STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI – 600 086

Institutional Learning Outcomes

Stella Maris College, an autonomous Catholic institution of higher education, is committed to the highest standards of academic excellence based on sound values and principles, where students are strengthened with whole person education to lead purposeful lives in service to the community and the nation.

The Institutional Learning Outcomes (ILOs) of Stella Maris College (SMC) reflect the broader mission and purpose of the institution. They are the overarching set of learning outcomes that all students, regardless of discipline, must achieve at graduation. All programme and course learning outcomes are mapped to the institutional outcomes, thus reflecting an overall alignment of values, knowledge and skills expected at programme completion. ILOs are designed to help guide individual departments and disciplines in the development of their programme learning outcomes.

The ILOs of SMC are formed by two components:

1. **Core commitments**: Knowledge and scholarship, values and principles, responsible citizenship, service to community
2. **Institutional values**: Quest for truth, spirit of selfless service, empowerment

Upon graduation, students of Stella Maris College will

- Display mastery of knowledge and skills in their core discipline (**Knowledge and Scholarship)**
- Exhibit in all actions and attitudes a commitment to truth and integrity in all contexts, both personal and professional (**Values and Principles)**
- Demonstrate knowledge about their role in society at local and global levels, and actively work for social and environmental justice (**Responsible Citizenship)**
- Engage in the process of self-discovery through a life-long process of learning (**Quest for truth**)
- Demonstrate readiness to serve those who are in need (**Spirit of selfless service**)
- Be able to function effectively and with confidence in personal and professional contexts **Empowerment)**

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Programme Learning Outcomes/Intended Programme Learning Outcomes

Graduates of a Master's Degree of Stella Maris College will have a comprehensive knowledge of their disciplines, with indepth knowledge of the underlying principles and concepts in one or more disciplines as a basis for independent lifelong learning.

At the end of a postgraduate programme students will be able to

- Demonstrate mastery in the discipline
- Demonstrate deep understanding of the broad principles of science and technology and apply them in varied contexts
- Demonstrate knowledge, understanding and professionalism required for the discipline
- Demonstrate capability to locate, evaluate, manage, and use information/data and research to develop and guide their own knowledge, learning, and practice
- Demonstrate the ability to organise a presentation in a coherent fashion
- Demonstrate the literacy and numeracy skills necessary to understand and interpret information/data and communicate according to the context
- Draw on multiple, relevant/interrelated fields of study to understand, analyse and solve problems
- Exhibit principled decision making and reasoning to identify creative solutions to ethical problems
- Practice/act in ways that show a commitment to social justice and the processes of peace/conflict resolution
- Demonstrate the skills to appropriately interact with people from a range of cultural, linguistic, and religious backgrounds
- Demonstrate an understanding of local, regional, national, and global issues
- Identify themselves as agents of change
- Demonstrate the ability to solve an issue
- Show self-awareness and emotional maturity
- Demonstrate career and leadership readiness
- Exhibit the ability to work in teams
- Demonstrate sensitivity and readiness to share their knowledge and capabilities with the marginalised and oppressed in their communities

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI 600 086

DEPARTMENT OF BIOINFORMATICS

PROGRAMME DESCRIPTION

The M.Sc. programme in Bioinformatics at Stella Maris College was started in the year 2002. The programme gives a strong interdisciplinary foundation to Biology and Informatics with courses like Molecular Biology, and ensures adequate Programming skills in C++, Perl, R and Python. The programme includes recent advancements and internationally demanding research cum job courses like Next Generation Sequencing Analysis, Big Data Analysis and Molecular Modeling and Computer Aided Drug Design. Other courses like Data Mining, Algorithms, Clinical Research Management and Systems Biology cover not only the theoretical aspects of the field, but also the practical essentials of Bioinformatics. The Summer Internship is an integral part of the course, and is done at the end of the first year where the students intern in reputed institutions such as IGIB, IBAB, NCBS, IIT-M, IISc, etc., where they are involved in live projects, and acquire hands-on experience in both wet lab and dry lab techniques and learn work ethics as well. The students are encouraged to choose their area of interest and work under the guidance of the faculty for their Master's Dissertation during the fourth semester.

PROGRAMME SPECIFIC LEARNING OUTCOMES

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

- Foster interdisciplinary research in the fields such as computer science, biosciences, mathematics, chemistry and physical sciences
- Interpret biological information computationally
- Develop programming skills in the languages of C++, Perl, Python and R
- Analyse genomic data and contribute to personalised medicine
- Demonstrate entrepreneurial skills
- Establish Bioinformatics start-ups
- Prepare scientific reports to publish and present quality research
- Evaluate the experimental raw data to infer molecular models

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M.Sc. DEGREE : BIOINFORMATICS

COURSES OF STUDY

(Effective from the academic year 2019-2020)

CHOICE BASED CREDIT SYSTEM

C-Credit, **L**-Lecture Hours, **T**-Tutorial Hours, **P**- Practical Hours, **Ex**-Exam Hours,
CA- Continous Assessment Marks, **ES**-End Semester Marks, **M**-Maximum Marks

Subject Code	Title of Course	C	L	T	P	Ex	CA	ES	M
SEMESTER-I									
19BI/PC/BM14	Biomolecules and Biochemistry	4	4	1	0	3	50	50	100
19BI/PC/EB14	Essentials of Bioinformatics	4	4	0	2	3	50	50	100
19BI/PC/CP14	Programming in C++ and Perl	4	3	0	2	3	50	50	100
19BI/PC/DB14	Database Management Systems	4	3	0	2	3	50	50	100
	SAP / SL	2	2	0	0	-	50	-	100
	Department Elective I								
SEMESTER-II									
19BI/PC/MB24	Molecular Biology	4	4	1	0	3	50	50	100
19BI/PC/P122	Molecular Biology-Practical	2	0	0	3	3	50	50	100
19BI/PC/GP24	Genomics and Proteomics	4	3	0	2	3	50	50	100
19BI/PC/RM24	Research Methodology	4	4	1	0	3	50	50	100
CD / ET	Value Education	2	2	0	0	-	50	-	100
19BI/PK/SS22	Soft Skills	2	2	0	0	-	50	-	100
	Department Elective II								
	Common Elective I								
SEMESTER-III									
19BI/PC/PR34	Python and R Programming	4	4	1	0	3	50	50	100
19BI/PC/P232	Python and R Programming-Practical	2	0	0	3	3	50	50	100
19BI/PC/AL34	Algorithms for Bioinformatics	4	4	1	0	3	50	50	100
19BI/PC/MC34	Molecular Modeling and Computer Aided Drug Deisgn	4	4	1	0	3	50	50	100
19BI/PC/P332	Molecular Modeling and Computer Aided Drug Design-Practical	2	0	0	3	3	50	50	100
CD / ET	Value Education	2	2	0	0	-	50	-	100
19BI/PN/SI32	Summer Internship	2	2	0	0	-	50	-	100
	Common Elective II								
SEMESTER-IV									
19BI/PC/AB44	Advances in Bioinformatics	4	4	1	0	3	50	50	100
19BI/PC/BD44	Big Data Analysis	4	4	1	0	3	50	50	100
19BI/PC/P442	Advances in Bioinformatics-Practical	2	0	0	3	3	50	50	100
19BI/PC/DS47	Dissertation	7	0	0	9	0	50	50	100
	Department Elective III								
Postgraduate Elective Courses Offered to Parent Department									
19BI/PE/CG15	Cell Biology and Genetics	5	4	1	0	3	50	50	100
19BI/PE/BS15	Biomathematics and Biostatistics	5	4	1	0	3	50	50	100
19BI/PE/DM15	Data Mining	5	4	1	0	3	50	50	100
19BI/PE/IM15	Immunoinformatics	5	4	1	0	3	50	50	100
19BI/PE/CR15	Basics of Clinical Research Management	5	4	1	0	3	50	50	100
19BI/PE/CI15	Cheminformatics	5	4	1	0	3	50	50	100
19BI/PE/BP15	Biophysics	5	4	1	0	3	50	50	100

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(Effective from the academic year 2019-2020)

CHOICE BASED CREDIT SYSTEM

C-Credit, **L**-Lecture Hours, **T**-Tutorial Hours, **P**- Practical Hours, **Ex**-Exam Hours, **CA**- Continous Assessment Marks, **ES**-End Semester Marks, **M**-Maximum Marks									
Postgraduate Elective Courses Offered to Other Departments									
19BI/PE/IB23	Introduction to Bioinformatics	3	3	0	0	3	50	50	100
19BI/PE/AP23	Applications of Bioinformatics	3	3	0	0	3	50	50	100
19BI/PE/CD23	Computer Aided Drug Design	3	3	0	0	3	50	50	100
Independent Elective Courses									
19BI/PI/PG24	Pharmacogenomics	4	0	0	0	3	0	100	100
19BI/PI/SB24	Systems Biology	4	0	0	0	3	0	100	100

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SYLLABUS
(Effective from the academic year 2019-2020)

BIOMOLECULES AND BIOCHEMISTRY

CODE: 19BI/PC/BM14 **CREDITS: 4**
L T P: 4 1 0
TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- To understand the concepts of the structure of biomolecules
- To understand the basics of metabolism and enzyme kinetics
- To give a basic understanding about the forces that determines the structure of biological macromolecules
- To provide knowledge about the techniques used in studying biological structure and function

COURSE LEARNING OUTCOMES

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

- Understand the importance of structural studies in bioinformatics and
- Gain an insight about the forces that determines the structure of biological macromolecules
- Apply the knowledge gained to interpret the properties of biological macromolecules
- Apply the recent advances in Biochemistry and Biophysical techniques in Clinical Chemistry and Life science Research

Unit 1 **(15 Hours)**

Biomolecules

1.1 Basics of Biomolecules - Structure and functions of Atoms, Molecules and Chemical bonds.
1.2 Biomolecule structures – Carbohydrates, Lipids, and Nucleic acids
1.3 Water - Properties and its importance in Biosystems

Unit 2 **(10 Hours)**

Metabolic Biochemistry

2.1 Carbohydrate metabolism – Glycolysis, Glycogen metabolism, TCA cycle, HMP shunt
2.2 Protein metabolism – Oxidative Deamination, Transamination and Urea Cycle
2.3 Fatty acid metabolism- β- oxidation and Biosynthesis of fatty acids. Xenobiotics and general detoxification methods in the body

Unit 3 **(15 Hours)**

Proteins

3.1 Proteins - Levels of organisation, Amino acid properties, peptide bonds, disulphide bridges and other conformations.

3.2 Four levels of protein structure, The Ramachandran Plot, Structure prediction by crystallography

3.3 Folding pathways. Domains, Motifs and their importance

Unit 4 **(10 Hours)**

Enzyme Kinetics and Bioenergetics

4.1 Enzyme action Mechanisms, Enzyme Kinetics, Michaelis-Menten Equation, significance of V max and Km, Line weaver-Burk plot

4.2 Competitive and non-competitive Inhibition, Feedback inhibition. Enzyme regulation. Allosteric modulation

4.3 Thermodynamics systems - laws of thermodynamics, statement and applications – concepts of entropy and enthalpy

Unit 5 **(15 Hours)**

Analytical Techniques

5.1 Principles and applications of Visible, UV, IR spectroscopy, Raman spectroscopy and Fluorescence spectroscopy

5.2 Nuclear Magnetic Resonance -The phenomenon, One dimensional and Two dimensional, NMR application to Macromolecules

5.3 Mass Spectrometry for protein and peptide analysis, MALDI-TOF Analyser, Tandem Mass Analyser, The Ion Trap Mass Analyser, Q-TOF Instrument

BOOKS FOR STUDY

Albert, L. Lehninger**,** *Biochemistry*, Worth Publishing, UK. 2012.

