

**CH. CHARAN SINGH UNIVERSITY, MEERUT**  
**DEPARTMENT OF MICROBIOLOGY**  
**Program: M.Sc.**  
**Program Code:BI**  
**Program (Specific): M.Sc. Bioinformatics**  
**Year of Implementation: 2016-2017**

### **Program Outcomes**

After successful completion of M.Sc. program, the students would be able

**PO1:**To get opportunities in higher education. They are also developed on the professional front. It also provides opportunities for career advancement in teaching, research, and industries.

**PO2:** An ability to acquire in-depth theoretical and practical knowledge of Biology, Computer Science, and Mathematics. Students will acquire knowledge of computer languages- PERL,C, SQL and JAVA and to write programs to solve biological problems.

**PO3:** To get introduced to the basic concepts of Bioinformatics and its significance in Biological data analysis. Students will become familiar with a wide variety of bioinformatics tools and softwares and apply these to conduct basic bioinformatics research and thus develop platform for molecularbiology experiments

**PO4:** An ability to acquire proficiency in tackling problems related to Biology using software or by development of new algorithms that help in addressing the biological challenges faced by humankind.

**PO5:** An ability to get an innovative perspective on Biology by providing support in terms of hardware, software and Big Data-handling.

**PO6:** An understanding of the intersection of life and information sciences, the core of shared concepts, language and skills the ability to speak the language of structure-function relationships, information theory, gene expression, and database queries.

### **Program Specific Outcomes**

**PSO1.**After successful completion of this program, the students would be able to apply knowledge of Bioinformatics in all the fields of learning, including higher research and its extensions. Gain multi-disciplinary knowledge and practical skills in computational, mathematical and biological sciences for challenging careers in academics, research, biotechnology,pharmaceutical and health care industries.

**PSO2.** Enhance knowledge in the scientific domains of Programming languages, Structural bioinformatics, Genomics, Proteomics, Systems biology, Bioethics, Biosafety, IPR, Molecular modeling and Drug discovery

**PSO3.** Apply the appropriate programming and analytical skills in big data analysis and make meaningful predictions.

**PSO4.** Design new algorithms and in-silico interventions to solve industrial and societal problems. Develop entrepreneurial skills and become professionals in various fields.

**PSO5.** Students will have analytical and scientific facet in the field of research Students will be able to identify societal problems and recognize the importance of designing scientifically sound and ethical research to solve societal problems.

**PSO6.**It makes them equipped with knowledge to crack lectureship and fellowship exams like UGC/ CSIR – NET, SET/ ISRO/DRDO and other competitive exams. Students will qualify for higher education and industry needs.



### Courses/ Papers and their Outcomes (COs)

| Semester | Course Code | Course Title  | Course Outcome  |
|----------|-------------|---|---|
| I        | BI-101      | <b>Basic of Bioinformatics, Computer system and 'C' Programming</b> | <p>After completion of this course, the student will be able to</p> <p><b>CO1.</b> Locate and use the main databases at the NCBI and EBI resources and know the difference between databases, tools, repositories and be able to use each one to extract specific information</p> <p><b>CO2.</b> Extract data from specific databases using accessions numbers and gene names.</p> <p><b>CO3.</b> Understand the types and functioning of computers. Apply in creation of folder, copying, renaming, deleting, searching, creating shortcuts, backup files using MS Windows.</p> <p><b>CO4.</b> Understand the components in data communication, compare and contrast types of networking and apply in maintenance applications of networking.</p> <p><b>CO5.</b> Demonstrate the syntaxes of C language. Design an algorithm for a given problem. Write and execute well-structured programs for simple application of real life. Identify and comprehend C documentation.</p> |
|          | BI-102      | <b>Biomathematics</b>   | <p><b>CO1.</b> Solve problems using Newton forward formula and Newton backward formula. Derive Gauss's formula and Stirling formula using Newton forward formula and Newton backward formula</p> <p><b>CO2.</b> To be well grounded in the basic manipulative skills level of Algebra, Calculus, Differential Equation, Number Theory, Analysis, Linear Algebra, Graph Theory .</p> <p><b>CO3.</b> To gain experience investigating the real world problems and learn to how to apply mathematical ideas and models to those problems.</p> <p><b>CO4.</b> Use mathematical and statistical techniques to solve welldefined problems and present their mathematical work.</p> <p><b>CO5.</b> Read, understand and construct correct mathematical and statistical proofs and use the library and electronic data-bases to employ information on mathematical problems</p>   |
|          | BI-103      | <b>Biological Database System</b>                                   | <p><b>CO1.</b> To gain knowledge about various Biological databases that provide information about nucleic acids and protein</p>  |

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|           |        |   | <p><b>CO2.</b>Introduction to Biological databases and database systems.Overview about types and Biological data and database search tools.</p> <p><b>CO3.</b> Describe about the different types of Biological database</p> <p><b>CO4.</b> Explain about different types of protein and other organism specific databases.</p> <p><b>CO5.</b> Overview about pathway and enzyme databases, Sequence submission tools.</p>  |
|           | BI-104 | <b>Microbiology &amp; Immunology</b>          | <p><b>CO1.</b> Knowledge on historical perspective of Microbiology Basic knowledge on different structure of microbes</p> <p><b>CO2.</b> Differentiate the morphology of different algae and fungi Ideas on different type of microscope</p> <p><b>CO3.</b> Students will be able to describe the cell mediated and humoral immunity and the role of lymphoid organs in the differentiation and maturation of T and B lymphocytes</p> <p><b>CO4.</b>Students will be able to explain the types of antigens and antibodies. The mechanism of antigen and antibody reaction including agglutination and opsonization</p> <p><b>CO5.</b>Students will be able to describe the hypersensitivity types, immunodeficiency diseases and role of major histocompatibility complex in transplantation reaction</p> |
|           | BI-105 | <b>Practical</b>                              | BI-101to BI-105   |
| <b>II</b> | BI-201 | <b>Operating System through Unix/Linux</b>    | <p><b>CO1.</b> Recall the concepts of file management.</p> <p><b>CO2.</b> Apply security aspects in appropriate Situations.</p> <p><b>CO3.</b> Explore various other operating systems.</p> <p><b>CO4.</b> Apply knowledge gained through processor scheduling to other applications. Analyze limitations of operating systems</p> <p><b>CO5.</b> To run most bioinformatics applications, users need to access remote Linux machines, such as supercomputer clusters that provide much larger computing resources.</p>   |
|           | BI-202 | <b>Object Oriented Programming with 'C++'</b> | <p><b>CO1.</b> To describe the advantages of a high level language like C/C++, the programming process, and the compilation process. Describe and compare machine language and a high level language Discuss the advantages of a high-level language</p> <p><b>CO2.</b> To describe and use software tools in the programming process Describe the functions of an IDE.Use an IDE to compile,</p>   |

