STELLA MARIS COLLEGE
(AUTONOMOUS), CHENNAI - INDIA

M.Sc. Degree
BIOINFORMATICS
(CHOICE BASED CREDIT SYSTEM)

OUTCOME BASED EDUCATION (OBE)
LEARNING OUTCOME BASED CURRICULUM FRAMEWORK (LOCF)

SYLLABUS
(Effective from the academic year 2023 - 2024)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI – 600 086

VISION STATEMENT

The vision of the College is to build a vibrant and inclusive learning community in a culture of excellence sustained by a sound value system that promotes responsible citizenship and effects social change.

MISSION STATEMENT

The mission of the College is to empower young women to face the challenges of life with courage and commitment, to be builders of a humane and just society, and to promote a learning community in which all, especially those from less privileged backgrounds, feel part of the collaborative high quality educational process which is value based and leads to holistic growth.

EDUCATIONAL OBJECTIVES OF THE INSTITUTION

- To offer a globally relevant curriculum and promote academic excellence, equipping graduates with a comprehensive understanding of their domain of study, leading to research and innovation
- To promote professional skill development and entrepreneurship, empowering graduates to achieve professional excellence, employability, entrepreneurship and leadership qualities
- To provide a vibrant and inclusive teaching-learning environment where graduates are imbued with a strong desire for academic growth and become lifelong learners
- To contribute towards nation building by fostering in graduates a respect for values, ethics and diversity
- To be environmentally conscious and sustainable, inspiring graduates to fulfil their social and civic responsibilities

POSTGRADUATE PROGRAMME OUTCOMES (POS)

On successful completion of the Programme, postgraduates will

PO 1	acquire in-depth and advanced knowledge in their chosen field of study, encompassing relevant theories, concepts, methodologies, and research findings.
PO 2	demonstrate competency in research and writing, with intellectual independence for critical enquiry/scientific reasoning, problem solving and innovative thinking.
PO 3	synthesise their domain knowledge with that of other relevant disciplines, to meet the challenges of higher studies/academia/work, in local and global contexts.
PO 4	display proficiency in communication and academic writing for coherent, contextual and independent exposition of knowledge and ideas.
PO 5	demonstrate enhanced professional and entrepreneurial skills, and the ability for life-long learning.
PO 6	use relevant digital/technological skills, and display leadership traits and creativity to contribute individually or collaboratively in local, national and global contexts.
PO 7	engage sensitively with a range of socio-cultural and ethical issues, and use their disciplinary knowledge in contributing to environmental causes and sustainable development.
PO 8	display self-awareness, attitudes of inclusivity, and effectively engage in a multicultural society with respect for democracy, peace and diversity.

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 Data 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, 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.

VISION OF THE DEPARTMENT

- To be recognised as a distinctive Centre for Bioinformatics and build an informed community of purpose driven Bioinformatics professionals with social responsibility, accountability and integrity

MISSION OF THE DEPARTMENT

- To provide insight for students in the field of Bioinformatics
- To prepare the students to handle Big-Data conducive to transform human health and wellness
- To empower young women in STEM by providing necessary technological skills to handle biological, chemical data, integrate multiomics, develop drugs and perform clinical research
- To encourage students to start Bioinformatics start-ups and enhance entrepreneurial skills with social concern

PROGRAMME SPECIFIC OUTCOME (PSO)

On successful completion of the M.Sc. Bioinformatics programme, the students will be able to:

PSO 1	Attain a strong foundation of the interdisciplinary sciences including computer science, biosciences, mathematics, chemistry and physical sciences
PSO 2	Develop programming skills, interpret biological information computationally and evolve into a professional with integrated skills from multiple fields
PSO 3	Analyse omics data, evaluate the experimental raw data to infer molecular models and contribute to personalised medicine
PSO 4	Establish proficiency in handling huge biological data using software and standardised data analysis pipelines to address the present scientific challenges
PSO 5	Cultivate and strengthen the ability to develop accelerated and precise technologies in resolving the biological, environmental and health care problems

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DISTRIBUTION OF CREDITS AND HOURS

M.Sc. Bioinformatics 2023-2024

Courses	**Semester 1**		**Semester 2**		**Semester 3**		**Semester 4**		**Total Credits**	**Total Hours**
	C	**H**	**C**	**H**	**C**	**H**	**C**	**H**		
PC	4	5	4	5	4	5	4	5	16	20
	4	6	4	5	4	5	4	5	16	21
	4	5	4	5	4	5	4	5	16	20
	4	5							4	5
PC Practical					2	3			2	3
			2	3	2	3			4	6
Dissertation							5	8	5	8
PE-dept.	5	5	5	5			5	5	15	15
PE-Common			3	3	3	3			6	6
PV			2	2	2	2			4	4
PK			2	2					2	2
PA	2	2							2	2
PN					2				2	0
Library		2				4		2		8
TOTAL	23	30	26	30	23	30	22	30	94	120

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI 600 086

M.Sc. DEGREE: BIOINFORMATICS

COURSES OF STUDY

(Effective from the academic year 2023-2024)

CHOICE BASED CREDIT SYSTEM

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

Subject Code	Title of Course	C	L	T	P	Ex	CA	ES	M
SEMESTER-I									
23BI/PC/BM14	Biomolecules and Biochemistry	4	4	1	0	3	50	50	100
23BI/PC/EB14	Essentials of Bioinformatics	4	4	0	2	3	50	50	100
23BI/PC/CP14	Programming in C++ and Perl	4	3	0	2	3	50	50	100
23BI/PC/DB14	Database Management Systems	4	3	0	2	3	50	50	100
	PA/PL								
	Department Elective I								
SEMESTER-II									
23BI/PC/MB24	Molecular Biology	4	4	1	0	3	50	50	100
23BI/PC/GT24	Genomics and Transcriptomics	4	3	0	2	3	50	50	100
23BI/PC/PR24	Python and R Programming	4	4	1	0	3	50	50	100
23BI/PC/P122	Python and R Programming - Practical	2	0	0	3	3	50	50	100
23BI/PK/SS22	Soft Skills	2	2	0	0	-	50	-	100
CD / ET	Value Education								
	Department Elective II								
	Common Elective I								
SEMESTER-III									
23BI/PC/PM34	Proteomics and Metabolomics	4	3	0	2	3	50	50	100
23BI/PC/MA34	Machine Learning, Deep Learning and Artificial Intelligence	4	4	1	0	3	50	50	100
23BI/PC/MC34	Molecular Modeling and Computer Aided Drug Design	4	4	1	0	3	50	50	100
23BI/PC/P232	Molecular Modeling and Computer Aided Drug Design - Practical	2	0	0	3	3	50	50	100
23BI/PC/P332	Molecular Biology - Practical	2	0	0	3	3	50	50	100
23BI/PN/SI32	Summer Internship								
CD / ET	Value Education								
	Common Elective II								
SEMESTER-IV									
23BI/PC/AB44	Applied Bioinformatics	4	4	1	0	3	50	50	100
23BI/PC/BD44	Big Data Analysis	4	4	1	0	3	50	50	100
23BI/PC/SM44	Systems Biology	4	4	1	0	3	50	50	100
23BI/PC/DS45	Dissertation	5	0	0	8	0	50	50	100
	Department Elective III								
Postgraduate Elective Courses Offered to Parent Department									
23BI/PE/CG15	Cell Biology and Genetics	5	4	1	0	3	50	50	100
23BI/PE/BS15	Biomathematics and Biostatistics	5	4	1	0	3	50	50	100
23BI/PE/RM15	Research Methodology, Bioethics and IPR	5	4	1	0	3	50	50	100
23BI/PE/IM15	Immunoinformatics	5	4	1	0	3	50	50	100
23BI/PE/CR15	Clinical Research Management	5	4	1	0	3	50	50	100
23BI/PE/SB15	Structural Bioinformatics	5	4	1	0	3	50	50	100

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M.Sc. DEGREE: BIOINFORMATICS

COURSES OF STUDY

(Effective from the academic year 2023-2024)

CHOICE BASED CREDIT SYSTEM

C-Credit, **L**-Lecture Hours, **T**-Tutorial Hours, **P**- Practical Hours, **Ex**-Exam Hours, **CA**- Continuous Assessment Marks, **ES**-End Semester Marks, **M**-Maximum Marks									
23BI/PE/AL15	Algorithms for Bioinformatics	5	4	1	0	3	50	50	100
Postgraduate Elective Courses Offered to Other Departments									
23BI/PE/IB23	Introduction to Bioinformatics	3	3	0	0	3	50	50	100
23BI/PE/AP23	Applications of Bioinformatics	3	3	0	0	3	50	50	100
23BI/PE/CD23	Computer Aided Drug Design	3	3	0	0	3	50	50	100
The Department will offer one Social Awareness Course									
Social Awareness									
23BI/PA/RD12	Rights of Differently Abled	2	2	0	0	-	50	-	100
23BI/PA/CR12	Child Rights	2	2	0	0	-	50	-	100
23BI/PA/CA12	Civic Awareness	2	2	0	0	-	50	-	100
23BI/PA/HW12	Health and Wellbeing	2	2	0	0	-	50	-	100
23BI/PA/LC12	Learning from Communities	2	2	0	0	-	50	-	100
23BI/PA/RR12	Rural Realities	2	2	0	0	-	50	-	100
23BI/PA/SE12	Social and Economic Issues	2	2	0	0	-	50	-	100
23BI/PA/UR12	Urban Realities	2	2	0	0	-	50	-	100
23BI/PA/SZ12	Care of Senior Citizens	2	2	0	0	-	50	-	100
Independent Elective Courses									
23BI/PI/TB24	Translational Bioinformatics	4	0	0	0	3	0	100	100
23BI/PI/JV24	Java for Bioinformatics	4	0	0	0	3	0	100	100

