SRM
UNIVERSITY
(Under section 3 of UGC Act 1956)

M. Tech. (Full Time) - GENOME INFORMATICS
CURRICULUM & SYLLABUS (2014-2015)

DEPARTMENT OF BIOINFORMATICS
SCHOOL OF BIOENGINEERING
FACULTY OF ENGINEERING & TECHNOLOGY
SRM UNIVERSITY, KATTANKULATHUR, CHENNAI
TAMIL NADU, INDIA 603 203

DEPARTMENT OF DEPARTMENT OF BIOINFORMATICS
SRM UNIVERSITY
M.Tech. GENOME INFORMATICS (FULL TIME)
CURRICULUM & SYLLABUS (2014-2015)

Semester I

Code	Category	Course	L	T	P	C
GI2001	C	Structural and Functional Genomics	3	0	2	4
GI2002	C	Genome Analysis	3	0	2	4
GI2003	C	Scripting languages for Genomics	3	0	2	4
MA2016	S	Numerical and Bio statistical Methods	3	0	0	3
E1	E	Program Elective I	3	0	0	3
Total			16	0	6	18
Total contact hours			22			18

Semester II

Code	Category	Course	L	T	P	C
GI2004	C	Next Generation Sequencing and Analysis	3	0	2	4
GI2005	C	Algorithms for Life Sciences	3	2	0	4
GI2006	C	R Programming	3	0	2	4
E2	E	Program Elective II	3	0	0	3
E3	E	Program Elective III	3	0	0	3
Total			15	2	6	18
Total Contact Hours			23			18

SEMESTER III

Code	Category	Course	L	T	P	C
E4	E	Program Elective IV	3	0	0	3
E5	E	Program Elective V	3	0	0	3
E6	E	Program Elective VI	2	0	2	3
E7	E	Interdisciplinary Elective	3	0	3	3
GI2047	C	Seminar	0	0	1	1
GI2048	C	Industrial Training	0	1	1	1
GI2049	P	Project – Phase I	0	0	12	6
Total			10	1	20	20
Total contact hours			31			20

SEMESTER IV

Code	Category	Course	L	T	P	C
GI2050	P	Project -- Phase II	0	0	32	16
Total						
Total contact hours			32			16
Total credits to be earned for the award of degree			72			

C - Core Course
PE - Program Elective
S- Supportive Course
IE- Interdisciplinary Elective

CONTACT HOUR/CREDIT:
L : Lecture Hours per week
P : Practical Hours per week
T: Tutorial Hours per week
C: Credit

ELECTIVES

	Code	Course	L	T	P	C
1	GI2101	Human Genetics	3	0	0	3
2	GI2102	Cancer Genomics	3	0	0	3
3	GI2103	Genome Technologies	3	0	0	3
4	GI2104	Genetic Diseases & Disorders	3	0	0	3
5	GI2105	Medical Annotation of SNPs	3	0	0	3
6	GI2106	Applications of Next Generation Sequencing Technologies	3	0	0	3
7	GI2107	Genetic Counseling & ELSI	3	0	0	3
8	GI2108	Metagenomics	3	0	0	3
9	GI2109	Database Management Systems	3	0	0	3
10	GI2110	Molecular Diagnostics	3	0	0	3
11	GI2111	Agri-genomics	3	0	0	3
12	GI2112	Epigenetics & Epigenomics	3	0	0	3
13	GI2113	1000 Genome Project	3	0	0	3
14	GI2114	Pharmacogenomics and Personalized Medicine	3	0	0	3
15	GI2115	Microarray Bioinformatics	3	0	0	3
16	GI2116	High Performance & Cloud computing	3	0	0	3
17	GI2117	Perl For Genomics	2	0	2	3
18	GI2118	Python	2	0	2	3

SEMESTER I

Course Code	Course Title	L	T	P	C
GI2001	STRUCTURAL AND FUNCTIONAL GENOMICS	3	0	2	4
	Total Contact Hours- 75				

PURPOSE
This course imparts knowledge on understanding genomes, sequences, and how all genes contribute to life, as opposed to single genes. This course aims to provide a state of the art working knowledge of these techniques, including: comparative genomics, microarray expression analysis .The detailed analysis of the techniques involved for quantifying gene will enable students to perform the assays for detection of gene expression.
INSTRUCTIONAL OBJECTIVES
To acquire the knowledge about genome anatomies
To understand the techniques of genomics to study gene expression.
To apply the techniques to study gene expression

UNIT I - GENOME ANATOMIES (9 Hours)

Genomes, Transcriptomes and Proteomes, The Human Genome, Why is the Human Genome Project Important? Genome Anatomies, an Overview, the Anatomy of the Eukaryotic and Prokaryotic Genome, the Repetitive DNA Content of Genomes. How genes work, Gene-protein relations, Genetic fine structure, Mutational sites Complementation

UNIT II - GENOME MAPPING AND COMPARISION (9 Hours)

Mapping Genomes, Genetic and Physical Maps, Sequencing Genomes, the Methodology for DNA Sequencing, Assembly of a Contiguous DNA Sequence, understanding a Genome Sequence, Locating the Genes in a Genome Sequence, Determining the Functions of Individual Genes, Global Studies of Genome Activity, comparative genomics

UNIT III - GENOME EXPRESSION AND REGULATION (9 Hours)

How Genomes Function, Accessing the Genome, Inside the Nucleus, Chromatin Modifications and Genome Expression, Assembly of the Transcription Initiation Complex, The Importance of DNA-binding Protein-DNA-Protein Interactions During Transcription. Initiation-Regulation of Transcription, Synthesis and Processing of the Proteome, The Role of tRNA in Protein Synthesis, The Role of the Ribosome in Protein Synthesis, Post-translational Processing of Proteins, Protein Degradation. RNA polymerase II, Cofactors, Chromatin, HATS and HDACS, Core promoter

elements in Transcription, Transcriptional Activators, Repressors, Cytokine regulated transcription, Nuclear receptors, HOX genes, NF-κB. Methods for gene expression analysis; DNA array for global expression profile; Types of DNA arrays, Array databases; Applications of DNA microarray

UNIT IV - THE HUMAN GENOME AND MOLECULAR PHYLOGENY (9 Hours)

How Genomes Evolve, Acquisition of New Genes, Non-coding DNA and Genome Evolution, The Human Genome: the Last 5 Million Years- Molecular Phylogenetics- Origins, Applications of Molecular Phylogenetics

UNIT V - RNA WORLD AND ITS STRUCTURE (9 Hours)

Riboswitches and the RNA World, Riboswitches: Structures and Mechanisms, Ribozymes, Noncoding RNPs of Viral Origin, Spliceosome Structure and Function, Folding and Finding RNA Secondary Structure, Predicting and Modeling RNA Architecture, *In Vivo* RNAi, miRNA biogenesis, miRNA in human disease-cancer, cardiovascular, metabolic disorders, epigenetics- miRNA as therapeutic targets. Principles, Technical Considerations in the Use of iRNA- Design and Synthesis of Small Interfering RNAs, Applications of iRNA to Establishing Gene Function- Signal Transduction, Therapeutic Applications of iRNA, in Biology and Medicine.

LIST OF EXPERIMENTS (30 Hours)

1. Genomic DNA Isolation
2. PCR Amplification
3. Contig Assembly
4. DNA Sequencing
5. Mapping In Bacterial System Conjugation
6. RFLP
7. RAPD
8. Detection Of SNPs
9. Physical Mapping of the Genome

TEXTBOOKS

1. Primrose S.B. and Twyman R.M, *"Principles of Gene Manipulation and Genomics"*, Blackwell Publishing Company, Oxford, UK, Seventh Edition, 2006.
2. Sahai S. *"Genomics and Proteomics",* Functional and Computational Aspects, Kluwer Academic Publishers, New York, 2002.

REFERENCES

1. Baxevanis A.D. and B.F. Francis Ouellellette, *"Bioinformatics A Practical"* Guide to the Analysis of Genes and Proteins, John Wiley & Sons, UK, Third Edition, 2005.
2. Jonathan Pevsner, *"Bioinformatics and Functional Genomics"*, John Wiley & Sons, Second Edition, 2009.

Course Code	Course Title	L	T	P	C
GI2002	GENOME ANALYSIS	3	0	2	4
	Total Contact Hours – 75				

PURPOSE
This course is designed to give a opportunity to study the sequence alignment methods and apply this knowledge to analyze data in research
INSTRUCTIONAL OBJECTIVES
To learn the basic databases and data formats
To grasp the significance of sequence alignment methods
To Understand the concept of phylogenetic analysis

UNIT I - SEQUENCE FORMATS (9 Hours)

DNA Sequencing databases, Sequence analysis programs, Pairwise sequence alignment, Multiple sequence alignment, The first complete genome sequence and database, DNA sequencing, Genomic sequencing, Sequencing cDNA Libraries of expressed genes, Accuracy and computers storage of sequence, Sequence formats, Conversions of one sequence format to others.

UNIT II - SEQUENCE ALIGNMENT (9 Hours)

Significance of sequence alignment, Methods and tools for pair wise sequence alignment, Use of scoring matrices and gap penalties, use of multiple sequence alignment, methods and tools for multiple sequence alignment, RNA Structure prediction - basics, features and methods of RNA Secondary structure prediction

UNIT III - DATABASE SEARCHING AND PHYLOGENETIC PREDICTION (9 Hours)

Database searching for similar sequences –Introduction, FASTA, BLAST, Bayes block aligner, Scoring matrix or Profile, Other methods for comparing databases of sequences and patterns, Genome complexity and phylogenetic analysis, The Concept of evolutionary trees, Methods for phylogenetic prediction.

