# Scheme of Teaching

# &

# Detailed Syllabus

## For

# Masters in Technology
# Bioinformatics

# M. Tech (BI)

## (Two Year Program)
(w.e.f. Academic Session 2018–19)

## School of Engineering & Technology
## Shobhit Institute of Engineering & Technology
### (Deemed to-be University)
### NH-58, Modipuram, Meerut (U.P.) – 250110

Website: www.shobhituniversity.ac.in

# M.Tech. Bioinformatics

**Overview:** M.Tech. Bio-informatics **or** Master of Technology in Bio-informatics is a postgraduate Bio-informatics course. Bio-informatics is the application of statistics and computer science to the field of molecular biology. The program provides competence in computational biology/bio-informatics by providing training in the areas of molecular biology, information technology, statistics and bio-informatics. The program also offers hands-on expertise in the essential multi-disciplinary fields of genomics, proteomics, protein engineering, metabolic pathway engineering, Pharmacogenomics, the discovery of new drugs and vaccines, molecular diagnostic kits, Agro-biotechnology that comprise the core of Bioinformatics.

**Program Outcome:** Bioinformatics has a strong interdisciplinary character. It can be considered to be a confluence of Biology, Computer Science, Information Technology, Mathematics, Chemistry, Physics, and Medicine with the objectives of developing tools to analyze biological, biochemical, biophysical data and to generate new knowledge in these areas. It is a fact that persons trained and skilled in these multifarious ways do not exist, and if this area is to develop in our country these persons will have to be trained and produced. An ability to independently carry out research /investigation and development work to solve practical problems related to Production and Industrial Engineering

**PO1.** An ability to write and present a substantial technical report/document

**PO2.** After the completion of this course students have the option to go for higher studies i.e. M. Tech. and then do some research for the welfare of mankind.

**PO3.** After higher studies students can join as scientist and can even look for professional job oriented courses.

**PO4.** After the completion of M.tech. Degrees there are various other options available for the science students. Often, in some reputed universities or colleges in India and abroad the students are recruited directly by big MNC's after their completion of the course.

**PO5.** Apart from the research jobs, students can also work or get jobs in Marketing, Business & Other technical

**Program Specific Outcome:** Some of the common job roles and responsibilities of a Bioinformatics scientist are:

**PSO1.** Attain theoretical and practical knowledge base, technical proficiency, and communication skills for employment in the biotechnology field

**PSO2.** Integrate the course work knowledge to research and industry based work.

**PSO3.** Development and utilization of critical thinking skills

**PSO4.** Interpret and analyze new scientific discoveries and technologies relevant to biotechnology

**PSO5.** Assess and apply established and emerging biotechnology techniques used for commercial development

**PSO6.** Development of an awareness and sensitivity to ethical issues in bioinformatics.

**PSO7.** Inspire to generate hypotheses, design approaches to test them, and interpret the data from those tests to reach valid conclusions.

**PSO8.** To provide in-depth knowledge in the area of bioinformatics and computational biology.

**PSO9.** To provide knowledge regarding the use of IT in the field of bioinformatics.

**Eligibility Criteria:**

A graduate student having completed any of the following with minimum 50% marks in B.E / B.Tech Biotechnology / Bioinformatics / Chemical Engineering / Computer Science / Computer Engineering / Bioinformatics Engineering / Bioprocess Technology / B.Pharm / M.B.B.S. / B.D.S. / M. V. Sc. or M. Sc. and equivalent.

**Credit Distribution:**

| S.No. | Criteria | I | II | III | IV | Total |
|-------|----------|---|----|-----|----|----|-------|
| 1. | **Core Bioinformatics (BBM)** | 14 | 18 | 8 | | 40 |
| 2. | **Departmental Elective** | 4 | | 8 | | 12 |
| 3. | **Seminars** | 2 | 2 | | | 4 |
| 4. | **Project** | | | 4 | | 4 |
| 5. | **Dissertation** | | | | 14 | 14 |
| | **Total** | **20** | **20** | **20** | **14** | **74** |

**SHOBHIT INSTITUTE OF ENGINEERING AND TECHNOLOGY, MEERUT**
**School of Biological Engineering and Life Sciences**

**Department of Bioinformatics and Bioinformatics Engineering**

**Bioinformatics Syllabus (M.Tech.)**

| Subject | | L | T | P | Credit |
|---|---|---|---|---|---|
| **Semester I** | | | | | |
| BIMT 501 | Concepts In Biotechnology | 3 | 1 | 0 | 4.0 |
| BIMT 503 | Essential Bioinformatics | 3 | 1 | 0 | 4.0 |
| BIMT 505 | Biostatistics | 3 | 1 | 0 | 4.0 |
| BIMT 521/523/525 | Java And Web Based Tools/ Genomics And Proteomics/ Advanced Data Structure | 3 | 1 | 0 | 4.0 |
| BIMT 551 | Bioinformatics Lab | 0 | 0 | 3 | 2.0 |
| BIMT 581 | Seminar | 0 | 0 | 3 | 2.0 |
| **Total** | | | | | 20.0 |
| **Semester II** | | | | | |
| BIMT 502 | Programming Language, Algorithm And Tools | 3 | 1 | 0 | 4.0 |
| BIMT 504 | Sequence And Structure Database | 3 | 1 | 0 | 4.0 |
| BIMT 506 | Mathematical Modelling And Advanced Statistics | 3 | 1 | 0 | 4.0 |
| BIMT 508 | Biomolecular Modeling And Simulation | 3 | 1 | 0 | 4.0 |
| BIMT 552 | Programming Language Lab | 0 | 0 | 3 | 2.0 |
| BIMT -582 | Seminars | 0 | 0 | 3 | 2.0 |
| **Total** | | | | | 20.0 |
| **Semester III** | | | | | |
| BIMT 601 | Computational Biology | 3 | 1 | 0 | 4.0 |
| BIMT 603 | Advanced Computer Aided Drug Designing | 3 | 1 | 0 | 4.0 |
| BIMT 621/623 | Bio-Python/ Molecular Phylogeny | 3 | 1 | 0 | 4.0 |
| BIMT 625/627 | Immunoinforamtics/ Chemoinformatics | 3 | 1 | 0 | 4.0 |
| BIMT 671 | Minor Project/Seminar | 0 | 0 | 8 | 4.0 |
| **Total** | | | | | 20.0 |
| **Semester IV** | | | | | |
| BIMT 692 | Dissertation | 0 | 0 | 28 | 14.0 |
| | | | **Total** | | 14.0 |
| | | | **Grand Total** | | 74.0 |

**Changes**: Advanced Data Structure in I Sem; Programming Language, Algorithm And Tools in II Sem Bio-Python Molecular Phylogeny in III Sem

| Course code | **BIMT-501** | | | |
|---|---|---|---|---|
| Category | Core Bioinformatics | | | |
| **Course title** | **Concepts in Biotechnology** | | | |
| **Scheme and Credits** | **Credit** | **L** | **T** | **P** |
| | 4 | 4 | 0 | 0 |
| **Pre-requisites (if any)** | Basic Knowledge of Biology | | | |
| **Objectives** | Evaluate scientific information presented in the media. Discover the relationship of biology to everyday experiences. | | | |
| **Outcomes** | 1. Demonstrate understanding and use of the Scientific Method<br>2. Generate Information by Observation, experimentation, Reflection, Reasoning<br>3. Read and Construction tabular and Graphical Data<br>4. Transfer Information to new settings<br>5. Analyze, Synthesize, Evaluate, Apply Information to solve problems<br>6. Understand how Scientific Theories are formulated, tested, validated<br>7. Recognize Similarities and Differences between scientific knowledge and other forms of knowledge | | | |
| | | | | |
| **Unit I** | Introduction to Biology; Macromolecules; Carbonchemistry; Proteins: Structure, folding, catalysis; Nucleic acids: DNA & RNA; storage and transfer of genetic information; Lipids: membranes, structure & function; Carbohydrate chemistry, energy storage, building blocks. | **08** | | |
| **Unit II** | Cell Structure: Eukaryotic and Prokaryotic cells, plant and animal cells, structure of nucleus, mitochondria, ribosomes, Golgi bodies, lysosomes, endoplasmic reticulum, chloroplast, vacuoles; Cell cycle and cell division: Different phases of cell cycle, cell division: Mitosis and meiosis. Mendelian law of inheritance: Monohybrid and dihybrid inheritance, law of segregation and independent assortment; Gene Interaction; Multiple alleles, supplementary and complementary genes, epistasis. Identification of genetic material: classical experiments; chromosome structure and organization, chemical composition of chromatin, structural organization of nucleosomes, heterochromatin, polytene and lamp-brush chromosomes, human chromosomes, chromosomal disorders. | **08** | | |
| **Unit III** | Scope and History of microbiology, Introduction to the structure and functions of microorganism: Bacteria, Viruses, Fungi and Protozoan's. Microscopy and microbialtechniques: Study of microscopes; sterilization techniques: Heat, steam, Radiation, Filtration and chemical methods; Pure culture techniques: Serial Dilution, Streak, Spread, Pour Plate. Immune System, Innate and adaptive immunity, antigens and antibodies; types of immune response, hypersensitivity. Humoral immunity: B-lymphocytes, Immunoglobulin classes, Major Histocompatibility Complex (MHC). Cell mediated immunity. Thymus derived lymphocytes (T-cells), Antigen presenting cells (APC); Immunity to infection, Cytokines. | **08** | | |
| **Unit IV** | Scope of agricultural biotechnology, Role of Micorbes in agriculture, Biopesticides, Bio fertilizers (Nitrogen fixing microbes), GM crops. Plant metabolic engineering and industrial products: Molecular farming for the production of industrial enzymes, biodegradable plastics, antibodies, edible vaccines. Metabolic engineering of plants for the production of fatty acids, | **08** | | |

| | | industrial oils, flavonoids etc. Basic aspects of Food & Nutrition | |
|---|---|---|---|
| **Unit V** | | Industrially important Microorganisms, Preservation techniques, Different media for fermentation, basic structure of fermentor and different types. Types of fermentation processes (surface, submerged, and solid state) and their products (ethanol, citric acid, lactic acid, enzymes, antibiotics) Biological treatment of waste water, primary, secondary and tertiary treatments. Bio indicators, Bioremediation of xenobiotic compounds, Bioleaching of minerals from ores, Bio-sorption of toxic metals. Solid waste management. Biofuel production from agricultural wastes | **08** |