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M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023-2024)

BIOMOLECULES AND BIOCHEMISTRY

CODE: 23BI/PC/BM14 **CREDITS: 4**

L T P : 4 1 0

TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- to acquire the knowledge on structure, function and metabolism of biomolecules
- to understand the enzyme kinetics and techniques used in biomolecules analytical purpose
- to foster the fundamental understanding on how the structures of biomolecules and their interactions lead to cell function and malfunction
- to understand the physical and chemical properties of molecules and their state of occurrence in biological system
- to undertake investigations and to perform analysis in order to obtain required information for solving the biological problems

COURSE LEARNING OUTCOMES

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

COs	DESCRIPTION	CL
CO1	define the structure, function, concepts of Biomolecules and relate the importance of the biomolecules	K1, K2
CO2	illustrate the intricacies of metabolic pathways and inculcate effective reasoning capability	K3
CO3	demonstrate the importance of enzymes and enzyme kinetics to inter-relate their role in normal vs diseased condition	K4
CO4	interpret the primary to highly complex structures of protein and its folding mechanisms in evaluating the research questions	K5
CO5	examine the nature of biomolecules, xenobiotics and the applications of various analytical techniques	K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**Introduction to Biomolecules** 1.1. Biomolecules - Structure and functions of Atoms and Molecules 1.2. Chemical bonds - Covalent and non-covalent interactions, acid base concept and buffers, pH, water - properties and its importance 1.3. Bioenergetics - Thermodynamics systems - laws of thermodynamics, entropy and enthalpy, concepts of free energy	K1-K4 K2-K5 K3-K6	15	1-5
2	**Carbohydrates, Lipids and Nucleic acid** 2.1. Structures, types and Functions of Carbohydrates 2.2. Structure, types and function of Lipids and nucleic acids 2.3. Carbohydrate and Lipid metabolism – Glycolysis, Glycogen metabolism, TCA cycle, β-oxidation	K1-K4 K2-K5 K3-K6	15	1-5
3	**Proteins** 3.1. Structures and properties of amino acids, Peptide bonds, disulphide bridges and other conformations. 3.2. Protein structure levels- primary, secondary, tertiary, quaternary. Ramachandran plot. 3.3. Protein folding pathways, classifications of proteins.	K1-K4 K2-K5 K3-K6	15	1-5
4	**Enzymes and Enzyme Kinetics** 4.1 Nomenclature, Classification of enzymes, Enzyme specificity, Cofactors, Coenzyme and Prosthetic group 4.2 Enzyme Kinetics, Michaelis-Menten Equation, significance of Vmaxand Km, Enzyme inhibition Competitiveand non-competitive Inhibition, Feedback inhibition. Enzyme regulation. Allosteric modulation. 4.3 Extraction and purification of enzymes, Immobilized enzymes, Application of enzymes in medicine and industry	K1-K4 K2-K5 K3-K6	10	1-5
5	**Xenobiotics and Analytical Techniques** 5.1. Xenobiotics and general detoxification methods in the body. 5.2. Principles, types and applications of Spectroscopy, Nuclear Magnetic Resonance- The phenomenon, types and applications 5.3. Mass Spectrometry for protein and peptide analysis, MALDI-TOF Analyser, Tandem Mass Analyser, The Ion Trap Mass Analyser, Q-TOF Instrument	K1-K4 K2-K5 K3-K6	15	1-5

BOOKS FOR STUDY

Victor W.Rodwell, David Bender, Kathleen M.Botham, Peter J.Kennelly, P.Anthony Well, Harper's Illustrated Biochemistry, McGraw Hill / Medical; New York,USA, 32nd ed., 2022.
David L.Nelson, Michael M.Cox, Lehninger Principles of Biochemistry, W H Freeman & Co; New York, USA, 8th ed., 2021.
Thomas. E. Creighton, Proteins: Structures and molecular properties, W. H. Freeman, New York, USA, 2018.
Narayanan P. Essentials of Biophysics Mumbai, India: Anshan Ltd; 2nd ed., 2010.

BOOKS FOR REFERENCE

Champe, Pamela C, Richard A. Harvey and Denise R. Ferrier. Lippincott's Illustrated Reviews: Biochemistry, India: J.P. Brothers Medical Publishers, Philadelphia, 7th ed., 2016.
Lubert and Stryer. Biochemistry, WH Freeman; New York, USA 9th ed. 2019.
Voet, D. and Voet, G. Biochemistry, New York (USA): Wiley; 4th ed., 2010.
Bengt Nolting. Methods in Modern Biophysics, Springer, Germany, 2004.

JOURNALS

Journal of Biochemistry
Indian Journal of Clinical Biochemistry
Biochemistry
Biophysical Journal
European Biophysics Journal
Journal of Biophysics

WEB SOURCES

http://www.biophysics.org/Education/Careers/CareersinBiophysics/tabid/112/Default.aspx
http://www.rcsb.org/pdb/101/static101.do?p=education_discussion/Looking-at-Structures/methods.html
http://www2.chemistry.msu.edu/faculty/reusch/VirtTxtJml/Spectrpy/MassSpec/masspec1.htm
www.themedicalbiochemistrypage.org
www.biochemistry.org

Pattern of Assessment

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

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs) to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/BM14												
	Course Title: BIOMOLECULES AND BIOCHEMISTRY												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	2	2	1	2	2	1	1	1	1	1	2	2	2
CO 2	3	3	2	2	1	1	1	1	2	1	3	2	3
CO 3	3	3	2	2	2	1	1	1	3	2	3	1	3
CO 4	3	2	3	2	1	2	1	1	2	1	3	1	3
CO 5	3	3	3	2	2	1	1	1	2	2	3	2	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

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M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023-2024)

ESSENTIALS OF BIOINFORMATICS

CODE: 23BI/PC/EB14 **CREDITS: 4**

L T P : 4 0 2

TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- to provide an integrative approach to the understanding of both theory and practice of bioinformatics
- to apply biological concepts at different levels to study gene / protein analysis, and the proteins implicated in diseases
- to understand the evolution of the life through phylogenetic analysis
- to perform comparative sequence analysis through different alignment approach and bring the meaningful information from the aligned sequences
- to access different biological databases and retrieve the required specific information

COURSE LEARNING OUTCOMES

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

COs	DESCRIPTION	CL
CO1	recognize and relate the biological databases, tools and software to be used in the interdisciplinary fields	K1, K2
CO2	infer the required information from different databases and utilise the fundamental tools in bioinformatics analysis	K3
CO3	compare and identify the differences in sequences to interpret their role in health and disease	K4
CO4	perform a complete analysis of the genes and protein to provide innovative research outcomes	K5
CO5	examine the gene, protein sequences and offer solutions to the health care problems	K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**Basics of Bioinformatics** 1.1. Introduction to Bioinformatics; Computers in Biology to understand Biological System; Concept of open resources in Bioinformatics. Biological databases 1.2. Concept of reference genome. Genome sequencing - human genome project- versions hg19, hg38, T2T. Role of bioinformatics in human genome projects. Other genome projects- 1000 genomes, Encode, Indian genome project. 1.3. Browsers and visualizers- UCSC, IGV, JBrowse, the Wellcome Trust Sanger Institute (WTSI), ENSEMBL, NCBI Map viewer	K1- K3 K2– K4 K5- K6	8	1-5
2	**Introduction to Biological Databases** 2.1. Type of Databases, Public Biological Databases –. Primary Nucleotide Sequence Databases: EMBL, GenBank, DDBJ 2.2. Secondary Nucleotide Sequence Databases: UniGene, Sequence Submission Methods and Tools (Sequin, Sakura, Bankit) 2.3. Sequence Retrieval Systems (Entrez & SRS); Sequence File Formats and Conversion Tools.	K1, K2 K3, K4 K5, K6	10	1-5
3	**Introduction to Sequence Alignment** 3.1. Protein and nucleotide alignment, Homology, Similarity, Identity, Pairwise alignments: Dot Plots, Scoring Matrix-PAM, BLOSUM, Gap Penalty 3.2. Dynamics programming - Alignment Algorithms: Global Sequence Alignment: Needle man-Wunsch Algorithm. Local Sequence Alignment: Smith –Waterman Algorithm. Rapid, Heuristic Versions of Smith Waterman: FASTA 3.3. Basic Local Alignment Search Tool - BLAST Search Steps, Search Strategy, E Value, Raw Scores and Bit Scores, Ensembl BLAST, TIGR BLAST, PSI-BLAST	K1, K2 K3, K4 K5, K6	10	1-5
4	**Multiple Sequence Alignment and Phylogeny** 4.1. Definition of Multiple Sequence Alignment. Tools of Multiple Sequence Alignment Programs and their algorithms - Clustal, Phylip, MAFT, Hidden Markov Models 4.2. Evolutionary analysis, Relationship of Phylogenetic Analysis to Sequence Alignment, Genome Complexity. Bootstrap, Tree Construction Methods. Neighbor-Joining Method, Unweighted Pair Group Method with Arithmetic Mean (UPGMA) 4.3. Character based methods: Maximum Parsimony Method and Maximum-Likelihood Method	K1, K2 K3, K4 K5, K6	12	1-5

