate molecular weight

8. Which software is widely used for drawing chemical structures? (CO2, K1)

(a) PyMol (b) RasMol

(c) ChemDraw (d) AutoDock

9. ADMET studies are important in ________ field? (CO2, K2)

(a) Organic synthesis (b) Inorganic analysis

(c) Polymer chemistry (d) Drug discovery

10. QSAR studies establish relationships between ________ (CO1, K1)

(a) Genes and proteins

(b) Structure and biological activity

(c) Atoms and bonds

(d) Reactions and catalysts

Part B (5 × 5 = 25)

Answer **all** the questions not more than 500 words each

11. (a) Explain the scope and applications of chemoinformatics in drug discovery. (CO1, K3)

Or

(b) Discuss the role of molecular modelling in structure elucidation. (CO1, K2)

12. (a) Describe molecular representation using graph-theoretical approaches. (CO2, K3)

Or

(b) Compare 2D and 3D molecular representations with examples. (CO2, K4)

13. (a) Explain the importance of chemical and bioactivity databases. (CO3, K3)

Or

(b) Describe the features and applications of ChEMBL database. (CO3, K2)

14. (a) Explain similarity search methods used in chemoinformatics. (CO4, K3)

Or

(b) Describe the role of molecular visualization tools in research. (CO4, K3)

15. (a) Discuss the importance of ADMET prediction in pharmaceutical research. (CO5, K2)

Or

(b) Evaluate the challenges associated with reproducibility in chemoinformatics. (CO5, K5)

Part C (5 × 8 = 40)

Answer **all** the questions not more than 1000 words each

16. (a) Analyse the evolution and future prospects of chemoinformatics in scientific research. (CO1, K3)

Or

(b) Evaluate the role of computational chemistry in materials science and environmental chemistry. (CO1, K5)

17. (a) Analyse different chemical structure representation methods used in chemoinformatics. (CO2, K4)

Or

(b) Evaluate the role of pharmacophore modelling in drug design. (CO2, K4)

18. (a) Analyse the role of toxicological and patent databases in chemoinformatics research. (CO3, K4)

Or

(b) Evaluate the significance of integrating multiple chemical databases. (CO3, K5)

19. (a) Analyse various chemical structure search strategies and their applications. (CO4, K5)

Or

(b) Evaluate the importance of molecular descriptors in structure—activity studies. (CO4, K4)

20. (a) Critically analyse applications of chemoinformatics in personalized medicine. (CO5, K5)

Or

(b) Propose strategies to overcome challenges in data interpretation and reproducibility. (CO5, K6)

R4989

Sub. Code
502401

M.Sc. DEGREE EXAMINATION, APRIL – 2026

Fourth Semester

Bioinformatics

MACHINE LEARNING AND ARTIFICIAL INTELLIGENCE

(CBCS – 2022 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

Answer **all** the following objective type questions by choosing the correct option.

1. In a search algorithm informed search is (CO2, K1)

   (a) Depth first search

   (b) Breadth first search

   (c) A*search

   (d) Uniform cost search

2. The path finding problem is defined as ———— (CO2, K2)

   (a) Finding shortest route on a map

   (b) Scheduling and puzzle solving

   (c) Travelling sales man problem

   (d) Navigating a maze

3. The valid predicate logic expression is (CO4, K6)

(a) $\forall X$ student $(X) \rightarrow$ studies (x)

(b) $X + Y = Z$

(c) If X then Y

(d) All $(X,Y)\rightarrow$

4. A predicate is an expression of one or more ———— (CO2, K3)

(a) Statement (b) Calculation

(c) Measurement (d) Variable

5. The process of removing branches or nodes from a decision tree to improve its generalization and prevent overfitting is called ———— (CO1, K2)

(a) Splitting (b) Pruning

(c) Branching (d) Clustering

6. ———— is used to predict a continuous value by finding the best-fit straight line between input and output values (CO2, K1)

(a) Logistic regression

(b) Decision Tree

(c) Linear Regression

(d) Support vector machine

7. ———— that involves finding pattern in unlabeled data. (CO3, K2)

   (a) Supervised Learning

   (b) Unsupervised learning

   (c) Reinforcement Learning

   (d) Q-Learning

8. Support Vector Machine is primarily used for ———— (CO2, K1)

   (a) classification

   (b) clustering

   (c) data generation

   (d) association

9. The key feature of the Focused learning (FOCL) algorithm is (CO2, K2)

   (a) Using supervised learning

   (b) Combines logical rules with data driven learning

   (c) It relies on deep learning techniques

   (d) It uses decision tree-based approach

10. To update values in Q learning algorithm is ———— (CO2, K2)

   (a) Bellman Equation

   (b) Gradient descent

   (c) Linear regression

   (d) Convolutional neural network

Part B (5 × 5 = 25)

Answer **all** questions not more than 500 words each.

11. (a) Describe the characteristics for defining problems in AI. (CO2, K2)

Or

(b) State the performance methods for analyzing search algorithm. (CO3, K3)

12. (a) Explain quantifiers in predicate logic. (CO1, K2)

Or

(b) Outline resolution with an example. (CO3, K3)

13. (a) Elaborate on Machine Learning approaches. (CO4, K3)

Or

(b) What is inductive bias in machine learning. (CO5, K4)

14. (a) Elaborate on kernel in support vector machines. (CO4, K2)

Or

(b) Describe various distance-based similarity metrices in Clustering. (CO4, K4)

15. (a) Explain inductive learning algorithm. (CO4, K4)

Or

(b) State the Advantages of Reinforcement Learning Approach. (CO3, K2)

Part C (5 × 8 = 40)

Answer **all** questions not more than 1000 words each.

