R1012

Sub. Code
502201

M.Sc. DEGREE EXAMINATION, APRIL – 2024

Second Semester

Bioinformatics

PHYLOGENY AND PHYLOGENOMICS

(CBCS – 2022 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

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

1. Molecular divergence between two species is primarily caused by (CO1, K1)

   (a) Gene flow

   (b) Adaptive radiation

   (c) Accumulation of genetic differences over time

   (d) Convergent evolution

2. Adaptive radiation is most likely to occur when: (CO1, K2)

   (a) Species are in direct competition for resources

   (b) There are limited environmental opportunities and niches

   (c) There is a sudden change in environmental conditions

   (d) There is no variation in the population

3. The Smith-Waterman algorithm is most suitable for: (CO2, K1)

(a) Identifying conserved motifs in sequences

(b) Aligning highly similar sequences

(c) Local sequence alignment

(d) Global sequence alignment

4. In a multiple sequence alignment, what symbol is typically used to represent a gap? (CO2, K1)

(a) - (b) *

(c) : (d) #

5. Which method is commonly used to classify protein sequences based on the presence of specific motifs? (CO3, K2)

(a) Sequence logos

(b) Regular expressions

(c) Hidden Markov models

(d) Probabilistic patterns

6. GRAIL is a computational tool used for: (CO3, K1)

(a) Gene discovery using Fourier analysis

(b) Gene discovery using Hidden Markov Models

(c) Gene discovery using artificial neural networks

(d) Gene discovery using statistical methods

7. Which algorithm aims to find the tree that requires the fewest evolutionary changes? (CO4, K2)

(a) Maximum Parsimony

(b) UPGMA

(c) Transformed Distance

(d) Neighbor-Joining

8. Which parameter is optimized in the maximum likelihood algorithm to infer the phylogenetic tree? (CO4, K1)

(a) Branch lengths

(b) Substitution rate

(c) Likelihood function

(d) Confidence intervals

9. PileUp is a software tool primarily used for: (CO5, K1)

(a) Constructing phylogenetic trees

(b) Pairwise sequence alignment

(c) Multiple sequence alignment

(d) Identifying protein motifs

10. What is one common application of phylogenetic analysis in biology? (CO5, K1)

(a) Identifying protein structures

(b) Predicting gene expression levels

(c) Understanding evolutionary relationships

(d) Analyzing metabolic pathways

Part B $(5 \times 5 = 25)$

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

11. (a) Define neutral evolution and explain its significance in molecular evolution. (CO1, K2)

Or

(b) Discuss the process of gene duplication and divergence. (CO1, K3)

12. (a) Define heterologs, orthologs, paralogs, xenologs and explain their significance in sequence analysis. (CO2, K4)

Or

(b) Discuss the significance of gap penalties in sequence alignment and discuss how they influence the alignment process. (CO2, K4)

13. (a) Outline the different pattern representations in protein sequences. (CO3, K2)

Or

(b) Discuss the application of Fourier analysis in gene discovery. (CO3, K4)

14. (a) Explain the different types of phylogenetic tree representations. (CO4, K2)

Or

(b) Describe the assumptions of Maximum Parsimony algorithm in phylogenetic analysis. (CO4, K3)

15. (a) Discuss the algorithm of CLUSTALW and its applications. (CO5, K4)

Or

(b) Write a note on the Phylogenetic analysis of ancient DNA. (CO5, K3)

Part C ($5 \times 8 = 40$)

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

16. (a) Discuss the various molecular tools in phylogeny, and its classification. (CO1, K3)

Or

(b) Discuss the concept of natural selection and its role in changing gene frequency within populations. (CO1, K4)

17. (a) Discuss the Smith-Waterman algorithm in sequence alignment. Provide a step-by-step example to illustrate how the algorithm identifies local similarities between sequences. (CO2, K3)

Or

(b) Compare and contrast PAM and BLOSUM substitution matrices, discussing their applications and differences in evolutionary modeling. (CO2, K5)

18. (a) Explain the methods of pattern discovery in protein and DNA sequences for identifying functional motifs and domains. (CO3, K3)

Or

(b) Discuss the use of artificial neural networks and HMM in gene discovery. (CO3, K4)

19. (a) Discuss the steps in constructing a Phylogenetic tree and its importance in evolutionary analysis. (CO4, K4)

Or

(b) Explain the Bootstrapping and maximum likelihood algorithms of phylogenetic analysis. (CO4, K3)