UNIT	CONTENT	CL	Hrs	CO
5	**Specialised databases** 5.1. Literature databases and biomedical databases – PubMed, OMIM, Metabolic database- KEGG, Metacyc, Reactome 5.2. Protein domain and motif prediction. Databases and tools to infer STS, EST, CDS, ORF, Domains and motifs. Protein structure databases - PDB, SCOP, CATH. Small molecule databases - Zinc, PubChem, Drug Bank. 5.3. Homologs, paralogs, xenologs, orthologs, COG databases, Plant and Animal databases. Model organism databases - SGD, MGD, ZFIN	K1, K2 K3, K4 K5, K6	10	1-5
	Practical Component Primary Nucleotide Sequence Databases: NCBI, EMBL, DDBJ Protein Sequence Databases – PIR, RefSeq, UniProt Protein Structure Databases – PDB, CATH, SCOP Protein Visualization Tools- Rasmol, Swiss PDB Viewer, PyMol Small molecular databases - PubChem, zinc, Drug Bank Genome browsers - UCSC, ENSEMBL, ENCODE, IGV Basic Local Alignment Search Tool (BLAST), Pairwise and Multiple Sequence Alignment Tools: EMBOSS, Clustal W and Clustal Omega Phylogenetic Tree Construction Tool: MEGA Software, Phylip, MAFT	K1- K2, K3 - K4 K5 - K6	15	1-5

BOOKS FOR STUDY

Lesk, Arthur M. Introduction to Bioinformatics. OUP Oxford; USA 5th ed., 2019.
David W.Mount. Bioinformatics Sequence and Genome Analysis. Cold Spring Harbor Laboratory Press, US; 2nd ed., 2004.
Pevsner, Jonathan. Bioinformatics and Functional Genomics. Wiley publications, New York, USA, 3rd ed., 2015.
Baxevanis, Andreas, D. and Francis B.F. Ouellette, Bioinformatics- A Practical Guide to the Analysis of Genes and Proteins. Wiley publications, New York, USA, 2nd ed., 2004.

BOOKS FOR REFERENCE:

Chen and Yi-Ping Phoebe. Bioinformatics Technologies. Springer, Germany 2005.
Durbin, R., S. Eddy, A. Krogh and G. Mitchison. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids. Cambridge University Press, Oxford, USA, 2005.
Higgins, Des and Willie Taylor. Bioinformatics –Sequence, Structure and Databanks – Practical Approach. Oxford University Press, USA, 2001.
Richard Blum, Linux Command Line and Shell Scripting Bible, Wiley, New York, USA, 3rd ed., 2021.
Baldi, P. and Brunak, S. Bioinformatics: Machine Learning Approach. MIT Press, Cambridge, US 2003.

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: **Total Marks: 50** **Duration: 90 minutes**

Sections	Cognitive levels	Marks	Pattern
Theory			
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K5, K6	10	2 X 5 = 10 (Internal choice) Answers in about 500 words
Practical			
A	K3, K4	10	2 X 5 =10 (All questions to be answered)
B	K5, K6	10	1 x 10 =10 (All questions to be answered)
	Record & Viva	5	
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs, open book tests/ Tests	K1 - K2	CO1-CO2	20
	K3 - K4	CO3-CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Mark allocation	Pattern
Theory			
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K5, K6	20	4 X 5 = 20 (Internal choice) Answers in about 500 words
Practical			
A	K3, K4	20	2 X 10 =20 (All questions to be answered)
B	K5, K6	20	2 x 10 =20 (All questions to be answered)
	Record & Viva	10	
	Total	100	

Mapping of Course Outcomes (COs) to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/EB14												
	Course Title: ESSENTIALS OF BIOINFORMATICS												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	1	2	3	1	1	3	1	1	3	3	2	1	3
CO 2	3	1	3	1	3	1	2	1	3	2	3	2	2
CO 3	3	2	3	2	1	2	2	1	1	1	3	3	3
CO 4	3	2	3	2	2	3	3	1	2	1	3	3	3
CO 5	3	1	3	2	2	1	2	1	3	3	3	3	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

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M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023-2024)

PROGRAMMING IN C++ AND PERL

CODE: 23BI/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
- to provide fundamentals on using programming languages for editing the dna and protein sequences
- to utilize bioperl modules to build a pipeline and process biological data

COURSE LEARNING OUTCOMES

On successful completion of the course, student will be able

COs	DESCRIPTION	CL
CO1	explain the basics of programming to handle multitudes of data	K1, K2
CO2	relate the necessity for programming in handling high volumes of data from various fields of science	K3
CO3	solve biological problems with c++ and perl scripts	K4
CO4	apply programing to analyse genomic, proteomic sequences and structure to aid innovative research solutions	K5
CO5	elaborate use of bio-perl in precisely solving complex problems in bioinformatics	K6

CL – Cognitive Level

K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Introduction to Programming language** 1.1. Machine/Assembly Language, Higher Level Languages, Simple and Compound Data, Code: Syntax and Semantics 1.2. 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++.	K1- K3 K2 – K4 K4- K6	8	1-5
2	**Object Oriented Programming** 2.1. Using Objects, Classes, Encapsulation, Inheritance, Abstraction and Polymorphism. Friend functions 2.2. String and file operations– creating string objects, Standard Streams – string and Files, Open, close, EOF, updating files and error Handling 2.3. String manipulation- String operators Manipulating String, String characteristics, Comparing and Swapping	K1, K2 K3, K4 K5, K6	10	1-5
3	**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	K1, K2 K3, K4 K5, K6	10	1-5
4	**Subroutines and File Handling** 4.1. Subroutines- Defining Subroutines, Returning Values, Using Arguments 4.2. Files- Overview and working with File handles, Closing the files, printing, renaming files 4.3. Various Ways of Opening a Perl File Handlers- Normal Scalar variable, Use Perl IO, Open the Standard Input and Standard Output, Use Sysopen ().	K1, K2 K3, K4 K5, K6	12	1-5
5	**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	K1, K2 K3, K4 K5, K6	10	1-5

UNIT	CONTENT	CL	Hrs	CO
	Practical components **C++** Find the area and circumference of a circle Armstrong Number Prime Number An example with classes and object Checking for palindrome of a given string (without using the built in string function) **Perl** Use regular expressions to modify a sequence of letters in sentences Convert DNA to RNA (transcription) Translate the given RNA sequence Calculate the frequency of bases **Bioperl** Using Bioperl retrieve a sequence from database Using Bioperl Convert DNA to Protein (Translation) Using Bioperl retrieve a subset of sequences, domain and motif regions from the given protein sequence	K1, K2 K3, K4 K5- K6 K1 - K4 K5, K6	15	1-5

BOOKS FOR STUDY

E. Balagurusamy. Object Oriented Programming with C++. Tata McGraw- Hill, India, 8th ed., 2020.

Tisdall James D. Beginning Perl for Bioinformatics. O'Reilly and Associates, US 1st ed., 2001.

BOOKS FOR REFERENCE

Conrod Bessant, Ian Shadforth and Darren Oakley. Building Bioinformatics Solutions with Perl, R and MySQL**.** Oxford University Press, US 1st ed., 2010.

Bjarne, Stroustrup. The C++ Programming Language. Addison Wesley, 4th ed., UK, 2013.

Holzner and Steven. Perl Black Book. Dream Tech Press, India 2nd ed., 2004.

Hubbard, John. Programming with C++, Schaum's Outline Series. Tata McGraw Hill, USA 2nd ed., 2000.

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: **Total Marks: 50** **Duration: 90 minutes**

Sections	Cognitive levels	Marks	Pattern
Theory			
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K5, K6	10	2 X 5 = 10 (Internal choice) Answers in about 500 words
Practical			
A	K3, K4	10	2 X 5 =10 (All questions to be answered)
B	K5, K6	10	1 x 10 =10 (All questions to be answered)
	Record & Viva	5	
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs, open book tests/ Tests	K1 - K2	CO1-CO2	20
	K3 - K4	CO3-CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Mark allocation	Pattern
Theory			
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K5, K6	20	4 X 5 = 20 (Internal choice) Answers in about 500 words
Practical			
A	K3, K4	20	2 X 10 =20 (All questions to be answered)
B	K5, K6	20	2 x 10 =20 (All questions to be answered)
	Record & Viva	10	
	Total	100	

Mapping of Course Outcomes (COs) to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/CP14												
	Course Title: PROGRAMMING IN C++ AND PERL												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	2	1	1	1	2	2	2	1	3	3	2	2	2
CO 2	3	2	1	1	2	2	1	1	3	2	2	3	2
CO 3	3	3	2	2	1	2	2	1	2	2	3	2	3
CO 4	3	3	3	2	2	2	1	2	3	3	2	2	2
CO 5	3	3	2	1	2	2	2	1	3	2	2	2	2

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023-2024)

DATABASE MANAGEMENT SYSTEMS

CODE: 23BI/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 and databases
- to familiarize the basic database storage structure and access techniques
- to apply the concepts of NoSQL and MongoDB to utilize the preferred schemas and the specific technical requirements

COURSE LEARNING OUTCOMES

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

COs	DESCRIPTION	CL
CO1	explain the working of different operating systems to analyse various data types	K1, K2
CO2	compare the data models and schemas in dbms for a variety of datasets	K3
CO3	create entity- relationship between multiple data tables and write sql queries to develop databases	K4
CO4	compare various rdbms tools, nosql databases in the context of research problems	K5
CO5	design databases using the knowledge of sql to provide feasible solutions	K6
CL – Cognitive Level K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create		

