University of North Bengal
Department of Bioinformatics

CHOICE BASED CREDIT SYSTEM (CBCS) SYLLABUS FOR M.SC.
Duration: Two years (Four Semesters); Total marks 1600 [64 CREDITS]
ACADEMIC YEAR 2021-2022

Semester I

Sem	Crs	Course	Course code	Paper type	Course name	Course type	Full Marks (External)	Full marks (Practical)	Full marks (Internal)	Total FM	Credit	Paper Sequence
1	332	M.Sc. in Bioinformatics	BINF-CT-101	T	Fundamentals of cell biology and genetics	Core theory	50		25	75	3.0	1
			BINF-CT-102A	T	Molecular Biology		25		25	75	3.0	2
			BINF-CT-102B	T	Biochemistry		25					3
			BINF-CT-103A	T	Basic Bioinformatics		25		25	75	3.0	4
			BINF-CT-103B	T	Basic Computer application		25					5
			BINF-CP-104	P	Fundamentals of cell biology and genetics	Core practical		50		50	2.0	6
			BINF-CP-105	P	Molecular Biology and Biochemistry			50		50	2.0	7
			BINF-CP-106	P	Basic Bioinformatics and Basic Computer Application			50		50	2.0	8
			BINF-CP-107	P	Assignments			25		25	1.0	9
						Total	150	175	75	400	16.0	

Semester II

Sem	Crs	Course	Course code	Paper type	Course name	Course type	Full Marks (External)	Full marks (Practical)	Full marks (Internal)	Total FM	Credit	Paper Sequence
2	332	M.Sc. in Bioinformatics	BINF-CT-201	T	Genomics and Proteomics	Core theory	50		25	75	3.0	1
			BINF-CT-202	T	Basic statistical techniques for Bioinformatics		50		25	75	3.0	2
			BINF-CT-203	T	Computer programming for Bioinformatics		50		25	75	3.0	3
			BINF-CP-204	P	Genomics and Proteomics	Core practical		50		50	2.0	4
			BINF-CP-205	P	Basic statistical techniques for Bioinformatics			50		50	2.0	5
			BINF-CP-206	P	Computer programming for Bioinformatics			50		50	2.0	6
			BINF-CP-207	P	Seminar/Assignments			25		25	1.0	7
						Total	150	175	75	400	16.0	

Semester III

Sem	Crs	Course	Course code	Paper type	Course name	Course type	Full Marks (External)	Full marks (Practical)	Full marks (Internal)	Total FM	Credit	Paper Sequence
3	332	M.Sc. in Bioinformatics	BINF-CT-301	T	Structural Bioinformatics	Core theory	50		25	75	3.0	1
			BINF-CT-302	T	Database management systems		50		25	75	3.0	2
			BINF-ET-303A	S	Evolutionary biology	*Elective theory (Choose any one)	50		25	75	3.0	3
			BINF-ET-303B	S	NGS and expression data analysis							
			BINF-ET-303C	S	Advance computer programming for Bioinformatics							
			BINF-ET-303D	S	Data Mining and Machine learning techniques for Bioinformatics							
			BINF-CP-304	P	Structural Bioinformatics	Core practical		50		50	2.0	4
			BINF-CP-305	P	Database management Systems			50		50	2.0	5
			BINF-EP-306	P	Corresponding to Elective Paper BINF-ET-303			50		50	2.0	6
			BINF-CP-307	P	Seminar/Assignments			25		25	1.0	7
						Total	150	175	75	400	16.0	

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Semester IV

Sem	Crs	Course	Course code	Paper type	Course name	Course type	Full Marks (External)	Full marks (Practical)	Full marks (Internal)	Total FM	Credit	Paper Sequence
4	332	M.Sc. in Bioinformatics	BINF-CT-401	T	Research Methodology & Scientific Writing	Core theory	50		25	75	3.0	1
			BINF-CT-402	T	Bioethics , Biosafety and IPR		50		25	75	3.0	2
			BIF-ET-403A	S	Chemo-informatics and Drug designing	*Elective theory (Choose any one)	50		25	75	3.0	3
			BIF-ET-403B	S	System Biology							
			BIF-ET-403C	S	Web-based Programming							
			BIF-ET-403D	S	Python programming for bioinformatics							
			BINF-CP-404	P	Dissertation/Review/Project work and viva	Practical		100		100	4.0	4
			BINF-CP-405	P	Industry visit/institute visit/Internship			25		25	1.0	5
			BINF-CP-406	P	Comprehensive viva			50		50	2.0	6
						Total	150	175	75	400	16.0	

Detailed Syllabus of M.Sc. in Bioinformatics:

Semester-I

BINF-CT-101	**Fundamentals of Cell Biology and Genetics**
Unit-1	Basics of cell biology: Structure and Functions of Cellular Organelles, Cell Cycle, Chromosome Structure, Cellular Metabolic Pathways
Unit-2	Genetic organization of prokaryotes and eukaryotes including nuclear genome and organelle genome; DNA as the genetic material (experimental evidences); central dogma; genome complexity; C-value paradox, Cot value, repetitive DNA, satellite DNA; gene structure in prokaryotes and eukaryotes; split genes, overlapping genes, pseudogenes
Unit-3	Condensation of chromosome, Lampbrush chromosome, Polytene chromosome, Supercoiling of DNA, nucleosomes, DNA methylation, genetic imprinting, epigenetic inheritance, Transposable elements, types of transposable elements, mechanism of transposition, retroposons and its types.
Unit-4	Introduction, concepts and theories of Mendelian genetics, chromosome theory of inheritance, Non Mendelian Inheritance, gene interaction, linkage and crossing over, twopoint and three point mapping, linkage map
Unit-5	Chromosome structure, organization, and classification, normal karyotype, chromosomal abnormalities, mutations and repair, idiogram, imprinting
Unit-6	Gene pools, allele frequencies, Hardy Weinberg equation, non random breeding, genetic drift, gene flow, selection, speciation. Protein and DNA sequence polymorphism, mutation detection, analysis of DNA length polymorphism, analysis of single nucleotide polymorphisms
Suggested readings	B. Alberts et. al.; Molecular biology of the cell; Taylor & Francis Publishers, 2014.; 6th edition. T. A. Brown; Genomes 3; Oxford: WileyLiss, 2007; 3rd edition G. M. Cooper and R. E. Hausman; The cell: A molecular approach; ASM Press, 2009; 5th edition - Hickey G. I. , Fletcher H. L., Winter P. Instant Notes: Genetics 3rd Edn. Publisher: Taylor & Francis group, 2007.
BINF-CT-102A	**Molecular Biology**
Unit-1	DNA Replication: Prokaryotic and eukaryotic DNA replication, Mechanics of DNA replication, enzymes and accessory proteins involved in DNA replication and DNA repair. Transcription: Prokaryotic transcription, Eukaryotic transcription, RNA polymerase, Regulatory elements in mechanisms of transcription regulation, Transcriptional and post-transcriptional gene silencing. Modifications in RNA: 5'-Cap formation, Transcription termination, 3'-end processing and polyadenylation, Splicing, Editing, Nuclear export of mRNA, mRNA stability
Unit-2	Translation: Prokaryotic and eukaryotic translation, the translation machinery, Mechanisms of initiation, elongation and termination, Regulation of translation, co- and post translational modifications of proteins.
Unit-3	Molecular markers in genome analysis: RFLP, RAPD and AFLP analysis, Molecular markers linked to disease resistance genes, Application of RFLP in