20. (a) Explain the dynamic programming algorithm of PileUp for aligning DNA and protein sequences. (CO5, K3)

Or

(b) Describe the steps involved in constructing a dendrogram, its interpretation and treeview tools. (CO5, K4)

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R1013

Sub. Code
502202

M.Sc. DEGREE EXAMINATION, APRIL – 2024

Second Semester

Bioinformatics

MOLECULAR MODELING AND DRUG DESIGN

(CBCS – 2022 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

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

1. What is the primary purpose of target identification in drug discovery? (CO1, K1)

   (a) Lead optimization

   (b) Finding new drug targets

   (c) Target validation

   (d) Phase HI clinical trials

2. During which phase of drug discovery does lead identification typically occur? (CO1, K2)

   (a) Target identification

   (b) Phase I clinical trials

   (c) Lead optimization

   (d) Phase II clinical trials

3. What is the primary function of a potential energy surface in molecular modeling? (CO2, K2)

   (a) Describing the electronic structure of atoms

   (b) Predicting the probability of molecular reactions

   (c) Mapping the relationship between molecular conformations and energy

   (d) Analyzing molecular dynamics simulations

4. Which principle of quantum mechanics is used to describe the behavior of electrons in atoms and molecules? (CO2, K1)

   (a) Newton's laws

   (b) Schrödinger equation

   (c) Heisenberg uncertainty principle

   (d) Pauli exclusion principle

5. Which process involves adjusting the positions of atoms in a protein structure to minimize steric clashes and improve energetics? (CO3, K1)

   (a) Structure Validation

   (b) Ramachandran Plotting

   (c) Loop Refinement

   (d) Secondary structure Prediction

6. In a Ramachandran Plot, which regions correspond to allowed and disallowed regions for the backbone torsion angles of amino acids in a protein? (CO3, K2)

   (a) The left and right quadrants, respectively

   (b) The upper and lower quadrants, respectively

   (c) The upper left and lower right quadrants, respectively

   (d) The upper right and lower left quadrants, respectively

7. Which of the following best describes a pharmacophore?

(a) A three-dimensional arrangement of atoms and functional groups essential for biological activity

(b) A two-dimensional representation of a drug molecule's structure

(c) The process of identifying potential drug targets in a biological system

(d) A statistical model used to predict drug-receptor interactions

8. What distinguishes HTVS from traditional virtual screening approaches? (CO4, K2)

(a) HTVS requires experimental validation of hits

(b) HTVS screens larger compound libraries

(c) HTVS focuses on low-affinity ligands

(d) HTVS is more time-consuming

9. Prodrugs are inactive compounds that are converted into active drugs through: (CO5, K1)

(a) Enzymatic hydrolysis

(b) Enzymatic oxidation

(c) Enzyme inhibition

(d) Enzyme induction

10. Which phase of drug metabolism involves reactions that introduce or expose functional groups such as hydroxyl, amino, or carboxyl groups? (CO5, K3)

(a) Phase I metabolism

(b) Phase II metabolism

(c) Phase III metabolism

(d) Phase IV metabolism

Part B (5 × 5 = 25)

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

11. (a) Describe the objective of the preclinical phase in drug discovery and briefly outline the key steps involved? (CO1, K3)

Or

(b) Explain the significance of target identification in the drug discovery process and discuss two common methods used for target identification? (CO1, K4)

12. (a) Discuss the significance of potential energy surface in molecular modeling. (CO2, K4)

Or

(b) Write a note on the importance of hydrogen bonding in molecular mechanics. (CO2, K2)

13. (a) Give an account on the secondary structure prediction methods. (CO3, K3)

Or

(b) Discuss the significance of Ramachandran plot in structure validation. (CO3, K4)

14. (a) What is pharmacophore identification and mapping in drug design? (CO4, K1)

Or

(b) Explain the methods commonly used to identify lead compounds in drug discovery. (CO4, K2)

15. (a) Differentiate between competitive and non-competitive enzyme inhibition. (CO5, K3)

Or

(b) Write a note on Drug-receptor interactions and mechanism of action. (CO5, K2)

Part C (5 × 8 = 40)

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

16. (a) Explain the various phases involved in the process of drug discovery. (CO1, K2)

Or

(b) Describe the importance of Pharmacoinformatics in drug discovery process. (CO1, K3)

17. (a) Describe the fundamental principles of quantum mechanics and its relevance to molecular modeling. (CO2, K4)