UNIT	CONTENT	CL	Hrs	CO
1	**Introduction to Files, Databases and Linux** 1.1 Introduction to File and Database systems- Record Storage and Primary File Organization- Secondary Storage Devices. 1.2. Linux basics commands. Working with Files, Text Editors, I/O Redirections, Pipes, Filters, and Wildcards. 1.3 Changing Access Rights. Bash scripting, loops, text mining, Awk, sed and grep. Editors- vim, nano, gedit.	K1, K2 K3-K4 K5-K6	8	1-5
2	**Introduction to Database Systems** 2.1 Introduction to Database Systems, Architecture, Data Models, Layers and Types of Database Management Systems 2.2. Operations on Files- Heap File- Sorted Files- Hashing Techniques – Index Structure for Files. Different Types of Indexes- B-Tree - B+Tree. Database System Structure, Data Models, database schemas. 2.3. Database Normalisation and denormalization for Relational Databases (up to BCNF) .	K1, K2 K3-K4 K5-K6	10	1-5
3	**SQL** 3.1. Data Definition Language, Data Manipulation Language, Transaction Control and Data Control Language Grant and Revoke Privilege Command. 3.2. Set Operators, Joins-Kinds of Joins, Table Aliases, Sub queries, Multiple and Correlated Sub Queries. 3.3. Functions-Single Row, Date, Character, Numeric, Conversion, Group Functions. Constraints-Domain, Equity, Referential Integrity Constraints	K1, K2 K3-K4 K5-K6	10	1-5
4	**RDBMS and No SQL databases** 4.1. Text and Multimedia Databases - Basic Concepts and Applications, Types of DBMS-Network, object oriented, graph based. Overview of RDBMs, Advantages of RDBMs Over DBMs. 4.2. Establishing relations between tables. Entity relationship concepts. Keys in linking relational databases - primary, foreign, super, candidate keys. 4.3. Brief history of No SQL databases. Features of No SQL, differences and advantages of No SQL over RDBMS. Types and misconceptions in No SQL databases. No SQL vs SQL.	K1, K2 K3-K4 K5-K6	12	1-5
5	**Recent trends in databases** 5.1. MongoDB, web development with MongoDB, install MongoDB, shell commands. 5.2. How can you store a DNA sequence using MongoDB? Role of MongoDB in 1000 genomes projects, MongoDB or Redis for biomedical data. 5.3 Database file formats- JSON, BSON, Creating uniprot mongodb, querying and retrieving protein sequences.	K1, K2 K3-K4 K5-K6	10	1-5

UNIT	CONTENT	CL	Hrs	CO
	Practical Components **Linux** Linux- create directory, move directory, remove directory and create files, move files, copy files Linux – using wildcard characters and sort files Linux - changing user rights **SQL** Create – a table and insert values using SQL Create subqueries with a where clause Create queries with constraints – NOT NULL and, DEFAULT Queries with Joins and functions Queries with primary and foreign keys	 K1-K4 K5- K6 K1- K4 K5- K6	15	1-5

BOOKS FOR STUDY

Ramakrishnan Raghu and Gehrke Johannes. Database Management Systems**,** McGraw–Hill, UK, 3rd ed., 2002

Kristina Chodorow, Michael Dirolf, MongoDB: The definitive guide, O'Reilly Media, Inc., USA,1st ed., 2010.

Gerardus Blokdyk, NoSQL A Complete Guide, 5Starcooks, Australia, 2020.

BOOKS FOR REFERENCE

Harrison Guy, Next Generation Databases: Nosqland Big Data, Apress publishers, India, 1st ed., 2018.

Anthony DeBarros, Practical SQL, No Starch Press, USA, 1st ed., 2018.

Anthony Molinaro, Robert de Graaf, SQL Cookbook, O'Reilly, USA, 1st ed., 2006.

Thomas Nield, Getting Started with SQL: A Hands-On Approach for Beginners, O′Reilly, USA, 1st ed., 2016.

Rick Copeland, MongoDB Applied Design Patterns: Practical use cases with the leading NoSQL database O'Reilly, USA,1st ed., 2013.

JOURNALS

International Journal of Database Management Systems

Journal of Database Management

Journal of Advanced Database Management & Systems

International Journal of Intelligent Information and Database Systems

WEB RESOURCES

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

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

www.odbms.org/

http://www.comptechdoc.org/os/linux/usersguide/linux_ugbasics.html

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

Pattern of Assessment

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

Sections	Cognitive levels	Marks	Pattern
Theory			
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K5, K6	10	2 X 5 = 10 (Internal choice) Answers in about 500 words
Practical			
A	K3, K4	10	2 X 5 =10 (All questions to be answered)
B	K5, K6	10	1 x 10 =10 (All questions to be answered)
	Record & Viva	5	
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs, open book tests/ Tests	K1 - K2	CO1-CO2	20
	K3 - K4	CO3-CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Mark allocation	Pattern
Theory			
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K5, K6	20	4 X 5 = 20 (Internal choice) Answers in about 500 words
Practical			
A	K3, K4	20	2 X 10 =20 (All questions to be answered)
B	K5, K6	20	2 x 10 =20 (All questions to be answered)
	Record & Viva	10	
	Total	100	

Mapping of Course Outcomes (COs)
to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/DB14												
	Course Title: DATABASE MANAGEMENT SYSTEMS												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	2	1	3	1	3	3	1	2	3	3	2	3	1
CO 2	1	1	3	2	3	3	1	1	3	2	2	3	1
CO 3	3	2	3	2	3	3	2	1	2	3	3	3	2
CO 4	2	2	3	1	3	1	1	1	3	3	1	3	2
CO 5	3	2	3	2	3	3	1	1	3	3	3	3	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

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M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023–2024)

MOLECULAR BIOLOGY

CODE: 23BI/PC/MB24 **CREDITS: 4**

L T P: 4 1 0

TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- to explore the structural organisation of chromosomes and genes
- to understand the general principles of genes at the molecular level of different organisms
- to acquire knowledge on dna, rna replication, mutations and transcriptional controls
- to familiarize the various levels of gene regulation and protein function
- to analyse the various genetic and molecular mechanisms involved in cancer signalling

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	grasp the functions of the prokaryotic and eukaryotic genome mechanisms at the molecular level	K1
CO2	represent and illustrate the structural organization of genes and the control of gene expression	K2
CO3	interpret the significance of central dogma of life	K3,K4
CO4	relate and analyse the protein synthesis mechanism	K4,K5
CO5	link the concepts of molecular signaling to a better understanding of diseases, including cancer	K5,K6

CL – Cognitive Level

K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Structure and Organisation of Genes and Chromosomes** 1.1. DNA-Structure and Conformations, Chromosomes – Structure and Functions 1.2. Cell division - Mitosis and meiosis, Cell cycle regulation, Check points 1.3. Organisation of Genomes - Coding Sequences, Repetitive Sequences, transposons	K1-K3 K2-K5 K5-K6	10	1-5

UNIT	CONTENT	CL	Hrs	CO
2	**Organelle, Bacterial and Viral Genome** 2.1. Mitochondrion and Chloroplast Genome - Organisation and Function 2.2. Bacteria - Cells structure and bacterial genetics 2.3. Virus - Structure, Viral genome, Viroids and Prions	K1-K3 K2-K5 K5-K6	13	1-5
3	**Replication and Transcription** 3.1. DNA replication, Mutations, DNA damage and repair mechanisms in prokaryotes and eukaryotes 3.2. Transcription- Eukaryotes and Prokaryotes, Transcriptional control by regulatory proteins, RNA polymerases 3.3. Post Transcriptional Regulation - DNA Methylation, Histone modification - Capping, RNA editing, Splicing, and Polyadenylation	K1-K4 K2-K5 K5-K6	15	1-5
4	**Translation** 4.1. RNA- Types, structure and functions, Ribosomes – Structure and Assembly 4.2. Translational Regulation - Regulation of gene expression in Prokaryotes (Operon) and Eukaryotes, Genetic code, Gene Silencing 4.3. Post- translational modifications of proteins	K1-K3 K2-K6 K5-K6	12	1-5
5	**Cell Signalling and Cancer** 5.1. Cell signalling – Signalling molecules, Receptors - Hormones receptors, cell surface receptor, G-protein coupled receptors, signal transduction pathways 5.2. Cancer Biology- Characteristics and genetic basis of cancers, Proto-oncogene, Oncogenes, Tumor Suppressor Genes 5.3. Oncogenesis - Cancer Immunotherapy, Regulation of Cell Death, Apoptosis	K1-K3 K2-K6 K5-K6	15	1-5

BOOKS FOR STUDY

Harvey Lodish, Arnold Berk, Chris A. Kaiser, Monty Krieger, Anthony Bretscher, Hidde Ploegh. *Molecular Cell Biology.* USA: W. H. Freeman, Eighth edition, 2016.

Wolfe, Stephen L. *Molecular and Cellular Biology.* USA: Wadsworth, 2005.

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

BOOKS FOR REFERENCE

Cooper, Geoffrey M. and Robert E. Hausman**.** *The Cell, A Molecular Approach***.** USA: Sinauer Associates, 2004.

Harvey Lodish, Arnold Berk, Chris A. Kaiser, Monty Krieger, Matthew P. Scott, Anthony Bretscher, Hidde Ploegh and Paul Matsudaira. *Molecular Cell Biology.* USA: W.H.freeman, 2008.

Watson, James, D. *Molecular Biology of the Gene***.** UK: Pearson, Seventh edition, 2017.

Darnell, James, Harvey Lodish and David Baltimore. *Molecular and Cell Biology,* Scientific American Books, USA: W.H. Freeman, 2004.