16. (a) Explain Heuristic Search algorithm. (CO2, K2)

Or

(b) Illustrate state space representation for solving Monkey Banana problem. (CO3, K3)

17. (a) Describe the logical connectivity in predicate logic with an example. (CO3, K5)

Or

(b) Summarize the knowledge representation structures frames and semantic network. (CO5, K4)

18. (a) Discuss the issues and challenges in modelling machine learning algorithm. (CO5, K4)

Or

(b) Explain decision tree algorithm with feature selection metrices. (CO2, K5)

19. (a) Elaborate on Naive Bayes Classifier. (CO2, K2)

Or

(b) Explain DBSCAN algorithm. (CO3, K2)

20. (a) Describe Explanation Based Learning with an Use case. (CO3, K3)

Or

(b) Compare Q-Learning Vs Temporal difference learning approaches. (CO5, K5)

———————

R4990

Sub. Code
502402

M.Sc. DEGREE EXAMINATION, APRIL – 2026

Fourth Semester

Bioinformatics

SYSTEMS BIOLOGY

(CBCS – 2022 onwards)

Time : 3 Hours   Maximum : 75 Marks

Part A   (10 × 1 = 10)

Answer **all** questions by choosing the correct option.

1. Which technique is used to separate proteins based on their isoelectric point and molecular weight? (CO1, K2)

   (a) Mass spectrometry

   (b) 2D gel electrophoresis

   (c) qRT-PCR

   (d) MALDI TOF MS

2. Which clinical application is not typically associated with proteomics? (CO1, K2)

   (a) Biomarker discovery

   (b) Diabetes profiling

   (c) Protein folding studies

   (d) Infectious disease profiling

3. Which database is commonly used for protein-protein interaction studies? (CO2, K3)

   (a) STRING

   (b) BLAST

   (c) InterPro

   (d) KEGG Autosomal dominant

4. The main purpose of protein arrays is to (CO2, K3)

   (a) Detect protein-protein interactions

   (b) Sequence DNA

   (c) Perform lipid analysis

   (d) Identify carbohydrates

5. Which of the following is an example of a regulatory network? (CO3, K4)

   (a) Neural network models

   (b) Metabolic fluxes

   (c) DNA sequencing models

   (d) Protein folding pathways

6. Which method is most commonly used for protein binding site analysis? (CO3, K4)

   (a) Mass spectrometry

   (b) Network theory and algorithms

   (c) Protein microarrays

   (d) qRT-PCR

7. What is the primary focus of glycan microarrays? (CO4, K4)

   (a) Protein sequencing

   (b) Carbohydrate interactions

   (c) Metabolomics analysis

   (d) Regulatory networks

8. The study of biomolecules in fluxomics focuses on (CO4, K4)

   (a) Metabolic flux in living systems

   (b) DNA mutation analysis

   (c) Neural networks in cells

   (d) Gene regulatory pathways

9. Which of the following is used for simulating cellular subsystems? (CO5, K2)

   (a) STRING

   (b) KEGG

   (c) GROMOS

   (d) Interpro

10. What is the main characteristic of a scale-free network? (CO5, K2)

   (a) All nodes have the same degree

   (b) Some nodes act as hubs with a high number of connections

   (c) All connections are random

   (d) No connections exist

Part B (5 × 5 = 25)

Answer **all** questions not more than 500 words each.

11. (a) How are body fluid profiles useful in clinical proteomics? (CO1, K2)

Or

(b) Describe the principle and applications of qRT-PCR in clinical proteomics. (CO1, K2)

12. (a) How does the Interpro database contribute to protein-protein interaction studies? (CO2, K3)

Or

(b) Explain the basic principles behind protein-protein interaction modeling. (CO2, K3)

13. (a) Explain the role of neural network models in studying protein interaction networks. (CO3, K4)

Or

(b) What is the application of network theory in analyzing structures of regulatory networks? (CO3, K4)

14. (a) What are the differences between glycomics, lipidomics and fluxomics? (CO4, K4)

Or

(b) Explain the importance of glycomics in studying glycoproteins and glycolipids. (CO4, K4)

15. (a) How does V-CELL software help in simulating cellular subsystems? (CO5, K2)

Or

(b) What are the advantages of computer simulations in modeling whole cells? (CO5, K2)

Part C (5 × 8 = 40)

Answer **all** questions not more than 1000 words each.

16. (a) Explain in detail the proteomic techniques such as mass spectrometry, 2D gel electrophoresis and protein microarrays. (CO1, K2)

Or

(b) Explain the significance of proteomics in personalized medicine and therapeutic development. (CO1, K2)

17. (a) Describe in detail the computational tools used for proteomics data analysis, including ExPASy Proteomics Server, STRING, and DIP databases. (CO2, K3)

Or

(b) Discuss the role of bioinformatics in identifying and analyzing polypeptides and protein-protein interactions. (CO2, K3)

18. (a) Explain the structure and function of regulatory networks in systems biology with examples. (CO3, K4)

Or

(b) Discuss the application of network theory and algorithms in analyzing protein complexes and regulatory networks. (CO3, K4)

19. (a) Explain the challenges and promises of glycomics in understanding biomolecular interactions, with a focus on glycoproteins and glycolipids. (CO4, K4)

Or

(b) Describe the techniques and applications of glycan microarrays in glycomics studies. (CO4, K4)

20. (a) Discuss in detail the differences between random and scale-free networks, and explain their applications in biological systems. (CO5, K2)

Or

(b) Discuss the integration of metabolic pathway databases such as KEGG, MetaCyc, and AraCyc for studying biochemical pathways. (CO5, K2)