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PSO 2 | PSO 3 | PSO 4 | PSO 5 | PSO 6 | PSO 7 | PSO 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CO 1** | 1 | 2 | 2 | 1 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | 1 | 1 |
| **CO 2** | 1 | 1 | 2 | 3 | 2 | 1 | 2 | 3 | 2 | 3 | 2 | 1 | 2 | 2 |
| **CO 3** | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 2 | 2 | 3 | 2 | 2 |
| **CO 4** | 2 | 2 | 3 | 1 | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 |
| **CO 5** | 3 | 2 | 1 | 3 | 1 | 1 | 3 | 2 | 1 | 1 | 1 | 2 | 2 | 2 |
| **CO 6** | 2 | 2 | 3 | 1 | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 2 | 2 | 2 |
| **CO 7** | 1 | 2 | 2 | 1 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | 1 | 1 |
| **Average** | 1.9 | 1.9 | 2.1 | 1.7 | 1.9 | 1.7 | 1.6 | 1.7 | 1.7 | 1.4 | 1.3 | 2.0 | 1.7 | 1.7 |

| **References** | 1. Fleet, G. H. (1993). *Wine microbiology and biotechnology*. CRC Press. 2. Buchholz, K., & Collins, J. (2014). *Concepts in biotechnology: history, science and business*. John Wiley & Sons. 3. Balasubramanian, D. (2004). *Concepts in biotechnology*. Universities Press. |
|---|---|

| Course code | **BIMT-503/ BIMT-551** | | | | |
|---|---|---|---|---|---|
| Category | Core Bioinformatics | | | | |
| **Course title** | **ESSENTIAL OF BIOINFORMATICS/ BIOINFORMATICS LAB** | | | | |
| **Scheme and Credits** | **Credit** | **L** | **T** | **P** | |
| | 4 | 4 | 0 | 0 | |
| **Pre-requisites (if any)** | Basic knowledge of Biotechnology and Computers | | | | |
| **Objectives** | Bioinformatics is the science of storing, extracting, organizing, analyzing, interpreting and using information. The approaches to the discipline of bioinformatics incorporate expertise from the biological sciences, computer science and mathematics. The major in bioinformatics is designed for students interested in molecular biology and genetics, information technologies and computer science. | | | | |
| **Outcomes** | A student completing a major in Bioinformatics shall be able to apply: <br><br> 1. knowledge and awareness of the basic principles and concepts of biology, computer science and mathematics <br> 2. existing software effectively to extract information from large databases and to use this information in computer modeling <br> 3. problem-solving skills, including the ability to develop new algorithms and analysis methods <br> 4. 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 | | | | |
| | | | | | |
| **Unit I** | Bioinformatics & Biological Databases: Introduction to Bioinformatics, Goals, Scope, Applications in biological science and medicine and Limitations,a) Sequence Databases b) Structure Databases c) Special Databases and applications: Genome, Microarray, Metabolic pathway, motif, multiple sequence alignment and domain databases. Mapping  databases – genome wide maps. Chromosome specific human maps. Applications of these databases. Database Similarity Searching: Unique Requirements of Database Searching. Heuristic Databasesearching, Basic Local Alignment Search Tool (BLAST), FASTA, Comparison of FASTA and BLAST, Database Searching with the Smith–Waterman Method. | | **08** | | |
| **Unit II** | Sequence Alignment: Evolutionary basis, Homology vs Similarity, Similarity vs Identity. Types of Sequence alignment - Pairwise and Multiple sequence alignment, Alignment algorithms, Scoring matrices, Statistical significance of sequence alignment. Multiple Sequence Alignment: Scoring function, Exhaustive algorithms, Heuristic algorithms, Practical issues. Profiles and Hidden Markov Models: Position-Specific scoring matrices, Profiles, Markov Model and Hidden Markov Model. | | **08** | | |
| **Unit III** | Prediction Motifs and Domains: Motif and Domain databases, Identification of Motifs and Domains in Multiple Sequence Alignment using Regular expressions, Motif and Domain Databases statistical models, Protein Family databases, Motif Discovery in unaligned sequences. Sequence logos. Gene and Promoter Prediction: Promoter and Regulatory elements in Prokaryotes and Eukaryotes. Promoter and Regulatory element prediction – algorithms. Gene prediction. Gene prediction in Prokaryotes and Eukaryotes. Categories of Gene Prediction | | **08** | | |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Unit IV | | Predictive Methods: Predictive methods using Nucleic acid sequence – DNA framework, Maskingof repetitive DNA, predicting RNA secondary structure, Finding RNA genes, Detection Offunctional sites and Codon bias in the DNA. Predictive methods using protein sequence –Proteiidentity and Physical properties. Structure prediction - Prediction of secondary structure of protein, Antigenic sites, Active sites, Folding classes, specialized structures and Tertiary structures. Discussions with case studies. Concepts involved in insilico Primer Designing and developing Restriction Maps. | | | | | | | | | | | | 08 |
| Unit V | | Molecular Phylogenetic: Phylogenetics Basics. Molecular Evolution and Molecular Phylogenetics - Terminology, Gene Phylogeny vs Species Phylogeny, Forms of Tree Representation. Phylogenetic Tree Construction Methods and Programs - Distance-Based Methods, Character- Based Methods. Phylogenetic Tree evaluation methods. Phylogenetic analysis software and algorithms. Bootstrap methods.. | | | | | | | | | | | | 08 |

Programs. Prediction algorithms. Discussions with case studies.

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PS O 2 | PSO 3 | PSO 4 | PS O 5 | PS O 6 | PS O 7 | PS O 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CO 1 | 1 | 3 | 2 | 1 | 2 | 3 | 1 | 1 | 1 | 1 | 1 | 2 | 1 | 3 |
| CO 2 | 2 | 1 | 2 | - | 2 | 2 | - | 3 | 2 | 2 | - | 1 | 1 | 2 |
| CO 3 | 2 | 2 | 3 | 1 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | - | 2 | 2 |
| CO 4 | 1 | 2 | 2 | 2 | 2 | 1 | 1 | 1 | 2 | 1 | 1 | 2 | 1 | - |
| Average | 1.5 | 2.0 | 2.3 | 1.0 | 2.0 | 2.0 | 0.8 | 1.5 | 1.8 | 1.3 | 0.8 | 1.3 | 1.3 | 1.8 |

**References**

1. Xiong, J. (2006). *Essential bioinformatics*. Cambridge University Press.
2. Augen, J. (2004). *Bioinformatics in the post-genomic era: Genome, transcriptome, proteome, and information-based medicine*. Addison-Wesley Professional.
3. Posada, D. (Ed.). (2009). *Bioinformatics for DNA sequence analysis*. New York: Humana Press.

| Course code | **BIMT-505** |
|---|---|
| Category | Core Bioinformatics |
| **Course title** | **Biostatistics** |

| **Scheme and Credits** | **Credit** | **L** | **T** | **P** | |
|---|---|---|---|---|---|
| | 4 | 4 | 0 | 0 | |

| **Pre-requisites (if any)** | Basic knowledge of Mathematical tools |
|---|---|
| **Objectives** | In public health work, one may be concerned with planning of experiments and the analysis of their results. Therefore, one has to deal with statistical data analyses that come from no deliberate experiment but that arise because of the data collected from the population in the course of public health study and survey. This course therefore provides training to the students on how to conduct epidemiological surveys, design questionnaire and analyze the data. The students will get hands-on-training on 'R', a free software environment for statistical computing and graphics. |
| **Outcomes** | After the completion of this course students would be able to:<br>1. use and interpret results of, descriptive statistical methods effectively.<br>2. Explain the principal methods of statistical inference and design.<br>**3.** Read and learn new statistical procedures independently. |
| | |

| Unit I | Descriptive statistics, quantitative parameters and inferential statistics. Events and samples spaces, algebra of events, Venn diagram, random events, axiomatic definition of probability, probability as relative frequency. Independence, mutually exclusiveevents, conditional events, Bayes' rule and theorem, counting-permutation-combination andprobability, application to diagnostics, types of errors, evaluation of odds and risks. | **08** |
|---|---|---|
| **Unit II** | Random variables as functions, discrete and continuous random variables, probability mass function, common discrete distributions – Bernouli, Binomial, Geometric, Poisson, ztransform, marginal and joint distributions, applications, Continuous random variables and distributions, Normal, exponential and gamma, Chi Square, t, and F distributions, characteristic/moment-generating functions Estimation of mean and variance and their distributions, Central Limit Theorem and sample size, confidence intervals, applications | **08** |
| **Unit III** | Testing for single or two populations for the mean with and without knowledge of variance, Normal and Student `t' test, Chi Square/F test for the variance of one/two populations, G. Independence of attributes and Chi Square test for goodness of fit. Experimental design: randomization, factorial, Latin square, and sequential cross-over design, F Test and Applications. | **08** |
| **Unit IV** | Non-parametric and distribution-free statistics, some important nonparametric tests; sign test, Wilcoxon's rank test and Spearman's rank, correlation. Classification (differential diagnosis), | **08** |
| **Unit V** | sequential clinical trials, and other applications. Introduction to regression and time-series, data mining for patterns, analytics. Laboratory sessions for descriptive statistics, testing and experimental design, using open source software R | **08** |