Or

(b) Discuss in detail, the key features of molecular mechanics in molecular modeling. (CO2, K2)

18. (a) Discuss the different methods of protein structure prediction. (CO3, K2)

Or

(b) Describe Geometry optimisation and loop refinement with respect to structure prediction. (CO3, K2)

19. (a) Discuss the workflow of virtual screening in drug discovery, including the steps involved in high-through put virtual screening (HTVS) and its significance in lead identification. (CO4, K4)

Or

(b) Explain the principles of QSAR and molecular descriptors in drug design. (CO4, K3)

20. (a) Discuss the various phases of drug metabolism in pharmacology. (CO5, K2)

Or

(b) Explain the fundamental principle of ADME-T properties of drug molecules. (CO5, K3)

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R1014

Sub. Code
502203

M.Sc. DEGREE EXAMINATION, APRIL – 2024

Second Semester

Bioinformatics

COMPUTATIONAL BIOLOGY

(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. What is the primary challenge in developing biosimilars compared to small molecule generics? (CO1, K1)

   (a) Cost of production

   (b) Complexity of manufacturing and characterization

   (c) Regulatory requirements

   (d) Market demand

2. In biosimilar development, what is the term for the comparative clinical trials conducted to demonstrate similarity with the reference product? (CO1, K2)

   (a) Pre-clinical trials

   (b) Phase I trials

   (c) Phase II trials

   (d) Phase III trials

3. What is the primary goal of sequence alignment in bioinformatics? (CO2, K2)

(a) Identifying genetic mutations

(b) Comparing protein structures

(c) Finding similarities between biological sequences

(d) Determining gene expression levels

4. Which type of sequence alignment is used to find the best match between two sequences without considering gaps? (CO2, K2)

(a) Global alignment

(b) Local alignment

(c) Semi-global alignment

(d) Overlapping alignment

5. What is the purpose of dynamic programming in sequence alignment algorithms? (CO3, K1)

(a) To identify conserved domains

(b) To optimize the alignment score

(c) To speed up the alignment process

(d) To ignore gaps in the alignment

6. What does the acronym "HMM" stand for in the context of sequence algorithms? (CO3, K1)

(a) 'Hidden Markov Model

(b) Heuristic Matching Method

(c) High-Speed Mapping

(d) Hybrid Model for Matching

7. What is the typical sequence recognition pattern for restriction enzymes? (CO4, K1)

(a) Palindromic sequences

(b) Random sequences

(c) A/T-rich sequences

(d) Single-stranded sequences

8. In a restriction map, what does the distance between two restriction sites represent? (CO4, K2)

(a) The number of nucleotides in the recognition sequence

(b) The size of the DNA fragment between the two sites

(c) The degree of methylation in the DNA

(d) The location of the restriction enzyme on the chromosome

9. What is the primary goal of synthetic biology? (CO5, K2)

(a) Cloning existing organisms

(b) Engineering biological systems for useful purposes

(c) Studying natural ecosystems

(d) Observing genetic mutations in natural populations

10. Which term refers to the design and construction of new biological parts, devices, and systems that do not exist in the natural world? (CO5, K1)

(a) Genetic engineering

(b) Metabolic engineering

(c) Synthetic biology

(d) Bioprocessing

Part B (5 × 5 = 25)

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

11. (a) How do different expression systems impact the production of genetically engineered biosimilars? (CO1, K2)

Or

(b) What challenges are specific to the clinical development of genetically engineered biosimilars? (CO1, K3)

12. (a) Explain the terms "homologous sequences" and "conserved regions" in the context of sequence alignment. (CO2, K2)

Or

(b) Describe the algorithmic steps involved in pairwise sequence alignment. (CO2, K2)

13. (a) How does dynamic programming optimize the alignment process in terms of time and space complexity? (CO3, K3)

Or

(b) How is k-mer analysis used for sequence data representation and analysis? (CO2, K3)

14. (a) What are the challenges in extending sequence alignment algorithms to multiple sequences? (CO3, K4)

Or

(b) Discuss the role of restriction enzymes in the generation of restriction maps. (CO3, K4)

15. (a) Discuss the role of gene editing technologies, such as CRISPR-Cas9, in synthetic biology. (CO5, K4)

Or

(b) Provide examples of biochemical compounds where aromaticity plays a crucial role. (CO5, K3)

Part C ($5 \times 8 = 40$)

