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| M.Sc.,  BIOINFORMATICS |
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| **SYLLABUS** |
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| **FROM THE ACADEMIC YEAR**  **2023 - 2024** |
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| **TAMILNADU STATE COUNCIL FOR HIGHER EDUCATION, CHENNAI – 600 005** |
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| **TANSCHE REGULATIONS ON LEARNING OUTCOMES-BASED CURRICULUM FRAMEWORK FOR POSTGRADUATE EDUCATION** | |
| **Programme** | **M.Sc. BIO - INFORMATICS** |
| **Programme Code** |  |
| **Duration** | **2 years for PG** |
| **Programme Outcomes (Pos)** | **PO1: Problem Solving Skill**  Apply knowledge of Management theories and Human Resource practices to solve business problems through research in Global context.  **PO2: Decision Making Skill**  Foster analytical and critical thinking abilities for data-based decision-making.  **PO3: Ethical Value**  Ability to incorporate quality, ethical and legal value-based perspectives to all organizational activities.  **PO4: Communication Skill**  Ability to develop communication, managerial and interpersonal skills.  **PO5: Individual and Team Leadership Skill**  Capability to lead themselves and the team to achieve organizational goals.  **PO6: Employability Skill**  Inculcate contemporary business practices to enhance employability skills in the competitive environment.  **PO7: Entrepreneurial Skill**  Equip with skills and competencies to become an entrepreneur.  **PO8: Contribution to Society**  Succeed in career endeavors and contribute significantly to society.  **PO 9 Multicultural competence**  Possess knowledge of the values and beliefs of multiple cultures and  a global perspective.  **PO 10: Moral and ethical awareness/reasoning**  Ability to embrace moral/ethical values in conducting one’s life. |
| **Programme Specific Outcomes**  **(PSOs)** | **PSO1 – Placement**  To prepare the students who will demonstrate respectful engagement with others’ ideas, behaviors, beliefs and apply diverse frames of reference to decisions and actions.  **PSO 2 - Entrepreneur**  To create effective entrepreneurs by enhancing their critical thinking, problem solving, decision making and leadership skill that will facilitate startups and high potential organizations.  **PSO3 – Research and Development**  Design and implement HR systems and practices grounded in research that comply with employment laws, leading the organization towards growth and development.  **PSO4 – Contribution to Business World**  To produce employable, ethical and innovative professionals to sustain in the dynamic business world.  **PSO 5 – Contribution to the Society**  To contribute to the development of the society by collaborating with stakeholders for mutual benefit. |

**Template for P.G., Programmes**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Semester–I** | **Credit** | **Hours** | **Semester-II** | **Credit** | **Hours** | **Semester-III** | **Credit** | **Hours** | **Semester–IV** | **Credit** | **Hours** |
| 1.1. Core-I | 5 | 7 | 2.1. Core-IV | 5 | 6 | 3.1. Core-VII | 5 | 6 | 4.1. Core-XI | 5 | 6 |
| 1.2 Core-II | 5 | 7 | 2.2 Core-V | 5 | 6 | 3.2 Core-VIII | 5 | 6 | 4.2 Core-XII | 5 | 6 |
| 1.3 Core – III | 4 | 6 | 2.3 Core – VI | 4 | 6 | 3.3 Core – IX | 5 | 6 | 4.3 Project with viva voce | 7 | 10 |
| 1.4 Discipline Centric  Elective -I | 3 | 5 | 2.4 Discipline Centric  Elective – III | 3 | 4 | 3.4 Core – X | 4 | 6 | 4.4Elective - VI (Industry / Entrepreneurship)  20% Theory  80% Practical | 3 | 4 |
| 1.5 Generic Elective-II: | 3 | 5 | 2.5 Generic Elective -IV: | 3 | 4 | 3.5 Discipline Centric Elective - V | 3 | 3 | 4.5 Skill Enhancement course / Professional Competency Skill | 2 | 4 |
|  |  |  | 2.6 NME I | 2 | 4 | 3.6 NME II | 2 | 3 | 4.6 Extension Activity | 1 |  |
|  |  |  |  |  |  | 3.7 Internship/ Industrial Activity | 2 | - |  |  |  |
|  | **20** | **30** |  | **22** | **30** |  | **26** | **30** |  | **23** | **30** |
| **Total Credit Points -91** | | | | | | | | | | | |

**Choice Based Credit System (CBCS), Learning Outcomes Based Curriculum Framework (LOCF) Guideline Based Credits and Hours Distribution System**

**for all Post – Graduate Courses including Lab Hours**

**First Year – Semester – I**

|  |  |  |  |
| --- | --- | --- | --- |
| **Part** | **List of Courses** | **Credits** | **No. of Hours** |
|  | Core – I | 5 | 7 |
| Core – II | 5 | 7 |
| Core – III | 4 | 6 |
| Elective – I | 3 | 5 |
| Elective – II | 3 | 5 |
|  |  | **20** | **30** |

**Semester-II**

|  |  |  |  |
| --- | --- | --- | --- |
| **Part** | **List of Courses** | **Credits** | **No. of Hours** |
|  | Core – IV | 5 | 6 |
| Core – V | 5 | 6 |
| Core – VI | 4 | 6 |
| Elective – III | 3 | 4 |
| Elective – IV | 3 | 4 |
| Skill Enhancement Course [SEC] - I | 2 | 4 |
|  |  | **22** | **30** |

**Second Year – Semester – III**

|  |  |  |  |
| --- | --- | --- | --- |
| **Part** | **List of Courses** | **Credits** | **No. of Hours** |
|  | Core – VII | 5 | 6 |
| Core – VIII | 5 | 6 |
| Core – IX | 5 | 6 |
| Core (Industry Module) – X | 4 | 6 |
| Elective – V | 3 | 3 |
| Skill Enhancement Course - II | 2 | 3 |
|  | Internship / Industrial Activity [Credits] | 2 | - |
|  |  | **26** | **30** |

**Semester-IV**

|  |  |  |  |
| --- | --- | --- | --- |
| **Part** | **List of Courses** | **Credits** | **No. of Hours** |
|  | Core – XI | 5 | 6 |
| Core – XII | 5 | 6 |
| Project with VIVA VOCE | 7 | 10 |
| Elective – VI (Industry Entrepreneurship) | 3 | 4 |
| Skill Enhancement Course – III / Professional Competency Skill | 2 | 4 |
| Extension Activity | 1 | - |
|  |  | **23** | **30** |

**Total 91 Credits for PG Courses**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **M.Sc. Bioinformatics**  **The Course of Study and the scheme of evaluation**  **Choice Based Credit System** | | | | | | | |
| **C-**Credits, **H**- hours of instruction/week, **Ex**-Exam Hours,  **IA-** Internal Assessment Marks, **ES**-End Semester Marks, **T**-Total Marks | | | | | | | |
| **Subject Type** | **Title of Course** | **C** | **H** | **Ex** | **IA** | **ES** | **T** |
| **SEMESTER I** | | | | | | | |
| **Core Course I** | Introduction to Bioinformatics | 5 | 7 | 3 | 25 | 75 | 100 |
| **Core Course II** | Programming in Linux, C++ and Perl | 5 | 7 | 3 | 25 | 75 | 100 |
| **Core Course III** | Cell and Molecular Biology | 4 | 6 | 3 | 25 | 75 | 100 |
| **Generic/Department specific Elective Course (G/DSEC) I** | Choose from the list below | 3 | 5 | 3 | 25 | 75 | 100 |
| **Generic / Department specific Elective Course (G/DSEC) II** | Choose from the list below | 3 | 5 | 3 | 25 | 75 | 100 |
| **Value Added Course I** | Programming in Linux, C++ and Perl - Practical |  |  |  |  |  |  |
| **SEMESTER II** | | | | | | | |
| **Core Course IV** | Biomolecules and Biochemistry | 5 | 6 | 3 | 25 | 75 | 100 |
| **Core Course V** | Python and R Programming | 5 | 6 | 3 | 25 | 75 | 100 |
| **Core Course VI** | Genomics and Transcriptomics | 4 | 6 | 3 | 25 | 75 | 100 |
| **Generic /Department specific Elective Course (G/DSEC) III** | Choose from the list below | 3 | 4 | 3 | 25 | 75 | 100 |
| **Generic /Department specific Elective Course (G/DSEC) IV** | Choose from the list below | 3 | 4 | 3 | 25 | 75 | 100 |
| NME I |  | 2 | 4 | - | - | - | - |
| **SEMESTER III** | | | | | | | |
| **Core Course VII** | Laboratory course - Programming in Python, R, Genomics and Transcriptomics | 5 | 6 | 3 | 25 | 75 | 100 |
| **Core Course VIII** | Molecular Modeling and Computer Aided drug design | 5 | 6 | 3 | 25 | 75 | 100 |
| **Core Course IX** | Proteomics and Metabolomics | 5 | 6 | 3 | 25 | 75 | 100 |
| **Core X**  **Industry Module** | Laboratory course - Molecular Modeling and Computer Aided Drug Design, Proteomics and metabolomics | 4 | 6 | 3 | 25 | 75 | 100 |
| **Generic /Department specific Elective Course (G/DSEC) V** | Choose from the list below | 3 | 5 | 3 | 25 | 75 | 100 |
| **Skill Enhancement Course (SEC) II** | Big data analytics and Computing - Practical | 2 | 3 | 3 | 25 | 75 | 100 |
| **Summer Internship** |  | 2 | - | - | - | - | - |
| **SEMESTER IV** | | | | | | | |
| **Core Course XI** | Database Management Systems | 5 | 6 | 3 | 25 | 75 | 100 |
| **Core Course XII** | Computational Biology | 5 | 6 | 3 | 25 | 75 | 100 |
| **Project and Viva-voce** |  | 7 | 10 | - | 25 | 75 | 100 |
| **Generic /Department specific Elective Course (G/DSEC) VI** | Choose from the list below | 3 | 4 | 3 | 25 | 75 | 100 |
| **Skill Enhancement Course / Professional Competency Skill** |  | 2 | 4 | - | - | - | - |
| **Extension Activity** |  | 1 | - |  |  |  |  |
| **Total Credits 91** | | | | | | | |
| **Department specific Elective course (DSEC)** | | | | | | | |
|  | Biomathematics and Biostatistics | | | | | | |
|  | Structural Bioinformatics | | | | | | |
|  | Data warehouse and Data mining | | | | | | |
|  | Research Methodology, IPR and Bioethics | | | | | | |
|  | Lipidomics and Glycomics | | | | | | |
|  | Network Biology and visualisation | | | | | | |
|  | Translational Bioinformatics | | | | | | |
|  | Medical and population genomics | | | | | | |
|  | Cancer Genomics | | | | | | |
|  | Basics of Clinical Research Management | | | | | | |
|  | Biodiversity, Agriculture and ecosystem Informatics | | | | | | |
|  | Systems Biology | | | | | | |
|  | Java Programming | | | | | | |
|  | Precision Medicine | | | | | | |
| **Generic elective course (GEC)** | | | | | | | |
|  | Basic Bioinformatics | | | | | | |
|  | Immunoinformatics | | | | | | |
|  | Applications of Bioinformatics | | | | | | |
|  | Cheminformatics | | | | | | |
|  | Pharmacogenomics | | | | | | |
|  | Computer aided drug design | | | | | | |

**SEMESTER - I**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core I** | **Introduction to Bioinformatics** | **5** | **7** | **65** |

**OBJECTIVES OF THE COURSE**

* To provide an integrative approach to the understanding of both theory and practice of bioinformatics
* To apply biological concepts at different levels to study gene / protein analysis, and the proteins implicated in diseases
* To understand the evolution of the life

**COURSE LEARNING OUTCOMES**

On successful completion of the course, students will be able to

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Recognize and relate the biological databases, tools and softwares to be used in the field of Bioinformatics | K1 |
| CO2 | Perceive the different databases, fundamental tools in bioinformatics and infer the required information and acquire hands on practice | K2 |
| CO3 | Compare and identify the differences in sequences and structure | K3 |
| CO4 | Perform a complete analysis of the genes and protein | K4 |
| CO5 | Apply the knowledge obtained from gene and protein sequence analysis to other clinical conditions | K5, K6 |

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| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Basics of Bioinformatics**  Introduction to Bioinformatics; Computers in Biology to understand Biological System; Concept of open resources in Bioinformatics. Biological databases – NCBI, NCBI, EBI, CMBI, OMIM | 12 | CO 1-5 |
| 2 | **Introduction to Biological Databases**  Type of Databases, Public Biological Databases –. Primary Nucleotide Sequence Databases: EMBL, GenBank, DDBJ, Secondary Nucleotide Sequence Databases: UniGene, SGD. Sequence Submission Methods and Tools (Sequin, Sakura, Bankit), Sequence Retrieval Systems (Entrez & SRS); Sequence File Formats and Conversion Tools. Finding Scientific Articles using Pubmed. | 13 | CO 1-5 |
| 3 | **Introduction to Sequence Alignment**  Protein and nucleotide alignment, Homology, Similarity, Identity, Pairwise alignments: Dot Plots, Scoring Matrix-PAM, BLOSUM, Gap Penalty, Dynamics programming - Alignment Algorithms: Global Sequence Alignment: Needleman-Wunch Algorithm. Local Sequence Alignment: Smith –Waterman Algorithm. Rapid, Heuristic Versions of Smith Waterman: FASTA, Basic Local Alignment Search Tool, BLAST Search Steps, Search Strategy, E Value, Raw Scores and Bit Scores, Ensembl BLAST, TIGR BLAST, PSI-BLAST- Practical and theory | 15 | CO 1-5 |
| 4 | **Multiple Sequence Alignment and phylogeny**  Definition of Multiple Sequence Alignment. Tools of Multiple Sequence Alignment Programs, Clutsal, Phylip, MAFT. Hidden markov models.  Evolutionary analysis, Relationship of Phylogenetic Analysis to Sequence Alignment, Genome Complexity. Bootstrap, Tree construction Methods. Neighbor-Joining Method, Unweighted Pair Group Method with Arithmetic Mean (UPGMA), Character based methods: Maximum Parsimony Method and Maximum-Likelihood Method | 15 | CO 1-5 |
| 5 | **Specialised databases**  Literature databases and biomedical databases – pubmed, OMIM, Metabolic database- KEGG, Metacyc, reactome, Protein domain and motif prediction. Databases and tools to infer STS, EST, CDS, ORF, Domains and motifs- Interpro, Prosite. Protein structure databases -CATH, SCOP, Homologs, paralogs, xenologs, orthologs, COG. | 5 | CO  1-5 |
| Self study | Concepts from ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

**BOOKS FOR STUDY**

### Richard Blum, Linux Command Line and Shell Scripting Bible, 3rd Edition, Wiley, 816

### Pevsner, Jonathan. Bioinformatics and Functional Genomics. USA: John Wiley,2009.

* Baxevanis, Andreas, D. and Francis B.F. Ouellette, Bioinformatics- A Practical Guide to the Analysis of Genes and Proteins. NewYork: John Wiley, 2004.
* David W.Mount. Bioinformatics Sequence and Genome Analysis. :CBS Publishers,2003.

**BOOKS FOR REFERENCE:**

* Baldi, P. and Brunak, S. Bioinformatics: Machine Learning Approach.USA: MIT Press, 2003.
* Chen and Yi-Ping Phoebe. Bioinformatics Technologies. Germany: Springer, 2005.
* Durbin, R., S. Eddy, A. Krogh and G. Mitchison. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids. USA: Cambridge University Press, 2005.
* Higgins, Des and Willie Taylor. Bioinformatics –Sequence, Structure and Databanks – Practical Approach. London: Oxford University Press, 2001.
* Lesk, Arthur M. Introduction to Bioinformatics. UK: Oxford University Press, 2014.

**JOURNALS**

BMC Bioinformatics

Bioinformatics

Journal of Bioinformatics and Computational Biology

Journal of Biomedical Informatics

Journal of Integrative Bioinformatics

**WEB RESOURCES**

http://bioinformaticsweb.net/tools.html

https://www.bits.vib.be/index.php/training/122-basic-bioinformatics

http://bioinformaticssoftwareandtools.co.in/

http://www.genscript.com/tools.html

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|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 2 | 3 | 2 | 1 | 3 | 3 | 3 | 2 |
| CLO2 | 1 | 1 | 2 | 2 | 2 | 2 | 1 | 2 | 2 |
| CLO3 | 2 | 2 | 2 | 1 | 3 | 3 | 1 | 3 | 3 |
| CLO4 | 3 | 3 | 3 | 3 | 3 | 3 | 1 | 3 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 3 |
| Weightage | 12 | 11 | 13 | 11 | 12 | 14 | 8 | 14 | 13 |
| Weighted percentage of Course Contribution to PSOs | 2.4 | 2.2 | 2.6 | 2.2 | 2.4 | 2.8 | 1.6 | 2.8 | 2.6 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-solving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

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| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core II** | **Programming in Linux/Unix, C++ and Perl** | **4** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To facilitate the students in gaining programming skills with both linux and windows operating systems.
* To enable the students to design and execute C++ and Perl scripts
* To interpolate biological demands through programming

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| 1 | Recognize and recall the basics of programming in biology | K1, K2 |
| 2 | Relate the necessity of using Linux based operating systems | K3,K4 |
| 3 | Access biological concepts with C++ and Perl scripts | K4 |
| 4 | Apply programing to analyse genomic sequences and process them | K5, K6 |
| 5 | Utilise the BioPerl knowledge to solve complex problems in Bioinformatics | K5, K6 |

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| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Introduction to Programming language and Linux/Unix**  Machine/Assembly Language, Higher Level Languages. Operating systems - Windows and Linux/Unix. Properties of Linux/Unix, Desktop Environment, Linux basics commands. Working with Files, Text Editors, I/O Redirections, Pipes, Filters, and Wildcards. Changing Access Rights. Bash scripting, loops, text mining, Awk, sed and grep. Editors- vim, nano, gedit. | 12 | CO 1-5 |
| 2 | **Introduction to C++**  Simple and Compound Data, Code: Syntax and Semantics, Programming in C++: C++ Characteristics, Tokens, Keywords, Identifiers and Constants, Basic Data Types, User Defined Data Types, Derived Data Types, Expressions and Control Structures, Functions and Variables: Scope, Declaration and Definition, Arrays and Strings in C++. | 13 | CO 1-5 |
| 3 | **Object Oriented Programming**  Using Objects, Classes, Encapsulation, Inheritance, Abstraction and Polymorphism. Friend functions, String and file operations– creating string objects, Standard Streams – string and Files, Open, close, EOF, updating files and error Handling, String manipulation- String operators Manipulating String, String characteristics, Comparing and Swapping. | 10 | CO 1-5 |
| 4 | **Introduction to Perl Programming**  Introduction, Statements and Declarations, Default Variable, Expressions, Statements, Operators in Perl, Control Structures, Variable Types and Data types– Scalar, Arrays, Hashes. Functions- split, join, length, lcfirst, ucfirst, index and exists, Creating Regular Expressions-Characters, Character Classes, Alternative Match Patterns, Quantifiers, Assertions, Back References, Modifiers and Translator. Subroutines. | 13 | CO 1-5 |
| 5 | **File Handling and Bioperl**  Files- Overview and working with File handles, Closing the files, printing, renaming files, Various Ways of Opening a Perl File Handles.  **Bioperl**  Introduction to Bioperl: Installation Procedures, Architecture, Uses of Bioperl, Modules of bioperl- seq, seqio, alignio, db, Modules of Bioperl – Annotation, location, tools - practical | 12 | CO 1-5 |
| Self study | Concepts from ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

**BOOKS FOR STUDY**

* E. Balagurusamy. *Object Oriented Programming with C++*. New Delhi: Tata McGraw- Hill, 2017.
* Tisdall James D. *Beginning Perl for Bioinformatics.* USA: O’Reilly and Associates, 2014.

### Jason Cannon, Linux for Beginners: An Introduction to the Linux Operating System and Command Line, 1st edition, 204 pages.

**BOOKS FOR REFERENCE**

* Conrod Bessant, Ian Shadforth and Darren Oakley. *Building Bioinformatics Solutions with Perl, R and MySQL***.** New York: Oxford University Press, 2014.
* Bjarne, Stroustrup. *The C++ Programming Language*. India: Addison Wesley, 2013.
* Holzner and Steven. *Perl Black Book*. India: Dream Tech Press, 2006.
* Hubbard, John. *Programming with C++, Schaum’s Outline Series*. New Delhi: Tata McGraw Hill, 2003.
* Tisdall James D. *Beginning Perl for Bioinformatics.* USA: O’Reilly and Associates, 2003.
* Ellen Siever, Weber, Stephen Figgins, Robert, Arnold Robbins *Linux in a Nutshell-ADesktop Quick Reference.* USA: O’Reilly and Associates, 2006
* Sanjeev Sofat. *Object Oriented Programming Using C++,* India : Cyber Tech. Publication, 2009.

**JOURNALS**

C/C++ Users Journal

International Journal of Computer Applications

Computer Methods and Programs in Biomedicine

Perl in communities

**WEB RESOURCES**

http://www.cplusplus.com/doc/tutorial/

http://www.cprogramming.com/

http://www.stroustrup.com/4th.html

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 3 | 1 | 3 | 1 | 3 | 1 | 3 | 2 |
| CLO2 | 3 | 1 | 2 | 1 | 2 | 2 | 1 | 3 | 2 |
| CLO3 | 3 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 |
| CLO4 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| Weightage | 14 | 12 | 11 | 12 | 11 | 14 | 11 | 15 | 13 |
| Weighted percentage of Course Contribution to PSOs | 2.8 | 2.4 | 2.2 | 2.4 | 2.2 | 2.8 | 2.2 | 3 | 2.6 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, Finding errors from the script.