	forensic disease. prognosis, genetic counseling, Pedigree, varietal etc
Unit-4	Genome Sequencing: Genome sizes., organelle genomes, Genomic libraries, YAC, BAC libraries, Strategies for sequencing genome
Suggested readings	- Bruce Alberts, Alexander Johnson, Julian Lewis; Molecular Biology of the Cell; Taylor & Francis Group / Spon Press (2015); 6th Ed. - Benjamin Lewin; Genes IX; Jones and Bartlett Publishers - James D Watson, Tania A Baker, Stephen P Bell; Molecular Biology of the Gene; Pearson Education Limited 2017 - Gerald Karp; Cell and Molecular Biology; John Wiley 2013; 5th Edition; H. Lodish, A. Berk, S. L. Zipursky, P. Matsudaira, D. Baltimore and J. Darnell; Molecular Cell Biology; W. H. Freeman & Comp., 2007; 6th edition
BINF-CT-102B	**Biochemistry**
Unit-1	Principles of physical chemistry applied to biochemistry: chemical forces, hydrophilic and hydrophobic forces, van der Waal's forces, electrostatic interaction, hydrogen bonding. Acids and bases – definitions, chemical equilibrium, ionic product of water, pH, pKa, acid titration curves and buffer solutions. Introduction to thermochemistry – energy, enthalpy and entropy, different types of systems, laws of thermodynamics, spontaneous reactions
Unit-2	Structures and conformations of nucleosides, nucleotides and dinucleosides, base pairs, base triples and base quartets; Unique properties of Watson and Crick pairs and duplex DNA structure, Non Watson and Crick base pairs, DNA structural polymorphism B-DNA, A-DNA, Z-DNA. Structure of duplex RNA, Structure of yeast tRNAPhe; RNA structural motifs−U turn, hairpins, pseudoknot; structure of hammerhead ribozyme, antisense oligonucleotides and small interfering RNA
Unit-3	Structure, properties and classification of amino acids, peptide conformation and Ramachandran map, secondary structural motifs, super secondary structural motifs and domains, tertiary and quaternary structures of proteins. Structure-function correlation of a few globular, fibril proteins, membrane proteins and transporters
Unit-4	What is the protein folding problem? Anfinsen's experiments, Levinthal paradox and free energy funnel, folding intermediates, protein misfolding, roles of chaperones and chaperonins
Suggested readings	R. Myers; Basics of Chemistry; Greenwood Press, USA, 2003. - D.L. Nelson and M.M. Cox; Principles of Biochemistry; 5th edition, Freeman & Co. NY, 2008. L. Stryer; Biochemistry, 5th edition, W H Freeman & Co, 2002. C. Branden and J. Tooze; Introduction to Protein Structure; Garland Publishing, NY, 1991. W. Saenger; Principles of Nucleic Acid Structure; SpringerVerlag, NY, 1984.
BINF-CT-103A	**Basic Bioinformatics**
Unit-1	Introduction and scope of Bioinformatics, DNA and protein sequences, genome and transcriptome, extracting, collecting and storing sequences; various file

	formats for bio-molecular sequences: GenBank, FASTA, GCG, MSF, NBRF-PIR.
Unit-2	Introduction to Biological Databases; nucleic acid sequence databases: GenBank, EMBL, DDBJ; protein sequence databases: Uniprot-KB: SWISS-PROT, TrEMBL; repositories for high throughput genomic sequences: EST, STS GSS; Genome databases at NCBI, EBI, TIGR, SANGER; structure databases: PDB, NDB, PubChem, ChemBank. Identification and interpretation of patterns in sequences; sequence patterns: InterPro, Prosite, Pfam, ProDom; structure patterns: FSSP, DSSP.
Unit-3	Pairwise and Multiple sequence alignments: basic concepts of sequence alignment, Use of pairwise alignments and Multiple sequence alignment for analysis of Nucleic acid and protein sequences and interpretation of results. Algorithms used in sequence alignments- Needleman–Wunsch algorithm & Smith–Waterman algorithm. Sequence-based Database Searches: BLAST and FASTA , various versions of basic BLAST
Unit-4	Dot plot, basic concepts of sequence similarity, identity and homology, definitions of homologues, orthologues, paralogues; Scoring matrices: basic concept of a scoring matrix, PAM and BLOSUM series
Suggested readings	● N. Gautham; Bioinformatics: Databases and Algorithms; Alpha Science, 2006. ● D. W. Mount; Bioinformatics Sequence and Genome Analysis; Cold Spring Laboratory Press, 2001. ● A. M Lesk; Introduction to Bioinformatics; Oxford University Press, 2002. ● J. Bedell, I. Korf and M. Yandell; BLAST; O'Reilly Press, 2003. ● J. M. Keith; Bioinformatics Vol. 1, Data, sequence analysis & evolution; Humana Press, 2008. ● R. Durbin; Biological sequence analysis; Cambridge University Press, 1998
BINF-CT-103B	**Basic Computer Application**
Unit 1	Computer Fundamentals - Number systems; Representation of integers, fixed and floating point numbers, character representation: ASCII, EBCDIC. Functional units of computer, I/O devices, Computer memory, primary and secondary memories; Concepts of Hardware and Software.
Unit 2	Basics of Operating System; Popular Operating Systems (Windows, Linux, DOS); Basic commands of DOS operating system, File management in DOS, Linux Operating System Layers, The Linux Shell (different kinds of shell), Process: (parent and child processes), Files and Directories (File Structure and directory structure), Interaction with System, shell commands, Regular expressions of Linux (awk, grep, sed)
Unit 3	Basic of Computer networks; Types of Networking - LAN, MAN, WAN; Data communication; ISO-OSI references model, TCP/IP reference model. Concept of Internet; WWW and Web Browsers; Search Engines; Understanding URL, Internet protocol- FTP, SMTP. Web page designing – HTML.
Unit 4	Computer graphics basics; Graphics I/P Devices; Development of computer graphics: Basic graphics system and standards.