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

Lewin and Benjamin. *Genes IX*, UK: Oxford University Press, 2009.

Roitte, Ivan M., Brostoff, Jonathan and Male, David K. *Immunology.* Philadelphia: J.B. Lippi ncott, 1990.

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

WEB SOURCES

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/

JOURNALS

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

Pattern of Assessment

Continuous Assessment: Total Marks: 50 Duration: 90 minutes

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs)
to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/MB24												
	Course Title: MOLECULAR BIOLOGY												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	3	3	2	2	2	1	1	3	1	2	1	3
CO 2	3	3	3	3	3	3	2	2	3	3	3	2	3
CO 3	3	3	3	3	3	3	2	2	3	2	3	1	3
CO 4	3	3	2	2	3	2	1	1	3	2	3	1	3
CO 5	3	3	3	3	3	3	2	2	3	3	3	2	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023-2024)

GENOMICS AND TRANSCRIPTOMICS

CODE: 23BI/PC/GT24 **CREDITS: 4**

L T P: 3 0 2

TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- to provide an insight into the complete genome sequences of a model organisms and human genome through comparative and functional genomics
- to acquaint knowledge on functional genomics techniques such as microarrays, est, sage and interpret data obtained through high throughput expression studies
- to provide hands on experience of handling the genomic datasets
- to obtain and analyse information and data relating to specific genes, next generation sequencing tools and next generation mapping portals
- to instill students to utilize bioinformatic pipelines for the characterization and quantification of RNAs and annotations at the genome level and make new discoveries

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	acquaint the fundamental concepts of genome sequencing, file formats and data analysis	K1
CO2	perform powerful computational and statistical methods to decode the functional information hidden in DNA and RNA sequences	K2
CO3	experiential knowledge on Next generation sequencing and gene editing techniques	K3
CO4	exploit the mechanisms of genomics and transcriptomics to deal with the growing demand for multiomics	K4
CO5	apply functional genomics techniques to analyse data from biological system	K5, K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**Genome Sequencing and Sequence File Formats** 1.1. Understanding a Genome sequence, Locating the genes in a Genome Sequence, Genome Sequencing technologies - Conventional Sequencing techniques 1.2. Next generation sequencing technology- Whole Genome Shotgun Sequencing, Exome and amplicon sequencing, Genome assembly, Comparative Genomics 1.3. File formats- FASTQ, SAM/BAM, VCF, GFF/GTF, and BED. Databases and tools, Variations at the Level of individual Nucleotides, Duplications, Indels, Rates and patterns of Nucleotide substitution, Molecular Clocks	K1- K3 K2– K4 K5- K6	8	1-5
2	**Epigenetic and Metagenome sequence analysis** 2.1. Genome variant analysis- GATK pipeline, concepts of genome wide association studies (GWAS) 2.2. Metagenome analysis- amplicon and shotgun metagenome, Alpha and Beta diversity, rarefaction curves and metrics, Logical steps for metagenome analysis, Taxonomical classification- silvaDB, green genes 2.3. Epigenomics, Local chromatin dynamics and epigenetic modifications, analysis of regulatory sequence motifs, transcription factor - DNA interaction	K1, K2 K3, K4 K5, K6	10	1-5
3	**Genome Editing** 3.1. Genome editing technologies - Clustered regularly interspaced short palindromic repeats (CRISPR) CAS 9 technology, Variants of CAS 9 nuclease, selection of targets from sequences 3.2. Guide RNA design, recognition sequences, Best practices in SgRNA design, Repair and data analysis of the edited genome, Therapeutic applications. 3.3. Targeted mutagenesis- Transcription activator-like effector nuclease (Talens), Zinc Finger Nuclease (ZFNs) Technology. Recent innovations in genome editing in agriculture, diseases and healthcare	K1, K2 K3, K4 K5, K6	10	1-5
4	**Transcriptomics** 4.1. Transcriptomics - microarray technology and gene expression, SAGE, Applications of Microarrays in Medicine, Databases - GEO, array express 4.2. Next generation Sequencing -RNA isolation and purification, RIN number. Bulk RNA sequencing, single-cell RNA sequencing, small RNA sequencing 4.3. Importance of gene silencing, miRNA, siRNA, lncRNA, competing endogenous RNA	K1, K2 K3, K4 K5, K6	12	1-5
5	**Transcriptomic Gene Annotation** 5.1. Data analysis- Quality check- fastqc, multi fastqc and trimming of adapters – trimmomatic, cutadapt 5.2. Generation of contigs and scaffolds- Assembly using genome assemblers and alignment of sequences, Samtools and bowtie 5.3. Competing endogenous RNA network, Predicting DEGs and ontology analysis, Statistics behind DGE analysis. Gene annotations and protein interaction network prediction	K1, K2 K3, K4 K5, K6	10	1-5

UNIT	CONTENT	CL	Hrs	CO
	Practical Component Genome databases of plants, animals and pathogens, Gene Prediction by ORF analysis, Gen scan, UCSC Genome Browser DNA markers - dbSNP, EST Clustering databases - DBEST, UNIGene, Epigenetic data analysis, EWAS atlas, PWM and DNA binding motifs- signature logo generation Command line SRA download, fastqc, trimmomatic and assembly GATK pipeline. Metagenomics - In silico -Mg RAST, Kaiju web server, Galaxy server Differential gene expression analysis –RNA seq, microarray datasets- volcano plot, heatmap, DEGs and annotations – Geo2R, Biojupies. Small RNA network- using cytoscape, Crispr – sg RNA design- Chop Chop	K1- K2 K3 - K4 K5 - K6	15	1-5

BOOKS FOR STUDY

Head, Steven R., Ordoukhanian, Phillip, Salomon, Daniel R, Next Generation Sequencing Methods and Protocols, Germany, 1st ed., Springer, 2018

Eija Korpelainen, Jarno Tuimala, Panu Somervuo, Mikael Huss, Garry Wong, RNA-seq Data Analysis: A Practical Approach, UK, 1st ed., Taylor and Francis publishers, 2014

Arthur Lesk M. Introduction to Genomics. New York, 3rd ed., Oxford university press, 2017.

Leland Hartwell, Michael L. Goldberg and Janice Fischer. Genetics: From Genes to Genomes. USA, 6th ed., McGraw-Hill Publishing Company. 2017

BOOKS FOR REFERENCE:

Vijai Singh, Pawan K.Dhar, Genome Engineering via CRISPR-CAS9 system, 1st ed., Academic Press Inc., 2020.

Jiaqian Wu, Transcriptomics and Gene regulation, 1st ed., Springer, 2016.

Muniyandi Nagarajan, Metagenomics: Perspectives, Methods and Applications, USA, 1st ed., Academic Press, 2017.

JOURNALS

Genome Research
Genome medicine
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
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4678780/
https://crisprtx.com/gene-editing/crispr-cas9

Pattern of Assessment

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

Sections	Cognitive levels	Marks	Pattern
Theory			
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K5, K6	10	2 X 5 = 10 (Internal choice) Answers in about 500 words
Practical			
A	K3, K4	10	2 X 5 =10 (All questions to be answered)
B	K5, K6	10	1 x 10 =10 (All questions to be answered)
	Record & Viva	5	
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs, open book tests/ Tests	K1 - K2	CO1-CO2	20
	K3 - K4	CO3-CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Mark allocation	Pattern
Theory			
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K5, K6	20	4 X 5 = 20 (Internal choice) Answers in about 500 words
Practical			
A	K3, K4	20	2 X 10 =20 (All questions to be answered)
B	K5, K6	20	2 x 10 =20 (All questions to be answered)
	Record &Viva	10	
	Total	100	

Mapping of Course Outcomes (COs) to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/GT24												
	Course Title: GENOMICS AND TRANSCRIPTOMICS												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	2	3	2	3	3	1	1	2	1	3	3	3
CO 2	3	2	3	1	3	3	1	2	2	2	3	3	3
CO 3	2	2	3	3	3	2	2	2	2	2	3	3	3
CO 4	3	3	3	2	3	3	1	2	2	3	3	3	3
CO 5	3	2	3	2	3	3	1	2	3	3	3	3	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI – 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023–2024)

PYTHON AND R PROGRAMMING

CODE: 23BI/PC/PR24 **CREDITS: 4**

L T P: 4 1 0

TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- to demonstrate how to locate and download files for data analysis involving genes and transcriptomes
- to select datasets, open files and pre-process data using python and r language
- to develop and write python and r scripts to replace missing values
- to write r scripts to normalize data, discretize data, and sample data
- to use biopython and bioconductor packages to analyze biological data

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	relate the necessity for programming in biology	K1
CO2	handling biological concepts with python and r scripts	K2
CO3	apply r and python programming to analyze genomic sequences	K3
CO4	gain efficient programming skills to handle missing values and impute values in data	K4
CO5	perform genomic data analysis and visualize them using python and r	K5, K6

CL – Cognitive Level
K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Introduction to Python** 1.1. Installation of Python and Jupyter notebooks 1.2. Variables- list, tuples, sets, dictionary, matrix, dataframe. handling strings, Functions, control structures, operators, Pandas, Numpy and Scipy 1.3. Fasta files, Parsing DNA and protein information, Gene locations splices, extracting all gene locations. Object Oriented Programming in Python. Constructors, Type(), Issubclass(), Super()	K1 K2-K4 K4-K6	12	1-5