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PSO 2 | PSO 3 | PSO 4 | PSO 5 | PSO 6 | PSO 7 | PSO 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CO 1** | 1 | 1 | 1 | 1 | 2 | 2 | 3 | 1 | 1 | 1 | 1 | 2 | 1 | 2 |
| **CO 2** | 3 | - | 2 | 2 | 1 | 1 | 2 | 3 | 2 | 2 | 2 | 1 | 1 | 2 |

| CO 3 | 1 | 2 | - | 1 | 1 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Average | 1.7 | 1.0 | 1.0 | 1.3 | 1.3 | 1.7 | 2.0 | 1.7 | 1.7 | 1.3 | 1.3 | 1.7 | 1.3 | 2.0 |

| References | 1. Martin Bland: An Introduction to Medical Statistics, Oxford University Press, 1995. |
|---|---|
| | 2. Wayne Daniel: Biostatistics: Foundation for Analysis in the Health Sciences, 5th Ed., |
| | 3. John Wiley & Sons, New York, 2009. 9th Edition |
| | 4. Marcello Pagano, Principles of Biostatistics, Cengage Learning India, 2000, 2$^{nd}$Edition |
| | 5. P. G. Hoel, S. C. Port, and C. J. Stone, Introduction to Statistical Theory, Universal Book Stall, New Delhi, 1994 |

| Course code | **BIMT-521** |
|---|---|
| Category | Departmental Elective |
| **Course title** | **JAVA AND WEB BASED TOOLS** |

| **Scheme and Credits** | **Credit** | **L** | **T** | **P** | |
|---|---|---|---|---|---|
| | 4 | 4 | 0 | 0 | |

| **Pre-requisites (if any)** | Basic knowledge of Languages |
|---|---|
| **Objectives** | Objective of this course is to learn the development of Enterprise based applications, using EJB: Stateful, Stateless and Entity Beans. 8. To make the students familiar with Struts frameworks, which gives the opportunity to reuse the codes for quick development? |
| **Outcomes** | 1. To learn the graphics and animation on the web pages, using Java Applets<br>2. To learn and design a full set of Event driven UI widgets and other components, including windows, menus, buttons, checkboxes, text fields, scrollbars and scrolling lists, using Abstract Windowing Toolkit (AWT) & Swings<br>3. To learn Java Data Base Connectivity (JDBC) so as to retrieve and manipulate the information on any relational database through Java programs.<br>4. To learn the server side programming using Servlets and JSP.<br>5. To learn Java Bean so as to make the reusable software components<br>6. To learn the invocation of the remote methods in an application using RMI<br>7. To learn Hibernate for the mapping of Java classes and objects associations to the relational database tables. |

| Unit I | Introduction to Java: Java and Java applications. Java Development Kit (JDK). Byte Code, JVM; Object-oriented programming. Simple Java programs. Data types and Tokens: Boolean variables, int, long,char, operators, arrays, white spaces, literals, assigning values. Creating and destroying objects. Access specifiers. Operators and Expressions: Arithmetic Operators, Bitwise operators, Relational operators, Assignment Operator, The ? Operator; Operator Precedence.Logical expression. Type casting, Strings. Control Statements: Selection statements, iteration statements, Jump Statements. | **08** |
|---|---|---|
| Unit II | Classes, Inheritance, Exceptions: Classes. Classes in Java - Declaring a class, Class name, Super classes, Constructors. Creating instances of class. Inner classes. Inheritance: Simple, multiple, and multilevel inheritance; Overriding, overloading. Exception handling: Exception handling in Java. Multi- Threaded Programming: Multi Programming: Extending threads; Implementing rentable. Synchronization, Changing state of the thread. Bounded buffer problems, Read-write problem, Producer-Consumer problems. Event Handling: Two event handling mechanisms, Delegation event model, Event classes; Sources of events; Event listener interfaces. Delegation event model; Adapter classes; Inner classes. | **08** |
| Unit III | Applets: The Applet Class: Two types of Applets, Applet basics, Applet Architecture, An Applet skeleton; The HTML APPLET tag; Passing parameters to Applets, Simple Applet display methods; Requesting repainting; Using the Status Window. getDocumentbase() and getCodebase(); ApletContext and showDocument(); The AudioClipInterface; The AppletStub Interface; Drawing Lines; Drawing Other Stuff; Color; Mouse Input; Keyboard Input and Output to the Console. Threads and Animation, Backbuffers, Graphics, and Painting; Clocks. Playing with text: Introduction to 2D arrays and hyperlinks, 3D Graphics | **08** |

| | | |
|---|---|---|
| | - Basic classes. | |
| **Unit IV** | Java 2 Enterprise Edition Overview, Database Access: Overview of J2EE and J2SE. The Concept of JDBC; JDBC Driver Types; JDBC Packages; A Brief Overview of the JDBC process; Database Connection; Associating the JDBC/ODBC Bridge with the Database; Statement Objects; ResultSet; Transaction | 08 |
| **Unit V** | Servlets: Background; The Life Cycle of a Servlet; Using Tomcat for Servlet Development; Simple Servlet; The Servlet API. The Javax.servlet Package. Reading Servlet Parameter, Javax.servlet.httppackage, Handling HTTP Requests and Responses. Cookies and Session Tracking. | 08 |

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PSO 2 | PSO 3 | PSO 4 | PSO 5 | PSO 6 | PSO 7 | PSO 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CO 1** | 1 | 1 | 1 | 1 | 2 | 2 | 3 | 1 | 1 | 1 | 1 | 2 | 1 | 2 |
| **CO 2** | 3 | - | 2 | 2 | 1 | 1 | 2 | 3 | 2 | 2 | 2 | 1 | 1 | 2 |
| **CO 3** | 1 | 2 | - | 1 | 1 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **CO 4** | 1 | 1 | 1 | 1 | 2 | 2 | 3 | 1 | 1 | 1 | 1 | 2 | 1 | 2 |
| **CO 5** | 3 | - | 2 | 2 | 1 | 1 | 2 | 3 | 2 | 2 | 2 | 1 | 1 | 2 |
| **CO 6** | 1 | 2 | - | 1 | 1 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **CO 7** | 1 | 2 | - | 1 | 1 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **Average** | 1.6 | 1.1 | 0.9 | 1.3 | 1.3 | 1.7 | 1.9 | 1.6 | 1.7 | 1.3 | 1.3 | 1.7 | 1.4 | 2.0 |

| **References** | 1. **Bloch, J. (2008).** *Effective java (the java series)*. **Prentice Hall PTR.**<br>2. Pigeaud, T. G. T. (2013). *Islamic States in Java 1500–1700: Eight Dutch Books and Articles by Dr HJ de Graaf*. Springer Science & Business Media.<br>3. Jaworski, J. (1999). *Java 2 Platform Unleashed* (Vol. 19). Sams. |
|---|---|

| Course code | **BIMT-521** | | | | |
|---|---|---|---|---|---|
| Category | Departmental Elective | | | | |
| **Course title** | **GENOMICS AND PROTEOMICS** | | | | |
| **Scheme and Credits** | **Credit** | **L** | **T** | **P** | |
| | 4 | 4 | 0 | 0 | |
| **Pre-requisites (if any)** | Biology, genetics | | | | |
| **Objectives** | Genomics, proteomics and bioinformatics are the cornerstones of the so-called 'Omics technologies that are routinely applied in medical research and throughout the drug-development process. In recent years genomic and proteomic technologies, combined with bioinformatics, and rapid progress in high throughput technologies, have made it possible to study gene regulation and protein function in high throughput. In contrast to studies of single genes or single proteins, genomic and proteomic methods simultaneously investigate large numbers of genes or proteins in one single experiment. | | | | |
| **Outcomes** | Student would be able to: <br> 1. be able to describe the development of Omics technologies, with emphasis on genomics and proteomics; <br> 2. Be able to synthesise information to discuss the key technological developments that enabled modern genomic and proteomic studies; <br> 3. be able to describe advanced genomics and proteomics technologies and the ways in which their data are stored; <br> 4. be able to use bioinformatics techniques to query examples of genomic and proteomic databases to analyse cell biology; <br> 5. be able to describe the different types of genome variation and their relationship to human diseases; <br> 6. be able to discuss how biological systems information relating to genes, proteins and cellular structures can be used to model living cells, and even to create new synthetic cells. | | | | |
| | | | | | |
| **Unit I** | Genome of eukaryotes, Genome of prokaryotes, organelle genome, C-value paradox, packing of DNA into chromosomes, gene families, pseudogene, genome of bacteriophage, eukaryotic virus, mobile genetic elements, repetitive DNA content. | | | | **08** |
| **Unit II** | Maxam and Gilbert degradation method, Sanger's dideoxy chain termination method, automated DNA sequencing, pyrosequencing, sequencing by hybridization, fully sequenced genome, SAGE, PFGE, expression and gene silencing | | | | **08** |
| **Unit III** | Insertional mutagenesis, T-DNA, transposon insertion, expressed sequence tag, contig, unigene, gene expression profiling by microarray, genome evalution. | | | | **08** |
| **Unit IV** | Basic principles of protein structure, primary, secondary, tertiary and quaternary structure, post translational modification, Ramachandran plot, protein folding, protein disulfide isomerism. | | | | **08** |
| **Unit V** | : SDS-PAGE, 2D-PAGE, ICAT (isotope coded affinity tag), X-ray crystallography, NMR spectroscopy, isoelectric focusing, mass spectroscopy, MALDI-TOF, protein chips, antibody microarray, protein microarray, application of protein chip in microarray, protein expression profiling, identification of | | | | **08** |

