DPU

Dr. D. Y. PATIL VIDYAPEETH, PUNE

(DEEMED UNIVERSITY)

SYLLABUS

FOR

M. Sc. BIOINORMATICS

2014-15

SEMESTER I

Code	Subject	L	T	P	Hr	Cr
MSI 101	Cell biology	3	1	0	4	4
MSI 102	Introduction to computers and C programming	3	0	4	7	5
MSI 103	Biostatistics	3	0	2	5	4
MSI 104	Biological Chemistry	3	1	0	4	4
MSI 105	Bioinformatics resources and applications	3	1	2	8	5
MSI 106	Molecular biology and genetic engineering	3	0	0	3	3
Total		**18**	**3**	**8**	**31**	**25**

SEMESTER II

Code	Subject	L	T	P	Hr	Cr
MSI 201	Molecular modeling and dynamics	3	1	4	8	6
MSI 202	Perl and Bioperl	3	0	2	5	4
MSI 203	Design and analysis of algorithms	3	0	2	5	4
MSI 204	C++ and R programming	3	0	4	7	5
MSI 205	Database management	3	0	4	7	5
MSI 206	Genomics and Proteomics	3	1	0	4	4
Total		**18**	**2**	**16**	**36**	**28**

SEMESTER III

Code	Subject	L	T	P	Hr	Cr
MSI 301	Chemoinformatics and drug design	3	1	4	8	6
MSI 302	Sequence analysis and Phylogenetics	3	0	4	7	5
MSI 303	Elective	3	0	0	3	3
MSI 304	Seminars and Research Methodology	3	0	0	3	3
MSI 305	Systems biology	3	0	4	7	5
MSI 306	Java and Bio-Java	3	0	4	7	5
Total		**18**	**1**	**16**	**35**	**27**

Elective: Networks and Cloud Computing, Machine learning in Bioinformatics

Semester IV

Particulars	Credit
Project(6 Months duration)	**25**

Total Credits for Sem. I to Sem. IV	**105**

SEMESTER I

Code	Subject	L	T	P	Hr	Cr
MSI 101	Cell biology	3	1	0	4	4
MSI 102	Introduction to computers and C programming	3	0	4	7	5
MSI 103	Biostatistics	3	0	2	5	4
MSI 104	Biological Chemistry	3	1	0	4	4
MSI 105	Bioinformatics resources and applications	3	1	2	8	5
MSI 106	Molecular biology and genetic engineering	3	0	0	3	3
Total		**18**	**3**	**8**	**31**	**25**

COURSE TITLE: CELL BIOLOGY

TOTAL LECTURE Hr. = 46

COURSE CODE : MSI 101	**L**	**T**	**P**	**Hr**	**C**
MARKS: 100	**3**	**0**	**0**	**3**	**3**

OBJECTIVE

The objective of this course is:

To create general understanding about the structure, functions, cell signaling and cell interaction in organisms.

LEARNING OUTCOME

At the end of the course, the students will be familiar with cell science. This would help the student for understanding of the cellular structure and properties, diseases associated with cells, for applications at various fields.

PREREQUISITES

This is an introductory course. Graduate level knowledge of life sciences is sufficient for undertaking this course.

COURSE DESCRIPTION:

Sr. No.	**Topics**	**Detail syllabus**	**No. of lectures**
1	Cell	Cell concept, Cell Theory Structural organization of Prokaryotic, plant and animal cell	4
2	Cell Organelles	Cytoskeleton and subcellular organelles	6
3	Cell cycle and Cell division	Regulation Cell cycle, Mitosis, Meiosis, Apoptosis, Cancer	8
4	Biomembranes and electrophysiology	Biomembranes- Structure, Chemistry and Functions Electrical properties of membranes	6
5	Intracellular compartments and	Intracellular compartments and protein trafficking	6

	protein trafficking		
4	Cell communication	Mechanisms of cell signaling Signal transduction Major signaling pathways	10
5	Cell- cell interaction and cell matrix interaction	Cell- junctions Cell adhesion Extracellular matrix	6
	Total		**46**

METHODOLOGY

The course will be covered through lectures using power point presentations and overhead projectors. There would be special discussion component in teaching. Students would be divided in groups and quiz competitions would be held. This would teach them group activity. .In tutorials, there would be discussion on the topics. There will be class tests and home assignments.
Evaluation Scheme (Theory)

EXAMINATION SCHEME

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

BOOKS RECOMMENDED:

1. Alberts et. al. 2008, Molecular Biology of the Cell. Fifth Edition. Garland Science.
2. Lodish et. al. 2004, Molecular Cell Biology. Fifth Edition, Freeman.
3. Karp 2002, Cell and Molecular Biology. John Wiley.
4. Pollard & Earnshaw 2002, Cell Biology. Saunders.
5. Tobin & Morcel 1997, Asking about Cells. Saunders.
6. Benjamin Levin et al. 2007, Cells. Jones and Bartlett

COURSE TITLE : INTRODUCTION TO COMPUTERS AND C PROGRAMMING **TOTAL LECTURE Hr. = 46**

COURSE CODE : MSI 102	**L**	**T**	**P**	**Hr**	**C**
MARKS: 100	**3**	**1**	**0**	**4**	**5**

THE OBJECTIVE OF THE COURSE IS

- To familiarize the students with computers and programming concepts.
- To introduce basic concepts in: hardware, software and its implementation.
- To introduce concepts of World Wide Web (Internet) etc.
- Programming module is intended to familiarize them with computer logic and solution of real world problems using computers**.**

LEARNING OUTCOME:

At the end of this course student would be able to understand basic principles of Computing, and Programming**.**

PREREQUISITES:

The course is of introductory nature and there are no prerequisites for the course.

COURSE DESCRIPTION

Sr. No.	**Topics**	**Detail syllabus**	**No. of lectures**
1	Basic Organization of Computers	Introduction to Computer, historical background, Block diagram of a Computer, parts of Computer, their integration and function.	2
2	Hardware	Computer hardware, different types of I/O devices, motherboard, BIOS, Primary and Secondary Memory, different types of Printers, Storage Media, their sizes and use.	4

3	Software	Introduction to software, Application software (Packaged & Customized) and System Software (OS & Utilities).	2
4	Types of Computer	Difference between Super Computer, Mini Computer and a Micro Computer and their applications.	2
5	Data representation in Computers	Introduction to Binary, Octal and Hexadecimal Number System	2
6	Operating System & Interface	OS, tasks performed by OS , Introduction to DOS, Windows and Linux/UNIX	2
7	Internet, WWW,	Internet, DNS and name resolution. History of Internet. IP Addressing scheme and its relation to the Internet.	1
8	HTML	Basic HTML tags	2
9	Introduction to C and Data types	An overview of C , C expressions, Operators, Integers long and short, Integers, signed and unsigned, Chars, signed and unsigned, Floats and doubles	2
10	The Decision controls in C	The 'if' statements within *if* Multiple statements within *if* The '*if-else'* statement The ! operator Hierarchy of Logical Operators The Conditional Operators	2
11	Loop control structures:	Loops, The '*While'* Loop, The '*for'* loop Nesting of Loops Multiple Initializations in the for loop The '*Odd'* Loop, The '*break'* statement The '*continue'* statement, The '*do-while'* statement	4