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|  |        |  | <p>load, save, and debug a C/C++ program</p> <p><b>CO3.</b> The bioinformatics library libcov is a collection of C++ classes that provides a high and low-level interface to maximum likelihood phylogenetics, sequence analysis and a data structure for structural biological methods</p> <p><b>CO4.</b> Describe the fundamental components of a C/C++ program (e.g.,. source files, header files, main() function, functions, and libraries). Explain and apply fundamental syntax rules for identifiers, declarations, expressions, statements, and functions</p> <p><b>CO5.</b> To demonstrate an understanding of primitive data types, values, operators and expressions in C/C++. Discuss the representation and appropriate use of primitive data types.</p>  |
|  | BI-203 | <b>Sequence Analysis</b>                           | <p><b>CO1.</b> The student should be able to understand basic research methods in bioinformatics. The student will choose biological data, submission and retrieval it from databases and design databases to store the information.</p> <p><b>CO2.</b> The students will be able to demonstrate the most important bioinformatics databases, perform text- and sequence-based searches, and analyze the results in light of molecular biological knowledge.</p> <p><b>CO3.</b> The students will be able to experiment pair wise and multiple sequence alignment and will analyze the secondary and tertiary structures of protein sequences.</p> <p><b>CO4.</b> The student should understand the data structure (databases) used in bioinformatics and interpret the information (especially: find genes; determine their functions), understand and be aware of current research and problems relating to this area.</p> <p><b>CO5.</b> Understand algorithms and applying tools in sequence analysis. Apply bioinformatics tools and interpret results</p> |
|  | BI-204 | <b>Molecular Biology &amp; Genetic Engineering</b> | <p><b>CO1.</b> Understand the Molecular biology and molecular biology.</p> <p><b>CO2.</b> .Understand the cell divisions and types of mutation. Understand the structure and function of the cells.</p> <p><b>CO3.</b> Understand the term cell signalling. Aware the students for Cancer.</p> <p><b>CO4.</b> Understand the Tools and Techniques in Molecular Biology.</p> <p><b>CO5.</b> Understand the term ELISA technique</p>  |

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|            |        |   | and DNA finger printing.   |
|            | BI-205 | <b>Practical</b>  | BI-201 to BI-205   |
| <b>III</b> | BI-301 | <b>Statistical Analysis and Optimization Techniques</b> | <p><b>CO1.</b> Understand the sampling methods, data collection methods and data classification. Analyze the data classification types and the application of statistical analysis.</p> <p><b>CO2.</b> Apply the statistical tests of significance and descriptive measures to interpret the results and draw conclusions.</p> <p><b>CO3.</b> Prepare algorithms and optimization techniques for the analysis and design of Statistical software.</p> <p><b>CO4.</b> Design the tools for collection; identify the samples, interpretation of data with the use of tables and pictorial representations</p> <p><b>CO5.</b> Biostatistics can be applied in major areas of drug design and discovery for example to evaluate the different hypotheses using ANOVA, t-test, correlation and regression generated during the exercise of computational technique.</p>   |
|            | BI-302 | <b>Biocomputing Programming</b>                         | <p><b>CO1.</b> Concepts of computer programming languages like C, JAVA helps in solving different complex problem in biology or data Analysis.</p> <p><b>CO2.</b> Knowledge of Traditional HTML interfaces for input to and output from Bioinformatics analysis on the Web are highly variable in style, content and data formats.</p> <p><b>CO3.</b> Knowledge of PHP There is an extremely rich variety of programming languages, web development frameworks, tools and libraries for “general” web development that are perfectly fit to handle Bioinformatics data.</p> <p><b>CO4.</b> Arithmetic and logical operators; Conditional statement and Loops; Regular Expressions; Function and subroutines Application of PERL in Bioinformatics; concatenating DNA fragments; DNA to RNA; Reading protein Files; Finding motifs; ORFs; DNA to protein</p> <p><b>CO5.</b> Introduction to PERL as scripting language; variables; Array; Initialization and manipulation</p> |
|            | BI-303 | <b>Structural Biology &amp; Molecular Modeling</b>      | <p><b>CO1.</b> Design the process steps leading to determination of crystal structures of small and macro molecules.</p> <p><b>CO2.</b> Explain the differences between crystallization of small molecules and</p>   |

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|  |        |   | <p>macromolecules; choose proper methods for protein crystallization. Introduction to the concept of molecular modeling.</p> <p><b>CO3.</b> Define electron density maps and choose the proper algorithms for structure refinement. Use specific crystallographic software for structure visualization and refinement. Validate the final structures. Describe about the concept of Molecular mechanics Explain about various methods used in energy minimization</p> <p><b>CO4.</b> Explicate about interactions that modulate protein-protein complexes (small-molecule, nucleic acids, iomolecules) which later on can be designed as therapeutic markers. escribe about various methods used in molecular dynamics and simulation.</p> <p><b>CO5.</b> They will be very capable to present the docking strategies. based on the ligand, receptor and de novo ligand design. Understanding of the ADME prediction, visualization tools, Pharmacophores and sequence analysis They would have the capacity to comprehend the Finger print searching, QSAR and Biological database usage.</p>                                       |
|  | BI-304 | <b>Genomics, Proteomics &amp; Systems Biology</b> | <p><b>CO1.</b> Understand the term genome and the methods of genetic and physical mapping. Learn about different methods of DNA sequencing, genome annotation, and gene prediction. Understand the concepts of structural, functional, and comparative genomics; and gain knowledge about the applications of comparative genomics.</p> <p><b>CO2.</b> Understand the concept of microarray data analysis for gene expression and will gain knowledge about the bioinformatics tools used in microarray data analysis.</p> <p><b>CO3.</b> The student should be able to investigate computational methods for genomic data and analyze metabolomic, proteomics, and protein-protein interaction experiments.</p> <p><b>CO4.</b> Discuss the practical aspects of protein-protein interactions using online tools of Expert Protein Analysis System (ExPASy).</p> <p><b>CO5.</b> To provide a system level understanding of complex interactions within biological systems and to model the biological systems employing computational and mathematical concepts. Introduction to systems Biology, its significance, applications</p> |

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|           |        |   | and experimental procedures. |
|           | BI-305 | <b>Practical</b>  | BI-301 to BI-305             |
| <b>IV</b> | BI-401 | <b>Project VIVA</b>   |                              |
|           | BI-402 | <b>Bioinformatics<br/>(short questions<br/>including<br/>objective type</b> |                              |
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## Course Structure and Evaluation Scheme

Course Duration: Four Semesters

Course Type: Self Finance Scheme

Pass Percentage: Theory-30%, Practical-30% Overall-40% (mention as Bioinformatics/  
M.Sc.)