**Application (K3) -** Suggest idea/concept with examples, Write a code to solve biological problems, Observe, Explain.

**Analyse(K4) –** Problem-solving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons/ writing codes and scripts

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core III** | **Cell and Molecular Biology** | **4** | **5** | **65** |

## OBJECTIVES OF THE COURSE

* To understand the general principles of gene organisation and expression
* To explore various levels of gene regulation and protein function
* To analyse various genetic and molecular changes that occur in a normal cell

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Grasp the functions of the prokaryotic and eukaryotic cell and cell cycle mechanisms at the molecular level | K1 |
| CO2 | Explore and analyse the structural organisation of genes and the control of gene expression | K2 |
| CO3 | Interpret the significance of central dogma of life | K3 |
| CO4 | Appreciate the molecular mechanisms involved in cancer signalling | K4 |
| CO5 | Link the concepts of cell and molecular biology to a better understanding of diseases, including cancer | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Cellular Organisation**  Prokaryotic and Eukaryotic cell - Characteristics, Membrane structure and function - lipid bilayer, osmosis, ion channels, active transport, membrane pumps, Structural organisation and function of intracellular organelles, Cell division - Mitosis and meiosis, Cell cycle regulation, Check points. | 12 | CO 1-5 |
| 2 | **Structural organisation of Chromosomes and Genes**  DNA-Structure and Conformations, Chromosomes – Functions, Organisation of Genomes - Coding Sequences, Repetitive Sequences, transposons, Mitochondria and Chloroplast Genome - Organisation and Function, Bacteria - Cells structure and bacterial genetics, Virus - Structure, Viral genome, Viroids and Prions. | 15 | CO 1-5 |
| 3 | **Replication and Transcription**  DNA replication, Mutations, DNA damage and repair mechanisms in prokaryotes and eukaryotes, Transcription- Transcriptional Control by Regulatory Proteins, RNA polymerases, Post Transcriptional Regulation - DNA Methylation, Histone Modification, - capping, RNA editing, splicing, and polyadenylation. | 10 | CO 1-5 |
| 4 | Translation RNA- Types, structure and functions,Ribosomes – Structure and Assembly, Translational Regulation - Regulation of gene expression in Prokaryotes (Operon) and Eukaryotes, Genetic code, Gene Silencing, Post- translational modification of proteins. | 10 | CO 1-5 |
| 5 | **Cell Signalling and Cancer**  Cell signalling – Signalling molecules, Receptors - Hormones receptors, cell surface receptor, G-protein coupled receptors, signal transduction pathways, Cancer Biology- Characteristics and genetic basis of cancers, Proto-oncogene, Oncogenes, Tumour Suppressor Genes, Oncogenesis - Cancer Immunotherapy, Regulation of Cell Death, Apoptosis. | 13 | CO 1-5 |
| Self study | Concepts from CSIR NET (lifesciences) and ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

## BOOKS FOR STUDY

* Harvey Lodish, Arnold Berk, Chris A. Kaiser, Monty Krieger, Anthony Bretscher, Hidde Ploegh. *Molecular Cell Biology.* USA: W. H. Freeman, Eighth edition, 2016.
* Wolfe, Stephen L. *Molecular and Cellular Biology.* USA: Wadsworth, 2005.
* Watson, James, D. *Molecular Biology of the Gene****.*** USA: The Benjamin Cummings Publishing Company, 2007.

#### BOOKS FOR REFERENCE

* Cooper, Geoffrey M. and Robert E. Hausman***.*** *The Cell, A Molecular Approach****.*** USA: Sinauer Associates, 2004.
* Harvey Lodish, Arnold Berk, Chris A. Kaiser, Monty Krieger, Matthew P. Scott, Anthony Bretscher, Hidde Ploegh and Paul Matsudaira. *Molecular Cell Biology.* USA: W.H.freeman, 2008.
* Watson, James, D. *Molecular Biology of the Gene****.*** UK: Pearson, Seventh edition, 2017.
* Darnell, James, Harvey Lodish and David Baltimore. *Molecular and Cell Biology*, Scientific American Books, USA: W.H. Freeman, 2004.
* Karp and Gerald. *Cell and Molecular Biology- Concepts and Experiments*, USA: John Wiley, 2013.
* Lewin and Benjamin. *Genes IX*, UK: Oxford University Press, 2009.
* Roitte, Ivan M., Brostoff, Jonathan and Male, David K. *Immunology.* Philadelphia: J.B. Lippincott, 1990.
* Purvis, William K, David Sadava, Craig Heller and Gordan H. Orians. *Life: The Science of Biology.* USA: Sinauer, 2004.

**JOURNALS**

### Journal of Molecular Biology

Molecular Biology

### Journal of Genetics and Genomics

*BMC Cell Biology*

**WEB SOURCES**

www.cellbio.com

www.molbiolcell.org

www.sciencedirect.com

http://www.nature.com/scitable/topic/cell-biology-13906536

http://www.biology.arizona.edu/cell\_bio/cell\_bio.html

http://ghr.nlm.nih.gov/

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 2 | 1 | 1 | 2 | 3 | 1 | 1 | 3 |
| CLO2 | 2 | 2 | 3 | 2 | 1 | 2 | 2 | 2 | 3 |
| CLO3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 |
| CLO4 | 3 | 1 | 2 | 3 | 2 | 3 | 2 | 2 | 3 |
| CLO5 | 3 | 2 | 3 | 2 | 3 | 2 | 3 | 2 | 3 |
| Weightage | 13 | 10 | 13 | 11 | 11 | 12 | 10 | 10 | 15 |
| Weighted percentage of Course Contribution to PSOs | 2.6 | 2 | 2.6 | 2.2 | 2.2 | 2.4 | 2 | 2 | 3 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Skill enhancement Course I** | **Molecular Biology and Bioinformatics Practical** | **2** | **3** | **39** |

**OBJECTIVES OF THE COURSE**

* To provide an integrative approach to the understanding of both theory and practice of bioinformatics
* To apply biological concepts at different levels to study gene / protein analysis, and the proteins implicated in diseases
* To understand the evolution of the life
* To identify subcellular structures, organelles and understand their functions
* To provide practical experience of the various techniques involved in Molecular Biology and Biochemistry
* To perform a range of molecular techniques used for the isolation, estimation, purification of biomolecules

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Learn to use a variety of softwares, tools and databases available for bioinformatics | K1 |
| CO2 | Handle a wide range of open source tools in bioinformatics | K2 |
| CO3 | * Utilise laboratory skills to enhance understanding of cell structure and function while participating in a group environment * Develop responsible conduct of laboratory skills appropriate to the field of cell and molecular biology * Apply the molecular biology techniques to biotechnological approaches | K3 |
| CO4 | Gain efficient sequence and structure processing skills | K4 |
| CO5 | Perform genomic data analysis | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Biological Databases**  Primary Nucleotide Sequence Databases: NCBI, EMBL, DDBJ  Protein Sequence Databases – PIR, RefSeq, UniProt  Protein Structure Databases – PDB | 8 | CO1-5 |
| 2 | **Sequence Analysis**  Basic Local Alignment Search Tool (BLAST), Pairwise and Multiple Sequence Alignment Tools: EMBOSS, Clustal W and Clustal Omega  Protein Visualization Tools- Rasmol, Swiss PDB Viewer, PyMol  Phylogenetic Tree Construction Tool: MEGA Software, Phylip, MAFFT | 10 | CO1-5 |
| 3 | **Molecular biology -Cellular Organelles**  Cell Fraction and Extraction of cell organelles - Chloroplast  Extraction of DNA from Onion, Extraction of RNA from Yeast  Estimation of DNA and RNA | 7 | CO1-5 |
| 4 | **Protein Analysis**  Estimation of Mitochondria by Assessing the Marker Enzyme  Denaturing Proteins and Identification of Amino Acids by Thin Layer Chromatography  Estimation of Proteins by Lowry’s Method | 7 | CO1-5 |
| 5 | **Molecular techniques**  Amplification of DNA by PCR  Electrophoretic Techniques: Agarose Gel Electrophoresis,  SDS PAGE | 7 | CO1-5 |

#### BOOKS FOR REFERENCE:

* Wilson, K; Walker, J.*Principles and techniques of Biochemistry and Molecular Biology.*USA: Cold Spring Harbor Laboratory Press, 2010.
* Sambrook, J; Russel, DW. *MolecularCloning*. USA: Cold Spring Harbor Laboratory Press, 2001
* Sadasivam, S. and Manickam, A. *Biochemical Methods***.** India: New Age International, 2009.
* Wilson, K; Walker, J.*Principles and techniques of Biochemistry and Molecular Biology.*USA: Cold Spring Harbor Laboratory Press, Eighth edition, 2010.
* Swati Agarwal, Suphiya Khan. Advanced Lab Practices in Biochemistry & Molecular Biology. India: I K International Publishing House, 2018.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 2 | 2 | 3 | 1 | 3 | 2 | 3 | 1 |
| CLO2 | 3 | 2 | 3 | 3 | 2 | 3 | 2 | 3 | 1 |
| CLO3 | 1 | 3 | 2 | 3 | 3 | 3 | 2 | 1 | 2 |
| CLO4 | 2 | 3 | 3 | 3 | 2 | 3 | 2 | 1 | 3 |
| CLO5 | 2 | 3 | 3 | 3 | 2 | 3 | 2 | 2 | 3 |
| Weightage | 11 | 13 | 13 | 15 | 10 | 15 | 10 | 10 | 10 |
| Weighted percentage of Course Contribution to PSOs | 2.2 | 2.6 | 2.6 | 3 | 2 | 3 | 2 | 2 | 2 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Recall (K1) & Understand/ Comprehend (K2) -** Working performance and continuous practice of codes/ scripts/ softwares/ tools/ experiment handling

**Application (K3) -** Solve problems/ execute codes/ debugging, Observe, Explain the methods/ identify spotters.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Maintenance of observation book, records, Critique or justify the methods with pros and cons.

**Create (K6) –** Check knowledge in specific or offbeat situations, viva voce.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Value Added Course I** | **Programming in Linux/Unix, C++ and Perl- Practical** | **4** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To facilitate the students in gaining programming skills.
* To enable the students to design and execute Linux, C++ and Perl scripts
* To interpolate biological demands through programming

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Learn the basics of programing and working with Linux/Unix | K1 |
| CO2 | Relate the necessity for programming in biology | K2 |
| CO3 | Handling biological concepts with C++ and Perl scripts | K3 |
| CO4 | Apply programing to analyse genomic sequences | K4 |
| CO5 | Understand Bio-Perl and their application in bioinformatics to handle the complex data | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Linux**  Create directory, move directory, remove directory, create files, move files, copy files, using wild card characters and changing user rights. All basic linux commands.  Differences of using awk, sed and bash. Usage of editors | 8 | CO 1-5 |
| 2 | **C++**  Find the area and circumference of a circle  Armstrong Number  Prime Number  Fibonacci series  Program to find factorial of numbers | 7 | CO1-5 |
| 3 | **C++ objects and strings**  An example with classes and object  Checking for palindrome of a given string (without using the built in string function)  Arrange the given names in alphabetical order  Program to find length of the string  Program to compare two strings  Program to swap two strings | 7 | CO1-5 |
| 4 | **Perl Basics**  Program to print the elements of a array  Program to take an element off the end of an array  Program to reverse an array  Use regular expressions to modify a sequence of letters in sentences.  Program to use subroutines  **Perl for Bioinformatics**  Convert DNA to RNA (transcription)  Translate the given RNA sequence  Calculate the frequency of bases  Find the reverse complement of the DNA sequence  Program to find the percentage of G and C in a DNA sequence  Program to append ATGC to a DNA sequence using subroutines  Program to concatenate two strings using subroutines | 10 | CO1-5 |
| 5 | **Bioperl**  Using Bioperl retrieve a sequence from database  Using Bioperl Convert DNA to Protein (Translation)  Using Bioperl retrieve last 30 amino acids from the given protein sequence  Using Bioperl run BLAST locally | 7 | CO1-5 |

**BOOKS FOR STUDY**

* E. Balagurusamy. *Object Oriented Programming with C++*. New Delhi: Tata McGraw- Hill, 2017.
* Tisdall James D. *Beginning Perl for Bioinformatics.* USA: O’Reilly and Associates, 2014.

**BOOKS FOR REFERENCE**

* Conrod Bessant, Ian Shadforth and Darren Oakley. *Building Bioinformatics Solutions with Perl, R and MySQL***.** New York: Oxford University Press, 2014.
* Bjarne, Stroustrup. *The C++ Programming Language*. India: Addison Wesley, 2013.
* Holzner and Steven. *Perl Black Book*. India: Dream Tech Press, 2006.
* Hubbard, John. *Programming with C++, Schaum’s Outline Series*. New Delhi: Tata McGraw Hill, 2003.
* Tisdall James D. *Beginning Perl for Bioinformatics.* USA: O’Reilly and Associates, 2003.
* Ellen Siever, Weber, Stephen Figgins, Robert, Arnold Robbins*Linux in a Nutshell-ADesktop Quick Reference.* USA: O’Reilly and Associates, 2006
* Sanjeev Sofat. *Object Oriented Programming Using C++,* India : Cyber Tech. Publication, 2009.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 3 | 2 | 2 | 1 | 3 | 1 | 3 | 2 |
| CLO2 | 2 | 3 | 2 | 2 | 2 | 3 | 2 | 3 | 2 |
| CLO3 | 2 | 3 | 3 | 3 | 2 | 2 | 2 | 3 | 3 |
| CLO4 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 |
| Weightage | 11 | 15 | 13 | 13 | 11 | 12 | 9 | 15 | 13 |
| Weighted percentage of Course Contribution to PSOs | 2.2 | 3 | 2.6 | 2.6 | 2.2 | 2.4 | 1.8 | 3 | 2.6 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) & Understand/ Comprehend (K2) -** Working performance and continuous practice of codes/ scripts/ softwares/ tools

**Application (K3) -** Solve problems/ execute codes/ debugging, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Maintenance of observation book, records, Critique or justify the methods with pros and cons.

**Create (K6) –** Check knowledge in specific or offbeat situations, viva voce.

**SEMESTER II**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core IV** | **Biomolecules and Biochemistry** | **4** | **5** | **65** |

## OBJECTIVES OF THE COURSE

* To acquire the knowledge on structure, function and metabolism of biomolecules
* To understand the enzyme kinetics and techniques used in biomolecule analytical procedures

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Understand the structure, function and concepts of Biomolecules | K1 |
| CO2 | Relate the importance of each biomolecule and inter-connectivity in their metabolism | K2 |
| CO3 | Demonstrate the significance of primary to highly complex structure of protein and their folding mechanisms | K3 |
| CO4 | Interpret the importance of enzymes and enzyme kinetics to inter-relate their role in normal vs diseased condition | K4 |
| CO5 | Infer the ways to examine and identify biomolecules, xenobiotics, drugs through various analytical techniques | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Introduction to Biomolecules**  Biomolecules - Structure and functions of Atoms and Molecules  Chemical bonds - Van der Waals, electrostatic, hydrogen bonding, hydrophobic interactions, acid base concept and buffers, pH, Water - Properties and its importance.  Bioenergetics - Thermodynamics systems - laws of thermodynamics, entropy and enthalpy, standard free energy, ATP. | 15 | CO1-5 |
| 2 | **Carbohydrates, Lipids and Nucleic acid**  Structures and Functions of Carbohydrates, Lipids, and Nucleic acids  Carbohydrate metabolism – Glycolysis, Glycogen metabolism, TCA cycle, HMP shunt  Fatty acid and Nucleic acid metabolism- β- oxidation and Biosynthesis of fatty acids, De novo pathway and salvage pathway | 15 | CO1-5 |
| 3 | **Proteins**  Proteins - Levels of organisation**,** Amino acid properties, amino acid types.Peptide bonds, disulphide bridges and other conformations. Amino acid and protein metabolism – Oxidative Deamination, Transamination and Urea Cycle | 15 | CO1-5 |
| 4 | **Enzymes and Enzyme Kinetics**  Nomenclature, Classification of enzymes, Enzyme specificity, Cofactors, Coenzyme and Prosthetic group  Enzyme Kinetics, Michaelis-Menten Equation, significance of Vmax and Km, Enzyme inhibition **-**Competitive and non-competitive Inhibition, Feedback inhibition. Enzyme regulation. Allosteric modulation.  Extraction and purification of enzymes, Immobilized enzymes, Application of enzymes in medicine and industry | 10 | CO1-5 |
| 5 | **Xenobiotics and Analytical Techniques**  Xenobiotics and general detoxification methods in the body  Principles, types and applications of Spectroscopy, Nuclear Magnetic Resonance- The phenomenon, types and applications  Mass Spectrometry for protein and peptide analysis, MALDI-TOF Analyser, Tandem Mass Analyser, The Ion Trap Mass Analyser, Q-TOF Instrument | 10 | CO1-5 |
| Self study | Concepts from CSIR NET (lifesciences) and ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

## BOOKS FOR STUDY

#### Albert, L. Lehninger et al, Biochemistry, Worth Publishing, UK. 2012.

#### Thomas. E. Creighton, Proteins, W. H. Freeman, New York.2012.

#### Igor, Serdyuk, Nathan R. Zaccai and Joseph Zaccai. Methods in Molecular Physics.UK: Cambridge University Press, 2007.

#### Narayanan P. Introductory Biophysics Mumbai, India: New Age Publishing Co., 2005

#### Kensal E.vanHolde, Johnson Curtis W. and Ho Shing P.Principles of Physical Biochemistry, USA: Prentice Hall International Inc., 2005

#### BOOKS FOR REFERENCE

* Champe, Pamela C, Richard A. Harvey and Denise R. Ferrier. Lippincott’s Illustrated Reviews: Biochemistry, India: J.P. Brothers Medical Publishers, 2013.
* Garrett, H. Reginald and Grisham, M. Charles. Biochemistry.USA: Thomson–BroCole, 2012.
* Jeremy, M. Berg. Biochemistry**,** New York: W.H. Freeman, 2010.
* Lubert and Stryer. Biochemistry**,** New York: W.H. Freeman, 2012.
* Voet, D. and Voet, G. Biochemistry, New York: John Wiley and Sons Inc, 2012.
* Bengt Nolting. Methods in Modern Biophysics, Germany: Springer, 2004.
* D.Freifelder. Physical Biochemistry. New York, USA: W.H.Freeman and Company, 1982.
* Banwell C.N. Fundamentals of Molecular Spectroscopy. New DelhiIndia: Tata McGraw-Hill Publishing Company Lt., 1994.
* D.Sherwood, Crystals, X-rays and Proteins. London, UK: Longman Group Lts., 1976.

**JOURNALS**

Journal of Biochemistry

Indian Journal of Clinical Biochemistry

Biochemistry

Biophysical Journal

European Biophysics Journal

Journal of Biophysics

**WEB SOURCES**

http://www.biophysics.org/Education/Careers/CareersinBiophysics/tabid/112/Default.aspx

http://www.rcsb.org/pdb/101/static101.do?p=education\_discussion/Looking-at-Structures/methods.html

http://www2.chemistry.msu.edu/faculty/reusch/VirtTxtJml/Spectrpy/MassSpec/masspec1.htm

www.themedicalbiochemistrypage.org

*www.biochemistry.org*

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 1 | 3 | 2 | 3 | 3 | 3 | 2 | 1 |
| CLO2 | 2 | 1 | 3 | 1 | 3 | 3 | 3 | 2 | 1 |
| CLO3 | 3 | 2 | 3 | 1 | 3 | 3 | 3 | 2 | 1 |
| CLO4 | 1 | 2 | 3 | 2 | 3 | 3 | 3 | 2 | 1 |
| CLO5 | 3 | 1 | 2 | 3 | 3 | 3 | 3 | 2 | 1 |
| Weightage | 12 | 7 | 14 | 9 | 15 | 15 | 15 | 10 | 5 |
| Weighted percentage of Course Contribution to PSOs | 2.2 | 1.4 | 2.8 | 1.8 | 3 | 3 | 3 | 2 | 1 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

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| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core V** | **Python and R programming** | **4** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To demonstrate how to locate and download files for data analysis involving genes and medicine
* Select datasets, open files and pre-process data using Python and R language

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Relate the necessity for programming in biology | K1 |
| CO2 | Handling biological concepts with Python and R scripts | K2 |
| CO3 | Apply R and Python programming to analyse genomic sequences | K3 |
| CO4 | Gain efficient programming skills to handle missing values and impute values in data | K4 |
| CO5 | Perform genomic data analysis and visualise them using Python and R | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Introduction to Python**  Installation of Python and Jupyter notebooks.  Variables- list, tuples, sets, dictionary, matrix, dataframe. handling strings, Functions, control structures, operators, Pandas, Numpy and Scipy  Fasta files, Parsing DNA and protein information, Gene locations splices, extracting all gene locations. Object Oriented Programming in Python. Constructors, Type(), Issubclass(), Super(). | 12 | CO1-5 |
| 2 | **Biopython**  Getting started and installation of modules and packages, Coding DNA, proteins, extracting translations**,** Modules- Bio Import, Bio Seq, Bio Align**.**  Plot ABI traces, Retrieve and Annotate Entrez gene | 13 | CO1-5 |
| 3 | **Data Visualization**  Getting Started with Pandas, Matplotlib, scki-kit learn.  Visualisation using Matplotlib and scikit learn – Line Plots- Scatter Plots-Visualizing Errors-Density and Contour Plots-Histogram, Binnings and Density -Customizing Color Bars. Customising Plot Legends -Multiple Subplots-Text and Annotation-Customizing Ticks. | 15 | CO1-5 |
| 4 | **R programming**  R as a statistical Calculator, Creating Objects and Assigning Values. Vectors, matrices, factors, levels, dataframes. Graphics: Simple Plotting, Advanced Plotting - ggplot, Using Color in Plots.Using Subscripts and Superscripts in Graph Labels, Interactive Graphics, Saving Graphical Output, Loops**.** | 10 | CO1-5 |
| 5 | **Bioconductor**  Introduction, Bioconductor Packages, Bio strings, Biomart  Bioconductor packages for protein- protein interaction graphs, gene variation packages, genomic ranges, genomic alignments, genomic annotations. Biomedical data science in R- BioML(R). Data wrangling with Tidyverse and shiny | 15 | CO1-5 |

**BOOKS FOR STUDY**

* Robert Gentleman*, R programming for Bioinformatics*, CRC Press, 2016
* Jason Kinser. *Python for Bioinformatics*. Massachusetts: Jones and Barlett Publishers, 2009.
* Mitchell L Model. *Bioinformatics Programming Using Python***.** USA**:** O’Reilly Media Publication, 2009.

**BOOKS FOR REFERENCE**

* Mark Lutz. *Learning Python.* USA: O’Reilly Media Publication, 2009.
* Martin C Brown. *Python: The Complete Reference*. Osborne: McGraw-Hill Media, 2001
* Gentleman R, Carey V.J, Huber W, Irizarry, RA, and Dudoit, S. *Bioinformatics and Computational Biology Solutions Using R and Bioconductor.* New York: Springer, 2008.