UNIT	CONTENT	CL	Hrs	CO
2	**Biopython** 2.1 Getting started and installation of modules and packages, Coding DNA, proteins, extracting translations. 2.2 Modules- Bio Import, Bio Seq, Bio Align 2.3 Plot ABI traces, Retrieve and Annotate Entrez gene	K1-K3 K3-K4 K5-K6	12	1-5
3	**Data Visualization** 3.1 Getting Started with Pandas, Matplotlib, scki-kit learn. 3.2 Visualisation using Matplotlib and scikit learn – Line Plots-Scatter Plots-Visualizing Errors-Density and Contour Plots-Histogram, Binnings and Density -Customizing Color Bars. 3.3 Customising Plot Legends -Multiple Subplots-Text and Annotation-Customizing Ticks.	K1-K3 K5-K6 K4-K6	15	1-5
4	**R programming** 4.1 R as a statistical Calculator, Creating Objects and Assigning Values. 4.2 Vectors, matrices, factors, levels, dataframes. 4.3 Graphics: Simple Plotting, Advanced Plotting - ggplot, Using Color in Plots. Using Subscripts and Superscripts in Graph Labels, Interactive Graphics, Saving Graphical Output, Loops**.**	K1 K2-K4 K5-K6	13	1-5
5	**Bioconductor** 5.1 Introduction, Bioconductor Packages, Bio strings, Biomart 5.2 Bioconductor packages for protein- protein interaction graphs, gene variation packages, genomic ranges, genomic alignments, genomic annotations. 5.3 Biomedical data science in R- BioML(R). Data wrangling with Tidyverse and shiny	K1-K3 K2-K4 K5-K6	13	1-5

BOOKS FOR STUDY

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

BOOKS FOR REFERENCE

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

WEB SOURCES

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/

JOURNALS

The Python Papers Source Codes
The Python Papers Anthology
Python Journal
The R Journal

Pattern of Assessment

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

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs) to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/PR24												
	Course Title: PYTHON AND R PROGRAMMING												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	3	3	2	2	2	2	1	3	3	3	2	2
CO 2	3	3	2	3	2	2	2	1	3	3	3	2	2
CO 3	3	3	3	3	3	2	1	1	3	2	3	2	2
CO 4	3	3	2	2	2	2	1	1	3	3	2	2	2
CO 5	3	3	3	3	2	2	1	1	3	2	3	2	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI – 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2023–2024)

PYTHON AND R PROGRAMMING – PRACTICAL

CODE: 23BI/PC/P122 **CREDITS: 2**
L T P: 0 0 3
TOTAL TEACHING HOURS: 39

OBJECTIVES OF THE COURSE

- to use python and r languages for dataset retrieval and accession
- to analyze biological data using biopython and bioconductor packages
- to develop and write python and r scripts to access biological databases
- to perform normalization and discretization of sample data
- to use Python and R languages for graphical visualization of biological data

COURSE LEARNING OUTCOMES (COs)
On successful completion of the course, students will be able to

COs	DESCRIPTION	CL
CO1	relate the necessity for programming in biology, Handling biological concepts with Python and R scripts	K1
CO2	perform and distinguish genomic and transcriptomic data analysis	K2
CO3	apply programing to analyze genomic sequences and process the information	K3
CO4	gain efficient programming skills by solving biological problems	K4
CO5	perform biological data analysis using python and R language	K5,K6

CL – Cognitive Level
K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Basics of Python** 1.1 Creating tuples, lists, sets, dataframes 1.2 Importing Data, Data Frames, Handling Missing Data 1.3 Data visualization – volcano, PCA plot, heatmap**,** Object oriented python – displaying genomic coordinates	K1-K3 K2-K4 K5-K6	7	1-5
2	**Biopython** 2.1 Counting the base frequency**,** Plotting ABI traces**,** To transcribe and translate a sequence 2.2 Biopython- using Bioseq –Sequence reading and writing**,** Biopython using Bio.Genbank – reading entries 2.3 Using BioALign to perform pairwise and multiple sequence alignment	K1-K3 K5-K6 K3-K4	8	1-5

UNIT	CONTENT	CL	Hrs	CO
3	**Basics of R** 3.1 Creating vectors, matrix, factors, list, dataframes 3.2 Plots – simple –bar, pie, line etc., 3.3. Setting up axis and labels	K1-K4 K5-K6	8	1-5
4	**Advanced plotting** 4.1 GGplot – geom point, jitter, geom bar, geom line. 4.2. PCA, heat maps, Clustering 4.3. Data analysis - Importing Data, Data Frames, Handling Missing Data	K5-K6 K2-K4	8	1-5
5	**Bioconductor** 5.1 Bioconductor packages- bioclite, Biostring, Biomart, protein -protein network graphs 5.2 Microarray data analysis – Limma/edgeR/DESEQ2 5.3 Microbiome data analysis- vegan/ phyloseq	K1-K3 K2-K4 K5-K6	8	1-5

BOOKS FOR STUDY

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

BOOKS FOR REFERENCE

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

WEB SOURCES

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/

JOURNALS

The Python Papers Source Codes
The Python Papers Anthology
Python Journal
The R Journal

PATTERN OF ASSESSMENT

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

Sections	Cognitive levels	Marks	Pattern
A	K3, K4	10	2 X 5 =10 (All questions to be answered)
B	K5, K6	30	2 x 15 = 30 (All questions to be answered)
Record		5	
Viva		5	
	Total	50	

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

Sections	Cognitive levels	Marks	Pattern
A	K3, K4	50	5 X 10 =50 (All questions to be answered)
B	K5, K6	30	2 x 15 = 30 (All questions to be answered)
Record		10	
Viva		10	
	Total	100	

Mapping of Course Outcomes (COs)
to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/P122												
	Course Title: PYTHON AND R PROGRAMMING - PRACTICAL												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	3	3	2	3	2	2	1	3	3	3	2	2
CO 2	3	3	2	3	2	2	2	1	3	3	3	2	2
CO 3	3	3	3	3	3	2	1	1	3	2	3	2	2
CO 4	3	3	2	2	2	2	1	1	3	3	2	2	2
CO 5	3	3	3	3	2	2	1	1	3	2	3	2	2

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023 -2024)

SOFT SKILLS

CODE: 23BI/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 (COs)

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

COs	DESCRIPTION	CL
CO1	communicate with confidence and poise	K1
CO2	accept themselves and improve on their weaknesses	K2
CO3	work more effectively and complete activities on time	K3
CO4	work more effectively and complete activities on time	K4
CO5	plan their future with clarity and focus	K5,K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**Behavioural Traits** 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	K1-K6	6	1-5
2	**Team Work** 2.1. Interpersonal Skills 2.2. People Management 2.3. Creative Thinking 2.4. Critical Thinking 2.5. Experiential Learning – Based on activities	K1-K6	5	1-5

UNIT	CONTENT	CL	Hrs	CO
3	**Time Management** 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	K1-K6	5	1-5
4	**Conflict Resolution** 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	K1-K6	5	1-5
5	**Career Mapping** 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	K1-K6	5	1-5

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

Other Components: Total Marks: 50

Categories of other components	Cognitive levels	Marks allocation
Quiz/MCQs, open book tests/ Tests	K1 - K2	10
Assignment, Mini projects, Debate.	K3 - K4	20
Critique a concept/ Seminar/ Group Presentation	K5 - K6	20

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI – 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023–2024)

PROTEOMICS AND METABOLOMICS

CODE: 23BI/PC/PM34 **CREDITS: 4**

L T P: 3 0 2

TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- to provide an insight into the complete proteome and metabolome map of humans
- to instill methods of protein modeling and validation
- to foster knowledge on the significance of protein interactions in disease conditions
- to acquaint knowledge on various experimental and computational techniques available for proteomic and metabolomic profiling
- to develop an understanding of the entire protein/metabolome components of a cell through analytical approaches, Data mining and other software tools

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	gain an insight of the basic and advanced concepts and applications of proteomics and metabolomics	K1
CO2	understand the mechanisms of integrating proteomics and metabolomic data with the previously learnt omics techniques	K2
CO3	apply functional genomics techniques to analyze proteome and metabolome data for biological system	K3
CO4	deduce differential abundances in proteome and metabolome during health and disease	K4
CO5	analyze the proteomic and metabolomic interactions in complex disease	K5, K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**Proteomics** 1.1. Introduction to Proteomics - Proteins structure, Organization of protein structure, structural conformation of proteins, three dimensional structures of proteins. 1.2. Protein extraction and purification - 1D and 2D-gel electrophoresis, Mass Spectrometry - ESI, MALDI, Software for Matching MS Data with Specific Protein Sequences, Peptide sequencing by tandem mass spectrometry 1.3. Preparative IEF, Protein Digestion Techniques, Protein structure prediction - Elementary Description of Crystallography - Crystal Growth, Data Collection, Structure Solution, Refinement and Interpretation	K1-K2 K2-K3 K3-K6	10	1-2 2-3 3-5