Thomas. E. Creighton, *Protein*s**,** 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

WEBSITES

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

PATTERN OF ASSESSMENT

Continuous Assessment: Total Marks: 50 Duration: 90 mins.
Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: Total Marks: 50
Assignment/Open book test/Case study/Clinical implications of metabolic pathways/ Diagnostic applications of biochemicals/Role of Biomarkers

End Semester Examination: Total Marks: 100 Duration: 3 Hours
Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

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SYLLABUS
(Effective from the academic year 2019 -2020)

ESSENTIALS OF BIOINFORMATICS

CODE: 19BI/PC/EB14 **CREDITS: 4**
L T P: 4 0 2
TOTAL TEACHING HOURS: 78

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, the student will be able to

- Better understanding of the bioinformatics concepts
- Applications of the gene and protein sequence analysis
- Apprehending the different databases in bioinformatics
- Perform a complete analysis of the genes and protein
- Compare and identify the differences in sequences

Unit 1 **(16 Hours)**

Introduction to Biological Databases

1.1 Type of Databases, Public Biological Databases – NCBI, EBI, CMBI, OMIM. Primary Nucleotide Sequence Databases: EMBL, GenBank, DDBJ

1.2 Secondary Nucleotide Sequence Databases: UniGene, SGD. Sequence Submission Methods and Tools (Sequin, Sakura, Bankit)

1.3 Sequence Retrieval Systems (Entrez & SRS); Sequence File Formats and Conversion Tools. Finding Scientific Articles, Using Pubmed

Unit 2 **(16 Hours)**

Introduction to Sequence Alignment

2.1 Protein Alignment, Homology, Similarity, Identity, Gaps

2.2 Pairwise alignments: Dot Plots, Scoring Matrix-PAM, BLOSUM, Gap Penalty

2.3 Dynamics programming - Alignment Algorithms: Global Sequence Alignment: Needleman-Wunsch Algorithm. Local Sequence Alignment: Smith –Waterman Algorithm. Rapid, Heuristic Versions of Smith Waterman: FASTA

Unit 3 **(16 Hours)**

Basic Local Alignment Search Tool

3.1 BLAST Search Steps, Search Strategy, General concepts

3.2 BLAST Algorithm: Local Alignment Search Statistics and E Value. Raw Scores and Bit Scores, Relation between E and P Values. Gapped Alignments in BLAST, Evaluation of Results

3.3 Advanced BLAST Searching-Specialised BLAST sites: - Organism Specific BLAST Sites, Ensemble BLAST, TIGR BLAST, PSI-BLAST

Unit 4 **(15 Hours)**

Multiple Sequence Alignment

4.1 Definition of Multiple Sequence Alignment

4.2 Databases of Multiple Sequence Alignment Programs- BLOCKS, PRINTS

4.3 Integrated Multiple Sequence Alignment Resources: InterPro, iProClass

Unit 5 **(15 Hours)**

Evolutionary Analysis

5.1 Introduction to Evolutionary Analysis, Bootstrap, Tree Construction Methods

5.2 Neighbor-Joining Method, Unweighted Pair Group Method with Arithmetic Mean (UPGMA)

5.3 Maximum Parsimony Method and Maximum-Likelihood Method

BOOKS FOR STUDY

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

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes

Theory:

Section A – 15 x 1 = 15 Marks (All questions to be answered)
Section B – 2 x 5 = 10 Marks (2 out of 4 to be answered)

Practical:

Section C – 2 x 10 = 20 Marks
1 x 5 = 5 Marks

Other Components: Total Marks: 50

Assignment/Test/Seminars

End Semester Examination: Total Marks: 100 Duration: 3 hours

Theory:

Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 2 x 15 = 30 Marks (2 out of 4 to be answered)

Practical:

Section C – 5 x 10 = 50 Marks

Questions comprising the following:
Primary Nucleotide Sequence Databases: NCBI, EMBL, DDBJ
Basic Local Alignment Search Tool (BLAST)
Protein Sequence Databases – PIR, RefSeq, Swiss-Prot
Protein Structure Databases – PDB
Protein Family Databases –Pfam, TIGRFAM
Protein Visualization Tools- Rasmol, Swiss PDB Viewer
Specialized Database -IMGT
Multiple Sequence Alignment Tools: Clustal W
Phylogenetic Tree Construction Tool: MEGA

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SYLLABUS
(Effective from the academic year 2019 -2020)

PROGRAMMING IN C++ AND PERL

CODE: 19BI/PC/CP14 **CREDITS : 4**
L T P : 3 0 2
TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- To facilitate the students in gaining programming skills.
- 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 to

- Learn the basics of programing
- Relate the necessity for programming in biology
- Handling biological concepts with C++ and Perl scripts
- Apply programing to analyze genomic sequences
- Understand Bio-Perl and their application in bioinformatics to handle the complex data

Unit 1 **(12 Hours)**

Introduction to Programming language

1.1 Introduction to Programming, Machine/Assembly Language, Higher Level Languages, Simple and Compound Data, Code: Syntax and Semantics

1.2 Introduction to Programming in C++: C++ Characteristics, Tokens, Keywords, Identifiers and Constants, Basic Data Types, User Defined Data Types, Derived Data Types, Expressions and Control Structures

1.3 Functions and Variables: Scope, Declaration and Definition, Arrays and Strings in C++

Unit 2 **(13 Hours)**

Object Oriented Programming – C++

2.1 Object Oriented Programming – Using Objects, Classes, Encapsulation, Inheritance, Abstraction and Polymorphism. Using Constructors, Destructors, Friend functions

2.2 String manipulation – creating string objects, Standard Streams, String operators Manipulating String, String characteristics, Comparing and Swapping

2.3 Working with files – File streams, Open, close, EOF, updating files and error Handling.

Unit 3 **(15 Hours)**

Introduction to Perl Programming

3.1 Introduction, Statements and Declarations, Default Variable, Expressions, Statements, Operators in Perl, Control Structures

3.2 Variable Types and Data types– Scalar, Arrays, Hashes. Functions- split, join, length, lcfirst, ucfirst, index and exists

3.3 Creating Regular Expressions-Characters, Character Classes, Alternative Match Patterns, Quantifiers, Assertions, Back References, Modifiers and Translator

Unit 4 **(13 Hours)**

Subroutines and File Handling

4.1 Subroutines- Defining Subroutines, Returning Values, Using Arguments

4.2 Files- Overview and working with File handles, Various Ways of Opening a Perl File Handlers- Normal Scalar variable, Use Perl IO, Open the Standard Input and Standard Output, Use Sysopen (). Closing the files, printing, renaming files

4.3 Reading and writing perl – arrays and hash files

Unit 5 **(12 Hours)**

Bioperl

5.1 Introduction to Bioperl: Installation Procedures, Architecture, Uses of Bioperl

5.2 Modules of bioperl- seq, seqio, alignio, db

5.3 Modules of Bioperl – Annotation, location, tools

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.

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

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes
Theory:
Section A – 15 x 1 = 15 Marks (All questions to be answered)
Section B – 2 x 5 = 10 Marks (2 out of 4 to be answered)
Practical:
Section C – 2 x 12.5 = 25 Marks

Other Components: Total Marks: 50
Assignment/Test/Seminars

End Semester Examination: Total Marks: 100 Duration: 3 hours
Theory:
Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 2 x 15 = 30 Marks (2 out of 4 to be answered)
Practical:
Section C – 4 x 10 = 40 Marks
Record and Viva – 10 Marks

Questions comprising the following:
Find the area and circumference of a circle
Armstrong Number
Prime Number
Convert DNA to RNA (transcription)
Calculate the frequency of bases
Find the reverse complement of the DNA sequence
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

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SYLLABUS
(Effective from the academic year 2019 -2020)

DATABASE MANAGEMENT SYSTEMS

CODE : 19BI/PC/DB14 **CREDITS : 4**
L T P : 3 0 2
TOTAL TEACHING HOURS : 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

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

- Understand data models and schemas in DBMS
- Skills to Create, update, retrieve and Manage data
- Handle files and databases
- Gain efficient skills on Atomicity, Consistency, Isolation, and Durability
- Clear understanding and usage of SQLanguage

Unit 1 **(12 Hours)**

Introduction to Database Systems and Linux

1.1 Introduction to File and Database systems- Database System Structure, Data Models Introduction to Network Models – ER Model. Relational Model

1.2 Introduction to Linux Operating System, Properties of Linux, Desktop Environment, Linux basics commands

1.3 Working With Files, Text Editors, I/O Redirections, Pipes, Filters, and Wildcards. Changing Access Rights

Unit 2 **(13 Hours)**

SQL definition and Normalization

2.1 SQL – Data Definition- Queries in SQL- Updates- Views – Integrity and Security

2.2 Relational Database design – Functional dependences and Normalization for Relational Databases (up to BCNF)

2.3 Query Forms

Unit 3 **(15 Hours)**

Files and RDBMS

3.1 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 – Query Processing

3.2 Multimedia Databases - Basic Concepts and Applications. Indexing and Hashing. Text Databases
3.3 Overview of RDBMs, Advantages of RDBMs Over DBMs - Data Mining

Unit 4 (13 Hours)

Data Definition and Manipulation Language

4.1 Data Definition Language, Data Manipulation Language, Transaction Control and Data Control Language Grant and Revoke Privilege Command
4.2 Set Operators, Joins-Kinds of Joins, Table Aliases, Sub queries, Multiple and Correlated Sub Queries
4.3 Functions-Single Row, Date, Character, Numeric, Conversion, Group Functions

Unit 5 (12 Hours)

Constraints and MySQL

5.1 Constraints-Domain, Equity, Referential Integrity Constraints
5.2 Locks -Types of Locks, Table Partitions, Synonym
5.3 Introduction to PL/SQL, Introduction, MySQL as an RDBMS Tool, Data types and Commands

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
International Journal of Computer Science and Information

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

PATTERN OF ASSESSMENT

Continuous Assessment: **Total Marks: 50** **Duration: 90 mins.**

Theory:
Section A – 15 x 1 = 15 Marks (All questions to be answered)
Section B – 5 x 2 = 10 Marks (2 out of 4 to be answered)

Practical:
Section C – 2 x 12.5 = 25 Marks

Other Components: **Total Marks: 50**
Seminars/Group discussion/Assignments/Problem solving

End Semester Examination: **Total Marks: 100** **Duration: 3 Hours**

The question paper pattern: theory and practical

Theory:
Section A – 30 x 1 = 30 Marks (All questions to be answered)
Section B – 10 x 2 = 20 Marks (2 out of 4 to be answered)

Practical:
Section C – 2 x 25 = 50 Marks (2 out of 3 to be answered)

Question comprising the following:

Display the output for the given query,
Error finding,
Output of the given programme,
Find the missing statements in a given programme.