Attendance Criterion: As per the norms decided by the statutory body

Maximum marks: 2000

Percentage range for Division: I- 60%,

Percentage range for Division: II- 45%,

Percentage range for Division: III- 33%,

Marks Range for Grades:NIL



| Sem.       | Course Code                      | Course Title   | Duration | Lecture Duration | Lect./Weak (Th+Tu+Pr) | Max. Marks=100 (Ext.+ Int.) | Credits    | External Exam duration |
|------------|----------------------------------|--|----------|------------------|-----------------------|-----------------------------|------------|------------------------|
| <b>I</b>   | BI 101                           | Basic of Bioinformatics, Computer system and 'C' Programming | 90 hours | 60 minutes       | 6                     | 50+50                       | <b>NIL</b> | 3 hours                |
|            | BI 102                           | Biomathematics   | 90 hours | 60 minutes       | 6                     | 50+50                       | <b>NIL</b> | 3 hours                |
|            | BI 103                           | Biological Database System                                   | 90 hours | 60 minutes       | 6                     | 50+50                       | <b>NIL</b> | 3 hours                |
|            | BI 104                           | Microbiology & Immunology                                    | 90 hours | 60 minutes       | 6                     | 50+50                       | <b>NIL</b> | 3 hours                |
|            | BI 105                           | Practical  | 25 hours | 120 minutes      | -                     | 100                         | <b>NIL</b> | 5 hours                |
|            | <b>Max. Marks of Semester-I</b>  |  |          |                  |                       |                             | <b>500</b> |                        |
| <b>II</b>  | BI 201                           | Operating System through Unix/Linux                          | 90 hours | 60 minutes       | 6                     | 50+50                       | <b>NIL</b> | 3 hours                |
|            | BI 202                           | Object Oriented Programming with 'C++'                       | 90 hours | 60 minutes       | 6                     | 50+50                       | <b>NIL</b> | 3 hours                |
|            | BI 203                           | Sequence Analysis  | 90 hours | 60 minutes       | 6                     | 50+50                       | <b>NIL</b> | 3 hours                |
|            | BI 204                           | Molecular Biology & Genetic Engineering                      | 90 hours | 60 minutes       | 6                     | 50+50                       | <b>NIL</b> | 3 hours                |
|            | BI 205                           | Practical  | 25 hours | 120 minutes      | -                     | 100                         | <b>NIL</b> | 5 hours                |
|            | <b>Max. Marks of Semester-II</b> |  |          |                  |                       |                             | <b>500</b> |                        |
| <b>III</b> | BI 301                           | Statistical Analysis and Optimization                        | 90 hours | 60 minutes       | 6                     | 50+50                       | <b>NIL</b> | 3 hours                |
|            | BI 302                           | Biocomputing Programming                                     | 90 hours | 60 minutes       | 6                     | 50+50                       | <b>NIL</b> | 3 hours                |
|            | BI 303                           | Structural Biology & Molecular Modeling Analysis             | 90 hours | 60 minutes       | 6                     | 50+50                       | <b>NIL</b> | 3 hours                |
|            | BI 304                           | Genomics, Proteomics & Systems                               | 90 hours | 60 minutes       | 6                     | 50+50                       | <b>NIL</b> | 3 hours                |

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|-----------|-----------------------------------|---|--------------|-------------|---|------------|------------|---------|
|           |                                   | Biology   |              |             |   |            |            |         |
|           | BI 305                            | Practical   | 25 hours     | 120 minutes | - | 100        | <b>NIL</b> | 5 hours |
|           | <b>Max. Marks of Semester-III</b> |   |              |             |   | <b>500</b> |            |         |
| <b>IV</b> | BI 401                            | Project Report include Viva-voce                          | 4 to 6 Month | -           | - | 400        | <b>NIL</b> | 4 hours |
|           | BI 402                            | Bioinformatics (short questions including objective type) | -            | -           | - | 100        | <b>NIL</b> | 1 hours |
|           | <b>Max. Marks of Semester-IV</b>  |   |              |             |   | <b>500</b> |            |         |

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**Syllabus**

| Semester | Course Code | Course Title   | Syllabus  |
|----------|-------------|--|---|
| <b>I</b> | BI 101      | <b>Basics of Bioinformatics, Computer system and 'C' Programming</b> | <p><b>Unit I- Introduction to Bioinformatics</b> Definition &amp; Concept; Human Genome Project; Role of Bioinformatics, Introduction of Internet in Biology &amp; Objectivity; Services of Internet used for Biological Data (E-Mail, File Transfer Protocol, Usenet, Telnet). Important bioinformatics resources (NCBI, EBI, SIB).</p> <p><b>Unit II- Computer System-</b> Definition and characteristics, Components (Input/Output unit, Control Unit, Primary Storage Unit, Arithmetic and Logic Unit), Types of Memory, Communication Pathways (Control Bus, Address Bus, Data Bus), Classification of Computers (according to logic &amp; size), Generation of Computers; Introduction to Software, Classification of Software, Translators (Compiler &amp; Interpreter); Number Systems; Logic Gates.</p> <p><b>Unit III- Networking-</b> Definition, Client/Server, Types (LAN, WAN, MAN); Network Connecting Devices; Topologies (Bus Network, Ring Network, Star Network, Mesh Network, Tree Network) and their advantages &amp; disadvantages. Elements of Networking (Network Services such as File Services, Database Services, Print Services, Application Services); Transmission Medias (Coaxial Cable, Fiber Optics, Twisted Pair).</p> <p><b>Unit IV- Functional Structure of Programming in C:</b> Concepts of flowcharting and algorithm development; Tokens in C (Constant, Variable &amp; Keywords); Data types; Operators (Arithmetic Operators, Relational Operators, Increment Operators, Decrement Operators, Assignment Operators &amp; Conditional Operators), if statement; if-else statement; switch statement; for statement; while statement; do-while statement; Odd Looping.</p> <p><b>Unit V-Arrays in C:</b> One Dimensional Array; Two</p> |