**JOURNALS**

The Python Papers Source Codes

The Python Papers Anthology

Python Journal

The R Journal

**WEB RESOURCES**

www.sthurlow.com/python/

www.learnpython.org

www.codecademy.com/en/tracks/python

https://docs.python.org/2/tutorial/

www.pyschools.com/

http://cran.r-project.org/doc/Rnews/

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 3 | 3 | 3 | 2 | 3 | 2 | 3 | 2 |
| CLO2 | 2 | 3 | 3 | 3 | 1 | 3 | 2 | 3 | 2 |
| CLO3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 3 |
| CLO4 | 1 | 3 | 1 | 3 | 2 | 3 | 1 | 3 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| Weightage | 10 | 15 | 14 | 15 | 11 | 15 | 10 | 15 | 13 |
| Weighted percentage of Course Contribution to PSOs | 2 | 3 | 2.8 | 3 | 2.2 | 3 | 2 | 3 | 2.6 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview, identify errors from the script.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas, write scripts and codes to solve biological problems.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core VI** | **Genomics and transcriptomics** | **4** | **5** | **65** |

## OBJECTIVES OF THE COURSE

* To provide an insight into the complete genome sequences of a few organisms as well as the Human genome through Comparative and Functional genomics
* To acquaint knowledge on functional genomics techniques such as microarrays, EST, SAGE and interpret data obtained through high throughput expression studies
* To provide hands on experience of handling the genomic datasets

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Acquaint the fundamental concepts of genome sequencing, file formats and data analysis | K1 |
| CO2 | Perform powerful computational and statistical methods to decode the functional information hidden in DNA and RNAsequences. | K2 |
| CO3 | Experiential knowledge on Next generation sequencing and gene editing techniques | K3 |
| CO4 | Exploit the mechanisms of genomics and transcriptomics to deal with the growing demand for multiomics | K4 |
| CO5 | Apply functional genomics techniques to analyse data from biological system | K5, K6 |

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| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Genome Sequencing and Sequence File Formats**  Understanding a Genome sequence, Locating the genes in a Genome Sequence, Genome Sequencing technologies - Conventional Sequencing techniques, Next generation sequencing technology- Whole Genome Shotgun Sequencing, Exome and amplicon sequencing, Genome assembly, Comparative Genomics - Genome Sequencing Projects, Variations at the Level of individual Nucleotides, Duplications, Indels, Rates and patterns of Nucleotide substitution, Molecular Clocks, Sequence formats and tools, Different file formats- FASTQ, SAM/BAM, VCF, GFF/GTF, BED. Databases and tools. | 10 | CO1-5 |
| 2 | **Epigenetic and Metagenome sequence analysis**  Genome variant analysis- GATK pipeline, concepts of genome wide association studies (GWAS).  Metagenome analysis- Introduction and biological background, amplicon and shotgun metagenome. Alpha and Beta diversity, rarefaction curves and metrics. Logical steps for metagenome analysis. Culturable microbes- Isolation and cultivation of bacteria from environmental samples (in vitro methods), Taxonomical classification- silvaDB, green genes.  Epigenomics, Local chromatin dynamics and epigenetic modifications, analysis of regulatory sequence motifs, transcription factor - DNA interaction | 15 | CO1-5 |
| 3 | **Genome Editing**  Genome editing technologies -CRISPR CAS 9 technology- cas9, selection of targets from sequences, Guide RNA design, recognition sequences, Best practices in SgRNA design, Repair and data analysis of the edited genome, Therapeutic applications. Targeted mutagenesis- Talens, ZFNs. Recent innovations in genome editing in agriculture, diseases and healthcare. | 15 | CO1-5 |
| 4 | **Transcriptomics**  Transcriptomics –microarray technology and gene expression, SAGE, Applications of Microarrays in Medicine, Databases – GEO, array express. RNA dynamics.  Next generation Sequencing -RNA isolation and purification, RIN number. Bulk RNA sequencing, single-cell RNA sequencing, small RNA sequencing,  Importance of gene silencing, miRNA, siRNA, lncRNA, competing endogenous RNA. | 15 | CO1-5 |
| 5 | **Transcriptomic Gene Annotation**  Data analysis- Quality check- fastqc, multi fastqc and trimming of adapters – trimmomatic, cutadapt, Samtools and bowtie, Assembly using genome assemblers and alignment of sequences. Generation of contigs and scaffolds. Competing endogenous RNA network, Predicting DEGs and ontology analysis, Statistics behind DGE analysis. Gene annotations and protein interaction network prediction | 15 | CO1-5 |
| Self study | Concepts from CSIR NET (lifesciences) and ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

## BOOKS FOR STUDY

* Head, Steven R., Ordoukhanian, Phillip, Salomon, Daniel R, Next Generation Sequencing Methods and Protocols, Springer, 2018
* Eija Korpelainen, Jarno Tuimala, Panu Somervuo, Mikael Huss, Garry Wong, RNA-seq Data Analysis: A Practical Approach, Taylor and Francis publishers, 2017
* Arthur Lesk M. Introduction to Genomics. New York: Oxford university press, Third edition, 2017.
* Leland Hartwell, Michael L. Goldberg and Janice Fischer. Genetics: From Genes to Genomes. USA:McGraw-Hill Publishing Company. 2018

#### BOOKS FOR REFERENCE

* Brown P. O and Botstein D. Exploring the new world of the genome with DNA microarrays. USA: Nat. Genet, 1999.
* Collado Vides Julio and Ralf Hofstadter. Gene Regulation and Metabolism – Post Genomic Computational Approaches. India: Ane Books, 2004.

**JOURNALS**

Journal of Biochemistry

Indian Journal of Clinical Biochemistry

Genomics, Proteomics & Bioinformatics

Journal of Data Mining in Genomics & Proteomics

Human Genomics and Proteomics

Journal of Proteomics and Genomics

**WEB SOURCES**

http://www.oncolink.org/resources/article.cfm?id=326

http://www.nature.com/nature/journal/v422/n6928/full/nature01510.html

http://www.ch.ic.ac.uk/local/organic/mod/

<http://www.chemcomp.com/MOE-Molecular_Modeling_and_Simulations.htm>

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 1 | 2 | 1 | 1 | 2 | 2 | 2 | 3 |
| CLO2 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 3 |
| CLO3 | 3 | 3 | 2 | 3 | 2 | 3 | 2 | 1 | 3 |
| CLO4 | 3 | 2 | 3 | 3 | 3 | 3 | 2 | 1 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 |
| Weightage | 15 | 12 | 13 | 14 | 11 | 13 | 10 | 8 | 15 |
| Weighted percentage of Course Contribution to PSOs | 3 | 2.4 | 2.6 | 2.8 | 2.2 | 2.6 | 2 | 1.6 | 3 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core VII** | **Laboratory course - Genomics, transcriptomics, Python and R programming** | **4** | **5** | **65** |

**OBJECTIVE OF THE COURSE**

* To demonstrate how to locate and download files for data analysis involving genes and transcriptomes
* To appreciate the analysis of genomic and transcriptomic data with both command line and GUI options
* Demonstrate how to locate and download files for data analysis involving genes
* Select datasets, open files and pre-process data using Python and R language
* Develop and write python and R scripts to replace missing values, normalise data, discretize data, and sample data
* Use biopython and bioconductor packages to analyse biological data

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Relate the necessity for programming in biology, Handling biological concepts with Python and R scripts | K1 |
| CO2 | Perform and distinguish genomic and transcriptomic data analysis | K2 |
| CO3 | Apply programing to analyse genomic sequences and process the information | K3 |
| CO4 | Gain efficient programming skills by solving biological problems | K4 |
| CO5 | Perform biological data analysis using python and R language | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Genomics**  Genome databases of plants, animals and pathogens  Clusters of Orthologous Groups (COGs)  Gene Prediction by ORF analysis, Gen scan, UCSC Genome Browser  DNA markers - dbSNP, Restriction mapping  EST Clustering databases - DBEST, UNIGene  Epigenetic data analysis  EWAS atlas  PWM and DNA binding motifs- signature logo generation | 10 | CO1-5 |
| 2 | Command line SRA download, fastqc, trimmomatic and assembly GATK pipeline.  Metagenomics - Culturable microbes- Isolation and cultivation of bacteria from environmental samples. In silico -Mg RAST, Kaiju web server, Galaxy server | 10 | CO1-5 |
| 3 | **Transcriptomics**  Differential gene expression analysis –RNA seq, microarray datasets- volcano plot, heatmap, DEGs and annotations – Geo2R, Biojupies  Small RNA network- using cytoscape  Crispr – sg RNA design- Chop Chop | 15 | CO1-5 |
| 4 | **Basics of Python**  Creating tuples, lists, sets, dataframes  Importing Data, Data Frames, Handling Missing Data  Data visualization – volcano, PCA plot, heatmap  Object oriented python – displaying genomic coordinates  **Biopython**  Counting the base frequency  Plotting ABI traces  To transcribe and translate a sequence  Biopython- using Bioseq –Sequence reading and writing  Biopython using Bio.Genbank – reading entries  Using BioALign to perform pairwise and multiple sequence alignment | 15 | CO1-5 |
| 5 | **Basics of R**  Creating vectors, matrix, factors, list, dataframes  Plots – simple –bar, pie, line etc., setting up axis and labels  **Advanced plotting**  GGplot – geom point, jitter, geom bar, geom line.  PCA, heat maps, Clustering  **Data analysis**  Importing Data, Data Frames, Handling Missing Data  **Bioconductor**  Bioconductor packages- bioclite, Biostring  Bioconductor packages – Biomart, protein -protein network graphs  Microarray data analysis – Limma/edgeR/DESEQ2  Microbiome data analysis- vegan/ phyloseq | 15 | CO1-5 |

**BOOKS FOR STUDY**

* Robert Gentleman*, R programming for Bioinformatics*, CRC Press, 2016
* Jason Kinser. *Python for Bioinformatics*. Massachusetts: Jones and Barlett Publishers, 2009
* Arthur Lesk M. *Introduction to Genomics***.** New York: Oxford university press, Third edition, 2017.
* Brown, T. A. *Genomes -3*. USA: John Wiley and Sons inc., 2006.
* Robert Gentleman*, R programming for Bioinformatics*, CRC Press, 2016
* Jason Kinser. *Python for Bioinformatics*. Massachusetts: Jones and Barlett Publishers, 2009

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 2 | 3 | 2 | 1 | 1 | 3 | 2 | 3 | 2 |
| CLO2 | 2 | 3 | 2 | 3 | 2 | 2 | 2 | 3 | 3 |
| CLO3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 |
| CLO4 | 2 | 3 | 3 | 2 | 2 | 3 | 1 | 3 | 2 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 3 |
| Weightage | 12 | 15 | 14 | 12 | 11 | 12 | 10 | 15 | 13 |
| Weighted percentage of Course Contribution to PSOs | 2.4 | 3 | 2.8 | 2.4 | 2.2 | 2.4 | 2 | 3 | 2.6 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) & Understand/ Comprehend (K2) -** Working performance and continuous practice of codes/ scripts/ softwares/ tools

**Application (K3) -** Solve problems/ execute codes/ debugging, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Maintenance of observation book, records, Critique or justify the methods with pros and cons.

**Create (K6) –** Check knowledge in specific or offbeat situations, viva voce.

**SEMESTER – III**

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| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core VIII** | **Molecular Modelling and computer aided drug design** | **4** | **5** | **65** |

## OBJECTIVES OF THE COURSE

* To provide clear concepts on bond angle, bond stretching, bond distance and role of different types of bonds in interactions
* To provide a theoretical background to the various methods of molecular modelling, mechanics and interaction
* To develop and understand the mechanism of drug design using computers

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Interpret the protein structural features, minimise the energy and simulate to attain the stability for its importance in drug action | K1 |
| CO2 | Construct and analyse the molecular dynamics and Monte Carlo simulation methods | K2 |
| CO3 | Compare, categorise and examine the concepts of molecular interactions and QSAR studies | K3 |
| CO4 | Determine the functional disease targets and interpret the target-ligand interactions | K4 |
| CO5 | Apply the knowledge towards design and development of potential lead molecules | K5, K6 |

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| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Molecular Mechanics**  Concepts in Molecular Modeling **-** Molecular Representations, Coordinate Systems, Potential Energy Surfaces, Molecular Mechanics, Force fields - Bond Length, Bond Angle and Torsion Angle potential Non- bonded interactions-Van der Waals and Electrostatic Potential – Hydrogen Bonding Terms | 10 | CO 1-5 |
| 2 | **Energy Minimization Methods**  Energy Minimization- Derivative and Non-Derivative Energy Minimization Methods, Calculation of Simple Thermodynamic Properties, Computer Simulation, Boundaries, Monitoring the Equilibration, Long Range Forces, Analysing the Results of Simulation and Estimating Errors | 15 | CO 1-5 |
| 3 | **Pharmacophores**  Molecular structures, representation – SMILES, InChi keys, Chemical Fingerprint generation, Tanimoto coefficient, Molecular structure similarity and diversity, Molecular Descriptors – 1D, 2D, 3D, 4D, CoMFA, COMSIA, QSAR, 3D QSAR, ADMET prediction, 3D Pharmacophore identification and mapping, Ligand-based and structure based pharmacophores, Chemical libraries, Scaffold hopping | 15 | CO 1-5 |
| 4 | **Molecular Docking**  Drug discovery and development, computational approaches in drug discovery, Structure Based Drug Design - Target Discovery and Validation, Active Site Prediction, Lead identification and Optimization, De Novo Drug Design, Molecular docking and high throughput virtual screening | 15 | CO 1-5 |
| 5 | **Molecular Dynamics and Monte Carlo Simulations**  Molecular Dynamics Using Simple Model, Molecular Dynamics with Continuous Potentials, Molecular Dynamics at Constant Temperature and Pressure, Incorporating Solvent effects into Molecular Dynamics, Conformational Changes from Molecular Dynamics Simulation, Monte Carlo Simulation of Molecules, Calculation of Chemical Potential- Gibbs Ensemble Molecular dynamics of the docked complex using Gromacs/ AMBER/ NAMD | 15 | CO1-5 |
| Self Study | Concepts from ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

## BOOKS FOR STUDY

### N. Claude Cohen. Guidebook on Molecular Modelling In Drug Design. California: Academic Press, 2006.

* Andrew R. Leach. Molecular Modeling: Principles and Applications. USA: Prentice Hall, 2007.
* Daan Frenkel and Berend Smit. Understanding Molecular Simulation: From Algorithms to applications. USA: Academic Press, 2002.
* Claudio N. Cavasotto. In Silico Drug Discovery and Design: Theory, Methods, Challenges, and Applications. USA: Taylor & Francis Group, 2017

#### BOOKS FOR REFERENCE

* Charifson P S. Practical Application of Computer Aided Drug Design. New York:
* Dekker, 1997
* Alan Hinchliffe. Molecular Modelling for Beginners. USA: John Wiley & Sons, 2008
* Sivasamy Ramasamy. Molecular Modeling. India: LAMBERT Academic Publishing, 2015
* Luca Monticelli, Emppu Salonen. Biomolecular Simulations: Methods and Protocols. USA: Humana Press, 2016.

**JOURNALS**

Journal of Molecular Modeling

Journal of Molecular Graphics and Modelling

Journal of Computer-Aided Molecular Design

Current Computer Aided-Drug Design

**WEB SOURCES**

http://accessengineeringlibrary.com/browse/computer-aided-drug-design-and-delivery

systems

http://www.southernresearch.org/life-sciences/lead-discovery-and-optimization/medicinal-

chemistry/computational-chemistry

http://www.ch.ic.ac.uk/local/organic/mod/

http://www.chemcomp.com/MOE-Molecular\_Modeling\_and\_Simulations.htm

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 3 | 3 | 1 | 1 | 2 | 2 | 1 | 3 |
| CLO2 | 2 | 3 | 2 | 3 | 1 | 2 | 2 | 1 | 2 |
| CLO3 | 2 | 3 | 3 | 3 | 2 | 3 | 2 | 3 | 2 |
| CLO4 | 2 | 3 | 2 | 2 | 3 | 3 | 2 | 1 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 |
| Weightage | 12 | 15 | 13 | 12 | 10 | 13 | 10 | 9 | 13 |
| Weighted percentage of Course Contribution to PSOs | 2.4 | 3 | 2.6 | 2.4 | 2 | 2.6 | 2 | 1.8 | 2.6 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core IX** | **Proteomics and metabolomics** | **4** | **5** | **65** |

#### OBJECTIVES OF THE COURSE

* To provide an insight into the complete proteome and metabolome map of Humans.
* To acquaint knowledge on various experimental and computational techniques available for proteomic and metabolomic profiling
* To develop an understanding of the entire protein/metabolome components of a cell through analytical approaches, Data mining and other software tools

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Gain an insight of the basic and advanced concepts and applications of proteomics and metabolomics | K1 |
| CO2 | Understand the mechanisms of integrating proteomics and metabolomic data with the previously learnt omics techniques | K2 |
| CO3 | Apply functional genomics techniques to analyse proteome and metabolome data for biological system | K3 |
| CO4 | Deduce differential abundances in proteome and metabolome during health and disease. | K4 |
| CO5 | Analyse the proteomic and metabolomic interactions in complex disease | K5, K6 |

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| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Proteomics**  Introduction to Proteomics - Proteins structure, Organization of protein structure, structural conformation of proteins, three dimensional structures of proteins, Protein extraction and purification - 1D and 2D-gel electrophoresis (in vitro), Mass Spectrometry - ESI, MALDI, Extraction of proteins from plant sources, Software for Matching MS Data with Specific Protein Sequences, Peptide sequencing by tandem mass spectrometry, Preparative IEF, Protein Digestion Techniques, Protein structure prediction - Elementary Description of Crystallography – Crystal Growth, Data Collection, Structure Solution, Refinement and Interpretation | 12 | CO1-5 |
| 2 | **Computational proteomics**  Protein Structure prediction - Secondary Structure Prediction, Homology modelling, Structure validation tools - Ramachandran Plot, Threading and *ab initio* method, Tools for Structure prediction; Protein structural visualisation; Geometry optimization and Loop refinement, AI based methods- alpha fold, alpha meet.  Proteogenomics - overview, applications and computational resources available. | 12 | CO1-5 |
| 3 | **Protein -protein interactions**  Proteomic interactions - Yeast Two-Hybrid, Mammalian Screen Methods and Co-Immuno Precipitation techniques, Protein-Protein Interactions, chaperones, protein misfolding in diseases and Protein Complexes. Databases and proteomic tools, Post translational modifications, top down and bottom up approaches in proteomics. Data analysis in proteomics, Applications of proteomics in Biomarker discovery, personalised medicine, astrobiology, paleo proteomics | 13 | CO1-5 |
| 4 | **Metabolomics**  Metabolite to metabolome and metabolic reactions, importance of metabolomics and designing a metabolome study. Metabolomic databases and web resources, Experimental methods in metabolome generation-Extraction of plant/bacterial secondary metabolites (in vitro), MS based approaches, targeted and untargeted metabolomics, experimental errors, Metabolomic categories - Lipidomics, glycomics, Fluxomics, metabolic modelling, genome scale metabolic modelling. | 10 | CO1-5 |
| 5 | **Computational Analysis of Metabolomics**  Generation of metabolome data, over representation analysis and disease based enrichment analysis, Statistical analysis in metabolomics – univariate and multivariate analysis, dimensionality reduction and differential abundance of metabolomics. Functional annotation, Softwares and tools for metabolome analysis - Mzime, metabolome analyst, paintomics | 10 | CO1-5 |
| Self study | Concepts from CSIR NET (Lifesciences) and ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

**BOOKS FOR STUDY**

* Lesk Arthur M. *Introduction to Protein Science: Architecture, Function and Genomics*. New York: Oxford university press, 2016
* Pennington S and M. J. Dunn. *Proteomics: From Proteins Sequence to Function*. Germany: Springer Publications, 2001
* Palzkill and Timothy. *Proteomics*. USA: Kluwer Academic Publishers, 2013.
* Daniel C. Leibler. *Introduction to Proteomics: Tools for New Biology***.** USA: Humana Press, 2002**.**
* Srivastava Sudhir. *Informatics in Proteomics*. USA: Taylor & Francis Group, 2005.

**BOOKS FOR REFERENCE**

* Collado Vides Julio and Ralf Hofstadter. *Gene Regulation and Metabolism – Post Genomic Computational Approaches*. India: Ane Books, 2004.
* Dale, Jeremy W and Malcolm von Schantz. *From Genes to Genomes – Concepts and Applications of DNA Technology*. USA: John Wiley and Sons, 2012.
* Griffiths, A.J.F, Miller, J.H, Suzuki, D.T. Lewontin, R. C. and Gelbart, W.M. *An Introduction to Genetic Analysis*. USA: W.H. Freeman, 1996.
* Golemis and Erica. *Protein-Protein Interaction*. USA: CSHL, 2005.

**JOURNALS**

*Genomics, Proteomics & Bioinformatics*

Journal of Data Mining in Genomics & Proteomics

*Human Genomics and Proteomics*

Journal of Proteomics and Genomics

**WEB RESOURCES**

http://www.oncolink.org/resources/article.cfm?id=326

http://www.nature.com/nature/journal/v422/n6928/full/nature01510.html

http://proteomics.cancer.gov/whatisproteomics

http://www.isaaa.org/resources/publications/pocketk/15/default.asp

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 3 | 3 | 2 | 1 | 3 | 2 | 2 | 3 |
| CLO2 | 2 | 3 | 3 | 3 | 2 | 2 | 2 | 2 | 3 |
| CLO3 | 1 | 3 | 3 | 2 | 2 | 3 | 2 | 2 | 3 |
| CLO4 | 2 | 2 | 3 | 1 | 3 | 3 | 2 | 2 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 |
| Weightage | 11 | 13 | 15 | 11 | 11 | 14 | 10 | 10 | 15 |
| Weighted percentage of Course Contribution to PSOs | 2.2 | 2.8 | 3 | 2.2 | 2.2 | 2.8 | 2 | 2 | 3 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

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| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core X** | **Big Data analytics** | **4** | **5** | **65** |

#### OBJECTIVES OF THE COURSE

* To develop a quantitative understanding of how Data Science in Bioinformatics plays a role in the current decade
* To understand the various aspects of data science and applying them in health care
* To obtain adequate knowledge of machine learning approaches

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Collect meaningful values out of big biological data | K1 |
| CO2 | Describe the Big Data landscape including examples of real world big data problems | K2 |
| CO3 | Identify what are and what are not big data problems and be able to recast big data problems as data science questions | K3 |
| CO4 | Apply the skills of Hadoop and spark technology to solve the data science questions | K4 |
| CO5 | Create pipelines for data analysis and reusable methods | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Introduction to Big data**  Characteristics, data structures and data repositories; What is big data? What makes big data valuable Example of Big Data. Where Does Big Data Come From? Machine-Generated Data and Advantages. Characteristics of big data Volume, Variety, Velocity. Characteristics of Big Data – Veracity, Valence and Value. Getting value out of big data using a 5-step process to structure your analysis. | 12 | CO 1-5 |
| 2 | **Big data in healthcare**  Data Science in Biomedicine and Healthcare. Sequence Processing, Medical Image Analysis, Natural Language Processing. Network Modelling and Probabilistic Modelling. Concepts of Hadoop and spark. Introduction to Hadoop systems, The Hadoop Distributed File System: A Storage System for Big Data, YARN: A Resource Manager for Hadoop. MapReduce: Simple Programming for Big Results. Introduction to Spark for big data analysis. Pyspark in solving big data. | 12 | CO 1-5 |
| 3 | **Biological data analysis**  ChIPseq - Introduction and biological theories on ChIPseq analysis. DNA fragment evaluation. Peak identification. Two condition comparison. Saturation analysis. Motif finding and related theories.  ATAC sequencing, Bisulfite sequencing for big biological data. Integrating Multiomics big data. Seqware, distmap, read annotation pipelines. | 15 | CO 1-5 |
| 4 | Computer clustersIntroduction to essential computing, Distributed computing systems. An oversimplified, but useful, view of a computing cluster, Essential Unix/Linux Terminal Knowledge, Clusters, parallel, supercomputers, workstations, HPC.Cluster computing and the job scheduler, High performance computer clustering (HPCC), learning about the resources on HPCC, Getting compute resources allocated to your jobs on an HPCC. Cloud computing - Cloud Primer, Cloud Foundations, containerization, Cloud Security & Migration. Available cloud services – AWS or google cloud. | 10 | CO 1-5 |
| 5 | Workflows and pipelines Introduction to Snake make and next flow**-** installation, rules, directives: input, output, shell, script, target files, fundamental best-practices of bioinformatics pipeline development.  History of containers, what are containers? Containers vs. virtual machines. Docker -Concept of and the difference between Docker & Singularity containers, Git and version control - github learning lab, git cheat sheet and best practices, REST- API. | 13 | CO 1-5 |

**BOOKS FOR STUDY**

* Teschendorff, A. E. (Ed.). (2015). Computational and Statistical Epigenomics. Springer Netherlands.
* Xiong, M. (2017). Big data in omics and imaging: Association analysis. Chapman and Hall/CRC.
* Ye, S. Q. (Ed.). (2016). Big data analysis for bioinformatics and biomedical discoveries. CRC Press

**BOOKS FOR REFERENCE**

* Paul Gerrard and Radia M. Johnson. Mastering Scientific Computing with R. Packt Publishing, UK, 2015.
* P.P. Sinha. Bioinformatics with R Cookbook. Packt Publishing, UK, 2014.
* Mandoiu, I., & Zelikovsky, A. (2016). Computational Methods for Next Generation Sequencing Data 50 Analysis.
* John Wiley & Sons. Peter, D. (2015 ). Introductory statistics with R (2 nd ed.). Springer Science & Business Media.

