Department of Bioinformatics
School of Earth, Biological and Environmental Sciences
Central University of South Bihar
Syllabus of M.Sc. Bioinformatics
Session-2018 onwards

Introduction

Bioinformatics is a rapidly growing field of interdisciplinary study at the interface of biology and Information technology. As such, Bioinformatics brings together Molecular biology with areas from Statistics, Mathematics, and Computer science. Bioinformatics now entails the creation and advancement of databases, algorithms, computational and statistical techniques, and theory to solve formal and practical problems arising from the management and analysis of biological data. Considering the interdisciplinary nature of Bioinformatics, this master programme shall have a major component from related subjects under one umbrella.

Objectives

The core objective of the programme is to provide quality education to the graduates, who want to pursue their career in the emerging areas of Bioinformatics and Computational Biology.

- To serve as a nodal point for Bioinformatics and its applications
- To provide industry interface to the students for research project
- To build skilled manpower for drug design and pharmaceutical industry

Target Group and Eligibility

Bachelor degree in Biological Science/ Agricultural Science/ Pharmaceutical Science/ Veterinary Science/ Medical Science/ Mathematics/ Physics/ Chemistry/ Computer Science/ Information Technology or any other related discipline.

Duration: Two Years (Four Semester) – Full Time

Umesh Singh

11.7.18

11/7/18

Rakesh Kumar
11/7/18

M Singh 11/07/2018

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Course Structure of M.Sc. Bioinformatics

Total Credits: 96

Semester I **(24 Credits)**

Course Code	Course title	Credits		
Core Courses		L	T	P
MSBIS1001C04	Introduction to Bioinformatics	2	1	1
MSBIS1002C04	Cell and Molecular Biology	3	1	0
MSBIS1003C04	Mathematics and Statistics with R	2	1	1
MSBIS1004C04	Linux and Shell Programming	2	1	1
MSBIS1005C04	Programming with C	2	1	1
	One elective course of 4 credits from parent or other department			
MSBIS1006S00	Plantation of Trees	Non- credit		

Student may choose any related course/elective including wet laboratory practicals during semester I and II from other department.

Semester II **(24 Credits)**

Course Code	Course title	Credits		
Core Courses		L	T	P
MSBIS2001C04	Algorithms in Bioinformatics	3	0	1
MSBIS2002C04	Biomolecular Modelling & Simulations	3	0	1
MSBIS2003C04	Programming with Perl	2	1	1
MSBIS2004C04	Genetics and Genomics	3	1	0
MSBIS2005C04	Evolution and Molecular Phylogeny	3	1	0
	One elective course of 4 credits from parent or other department			
MSBIS2006S00	Swachh Bharat Abhiyan	Non- credit		

Students wish to go for summer training (non-credit) may join the same at the end of II semester and present work done during summer training within one week of the commencement of semester III.

Experts from industry / alumni placed at various institutions may be called for guest lecture and interaction to get update on requirement in industry.

Educational/Industrial tour or Excursion may be made to visit institutes/industries/laboratories based on availability of funds or otherwise. If excursion took place, student has to submit a report (10 marks) within a week that will be the part of continuous assessment of a specific course decided by faculty council.

Semester III **(24 Credits)**

Course Code	Course title	Credits		
Core Courses		L	T	P
MSBIS3001C04	Chemoinformatics and Drug Design	3	0	1
MSBIS3002C04	Transcriptomics and Proteomics	3	0	1
MSBIS3003C04	DBMS and Web Technology	2	1	1
MSBIS3004C04	Minor Project (Review of Literature, Seminar, and Research Problem Definition)	4		
	Two elective courses of 8 credits from parent or other department			
MSBIS3005S00	Village based Skills	Non- credit		
MSBIS3006S00	Human Molecules Genetics (SWAYAM Course)	Non- credit		

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Semester IV **(24 Credits)**

Course Code	**Course title**	**Credits**
MSBIS4001C24	Dissertation	24

Student would have choice to carry out dissertation internally or externally.

Course Code	**Course title**	**Credits**		
Elective Courses		L	T	P
MSBIS1001E04	Biochemistry and Immunology	3	1	0
MSBIS2001E04	Whole exome sequencing data analysis	3	0	1
MSBIS3001E04	Big Data Analytics and Health Informatics	4	0	0
MSBIS3002E04	Programming with Python	2	1	1
MSBIS3003E04	Systems Biology	2	1	1

C: Core Course; E: Elective Course; S: Self-study/Skill Course

An elective will run if opted by 33% of the students enrolled in the programme.

Inter department elective: Any theory course and related practical may be opted by a student from school

Inter school course: MSBIS1004C04, MSBIS1005C04, MSBIS3003C04

Skill based course: MSBIS1001C04, MSBIS1005C04, MSBIS2002C04, MSBIS2003C04, MSBIS3001C04, MSBIS3003C04

Umesh Singh
11/07/2018

11/07/18

11.7.18

11/07/18 Rakesh Kumar
11/7/18

M Singh
11/07/2018

11/07/18

INTRODUCTION TO BIOINFORMATICS

Course Details			
Course Title: INTRODUCTION TO BIOINFORMATICS			
Course Code	MSBIS1001C04	**Credits**	4
L + T + P	2 + 1 + 1	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	30 (L) + 15 (T) + 30 (P) Hours
Methods of Content Interaction	Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

The course introduces Bioinformatics in general and online resources related to sequences, structures, pathway, and genome databases in particular to the students.

Learning Outcomes

- After completing the course the student will recognize various online bioinformatics resources, able to retrieve relevant information from biological databases and also learn to differentiate between file formats to store biological data.

Course Contents

Unit 1: **(50% Weightage)**

General Introduction and history of bioinformatics, advanced internet search, overview of bioinformatics resources on the web NCBI / EXPASY, DNA and protein sequence database: GenBank, Searching GenBank through Entrez search engine, SwissProt, sequence submission, various file formats in bioinformatics, bibliographic resource and literature database.

Unit 2: (50% Weightage)

PROSITE, Pfam, PDB, SCOP, small molecule database: ZINC, Natural product database, Biochemical pathway database: KEGG, Gene expression and genome databases, Interaction databases, Gene ontology: ontology structure, ontology relations, cellular component, molecular function and biological process ontology, Patenting and IPR issues in bioinformatics.

List of practical

1. Practicals based on retrieval of nucleotide/protein sequences from biological databases NCBI and SwissProt (Gene, protein, CDS, EST)
2. Study of various file formats to store biological data (Fasta, GenBank, GenPept, PDB)
3. Explore online resources including KEGG, GO Consortium
4. Advanced internet search on biological data using Entrez
5. Data retrieval from P-FAM, PRINTS**,** SCOP, CATH
6. Genome Databases and related data resources (EST, STS, GSS, HSS etc.)
7. Genome browsers and Data Visualization: UCSC genome browser, NCBI genome browser, Ensembl genome browser, Map Viewer
8. Retrieving sequences and annotation with help of genome browsers
9. Downloading sequence data in bulk

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
1-2	General Introduction and history of bioinformatics
3-4	Advanced internet search
5-7	Overview of bioinformatics resources on the web NCBI / EXPASY
8	DNA and protein sequence database
9	GenBank
10	Searching GenBank through Entrez search engine
11	SwissProt
12	Sequence submission
13-14	Various file formats in bioinformatics
15	Bibliographic resource and literature database

16	Continuous assessment (Class Test I)
17	PROSITE
18	Pfam
19	PDB
20	SCOP
21	Small molecule database: ZINC
22	Natural product database
23	Biochemical pathway database: KEGG
24-25	Gene expression and genome databases
26	Interaction databases; Continuous assessment (Assignment)
27-28	Gene ontology: ontology structure, ontology relations, cellular component, molecular function and biological process ontology
29	Patenting and IPR issues in bioinformatics
30	Continuous assessment (Class Test II)
15 Hours	Tutorials
30 Hours	Practicals

Suggested References:

- Attwood T, Parry-Smith DJ (2001) Introduction to Bioinformatics. Pearson Education
- Claverie JM, Notredame C (2003) Bioinformatics for Dummies. John Wiley & Sons
- Mount DW (2001) Bioinformatics: Sequence and Genome Analysis. Cold Spring Harbor Laboratory Press
- Sharma V, Munjal A, Shanker A (2016) A Text Book of Bioinformatics. Rastogi Publications
- Singh HB (2016) Intellectual Property Issues In Biotechnology. CABI

CELL AND MOLECULAR BIOLOGY

Course Details			
Course Title: Cell and Molecular Biology			
Course Code	MSBIS1002C04	Cell and Molecular Biology	4
L + T + P	3 + 1 + 0	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	45 (L) +15 (T) Hours
Methods of Content Interaction	Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students, individual and group drills, group and individual field based assignments followed by workshops and seminar presentation.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

- To introduce the students to classical and modern concepts in cell and molecular biology
- To learn their application in biological research.
- To understand molecular level mechanism and cellular processes.
- To understand the concept of cell and molecular biology in bioinformatics as one of important key applied areas and its uses in biological research

Learning Outcomes

After completion of the course the learners will be able to:

- Understand the concepts of cell and molecular biology and to utilize them in bioinformatics applications.
- Basic as well as advanced application of Cell and Molecular Biology in Biological application

- To Understand the connection of Applied areas of cell and molecular biology and Bioinformatics for human diseases and health

Course Contents

Unit 1: Cell and its structural Organization (25 % Weightage)

Prokaryotic and eukaryotic cells, physical structure of model membranes in prokaryotes and eukaryotes, lipid bilayer, membrane proteins, Structural organization and functions of cell organelles: nucleus, mitochondria, Golgi bodies, endoplasmic reticulum, lysosomes, Chloroplast, Structure of chromatin and chromosomes.

Unit 2: Nucleus and its Content (25 % Weightage)

Nucleic acids: structure properties and function of DNA, RNA, and their forms, Conformation of nucleic acids, Replication of DNA in prokaryotes and eukaryotes, Chromatin and its remodelling, Transcription and its machinery: RNA polymerases, formation of initiation complex, elongation and termination of transcription. Regulation of transcription: activators (enhancers) and repressors, Gene silencing.

Unit 3: Transcription, Translational Mechanism and its control (25 % Weightage)

Genetic code, Mechanism of translation: Initiation, elongation and termination factors and translational proof-reading in prokaryotes. Regulation of translation, posttranslational modifications of proteins. Protein trafficking and transport, Control of gene expression at transcription and translation level: Regulation of gene expression in prokaryotes and eukaryotes.

Unit 4: Cell Communications, receptors and its messengers (25 % Weightage)

Cell signaling, Hormones and their receptors, cell surface receptor, signaling through G-protein coupled receptors, modulation of G-proteins through small molecules, activators, and antagonism, signal transduction pathways, second messengers, and regulation of signaling pathways.