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PS O 2 | PSO 3 | PSO 4 | PS O 5 | PS O 6 | PS O 7 | PS O 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | protein-protein interaction, multiprotein complexes | | | | | | | | | | | | | |
| CO 1 | 1 | 1 | 1 | 2 | 1 | 2 | 3 | 1 | 1 | 1 | 1 | 2 | 1 | 2 |
| CO 2 | 2 | 2 | 2 | 2 | 1 | 2 | 2 | 2 | 2 | 2 | 2 | 1 | 1 | 2 |
| CO 3 | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| CO 4 | 1 | 1 | 1 | 2 | 1 | 2 | 3 | 1 | - | 1 | 1 | 2 | 1 | 2 |
| CO 5 | 2 | 2 | - | 1 | 1 | 2 | 1 | 3 | 2 | - | 2 | 1 | 1 | 2 |
| CO 6 | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | - | 2 |
| Average | 1.7 | 1.3 | 1.0 | 1.8 | 1.3 | 2.0 | 1.8 | 1.5 | 1.5 | 1.0 | 1.3 | 1.7 | 1.0 | 2.0 |

| References | 1. Brown, T.A. 2008. Gene cloning and DNA analysis: an Introduction (5th eds.) Blackwell science Ltd.<br><br>2. Brown, T.A. 2007. Genome 3 (3rd eds) Garland science publishing.<br><br>3. Primrose, S.B. and Twyman, R.M. Principle of gene manipulation and genomics (7th eds.) black well Publishing.<br><br>4. Winnacker, Ernst-L. 2003. Form gene to clone introduction to gene technology Panima Publishing crop, New Delhi.<br><br>5. Alberts, B., Johnson, A., Lewis, J., Raff, M., Roberts, K., Walter, P. 2008. Molecular Biology of Cell (5th eds.). Garland Sciences.<br>6. Benjamin Lewin. 2008. Genes IX. Oxford University Press.<br>7. Lodish, H., Berk, A., Kaiser, C.A., Krieger, M., Scott, M.P., Bretscher, A., Ploegh, H. and Matsudaira, P. 2008. Molecular Biology (6th eds.). |
|---|---|
| **Course code** | **BIMT-521** |
| Category | Departmental Elective |
| **Course title** | **ADVANCED DATA STRUCTURE** |
| **Scheme and Credits** | Credit: 4    L: 4    T: 0    P: 0 |
| **Pre-requisites (if any)** | Basic knowledge of Programming and Computers |
| **Objectives** | Objective is to Learn the notions of data structure, Abstract Data Type. Understand Big(O) notation and role of algorithm complexity in computing |
| **Outcomes** | 1. To evaluate various methods of linked list formulation. Also explore different kinds of linked lists and their applications in day to day problem solving.<br>2. To evaluate various methods stack formulation. Also explore different kinds stacks and their applications and implementations in day to day problem solving.<br>3. To evaluate various formulation of queues. Also explore different kinds queues and their applications and implementations in simulations.<br>4. To learn Sorting: Insertion sort, merge sort, Heaps and heap sort, Quick sort, Linear sort, priority queqe, order statistics, lower bounds for sorting<br>5. To learn Searching: Balanced tree, red-black tree, lower bounds for searching<br>6. To learn Graph: representation and algorithms, Breadth-first search (BFS), Depth-first search (DFS), topological sorting, Shortest Paths, Single-source shortest paths problem, Dijkstra, |

| | | 7. | To explore hashing, and various implementations of searching and hashing algorithms. | |
|---|---|---|---|---|

| | | |
|---|---|---|
| **Unit I** | **Introduction:** Algorithms, analysis of algorithms, design of algorithms, and complexity of algorithms, asymptotic notations, growth of function, recurrences, sorting in polynomial time: insertion sort, merge sort, heap sort, and quick sort, sorting in linear time: counting sort, radix sort, bucket sort. | **08** |
| **Unit II** | **Elementary Data Structure**: Stacks, queues, linked list, binary search tree, hash table. **Advanced Data Structure**: Red Black Trees, splay Trees, augmenting data structure, binomial heap, B-tree, Fibonacci heap, and data structure for disjoint set ,dictionaries and priority queues. | **08** |
| **Unit III** | **Advanced design and analysis techniques:** Dynamic programming, Greedy algorithm, backtracking, branch-and-bound. | **08** |
| **Unit IV** | **Graph Algorithms**: Elementary graph algorithms, breadth first search, depth first search, minimum spanning tree, Kruskal's algorithms, Prim's algorithms, single source shortest path, all pair shortest path, ,maximum flow and traveling salesman problem | **08** |
| **Unit V** | Randomized Algorithms, String Matching, NP-Hard and NP-Completeness | **08** |

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PS O 2 | PSO 3 | PSO 4 | PS O 5 | PS O 6 | PS O 7 | PS O 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CO 1** | 1 | 1 | 1 | 2 | 1 | 2 | 3 | 1 | 1 | 1 | 1 | 2 | 1 | 2 |
| **CO 2** | 3 | 3 | 2 | 2 | 1 | 2 | 2 | 2 | 2 | - | 2 | 1 | 1 | 2 |
| **CO 3** | 2 | 1 | 1 | 3 | 2 | 2 | 2 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **CO 4** | 1 | 1 | 1 | 2 | 1 | 2 | 3 | 1 | 2 | 1 | 1 | 2 | 3 | 2 |
| **CO 5** | 2 | 2 | - | 1 | 1 | 2 | 1 | 3 | 2 | - | 2 | 1 | 1 | 2 |
| **CO 6** | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | - | 2 |
| **CO 7** | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **Average** | 1.9 | 1.4 | 1.0 | 2.0 | 1.4 | 2.0 | 1.9 | 1.4 | 1.9 | 0.7 | 1.3 | 1.7 | 1.4 | 2.0 |

| **References** | 1. Horowitz, S. Fundamentals of Computer Algorithms, Publisher Golgotia.<br>2. Leiserson, C. et al., Introduction to Algorithms, Publisher PHI.<br>3. Bratley, B., Fundamental of Algorithms, Publisher PHI<br>4. Goodrich, M. T. et al,.Algorithms Design, Publisher John Wiley<br>5. Aho A. V. et al., The Design and analysis of Algorithms, Publisher Pearson Education |
|---|---|

| Course code | **BIMT-502/ BIMT 552** |
|---|---|
| Category | Core Bioinformatics |
| **Course title** | **PROGRAMMING LANGUAGE, ALGORITHM AND TOOLS/ PROGRAMMING LANGUAGE LAB** |

| **Scheme and Credits** | **Credit** | **L** | **T** | **P** | |
|---|---|---|---|---|---|
| | 4+2 | 4 | 0 | 4 | |

| **Pre-requisites (if any)** | Basic knowledge of Programming and Computers |
|---|---|
| **Objectives** | Objective of this course is to learn the use of pointers to pass arguments to functions by reference. The close relationships among pointers, arrays and strings. To use pointers to functions. To define and use arrays of strings. 8. To use input and output streams. To use all print formatting capabilities. To use all input formatting capabilities. To print with field widths and precisions. To use formatting flags in the printf format control string. To output literals and escape sequences. To format input using scanf. How C provides a foundation for further study of programming languages in general and of C++, Java and C# in particular. Traditional view of computer hardware and its functioning. Bit manipulations. Number conversion. Floating point data manipulations. |
| **Outcomes** | 1. To use simple input and output statements. To use the for and do…while repetition statements to execute statements repeatedly. <br> 2. To understand multiple selection using the switch selection statement. To use the break and continue statements to alter the flow of control. To use the logical operators to form complex conditional expressions in control statements. To avoid the consequences of confusing the equality and assignment operators. <br> 3. How the function call/return mechanism is supported by the function call stack and activation records. Simulation techniques using random number generation. <br> 4. To pass arrays to functions. To use arrays to store, sort and search lists and tables of values. <br> 5. To use the array data structure to represent lists and tables of values. <br> 6. To define an array, initialize an array and refer to individual elements of an array. <br> 7. To define symbolic constants. To pass arrays to functions. <br> 8. To use arrays to store, sort and search lists and tables of values. <br> 9. To define and manipulate multiple-subscripted arrays |

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| **Unit I** | **Introduction:** Perl overview, Perl parsing rules, variables and data, statements and control Structure, sequence and string, motif and loop, while loop, for loop, until loop, filehandles , opening and closing files, reading and writing filehandles, hashes. | **08** |
| **Unit II** | **Regular Expressions:** simple characters, * special character, . character, \| character, Grouping with ()s, anchor characters, pattern matching, regular expression shortcuts, defining subroutines, returning values, using arguments, inheritance in Perl, polymorphism in Perl. | **08** |
| **Unit III** | **Alignments:** Pairwise sequence alignment, global alignment or Needleman-Wunch algoritnm, local alignment or Smith-Waterman algorithm, multiple sequence alignments, progressive methods of multiple sequence alignment, CLUSTALW, PILEUP, | **08** |
| **Unit IV** | **Scoring Matrices:** Basicconceptof sequence similarity, identity and homology, distance matrix, similarity matrix, scoring matrices for similarity searches, | **08** |

| | | PAM250 scoring matrix, BLOSUM62 scoring matrix, other scoring matrices, position-specific scoring matrices, information content of the PSSM, sequence logos. | |
|---|---|---|---|
| **Unit V** | | Iterative methods of multiple sequence alignment, iterative methods of multiple sequence alignment, genetic algorithm, hidden markov models of multiple sequence alignment, profile analysis, block analysis, extraction of blocks from a global or local multiple sequence alignment, pattern searching. | **08** |