UNIT	CONTENT	CL	Hrs	CO
2	**Computational proteomics**		10	
	2.1. Protein Structure prediction - Secondary Structure Prediction, Homology modelling, Structure validation tools - Ramachandran Plot, Threading and *ab initio* method, Tools for Structure prediction	K1-K3		1-3
	2.2. Protein structural visualization; Geometry optimization and Loop refinement, AI based methods- alpha fold, alpha meet	K3		3
	2.3. Proteogenomics - overview, applications and computational resources available	K4-K6		4-5
3	**Protein -protein interactions**		10	
	3.1. Proteomic interactions - Yeast Two-Hybrid, Mammalian Screen Methods and Co-Immuno Precipitation techniques	K1-K3		1-3
	3.2. Protein-Protein Interactions, chaperones, protein misfolding in diseases and protein complexes. Databases and proteomic tools	K3-K6		3-5
	3.3. Post translational modifications, top down and bottom up approaches in proteomics. Data analysis in proteomics, Applications of proteomics in Biomarker discovery, personalized medicine, astrobiology, paleo proteomics	K4-K6		5
4	**Metabolomics**		12	
	4.1. Metabolite to metabolome and metabolic reactions, importance of metabolomics and designing a metabolome study	K1-K3		1-3
	4.2. Metabolomic databases and web resources, Experimental methods in metabolome generation-Plant/bacterial secondary metabolites, MS based approaches, targeted and untargeted metabolomics, and experimental errors.	K3-K4		3-4
	4.3. Metabolomic categories - Lipidomics, Glycomics, Fluxomics, genome scale metabolic modelling	K4-K6		4-5
5	**Computational Analysis of Metabolomics**		13	
	5.1. Generation of metabolome data, over representation analysis and disease-based enrichment analysis.	K1-K3		1-3
	5.2. Statistical analysis in metabolomics – univariate and multivariate analysis, dimensionality reduction and differential abundance of metabolomics.	K4-K6		4-5 2-3
	5.3. Functional annotation, Softwares and tools for metabolome analysis - Mzime, metabolome analyst, paintomics.	K2-K3		

UNIT	CONTENT	CL	Hrs	CO
	Practical component Metabolic pathway database – KEGG, PharmGKB, Pubchem Protein classification and structure analysis –Chou fasman, GOR, Procheck Protein motif and domain search – PROSITE, PDBeMotif, MASCOT Homology modelling – Swiss model, Modeller software Secondary structure prediction – JPRED, MFOLD Protein–Protein interaction analysis – DIP, STRING, BIND, Expasy, Cytoscape	K1,K2 K3,K4 K5,K6	10	1-5

BOOKS FOR STUDY

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

Pennington S and M. J. Dunn. *Proteomics: From Proteins Sequence to Function*. Germany: Springer Publications, 2001

Palzkill and Timothy. *Proteomics*. USA: Kluwer Academic Publishers, 2013.

Daniel C. Leibler. *Introduction to Proteomics: Tools for New Biology***.** USA: Humana Press, 2002**.**

Srivastava Sudhir. *Informatics in Proteomics*. USA: Taylor & Francis Group, 2005.

BOOKS FOR REFERENCE

Collado Vides Julio and Ralf Hofstadter. *Gene Regulation and Metabolism – Post Genomic Computational Approaches*. India: Ane Books, 2004.

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

Griffiths, A.J.F, Miller, J.H, Suzuki, D.T. Lewontin, R. C. and Gelbart, W.M. *An Introduction to Genetic Analysis*. USA: W.H. Freeman, 1996.

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

WEB SOURCES

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

JOURNALS

Genomics, Proteomics & Bioinformatics
Journal of Data Mining in Genomics & Proteomics
Human Genomics and Proteomics
Journal of Proteomics and Genomics

PATTERN OF ASSESSMENT

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

Sections	Cognitive levels	Marks	Pattern
Theory			
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K5, K6	10	2 X 5 = 10 (Internal choice) Answers in about 500 words
Practical			
A	K3, K4	10	2 X 5 =10 (All questions to be answered)
B	K5, K6	10	1 x 10 =10 (All questions to be answered)
	Record & Viva	5	
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs, open book tests/ Tests	K1 - K2	CO1-CO2	20
	K3 - K4	CO3-CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Mark allocation	Pattern
Theory			
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K5, K6	20	4 X 5 = 20 (Internal choice) Answers in about 500 words
Practical			
A	K3, K4	20	2 X 10 =20 (All questions to be answered)
B	K5, K6	20	2 x 10 =20 (All questions to be answered)
	Record & Viva	10	
	Total	100	

Mapping of Course Outcomes (COs) to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/PM34												
	Course Title: PROTEOMICS AND METABOLOMICS												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	2	2	1	3	2	2	1	1	1	1	2	2	2
CO 2	3	3	2	3	2	1	1	1	2	1	3	2	3
CO 3	3	3	2	3	2	2	1	1	3	2	3	1	2
CO 4	3	3	3	3	2	1	1	1	2	1	3	1	1
CO 5	3	2	3	3	2	2	1	1	2	2	3	2	2

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023-2024)

MACHINE LEARNING, DEEP LEARNING AND ARTIFICIAL INTELLIGENCE

CODE: 23BI/PC/MA34 **CREDITS: 4**

L T P : 4 1 0

TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- to provide an insight in discovering pattern in the data and to make predictions as well as to intricate patterns for solving healthcare problems
- to identify objects from large datasets and to perform complex tasks with increasing accuracy
- to identify the precise 3d geometry of biological molecules and enhance the ability of biological research for better disease diagnosis
- to annotate biological databases and retrieve the key information hidden in the data.
- to construct model in order to identify the patterns and relationships in data and apply in the AI tool development

COURSE LEARNING OUTCOMES

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

COs	DESCRIPTION	CL
CO1	demonstrate the fundamental knowledge on concepts of machine learning and deep learning	K1, K2
CO2	utilise the different libraries available to understand the fundamental prerequisite for ml and dl	K3
CO3	identify the right method of classification and clustering analysis specific for the datasets	K4
CO4	enable to build a model and examine their performance using various statistical methods by training and testing to culminate artificial intelligence	K5
CO5	apply the ml, dl and ai concepts to solve problems in biology and medicine	K6

CL – Cognitive Level

K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Data Types and Preprocessing** 1.1. Different Forms–statistics, data mining, data analysis, data science, Statistics vs. Data Mining vs. Data Analytics vs. Data Science. 1.2. Machine Learning perspectives of data–Scales of Measurement, data imputation, dealing with missing data, normalising data, feature generation. 1.3. Machine Learning Categories-supervised, unsupervised, reinforcement learning.	K1-K4 K2-K5 K3-K6	10	1-5
2	**Machine Learning** 2.1. Exploratory data analysis –multivariate and univariate analysis, Supervised Learning concepts- Regression, correlation and causation. 2.2. Supervised Learning – Classification, ROC curve, Evaluating a Classification Model Performance, SVM, SOM and KNN. 2.3. Unsupervised learning – K means, Hierarchical and random forest, evaluation – cross fold K validation.	K1-K4 K2-K5 K3-K6	15	1-5
3	**Building and Evaluating Model** 3.1. Ensemble methods- bagging, boosting, Ensemble voting, stacking. 3.2. Text mining, data assemble, Data Preprocessing (Text) - Convert to Lowercase and Tokenize, Removing Noise, Part of Speech (PoS) Tagging, Stemming, Lemmatization, N-grams, Word2Vec, FastText, Glove. 3.3. Transformer based architecture and models, Data Exploration, model building and evaluation.	K1-K4 K2-K5 K3-K6	15	1-5
4	**Deep Learning and Artificial Intelligence** 4.1. Artificial Neural Network (ANN), Image Recognition with Deep Learning and Neural Networks, Perceptron– Single Artificial Neuron, Multilayer Perceptrons (Feedforward Neural Network). 4.2. Restricted Boltzmann Machines (RBM), Multilayer Perceptrons (MLP) Using Keras, tensor flow, Autoencoders. 4.3 Convolution Neural Network (CNN), Recurrent Neural Network (RNN), Long Short- Term Memory (LSTM), Transfer Learning and Reinforcement Learning	K1-K4 K2-K5 K3-K6	10	1-5
5	**Applications of ML, DL and AI** 5.1. ML, DL and AI in drug discovery and development 5.2. Approaches of ML, DL and AI in medical diagnosis and personalized medicine 5.3. Implementation of ML, DL and AI in disease prediction and prevention	K1-K4 K2-K5 K3-K6	15	1-5

BOOKS FOR STUDY

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

Andreas Muller, Introduction to Machine Learning with Python a guide for data scientists, O'Reilly, 2016

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

BOOKS FOR REFERENCE

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

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

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

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

JOURNALS

Journal of Machine Learning Research
Journal of Artificial Intelligence Research
Applied Artificial Intelligence
International Journal on Artificial Intelligence Tools

WEB SOURCES

https://www.futurelearn.com/courses/artificial-intelligence-in-bioinformatics
https://towardsdatascience.com/ai-in-bioinformatics-a1acdc3cdd89#:~:text=AI%20in20bioinformatics%20includes%20both,as%20well%20as%20complex%20systems.
https://addepto.com/blog/the-role-of-machine-learning-in-bioinformatics-and-biology/

PATTERN OF ASSESSMENT

Continuous Assessment: Total Marks: 50 Duration:90 minutes

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs)
to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/MA34												
	Course Title: MACHINE LEARNING, DEEP LEARNING AND ARTIFICIAL INTELLIGENCE												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	3	3	2	3	2	1	1	3	3	3	3	2
CO 2	3	2	3	2	3	3	2	1	3	3	3	3	3
CO 3	3	3	3	2	3	3	2	1	3	2	2	2	3
CO 4	3	2	2	3	3	3	2	2	3	2	3	2	3
CO 5	2	2	3	2	2	2	1	1	3	2	3	3	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023 -2024)

MOLECULAR MODELING AND COMPUTER AIDED DRUG DESIGN

CODE: 23BI/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 understand theoretical background to the various methods of energy minimization
- to instill molecular modelling mechanics and interaction
- to develop and understand the mechanism of drug design using computers
- to acquire knowledge on molecular dynamics and monte carlo simulations