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

16. (a) Discuss the role of genetic modifications in biosimilars. How do developers introduce and manage genetic changes while ensuring similarity to the reference product? (CO1, K5)

Or

(b) Describe the step-by-step process involved in the development of biosimilars, from initial concept to market approval. Discuss key considerations at each stage. (CO1, K5)

17. (a) Discuss the role of scoring systems in sequence alignment algorithms. (CO2, K4)

Or

(b) Compare and contrast the Needleman-Wunsch and Smith-Waterman algorithms. (CO2, K4)

18. (a) Provide examples of how HMMs are used in bioinformatics, particularly in sequence analysis and structural prediction. (CO3, K4)

Or

(b) Explain the step-by-step process of constructing a dot plot. (CO3, K2)

19. (a) Describe how restriction maps are compared between different DNA samples or organisms. (CO4, K4)

Or

(b) Discuss the design considerations for vectors used in protein expression systems. (CO4, K5)

20. (a) How are these plasmids engineered for specific functions, such as biosynthesis pathways or gene circuits? (CO5, K5)

Or

(b) How can quantum algorithms be applied to solve computational biology problems more efficiently than classical algorithms? (CO5, K5)

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R1015

Sub. Code
502204

M.Sc. DEGREE EXAMINATION, APRIL – 2024

Second Semester

Bioinformatics

PROGRAMMING IN SCRIPTING LANGUAGES (PYTHON, PERL & R)

(CBCS – 2022 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

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

1. The sequence is one of basic structures in _____. (CO1, K1)

   (a) Manual Programming
   (b) Computer Programming
   (c) Dynamic Programming
   (d) System Programming

2. _____ is an object oriented high level language, interpreted, dynamic and multipurpose language. (CO2, K1)

   (a) JAVA (b) Python
   (c) C# (d) C++

3. There are _____ variables in perl. (CO1, K1)

   (a) 2 (b) 3
   (c) 5 (d) 6

4. The engine that translates and runs python is called the python ————————. (CO2, K1)

(a) Source code (b) Interpreter

(c) Compiler (d) Programming code

5. A value is one of the fundamental things like, a letter or a number that program manipulates (CO3, K1)

(a) Numeric (b) Value

(c) Alphanumeric (d) Data

6. Identifiers can be a _____, in a lower case (a to z) (or) Uppercase (A to Z). (CO3, K1)

(a) Combination of letter

(b) Symbol

(c) Arithmatic

(d) Numeric

7. Multiple statement and end of the statement in python, is marked by _____ character. (CO4, K1)

(a) New line (b) Termination

(c) Interpreter (d) Source code

8. Function can be invoked in _____. (CO4, K1)

(a) Program section

(b) Section of program

(c) Intermediate program

(d) End of program

9. An expression is combination of values, variable, operators and function calls (CO5, K1)

(a) >>>1 + 1 = 2 (b) <<< 2 + 2 = 4

(c) >>> 3 + 3 = 6 (d) <<< 2 + 1 = 3

10. The break statement is executed ———————— (CO5, K1)

(a) out of the loop (b) end of the loop

(c) terminate the loop (d) intermediate loop

Part B (5 × 5 = 25)

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

11. (a) Write an account on Pointers and Hierarchy of operators in Perl. (CO1, K2)

Or

(b) Write a code for Sub-routines in perl. (CO1, K3)

12. (a) Give an account on String functions and methods in python. (CO2, K3)

Or

(b) Describe the conditionals in Python. (CO2, K3)

13. (a) Write a code for literal matching in python. (CO3, K4)

Or

(b) Explain the Split and Join function in python. (CO3, K3)

14. (a) Describe the lists, arrays and tuples in python. (CO4, K4)

Or

(b) Explain the Greedy algorithm. (CO4, K3)

15. (a) Write a note on Debugging using R. (CO5, K4)

Or

(b) Explain the Loop functions in R. (CO5, K3)

Part C (5 × 8 = 40)

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

16. (a) Explain in detail about control structures in PERL. (CO1, K4)

Or

(b) Describe the Database connections and operations. (CO1, K4)

17. (a) Explain the detail, Control flow structures in python and write a code for decision- making. (CO2, K4)

Or

(b) Describe the data types and variables in python. (CO2, K3)

18. (a) Discuss file handling and sub-routines in python with codes. (CO3, K4)

Or

(b) Describe the concept and uses of Regular Expressions in python and Write a code for Pattern matching. (CO3, K5)