12	Case control structure	Decisions using switch, The *goto* statement	1
13	Functions	What is a function? Why Use Functions, Passing values between functions, Scope of functions	2
14	Array & strings:	Single-dimension Arrays, Generating a Pointer to an array, Passing single-dimension arrays to functions Strings, Two-dimensional Arrays, Arrays of Strings Multidimensional Arrays, Array Initialization Variable-Length arrays	6
15	Puppeting on strings:	What are Strings? More about Strings, Pointers and Strings, Standard Library String functions, Two, Dimensional Array of Characters, Array of pointers to Strings, Limitations of Array of Pointers to String	4
16	Pointers:	What are pointers?, Pointer variables, The pointer Operators, Pointer Expressions, Pointers and Arrays, Initializing Pointers, Pointers to Functions, C's Dynamic Allocation Arrays, Problems with Pointers	2
17	I/O in C:	Types of I/O, Console I/O Functions, Disk I/O functions, I/O under windows.	2
18	Structures, Union, Enumeration & type definition:	Structures, Arrays of structures Passing structures to functions, Structure Pointers Unions, Bit-Fields, Enumerations, Typedef	4
Total Number of Lectures			**46**

METHODOLOGY

The course would be taught through lectures, demonstrations and practical classes.

EXAMINATION SCHEME

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

BOOKS RECOMMENDED:

- Introduction to Computers by Norton
- Fundamentals of Computers by Raja Raman
- Computers Fundamentals by Sinha
- Introduction to Computers by Subramanian
- The complete reference of C 4th edition by Herbert Schildt
- Let us C By Yashwant Kanitakar
- C- programming by Balaguruswamy
- Data Structure by Kanitakar
- Pointers in C by Kanitakar
- Data Structure C and C++ by Taneumbam.
- C programming by Keinighan and Ritchite

COURSE TITLE: BIOSTATISTICS
TOTAL LECTURE HR. = 45

COURSE CODE : MSI 103	**L**	**T**	**P**	**Hr**	**C**
MARKS:150	**3**	**0**	**2**	**4**	**4**

OBJECTIVE
The objective of the course is to familiarize the student with basic concepts in mathematics & statistics

LEARNING OUTCOME
At the end of the course, the students will have sufficient understanding of different mathematics and statistical tools used in Biotechnology. This knowledge would be applicable in different industries

PREREQUISITES
Students should be familiar with school level mathematics to take up this course. In case they do not have mathematics at the twelfth level they would be helped by the teacher

COURSE DESCRIPTION:

Sr. No.	**Topics**	**Detail syllabus**	**No. of lectures**
1	Bio-Statistics: Introduction	• Scope, application and use of statistics, • Collection and classification of data, • Census and sampling graphs and diagrams, • Arithmetic mean, median standard deviation.	7
2	Correlation and regression:	For ungrouped data, scatter diagram, • Calculation and interpretation of correlation coefficient • linear regression coefficient, nonlinear relationship transformable to linear.	7

3	Population parameters and sample statistics	Sample techniques, simple random sampling • stratified random sampling, systematic sampling, and • standard error of mean	7
4	Estimation, point and interval, confidence interval for population mean and proportion	Estimation, • Point and interval, • Confidence interval for population • mean and proportion	7
5	Hypothesis testing	Type I and Type II errors levels of significance, • One-tiled and two-tailed tests, • Application to single mean and single proportion , • Equality of population means and two population proportions	6
6	Chi square test for independent attribute in R x C table, special case of 2 x 2 table	Chi square test for independent attribute in R x C table, • special case of 2 x 2 table	5
7	Variance ratio, F-test, Fishers Z test, ANOVA	Variance ratio, • F-test, • Fishers Z test, • ANOVA	6
	Total		**45**

METHODOLOGY

The course will be covered through lectures and assignments. They would be given problems to solve in the class room on the board where everybody can participate. There will be two class tests/ and home assignments. They would be taught the use of statistical software

EXAMINATION SCHEME

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

BOOKS RECOMMENDED:

- Statistic by S. G. Gupta
- Statistical Method in Biology by Bailey.
- Mathematics for Biological Science by Jagdish Arya and Ladner.
- Numerical methods by E. Balguruswamy.
- Statistics from biologist by Campbell

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COURSE TITLE: BIOLOGICAL CHEMISTRY

TOTAL LECTURE HR. = 44

COURSE CODE : MSI 104 **L T P HR C**

MARKS:100 **3 1 0 4 4**

OBJECTIVE

The objective of this course is:

To create general understanding about bio-molecules their synthesis, metabolism and interactions in relation to living systems.

To familiarize the student with basic concepts in bioenergetics and lipid metabolism.

LEARNING OUTCOME

At the end of the course, the students will have sufficient scientific understanding of the basic concepts in biochemical processes. This would enable him to understand use of biochemical methods in understanding synthesis of various products

PREREQUISITES

This is an introductory course at the masters level. Graduate level knowledge of chemistry and life sciences is sufficient.

COURSE DESCRIPTION:

Sr. No.	**Topics**	**Detail syllabus**	**No. of lectures**
1	Biomolecules	Introduction to Biomolecules and role of biomolecules in metabolism.	10
2	Lipid Metabolism:	Biosynthesis of lipids: Requirements of carbon dioxide and citrate for biosynthesis, Formation of Malonyl CoA Fatty acid synthase complex, Regulation of biosynthesis. Fatty acid oxidation**:** β-oxidation of fatty acids monounsaturated and polyunsaturated fatty acids. Energetic of β-oxidation, Ketone	8

		bodies	
3	Triglycerides and phospholipids biosynthesis:	Biosynthesis of triacylglycerides, membrane phospholipids,Plasmalogens, Sphingolipids. Biosynthesis of cholesterol and steroid hormones, bile salts	6
4	Glycogen metabolism	Biosynthesis and degradation of glycogen and its regulation.	4
5	Biosynthesis and degradation of amino acids	Conversion of nitrogen to NH4 by microorganisms, Conversion of ammonia into amino acids by way of glutamate & glutamine, Conversion of citric acid intermediates to amino acids, glutamate as precursor of glutamine, proline & arginine, Conversion of 3-phosho glycerate to serine, synthesis of cysteine from serine & homocysteine. Biosynthesis of aromatic acids and one carbon atom transfer by folic acid	8
6	Biosynthesis and degradation of purine, pyrimidine nucleotides, regulation	Denovo and Salvage Pathways Purine biosynthesis: formation of PRPP, Biosynthesis of IMP, Purine nucleotide interconversions, Regulation of purine biosynthesis Pyrimidine biosynthesis: assembly of the pyrimidine nucleus, synthesis of di & tri phosphates, formation of deoxy ribonucleotides, thymine biosynthesis. Degradation of purines & pyrimidines , uric acid & urea	8
	Total		**44**

METHODOLOGY

The course will be covered through lectures supported by tutorials. In tutorials, apart from the discussion on the topics covered in lectures, assignments in the form of questions will be given. Normally a student's is expected to complete the assignment by himself, however if needed, difficulties will be discussed in the tutorial classes. There will be two class tests/ and surprise test conducted during the tutorial classes.