	Raster scan and random scan graphics, Frame buffer and bit operations, Concepts in raster graphics; Points, Lines and Curves; Scan conversion; Line-drawing algorithms; Circle and ellipse generation; Polygon filling; Conic-section generation. Three-dimensional concepts: 3-D representations and transformations; 3-D viewing; Algorithm for 3-D volumes, Spline curves and surfaces.
Suggested readings	● Buyens, Jim. 2002. Microsoft FrontPage -Inside Out. Microsoft Press. ● Cox, V., Wermers L. and Reding E. E. 2006. HTML Illustrated Complete. Course Technology. ● Niederst, J. 2001. Web Design in a Nutshell. O'Reilly Media, Inc. ● Tanenbaum, A.S. 2003. Computer Networks. Prentice Hall of India, New Delhi.
BINF-CP-104	**Fundamentals of cell biology and genetics (Practical)**
	● Orcein and Feulgen staining of metaphase plates; preparation of karyotype and idiogram. ● Linear differentiation of chromosomes through G-banding, C-banding and Q-banding ● Study of Meiotic chromosome complements ● Induction of polyploidy using colchicine; different methods of application of colchicine ● Microscopic studies of microbial morphology (shape, size, arrangement etc.) and Microbial staining techniques (Simple staining; Gram staining; Flagella staining; Cell wall staining; Negative staining) ● Probability and chi-square test for genetic analyses for goodness of fit ● Human genetics- study of simple human traits
BINF-CP-105	**Biochemistry and Molecular Biology (Practical)**
	● Standard buffer solution preparation and pH determination ● Estimation of protein concentration using Lowry and Bradford methods ● Separation of plant pigments by thin layer chromatography ● Isolation of genomic and plasmid DNA and analysis by agarose gel electrophoresis ● Separation of proteins by SDSPAGE, followed by silver staining ● PCR and RAPD analysis. ● PCR primer designing; Plasmid vector designing
BINF-CP-106	**Basic Bioinformatics and Computer application(Practical)**
	● Retrieval of DNA/RNA/protein sequences from databases; Biological sequence editing and analysis; Data mining tools ● Exploring the integrated database system at NCBI server and querying the PUBMED and GenBank databases using the ENTREZ search engine ● Sequence alignment: database searches (BLAST, FASTA etc.), PSA and MSA ● Phylogenetic tree construction, Bootstrapping ● Codon Usage analysis bias prediction ● Network and mail configuration ● Web page designing using HTML; Designing static website with features like tables, hyperlink among pages, pictures, frames and layers ● Shell: Basic commands of a shell, internal vs external commands (working on multiple shell commands and understanding of how it interacts with Linux) ● Shell programming (working on core shell programming in sync with Linux)

BINF-CP-107	Assignments
	Four (4) assignments based on application of basic bioinformatics tools and databases for analyzing experimental data. Students have to complete the assignment individually in stipulated time.

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Semester-II

BINF-CT-201	**Genomics and Proteomics**
Unit 1	History of genomics; genome projects of model organisms; human genome structure and comparative, genomics. Genomic elements, SNPs and genome-wide association studies
Unit 2	Principle of and output from Sanger's dideoxy method versus NGS; shotgun sequencing method and library preparations, comparative study of standard NGS methods
Unit 3	Methylation of DNA and genetics; histone modifications, HATs and HDACs in the context of gene expression regulation. ChIP-chip and ChIPseq techniques; miRNA, siRNA and piRNAs. Alternative splicing: basic concept and significance, prevalence across species and human tissues, types and mechanisms
Unit 4	Introduction to metabolomics: metabolome, metabonomics, metabolite profiling, metabolome fingerprinting, role of biomarker in metabolomics, tools of metabolome studies: NMR, MS, GC, LC, IR and its application, metabolome projects of plant and human, future prospective of metabolomics
Unit 5	Proteome profiling methods, 2-D electrophoresis image comparisons; yeast two hybrid system, protein arrays, mass spectrometry data processing and analysis; pathway analysis and identifying Protein-protein interactions with mass scale expression data.
Suggested readings	T. A. Brown; Genomes; Bios Scientific Publishers Limited, 2002. B. R. Korf and M. B. Irons; Human Genetics and Genomics; Wiley, 2013, 4th edition. A. M. Lesk; Introduction to Genomics; Oxford University Press, 2012, 2nd edition J. P. Tremblay and J. Paul; An Introduction to Data Structures with Applications; McGraw Hill, 1984, 2nd edition. 2. G. P. Quinn and M. J. Keough; Experimental Design and Data Analysis for Biologists; Cambridge University Press, 2002 A. Zhang, Advanced Analysis of Gene Expression Microarray Data; World Scientific Publishing, 2006 N. RodriguezEzpeleta; Bioinformatics for High Throughput Sequencing; Springer; 2012.
BINF-CT-202	**Basic statistical techniques for Bioinformatics**
Unit 1	Basic concepts of statistics, data presentation and tabulation; Box-plot, Stem and leaf plot Descriptive statistics: measures of central tendency; measures of dispersion.
Unit 2	Theory of probability; Random variable; Discrete and continuous probability distribution. Fitting of distributions: Binomial, Poisson and Normal. Testing of hypothesis; t-test, chi-square test, F-test.