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2019 -2020)

MOLECULAR BIOLOGY

CODE: 19BI/PC/MB24 **CREDITS : 4**

L T P : 4 1 0

TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

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

COURSE LEARNING OUTCOMES

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

- Represent and illustrate the structural organization of genes and the control of gene expression
- Explore the prokaryotic and eukaryotic protein synthesis mechanism
- Conceptualize mechanisms of signal transduction, cell cycle and cell death
- Link the concepts of cell and molecular biology to a better understanding of diseases, including cancer

Unit 1 (15 Hours)

Structure and Organisation of Genes and Chromosomes

1.1 DNA-Structure and Conformations, Histones and Non-Histones, Chromosomes - Structure and Function of Chromosomes

1.2 Cell division - Mitosis and meiosis, Cell cycle regulation, Check points

1.3 Organisation of Genomes –Coding Sequences, Repetitive Sequences, transposons

Unit 2 (15 Hours)

Replication and Transcription

2.1 DNA replication, repair and recombination, DNA damage and repair mechanisms in prokaryotes and eukaryotes, Mutations

2.2 Transcription: Eukaryotes and Prokaryotes, Genetic code, Transcriptional Control by Regulatory Proteins, Steroid Hormone Receptors - Heat Shock Genes- Homeotic Genes

2.3 Mechanisms Modifying Transcriptional Control – DNA Methylation, Histone Modification, Post Transcriptional Regulation

Unit 3 **(12 Hours)**

Translation

3.1 RNA- Types, structure and functions, Ribosomes – Structure and Assembly

3.2 Translational Regulation - Regulation of gene expression in Prokaryotes (Operon) and Eukaryotes, Gene Silencing

3.3 Genetic Control of Vertebrate Immune System

Unit 4 **(10 Hours)**

Organelle Genome

4.1 Mitochondrion genome – Organisation and Function

4.2 Chloroplast genome – Organisation and Function

4.3 Transcription and Translation in Mitochondria

Unit 5 **(13 Hours)**

Cell Signalling and Cancer

5.1 Cell signalling – Signalling molecules, Receptors - Hormones receptors, cell surface receptor, signal transduction pathways, regulation of signalling pathways

5.2 Cancer Biology- Characteristics of Cancer, Genetic basis of cancers, Proto-oncogene, Oncogenes, Tumor Suppressor Genes, Tumor Metastasis

5.3 Oncogenesis - Cancer Immunotherapy, Regulation of Cell Death, Apoptosis

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/

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes

Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: Total Marks: 50

Assignment/Test/Seminars

End Semester Examination: Total Marks: 100 Duration: 3 hours

Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

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SYLLABUS
(Effective from the academic year 2019 -2020)

MOLECULAR BIOLOGY PRACTICAL

CODE: 19BI/PC/P122 **CREDITS : 2**
L T P : 0 0 3
TOTAL HOURS : 39

OBJECTIVE OF THE COURSE:

- 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

- Utilize 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

Unit 1 **(8 Hours)**

1.1 Cell Fraction and Extraction of cell organelles
1.2 Isolation of Sub-Cellular Organelles and Particles –Mitochondria and Chloroplast

Unit 2 **(10 Hours)**

2.1 Extraction of DNA from Onion, Extraction of RNA from Yeast
2.2 Estimation of DNA and RNA
2.3 Estimation of Proteins by Lowry's Method

Unit 3 **(7 Hours)**

3.1 Estimation of Mitochondria by Assessing The Marker Enzyme
3.2 Denaturing Proteins and Identification of Amino Acids by Thin Layer Chromatography

Unit 4 **(7 Hours)**

4.1 Isolation of Plasmid DNA (Demo)
4.2 Amplification of DNA by PCR

Unit 5 **(7 Hours)**

5.1 Electrophoretic Techniques: Agarose Gel Electrophoresis, SDS PAGE (Demo)
5.2 Southern Blotting (Demo)

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. *Molecular Cloning*. 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.

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes

Spotters 2 in number each carrying 5 marks totalling 10 marks

Any two experiments each carrying 15 marks each - 5 marks for procedure, 5 marks for the result and 5 marks for the conduct of the experiment

Viva - 5 marks

Record - 5 marks

End Semester Examination Total Marks: 100 Duration: 3 hours

Spotters 4 in number each carrying 5 marks totalling 20 marks

Any two experiments each carrying 30 marks each—10 marks for procedure, 10 marks for the result and 10 marks for the conduct of the experiment

Viva - 10 marks

Record - 10 marks

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2019 -2020)

GENOMICS AND PROTEOMICS

CODE: 19BI/PC/GP24 **CREDITS : 4**
L T P : 3 0 2
TOTAL CONTACT HOURS: 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 develop an understanding of the entire protein complement 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

- Gain an insight of the basic and advanced concepts and applications of sequencing technologies
- Understand the mechanisms of genomics and proteomics and exploit the same in the growing field of omics
- Apply functional genomics techniques to analyse data for biological system
- Implement techniques and database search to analyze complex protein samples
- Analyze the proteomic interactions in complex diseases

Unit 1 (13 Hours)

Genomics

1.1 Understanding a Genome sequence, Locating the genes in a Genome Sequence, Gene location by Sequence Inspection, Experimental Techniques for Gene Location, Determining the Functions of Individual Genes

1.2 Genome Sequencing technologies - Conventional Sequencing techniques (Maxam Gilbert and Sanger Sequencing), Whole Genome Shotgun Sequencing, Genome assembly, Genome annotation and Genome databases

1.3 Rates and patterns of Nucleotide substitution, Molecular Clocks, Local Clocks**,** Computer Analysis of a Gene Function, Assigning Gene Function by Experimental Analysis

Unit 2 (12 Hours)

Comparative Genomics

2.1 Comparative Genomics - Genome Sequencing Projects, Variations at the Level of individual Nucleotides, Duplications, Comparisons at the Chromosome Level: Synteny, Genomes of Chimpanzees and Humans

2.2 Phylogenetic Analysis - Relationship of Phylogenetic Analysis to Sequence Alignment, Genome Complexity and Phylogenetic Analysis, Maximum Parsimony Method, Distance Methods, Gene Prediction by ORF analysis

2.3 Gene mapping - pedigree analysis, Application of DNA markers - RFLPs, SNPs, Physical mapping - Restriction mapping, Fluorescent *in situ* hybridization, Assessing genomic variations

Unit 3 **(15 Hours)**

Functional Genomics

3.1 Transcriptomes and analysis - Micro Array technology, SAGE, Applications of Microarrays In Medicine, Databases – GEO, MAML

3.2 ESTs Generation, EST Clustering and Assembly, EST databases (DB-EST, UNIGene)

3.3 KEGG and Metabolic Pathways, Regulatory Networks, Sequence based and structure-based approaches to assign gene functions, Role of databases in function assignment, Structural changes in sequences by the influence of polymorphisms (dbSNPs)

Unit 4 **(13 Hours)**

Proteomics

4.1 Introduction to Proteomics - Proteins structure, Organization of protein structure, structural conformation of proteins, three dimensional structures of proteins

4.2 Analytical tools in Proteomics - 1D and 2D-gel electrophoresis, Mass Spectrometry - ESI, MALDI etc., Software for Matching MS Data with Specific Protein Sequences, Peptide sequencing by tandem mass spectrometry

4.3 Preparative IEF, HPLC, Tandem LC/ MS-MS, Protein Digestion Techniques

Unit 5 **(12 Hours)**

Application of Proteomics

5.1 Proteomic interactions - Yeast Two-Hybrid, Mammalian Screen Methods and Co-Immuno Precipitation techniques

5.2 Protein-Protein Interactions and Protein Complexes, Databases and proteomic tools

5.3 Protein Interaction Networks and Protein Pathways, Mapping Protein modifications

BOOKS FOR STUDY

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.

Leland Hartwell, Michael L. Goldberg and Janice Fischer. *Genetics: From Genes to Genomes.* USA:McGraw-Hill Publishing Company. 2018

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

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.

Dale, Jeremy W and Malcolm von Schantz. *From Genes to Genomes – Concepts and Applications of DNA Technology*. USA: John Wiley and Sons, 2012.

Arthur Lesk M. *Introduction to Genomics***.** New York: Oxford university press, 2008.

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.

Hunt Stephen P and Livesey Fredrick J. *Functional Genomics -A Practical Approach*. Great Britain: Oxford University Press, 2000.

Golemis and Erica. *Protein-Protein Interaction*. USA: CSHL, 2005.

Lesk Arthur M. *Introduction to Protein Science: Architecture, Function and Genomics*. New York: Oxford university press, 2016.

Mount David W. *Bioinformatics: Sequence and Genome Analysis*, USA: Cold Spring Harbor Lab., 2005.

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.

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

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes
Theory:
Section A – 15 x 1 = 15 Marks (All questions to be answered)
Section B – 2 x 5 = 10 Marks (2 out of 4 to be answered)

Practical:
Section C – 5 x 5 = 25 Marks

Other Components: Total Marks: 50
Assignment/Test/Seminars

End Semester Examination: Total Marks: 100 Duration: 3 hours
Theory:
Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 2 x 15 = 30 Marks (2 out of 4 to be answered)

Practical:
Section C – 5 x 10 = 50 Marks

Questions comprising the following:
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
Transcriptomes analysis - Micro Array data analysis, GEO
EST Clustering databases - DBEST, UNIGene
Metabolic pathway database – KEGG, PharmGKB
Protein classification and structure analysis - CATH, SCOP
Protein Motif and Domain search - PROSITE, PDBeMotif
Protein - protein interaction analysis - DIP, STRING, BIND

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M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2019 -2024)

RESEARCH METHODOLOGY

CODE: 19BI/PC/RM24 **CREDITS : 4**
L T P : 4 1 0
TOTAL TEACHING HOURS : 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, the student will be able to

- Better understanding of the research methods
- Design an action plan of research
- Acquire skills of writing a research manuscript
- Application of statistical study in research
- Understand the ethics in writing research work

Unit 1 **(15 Hours)**

Types of Data and research problem identification

1.1 Data Collection, Sampling. Sources of Data Primary, Secondary and Tertiary Sources Classification and Presentation of Data

1.2 Documents, Types of Documents, Archives, Chronologies

1.3 Definition of Research and Research Methodology. Principles and Practice of Research. Exploring the Broad Area – Using the Library and Online Resources. Identifying The Research Problem

Unit 2 **(15 Hours)**

Scientific Communication

2.1 Literature Review - Its Relevance and Importance in Directing Research. Citations – Types Of Citations, Bibliography and End Matters, Editing and Proof Reading

2.2 Action Plan, Design and Pilot Study Undertaking a Research Project, Writing a Research grant Proposal, writing papers and posters, Format of thesis

2.3 Paper critiquing- the Purpose and the Methodology of Paper Critiquing

Unit 3 **(10 Hours)**

Writing well

3.1 Writing for non- native audiences, usage of simple sentences, untangle long noun phrases, make complete sentences.

3.2 Use of punctuations- comma, colon, semicolon, dash and periods.

3.3 Creating non-textual information- acquiring, processing and printing illustrations. Concepts of mind maps.

Unit 4 **(12 Hours)**

Bioethics

4.1 Introduction. Intellectual Property Rights (IPR) and Patents, TRIPS

4.2 Case studies on Patents (Basmati, Turmeric and Neem), ethics in science practicals

4.3 Plagiarism and Common Errors in Scientific Writing. Misconduct in science

Unit 5 **(13 Hours)**

Tools for research

5.1 Use of Encyclopaedias, Research Guides, Handbook etc., Academic Databases for Computer Science Discipline.

5.2 Use of tools / techniques for Research: methods to search required information effectively, Reference Management Software like Zotero/ Mendeley,

5.3 Software for paper formatting like LaTeX/MS Office, Software for detection of Plagiarism

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

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes
Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: Total Marks: 50
Assignment/Test/Seminars

End Semester Examination: Total Marks: 100 Duration: 3 hours
Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2019 -2020)

SOFT SKILLS

CODE: 19BI/PK/SS22 **CREDITS: 2**
L T P: 2 0 0
TOTAL TEACHING HOURS: 26

OBJECTIVES OF THE COURSE

- To empower students and create opportunities for self-development.
- To instill confidence in students to face challenges.
- To manage emotions and resolve conflicts.
- Top organize activities and manage time.
- To set goals and plan ahead.