19. (a) Describe the files and exceptions with respect to python. (CO4, K4)

Or

(b) Explain in detail, the Pattern matching algorithm. (CO4, K5)

20. (a) Explain in detail, the different data visualisations methods used in data analytics. (CO5, K4)

Or

(b) Discuss in detail, the String Operations commonly used in R. (CO5, K4)

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R1016

Sub. Code
502401

M.Sc. DEGREE EXAMINATION, APRIL – 2024

Fourth Semester

Bioinformatics

MACHINE LEARNING AND ARTIFICIAL INTELLIGENCE

(CBCS – 2022 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A ($10 \times 1 = 10$)

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

1. Which of the following best describes a well-defined problem? (CO1, K1)

   (a) A problem with unclear objectives

   (b) A problem with multiple possible solutions

   (c) A problem with clearly stated goals and constraints

   (d) A problem that lacks data

2. Choose the correct example of a heuristic search method? (CO1, K1)

   (a) Depth-first search

   (b) Breadth-first search

   (c) Dijkstra's algorithm

   (d) Greedy algorithm

3. The knowledge representation technique is used to encode the rules of a game is ———————— (CO2, K1)

(a) Expert systems

(b) Fuzzy logic

(c) Semantic networks

(d) Rule-based systems

4. Which logical connective is used to represent conjunction in predicate logic? (CO2, K1)

(a) $\exists$ (b) $\vee$

(c) $\rightarrow$ (d) $\wedge$

5. The role of inductive bias in machine learning is described by ———————— (CO3, K1)

(a) It helps minimize bias and variance simultaneously.

(b) It allows the model to generalize beyond the training data.

(c) It increases the likelihood of overfitting.

(d) It eliminates the need for feature engineering.

6. In a decision tree, what does each internal node represent? (CO3, K2)

(a) A feature or attribute

(b) A prediction or decision

(c) A leaf node

(d) A root node

7. Support Vector Machine (SYM) is primarily used for (CO4, K3)

(a) Classification

(b) Regression

(c) Clustering

(d) Dimensionality reduction

8. What is the primary objective of regression analysis? (CO4, K1)

(a) To classify data points into different categories

(b) To predict the value of a dependent variable based on one or more independent variables

(c) To find the mean of a dataset

(d) To calculate the standard deviation of a dataset

9. ———— is a key characteristic of Explanation-based Learning? (CO5, K2)

(a) Learning from labeled examples

(b) Generalizing from specific instances

(c) Utilizing prior knowledge to derive explanations

(d) Minimizing prediction errors

10. The following algorithm is used for learning optimal policies in reinforcement learning is ———— (CO5, K1)

(a) Q-Learning

(b) Supervised Learning

(c) Unsupervised Learning

(d) Decision Trees

Part B (5 × 5 = 25)

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

11. (a) Explain Production System with an example. (CO1, K2)

Or

(b) Compare Heuristic functions Vs Hill Climbing Approaches. (CO1, K4)

12. (a) Explain the Quantifiers used to represent predicate Logic. (CO2, K2)

Or

(b) Outline on the applications of predicate calculus. (CO2, K2)

13. (a) Elaborate on Candidate Elimination method with example. (CO3, K3)

Or

(b) Discuss the demerits of Inductive Bias. (CO3, K2)

14. (a) Explain Bayes Rule with an example. (CO4, K2)

Or

(b) Discuss the various distance measures specific to data attribute type. (CO4, K3)

15. (a) Compare Analytical Learning Vs Explanation Base Learning. (CO5, K3)

Or

(b) Interpret Bellman equation in Q-Learning. (CO5, K6)

Part C (5 × 8 = 40)

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

16. (a) Explain problem state representation for tic-tac-toe. (CO1, K6)

Or

(b) Explain the key components of constraint satisfaction problem. (CO1, K4)

17. (a) Explain knowledge representation using predicate logic with an example. (CO2, K3)

Or

(b) Elaborate the various knowledge representation formats and state the advantages and limitation. (CO2, K4)

18. (a) Discuss the challenges in learning problems with respect to machine learning (CO3, K3)

Or

(b) Explain the Heuristic search to find shortest path with an example. (CO3, K3)

19. (a) Describe the steps required to be followed to formulate Regression model. (CO4, K5)

Or

(b) Discuss distance-based clustering approach k-means and k-medoids. (CO4, K3)