	Non-parametric tests - Sign, Wilcoxon, Mann-Whitney Utest, Wald Wolfowitz run test, Run test for the randomness of a sequence. Median test, KruskalWallis test.
Unit 3	Statistical Inference: Properties of estimation theory, Methods of estimation; Maximum likelihood estimation, Ordinary least square, Confidence Intervals, Classical Hypothesis Testing, P-Values, Testing for the Parameters in a Multinomial Distribution, Association tests, Likelihood Ratios. Differential Expression – Multiple Genes: The False Discovery Rate (FDR), Bootstrap Methods: Estimation and Confidence Intervals, Bayesian inference: Monte Carlo Markov Chain, The Hastings–Metropolis Algorithm, Gibbs Sampling;
Unit 4	Concept of sampling; sampling and complete enumeration; sampling from finite population; simple random sampling (SRS). Concepts of correlation and regression; Rank correlation, partial correlation coefficient, linear regression model; ordinary least square method and generalized least square method for parameter estimation. Analysis of variance (ANOVA), Analysis of covariance (ANCOVA)
Suggested readings	● Gupta, S.C. and Kapoor, V.K. 2007. Fundamentals of Mathematical Statistics. Sultan Chand and Sons. ● Campbell, R.A. 1974. Statistics for Biologists. Cambridge University Press. ● W. Warren John Ewens, Gregory Robert Grant 2001. Statistical Methods in Bioinformatics: An Introduction. Springer
BINF-CT-203	**Computer programming for Bioinformatics**
Unit 1	Techniques of problem solving, Algorithm development, Flowcharting, Stepwise refinement. Concepts of programming language, types of programming language, imperative language, procedural programming language and object oriented programming language. Compiler, Interpreter, Loader and Linker.
Unit 2	Procedural programming language; C programming language, data types, keywords, operators and expressions; I/O library function, control statements, function, function prototype, type of functions; local and global variables.
Unit 3	Structured programming; Object oriented programming, C++ and Java; Classes, objects, Abstract data types, Data types, Operators (Arithmetic, Logical and Comparison) and expressions. Branching and iteration, Arrays, Object/Message paradigm. Data encapsulation- modules and interfaces; Polymorphism - Static and dynamic binding, Inheritance: class and object inheritance.
Unit 4	Perl: Introduction, Scalar, Arrays and List Data, Control Structures, Hashes, String Handling, Regular Expressions; Subroutines, File handling, Directory Access and Formatting, CGI Programming: CGI Module, Passing Parameters via CGI and Perl, Object oriented, Creating Objects.
Suggested readings	● Petersen, R. 2007. Linux: The Complete Reference, Sixth Edition. Mcgraw-Hill Education. ● Sethi, R., 1996, Programming Languages, Addison-Wesl. ● Gottfried, B.S., 1998 Schaum's Outline of Theory and Problems of Programming with C, McGraw-Hill. ● James Tisdall. 2001. Beginning Perl for Bioinformatics. O-Reilly. ● Randal L. Schwartz, Tom Phoenix, brian d foy. 2008 .Learning Perl. O-Reilly.
BINF-CP-204	**Data analysis in Genomics and Proteomics (Practical)**
	● Explore comparative genomics resources and NCBI and EBI

	- Assembling and editing of Genomic data; Genome alignment and analysis tools- BWA (BurrowsWheeler Aligner), SAMtools, GATK (The Genome Analysis Toolkit), IGV (Integrative Genomics Viewer) - Assembling short reads from a organism using VELVET; computing N50/L50, coverage and length of longest contig. - Annotate a given assembled genome using gene prediction tools including GenScan and Augustus; BLAST the predicted genes against databases for functional annotation - Explore and query SNP and SNP-related databases - Map reads from CHiPseq experiment to the respective reference genome and identify peaks using MACS - Explore and query the protein-protein interaction databases like DIP, PPI Server, GRID, InterPreTS etc.
BINF-CP-205	**Basic statistical techniques (Practical)**
	- Data analysis using descriptive statistics measures in Microsoft excel - Correlation studies of data - Error analysis and error bars - Binomial, Poisson and Gaussian distrbutions and deviates - Testing of hypothesis using t-test, F-test, chi-square test - Nonparametric tests – Wilcoxon Mann Whitney tests, Kruskal Wallis test - Fitting of regression model and parameter estimation using OLS and GLS - Application of ANOVA and ANCOVA in Bioinformatics - R graphics library: Line plots, histograms, pie charts, bar plots and other plots
BINF-CP-206	**Computer programming (Practical)**
	- Writing C script, variable declaration, functions, arithmetic and logical operations - Working with arrays single and multi dimensional; control/condition statements; iterations and looping - Programming in Java, declaring objects, methods and constructor, packages and arrays, multithreading, file handling, exception handling. - Designing PERL program for analysis of nucleotide and protein sequences; Uses of Scalar and Array Variables to manipulate DNA/RNA/Protein sequence data - Reading a sequence data from a file and writing the results to a file; Concatenation DNA fragments, Transcribing DNA into RNA; Calculating the Reverse complement of a DNA strand; Uses of subroutine to read FASTA files - Uses of Regular Expressions - Uses of Bio-PERL modules for sequence manipulation, accessing local database
BINF-CP-207	**Seminar/Assignment**
	A seminar topic will be allotted to individual student according to his/her area of interest (students are also suggested to propose topics with relevant published information during the time of allotment), on which a ppt presentation may be produced as per schedule. Assignments may also be given to students based on relevant topics.

Semester-III

BINF-CT-301	**Structural Bioinformatics**

Unit- 1	Proteins: Amino acid components and structural features; Primary, secondary, tertiary, quarternary and supra-molecular structures; Non-covalent interactions in relation to structural conformation; Ramachandran plots; Secondary structures, motifs and folds; Amino acid sequencing and purification strategies
Unit-2	Methods for determining structure of biomolecules (X-ray, CD, NMR, IR, UV Visible, Fluorescence, SEM etc) and their limitations.
Unit-3	Molecular structures – visualizing and graphical representations. Calculation of geometric parameters (bond distance, bond angle, dihedral angle). Identifying intramolecular and inter molecular interactions from crystal structures (using GUI).
Unit-4	Protein structures comparison and alignment: general approach, comparison algorithm and optimization (CE, VAST, DALI), concept of coordinate transformation, RMSD, Z score for structural comparison; identifying structural domains in protein, first and second-generation algorithms for domain assignments, domain assignment based on graph theoretical methods, Prediction of binding sites and characterization.
Unit-5	Prediction of protein structure from sequences- Homology modelling, Fold recognition and Ab-initio method; functional sites prediction; Protein folding problem; Secondary structure analysis and prediction; motifs, profiles, patterns and fingerprints search, protein structural databases (PDB)
Unit-6	Molecular dynamics: -Introduction, Newton's equation of motion, equilibrium point, radial distribution function, pair correlation functions, MD methodology, periodic box, algorithm for time dependence; leapfrog algorithm, Verlet algorithm, Boltzman velocity, time steps, duration of the MD run. Starting structure, analysis of MD job, uses in drug designing, ligand protein interactions.
Suggested readings	● F. J Burkowski; Structural Bioinformatics An Algorithmic Approach; CRC Press, 2009 ● P. E. Bourne and J. Gu; Structural bioinformatics; 2nd edition. John Wiley and Sons. 2009. ● A. Leach; Molecular modelling – principles and applications; Pearson Education Ltd, 2001 ● M.J.E Sternberg; Protein Structure Prediction: A Practical Approach. Publisher: USA; Oxford University Press, 1997
BINF-CT-302	**Database management systems**
Unit 1	Database system - Operational Data, Characteristics of database approach, architecture. Overview of DBMS; Data associations - Entities, Attributes and Associations, Relationship among Entities, Representation of Associations and Relationship, Data Model classification.
Unit 2	Entity Relationship model; Relational Data Structure- Relations, Domains and Attributes, Relational Algebra and Operations, Retrieval Operations. Relational Database Design - Anomalies in a Database, Normalization Theory, and Normal forms; Query processing and optimization; Security, backup and recovery.
Unit 3	Distributed Databases- concepts, architecture, design; Object Oriented databases; Structured Query Language (SQL) - Data Definition Language (DDL), Data Manipulation Language (DML) and Query by example.

