R6713	Sub. Code
	502201

M.Sc. DEGREE EXAMINATION, APRIL – 2022

Second Semester

Bioinformatics

PHYLOGENY AND PHYLOGENOMICS

(CBCS – 2019 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

1. Difference between bottleneck effect and founder's effect.
2. Difference between convergent evolution and co-evolution.
3. Difference between paralogs and orthologs.
4. Difference between PAM matrix and BLOSUM matrix.
5. What is a protein motif?
6. What is Markov Model?
7. What is a clade?
8. How is jacknifing used in phylogenetics?
9. Name two tools for visualization and plotting of phylogenetic tree.
10. Write any three applications of phylogenetic analysis.

Part B (5 × 5 = 25)

Answer **all** the following questions choosing either (a) or (b).

11. (a) Describe the various ways in which new genes and proteins are acquired or evolved.

Or

(b) Describe adaptive radiation with a suitable example

12. (a) What is MSA? Explain the terms progressive and hierarchical MSA.

Or

(b) Explain the algorithm of FASTA.

13. (a) Explain gene discovery using Fourier analysis.

Or

(b) Explain how artificial neural networks are used for gene discovery.

14. (a) Explain the various components of a phylogenetic tree, Differentiate between rooted and unrooted trees.

Or

(b) Explain distance-based methods for phylogenetic tree reconstruction.

15. (a) Explain role of ClustalW for phylogenetic analysis.

Or

(b) Describes the trees obtained using DNA seq. vs protein seq. vs Full genome.

Part C

(3 × 10 = 30)

Answer any **three** questions.

16. Explain molecular evolution and the various methods by which organisms have evolved over the course of time.

17. Explain the algorithm for dynamic programming with suitable examples.

18. Write and explain about the different sequence pattern representations used for pattern discovery and classification in protein and DNA sequences.

19. Explain the algorithm:

    (a) Bootstrapping Method

    (b) SAM method.

20. Write the algorithm and their application in phylogenetic analysis:

    (a) MUSCLE

    (b) MAFFT

    (c) Pileup

———————

R6714	Sub. Code
	502202

M.Sc. DEGREE EXAMINATION, APRIL – 2022

Second Semester

Bioinformatics

MOLECULAR MODELING AND DRUG DESIGN

(CBCS – 2019 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

1. List various classes of drug targets.

2. List any two disease condition, drug for their treatment and their targets.

3. What is a force field?

4. What is inter and intra molecular interactions?

5. What is geometry optimization?

6. Sketch a representative Ramachandran plot.

7. List four pharamcophore features.

8. What is virtual screening?

9. What is an agonist?

10. What is ADMET?

Part B (5 × 5 = 25)

Answer **all** the questions, choosing either (a) or (b).

11. (a) Discuss the various stages of new drug discovery process.

Or

(b) How is a lead optimized using computational methods? Explain.

12. (a) What is the basis of drug – target interaction?

Or

(b) Discuss the features of PES.

13. (a) Discuss about various structure validation tools.

Or

(b) Discuss about the tools available for structure visualization.

14. (a) Explain in detail QSAR study.

Or

(b) What is *de novo* drug design? Explain along with advantages and disadvantages.

15. (a) Explain the concept of hard and soft drugs with examples.

Or

(b) What is the relevance of drugs metabolism for biological activity of a drug. Explain in detail.

Part C

(3 × 10 = 30)

Answer any **three** questions.

16. Discuss the role of computational methods in various stages of drug discovery.

17. Explain in detail the energy terms in a force field equation.

18. Discuss homology modeling concept in detail.

19. Discuss various computational approaches for lead identification.

20. Discuss in detail how an orally administered drug produce it's effect.

———————

R6715

Sub. Code
502203

M.Sc. DEGREE EXAMINATION, APRIL – 2022

Second Semester

Bioinformatics

COMPUTATIONAL BIOLOGY

(CBCS – 2019 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

1. Define biosimilars.
2. What is expression system?
3. Difference between local and global alignment.
4. Write the applications of substitution matrices.
5. Name any two tools that use the dynamic programming algorithm for sequence alignment.
6. What is E-value? How does it affect the alignment results?
7. Differentiate between pairwise and multiple sequence alignment.
8. What is Restriction-map Graph?
9. What is computational synthetic biology?
10. What is codon optimization?

Part B (5 × 5 = 25)

Answer **all** questions choosing either (a) or (b).

11. (a) What are the critical manufacturing parameters for biosimilars?

Or

(b) Write the concept of an expression cassette.

12. (a) What is local alignment and how to normalize it?

Or

(b) Write the differences between PAM and BLOSUM matrix.

13. (a) Explain the Baysesian method for sequence alignment.

Or

(b) Describe the statistics to estimate significance of an alignment.

14. (a) What are the various problems that arise in multiple maps-double design?

Or

(b) Write about interval graphs. Explain with a suitable example.

15. (a) What is molecular orbital theory?

Or

(b) Write about the ethical issues of synthetic biology.

Part C (3 × 10 = 30)

Answer any **three** questions.

16. Explain in detail the clinical and non-clinical aspects of biosmilars.

17. Write the nature and scopes of computational biology,

18. Write on the following:

    (a) Markov Chain Model

    (b) Hidden Markov Model

    (c) Kernal Methods.