Content Interaction Plan:

Lecture cum Discussion **(Each session of 1 Hour)**	**Unit/Topic/Sub-Topic**
(Unit I)1-2	Prokaryotic and eukaryotic cells
2-4	Physical structure of model membranes in prokaryotes and eukaryotes
4-5	Lipid bilayer, membrane proteins
5-7	Structural organization and functions of cell organelles: nucleus
7-11	Structural organization and functions of cell organelles: Mitochondria, Golgi bodies, endoplasmic reticulum, lysosomes, Chloroplast
12	**CONTINUOUS ASSESSMENT : 01**
(Unit –II) 13-14	Nucleic acids: structure properties and function of DNA, RNA, and their forms
14-15	Conformation of nucleic acids
15-17	Replication of DNA in prokaryotes and eukaryotes
17-18	Chromatin and its remodelling
18-19	Transcription and its machinery: RNA polymerases
19-20	Formation of initiation complex
20-21	Elongation and termination of transcription
21-23	Regulation of transcription: activators (enhancers) and repressors, Gene silencing
24	**CONTINUOUS ASSESSMENT : 02**
(Unit –III) 25-27	Genetic code, Mechanism of translation: Initiation, elongation and termination factors
27-28	Translational proof-reading in prokaryotes
28-30	Regulation of translation, posttranslational modifications of proteins
30-32	Protein trafficking and transport
32-34	Control of gene expression at transcription and translation level
34-35	Regulation of gene expression in prokaryotes and eukaryotes
(Unit –IV) 35-36	Cell signaling
36-37	Hormones and their receptors
38-39	Cell surface receptor
39-40	Signaling through G-protein coupled receptors

40-41	Modulation of G-proteins through small molecules
41-42	Activators, and antagonism
42-43	Signal transduction pathways
43-44	Second messengers
44-45	Regulation of signaling pathways.
	CONTINUOUS ASSESSMENT : 03
45-60	Tutorials

Suggested References:

1. Brown TA (2000) Genomes 2. BIOS Scientific Publishers Ltd, New York
2. Bruce A, Alexander J, Julian L, Martin R, Roberts K, Peter W (2008) Molecular Biology of the Cell (5th Edition). Garland Science
3. Bruce A, Dennis B, Karen H, Alexander JD, Julian, Martin LR, Roberts K, Peter W (2010) Essential Cell Biology (3rd Edition). Garland Science
4. Cooper GM, Hausman RE (2013) The Cell: A Molecular Approach. Sinauer Associates
5. Harris ELV, Angal S (1990) Protein Purification Applications: A Practical Approach. Oxford University Press
6. Michael RL, Stuart EB, Chih-duen CP, Richard CW(1990) Protein Purification: From Molecular Mechanisms to Large-Scale Processes (Acs Symposium Series). An American Chemical Society Publication
7. Sambrook J, Fritsch EF, Maniatis T (1989) Molecular Cloning: A Laboratory Manual (3 Volume Set; Edition 2nd). Cold Spring Harbor Laboratory Press
8. Sambrook JF, Russell DW (2001) Molecular Cloning: A Laboratory Manual (3rd Edition). Cold Spring Harbor Laboratory Press
9. Watson JD (2001) The Double Helix: A Personal Account of the Discovery of the Structure of DNA. Simon & Schuster
10. Watson JD, Baker TA, Bell Stephen P, Gann A, Levine, Richard ML (2008) Molecular Biology of the Gene (6th Edition). Cold Spring Harbor Laboratory Press
11. Wilson K, Walker J (2005) Principles and Techniques of Biochemistry and Molecular Biology. Cambridge University Press

Mathematics and Statistics with R

Course Details			
Course Title: Mathematics and Statistics with R			
Course Code	MSBIS1003C04	**Credits**	4
L + T + P	2 + 1 + 1	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	45 (L) + 15 (T) + 30 (P) Hours
Methods of Content Interaction	Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students, hands-on practical sessions, individual and group drills, seminar presentation.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

This course is designed to provide student's basic understanding of mathematical and statistical concepts required for biological data analysis.

Learning Outcomes

After completion of the course the learners will be able to solve linear equation with help of matrices. Calculate descriptive statistics of given data. Perform probability calculations. Calculate sensitivity and specificity of a diagnostics test. Perform testing of hypothesis in relation to biological problems. Understand correlation and its importance in solving biological problems

Course Contents

UNIT I: (15% Weightage)

Sequences and series (Ap, GP, HP), Limits and continuity, Vector - addition, subtraction, multiplication and their geometric understanding, Matrices and its types, their eigenvalues and eigen vectors, transposition and inverse of matrices, Cayley–Hamilton theorem.

UNIT II: (15 % Weightage)

Measure of central tendency: arithmetic mean, harmonic mean, geometric mean, weighted mean, median and mode of grouped and ungrouped data. Measure of dispersion: standard deviation and variance, Coefficients of dispersion and variance, Measure of skewness and kurtosis.

UNIT III: (35 % Weightage)

Probability: Classical, frequency and axiomatic approach of calculating probabilities. Conditional probability and Bayes theorem. Random variable and probability distribution: discrete and continuous random variables, probability mass function and probability density function, cumulative distribution function for discrete and continuous random variables. Binomial, normal, Chi-square, t and F distribution.

UNIT IV: (35% Weightage)

Sampling theory: Population and sample, random sample, population parameters, Sample statistics, sampling distribution of means, sampling distribution of proportion, sampling distributions of differences and sums, sample variance. Estimation: unbiased, maximum likelihood, Bayesian. Test of hypothesis and significance: Type I and type II error, Power of test, P-values. Curve fitting and regression: method of least squares, standard error of estimate, correlation coefficients, Analysis of variance, nonparametric tests.

List of Practicals

1. Introduction to R-Statistical software. Vectors and assignments, Vector arithmetics, generating regular sequences, logical vectors, character vector, selecting and modifying subset of a data set. Other objects in R: factors, arrays, matrices, list, data.frame and functions. R-objects their mode and attributes. Reading data from files.
2. Determinants of 2 by 2 single digit matrices. Transpose of an array.
3. Performing matrix multiplication in 'R', solving linear equations with help of 'R'.
4. Calculation of Eigenvalues and Eigenvectors in 'R'.
5. Examining the distribution of a set of data.
6. Calculating probabilities and p-values.
7. One and two sample test.
8. Generating good quality plots in 'R': scattered plot, bar plot, histogram, pi-chart, density plot and boxplots.

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
1-2	Sequences and series (Ap, GP, HP), Limits and continuity
2-3	Vector - addition, subtraction, multiplication and their geometric

	understanding
3-7	Matrices and its types, their eigenvalues and eigen vectors, transposition and inverse of matrices, Cayley–Hamilton theorem
8-9	Measure of central tendency: arithmetic mean, harmonic mean, geometric mean, weighted mean
10	median and mode of grouped and ungrouped data
11-12	standard deviation and variance, Coefficients of dispersion and variance
13-14	Measure of skewness and kurtosis
15	Continuous Assessment I
16-17	Classical, frequency and axiomatic approach of calculating probabilities
18-22	Conditional probability and Bayes theorem
23-25	discrete and continuous random variables, p.m.f, p.d.f and c.d.f.
26-28	Binomial, normal, Chi-square, t and F distribution
29	Population and sample, random sample, population parameters, Sample statistics
30	Continuous Assessment II
31-34	sampling distribution of means, sampling distribution of proportion
35-36	Estimation: unbiased, maximum likelihood, Bayesian
37-41	Test of hypothesis and significance: Type I and type II error, Power of test, P-values
41-42	Curve fitting and regression: method of least squares, standard error of estimate
43-44	correlation coefficients, Analysis of variance, nonparametric tests
45	Continuous Assessment III
30 Hours	Practical

- Suggested References:

- Daniel WW (2009) Biostatistics: A Foundation for Analysis in the Health Sciences. Wiley
- Das KK (2010) An introduction to probability theory. Asian Books Pvt Ltd
- Das NG (2008) Statistical methods. Mcgraw Hill Education
- George A (2012) Mathematical methods for physicists. Orlando Academic Press
- Nabendu P, Sahadeb S (2005) Statistics: Concepts and Applications. PHI Learning Pvt Ltd
- Rosner B (2010) Fundamentals of Biostatistics. Cengage Learning Inc
- Stephenson G, Radmore PM (1990) Advanced Mathematical Methods for Engineering and Science Students. Cambridge University Press
- Wang X (2016) Next Generation Sequencing Data Analysis. CRC Press

Linux and Shell programming

Course Details			
Course Title: Linux and Shell programming			
Course Code	MSBIS1004C04	Linux and Shell Programming	4
L + T + P	2 + 1 + 1	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	30 (L) +15(T) + 30 (P) Hours
Methods of Content Interaction	Lecture, Tutorials, Practical, Group discussion; self-study, seminar, presentations and assignment class based as well as take-home type by students,		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

- Enable students to understand concept of computer architecture, generation and its history.
- Understanding the concept of operating system.
- To make student aware of Unix/Linux operating system.
- Concept of shell and its power to automate job write shell scripts to solve bioinformatics problems.

Learning Outcomes

- After completion of the course the learners will be able to:
- Understand computer system architecture.
- Have an idea of operating system, specifically Linux and its advantages over other OS
- Have an idea of several command and utility of Linux.
- Able to write shell scripts for various bioinformatics applications and automate the job.

Course Contents

Unit 1: (50 % Weightage)

Fundamentals of computers and software systems: Types of computers, Operating Systems, Languages, Computer Networks, Internet technology, Remote Login (telnet, ssh, ftp etc.). Introduction to Linux OS, File Management, Directories, File Permissions, Environment Setting, Basic Utilities commands: cp, mv, cd, ls, rm, clear, lp/lpr, cat, pwd, Pipe and Filters: Grep, SED, AWK, Compiling and Running the Source Code, Make and Makefile

Unit 2: (50 % Weightage)

Introduction to shell in Linux operating system. Types of shells and their comparison. Shell functionality environment, writing script & executing basic script, debugging, Variables, and mathematical operators. Conditional statements, if, else elif. Logical operators, AND, OR, NOT. Loops While, For, Until, Break & continue. Functions & file manipulations Processing file line by line, opening reading and writing a file/ directory. Regular Expression & Filters: concept of regular expression Grep, cut , sort commands Grep patterns.

Lists of Practical's

- Computer hardware architecture, components
- Editors and writing scripts using gedit, Vi and Vim editor.
- Major Linux commands: cp, mv, cd, ls, rm, clear, lp/lpr, cat, pwd,
- Pipe and Filters: Grep, SED, AWK.
- Shell scripting
- Variables, operators, (mathematicsl and logical)
- Conditional and logical statements (if, else, elif, while)
- Loops (for and while), break & continue
- File manipulation
- Pipes and filters automation using Shell

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
(Unit I)1-2	Fundamentals of computers and software systems: Types of computers,

2-4	Operating Systems, Languages, Computer Networks, Internet technology.
5-6	Remote Login (telnet, ssh, ftp etc.). Introduction to Linux OS,
7-10	File Management, Directories, File Permissions, Basic Utilities commands: cp, mv, cd, ls, rm, clear, lp/lpr, cat, pwd
11-15	Pipe and Filters: Grep, SED, AWK, Compiling and Running the Source Code, Make and Makefile
16	**CONTINUOUS ASSESSMENT : 01**
(Unit –II) 17-18	Introduction to shell in Linux operating system. Types of shells and their comparison.
18-19	Shell functionality environment, writing script & executing basic script, debugging,
19-21	Variables, and mathematical operators. Conditional statements, if, else elif,
22-24	Logical operators, AND, OR, NOT. Loops While, For, Until, Break & continue.
25-27	Functions & file manipulations Processing file line by line, opening reading and writing a file/ directory
28-29	Regular Expression & Filters: concept of regular expression Grep, cut, sort commands Grep patterns.
30	**CONTINUOUS ASSESSMENT : 02**
15 Hours	**Tutorial**
30 hours	Practicals

Suggested References:

1. Jerry P, Shelley P, O’Reilly T, Loukides M (2002) Unix Power Tools (3rd Edition). O’Reilly Media
2. Neil M, Stones R (2004) Beginning Linux Programming (3rd Edition). Wiley Dreamtech India Pvt Ltd
3. Richard Blum C Bresnahan (2015) Linux Command Line and Shell Scripting, Wiley
4. Christopher Negus, Linux Bible, 9th edition , Wiley

PROGRAMMING WITH C

Course Details			
Course Title: Programming with C			
Course Code	MSBIS1002C04	**Credits**	4
L + T + P	2 + 1 + 1	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	30 (L) + 15 (T) + 30 (P) Hours
Methods of Content Interaction	Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students, individual and group drills, group and individual field based assignments followed by workshops and seminar presentation.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

- To acquaint the students with basic concepts of programming.
- To expose the students with C language syntax and its data structure.

Learning Outcomes

After completion of the course the learners will be able to:

- Write and execute programs in C language.