EXAMINATION SCHEME

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

BOOKS RECOMMENDED:

Biochemistry by Leininger

COURSE TITLE: BIOINFORMATICS RESOURCES AND APPLICATIONS **TOTAL LECTURE HR. = 46**
COURSE CODE : MSI 105 **L T P Hr C**
MARKS: 200 **3 0 4 7 5**

OBJECTIVE:
The objective of this course is:
To create general understanding about different bioinformatics resources

LEARNING OUTCOME:
At the end of the course, the students will have an idea on the general overview of different resources and its application related to bioinformatics.

PREREQUISITES:
This is an introductory course at the master's level. Basic knowledge on computers and internet required.

COURSE DESCRIPTION:

Sr. No.	Topics	Detailed syllabus	No. of Lectures
1	Overview of Bioinformatics	Scope and fields of Bioinformatics Contribution to different problems in biology	4
2	Sequence formats	GenBank DNA Sequence Entry,EMBL, SwissProt, FASTA, NBRF/PIR, Stanford University/Intelligenetics,Genetic Computer Group and Genetic Data Environment sequence formats. conversion of sequence formats. Multiple sequence format.	8
3	Retrieval of Biological Data	Data retrieval with Entrez and DBGET/ LinkDB Data retrieval with SRS etc.	6

4	Introduction to nucleic acid and protein databases	NCBI EMBL DDBJ EBI NBRF-PIR, SWISSPROT, PDB	8
4	Genome databases	The Institute of Genome Research (TIGR), GOLD Ensemble, Organism specific databases, etc.	5
5	Protein-Protein Interaction databases and software	DIP (Database of Interacting Proteins), PPI Server, BIND- Bimolecular Interaction Network Database, PIM- Hybrigenics, PathCalling Yeast Interaction Database, MINT- a Molecular Interactions Database, GRID- The General Repository for Interaction Datasets InterPreTS-protein interaction prediction through tertiary structure	5
6	Introduction to phylogenesis	Phylogenetics, cladistics and ontology Building phylogenetics trees Evolution of macromolecular sequences	4
7	Introduction to structural Bioinformatics	Amino acids, Polypeptide Composition Secondary Composition Backbone flexibility □ & ψ Angles, Ramchandran Plot Tertiary & Quaternary Structure Hydrophobicity Disulphide bonds	4

		Active Sites	
8	Introduction to	Homology Analogy Orthology Paralogy Xenology	2
		Total Lectures	**46**

Methodology

The course will be covered through lectures supported by practicals. In tutorials, apart from the discussion on the topics covered in lectures, assignments in the form of questions will be given. Normally a student's is expected to complete the assignment by himself, however if needed, difficulties will be discussed in the tutorial classes. There will be two class tests/ and surprise test conducted during the tutorial classes.

EXAMINATION SCHEME

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

PRACTICALS

1. Retrieval of sequences from NCBI, EBI and EMBL databases.
2. Retrieval of sequences from NBRF-PIR, SWISSPROT and Pdatabases.
3. Transition and Translation of sequences.
4. Retrieval of genome from genome databases.
5. Exploring DIP and PPI.
6. Exploring BIND and PIM.
7. Exploring MINT and GRID.
8. Analysis of phylogenetic tree.
9. Exploring PDB file.
10. Analysis of active site by pymol

COURSE TITLE: MOLECULAR BIOLOGY AND GENETIC ENGINEERING **TOTAL LECTURE HR. = 48**

COURSE CODE : MSI 106	**L**	**T**	**P**	**HR**	**C**
MARKS:100	**3**	**1**	**0**	**4**	**4**

OBJECTIVE:

The objective of the course is to prepare students competent in the subject through in-depth lectures & laboratory practicals. The objective of the course is to create a general motivation amongst students to critically analyze the problem, and how to apply the knowledge of molecular biology to solve the problems. To prepare them to think independently for developing new research projects through the literature review on a topic of their interest, writing a review article on a topic, and making 15-minutes presentation to the class.

LEARNING OUTCOME:

At the end of the semester, it is expected that students understood the basic genetic mechanisms such as DNA and chromosomes, replication, DNA repair and recombination, gene expression and regulation, and how to apply molecular knowledge to solve a critical problem. It is expected that they will be more confident to develop independent research projects either for pursuing their higher education or for industrial applications.

PRE-REQUISITES:

This is an advanced level course. Students must have an understanding of introductory undergraduate level courses such as in Biochemistry, Chemistry, Biology, Microbiology, Plant and Animal Biology.

COURSE DESCRIPTION

Sr. No.	**Topics**	**Detail syllabus**	**Hrs.**
1	DNA & chromosomes	Chromosomal DNA and its packing in the chromatin fiber The global structure of chromosomes	4 4
2	DNA Replication	DNA replication mechanis The initiation and completion of	3 3

	and Repair	DNA replication in chromosomes DNA repair	 4
3	Recombination	General recombination Site specific recombination	4 3
4	Transcription and translation	DNA to RNA RNA to protein	4 4
5	Gene Expression	DNA binding mitosis in gene regulatory How genetic switches work Post transcriptional control.	3 3 4
6	Comparative genomics and the evolution	Comparative genome Evolution	4 4
7	Methods in molecular biology	Isolation, cloning & sequencing DNA Analyzing protein structure & function Studying gene expression & function	4 4 4
8	Topic write-up and 15 minutes presentation	Students will select the Topic of their interest (to be decided in the mid of semester)	4
		Total Hours	**48**

METHODOLOGY:
The course will be covered through lectures supported by tutorials and laboratory practicals. Students will be given a seminar topic of their own interest in the subject of Molecular Biology. Students are expected to collect review, write a review article and make 15 minutes power point presentation. Students will be evaluated based on two class tests, lecture and laboratory attendance, class participation, write-up and power point submission and presentation.
Evaluation Scheme (Theory)

EXAMINATION SCHEME

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

BOOKS RECOMMENDED:

- Molecular Biology of the Gene – Watson
- Genes – Lewin
- Molecular Biology of the Cell – Watson
- Recombinant DNA Technology – Watson

SEMESTER II

Code	Subject	L	T	P	Hr	Cr
MSI201	Molecular modeling and dynamics	3	1	4	8	6
MSI202	Perl and Bioperl	3	0	2	5	4
MSI203	Design and analysis of algorithms	3	0	2	5	4
MSI204	C++ and R programming	3	0	4	7	5
MSI205	Database management	3	0	4	7	5
MSI206	Genomics and Proteomics	3	1	0	4	4
Total		**18**	**2**	**16**	**36**	**28**

COURSE TITLE: CHEMOINFORMATICS AND MODELING IN DRUG DISCOVERY **TOTAL LECTURE HR. = 48**
COURSE CODE :MSI 201 **L T P HR C**
MARKS: 100 **3 1 4 8 6**

OBJECTIVE OF THE COURSE:
The objective of the course is to familiarize the students with Chemoinformatics and molecular modelling concepts.

