R–4610

Sub. Code
502201

M.Sc. DEGREE EXAMINATION, APRIL 2021

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 allopatricity and sympatricity.

2. What are homologous genes? Write the types of homology.

3. Difference between heterlogs and xenologs.

4. What is gap penalty? What is its significance in sequence alignment?

5. Explain how regular expressions are used for motif searching.

6. How is Gene Scan used?

7. Define a phylogenetic tree with respect to evolution.

8. Write the steps in constructing a phylogenetic tree.

9. Define a dendogram.

10. Write two different softwares available for phylogenetic analysis.

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

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

11. (a) Briefly describe molecular clock hypothesis with a suitable example.

Or

(b) Describe the concepts of neutral evolution.

12. (a) Explain the algorithm of BLAST.

Or

(b) What is local and global alignment? Explain the conditions in which they can be used.

13. (a) Write the different methods of gene discovery.

Or

(b) What is Hidden Markov Model (HMM) and what are its applications to analyse protein sequences?

14. (a) Explain character-based methods for phylogenetic tree reconstruction.

Or

(b) What is a consensus tree? Explain its types.

15. (a) Define PHYLIP and its applications.

Or

(b) Write short notes on evolutionary trace analysis.

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.

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R–4611

Sub. Code
502202

M.Sc. DEGREE EXAMINATION, APRIL 2021

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. What is a lead molecule?

2. When patients are used for Phase I testing?

3. What is potential energy surface?

4. Illustrate with an example electrostatic interaction between a drug and a target.

5. What is loop refinement?

6. List four tools for structure prediction.

7. What is HTVS?

8. What is a dependent and independent variable in QSAR study?

9. What is an antagonist?

10. What is meant by ADMET property of a drug?

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

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

11. (a) What are the methods available for drug targets identification? Explain.

Or

(b) Why a lead need to he optimized and how it is done?

12. (a) Discuss the differences between molecular and quantum mechanics. How they are useful?

Or

(b) What is force field equation? Explain the energy terms in it.

13. (a) How to predict the secondary structure elements of a protein? Explain.

Or

(b) Explain the concept behind Ramachandran plot and how it is useful.

14. (a) How will you carry out pharmacophore based screening of a database. Explain its advantage.

Or

(b) Discuss various descriptors used in QSAR study.

15. (a) Discuss Phase I and Phase II drug transformations.

Or

(b) What is Lipinski rule? How can we calculate it for a molecule?

Part C (3 × 10 = 30)

Answer any **three** questions.

16. In a step-by-step manner explain new drug discovery process.

17. Discuss molecular mechanics concept in detail and how it is useful.

18. What are the methods available for predicting 3D structure of a protein? Explain.

19. How is a docking experiments performed for lead identification and optimization? Explain in detail.

20. Discuss the molecular basis of how drugs work.

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R–4612

Sub. Code
502203

M.Sc. DEGREE EXAMINATION, APRIL 2021

Second Semester

Bioinformatics

COMPUTATIONAL BIOLOGY

(CBCS – 2019 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

1. Write a few examples of genetically engineered products of biosimilars.
2. What are the different types of vectors used?
3. What is maximizing vs minimizing score?
4. What is pairwise sequence alignment? What is it used for?
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 border block graph?
9. Define polyelectron atoms and molecules. Write a few examples.
10. What is Huckel theory?

Part B (5 × 5 = 25)

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

11. (a) What are the different challenges for conversion and formulation of biosimilars?

Or

(b) What are the various molecular complexities of biosimilars?

12. (a) Define and differentiate between overlap and banded alignment.

Or

(b) Explain similarity and distance measures.

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

Or

(b) Write a short note on sequence pattern representation.

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

Or

(b) What do you mean by overlap equivalence and overlap size equivalence?

15. (a) Explain the various Logic Gates in biology using suitable examples.

Or

(b) Explain about the operon system.

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.

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R–4613

Sub. Code
502204

M.Sc. DEGREE EXAMINATION, APRIL 2021

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.

1. History Perl and its Features.

2. Define Array and its Syntax in Perl.

3. What are a Function Parameters and Arguments in Python?

4. Define Subroutines in Python.

5. What is a use of Regular Expression in Python?

6. Rule of Variable and Identifier in Python.

7. Write the Syntax for String in Python.

8. Define Nuts and Bolts.

9. What are basic objects and classes of R?

10. List out Python Comments with an Example.

Part B (5 × 5 = 25)

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

11. (a) Explain interpolative context in perl.