**JOURNALS**

BMC: Big data Analytics

Journal of Bigdata, Springer  
Big Data Research, Elseiver

**WEBSITES**

<https://hevodata.com/learn/top-21-hadoop-big-data-tools/>

[https://www.cloudxlab.com](https://www.cloudxlab.com/)

[https://www.abinitio.com](https://www.abinitio.com/)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 2 | 3 | 2 | 1 | 2 | 1 | 3 | 3 |
| CLO2 | 3 | 2 | 3 | 3 | 2 | 3 | 1 | 3 | 3 |
| CLO3 | 2 | 3 | 3 | 3 | 1 | 3 | 2 | 3 | 2 |
| CLO4 | 3 | 2 | 3 | 3 | 2 | 3 | 3 | 3 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 3 | 3 |
| Weightage | 12 | 12 | 15 | 14 | 8 | 14 | 10 | 15 | 14 |
| Weighted percentage of Course Contribution to PSOs | 2.2 | 2.2 | 3 | 2.8 | 1.6 | 2.8 | 2 | 3 | 2.8 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core Industry module I** | **Laboratory course Molecular Modelling, computer aided drug design, Proteomics and metabolomics** | **4** | **5** | **65** |

#### OBJECTIVES OF THE COURSE

* To provide practical experience in the analysis of protein sequences
* To understand the use of informatics in drug design and development, finding new targets to treat disease.
* To gain insights on protein-ligand docking and knowledge-based scoring functions

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Understand the mechanics and dynamics of molecules | K1 |
| CO2 | Gain practice in macromolecular simulations and perform research work in the area of computational drug design | K2 |
| CO3 | Extract and analyse the proteomic and metabolomic data experimentally | K3 |
| CO4 | Model the target structures and validate them | K4 |
| CO5 | In silico identification of lead molecules through molecular docking, pharmacophores and molecular dynamics | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Proteomics**  Protein extraction and purification steps, 2D-gel electrophoresis (in vitro), Protein interaction and property calculation –String, Expasy tools.  Protein motif prediction and position weight matrix calculation. Peptide mass fingerprint – Mascot database and Propensity score calculation. Protein structure prediction tools – secondary – Chou fasman and GOR. Homology modelling - Swiss model, Modeller software. Protein structure validation – Rampage, Procheck. Protein protein interaction viewer. | 15 | CO1-5 |
| 2 | **Metabolomics**  Extraction of plant/bacterial secondary metabolites (in vitro), Ligand Search – Pubchem, Drug bank, CHEMBL, ZINC databases, metabolome analyst, paintomics. Chemical drawing package – Marvin Sketch, Chemdraw. ADME prediction – Online tools (Swiss ADME, etc.,). QSAR model prediction – In Silico tools. Pharmacophore mapping. | 10 | CO1-5 |
| 3 | **Molecular Visualisation:** Pymol and Chimera, Pdb file format and Parsing Visualizing a molecule in different representations Identifying interacting residues (protein and ligand interactions) Measuring distances between atoms B-factor visualisation Image tracing and preparation  Geometry Optimization using SwissPdb Viewer Energy Minimization of protein molecule Determining Maxima and Minima energy points | 15 | CO1-5 |
| 4 | Binding Site Identification Different approaches for binding site identification Tools - Cast-P, POCASA, 3D ligand site, Metapocket, Ghecom, Structure based Drug Design Molecular docking using AutoDock vina and pyrx. | 15 | CO1-5 |
| 5 | Molecular dynamics using GROMACS/NAMD/ AMBER | 10 | CO1-5 |

**BOOKS FOR STUDY**

* B.Patwaradhan.2007. Drug discovery and development. New India publishing agency, New Delhi.
* Andrew R. Leach Molecular Modeling: Principles and Applications.
* L.Shargel and A.B.C.Yu.1999. Applied Biopharmaceutics and Pharmacology. McGrawHill, New York.
* Jin Xiong. Essential Bioinformatics. Cambridge University Press.

**BOOKS FOR REFERENCE**

* J.H. Block and J.M. Beale Jr. 2004. Organic medicinal and Pharmaceutical chemistry. Lippincott Williams and Wilkins, New York.
* Rothstein, Pharmacogenomics: Social, ethical and clinical dimensions, Wiley Less.
* D.M. Brown.2004. Drug delivery systems in Cancer therapy. Humana press, Totowa, New Jersey

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 2 | 3 | 2 | 1 | 2 | 3 | 1 | 2 |
| CLO2 | 3 | 2 | 2 | 3 | 2 | 3 | 3 | 1 | 2 |
| CLO3 | 3 | 1 | 3 | 3 | 1 | 3 | 3 | 1 | 2 |
| CLO4 | 3 | 2 | 2 | 1 | 3 | 2 | 3 | 1 | 2 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 1 | 2 |
| Weightage | 15 | 10 | 13 | 1 | 10 | 12 | 15 | 5 | 10 |
| Weighted percentage of Course Contribution to PSOs | 3 | 2 | 2.8 | 2.4 | 2 | 2.2 | 3 | 1 | 2 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) & Understand/ Comprehend (K2) -** Working performance and continuous practice of codes/ scripts/ softwares/ tools

**Application (K3) -** Solve problems/ execute codes/ debugging, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Maintenance of observation book, records, Critique or justify the methods with pros and cons.

**Create (K6) –** Check knowledge in specific or offbeat situations, viva voce.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Skill Enhancement Course II** | **Big data analytics and Computing practical** | **2** | **3** | **39** |

(This Practical paper can be modified as per the Institute’s infrastructure availability)

#### OBJECTIVES OF THE COURSE

* To provide students with the basic knowledge of computing resources and biological data handling.
* To facilitate the students to attain skills in working with cluster computing, command line based tools, sequence matching and appreciate its various biomedical applications.

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Learn to install bioinformatics packages in linux | K1 |
| CO2 | Develop command line programming skills in linux | K2 |
| CO3 | Create pipelines for data analysis and reusable methods | K3 |
| CO4 | Justify the uses of HPC and cluster computers | K4 |
| CO5 | Appreciate the ML based methods in biological data handling | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | Linux  Installation of bioinformatics packages – anaconda/ jupyter notebooks/RDkit/ Qiime.  Linux and shell commands for cluster computing - *man, sinfo, cat, sbatch, squeue,*  Submitting jobs and job scheduler | 8 | CO 1-5 |
| 2 | Exploratory big data analysis with pandas  Chip seq data analysis  Using Spark to analyse big data (Pyspark python package)  (Additional topics can be included) | 10 | CO 1-5 |
| 3 | Locate and download files for data analysis involving genes and medicine. Open files and preprocess data. Write R/python scripts to replace missing values, normalise data, discretize data, and sample data. Select features from highly dimensional datasets. Evaluate the performance of feature selection methods | 7 | CO 1-5 |
| 4 | Creating confusion matrix (Python or R Packages or Weka can be used)  ROC curves  Supervised algorithm - K- means clustering  Unsupervised algorithm -Random forest  (Topics can be modified) | 7 | CO 1-5 |
| 5 | Containers and workflow for reproducible research – snake make/ nextflow/knime  Using dockers/ git/version control | 7 | CO 1-5 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 2 | 3 | 2 | 1 | 2 | 3 | 1 | 2 |
| CLO2 | 3 | 2 | 2 | 3 | 2 | 3 | 3 | 1 | 2 |
| CLO3 | 3 | 1 | 3 | 3 | 1 | 3 | 3 | 1 | 2 |
| CLO4 | 3 | 2 | 2 | 1 | 3 | 2 | 3 | 1 | 2 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 1 | 2 |
| Weightage | 15 | 10 | 13 | 1 | 10 | 12 | 15 | 5 | 10 |
| Weighted percentage of Course Contribution to PSOs | 3 | 2 | 2.8 | 2.4 | 2 | 2.2 | 3 | 1 | 2 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) &Understand/ Comprehend (K2) -** Working performance and continuous practice of codes/ scripts/ softwares/ tools

**Application (K3) -** Solve problems/ execute codes/ debugging, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Maintenance of observation book, records, Critique or justify the methods with pros and cons.

**Create (K6) –** Check knowledge in specific or offbeat situations, viva voce.

**SEMESTER – IV**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core XI** | **Database management systems** | **4** | **5** | **65** |

## OBJECTIVES OF THE COURSE

* To introduce the basic concepts of Relational Database Management System and Client / Server Environment
* To be trained in designing databases and manipulating them for biological applications
* To understand the working knowledge of Linux environment and databases

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Learn the database formats and types | K1 |
| CO2 | Understand data models and schemas in DBMS | K2 |
| CO3 | Create, update, retrieve and Manage data to develop databases | K3 |
| CO4 | Determine the problems of Atomicity, Consistency, Isolation, and Durability | K4 |
| CO5 | Apply the knowledge towards the usage of SQLanguage and appreciate the differences between RDBMS, NoSQL databases. | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Introduction to Database Systems - SQL query**  Introduction to File and Database systems- Record Storage And Primary File Organization- Secondary Storage Devices- Operations on Files- Heap File- Sorted Files- Hashing Techniques – Index Structure For Files –Different Types Of Indexes- B-Tree - B+Tree.  Database System Structure, Data Models, database schemas. Database Normalisation and denormalization for Relational Databases (up to BCNF) . | 15 | CO 1-5 |
| 2 | **SQL - Practical component included**  Data Definition Language, Data Manipulation Language, Transaction Control and Data Control Language Grant and Revoke Privilege Command. Set Operators, Joins-Kinds of Joins, Table Aliases, Sub queries, Multiple and Correlated Sub Queries. Functions-Single Row, Date, Character, Numeric, Conversion, Group Functions. Constraints-Domain, Equity, Referential Integrity Constraints  (All SQL concepts - both theory and Practice) | 15 | CO 1-5 |
| 3 | **RDBMS**  Text and Multimedia Databases - Basic Concepts and Applications, Types of DBMS-Network, object oriented, graph based. Overview of RDBMs, Advantages of RDBMs Over DBMs. Establishing relations between tables. Entity relationship concepts. Keys in linking relational databases - primary, foreign, super, candidate keys. | 15 | CO 1-5 |
| 4 | **No SQL databases**  Brief history of No SQL databases. Features of No SQL, differences and advantages of No SQL over RDBMS. Types and misconceptions in No SQL databases. No SQL vs SQL. | 10 | CO 1-5 |
| 5 | **Recent trends in databases**  MongoDB, web development with MongoDB, install MongoDB, shell commands. How can you store a DNA sequence using MongoDB? Role of MongoDB in 1000 genomes projects, MongoDB or Redis for biomedical data. Database file formats- JSON, BSON, Creating uniprot mongodb, querying and retrieving protein sequences. | 10 | CO 1-5 |
| Self study | Concepts for ASRB - NET Bioinformatics related to DBMS to be discussed and taught | 5 |  |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 3 | 3 | 1 | 1 | 3 | 1 | 3 | 2 |
| CLO2 | 2 | 2 | 2 | 1 | 1 | 3 | 1 | 3 | 2 |
| CLO3 | 2 | 3 | 3 | 2 | 2 | 3 | 1 | 3 | 2 |
| CLO4 | 2 | 2 | 2 | 2 | 2 | 3 | 1 | 3 | 2 |
| CLO5 | 2 | 2 | 3 | 3 | 2 | 3 | 1 | 3 | 2 |
| Weightage | 9 | 12 | 13 | 9 | 8 | 15 | 5 | 15 | 10 |
| Weighted percentage of Course Contribution to PSOs | 1.8 | 2.2 | 2.6 | 1.8 | 1.6 | 3 | 1 | 3 | 2 |

**BOOKS FOR STUDY**

* Ramakrishnan Raghu and Gehrke Johannes. *Database Management Systems***,** USA: McGraw–Hill, 2003

**BOOKS FOR REFERENCE**

* George Koch and Kevin Loney.*Oracle 8 - The Complete Reference***,** USA: Tata McGraw – Hill, 2000.
* Kyte, Thomas. *Expert Oracle Database Architecture- 9i and 10g Programming Techniques and Solutions*. USA: Berkeley press, 2006.
* Michael Abbey and Michael J. Correy.*Oracle 8i - A Beginners Guide.* USA :McGraw-Hill, 1999.

**JOURNALS**

International Journal of Database Management Systems

Journal of Database Management

Journal of Advanced Database Management & Systems

International Journal of Intelligent Information and Database Systems

**WEB RESOURCES**

www.oracle.com/technetwork/oem/db-mgmt/db-mgmt-093445.html

http://education-portal.com/academy/lesson/what-is-a-database-management-system-

purpose-and-function.html

www.odbms.org/

http://www.comptechdoc.org/os/linux/usersguide/linux\_ugbasics.html

http://www.dummies.com/how-to/content/common-linux-commands.html

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core XII** | **Computational Biology** | **4** | **5** | **65** |

#### OBJECTIVES OF THE COURSE

* To provide students with the basic knowledge of algorithms, computational biology and their advances in biology.
* To facilitate the students to attain skills in solving biological problems with algorithms, computational biology, sequence matching and learn its various biomedical applications.

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Understand the working of bioinformatics algorithms | K1 |
| CO2 | Describe the divide-and-conquer paradigm and explain when an algorithmic design situation calls for it. | K2 |
| CO3 | Apply the algorithms and design techniques to solve problems | K3 |
| CO4 | Employ the important algorithmic design paradigms and methods of biomedical data analysis. | K4 |
| CO5 | Solve current biological research problems using computational approaches | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Introduction**  Algorithms and Complexity. Definition, Biological Algorithms versus Computer Algorithms, Fast versus Slow Algorithms Big-O Notation. Algorithm Design Techniques Exhaustive Search Branch-and-Bound Algorithms Greedy Algorithms. Dynamic Programming Divide-and-Conquer Algorithms Machine Learning Randomised Algorithms. Linear and non linear algorithms, stack, queries, linked list. | 12 | CO1-5 |
| 2 | **Sequence Alignment**  Longest Common Subsequences - Global Sequence Alignment- Local Sequence Alignment. Graph Algorithms- Graphs and Genetics- DNA Sequencing Shortest Superstring Problem. DNA Arrays as an Alternative Sequencing Technique. Sequencing by Hybridization | 12 | CO1-5 |
| 3 | **Clustering**  Gene Expression Analysis. Hierarchical Clustering -k-Means Clustering- Clustering and Corrupted Cliques. Evolutionary Trees - Distance-Based Tree Reconstruction Reconstructing Trees from Additive Matrices. | 10 | CO1-5 |
| 4 | Evolutionary Trees and Character-Based Tree Reconstruction, Keyword Trees and Suffix Trees. Querying a Binary search tree, Insertion and Deletion, Tree Traversals, AVL-Trees, Rotations, Insertion, Deletion, B-trees. | 10 | CO1-5 |
| 5 | Heuristic Similarity Search Algorithms. Regulatory Motifs in DNA Sequences Profiles: The Motif Finding Problem Search Trees, String matching algorithm. Bayesian method, progressive method, Markov chain model, Hidden Markov Models and Kernel methods. | 13 | CO1-5 |
| Self study | Concepts from ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

**BOOKS FOR STUDY**

Fundamentals of Algorithms by E. Horowitz and S. Sahani., Galgotia Book source Pvt. Ltd. 1999.

Introduction to Algorithms, Cormen, Thomas H.; Leiserson, Charles E.; Rivest, Ronald L.; Stein, Clifford (2009) [1990], MIT Press and McGraw-Hill, 2016

**BOOKS FOR REFERENCE**

Data Structures by Seymour Lipschutz., Tata Mc-Graw-Hill publication. 2007 2. Introduction to Algorithms (3rd Ed.) by T .H. Cormen, C. E. Leiserson, R .L. Rivest., The MIT Press. 2007

**JOURNALS**

# Algorithms for Molecular Biology

# Journal of Computational Intelligence in Bioinformatics

# International Journal of Bioinformatics Research and Applications

Developments in Bioinformatics Algorithms

**WEB RESOURCES**

http://www.comp.nus.edu.sg/~ksung/algo\_in\_bioinfo/

http://bioinformaticsalgorithms.com/

http://bix.ucsd.edu/bioalgorithms/presentations/Ch08\_GraphsDNAseq.pdf

http://www.ait-budapest.com/advanced-algorithms-for-bioinformatics

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 2 | 1 | 1 | 2 | 3 | 2 | 3 | 2 |
| CLO2 | 2 | 3 | 3 | 2 | 1 | 3 | 2 | 3 | 3 |
| CLO3 | 3 | 3 | 3 | 2 | 2 | 3 | 2 | 3 | 3 |
| CLO4 | 3 | 3 | 3 | 2 | 2 | 3 | 2 | 3 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 2 | 3 | 2 | 3 | 3 |
| Weightage | 12 | 14 | 14 | 10 | 9 | 15 | 10 | 15 | 14 |
| Weighted percentage of Course Contribution to PSOs | 2.2 | 2.8 | 2.8 | 2 | 1.8 | 3 | 2 | 3 | 2.8 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Core XIII** | **Machine Learning, Deep learning and Artificial intelligence** | **4** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To provide an insight in discovering pattern in the data and to make predictions as well as to intricate patterns for solving healthcare problems
* To identify objects from large datasets and to perform complex tasks with increasing accuracy
* To identify the precise 3D geometry of biological molecules and enhance the ability of biological research for better disease diagnosis

**COURSE LEARNING OUTCOMES**

On successful completion of the course, students will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Demonstrate the fundamental knowledge on concepts of machine learning, deep learning and artificial intelligence | K1 |
| CO2 | Utilise the different libraries available to understand the fundamental prerequisite for ML, DL and AI | K2 |
| CO3 | Identify the right method of classification and clustering analysis specific for the datasets | K3 |
| CO4 | Enable to build a model and examine their performance using various statistical methods by training and testing | K4 |
| CO5 | Apply the ML, DL and AI concepts to solve problems in biology and medicine | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **History and evolution**  Different Forms–statistics, data mining, data analysis, data science, Statistics vs. Data Mining vs. Data Analytics vs. Data Science. Similarities and Differences between Machine learning, Deep learning and Artificial intelligence, Machine Learning perspectives of data–Scales of Measurement, data imputation, dealing with missing data, normalising data, feature generation, Machine Learning Categories-supervised, unsupervised, reinforcement learning | 10 | CO1-5 |
| 2 | **Machine learning**  Exploratory data analysis –multivariate and univariate analysis, Supervised Learning– Regression – correlation and causation, Supervised Learning – Classification, ROC curve, Evaluating a Classification Model Performance, SVM, SOM and KNN, Unsupervised learning – K means, Hierarchical and random forest, evaluation – cross fold K validation. | 15 | CO1-5 |
| 3 | **Building and evaluating model**  Ensemble methods- bragging, boosting, Ensemble voting, stacking, Text mining, data assemble, Data Preprocessing (Text) - Convert to LowerCase and Tokenize, Removing Noise, Part of Speech (PoS) Tagging, Stemming, Lemmatization, N-grams, Bag of Words (BoW), Term Frequency-Inverse Document Frequency (TF-IDF), Data Exploration, model building and evaluation | 15 | CO1-5 |
| 4 | **Deep and Reinforcement Learning**  Artificial Neural Network (ANN) What Goes Behind, When Computers Look at an Image, Perceptron–Single Artificial Neuron, Multilayer Perceptrons (Feedforward Neural Network). Restricted Boltzmann Machines (RBM), MLP Using Keras, tensor flow, Autoencoders, Convolution Neural Network (CNN), Recurrent Neural Network (RNN), Long Short-Term Memory(LSTM), Transfer Learning and Reinforcement Learning, challenges and future perspectives of DL | 10 | CO1-5 |
| 5 | **Artificial intelligence**  AI and Bioinformatics, applications and methods of AI in genome sequencing, protein homology modelling and structure prediction, AI in drug discovery and drug repurposing, Natural language processing, AI in multiomics integration, medical imaging and diagnosis, AI in healthcare and personalised medicine, Innovations in Biology with AI- deep variant, deep mind, atom wise, cell profile, ChatGPT, Future directions of AI in healthcare. ICMR guidelines on using AI for healthcare | 10 | CO1-5 |
| Self study | Concepts from ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

**BOOKS FOR STUDY**

# Stuart Russel and Peter Norvig, Artificial Intelligence: A Modern Approach (Prentice Hall Series in Artificial Intelligence), 4th Eds., 2010.