19. Explain in detail the Casette transformation of restriction map with example.

20. Explain in detail the use of ab-initio and semi-emperical methods in computational quantum mechanics.

———————

R6716

Sub. Code
502204

M.Sc. DEGREE EXAMINATION, APRIL – 2022

Second Semester

Bioinformatics

PROGRAMMING IN SCRIPTING LANGUAGES (PYTHON, PERL & R)

(CBCS – 2019 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

All questions carry equal marks.

1. What are the warning options used in Perl to reduce or avoid the errors?

2. List the prefix dereferencer in Perl.

3. Analyze different ways to manipulate strings in Python.

4. Justify the effects of slicing operations on an array in Python.

5. Illustrate negative indexing in list with an example.

6. Classify the Python accessing elements in a tuples.

7. What will be the output of print str[2:5] if str= 'Welcome to the world!'?

8. List the syntax for function call with and without arguments.

9. What are data frames in R? Give an example.

10. What is the role of missing data in R?

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

Answer **all** questions choosing either (a) or (b).

All questions carry equal marks.

11. (a) Differentiate between the following control statements of Perl.

(i) If and unless

(ii) While and until

(iii) Next and last

Or

(b) List out the categories of Perl functions and write any two functions for each category.

12. (a) Describe the different access modes of the files with an example.

Or

(b) Formulate the difference between type casting and type coercion in python with suitable example.

13. (a) Investigate on mutability and immutability in python.

Or

(b) Discuss the methods to manipulate arrays in python.

14. (a) Distinguish between max( ) and pmax() functions in R.

Or

(b) Discuss about any five math functions used in R with necessary examples.

15. (a) Write code snippets in Python to perform the following

(i) Accessing Elements of a Tuple (2.5)

(ii) Modifying Elements of a Tuple (2.5)

Or

(b) Write a python program to find the sum of 'n' numbers.

Part C ($3 \times 10 = 30$)

Answer any **three** questions.

All questions carry equal marks.

16. (a) How do you activate Perl debugger? What does it do? (4)

(b) List and explain any six Perl debugger commands.(6)

17. Discuss inheritance in Python programming language. Write a Python program to demonstrate the use of super() function.

18. Explain Values and types supported in Python.

19. Find the area and perimeter of a circle using functions. Prompt the user for input.

20. Explain in details various looping statements in R.

———————

R6717	Sub. Code
	502401

M.Sc. DEGREE EXAMINATION, APRIL – 2022

Fourth Semester

Bioinformatics

MACHINE LEARNING AND ARTIFICIAL INTELLIGENCE

(CBCS – 2019 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

1. Define Hill climbing search
2. State the significance of using heuristic functions.
3. What is game playing?
4. What are the four properties of knowledge representation
5. Differentiate supervised and unsupervised learning
6. Define knowledge based inductive learning
7. Define clustering
8. What is called SVM?
9. Define first order rules.
10. What is meant by Q-Learning

Part B (5 × 5 = 25)

Answer **all** questions choosing either (a) or (b).

11. (a) Differentiate BES and DFS.

Or

(b) Explain the following uninformed search strategies with examples.

(i) Breadth First Search

(ii) Depth First Search

12. (a) Explain approaches to knowledge representation

Or

(b) Illustrate the use of first order logic to represent the knowledge.

13. (a) Explain the concept of learning using decision trees.

Or

(b) Explain in detail about heuristic space search procedure.

14. (a) Explain the various distance based clustering methods.

Or

(b) What are the functionalities of classification and regression with diagram?

15. (a) Explain the concept of reinforcement learning.

Or

(b) Describe multithreading models with suitable use case scenario.

Part C

(3 × 10 = 30)

Answer any **three** questions.

All questions carry equal marks.

16. Explain briefly about Hill Climbing and Constraint satisfaction

17. Enumerate the practical uses of knowledge representation.

18. Explain about Heuristic space search with proof.

19. Describe in detail about K-Nearest Neighbor algorithm.

20. Discuss the functionalities of sequential covering algorithm.

———————

R6718	Sub. Code
	502402

M.Sc. DEGREE EXAMINATION, APRIL – 2022.

Fourth Semester

Bioinformatics

SYSTEMS BIOLOGY

(CBCS – 2019 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

1. What is 2D gel electrophoresis?

2. List the lipid profiles.

3. Explain protein - protein interaction.

4. Write about pro database.

5. Define neural network.

6. Enumerate the tools to detect protein binary sites.

7. What are glycan determinants?

8. Write the functions of glycolipids.

9. What is E cell?

10. Write the functions of KEGG database.

Part B (5 × 5 = 25)

Answer **all** questions, choosing either (a) or (b).

11. (a) Discuss the scope of proteomics.

Or

(b) Give a short note on protein microarray.

12. (a) Justify the functions of STRINGS modelling in biological systems.

Or

(b) "ExPASy proteomics server" – Discuss.

13. (a) Highlight the importance of protein interaction network.

Or

(b) Elaborate the function of regulatory networks.

14. (a) Explain about lipidomics analysis.

Or

(b) Write about glycan recognition molecules.

15. (a) Give a short note on the importance of integrating networks.

Or

(b) Write a short note about signal transduction network.

Part C (3 × 10 = 30)

Answer any **three** questions.

16. Write a detail note about protein sequencing.

17. List out the bioinformatics tools for analysis proteomics data.

18. Elaborate briefly about neural network models.

19. Justify the transcriptomics analysis and its application in animal research.

20. Explain about human erythrocyte model and its application.

———————