COURSE LEARNING OUTCOMES

- Communicate with confidence and poise.
- Accept themselves and improve on their weaknesses.
- Strengthen their relationships through confronting and solving problems.
- Work more effectively and complete activities on time.
- Plan their future with clarity and focus.

Unit 1

Behavioural Traits **(6 Hours)**

1.1 Self Awareness
1.2 Communication Skills –Verbal and Non Verbal
1.3 Leadership Qualities
1.4 Etiquette and Good Manners
1.5 Experiential Learning –Based on activities

Unit 2

Team Work **(5 Hours)**

2.1. Interpersonal Skills
2.2. People Management
2.3. Creative Thinking
2.4. Critical Thinking
2.5. Experiential Learning – Based on activities

Unit 3

Time Management **(5 Hours)**

3.1. Importance of time management
3.2. Planning and Prioritizing
3.3. Organizing skills
3.4. Action Plan
3.5. Experiential Learning – Based on activities

Unit 4

Conflict Resolution **(5 Hours)**

4.1. Reasons for conflict
4.2. Consequences of conflict
4.3. Managing emotions
4.4. Methods of resolving conflicts
4.5. Experiential Learning – Based on activities

Unit 5

Career Mapping **(5 Hours)**

5.1. Goal Setting and Decision Making
5.2. Career Planning
5.3. Resume Writing
5.4. Handling Interviews
5.5. Experiential Learning – Based on activities

Workshop on Societal Analysis

BOOKS FOR REFERENCE

Khera. Shiv. *You Can Win*. New Delhi: Macmillan India, 2002.

Mishra. Rajiv. K. *Personality Development: Transform Yourself*. New Delhi: Rupa 2004.

Newstorm, John. W. and Scannell. Edward. E. *Games Trainers Play: Experiential Learning*. New Delhi: Tata McGraw Hill, 1980.

PATTERN OF EVALUATION

Internal Assessment: **Total Marks: 50**

Quiz / Group Presentation /Assignment

No End Semester Examination

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
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SYLLABUS
(Effective from the academic year 2019 -2020)

PYTHON AND R PROGRAMMING

CODE: 19BI/PC/PR34 **CREDITS : 4**
L T P : 4 1 0
TOTAL TEACHING HOURS : 65

OBJECTIVES OF THE COURSE

- 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
- Develop and write R scripts to replace missing values, normalize data, discretize data, and sample data

COURSE LEARNING OUTCOMES

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

- Relate the necessity for programming in biology
- Handling biological concepts with Python and R scripts
- Apply programing to analyse genomic sequences
- Gain efficient programming skills
- Perform genomic data analysis

Unit 1 **(12 Hours)**

Introduction to Python

1.1 Installation of Python, Variables, types, strings, Jupiter notebooks

1.2 Objects, functions, control structures, operators, Numpy and Scipy

1.3 Fasta files, Parsing DNA and protein information, Gene locations splices, extracting all gene locations

Unit 2 **(12 Hours)**

Biopython

2.1 Getting started and installation, Coding DNA, proteins, extracting translations

2.2 Modules- Bio Import, Bio Seq, Bio Align

2.3 Plot ABI traces, Retreive and Annotate Entrez gene

Unit 3 **(15 Hours)**

R programming

3.1 Introduction to R, Installing R, Loops

3.2 R as a Deluxe Calculator, Creating Objects and Assigning Values

3.3 Graphics: Simple Plotting, Advanced Plotting, Using Color in Plots, Using Subscripts and Superscripts in Graph Labels, Interactive Graphics, Saving Graphical Output, Loops

Unit 4 **(13 Hours)**

Gene Expression Data Analysis

4.1 Feature selection models, Data Preprocessing, Normalization- methods

4.2 Data reduction, data sampling, Heatmaps

4.3 Classification based on analogy, rules, probabilities, statistics and prediction with R

Unit 5 **(13 Hours)**

Bioconductor

5.1 Introduction, Bioconductor Packages

5.2 Expression set, data annotation biomart

5.3 Applications of R in Phylogenetics and Sequence analysis

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/

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes

Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: **Total Marks: 50**
Assignment/Test/Seminars

End Semester Examination: **Total Marks: 100** **Duration: 3 hours**

Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

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M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2019 -2020)

PYTHON AND R PROGRAMMING PRACTICAL

CODE: 19BI/PC/P232 **CREDITS : 2**
L T P : 0 0 3
TOTAL HOURS: 39

OBJECTIVE OF THE COURSE

- 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
- Develop and write R scripts to replace missing values, normalize data, discretize data, and sample data

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

- Relate the necessity for programming in biology
- Handling biological concepts with Python and R scripts
- Apply programing to analyse genomic sequences
- Gain efficient programming skills
- Perform Microarray data analysis using R language

Unit 1 **(7 Hours)**
Basics of Python
1.1 Counting letters in DNA strings
1.2 Write a Python program related to Bioinformatics transcription

Unit 2 **(8 Hours)**
Biopython
2.1 Biopython- using Bioseq –Sequence reading and writing
2.2 Biopython using Bio.Genbank – reading enteries

Unit 3 **(8 Hours)**
Basics of R
3.1 Creating vectors and dataframes
3.2 Plots – simple and advanced plots

Unit 4 **(8 Hours)**
Bioconductor
4.1 Bioconductor packages- bioclite, biostrings
4.2 Bioconductor packages- edge r

Unit 5 **(8 Hours)**

Data Analysis

5.1 Data Manipulation and visualization

5.2 Microarray data analysis – Limma

BOOKS FOR STUDY

Robert Gentleman, *R programming for Bioinformatics*, CRC Press, 2016

Jason Kinser. *Python for Bioinformatics*. Massachusetts: Jones and Barlett Publishers, 2009

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes

Part - A - Programs	3X 10- 30 marks
Part- B Programs and error handling	2X5 - 10 marks
Viva -	5 marks
Record -	5 marks

End Semester Examination Total Marks: 100 Duration: 3 Hours

Part - A - Programs -	3X 20- 60 marks
Part- B Programs and error handling	2X10 - 20 marks
Viva -	10 marks
Record -	10 marks

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2019 -2020)

ALGORITHMS FOR BIOINFORMATICS

CODE: 19BI/PC/AL34 **CREDITS : 4**
L T P : 4 1 0
TOTAL TEACHING HOURS : 65

OBJECTIVES OF THE COURSE

- To develop a quantitative understanding of how living things are built
- To raise the awareness of the impact of algorithms on the efficiency of the system
- To develop skills to analyse algorithms related to Bioinformatics

COURSE LEARNING OUTCOMES

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

- Know the main problems in the field of bioinformatics and computational molecular biology
- Analyse the correctness of algorithms and how it works
- Describe the divide-and-conquer paradigm and explain when an algorithmic design situation calls for it.
- Apply the algorithms and design techniques to solve problems
- Analyse the complexities of various problems in different domains

Unit 1 **(10 Hours)**

Introduction

1.1 Algorithms and Complexity. Definition, Biological Algorithms versus Computer Algorithms, Fast versus Slow Algorithms Big-O Notation

1.2 Algorithm Design Techniques Exhaustive Search Branch-and-Bound Algorithms Greedy Algorithms

1.3 Dynamic Programming Divide-and-Conquer Algorithms Machine Learning Randomized Algorithms

Unit 2 **(10 Hours)**

Restriction Mapping

2.1 Impractical Restriction Mapping Algorithms, Practical Restriction Mapping Algorithm

2.2 Regulatory Motifs in DNA Sequences Profiles: The Motif Finding Problem Search Trees

2.3 Finding a Median String. String matching algorithm

Unit 3 **(15 Hours)**

Sequence Alignment

3.1 Longest Common Subsequences - Global Sequence Alignment- Local Sequence Alignment

3.2 Graph Algorithms- Graphs and Genetics- DNA Sequencing Shortest Superstring Problem

3.3 DNA Arrays as an Alternative Sequencing Technique. Sequencing by Hybridization

Unit 4 **(15 Hours)**

Clustering and Evolutionary Trees

4.1 Gene Expression Analysis. Hierarchical Clustering -k-Means Clustering- Clustering and Corrupted Cliques

4.2 Evolutionary Trees - Distance-Based Tree Reconstruction Reconstructing Trees from Additive Matrices. Evolutionary Trees and Hierarchical Clustering Character-Based Tree Reconstruction

4.3 Secondary Structure Prediction methods, Artificial Neural Networks

Unit 5 **(15 Hours)**

Pattern Matching

5.1 Combinatorial Pattern Matching. - Identical, Similar and Distant Repeats Finding methods. Exact Pattern Matching

5.2 Keyword Trees and Suffix Trees. Heuristic Similarity Search Algorithms

5.3 BLAST: Comparing a Sequence against a Database

BOOKS FOR STUDY

Neil C Jones and Pavel A. Pevzner. *An Introduction to Bioinformatics Algorithms***.** USA: MIT press, 2011.

Pavel A. Pevzner. *Computational Molecular Biology- An algorithmic approach***.** USA: MIT press, 2004.

BOOKS FOR REFERENCE

Alfred V. Aho, John E. Hopcroft and Jefferey D.Ullman. *Data Structures and Algorithms.* London: Addison Wesley,1983.

Clark, John and Derek Allan Holton. *A First Look at Graph Theory*. Singapore: Singapore Publishers,1995.

Horowitz, Ellis, and Sartag Sahni. *Fundamentals of Computer Algorithms*. New Delhi: Galgotia Publications,1994.

Jeffrey J. McConnell. *Analysis of Algorithm*. New Delhi: Narosa Publishing House, 2002.

Thomas H. Cormen, Charles E. Leiserson and Ronald L. Rivest. *Introduction to Algorithms*. New Delhi: Prentice Hall of India, 1990.

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

PATTERN OF ASSESSMENT

Continuous Assessment: Total Marks: 50 Duration: 90 minutes
Section A: $5 \times 10 = 50$ (7 questions to be set)

Other Components: Total Marks: 50
Seminars/Assignments/Problem solving

End Semester Examination: Total Marks: 100 Duration: 3 Hours
Section A: $10 \times 10 = 100$ (12 questions to be set)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2019 -2020)

MOLECULAR MODELING AND COMPUTER AIDED DRUG DESIGN

CODE: 19BI/PC/MC34 **CREDITS : 4**
L T P : 4 1 0
TOTAL TEACHING HOURS : 65

OBJECTIVES OF THE COURSE

- To provide clear concepts on bond angle, bond stretching, bond distance and role on 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

- Perform protein structure prediction and understand energy simulation methods and its importance in drug action
- Gain insight on the molecular dynamics and Monte Carlo simulation methods
- Understand the concept of molecular interactions and QSAR studies
- Apply the knowledge gained to find new targets and design drug to treat diseases
- Learn the concept of drug development

Unit 1 **(13 Hours)**

Molecular Mechanics

1.1 Concepts in Molecular Modeling - Molecular Representations, Coordinate Systems, Potential Energy Surfaces

1.2 Molecular Mechanics, Force fields - Bond Length, Bond Angle and Torsion Angle potential

1.3 Non- bonded interactions-Van der Waals and Electrostatic Potential – Hydrogen Bonding Terms

Unit 2 **(12 Hours)**

Energy Minimization Methods

2.1 Energy Minimization- Derivative and Non-derivative Energy Minimization Methods

2.2 Calculation of Simple Thermodynamic Properties, Computer Simulation, Boundaries, Monitoring the Equilibration, Long Range Forces