LEARNING OUTCOME
At the end of the course, the students will have sufficient knowledge of how the molecules could be built and what are the various details associated with the field.

PREREQUISITES
Since course deals with molecular modeling students should have basics of Maths, Physics and Chemistry of molecules.

COURSE DESCRIPTION

Sr. No.	Topics	Detail syllabus	No. of Lectures
1.	Introduction to Molecular Modeling	Introduction to molecular modeling	2
2	Mathematical concepts in Molecular Modeling	Series expansion, Vectors, matrices, eigen vectors and eigen values, complex numbers, Lagrange multipliers, multiple integrals, basics of statistics and fourier series, taylor series	14
3	Introduction to Structure representation ans structure database	Building of small molecules, co-ordinate system for structure representation, Building of Biopolymers and oligopeptides, PDB, CSD	8
4	Optimization of geometries of	Energy minimization by systematic search method	10

	small molecules	Plotting conformation energy contours (Ramachandran plot), and finding out minimum energy conformation Gradient based Energy minimization, Molecular mechanics approach, Molecular Dynamics method, Monte Carlo method Genetic algorithm	
5	Use of Quantum chemical methods for geometry optimization	Schrödinger equation Basic Formalism in quantum mechanics Schrödinger equation for a multi- electron atom Schrödinger equation for a molecule Hartree- Fock Method, Different MO methods Molecular electrostatic potential Optimization of geometries of small molecules Quantum chemical indices	14
Total lectures			**48**

METHODOLOGY

The course will be covered through lectures, demonstration and practicals.

EXAMINATION SCHEME

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

BOOKS RECOMMENDED:

- Molecular modeling by Andrew Leach
- Introduction to Computational Chemistry by Frank Jensen, Wiley publication.
- Handbook of Cheminformatics by John Gasteger by Wiley publications.

PRACTICALS IN CHEMOINFORMATICS AND MODELING IN DRUG DISCOVERY

- Exploring of different databases
- Molecular graphics
- Structure drawing using hyperchem, vLife and MOE
- Viewing macromolecules in Pymol.
- Calculation of Bond length, bond angle and torsion angle
- Force Field generation and energy minimization
- Molecular Dynamics studies on proteins using Hyperchem and MOE
- Gromacs installation and dynamics of Speptide.
- Study of Molecular Dynamics and Simulation of given protein (RMSD, RMSF, Energies)
- Comparative study of trajectories at different intervals.
- Dynamics of protein with drug.

PRACTICAL EVALUATIONS

Practical work is evaluated while it is being carried out. The evaluation done for each practical session will be consolidated into a final evaluation. Equal weight age will be given to each session in the final evaluation. In case of a deviation from this guideline, the course coordinator will make an appropriate note in the Course Description.

COURSE TITLE: PERL AND BIOPERL

TOTAL LECTURE HR. = 48

COURSE CODE : MSI 202 **L T P HR C**

MARKS: 100 **3 0 4 5 4**

OBJECTIVE:

To understand how the Perl and Bioperl scripts are useful in biological sciences like biotechnology plant and plant biotechnology to solve the related problems.

To familiarize Perl scripts for genomic and proteomic analysis.

LEARNING OUTCOME:

At the end of the course, the students will have understanding of the Perl and Bioperl scripts and how to apply the same in biological problems, how to make biological database using different modules used in Perl.

PREREQUISITES:

Student should know C programming and logic behind the scripts. Also its application in biology.

COURSE DESCRIPTION:

Sr. No	Topics	Detail Syllabus	No. Of Lectures
1.	Introduction and Installation	Introduction to Perl, Use of Perl in Bioinformatics, History, Availability Support and Basic Concepts	02
2.	Scalar Data	Number, String, Scalar Operators, Scalar Variables, Scalar Operators, Functions	02
3.	Control Structure	Conditions and loops	02

4	Arrays and List Data	Basic Concepts, Assigning Values To An Array, Accessing Array Elements, Array Functions, Command Line Arguments	03
5	Hashes	What is Hash? Why use Hash? Hash element access, Modifying Hashes ,The hash as whole, Hash Assignment, Hash function	03
6	Subroutine	Defining and invoking a user function (subroutine),Return values, Arguments ,Private variables in subroutines, The local operator, The difference between local and my	03
7	Basic I/O	Introduction, File handles, Input from standard input, Input from the diamond ()/) operator, The invocation arguments, Output to standard output, File Operators	04
8	Directory Access	Moving around the directory tree, Globbing, An alternate syntax for globbing, Directory handles, Skipping some files with dirhandles	02
9	Manipulating Files and Directories	Removing a file, Renaming a file, Creating a link to a file, Making and removing directories, Modifying permissions and ownership, Changing timestamps	02

10	Regular Expressions	Use of regular expression, Using simple patterns, Matching operators Substitution and transliterate, Metacharacters	04
11	Process Management	The system operator, The exec operator, Backquotes in scalar context Backquotes in list context, Processes as filehandles, The fork and wait operators ,The fork and wait operators in Perl Sending and receiving signals	04
12	References	Introduction, Summary of References, Array References, Anonymous Arrays, Anonymous Hashes Higher Dimensional Arrays, Complex Hashes, References and Subroutines, Anonymous Subroutines	04
13	Object-Oriented Programming	Introduction, Object-Oriented Vocabulary, The class Definition, Defining and Using Objects, Information Hiding, Instance Methods, Destructors, Class Methods, inheritance, Polymorphism, Documenting Perl Code	04
14	Advanced features in Perl	Advanced features in Perl, Advanced functions, operators files and directories, Introduction to modules	02

15	Using Perl for CGI	What is CGI?, Web Servers and Browsers, HTML, HTML Forms, Form Elements, A Typical CGI Application, CGI Input CGI Output, Using the CGI.pm Module	02
16	Using DBM module		03
17	Using Bioperl Modules		02
Total Lectures			**48**

EXAMINATION SCHEME

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

COURSE TITLE: INTRODUCTION TO ALGORITHMS IN BIOINFORMATICS **TOTAL LECTURE HR. = 48**
COURSE CODE : MSI203 **L T P Hr C**
MARKS: 100 **3 1 0 4 4**

OBJECTIVE OF THE COURSE:
The objective of the course is to familiarize the students with algorithms in Bioinformatics which includes sequence analysis and its application to life science research, bacteria and viruses, their structures, metabolism, diseases caused by bacteria and viruses and their control.

LEARNING OUTCOME
At the end of the course, the students will have sufficient scientific understanding of algorithms in Bioinformatics**.**

PREREQUISITES
Since the course is mid level in nature, so minimum basics of Bioinformatics and good understanding of Biotechnology, Mathematics and Statistics.