* Michael Bowels, Machine Learning in Python: Essential Techniques for Predictive Analysis, Wiley publications, 2015

# Andreas Muller, Introduction to Machine Learning with Python a guide for data scientists, 2016

* François Chollet, Deep Learning with Python, 2nd eds., Manning publications, 2021

**BOOKS FOR REFERENCE:**

# Aurélien Géron, Hands-On Machine Learning with Scikit-Learn, Keras, and TensorFlow: Concepts, Tools, and Techniques to Build Intelligent Systems, Third Edition, 2022

* John Patterson, Deep Learning: A Practitioner's Approach (Greyscale Indian Edition), 2017

# Seth Weidman, Deep Learning from Scratch: Building with Python from First Principles, O’Reilly, 2019.

* Ian Goodfellow, Yoshua Bengio and Aaron Courville, Deep Learning, MIT Press, 2016

**JOURNALS**

Journal of Machine Learning Research

Journal of Artificial Intelligence Research

Applied Artificial Intelligence

International Journal on Artificial Intelligence Tools

**WEB RESOURCES**

https://www.futurelearn.com/courses/artificial-intelligence-in-bioinformatics

https://towardsdatascience.com/ai-in-bioinformatics-a1acdc3cdd89#:~:text=AI%20in20bioinformatics%20includes%20both,as%20well%20as%20complex%20systems.

https://addepto.com/blog/the-role-of-machine-learning-in-bioinformatics-and-biology/

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 2 | 1 | 1 | 1 | 3 | 1 | 3 | 2 |
| CLO2 | 2 | 2 | 2 | 2 | 2 | 3 | 1 | 3 | 2 |
| CLO3 | 2 | 3 | 3 | 3 | 2 | 3 | 1 | 3 | 3 |
| CLO4 | 3 | 3 | 3 | 2 | 2 | 3 | 1 | 3 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 3 |
| Weightage | 11 | 13 | 12 | 11 | 10 | 15 | 6 | 15 | 13 |
| Weighted percentage of Course Contribution to PSOs | 2.2 | 2.8 | 3 | 2.2 | 2 | 3 | 1.2 | 3 | 2.6 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

**DEPARTMENT SPECIFIC ELECTIVE COURSES**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective I** | **Biomathematics and biostatistics** | **3** | **5** | **65** |

# **OBJECTIVES OF THE COURSE**

* To enhance the skills in mathematics those are essential for learning Bioinformatics
* To understand and implement various mathematical techniques being applied in analysing information of biological data
* To understand statistical methods in its several forms is the basis of biological research
* To introduce the various statistical techniques useful for handling quantitative data

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Understand the importance of mathematics for research based problems | K1 |
| CO2 | Apply the different statistical tests for the research | K2 |
| CO3 | Learn to solve aptitude based problems in competitive exams | K3 |
| CO4 | Gain skills on solving the population genetics equations | K4 |
| CO5 | Apply the regression and correlation techniques to interpret Drug activity based on QSAR | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Set Theory and Vectors**  Introduction, Representation of a Set, Set Operations - Types of Sets, Subsets, Complement of Sets, Union and Intersection of Sets, Difference of Sets, De Morgan’s Law, Venn diagram, Cartesian Product of Sets, Vectors Additions, Subtraction, Dot, Cross, Magnitude, Scalar Triple Product. | 15 | CO1-5 |
| 2 | **Matrices, Relations and Functions**  Matrix, Basic Operations, Transpose, Square matrices, Non Singular Matrices, Inverse of a Matrix, Determinants, Elementary Applications, Relations and Functions - Linear Function, Polynomials and Differences | 10 | CO1-5 |
| 3 | **Probability**  Rules of probability, Theorems of probability, Addition and Multiplication Theorem, Probability distributions: Binomial distribution, Poisson distribution, Normal distribution, Binomial Coefficient, Permutations, Combinations, Identities Applications. | 10 | CO1-5 |
| 4 | Introduction to Biostatistics Scope, collection, classification and tabulation, Graphical representation of data- measures of location and dispersion -Diagrammatic and Graphical Presentation of data, Types of data, Frequency distribution: Discrete and continuous frequency distribution. Mean-Median- Mode, Measures of dispersion- Standard Deviation, Coefficient of variation, Range | 12 | CO1-5 |
| 5 | **Application and Testing**  Sampling techniques, Sampling Distribution, Standard error, testing of hypotheses, Null Hypothesis, Correlation - Types of Correlation-Simple, Linear and Nonlinear- Pearson’s Coefficient Correlation, Regression analysis- Types of Regression, Regression Equations.  c2 test, t-test, Analysis of Variance (ANOVA), Population Genetics: Hardy-Weinberg principle. | 13 | CO1-5 |
| Self study | Concepts from CSIR- NET (lifesciences) and ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

**BOOKS FOR STUDY**

* Jae K.Lee, Statistical Bioinformatics for Biomedical and Life Science Researchers, John Wiley & Sons Publications, USA, 2010
* Rao P. S. S. Sundar, Introduction To Biostatistics And Research Methods, Prentice Hall, India, 2009.
* Veer Bala Rastogi, Fundamentals of Biostatistics, Ane Books Pvt Ltd, New Delhi, 2010.
* Basu, A.K., (2003), Introduction to Stochastic Process, Narosa Publishing House, New Delhi, India
* Gurumani, N., (2004), An Introduction to Biostatistics, M.J. P. Publishers, Chennai,India.
* Lipschutz S. and Lipson, M.L. Discrete Mathematics, New York: McGraw Hill Book Company, 2001.
* Narayanan S. and Manicavachagam Pillay, T. K., Ancillary Mathematics- Book II, India: S. Viswanathan Printers and Publishers, 2002.
* Negi, K.S., Biostatistics, AITBS Publishers and Distributors, New Delhi, India. 2002

**BOOKS FOR REFERENCE**

* Vittal, P.R. Allied Mathematics, India: Margham Publishers, 2001.
* Papoulis, Athanasios and S. Unnikrishnan Pillai, Probability, Random Variables and Stochastic Processes, (4th Ed.) Tata McGraw Hill Pub. Co. India. 2002
* J. Richard, Sundar P. S. S. Rao, An Introduction To Biostatistics: A Manual For Students In Health Sciences, 3rd Edn, Prentice Hall, India. 2004
* Bernard Rosner, Fundamentals of Biostatistics, Duxbury Press, USA. 2010
* B. Antonisamy, Solomon Christopher, P. Prasanna Samuel. Biostatistics: principles and practice, Tata McGraw Hill Pub. Co. India. 2010

**JOURNALS**

The Journal of Mathematical Behavior

Mathematical Journals

The College Mathematics Journal

International Journal of Mathematics and Statistics Studies

**WEBSITES**

http://mathworld.wolfram.com/Integral.html

http://www-math.mit.edu/~djk/calculus\_beginners/

http://mathworld.wolfram.com/Probability.html

https://www.math.hmc.edu/calculus/tutorials/matrixalgebra/

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 1 | 3 | 2 | 1 | 3 | 3 | 1 | 3 |
| CLO2 | 2 | 3 | 3 | 3 | 2 | 3 | 3 | 1 | 3 |
| CLO3 | 2 | 3 | 3 | 3 | 2 | 3 | 3 | 1 | 2 |
| CLO4 | 2 | 2 | 3 | 2 | 3 | 3 | 3 | 2 | 3 |
| CLO5 | 2 | 1 | 2 | 2 | 3 | 3 | 3 | 2 | 3 |
| Weightage | 11 | 10 | 14 | 12 | 11 | 15 | 15 | 7 | 14 |
| Weighted percentage of course contribution to PSOs | 2.2 | 2 | 2.8 | 2.4 | 2.2 | 3 | 3 | 1.4 | 2.8 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective II** | **Structural Bioinformatics** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To develop new ways for analysing biological macromolecular data in order to address biological problems and discover new information
* To understand the factors that influence and determine the function of biological macromolecules
* To create general-purpose methods for manipulating information about biological macromolecules and the application of these methods to solve problems in biology

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Recognize the fundamental structural and functional concepts of DNA and RNA molecules | K1 |
| CO2 | Demonstrate the relativity and mechanisms of DNA molecules with protein molecules | K2 |
| CO3 | Utilise the knowledge on the structure and properties of protein molecules and identify them computationally using variety of tools | K3 |
| CO4 | Infer the functions, similarity, structural properties and their interactions in complex with other biological molecules using bioinformatics tools and databases | K4 |
| CO5 | Measure the importance of peptides to proteins in the body functions and apply for solving biological problems | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **Unit** | **Contents** | **Hrs** | **CO1** |
| 1 | **Introduction**  Introduction to Molecular structures including genes and gene products: protein, DNA, and RNA structure. structure representation, comparison of structures, visualisation, and modelling, DNA sequence and structures- complementarity, Chargaff’s rule, other base pairs in sequence, reverse complementarity, palindromic sequences, RNA sequences, types and structures – mRNA, tRNA, rRNA, miRNA, siRNA, circRNA, lncRNA, sg RNAs | 10 | CO 1-5 |
| 2 | **Nucleic acids**  DNA – chromosome structure and architecture, Intron-exon boundary, histones, euchromatin, heterochromatin, CpG islands, methylated DNA structures, Computational Structure prediction –RNA Structure determination methods, RNA structural refinement, predicting targets for inhibitory RNAs, Reading frames; Codon Usage analysis; Translational and transcriptional signals, Splice site identification, Gene prediction methods and RNA fold analysis | 10 | CO1-5 |
| 3 | **Proteins**  Protein sequences and structure fundamentals, Amino acids – types, single letter codes, essential and non-essential amino acids, Protein sequence analysis-Compositional analysis, Hydrophobicity profiles, Amphiphilicity detection, Moment analysis, Transmembrane prediction methods, Protein function prediction, motifs and domains, predicting binding site geometry and evolution. Patterns and fingerprints. Point based and surface based binding site matching,    Pattern based search using MeMe and PRATT); Motif-based search using ScanProsite and eMOTIF; Profile-based database searches using PSI-BLAST and HMMer. | 15 | CO1-5 |
| 4 | **Structural Properties of Proteins**  Protein structure determination - Secondary structure prediction methods – Chou fasman and GOR, tertiary structure prediction - ab initio modelling, threading, fold recognition, Protein-protein and protein-nucleic acid interactions, Protein structure refinement, comparison of structures. Prediction of Coiled coils, Low complexity, non-globular, and disordered regions, Contact prediction, Alternative splicing and protein structure, Target selection for diseases, CATH and SCOP, identification of Extreme environments, Protein-protein interactions, Protein evolution, Structure-function relationships in proteins, Functionally important residues, Local sequence motifs, Exons and domains, Mutations and their effect on structures | 15 | CO1-5 |
| 5 | **Peptides and Proteogenomics**  Peptide modelling - Signal peptides, natural peptides, Proteome - peptide repositories – PRIDE DB, peptide modelling, epitope and antibody structures, Peptide- protein docking, Databases and tools for identifying protein- peptide interactions, network analysis, Tools and softwares to predict protein-protein and protein-peptide interactions. Protein complex modelling approaches, Proteogenomics - Proteogenomics overview, Phenotype- Genotype, Gene expression, Proteogenomics approach to unravel proteoforms, Sequence centric proteogenomics, ProTIGY. | 15 | CO1-5 |
| Self study | Concepts from CSIR NET (Lifesciences) and ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

**BOOKS FOR STUDY**

Jenny Gu, Philip E. Bourne, Structural Bioinformatics, 2nd Ed., 2009. ISBN: 978-0-470-18105-8

**BOOKS FOR REFERENCE**

Zoltan Gaspari, Structural Bioinformatics, Methods and Protocols, Springer publication, 2020.

Forbes J. Burkowski, Structural Bioinformatics An algorithmic approach, 2009. Taylor and Francis Publication.

**JOURNALS**

Journal of Structural Biology

BMC Structural Biology

Computational and Structural Biotechnology Journal

Journal of Molecular Biology

**WEBSITES**

<https://ball-project.org/ballaxy/>

<https://bio.tools/bioinfo3d>

<https://computomics.com/services/megan6.html>

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 2 | 1 | 2 | 2 | 3 | 2 | 1 | 3 |
| CLO2 | 2 | 2 | 1 | 1 | 1 | 3 | 1 | 1 | 3 |
| CLO3 | 3 | 2 | 3 | 3 | 2 | 3 | 3 | 1 | 3 |
| CLO4 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 1 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 1 | 3 |
| Weightage | 12 | 12 | 11 | 12 | 11 | 15 | 12 | 5 | 15 |
| Weighted percentage of course contribution to PSOs | 2.4 | 2.4 | 2.2 | 2.4 | 2.2 | 3 | 2.4 | 1 | 3 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective III** | **Data warehouse and Data mining** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To provide an insight to Data mining
* To introduce the techniques used in data mining
* To understand these techniques in collecting and sorting of data

**Course Learning outcomes**

On successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Understand data mining principles and techniques for a cutting edge business intelligence method and acquaintance. | K1 |
| CO2 | Understand concepts of Data warehousing, components of data warehousing and design schemas | K2 |
| CO3 | Gain insight into the field of Bioinformatics from theoretical models to finished software | K3 |
| CO4 | Integrate existing tools to create productive information environment for bioinformatics practice | K4 |
| CO5 | Measure how open source can be powerful in creating web-based applications in Bioinformatics | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **Unit** | **Contents** | **Hrs** | **CO1** |
| 1 | **Concepts**  Need for data warehousing, Basic elements of data warehousing, Planning and Requirements: Project planning and management, Collecting the requirements. Architecture and Infrastructure: Architectural components, Infrastructure and metadata. | 15 | CO1-5 |
| 2 | **Data Design And Data Representation**  Principles of dimensional modeling, Dimensional modeling advanced topics, data extraction, transformation and loading, data quality. Information Access and Delivery: Matching information to classes of users, OLAP in data warehouse, Data warehousing and the web. Implementation and Maintenance: Physical design process, data warehouse deployment, growth and maintenance. | 10 | CO1-5 |
| 3 | **Data mining Introduction**  Classification of data, Relational databases. Data warehouses. Transactional databases. Advanced database systems and advanced database applications. Data mining functionalities. Concept /class description. Characterization and discrimination. Association analysis. Knowledge Discovery: KDD Process. Web Mining: Web Content Mining, Web Structure Mining, Web Usage mining | 15 | CO1-5 |
| 4 | **Data Processing**  Data Preprocessing. Data integration and transformation, Data reduction. Association rule mining.  The Apriori algorithm: Finding frequent item sets from association mining to correlation analysis. Classification and Prediction Classification by backpropagation association-based classification and other classification methods | 10 | CO1-5 |
| 5 | **Advanced Topics**  Spatial mining, temporal mining. Visualisation: Data generalisation and summarization-based characterization, Analytical characterization: analysis of attribute relevance, mining class comparisons: Discriminating between different classes, mining descriptive statistical measures in large databases Data Mining Primitives, Languages, and System Architectures: Data mining primitives, Query language, Designing GUI based on a data mining query language. | 10 | CO1-5 |
| Self study | Concepts from ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

**BOOKS FOR STUDY**

* Jiawei Han and Micheline Kamber. *Data Mining: Concepts and Techniques*, USA: Morgan Kaufmann Publishers, 2011.
* Hu, X., & Pan, Y. (Eds.). (2007). Knowledge discovery in bioinformatics: techniques, methods, and applications (Vol. 5). John Wiley & Sons.
* Inmon, W. H. (2005). Building the data warehouse. John wiley & sons. Mallach Efrem, G. (2002). Decision Support and Data Warehouse System. Tata McGrawHill, 424- 456.
* Ross, M., & Kimball, R. (2013). The data warehouse toolkit: the complete guide to dimensional 45 modeling. Wiley

**Books for reference**

* Berry, M. W., & Kogan, J. (Eds.). (2010). Text mining: applications and theory. John Wiley & Sons.
* Dunham, M.H. (2006). Data Mining Introductory and Advanced Topics. Pearson Education. Feldman, R & Sanger, J. (2007). The Text Mining Handbook: Advanced approaches in analyzing unstructured data. Cambridge University Press.
* Han, J., Kamber, M., & Pei, J. (2011). Data mining concepts and techniques third edition. The Morgan Kaufmann Series in Data Management Systems, 83-124.

**JOURNALS**

# Data Mining in Bioinformatics

International Journal of Data Mining and Bioinformatics

**WEB RESOURCES**

http://www.bioinformaticszen.com/post/an-introduction-to-data-mining-in-bioinformatics/

http://biit.cs.ut.ee/

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 2 | 3 | 1 | 1 | 3 | 2 | 3 | 1 |
| CLO2 | 1 | 3 | 1 | 2 | 1 | 3 | 1 | 2 | 3 |
| CLO3 | 3 | 2 | 2 | 3 | 3 | 3 | 3 | 2 | 1 |
| CLO4 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 2 |
| CLO5 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 2 | 3 |
| Weightage | 11 | 13 | 12 | 12 | 10 | 15 | 12 | 5 | 10 |
| Weighted percentage of course contribution to PSOs | 2.2 | 2.6 | 2.4 | 2.4 | 2 | 3 | 2.4 | 1 | 2 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective IV** | **Research methodology, IPR and Bioethics** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To describe and express the role and importance of research in basic and applied sciences
* To facilitate writing of research proposals / projects and apply for grants in the field of bioinformatics
* To understand the analytical tests to be applied for research

**COURSE LEARNING OUTCOMES**

On successful completion of the course, students will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Better understanding of the research methods | K1 |
| CO2 | Design an action plan of research | K2 |
| CO3 | Acquire skills of writing a research manuscript | K3 |
| CO4 | Application of statistical study in research | K4 |
| CO5 | Understand the ethics in writing research work | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Types of Data and research problem identification**  Data Collection, Sources of Data- Primary, Secondary and Tertiary Sources, Sampling Methods- Probability and non-probability methods, Sample size and Sampling error, Definition of Research, Types of research, Research Methodology, Principles and Practice of Research, Identifying The Research Problem, Research Design: Exploratory, Descriptive and Experimental Research Design | 10 | CO 1-5 |
| 2 | **Scientific Communication**  Literature Review - Its Relevance and Importance in Directing Research. Citations – Types of Citations, Bibliography and End Matters, Editing and Proofreading, Action Plan, Design and Pilot Study Undertaking a Research Project, Writing a Research grant Proposal, Format of thesis, Scholarly Communication: IMRaD concepts for papers, and Poster and Oral Presentation, the Purpose and the Methods of Paper Critiquing. | 15 | CO 1-5 |
| 3 | **Writing well**  Writing for non- native audiences, usage of simple sentences, untangle long noun phrases, make complete sentences, Use of punctuations- comma, colon, semicolon, dash and periods, Creating non-textual information- acquiring, processing and printing illustrations. Concepts of mind maps. Use of Encyclopedias, Research Guides, Handbook etc., Academic Databases for Computer Science Discipline, Use of tools / techniques for Research: methods to search required information effectively, Reference Management Software like Zotero/ Mendeley, Software for paper formatting like LaTeX/MS Office, Software for detection of Plagiarism | 15 | CO 1-5 |
| 4 | **Bioethics**  Introduction. Intellectual Property Rights (IPR) and Patents, TRIPS, Case studies on Patents (Basmati, Turmeric and Neem), ethics in science practicals, Plagiarism and Common Errors in Scientific Writing. Misconduct in science. Ethical issues related to embryonic stem cells, Genetic testing and screening, human clinical trials and drug testing. | 15 | CO 1-5 |
| 5 | **IPR, Patent, copyrights and trademarks**  Introduction of IPR, General Agreement on Trade and Tariff (GATT) and World Trade Organizations. Establishment and functions of GATT, World Trade Organization (WTO) and World International Property Organization (WIPO). WTO Summits, Role of Integrated Business Solution Center (IBSC) and Review Committee on Genetic Manipulation (RCGM), Production of Plant variety and farmers right act. TRIPS, Different types of intellectual property rights (IPR), Patents, Trade mark, Trade secret copyright, Geographical distribution on biological diversity, Obligations, Production of Traditional Knowledge, Impact of GM Crops and GM Foods. | 10 | CO 1-5 |

**BOOKS FOR STUDY**

### Gopalan, R. Thesis Writing. India: Vijay Nicole Imprints Private Limited, 2005.

* Gurumani, N. Research Methodology for Biological Sciences. India MJ Publishers, 2010.