2.3 Analyzing the Results of Simulation and Estimating Errors

Unit 3 **(15 Hours)**

Molecular Dynamics and Monte Carlo Simulations

3.1 Molecular Dynamics Using Simple Model, Molecular Dynamics with Continuous Potentials

3.2 Molecular Dynamics at Constant Temperature and Pressure, Incorporating Solvent effects into Molecular Dynamics, Conformational Changes From Molecular Dynamics Simulation

3.3 Monte Carlo Simulation of Molecules, Calculation of Chemical Potential-Simulating Phase Equilibria by Gibbs Ensemble Monte Carlo Method

Unit 4 **(12 Hours)**

Molecular Modeling and Structure Analysis

4.1 Protein Structure prediction - Secondary Structure Prediction, Homology modeling

4.2 Threading and *ab initio* method, Tools for Structure prediction; Protein structural visualization; Geometry optimization and Loop refinement

4.3 Structure validation tools - Ramachandran Plot.

Unit 5 **(13 Hours)**

Molecular Docking

5.1 Molecular Docking -Structure Based Drug Design - Target Discovery and Validation, Active Site Prediction, Lead identification and Optimization, De Novo Drug Design

5.2 Molecular Descriptors - QSAR, 3D Pharmacophore identification and mapping

5.3 Ligand-based drug designing approaches: Lead Designing, High Throughput Screening (HTS), Chemical libraries, ADME prediction

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 RESOURCES

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

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes

Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: Total Marks: 50

Assignment/Test/Seminars

End Semester Examination: Total Marks: 100 Duration: 3 hours

Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2019 -2020)

MOLECULAR MODELING AND COMPUTER AIDED DRUG DESIGN PRACTICAL

CODE: 19BI/PC/P332 **CREDITS : 2**

L T P : 0 0 3

TOTAL TEACHING HOURS : 39

OBJECTIVE 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; mechanism of drug designing
- 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

- Perform, understand, and interpret the results of the calculations and bring them in a publication ready form
- Understand the importance of drug-like properties and their prediction
- Describe the use of lead candidates and database representations
- Apply Molecular modeling and molecular dynamics methods to study structure from sequence

Unit 1 **(8 Hours)**

1.1 Drug target identification - structural databases, RCSB PDB

1.2 Drug target databases, Protein function prediction tools – RaptorX and online other tools)

Unit 2 **(8 Hours)**

2.1 Homology modeling - Swiss model, Modeller software

2.2 Protein structure validation – Rampage, Procheck

Unit 3 **(7Hours)**

3.1 Ligand Search – Pubchem, Drug bank, CHEMBL, ZINC databases

3.2 Chemical drawing package – Marvin Sketch, Chemdraw

Unit 4 **(8 Hours)**

4.1 ADME prediction – Online tools (Swiss ADME, etc.,)

4.2 QSAR model prediction – In Silico tools

Unit 5 **(8 Hours)**

5.1 Protein Active site prediction – (CASTp and online tools)

5.2 Molecular Docking – Auto dock, Argus Lab and other docking software, Scoring Functions, Simple Interaction Energies, Visualizing tools – Pymol, Rasmol

BOOKS FOR REFERENCE:

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

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

Luca Monticelli, Emppu Salonen. Biomolecular Simulations: Methods and Protocols. USA: Humana Press, 2016**.**

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes

Two out of four questions to be answered	(2 X 20=40)
Viva -	5 marks
Record -	5 marks

End Semester Examination Total Marks: 100 Duration: 3 Hours

Four out of five questions to be answered	(4 X 20=80)
Viva -	10 marks
Record -	10 marks

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2019 -2020)

SUMMER INTERNSHIP

CODE: 19BI/PN/SI32 **CREDITS: 2**

OBJECTIVES OF THE COURSE

- To enable students to gain experiential learning in the field of Bioinformatics
- To acquire hands on training in Bioinformatics Softwares

The Summer Internship program is for a minimum period of three weeks. The students are expected to have regular attendance in their respective Institutes and submit a report to the Department reporting the experiments they have observed/conducted. The students are expected to give a seminar presentation in the third semester of the work they have observed/conducted.

Guidelines for Evaluation

The maximum marks for the Summer Internship is 50 and is divided into the following:

a) Log Book (20 Marks)
b) Seminar presentation (15 Marks)
c) Attendance (15 Marks)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2019 -2020)

ADVANCES IN BIOINFORMATICS

CODE: 19BI/PC/AB44 **CREDITS : 4**
L T P : 4 1 0
TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- To develop a quantitative understanding of recent and emerging fields of Bioinformatics
- To provide Hands on experience of handling the genomic and proteomic datasets
- To provide a better understanding of data and its applications in Bioinformatics

COURSE LEARNING OUTCOMES

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

- Students will be able to analyse the raw reads of sequences
- Understand the analysis of gene expression
- Experiential knowledge on gene editing techniques
- Perform genomic data analysis
- Learn the skills of cancer genomic data analysis

Unit 1 **(10 Hours)**

Next Generation Sequencing

1.1 Introduction to Next-generation sequencing. History and Future of DNA Sequencing
1.2 Introduction to Linux commands and Different Platforms and Applications
1.3 Different file formats – FASTQ, SAM, BAM, GFF, Databases and tools – UCSC genome, Galaxy, SRA, NCBI refseq, ENA, FastQC, Bowtie

Unit 2 **(12 Hours)**

Metagenomics

2.1 Metagenomics – Introduction and biological background, case studies of recent research
2.2 Alpha and Beta diversity of metagenomic studies
2.3 Analysis of metagenome data and logical steps for metagenome analysis

Unit 3 **(15 Hours)**

Transcriptomics

3.1 Introduction and Biological background, case studies of recent research
3.2 Quantifying RNA: RNA seq and other techniques. Generating expression table
3.3 Logical steps for analysing RNA seq data – differential expression and factor regression analysis

Unit 4

Epigenetics **(15 Hours)**

4.1 Gene regulatory dynamics from analysis of regulatory sequence motifs, transcription factor-DNA interaction,

4.2 Local chromatin dynamics and epigenetic modifications, RNA dynamics at the level of transcription and post-transcriptional processing,

4.3 3D dynamics of chromatin and the resulting gene regulatory dynamics on daily and development time scales

Unit 5 **(13 Hours)**

Crispr- Cas 9

5.1 Introduction to Crispr, cas9, selection of targets from sequences

5.2 Targeted mutagenesis – guide RNA design, recognition sequences

5.3 Repair and data analysis of the edited genome, Therapeutic applications

BOOK 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

BOOKS FOR REFERENCE

Takashi Yamamoto. *Targeted Genome Editing Using Site-Specific Nucleases: ZFNs, TALENs, and the CRISPR/Cas9 System*, 2015

Jennifer Doudna, Prashant Mali, *CRISPR-Cas: A Laboratory Manual,* Cold Spring Harbor Laboratory Press, 2016

Richard Cummings, J. Pierce, *Handbook of Glycomics*, Academic Press, 2009 ISBN: 9780123736000

WEB RESOURCES

http://www.ebi.ac.uk/training/online/course/ebi-next-generation-sequencing-practicalcourse/what-you-will-learn/what-next-generation-dna-
http://www.personal.psu.edu/iua1/courses/2014-BMMB-852.html
https://www.illumina.com/science/technology/next-generation-sequencing.html
https://bitesizebio.com/21193/a-beginners-guide-to-next-generation-sequencing-ngs-technology/
https://edu.t-bio.info/courses

JOURNALS

Next generation sequencing

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes

Theory:

Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 5 x 2 = 10 Marks (2 out of 4 to be answered)
Section C – 2 x 10 = 20 Marks

Other Components: Total Marks: 50

Assignment/Test/Seminars

End Semester Examination: Total Marks: 100 Duration: 3 hours

Theory:

Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (2 out of 4 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 3 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2019 -2020)

BIG DATA ANALYSIS

CODE: 19BI/PC/BD44 **CREDITS : 4**
L T P : 4 1 0
TOTAL TEACHING HOURS : 65

OBJECTIVES OF THE COURSE

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

OUTCOMES OF THE COURSE

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

- Describe the Big Data landscape including examples of real world big data problems
- Explain the V's of Big Data and impacts of data collection, monitoring, storage, analysis and reporting
- Identify what are and what are not big data problems and be able to recast big data problems as data science questions
- Gain skills of Hadoop technology
- Learn to get value out of bigdata

Unit 1 **(12 Hours)**

Introduction to Data Science

1.1 Introduction to data science, Case Studies: Data Science in Biomedicine and Healthcare
1.2 Sequence Processing, Medical Image Analysis, Natural Language Processing
1.3 Network Modelling and Probabilistic Modelling

Unit 2 **(15 Hours)**

Big Data

2.1 What is big data? What makes big data valuable Example of Big Data
2.2 Where Does Big Data Come From? Machine-Generated Data and Advantages
2.3 Big Data Generated by People, organization of Generated Data, integrating the data

Unit 3 **(13 Hours)**

Characteristics of Big Data

3.1 Characteristics of big data Volume, Variety, Velocity
3.2 Characteristics of Big Data – Veracity, Valence and Value
3.3 Getting value out of big data using a 5-step process to structure your analysis

Unit 4 **(12 Hours)**

Data Science: Getting Value out of Big Data

4.1 Building a Big Data Strategy, How does big data science happen? Five Components of Data Science

4.2 Steps in the Data Science - Acquiring Data , preprocessing and Exploring Data

4.3 Analyzing Data, Communicating Results, Turning Insights into Action

Unit 5 **(13 Hours)**

Big data systems and Hadoop

5.1 What is a Distributed File System? Scalable Computing over the Internet, Programming Models for Big Data6m

5.2 Introduction to Hadoop systems, The Hadoop Distributed File System: A Storage System for Big Data, YARN: A Resource Manager for Hadoop

5.3 MapReduce: Simple Programming for Big Results, When to Reconsider Hadoop? Cloud Computing: An Important Big Data Enabler

BOOKS FOR STUDY

Peter Guerra and Kirk Borne, *Ten Signs of Data Science Maturity*, O'Reily media Pvt ltd, 2016,

Tom White, *Hadoop: The Definitive Guide" Third Edition*, O'reily Media, 2012.

Seema Acharya, Subhasini Chellappan, *Big Data Analytics*, Wiley 2015.

BOOKS FOR REFERENCE

Howard Wen, *Big Ethics for Big Data*, O'Reilly Media

Michael Mineli, Michele Chambers, Ambiga Dhiraj, *Big Data, Big Analytics: Emerging Business Intelligence and Analytic Trends for Today's Businesses*, Wiley Publications, 2013.

Judith S.Hurwitz, Alan Nugent, Fern Halper, Marcia Kaufman **,** *Big Data for Dummies*, 2015

JOURNALS

Journal of Bigdata, Springer
Big Data Research, Elseiver

WEB RESOURCES

https://www.coursera.org/learn/big-data-introduction/home/welcome
https://www.coursera.org/learn/bioconductor?action=enroll&authMode=login

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes
Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: Total Marks: 50
Assignment/Test/Seminars

End Semester Examination: Total Marks: 100 Duration: 3 hours
Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2019 -2020)

ADVANCES IN BIOINFORMATICS PRACTICAL

CODE: 19BI/PC/P442 **CREDITS : 2**
L T P : 0 0 3
TOTAL HOURS: 39

OBJECTIVES OF THE COURSE

- Demonstrate how to locate and download files for data analysis involving genes and medicine
- Select datasets and pre-process data using
- Develop and replace missing values, normalize data, discretize data, and sample data

COURSE LEARNING OUTCOMES

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

- Analyse genomic sequences
- Handle raw data
- Understand the steps of data assembling
- Learn RNA sequence analysis
- Understand and design sg RNA for genome editing

Unit 1 **(7 Hours)**
Basics of NGS
1.1 Introduction to UNIX commands and Virtual machine

Unit 2 **(8 Hours)**
Metagenomics
2.1 Analysis of metagenomic raw data using galaxy

Unit 3 **(8 Hours)**
Transcriptomics
3.1 Cancer data analysis using Webmev

Unit 4 **(8 Hours)**
RNA seq analysis
4.1 RNA seq analysis using Biojupies

Unit 5 **(8 Hours)**
Crispr cas 9
5.1 Small guide RNA design – Chop Chop, primerX

BOOKS FOR STUDY

Head**,** Steven R**.,** Ordoukhanian, Phillip, Salomon, Daniel R, *Next Generation Sequencing*

Methods and Protocols, Springer Protocols, Humana Press, 2018.