COURSE CONTENT:

Sr. No.	**Topics**	**Detail syllabus**	**No. of Lectures**
1	The history of genome rearrangement	Discovering genes and genome rearrangement, Research on genome rearrangement in the bioinformatics area	02
2	Genome rearrangement by double cut & join (DCJ) operations	What is the DCJ distance, shortest DCJ sorting path, DCJ operations.	04
3	The Hannenhalli Pevzner (Bergeron)	Theorems of Hannenhalli Pevzner, smallest hurdle, shortest reversal sorting paths, black and white graphs.	05

	theory		
4	Sorting by block interchanges	block interchange distance, shortest block interchange, shortest block interchange sorting scenarios	03
5	Sorting by transpositions	What is transposition, transposition distance, breakpoint, 5-long cycle, 3-long and 1-long cycle, Algorithm 1.5-sort, transposition diameter	06
6	The principle of dynamic programming	dynamic programming algorithm	01
7	Pairwise sequence alignment	Pairwise sequence alignment with linear gap penalty, Pairwise sequence alignment with arbitrary gap penalty, Pairwise sequence alignment with arbitrary gap penalty, Similarity and local alignment	06
8	Multiple sequence alignment	multiple sequence alignment, rooted binary tree, iterative sequence alignment algorithm	04
9	Dynamic programming on trees	The large and the small parsimony problem, Felsenstein's algorithm for calculating the likelihood of a tree, Sankoff-Rousseau algorithm., Fitch algorithm	05
10	Transformational grammars	The Chomsky hierarchy of transformational grammars, Stochastic regular grammars and Hidden Markov Models, Stochastic Context Free Grammars, CYK (Cocke-Younger-Kasami) algorithm, Forward and the Viterbi	05

		algorithms	
11	RNA secondary structure prediction	The Nussinov algorithm, The Knudsen-Hein grammar	02
12	Graphical degree sequences	The Havel-Hakimi theorem, The swap Markov chain	02
Total Lectures			**45**

METHODOLOGY

The course would be taught through lectures, demonstrations and practicals.

EXAMINATION SCHEME

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

BOOKS RECOMMENDED:

- An Introduction to Bioinformatics Algorithms By Neil C. Jones, Pavel Pevzner
- Algorithms in Bioinformatics: A Practical Introduction By Wing-Kin Sung
- Algorithms in Bioinformatics by Costas S. Iliopoulos, Kunsoo Park, Kathleen Steinhöfel
- Bioinformatics: Databases and Algorithms by N. Gautham
- Algorithmic Aspects of Bioinformatics By Springer, 06-Jun-2007 - 406 pages
- Algorithms in Bioinformatics: 4th International Workshop, WABI 2004, Bergen, Norway, September 17-21, 2004, Proceedings, Volume 4

COURSE TITLE: OOPS WITH C++ AND INTRO. R LANGUAGE **TOTAL LECTURE HR. = 48**

COURSE CODE : MSI 204	**L**	**T**	**P**	**Hr**	**C**
MARKS: 100	**3**	**0**	**4**	**7**	**5**

OBJECTIVE:

The objective of the course is to make the student familiar with Object Oriented Concepts, R- Programming. Students can develop the programs, graphics, using R.

LEARNING OUTCOME:

At the end of the semester, it is expected that students understood the basic knowledge about R-programming language, OOP concepts.

PRE-REQUISITES:

Students are expected to have an understanding of basic OOP concepts, as well as basic programming knowledge.

COURSE CONTENT:

Sr.No	Topic	Description	Hrs.
1	Fundamentals of OOP's with C++	Introduction to OOP – Differences between OOP and procedure oriented Programming – classes, objects and methods – overview of inheritance, Abstraction and polymorphism.Structure of a C and C++ program – pre-processor directives – data types and declaration – expressions and operator precedence – program flow control – functions – scope of variables – default arguments – dynamic allocation – new and delete operators.	5

2	Classes and Objects and Functions in C++	Introduction to classes and Objects, accessing class members, member functions, Arrays in c++, static data members and member functions, friendly functions, constructors and destructors. Main function, call by reference, return by reference, Inline functions. Default arguments, const arguments, friend and virtual functions.	5
3	Polymorphism & Inheritance	Overloading functions and operators – Run time polymorphism – overloading new and delete operators. Derived classes – syntax of derived classes – access to the base class – overloading inherited member functions – multiple inheritance – virtual base class.	5
4	Pointers and Virtual functions and Exception Handling in C++	Introduction, Pointers to Objects, this pointer, pointers to derived classes, virtual functions, pure virtual functions. Benefits of exception handling – troubles with standard C functions (set jmp and long jmp) – proposed exception handling mechanism for C++.	5
5	Managing Console I/O Operations & working with files.	Standard I/O Using C functions , steam I/O in C++, manipulators , formatted I/O , Overloading << and >> operators – File I/O Files introduction, classes for file stream operation, opening and losing a file. Command line arguments.	5
6	Introduction to	How R works, Creating, listing	7

	R Lang	and deleting the objects in memory, Data with R,	
7	Graphics with R	Managing graphics, Graphical functions, Low-level plotting commands, Graphical parameters, practical example, The grid and lattice packages	5
8	Statistical analyses with R	A simple example of analysis of varience, Formulae, Generic Functions, Packages.	6
9	Programming with R	Loops and vectorization, programs in R, Writing your own functions	5
Total			48

EXAMINATION SCHEME (THEORY)

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

BOOKS RECOMMENDED

- OOP's with C++ programming by E. Balguruswamy.
- C++, The Complete Reference, 4th Edition, Herbert Schildt, TMH
- An Introduction to R: A Programming Environment for Data Analysis and Graphics. Author(s) William N Venables, David M Smith
- Publisher: Network Theory Ltd.; 2nd edition (May 1, 2009); eBook (Version 2.15.1, June 22, 2012)
- Beginning R : The Statistical Programming Language by Mark Gardener, Publisher: Wiley (2013)
- Using R for Data Analysis and Graphics, Author(s) J H Main Donald, Publisher: Australian National University (2008).

LIST OF PRACTICAL'S IN OOPS WITH C++ AND INTRO. R LANGUAGE :

- Defining a class, data members (private, public and protected) and methods.
- Dynamic memory allocation
- Pointers and Classes
- Operator overloading
- Inheritance and polymorphism
- Templates
- Exception handling
- Console I/O operations
- Files and Streams
- R-Language example programs based on topic wise.

PRACTICAL TRAINING (TWO HOURS PER WEEK) MARKS 100

- The course will also have a practical component. The practical training would be in the area of data types, operators, IO streams, loops, R-Graphics, Statistical analyses with R. etc.

COURSE TITLE: DATA BASE MANAGEMENT SYSTEM

TOTAL LECTURE HR. = 48

COURSE CODE : MSI 205 **L T P Hr C**

MARKS: 100 **3 0 4 7 5**

OBJECTIVE:

To create Database Tables, Store the data, Retrieve the data in Data Base Management System. To understand about Database design process. To know about Database System in detail.

LEARNING OUTCOME :

At the end of the course, the students will have sufficient scientific understanding of the basic concepts in DBMS.