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PS O 2 | PSO 3 | PSO 4 | PS O 5 | PS O 6 | PS O 7 | PS O 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CO 1** | 1 | 1 | 1 | 2 | 1 | 2 | 3 | 1 | 1 | 1 | 1 | 2 | 1 | 2 |
| **CO 2** | 3 | 3 | 2 | 2 | 1 | 2 | 2 | 2 | 2 | - | 2 | 1 | 1 | 2 |
| **CO 3** | 2 | 1 | 1 | 3 | 2 | 2 | 2 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **CO 4** | 1 | 1 | 1 | 2 | 1 | 2 | 3 | 1 | 2 | 1 | 1 | 2 | 3 | 2 |
| **CO 5** | 2 | 2 | - | 1 | 1 | 2 | 1 | 3 | 2 | - | 2 | 1 | 1 | 2 |
| **CO 6** | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | - | 2 |
| **CO 7** | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **CO 8** | 2 | 1 | 1 | 3 | 2 | 2 | 2 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **CO 9** | 1 | 1 | 1 | 2 | 1 | 2 | 3 | 1 | 2 | 1 | 1 | 2 | 3 | 2 |
| **Average** | 1.8 | 1.3 | 1.0 | 2.1 | 1.4 | 2.0 | 2.0 | 1.3 | 1.9 | 0.8 | 1.2 | 1.8 | 1.7 | 2.0 |

| **References** | 1. Kuhn, B.M.(2001) Picking Up Perl (12th eds.) published by the Free Software Foundation<br>2. Mount, W. D.2005. Bioinformatics: Sequence and genomic analysis (2nd eds.) CBS publishers and distributors New Delhi.<br>**3.** Conway D.2000. Object oriented Perl. Manning Publications. |
|---|---|

| Course code | **BIMT-504** |
|---|---|
| Category | Core Bioinformatics |
| **Course title** | **SEQUENCE AND STRUCTURE DATABASE** |

| **Scheme and Credits** | **Credit** | **L** | **T** | **P** | |
|---|---|---|---|---|---|
| | 4 | 4 | 0 | 0 | |

| **Pre-requisites (if any)** | Basic knowledge of Programming and Computers |
|---|---|

| **Objectives** | The aim for this course is to give students knowledge of and competence in use of bioinformatical methods central to conduction of molecular biological research projects. The course has emphasis on bioinformatics related to exploration of proteins and includes analyses of sequences, database searches, sequence comparison, visualization and analysis of protein structures, and introduction to phylogenetic analyses. The students will get an introduction to the theoretical foundations for a few key methods. The course will also give an introduction to analysis of DNA sequences, genes and genomes, gene expression and systems biology. Through practical exercises, the course aims to give students a basic competences in the use of bioinformatical tools. The course emphasizes the the learning of bioinformatical tools in light of the student's knowledge of molecular biology. |
|---|---|
| **Outcomes** | On completion of the course the student should have the following learning outcomes defined in terms of knowledge, skills and general competence: <br> **1.** The student can explain which type of data is available from the most common protein sequence and structure databases (UniProt, GenBank, Protein Data Bank, CATH). <br> **2.** The candidate can explain the theories underlying the most common methods for sequence searches and sequence alignments, and in particular knows the principle and main steps for pairwise and multiple sequence alignments; <br> **3.** The student can explain and is able to apply the main steps of dynamic programing for/to simple alignments of short sequences; <br> **4.** The student can list methods to uncover structure-function relationship in proteins and knows their underlying principles; <br> **5.** The student can explain the principles of computational methods for the prediction of secondary structure elements from protein sequence, prediction and modeling of three-dimensional protein structures (homology modeling, threading and ab initio methods). |

| | | |
|---|---|---|
| **Unit I** | Data base: Introduction, types of database, Application of biological database, classification schema of biological database, database search: genome database search and Protein database search, sequence file format. | **08** |
| **Unit II** | Nucleotide Sequence Database: Introduction, Primary & Secondary database, format vs. content: computer vs. humans, GenBank Flat File dissection, GCG, ACDEB, major Bioinformatics Resources: NCBI, EBI, GeneBank, DDBJ the knowledge of various databases and Bioinformatics tools available at these resources like BLAST and algorithm, NCBI BLAST and WU BLAST, ORF etc. SIFT tool for SNPS detection, submitting DNA sequences to the databases introduction, where to submit, what to submit, how to submit on the world wide web, how to submit with sequin, PubMed, PubMed central, public library of sciences etc. introduction, SeqIDS, Bioseq: sequences, Bioseqsets: collections of | **08** |

| | | sequences, Seq. Annot: annotating the sequences | |
|---|---|---|---|
| **Unit III** | | Protein sequence and structure databases: Introduction to structures and sequence, PDB, MMDB, structure file formats, visualizing structural information, database structure viewers. protein sequence databases: Expasy: SWISSPROT, feature of SWISSPROT, TrEMBL, PIR, and genome databases at NCBI: Unigene and homologene, TIGR, SANGER, high throughput genomic sequences EST, STS GSS, etc. | **08** |
| **Unit IV** | | Derived databases: composite database conserved domain database (CDD), E-MSD (European Bioinformatics Institute's Macromolecular Structure Database),protein secondary database like PROSITE, PRINT, BLOCK, PRODOM etc, gene expression database, chemical database, biochemical pathway database like KEGG and pathDB . | **08** |
| **Unit V** | | Structural Bioinformatics: the relationship of protein 3-D structure to protein function, data deposition tool, classification of proteins of known 3-D Structure: CATH and SCOP, Alignment of 3-D structure of Proteins: VAST, DALI, DSSP, FSSP and PALI. Annotating and analyzing whole Genome Sequences: Genome Annotation MAGPIE, Genome comparison Pipmaker, MUMer, DNA, Structure analysis databases like Procheck,WHAT IF and WHAT CHECK | **08** |

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PSO 2 | PSO 3 | PSO 4 | PSO 5 | PSO 6 | PSO 7 | PSO 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CO 1** | 1 | 1 | 1 | 2 | 1 | 2 | 3 | 1 | 1 | 1 | 1 | 2 | 1 | 2 |
| **CO 2** | 3 | 3 | 2 | 2 | 1 | 2 | 2 | 2 | 2 | - | 2 | 1 | 1 | 2 |
| **CO 3** | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | - | 2 |
| **CO 4** | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **CO 5** | 2 | 1 | 1 | 3 | 2 | 2 | 2 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **Average** | 2 | 1.4 | 1.2 | 2.2 | 1.6 | 2 | 1.8 | 1.2 | 1.8 | 1 | 1.2 | 1.8 | 1.5 | 2 |

| **References** | 1. Mount, W. D.2005. Bioinformatics: Sequence and genomic analysis (2nd eds.) CBS publishers and distributors New Delhi.  2. westhead D.R., Parish J.H. and Twyman R.M. 2003. Instant notes: Bioinformatics BIOS Scientific Publishers Ltd.  3. Rastogi, S.C., Mendiratta, N. and Rastogi, P. 2007. Bioinformatics: concept skill and applications |
|---|---|

| Course code | **BIMT-506** |
|---|---|
| Category | Core Bioinformatics |
| **Course title** | **MATHEMATICAL MODELLING AND ADVANCED STATISTICS** |

| **Scheme and Credits** | **Credit** | **L** | **T** | **P** | |
|---|---|---|---|---|---|
| | 4 | 4 | 0 | 0 | |

| **Pre-requisites (if any)** | Basics of Biostatistics |
|---|---|
| **Objectives** | Objective of this course is to inculcate the student with mathematical reasoning by justifying and generalizing patterns and relationships and to Explain and apply basic concepts of probability, andFormulate questions that can be addressed with data and collect, organize, and display relevant data to answer them. |
| **Outcomes** | 1. Solve open-ended elementary school problems in using visualization and statistical reasoning,<br>2. Demonstrate the use of mathematical reasoning by justifying and generalizing patterns and relationships,<br>3. Identify, explain, and evaluate the use of elementary classroom manipulatives to model geometry, probability and statistics,<br>4. Explain relationships among measurable attributes of objects and determine measurements,<br>5. Analyze characteristic and properties of two- and three-dimensional geometric shapes and develop mathematical arguments about geometric relationships,<br>6. Apply transformations and use symmetry to analyze mathematical situations, |

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|---|---|---|
| **Unit I** | **Introduction to statistics:** Definition of statistics, diagrammatic and graphical representation of data, measure of central tendency, dispersion, skewness and kurtosis | **08** |
| **Unit II** | **Applied statistics:** Introduction, discrete and continuous random variable, addition and multiplication theorem, introduction to correlation and regression analysis, simple linear regression analysis, multiple linear regression analysis | **08** |
| **Unit III** | **Introduction to sampling inference probability**: sampling distribution, large and small distribution, significance test of a sample mean, significance test of a difference between sample mean. | **08** |
| **Unit IV** | **Application in biosystem:** Introduction to mathematical models and simulation techniques, logistic equation, Lotka-Voltera equation, butterfly effect, chaotic theory, fractals, optimization techniques, genetic algorithm, simulated annealing, Mote Carlo simulation. | **08** |
| **Unit V** | **Models for interacting populations:** Predator–Prey models: Lotka–Volterra systems, realistic Predator–Prey models, analysis of a Predator–Prey model with limit cycle, periodic behaviour, parameter domains of stability, discrete growth models for interacting populations, use and abuse of fractals. | **08** |