**BOOKS FOR REFERENCE:**

* Pence, G.E. Classic Cases in Medical Ethics.India: McGraw-Hill, 2004.
* Kothari C R. Research Methodology, Methods and Techniques. India: Wishwa Prakashan, 2009

**JOURNALS**

The Journal of Communication

International Association for Media and Communication Research

Indian Journal of Science Communication

**WEB RESOURCES**

http://www.palgrave.com/studentstudyskills/page/choosing-appropriate-researchmethodologies/

https://explorable.com/research-methodology

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 3 | 2 | 2 | 1 | 3 | 3 | 1 | 3 |
| CLO2 | 2 | 3 | 3 | 3 | 2 | 3 | 3 | 1 | 3 |
| CLO3 | 2 | 3 | 2 | 3 | 2 | 3 | 3 | 1 | 3 |
| CLO4 | 1 | 2 | 3 | 3 | 2 | 3 | 3 | 1 | 3 |
| CLO5 | 3 | 2 | 3 | 3 | 3 | 3 | 3 | 1 | 3 |
| Weightage | 11 | 13 | 13 | 14 | 10 | 15 | 15 | 8 | 15 |
| Weighted percentage of Course Contribution to PSOs | 2.2 | 2.6 | 2.6 | 2.8 | 2 | 3 | 3 | 1 | 3 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective V** | **Lipidomics and Glycomics** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To describe and express the role and importance of lipidomics and glycomics
* To facilitate the inclusion of multiomics based approaches in disease diagnosis
* To understand the analytical methods available for lipidomics and glycomic profiling

**COURSE LEARNING OUTCOMES**

On successful completion of the course, students will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Understand of the basic concepts of lipidomics and glycomics | K1, K2 |
| CO2 | Design an action plan of research | K3 |
| CO3 | Acquire skills on analysing lipidomic and glycomic data | K4 |
| CO4 | Application of statistics in omics research | K5 |
| CO5 | Apply the tools to infer the lipidomic and glycomic profiles during diseases | K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **Unit** | **Contents** | **Hrs** | **COs** |
| 1 | Lipidomics: objectives and relevance in the context of Systems Biology. Basic principles of lipid organisation in supramolecular structures. The architecture of the membrane: dependence on lipid composition; disturbing and regulatory agents; the role of lipids in the topological organisation of membrane proteins; lipid-lipid, and lipid-protein interactions. | 10 | CO1-5 |
| 2 | Lipid rafts and caveolae. Lipids and membranes as targets for drug action and toxicity. Changes in membrane lipid composition as an adaptive response under environmental pressure (temperature, pressure, dehydration, presence of xenobiotics). Bioactive lipids, mediators or second messengers and cell signalling. | 15 | CO1-5 |
| 3 | Changes in metabolism, homeostasis and lipid trafficking in metabolic diseases, neurological disorders and cancer. Recent advances in functional lipidomics: the mitochondrial lipidome as an example. Targeted and untargeted lipidomics. Quantification of lipids and Comprehensive lipid profiling and quantitation is a system-based study of all possible lipid classes in the biological system. | 15 | CO1-5 |
| 4 | Introduction to glycans and glycobiology. Glycome, glycoproteomics, glyco lipidomics and glycomics. Glyco profiling, Glycan class characterization, experimental methods in glycomics profiling - Mass spectrometry based Profiling of N- and O-Linked Glycans. Glycan modifications. Glycosylation as biomarkers of diseases | 15 | CO1-5 |
| 5 | Databases and tools for lipidomics and glycomic profiling- glycocan, Gly Space alliance, GlyToucan, Glyco Expasy, CCSD. Lipid home, Lipid maps, Lipid bank, Swiss lipids. | 10 | CO1-5 |

**BOOKS FOR STUDY**

* [Xianlin Han](https://onlinelibrary.wiley.com/authored-by/), Lipidomics: Comprehensive Mass Spectrometry of Lipids, April 2016, Print ISBN:9781118893128 |Online ISBN:9781119085263 |DOI:10.1002/9781119085263, John Wiley & Sons, Inc
* Paul wood, Lipidomics, [Neuromethods](https://www.springer.com/series/7657) (NM, volume 125), 2017, Springer
* Giera, M. William Griffiths, Yuqin Wang (Eds.): Lipidomics: current and emerging techniques. *Anal Bioanal Chem* 412, 7371–7372 (2020). <https://doi.org/10.1007/s00216-020-02871-7>

**BOOKS FOR REFERENCE**

# [Xiangdong Wang](https://www.amazon.in/s/ref=dp_byline_sr_book_1?ie=UTF8&field-author=Xiangdong+Wang&search-alias=stripbooks) (Editor), [Duojiao Wu](https://www.amazon.in/s/ref=dp_byline_sr_book_2?ie=UTF8&field-author=Duojiao+Wu&search-alias=stripbooks) (Editor), [Huali Shen](https://www.amazon.in/s/ref=dp_byline_sr_book_3?ie=UTF8&field-author=Huali+Shen&search-alias=stripbooks) (Editor), Lipidomics in Health & Disease: Methods & Application: 14 (Translational Bioinformatics, Springer publications

* Editors: Richard Cummings, J. Pierce, Handbook of Glycomics, 1st Edition - September 15, 2009, Elseiver, ISBN: 9780123736000
* Von Der Lieth, Bioinformatics for Glycobiology & Glycomics: An Introduction, 2009.Wiley publishers

**WEBSITES**

[www.lipotype.com](http://www.lipotype.com)

https://glycocan.eu/

<https://www.swisslipids.org/#/>

<http://www.glyspace.org/>

<https://glytoucan.org/>

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 2 | 1 | 1 | 2 | 3 | 3 | 1 | 1 |
| CLO2 | 2 | 1 | 2 | 3 | 1 | 3 | 1 | 1 | 1 |
| CLO3 | 2 | 3 | 2 | 3 | 2 | 2 | 3 | 2 | 3 |
| CLO4 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| Weightage | 11 | 12 | 11 | 13 | 11 | 13 | 13 | 10 | 11 |
| Weighted percentage of Course Contribution to PSOs | 2.2 | 2.4 | 2.2 | 2.6 | 2.2 | 2.6 | 2.6 | 2 | 2.2 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

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| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective VI** | **Network biology and visualisation** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To describe and express the role and importance of networks in biology
* To facilitate the inclusion of graph theory and networks in disease diagnosis
* To understand the analytical methods available for Network prediction and visualisation

**COURSE LEARNING OUTCOMES**

On successful completion of the course, students will be able to

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Understand of the basic concepts of graph theory | K1 |
| CO2 | Learn available algorithm for creating networks | K2 |
| CO3 | Create biological networks from clinical data | K3 |
| CO4 | Infer functional association networks | K4 |
| CO5 | Justify the use of genome scale networks in clinical settings | K5, K6 |

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| --- | --- | --- | --- |
| **Unit** | **Contents** | **Hrs** | **COs** |
| 1 | Introduction to graph theory, Probabilistic graphical model representation of molecular networks. Bayesian networks. Graphical Gaussian models. Network-based data integration and interpretation. Random walk on the graph. Diffusion on graphs. Graph kernels. Clustering and supervised classification | 10 | CO 1-5 |
| 2 | Network theory and algorithms. Network versus matrix representations. Weighted and directed networks. Edges based on “co-citation” and correlation Bipartite networks and hypergraphs. Degree and cluster coefficient. Protein interaction graphs- Spatial interaction analysis (APEX) Residue contact maps. Domain-domain and protein structural interactions | 10 | CO 1-5 |
| 3 | Introduction: why biological networks? Molecular networks bridge genotype to phenotype. Networks as the next phase of the Genome Project. Types of biological networks Network databases and the NDEx cloud. | 10 | CO 1-5 |
| 4 | Genetic interaction networks. Epistasis versus epistacy; Statistical genetic interactions. Dependency maps and Mutual exclusivity. Epistatic miniarrays Combinatorial CRISPR. Functional association networks (FANs) | 10 | CO 1-5 |
| 5 | Genome-scale modelling and network integration. Evolution of molecular networks. Software- cytoscape. Networks as guiding tools. Types of graph alignment problems. Network layout and visualisation. Properties of good visualisations. Force-directed graph layout Eades algorithm. Kamada & Kawaii algorithm. Hyperbolic & spherical layout. Other layouts | 15 | CO 1-5 |

**BOOKS FOR REFERENCE:**

* Edited by [Narsis A. Kiani](https://www.cambridge.org/core/search?filters%5BauthorTerms%5D=Narsis%20A.%20Kiani&eventCode=SE-AU), Karolinska Institutet, Stockholm, [David Gomez-Cabrero](https://www.cambridge.org/core/search?filters%5BauthorTerms%5D=David%20Gomez-Cabrero&eventCode=SE-AU), King's College London, [Ginestra Bianconi](https://www.cambridge.org/core/search?filters%5BauthorTerms%5D=Ginestra%20Bianconi&eventCode=SE-AU), Networks of Networks in Biology, 2021,ISBN: 9781108553711, <https://doi.org/10.1017/9781108553711>, Cambridge University Press

Alpan Raval, Animesh Ray, Introduction to Biological Networks, 2016, ISBN: 9781420010367, Chapman and Hall/CR

# **JOURNALS**

* Journal of network biology

Journal of health informatics and network biology

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **POs** | | | | | | **PSOs** | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 2 | 1 | 1 | 2 | 2 | 3 | 1 | 3 | 2 |
| CLO2 | 2 | 1 | 2 | 1 | 1 | 3 | 1 | 3 | 2 |
| CLO3 | 2 | 3 | 2 | 2 | 3 | 2 | 2 | 3 | 3 |
| CLO4 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 3 |
| Weightage | 12 | 11 | 11 | 11 | 12 | 13 | 8 | 14 | 13 |
| Weighted percentage of Course Contribution to PSOs | 2.4 | 2.2 | 2.2 | 2.2 | 2.4 | 2.6 | 1.6 | 2.8 | 2.6 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

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| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective VII** | **Translational Bioinformatics** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To develop a quantitative understanding of recent and emerging fields of Bioinformatics
* To provide a platform for knowledge on imminent concepts to serve the present societal requirements
* To provide a better understanding of data and its applications in Bioinformatics

**COURSE LEARNING OUTCOMES**

On successful completion of the course, students will be able to

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Apply knowledge of bioinformatics data exploration | K1, K2 |
| CO2 | Analyse, interpret and appraise bioinformatics research data | K3 |
| CO3 | Critically appraise the key concepts and conclusions from disease models | K4 |
| CO4 | Infer functional association networks | K5 |
| CO5 | Justify the use of genome scale networks in clinical settings | K6 |

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| --- | --- | --- | --- |
| **Unit** | **Contents** | **Hours** | **CO** |
| 1 | Overview of bioinformatics and principal applications: sequencing, Microarray, ‘omics’ fields, systems biology, data mining. Relationships to diseases and health. Data-driven Disease Biology. Translational Bioinformatics: Past, Present, and Future. | 10 | CO 1-5 |
| 2 | Biomedical Knowledge Integration. Data, Molecules, and Diseases, Computational Causal Analytics, Transforming patient care. Omics based approaches in diagnosis and treatment. Health informatics and the influence on the delivery of healthcare. The electronic patient record and the importance of coding healthcare delivery consultations. The management of multi-dimensional and heterogeneous data sets. | 15 | CO 1-5 |
| 3 | Biomedical image analysis- Picture archive communication system (PACS) design and implementation; clinical PACS-based imaging informatics; telemedicine/teleradiology; image content indexing, image data mining; grid computing in large-scale imaging informatics; image-assisted diagnosis, surgery and therapy. | 15 | CO 1-5 |
| 4 | Disease informatics- Small molecules and diseases. Cause and treatment of diseases. The Small Molecule Pathway Database (SMPDB). Toxin and Toxin-Target Database (T3DB), Poly Search and Metabolite Set Enrichment Analysis.  Protein interaction and diseases - molecular and genetic basis of diseases. Protein-DNA interaction disruptions, Protein misfolding problems. Network based approaches in complex diseases. | 15 | CO 1-5 |
| 5 | Biological Knowledge Assembly and Interpretation **-** Gene Set-Wise Differential Expression Analysis, Gene set enrichment analysis. Differential coexpression analysis. Statistical inferences- p values, hyper parametric test, Bonferroni corrections, Benjamini Hochberg corrections. False drug discovery rate. | 15 | CO 1-5 |

**Books for reference**

* Maricel Kann (Ed), Fran Lewitter (Ed), [PLOS Computational Biology: Translational Bioinformatics, 2016.](http://collections.plos.org/translational-bioinformatics)  
  Trevor Hastie, Robert Tibshirani and Jerome Friedman, [The Elements of Statistical Learning: Data Mining, Inference, and Prediction](http://web.stanford.edu/~hastie/pub.htm)(Second Edition) 2009.

**Website**

<http://web.stanford.edu/~hastie/pub.html>

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **POs** | | | | | | **PSOs** | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 2 | 1 | 1 | 2 | 2 | 3 | 1 | 3 | 2 |
| CLO2 | 2 | 3 | 2 | 1 | 1 | 3 | 1 | 3 | 2 |
| CLO3 | 2 | 3 | 2 | 2 | 3 | 2 | 2 | 3 | 3 |
| CLO4 | 2 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 3 | 3 |
| Weightage | 11 | 13 | 11 | 11 | 12 | 13 | 8 | 14 | 13 |
| Weighted percentage of Course Contribution to PSOs | 2.2 | 2.6 | 2.2 | 2.2 | 2.4 | 2.6 | 1.6 | 2.8 | 2.6 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short  summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

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| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective VIII** | **Medical and population genomics** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To infer the genome function based on inter-individual variability or gene mutations in human cells and tissues to study cellular and disease phenotypes and their genetic architecture.
* To identify associations between single nucleotide polymorphisms (SNPs) and phenotypic traits within a population community
* To provide the principle knowledge of medical genetics and genomics to evaluate and interpret appropriate genetic investigations for individuals and families with genetic disease.

**Course learning outcomes**

On successful completion of the course, the student will be able to

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Understand the dominant disorders, trait variants, the mode of inheritance of a disease for the prediction of probability of disease appearance | K1 |
| CO2 | Determine the genetic mutations needed to be interrogated using ultra-high throughput sequencing technology | K2 |
| CO3 | Measure the clinically relevant variant phenotype of an individual and relate to pathogenicity with ACMG and AMP guidelines | K3 |
| CO4 | Apply the genetic principles to medical practice like inheritance, mapping disease genes | K4 |
| CO5 | Utilise the resources and medical genetics knowledge for diagnosis, prevention, treatment and surveillance | K5, K6 |

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| **Unit** | **Contents** | **Hrs** | **CO1** |
| 1 | **Genetics**  Introduction -Landmarks in the history of genetics, Principles in human genetics, Single locus (Mendelian) versus multi-locus (quantitative/complex) inheritance, Chromosome theory of inheritance (segregation and independent assortment), Introduction to Ecological Genetics and Polymorphism, Phenotypic & genotypic polymorphisms, Transient polymorphism, Balanced polymorphisms, Pedigree analysis- Models explaining the maintenance of genetic polymorphism, Relationship between sickle cell and malaria, X-linked polymorphism, Selection due to infectious diseases and its association with blood groups and other. Hardy-Weinberg principle | 15 | CO 1-5 |
| 2 | **Genomics**  Next generation sequencing and population genomics, Human genome projects and their updated versions, recent human genome reference sequence- T2T human genome, High-throughput sequencing data: Whole exome sequencing - new genomic and analytical methods for improving the diagnosis of patients affected by rare, severe genetic diseases, Data formats (fastq, nexus, phylip, BAM, SAM, mpileup, VCF, etc.). anitation: filtering of low quality and low complexity reads, adapter removal and checking for contamination | 10 | CO 1-5 |
| 3 | GuidelinesIntroduction to ACMG & AMP Guidelines for Interpretation of Sequence Variants, Annotation of variants as per the guidelines. The Human Genome Variation Society (HGVS) nomenclature, Interchanging variant nomenclature and syntax checking, Variant curation from literature, annotation of variant, Copy number variants- Guidelines for interpretation of copy number variants – predictors, evaluators, partial overlap, complete overlap, Overview of major achievements and current goals of population genomics – tools and databases – clinvar, dbSN, fastSIMCOAL and ABC Toolbox | 10 | CO1-5 |
| 4 | **P4 medicine** P4 Medicine - Preventive, participatory, predictive and personalised medicine. WGS or WES or Candidate /targeted gene panels. Interpretation of a genetic report, Genetic Disorders – Sickle cell anaemia. Immunodeficiency disorders - Autoimmune Lymphoproliferative Syndrome. Rare Genetic Diseases and mitochondrial diseases. Applications of Genome Editing, Genome projects- Genome England, 100,000 genome project, Australian genome project, Indigenomes and other genome projects. | 15 | CO1-5 |
| 5 | **Genetic counselling**  Genetic counselling and human population genetics, Human population genetics and Forensics, Define roles for a genetic counsellor in a genetic clinical laboratory. Clinical laboratories are a common work setting for genetic counsellors, to differentiate between hereditary and acquired genetic changes associated with cancer. Analyse the goals associated with acquired change genetic testing. Identify genes associated with oncogenesis, Identification of biomarkers and hub genes, Regulatory landscape for clinical laboratories including CMS, CDC, FDA, CLIA, and CAP roles. | 10 | CO 1-5 |
| Self study | Concepts from CSIR NET (lifesciences) and ASRB-NET Bioinformatics related to this course can be discussed and taught | 5 |  |

**Books for reference**

* Om P. Rajora, Population Genomics, 2020, Springer. 978-3-030-04589-0
* [Emmanuel Paradis](https://www.google.co.in/search?tbo=p&tbm=bks&q=inauthor:%22Emmanuel+Paradis%22), Population Genomics with R, 2020, CRC press.

**Websites**

<http://guardian.meragenome.com/news-updates/genomicvariantanalysisclinicalinterpretation>

<https://www.broadinstitute.org/medical-population-genetics>

<https://www.genome.gov/genetics-glossary/Population-Genomics>

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **POs** | | | | | | **PSOs** | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 2 | 2 | 1 | 2 | 3 | 2 | 1 | 3 |
| CLO2 | 3 | 1 | 3 | 2 | 1 | 3 | 2 | 1 | 3 |
| CLO3 | 3 | 3 | 2 | 2 | 3 | 3 | 2 | 1 | 3 |
| CLO4 | 3 | 3 | 3 | 3 | 2 | 2 | 2 | 1 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| Weightage | 13 | 12 | 13 | 14 | 11 | 14 | 11 | 7 | 15 |
| Weighted percentage of Course Contribution to PSOs | 2.6 | 2.4 | 2.6 | 2.8 | 2.2 | 2.8 | 2.2 | 1.4 | 3 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

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| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective IX** | **Cancer Genomics** | **3** | **5** | **65** |

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Understanding of major concepts of Oncogenes and Tumour Suppressor genes | K1 |
| CO2 | Appreciate the variety of tumour types and their mechanisms | K2 |
| CO3 | Justify the recent research trends in Cancer Genetics and novel genetic approaches to the cancer problem. | K3 |
| CO4 | Distinguish the major steps in cancer development and progression and their relationship to disease mechanisms and therapeutic strategies | K4 |
| CO5 | Describe the major clinical-translational areas of research in cancer biology and the goals of biomedical research in these areas | K5, K6 |

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| --- | --- | --- | --- |
| **Unit** | **Contents** | **Hrs** | **CO1** |
| 1 | Introduction to the biology and history of cancer. - history, features of cancer, cancer as a genetic disease.  Causes and types of cancer. The discovery of oncogenes. - tumour viruses, chemically induced oncogenes. Cancer terminology and definitions | 10 | CO 1-5 |
| 2 | Carcinogenesis - chemical and physical carcinogenesis, molecular pathways in carcinogenesis, Apoptosis and cancer. Mutagens, genetic variants. Variants of unknown significance and driver mutations in carcinogenesis | 12 | CO 1-5 |
| 3 | Familial cancers  The discovery of tumour suppressor genes. - loss of heterozygosity - case studies of retinal cancer (Rb), breast cancer, colorectal cancer, lung cancer- Small cell and non small cell lung cancers, other cancer types. Biomarkers in cancer types. | 13 | CO 1-5 |
| 4 | Other pathways in cancer - epigenetics - angiogenesis - telomeres Multiple mutations and the evolution of metastases. - multiple mutations in cancer - metastasis.  DNA repair and cancer. Tumour microenvironment, liquid biopsy based diagnostics, molecular targets and therapeutics | 15 | CO 1-5 |
| 5 | Databases and tools to analyse cancer data- TCGA, cBioportal, GTEX, HPA, Reactome, UALCAN, Oncomine, KM plotter, COSMIC. Kaplan meier survival plots. Analysing Big Data of Cancer Genomics. Application of next generation sequencing technologies in diagnosis and prediction of cancer genes. Identification of Methylation sites, Expression profiles, pathway analysis. | 15 | CO 1-5 |

**BOOKS FOR STUDY**

* Pezzella et al., Oxford textbook of cancer biology, 2020, Oxford Publications, Pages – 504.
* Jim Kim, Cancer genetics and genomics for personalized medicine, 1st Eds. New York Publications, Taylor and Francis group, 2017, Pages- 300.
* Graham Dellaire, Jason N. Berman and Robert J. Arceci, Cancer Genomics, from bench to personalized medicine, Springer Publications, 2014.

**JOURNALS**

Cancer genomics

Cancer genomics and proteomics

Cancer genetics

**WEBSITE**

<https://www.cbioportal.org/>

<https://cancer.sanger.ac.uk/cosmic>

<https://www.mycancergenome.org/>

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **POs** | | | | | | **PSOs** | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 2 | 3 | 2 | 1 | 3 | 2 | 1 | 3 |
| CLO2 | 2 | 1 | 2 | 2 | 1 | 3 | 1 | 1 | 3 |
| CLO3 | 2 | 3 | 3 | 3 | 3 | 3 | 2 | 2 | 3 |
| CLO4 | 3 | 3 | 2 | 3 | 3 | 3 | 2 | 2 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| Weightage | 11 | 12 | 13 | 13 | 11 | 15 | 10 | 9 | 15 |
| Weighted percentage of Course Contribution to PSOs | 2.2 | 2.4 | 2.6 | 2.6 | 2.2 | 3 | 2 | 1.8 | 3 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

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| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective X** | **Basics of clinical research management** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To give a basic understanding about clinical research
* To understand the various aspects of clinical research management
* To be conversant with the regulations in clinical management

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Evaluate critical global regulatory and health care issues that challenge and influence biopharmaceutical product development | K1 |
| CO2 | Understand the drug development process and its importance in clinical trials | K2 |
| CO3 | Forecast the resources necessary for regulatory submission and comprehend regulatory Affairs procedure in clinical research | K3 |
| CO4 | Enrich the student role and responsibility of project manager in clinical trials | K4 |
| CO5 | Understand the basic statistical principles, concepts, and methods for clinical data analysis and reporting | K5, K6 |

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| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Clinical Research**  History of drug development - Pharmaco-epidemiology,  Issues in Clinical Trials. Nuremberg Code, Declaration of Helsinki, International Conference of Harmonization and Good Clinical Practice, Clinical trials – History of clinical trials. Stages of Clinical trials. | 10 | CO1-5 |
| 2 | **Pharmacology and Drug Development**  Introduction to Drug Discovery and Development, Approaches, Sources of Drugs, Databases for drug search, Pharmacokinetics and pharmacodynamics, Toxicological requirements, Emerging technologies in Drug Discovery**,** Preclinical Testing, and Clinical Trials. | 10 | CO1-5 |
| 3 | **Regulations in Clinical Research**  Evolution and History of Regulations in Clinical Research, US FDA Regulations, IND, NDA, ANDA, FDA Audits and Inspections, European Regulatory Affairs, Organization and Functions, Indian Regulatory system, Schedule Y- Rules and Regulations, Post Drug Approval Activities, PMS. | 15 | CO1-5 |
| 4 | **Clinical Trial Management**  Role of Ethics Committees and Institutional Review Boards. Special populations; women elderly and children, Designing of Protocol, SOP, ICF, Pharmacovigilance, Project management Documentation, Monitoring, Audits, Inspections, Fraud and Misconduct, Roles and Responsibilities of Clinical Research Professionals. | 15 | CO1-5 |
| 5 | **Clinical Data Management**  Importance of CDM in clinical research, Clinical Data Entry**,** CRF, e-CRF, Statistical considerations at the design, analysis and reporting stage, Data validation, SAE reconciliation, Quality Assurance | 15 | CO1-5 |

**BOOKS FOR STUDY**

Lori A. Nesbitt. Clinical Research What It Is and How It Works. UK: Jones Barlett Publishers, 2006.

Richard K. Rondel, Sheila A. Varley, Colin F. Webb. Clinical Data Management. UK: John Wiley, 2013.

Steven Piantadosi. Clinical Trails A Methodologic Perspective. UK: John Wiley, 2005.

**BOOKS FOR REFERENCE**

Russ B. Altman, David Flockhart, David B. Goldstein Principles of Pharmacogenetics and Pharmacogenomics. UK: John Wiley, 2012.

Martin M. Zdanowicz. Concepts in Pharmacogenomics. UK: Mc Graw Hill, 2010.