Course Contents

UNIT I: Basics, Data Type, Variables & Control Statements in C (25% Weightage)

- History and Features of C, Role of Compiler, Structure of a C Program, Writing C Programs, Building an Executable Version of a C Program, Running and Debugging a C Program
- Data Types, Variable and Operators, Preprocessor Directives Input and Output Operators

- Reading/Writing Characters , Formatted input/output Function
- Control Statements: IF, IF-ELSE and IF-ELSIF-ELSE Statements, Nesting of IF-ELSE Statements, SWITCH, DO-WHILE, WHILE and FOR Statements

UNIT II: Arrays, Strings and Pointers in C (25% Weightage)

- One Dimensional, Two Dimensional and Multi-Dimensional Arrays
- String Handling: Reading and Writing Strings, String Handling Functions
- Understanding Pointers, Pointer expressions, Pointer and Arrays, Pointers to Functions

UNIT III: Functions in C (25% Weightage)

- Function Basics, Advantage of Function, User defined and standard functions, Function prototypes
- Parameter passing, Call-by-value, Call-by-reference, Recursion, Variable Storage Classes

UNIT IV: Dynamic Memory allocation and File Management in C (25% Weightage)

- Introduction to Dynamic Memory Allocation, Malloc, Calloc, Realloc and Free functions
- Introduction to File Management, Opening/Closing a File, Input/Output operations on Files, Error Handling During I/O Operations

List of Practicals

C programs for the following:

- To find simple and compound interest.
- For swapping 2 numbers.
- To find leap year.
- To find largest/smallest of given 3 numbers.
- To find sum and average of given 3 numbers.
- To find square and cube of given number.
- For calculation of factorial for a given number
- To search given number in an array.
- For calculator application.
- To find whether given character vowel or not.
- To find sum of n numbers.
- To check if the number is odd or even.
- To print numbers from 1 to 100.
- To insert an element into an array.
- To delete an element from an array.
- For matrix addition and matrix multiplication.
- For string comparison, string copying and calculation string length
- For sorting an array using bubble sort/selection sort.

- For taking input from a file and writing output in a file.

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
1-2	History and Features of C, Role of Compiler, Structure of a C Program, Writing C Programs, Building an Executable Version of a C Program, Running and Debugging a C Program.
3-4	Data Types, Variable and Operators, Pre-processor Directives Input and Output Operators.
5-6	Reading/Writing Characters Formatted input/output Function.
7-11	Control Statements: IF, IF-ELSE and IF-ELSIF-ELSE Statements, Nesting of IF-ELSE Statements, SWITCH, DO-WHILE, WHILE and FOR Statements.
12-14	One Dimensional, Two Dimensional and Multi-Dimensional Arrays.
15-17	String Handling: Reading and Writing Strings, String Handling Functions.
18-19	Understanding Pointers, Pointer expressions, Pointer and Arrays, Pointers to Functions.
20-21	Function Basics, Advantage of Function, User defined and standard functions, Function prototypes.
22-25	Parameter passing, Call-by-value, Call-by-reference, Recursion, Variable Storage Classes.
26-27	Introduction to Dynamic Memory Allocation, Malloc, Calloc, Realloc and Free functions.
28-30	Introduction to File Management, Opening/Closing a File, Input/Output operations on Files, Error Handling During I/O Operations.
15 Hours	Tutorials
30 Hours	Practicals

Suggested References:

- *Hutchinson RC, Just RB (1998) Programming using the C Language. McGraw-Hill*
- *Kernighan BW, Ritchie DM (1988) The C Programming Language. Prentice-Hall*
- *Balagurusamy E (2017) Programming in ANSI C. (Seventh Edition) McGraw-Hill*
- *Kanetkar Y (2016)Let Us C. (Fifteenth Edition) BPB Publications*

Algorithms in Bioinformatics

Course Details			
Course Title: Algorithms in Bioinformatics			
Course Code	MSBIS2001C04	Algorithms in Bioinformatics	4
L + T + P	3 + 0 + 1	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	45 (L) + 30 (P) Hours
Methods of Content Interaction	Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students, individual and group drills, group and individual field based assignments followed by workshops and seminar presentation.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

- To deals with various algorithms used to solve biological problems
- To understand the algorithms for sequence alignment, promoter and gene prediction.
- To learn machine learning algorithms to build their own computational biology models.
- To Articulate the trade-offs behind algorithms in bioinformatics
- Locate and critically evaluate scientific information

Learning Outcomes

After completion of the course the learners will be able to:

- Familiar with the use of various computational algorithms
- Algorithms use in solving biological problems.
- Students will be able to design and analyze their algorithms.

- Apply one of the paradigms presented in class to solve real-world problems
- Present scientific content to a small technical audience

Course Contents

Unit 1: **(25 % Weightage)**

A brief introduction to algorithms, history & concept, introduction to Dynamic programming, Divide & conquer, Bruitforce and Greedy algorithms. Representation of algorithms flowchart & pseudocode. Concept of Homologous, orthologous, paralogous and Xenologous sequences, Alignment of pair of sequences, and gap penalties, dot plot method, dynamic programming algorithm as applicable to global (Needleman-Wunsch) and local (Smith - Waterman) sequence alignment. Database searching for similar sequences: Heuristic algorithm FASTA, BLAST and their types.

Unit 2: **(25 % Weightage)**

Multiple sequence alignment (MSA), dynamic programming for MSA, heuristic approach to MSA, progressive sequence alignments method, Clustal W/X, Branch and bound and other methods for MSA, Consensus sequence & PSSM, Scoring matrices (PAM and BLOSUM) Whole genome alignments: concepts and applications, Cluster of Orthologous Groups.

Unit 3: **(25 % Weightage)**

Promoter prediction in prokaryote and eukaryotes, Prediction of genes and gene structure for prokaryotic and eukaryotic organisms, sequence and structural motifs and motif prediction tools RNA structure prediction algorithms, Prediction of splice sites.

Unit 4: **(25 % Weightage)**

Application of machine learning Techniques (Genetic algorithms, Markov chain and Hidden markov models, Neural networks, Graph matching algorithms, Support vector machine, Nearest-neighbour methods (clustering).

List of Practicals

1. Finding similar sequences (DNA/proteins) in databases: use of different version of BLAST and interpretation of BLAST results.
2. Multiple sequence alignments using web-based and stand-alone version of CLUSTAL. Interpretation of results to identify conserved and variable regions and correlate them with physico-chemical & structural properties.
3. Prediction of ORFs.

4. Gene Prediction in prokaryotes and eukaryotes.
5. Primer designing.
6. Prediction of promoters using Neural Network Promoter Prediction (NNPP).
7. Prediction of alternate splice sites using methods such as Splice Site Prediction by Neural Network.
8. Using sequence-based and structure-based Function Annotation Servers such: ProKnow (http://www.doe-BIS.ucla.edu/Services/ProKnow/), Joined Assembly of Function Annotations (JAFA) at http://jafa.burnham.org/learnMore.html.
9. Predicting protein function from 3D structure using ProFunc.

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
1-2	A brief introduction to algorithms, history & concept, introduction to Dynamic programming, Divide & conquer, Bruitforce and Greedy algorithms.
3-4	Representation of algorithms flowchart & pseudocode Homologous, orthologous, paralogous and Xenologous sequences
5-6	Alignment of pair of sequences, and gap penalties ,Dot plot method
7-8	Dynamic programming algorithm as applicable to global (Needleman-Wunsch) and local (Smith - Waterman) sequence alignment
8-9	Database searching for similar sequences: Heuristic algorithm FASTA, BLAST and their types.
10	**CONTINUOUS ASSESSMENT : 01**
11	Multiple sequence alignment (MSA)
12-13	Dynamic programming for MSA
13-15	Heuristic approach to MSA, Consensus sequence & PSSM, Scoring matrices
16	Progressive sequence alignments method
17	Clustal W/X
18	Branch and bound and other methods for MSA
19	Whole genome alignments: concepts and applications,
20	Cluster of Orthologous Groups
21	**CONTINUOUS ASSESSMENT : 02**

22	Promoter prediction in prokaryote and eukaryotes
23	Prediction of genes and gene structure for prokaryotic organisms
24	Prediction of genes and gene structure for eukaryotic organisms
25-26	Sequence and structural motifs and motif prediction tools. RNA structure prediction algorithms
27	Software Information and demo
28	Prediction of splice sites.
29	Application of machine learning Techniques: Genetic algorithms
30	Application of machine learning Techniques: Markov chain and Hidden markov models
31	Application of machine learning Techniques: Neural networks
32-34	Application of machine learning Techniques: Graph matching algorithms
35-36	Application of machine learning Techniques : Support vector machine
37-38	Application of machine learning Techniques: Nearest-neighbour methods (clustering).
39-41	Application of machine learning Techniques: Nearest-neighbour methods (clustering).
42-43	Problem Discussion
44	Problem Discussion
45	**CONTINUOUS ASSESSMENT : 03**
30 Hrs	**Practicals**

Suggested References:

1. Cormen TH, Leiserson CE, Rivest RL, Stein C (2009) Introduction to Algorithms. The MIT Press
2. Dey DK, Ghosh S, Mallick BK (2010) Bayesian Modelling in Bioinformatics. Chapman and Hall
3. Gusfield D (1997) Algorithms on Strings, Trees, and Sequences. Cambridge University Press
4. Jones NC, Pevzner PA (2004) An Introduction to Bioinformatics Algorithms. The MIT Press
5. Klir GJ, Yuan B (1995) Fuzzy Sets and Fuzzy Logic: Theory and Applications. Prentice Hall
6. Mitchell T (1997) Machine Learning. The McGraw-Hill Company
7. Mitra S, Dutta S, Perkins T, Michailidis G (2008) Introduction to Machine learning and

Bioinformatics. Chapman and Hall

8. Mount DW (2001) Bioinformatics: Sequence and Genome Analysis. Cold Spring Harbor Laboratory Press
9. Rao SS (1991) Optimization: Theory and applications. Wiley Eastern Ltd
10. Sharma V, Munjal A, Shanker A (2016) A Text Book of Bioinformatics. Rastogi Publications
11. Waterman M (1995) Introduction to Computational Biology: Maps, sequences and genomes. Chapman & Hall
12. Witten IH, Frank E, Hall MA, Pal CJ (2011) Data Mining: Practical Machine Learning Tools and Techniques. Morgan Kaufmann

Biomolecular Modeling and Simulation

Course Details			
Course Title: Biomolecular Modeling and Simulation			
Course Code	MSBIS2002C04	**Credits**	4
L + T + P	3 + 0+ 1	**Course Duration**	One Semester
Semester	Even	**Contact Hours**	45 (L) + 30 (P) Hours
Methods of Content Interaction	Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students, individual and group drills, group and individual assignments followed by paper presentation.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

- The course will impart essential training in the area of molecular modelling, simulation, structure determination and prediction to add in research in pharmaceutical and biological sciences. Further, the present course aims to introduce about concepts, algorithms and software’s in structural biology and protein modelling.

Learning Outcomes

- The student would be able to understand, model and analyze structure of small and macro molecules.
- Students would be able to predict the structures and grasp the idea of experimental structure and determination using x-ray crystallography.
- Student would develop hands on experience in molecular simulation.

Course Contents

UNIT I: Nomenclature and overview of molecular modeling (25% Weightage)

- Nomenclature & terms used in molecular modelling, stereochemistry, CIP/CORN rule, ring puckering, chirality, Computer representation & visualization of molecules, internal, orthogonal and fractional coordinates, Steric criteria, Hard and soft spheres model, Atomic, ionic, covalent and van der Waal radii, Calculation of molecular geometry – bond length, angle and torsion angles, Calculation of molecular volumes & surfaces - van der Waals, Connolly and solvent accessible surfaces, Ramachandran Map, Overview of experimental techniques to study macromolecular structures: X-ray crystallography, NMR &Cryo-electron microscopy, Structure consistency and validation tools: Procheck, WhatIF, &MolProbity.

UNIT II: 2D and 3D structure prediction methods (25% Weightage)

- Principles of protein folding, Anfinsen paradigm, Levinthal paradox and Folding Funnel, Structural Classes, Motifs, Folds and Domain, Protein Secondary Structure Prediction Methods: Chou and Fasman, GOR, Neural Network & nearest neighbour methods, Tertiary structure prediction: homology modelling, fold recognition (threading) and ab initio methods, Structural comparison & alignment methods, VAST & DALI, Macromolecular interactions & Protein-Protein docking.

UNIT III: Overview of molecular modeling and energy minimization (25 % Weightage)

- Brief overview of molecular modelling methods: molecular mechanics, semi-empirical, DFT, and *ab initio* methods; empirical potential functions; ball-and-spring model, harmonic approximation, bond length, angle, torsional, out-of-plane and cross terms, Electrostatics of biomolecules, hydrogen bonding and salt-bridges, Popular force fields - MM, AMBER, CHARMM, OPLS, NAMD, GROMACS, parameterization problem, Energy Minimization: Golden section, derivative based method (SD, CG, Newton-Raphson).