	PL/SQL - Stored procedure, Database triggers; Relational Data Base Management Package.
Unit 4	Transaction management: ACID properties, serializability and concurrency control, Lock based concurrency control (2PL, Deadlocks), Time stamping methods, optimistic methods, database recovery management.
Suggested readings	● Date, C. J. 2000. Introduction to Database System. Addison Wesley. ● Desai, B. C. 2000. Introduction to Database Systems. Galgotia Publications, New Delhi. ● Elmasri and Navathe. 2006. Fundamentals of Database Systems. Addison Wesley. ● Garcia-Molina, H., Ullman, J. D. and Widom J. 2002. Database Systems: The Complete Book. Prentice Hall.
BINF-ET-303	**Elective Theory Course (Any one of the following)**
BINF-ET-303A	**Evolutionary Biology**
Unit-1	Background Knowledge: Evolutionary Biology – From atoms to molecules to life, Hypothesis of evolution, Darwin's theory of evolution, From taxonomy to molecular phylogenetics – Linnaeus' classification systems- Whittaker's five kingdom system.
Unit-2	Tree concept: Molecular data as molecular fossils; Molecular-clock-hypothesis; The terminology of phylogenetics- Trees, Root, branches, Node, Leaf, Clade; lineage sorting, orthology, paralogy, xenology; "basal" lineages, crown vs. stem groups, Phylogram vs. cladogram
Unit-3	Molecular phylogeny : Gene phylogeny vs. species phylogeny; Different types of trees- rooted vs. unrooted trees, dichotomy vs. polytomy, monophyletic vs. paraphyletic, ultra- metric vs. unconstrained; Constructing molecular phylogenetic trees-Choice of molecular markers
Unit-4	Phylogenetic Algorithms: Clustering based methods-UPGMA and neighbor joining, Optimality based: Fitch-Margoliash and minimum evolution algorithm; Character based methods- Maximum Parsimony (MP) and Maximum Likelihood (ML) methods; Bayesian inference, Evaluation of phylogenetic trees-reliability and significance; Boot strapping; Jackknifing
Unit-5	Phylogenetic software & applications: Multiple sequence alignment & Tree building software - ClustalW, Mega, Phylip, Phylodraw, Phyml, RaxML; Case studies- Phylip/Mega
Unit-6	Comparative methods for detection of species / organism relationships -Gene duplication, Horizontal transfer, Domain evolution
Suggested readings	● L. Bromham ; Reading the Story in DNA: A Beginner's Guide to Molecular Evolution; Oxford University Press, 2008 ● G. Bernardi; Structural and Evolutionary Genomics: Natural Selection in Genome Evolution (New Comprehensive Biochemistry); Elsevier Science, 2005. ● M. Salemi and Anne-Mieke Vandamme; The phylogenetic handbook: a practical approach to DNA and protein phylogeny; Cambridge University Press, 2003 ● L. Patthy; Protein Evolution; Blackwell Science Ltd., 1999. ● D. Graur and W.H Li; Fundamentals of molecular evolution ; Sinauer Associates, 1991.
BINF-ET-303B	**NGS and expression data analysis**

Unit-1	Overview of next generation sequencing technology (Roche/454 FLX, Illumina Genome Analyzer, SOLiDTM sequencing, Ion TorrentTM, Nanopore), data processing, NGS and genetics of complex disease, exome sequencing, Overview of RNA-seq experiments and data analysis	
Unit-2	NGS Data Quality Control methods, NGS Data Structure, Resources and Repositories, genome annotations, haplotyping (concepts and application), SNP technologies (platforms and analysis)	
Unit-3	Overview of metagenomics principles, microbial and ecological aspects underlying metagenomic experiments; 16SrRNA data analysis, clustering/phylogenetic tree based of alignment, clustering based on composition. Concepts behind self organizing maps, principal component and other clustering tools	
Unit-4	DNA microarray- understanding of microarray data, normalizing microarray data, detecting differential gene expression, correlation of gene expression data to biological process and computational analysis tools (especially clustering approaches); expression analysis using RNAseq data	
Unit-5	MicroRNA and genomewide profiling: miRNA and human disease, significance of miRNA profiling, genomewide profiling of miRNA by microarray. RNAi: what are RNAi and siRNA, RNAi mechanism, siRNA applications, siRNA design, siRNA resources, siRNA information	
Unit-6	Metabolic pathway analysis: macromolecular networks, topology of macromolecular networks, modulatory and dynamics of macromolecular networks, inference of regulatory networks, simulation of molecular networks, simulation of biological processes	
Suggested readings	● G.P. Quinn and M. J. Keough; Experimental design and data analysis for biologists; Cambridge University Press, 2002. ● S. Knudsen; Guide to analysis of DNA microarray data; Wiley, 2nd edition, 2004 ● N. RodriguezEzpeleta; Bioinformatics for High Throughput Sequencing; Springer; 2012. ● Y. M. Kwon and S. C. Ricke; HighThroughput Next Generation Sequencing: Methods and Applications; Humana Press; 2011. ● S. M. Brown; Next Generation DNA Sequencing Informatics; Cold Spring Harbor Laboratory Press;2013	
BINF-ET-303C	**Advance computer programming for Bioinformatics**	
Unit 1	Overview of Parallel Computing, Concepts and Terminology. Parallel Computer Memory Architectures, Parallel Programming Models: parallelizing compilers, parallel languages, message-passing, virtual shared memory, object-oriented programming, and programming skeletons.	
Unit 2	Bioperl: Introduction, Modules: SeqIO, SearchIO, Seq Feature, Finding introns, Alignments, LiveSeq and Tree.	
Unit 3	R: open-source language and environment for statistical computing and graphics Bioconductor - open-source software for the analysis of biomedical and genomic data, mainly R packages. Analysis of microarray data, Next Generation Sequencing (NGS) data etc.	
Unit 4	Introduction to Python Programming, Features of Python, Python interpreter interactive and non-interactive mode.	