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|  |        |                       | <p>Dimensional Array; String Handling in Array (Declaration of String Variable, Printing of a string, Concatenation of a String, Comparison of the String). Built-in Functions &amp; User Defined Functions (Definition; syntax; main function; printf function; scanf function; getchar function; getche function; putchar function; strcmp function; strcpy function; strcat function; strlen function; Declaration and definition of User-Defined Function; Call by Value; Call by Reference; Recursion); Pointers in C (Definition; Objectivity; Initialization of Pointers; Pointers &amp; Array; Pointers &amp; Function).</p> <p><b>Suggested Readings (Latest Editions):</b></p> <ul style="list-style-type: none"> <li>• <i>J.B. Dixit. 2009 Computer fundamentals and programming in 'C'. LP Publication</i></li> <li>• <i>Guigo R. Ed. &amp; Gusfield. 2014. Algorithm in Bioinformatics. O.Ed. Berlin. Springer-Verlog</i></li> <li>• <i>Yashavant Kanetkar, 13th Edition, 2016, Let Us C/C++, Paperback.</i></li> <li>• <i>E. Balaguruswami. 5th Edition . 2008. Programming in ANSI 'C'. Tata Mac Graw Hill.</i></li> <li>• <i>Sharma, Munjal and Shankar.2007. A Text book of bioinformatics. Rastogi Publications.</i></li> <li>• <i>P.K. Sinha. 2016. Fundamental of computers. BPB publication.</i></li> </ul> |
|  | BI 102 | <b>Biomathematics</b> | <p><b>Unit I: - Matrices:</b> Algebra of matrices, transpose and inverse of a matrix, determinants. Arithmetic and Geometric Series, Binomial Theorem. Permutation and combinations. Introduction to set theory, Functions, Polynomials, limits and continuity.</p> <p><b>Unit II: - Differentiation and Integration:</b> Derivative of simple algebraic and trigonometric functions. Maxima and minima. Integration of some standard functions. Integral by parts. Applications of Integral calculus in biology. Definite integral. Ordinary differential equations (first order) - example from biology.</p> <p><b>Unit III: - 2D Coordinate Geometry:</b> Equation of a line, circle, ellipse, parabola, and hyperbola. 3D geometry: Equation of sphere, cone.</p> <p><b>Unit IV:- Numerical Analysis:</b> Gaussian Elimination and Gauss Jordan Methods for the solution of system of linear equations. Solution of Algebraic and Transcendental</p>   |

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|        |                                   |  | <p>Equations by Bisection Method and Newton- Raphson Method.</p> <p><b>Unit V: - Interpolation:</b> Newton’s formulae, Lagrange’s formula. Curve fitting by Method of least squares. Numerical differentiation using Newton formulae. Numerical Integration: Trapezoidal rule, Simpson’s 1/3 and 3/8 rules.</p> <p><b>Suggested Readings (Latest Editions):</b></p> <ul style="list-style-type: none"> <li>• <i>J. D. Murray. 2014. Mathematical Biology. Springer Verla.</i></li> <li>• <i>Segal, L. 2012. Mathematical Models in Molecular and Cellular Biology Cambridge: Cambridge University Press.</i></li> <li>• <i>Balaguruswamy. 2016. Numerical Methods . TMH.</i></li> <li>• <i>V Rajaraman. 2007. Computer oriented numerical methods. Printice hall India.</i></li> <li>• <i>S. C. Gupta. 2009. Fundamental of Methametics . Sutanchand &amp; Sons Publication.</i></li> <li>• <i>A.R. Vasistha. 2014. Matrices. Krishna Publication.</i></li> </ul>  |
| BI 103 | <b>Biological Database System</b> |  | <p><b>Unit I:- Database System-</b> Definition; Purpose of Database System; Advantages of Database System; Components of Database System (., Hardware, Software &amp; Users), Database Administrator; Data Administrator; Data Models (Relational, Network, Hierarchical); Three Level Architecture for Database System (Internal Level; Conceptual Level; External Level); Data Independence; Data Abstraction; Mapping; Data Definition Language; Data Manipulation Language; Data Sub Language; Role of Schemas in Three Level Architecture; Client/Server architecture; Distributed Processing; Database Technologies (Flat Files, Relational &amp; Object).</p> <p><b>Unit II:- Relational Database-</b> Definition; Relational Data Model (Binary, Ternary, Quaternary &amp; n-ary Relation); Important terms in Relational database system (Tuple, Records, Fields, Domain, Degrees, Cardinality); Keys(Primary Key, Candidate Key, Composite Key, Foreign Key&amp; Alternate Key).</p> <p><b>Unit III:- Structured Query Language-</b> Creating Table; Applying Column &amp; Table Constraints; Inserting Values in Table; Deletion(of Rows &amp; Table); Updating Values; Altering Table; Retrieving Values from Table; Revoke Command;</p> |

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|        |                                      |  | <p>Drop Command; Grant Command; Commit Command; Rollback Command.</p> <p><b>Unit IV:- Biological Database-</b> Primary Database &amp; Secondary Database; Submitting Sequence to the Database and Information Retrieval through LocusLink; Sequence Databases (EMBL, GenBank, DDBJ).</p> <p><b>Unit V: - Protein and other databases:</b> SWISS-PROT, PIR, TrEMBL); Protein Family/Domain Databases (PROSITE, Pfam, PRINTS &amp; SMART), cDNA Libraries and ESTs &amp; Structure Database (PDB, CATH, SCOP).</p> <p><b>Suggested Readings (Latest Editions):</b></p> <ul style="list-style-type: none"> <li>• <i>Ivan Bayross. 2010. SQL, PL/SQL the programming language of Oracle., BPB Publication</i></li> <li>• <i>C.J. Date. 2010. An introduction to database systems. Addison Wesley</i></li> <li>• <i>Orpipa Bosu and Simminder Kaur, Thukaral. 2009. Bioinformatics: Database, tools and algorithms. Oxford Publications</i></li> <li>• <i>Hanery Korth and Abraham Silberchaltz. 2013. Database system concepts. Tata Mac Graw Hill</i></li> <li>• <i>Baxevanis, A.D. and Ouellette. 2004. Bioinformatics: A practical guide to the analysis of the gene and protein b. B.F.F, New York, John Wiley and Sons, Inc Publication</i></li> <li>• <i>Atwood, T.K. and Aprry-Smith. 2003. Introduction to Bioinformatics. D.J. Delhi, Pearson education (Singapore)</i></li> </ul> |
| BI 104 | <b>Microbiology &amp; Immunology</b> |  | <p><b>Unit I :</b> Discovery of microbial world, controversy over spontaneous generation; origin of life. Microbial evolution and diversity; five kingdom and eight-kingdom classification.</p> <p><b>Unit II :</b> General account of prokaryotes: structural organization of Eubacteria and Archae (cell membrane, cytoplasmic matrix, inclusion bodies, nucleoid, flagella, pilli and endospore); General characters of eukaryotic microbes, structure and organization of a typical eukaryotic cell, Evolutionary relationship of each group based on modern systems of classification.</p> <p><b>Unit III :</b> History and discovery of viruses; nature of viruses; General characters of viruses; Nomenclature and</p>   |

