D 1714

Q.P. Code: [D 07 PBI 01]

(For the candidates admitted from 2007 onwards)

M.Sc. DEGREE EXAMINATION, DECEMBER 2010.

First Year

#### Bioinformatics

## FUNDAMENTALS OF BIOLOGICAL SYSTEMS

Time: Three hours Maximum: 100 marks

Answer any FIVE questions.

All questions carry equal marks.

 $(5 \times 20 = 100)$ 

- Explain various mechanisms of transport of ions across plasma membrane.
- Describe the structure of prokaryotic and eukaryotic cells with near th grams.
- 3. Describe the double helical structure of DNA.
- Explain the different types of isomers in carbohydrates.

- Explain the mechanism of carbon dioxide fixation by Calvin pathway.
- Give a detailed account on coenzymes and metal cofactors.
- 7. Explain in detail the mechanism of enzyme action.
- 8. Explain the mech mism of DNA replication.

D 1714

Reg. No.:

D 1715

Q.P. Code: [D 07 PBI 02]

(For the candidates admitted from 2007 onwards)

M.Sc. DEGREE EXAMINATION, DECEMBER 2010.

First Year

Bioinformatics

COMPUTATIONAL METHODS FOR SEQUENCE ANALYSIS

Time: Three hours

Maximum: 100 marks

### SECTION A

Answer any FIVE questions.

 $(5 \times 20 = 100)$ 

- Give a brief account on various available biological databases, data formats
- Compare and contrast the PAM and BLOSUM in mutation analysis between two homologous DNA sequences.
- Explain the strategies of Bootstrapping in the evolutionary analysis of different organisms.

- 4. How will you proceed with the identification of regulatory regions in prokaryotic and eukaryotic genes?
- Describe the concepts and secondary structure prediction of RNA using HMM.
- Discuss the methodology, significant advantages and disadvantages of dot plot.
- Highlight the applications of bioinformatics in various i elds.
- 8. Write brief notes on rooted and unrooted tree representation in evolutionary analysis of different organisms.

D 1715

Reg. No. : .....

D 1751

Q.P. Code : [D 07 PBI 03]

(For the candidates admitted from 2007 onwards)

M.Sc. DEGREE EXAMINATION, DECEMBER 2010.

First Year

Bioinformatics

PROGRAMMING IN C AND PERL

Time: Three hours Maximum: 100 marks

Carefully read the questions.

Write the program code wherever necessary.

Answer any FIVE questions.

All questions carry equal marks

- Explain in detail about the colowing with suitable examples.
  - (a) Keywords and identifiers
  - (b) Rules for naming the variables
  - (c) Symbolic constant
  - (d) Data types and qualifiers.

- Describe in detail about the different looping statements available in C, with suitable example programs.
- Write a simple C program to calculate the different arithmetic functions using switch-case statement.
- Write a C program to calculate the average of given mark of n students using function.
- 5. We to the syntax for declaration of one and two dimensional arrays in C. Write a C program to find the addition of given two matrices.
- Write syntax for opening, updating and closing a file in C. Discuss about the command line arguments in C.
- Discuss in detail about the different operators used in Perl. Explain the Hashes and Lists with suitable example.
- What is regular expression? Write any five regular expression symbols and describe their uses in pattern matching.

		Reg. No.:					
	D 17	16	Q.P. Code	: [D 07 P	BI 04]		
	(Fo	(For the candidates admitted from 2007 onwards)  M.Sc. DEGREE EXAMUNATION, DECEMBER 2010.  First Year  Bioinformatics  MOLECULAR INTERACTIONS					
	M.Sc						
	Dma.	Three hours		mum: 100	marks		
WWW.studyouic		Answer any FIVE questions out of Eight. $(5 \times 20 = 100 \text{ marks})$					
1913	1. (a		near combinat	ion of	atomic		
CiU		orbitals.			(5)		
	(b	) Write a note	e on resonance st	ructures.	(15)		
	2. E	Explain VSEPR theory with suitable examples.					
- N	3. Di	Discuss in detail					
	(a) principle and significance of protein folding (9)						
	(b)	hydrophobic	interactions		(4)		