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes

Data analysis any two methods	2X20= 40 marks
Viva -	5 marks
Record -	5 marks

End Semester Examination Total Marks: 100 Duration: 3 Hours

Data analysis any two methods	2X40= 80 marks
Viva -	10 marks
Record -	10 marks

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2019 -2020)

DISSERTATION

CODE: 19BI/PC/DS47 **CREDITS: 7**

The Dissertation shall contain at least 50 pages and shall be typed with double spacing.

The format for the thesis is as follows:

1. Cover page shall contain
   a) Title of the dissertation
   b) Name of the Candidate
   c) Department of Bioinformatics
      Stella Maris College (Autonomous), Chennai – 86
   d) Month, Year

2. The dissertation shall contain
   a) Contents page
   b) i. Certificate page
      ii. Acknowledgement page
   c) At least 5 Chapters including an introduction, Review of Literature, Materials and Methods, Result and Discussion and Summary
   d) List of figures / list of abbreviations (if needed) shall be given as an appendix
   e) Bibliography shall be given in alphabetical / chronological order at the end.

3. Each candidate may prepare 3 hard copy and one soft copy of the thesis, one copy for her and submit 2 copies to the Head of the department 15 days before the commencement of the fourth semester examination.

4. The candidate may be advised that the dissertation will be valued and given credit on the criteria of
   a) Motivation towards the chosen area / formulation of the problem
   b) Methodology and Analysis
   c) Capacity to interpret the results obtained

5. The Controller of Examination is requested to arrange for the valuation of the Dissertation as well as the conduct of the Viva – Voce at the college where the candidates take examinations, within two weeks of the last date of

examination for M.Sc. Degree. The panel of examiners will consist of an external examiner and the guide. The guidelines for the Viva-Voce examiners would be that a) They will satisfy themselves that this is a work of the candidate as certified by the department b) The thesis is in the given form and c) The candidate has clear understanding of the concepts, discussed in the thesis.

PATTERN OF ASSESSMENT

Continuous Assessment : **Total Marks: 50**

Periodic review	25 marks
Presentation	25 marks

End Semester Examination: **Total Marks: 100**

i.	Style, format and neatness in presentation	15
ii	Chapterization, logic and reasoning	10
iii	Methodology – Analysis and interpretation	25
iv	Viva	50

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2019 -2020)

CELL BIOLOGY AND GENETICS

CODE: 19BI/PE/CG15 **CREDITS : 5**
L T P : 4 1 0
TOTAL TEACHING HOURS:65

OBJECTIVES OF THE COURSE

- To understand the structure and function of the basic unit of life
- To gain knowledge about the Cell and all its components in both Prokaryotic and Eukaryotic cells
- To familiarize the students with the basic concepts of Genetics

COURSE LEARNING OUTCOMES

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

- Understand the functions of the cell at the molecular level
- Represent and illustrate the structural organization of genes and the control of gene expression
- Explore the prokaryotic and eukaryotic protein synthesis mechanism
- Conceptualize mechanisms of signal transduction, cell cycle and cell death
- Link the concepts of cell and molecular biology to a better understanding of diseases, including cancer

Unit 1 **(10 Hours)**

Prokaryotic and Eukaryotic cells

1.1 Introduction - Prokaryotic and Eukaryotic cell - Characteristics, Similarities and differences
1.2 Bacteria Cells - Structure, organisation and bacterial genetics
1.3 Virus - Structure, Viral Infective cycles, origin and significance, Viroids and Prions

Unit 2 **(15 Hours)**

Organelles

2.1 Structure and function of Mitochondria, Plastids (i.e. chloroplasts), Endoplasmic Reticulum Golgi bodies, Lysosomes and Peroxisomes
2.2 DNA -Structure – conformations, Histones and Non-Histones, Nuclear matrix and Lamins; Nuclear envelope, Pore complexes, transport through the envelope
2.3 RNA- Types, Ribosomes – Structure, Assembly of polypeptides on Ribosomes

Unit 3 **(15 Hours)**

Cytoskeleton

3.1 Structure of the Cell Wall

3.2 Structure and Role of Microtubules and Microfilaments in cells -cell-cell interactions- cell adhesion, tight junctions and plasmodesmata

3.3 Introduction to Membranes - Structure, Function, and Communication: Roles of membranes in eukaryotic cells; Membrane structure and composition, The Plasma Membrane - Fluid Mosaic Model

Unit 4 **(13 Hours)**

Multiple alleles

4.1 Human blood groups (A, B, AB, O, M, N and H) and Rh factor - Inheritance and significance

4.2 Gene Linkage and Recombination**:** Coupling and repulsion hypothesis Linkage in *Drosophila* Cytological proof of crossing over - Example – *Drosophila*

4.3 Mapping: Locating genes along a chromosome: Two - point and three - point crosses

Unit 5 **(12 Hours)**

Cell Cycle and Karyotyping

5.1 Chromosomes- Structure and function, Centromers and Telomers, Cell Cycle-Mitosis and Meiosis

5.2 Karyotyping, Sex determination in Human - Barr body - Importance of Y Chromosome - Klinefelters' and Turners' Syndromes

5.3 Inter –sexuality Linked Inheritance: Colour blindness and Haemophilia Y - linked genes

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.

Klug, William, S. and Michael R. Cummings. *Concepts of Genetics.* USA: Prentice Hall, 2008.

Purvis, William K, David Sadava, Craig Heller and Gordan H. Orians. *Life: The Science of Biology.* USA : Sinauer, 2004.

BOOKS FOR REFERENCES

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, 2000.

Karp and Gerald. *Cell and Molecular Biology- Concepts and Experiments*, USA : John Wiley, 2013.

Karp, Gerald and Nancy L. Puritt, *Cell and Molecular Biology- Concepts and Experiments*, USA: John Wiley, 2004.

Lodish Harvey, Arnold Berk, Paul Matsudaira, Chris A. Kaiser, Monte Krieger, Mathew P. Scott, S. Lawrence Zipursky and James Darnell. *Molecular Cell Biology*. USA: W.H. Freeman,2004.

Burns, George W., and Botto, Paul J. *The Science of Genetics.* USA: Macmillan Publishing Company, 1989.

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.

Watson, James, D. *Molecular Biology of the Gene***.** USA : The Benjamin Cummings Publishing Company,2007.

JOURNALS

Journal of Molecular Biology
Journal of Genetics and Genomics
BMC Cell Biology

WEB SOURCES

www.cellbio.com
www.molbiolcell.org
www.sciencedirect.com
http://www.biology.arizona.edu/cell_bio/cell_bio.html

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes
Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: Total Marks:50
Assignment/Quiz/Case studies/Seminars

End Semester Examination: Total Marks: 100 Duration: 3 Hours
Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2019-2020)

BIOMATHEMATICS AND BIOSTATISTICS

CODE: 19BI/PE/BS15 **CREDITS: 5**
L T P: 4 1 0
TOTAL TEACHING HOURS: 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 analyzing 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

- Understand the importance of mathematics for research based problems
- Apply the different statistical tests for the research
- Learn to solve aptitude based problems in competitive exams
- Gain skills on solving the population genetics equations
- Apply the regression and correlation techniques to interpret Drug activity based on QSAR

Unit 1 **(15 Hours)**

Set Theory and Matrices

1.1 Introduction, Representation of a Set, Set Operations - Types of Sets, Subsets, Complement of Sets, Union and Intersection of Sets, Difference of Sets
1.2 De Morgan's Law, Venn diagram, Cartesian Product of Sets
1.3 Matrix, Basic Operations, Transpose, square matrices, Non Singular Matrices, Inverse of a Matrix, Determinants, Elementary Applications

Unit 2 **(10 Hours)**

Relations and Functions

2.1 Introduction – Product sets, Relations
2.2 Functions – Linear Function
2.3 Related Functions – Polynomials and Differences

Unit 3 **(15 Hours)**

Probability

3.1 Rules of probability, Theorems of probability, Addition and Multiplication Theorem
3.2 Probability distributions: Binomial distribution, Poisson distribution, Normal distribution.
3.3 Binomial Co-efficient, Permutations, Combinations, Identities Applications

Unit 4 **(12 Hours)**

Introduction to Biostatistics

4.1 Scope, collection, classification and tabulation, Graphical representation of data-measures of location and dispersion -Diagrammatic and Graphical Presentation of data, Types of data, Significance and uses of diagrammatic representation-limitations.

4.2 Frequency distribution: Discrete and continuous frequency distribution. Mean-Median- Mode.

4.3 Measures of dispersion- Standard Deviation, Coefficient of variation, Range

Unit 5 **(13 Hours)**

Application and Testing

5.1 Sampling techniques, Sampling Distribution, Standard error, testing of hypotheses, Null Hypothesis

5.2 Correlation - Types of correlation-Simple, Linear and Nonlinear- Pearson's Coefficient Correlation, Regression analysis- Types of Regression, Regression Equation of X on Y

5.3 χ^2 test, t-test, Analysis of Variance (ANOVA), Population Genetics: Hardy–Weinberg principle

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*, (4^{th} 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/

PATTERN OF ASSESSMENT

Continuous Assessment: **Total Marks: 50** **Duration: 90 mins.**
Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: **Total Marks: 50**
Assignment/Class Test

End Semester Examination: **Total Marks: 100** **Duration: 3 Hours**
Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

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SYLLABUS
(Effective from the academic year 2019 -2020)

DATA MINING

CODE: 19BI/PE/DM15 **CREDITS : 5**
L T P : 4 1 0
TOTAL TEACHING HOURS : 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

- Gain insight into the field of Bioinformatics from theoretical models to finished software
- Understand how software design and methods can be integrated with existing tools to create productive information environment for bioinformatics practice
- Understand how open source can be powerful in creating web-based applications in Bioinformatics
- Understand important roles of programming languages and databases in Bioinformatics software development and service

Unit 1 **(10 Hours)**

Data mining

1.1 Introduction: Classification of data, Relational databases. Data warehouses Transactional databases .Advanced database systems and advanced database applications.

1.2 Data mining functionalities. Concept /class description.

1.3 Characterization and discrimination. Association analysis

Unit 2 **(10 Hours)**

2.1 Classification and prediction -Clustering analysis. Evolution and deviation analysis

2.2 Classification of data mining systems. Major issues in data mining

2.3 Multimedia data mining. Spatial data mining. Text mining

Unit 3 **(15 Hours)**

Data Processing

3.1 Data Preprocessing. Data integration and transformation, Data reduction. Association rule mining.

3.2 The Apriori algorithm: Finding frequent item sets From association mining to correlation analysis

3.3 Classification and Prediction Classification by back propagation association-based classification and other classification methods

Unit 4 **(15 Hours)**

Clustering

4.1 Clustering – cluster analysis – Types of clustering methods- Types of data in clustering analysis

4.2 A categorization of major clustering methods. Hierarchical methods. Density Based clustering methods. Grid based methods. Outlier analysis.