COURSE DESCRIPTION :

Sr. No.	Topics	Detail syllabus	No. of Lectures
1	Introduction to DBMS	What is Data Actually? What is Information Actually? What is Metadata Actually? Database Architecture, Advantages of DBMS, Database models and Their Timelines.	03
2	Introduction to RDBMS	Features of RDBMS Properties of RDBMS Types of Relations. E-R Diagram. Normalization.	04
3	Introduction to SQLDatabase Object:	Features of SQL, Data Types in Oracle, Sub Language Commands: DDL,DML, TCL,DCL	07
4	FSCS in SQL	Functions, Sequences, Constraints,	08

		Synonyms.	
5	Joins and Views & Locks	Equi Joins, Outer Joins, Simple view and Complex View, What is Lock? Types of Locks,	07
6	Sub Quires	Types of SubQuires, Applying Group Functions in Sub Quires, The Impact of Having Clause in Sub Quires, IN, ANY/SOME, ALL Operations in Sub Quires.	05
7	PL/SQL	Introduction to Programming Languages, Introduction to PL/SQL, Advantages of PL/SQL, PL/SQL Architecture, Condition statements in PL/SQL, Loop's in PL/SQL, Cursor Management in PL/SQL.	07
8	Advanced PL/SQL	Procedures in PL/SQL, Functions in PL/SQL, Packages in PL/SQL, Exception in PL/SQL, Database Triggers in PL/SQL.	07
Total Lectures			**48**

EXAMINATION SCHEME (THEORY)

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

LIST OF PRACTICAL'S:-

- Data Definition Language (DDL).
- Data Manipulation Language (DML).
- Transaction Control Language (TCL).
- Data Control Language (DCL).
- Working with Functions.
- Working with Sequences.
- Working with Constraints.
- Working with Synonyms.
- Working with Views, Joins and Locks.
- Working with Sub Quires
- Working with PL/SQL

BOOKS RECOMMENDED:-

- DataBase Systems, 3rd Edition, Thomas connolly
- DBMS Black book

COURSE TITLE: GENOMICS AND PROTEOMICS

TOTAL LECTURE HR. = 45

COURSE CODE: MSI206 **L T P Hr C**

MARKS: 100 **3 1 0 4 4**

OBJECTIVE OF THE COURSE:

The objective of the course is to familiarize the students with Bioinformatics basics of sequence analysis and its application to life science research, bacteria and viruses, their structures, metabolism, diseases caused by bacteria and viruses and their control.

LEARNING OUTCOME

At the end of the course, the students will have sufficient scientific understanding of Sequence analysis, Genomics and Proteomics.

PREREQUISITES

Since the course is mid level in nature, so minimum Basics of Bioinformatics and good understanding of Biotechnology.

COURSE CONTENT:

Sr. No.	Topics	Detail syllabus	No. of Lectures
1	DNA and Genome sequencing	Organization of genome, genome structure, Genome projects, next generation sequencing, Genome sequencing, Raw data & Assembly.	04
2	Genome and genome projects	Eukaryotic and prokaryotic genome projects, human genetic disease projects	05
3	Genome Comparisons and tools	Genome alignments, MUMmer, PIPMAKER, VISTA, other genome comparison tools.	4
4	Comparative Genomics	Comparison of Gene Order, Comparative Genomics and Comparative Genomics Databases	4

5	Single Nucleotide Polymorphism	SNPs and its Applications. SNP Maps in population studies.	02
6	Functional Genomics	Expression, regulation and cloning disease genes Vs normal genes.	03
7	Microarray based technique	Analysis of gene expression at RNA and protein level DNA Fingerprinting & DNA Foot printing	04
8	Pharmacogenetics	Genetics of drug metabolism and therapeutic targets	04
9	Overview of Proteomics	Experimental Techniques, Bioinformatics Approaches	05
10	Protein chips	Protein Chips and Functional Proteomics, Applications of Proteomics in disease diagnosis, drug development and plant biotechnology	04
11	Protein protein interaction methods	Proteome profiling methods, yeast two-hybrid, mass, spectrometry data processing and analysis	04
12	Proteome analysis and prediction of epitopes on genomic scale	Proteome analysis and prediction of epitopes on genomic scale	02
Total Lectures			**45**

METHODOLOGY

The course would be taught through lectures, demonstrations and practicals.

EXAMINATION SCHEME (THEORY)

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

BOOKS RECOMMENDED :

- Introduction to Bioinformatics By T.K. Attwood & D.L. Parry-Smith
- Bioinformatics By Arthur Lesk.
- Instant notes in Bioinformatics
- Fundamental Concepts of Bioinformatics By Krane & Raymer
- Introduction to Bioinformatics By S. Sundara Rajan & R. Balaji.
- Bioinformatics By Baxevanis
- Discovering Genomics, Proteomics, and Bioinformatics by A. Malcolm
- Applying Genomic and Proteomic Microarray Technology in Drug Discovery by Robert S. Matson
- Genomics, Proteomics and Vaccines by Guido Grandi
  Guide to human genome computing by Bishop, MJ.
- Computational methods in genome research by Suhai,S.
- Theoretical and computational methods in genome research by Suhai,S

SEMESTER III

Code	Subject	L	T	P	Hr	Cr
MSI301	Chemoinformatics and drug design	3	1	4	8	6
MSI302	Sequence analysis and Phylogenetics	3	0	4	7	5
MSI303	Elective	3	0	0	3	3
MSI304	Seminars and Research Methodology	3	0	0	3	3
MSI305	Systems biology	3	0	4	7	5
MSI306	Java and Bio-Java	3	0	4	7	5
Total		**18**	**1**	**16**	**35**	**27**

Elective: Networks and Cloud Computing, Machine learning in Bioinformatics

COURSE TITLE: CHEMOINFORMATICS AND DRUG DESIGN **TOTAL LECTURE HR. = 44**
COURSE CODE : MSI301 **L T P HR C**
MARKS: 100 **3 1 4 8 6**

OBJECTIVE :
The objective of this course is to familiarize the student with the concepts and physical principles involved in Biochemistry. They would learn topics such as: Osmosis, diffusion, dialysis, Redox potential, etc. They would be made to understand the nature of chemical bonds and its relevance in stabilization of the molecules.

LEARNING OUTCOME :
At the end of the course, the students will be able to use different Biophysica techniques and principles used in Biochemistry

PREREQUISITES :
This is the first introductory course and there are no prerequisites.

COURSE DESCRIPTION

Sr. No.	Topics	Detail syllabus	No. of Lectures
1	Introduction to Cheminformatics	Introduction to Chemo-informatics and modeling	2
2	Molecular Structure representation	-General introduction to chemical structures, line notation, graph theory, connection tables -standard structure exchange formats, structure searching -SMARTS, SMIRKS, SMILES, Mol and SDF -Special structure representations- Hash codes, fingerprints, fragmnent coding	12
3	Data	-Datatypes -dataprocessing -data analysis tools	10

		-multiple linear regression - simulated annealing -principle component PLS -PCA -ANN -KNN -SVM -AI -Data mining	
4.	Databases	Structure, Reaction, Literature, Chemical, Scisearch, Medline, and Beilstein.	6
5	Chemical properties	Matrix for calculation of Indexs, Electrotopological index, Introduction to shape indices	6
6	Drug Discovery	QSAR, QSPR, Pharmacophore, Docking, Therapeutic proteins.	8
Total lectures			**44**

METHODOLOGY

The course will be covered through lectures supported by tutorials. In tutorials, students would be made to analyze data related to different Biophysical techniques. They would be also made to compute molecular properties based on bonds.