UNIT IV: Molecular dynamics methods (25%Weightage)

- Molecular Dynamics: Steps in typical MD simulations, minimization, equilibration and data collection, velocity scaling, periodic boundary condition, Numerical integrators, verlet algorithm, analysis of trajectories, Solvation, water and membrane models, implicit and explicit solvation model, Monte carlo (MC) methods, conformation search procedure, Types of dynamics simulations: adiabatic, constant T, simulated annealing, Free energy perturbation method, brief introduction of metadynamics, coarse graned and MM-GBSA

List of Practicals:

Molecular modelling and molecular dynamics Lab

- Exploring the Database & searches on PDB and CSD, WHATIF, ExPasy.
- Methods for prediction of secondary structure of proteins: Prediction of secondary structures of proteins using at least 2 different methods with analysis and interpretation of the results. Comparison of the performance of the different methods for various classes of proteins.
- Methods for prediction tertiary structure of proteins along with analysis and interpretation of results: Homology modelling: Modeller, SWISS MODEL, SWISS PDBViewer; Fold recognition methods: PHYRE, I-TASSER, Verify 3D.
- Use of Steepest Decent and Conjugate Gradient for energy minimization of biomolecule.
- MD Using GROMACS or DESMOND: MD in vacuum, MD using implicit solvent, MD using explicit solvent with PBC/layer of solvent.
- Visualization and analysis of MD trajectory data (DS tools & VMD or Maestro). Protein ligand simulations.

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
Unit I 1-3	Nomenclature & terms used in molecular modelling, stereochemistry, CIP/CORN rule, ring puckering, chirality, Computer representation & visualization of molecules, internal, orthogonal and fractional coordinates, Steric criteria, Hard and soft spheres model, Atomic, ionic, covalent and van der Waal radii
4-5	Calculation of molecular geometry – bond length, angle and torsion angles, Calculation of molecular volumes & surfaces - van der Waals, Connolly and solvent accessible surfaces
5-6	Overview of experimental techniques to study macromolecular structures: X-ray crystallography, NMR &Cryo-electron microscopy
7-11	Structure consistency and validation tools: Procheck, WhatIF, & MolProbity.
Unit-2 12-13	Principles of protein folding, Anfinsen paradigm, Levinthal paradox and Folding Funnel, Structural Classes, Motifs, Folds and Domain

14-16	Protein Secondary Structure Prediction Methods: Chou and Fasman, GOR, Neural Network & nearest neighbour methods
17-22	Tertiary structure prediction: homology modelling, fold recognition (threading) and ab initio methods
23	Structural comparison & alignment methods, VAST & DALI,
Unit-3 24-25	Brief overview of molecular modelling methods: molecular mechanics, semi-empirical, DFT, and ab initio methods
26-30	empirical potential functions; ball-and-spring model, harmonic approximation, bond length, angle, torsional, out-of-plane and cross terms, Electrostatics of biomolecules, hydrogen bonding and salt-bridges,
31-32	Popular force fields - MM, AMBER, CHARMM, OPLS, NAMD, GROMACS, parameterization problem
33-34	Energy Minimization: Golden section, derivative based method (SD, CG, Newton-Raphson).
Unit-4 35-39	Molecular Dynamics: Steps in typical MD simulations, minimization, equilibration and data collection, velocity scaling, periodic boundary condition, Numerical integrators, verlet algorithm, analysis of trajectories
40-41	Solvation, water and membrane models, implicit and explicit solvation model
42-43	Monte carlo (MC) methods, conformation search procedure, Types of dynamics simulations: adiabatic, constant T, simulated annealing
44-45	Free energy perturbation method, brief introduction of metadynamics, coarse graned and MM-GBSA

- <u>Suggested References:</u>

1. Bourne PE, Weissig H (2003) Structural Bioinformatics (Methods of Biochemical Analysis, V. 44). Wiley-Liss Publisher
2. Branden CI, Tooze J (1999) Introduction to Protein Structure. Garland Publishing Inc, New York
3. Dieter HH, Wolfgang S, Didier R, Gerd F (2003) Molecular Modelling: Basic Principles and Applications. Wiley-VCH
4. Glusker JP, Trueblood KN (1994) Crystal Structure Analysis: A Primer. Oxford University Press
5. Jensen F (2017) Introduction to Computational Chemistry. John Wiley & Sons

6. Leach A (2001) Molecular Modelling: Principles and Applications. Prentice-Hall
7. Lewars EG (2003) Computational Chemistry. Kluwer Academic Publishers
8. Ramakrishnan C (2001) Ramachandran and his Map. Resonance – J Sci Edu 6:48-56.
9. RappéAK, Casewit CJ (1997) Molecular Mechanics across Chemistry. University Science Book
10. Richard FA (2002) Computational Methods for Protein Folding: Advances in Chemical Physics. John Wiley & Sons
11. SchleyerPvR (1998) Encyclopaedia of Computational Chemistry. John Wiley & Sons
12. Sternberg MJE (1997) Protein Structure Prediction: A Practical Approach. Oxford University Press
13. Young DC (2001) Computational Chemistry: A Practical Guide for Applying Techniques to Real World Problems. John Wiley & Sons

PROGRAMMING WITH PERL

<table>
<tr><th colspan="4">Course Details</th></tr>
<tr><th colspan="4">Course Title: Programming with Perl</th></tr>
<tr><td>Course Code</td><td>MSBIS2003C04</td><td>Credits</td><td>4</td></tr>
<tr><td>L + T + P</td><td>2 + 1 + 1</td><td>Course Duration</td><td>One Semester</td></tr>
<tr><td>Semester</td><td>Even</td><td>Contact Hours</td><td>30 (L) + 15 (T) + 30 (P) Hours</td></tr>
<tr><td>Methods of Content Interaction</td><td colspan="3">Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students, individual and group drills, group and individual field based assignments followed by workshops and seminar presentation.</td></tr>
<tr><td>Assessment and Evaluation</td><td colspan="3">• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades)
• 70% - End Term External Examination (University Examination)</td></tr>
</table>

Course Objectives

- To acquaint the students with basic concepts of Perl scripting.
- Enable students to write Perl scripts for bioinformatics applications.

Learning Outcomes

After completion of the course the learners will be able to:

- On successful completion, students will be equipped with designing and writing Perl scripts that will help in their work and research.

Course Contents

UNIT I: Introduction to Perl, Scalar, Array and List Data (25% Weightage)

- Introduction to Perl, Use of Perl in Bioinformatics, History of Perl, Availability, Support, Basic Concepts.

- Introduction to Scalar Data, Numbers, Strings, Scalar Variables, Scalar Operators and Functions.
- Introduction to Arrays and List Data, Literal Representation, Variables, Array Operators and Functions, Scalar and List Context.

UNIT II: Control Structures and Basic I/O File handles (25% Weightage)

- Control Structures: Statement Blocks, Introduction to Hashes, Hash Variables, Literal Representation of a Hash, Hash Functions, Hash Slices.
- Basic I/O File handles and File Tests, File Manipulation, Directory Manipulation. Formatting Data: Sorting, Transliteration.

UNIT III: Regular Expressions and Subroutines in Perl (25% Weightage)

- Regular Expressions: Concepts about Regular Expressions, Simple uses of Regular Expressions, Patterns, Matching Operator, Substitutions, the split and join Functions.
- Subroutines: System and User Functions, The local Operator, Variable-length Parameter Lists, Notes on Lexical Variables.

UNIT IV: Database Manipulation, CGI Programming and Bioperl (25% Weightage)

- Database Manipulation: DBM Databases and DBM Hashes, Opening and Closing DBM Hashes, Fixed-Length Random-Access Databases, Variable-Length (Text) Databases, Win32 Database Interfaces.
- CGI Programming: The CGI.pm Module, Your CGI Program in Context, Simplest CGI Program, Passing Parameters via CGI, Perl and the Web.
- Bioperl: Introduction, Installation procedures, Architecture, Uses of Bioperl.

List of Practicals

- Basics of Perl scripting: declaration, initialization and printing: Scalar Variable, Array Variable and Hash Variables.
- Manipulation of array variable using Join, Split, Splice, Sort, Merging, Pop, Push, Shift and Unshift function.
- Concatenating DNA fragment.
- Calculating the number of bases in the DNA string.
- Transcribing DNA to RNA.
- Reverse Complement of DNA string.
- Searching motifs.

- Using loops in perl scripting: for, while, do- while, foreach, until, unless etc.
- Counting DNA bases present in file containing DNA string.
- Using Subroutines in perl scripting.
- Finding STOP codons in a DNA string.
- Mutating DNA string at random positions.
- Generating random DNA sequence of specific length.
- Counting nucleotide in DNA string using subroutine.
- Calculating average percentage identity between pairs of random DNA sequence.
- Translation of DNA string using regular expression and hashes.
- Extracting DNA from FASTA files using regular expression.
- Extracting Data from a local RDBMS database server.

Content Interaction Plan:

Lecture cum Discussion **(Each session of 1 Hour)**	**Unit/Topic/Sub-Topic**
1-2	Introduction to Perl, Use of Perl in Bioinformatics, History of Perl, Availability, Support, Basic Concepts.
3-5	Introduction to Scalar Data, Numbers, Strings, Scalar Variables, Scalar Operators and Functions.
6-8	Introduction to Arrays and List Data, Literal Representation, Variables, Array Operators and Functions, Scalar and List Context.
9-11	Control Structures: Statement Blocks, Introduction to Hashes, Hash Variables, Literal Representation of a Hash, Hash Functions, Hash Slices.
12-14	Basic I/O File handles and File Tests, File Manipulation, Directory Manipulation. Formatting Data: Sorting, Transliteration.
15-17	Regular Expressions: Concepts about Regular Expressions, Simple uses of Regular Expressions, Patterns, Matching Operator, Substitutions, the split and join Functions.
18-21	Subroutines: System and User Functions, The local Operator, Variable-length Parameter Lists, Notes on Lexical Variables.

22-24	Database Manipulation: DBM Databases and DBM Hashes, Opening and Closing DBM Hashes, Fixed-Length Random-Access Databases, Variable-Length (Text) Databases, Win32 Database Interfaces.
25-27	CGI Programming: The CGI.pm Module, Your CGI Program in Context, Simplest CGI Program, Passing Parameters via CGI, Perl and the Web.
28-30	Bioperl: Introduction, Installation procedures, Architecture, Uses of Bioperl.
15 Hours	Tutorials
30 Hours	Practicals

Suggested References:

- Bal HP (2003) Perl programming for Bioinformatics. Tata McGraw-Hill
- Curtis JD (2003) Perl programming for biologists. John Wiley & Sons
- Moorhouse M, Barry P (2004) Bioinformatics Biocomputing and Perl: an introduction to bioinformatics computing skills and practice. John Wiley & Sons
- Schwartz RL, Phoenix T (2011) Learning Perl. Shroff Publishers and Distributors
- Tisdall JD (2001) Beginning Perl for bioinformatics. Shroff Publishers and Distributors

GENETICS AND GENOMICS

Course Details			
Course Title: Genetics and Genomics			
Course Code	MSBIS2004C04	**Credits**	4
L + T + P	3 +1 + 0	**Course Duration**	One Semester
Semester	Even	**Contact Hours**	45 (L) + 15 (T) Hours
Methods of Content Interaction	Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

The course is designed to provide the students basic understanding of genetics concepts from mendelian to modern era and importance of genome and sequencing technologies.

Learning Outcomes

The student will be able to understand the gene and its modular structure, mutation and its role in genome evolution, genetic and physical map, and complexities in genome sequencing.

Course Contents

Unit 1: **(30% Weightage)**

Mendelian principles: Dominance, segregation, independent assortment, Concept of gene: Allele, multiple alleles, pseudoallele, complementation tests Extensions of Mendelian principles: Codominance, incomplete dominance, gene interactions, pleiotropy, genomic imprinting, penetrance and expressivity, phenocopy, linkage and crossing over, sex linkage, sex limited and sex influenced characters.

Unit 2: **(20% Weightage)**

Mutation: Types, causes and detection, mutant types – lethal, conditional, biochemical, loss of function, gain of function, germinal verses somatic mutants, insertional mutagenesis. Structural and numerical alterations of chromosomes: Deletion, duplication, inversion, translocation, ploidy and their genetic implications. Recombination: Homologous and non-homologous recombination including transposition.