	Functions: Introduction, Defining and Calling a Void Function, Designing a Program to Use Functions, Local Variables, Passing Arguments to Functions, Global Variables and Global Constants, Value-Returning Functions Generating Random Numbers, Writing Our Own Value-Returning Functions, The math Module, Storing Functions in Modules. Application of Biopython in Bioinformatics.
Suggested readings	● Sriram Srinivasan.1997. Advanced Perl Programming. O-Reilly. ● Tim Bunce and Alligator Descartes. 2000. Programming the Perl DBI. O-Reilly. ● Kinser J. 2008 Python for Bioinformatics, Series in Biomedical Informatics, Jones & Bartlett. ● Robert Orfali and Dan Harkey. 1999 .Client/Server Programming with JAVA and CORBA. John Wiley.
BINF-ET-303D	**Data mining and Machine learning techniques for Bioinformatics**
Unit 1	Overview of machine learning techniques; supervised and unsupervised techniques. Empirical Risk Minimization, Structural Risk Minimization; Measuring the accuracy of learned hypotheses. Comparing learning algorithms: cross-validation, learning curves, and statistical hypothesis testing.
Unit 2	Classification: Decision tree, Bayesian, Rule based classification, ANN, SVM, KNN; Case based reasoning and Applications in Bioinformatics. Clustering: Partition Methods, Heirarchical methods, Density based methods, Grid based clustering, Model based clustering, clustering of high dimensional data, constraints based clustering, Analysis of MD trajectories, Protein Array data Analysis.
Unit 3	Dimensional Reduction Techniques, Methods of Feature Selection, Resampling Techniques, Elements of Text Mining and Web Mining, Soft Computing and Fuzzy logic system & application in bioinformatics.
Unit 4	Introduction to Data mining, Data mining Functionalities, Classification of Data mining Systems, Data Mining Task Primitives, Integration of Data mining systems, Major issues of Data mining. Data mining: Basic concepts of Knowledge discovery and Data Mining, Application of data mining in bioinformatics. Data Preprocessing, Data Cleaning, Data Integration and Transformation, Data Reduction, Data discretization and concept hierarchy generation.
Suggested readings	● Witten, H. I., Frank, E. and Hall, M. A. 2011. Data Mining: Practical Machine Learning Tools and Techniques. ● Hastie, T., Tibshirani, R., Friedman, J. H. 2009. The Elements of Statistical Learning: Data Mining Interface and Prediction. ● Clarke, S. B., Fokoue, E. and Zhang, H. H. 2009 Principles and Theory for Data Mining and Machine Learning.
BINF-CP-304	**Structural Bioinformatics (Practical)**
	● Evaluation and visualization of 3D structure of biomolecules using open source resources ● Introduction to PDB files – editing-fixing Non-standard residues and alternate conformers. Extracting sequence from coordinates. Editing PDB files – chain ids, residue numbers etc.

	- Inducing point mutations and analyzing molecular interactions, intra and inter molecular interactions, salt bridges and crystal contacts - Calculation of RMSD between two protein structures using C-alpha, main chain atoms, all common atoms as equivalent pairs. - Homology modelling using MODELLER. - Evaluation and Validation of protein models using Procheck, WHATIF, VERIFY 3D - Molecular simulation studies in vacuo, implicit solvent as well as explicit solvent methods using GROMACS. Analysing a molecular dynamics trajectory.
BINF-CP-305	**Database management systems (Practical)**
	- E-R diagram construction; - SQL - Command Syntax, SQL constraints, Data types, DDL Statements, DML Statements, - SQL-expressions, Creating database using SQL, CREAT, DROP or DELETE table - SQL operators, SELECT, INSERT, WHERE, AND, OR. - SQL UPDATE query, DELETE query - Integrity constraints; Triggers, creating stored procedures/ functions; - Normalization of database and Case study on a database design and implementation using SQL and Oracle. - Relational DBMS using SQL. - SQL Transactional control commands, COMMIT, ROLLBACK, SAVEPOINT, SET TRANSACTION.
BINF-EP-306	**Corresponding to Elective Paper BINF-ET-303**
	Evolutionary Biology (Practical) - Reconstruction of phylogenetic trees using molecular data – UPGMA, Neighbour-joining, Maximum parsimony and Maximum likelihood method - Using bootstrapping tool to generate multiple datasets from the original input data & generation of consensus tree - Plotting, visualizing & formatting phylogenetic trees: TreeView and FigTree - Molecular divergence or clock analysis - Reconstruction of phylogenetic trees using whole genome data of viruses - Numerical taxonomy & Bacterial identification using matrices - Identification of horizontal gene transfer events from phylogenetic trees
	NGS and expression data analysis (Practical) - Exploring the Gene expression databases like GEO, SRA etc - Microarray data analysis- understanding of microarray data, normalizing microarray data, detecting differential gene expression - Mapping RNAseq dataset onto the reference genome; extract read counts per gene using a gtf file; compute RPKM; find out genes differentially expressed between two samples; identify biomarker using DESeq (R package). - Map RNAseq reads to the reference genome using Tophat to identify differential splice events and fusion transcripts.

	• Assemble two transcriptomes using Trinity and compare the gene expression using cufflink, cuffdiff family of tools • Classify the phylum using a dataset of 16SrRNA sequencing of a microbiome using QIIME; identify differential microbial population between two samples both at the OUT level and abundance
	Advance computer programming for Bioinformatics (Practical)
	• Sequence analysis and alignment using Bioperl • Parallel Programming with MPI, Parallel Programming with OpenMP. • R programming for analysing gene expression data, RNA seq data. • Bio-conductor and R package for analysis of biological data • Declaring function in R, creating package in R. • Basic syntax; variables; operators (basic python programming) • Decision making; loops (selection and iterations in python programming) • Numbers, lists, strings, tuples and dictionary (advanced data structures in python programming). • Functions in python; modules in python (function and module orientation in python programming)
	Data mining and Machine learning techniques for Bioinformatics (Practical)
	• Generalized linear model prediction based on real data, error minimization of the model and cross validation using ROC curve. • Regularized regression model , Ridge regression, LASSO for prediction • Decision tree, random forest based prediction • Classification techniques: ANN, SVM, KNN. • Case based reasoning and its applications on biological data. • Clustering techniques; Clustering of high dimensional data; clustering of gene expression data. • Dimensional reduction techniques; Principal component analysis, feature selection technique. • Re-sampling techniques; bootstrap for estimation and model validation. Text mining and Web mining. Soft Computing and Fuzzy logic system and application in bioinformatics
BINF-CP-307	**Seminar/Assignment**
	A seminar topic will be allotted to individual student according to his/her area of interest (students are also suggested to propose topics with relevant published information during the time of allotment), on which a ppt presentation may be produced as per schedule. Assignments may also be given to students based on relevant topics.