4.3 Data Mining applications and trends in data mining – Data mining applications in biotechnology and bioinformatics

Unit 5 **(15 Hours)**

Neural networks and machine learning

5.1 Introduction to Neural networks, learning rules

5.2 Classification Analysis, learning algorithm and model evaluation

5.3 SOM and SVM techniques in data mining

BOOKS FOR STUDY

Jiawei Han and Micheline Kamber. *Data Mining: Concepts and Techniques,* USA: Morgan Kaufmann Publishers, 2011.

BOOKS FOR REFERENCE

Oliviero carugo and Frank Eisenhaber. *Data Ming techniques for life sciences.* Singapore: Humana Press, 2009.

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/

PATTERN OF ASSESSMENT

Continuous Assessment: Total Marks: 50 Duration: 90 minutes.
Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: Total Marks:50
Assignment/Case study/Seminars

End Semester Examination: Total Marks: 100 Duration: 3 Hours
Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

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SYLLABUS
(Effective from the academic year 2019 -2020)

IMMUNOINFORMATICS

CODE: 19BI/PE/IM15 **CREDITS : 5**
L T P: 4 1 0
TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- 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

COURSE LEARNING OUTCOMES

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

- Understand the application of information technology to immunology
- Study informatics-based approaches for prediction of epitopes and immuno-diagnostic tools
- Gain knowledge about computer aided vaccine design

Unit 1

Immune System **(10 Hours)**

1.1 Introduction to Immune System - Adaptive and Innate Immunity
1.2 Cells of the Immune System, Soluble Mediators of Immunity, Cell and Antibody mediated immunity
1.3 Immune Responses - Inflammation, Immunopathology, Auto immune diseases, Vaccines

Unit 2

Antigens and Antibodies **(15 Hours)**

2.1 Immunoglobulin classes and subclasses, Major Histocompatibility Complex (MHC) its Polymorphism, Causes for Polymorphism, MHC Supertypes
2.2 Antigen types – Epitope, Affinity Maturation, Epitope mapping
2.3 B-cell and T-cell Epitope Prediction, Recognition of Antigen by B cells. Neutralizing Antibody

Unit 3

Computational Immunology **(10 Hours)**

3.1 Computational Immunology - Databases in Immunology, dbMHC-MHC database at NCBI
3.2 T-cell epitope databases, B-cell epitope databases, SYFPEITHI MHC-presented epitopes
3.3 IMGT Immunoinformatics, IMGT International ImMunoGeneTics Information System. HLA Nomenclature and the IMGT/HLA Sequence Database

Unit 4 **(15 Hours)**

Vaccine Design

4.1 From immunome to Vaccine – Prediction of immunogenicity, Vaccine design tools
4.2 Reverse Vaccinology and Immunoinformatics, Peptides with Antimicrobial Activity or Antibiotic Peptides
4.3 Functional Prospecting of Genes and Transcripts, Future of Computational Modelling and Prediction Systems in Clinical Immunology

Unit 5

Viral Bioinformatics **(15 Hours)**

5.1 Viral Bioinformatics - Computational Views of Hosts and Pathogens using VIDA
5.2 Drug Discovery - Introduction, Conventional Drug Design Approaches, Lipinski rule, Pharmacophore Kinetics and Dynamics, ADME Properties
5.3 Applications of Computer Based Drug Discovery

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.

Christian Schönbach, ShobaRanganathan, and Vladimir Brusic. *Immunoinformatics (Immunomics Reviews)* USA: Humana Press, 2010.

BOOKS FOR REFERENCE

Kenneth Murphy. *Janeway's Immunobiology*, UK: Garland Science, 2014.

Robert A. Meyer. *Immunology - from cell biology to disease***.**Germany: Wiley VCH, 2007.

Richard A. Goldsby, Thomas .J Kindt, Barbara A. Osborne & Janis Kuby. *Immunology*. USA: WH Freeman Company, 2013.

JOURNALS

Immunology
Immunoinformatics
Journal of Computational Biology

WEB RESOURCES

http://www.imgt.org/Immunoinformatics.html
http://rsob.royalsocietypublishing.org/content/3/1/120139

http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.0020071
http://omicsonline.com/immunoinformatics.php

PATTERN OF ASSESSMENT

Continuous Assessment: Total Marks: 50 Duration: 90 minutes
Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: Total Marks:50
Assignment/Tests/Seminars

End Semester Examination: Total Marks: 100 Duration: 3 hours
Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

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SYLLABUS
(Effective from the academic year 2019-2020)

BASICS OF CLINICAL RESEARCH MANAGEMENT

CODE:19BI/PE/CR15 **CREDITS : 5**
L T P : 4 1 0
TOTAL PRACTICAL HOURS : 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

- Evaluate critical global regulatory and health care issues that challenge and influence biopharmaceutical product development
- Understand the basic statistical principles, concepts, and methods for clinical data analysis and reporting
- Forecast the resources necessary for developing and managing clinical trials
- Demonstrate advanced critical thinking skills necessary to enhance employment opportunities or advance within the biopharmaceutical industry

Unit 1 **(10 Hours)**

Clinical Research

1.1 History of drug development - Pharmaco-epidemiology
1.2 Issues in Clinical Trials. Nuremberg Code, Declaration of Helsinki, International Conference of Harmonization and Good Clinical Practice
1.3 Clinical trials – History of clinical trials. Stages of Clinical trials

Unit 2 **(10 Hours)**

Pharmacology and Drug Development

2.1 Introduction to Drug Discovery and Development, Approaches, Sources of Drugs, Databases for drug search
2.2 Pharmacokinetics and pharmacodynamics, Toxicological requirements
2.3 Emerging technologies in Drug Discovery**,** Preclinical Testing, Clinical Trials

Unit 3 **(15 Hours)**

Regulations in Clinical Research

3.1 Evolution and History of Regulations in Clinical Research, US FDA Regulations, IND, NDA, ANDA, FDA Audits and Inspections
3.2 European Regulatory Affairs, Organization and Functions
3.3 INDIAN Regulatory system, Schedule Y- Rules and Regulations, Post Drug Approval Activities, PMS

Unit 4 **(15 Hours)**

Clinical Trial Management

4.1 Role of Ethics Committees and Institutional Review Boards. Special populations; women elderly and children

4.2 Designing of Protocol, SOP, ICF, Pharmacovigilance

4.3 Project management Documentation, Monitoring, Audits, Inspections, Fraud and Misconduct, Roles and Responsibilities of Clinical Research Professionals

Unit 5 **(15 Hours)**

Clinical Data Management

5.1 Importance of CDM in clinical research, Clinical Data Entry**,** CRF, e-CRF

5.2 Statistical considerations at the design, analysis and reporting stage.

5.3 Data validation, SAE reconciliation, Quality Assurance

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

PATTERN OF ASSESSMENT

Continuous Assessment: Total Marks: 50 Duration: 90 mins.

Section A – 10 x 1 = 10 Marks (All questions to be answered)

Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)

Section C – 1 x 20 = 20 Marks (1out of 2 to be answered)

Other Components: Total Marks: 50

Seminars/Quiz/Group discussion//Assignments/Case studies, etc.

End Semester Examination **Total Marks: 100** **Duration: 3 Hours**

Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

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SYLLABUS
(Effective from the academic year 2019 -2020)

CHEMINFORMATICS

CODE: 19BI/PE/CI15 **CREDITS : 5**
L T P: 4 1 0
TOTAL TEACHING HOURS: 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

- Gain skills to analyse the properties of small molecules
- Design the biological targets and properties of the small molecule under investigation
- Better understanding of the drug discovery and development process
- Apply the concepts to create novel leads

Unit 1 **(15 Hours)**

Introduction

1.1 Introduction to Cheminformatics, History and Evolution of Cheminformatics, Use of Cheminformatics, Prospects of Cheminformatics
1.2 Databases: Chemical Structure Databases (PubChem, Drug bank)
1.3 Modelling of small molecules and Structure Elucidation

Unit 2 **(10 Hours)**

Representation of Molecules

2.1 Representation of Molecules and Chemical Reactions
2.2 Different Types of Notations, SMILES Coding, Structure of Mol files and Sdf files (Molecular converter, SMILES Translator)
2.3 Similarity Search of the Molecule

Unit 3 **(15 Hours)**

Cheminformatics databases

3.1 Structure databases; Reaction Databases; Literature Databases; Medline; GenBank
3.2 PIR; CAS Registry; National Cancer Institute (NCI) Database
3.3 Databases of Small Molecules (ZINC)

Unit 4 **(10 Hours)**

Searching Chemical Structure

4.1 Searching Chemical Structure: Full Structure Search; Sub Structure Search; Similarity Search
4.2 Three dimensional Search Methods. Structure Visualization

4.3 Drawing the Chemical Structure: 2D and 3D Drawing Tools (ACD Chemsketch) Structure Optimization

Unit 5 (15 Hours)

Applications of Cheminformatics tools

5.1 Definition of drugs, Structure-Based Drug Design, QSAR

5.2 Pharmacophore Design, Ligand-Based Design, De Novo Drug Design Virtual Screening / Docking of Ligands

5.3 Protein structure-Fragment-Based Drug Design, ADMET Prediction

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

PATTERN OF ASSESSMENT

Continuous Assessment: **Total Marks: 50** **Duration: 90 mins.**
Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: **Total Marks: 50**
Assignment/Case study/Seminars

End Semester Examination: **Total Marks:100** **Duration: 3 Hours**
Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

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SYLLABUS
(Effective from the academic year 2019-2020)

BIOPHYSICS

CODE: 19BI/PE/BP15 **CREDITS: 5**
L T P: 4 1 0
TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- To give a basic understanding about the forces that determines the structure of biological macromolecules
- To provide knowledge about the techniques used in studying biological structure and function
- To understand the behaviour and properties of biological macromolecules

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

- Understand the importance of structural studies in bioinformatics
- Gain an insight about the forces that determines the structure of biological macromolecules
- Apply the knowledge gained to interpret the properties of biological macromolecules
- Apply the recent advances in Biophysical techniques in Life science Research

Unit 1

Introduction **(10 Hours)**

1.1 Atoms, Molecules and Chemical Bonds
1.2 Bohr Model of the Atom, Atomic Spectra, De Broglie Theory of Matter Waves, Schrödinger Wave Equation, Atomic and Molecular Orbitals, Hybrid Orbitals
1.3 Thermodynamics Systems – Laws of Thermodynamics – Statement and Applications – Concepts of Entropy and Enthalpy

Unit 2

Spectroscopy **(15 Hours)**

2.1 Visible, UV And IR Spectroscopy
2.2 Raman Spectroscopy –'Fingerprinting' Using Raman Spectra – Complementarity of Raman and IR Spectroscopy
2.3 Fluorescence Spectroscopy – Principles and Applications only for all

Unit 3

Nuclear Magnetic Resonance **(15 Hours)**

3.1 The Phenomenon, Spin-Spin Interaction
3.2 Relaxation and Nuclear Overhauser Effect, Chemical Shift, Measuring the Spectrum
3.3 One Dimensional and Two Dimensional NMR, NMR Application to Macromolecules

Unit 4

Mass Spectrometry **(15 Hours)**

4.1 Mass Spectrometry for Protein and Peptide Analysis

4.2 MALDI-TOF Analyzer, Tandem Mass Analyzer, The Ion Trap Mass Analyzer, Q-TOF Instrument

4.3 Protein identification by Peptide Mass Fingerprinting, Peptide Sequence Analysis by TMS

Unit 5

Crystallography and Microscopy **(10 Hours)**

5.1 Elementary Description of Crystallography – Crystal Growth, Data Collection, Structure Solution, Refinement and Interpretation – Concept of Resolution

5.2 AFM: Atomic Force Microscopy Basic Principle and Application

5.3 CFM: Chemical Force Microscopy Basic Principles and Applications

BOOKS FOR STUDY

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

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.