	(c)	beta turns	(4)	8.	Exp	Explain:	
	(d)	disulphide bridges	(3)		(a)	non-banded i	
4.	(a)	Write a detailed note on metallo p	roteins. (12)		(b)	type of helices	
	(b)	Explain DNA-protein interactions.	(8)		(c) (d)	partial ionic c	
5.	Def	ine:			(4)	<u>C</u>	
	(a)	chemical shift				AiD.	
	(b)	condition and selection role of IR			Vi	10,	
	(c)	auxochrome and chromophote		6:	9,		
	(d)	Beer-Lambert's law	10,-01				
	(e)	Circular dicbroism (5 ×	4 = 20)				
6.	(a)	Write the applications of macromolecules.	4 = 20, 0 to (10)				
	(b)	Explain the principle of MAR spectro	oscopy. (10)				
7.	(a)	Write a note on valence bond theory.	(10)				
	(b)	Explain the formation and stabil electrovalent band.	ity of (10)				

#### 8. Explain:

- non-banded interatctions
- type of helices (b)
- partial ionic character of covalent bands (c)

3

 $(4 \times 5 = 20)$ vander waals forces.

D 1717

Q.P. Code: [DO 7 PBI 05]

(For the candidates admitted from 2007 onwards)

M.Sc. DEGREE EXAMINATION, DECEMBER 2010.

Second Year

Bioinformatics

GENOMICS AND PROTEOMICS

Time: Three hours Maximum: 100 marks

Answer any FIVE of the following questions.

- 1. Describe the gene prediction approaches:
- How will you perform genome or alysis? Describe the tools.
- Give an account of the approaches to Gene Expression analysis.
- Illustrate how you will analyse expression and regulation of entire set of genes.

- 5. Describe the methods of comparative genomics.
- Describe the softwares employed to analyse protein structures.
- Discuss the Molecular Modelling Databases that are available to you
- Discuss the rieans of experimentally analysing proteins in a laboratory.

D 1718

Q.P. Code: [D 07 PBI 06]

(For the candidates admitted from 2007 onwards)

M.Sc. DEGREE EXAMINATION, DECEMBER 2010.

Second Year

Bio-informatics

# SYSTEMS BIOLOGY

Time: Three hours

Maximum: 100 marks

Answer any FIVE of the following questions.

(5 × 20 = 100

- 1. Throw light on the integration of the bioch mical networking of a cell.
- 2. Explain the applications of micro-array analysis
- Discuss the metabolome of an organism with a suitable illustration.
- 4. How will you translate the biochemical networks into linear algebra?
- Explain the principles and advantages of whole cell simulation studies.

- Describe the types and relationship exhibited in protein-ligand binding events.
- 7. How are macromolecular associations/interactions predicted?
- 8. Explain the gene discovery process.

D 1752

Q.P. Code: [D 07 PBI 07]

(For the candidates admitted from 2007 onwards)

M.Sc. DEGREE EXAMINATION, DECEMBER 2010.

Second Year

Bioinformatics

PROGRAMMING IN VISUAL BASIC WITH, RDBMS

Time: Three hours Maximum: 100 marks

Answer any FIVE questions.

- Describe in detail about the schemes of E-R models.
- Explain about application of Network Data Model and Hierarchical Data No. el.
- Discuss in detail about the different data definition languages.

- Explain in detail about the following Visual Basic concepts with a suitable example:
  - (a) Data types
  - (b) Strings
  - (c) Constants
  - (d) Data arrays
- 5. What is locoing statement? Explain the looping statements of Visual Basic.
- 6. Write a suitable program using different types of boxes available in Visual Basic.
  - Describe in detail about the data connectivity and explain how it is achieved in Visual Basic.
- Write short notes on :
  - (a) VB scripting and
  - (b) ASP and its applications.

D 1719

Q.P. Code: [D 07 PBI 08]

(For the candidates admitted from 2007 onwards)

M.Sc. DEGREE EXAMINATION, DECEMBER 2010.

Second Year

Bio-informatics

MOLECULAR MODELLING AND COMPUTER AIDED DRUG DESIGN

Time: Three hours

Maximum: 100 marks

Answer any FIVE questions.

- 1. Write notes on molecular structure, internal energy and molecular graphics.
- Explain Hartee Fock equations and its role in molecular modelling.
- Discuss the principles and applications of molecular modelling.
- Explain bond streching, angle bending and non-bonded interactions.

- Give a detailed account on energy minimization methods and applications.
- Discuss about the methods of molecular dynamic simulation.
- Give a detailed account on SAR and QSAR studies and their implications.
- Explain the structure based drug design for all classes of argets.