UNIT IV - GENE PREDICTION AND GENOME REARRANGEMENT (9 Hours)

Introduction, testing the reliability of an ORF Prediction, gene prediction methods and tools, The Biological Problem, Permutations .Analyzing Genomes with Reversals of Oriented Conserved Segments , Applications to Complex Genomes

UNIT V - COMPARATIVE GENOMICS (9 Hours)

Genome anatomy: prokaryotic genomes, Eukaryotic Genomes, Sequence assembly and gene identification, Comparative genomics, functional classification of genes.

LIST OF EXPERIMENTS (30 Hours)

1. Nucleotide databases
2. Biological data Formats
3. Pairwise sequence alignment
4. Sequence similarity searching
5. Multiple sequence alignment and editing
6. Phylogenetic analysis and Evaluation of trees
7. Gene prediction tools
8. RNA Structure Prediction
9. Comparative Genomics

TEXTBOOKS

1. David W Mount, *"Bioinformatics sequence and Genome analysis"*, Second Edition, Cold Spring Harbor Laboratory Press, 2013.
2. Richard C. Deonier, Simon Tavaré, and Michael S. Waterman, *"Computational Genome Analysis: An Introduction"*, Springer, 2010.

REFERENCES

1. Richard Durbin, Sean R. Eddy, Anders Krogh, and Graeme Mitchison, *"Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids"*, Cambridge University Press, 1998

Course Code	Course Title	L	T	P	C
GI2003	Scripting Languages	3	0	2	4
	Total Contact Hours - 75				
PURPOSE					
The course imparts knowledge on learn the concepts of scripting languages through Unix shell programming, JavaScript, HTML and XML.					
To learn how scripting can be effectively used for handling documents and data.					
INSTRUCTIONAL OBJECTIVES					
To get an understanding of the Unix/Linux operating systems					
To understand and apply Unix shell scripting concepts					
To understand and apply the concepts of JavaScript					
To understand and apply XML scripting					

UNIT I - UNIX/Linux Operating System (9 Hours)

UNIX architecture, File system, directory and file handling commands. Basic File attributes, Text editors: the Vi editor. Filters head, tail, cut, paste, sort, uniq, grep with regular expressions.

UNIT II - UNIX Shell Scripts (9 Hours)

Shell scripts – read, exit, logical operators, conditional operators, evaluating operations using test, the case condition. Looping with 'while' and 'for'. Example scripts for the above.

UNIT III - JavaScript (9 Hours)

Core JavaScript Concepts, Introduction to JavaScript, Variables in JavaScript, Types of constants in JavaScript, Expressions and Conditions, Relational operators Data types, Flow control, Functions, Objects, Data type conversion and equality, Forms and Data

UNIT IV - HTML Scripts (9 Hours)

Fundamentals of HTML, Links and Addressing, HTML and Images, Backgrounds, Colors and Text, Introduction to Layout, Advanced Layout Tables, Frames, Forms.

UNIT V - Extensible Markup Language (XML) (9 Hours)

Fundamentals of XML, Origins and Goals of XML, Creating Documents, Viewing XML, Testing XML, Transformation, Markup and Core Concepts: The Anatomy of a Document Elements, Attributes, Namespaces, Entities. Current applications of XML

LIST OF EXPERIMENTS (30 Hours)

1. Unix/Linux Command Line mode, file and directory handling
2. Vi Editor
3. Unix filter commands
4. Unix shell scripts – conditional operators
5. Unix shell scripts – looping, string handling
6. JavaScript variables and data types
7. JavaScript Functions, Events
8. HTML links, image handling,
9. HTML tables, formatting,
10. XML creating documents
11. Testing XML

TEXTBOOKS

1. Sumitabha Das, *"Unix Concepts and Applications"*, McGraw - Hill; 4 edition. Units I and II – Chapters in book 1,2,3,4,7,10,14, (2006).
2. Paul Wilton & Jeremy Mc, *"Peak Beginning Java script"*, John Wiley & Sons, 4th Edition. Unit III – Chapters in book 1, 2, 5, (2009).
3. Thomas A. Powell, *"Html & CSS:"* The Complete Reference 5th Edition – Tata McGraw – Hill, Unit IV – Chapters in book 1, 2, (2010).
4. Erik T. Ray, *"Learning XML"*, Second Edition - O'Reilly Media. Unit V – Chapters in book 1, 2, (2003).

REFERENCES

1. *"UNIX"*, The Complete Reference, Second Edition (Complete Reference Series) Paperback, Kenneth Rosen, Douglas Host et al. McGraw-Hill. 2006.
2. *"JavaScript"*, the Complete Reference 3rd Edition, Thomas Powell, Fritz Schneider McGraw Hill, 2012.
3. *"HTML & XHTML"*, The Complete Reference, Thomas Powell - Osborne Complete Reference Series 2003.

Course Code	Course Title	L	T	P	C
MA2016	NUMERICAL AND BIOSTATISTICAL METHODS	3	0	0	3
	Total Contact Hours – 45				

PURPOSE
To provide an understanding of statistical methods and numerical methods.
INSTRUCTIONAL OBJECTIVES
Know the techniques of numerical methods
Learn the basics of Biostatistics
Understand the concept of hypothesis

UNIT I - NUMERICAL CALCULATIONS (9 Hours)

Numerical calculation: introduction and fundamental concepts, numerical methods for linear equation and matrices, Crammers rule, Gaussian elimination method , Crouts method, Similarity transformation, Eigen values and Eigen vectors of a matrix, Numerical solution of differential and integral equations.

UNIT II - BIOSTATISTICS (9 Hours)

Biostatistics: Introduction to Biostatistics, Distributions – Binomial, Poisson and Normal, Handling Univariate, Bivariate and Multivariate data- Introduction to Probabilities, Interval Estimation.

UNIT III - TESTING OF HYPOTHESIS (9 Hours)

Hypothesis testing: Testing hypothesis, Examining relationships using Correlation & Regression.

UNIT IV - ANALYSIS OF VARIANCE (9 Hours)

Analysis of Variance, Multiple Correlation, PCA, Factor analysis, Discriminant functional analysis.

UNIT V - DESIGN EXPERIMENTS (9 Hours)

Concepts & Methods of Design Experiments, Randomization & Blocking, Analysis of variance, Factorial & Fractional designs, Taguchi's concepts & Methods and second order designs.

TEXTBOOKS

1. George W. Collins, II, *"Fundamental Numerical Methods and data analysis"*, Harvard University Press, 2003.
2. Hildebrand. F.B, *"Introduction to Numerical Analysis"*, McGraw- Hill Book Co, 1956.

REFERENCES
1. Hamming R.W, *"Numerical methods for scientists and engineers"*, McGraw Hill Book Co; 1962.
2. Daniel W.W, *"Biostatistics a Foundation for Analysis in the Health Sciences"*, John Wiley & Sons, 2000.
3. Warren J. Ewens, Gregory R. Grant, *"Statistical methods in Bioinformatics: An Introduction"*, 2nd Edition, Springer 2004.

SEMESTER II

Course Code	Course Title	L	T	P	C
GI2004	NEXT GENERATION SEQUENCING AND ANALYSIS	3	0	2	4
	Total Contact Hours -75				
PURPOSE					
This course provides knowledge to handle biological data generated by the sequencing projects and its analysis.					
INSTRUCTIONAL OBJECTIVES					
To provide general and unique aspects of the sequencing methods.					
To understand the concepts of NGS.					
To understand the analysis of NGS data.					

UNIT I - DNA Sequencing (9 Hours)

DNA Sequencing, First generation DNA sequencers, Drawbacks of the first generation sequencing methods.

UNIT II - NGS (9 Hours)

Emergence of Next generation sequencing, 454 Pyro-sequencing, Illumina Genome Analyzer, Applied Biosystems Sequencing, Ion Torrent Sequencing, Polonator Technology, Nanopore Sequencing, Single Molecule Real Time DNA sequencing, Comparison of Next generation sequencing techniques, Drawbacks of NGS, NGS File formats, & applications.

UNIT III - ASSEMBLY OF SEQUENCE DATA (9 Hours)

De novo Genome sequence assembly, Reference sequence assembly, Challenges of Genome assembly, Use of paired – end reads in the assembly, Data Preprocessing methods and sequencing read correction methods, Assembly Errors, Evaluation of assembly methods.

UNIT IV - APPLICATIONS OF NGS (9 Hours)

Transcriptome (RNA) sequencing, Exome sequencing, Genome Annotation, Using NGS to detect sequence variants, ChIP-sequence, Biological theories on ChIP-sequence analysis, Understanding the non – coding genome, Disease gene identification, DNA fragment evaluation, Peak identification, Two condition comparison, Saturation analysis, Motif finding and related theories.

UNIT V - NGS DATABASES AND ANALYSIS OF NGS DATA (9 Hours)

NGS databases, Sequence Analysis: Pairwise and multiple sequence alignment methods.

LIST OF EXPERIMENTS (30 Hours)

1. Ion Torrent Sequencing'
2. NGS file formats
3. Reference Assembly
4. Genome Annotation
5. De Novo & Reference Assembly
6. Chip – Seq
7. Identification of SNPs
8. Disease gene Identification
9. NGS databases

TEXTBOOKS

1. Ali Masoudi-Nejad, Zahra Narimani, Nazanin Hosseinkhan; *"Next Generation Sequencing and Sequence Assembly"*, Methodologies and Algorithms, Springer; 2013.
2. Stuart M. Brown, *"Next-Generation DNA Sequencing Informatics"*, Cold Spring Harbor Laboratory Press, 2013.