Unit 3: **(30% Weightage)**

Genome sequencing: Genetic and physical mapping. Molecular markers: RFLP, RAPD, AFLPs, SSRs. Recombinant DNA technology: Cloning strategies, vectors: YAC and BAC, screening of recombinants. Methods of DNA sequencing: Sanger's/dideoxy method, Maxam-Gilbert/chemical method. Sequence assembly: shotgun and clone contig approach.

Unit 4: **(20% Weightage)**

Next Generation sequencing & assembly: NGS Platforms based on pyrosequencing, sequencing by synthesis, emulsion PCR approach with small magnetic beads and single molecule real time (SMRT) sequencing; Genome assembly algorithms, De-novo assembly algorithms.

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
1-3	Mendelian principles: Dominance, segregation, independent assortment
4-5	Concept of gene: Allele, multiple alleles, pseudoallele, complementation tests
6-7	Extensions of Mendelian principles: Codominance, incomplete dominance
8-9	Gene interactions, pleiotropy, genomic imprinting, penetrance and expressivity, phenocopy
10-11	Linkage and crossing over
12	Sex linkage, Sex limited and sex influenced characters
13	Mutation: Types, causes and detection
14	Mutant types – lethal, conditional, biochemical

15	Continuous Assessment (Class test I)
16	Loss of function, gain of function
17	Germinal verses somatic mutants
18	Insertional mutagenesis
19	Structural and numerical alterations of chromosomes
20	Deletion, duplication, inversion, translocation
21	Ploidy and their genetic implications
22-23	Recombination: Homologous and non-homologous recombination including transposition
24-25	Genome sequencing: Genetic and physical mapping
26-27	Molecular markers: RFLP, RAPD, AFLPs, SSRs
28	Recombinant DNA technology: Cloning strategies
29-30	Vectors: YAC and BAC
31	Screening of recombinants
32	Methods of DNA sequencing: Sanger's/dideoxy method, Maxam-Gilbert/chemical method
33-34	Sequence assembly: shotgun and clone contig approach
35	Continuous Assessment (Class test II)
36-37	Next Generation sequencing & assembly
38	NGS Platforms based on pyrosequencing
39	Sequencing by synthesis
40	Emulsion PCR approach with small magnetic beads
41	Single molecule real time (SMRT) sequencing
42-43	Genome assembly algorithms
44	De-novo assembly algorithms
45	Revision of required topics and Continuous Assessment (Assignment)

Suggested References:

- Booker R (2011) Genetics: Analysis and Principles. McGraw-Hill
- Brown TA (2000) Genomes 2. BIOS Scientific Publishers Ltd
- Gardner EJ, Simmons MJ, Snustad DP (2006) Principles of Genetics. Wiley
- Primrose SB, Twyman RM (2006) Principles of Gene Manipulation and Genomics. Oxford

press

- Watson JD, Baker TA, Bell SP, Gann A, Levine M, Losick R (2014) Molecular Biology of the Gene (7th Edition). Pearson
- Weaver RF (2007) Molecular biology. McGraw-Hill Higher Education

Evolution and Molecular Phylogeny

Course Details			
Course Title: Evolution and Molecular Phylogeny			
Course Code	MSBIS2005C04	Evolution and Molecular Phylogeny	4
L + T + P	3 + 1 + 0	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	45 (L) +15(T)
Methods of Content Interaction	Lecture, Tutorials, Practical, Group discussion; self-study, seminar, presentations and assignment class based as well as take-home type by students,		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

- To understand the concept & fundamental of classical evolution principles and theories.
- To understand Molecular basis of Evolution, theories, Phylogeny and molecular clock.
- To be able to explain the various approaches and algorithm to inferring molecular phylogeny among organisms.

Learning Outcomes

- The Students will be able to understand the theoretical aspects of classical, molecular evolution and applications.
- Measuring the rate of evolution and concept of molecular clock hypothesis.
- Various algorithms and their comparison for deducing phylogenetic tree among species.

Course Contents

Unit 1: **(33 % Weightage)**

Foundations in Molecular Evolution: Evolution, natural selection, convergent evolution, co-evolution. Evolution of genes in populations. Hardy-Weinberg equilibrium. Mutation; Migration;

Selection; Genetic drift; measures of genetic diversity. The neutral and nearly-neutral theories of molecular evolution.

Unit 2: **(33 % Weightage)**

Evolution of genome and gene families: Lateral gene transfer and transposition. Chromosomal evolution: Genome duplications, Domain shuffling, concerted evolution and molecular drive Calculating evolutionary distances among sequences; correlation and models. Molecular clocks. Molecular phylogenetics: Concepts, types of trees, rooting, clades, reconstructing character evolution, consensus trees. Parsimony and distance based phylogenetic methods, Maximum likelihood and Bayesian phylogenetics.

Unit 3: **(34 % Weightage)**

Phylogenetic analysis algorithms: Distance-based: UPGMA, Neighbor-Joining, Maximum Parsimony, Reliability of trees: Bootstrap, Jackknife, randomization tests. Phylogenetic trees and their comparison: Definition and description, various types of trees; Consensus tree, Data partitioning and conation, Robinson-Foulds distance, Patristic distance. Probabilistic models and associated algorithms: Probabilistic models of evolution, Maximum likelihood algorithm.

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
(Unit I)1-2	Concept of organic Evolution, theories of evolution, natural selection
2-4	Convergent evolution, co-evolution. Evolution of genes in populations..
5-6	Hardy-Weinberg equilibrium.
7-10	Mutation; Migration; Selection; Genetic drift; measures of genetic diversity
11-14	The neutral and nearly-neutral theories of molecular evolution.
(Unit II)15-17	Evolution of genome and gene families: Lateral gene transfer and transposition
17-20	Chromosomal evolution: Genome duplications, Domain shuffling, concerted evolution and molecular drive
21	**CONTINUOUS ASSESSMENT : 01**
22-25	Calculating evolutionary distances among sequences; correlation and models. Molecular clocks hypothesis.

26-28	Concepts, types of trees, rooting, clades, reconstructing character evolution, consensus trees.
28-30	Parsimony and distance based phylogenetic methods, Maximum likelihood and Bayesian phylogenetics.
22-24	Calculating evolutionary distances among sequences; correlation and models & Molecular clocks.
25-27	Concepts, types of trees, rooting, clades, reconstructing character evolution, consensus trees.
28-29	Parsimony and distance based phylogenetic methods, Maximum likelihood and Bayesian phylogenetics.
30	**CONTINUOUS ASSESSMENT : 02**
31-33	Phylogenetic analysis algorithms: Distance-based: UPGMA, Neighbor-Joining
34-37	Maximum Parsimoney, Maximum likelihood
38-40	Reliability of trees: Bootstrap, Jackknife, randomization tests.
41-43	Various types of trees; Consensus tree, Data partitioning and conation, Robinson-Foulds distance,
44-45	Probabilistic models and associated algorithms: Probabilistic models of evolution, Maximum likelihood algorithm.
46	**CONTINUOUS ASSESSMENT : 03**
15 Hours	**Tutorial**

Suggested References:

5. Dan G, Wen-Hsiung L (2001) Fundamentals of molecular evolution. Willey-VCH
6. Marco S, Anne-Mieke V (2003) The phylogenetic handbook: a practical approach to DNA and protein phylogeny. Cambridge University Press
7. Takahata N, Clark AG (1993) Mechanisms of molecular evolution: introduction to molecular paleopopulation biology. Japan Scientific Societies Press and Sinauer Associates
8. Bernardi G (2005) Structural and evolutionary genomics, Volume 37: natural selection in genome evolution (new comprehensive biochemistry). Elsevier Science, Netherland
9. Ahron Oren (2010) Molecular phylogeny of Microorganism. Academic press
10. Nei & Sudhir Kumar (2000) Molecular Evolution and Phylogenetics. Oxford University Press

Chemoinformatics and Drug Design

Course Details			
Course Title: **Chemoinformatics and Drug Design**			
Course Code	MSBIS3001C04	**Credits**	4
L + T + P	3 + 0 + 1	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	45 (L) + 30(P) Hours
Methods of Content Interaction	Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students, individual and group drills, group and individual field based assignments followed by research paper presentation.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

- To train students in the area of drug discovery & chemoinformatics for pharmaceutical research. The course is designed to provide basic understanding of computational drug design and applicability of tools for novel drug discovery.

Learning Outcomes

- Students would be able to get insights on the modern drug discovery and development process. Students would be able to develop basic skills in drug design and apply it in pharmaceutical industry.

Course Contents

UNIT I: Chemoinformatics & chemical data formats **(25% Weightage)**

Introduction to Chemoinformatics: aims and scope. Role of Chemoinformatics in pharmaceutical/chemical research. Chemical Structure representation: 1D, 2D and 3D structures; Molecular file formats (SMILES, InChI, WLN, SDF, MOL, CIF), Chemical Structure based

Search techniques: Exact, Substructure and similar structure searches. Molecular Descriptors (1D, 2D and 3D), Topological, electrotopological and shape indices.

UNIT II: Ligand-based Drug Design **(25% Weightage)**

Chemical Databases and Retrieval methods. Molecular Database Screening: (Lipinski Rule: Drug/Lead like molecules), IC_{50}, pIC50, Ki, LD_{50}, History of SAR & QSAR, Quantitative Structure Activity/Property/Toxicity Relationship Studies: 2D & 3D QSAR, CoMFA and CoMSIA, Training & Test Data sets, validation, Pharmacophore Modelling: Pharmacophore definition and classes (HBA, HBD, Aromatic etc.), Identification of pharmacophore features, Building 2D/3D pharmacophore hypothesis, Searching databases using pharmacophores, receptor-based pharmacophores, Shape-based screening.

UNIT III: Structure-Based Drug Design: **(25 % Weightage)**

Structure-Based Drug Design: Molecular Targets, GPCR as important Drug target. Agonists and antagonist, Lead identification & optimization, Active site analysis, Molecular Docking, Protein & Ligand preparation, Rigid and flexible (induced-fit) & quantum polarized docking, Virtual screening and analysis of results, Compound Library ZINC, Maybridge Pubchem, Asinex, Library generation (focused & diverse). Combinatorial & Fragment libraries: Molecular Scaffolds, combinatorial library generation. Scaffold hoping, *de novo* ligand design.

UNIT IV: Computational medicinal chemistry: **(25% Weightage)**

Computational medicinal chemistry: Approaches & various phases of novel drug discovery, Clinical trials, Classification of drug, Multidrug Resistance (MDR), pharmacokinetics: introduction to drug absorption, disposition, metabolism, elimination, toxicity (ADMET), ADMET and molecular properties prediction, prediction of site of metabolism (SOM), concept of prodrug & soft drug. Pharmacodynamics: mechanism of drug action, dose-response relationship, drug potency and efficacy, Pharmacogenetics: the genetics of drug metabolism, Introduction to biologics, Residue scanning, hot-spot identification, antibody design and modelling.

List of Practical

- Practical session for chemical structure representation and storage in special file formats (SMILES,WLN, sd and mol).
- Importance of 3D structures and method of generation from 1D & 2D representations.
- Substructure/Exact/similar structure based searching.
- Property based search of molecular databases.