Semester-IV

BINF-CT-401	**Research Methodology and Scientific Writing**
Unit- 1	Introduction to Research- Definition, Objectives and Characteristics of research, Types of Research- Basic, Applied and Action research, Exploratory and Descriptive, Ex-post facto research

Unit-2	Identification of Research Problem Sources of research problem, Criteria for the selection of research problem. Research design, Rationale, Statement of problem, Setting objectives. Definition of concepts, operational definition, variables independent and dependent, control and intervening variables, limitations and delimitation. Hypothesis - Meaning and importance, types of hypotheses
Unit- 3	Methods of Collecting Primary Data- Questionnaire, preparation of schedules, interview method, case study method, experimentation method and sources of secondary data. Editing and Coding the Data. Organization of Data - Classification - meaning and objectives, types of classification. Representation of Data - Diagrammatic and graphical representation - significance of diagrams and graphs
Unit-4	Introduction to Biostatistics: Variable and attribute; Population vs. sample; Census vs sample survey; Arrangement of data; Frequency distribution. Graphical presentation of data: Line diagram; Bar diagram; Pie chart; Histogram, Level of significance, Probability, Normal distribution, Error of inference, Student's t-test, Paired t-test, Fisher's t-test, Chi-square test. Introduction to SPSS
Unit-5	Introduction - Types of scientific writings - Thesis or dissertation writing – Research paper writing; Types of publications - Open access and subscription based resources; Scientific paper writing - Choosing a journal- Instructions to authors - Structure and Style- Authorships –figures tables with legends - References and citations - Acknowledgements- Conflict of interest; Peer review mechanism and publication process; Scientometric Analyses of a paper/journal; Ethics in publishing and Plagiarism issues. Use of software for Reference Management – (Mendeley/endnote) and detection of Plagiarism (turnitin)
Suggested readings	R. A. Day; Scientific English: A Guide for Scientists and other Professionals. Greenwood Press; 3rd Revised edition, 2011. Y.N. Bui; How to Write a Master's Thesis Paperback; 2nd edition, 2013.
BINF-CT-402	**Bioethics , Biosafety and IPR**
Unit-1	Good laboratory practice, Good manufacturing practice and National and International regulations - Regulations for recombinant DNA research and manufacturing process - Bio-safety and Bioethics - Regulations for clinical trials, Documentation and Compliance, in India and selected countries - Rules for import and export of biological materials.
Unit-2	The importance and needs of bioethics; Bioethical business practices; Laws and bioethics; Environmental protection; Creating awareness and safeguarding health of consumers; Fair trade practices; Combating plagiarism; Various ethical issues related to genetic studies, human genome project-stem cell applications and ethical issues in stem cell research- cloning- instrumentality
Unit-3	Concept of property, rights/protection, duties, and their correlation; History and evaluation of intellectual property rights (IPR); Distinction among various forms of IPR, WTO - Definition — Functions- International treaties for IPR Protection.
Unit-4	Introduction to patents; Key concepts; International Law of Patents; Indian Patent Act and practice**;** Patentability; Types of patents**;** Procedure of obtaining patents- Rights of patents- Infringement of patent rights.
Unit-5	Other forms of IPR protection: Copyright - Trademark - Designs - Importance in Indian Scenario & laws in India for IPR protection.
Suggested readings	● J. Pila; The Subject Matter of Intellectual Property; Oxford University Press, 2017.

	● N. S. Sreenivasulu; Intellectual Property Law Dynamic Interfaces; Aggarwal Law House, 2017. ● K. C. Kankanala; Fundamentals of Intellectual Property (FUN IP); Published by Dr. Kalyan C. Kankanala, 2013. ● K. C. Kankanala; Indian Patent Law and Practice (Oxford India Paperbacks); Oxford India Paperbacks, 2012. ● All (updated) statutes: Trade Marks Act 1999; Indian Copyright Act 1957; Design Act of 2000; Patents Act 1970
BINF-ET-403	**Elective Theory Course (Any one of the following)**
BINF-ET-403A	**Chemo-informatics and Drug designing**
Unit-1	Basic concepts and application of Cheminformatics. Manipulations in 2D and 3D structures of chemical compounds, representation of chemical reactions, molecular descriptors, calculations of physical and chemical data, calculation of structural deciphers. In silico representation of chemical information (SMILES, IchI, SDF, MOL, PDB, PDBQT, etc), Computer-oriented chemical compounds nomenclature, Computer-Assisted structure elucidation. Molecular drawing and interactive visualization, Chemical name and formula searching.
Unit-2	Cheminformatics Databases, Chemical Database Design, Bio Catalysts Database, The MOS Database, SolidPhase Synthesis Database, Compound Databases (ZINC, PubChem, ChEMBL, DrugBank, etc.).Chemistry & Information technology, chemical data collation, retrieval, analysis & interpretation, hypothesis generation & validation, development of structure activity/property relationships, artificial intelligence techniques in chemistry. Building molecules on a computer, quantum and molecular mechanics methods for geometry optimization, Simulation methods for molecules and material
Unit-3	Introduction to drug discovery, Current approaches and philosophies in drug design, Molecular Modelling and virtual screening techniques, lead identification, Concept of pharmacophore mapping and pharmacophore-based Screening, Analysis of the receptor, Docking: Rigid docking, flexible docking, manual docking, docking based screening, Scoring Functions, Binding energy calculations De novo drug design., Drug likeness screening, ADMET properties.
Unit-4	SAR versus QSAR, QSAR methodology, Quantum-chemical descriptors, COMFA and COMSIA. Molecular mechanisms of diseases and drug action. Pharmacokinetics: Models and Applications, Drug–receptor interactions. Pharmacodynamics, Biomolecular interactions and binding thermodynamics, Biochemical and cell-based assays. Molecular recognition and specificity
Suggested readings	● Cramer CJ (2004) "Essentials of Computational Chemistry: Theories and Models", Wiley-Blackwell ● Gilani HG, Samper KG and Haghi RK (2012) "Chemoinformatics: Advanced Control and Computational Techniques", CRC Press ● Bajorath JB (2004) "Chemoinformatics-Concepts, Methods, and Tools for Drug Discovery", Springer ● Vogel H (2007) "Drug Discovery and Evaluation: Pharmacological Assays", Springer ● Czechtizky W and Hamley P (2016) "Small Molecule Medicinal Chemistry: Strategies and Technologies", John Wiley & Sons