REFERENCES

1. Mark I. Rees, *"Challenges and Opportunities of Next-generation Sequencing for Biomedical Research"*, Academic Press, 2012.

Course Code	Course Title	L	T	P	C
GI2005	ALGORITHMS FOR LIFE SCIENCES	3	2	0	4
	Total Contact Hours – 75				
PURPOSE					
The purpose of this subject is to understand the basic algorithms behind the methods and tools available for data analysis and develop new tools.					
INSTRUCTIONAL OBJECTIVES					
Understand the basics of genomics and algorithms					
To understand the algorithms in sequencing and data integration					
To understand the algorithms for comparative analysis and data mining					
To develop new algorithms for data analysis					

UNIT I - DYNAMIC PROGRAMMING ALGORITHMS (9 Hours)

Algorithms - Dynamic Programming, Sequence Alignment: Edit distance, LCS PAM and BLOSUM Scoring Matrices. Global alignments: Needleman Wunsch Algorithm, Local Alignments: Smith Waterman Algorithm, Gap Penalties.

UNIT II - GRAPH ALGORITHMS (9 Hours)

Graph Algorithms, SBH and Eulerian Paths, De-novo Peptide Sequencing: Longest Paths and. Space Efficient Alignment Algorithms. Fast LCS using Table Lookup.

UNIT III - PATTERN MATCHING AND CLUSTERING (9 Hours)

Exact Pattern Matching: KMP Algorithm, Keyword Trees, Aho-Corasick Algorithm. Clustering Basics: Hierarchical Clustering, Multiple Sequence Alignment: CLUSTAL, Center-based Clustering, Clustering via Cliques.

UNIT IV - EVOLUTIONARY TREES AND PHYLOGENY (9 Hours)

Evolutionary Trees and Ultra metrics, Additive distance trees, Perfect Phylogeny Problem. Small Parsimony Problem, Nearest Neighbor Interchange.

UNIT V - HIDDEN MARKOV MODELS, RANDOMIZED ALGORITHMS (9 Hours)

Hidden Markov Models: Basics, Forward and Backward (Viterbi) Algorithms. Randomized algorithms and their applications, Data Mining algorithms.

TUTORIALS (30 Hours)

TEXTBOOKS

1. Neil C. Jones and Pavel A. Pevzner, *"An Introduction to Bioinformatics Algorithms"*, MIT Press, 2005.
2. Gus fields D, "*Algorithms on strings, trees and sequences: Computer Science and Computational Biology*", Cambridge University Press, 1997.

REFERENCES

1. Steffen Schulze-Kremer, *"Molecular Bioinformatics: Algorithms and Applications"*, Walter de Gruyter, 1996.
2. Wing-kin Sung, *"Algorithms in Bioinformatics: A Practical Introduction"*, CRC Press, 2011.
3. Richard Durbin, Sean R. Eddy, Anders Krogh, "Graeme Mitchison, *"Biological Sequence Analysis: Probabilistic Models of Protein"*, Cambridge University Press, 2005.

Course Code	Course Title	L	T	P	C
GI2006	R PROGRAMMING	3	0	2	4
	Total Contact Hours: 75				
PURPOSE					
This course provides knowledge to handle biological problems in Bioinformatics and computational biology					
INSTRUCTIONAL OBJECTIVES					
Providing general properties and unique aspects of the R language					
To teach Object Oriented programming in R					
To teach methods for getting of data in and out					
To provide knowledge how to how to write own software packages					

UNIT I - R LANGUAGE (9 Hours)

Motivation of R, Attributes and some special values, Types of objects, Sequence generating and vector subsetting, Types of functions, Data Structures, Managing R session, Evaluations.

UNIT II - OBJECT ORIENTED PROGRAMMING IN R (9 Hours)

OOP in R, Basics of OOP, S3 OOP, S4 OOP, Documentation, Debugging, Managing S3 and S4 together.

UNIT III - INPUT AND OUTPUT IN R (9 Hours)

Basic file handling, connections, File input and output, Tools for accessing files on the Internet.

UNIT IV - WORKING WITH CHARACTER DATA (9 Hours)

Built-in Capabilities, Regular Expression, Prefix, Suffix and Substrings, Biological sequences, Matching patterns.

UNIT V - R PACKAGES (9 Hours)

Package basics, Package Management and authoring, Initialization, Debugging and Profiling

LIST OF EXPERIMENTS (30 Hours)

1. Getting data into R
2. Extracting subsets of data frames by value
3. Sorting data, Merging data, and Exporting data
4. Simple functions: tapply, sapply, summary, table
5. Basic plotting tools
6. Revisiting the plot function
7. Loops
8. Functions and If Statements
9. Analysis of variance
10. Test of Significance

TEXTBOOKS

1. Robert G, *"R programming in Bioinformatics"*, CRC press, Taylor and Francis Group, USA, 2008.
2. Own J, Robert. M, and Andrew R., *"Introduction to Scientific programming and simulation using R"*, CRC Press, Taylor and Francis Group, USA, 2014.

REFERENCES

1. Norman M. And Norman S. Matloff *"The Art of R programming: A tour of statistical software Design",* No Starch Press Inc, USA, 2011.

SEMESTER III

Course Code	Course Title	L	T	P	C
GI2047	SEMINAR	0	0	1	1

PURPOSE

This course gives an opportunity to present what they have learnt to an audience. This will train the students in giving scientific presentations.

INSTRUCTIONAL OBJECTIVES

Teach the students to learn prepare for scientific presentations and present it to an audience and face the discussions.

TOPICS:

1. NGS
2. Pharmacogenomics
3. Transcriptomics

4. RNAi
5. Agrigenomics
6. Programming languages for life sciences
7. Metagenomics

Course Code	Course Title	L	T	P	C
GI2048	INDUSTRIAL TRAINING	0	1	1	1
	Three Weeks practical training in industry				
PURPOSE					
This course gives an opportunity to the students to get exposure to the genomics / genome informatics industry / Research institutions. This will help the students to get hands on training in carrying out scientific activities at Bioinformatics Industries.					
INSTRUCTIONAL OBJECTIVES					
To help the students to get exposure to genomics / genome informatics / bioinformatics industry.					
Enable the students to get hands on training at genomics / genome informatics / bioinformatics industry.					

The student has to undergo Industrial Training for a period of three weeks during summer vacation between II and III semesters. At the end of the training student will submit a report as per the prescribed format to the department which will be evaluated.

Course Code	Course Title	L	T	P	C
GI2049	PROJECT WORK PHASE I (III Semester)	0	0	12	6
GI2050	PROJECT WORK PHASE II (IV Semester)	0	0	32	16
PURPOSE					
To undertake research in an area related to the program of study					
INSTRUCTIONAL OBJECTIVES					
The student shall be capable of identifying a problem related to the program of study and carry out wholesome research on it leading to findings which will facilitate development of a new/improved product, process for the benefit of the society.					

M. Tech projects should be socially relevant and research oriented. Each student is expected to do an individual project. The project work is carried out in two phases, Phase I in III semester where it is compulsory for the student to have research methodology as one of the components; and Phase II in semester IV. Phase II of the project work shall be in continuation of Phase I only. At the completion of a project the student will submit a project report, which will be evaluated (end semester assessment) by duly appointed examiner(s). This evaluation will be based on the

project report and a viva voce examination on the project. The method of assessment for both Phase I and II is shown in the following table:

Assessment	Tool	Weightage
In - semester	I review	10%
	II review	15%
	III review	35%
End semester	Final viva voce examination	40%

Student will be allowed to appear in the final viva voce examination only if he / she has submitted his / her project work in the form of paper for presentation / publication in a journal and produced the proof of acknowledgement of receipt of paper from the organizers / publishers.

PROGRAM ELECTIVES

Course Code	Course Title	L	T	P	C
GI2101	HUMAN GENETICS	3	0	0	3
	Total Contact Hours: 45				
PURPOSE					
To understand the genetic makeup of human genome					
INSTRUCTIONAL OBJECTIVES					
To Provide understanding of the concepts and scientific methods of modern genetics					
To develop conceptual skills to address questions in genetics research and clinical practice					

UNIT I - ORGANIZATION OF THE HUMAN GENOME AND GENE EXPRESSION (9 Hours)

General organization of the human genome, Organization and distribution of human genes, Human multigene families and repetitive coding DNA, Extragenic repeated DNA sequences and transposable elements, Human gene expression, An overview of gene expression in human cells, Control of gene expression by binding of *trans*-acting protein factors to *cis*-acting regulatory sequences in DNA and RNA, Alternative transcription and processing of individual genes, Asymmetry as a means of establishing differential gene expression and DNA methylation as means of perpetuating differential expression, Long-range control of gene expression and imprinting, The unique organization and expression of Ig and TCR genes

UNIT II - INSTABILITY OF THE HUMAN GENOME: MUTATION AND DNA REPAIR (9 Hours)

An overview of mutation, polymorphism, and DNA repair, Simple mutations, Genetic mechanisms which result in sequence exchanges between repeats, Pathogenic mutations, The pathogenic potential of repeated sequences, DNA repair

UNIT III - PHYSICAL AND TRANSCRIPT MAPPING (9 Hours)

Low and High resolution physical mapping: chromatin and DNA fiber FISH and restriction mapping, Assembly of clone contigs, Constructing transcript maps and identifying genes in cloned DNA

UNIT IV - GENETIC MAPPING OF MENDELIAN CHARACTERS (9 Hours)

Recombinants and non-recombinants, Genetic markers, Two-point mapping, Multipoint mapping, Standard lod score analysis

UNIT V - GENETIC MAPPING OF COMPLEX CHARACTERS (9 Hours)

Parametric linkage analysis and complex diseases, r, Thresholds of significance - an important consideration in analysis of complex diseases, Strategies for complex disease mapping - combination of linkage and association techniques

TEXTBOOK

1. Tom Strachan and Andre, *"Human and Molecular Genetics"*, 4th Edition, Garland Science, 2011.

REFERENCES

1. Bruce R. Korf, Mira B. Irons, *"Human Genetics and Genomics"*, Includes Wiley E-Text, 4th Edition, Wiley-Blackwell January, 2013.
2. Speicher, Michael, Antonarakis, Stylianos E., Motulsky, Arno G. (Eds.), *"Vogel and Motulsky's Human Genetics, Problems and Approaches",* 4th ed. 2010.

