R–3004

Sub. Code
502201

M.Sc. DEGREE EXAMINATION, APRIL 2019

Second Semester

Bio Informatics

ALGORITHM AND COMPUTATIONAL BIOLOGY

(CBCS – 2018 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

All questions carry equal marks.

1. What is meant by strongly connected graph and give an example?

2. Define topological sort.

3. Define Xenolog.

4. Compare PAM250 and BLOSUM62 matrix.

5. How you will construct GenePlot?

6. What is the main advantage of gap penalties in the sequence analysis?

7. What is Flexible gap in Pattern discovery?

8. Define Pattern width.

9. How homology modelling is different from *Ab initio* modelling?

10. Define Super secondary structure.

Part B (5 × 5 = 25)

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

All questions carry equal marks.

11. (a) Describe the basic operations on string in detail.

Or

(b) Differentiate algorithm and program.

12. (a) Explain the working of BLAST based on your knowledge of sequence alignment.

Or

(b) Explain the concept of scoring matrices for aligning amino acid sequences. Briefly explain how PAM is derived?

13. (a) Describe in brief about the ways of aligning multiple sequences.

Or

(b) Write down major differences between PAM and BLOSUM substitution matrices.

14. (a) Write short notes on Pattern discovery vs. Pattern matching.

Or

(b) Discuss the role of GeneScan in gene discovery.

15. (a) How Chou-Fasman and GOR methods predict secondary structure of protein from amino acid sequence?

Or

(b) Write some short notes on (i) FSSP (ii) VAST (iii) DALI.

Part C (3 × 10 = 30)

Answer any **three** questions.

All questions carry equal marks.

16. Explain dynamic programming approach for

(a) Salesman problem

(b) Hamiltonian path problem.

17. How Needleman-Wunsch and smith-waterman algorithms used for sequence alignment? Explain with the help of suitable example.

18. Explain in details about progressive approach of MSA and add key points on advantages and disadvantages for the same.

19. Explain how a simple prediction strategy can be developed using a first order Markov Chain model for discriminating biologically important functional site?

20. Explain the structural hierarchy of protein structures with suitable examples. Discuss the reversible protein denaturation and protein folding.

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R–3005	Sub. Code 502202

M.Sc. DEGREE EXAMINATION, APRIL 2019

Second Semester

Bio Informatics

COMPUTATIONAL APPROACHES TO PHYLOGENY

(CBCS – 2018 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

All questions carry equal marks.

1. Define molecular evolution.

2. What is molecular clock hypothesis?

3. What is Data partitioning?

4. What is greedy consensus tree?

5. How multiple sequence alignment used for phylogenetic analysis?

6. What do you mean by transformed distance?

7. What are Ultrametric trees?

8. What is bootstrap value?

9. Write any two uses of phylogenetic trees.

10. Write any two tools used for phylogenetic analysis.

Part B (5 × 5 = 25)

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

All questions carry equal marks.

11. (a) What are the advantages of using proteins sequences while constructing phylogenetic tree?

Or

(b) Write short notes on Adaptive radiation and Genetic draft.

12. (a) Write short notes on Data partitioning and combination.

Or

(b) To build a phylogenetic tree for a set of related sequences, what are the basic steps to be carried out? Explain with a suitable example.

13. (a) What is an outgroup? How to select one?

Or

(b) What is maximum parsimony method? How do you find out ancestral sequence for a set of DNA sequences?

14. (a) Write the fundamental differences Between the Methods of Maximum Likelihood and Maximum Posterior Probability in Phylogenetics.

Or

(b) What is dandrogram? How you will interpret dandrogram?

15. (a) Explain the working principle of Jackknife test and Add some points on potential problem with the bootstrap.

Or

(b) How do you analyze phylogenetic trees results from Treeview?

Part C (3 × 10 = 30)

Answer any **three** questions.

16. What is molecular evolution and explain the evolution of DNA and RNA, amino acids, codon, and protein?

17. Write in detail about computational approaches for constructing consensus tress.

18. What are the steps involved in phylogenetic analysis? Explain UPGA method with an example. What is the drawback of using UPGMA method in tree building?

19. What are the merits and demerits of distance-based and character based method? Discuss any one character based method in details.

20. How ClustalW and PileUp are used to find biologically significant features in sequences and to carry to out phylogenetic analysis?