**JOURNALS**

Journal of Clinical Research & Bioethics

Perspectives in Clinical Research

Asian Journal of Pharmaceutical and Clinical Research

**WEB RESOURCES**

http://hub.ucsf.edu/clinical-study-management

http://icmr.nic.in/ethical\_guidelines

http://www.niaaa.nih.gov/research/guidelines-and-resources/clinical-trial-regulations-policies-and-guidance

http://www.fda.gov/ScienceResearch/SpecialTopics/RunningClinicalTrials/ucm155713.html

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **POs** | | | | | | **PSOs** | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 2 | 3 | 3 | 3 | 2 | 3 | 1 | 2 |
| CLO2 | 3 | 1 | 2 | 2 | 3 | 3 | 3 | 1 | 3 |
| CLO3 | 1 | 3 | 3 | 3 | 2 | 2 | 2 | 1 | 2 |
| CLO4 | 2 | 3 | 2 | 3 | 3 | 2 | 1 | 1 | 2 |
| CLO5 | 3 | 2 | 3 | 3 | 3 | 3 | 2 | 1 | 3 |
| Weightage | 13 | 11 | 13 | 14 | 14 | 12 | 11 | 5 | 13 |
| Weighted percentage of Course Contribution to PSOs | 2.6 | 2.2 | 2.6 | 2.8 | 2.8 | 2.4 | 2.2 | 1 | 2.4 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective XI** | **Biodiversity, Agriculture and ecosystem Informatics** | **3** | **5** | **65** |

**OBJECTIVE OF THE COURSE**

* To make the students understand the basic Biological diversity of life.
* To know the distributed databases and web- accessible resources
* To analyse the software for identification of Assessing existing biodiversity databases
* To understand the probabilistic and deterministic method for analysing biodiversity data

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Describe the role of information technology in distributing biodiversity information. | K1 |
| CO2 | Learn the measures in biodiversity assessments and inventorying programmes. | K2 |
| CO3 | Interpret the morphological and molecular characterization of biodiversity | K3 |
| CO4 | Evaluate the Red data books and Biodiversity registers | K4 |
| CO5 | Portray basic research from epidemiology and public health on leading health conditions. | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Biodiversity**  Status, scope, types, monitoring and documentation; major drivers of biodiversity change; biodiversity management approaches. Uses of Biodiversity, Loss of biodiversity. Introduction to biodiversity database: endangered animals, endemism and Red data books- Biodiversity registers | 10 | CO1-5 |
| 2 | **Agriculture**  Comparative genomes of plant and model plants, Insect resistance, Improve nutritional quality, Grow drought resistant crops in poorer soils, Biodiversity of Indian medicinal plants. Phenomics, root- shoot axis, R genes. Informatics to improve maize and rice cultivation. Multiomics in agriculture. | 10 | CO1-5 |
| 3 | **Ecosystem structure**  Ecosystem function; energy flow and mineral cycling (C, N, P); primary production and decomposition; structure and function of some Indian ecosystems: terrestrial (forest, grassland) and aquatic (fresh water, marine, eustarine). Principles of conservation, major approaches to management, Indian case studies on conservation/management strategy (Project Tiger, Biosphere reserves). | 15 | CO1-5 |
| 4 | **Networks, databases and tools**  Designing information systems to support biodiversity conservation- Networks for distributing information- Distributed Databases and Web- Accessible Resources. Software for identification of Assessing existing biodiversity databases on the worldwide web- Probabilistic and deterministic identification, Delta, MicroIS, AVIS, ICTV. | 15 | CO1-5 |
| 5 | UNEP/GEF biodiversity data management project (BDM). – CBD and bioethics– General agreement on trade and traffics. Databases of interest -Integbio, NARO- (RAP-DB, TENOR) | 15 | CO1-5 |

**Books for reference**

* Dahiya., P,& Ahlawat, M. (2013). Environmental Science: A New Approach.Alpha Science.
* Fulekar, M. H. (Ed.). (2009). Bioinformatics: applications in life and environmental sciences. Springer Science & Business Media.
* Saha., T.K. (2013). Ecology and Environmental Biology. Books & Allied (P) Ltd. Singh, J. S.,
* Gupta, S. R., & Singh, S. P. (2006). Ecology, environment and resource conservation. Anamaya Publishers.
* Tandon, P., Abrol, Y. P., & Kumaria, S. (Eds.). (2007). Biodiversity and its significance. IK International Pvt Ltd.
* Biodiversity: Measurement & Estimation -Hawkswoth, D.I. (Ed.) (1995), Chapman & Hall,
* London. 2 Alice, 1990. A Biodiversity database system. Alice software partnership. Cnhos,
* D.A.L. Canhos, V.P and Kirsop, B.E (eds) 1994. Linking Mechanisms for biodiversity information, Tropical foundation, Tropical Foundation, Campinas, Brazil.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **POs** | | | | | | **PSOs** | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 1 | 2 | 2 | 3 | 3 | 3 | 1 | 2 |
| CLO2 | 3 | 1 | 2 | 3 | 3 | 2 | 3 | 1 | 2 |
| CLO3 | 3 | 3 | 1 | 3 | 3 | 3 | 3 | 2 | 3 |
| CLO4 | 3 | 2 | 2 | 2 | 3 | 2 | 3 | 2 | 2 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 2 | 3 |
| Weightage | 15 | 10 | 10 | 13 | 15 | 13 | 15 | 8 | 12 |
| Weighted percentage of Course Contribution to PSOs | 3 | 2 | 2 | 2.4 | 3 | 2.4 | 3 | 1.6 | 2.4 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions

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| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective XII** | **Systems Biology** | **3** | **5** | **65** |

**OBJECTIVE OF THE COURSE**

* To introduce the basic concepts of Systems biology
* To train the students in designing a new organism through modelling network concept

and manipulating them for biological applications

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| CO1 | Understand the principles of integrative analysis methods for biological system analysis and interactions. | K1 |
| CO2 | Appreciate the model behaviour concepts | K2 |
| CO3 | Model gene expressions and integrate them with other omics | K3 |
| CO4 | Simulate the cell environments and model a cell | K4 |
| CO5 | Develop synthetic biology applications for omics | K5, K6 |

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| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Introduction**  Introduction – Systems Biology is a Living Science  Properties of Models-Model Behaviour - Model development  Systems Biology is Data Integration | 10 | CO 1-5 |
| 2 | **Standard Models and Approaches in Systems Biology**  Standard Models and Approaches in Systems Biology  Enzyme Kinetics and Thermodynamics -Metabolic Networks. Structure of Intra- and Intercellular Communication-Receptor-Ligand Interactions | 10 | CO 1-5 |
| 3 | **Modelling of Gene Expression**  Modelling of Gene Expression**-**Modules of Gene Expression – Promoter Identification - General Promoter Structure- Sequence  Based Prediction of Promoter Representation of Gene  Network as Directed and Undirected Graphs  Bayesian Networks-Boolean Networks- Gene Expression Modeling with Stochastic Equations | 15 | CO 1-5 |
| 4 | Integrating Networks. Computer Simulation of the whole Cell. Human Erythrocyte Model and its applications. Software for Modeling, ECELL, VCELL and GROMOS. Simulation of cellular subsystems, network of metabolites and enzymes, Signal transduction networks, Gene 5 regulatory networks, metabolic pathways: databases such as KEGG, EMP, MetaCyc, AraCyc. | 15 | CO 1-5 |
| 5 | Introduction to Synthetic Biology. General concepts and enabling technologies. Biological Parts. Modularity and Standardization. Part repositories DNA synthesis and assembly. Genome Editing. Controlling Gene Expression and Protein Production. Gene synthesis and genetic engineering. Optogenetics. Gene therapy, Microbiome engineering, synthetic biosystems. | 15 | CO 1-5 |

**BOOKS FOR STUDY**

* E. Klipp, R. Herwig, A. Kowald, C. Wierling, H. Lehrach. *Systems Biology In Practice- Concepts, Implementation And Application*. Germany: Wiley-Vch Verlag Gmbh & Co.Kgaa, 2005.
* Andres Kriete And Roland Eils. *Computational Systems Biology*. Uk: Elsevier, 2005.

**BOOKS FOR REFERENCE**

* Uri Alon. *An Introduction To Systems Biology: Design Principles Of Biological Circuits*. London: Chapman & Hall/Crc, Taylor And Francis Group, 2006.
* Choi And Sangdun. *Introduction To Systems Biology*. Usa: Humana Press, 2007. Edda Klipp, Wolfram Liebermeister, Christoph Wierling, Axel Kowald, Hans Lehrach,
* Ralf Herwig. *Systems Biology: A Textbook*. Uk: Wiley- Vch.Edinburgh, 2009.
* Zoltan Szallasi, Joerg Stelling, Vipul Periwal. *Systems Modeling In Cellular Biology*. USA: Mit Press, 2006.
* Najarian, K., Najarian, S., Gharibzadeh, S., & Eichelberger, C. N. (2009). Systems biology and bioinformatics: a computational approach. CRC Press

**JOURNALS**

Current Synthetic and Systems Biology

Journal of Computer Science & Systems Biology

Eurasip Journal on Bioinformatics and Systems Biology

Bmc Systems Biology

**WEB RESOURCES**

http://Sysbio.Med.Harvard.Edu/

www.Systemsbiology.Org

www.Systemsbiology.Ucsd.Edu/

www.Sysbio.Org/

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **POs** | | | | | | **PSOs** | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 1 | 2 | 1 | 3 | 3 | 3 | 1 | 3 |
| CLO2 | 1 | 2 | 1 | 2 | 3 | 3 | 2 | 1 | 2 |
| CLO3 | 2 | 3 | 3 | 3 | 2 | 3 | 2 | 3 | 3 |
| CLO4 | 2 | 3 | 2 | 3 | 3 | 3 | 3 | 2 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 1 | 3 |
| Weightage | 11 | 12 | 11 | 12 | 14 | 15 | 13 | 8 | 14 |
| Weighted percentage of Course Contribution to PSOs | 2.2 | 2.4 | 2.2 | 2.4 | 2.8 | 3 | 2.6 | 1.6 | 2.8 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions

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| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective XIII** | **Java Programming** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To understand the concepts of Object Oriented Programming.
* To learn about the control structures, class with attributes and methods used in Java
* To understand the application of java in biological research

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to:

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| --- | --- | --- |
| **COs** | **Description** | **CL** |
| 1 | Understanding of the structure of the Java programming language. | K1, K2 |
| 2 | Apply the basic principles of creating a Java program. | K3,K4 |
| 3 | Differentiate various methods used in Java | K4 |
| 4 | Comprehend the relevance of Java in Biological applications | K5 |
| 5 | Decipher the uses of biojava pipelines in bioinformatics | K6 |

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| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Introduction to Java**  Java Basics: Importance and features of JAVA, Lexical elements of JAVA, Data types and Control structure, Program structure, Arrays, Command line input handling, OOPS, String Handling. | 10 | CO 1-5 |
| 2 | Package, Exception Handling and File Handling: Package concept, working with util package, Built-in Exceptions, Exception Handling, User Defined Exception, Streams in Java: FileInputStream, FileOutputStream, DataInputStream, DataOutputStream, Serialization. | 15 | CO 1-5 |
| 3 | JDBC and Applets: JDBC, Steps to connect database, Classes and Methods for Database connectivity and Data Manipulation, Applets: Importance of applets, Steps to build an applet, Applet class methods, applet life cycle, creation and execution of applets, Graphics class methods. | 15 | CO 1-5 |
| 4 | **Class and objects**  Defining a class and Creating objects – Accessing class members .  Constructors – Method overloading – Static members –Nesting of Methods – this keyword – Command line input. Inheritance: Defining inheritance and types of inheritance | 12 | CO 1-5 |
| 5 | **Biojava**: Concepts, Installation, Symbols &SymbolList, DNATools, MotifTools, RNATools, DNA to RNA conversion, Translation of DNA sequence to Protein sequence, proteomics classes: Calculate Mass and isoelectric point, Sequence I/O basics, Parsing, remote pdb file access | 13 | CO 1-5 |

**BOOKS FOR STUDY**

* E. Balagurusamy, “*Programming with Java*”, TataMc-Graw Hill, 5th Edition.
* Sagayaraj, Denis, Karthick and Gajalakshmi, “*Java Programming for Core and advanced learners*”, Universities Press (INDIA) Private Limited 2018.
* Herbert Schildt, 2017. Java – A Beginner’s Guide, 7th Edition, MCGRAW HILL. 2. Andreas Prlic, Andrew Yates, Spencer E. Bliven, et al., BioJava: on open-source framework for bioinformatics in 2012. Bioinformatics. 28(20): 2693-2695. https://www.biojava.org

**BOOKS FOR REFERENCE**

* [Bert Bates](https://www.amazon.com/Bert-Bates/e/B004APJL7O/ref=dp_byline_cont_book_1) , [Kathy Sierra](https://www.amazon.com/Kathy-Sierra/e/B001H6U55G/ref=dp_byline_cont_book_2),”*Head First Java: Your Brain on Java - A Learner's Guide1”,*1st Edition, O'Reilly Media
* [Herbert Schildt](https://www.amazon.com/Herbert-Schildt/e/B001H6PSMG/ref=dp_byline_cont_book_1) ,”*Java: A Beginner's Guide”,*8th Edition, McGraw Hill
* [Joshua Bloch](https://www.amazon.com/Joshua-Bloch/e/B001CDCVUG/ref=dp_byline_cont_book_1) ,”*Effective Java”,*3rd Edition, Addison-Wesley Professional
* Eric Freeman , [Elisabeth Robson](https://www.amazon.com/Elisabeth-Robson/e/B001H6Q046/ref=dp_byline_cont_book_2),”*Head First Design Patterns: Building Extensible and Maintainable Object-Oriented Software”,* 2nd Edition, O'Reilly Media

**JOURNALS**

Java Development Journal

Java World

Java Revisited

Journal of Bioinformatics and Computational Biology

**WEB RESOURCES**

NPTEL & MOOC courses titled Java

<https://nptel.ac.in/courses/106105191/>

<https://www.udacity.com/course/java-programming-basics--ud282>

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 1 | 3 | 2 | 1 | 1 | 3 | 1 | 3 | 1 |
| CLO2 | 1 | 3 | 2 | 2 | 1 | 3 | 1 | 3 | 1 |
| CLO3 | 1 | 3 | 2 | 2 | 1 | 3 | 1 | 3 | 1 |
| CLO4 | 3 | 3 | 3 | 3 | 2 | 2 | 3 | 3 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 3 | 3 |
| Weightage | 9 | 15 | 12 | 11 | 7 | 14 | 9 | 15 | 9 |
| Weighted percentage of course contribution to PSOs | 1.8 | 3 | 2.4 | 2.2 | 1.4 | 2.8 | 1.8 | 3 | 1.8 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

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| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Elective XIV** | **Precision medicine** | **2** | **3** | **0** |

**OBJECTIVES OF THE COURSE**

* To explore the possibilities, promises, and pitfalls of precision medicine, using real-world examples.
* To bridge the gap between basic and translational research and its practical clinical applications, which will help prepare any student interested in research or health professions careers.
* To provide students with knowledge about prolonging health and treating disease that will empower them to make shared informed decisions with their physicians.

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to:

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| 1 | Explain how the HGP has advanced technology in biomedical research | K1, K2 |
| 2 | Understand how the diversity of life evolves over time by processes (leading to) of genetic change, particularly the role of genetic and genomic variation throughout the genome in health and disease. | K3,K4 |
| 3 | Describe recent advances in disease risk prediction, molecular diagnosis and progression of diseases, and targeted therapies for individuals | K4 |
| 4 | Discuss the ethical, legal, and social implications of health privacy and policy laws for precision medicine. | K5 |
| 5 | Critically evaluate primary and secondary precision medicine research | K6 |

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| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | Introduction to Precision Medicine, the Human Genome, and Human Genomic Variation. Versions of human reference genomes. T2T genome. | 12 | CO 1-5 |
| 2 | Genomics technologies  Genome: Whole Exome Sequencing (WES)  Genome: Whole Genome Sequencing (WGS).  Pharmacogenomic, Epigenome, Chromatin Remodelling Factors, transcriptome, proteome, metabolome, microbiome concepts | 13 | CO 1-5 |
| 3 | Statistical concepts in personalised medicine: statistical concepts and skills important to clinical data analysis (odds ratios, relative risk, P values, multiple testing, sensitivity, specificity, ROCs. Adverse Drug Reactions/Hypersensitivity | 15 | CO 1-5 |
| 4 | Ethical, Legal, and Social Implications of Precision Medicine. HMX Pro Genetics – Cancer Genomics and Precision Oncology. Consumer Health Informatics and Healthcare Systems Engineering for Precision Health | 10 | CO 1-5 |
| 5 | Implementation of P4 medicine  Personalised, participatory, preparative and preventive medicine. Digital twin. Developing Evidence for PM & Designing PM Clinical Trials. Implementation Science & Costs of PM | 10 | CO 1-5 |
| Self study | Enlightening ideas to establish a start-up company with skills in personalised genomics can be encouraged and discussed | 5 |  |

**Books for reference**

* Arwood MJ, Chumnumwat S, Cavallari LH, Nutescu EA, Duarte JD. Implementing pharmacogenomics at your institution: establishment and overcoming implementation challenges. Clin Tranl Sci (2016) 00, 1- 14.
* Geoffrey Ginsburg and Huntington Willard, Genomic and Precision Medicine, 3rd Edition, 2016 The Language of Life: DNA and the Revolution in Personalized Medicine, Francis S. Collins, 2010

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

**Generic Elective courses – offered to non-major students**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Generic Elective I** | **Basic Bioinformatics** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To become familiar with bioinformatics and how it’s changing complex biological research
* To enable textual mining of biological literature and bioinformatics tools that are required to query biological data
* To understand the application of information technology in biological research

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to:

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| 1 | Have a better understanding of the bioinformatics concepts | K1, K2 |
| 2 | Emphasise the application of bioinformatics and biological databases to solve research problems | K3,K4 |
| 3 | Perform a complete analysis of the gene and protein | K4 |
| 4 | Understand the evolutionary concepts related to biological query | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Introduction to Bioinformatics**  Introduction to Bioinformatics, Classification of Biological Databases, Biological Data formats, Application of bioinformatics in various fields.  Introduction to single letter code of amino acids, symbols used in nucleotides. Data retrieval systems- Entrez and SRS | 8 | CO 1-5 |
| 2 | **Sequence and Structure Analysis**  Introduction to Sequence Alignment. BLAST, Multiple sequence alignment. Structural Databases-PDB and other online tools  Visualising tools-Rasmol,Pymol | 8 | CO 1-5 |
| 3 | **Phylogenetic Analysis**  Evolutionary Analysis: Distances, Cladistic and Phenetic methods. Clustering methods, Rooted and Unrooted tree representation. Tools for Phylogenetic tree construction | 7 | CO 1-5 |
| 4 | **Genomics and Proteomics**  Genome-Gene finding methods, Gene Prediction Tools - ORF finder, Genscan, Genemark. Gene variants, types of variants. Repeat Sequence Finder. Protein levels of organisation, structures and analysis tools- Expasy | 8 | CO 1-5 |
| 5 | **Pharmacy informatics**  Introduction to pharmacy informatics, Medical Transcription, Role of informatics to enhance the services provided by pharmaceutical care givers. Health Information Systems Architecture, Health Data Management, Medical Coding, Telemedicine and Telehealth, Ethics in medical informatics, Pharmacy systems and automation, Informatics applications in pharmacy, survey and evaluation of on-line resources. | 8 | CO 1-5 |

**BOOKS FOR STUDY**

* Pevsner and Jonathan.*Bioinformatics and Genomics Functional.* USA: John Wiley,2003.
* Baxevanis, Andreas D. and Francis B.F. Ouellette. *Bioinformatics- A Practical Guide to the Analysis of Genes and Proteins*. USA: John Wiley, 2001.
* David W. Mount. *Bioinformatics Sequence and Genome Analysis*. INDIA: CBS Publishers, 2003.

**BOOKS FOR REFERENCE**

* Baldi P. and Brunak S. *Bioinformatics: Machine Learning Approach*. USA: MIT Press, 2003.
* Chen, Yi-Ping Phoebe. *Bioinformatics Technologies*. Germany: Springer, 2005.
* Durbin R, S. Eddy, A. Krogh and G. Mitchison.*Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids.* USA: Cambridge University Press, 2005.
* Higgins, Des and Willie Taylor. *Bioinformatics – Sequence, Structure and Databanks – Practical Approach***.** UK: Oxford University Press, 2001.
* Lesk, Arthur M. *Introduction to Bioinformatics.* UK: Oxford University Press, 2014.

**JOURNALS**

BMC Bioinformatics

Bioinformatics

Journal of Bioinformatics and Computational Biology

Journal of Biomedical Informatics

Journal of Integrative Bioinformatics

PLoS Computational Biology

**WEB RESOURCES**

http://bioinformaticsweb.net/tools.html

https://www.bits.vib.be/index.php/training/122-basic-bioinformatics

http://bioinformaticssoftwareandtools.co.in/

http://www.genscript.com/tools.html

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 2 | 2 | 1 | 1 | 3 | 3 | 1 | 2 |
| CLO2 | 3 | 3 | 2 | 2 | 2 | 3 | 3 | 1 | 2 |
| CLO3 | 3 | 2 | 2 | 2 | 2 | 3 | 3 | 1 | 2 |
| CLO4 | 3 | 3 | 2 | 2 | 3 | 3 | 3 | 1 | 2 |
| CLO5 | 3 | 3 | 3 | 2 | 3 | 2 | 3 | 1 | 2 |
| Weightage | 15 | 13 | 11 | 9 | 11 | 14 | 15 | 5 | 10 |
| Weighted percentage of course contribution to PSOs | 3 | 2.4 | 2.2 | 1.8 | 2.2 | 2.8 | 3 | 1 | 2 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Generic Elective II** | **Immunoinformatics** | **3** | **5** | **65** |

## OBJECTIVES OF THE COURSE

* To be familiar with the use of a wide variety of internet applications and biological database
* To understand the immune system, its components and their functions
* To impart knowledge of immune responses to various pathogens by integrating genomics and proteomics with bioinformatics strategies
* To provide information about the methods used in immunological bioinformatics
* To understand the application of information technology to immunology

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to:

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| 1 | Understand the application of information technology to immunology | K1, K2 |
| 2 | Understand informatics-based approaches for prediction of epitopes and immuno-diagnostic tools | K2 |
| 3 | Apply the immunological data and to the sophisticated computational solutions available for immunological research | K3 |
| 4 | Emphasise the application of bioinformatics and biological databases to problem solving in real research problems | K4 |
| 5 | Comprehend knowledge about computer aided vaccine design and reverse vaccinology | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Immune System**  Introduction to Immune System - Adaptive and Innate Immunity. Cells of the Immune System, Soluble Mediators of Immunity, Cell and Antibody mediated immunity. Immune Responses - Inflammation, Immunopathology, Autoimmune diseases, Vaccines | 7 | CO 1-5 |
| 2 | **Antigens and Antibodies**  Immunoglobulin classes and subclasses, Major Histocompatibility Complex (MHC) its Polymorphism, Causes for Polymorphism, MHC Supertypes. Antigen types – Epitope, Affinity Maturation, Epitope mapping. B-cell and T-cell Epitope Prediction, Recognition of Antigen by B cells. Neutralising Antibody**.** | 8 | CO 1-5 |
| 3 | **Computational Immunology**  Computational Immunology **-** Databases in Immunology, dbMHC-MHC database at NCBI. T-cell epitope databases, B-cell epitope databases, SYFPEITHI MHC-presented epitopes. IMGT Immunoinformatics, IMGT International ImMunoGeneTics Information System. HLA Nomenclature and the IMGT/HLA Sequence Database | 8 | CO 1-5 |
| 4 | **Vaccine Design**  From immunome to Vaccine – Prediction of immunogenicity, Vaccine design tools. Reverse Vaccinology and Immunoinformatics, Peptides with Antimicrobial Activity or Antibiotic Peptides. Functional Prospecting of Genes and Transcripts, Future of Computational Modelling and Prediction Systems in Clinical Immunology. | 8 | CO 1-5 |
| 5 | **Viral Bioinformatics**  Viral Bioinformatics - Computational Views of Hosts and Pathogens using VIDA. Virus- human protein interaction databases. Virus- NCBI. GISAID database. Virus mint, Virus host database. Viral zone- Expasy | 8 | CO 1-5 |

**BOOKS FOR STUDY**

* Darren R. Flower. *Bioinformatics forImmunomics (Immunomics Reviews).* New York: Springer-Verlag, 2010.
* Abul K. Abbas, Andrew H. H. Lichtman, and Shiv Pillai. *Cellular and Molecular Immunology* USA: Elsevier, 2017.
* Andrew R. Leach, Valerie J. Gillet. *An Introduction to Chemoinformatics*.UK: Springer, 2007.