Course Code	Course Title	L	T	P	C
GI2102	CANCER GENOMICS	3	0	0	3
	Total Contact Hours: 45				

PURPOSE

Cancer Genomics addresses how recent technological advances in genomics are shaping how we diagnose and treat cancer. Understand techniques involved in analyzing cancer genomes

INSTRUCTIONAL OBJECTIVES

To provide in-depth knowledge in cancer Genome structure, analysis and interpretation

To highlight various techniques involved in understanding cancer genomes

UNIT I - CANCER AND GENOME REGULATION (9 Hours)

The Genomics, Epigenomics and Transcriptomics of Cancer, Somatic mutations, Transcription and Epigenetics Overview, Adult Solid Tumors: Lung Cancer, Breast Cancer, Prostate Cancer, Colon Cancer , Thyroid Cancer

UNIT II - METHODOLOGICAL APPROACHES AND BACKGROUND (9 Hours)

Expression Arrays, SNPs, Tissue micro-arrays (breast, ovarian), Next generation sequencing DNA sequence, RNA sequence, Epigenetic Analyses, Pharmacogenomics, Biomarker discovery through genomics, Preclinical models for genomics.

UNIT II - CANCER GENOME ANALYSIS (10 Hours)

Reciprocal Subtraction Differential RNA Display (RSDD), Rapid Subtraction Hybridization (RaSH) Differential Display as a Gene Profiling Tool, Serial Analysis of Gene Expression (SAGE) Gene Expression Profile Analysis of Tumors, cDNA Microarray and Bioinformatics Analysis, Complete Open Reading Frame (C-ORF) Technique. Chromatin Immunoprecipitation Assays: Artificial Chromosome Transfection, Monitoring Methylation and Gene Expression in Cancer.

UNIT IV - SPECIFIC CANCER CASE STUDIES (9 Hours)

Age Non-specific Tumors and Hematopoietic Malignancies ,ALL , AML, NHL, Multiple Myeloma, Brain Tumors, Pediatric Cancers, Neuroblastoma, Soft tissue sarcomas, Osteosarcoma, Wilms Tumors, Germline Mutations and Hereditary Cancer Syndromes .

UNIT V - ETHICS AND FUTURE DIRECTIONS (8 Hours)

The role of microRNAs and ultra-conserved non-coding RNAs in cancer, Environmental impact on cancer genomics, Bioinformatics and computational methods for data analysis, Genomic Resource Projects, The Cancer Genome Atlas (TCGA) International Cancer Genome Consortium (ICGC), Ethics of Genomics Research.

TEXTBOOKS

1. Paul B. Fisher Editor(s), *"Cancer Genomics and Proteomics: Methods and Protocols"*, Volume No. 383, Humana, 2007.
2. Dellaire, Berman Arceci, Editor(s), *"Cancer Genomics, From Bench to Personalized Medicine"*, Academic Press, 2013.

REFERENCE

1. Lewis J. Kleinsmith, *"Principles of Cancer Biology"*, Pearson new international edition 2014.

Course Code	Course Title	L	T	P	C
GI2103	GENOME TECHNOLOGIES	3	0	0	3
	Total Contact Hours – 45 Hours				
PURPOSE					
The course helps the students to grasp the new technologies associated with genome sequencing and analysis					
INSTRUCTIONAL OBJECTIVES					
Microarray technologies					
NGS technologies					
PCR technologies					
Allied technologies					

UNIT I - PAST & PRESENT OUTLOOK OF GENOME TECHNOLOGIES (9 Hours)

aCGH and SNP genotyping using microarray, Frontiers of Genomics, Challenges of genomics.

UNIT II - NGS TECHNOLOGIES (9 Hours)

SGS and TGS technologies, Illumina genome analyzer, Applied biosystems- Ligation based sequencing, 454 Roche GLS, Emerging sequencing technologies

UNIT III - INTERGRATED GENOME ANALYSIS TECHNOLOGIES 9 Hours)

Paired end ditags for Transcriptome and genome analysis, Paleo-genomics using 454 sequencing, ChipSeq for DNA protein interactions, microRNA NGS, DeepSAGE

UNIT IV - PCR (12 Hours)

Real time PCR principles and instrumentation, Relative Quantification methods of qPCR, PCR using SYBR green, PCR methods for scanning and genotyping genomes

UNIT V - ALLIED TECHNOLOGY (12 Hours)

Overview of n Counter Gene expression assay, Design and synthesis of code set, Protocol, SMRT sequencing, methods and applications

TEXTBOOKS

1. Michal Janitz, *"Next-Generation Genome Sequencing: Towards Personalized Medicine"*, John Wiley & Sons, 2011.
2. Zhanjiang (John) Liu, *"Aquaculture Genome Technology"*, John Wiley & Sons, 2008.

REFERENCES

1. Jeffrey Fisher and Mostafa Ronaghi *"The Current Status and Future Outlook for Genomic Technologies"*, Bridge-Linking Engineering and Society, https://www.nae.edu/File.aspx?id=41605 (UNIT 1)
2. Mahendar Thudi, Yupeng Li, Scott A. Jackson, Gregory D. May, and Rajeev K. Varshney, *"Current state-of-art of sequencing technologies for plant genomics research",* Briefings in Functional Genomics , 11 (1): 3-11, (UNIT 2), 2012.
3. Paul D. Brady and Joris R. Vermeesch, *"Genomic microarrays: a technology overview, Prenatal Diagnosis",* John Wiley & Sons ,32, 336–343, (UNIT 3), 2012.
4. Tefvik Dorak, *"Real-Time PCR"*, Taylor and Francis, (UNIT 4), 2007.
5. Meghana M. Kulkarni , *"Digital Multiplexed Gene Expression Analysis Using the NanoString nCounter System, Current protocols in molecular biology"*, Unit 25.B10, John Wiley & Sons, (UNIT 5), 2011.
6. Jonas Korlach, Stephen Turner, et al, *"Real-Time DNA Sequencing from Single Polymerase Molecules"*, Science , 323 (5910), 133-138. (UNIT 5), 2009.
7. Richard J Roberts, Mauricio O Carneiro , Michael C Schatz, *"The advantages of SMRT sequencing"*, *Genome Biology* , 14:405 , (UNIT 5), 2013.

Course Code	Course Title	L	T	P	C
GI2104	GENETIC DISEASES & DISORDERS	3	0	0	3
	Total Contact Hours - 45				
PURPOSE					
The course helps the students to understand genetic diseases					
INSTRUCTIONAL OBJECTIVES					
Genetic diseases and its causes					
Some molecular mechanisms of genetic disease					
Diagnoses of genetic diseases					
Genetic Disorders					

UNIT I - GENETIC DISEASES (9 Hours)

Mendel's law-Selection, Genetic Diversity, Epistatis, Complex Syndromes, Mutation-Variation types and copy number, Genetic code, Inbreeding, Genetic disorders, Types of genetic disorders, Databases for genetic disorders related genes and their manifestations.

UNIT II - SINGLE GENETIC DISORDERS (9 Hours)

Types of single genetic disorders, Molecular basis of disorders like Cystic fibrosis, Turner syndrome, Rett syndrome

UNIT III - COMPLEX GENETIC DISEASES (9 Hours)

Down syndrome, Obesity, mental retardation, epilepsy, Pseudoxanthoma elasticum

UNIT IV - METABOLIC DISORDERS (9 Hours)

Disorders of intermediary disorders, disorders of biosynthesis and breakdown of complex molecules, neurotransmitter defects, eye disorders, metabolic myopathies

UNIT V - GENETIC DISEASES OF THE INDIAN SUBCONTINENT (9 Hours)

Thalassaemias and other haemoglobinopathies, Inherited skeletal dysplasias and collagen diseases, Deafness and related syndrome, genetics of cancer, Epidemiology of genetic diseases

TEXTBOOKS

1. Dijana Plaseska-Karanfilska, *"Human Genetic Disease"*, In Tech Publishers, Croatia, Europe 2011.
2. Maria Puiu, *"Genetic Disorders"*, In Tech Publishers, Croatia, Europe 2013.

REFERENCES

1. Kenji Ikehara, *"Advances in the Study of Genetic Disorders",* In Tech Publishers, Croatia, Europe 2011.
2. Dhavendra Kumar, *"Genetic disorders of Indian Subcontinent",* Kluwer publications, India 2010.

Course Code	Course Title	L	T	P	C
GI2105	MEDICAL ANNOTATION OF SNPs	3	0	0	3
	Total Contact Hours - 45				

PURPOSE
This course is intended to provide the in-depth knowledge on Single Nucleotide Polymorphism (SNP) and its annotations.
INSTRUCTIONAL OBJECTIVES
To understand the potentials of SNPs
To have knowledge on SNP databases and data mining
To understand the application of various methods used in SNP discovery and analysis

UNIT I - SNP (6 Hours)

Single Nucleotide Polymorphism, Impact on Gene function and phenotype, SNP databases, Mining SNPs from DNA Sequence Data, Computational Approaches to SNP Discovery and Analysis.