| | **PO 1** | **PO 2** | **PO 3** | **PO 4** | **PO 5** | **PSO 1** | **PSO 2** | **PSO 3** | **PSO 4** | **PSO 5** | **PSO 6** | **PSO 7** | **PSO 8** | **PSO 9** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CO 1** | 1 | 2 | 1 | 2 | 1 | 3 | 3 | 2 | 1 | 1 | 1 | 2 | 1 | 2 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CO 2** | 2 | 2 | 1 | 3 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | - | 2 |
| **CO 3** | 3 | 3 | 2 | 2 | 1 | 1 | 2 | 2 | 3 | - | 2 | 1 | 1 | 2 |
| **CO 4** | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | - | 2 |
| **CO 5** | 2 | 1 | 2 | 2 | 2 | 2 | 2 | 1 | 2 | 1 | - | 2 | 2 | 2 |
| **CO 6** | 2 | 1 | 1 | - | 2 | 3 | 2 | 1 | 2 | 1 | 1 | - | 2 | 2 |
| **Average** | **2.0** | **1.7** | **1.3** | **2.2** | **1.7** | **2.2** | **1.8** | **1.3** | **2.0** | **1.0** | **1.2** | **1.8** | **1.5** | **2.0** |

| **References** | 1. Montgomery, D.C. and Runger, G.C. Applied statistics and probability for engineers(3rd eds.). John-Wiley and Sons Publication. 2. Prasad, S. 2004. Elements of biostatistics (1st ed.). Rastogi Publication. 3. Kapur, J.N. and Saxena, H.C. Mathematical statistics (1st ed.) S. Chand and Company Ltd |

| Course code | **BIMT-508** | | | |
|---|---|---|---|---|
| Category | Core Bioinformatics | | | |
| **Course title** | **BIOMOLECULAR MODELING AND SIMULATION** | | | |
| **Scheme and Credits** | **Credit** | **L** | **T** | **P** |
| | 4 | 4 | 0 | 0 |
| **Pre-requisites (if any)** | Basic knowledge of Language and Computers | | | |
| **Objectives** | The goal of this course is to teach students, from variety of backgrounds, the theoretical principles and practical skills in designing and running biomolecular simulations. Topics discussed in the course are divided into three modules. First module (thermodynamics and statistical mechanics of biomolecules) will lay down theoretical foundations to understand modern simulation approaches. Second module (simulation techniques) will consist of practical sessions in running simple simulations to study functional characteristics and dynamic behavior of proteins. Final module (modern trends in biomolecular simulation) will introduce some of the most exciting application areas of simulation such as computer-based drug design, protein folding and protein design. As part of the assessment, each student will complete an independent short simulation project of a protein system of interest, using techniques discussed in the course. As the emphasis is placed on students running their own simulations, minimal exposure to any programming language (python, perl, C++, fortran) and a mathematical package (R or Matlab) is a pre-requisite to attend this course. | | | |
| **Outcomes** | After the course, the student should be able to<br>1. Understand the basic concepts behind simulation methods and using right method and parameters for the right problem<br>2. Run small-scale simulations to calculate thermodynamic, statistical and conformational properties of biomolecules<br>3. Apply the methods on moderately difficult problems in areas such as protein-ligand binding, free energy calculations, folding simulations | | | |
| | | | | |
| **Unit I** | **Concepts in molecular modelling**: Coordinate systems, potential energy, molecular graphics, surfaces, SMILE format, Mol2 format. | **08** | | |
| **Unit II** | **Force fields:** Bond stretching, angle bending, introduction to non-bonded interactions, electrostatic interactions, Van der Waals interaction, hydrogen bonding in molecular mechanics, force field models for the simulation of liquid water, energy minimization, related methods for exploring the energy surface. | **08** | | |
| **Unit III** | **Computer simulation methods:** Calculation of simple thermodynamic properties, Phase Space, Long-range Forces, analyzing the Results of a Simulation and Estimating Errors. | **08** | | |
| **Unit IV** | **Molecular dynamics simulation method:** Molecular dynamics using simple model, molecular dynamics with continuous potentials, Monte Carlo Simulation Methods, calculating properties by integration. Metropolis method, implementation of the Metropolis Monte Carlo method, Monte carlo simulation of molecules, molecular modeling softwares – Insight II, DS modeling(Basic concepts only) | **08** | | |
| **Unit V** | **Protein Structure Prediction:** Sequence analysis, basic principles of protein structure, predicting protein structure, comparative or homology modeling, | **08** | | |

evaluating a comparative model, predicting protein structures by 'Threading', comparison of protein structure prediction methods: CASP, protein folding and unfolding.

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PS O 2 | PSO 3 | PSO 4 | PS O 5 | PS O 6 | PS O 7 | PS O 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CO 1 | 3 | 3 | 2 | 2 | 1 | 1 | 2 | 2 | 3 | - | 2 | 1 | 1 | 2 |
| CO 2 | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | - | 2 |
| CO 3 | 2 | 1 | 2 | 2 | 2 | 2 | 2 | 1 | 2 | 1 | - | 2 | 2 | 2 |
| Average | 2.3 | 1.7 | 1.7 | 2.0 | 1.7 | 1.7 | 1.7 | 1.3 | 2.3 | 1.0 | 1.5 | 1.7 | 1.5 | 2.0 |

| References | 1. Leach, A.R. 1996.Molecular Modelling Principles and Application, Longman. |
|---|---|
| | 2. Haile, J.M. Molecular Dynamics Simulation Elementary Methods, John Wiley and Sons, 1997T. Mappes, D. D Grazia, *Bioinformatics Ethics*, McGraw-Hill, 2005. |

| Course code | **BIMT-601** | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Category | Core Bioinformatics | | | | | | | | | | | | |
| **Course title** | **COMPUTATIONAL BIOLOGY** | | | | | | | | | | | | |

| **Scheme and Credits** | **Credit** | **L** | **T** | **P** | |
|---|---|---|---|---|---|
| | 4 | 4 | 0 | 0 | |

| **Pre-requisites (if any)** | Basic knowledge of Molecular Biology and Genetics |
|---|---|
| **Objectives** | This course will introduce the discipline of computational biology and drug design. It has been designed to explain the different aspects of nucleotide and protein sequence analyses, sequence alignments and their applications in understanding biology. The course will also emphasize on the strategic issues in drug discovery and development, principles of computational methods involved in lead generation virtual screening, quantitative structureactivity relationship and molecular docking. |
| **Outcomes** | Students would be able in   Sequence alignment and visualization   and  Phylogenetic and microarray analysis |

| Unit | | |
|---|---|---|
| **Unit I** | **Sequence alignment and database searching** Global and local alignments, statistical significance of alignments, scoring matrices and gap penalties, filtering, position specific scoring matrices, internet resources, Pairwise and multiple alignment, uses of pairwise and multiple sequence alignment, programs and methods for sequence alignment, pattern searching programs, family and superfamily representation, structural inference, dynamic programming algorithms, alignment by hidden Markov models, consensus word analysis, more complex scoring. | **08** |
| **Unit II** | **Phylogenetic prediction** Trees-splits and metrices on trees, tree interpretation, Distance – additive, ultrameric and nonadditive distances, tree building methods, phylogenetic analysis, parsimony, tree evaluation, maximum likelihood trees – continuous time markov chains, estimating the rate of change, likelihood and trees; analysis software. | **08** |
| **Unit III** | ESTs – databases, EST clustering, TIGER indices, gene prediction in genomic DNA, gene annotation, Protein identification, physical properties, motifs and patterns, structure, folding classes, structure classification, sequence assembly, global assembly. | **08** |
| **Unit IV** | Molecular modeling: PDB and MMDB, structure file formats, visualizing structural information, advance structure modeling, Internal and external co-ordinate system, cartesian and cylindrical polar co-ordinate system, Potential energy calculations using semiempirical potential energy function, Molecular mechanics and dynamics. | **08** |
| **Unit V** | Secondary structure prediction of proteins and RNA, Docking of Molecules, Knowledge base structure prediction, Molecular Design, structure similarity searching; prediction of buried residues in proteins; | **08** |

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PS O 2 | PSO 3 | PSO 4 | PS O 5 | PS O 6 | PS O 7 | PS O 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CO 1** | 3 | 3 | 2 | 2 | 1 | 1 | 2 | 2 | 3 | - | 2 | 1 | 1 | 2 |

| Averag e | 3 | | 3 | 2 | 2 | 1 | 1 | 2 | 2 | 3 | - | 2 | 1 | 1 | 2 |
|-----------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|

| | |
|---|---|
| **References** | 1. Baxevanis, D. A and Ouellette, F. B., Bioinformatics: A practical guide to the analysis of Genes and proteins, 2001, (IIndedi) a John Wiley & sons, inc., publication.<br>2. Mount, W. D.2005. Bioinformatics: Sequence and genomic analysis (2nd eds.) CBS publishers and distributors New Delhi.<br><br>3. Westhead D.R., Parish J.H. and Twyman R.M. 2003. Instant notes: Bioinformatics BIOS Scientific Publishers Ltd.<br><br>4. Rastogi, S.C., Mendiratta, N. and Rastogi, P. 2007. Bioinformatics: concept skill and applications |