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|  |  |  | <p>Classification of viruses;<br/>Bacteriophage: Structure and life cycle pattern of T-even phage;<br/>Genome organization of viruses.</p> <p><b>Unit IV :</b> Introduction to the immune system: Innate immunity; anatomic, physiological, phagocytic &amp; inflammatory barriers. Adaptive immunity; natural &amp; artificial immunity. Cells involved in immune response: lymphoid lineage (producing B &amp; T lymphocytes) &amp; Myeloid lineage (phagocytes: macrophages, neutrophils &amp; eosinophils. And auxillary cells; basophils, mast cells &amp; platelets). Organs involved in immune system: primary &amp; secondary lymphoid organs.</p> <p><b>Unit V :</b> Types of antigens; Structure &amp; types of Immunoglobulins, genetic diversity of immunoglobulins; Cytokines: B-cell biology: Antigen-Antibody binding, B-cell activation. T-cell biology: major histocompatibility complex molecules; Types of vaccines &amp; their characteristics; Immune disorders; Hybridoma technology, applications of monoclonal antibodies. Antigen-antibody reactions <i>in vitro</i>.</p> <p><b>Suggested Readings (Latest Editions):</b></p> <ul style="list-style-type: none"> <li>• Prescott - Harley - Klein -2007- Microbiology - IV Edition - International edition - McGraw Hill - ISBN0-07-115830-8.</li> <li>• D. J. Taylor - N. P. O. Green - G. W. Stout – Biological Sciences - III Edition - Ed. - R. Soper - Cambridge University Press - ISBN0 - 521 - 639239 (Low Price Paperback)</li> <li>• K. P. Talaro &amp; A. Talaro., Foundations in Microbiology, HI - International Edition. WCB / McGraw Hill –ISBN0, 697, 35452 . 0</li> <li>• Guntram Seltmann, Otto Holst Bacterial cell walls. Springer ISBN:3540426086</li> <li>• Nelson D. L. and Cox M. M. (2005) Lehninger's Principles of Biochemistry, Fourth edition, W. H. Freeman &amp; Co. New York.</li> <li>• White David Physiology and Biochemistry of Prokaryotes. 2nd Ed. Oxford University Press, New York.</li> <li>• Berg Jeremy, Tymoczko John, Stryer Lubert Biochemistry 4th Ed, W. H. Freeman, New York.</li> </ul> |
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| II | BI 201 | <b>Operating System through Unix/Linux</b> | <p><b>Unit I- Operating System:</b> Introduction: Windows and Unix/Linux, Definition; Concepts; Function of Operating System; Batch Processing; Multiprogrammed Batch System; Time Sharing System; Parallel System; Distributed System; Real Time System.</p> <p><b>Unit II- Process &amp; Memory Management:</b> Process; Process State(New, Running, Waiting, Ready, Termination); Process Control Block; Process Scheduling (Round Robin Scheduling, Priority Scheduling, Multiple Queues, Shortest Job Scheduling); Operations on Process; Basic Management of Memory; Swapping Virtual Memory; Paging.</p> <p><b>Unit III- Input/Output Management:</b> I/O Devices; Device Controllers; I/O Software; Device Drivers; Deadlock; Resources; Principles of Dead Lock; Detection and Recovery; Deadlock Prevention; Deadlock Avoidance.</p> <p><b>Unit IV- UNIX/LINUX Operating Systems:</b> Introduction; Concepts; Layers of UNIX; Role of System Administrator and Ordinary User; Tree Structure of UNIX; Root File System; /bin Directory; /dev Directory; /bin Directory; /etc Directory; /lib Directory; /proc Directory; /mnt Directory; /root Directory; /sbin Directory; /tmp Directory; /var Directory; Relative Path; Absolute Path; Creation of Directory; Creating file; removing file; Listing Files and Directories copying file; renaming file; Changing File Permission; Changing Directory Permission; Changing Group; Changing Owner; Pipe; Filters; pwd command; date command; head command; tail command less command; more command; grep command; VI Editor (Creating a new File; Inserting Text in File; Deleting Text in File; Copy , Cut &amp; Paste Text; Save File).</p> <p><b>Unit V- Shell Programming-</b> Variables(Configuration Variable &amp; Environmental Variable); Operators( Arithmetic Operator, Logical Operator, Relational Operator); Instruction(Sequence Control Instruction, Selection Control Instruction, Repetition or Loop Instruction); echo command; read command; output command.</p> <p><b>Suggested Readings (Latest Editions):</b></p> <ul style="list-style-type: none"> <li>• <i>Ramesh Bangia. 2015. Learning Unix. BPB Publication.</i></li> <li>• <i>Peter Baer Galvin. 2016. Operating System Concepts. BPB Publication</i></li> <li>• <i>Stuart E. Madnick. 2001. Operating System.</i></li> </ul> |
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|  |        |   | <p><i>Tata Mac Graw Hill.</i></p> <ul style="list-style-type: none"> <li>• <i>Kenneth H. Roshan. 2007. The complete reference Unix Tata Mac Graw Hill..</i></li> <li>• <i>D. M. Dhamethire. , 2011. System Programming and Operating Systems. Tata Mac Graw Hill.</i></li> <li>• <i>Kirrgcox. 2001. Red Hat Linux by. Printice Hill India.</i></li> <li>• <i>Andrew S. Talenbaum. 2008. Modern Operating system. Printice Hill India.</i></li> <li>• <i>Sumetabha Das. 2013. Unix (Concept and Application). Tata Mac Graw Hill.</i></li> </ul>  |
|  | BI 202 | <b>Object Oriented Programming with 'C++'</b> | <p><b>UNIT-I:</b> Introduction to Object-oriented programming, Concepts of object oriented programming: Objects, Classes, Data Abstraction, Data encapsulation, Inheritance, Polymorphism, Advantages of OOP, Application of OOP with C++.</p> <p><b>UNIT-II:</b> Introduction to C++, Token, Keywords, Identifiers, Data types (User define &amp; Derived Data types), Variables, Declaration of Variables, Operators, Scope resolution operator, Manipulators, Operator Overloading, Operator Precedence, Controlling Structures: Sequence structure, Selection structure(if....else if &amp; switch statement), Loop structure (for loop, while loop &amp; do-while loop).</p> <p><b>UNIT-III:</b>Function Prototyping, Call by reference, Friend function, Inline function, Outside function inline, Private Member functions, Public Member functions, Static class members: Static data member, Static member function, Object assignment, Passing objects to function, Objects as function arguments, Function &amp; operator overloading.</p> <p><b>UNIT-IV:</b> Array, Array of objects, Arrays within class, Pointers to object, Memory allocation, Initializing allocated memory, Allocating Array, Allocating objects. Constructor &amp; Destructor, Creating string objects, manipulating string objects, relational operators, string characteristics, comparing and swapping.</p> <p><b>UNIT-V:</b> Inheritance : Base class Access control, Inheritance &amp; protected members, Derived class, Protected base class inheritance, Single Inheritance, Multilevel Inheritance Inheritance, Multiple Inheritance, Hierarchical Inheritance, Hybrid Inheritance Virtual base classes . Virtual functions &amp; Polymorphism: Virtual function, Constructors in Derived Classes, Formatted &amp; Unformatted I/O operations.</p> |