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R–3006

Sub. Code
502203

M.Sc. DEGREE EXAMINATION, APRIL 2019

Second Semester

Bioinformatics

MOLECULAR MODELING AND DRUG DESIGN

(CBCS – 2018 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

1. What is a lead?

2. What is Phase I testing?

3. What is potential energy surface?

4. Illustrate H-bonds between a drug and a target.

5. What is a template structure?

6. List four tools for structure prediction.

7. What is a descriptor?

8. Write down a simple QSAR equation and explain the terms in it.

9. List out different drug-target interactions.

10. Expand ADME.

Part B (5 × 5 = 25)

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

11. (a) Write a note on drug target identification.

Or

(b) Write a note on lead optimization.

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

Or

(b) Write down the energy terms in a force field equation.

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

Or

(b) Discuss Ramachandran plot and its usefulness.

14. (a) Explain virtual screening protocol along with its application.

Or

(b) How is a ligand designed using de novo method? What is the disadvantage of this method?

15. (a) Discuss the working principle of a prodrug with an example.

Or

(b) How will you predict the drug-likeness of a molecule? Explain.

Part C (3 × 10 = 30)

Answer any **three** questions.

16. Discuss in detail with schematics various steps involved in discovering a new drug.

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

18. How will you construct a 3D model of a protein and validate the structure? Explain.

19. How is a pharmacophore model constructed and used. List out the advantages and disadvantages, in comparison to docking.

20. Discuss drug metabolism in detail and its significance in drug development.

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R–3007

Sub. Code
502401

M.Sc. DEGREE EXAMINATION, APRIL 2019

Fourth Semester

Bioinformatics

OMICS AND SYSTEMS BIOLOGY

(CBCS – 2016 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

1. What is the function of SYBER GREEN PCR mix?
2. Define a protein memory.
3. What is IMAGE consortium?
4. List out tools used for 2D gel analysis.
5. Define regulon.
6. What is consensus sequence?
7. Describe glycosylation sites.
8. What is lipid marker?
9. Describe Recon 2.0.
10. What are the salient features of human metabolome atlas?

Part B (5 × 5 = 25)

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

11. (a) How do you process the metabolite data?

Or

(b) Describe in details about the m/z based data analytical platforms.

12. (a) Write a short note on a protein array.

Or

(b) Explain briefly about the protein structural analysis tools.

13. (a) Describe in details about a network biology.

Or

(b) Give a brief outline on a neural network model.

14. (a) Explain and differentiate about the glycan determinants.

Or

(b) Discuss briefly about the fluxomic data analysis.

15. (a) Write down a human erythrocyte model.

Or

(b) Describe a short note on a constrain-based modeling.

Part C (3 × 10 = 30)

Answer any **three** questions.

16. Give a detail account on protein marker discovery and its clinical applications.

17. Explain in detail on the protein interaction databases.

18. Discus in details about regulatory network reconstruction methods.

19. Describe an essay on glycomics and its applications.

20. Write down short notes on whole cell modeling and simulation.

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R–3008

Sub. Code
502504

M.Sc. DEGREE EXAMINATION, APRIL 2019

Fourth Semester

Bioinformatics

OPEN SOURCE IN BIOINFORMATICS

(CBCS – 2016 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 2 = 20)

Answer **all** questions.

1. What are the uses of EMBOSS aliner?
2. Describe RNA family proteins.
3. What is CLC gene workbench?
4. List out tools used for protein secondary structure prediction.
5. Define a molecular phylogeny.
6. What is a consensus sequence?
7. Describe binding site analysis programs.
8. What is docking score?
9. Describe a protein-protein interaction network.
10. What are the salient features of bioconductor?

Part B (5 × 5 = 25)

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

11. (a) How do you annotate genome features?

Or

(b) Describe in details about the gene prediction programs.

12. (a) Write a short note on a proteomics tools.

Or

(b) Explain briefly about the tools used for prediction of sub-cellular localization.

13. (a) Describe in details about primer prediction tools.

Or

(b) Give a brief outline on sequence analysis software.

14. (a) Give short notes on structure visualization software.

Or

(b) Explain briefly about the molecular modeling tools.

15. (a) Write down a protein network analysis software.

Or

(b) Describe a short note on data mining software.

Part C (3 × 10 = 30)

Answer any **three** questions.

16. Give a detail account on the RNA structure prediction programs.

17. Explain in detail on the biological network analysis programs.

18. Discuss in details about phylogenetic programs.

19. Describe an essay on molecular docking software.

20. Write down short notes on chemoinformatics programs.