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|---|---|---|---|---|
| **Course code** | **BIMT-603** | | | |
| Category | Core Bioinformatics | | | |
| **Course title** | Advanced Computer Aided Drug Designing **(ADVANCE CADD)** | | | |
| **Scheme and Credits** | **Credit** | **L** | **T** | **P** |
| | 4 | 4 | 0 | 0 |
| **Pre-requisites (if any)** | | | | |
| **Objectives** | This course aims at application of modern in silico tools or information technology in different phases of drug discovery and design of new drug candidates by understanding the molecular basis of the interaction of small molecules with their targets. | | | |
| **Outcomes** | **1.** Students are introduced to the principles and practice of Molecular modeling and modern drug discovery.<br>**2.** An awareness of rational drug design, based on understanding of three-dimensional (3D) structures and physicochemical properties of drugs and receptors will be created. | | | |
| | | | | |
| **Unit I** | Introduction, history, discovery and development of drugs, strategies in drug discovery, ADMET, pre clinical trials and source of drugs- plant, marine, animal, synthetic. | **08** | | |
| **Unit II** | Molecular biology concepts in drug designing – structure, function and drug action on membrane and receptor molecule, membrane permeability, mode of action-enzyme inhibitors, activators, design of agonist and antagonists, receptor theories | **08** | | |

| Unit III | Physico chemical principles of drug action, drug – receptor interactions, Hansch analysis, COMFA-2D, 3D, COMSIA, free Wilson method, Topliss and Craigs model, morphological effects, drugs affecting CNS and drugs use- addiction, regulation, drugs affecting hormonal system- epinephrine, histamine | 08 |
|---|---|---|
| Unit IV | Concept of quantum mechanics, force fields, energy minimization, conformational search, molecular dynamics, ligand based drug designing, receptor based drug designing, analog approach, pharmacophore mapping, irrational drug design. | 08 |
| Unit V | Combinatorial library design –combinatorial libraries, optimization approaches, virtual library, pharmacophore based fingerprints, structure based library design, docking as virtual screening tool, regulatory affairs | 08 |

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PSO 2 | PSO 3 | PSO 4 | PSO 5 | PSO 6 | PSO 7 | PSO 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CO 1 | 3 | 2 | 2 | 1 | 1 | 1 | 2 | 2 | 3 | 2 | 2 | 1 | 1 | 2 |
| CO 2 | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| Average | 2.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 2.5 | 1.5 | 1.5 | 1.5 | 1.5 | 2 |

| References | 1. Haile, J.M. 1997. Molecular Dynamics Simulation Elementary Methods, John Wiley and Sons.<br>2. Leach. A. 1998. Molecular Modeling, Principles and Applications, Longman publications.<br>3. Doucet, P. J. and Weber, J. Computer-Aided Molecular Design: Theory and Applications. Academic Press. |
|---|---|

| Course code | BIMT-621 |
|---|---|
| Category | Departmental Elective |
| Course title | BIO-Python |
| Scheme and Credits | Credit: 4 — L: 4, T: 0, P: 0 |
| Pre-requisites (if any) | |
| Objectives | Objective of this course to aware the student with Biopython is the best-known Python library to process biological data. It will aware the students with sequences, NCBI queries, BLAST, trees, and 3D structures |
| Outcomes | 1. Understand what Biopython is and what it can do.<br>2. Learn how to get Biopython running.<br>3. Learn how to retrieve data records from NCBI.<br>4. Learn how to read and write sequence files.<br>5. Learn how to run BLAST from Python and read the results.<br>6. Learn how to read and write phylogenetic tree files.<br>7. Learn how to read and write 3D structure files.<br>8. Learn how to use the Biopython documentation, examples, and where to find help.<br>9. Understand what alternatives to Biopython exist and what they can do. |

| | | Introduction, Python programming language, interpreter, Python's basic data types, literals constant, error handling, lists. | | | | | | | | | | | | 08 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Unit I** | | | | | | | | | | | | | | | |

| **Unit II** | Conditional Statements, if-then, looping, while-loops, for-loops, break, continue, functions, arguments, function parameter, local variables, global variables, return values, operators, passing arguments, reference argument. | 08 |
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| **Unit III** | String processing, case changing method, string manipulation, string slices, string comparison, regular expression, non greedy matching, Module, make own module, import statement, loading, classes, creating instances. | 08 |
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| **Unit IV** | Biopython introduction, bio sequence, sequence reading, sequence writing, bio Swissprot,  Regular entries, bio genbank, reading entries, running blast, clustal W. | 08 |
|---|---|---|

| **Unit V** | Seq feature, slicing seq record, reading sequence file, writing sequence file, sequence alignment, single alignment, multiple alignment, ambiguous alignment. | 08 |
|---|---|---|

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PS O 2 | PSO 3 | PSO 4 | PS O 5 | PS O 6 | PS O 7 | PS O 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CO 1** | 1 | 1 | 1 | 2 | 1 | 2 | 3 | 1 | 1 | 1 | 1 | 2 | 1 | 2 |
| **CO 2** | 3 | 3 | 2 | 2 | 1 | 2 | 2 | 2 | 2 | - | 2 | 1 | 1 | 2 |
| **CO 3** | 2 | 1 | 1 | 3 | 2 | 2 | 2 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **CO 4** | 1 | 1 | 1 | 2 | 1 | 2 | 3 | 1 | 2 | 1 | 1 | 2 | 3 | 2 |
| **CO 5** | 2 | 2 | - | 1 | 1 | 2 | 1 | 3 | 2 | - | 2 | 1 | 1 | 2 |
| **CO 6** | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | - | 2 |
| **CO 7** | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **CO 8** | 2 | 1 | 1 | 3 | 2 | 2 | 2 | 1 | 2 | 1 | 1 | 2 | 2 | 2 |
| **CO 9** | 1 | 1 | 1 | 2 | 1 | 2 | 3 | 1 | 2 | 1 | 1 | 2 | 3 | 2 |
| **Average** | 1.8 | 1.3 | 1.0 | 2.1 | 1.4 | 2.0 | 2.0 | 1.3 | 1.9 | 0.8 | 1.2 | 1.8 | 1.7 | 2.0 |

| **References** | 1.  Brueck, D. and Tanner, S., Python 2.1 bible, hungry minds Inc.<br>2.  Schuerer, K. and Letondal, C., Python course in Bioinformatics, Pasteur Institute |
|---|---|

| Course code | BIMT-621 |
|---|---|
| Category | Departmental Elective |
| **Course title** | **MOLECULAR PHYLOGENY** |

| **Scheme and Credits** | **Credit** | **L** | **T** | **P** | |
|---|---|---|---|---|---|
| | 4 | 4 | 0 | 0 | |

| **Pre-requisites (if any)** | Basic knowledge of cell and Biology. |
|---|---|
| **Objectives** | Genetics having its roots in mathematics thanks to Mendel, appeals to students as one of the analytical branches of biology even in senior school. Basic concepts that are essential to understand inheritance will be taught, starting from the abstract factors to physical basis of inheritance. The course aims to communicate the pivotal role of Mendelian concepts in the development of the science of genetics and also the fact that nature is full of examples that deviate from Mendelian laws starting from linkage groups. Introduction of models and the way they have contributed to our understanding of genetics will provide a perception of how forward genetics has been used to understand the basis of continuity of information transfer that is applicable to not only to the simple life forms but also to humans. Most of the topics will be at the introductory level, which would motivate the students to understand the molecular basis of genotype to phenotype correlation. |
| **Outcomes** | The student will demonstrate knowledge of the basics principles of Mendelian genetics by: <br> 1. Discussing the progression of discovery from Classical to Modern Genetics. <br> 2. Defining basic concepts of Classical Genetics. <br> 3. Describing Mendel's experimental design. <br> 4. Utilizing conventional Mendelian genetic terminology. <br> 5. Explaining Mendel's principles ofsegregation, and independent assortment. <br> 6. Solving monohybridcross genetic outcomes utilizing branch diagrams and/or Punnett squares. <br> 7. Using testcrosses to identify parental genotype and confirm the principle ofsegregation. <br> 8. Solving dihybrid cross genetic outcomes utilizing branch diagrams and/or Punnett squares. <br> 9. Analyzing the results of multihybrid crosses to confirm the principle of Independent Assortment. <br> 10. Using the laws of probability to statistically analyze the outcomes of genetic crosses. |

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| **Unit I** | **Introduction to phylogenetic Analysis**: Terminology of phylogenetic trees root, internal nodes, internal branches, external branches, terminal nodes, rooted and unrooted trees, cladograms vs. phylograms, phylogeny, species trees, gene tree, characters, cladistics, evolutionary tree, properties of phylogenetic trees: Ultrametric trees and Additive trees | **08** |
| **Unit II** | **Distance matrix methods:** clustering, algorithms, measuring genetic change; models of sequence evolution, introduction to maximum likelihood, UPGMA, neighbor joining methods, Fitch-Margolish method | **08** |
| **Unit III** | **Character based method of phylogenetics**: Parsimony, maximum parsimony method, maximum likelihood method, Markov model, dynamic programming, analysis of true tree, Tree construction using partial distance matrices, consensus trees, Tree confidence, minimum distance trees. | **08** |
| **Unit IV** | **Model of molecular evolution:** Introduction to molecular, mode of evolutionary process, genome and biological network evolution, evolutionary change in nucleotide sequences, mathematical modeling of nucleotide substitution in a DNA sequence, Probabilistic models of evolution, derivation of the Jukes-Cantor model, Kimura's two-parameter model, introduction to Hidden Morkov model. | **08** |