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|  |        |                          | <p><b>Suggested Readings (Latest Editions):</b></p> <ul style="list-style-type: none"> <li>• E. Balaguruswami, <i>6th Edition . 2013</i>, Object Oriented Programming with ‘C++’, <i>Tata Mac Graw Hill</i>.</li> <li>• Yashavant Kanetkar, 13th Edition, 2016, Let Us C/C++, Paperback.</li> <li>• Robert Lafore, 4<sup>th</sup> Edition, 2008, Object Oriented Programming in ‘C++’, Paperback.</li> <li>• Scott Meyers, Latest Edition, Effective Modern C++, Paperback.</li> </ul>   |
|  | BI 203 | <b>Sequence Analysis</b> | <p><b>Unit I:</b> Sequence comparison algorithm, sequence scoring schemes (weight matrix as Identify scoring, genetic code scoring scheme chemical scoring, observed substitution matrix and Gap penalties.)</p> <p><b>Unit II:</b> Sequence database similarity searching algorithms, local alignment, global alignment, FASTA, BLAST (BLASTP, BLASTN, BLASTX, TBLASTN, TBLASTX) and similarity searching scores and their statistical interpretation.</p> <p><b>Unit III :</b> Motifs and Domains, algorithm for multiple alignments (CLUSTALx and CLUSTALW) Biological motifs (consensus, regular expression, profiles, PSSMs, HMMs and application for biological sequence similarity searching(PSI- &amp; PHI BLAST, motifs, patterns)).</p> <p><b>Unit IV:</b> Functional genomics Strategies for generating EST and full length insert, EST clustering and assembly, statistical analysis of EST and EST data, micro array (target selection/design, image analysis, data validation, statistical analysis).</p> <p><b>Unit V:</b> Phylogenetic prediction: Relationship of phylogenetic analysis to sequence alignment, Genome complexity and phylogenetic analysis, concept of evolutionary trees. Maximum parsimony method, distance method, maximum likelihood method.</p> <p><b>Suggested Readings (Latest Editions):</b></p> <ul style="list-style-type: none"> <li>• <i>Heijne, Gunnar Von. Sequence Analysis in Molecular biology: treasure troureor trivial Pursuit</i></li> <li>• <i>Koski, T. Dordrecht Kluwer. 2013. Hidden Markou Modles for Bioinformatics. Academic</i></li> </ul> |

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|  |        |  | <p><i>Publishers</i></p> <ul style="list-style-type: none"> <li>• <i>Darbin, R. Eddy, S. Krogh, A. &amp; Mithchison G.. 2010. Biological Sequence Analysis: Probabilistic models of Proteins and Nuclie acid Cambridge University Press, Cambridge</i></li> <li>• <i>Sharma, Munjal and Shankar. A Text book of bioinformatics.2009. Rastogi Publications</i></li> <li>• <i>Advances in Bioinformatics by M. S. Krishna Kumar</i></li> </ul>  |
|  | BI 204 | <b>Molecular Biology &amp; Genetic Engineering</b> | <p><b>Unit I-</b> Nucleic acids as genetic information carriers, DNA structure, types of DNA. DNA replication in prokaryotes &amp; eukaryotes. Structural features of RNA (mRNA, tRNA, rRNA). Transcription in prokaryotes &amp; eukaryotes.</p> <p><b>Unit II-</b> Regulation of gene expression. Basic features of the genetic code. Protein synthesis in prokaryotes and eukaryotes. Recombination: general principles. Plasmids (types of plasmids- F plasmids, R plasmids, Col plasmids &amp; Ti plasmid). Gene transfer mechanisms: transformation, transduction, and conjugation.</p> <p><b>Unit III-</b> Mutations: spontaneous mutation, Induced mutagenesis- mutagens (physical mutagens: non ionizing &amp; ionizing radiations; chemical mutagens: Base analogues, alkylating agents, deaminating agents, intercalating agents &amp; others), molecular mechanism of mutagenesis. DNA repair mechanism: repair by direct reversal, excision repair, recombinational repair &amp; SOS repair.</p> <p><b>Unit IV-</b> Basic steps of r-DNA technology. Restriction endonucleases. Cloning vectors: general properties, plasmids, bacteriophages, cosmids, shuttle vectors, bacterial artificial chromosomes. Eukaryotic cloning vectors for yeast, &amp; animal cells. Gene libraries: genomic library (Shot gun approach), c DNA library (Different methods for synthesizing c DNA molecules).</p> <p><b>Unit V-</b> Molecular Techniques; Principles, methods &amp; their applications in medical diagnosis -such as PCR, Southern Blotting, Northern Blotting, RFLP, RAPD, Western Blotting, DNA finger printing and DNA sequencing. Microbial genetic &amp; design of vaccines; for TB &amp; leprosy. DNA vaccines design &amp; advantages. Recombinant vaccines.</p> <p><b>Suggested Readings (Latest Editions):</b></p> <p>Maloy. Microbial Genetics. Jones and Bartlett Publishers.</p> <p>Dale JW. Molecular Genetics of Bacteria. John Wiley and Sons.</p> <p>Streips and Yasbin Modern Microbial Genetics. Niley Ltd.</p> |