BINF-ET-403B	**System Biology**
Unit 1	Introduction to biological networks, Graph theoretic modelling and analysis of biological networks; Discrete Dynamic modelling (Boolean networks, Petri nets); Continuous dynamic modelling (ODEs, stochastic simulation, etc.)
Unit 2	Mathematics of networks: Networks and their representation, adjacency matrix, weighted networks, bipartite networks; Measures and metrics: Clustering coefficient, centrality measures (degree, eigenvector); Random graphs, metabolic networks and flux balance analysis.
Unit 3	Generation of regulatory networks using WGCNA; Generation of protein interaction networks via the String database; Comparisons and interpretations of protein networks; Pathways and regulatory networks in the context gene/protein functions; Transcriptional regulation significance of non-coding RNAs ;Visualization of gene-gene interactions via Cytoscape
Unit 4	Probabilistic modelling (Probabilistic Boolean networks, Bayesian networks, Mutual Information); Network inference from experimental data, Genome-scale modelling and network integration; Evolution of molecular networks, Network-guided GWAS studies, FBA and epistasis detection, protein function prediction.
Suggested readings	● Junker, B. H. 2008.Analysis of Biological Networks. ● Koch, I. Reisig, W. Schreiber F. 2010. Modeling in Systems Bioloay: The Petri Net Approach. ● Ramadan, E.Y. 2008. Biological Networks: Modeling and Structural Analysis. ● Laubenbacher, R. 2007.Modeling and Simulation of Biological Networks.
BINF-ET-403C	**Web-based Programming**
Unit-1	Brief History of the Internet, WWW, Web System Architecture, Internet vs. Intranet, URL, Protocol used in Internet: TCP/IP, SMTP, PPP, HTTP(s), Services on the Internet, Web Servers, Overview of Web Authoring Tools, Design Frameworks
Unit-2	Introduction to HTML and HTML5, Basic Structures of a HTML/HTML5 Documents, HTML5 Semantic Elements: Header, Footer, Article, Section. Ordered & Unordered Lists, Hyperlinks, Working with Table, Working with Forms: Form and Input Tags, Text Box, Radio Button, Checkbox, Select Tag and Pull Down Lists, Hidden, Submit and Reset, Attributes of HTML5 Form Elements: Number, Date, Time, Calendar, Range, HTML5 Drag and Drop, Graphics: Canvas, SVG, Multimedia Elements: Audio, Video
Unit-3	Benefit of CSS, CSS Properties, CSS Styling: Background, Text Format, Controlling Fonts, Working with Lists and Tables, CSS ID and Class, Web Page Layout and Editing with CSS, Writing JavaScript into HTML, Basic Programming using JavaScript, JavaScript Client Validations, Dialog Boxes, Event Handling
Unit-4	Evaluation of PHP, Basic Syntax, Defining variable and constant, Data Types, Operator and Expression, Handling HTML Form With PHP: Capturing Form Data, Dealing with Multi-valued Field, Conditional Statement, Iterations, Arrays, Working with Functions: Call-by-value and Call-by-reference, Recursive Function, Working with String. String Matching with Regular Expression: Pattern Matching in PHP, Replacing Text, Splitting a String with a Regular Expression

Unit-5	Introduction to WAMP/XAMPP Server – Configuration and Web Application Deployment, PHP Server Variables, State Management - Query String (URL Rewriting), Hidden field, Cookies, Session. Database Connectivity with MySql: Connection with MySql Database, Basic Database Operations – Insert, Delete, Update and Select, Setting Query Parameter, Executing Query, Join.
Suggested readings	● Robert W. Sebesta, Programming the World Wide Web, Addison Wesley ● Ivan Bayross, HTML 5 and CSS 3 Made Simple, BPB ● Bayross, Web Enabled Commercial Application Development Using HTML, JavaScript, DHTML and PHP, BPB ● Dick Oliver, Michael Morrison, Sams Teach Yourself HTML and CSS in 24 Hours, Pearson Education
BINF-ET-403D	**Python programming for bioinformatics**
Unit-1	Introduction to python interpreter and interactive mode – Statement Read and Print commands – Evaluating expressions - Decision, Boolean Logic and Repetition structures syntax with examples in biological application
Unit-2	Defining and Calling a function - Fruitful functions (return value, parameters, local and global scope, function composition, recursion) – Examples in sequence analysis using function - Introduction to Modules. Regular Expression: Importance of patterns in biology – String manipulation using regular expressions (Extraction, splitting and matching).
Unit-3	Introduction to Lists – List slicing – Finding items in Lists with operator – Copying and Processing Lists – List built-in methods – Two Dimensional lists. Tuples: Basic tuple operations – creation, concatenation, repetition, slicing, immutable and deletion. Dictionaries: creation, accessing and processing - Dictionary methods
Unit-4	File objects – File built-in methods and attributes - Reading and writing files - command line arguments. Exception Handling: Errors and exceptions, Detecting and Handling Exceptions
Unit-5	Introduction to Bio-python, Installation, Inbuilt modules related to sequence objects, sequence annotation objects, sequence analysis, sequence input/output, sequence alignment objects and tools, Applications of Bio-python
Suggested readings	● Beazley, D. M. (2009).Python essential reference. Addison-Wesley Professional. ● Barry, P. (2010). Head First Python. "O'Reilly Media, Inc.". ● Punch, W. F., & Enbody, R. (2010). The practice of computing using python. Addison-Wesley Pub-lishing Company. ● Mark, S. (2009). Programming in Python 3. Pearson Education India. ● Lutz, M. (2013). Learning python. "O'Reilly Media, Inc.". ● Turnquist, G. L. (2011). Python Testing Cookbook. Packt Publishing Ltd.
BINF-CP-404	**Dissertation/Project Work and Viva**
	Each student will be required to undertake dissertation/review work assigned to him related to R&D in any area of Bioinformatics under the supervision of a faculty member. In principle, the research work is to be carried out by the student himself/herself taking advice from his/her supervisor when problem arises. The work will be allotted at the beginning of the fourth semester specifying the different aspects to be carried out by the student. At the end of the semester the student will submit a report on his work in typed and bound form.

	Evaluation shall include oral presentation and a viva-voce. Defense of the viva on the project should be done in presence of an external examiner along with the faculties **Marks distribution for project evaluation – Project Report: 50 Marks; Implementation: 50 Marks; Presentation + Viva-voce: 50 Marks**
BINF-CP-405	**Industry visit/institute visit/Internship**
	In-plant training in an industry which utilizes bioinformatics for R&D or an advanced centre of learning is to be undertaken by each student. A report on the training is required to be submitted.
BINF-CP-406	**Comprehensive Viva**
	Comprehensive viva-voce is to assess the overall knowledge of the student in the relevant field of Bioinformatics acquired over 2 years