UNIT II - MELTING BASED METHODS (6 Hours)

SNP Screening with Denaturing Gradient Gel Electrophoresis, Temporal Temperature Gradient Electrophoresis

UNIT III - CONFORMATION BASED METHODS (12 Hours)

Zn (II)–Cyclen and Phosphate-Affinity Polyacrylamide gel electrophoresis, SSCP analysis, Fluorescence SNP Detection, Detection of Mutations in Long DNA Fragments, Mismatch Oxidation Assay

UNIT IV - HIGH-THROUGHPUT METHODS - SNP GENOTYPING (12Hours)

Combining Tag SNPs and Molecular Beacons, SNP Genotyping by the 5'-Nuclease Reaction, TaqMan Method, Detection Using Trityl Mass Tags, Multiplex Single Base Primer Extension Assays, PCR Amplification on Magnetic Nanoparticles Using Dual-Color Hybridization

UNIT V - PCR BASED METHODS (9 Hours)

Restriction Enzyme Analysis of PCR Products, Allele-Specific PCR in SNP Genotyping, Modified Multiple Primer Extension Method, Detection of SNP by the Isothermal Smart Amplification Method

TEXTBOOK

1. Komar, Anton A. (Ed.), *"Single Nucleotide Polymorphisms: Methods and Protocols"*, Springer Methods in Molecular Biology (US), Volume 578, 2009.

REFERENCES

1. Pui-Yan Kwok, *"Single Nucleotide Polymorphisms: Methods and Protocols"*, Springer Science & Business Media (US), Volume 212, 2003.
2. Bethesda (MD), *"SNP FAQ Archive"*, National Center for Biotechnology Information (US), 2005.

Course Code	Course Title	L	T	P	C
GI2106	APPLICATION OF NEXT GENERATION SEQUENCING TECHNOLOGIES	3	0	0	3
	Total Contact Hours- 45				
PURPOSE					
This course provides knowledge to handle biological data generated by the sequencing projects and its analysis.					
INSTRUCTIONAL OBJECTIVES					
To know the application of NGS in various areas of research.					
To highlight the various techniques (software's and tools) used for NGS analysis.					
To provide in-depth understanding of the use of NGS in clinical and medical diagnostic approach					

UNIT I - NEXT GENERATION SEQUENCING (9 Hours)

Sanger sequencing principles - history and landmarks, of Sequencing Technology Platforms, A survey of next-generation sequencing technologies, A review of DNA enrichment technologies, Application of High-Throughput Sequencing, Application of NGS to the diagnosis of genetic disorders, Computational Infrastructure and Basic Data Analysis.

UNIT II - INTERACTION ANALYSIS OF CHIP-SEQ (9 Hours)

Base-Calling for Bioinformaticians, De Novo Short-read Assembly, Short-Read Mapping, DNA-Protein Interaction Analysis (CHIP-Sequence), Generation and Analysis of Genome-Wide DNA Methylation Maps, Differential Expression for RNA

Sequencing (RNA-Sequence) Data: Mapping, summarization, statistical Analysis and Experimental Design.

UNIT III - ANALYSIS OF METAGENOMIC DATA (9 Hours)

MicroRNA Expression Profiling and Discovery, Dissecting Splicing Regulatory Network by Integrative Analysis of CLIP-Sequence Data, Analysis of Metagenomic Data, NGS-based noninvasive prenatal diagnosis, Diagnosis of inherited neuromuscular disorders by NGS Application of NGS in hearing loss diagnosis.

UNIT IV - EXOME SEQUENCING (9 Hours)

Exome sequencing as a discovery and a diagnostic tool, Challenges of NGS based molecular diagnostics, NGS-Based Clinical Diagnosis of Genetically Heterogeneous Disorders, Molecular Diagnosis of Congenital Disorders of Glycosylation (CDG), NGS improves the Diagnosis of X-Linked Intellectual Disability (XLID), NGS Analysis of Heterogeneous Retinitis Pigmentosa.

UNIT V - NGS ANALYSIS OF THE WHOLE MITOCHONDRIAL GENOME (9 Hours)

NGS Analysis of the Whole Mitochondrial Genome, Noninvasive Prenatal Diagnosis Using Next-Generation Sequencing, High-Throughput Sequencing Data Analysis Software: Current state and future developments.

TEXTBOOKS

1. Valencia, C.A., Pervaiz, M.A., Husami, A., Qian, Y., Zhang, K, *"Next Generation Sequencing Technologies in Medical Genetics",* Springer, 2013.
2. Lee-Jun C. Wong*, "Next Generation Sequencing: Translation to Clinical Diagnostics"*, Springer, 2013.
3. Naiara Rodríguez-Ezpeleta, Michael Hackenberg, *"Bioinformatics for High Throughput Sequencing"*, Springer, 2012.

REFERENCES

1. Masoudi-Nejad, Ali, Narimani, Zahra, Hosseinkhan, Nazanin, *"Next Generation Sequencing and Sequence Assembly: Methodologies and Algorithms"*, Springer, 2013.
2. Wu, Wei, Choudhry, Hani (Eds.), *"Next Generation Sequencing in Cancer Research: Volume 1: Decoding the Cancer Genome",* Springer, 2013.

Course Code	Course Title	L	T	P	C
GI2107	GENETIC COUNSELING & ELSI	3	0	0	3
	Total Contact Hours - 45				
PURPOSE					
This course is intended to provide the in-depth knowledge on Genetic Counseling and its associated ethical, legal and social issues.					
INSTRUCTIONAL OBJECTIVES					
To be able to understand the processes involved in genetic counseling					
To have knowledge on Socio, ethical and legal issues					
To understand the application of genetic counseling in different cases					

UNIT I - GENETIC COUNSELING (9 Hours)

The Practice of Genetic Counseling, Definition and Goals, Components, Counseling Contexts and Situations, Providers, Professional and Educational Landmarks in Genetic Counseling , Professional Growth and Skill Acquisition, The Evolution of the Pedigree, Family History Basics, Constructing a Pedigree, Interpretation, Analysis,

UNIT II - CASE PREPARATION AND MANAGEMENT (10 Hours)

Interviewing, Core Qualities, Creating a Working Agreement, Verbal and Nonverbal Communication, Interviewing Techniques, Obtaining Pedigrees, Assessment, Billing Issues for Genetics Clinic Visits, Preparing a Case, Practice Guidelines, Finding Support /Advocacy Groups and Patient Resources, Risk Assessment, Counseling Aids, Genetic Testing, Referrals to Other Specialists / Family Members to Genetics Clinics

UNIT III - PSYCHOSOCIAL COUNSELING AND PATIENT EDUCATION (9 Hours)

Psychosocial Assessment and the Structure of a Session, Patient's Story, Achieving Dynamic Psychological Engagement: The Working Alliance, Disruptions in the Working Alliance, Discussions, Reactions and Psychologically Challenging Experiences, Counselees' Coping Styles, surrounding theories, Patient Education

UNIT IV - SOCIAL, ETHICAL AND LEGAL ISSUES (9 Hours)

Multicultural Counseling- Multicultural Competency, the Religion Factor, American Values Compared, Four Basic Core Values, Pregnancy, Birth, and Family, Beliefs About the Causes of Disease and Disorders, Communicating Across Cultural Boundaries, Ethical Issues, NSGC Code of Ethics, Legal Issues, Areas of Practice Raising Ethical and Legal Questions

UNIT V EVALUATION AND CASE STUDIES (8 Hours)

The Medical Genetics Evaluation- Components, Diagnostic Studies, Tools and Resources of the Clinical Geneticist, Impact of Human Genome Project for genetic

counselors, Case Studies-Pediatric Case (Cheryl Shuman), Reproductive Genetics Case (Donna F. Blumenthal), Cancer Genetics Case (Monica, L. Marvin)

TEXTBOOKS

1. Wendy R. Uhlmann, Jane L. Schuette, Beverly Yashar, "A Guide to Genetic Counseling", 2nd Edition, Wiley-Blackwell, USA, 2009.
2. Dianne M. Bartels, Bonnie S. Leroy, Arthur L. Caplan, "Genetic Counseling: Ethical Challenges and Consequences", Transaction Publishers, USA, 2010.

REFERENCES

1. Genetic Alliance, *"Making Sense of Your Genes-A Guide to Genetic Counseling"*, National Society of Genetic Counselors; Washington (DC): Genetic Alliance, 2008.
2. Bonnie S. LeRoy, Patricia M. Veach, Dianne M. Bartels, *"Genetic Counseling Practice: Advanced Concepts and Skills"*, John Wiley & Sons, USA, 2011.

Course Code	Course Title	L	T	P	C
GI2108	METAGENOMICS	3	0	0	3
	Total Contact Hours: 45				
PURPOSE					
This course Provides understanding the basics about microbial genome					
INSTRUCTIONAL OBJECTIVES					
To use metagenomic data to describe the taxonomic make-up, functional potential and ecological processes of microbial communities from a range of environments					
To Apply next generation sequencing technology to ecologically relevant projects					

UNIT I - EXPLORING MICROBIAL GENOME (9 Hours)

Bacterial genomes and basic functions, Mutations and phenotypes, Basics of genetic analysis, Implementation and suppression, transposons, Conjugation, Mechanisms of gene regulation

UNIT II - GENOMICS (9 Hours)

Genome sequence analysis, Annotation of genomes from sequence to consequence: *In silico* hypothesis generation and testing, the atlas visualisation of genome-wide information Comparative nucleic acid analysis, Representational display analysis of genome comparisons

UNIT III - FROM GENOMICS TO METAGENOMICS: FIRST STEPS (9 Hours)

Sequencing is just one kind of metagenomics, Pioneering Projects in metagenomics, The Acid Mine Drainage Project, The Sargasso Sea Metagenomic Survey and community, profiling, The Soil-resistome Project, the Human-Microbiome Project.