EXAMINATION SCHEME (THEORY)

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

BOOKS RECOMMENDED:

- Molecular modeling by Andrew Leach
- Introduction to Computational Chemistry by Frank Jensen, Wiley publication.
- Handbook of Cheminformatics by John Gasteger by Wiley publications**.**

PRACTICALS IN CHEMOINFORMATICS AND MODELING IN DRUG DISCOVERY

Structure representation in different file formats.

- Exploring databases and similarity searching.
- Calculation of E-state Index
- Calculation of Descriptors in MOE.
- QSAR study and analysis using Statistica
- QSAR study and analysis using MOE
- Pharmacophore generation in MOE
- Performing docking studies in MOE and FlexX
- Generating a QSAR and Pharmacophore model and correlating the results.
- Virtual Screening and Docking.

COURSE TITLE: SEQUENCE ANALYSIS & PHYLOGENETICS **TOTAL LECTURE HR. = 42**
COURSE CODE : MI 302 **L T P HR C**
MARKS: 100 **3 0 4 7 5**

COURSE DESCRIPTION:

Sr. No.	Topic	Details	No. of Lectures
1.	Overview on DNA and Protein sequencing	DNA, Genome sequencing, sequencing cDNA libraries, submission of sequences to databases.	4
2.	Biological basis of sequence analysis	Distance and similarity: Evolutionary basis for sequence alignment, Concepts for homology, analogy,	2
3.	Database similarity searches	BLAST FASTA PSI-BLAST algorithms PAM, BLOSUM	7
4.	Pairwise sequence allignment	Dot matrix, Needleman Wunsch and Smith Waterman algorithms	5
5	Sequence analysis Tools	DNA sequence analysis, protein sequence analysis, packages-GCG, Straden etc.,	2
6	Multiple sequence alignment	Clustering algorithm CLUSTAL W	04
7	Patterns Motifs, and Profiles	Derivation and searching, Derived Databases of patterns, motifs and profiles Prosite Blocks Prints Pfam	04
8	Predictive	Pattern searching,	2

	methods:	Evolutionary basis of sequence analysis, SMART, PRODOM	
9	Information theory and applications in biology-languages	Extron-intron finder, Sequence logo, Gene finding,	2
10	Markov chains	HMMs for motif searching. Using HMM's for structural feature recognition	2
11	Phylogenetic analysis	Biodiversity and phylogenetic analysis, Maximum likelihood, Parsimony, Nearest neighbor methods etc	5
12	Protein structure prediction	Homology modeling, secondary structure prediction tools	3
Total			**42**

EXAMINATION SCHEME (THEORY)

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

LIST OF PRACTICALS

1. Retrieval of sequences from various databases
2. Retrieval of homologous sequences
3. Exploring BLAST and FASTA
4. Generation of dot matrix and analysing the homology
5. Multiple Sequence alignment by online and offline software's.
6. Exploring databases for motifs and domains.
7. Exploring and analysing Gene and exon-intron from the given sequence using online tools.
8. Construction and analysis of phylogenetic tree.
9. Exploring Secondary structure prediction tools.
10. Homology modelling of given protein sequence.

TITLE OF THE COURSE: BIOINFORMATICS FOR SYSTEM BIOLOGY **TOTAL LECTURE HR. = 42**

COURSE CODE : MSI 303 **L T P Hr C**

MARKS: 100 **3 0 4 7 5**

OBJECTIVE OF THE COURSE:

The objective of the course is to familiarize the students with system biology approach

LEARNING OUTCOME

At the end of the course, the students will have sufficient knowledge of how

PREREQUISITES

Sr. No.	Topic	Description	Hrs
1	Introduction to computational Systems biology	Basic concepts of System biology, Enabling information and integration for systems biology, Databases for Systems biology, Natural language processing and ontology-enhanced biomedical literature mining for Systems Biology	8
2.	Foundations of biochemical network analysis and modeling	Introduction to computational models of biochemical reaction networks, Biological foundations of Signal transduction and the Systems biology perspective, Reconstruction of metabolic network from genome information and its structural and functional analysis, Metabolic Flux analysis, GEPASI, Gopher	12
3.	Computer simulations of dynamic networks	Discrete approach to network modeling, Gene networks: Estimation modeling and simulation, Computational models for circadian rhythms: Deterministic	10

		Versus Stochastic approaches.	
4.	Multi scale representation of cells and Emerging phenotypes	Spatio-temporal Systems biology, Cytomics-from Cell States to predictive medicine, The IUPS Physiome project, E-Cell Concept. Genesis tool and its applications	10
5.	Applications and perspectives of Systems biology	Developments and trends of Systems biology, Long and medium term goals of Systems biology, the potential applications of Systems biology, Microarray analysis and gene networks, BRB Array tool	8
Total			48

METHODOLOGY

The course would be taught through lectures, practicals and assignments.

EXAMINATION SCHEME (THEORY)

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

BOOKS RECOMMENDED:

1. Computational Systems Biology. By Andres Kriete, Roland Eils. Published by Academic Press, 2005, ISBN 012088786X.

2. Systems Biology: Applications And Perspectives. By Peter Bringmann.Published by Springer, 2007, ISBN 3540313389.

3. Systems Biology: Principles, Methods, and Concepts. By Andrzej K. Konopka. Published by CRC Press, 2007, ISBN 0824725204.

PRACTICALS LIST

Sr. No	Laboratory Exercise	Hr
1	Exploring metabolic pathways in KEGG	4
2	Drawing metabolic pathways in System biology workbench	4
3	Analysis of substrate conc. in Glycolytic enzymes in pathway	4
4	Applications of enzyme kinetics in metabolic pathway	4
5	Cell designer application to draw a gene network	4
6	Protein -ligand network mapping	4
7	Protein-protein interaction mapping and simulation	4
8	3D simulations for system biology networks with x-y plots	4
9	Explore the software Gillespie simulator for model simulaitons	4
10	Biomodel importer and analysis with jDesigner, jarnac	4
Total		**40**

COURSE TITLE: JAVA & BIO-JAVA

TOTAL LECTURE HR. = 48

COURSE CODE : MSI 304 **L T P HR C**

MARKS: 100 **3 0 4 7 5**

OBJECTIVE:

The objective of the course is to make the student familiar with Object Oriented Concepts, Java Programming. Students can develop the programs, graphics, animations using Java.

LEARNING OUTCOME:

At the end of the semester, it is expected that students understood the basic knowledge about Java programming language, OOP concepts. Students should develop small softwares using Java.

PRE-REQUISITES:

Students are expected to have an understanding of basic OOP concepts, as well as basic programming knowledge.