C.R.Cantor and P.Schimmel. *Biophysical Chemistry, Vol. I, II and III***.** New York, USA: W.H.Freeman and Company, 1985.

Sears F. W, Zemansky M.W and Young H.D. *College Physics*, Massachusetts, USA: Addison Wesley Publishing Company, 1985.

Leach A.R, *Molecular Dynamics Simulation.* New York, USA: John Wiley and Sons, 2001.

A.P. Gunning, A. R. Kirby, V. J. Morris. *Atomic Force Microscopy***.** London: Imperial College Press, 2009.

JOURNALS
Biophysical Journal
European Biophysics Journal
Journal of Biophysics

WEBSITES
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

PATTERN OF ASSESSMENT

Continuous Assessment: **Total Marks: 50** **Duration: 90 minutes**
Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: **Total Marks: 50**
Seminars
Assignment
Interpretation of results

End Semester Examination: **Total Marks: 100** **Duration: 3 Hours**
Section A – 20 x 1 = 20 Marks (All questions to be answered)
Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)
Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

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SYLLABUS

(Effective from the academic year 2019 -2020)

INTRODUCTION TO BIOINFORMATICS

CODE: 19BI/PE/IB23 **CREDITS : 3**

L T P : 3 0 0

TOTAL TEACHING HOURS : 39

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

- Better understanding of the bioinformatics concepts
- Emphasis the application of bioinformatics and biological databases to problem solving in real research problems
- Perform a complete analysis of the genes and protein
- Understand the evolutionary concepts related to biological query

Unit 1 **(8 Hours)**

Introduction to Bioinformatics

1.1 Introduction to Bioinformatics, Classification of biological databases, Biological data formats, Application of bioinformatics in various fields

1.2 Introduction to single letter code of amino acids, symbols used in nucleotides

1.3 Data retrieval systems- Entrez and SRS

Unit 2 **(8 Hours)**

Sequence and Structure analysis

2.1 Introduction to Sequence alignment. BLAST, Multiple sequence alignment

2.2 Structural Databases – PDB and other online tools

2.3 Visualizing tools – Rasmol, Pymol

Unit 3 **(7 Hours)**

Phylogenetic analysis

3.1 Evolutionary analysis: distances, Cladistic and Phenetic methods

3.2 Clustering Methods. Rooted and unrooted tree representation

3.3 Bootstrapping strategies, Tools for Phylogenetic tree construction

Unit 4 **(8 Hours)**

Genomics

4.1 Genome - Gene finding methods,
4.2 Gene prediction tools
4.3 Repeat Sequence finder

Unit 5 **(8 Hours)**

Proteomics

5.1 Proteomics - Protein structure – levels of organisation
5.2 Protein separation techniques – SDS-PAGE
5.3 Restriction Enzymes and Mapping

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

PATTERN OF ASSESSMENT

Continuous Assessment Test: Total Marks: 50 Duration: 90 minutes
Section A – 10 x 1 = 10 Marks (All questions to be answered)
Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Other Components: Total Marks:50
Assignment/Test/Seminars

End Semester Examination: Total Marks: 100 Duration: 3 Hours
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STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2019 -2020)

APPLICATIONS OF BIOINFORMATICS

CODE: 19BI/PE/AP23 **CREDITS : 3**
L T P : 3 0 0
TOTAL TEACHING HOURS: 39

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

- Examine factors that affect drug response and the application of pharmacogenetics to drug development and drug treatment
- Apply the immunological data and to the sophisticated computational solutions available for immunological research
- Emphasis the application of bioinformatics and biological databases to problem solving in real research problems

Unit 1 **(7 Hours)**

Introduction to Bioinformatics

1.1 Classification of biological data, and different data formats
1.2 Introduction to single letter codes of amino acids, symbols used in nucleotides
1.3 Bioinformatics Perspectives on Human Diseases

Unit 2 **(8 Hours)**

Bioinformatics databases

2.1 Overview of Biological Sequence Databases - NCBI, EMBI, DDBJ
2.2 Sequence Retrieval Systems (Entrez & SRS), Sequence Submission Methods and Tools (Sequin, Sakura, Bankit)
2.3 Finding Scientific Articles Using PubMed, Identification of disease genes, OMIM database

Unit 3 **(8 Hours)**

Pharmacogenomics

3.1 Introduction to Basic Concept of Pharmacogenomics, Application and Challenges in Pharmacogenomics, Personalized Medicine
3.2 Genetic Variation, Types of Variants, SNPs, Insertion/Deletions

3.3 Databases - Pharmacogenomics Knowledge Base (PharmGKB)

Unit 4 **(8 Hours)**

Computational Immunology

4.1 Introduction to Immune System - Adaptive and Innate Immunity, Cells of the Immune System

4.2 Major Histocompatibility Complex (MHC) its Polymorphism, Principles of B-cell and T-cell Epitope Prediction

4.3 Databases in Immunology, IMGT immunoinformatics

Unit 5 **(8 Hours)**

Applications of Cheminformatics Tools in Drug Design

5.1Definition of drugs - 2D and 3D Molecular Structures

5.2 Searching for Chemicals on the Internet (PubChem, eMolecules)

5.3 Chemical structure drawing tools

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.

Russ B. Altman, David Flockhart, David B. Goldstein. *Principles of Pharmacogenetics and Pharmacogenomic*.UK:Cambridge University Press, 2012.

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.

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

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End Semester Examination: Total Marks: 100 Duration: 3 Hours

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SYLLABUS
(Effective from the academic year 2019 -2020)

COMPUTER AIDED DRUG DESIGN

CODE: 19BI/PE/CD23 **CREDITS : 3**
L T P : 3 0 0
TOTAL TEACHING HOURS : 39

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

- Identify the key elements in drug and explain new methodologies for drug design
- Describe the role and importance of the various disciplines involved in the different phases of drug discovery and development
- Review and evaluate preclinical and clinical pharmaceutical studies
- Follow new ideas in utilizing main approaches of ligand screening methods

Unit 1 **(7 Hours)**

Drug Discovery and Development

1.1 Drug Development Process Overview - The Changing Landscape of drugs development
1.2 Drug Discovery Phases
1.3 Preclinical Phase studies

Unit 2 **(8 Hours)**

Regulations in Drug Discovery

2.1 FDA regulations on Drug Development
2.2 Indian Regulatory Systems
2.3 Ethical Considerations and Special Populations

Unit 3 **(8 Hours)**

Drug Target Identification

3.1 Computational inferences used to identify and validate small molecule drug targets
3.2 Databases for Drug targets, Retrieving protein structure and visualisation
3.3 Target Discovery and Validation, Active Site Prediction

Unit 4 **(8 Hours)**

Ligand Based Drug Design

4.1 Screening of lead molecules - Natural products and their analogues
4.2 Chemical Databases – PubChem, Drug Bank
4.3 Chemical file formats, Retrieving drug molecules

Unit 5 **(8 Hours)**

Pharmacokinetics and Molecular Docking

5.1 Pharmacokinetics - ADME Prediction
5.2 Pharmacodynamics
5.3 Molecular Docking - Scoring and evaluation

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/

PATTERN OF ASSESSMENT

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SYLLABUS
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PHARMACOGENOMICS

CODE:19BI/PI/PG24 **CREDITS : 4**

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

- Gain an insight on pharmacology linked to genomics
- Assess genetic polymorphisms and their importance in drug designing
- Understand structural influence in the Drug response
- Analyse different tools for pharmacogenomic analysis including ADME prediction

Unit 1

Pharmacogenomics

1.1 Pharmacogenomics- Introduction, basic concepts about genetic diseases
1.2 Personalized medicine- introduction and importance, The genetics of therapeutic targets and gene-based targets
1.3 Pharmacogenomics necessity in drug designing

Unit 2

Genetic Variation

2.1 Introduction to genetic variation, types of variants, SNPs, coding and cis/trans regulatory variants, insertion/deletions, Satellite DNA
2.2 Databases, National pharmacogenetics resources/efforts (PGRN), Pharmacogenomics Knowledge Base (PharmGKB)
2.3 Prediction of structural changes among sequences by the influence of polymorphisms.

Unit 3

Pharmacokinetics & Metabolism

3.1 Pharmacokinetics (PK), Pharmacodynamics (PD)
3.2 Tools for pharmacogenomics analysis
3.3 Definition of Toxicogenomics, Detoxification and poisoning. Preclinical Toxicology

Unit 4

Pharmacogenomics in Drug Discovery and Development

4.1 An Introduction to Drug Discovery and Development

4.2 Process in Structural Pharmacogenomics - Target Structure optimization, Validation, lead identification, ADME prediction, synthesis, assays and Clinical trials

4.3 Drug response to patients, Structural influence in the Drug response. Efficacy and metabolism of drugs, Drug metabolism pathways and adverse drug reactions

Unit 5

Micro array Analysis

5.1 DNA Microarray: Importance and definition, Designing a MicroArray Experiment: The Basic steps

5.2 Types of Microarray, NCBI and Microarray Data Management, GEO (Gene Expression Omnibus), MAML

5.3 The Promise of Microarray Technology in Treating Disease. Microarray Data, Expression Pattern, Visualizing Microarray Data

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

PATTERN OF ASSESSMENT

End Semester Examination: Total Marks: 100 Duration: 3 hours

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SYLLABUS
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SYSTEMS BIOLOGY

CODE: 19BI/PI/SB24 **CREDITS : 4**

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

Unit 1

Introduction

1.1 Introduction – Systems Biology is a Living Science
1.2 Properties of Models-Model Behaviour- Model Development
1.3 Systems Biology is Data Integration

Unit 2

Standard Models and Approaches in Systems Biology

2.1 Standard Models and Approaches in Systems Biology
2.2 Enzyme Kinetics and Thermodynamics-Metabolic Networks
2.3 Structure of Intra- and Intercellular Communication-Receptor-Ligand Interactions

Unit 3

Modeling of Gene Expression

3.1 Modeling of Gene Expression-Modules of Gene Expression – Promoter
3.2 Identification - General Promoter Structure- Sequence-Based Prediction of Promoter Representation of Gene Network as Directed and Undirected Graphs
3.3 Bayesian Networks-Boolean Networks- Gene Expression Modeling With Stochastic Equations

Unit 4

Analysis of Gene Expression Data

4.1 Analysis of Gene Expression Data- Introduction-DataCapture-DNA Array Platforms
4.2 Image Analysis and Data Quality Control-Grid Finding- Quantification of Signal Intensities- Signal Validity- Pre-processing-Global Measures
4.3 Linear Model Approaches- Nonlinear. Fold-change Analysis

Unit 5

Clustering Algorithms

5.1 Clustering Algorithms-Hierarchical Clustering- Self-organizing Maps

(SOMs).K-means- Validation of Gene Expression

5.2 Publication in the Era of Systems Biology- Systems Biology and Text Mining. Systems Biology in Medicine and Drug Development

5.3 Guiding the Design of New Organisms -Computational Limitations- Potential Dangers

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.

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/

PATTERN OF EVALUATION

End Semester Examination

Total Marks: 100 Duration: 3 Hours
Section A – 20 X 1 = 20 Marks (All Questions to be answered)
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