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|            |        |   | <p>Watson, JD, Hopkings NH, Roberts JW, Steitz JA and Weiner AM. Molecular Biology of the Gene. Benjamin / Cummings Publications Co. Inc. California.</p> <p>Lewin. Gene VII. Oxford University Press.</p> <p>Friedberg, C, Graham C, Walker and Wolfram S. DNA repair and mutagenesis. ASM Publications.</p> <p>Larry, Snyder and Wendy. Molecular Genetics of Bacteria. ASM Publications.</p>  |
| <b>III</b> | BI 301 | <b>Statistical Analysis and Optimization Techniques</b> | <p><b>Unit I:</b> Frequency distribution. Measures of central tendency and measures of dispersion. Correlation and regression: Scatter Diagram, Coefficient of Correlation, Rank correlation. Lines of Regression.</p> <p><b>Unit II :</b> Probability theory: Classical and Statistical definitions, conditional probability, Bayes' Theorem. Random variable, mathematical expectation. Probability Distributions: Binomial, Multinomial, Poisson and Normal Distribution. Introduction and Properties of 't', Chi-square and F distribution.</p> <p><b>Unit III :</b> Estimation: Population and sample, Different kinds of sampling. Fundamental concepts of estimation, Maximum Likelihood Estimation, Interval Estimation. Hypothesis testing: students t-test, Paired t-test, large sample tests, F-test, Chi-square test, Analysis of variance.</p> <p><b>Unit IV:</b> Multivariate analysis: Multiple correlation and Regression. Introduction to Principal component analysis, Discriminant analysis and Cluster Analysis. Applications: extracting clusters of functionally related genes from microarray results.</p> <p><b>Unit V:</b> Dynamic Programming, Gibbs sampling, Markov chains, Hidden Markov Model, Simulated annealing, Genetic algorithm. Applications of these methods in sequence alignments, Protein classification and structure prediction.</p> <p><b>Suggested Readings (Latest Editions):</b></p> <ul style="list-style-type: none"> <li>• Boca Raton, Ayyub B. M. &amp; McCuen, R H. 2003. <i>Probability statistics, and reliability for engineers.</i> CRC Press.</li> <li>• S.C.Gupta &amp; V.K. Kapoor.2004. <i>Fundamentals of Mathematical Statistics.</i></li> </ul> |

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|  |        |                                 | <p><i>Sultan Chand publication</i></p> <ul style="list-style-type: none"> <li>• Ewens, W. J. &amp; Grant, G. R.. 2012. <i>Statistical methods in bioinformatics: an introduction</i>. New York. Springer,.</li> <li>• S.C.Gupta &amp; V.K. Kapoor.2014. <i>Fundamentals of Applied Statistics</i> Sultan Chand publication</li> <li>• Ghosh, Subir.. 2012. <i>Statistical design and analysis of industrial experiments</i>.</li> <li>• <a href="#">David W. Mount, David Mount. 2004. <i>Bioinformatics: Sequence and Genome Analysis</i>.</a></li> </ul>   |
|  | BI 302 | <b>Biocomputing Programming</b> | <p><b>Unit I- Hyper Text Programming Language:</b><br/>Structure of HTML program(&lt;HTML&gt;, &lt;HEAD&gt;, &lt;TITLE&gt;, &lt;BODY&gt;); Titles &amp; Footer; Text Formatting(Paragraph break&lt;P&gt;, line break&lt;BR&gt;); Text Styles(Bold&lt;B&gt;, Italics&lt;I&gt;, Underline&lt;U&gt;); Font Style, Color &amp; Size; Image Tag(&lt;IMG&gt;); Table (&lt;TABLE&gt;, &lt;TR&gt;, &lt;TH&gt;, &lt;TD&gt;) &amp; Attributes( Border, Width, Align); Frames; Forms (Text Box, Check Box, Command Button, List Box); Anchors.</p> <p><b>Unit II- Java Script-</b> Data Types; Literals; Variables; Arrays; Operators (Arithmetic, Comparison, Logical, String, Assignment); Condition Check(if-then-else); looping(for, while); Functions(Built-in, user defined); scope of functions; Dialog Boxes( Alert Dialog Box, Prompt Dialog Box; Confirmed Dialog Box).</p> <p><b>Unit III- PERL-</b> Scalar Data; Scalar Variable; List Data &amp; Variable; Operators, &lt;STDIN&gt;; print &amp; printf; Arrays; Assigning values to Array elements, Accessing Array elements; Finding the length of an Array; Hashes; Accessing Hash elements; Deleting Hash elements; Conditionals (if &amp; elseif); while loop( while, until &amp; do); for loop; controlling loop (last, next &amp; redo); Manipulating Lists and Strings (Sorting, Searching, Modifying List Elements such as: push &amp; pop, shift &amp; unshift, splice, reverse, index, substr), Pattern Matching, File Handling.</p> <p><b>Unit IV- PHP Basics-</b> PHP Syntax, Variables, Strings, Constants, Operators, Echo / Print, Conditionals (if, if...else, if...elseif); Loops For, Foreach, While, Functions, string functions, user defined functions.</p> <p><b>Unit V- PHP Array &amp; MySQL-</b> Get length without using pre-defined functions, Array push and pull, Associative arrays, loop through arrays, Array Sorting without</p> |