UNIT IV - APPLICATION OF MICROBIAL GENOMICS (9 Hours)

Cloning the metagenome: Culture-independent access to the diversity and functions of the uncultivated microbial world, Reverse vaccinology: from genome to vaccine, Microbial genomics for antibiotic target discovery

UNIT V - CASE STUDIES (9 Hours)

Helicobacter pylori functional genomics *Streptomyces coelicolor* A3(2): from genome sequence to function, Functional analysis of the *Bacillus subtilis* genome, *Plasmodium falciparum* DNA microarrays and interpretation of data, Functional analysis of the *Plasmodium falciparum* genome using transfection, Chromosome fragmentation as an approach to whole genome analysis in trypanosomes

TEXTBOOK

1. Norman Grossblatt, (Ed), *"The new science of metagenomics"*, National Academic Press, Washington, 2007.

REFERENCES

1. Wren, B Dorrell, N, *"Functional Microbial Genomics: Methods in Microbiology"*, Academic Press Inc, 2002.
2. *"Metagenomics, Methods and Protocols"*, Streit, Wolfgang, Daniel, Rolf (Eds.) Springer, 2010.

Course Code	Course Title	L	T	P	C
GI2109	DATABASE MANAGEMENT SYSTEMS	3	0	0	3
	Total Contact Hours: 45				
PURPOSE					
This purpose of this course is to cover the fundamentals of database architecture, DBMS. Upon completion of this course, the students will get in-depth knowledge in Database design and techniques for the development of database applications in bioinformatics, to fulfill the biological needs.					
INSTRUCTIONAL OBJECTIVES					
To Analyze existing and future data processing needs					
To acquire good knowledge in DBMS and Database architecture					
To Identify the data integrity and security requirements					
To Apply DBMS to Bioinformatics					

UNIT I - DBMS & SQL (9 Hours)

Database and Database Users, Database system concepts and Architecture, The Relational Data Model and Relational Database Constraints, Basic SQL, SQL – Complex Queries, Triggers, Views and Scheme Modification, the relational algebra and relational calculus.

UNIT II - CONCEPTUAL MODELING AND DATABASE DESIGN (9 Hours)

Data Modeling using the entity-relationship(ER) model, the Enhanced entity-relationship (EER) model, Relational Database design by ER and EER to Relational Mapping, Practical database design methodology and use of UML diagrams.

UNIT III - OBJECT, OBJECT RELATIONAL AND XML (9 Hours)

Object and object- relational databases, XML: Extensible Markup Language, Database Programming Techniques- Introduction to SQL programming Techniques, Web Database programming using PHP, Database Design Theory and Normalization, Relational Database Design Algorithm and Further Dependencies.

UNIT IV - FILE STRUCTURES, INDEXING AND HASHING (9 Hours)

Disk storage, basic file structures and Hashing, Indexing structures for files, Query Processing and Optimization and Database Tuning – Algorithms for Query processing and optimization, Physical Database design and tuning, Transaction processing, Concurrency control and Recovery, Database security and Distributed databases.

UNIT V - ADVANCED DATABASE MODELS, SYSTEMS, AND APPLICATIONS (9 Hours)

Enhanced Data Models for Advanced applications, information retrieval and web search, Data Mining concepts, Overview of Data warehousing and OLAP

TEXTBOOKS

1. Ramez Elmasri, Shamkant B. Navathe, *"Fundamentals of Database Systems"*, Pearson Education Limited, 2013.
2. Raghu Ramakrishnan, Johannes Gehrke, *"Database Management Systems"*, McGraw-Hill higher education, 2003.
3. Avi Silberschatz, Henry F. Korth, S. Sudarshan, *"Database System Concepts"*, McGraw-Hill, Sixth Edition, 2010.

REFERENCE

1. Date C.J, *"An Introduction to Database Systems"* – Addison-Wesley, 8th Edition, 2003.

Course Code	Course Title	L	T	P	C
GI2110	MOLECULAR DIAGNOSTICS	3	0	0	3
	Total Contact Hours: 45				

PURPOSE
This course provides the knowledge on genomic and proteomic expression pattern and examines their relevance to the identification of disease-causing genes/mutations and the diagnosis of human genetic disorders.
INSTRUCTIONAL OBJECTIVES
To understand the structural organization of the human genome
To learning and understanding of molecular techniques
To understand gene mapping and linkage analysis.
To recognize the importance of molecular methods in genetic disorders

UNIT I - FUNDAMENTALS MOLECULAR DIAGNOSTICS (9 Hours)

Introduction Infection – mode of transmission in infections, types of infectious diseases. Philosophy and general approach to clinical specimens, Sample collection-method of collection, transport and processing of samples. Interpretation of results.

UNIT II - METHODS IN MOLECULAR DIAGNOSTICS (9 Hours)

Isolation and Purification of Nucleic acids- Principles and Methods. Molecular cloning, labeling of nucleic acids, hybridization.

UNIT III - DIAGNOSIS OF FUNGAL INFECTIONS (9 Hours)

Diagnosis of infection caused by *Streptococcus*, Coliforms, *Salmonella*, *Shigella*, *Vibrio*, and *Mycobacterium*. Diagnosis of fungal infections. Major fungal diseases: Dermetophytoses, Candidiosis and Aspergillosis.

UNIT IV - DIAGNOSIS OF VIRUS AN D PROTOZOAN DISEASES (9 Hours)

Diagnosis of DNA and RNA viruses. Pox viruses, Adenoviruses, Rhabdo Viruses, Hepatitis Viruses and Retroviruses. Diagnosis of Protozoan diseases: Amoebiosis, Malaria, Rypnosomiosis, Leishmaniasis.

UNIT V - APPLICATIONS OF MOLECULAR DIAGNOSTICS (9 Hours)

Advances in DNA sequencing- Pyrosequencing, Microarrays, Personalised Medicine Pharmacogenomics and proteomics.

TEXTBOOK

1. David E. Bruns, Edward R. Ashwood, Carl A. Burtis, *"Fundamentals of Molecular Diagnostics"*, Saunders Group, 2007.

REFERENCES

1. Lele Buckingham and Maribeth L. Flaws, *"Molecular Diagnostics: Fundamentals, Methods & Clinical applications"*, 2007.
2. Coleman W.B, *"Molecular Diagnostics for the Clinical Laboratorian"*, 2nd Ed.,. Humana Press 2006.

Course Code	Course Title	L	T	P	C
GI2111	AGRI-GENOMICS	3	0	0	3
	Total Contact Hours- 45				

PURPOSE

This course imparts knowledge on understanding genomes, sequences, and how all genes contribute to plant life and their diversity. Also introduces to resources available for insect genomics.

INSTRUCTIONAL OBJECTIVES

To acquire the knowledge about plant genome.

To understand and apply the techniques of genomics to study and improve plant variety.

To apply the techniques to study differential gene expression to develop new plant varieties.

UNIT I - PLANT BREEDING & COMPARATIVE GENOMICS (9 Hours)

Introduction to the Plant Breeding Process and Genomics; Overview of molecular breeding, the cultivar development process, and genetic gain; Sequence-based gene discovery and comparative genomics approaches; Demonstration of "*in silico*" gene discovery strategies; Databases for discovery of plant improvement genes

UNIT II - MOLECULAR MARKERS & PHENOTYPING (9 Hours)

DNA Sequence Variation and Genetic Diversity; Molecular marker development and genotyping methods; Applications of molecular markers to plant improvement; Demonstration of identifying sequence variation for molecular markers; Genetic diversity analysis of plant improvement genes; Gene Expression Variation; mRNA profiling – overview of methods and applications to plant improvement; Molecular phenol typing, regulatory networks, and systems biology approaches; Demonstration of RNA profiling data analyses; RNA expression profiling of plant improvement genes

UNIT III - EPIGENOMIC VARIATION (9 Hours)

Epigenomic Variation; Small RNAs and chromatin remodeling; Phenotypic impacts of epigenomic variation; Analysis of epigenomic datasets; Epigenomic variation of plant improvement genes.

UNIT IV - MAPPING (9 Hours)

Integrated Molecular Phenotyping; Genetic mapping and quantitative trait loci; Marker-assisted selection strategies targeted intervals and genomic selection; Demonstration of integrated molecular Phenotyping and genetic mapping; Genetic mapping of plant improvement genes; Directed Genetic Variation; Forward and reverse genetics methods; Transgenic product development; Strategies for Design of Transgenic Products; Functional analysis of plant improvement genes

UNIT V - INSECT GENOMICS (9 Hours)

Integrated Pest Management; Insect databases: Flybase, InsatDb, DroPhEA, DroSpeGe, VectorBase; Genes responsible for detoxification and molting process in insects; i5K & 1Kite; Commercializing Genetic Improvements; Golden Rice; Biotechnology regulation and intellectual property issues; Future prospects for genomics driven plant improvement.