- Quantitative Structure Activity/Property/Toxicity Relationship Studies.
- Pharmacophore hypothesis and searching.
- Virtual screening and Docking studies (Rigid, Flexible & library based).
- Design and analysis of focused combinatorial and fragment library.
- De-novo drug designing.
- Drug target and Vaccine target identification
- Residue scanning of Barnease-Barster protein interface and hot-spot identification

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
Unit-1 Lect-1-2	Introduction to Chemoinformatics: aims and scope. Role of Chemoinformatics in pharmaceutical/chemical research.
3-7	Role of Chemoinformatics in pharmaceutical/chemical research. Chemical Structure representation: 1D, 2D and 3D structures; Molecular file formats (SMILES, InChI, WLN, SDF, MOL, CIF)
8	Chemical Structure based Search techniques: Exact, Substructure and similar structure searches.
9-12	Molecular Descriptors (1D, 2D and 3D), Topological, electrotopological and shape indices.
Unit-2 Lect-13	Chemical Databases and Retrieval methods.
14	Molecular Database Screening: (Lipinski Rule: Drug/Lead like molecules),
15-17	History of SAR & QSAR, CoMFA and CoMISA,
18	IC_{50}, Ki, LD_{50},
19	Quantitative Structure Activity/Property/Toxicity Relationship Studies: 2D & 3D QSAR, Training & Test Data sets, validation,
20-23	Pharmacophore Modelling: Pharmacophore definition and classes (HBA, HBD, Aromatic etc.), Identification of pharmacophore features, Building 2D/3D pharmacophore hypothesis, Searching databases using pharmacophores, receptor-based pharmacophores, Shape-based

	screening.
Unit-3 24	Molecular Targets, GPCRs. Enzyme kinetics and interaction of enzymes with inhibitors, agonists and antagonist
25	Lead identification & optimization
26-29	Active site analysis, Molecular Docking, Protein & Ligand preparation and conformational analysis, Rigid and flexible (induced-fit) & quantum polarized docking
30-31	Virtual screening and analysis of results, Compound Library ZINC, Maybridge etc.,
32-34	Library generation (focused & diverse). Combinatorial & Fragment libraries: Molecular Scaffolds, Reagents-based combinatorial library generation. Scaffold hoping, Fragment-based, *Denovo* design
Unit-4 35-36	Computational medicinal chemistry: Approaches & various phases of novel drug discovery, Clinical trials, Classification of drug, antibiotics, antimalarial, antifungal, antidepressant, narcotics, sedatives, hypnotics, anxiolytics, Multidrug Resistance (MDR),
38-40	Pharmacokinetics: introduction to drug absorption, disposition, metabolism, elimination, toxicity (ADMET), ADMET and molecular properties prediction, prediction of site of metabolism (SOM), concept of prodrug & soft drug.
41-42	Pharmacodynamics: mechanism of drug action, dose-response relationship, drug potency and efficacy,
43-45	The genetics of drug metabolism. Introduction to biologics, Residue scanning, hot-spot identification, antibody design and modelling

- Suggested References:

1. Barry AB, Brian S, Guillermo M, Jürgen B (2006) Chemoinformatics: Theory, practice, & products. Springer
2. Holtje HD, Sippl D, Rognan, Folkers G (2008) Molecular modelling basic Principles and applications (3rd Edition). Wiley-VCH
3. Johann G, Engel TE (2003) Chemoinformatics: A Textbook. Wiley-VCH
4. Johann G, Thomas E (2004) Chemoinformatics: A textbook.: Willey-VCH
5. Leach AR, Gillet VJ (2003) An introduction to chemoinformatics. Kluwer

Academic.

6. Osman F Güner (2000) Pharmacophore Perception, Development, and Use in Drug Design. International University Line
7. Thomas L, Raimund M, Hugo K, Hendrik T (2002) Bioinformatics: From genomes to drugs Volume 1: Basic technologies. Wiley-VCH
8. Thomas L, Raimund M, Hugo K, Hendrik T (Series Editor) (2002) Bioinformatics: From genomes to drugs volume II: Applications. Wiley-VCH
9. Young DC (2009) Computational drug design: a guide for computational and medicinal chemists: John Wiley & Sons

Transcriptomics and Proteomics

Course Details			
Course Title: Transcriptomics and Proteomics			
Course Code	MSBIS3002C04	**Credits**	4
L + T + P	3 + 0 + 1	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	45 (L) + 30 (P) Hours
Methods of Content Interaction	Lecture, Group discussion; self-study, seminar, presentations by students, hands-on practical sessions, individual and group drills, seminar presentation.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

The course is designed to provide students the knowledge of current tools and techniques used in transcriptome and proteome research.

Learning Outcomes

Students will be able to understand the nature of transcriptome data, normalize it and perform differential expression analysis. Moreover, students will be able to compare 2D gel images for difference of protein expression.

Course Contents

UNIT I: (25% Weightage)

Goals of transcriptomics experiment. Understanding Microarray and Next generation sequencing data. Types of microarrays. Experimental design for comparing transcriptome, statistical power and number of replicates. Reproducibility of transcriptomic experiments. Data normalization methods.

UNIT II: (25 % Weightage)

Filtering of non-informative probes. Supervised and unsupervised clustering. Cluster validation. Generating Heatmaps. Finding genes differentially expressed between two conditions. Making sense of list of differentially expressed genes, Gene regulatory networks.

UNIT III: **(25 % Weightage)**

Proteome analysis: Proteomics in relation to transcriptomics and Systems Biology. Protein sequencing, Protein identification and characterization: Mass spectrometry. Differential display proteomics: comparison of 2D gel images to identify proteins differentially expressed between two conditions. Number of replicate and reproducibility related issues.

UNIT IV: **(25% Weightage)**

Cell mapping proteomics: finding protein protein interactions, Yeast two hybrid system. Phage display, Protein interaction maps, Protein networks. Protein microarrays, Protein-protein interactions: databases such as STRINGS, DIP, PPI server and tools for analysis of protein-protein interactions.

List of Practicals

- Transcriptome databases.
- Tools for Genomic Data Mining.
- Transcriptome data visualization and processing.
- Biomarker identification: Identification of differentially expressed genes with 'R' and Bioconductor. Analysis of 2D-gel image.
- Gel image manipulation, spot detection and quantification, spot matching, normalization, gel comparison and detection of differentially expressed spots.
- Mass spectrometry data analysis.

Content Interaction Plan:

Lecture cum Discussion **(Each session of 1 Hour)**	**Unit/Topic/Sub-Topic**
1-2	Understanding Microarray and Next generation sequencing data
2-6	Types of microarrays. Experimental design for comparing transcriptome, statistical power and number of replicates
7-10	Reproducibility of transcriptomic experiments. Data normalization methods
10-12	Filtering of non-informative probes. Supervised and unsupervised clustering

13	Cluster validation. Generating Heatmaps
13-16	Finding genes differentially expressed between two conditions
17-19	Making sense of list of differentially expressed genes, Gene regulatory networks
20-24	Proteomics in relation to transcriptomics and Systems Biology. Protein sequencing, Protein identification and characterization
24-30	Mass spectrometry. Differential display proteomics: comparison of 2D gel images to identify proteins differentially expressed between two conditions
31	Number of replicate and reproducibility related issues
32-36	finding protein protein interactions, Yeast two hybrid system
37-38	Phage display, Protein interaction maps
39-41	Protein microarrays, Protein-protein interactions:
42-45	databases such as STRINGS, DIP, PPI server and tools for analysis of protein-protein interactions.
30 Hours	*Practical*

- Suggested References:
- Bernhard OP (2007) Systems Biology: Properties of Reconstructed Networks. Cambridge University Press
- Brown SM (2013) Next-generation DNA sequencing Informatics. Cold Spring Harbor Laboratory Press
- Gentleman R (2005) Bioinformatics and Computational Biology Solutions Using R and Bioconductor. Springer
- Julio CV, Ralf H (2002) Gene Regulation and Metabolism: Post- Genomic Computational Approaches. The MIT Press
- Nelson DL, Cox M (2008) Lehninger Principles of Biochemistry (5th Edition). WH Freeman
- Simpson RJ (2002) Proteins and proteomics: A laboratory manual. Cold Spring Harbor Laboratory Press
- Smyth GK (2005) Limma: linear models for microarray data. In:Bioinformatics and Computational Biology Solutions using R and Bioconductor, Gentleman R, Carey V, Dudoit S, Irizarry R, Huber W (Eds.), Springer, pages 397–420.
- Stekel D (2003) Microarray Bioinformatics. Cambridge University Press
- Voet D, Voet JG, Pratt CW (2006) Fundamentals of Biochemistry: Life at the molecular Level (2nd Edition). John Wiley & Sons
- Wang J (2012) Next Generation Microarray Bioinformatics: Methods & Protocols. Humana Press
- Wang X (2016) Next Generation Sequencing Data Analysis. CRC Press

DBMS AND WEB TECHNOLOGY

Course Details			
Course Title: DBMS and Web Technology			
Course Code	MSBIS3003C04	**Credits**	4
L + T + P	2 + 1 + 1	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	30 (L) + 15 (T) + 30 (P) Hours
Methods of Content Interaction	Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students, individual and group drills, group and individual field based assignments followed by workshops and seminar presentation.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

- This course is intended to provide students with an in-depth understanding of the database management systems and to equip them with design and implementation of database applications.

Learning Outcomes

After completion of the course the learners will be able to:

- Understand basic database concepts of the relational data model. They will be able to construct database queries using SQL and designing web applications using PHP and HTML.

Course Contents

UNIT I: Introduction to databases, Data models and E-R model (25% Weightage)

- Introduction to databases, Database designing, data acquisition, Data Abstraction.
- Data Models: Relational Data Model, Network Data Model, Hierarchical Data Model.
- E-R Model: Entity and entity sets, Relations and relationship sets, E-R diagrams, Reducing E-R Diagrams to tables.

UNIT II: Data normalization, Indexing & Hashing and Data mining (25% Weightage)

- Data normalization, Basic concepts of Indexing and Hashing. Textual Databases, Introduction to Distributed Database Processing, Data warehousing and Data mining.
- Organizing biological species information using various database techniques. Need of meta-data standards.

UNIT III: MySQL Architecture and SQL statements (25% Weightage)

- MySQL Architecture. Objects - Tables, Views, Indexes, Sequences; Synonyms, Snapshots, Clusters. Database - Table space, Data files, Blocks, Extents, Segments; SQL DBA - Export-Import/SQL Monitor Backup & Recovery (Archiving), Physical Storage & Logical Storage.
- Select Statements, Data Definition Statements, Data Manipulation Statements, Data Control Statements.

UNIT IV: Introduction to Web technology, HTML and PHP (25% Weightage)

- Introduction to Web Technology, HTML, Basic Tags, CSS, Table and Forms.
- Introduction to PHP, Syntax, Operators, Variables, Constants, Control structure, Language construct and functions.
- Arrays-Enumerated Arrays, Associative array, array iteration, Multi-dimensional array.
- Array function, Date and Time functions, Web Features- Sessions, Forms, GET and POST data, database programming.

List of Practicals

- Based on "Data Definition Language". A set of SQL commands used to create table, modify table structure, drop table, rename table.

- Based on “Data Manipulation Language” A set of SQL commands used to change the data within the database. It consists of inserting of records in the tables, updation of all or specific set of records in tables, viewing the attributes of table’s column.
- Based on “Data Query Language” It allows extracting the data out of the database. Selecting the data from table using Arithmetic and logical operators. Range searching and pattern matching. Function, group function, scalar function.
- Based on defining Constraints. Types: I/O constraints like Primary Key, Foreign key, Null and Unique constraints. Business constraints like check constraints. Levels: Table level constraints, column level constraints, creating and deletion of constraints using the Alter Table clause.
- Based on using joins. Joining multiple tables, joining a table to itself.
- Based on using Indexes, Sequences.
- Based on Security Management using SQL, Granting rights on user objects such as Tables, Views, and Sequences. Revoking rights on user objects such as Tables, Views, and Sequences.

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
1-2	Introduction to databases, Database designing, data acquisition, Data Abstraction.
3-4	Data Models: Relational Data Model, Network Data Model, Hierarchical Data Model.
5-6	E-R Model: Entity and entity sets, Relations and relationship sets, E-R diagrams, Reducing E-R Diagrams to tables.
7-11	Data normalization, Basic concepts of Indexing and Hashing. Textual Databases. Introduction to Distributed Database Processing. Data warehousing and Data mining.
12-13	Organizing biological species information using various database techniques.