20. (a) Explain Sequential Covering algorithm workflow steps with an example. (CO5, K2)

Or

(b) Explain temporal difference learning techniques for any specific use case. (CO5, K3)

———————

R1017

Sub. Code
502402

M.Sc. DEGREE EXAMINATION, APRIL – 2024

Fourth Semester

Bioinformatics

SYSTEMS BIOLOGY

(CBCS – 2022 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 building blocks of proteins are ———— naturally occurring amino acids, small molecules that contain a free amino group (NH_2) and a free carboxyl group (COOH). (CO1, K1)

   (a) ten (b) twenty

   (c) nine (d) nineteen

2. A linear polymer of more than fifty amino acid residues is referred to as a ———— (CO1, K2)

   (a) dipeptide (b) oligopeptide

   (c) peptide (d) polypeptide

3. Which mass analyzer is most frequently used with protein sequencing method? (CO2, K2)

(a) Magnetic sector (b) Quadrupole

(c) MALDI-TOF (d) Ion trap

4. What is the deposition of cDNA into the inert structure called? (CO2, K1)

(a) DNA probes

(b) DNA polymerase

(c) DNA microarrays

(d) DNA fingerprinting

5. Proteomics refers to the study of ————————. (CO3, K1)

(a) Set of proteins in a specific region of the cell

(b) Biomolecules

(c) Set of proteins

(d) The entire set of expressed proteins in the cell

6. The computational methodology that tries to find the best matching between two molecules, a receptor and ligand are called ————————. (CO3, K1)

(a) Molecular fitting

(b) Molecular matching

(c) Molecular docking

(d) Molecule affinity checking

7. Which of the following is untrue regarding the STRING? (CO4, K1)

(a) Search Tool for the Retrieval of Interacting Genes/Proteins.

(b) Functional associations include only the direct protein-protein interactions.

(c) It is based on combined evidence of gene linkage, gene fusion and phylogenetic profiles.

(d) It is a web server that predicts gene and protein functional associations.

8. Which of the following requires for the simulation? (CO4, K1)

(a) Program (b) Model

(c) Process (d) Procedure

9. Correlation of gene expression for pairs of transiently interacting proteins is ———— compared to randomly chosen pairs of proteins. (CO5, K1)

(a) not significant

(b) only marginally significant

(c) totally significant

(d) significant to much extent

10. Disease related network variations entry point ———————— . (CO5, K1)

(a) KEGG NETWORK

(b) KEGG Enzyme

(c) KEGG GLYCAN

(d) KEGG COMPOUND

Part B ($5 \times 5 = 25$)

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

11. (a) Write about the Components of a complex mixture. (CO1, K2)

Or

(b) Describe in detailed account on ITC. (CO1, K3)

12. (a) Write notes on PPI Modeling in biological system. (CO2, K3)

Or

(b) Explain the ExPASy Proteomics server. (CO2, K2)

13. (a) Describe the protein binding site analysis. (CO3, K4)

Or

(b) Write down the Structure of regulatory networks. (CO3, K3)

14. (a) List out the applications of Lipidomics and Fluxomics. (CO4, K3)

Or

(b) Write a detailed note on the Challenge and Promise of Glycomics. (CO4, K4)

15. (a) Explain the Signal transduction networks. (CO5, K4)

Or

(b) Comment on Simulation of cellular subsystems. (CO5, K4)

Part C ($5 \times 8 = 40$)

Answer **all** the questions not more that 1000 words each.

16. (a) Describe the Protein sequencing techniques. (CO1, K2)

Or

(b) Write in detail about Body fluid profiles, Blood disease profiles and Diabetes profiles. (CO1, K4)

17. (a) Explain the principles and Computational methods for identification of polypeptides. (CO2, K2)

Or

(b) Give an elaborate account on Protein – Protein interactions. (CO2, K3)

18. (a) Write in detail about Protein network analysis in Cytoscape and Python. (CO3, K4)

Or

(b) Explain the Network theory and algorithms. (CO3, K3)

19. (a) Describe in detailed account on Transcriptomics and Metabolomics and its applications. (CO4, K4)

Or

(b) Explain in detail about identification of Carbohydrates, Glycan Microarrays and Glycan. (CO4, K5)

20. (a) Give an elaborate account on Human Erythrocyte Model and its applications. (CO5, K4)

Or

(b) Discuss in detailed account on metabolic pathways databases such as EMP and MetaCyc. (CO5, K3)

———————