TEXTBOOKS

1. Chakravarthy R., *"Agri Informatics: An Introduction"*, ICFAI University Press, 2006.
2. Chittaranjan Kole, Albert G., *"Principles and Practices of Plant Genomics: Advanced Genomics"*, Volume 3. Abbott. Science Publishers, 2010.

REFERENCES

1. Christopher A. Cullis, *"Plant Genomics and Proteomics"*, Wiley Publishers, 2007.
2. Hany A. El-Shemy, *"Plant Genomics"*, Horizon Scientific Press, 2009.
3. Poonam Chilana, Anu Sharma and Anil Rai, *"Insect genomic resources: status, availability and future"*, Current Science, Vol. 102, No. 4: 25, 2012.

Course Code	Course Title	L	T	P	C
GI2112	EPIGENETIC AND EPIGENOMICS	3	0	0	3
	Total Contact Hours- 45				

PURPOSE
This course imparts knowledge on understanding the importance of epigenetics and epigenomics; with importance to the organization, regulation, system and other relevant methodologies.
INSTRUCTIONAL OBJECTIVES
To acquire the knowledge about the epigenetic organization and regulation.
To impart knowledge on the epigenomic system
To impart knowledge on the methodologies and applications of the epigenetics and epigenomics.

UNIT I - EPIGENETIC ORGANIZATION (9 Hours)

Histone Modifications: Chromatin Dynamics and Higher Order Chromatin Organization, Heterochromatin and euchromatin-Organization, Boundaries, and Gene Regulation, Regulation of Gene Expression, Chromosome Territory Organization within the Nucleus.

UNIT II - EPIGENOME REGULATION (9 Hours)

The Cell Nucleus: Biogenesis, Structure, and Function, Molecular Genetics of Genomic Imprinting, Imprinting and the Epigenetic Asymmetry between Parental Genomes.

UNIT III - EPIGENOME SYSTEMS (9 Hours)

The Human Epigenome, Parental Genomic Imprinting in Flowering Plants, Prions as Epigenetic Regulators of Phenotype in Fungi, Methylomes.

UNIT IV - METHODOLOGIES IN EPIGENOME ANALYSIS (9 Hours)

RNA Methodologies, DNA Methylation Analysis by MALDI Mass Spectrometry, All Things ChIP: ChIP-chip, ChIP-Sequence, ChIP-PCR, Computational Epigenetics.

UNIT V - APPLICATIONS OF EPIGENETICS AND EPIGENOMICS (9 Hours)

Epigenetic Medicine ,Epigenetic Regulation in Pluripotent Stem Cells, Epigenetics of the Immune System Pharmaco-epigenomics to Improve Cancer Therapies, Epigenetics of Ciliates, Nuclear Transfer for Cloning Animals.

TEXTBOOKS

1. Nessa Carey, *"The epigenetics revolution"*, Columbia University Press, North America, 2011.
2. Jefferey M. Craig and Nicolas C. Wong, *"Epigenetics"*, A Reference manual, Caister Academic press, Norfolk, UK, 2011.

REFERENCES

1. Robert A. Myers, Wiley-Blackwell, *"Epigenetic regulation and Epigenomics"*, 2012.
2. Epigenomics: From Chromatin Biology to Therapeutics Krishnarao Appasani, Cambridge University Press, 2012.

Course Code	Course Title	L	T	P	C
GI2113	1000 GENOME PROJECT	3	0	0	3
	Total Contact Hours: 45				
PURPOSE					
To understand the recent breakthrough – 1000 genome project					
INSTRUCTIONAL OBJECTIVES					
To Provide understanding of project design and analysis					
To Learn about use and applications of data from 1000 genome project					

UNIT I - PROJECT DESIGN AND PILOT STUDIES (9 Hours)

1000 Genome Project, Project design, pilot studies, Low coverage, Assess strategy of sharing data across samples; 2 trios, Assess coverage and platforms and centers; 3 Gene regions, Assess methods for gene region capture project design and sample included

UNIT II - DATA RELEASED BY 1000 GENOME PROJECT (9 Hours)

Variant calls, Alignments, and raw sequence files downloading and browsing data.

UNIT III - ANALYSIS DESCRIPTION (9 Hours)

Recalibration, SNP calling, Low Coverage SNP Calling; Low Coverage Phasing; Trio SNP calling

UNIT IV - USE OF PROJECT DATA AND SAMPLES (9 Hours)

Genome-wide association (GWA) studies, risk variants, protective variants, linkage disequilibrium, variant associated with a disease, comparison of the allele frequencies, LD patterns in the 1000 Genomes data. 1000 Genomes data study recombination, natural selection, and population structure and admixture. Study of cellular phenotypes gene expression, epigenetic patterns, and drug response. Computational Mapping genome of cellular phenotypes, Heritability of phenotypes.

UNIT V - APPLICATION OF 1000 GENOME PROJECT (9 Hours)

Global analyses of Project data; Large-scale analyses of Project data; Methods development using Project data; Disease studies using Project data; Population comparisons using Project data.

REFERENCES

1. *"The 1000 Genomes Project Consortium"*, A map of human genome variation from population-scale sequencing; Nature 467:1061-73 (1061-1073), 2010.
2. *"Genomes Browser Orientation"*, http://browser.1000genomes.org; European Bioinformatics Institute 2011.

Course Code	Course Title	L	T	P	C
GI2114	PHARMACOGENOMICS AND PERSONALIZED MEDICINE	3	0	0	3
	Total Contact Hours - 45				

PURPOSE
This course is intended to provide the in-depth knowledge on Pharmacogenomics and Pharmacogenetics techniques and applications
INSTRUCTIONAL OBJECTIVES
To be able to understand the potentials of Pharmacogenomics
To have knowledge in technologies associated with pharmacogenomics
To understand the application of pharmacogenomics and pharmacogeneteics in disease management.

UNIT I - INTRODUCTION TO PERSONALIZED MEDICINE (9 Hours)

Historical aspects of Pharmacogenetics- Pharmacogenomics- Biomarkers- and the promise of personalized medicine, Pharmacogenetics at population level, Customized therapy, barriers

UNIT II - PHARMACOGENETICS OF ENZYEMS, RECEPTORS, TRANSPORTERS (9 Hours)

Pharmacogenetics of two clinically important polymorphic enzymes, CYP2D6 and TPMT polymorphisms, nuclear receptors, cell surface receptors

UNIT III - PHARMACOGENETICSOF TRANSPORTERS AND ION CHANNELS (9 Hours)

Organic anion and caution transporter family, PepT and MRP families, BCRP protein, Genetics and dynamics- anti arrhythmic drugs, sodium channel, QT prolongation

UNIT IV - TECHNOLOGIES IN PHARMACOGENOMICS (9 Hours)

Single Nucleotide Polymorphism, Introduction, Analysis, and SAGE, interethnic differences in drug response- Alcohol and aldehyde dehydrogenases

UNIT V - APPLICATIONS (9 Hours)

Identification of Pharmacogenomics Biomarker Classifiers in Cancer, Toxicogenomics Application to Oncology Drug Development, Strategies to Identify Pharmacogenomic Biomarkers: Candidate Gene, Pathway-Based, and Genome-Wide Approaches

TEXTBOOKS

1. Werner Kalow, Rachel F Tyndale, Urs A Meyer, *"Pharmacogenomics"*, Marcel Dekker Inc., USA, 2001.
2. Beverly A. Teicher, Federico Innocenti, *"Genomics and Pharmacogenomics in Anticancer Drug Development and Clinical Response"*. Springer, USA, 2008.

REFERENCES

1. Chakravarthy R, *"Pharmacogenomics: An Introduction"*, the ICFAI University Press, India, 2006.
2. Nadine Cohen, *"Pharmacogenomics and Personalized Medicine (Methods in Pharmacology and Toxicology)"*, Humana Press, USA, 2010.
3. Chiranjib Chakraborty, Atanu Bhattacharyya, *"Pharmacogenomics: An Approach to New Drug Development"*, Biotech Books, India, 2004.

Course Code	Course Title	L	T	P	C
GI2115 BI2104	MICROARRAY BIOINFORMATICS	3	0	0	3
	Total Contact Hours - 45				
PURPOSE					
This course gives the technical knowledge on Microarray techniques and data analysis					
INSTRUCTIONAL OBJECTIVES					
DNA Microarray and its statistical analysis					
Analysis of RNA data					
Statistical computing and Statistical Genetics					

UNIT I - DNA MICROARRAY (7 Hours)

The Technical Foundations, Why are Microarray Important? What is a DNA Microarray?, Designing a Microarray Experiment-The Basic steps, Types..

UNIT II - MICROARRAY DATABASES (8 Hours)

NCBI and Microarray Data Management, GEO (Gene Expression Omnibus), MAML, The benefits of GEO and MAML, The Promise of Microarray Technology in Treating Disease

UNIT III - MICROARRAY DATA NORMALIZATION (10 Hours)

Microarray Data Preprocessing, Data-Data normalization, Measuring Dissimilarity of Expression Pattern-Distance Motifs and Dissimilarity measures, Visualizing Microarray Data-Principal Component Analysis, Microarray Data.

UNIT IV - MICROARRAY DATA ANALYSIS (10 Hours)

K Means Clustering, Hierarchical Clustering, Self Organization Maps (SOM), Identifying Genes: Expressed usually in a sample- Expressed significantly in population-Expressed differently in two populations, Classifying Samples from two populations using Multilayer Perceptron, Support Vector Machines and their applications, Using genetic algorithm and Perceptron for feature selection and supervised classification.