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|  |        |  | <p>using pre-defined functions, MySQL datatypes, DML and DDL, Aggregate functions, Sub query and join.</p> <p><b>Suggested Readings (Latest Editions):</b></p> <ul style="list-style-type: none"> <li>• <i>Dick Oliver. 2014. HTML 4 in 24 hrs. Techmedia Publication</i></li> <li>• <i>Dick Oliver. 2014. JavaScript 4 in 24 hrs. Techmedia Publication</i></li> <li>• <i>Ivan Bayross. 2013. Web Enabled commercial application development using HTML, DHTML, JavaScript and PERL CGI. BPB Publication</i></li> <li>• <i>James Tisdall. 2012. Beginning perl for Bioinformatics. O-Reilly</i></li> <li>• <i>Cynthia Gibos, Per Jambeck. 2010. Developing Bioinformatics Computer Skills. O-Reilly</i></li> <li>• <i>Randal L. Schwartz, Tom Phoenix. 2008. Learning Perl. O-Reilly</i></li> <li>• <i>Techmedia Aldo. 2002. Perl programming, Wiley Publication.</i></li> <li>• <i>Eric C. Hermamm.2008. Mastering Perl 5. BPB Publication.</i></li> </ul>  |
|  | BI 303 | <b>Structural Biology &amp; Molecular Modeling</b> | <p><b>Unit I:</b> Macromolecular Structures: Protein - Primary, Secondary, Super secondary, Tertiary and Quaternary structure, Enzymes- Introduction, Michaelis Menton Kineteis, Enzyme regulation; Classification, Structure and function of Carbohydrates and lipids; 3D Viral structures.</p> <p><b>Unit II:</b> Methods to study 3D structure, Principles of crystallography, Co-ordinate systems, Fitting and refinement, Validation, Analysis of 3D structures, Methods for 3D structure prediction, Knowledge based &amp; Fold recognition; Principles of protein folding and methods to study protein folding.</p> <p><b>Unit III:</b> Basic concept of Bioenergetics; Thermodynamics principle in biology; energy rich bonds, Computational approaches in structural biology; Macromolecular interactions, Protein - Protein, Protein – Nucleic acids, Protein – carbohydrates.</p> <p><b>Unit IV:</b> Overview of molecular modelling - Introduction and challenges, Molecular modelling methods, Conformational searching, Potential energy maps, Ramachandran maps, Ab-initio methods, Semi-empirical methods, Empirical methods- Conformational analysis, Introduction and Methods, Molecular fitting, Energy Minimization, Non-</p> |

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|  |        |   | <p>derivative and derivative methods.</p> <p><b>Unit V:</b> Global optimization (simulated annealing, Tabu search, genetic algorithms), Applications of energy minimization, Molecular Mechanics, Conformations: global vs. local, Force fields: expressions for stretch, bond, torsion, etc., Description of various force fields: MM3, Dreiding, AMBER, CHARMM, Mechanics of Bio-macromolecules, Molecular Dynamics- Newton's equations for many particles, Verlet and related algorithms, Types of dynamics simulations: adiabatic, constant T, annealed, etc., Conformational searching using MD and other methods, Free energy calculations, Dynamics of Bio-macromolecules</p> <p><b>Suggested Readings (Latest Editions):</b></p> <ul style="list-style-type: none"> <li>• <i>Philip E. Bourne (Editor), Helge Weissig (Editor). 2003. Structural Bioinformatics - Methods of biochemical Analysis V. 44. New Jersey. Wiley-Liss.</i></li> <li>• <i>Jan Drenth. 2008. Principles of protein X-ray Crystallography Springer-Verlag.</i></li> <li>• <i>Branden, Carl &amp; Tooze, John , Introduction to Protein Structure. Garland Publishing.</i></li> <li>• <i>Friesner, R.A. Ed., Prigogine, L. Ed. &amp; Rice, S.A. New York. John wiley &amp; sons. 2002. Computational methods for protein folding : advances in chemical physics vol. 120. Inc. publication.</i></li> <li>• <i>Hans Dieter and Didier Rognan. 2003. Molecular Modeling: Basic Principles and application. Wiley VeH Gmbh and Co. KGA.</i></li> <li>• <i>Heilmeyer, L. &amp; Friedrich, P. Amsterdam . 2001. Protein modules in cellular signaling edited. IOS Press.</i></li> </ul> |
|  | BI 304 | <b>Genomics, Proteomics &amp; Systems Biology</b> | <p><b>Unit I:</b> Objective and Overview of Genome Comparisons, Genome Alignments, BLAST2, MUMmer, PipMaker, VISTA, Comparison of Gene Order, Comparative Genomics— Viruses, Microbes, Pathogens, Eukaryotes,</p> <p><b>Unit II:</b> Comparative Genomics Databases- COG, VirGen, CORG, HOBACGEN, Homophila, XREFdb, Gramene, Single Nucleotide Polymorphism, dbSNP and other SNP-related databases; An overview of pharmacogenomics.</p> <p><b>Unit III:</b> Definition, History and Scope of Proteomics, Experimental Techniques (SDS-PAGE, 2D-PAGE, X-ray crystallography, NMR spectroscopy, isoelectric focusing, mass spectroscopy, (MALDI), differential display, protein chips and antibody</p>   |

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|  |  |  | <p>microarrays, functional protein microarrays; resolution and identification of proteins), analysis of post translational modifications of proteins; Bioinformatics Approaches, Protein-Protein Interaction Networks, databases and software, DIP (Database of Interacting Proteins).</p> <p><b>Unit IV:</b> PPI Server, BIND - Biomolecular Interaction Network Database, PIM –Hybrigenics PathCalling Yeast Interaction Database, MINT - a Molecular Interactions Database, GRID - The General Repository for Interaction Datasets, InterPreTS - protein interaction prediction through tertiary structure.</p> <p><b>Unit V: Systems Biology:</b> Biological Systems-- System of Molecular Networks; Ecosystem, Elements of systems modeling, Gene regulatory network and the models; Computational modeling in biology.</p> <p><b>Suggested Readings (Latest Editions):</b></p> <ul style="list-style-type: none"> <li>• Hecker, M. &amp; Mullner, S., Berlin. 2003. Proteomics of microorganisms. Springer-Verlag.</li> <li>• Liebler, D.C. &amp; Yates, J.R. III. 2002. <i>Introduction to proteomics: tools for the new biologist.</i> New York. Humana Press.</li> <li>• Pennington, S. R. &amp; Dunn, M. J. 2002. <i>Proteomics: from protein sequence to function</i> New Delhi, Viva Books Private Ltd.</li> <li>• David Mount. 2004. <i>Bioinformatics: sequence and genome analysis.</i> cold springer harbour press.</li> <li>• Sankoff, D. &amp; Nadeau, J.H., Netherlands. 2004. <i>Comparative genomics: empirical and analytical approaches to gene order dynamics, map alignment and the evolution of gene families.</i> Kluwer Academic Publishers.</li> </ul> |
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