|        | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PS O 2 | PSO 3 | PSO 4 | PS O 5 | PS O 6 | PS O 7 | PS O 8 | PSO 9 |
|--------|------|------|------|------|------|-------|--------|-------|-------|--------|--------|--------|--------|-------|
| CO 1   | 1    | 1    | 1    | 2    | 1    | 2     | 3      | 1     | 1     | 1      | 1      | 2      | 1      | 2     |
| CO 2   | 2    | 3    | 2    | 2    | 1    | 2     | 2      | 2     | 2     | 3      | 2      | 1      | 1      | 2     |
| CO 3   | 1    | 1    | 1    | 3    | 2    | 3     | 2      | -     | 2     | 1      | 1      | 2      | -      | 3     |
| CO 4   | 1    | 1    | 1    | 2    | 1    | 2     | 3      | 1     | 2     | 1      | 1      | 2      | 3      | 2     |
| CO 5   | 2    | 2    | -    | 1    | 1    | 2     | 1      | 3     | 2     | 2      | 2      | 1      | 1      | 2     |
| CO 6   | 2    | 1    | 1    | 2    | 2    | 3     | 1      | 1     | 2     | 1      | 1      | 2      | -      | 2     |
| CO 7   | 2    | 1    | 1    | 2    | 2    | 2     | 1      | 1     | 2     | 1      | 1      | 2      | 2      | 3     |
| CO 8   | 2    | 1    | 1    | 3    | 2    | 2     | 2      | 1     | 2     | 1      | 1      | 2      | 2      | 2     |
| CO 9   | 1    | 1    | 2    | 2    | 1    | 2     | 3      | 1     | 2     | 1      | 1      | 2      | 3      | 3     |
| CO 10  | 1    | 2    | 2    | 1    | 1    | 2     | 1      | 3     | 2     | 2      | 2      | 1      | 1      | 2     |
| Average| 1.5  | 1.4  | 1.3  | 2.0  | 1.4  | 2.2   | 1.9    | 1.6   | 1.9   | 1.4    | 1.3    | 1.7    | 1.8    | 2.3   |

| Unit V | **Evaluation and softwares**: Perfect phylogeny, compatibility, bootstrap, Jacknife, PHYLIP, PAUP. | **08** |
|--------|------|------|

| References | 1. Mount, D.W. 2005. Bioinformatics: Sequence and genomic analysis (2ndeds.). CBS Publishers and Distributors, New Delhi. <br> 2. Roderic, D. M., Edward, C.M. Molecular evolution, A phylogenetic approach. Blackwell science. <br> 3. Westhead, Parish and Twyman. Instant notes in bioinformatics. <br> 4. Rastogi, S.C., Mendiratta, N. and Rastogi, P. 2007. Bioinformatics: concept, skill and applications (2ndeds.). CBS Publishers and distributors, New Delhi. |
|------------|---|

| Course code | **BIMT-623** | | | |
|---|---|---|---|---|
| Category | Departmental Elective | | | |
| **Course title** | **IMMUNOINFORAMTICS** | | | |
| **Scheme and Credits** | **Credit** | **L** | **T** | **P** |
| | 4 | 4 | 0 | 0 |
| **Pre-requisites (if any)** | Basic knowledge of cell and Biology. | | | |
| **Objectives** | The immune system distinguishes between self and foreign molecules and thus alerts and mediates protection against attack by potentially infectious organisms. Malfunctioning of the immune system leads to a number of disorders and diseases. Immunobiology is a comprehensive study of the organization and functioning of the immune system with its network of cells and molecules. Understanding the biology of the immune system is, therefore, key to developing strategies towards prevention and cure to a number of disorders and diseases that result due to interference in the functioning and regulation of the immune system. This paper covers the structure, organization, function and regulation of and by the immune system keeping the above aspects in mind. | | | |
| **Outcomes** | After going through this unit student shall be able to:<br>1. Trace the history and development of immunology.<br>2. Describe surface membrane barriers and their protective functions.<br>3. Explain the importance of phagocytosis and natural killer cells in innate body defense.<br>4. Describe the roles of different types of T cells, B cells and APCs. Compare and contrast the origin, maturation process, and general function of B and T lymphocytes. | | | |
| | | | | |
| **Unit I** | Immunology: Introduction: overview of the immune system: a case study, classification of immunity, concepts in immunology, antigens, antibodies, compliment system, antigen-antibody reactions, major histocompatibility complex, allele selection, antigen presentation, TAP, T cell receptors | | **08** | |
| **Unit II** | Advanced immunology: Immune effector mechanisms, cytokines, chemokines, hypersensitive reactions, immune system in health and disease, autoimmunity, transplantation immunology, classification of vaccine. | | **08** | |
| **Unit III** | HLA System in model organism: Defining HLA super types in: HLA–structural and modeling principles, HLA supertypes by GRID/CPCA, hierarchical clustering methods, structural sasis for HLA-A2 supertypes, clustering of MHC peptide-binding repertoires, HLA alleles- electrostatic distribution maps | | **08** | |
| **Unit IV** | In Silico Prediction of Immunogenicity : Databases searching, MHCDB(NCBI), IMGT, IMGT/HLA database, IPD, immuno polymorphism database, SYFPEITHI: database for searching and T-cell epitope prediction, mapping of T-cell epitopes, MHC binders, TAP binders, mapping of linear\B-cell epitopes in bcipep database, haptens, carrier proteins, anti-hapten antibodies. | | **08** | |
| **Unit V** | Prediction: Predicting peptide-MHC binding, peptide–MHC binding using profiles, machine learning techniques for MHC binders, artificial intelligence methods for predicting T-Cell epitopes, MHC-Class I and II binding affinity, MHC– molecular affinity and QSAR models, support vector machine for mhc-binding peptides, static energy analysis of MHC Class I and Class II peptide-binding affinity, nonlinear predictive modeling of MHC class II–peptide binding | | **08** | |

using bayesian, neural networks

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PS O 2 | PSO 3 | PSO 4 | PS O 5 | PS O 6 | PS O 7 | PS O 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CO 1 | 3 | 3 | 2 | 2 | 1 | 1 | 2 | 2 | 3 | - | 2 | 1 | 1 | 2 |
| CO 2 | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | - | 2 |
| CO 3 | 2 | 1 | 2 | 2 | 2 | 2 | 2 | 1 | 2 | 1 | - | 2 | 2 | 2 |
| CO 4 | 2 | 1 | 2 | 2 | 2 | 2 | 2 | 1 | 2 | 1 | - | 2 | 2 | 2 |
| Average | 2.3 | 1.5 | 1.8 | 2.0 | 1.8 | 1.8 | 1.8 | 1.3 | 2.3 | 0.8 | 0.8 | 1.8 | 1.3 | 2.0 |

| References | 1. Richard, A., Goldsby, Kindt, J.T., Barbara, A., Kubey, and Osborne, J., Immunology (5th eds) 2003, W.H. Freeman & Company<br>2. Roitt's Essential Immunology; Ivan M. Roitt, Peter J. Delves Blackwell Science Ltd., 10th Edition (2001)<br>3. arren R., Immunoinformatics: predicting Immunogenicity in-silico, Flower Humana Press.<br>4. Lydyard, P.M., Whelan, A. and Fanger, M.W. Instant Notes in Immunology (1st eds.), BIOS Scientific Publishers Ltd, 2003. |
|---|---|

| Course code | **BIMT-623** | | | |
|---|---|---|---|---|
| Category | Departmental Elective | | | |
| **Course title** | **CHEMOINFORMATICS** | | | |
| **Scheme and Credits** | **Credit** | **L** | **T** | **P** |
| | 4 | 4 | 0 | 0 |
| **Pre-requisites (if any)** | Biology and Bioinformatics | | | |
| **Objectives** | The objective of this course is to provide introduction to chemoinformatics, an interdisciplinary area on the interface of chemistry, informatics and biology. The student will be provided with understanding of fundamentals of chemoinformatics and its applications. Through lectures, hands-on exercises and assignments, the student is expected to achieve a good grasp of the concepts and applications of chemoinformatics. | | | |
| **Outcomes** | 1. Students are able to explain basic concepts of chemoinformatics.<br>2. Students are able to explain and implement computation of molecular descriptors and chemical similarity.<br>3. Students are able to classify small molecules and interpret results from chemoinformatics analysis. | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Unit I** | Introduction:scope of chemoinformatics, structure databases, reaction databases, biochemical pathway databases, searching chemical structure, full structure search, substructure search, screening, 3-dimensional structure method. | | | | | | | | | | | **08** |
| **Unit II** | Representation of chemical compound: Introduction, advantage and disadvantage, graph theory, matrix representation, Adjacency matrix, distance matrix, atom connectivity matrix, bond matrix, incidence matrix, bond-electron matrix, advantage and disadvantage of matrix, connection table, advantage and disadvantage of connection table. | | | | | | | | | | | **08** |
| **Unit III** | Standard structure exchange format: Structure of Mol file, Sdf file, PDB file, Morgan algorithm, Hash codes, application of hash code, stereochemistry in SMILE and Mol file | | | | | | | | | | | **08** |
| **Unit IV** | Molecular surface: Introduction, Van der Waal's surface, solvent accessible surface, solvent excluded surface, enzyme activity surface, method for data analysis, machine learning techniques, machine learning process, decision tree, chemomerices. | | | | | | | | | | | **08** |
| **Unit V** | Structure descriptors: introduction, classification of molecular descriptors, 1-D descriptors, 2-D descriptors, 3-D descriptors, distance and similarity measure, Method of data analysis. | | | | | | | | | | | **08** |

| | PO 1 | PO 2 | PO 3 | PO 4 | PO 5 | PSO 1 | PS O 2 | PSO 3 | PSO 4 | PS O 5 | PS O 6 | PS O 7 | PS O 8 | PSO 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CO 1** | 3 | 3 | 2 | 2 | 1 | 1 | 2 | 2 | 3 | - | 2 | 1 | 1 | 2 |
| **CO 2** | 2 | 1 | 1 | 2 | 2 | 2 | 1 | 1 | 2 | 1 | 1 | 2 | - | 2 |
| **CO 3** | 2 | 1 | 2 | 2 | 2 | 2 | 2 | 1 | 2 | 1 | - | 2 | 2 | 2 |
| **Average** | 2.3 | 1.7 | 1.7 | 2.0 | 1.7 | 1.7 | 1.7 | 1.3 | 2.3 | 1.0 | 1.5 | 1.7 | 1.5 | 2.0 |

| **References** | 1. Patrick, G. 2002. Instant notes medicinal chemistry (1st ed.). Viva Publication.<br><br>2. Gasteiger, J. and Engle, T. 2003. Chemoinformatics. |
|---|---|