Or

(b) Write a short note on Hashs in perl.

12. (a) Distinguish between break and Continue statement in Python.

Or

(b) Describe Python Operator and operator precedence with an Example.

13. (a) Shortly explain Fruitful Function and immutable in Python.

Or

(b) Explain interpreter and interactive mode in python language.

14. (a) Explain Types of arguments in Python.

Or

(b) Write any five python built-in Function.

15. (a) Give a note on loops in R programming with Examples.

Or

(b) Explain about Variables, constants and data types in R programming.

Part C (3 × 10 = 30)

Answer any **three** questions.

16. Describe Perl Operator and operator precedence with an Example.

17. Explain in detail about conditional statement and write the Syntax in python.

18. Describe the following Exception Handling Function in Python.

    (a) ZeroDivisionError

    (b) NamError

    (c) IndentationError

    (d) IOError

    (e) EOFError

19. Explain Python Package and Modules with its Syntax.

20. Explain the following R Programming.

    (a) Classification

    (b) Clustering

    (c) Data Visualization

    (d) Regression.

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R5459	Sub. Code 502401

M.Sc. DEGREE EXAMINATION, APRIL – 2021.

Fourth Semester

Bioinformatics

MACHINE LEARNING & ARTIFICIAL INTELLIGENCE
(CBCS-2019 ONWARDS)

Time : Three Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

1. Define BFS and DFS.

2. State the significance of control strategies in AI.

3. What is predicate logic?

4. What is the use of predicate calculus?

5. What is called as inductive bias?

6. Define concept learning

7. What is the feature of KNN?

8. What is meant by kernel space?

9. Define induction and deduction.

10. What is meant by reinforcement learning?

Part B (5 × 5 = 25)

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

11. (a) How to measure the performance and analysis of search algorithms.

Or

(b) Explain the following terminologies.

(i) Matching

(ii) Indexing

12. (a) Explain the usage of predicate calculus

Or

(b) Illustrate the various knowledge representation methods for game playing.

13. (a) Explain the concept of version spaces and candidate elimination.

Or

(b) Explain in detail about heuristic space search.

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

Or

(b) Explain in detail about K-Nearest Neighbour algorithm

15. (a) Explain the procedure of FOCL algorithm.

Or

(b) Describe temporal difference learning.

Part C

$(3 \times 10 = 30)$

Answer any **three** questions.

16. Explain briefly about various search and control strategies.

17. Enumerate the role of predicate calculus for knowledge representation.

18. Explain about decision tree learning with diagram.

19. Describe in detail about feature selection and classification methods.

20. Compare reinforcement learning, Q-Learning, Temporal difference learning.

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R5460	Sub. Code 502402

M.Sc. DEGREE EXAMINATION, APRIL – 2021

Fourth Semester

Bioinformatics

SYSTEMS BIOLOGY

(CBCS – 2019 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

1. Write any two key bottlenecks of proteomics.

2. What are amyloid proteins?

3. What is the role of melting curve in validating real-time qRT-PCR?

4. Differentiate receptor and ligand.

5. What do you mean by neural network models?

6. Define V-CELL.

7. How STRING imports data in protein-protein interactions?

8. Define fluxomics.

9. List any two consortium members of InterPro database.

10. Define gene regulatory network.

Part B (5 × 5 = 25)

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

11. (a) Write the principle and methodology of 2D gel electrophoresis.

Or

(b) Discuss the role of protein biomarker in diagnosis of infectious disease.

12. (a) Differentiate key elements between *de novo* and Edman degradation sequencing methods.

Or

(b) Write a note on the structures of regulatory networks.

13. (a) What are the biological applications of glycan microarray?

Or

(b) Give a note on the applications of human erythrocyte model.

14. (a) What is transcriptomics? What are its applications?

Or

(b) Define glycomics and describe its challenges.

15. (a) How MALDI-TOF is used in post-translational modification studies?

Or

(b) What is KEGG? Write about its categories.

Part C

$(3 \times 10 = 30)$

Answer any **three** questions.

16. Elaborate with neat diagram
    (a) Protein sequencing
    (b) QTrap MS/MS.

17. Write an account on computational methods for protein-protein interaction and their application.

18. Explain in detail about the applications of MetaCyc.

19. Write a large note on the principle, mechanism and application of real-time qRT-PCR.

20. Give an account on how computer simulation models are shaping the future of science.

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