	Need of meta-data standards.
14-16	MySQL Architecture. Objects - Tables, Views, Indexes, Sequences; Synonyms, Snapshots, Clusters. Database - Table space, Data files, Blocks, Extents, Segments; SQL DBA - Export-Import/SQL Monitor Backup & Recovery (Archiving), Physical Storage & Logical Storage.
17-20	Select Statements, Data Definition Statements, Data Manipulation Statements, Data Control Statements.
21-23	Introduction to Web Technology, HTML, Basic Tags, CSS, Table and Forms.
24-26	Introduction to PHP, Syntax, Operators, Variables, Constants, Control structure, Language construct and functions.
27-28	Arrays-Enumerated Arrays, Associative array, array iteration, Multi-dimensional array.
29-30	Array function, Date and Time functions, Web Features- Sessions, Forms, GET and POST data, database programming.
15 Hours	*Tutorials*
15 Hours	*Practicals*

Suggested References:

- Date CJ (1999) An Introduction to Database Systems (6th edition). Addison Wesley
- Ivan B (2003) SQL, PL/SQL The Programming Language of Oracle (2nd Edition). BPB
- Korth H, Silberschatz A (1997) Database System Concepts. Tata Mac-Graw Hill
- Silberschatz A, Korth HF, Sudarshan S (2002) Database system concepts (4th Edition). McGraw-Hill

Minor Project

Course Details			
Course Title: Minor Project (Review of Literature, Seminar and Problem Definition)			
Course Code	MSBIS3004C04	**Credits**	4
L + T + P	0 + 0 + 4	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	60 Hours
Methods of Content Interaction	Self-study and computational/experimental/Field work, seminar, presentations by students, research paper presentation.		
Assessment and Evaluation	• End Term - A seminar on the topic selected by student in consultation with guide. • A Synopsis to be submitted		

Course Objectives

- To orient students towards research methodology
- To introduce students about research problem formulation, planning of experiments
- To develop scientific communication skills

Learning Outcomes

- Students would be able to get insights on the research methodology adopted, and how to formulate the research problems and plan experiments.
- Students would be able to develop scientific communication and presentation skills.

Course Contents

Unit-1 Biological Research in Practice and Scientific Writing/ Presentation (Lectures-2Hr)

Literature Review, Introduction of bibliographic databases, Journals, Scientific resources and search engines, Journal Impact Factor, Citation Index, Writing a Scientific Paper

Unit-2: Self-study and computational/experimental/Field work, seminar presentation

Biochemistry and Immunology

Course Details			
Course Title: Biochemistry and Immunology			
Course Code	MSBIS1001E04	**Credits**	4
L + T + P	3 + 1 + 0	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	45 (L) + 15 (T) Hours
Methods of Content Interaction	Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students, individual and group drills, group and individual field based assignments followed by paper presentation.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

- To develop an understanding of the chemistry of building blocks (carbohydrate, lipids, amino acids and nucleic acids) and biological pathways in terms of regulation.
- To develop an understanding of our immune system, different types of immunity and immune cells. The students will learn about different diseases, immunodiagnostics and therapeutic approaches.

Learning Outcomes

After completion of the course the learners will be able to:

- The student will be able to understand primary catabolic and anabolic pathways pertaining to the carbohydrates, fats/lipids, amino acids, and nucleic acids and to identify the key regulatory points as well as the energetics of the reactions.

- The students will understand the basic concepts of how our immune system works, different techniques and their uses to diagnose the diseases and also think about its remediation employing different immune-based therapies.

Course Contents

UNIT I: Bioenergetics (25% Weightage)

Water as Universal solvent, hydrogen bond, Amino acids, pH, pKa, pI, Carbohydrate, Lipids. Bioenergetics: Laws of Thermodynamics and its Applications; Concept of free energy; High energy compounds; ATP as the main source of free energy in biological systems.

UNIT II: Biochemical Pathways (25% Weightage)

Glycolysis, Gluconeogenesis, Pentose Phosphate Pathway, Metabolism of Glycogen in animals, Citric Acid Cycle, Fatty Acid Catabolism, Oxidative Phosphorylation and Photophosphorylation. Enzymes and enzyme kinetics, enzyme regulation, isozymes.

UNIT III: Basics of Immunology (30 % Weightage)

Innate and adaptive immune system: Cells and molecules involved in innate and adaptive immunity, antigens, antigenicity and immunogenicity. B and T cell epitopes, structure and function of antibody molecules, generation of antibody diversity, monoclonal antibodies, antibody engineering, antigen-antibody interactions, MHC molecules, antigen processing and presentation.

UNIT IV: Applied Immunology (20%Weightage)

T cell receptors, humoral and cell-mediated immune responses, the complement system, Toll-like receptors, inflammation, hypersensitivity and autoimmunity, congenital and acquired immunodeficiencies, vaccines, Bioinformatics Tools and software in Immunology. Antibody generation, Detection of molecules using ELISA, RIA, western blot, immunoprecipitation.

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
	UNIT I: Bioenergetics
1-2	Water as Universal solvent, hydrogen bond etc
3-6	Amino acids, pH, pKa and pI,
7-9	Carbohydrate and Lipids.
10-11	Bioenergetics: Laws of Thermodynamics and its Applications; Concept of free energy; High energy compounds; ATP as the main source of free energy in biological systems.
	UNIT II: Biochemical Pathways
11-12	Glycolysis, Gluconeogenesis,
13-14	Metabolism of Glycogen in animals
15	Citric Acid Cycle,
16-18	Fatty Acid Catabolism,
18-19	Oxidative Phosphorylation and Photophosphorylation
20-23	Enzymes and enzyme kinetics, enzyme regulation, isozymes.
	UNIT III: Basics of Immunology
24-25	Innate and adaptive immune system, Cells and molecules involved in innate and adaptive immunity
26	Antigens, antigenicity and immunogenicity
27	B and T cell epitopes
28-29	Structure and function of antibody molecules
30	Generation of antibody diversity
31	Monoclonal antibodies
32	Antibody engineering, antigen-antibody interactions
33	MHC molecules

34-35	Antigen processing and presentation.
	UNIT IV: Applied Immunology
36-37	T cell receptors, humoral and cell-mediated immune responses
38	The complement system, Toll-like receptors
39-40	Inflammation, hypersensitivity and autoimmunity, congenital and acquired immunodeficiencies
41-42	Vaccines, Bioinformatics Tools and software in Immunology
43-44	Antibody generation, Detection of molecules using ELISA, RIA,
45	Western blot, immunoprecipitation
15 Hours	*Tutorials*

- **Suggested References:**
- Anastasi A. (1976). *Psychological testing*(4th ed.). New York: McMillan Pub Co.
- Bloom, B. S., Hastings, J. H., & Madaus, G. F. (1971). *Handbook on formative and summative evaluation of student learning*. New York: McGraw Hill.
- Cronbach, L. J. (1950).*Essentials of psychological testing*(3rded.). New York: Harper & Row publishers.
- Ebel, R. L.,&Frisbei, D. A. (1986).*Essentials of educational measurement.* New Delhi: Prentice Hall.
- Freeman, F. S. (1976). *Theory and practice of psychological testing*,(3rded.). New Delhi: Oxford & IBH Pub. Co.
- Guilford, J.P. (1954). *Psychometric methods*. New York: McGrawHill.
- Miller, M. D., Linn, R. L., & Gronlund, N. E. (2009). *Measurement and assessment in teaching* (10th ed.). New Jersey: Pearson Education Inc.
- Singh, A. K. (1986). *Tests, measurement and research methods in behavioural sciences.* New Delhi: McGraw Hill.
- Kindt T. J., Osborne B. A. and Goldby R. A. (2013) Kuby Immunology, 7th Edition.
- Delves P., Martin S., Burton D. and Roitt I (2011) Roitt's Essential Immunology (Essentials), 12th Edition.
- Murphy K. (2011) Janeway's Immunobiology, 8th Edition.

Whole exome sequencing data analysis

Course Details			
Course Title: Whole exome sequencing data analysis			
Course Code	MSBIS2001E04	**Credits**	4
L + T + P	3 + 0 + 1	**Course Duration**	One Semester
Semester	Even	**Contact Hours**	45 (L) + 30 (P) Hours
Methods of Content Interaction	Lecture, Group discussion; self-study, seminar, presentations by students, hands-on practical sessions, individual and group drills, group and individual field based assignments followed by workshops and seminar presentation.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

- To acquaint the students with the basic concepts and practices adopted for whole exome sequencing data analysis.
- To help the students understand, how WES helps to bridge cutting edge science and the delivery of genomic medicine in clinical practice.
- To orient the students with tools and techniques of WES data analysis.
- To develop skills and competencies to analyze and interpret WES data.
- To make the students understand how genomic medicine has impacted on a patients diagnosis, care and or treatment.

Learning Outcomes

After completion of the course the learners will be able to:

- Describe the wider issues affected by whole exome sequencing and Bioinformatics.

- Define the challenges and opportunities facing bioinformaticians in WES data analysis.
- Describe the steps involve in WES data analysis workflow.
- Explain how WES data is taken from the computational level to the human level
- Describe the importance of accuracy and precision in genomic data analysis.
- Evaluate quality of read sequences generated by NGS experiments.
- Align read sequences to reference genome.
- Perform variant calling given aligned read sequences.
- Triaging the variants.

Course Contents

UNIT I: Whole Exome sequencing data acquisition (25% Weightage)

- Exome sequencing techniques: Library preparation, Exome enrichment methods, cluster generation, sequencing and base calling.
- File format for sequencing data: FASTQ, BAM, SAM, VCF.

UNIT II: Exome data processing (25 % Weightage)

- Exome data analysis pipeline
- Quality control for raw read data: Phred quality score, FASTQC tool
- Tools for sequence read alignment: HISAT2 and Bowtie.
- Refining the alignment

UNIT III: Variant detection (25 % Weightage)

- Variant calling algorithms, variant annotation
- Removing common variants.
- Databases that capture the frequency of different variations in the population.

UNIT IV: Exome sequencing and ethical issues (25% Weightage)

- What is ethics and governance? Who owns the data?
- Difference between privacy and confidentiality.
- Data sharing and the law

List of Practicals

- Examining file format to store NGS data
- Performing quality control checks on raw sequencing reads
- Aligning reads to reference genome
- Variant calling
- Filtering common variants
- Generating repots for clinicians

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
1-2	Exome sequencing over view
3-6	Library preparation, Exome enrichment methods
7-9	cluster generation, sequencing and base calling
10-14	File format for sequencing data: FASTQ, BAM, SAM, VCF
14-15	Exome data analysis pipeline
16	Continuous Assessment I
17-19	Quality control for raw read data: Phred quality score, FASTQC tool
20-28	Tools for sequence read alignment: HISAT2 and Bowtie
29-30	Refining the alignment
31	Continuous Assessment II
32-35	Variant calling algorithms, variant annotation
36-37	Removing common variants
38-39	Databases that capture the frequency of different variations in the population
40-41	What is ethics and governance? Who owns the data?
42-43	Difference between privacy and confidentiality

44	Data sharing and the law
45	Continuous Assessment III
30 Hours	Practical

- Suggested References:

- Brown TA (2000) Genomes 2. BIOS Scientific Publishers Ltd, New York.
- Bruce A, Alexander J, Julian L, Martin R, Roberts K, Peter W (2008) Molecular Biology of the Cell (5th Edition). Garland Science
- Bruce A, Dennis B, Karen H, Alexander JD, Julian, Martin LR, Roberts K, Peter W (2010) Essential Cell Biology (3rd Edition). Garland Science
- Gentleman R (2005) Bioinformatics and Computational Biology Solutions Using R and Bioconductor. Springer.
- Landrum MJ, et al ClinVar: public archive of relationships among sequence variation and human phenotype. Nucleic Acids Res. 2014 Jan 1;42(1):D980-5. PubMed PMID: 24234437.
- Next-generation Sequencing in the Diagnosis of Metabolic Disease Marked by Pediatric Cataract. R. L. Gillespie et al Ophthalmology. 2016 Jan;123(1):217-20.
- Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology Genetics in Medicine 17;5 405-424 doi:10.1038/gim.2015.30.
- Wang J (2012) Next Generation Microarray Bioinformatics: Methods & Protocols. Humana Press
- Wang X (2016) Next Generation Sequencing Data Analysis. CRC Press

BIG DATA ANALYTICS AND HEALTH INFORMATICS

Course Details			
Course Title: BIG DATA ANALYTICS AND HEALTH INFORMATICS			
Course Code	MSBIS3001E04	**Credits**	4
L + T + P	4 + 0 + 0	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	60 (L) Hours
Methods of Content Interaction	Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

This course introduces the student to concepts of big data management, and other techniques that support big data analytics.

Learning Outcomes

- Students will learn to build and maintain reliable, scalable, distributed systems with Apache Hadoop, able to write Map-Reduce based applications, to design and build MongoDB based Big data Applications and learn MongoDB query language.