**BOOKS FOR REFERENCE**

* Christian Schönbach, ShobaRanganathan, and Vladimir Brusic. *Immunoinformatics (Immunomics Reviews)* USA: Humana Press, 2010.
* Kenneth Murphy. *Janeway's Immunobiology*, UK: Garland Science, 2014.
* Bunin, Barry A. Dordrecht. *Chemoinformatics: Theory, Practice, and Products*.UK: Springer, 2010.
* [Malay Das](https://www.amazon.in/s/ref=dp_byline_sr_ebooks_1?ie=UTF8&field-author=Malay+Das&text=Malay+Das&sort=relevancerank&search-alias=digital-text) , [Liuyin Ma](https://www.amazon.in/s/ref=dp_byline_sr_ebooks_2?ie=UTF8&field-author=Liuyin+Ma&text=Liuyin+Ma&sort=relevancerank&search-alias=digital-text) , [Amita Pal](https://www.amazon.in/s/ref=dp_byline_sr_ebooks_3?ie=UTF8&field-author=Amita+Pal&text=Amita+Pal&sort=relevancerank&search-alias=digital-text) , [Chittaranjan Kole](https://www.amazon.in/s/ref=dp_byline_sr_ebooks_4?ie=UTF8&field-author=Chittaranjan+Kole&text=Chittaranjan+Kole&sort=relevancerank&search-alias=digital-text) , “Genetics, Genomics and Breeding of Bamboos (Advances in Agri-Genomics) 1st Edition”, by CRC Press

**JOURNALS**

The Pharmacogenomics Journal

Pharmacogenomics and Personalized Medicine

Pharmacogenetics and Genomics

Immunoinformatics

BMC Genomics

Journal of Computational Biology

Chemoinformatics: Concepts, Methods, and Tools for Drug Discovery

International Journal of Chemoinformatics and Chemical Engineering

BMR Bioinformatics & Cheminformatics

**WEB RESOURCES**

http://www.imgt.org/Immunoinformatics.html

http://rsob.royalsocietypublishing.org/content/3/1/120139

http://ghr.nlm.nih.gov/handbook/genomicresearch/pharmacogenomics

https://www.pharmgkb.org/

http://cheminformatics.org/

<http://www.emolecules.com/info/molecular-informatics>

<https://www.illumina.com/areas-of-interest/agrigenomics.html>

<https://center-forward.org/genomics-agricultural-innovation/>

http://www.pmjournal.ir/

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 2 | 2 | 1 | 2 | 3 | 3 | 1 | 2 |
| CLO2 | 3 | 2 | 2 | 3 | 1 | 3 | 3 | 1 | 3 |
| CLO3 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 1 | 3 |
| CLO4 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 1 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 1 | 2 |
| Weightage | 15 | 13 | 13 | 14 | 10 | 15 | 15 | 5 | 13 |
| Weighted percentage of course contribution to PSOs | 3 | 2.6 | 2.6 | 2.8 | 2 | 3 | 3 | 1 | 2.4 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Generic Elective III** | **Applications of Bioinformatics** | **3** | **5** | **65** |

## 

## OBJECTIVES OF THE COURSE

* To be familiar with the use of a wide variety of internet applications and biological database
* To understand the basics of pharmacogenomics in the context of variability in drug response
* To introduce the basic concepts of using chemical structure databases
* To understand the application of information technology to immunology

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to:

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| 1 | Introduce the concepts of bioinformatics to anyone | K1 |
| 2 | Apply the nutritional information to genomics and vice versa | K2 |
| 3 | Emphasise the application of bioinformatics and biological databases to problem solving in real research problems | K3 |
| 4 | Imbibe the genome technologies to change breeding, monitor and protect the wild plant population | K4 |
| 5 | Infer the genetic composition of individual and improve the treatment strategies | K5, K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Introduction to Bioinformatics**  Classification of biological data, and different data formats  Introduction to single letter codes of amino acids, symbols used in nucleotides  Bioinformatics Perspectives on Human Diseases, Overview of Biological Sequence Databases - NCBI, EMBI, DDBJ | 7 | CO 1-5 |
| 2 | **Nutrigenomics**  Introduction-Background & Preventive Health. Applications -Nutrigenomics & gut health-prebiotics and probiotics. Nutrition linked to genes and phenotypes. Role of folate, choline, and vitamins B2, B6 and B12, in gene regulation. Databases -SGMD, Barleybase and others. Tools-Use of BioConductor,Booly. | 8 | CO 1-5 |
| 3 | **Pharmacogenomics**  Introduction to Basic Concept of Pharmacogenomics, Application and Challenges in Pharmacogenomics, Genetic Variation, Types of Variants, SNPs, Insertion/Deletions. Databases - Pharmacogenomics Knowledge Base (PharmGKB) | 8 | CO 1-5 |
| 4 | **Agrigenomics**  Genomics application in Agriculture- The advantages and outcomes. Wheat genomics program. Seed saving techniques. Genomic breeding, genetic engineering of plants. Development of high performance plants- Case study. Databases of interest -Integbio, NARO- (RAP-DB, TENOR),Tools- Parentage Testing, Marker assisted backcrossing. | 8 | CO 1-5 |
| 5 | Personalised Medicine Introduction- the use of GWAS(Genome Wide Association study). The use of AI in personalised medicine. Database-PreMedKb,Tools-Molecular Diagnostics and Molecular Imaging. Digital Twin | 8 | CO 1-5 |

**Books for reference**

* Russ B. Altman, David Flockhart, David B. Goldstein. *Principles of Pharmacogenetics and Pharmacogenomic*.UK:Cambridge University Press, 2012.
* [Bryce Mendelsohn](https://www.amazon.in/s/ref=dp_byline_sr_book_1?ie=UTF8&field-author=Bryce+Mendelsohn&search-alias=stripbooks), [Jeanette McCarthy](https://www.amazon.in/s/ref=dp_byline_sr_book_2?ie=UTF8&field-author=Jeanette+McCarthy&search-alias=stripbooks),”Precision Medicine: A Guide to Genomics in Clinical Practice (INTERNAL MEDICINE)”, Paperback,McGraw-Hill Education
* [Lynnette R. Ferguson](https://www.amazon.in/s/ref=dp_byline_sr_book_1?ie=UTF8&field-author=Lynnette+R.+Ferguson&search-alias=stripbooks),”Nutrigenomics and Nutrigenetics in Functional Foods and Personalized Nutrition”, CRC Press
* Bunin, Barry A. Dordrecht. *Chemoinformatics: Theory, Practice, and Products*.UK: Springer, 2010.

**Journals**

International Journal of Genomics

Agronomy Journal

The Ohio Journal of Science

### [Journal of Nutrigenetics and Nutrigenomics - Karger Publishers](https://www.karger.com/Journal/Home/275177)

Journal of Personalized Medicine

**Websites**

<http://www.emolecules.com/info/molecular-informatics>

<https://www.illumina.com/areas-of-interest/agrigenomics.html>

<https://center-forward.org/genomics-agricultural-innovation/>

http://www.pmjournal.ir/

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 2 | 3 | 2 | 1 | 3 | 3 | 1 | 3 |
| CLO2 | 3 | 2 | 1 | 2 | 1 | 3 | 3 | 1 | 3 |
| CLO3 | 3 | 2 | 3 | 2 | 1 | 3 | 3 | 1 | 2 |
| CLO4 | 3 | 3 | 3 | 2 | 3 | 3 | 3 | 1 | 2 |
| CLO5 | 3 | 3 | 3 | 2 | 3 | 3 | 3 | 1 | 3 |
| Weightage | 15 | 12 | 13 | 10 | 9 | 15 | 15 | 5 | 13 |
| Weighted percentage of course contribution to PSOs | 3 | 2.4 | 2.6 | 2 | 1.8 | 3 | 3 | 1 | 2.6 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Generic Elective IV** | **Cheminformatics** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To introduce the basic concepts of using chemical structure databases
* To apply the concepts and learn the use of Cheminformatics tools
* To understand the applications of Cheminformatics in drug design

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to:

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| 1 | Gain skills to analyse the properties of small molecules | K1, K2 |
| 2 | Design the biological targets and properties of the small molecule under investigation | K3,K4 |
| 3 | Better understanding of the drug discovery and development process | K4 |
| 4 | Apply the concepts to create novel leads | K5 |
| 5 | Compare the molecular data with drugs to predict therapeutic lead molecules | K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Introduction**  Introduction to Cheminformatics, History and Evolution of Cheminformatics, Use of Cheminformatics, Prospects of Cheminformatics. Databases: Chemical Structure Databases (PubChem, Drug bank). Modelling of small molecules and Structure Elucidation | 8 | CO 1-5 |
| 2 | **Representation of Molecules**  Representation of Molecules and Chemical Reactions. Different Types of Notations, SMILES Coding, Structure of Mol files and Sdf files (Molecular converter, SMILES Translator). Similarity Search of the Molecule | 8 | CO 1-5 |
| 3 | **Cheminformatics databases**  Structure databases; Reaction Databases; Literature Databases; Medline; GenBank. PIR; CAS Registry; National Cancer Institute (NCI) Database. Databases of Small Molecules (ZINC), pubchem, chemspider. | 7 | CO 1-5 |
| 4 | **Searching Chemical Structure**  Searching Chemical Structure: Full Structure Search; SubStructure Search; Similarity Search. Three dimensional Search Methods. Structure Visualisation. Drawing the Chemical Structure: 2D and 3D Drawing Tools (ACD Chemsketch) Structure Optimization | 8 | CO 1-5 |
| 5 | **Cheminformatics in drug design**  Definition of drugs, Structure-Based Drug Design, QSAR. Pharmacophore Design, Ligand-Based Design, De Novo Drug Design Virtual Screening / Docking of Ligands. Protein structure-Fragment-Based Drug Design, ADMET Prediction. | 8 | CO 1-5 |

**BOOKS FOR STUDY**

* Johann Gasteiger and Thomas Engel. *Chemoinformatics -A Textbook*. Germany: Wiley-VCH, 2003.
* Johann Gasteiger. *Handbook of Chemoinformatics-From Data to Knowledge,* Germany: Wiley-VCH, 2003.

**BOOKS FOR REFERENCE**

* Andrew R. Leach, Valerie J. Gillet. *An Introduction to Chemoinformatics*.UK: Springer, 2007.
* Bunin, Barry A. Dordrecht. *Chemoinformatics: Theory, Practice, and Products*.UK: Springer, 2010.
* Bajorath, Juergen,Totowa, N.J. *Chemoinformatics: Concepts, Methods, and Tools for Drug Discovery.* USA: Humana Press, 2004.
* Ekins, Sean, Hoboken, N.J. Computer *Applications in Pharmaceutical Research and Development.*Germany: Wiley, 2006.

**JOURNALS**

Journal of Cheminformatics

Chemoinformatics: Concepts, Methods, and Tools for Drug Discovery

International Journal of Chemoinformatics and Chemical Engineering

BMR Bioinformatics & Cheminformatics

The Journal of Chemical Information and Modeling

**WEB RESOURCES**

http://cheminformatics.org/

http://www.emolecules.com/info/molecular-informatics

http://accelrys.com/products/informatics/cheminformatics/

http://www.rasalsi.com/services\_drugdis.html

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 2 | 3 | 3 | 2 | 1 | 3 | 2 | 1 | 3 |
| CLO2 | 3 | 2 | 3 | 3 | 1 | 3 | 2 | 1 | 3 |
| CLO3 | 3 | 2 | 3 | 3 | 2 | 2 | 2 | 1 | 3 |
| CLO4 | 3 | 3 | 3 | 2 | 2 | 3 | 2 | 1 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 2 | 3 | 2 | 1 | 3 |
| Weightage | 14 | 13 | 15 | 13 | 8 | 14 | 10 | 5 | 15 |
| Weighted percentage of course contribution to PSOs | 2.8 | 2.6 | 3 | 2.6 | 1.6 | 2.8 | 2 | 1 | 3 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Generic Elective V** | **Pharmacogenomics** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To understand the basics of pharmacogenomics in the context of variability in drug response
* To examine factors that affect drug response and the application of pharmacogenetics to drug development and drug treatment
* To analyse the tools and databases related to pharmacogenomics

**COURSE LEARNING OUTCOMES**

On successful completion of the course, the student will be able to:

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| 1 | Gain an insight on pharmacology linked to genomics | K1, K2 |
| 2 | Assess genetic polymorphisms and their importance in drug designing | K3,K4 |
| 3 | Understand structural influence in the Drug response | K4 |
| 4 | Analyse different tools for pharmacogenomic analysis including ADME prediction | K5 |
| 5 | Apply the ADME prediction skills to investigate new lead molecules | K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Pharmacogenomics**  Pharmacogenomics- Introduction, basic concepts about genetic diseases  Personalized medicine- introduction and importance, The genetics of therapeutic targets and gene-based targets  Pharmacogenomics necessity in drug designing | 8 | CO 1-5 |
| 2 | **Genetic Variation**  Introduction to genetic variation, types of variants, SNPs, coding and cis/trans regulatory variants, insertion/deletions, Satellite DNA  Databases, National pharmacogenetics resources/efforts (PGRN), Pharmacogenomics Knowledge Base (PharmGKB)  Prediction of structural changes among sequences by the influence of polymorphisms. | 8 | CO 1-5 |
| 3 | **Pharmacokinetics & Metabolism**  Pharmacokinetics (PK), Pharmacodynamics (PD). Tools for pharmacogenomics analysis.  Definition of Toxicogenomics, Detoxification and poisoning. Preclinical Toxicology | 7 | CO 1-5 |
| 4 | **Pharmacogenomics in Drug Discovery and Development**  An Introduction to Drug Discovery and Development  Process in Structural Pharmacogenomics - Target Structure optimization, Validation, lead identification, ADME prediction, synthesis, assays and Clinical trials  Drug response to patients, Structural influence in the Drug response. Efficacy and metabolism of drugs, adverse drug reactions | 8 | CO 1-5 |
| 5 | **Microarray Analysis**  DNA Microarray: Importance and definition, Designing a MicroArray Experiment: The Basic steps  Types of Microarray, GEO (Gene Expression Omnibus).  The Promise of Microarray Technology in Treating Disease. Microarray Data, Expression Pattern, Visualizing Microarray Data. | 8 | CO 1-5 |

**BOOKS FOR STUDY**

* Russ B. Altman, David Flockhart, David B. Goldstein. *Principles of Pharmacogenetics and Pharmacogenomic*.UK:Cambridge University Press, 2012.
* Rapley R and Harbron S.*Molecular analysis and Genome discovery*. John Willey, 2004.

**BOOKS FOR REFERENCE**

* Lori A. Nesbitt.*Clinical Research What It Is and How It Works.*UK*:* Jones Barlett Publishers, 2004.
* Steven Piantadosi.*Clinical Trials A Methodologic Perspective*.UK:John Wiley, 2005.

# Martin M. Zdanowicz. *Concepts in Pharmacogenomics*.NewYork: McGraw Hill, 2010.

**JOURNALS**

The Pharmacogenomics Journal

American Journal of Pharmacogenomics

Pharmacogenomics and Personalized Medicine

*Pharmacogenetics and Genomics*

**WEB RESOURCES**

http://ghr.nlm.nih.gov/handbook/genomicresearch/pharmacogenomics

https://www.pharmgkb.org/

http://www.fda.gov/drugs/scienceresearch/researchareas/pharmacogenetics/ucm083378.htm

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 2 | 3 | 1 | 1 | 3 | 3 | 1 | 3 |
| CLO2 | 3 | 2 | 3 | 2 | 2 | 3 | 3 | 1 | 3 |
| CLO3 | 3 | 2 | 3 | 2 | 2 | 3 | 3 | 1 | 2 |
| CLO4 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 1 | 2 |
| CLO5 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 1 | 2 |
| Weightage | 15 | 12 | 15 | 11 | 9 | 15 | 15 | 5 | 12 |
| Weighted percentage of course contribution to PSOs | 3 | 2.4 | 3 | 2.2 | 1.8 | 3 | 3 | 1 | 2.4 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COURSE** | **TITLE** | **CREDITS** | **HOURS / WEEK** | **TOTAL TEACHING HOURS** |
| **Generic Elective VI** | **Computer aided drug design** | **3** | **5** | **65** |

**OBJECTIVES OF THE COURSE**

* To understand the general pathway for drug discovery and development
* To define new methodologies for analysis of ligands with their bound protein target
* To gain an in-depth overview of methods and techniques applied in computer assisted drug design (CADD)
* To learn about computer-aided drug design, safety evaluation, bioavailability and clinical trials

**COURSE LEARNING OUTCOMES**

On Successful completion of the course, the student will be able to

|  |  |  |
| --- | --- | --- |
| **COs** | **Description** | **CL** |
| 1 | Identify the key elements in drug and explain new methodologies for drug design | K1, K2 |
| 2 | Describe the role and importance of the various disciplines involved in the different phases of drug discovery and development | K3,K4 |
| 3 | Review and evaluate preclinical and clinical pharmaceutical studies | K4 |
| 4 | Follow new ideas in utilising main approaches of ligand screening methods | K5, K6 |
| 5 | Apply the ADME prediction skills to investigate new lead molecules | K6 |

|  |  |  |  |
| --- | --- | --- | --- |
| **UNIT** | **CONTENT** | **Hrs** | **CO** |
| 1 | **Drug Discovery and Development**  Drug Development Process Overview - The Changing Landscape of drugs development  Drug Discovery Phases  Preclinical Phase studies | 10 | CO 1-5 |
| 2 | **Regulations in Drug Discovery**  FDA regulations on Drug Development, Indian Regulatory Systems. Ethical Considerations and Special Populations. | 15 | CO 1-5 |
| 3 | **Drug Target Identification**  Computational inferences used to identify and validate small molecule drug targets  Databases for Drug targets, Retrieving protein structure and visualisation. Target Discovery and Validation, Active Site Prediction | 15 | CO 1-5 |
| 4 | **Ligand Based Drug Design**  Screening of lead molecules - Natural products and their analogues. Chemical Databases – PubChem, Drug Bank  Chemical file formats, Retrieving drug molecules | 15 | CO 1-5 |
| 5 | Pharmacokinetics and Molecular Docking Pharmacokinetics - ADME Prediction, Pharmacodynamics  Molecular Docking - Scoring and evaluation | 10 | CO 1-5 |

## BOOKS FOR STUDY

## Claudio N. Cavasotto*. In Silico Drug Discovery and Design: Theory, Methods, Challenges, and Applications*. USA: Taylor & Francis Group, 2017

* Charifson P S. *Practical Application of Computer Aided Drug Design***.** New York:

Dekker, 1997

#### BOOKS FOR REFERENCE

* Andrew R. Leach. *Molecular Modeling: Principles and Applications*. USA: Prentice Hall, 2007.
* Daan Frenkel and Berend Smit. *Understanding Molecular Simulation: From Algorithms to applications*. USA: Academic Press, 2002.
* Alan Hinchliffe. *Molecular Modelling for Beginners*. USA: John Wiley & Sons, 2008
* Luca Monticelli, Emppu Salonen*. Biomolecular Simulations: Methods and Protocols.* USA: Humana Press, 2016**.**

**JOURNALS**

# Journal of Molecular Graphics and Modelling

# Journal of Computer-Aided Molecular Design

Current Computer Aided-Drug Design

**WEB SOURCES**

http://accessengineeringlibrary.com/browse/computer-aided-drug-design-and-delivery systems

http://www.southernresearch.org/life-sciences/lead-discovery-and-optimization/medicinal-chemistry/computational-chemistry

http://www.ch.ic.ac.uk/local/organic/mod

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | POs | | | | | | PSOs | | |
|  | 1 | 2 | 3 | 4 | 5 | 6 | 1 | 2 | 3 |
| CLO1 | 3 | 3 | 3 | 3 | 1 | 3 | 3 | 1 | 3 |
| CLO2 | 3 | 2 | 3 | 3 | 1 | 3 | 3 | 1 | 3 |
| CLO3 | 3 | 2 | 2 | 2 | 3 | 3 | 3 | 1 | 3 |
| CLO4 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 1 | 3 |
| CLO5 | 3 | 3 | 3 | 3 | 2 | 3 | 3 | 1 | 3 |
| Weightage | 15 | 13 | 14 | 14 | 9 | 15 | 15 | 5 | 15 |
| Weighted percentage of course contribution to PSOs | 3 | 2.6 | 2.8 | 2.8 | 1.8 | 3 | 3 | 1 | 3 |

**Method of Evaluation**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Internal Assessment** | | | **End semester exams** | **Total** |
| **Test 1** | **Test 2** | **Other components (Seminars/quiz/assignments)** |
| 10 | 10 | 5 | 75 | 100 |

**Methods of assessment:**

**Recall (K1) -** Simple definitions, MCQ, Recall steps, Concept definitions.

**Understand/ Comprehend (K2) -** MCQ, True/False, Short essays, Concept explanations, short summary or overview.

**Application (K3) -** Suggest idea/concept with examples, Solve problems, Observe, Explain.

**Analyse(K4) –** Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

**Evaluate (K5) -** Longer essay/ Evaluation essay, Critique or justify with pros and cons

**Create (K6) –** Check knowledge in specific or offbeat situations, group discussions.

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