COURSE DESCRIPTION:

Sr. No.	Topics	Hrs
1	Working with basics Difference between C++ and JAVA, Features of java, Data types, variables and arrays, Operators, Conditions and loops, Introduction to classes and Methods, Typecasting, Access specifiers and access modifiers	5
2	OOPS concept in JAVA Abstraction, Polymorphism, Encapsulation Inheritance, Constructor	8
3	Exception handling Types of Exception handling	4
4	Java: Packages and interfaces	4
5	Multithreading concepts and I/O streams	3
6	AWT and Applets	6

	Graphics, fonts and colour Simple animation and threads More animation, Images and sound Managing Simple Events and interactivity User Interfaces with AWT	
7	Swings: Icons & Labels, Text Fields Buttons, Combo boxes, Trees, Tables	8
8	Bio Java: Writing Programs based on basic problems in Biotechnology.	10
	Total	**48**

EXAMINATION SCHEME (THEORY)

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

BOOKS RECOMMENDED:

- Building Java Applets for Netscape 2.0 by Tim Ritchey
- Hooked on Java by Arthur Van Hoff
- Internet World 60 minute Java by Ed Tittel, Java by Tim Ritchey
- Java Black Book
- The complete Idiot's Guide to Java script
- Complete Reference Java

LIST OF PRACTICAL'S IN JAVA:

- Using Diff-data types
- Using Abstraction
- Using Polymorphism
- Using Encapsulation
- Using Inheritance
- Using packages.
- Using Multithreading
- Using Exception handling
- Using Typecasting
- Using Access specifiers and access modifiers
- Applet programs.
- AWT programs
- Swings Programs
- Programs in Bio JAVA

COURSE TITLE: NETWORKING AND INTRODUCTION TO CLOUD COMPUTING **TOTAL LECTURE HR. = 48**
COURSE CODE : MSI 305 **L T P HR C**
MARKS: 100 **3 0 4 7 5**

OBJECTIVE
To communicate one node to other node, Share the data, retrieve the data from remote node in Network. To understand about network design process. To know about cloud computing in details.

LEARNING OUTCOME
At the end of the course, the students will have sufficient scientific understanding of the basic concepts in networking and cloud computing.

COURSE DESCRIPTION:

Sr. No.	Topics	Detail syllabus	No.of Lectures
1	Introduction to networking	Uses of Computer Networks, Network Hardware, Network Software, Reference Models,Example Networks, Network Standardization.	5
2	The Physical and Data Link Layer	The Theoretical Basis for Data Communication, Guided Transmission Media, Wireless Transmission, The Public Switched Telephone Network, The Mobile Telephone System, Data Link Layer Design Issues, Error Detection and Correction, Elementary Data Link Protocols, Sliding Window Protocols, Protocol Verification,	7
3	Medium	The Channel Allocation	7

	Access Control & The Network Layer	Problem, Multiple Access Protocols, Ethernet, Wireless LANs, Broadband Wireless, Bluetooth, Data Link Layer Switching. Network Layer Design Issues, Routing Algorithms, Congestion Control Algorithms, Internetworking,	
4	Transport and Application Layer	The Transport Service, Elements of Transport Protocols, A Simple Transport Protocol, The Internet Transport Protocols: UDP, The Internet Transport Protocols: TCP, DNS—The Domain Name System, Electronic Mail, The World Wide Web, Multimedia.	7
5	Introduction to Cloud computing	Cloud Computing (NIST Model) Introduction to Cloud Computing, History of Cloud Computing, Cloud service providers Properties, Characteristics & Disadvantages Pros and Cons of Cloud Computing, Benefits of Cloud Computing, Cloud computing vs. Cluster computing vs. Grid computing,Role of Open Standards	7
6	Cloud Computing Architecture	1) Cloud computing stack Comparison with traditional computing architecture (client/server), Services provided at various levels, How Cloud Computing Works, Role of Networks in Cloud	7

		computing, protocols used, Role of Web services . 2) Service Models (XaaS) Infrastructure as a Service(IaaS) Platform as a Service(PaaS) Software as a Service(SaaS) 3) Deployment Models Public cloud Private cloud Hybrid cloud Community cloud	
7	Network Security & Cloud Security	Cryptography, Symmetric-Key Algorithms, Public-Key Algorithms, Digital Signatures, Communication Security, E-Mail Security, Web Security. Infrastructure Security, Data security and Storage, Identity & Access Management, Access Control, Trust, Reputation, Risk, Authentication in cloud computing, Client access in cloud, Cloud contracting Model, Commercial and business considerations	8
Total Lectures			**48**

EXAMINATION SCHEME (THEORY)

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

LIST OF PRACTICAL'S:-

- Remote desktop,
- files sharing ,
- remote file transfer,
- ammy admin,
- Printer share,
- TeamViewer,
- packet tracer (draw LAN & configuration),
- Ip-scanner,
- internet dos cmd,
- online chating,
- online meeting,
- video calling.

BOOKS RECOMMENDED:-

- Cloud Computing Bible, Barrie Sosinsky, Wiley-India, 2010
- Cloud Computing: Principles and Paradigms, Editors: Rajkumar Buyya, James Broberg, Andrzej M. Goscinski, Wile, 2011
- Cloud Computing: Principles, Systems and Applications, Editors: Nikos Antonopoulos, Lee Gillam, Springer, 2012
- Cloud Security: A Comprehensive Guide to Secure Cloud Computing, Ronald L. Krutz, Russell Dean Vines, Wiley-India, 2010

COURSE TITLE: MACHINE LEARNING IN BIOINFORMATICS **TOTAL LECTURE HR. = 48**

COURSE CODE : MSI 306 **L T P HR C**

MARKS: 100 **3 0 4 7 5**

OBJECTIVE:

To make the students familiar with the different concepts and techniques that are put to use in the field of Bioinformatics.

LEARNING OUTCOME:

At the end of the course, the students will have sufficient scientific understanding of the basic concepts in concepts behind different machine learning techniques put to use in bioinformatics.

COURSE DESCRIPTION:

Sr. No.	Topics	Detail syllabus	No.of Lectures
1	Introduction to machine learning	Introduction to machine learning	3
2	Feature selection related to datamining	Feature selection related to datamining	4
3	Visualization of microarray data	Visualization of microarray data	6
4	Fuzzy gene mining	Fuzzy gene mining	5
5	Protein structre prediction methods	Sequence based prediction of residue level properties in proteins Consensus prediction for protein prediction, Kernel methods, Evolutionary kernel method	9
6	Probalistics models in Biosequences	Probalistics models in Biosequences	5
7	Motif refinement techniques	Motif refinement techniques	6

8	Neural networks and Supervised learning methods	Neural networks and Supervised learning methods	3
9	Machine learning Applications	Machine learning Applications	3
Total Lecture			**48**

EXAMINATION SCHEME (THEORY)

Examination	**Duration**	**Marks**
I Internal	45 minutes	15
II Internal	45 minutes	15
Teachers assessment		10
End Semester Exam	2 hours 30 minutes	60
Total		**100**

RECOMMENDED BOOKS:

- Machine Learning in Bioinformatics by Wiley Series in Bioinformatics, Yanqing Zhang, Jagath C. Rajapakse

SEMESTER IV

Particulars	**Credit**
Project(6 Months duration)	**25**