Course Contents

Unit 1: **(25% Weightage)**

Introduction to distributed file system, Big Data and its importance, Drivers for Big data, Big data applications. Algorithms using Map-reduce, Apache Hadoop & Hadoop EcoSystem, Moving Data in and out of Hadoop - Understanding inputs and outputs of MapReduce, Data Serialization, Relationship and Representations, Graph Databases, Big data analytics: Regression, Clustering & Classification, Building visualizations using Big Data, Case Studies.

Unit 2: **(25% Weightage)**

Introduction to NoSQL, Types of NoSQL databases, Advantages of NoSQL, Use of NoSQL, SQL vs NoSQL, Introduction to MongoDB key features, Core Server tools, MongoDB through the JavaScript's Shell, Creating and Querying through Indexes, Document-Oriented, principles of schema design, Constructing queries on Databases, collections and Documents, MongoDB Query Language.

Unit 3: **(25% Weightage)**

Overview of Medical Informatics, Healthcare Data, Information and Knowledge, Consumer Health Informatics, Online Medical Resources, Search Engines, Evidence Based Medicine and Clinical Practice Guidelines, Disease Management and Registries, Quality Improvement Strategies, Electronic Health Records, Practice Management Systems, Health Information Exchange.

Unit 4: **(25% Weightage)**

Data Standards, Privacy and Security, Health Information Ethics, Mobile Technology, Architectures of information Systems, Patient Safety and Health Information Technology, E-prescribing, Telehealth and Telemedicine, Picture Archiving and Communication Systems, E-Research , Public Health Informatics.

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
1-2	Introduction to distributed file system
3-4	Big Data and its importance
5	Drivers for Big data
6	Big data applications
7-8	Algorithms using Map-reduce
9-10	Apache Hadoop & Hadoop EcoSystem
11	Moving Data in and out of Hadoop, Understanding inputs and outputs of MapReduce
12	Data Serialization, Relationship and Representations, Graph Databases,

13-14	Big data analytics: Regression, Clustering & Classification, Building visualizations using Big Data, Case Studies
15	Continuous Assessment (Class Test I)
16	Introduction to NoSQL
17	Types of NoSQL databases
18	Advantages of NoSQL
19	Use of NoSQL
20	SQL vs NoSQL
21	Introduction to MongoDB key features
22	Core Server tools
23	MongoDB through the JavaScript's Shell
24-25	Creating and Querying through Indexes, Document-Oriented
26	Principles of schema design
27-28	Constructing queries on Databases
29	Collections and Documents
30	MongoDB Query Language
31	Overview of Medical Informatics, Healthcare Data
32	Information and Knowledge
33	Consumer Health Informatics
34	Online Medical Resources
35	Search Engines
35-36	Evidence Based Medicine and Clinical Practice Guidelines
37-38	Disease Management and Registries
39	Continuous Assessment (Class test 2/Assignment/ Problem solving)
40-41	Quality Improvement Strategies, Electronic Health Records
42-43	Practice Management Systems,
44-45	Health Information Exchange.
46	Data Standards
47	Privacy and Security
48	Health Information Ethics

49	Mobile Technology
50	Architectures of information Systems
51-52	Patient Safety and Health Information Technology
53	E-prescribing
54	Telehealth and Telemedicine
55-56	Picture Archiving and Communication Systems,
56-58	E-Research
59	Public Health Informatics
60	Continuous Assessment (Class test 3)

Suggested References:

- Viktor Mayer-Schönberger V, Cukier K (2013) Big Data: A Revolution That Will Transform How We Live, Work and Think. John Murray Publisher
- Banker K (2011) MongoDB in Action. Manning Publications
- Fowler A (2015) NoSQL For Dummies. John Wiley & Sons
- Ibm, Zikopoulos PC, Eaton C, Zikopoulos P (2012) Understanding Big Data: Analytics for Enterprise Class Hadoop and Streaming Data. McGraw-Hill Osborne
- Lublinsky B, Smith KT, Yakubovich A (2015) Professional Hadoop Solutions. Wiley/Wrox
- Sadalage PJ, Fowler M (2013) NoSQL Distilled: A Brief Guide to the Emerging World of Polyglot Persistence. Pearson Education
- White T (2012) HADOOP: The definitive Guide. O’Reilly
- White T (2012) HADOOP: The definitive Guide. O’Reilly
- Degoulet P, Fieschi M (2012) Introduction to clinical informatics. Springer
- John TF, Brian ED (Eds.) (2016) Clinical Informatics Study Guide. Springer
- Karen A, Fand L, Glaser J (2009) Managing Healthcare information systems. Josey bass publishers
- Shortliffe EH, Cimino JJ (2006) Biomedical informatics Computer Applications in health care and biomedicine. Springer

Programming with Python

Course Details			
Course Title: Programming with Python			
Course Code	MSBIS3002E04	Programming With Python	4
L + T + P	2 + 1 + 1	**Course Duration**	One Semester
Semester	Even	**Contact Hours**	30 (L) +15(T) + 30 (P) Hours
Methods of Content Interaction	Lecture, Tutorials, Practical Group discussion; self-study, seminar, presentations and assignment class based as well as take-home type by students,		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

- Enable students with Python Scripting.
- Identify/characterize/define a problem
- Design a program to solve the problem
- Create executable code
- Hone students programming capability to write scripts to solve bioinformatics problems

Learning Outcomes

- After completion of the course the learners will be able to:
- Understand Python programming syntax
- Apply python programming on various algorithm
- Able to write python scripts for various bioinformatics applications.

Course Contents

Unit 1: (35 % Weightage)

Introduction to python programming, Keywords & Identifier, Statements & Comments, Python Data Types (numbers, lists, tuples string and dictionary), Python I/O and Import, Python Operators and Operator Precedence, Conditional Statements if...else, for and while, loop, break and continue, Pass Statement, File Handling in python: File Operation (open, reading writing and closing of files), Directory handling, Use defined exception and it's handling.

Unit 2: (35 % Weightage)

Python functions: syntax, function call, types of functions, function arguments, recursion, anonymous functions, python module and packages, import and reloading module, importing module from packages, Object & Class in python: defining an Object and class in python, deleting attributes and objects, namespace and variable scopes, concept of python class, inheritance and method overriding, multiple inheritances, resolution order.

Lists of Practicals

- Python installation, Calling python from terminal
- Python Syntax
- Datatype and variables in Python,
- Conditional and Logical statements in Python
- Loops in Python (If, For, While Break and continue)
- File handling and file operation in Python
- Directory handling and its operation in Python
- Function, definition and calling
- Python modules and packages and its integration

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
(Unit I)1-2	Introduction to python programming, Keywords & Identifier, Statements & Comments
2-5	Python Data Types (numbers, lists, tuples string and dictionary)
5-6	Python I/O and Import, Python Operators and Operator Precedence

7-10	Conditional Statements if...else, for and while, loop, break and continue, Pass Statement
11-15	File Handling in python: File Operation (open, reading writing and closing of files), Directory handling, Use defined exception and it’s handling.
16	**CONTINUOUS ASSESSMENT : 01**
(Unit –II) 17-18	Python functions: syntax, function call, types of functions
18-19	Function arguments, recursion, anonymous functions, python
19-20	Python module and packages, import and reloading module, importing module from packages,
20-21	Object & Class in python: Defining an Object and class in Python,
21-22	Deleting attributes and objects, namespace and variable scopes,
22-26	Concept of python class, inheritance and method overriding,
27-29	Multiple inheritances, resolution order
30	**CONTINUOUS ASSESSMENT : 02**
15 Hours	**Tutorial**
30 hours	Practicals

Suggested References:

- David M, Beazley DM (2009) Python Essential Reference (4th Edition). Pearson Addison-Wesley Professional
- Downey AB (2009) Think Python: An Introduction to Software Design. Create Space Independent Publishing Platform
- Lutz M (2009) Learning Python (5th Edition). O’Reilly
- Kenneth A. Lambert, The Fundamentals of Python: First Programs, 2011, Cengage Learning, ISBN: 978-1111822705.

Systems Biology

Course Details			
Course Title: Systems Biology			
Course Code	MSBIS3003E04	**Credits**	4
L + T + P	2 + 1 + 1	**Course Duration**	One Semester
Semester	Odd	**Contact Hours**	30 (L) +15 (T)+ 30 (P)
Methods of Content Interaction	Lecture, Tutorials, Group discussion; self-study, seminar, presentations by students, individual and group drills, group and individual field based assignments followed by paper presentation.		
Assessment and Evaluation	• 30% - Continuous Internal Assessment (Formative in nature but also contributing to the final grades) • 70% - End Term External Examination (University Examination)		

Course Objectives

This course will provide an introduction to systems biology by focusing on the behaviors expected from interactions between only a few genes, taking examples from microbes to mammals. Cells are dynamic systems, and we will build intuition about the types of responses expected from different gene circuits by running, adapting, and analysing computer simulations. Throughout, the course will use such simulations and analysis as research tools to understand biology. After an introduction to motifs and modules, we will focus on the role of feedback in genetic networks and how feedback can sometimes create permanent switches, in, for example, stem cells, or at other times can generate oscillations such as circadian rhythms in neurons. We will show how these behaviors can be undermined when numbers of molecules become low, an effect that cells may exploit or regulate away. Finally, we discuss experimental techniques that allow direct comparison between simulations and real biological systems. Finally overall aims is to understand, design principles of biological circuits i.e. transcriptional, signal transduction, neuronal and developmental networks in unified way.

Learning Outcomes

- Students will gain an appreciation of how interactions between genes can explain some of the behaviour we see in cells.
- Students will gain an understanding of the different behaviours expected in dynamical systems and how to biochemically code for some of these behaviours.
- Students will develop skills in simulation and learn how to use computers as tools to help decide between different hypotheses

Course Contents

UNIT I: The Assessment and Evaluation Process (50% Weightage)

Gene Networks basic concepts, Transcription Networks: Basic concepts, Auto-regulation a network motif AR and NAR , The Feed-Forward Loop Network Motif, Coherent and In coherent FFL, Temporal programme and the global structure of transcription network, Network motifs in developmental, signal transduction and neuronal networks.

UNIT II: Tools of Assessment and Evaluation (50% Weightage)

FIFO, DOR, Global, Development, memory and irreversibility- signaling networks and neuron circuits-robustness,Robustness of protein circuits: The example of bacterial Chemotaxis, Robust patterning in development, Kinetic proofreading, Optimal Gene circuit design, Demand rules for gene regulation, Epilogue: simplicity in biol ogy, Cell Designer and SBML.

List of practicals

- Study of models in systems Biology, Defining model, Reaction Network, reaction kinetics, Kinetic law, paramer, and simulation
- Simulation and analysis of transcription network, signal transduction network, developmental network and metabolic network in cell designer/ cytoscape. Interpretations of simulation results biological context.
- Map Kinase and M Phase of cell Division Pathways simulation and interpretation.

Content Interaction Plan:

Lecture cum Discussion (Each session of 1 Hour)	**Unit/Topic/Sub-Topic**
Unit-1 1-5	Gene Networks basic concepts, Transcription Networks: Basic concepts, Auto-regulation a network motif AR and NAR , The Feed-Forward Loop Network Motif.
6-10	Temporal programme and the global structure of transcription network,
11-15	Coherent and In coherent FFL, Network motifs in developmental, signal transduction and neuronal networks.
Unit-2 16-17	FIFO, DOR, Global, Development
17-18	Memory and irreversibility of developmental network
19-20	signaling networks and neuron circuits
21-23	,Robustness of protein circuits: The example of bacterial Chemotaxis,
23-25	robustnessRobust patterning in development,
25-27	Kinetic proofreading,
27-29	Optimal Gene circuit design,
30	Demand rules for gene regulation, Epilogue: simplicity in biology,
15 Hours	Tutorials
Suggested References: • An introduction to systems biology, u alon (chapman & hall, 2006) • First steps in computational systems biology: a practical session in metabolic modeling and simulation*biochemistry and molecular biology education vol. 37, no. 3, pp. 178–181, 2009 https://iubmb.onlinelibrary.wiley.com/doi/pdf/10.1002/bmb.20281 • First steps in computational systems biology: a practical session in metabolic modeling and simulation. https://www.ncbi.nlm.nih.gov/pubmed/21567728	