UNIT V - MICROARRAY APPLICATIONS (10 Hours)

Gene Ontology and pathway analysis, Promoter analysis and gene regulatory network, Co expression analysis, CGH & Genotyping chips, Chromosome aberration and polymorphism via genome-wide scanning, Future direction of microarray approach, Pharmacogenomics, Toxicogenomics, Data mining.

TEXT BOOKS

1. Arun Jogota, *"Microarray Data Analysis and Visualization"*, The Bay Press, 2001.
2. Ernst Wit and John McClure, *"Statistics for Microarrays Design"*, Analysis and Inference, John Wiley & Sons, 2004.
3. Steen Knudsen, *"Guide to analysis of DNA Microarray data"*, John Wiley & Sons, 2004.

REFERENCES

1. Dov Stekel, *"Microarray Bioinformatics"*, Cambridge University Press, 2003.
2. Uwe R. Müller, Dan V. Nicolau, *"Microarray Technology and Its Applications"*, Springer, 2005.
3. Emanuele de Rinaldis, Armin Lahm, *"DNA Microarrays: Current applications"*, Horizon Scientific Press, 2007.

Course Code	Course Title	L	T	P	C
GI2116	HIGH PERFORMANCE & CLOUD COMPUTING	3	0	0	3
	Total Contact Hours - 45				

PURPOSE
The purpose of this subject is to impart knowledge on parallel computing and the concept of cloud computing.
INSTRUCTIONAL OBJECTIVES
To understand the paradigm of parallel computing.
To rethink about known algorithms in a parallel manner.
To understand the logic behind high performance computing and cloud computing.

UNIT I - PARALLEL COMPUTING (9 Hours)

Motivating Parallelism, Scope of Parallel Computing. Parallel Programming Platforms Implicit Parallelism: Dichotomy of Parallel Computing Platforms, Principles of Parallel Algorithm Design: Preliminaries, Decomposition Techniques, Characteristics of Tasks and Interactions.

UNIT II - BASIC COMMUNICATION OPERATIONS (9 Hours)

One-to-All Broadcast and All-to-One Reduction, All-to-All Broadcast and Reduction, All-Reduce and Prefix-Sum Operations, All-to-All Personalized Communication, Circular Shift, Improving the Speed of Some Communication Operations

UNIT III - MESSAGE-PASSING AND SHARED ADDRESS SPACE (9 Hours)

Principles of Message-Passing Programming, MPI: the Message Passing Interface, Topologies and Embedding, Overlapping Communication with Computation, Collective Communication and Computation Operations, Groups and Communicators. Programming Shared Address Space Platforms: Thread Basics: Creation and Termination, Synchronization Primitives in P threads, Controlling Thread and Synchronization Attributes, Thread Cancellation, Composite Synchronization Constructs, Open MP.

UNIT IV - ALGORITHMS (9 Hours)

Dense Matrix Algorithms, Sorting Algorithms Issues in Sorting on Parallel Computers, Sorting Networks, Bubble Sort and its Variants, Quicksort, Bucket and Sample Sort. Graph Algorithms: Definitions and Representation, Minimum Spanning Tree: Prim's Algorithm, Single-Source Shortest Paths: Dijkstra's Algorithm, All-Pairs Shortest Paths.

UNIT V - ADVANCED ALGORITHMS (9 Hours)

Search Algorithms for Discrete Optimization: Definitions and Examples, Sequential Search Algorithms, Depth-First Search Algorithms, Best-First Search Algorithms, Search Overhead Factor, Parallel Depth-First Search, Parallel Best-First Search. Dynamic Programming: Overview, Serial Monadic DP Formulations, Non serial Monadic DP Formulations, Serial Polyadic DP Formulations, Non serial Polyadic DP Formulations.

TEXTBOOKS

1. Ananth Grama et al., *"Introduction to Parallel Computing"*, Second Edition, Addison Wesley Publishing Company, 2003.
2. Peter Pacheco, *"Parallel Programming with MPI"*, Morgan Kaufmann Publishers, 1997.

REFERENCES

1. Georg Hager, *"Introduction to High Performance Computing for Scientists and Engineers"*, Chapman & Hall / CRC Computational Science, CRC Press. 2010
2. Jeffrey S. Vetter, *"Contemporary High Performance Computing: From Petascale toward Exascale",* Chapman & Hall / CRC Computational Science. CRC Press. 2013

Course Code	Course Title	L	T	P	C
GI2117	PERL FOR GENOMICS	2	0	2	3
	Total Contact Hours -45				
PURPOSE					
This course provides knowledge to handle biological problems in Bioinformatics and computational biology					
INSTRUCTIONAL OBJECTIVES					
To provide general properties and unique aspects of the perl language					
To understand Object oriented programming in perl					
To understand the implementation of Perl to NGS data.					

UNIT I - ELEMENTARY PERL (6 Hours)

Perl Introduction, Data types, Operators, Flow of control: conditional statements & loops, Array functions, Hash Traversal. Hash Tables, Scalar & list context.

UNIT II - FILE HANDLING & SUBROUTINES (6 Hours)

Subroutines, System and user defined functions, the local operator, variable-length parameter lists, lexical variables. File handling, Reading from and writing to files, File test operators, Special Variables.

UNIT III - PATTERN MATCHING (6 Hours)

Regular Expressions: Metacharacters & Metasymbols, Pattern Matching, substitution, transliteration, motif search, finding a substring, extracting and replacing a substring.

UNIT IV - APPLICATIONS IN GENOMICS I (6 Hours)

Genomic Perl: Transcription & Translation in perl, RNA secondary structures in perl, Alignment & similarity in perl, species prediction in perl, Substitution matrices in perl, Sequence databases and formats.

UNIT V - APPLICATIONS IN GENOMICS II (6 Hours)

Local alignment and the blast heuristics, statistics of blast database search, Multiple sequence alignment, protein motifs and prosite, coding sequence prediction with dicodons, Satellite identification, Restriction mapping, rearranging genomes and CGI.

TEXTBOOKS

1. Geoffrey Sampson, *"Perl for beginners"*, Geoffrey Sampson & Ventus Publishing ApS, 2010.
2. Mark Jason Dominus, Higher Order Perl, *"Transforming programs with programs"*; Morgan Kaufmann Publishers, 2005.

REFERENCES

1. Rex A. Dwyer, *"Genomic Perl: From Bioinformatics Basics to Working Code"* Cambridge University Press, 2003.
2. James Tisdall, *"Mastering Perl for Bioinformatics"*, O'Reilly Publications, 2003.
3. Brian D Foy, *"Mastering Perl"*, O'Reilly Publications, 2014.

LIST OF EXPERIMENTS (15 Hours)

1. Data types
2. Operators
3. Flow control
4. Built-in Functions
5. File handling
6. Pattern matching
7. Arrays
8. Lists
9. Multiple sequence alignment
10. Protein motifs
11. Fragment Assembly

Course Code	Course Title	L	T	P	C
GI2118	PYTHON	2	0	2	3
	Total Contact Hours -45				

PURPOSE
The purpose of this subject is to learn the python programming language and students should solve the biological problem using Python Programming.
INSTRUCTIONAL OBJECTIVES
To understand the basic of python programming
To learn the practical data management and manipulation tasks in python
To develop bioinformatics software development using Python programming

UNIT I - BASICS OF PYTHON (6 Hours)

Simple values – Booleans, Integers, Floats and Strings, Expressions – Numerical operators, Logical Operations, String Operations, Names, Functions and Modules – Assigning Names, Defining the functions – Function parameters, Comments and Documentation, Assertions, Default parameter values, Using Modules – Importing, Python Files.

UNIT II - COLLECTIONS & CONTROL STATEMENTS (6 Hours)

Sets, Sequences – Strings, Bytes and Bytearrays, Rangers, Tuples, Lists, Mappings – Dictionaries, Streams-Files & Generators, Collection-Related Expression Features – Comprehensions & Functional parameters, Control Statements – Conditionals, loops, Iterations, Exception Handlers, Extended Examples.

UNIT III - CLASSES & UTILITIES (6 Hours)

Defining Classes – Instance Attributes, Class Attributes, Class and Method Relationships – Decomposition, Inheritance, Utilities- System Environment, The File system, working with Text, Persistent Storage.

UNIT IV - PATTERN MATCHING, STRUCTURED TEXT (6 Hours)

Fundamental Syntax, The actions of the re Modules, results of re Functions and Methods, Putting it all together: Examples, Structured Text – HTML, XML.

UNIT V - WEB PROGRAMMING & RELATIONAL DATABASES (6 Hours)

Manipulating URLs, Opening Web Pages: web browser, Web clients, Web servers, Representation in Relational Databases, Using Relational Data, Structured Graphics – Introduction to Graphics Programming, GUI toolkits, Structured Graphics with tkinter, SVG with examples.

LIST OF EXPERIMENTS (15 Hours)

1. Overview of Python – Working with sequences

2. Parsing sequence file formats
3. Sequence objects
4. Sequence annotation objects
5. Slicing a sequence record
6. Parsing sequences from compressed files,
7. Sequence files as Dictionaries
8. Writing sequence and alignment files
9. Accessing and searching NCBI's Entrez databases
10. Analyzing the 3D structure using Python programming

TEXTBOOKS

1. Mitchell L. Model, *"Bioinformatics Programming using Python: Practical Programming for Biological Data"* , O'Reilly Media", 1st Edition, 2009.
2. Mark Lutz and David Ascher, *"Learning Python"*, O'Reilly Media, 5th Edition, 2013

REFERENCE

1. Jeff Chang et al, Biopython – *"Biopython Tutorial and Cookbook"*, Link: http://biopython.org/DIST/docs/tutorial/Tutorial.html, (2013)