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	interpret the protein structural features, minimise the energy and simulate to attain the stability for its importance in drug action	K1,K2
CO2	construct and analyse the molecular dynamics and monte carlo simulation methods	K2,K3
CO3	compare, categorise and examine the concepts of molecular interactions and qsar studies	K3,K4
CO4	determine the functional disease targets and interpret the target-ligand interactions	K4,K5
CO5	apply the knowledge towards design and development of potential lead molecules	K5,K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**Molecular Mechanics** 1.1. Concepts in Molecular Modeling - Molecular Representations, CoordinateSystems, 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 bond interactions	K1-K4 K2-K4 K5-K6	10	1-5
2	**Energy Minimization Methods** 2.1. Energy Minimization- Derivative and Non-Derivative Energy MinimizationMethods. 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.	K1-K4 K2-K4 K5-K6	10	1-5
3	**Pharmacophores** 3.1. Molecular structures, representation – SMILES, InChi keys, Chemical Fingerprint generation, Tanimoto coefficient. 3.2. Molecular structure similarity and diversity, Molecular Descriptors – 1D, 2D, 3D, 4D, CoMFA, COMSIA, QSAR, 3D QSAR, ADMET prediction. 3.3. 3D Pharmacophore identification and mapping, Ligand-based and structure based pharmacophores, Chemical libraries, Scaffold hopping	K1-K3 K2-K4 K5-K6	15	1-5
4	**Molecular Docking** 4.1. Drug discovery and development, computational approaches in drug discovery. 4.2. Structure Based Drug Design - Target Discovery and Validation, Active Site Prediction, Lead identification and Optimization, De Novo Drug Design. 4.3. Molecular docking and high throughput virtual screening.	K1-K3 K2-K4 K5-K6	15	1-5
5	**Molecular Dynamics and Monte Carlo Simulations** 5.1. Molecular Dynamics Using Simple Model, Molecular Dynamics with Continuous Potentials 5.2 Molecular Dynamics at Constant Temperature and Pressure Incorporating Solvent effects into Molecular Dynamics, Conformational Changes from Molecular Dynamics Simulation 5.3. Monte Carlo Simulation of Molecules, Calculation of Chemical Potential-Simulating Phase Equilibria by Gibbs Ensemble Monte Carlo Method	K1-K4 K2-K4 K5-K6	15	1-5

BOOKS FOR STUDY

N. Claude Cohen. *Guidebook on Molecular Modelling In Drug Design***.** California: AcademicPress, 2006.
Andrew R. Leach. *Molecular Modeling: Principles and Applications*. USA: Prentice Hall,2007.
Daan Frenkel and Berend Smit. *Understanding Molecular Simulation: From Algorithms toapplications*. 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 ModellingJournal 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: Total Marks: 50 Duration: 90 minutes

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs) to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/MC34												
	Course Title: MOLECULAR MODELING AND COMPUTER AIDED DRUG DESIGN												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	3	3	2	3	3	2	1	3	3	3	2	3
CO 2	3	3	3	3	2	3	1	1	3	2	2	2	2
CO 3	3	3	3	3	3	3	2	1	3	3	3	2	3
CO 4	3	3	3	3	3	3	2	1	3	3	3	2	3
CO 5	3	3	3	3	3	3	3	2	3	2	3	3	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2023 -2024)

MOLECULAR MODELING AND COMPUTER AIDED DRUG DESIGN- PRACTICAL

CODE: 23BI/PC/P232 **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 instill knowledge on pharmacophore mapping
- to understand the use of informatics in drug design and development
- to identify new drug targets to treat diseases
- to gain insights on protein-ligand docking and knowledge-based scoring functions for molecular simulations

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	understand the importance of drug-like properties and their prediction	K1,K2
CO2	describe the use of lead candidates and database representations	K2,K3
CO3	in silico identification of lead molecules through molecular docking, pharmacophore modeling	K3,K4
CO4	perform the mechanics and dynamics of molecules	K4,K5
CO5	gain practice in macromolecular simulations and perform research work in the area of computational drug design	K5,K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3– Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**Pharmacophore modeling** Ligand Search – PubChem, Drug bank, CHEMBL, ZINC databases. Chemical drawing package – Marvin Sketch. ADME prediction – Online tools (Swiss ADME, etc.). QSAR model prediction – In Silico tools. Pharmacophore mapping.	K1-K6	8	1-5
2	**Active site prediction** Binding Site Identification Different approaches for binding site identification Tools - Cast-P, POCASA, 3D ligand site, Metapocket, Ghecom.	K1-K6	8	1-5
3	**Molecular Docking** Structure Based Drug Design-Molecular docking using AutoDock and pyrx, Discovery Studio	K1-K6	8	1-5
4	**Molecular Visualisation:** Pymol and Chimera, Pdb file format and Parsing Visualizing a molecule in different representations Identifying interacting residues (protein and ligand interactions) Measuring distances between atoms B-factor visualisation Image tracing and preparation. Geometry Optimization using SwissPdb Viewer Energy Minimization of protein molecule, Determining Maxima and Minima energy points	K1-K6	7	1-5
5	**Molecular Dynamics** Molecular dynamics using GROMACS/NAMD/ AMBER, Discovery Studio (CHARMM)	K1-K6	8	1-5

BOOKS FOR REFERENCE:

N. Claude Cohen. *Guidebook on Molecular Modelling In Drug Design***.** California: AcademicPress, 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

Sections	Cognitive levels	Marks	Pattern
A	K3, K4	10	2 X 5 =10 (All questions to be answered)
B	K5, K6	30	2 x 15 = 30 (All questions to be answered)
Record		5	
Viva		5	
	Total	50	

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

Sections	Cognitive levels	Marks	Pattern
A	K3, K4	50	5 X 10 =50 (All questions to be answered)
B	K5, K6	30	2 x 15 = 30 (All questions to be answered)
Record		10	
Viva		10	
	Total	100	

Mapping of Course Outcomes (COs)
to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/P232												
	Course Title: MOLECULAR MODELING AND COMPUTER AIDED DRUG DESIGN-PRACTICAL												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	3	3	2	3	3	2	1	3	3	3	2	3
CO 2	3	3	3	3	3	3	2	1	3	3	3	3	3
CO 3	3	3	3	3	3	3	2	1	3	3	3	3	3
CO 4	3	3	3	2	3	2	1	1	3	2	3	3	3
CO 5	3	3	3	3	3	3	2	1	3	2	3	3	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023 -2024)

MOLECULAR BIOLOGY PRACTICAL

CODE: 23BI/PC/P332

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
- to instill practical knowledge on plant extraction and identification of secondary metabolites
- to understand the mechanism of sequencing of environmental samples through metagenomics approach

COURSE LEARNING OUTCOMES

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

COs	DESCRIPTION	CL
CO1	utilize laboratory skills to enhance understanding of cell structure and functionwhile participating in a group environment	K1,K2
CO2	develop responsible conduct of laboratory skills appropriate to the field of celland molecular biology	K2,K3
CO3	apply the molecular biology techniques to biotechnological approaches	K3,K4
CO4	perform the mechanics and dynamics of molecules	K4,K5
CO5	gain practice in macromolecular simulations and perform research work in the area of computational drug design	K5,K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	1.1. Cell Fraction and Extraction of cell organelles - Chloroplast 1.2. Extraction of DNA from Onion 1.3. Extraction of RNA from Yeast	K1-K6	8	1-5
2	2.1. Estimation of DNA and RNA 2.3. Estimation of Proteins by Lowry's Method 2.3. Estimation of Mitochondria by Assessing the Marker Enzyme	K1-K6	8	1-5

UNIT	CONTENT	CL	Hrs	CO
3	3.1. Denaturing Proteins and Identification of Amino Acids by Thin Layer Chromatography 3.2. Amplification of DNA by PCR 3.3. Electrophoretic Techniques: Agarose Gel Electrophoresis, SDS PAGE, Southern Blotting (Demo)	K1-K6	8	1-5
4	4.1. Plant sample extraction using solvents 4.2. Identification of secondary metabolites 4.3. Evaluation of secondary metabolites for therapeutic use	K1-K6	7	1-5
5	5.1. Sample collection from different environments 5.2. Microbial isolation and culture techniques 5.3. Metagenomics analysis	K1-K6	8	1-5

BOOKS FOR REFERENCE

Wilson, K; Walker, J. *Principles and techniques of Biochemistry and Molecular Biology.* USA: Cold Spring Harbor Laboratory Press, 2010.

Sambrook, J; Russel, DW. *Molecular Cloning*. USA: Cold Spring Harbor LaboratoryPress, 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 & MolecularBiology. India: I K International Publishing House, 2018.

PATTERN OF ASSESSMENT

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

Sections	Cognitive levels	Marks	Pattern
A	K3, K4	10	2 X 5 =10 (All questions to be answered)
B	K5, K6	30	2 x 15 = 30 (All questions to be answered)
Record		5	
Viva		5	
	Total	50	

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

Sections	Cognitive levels	Marks	Pattern
A	K3, K4	50	5 X 10 =50 (All questions to be answered)
B	K5, K6	30	2 x 15 = 30 (All questions to be answered)
Record		10	
Viva		10	
	Total	100	

Mapping of Course Outcomes (COs) to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/P332												
	Course Title: MOLECULAR BIOLOGY-PRACTICAL												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	2	3	2	3	2	3	1	3	2	1	1	2
CO 2	3	2	3	2	3	2	3	1	3	1	2	1	3
CO 3	3	3	3	3	3	2	3	2	3	2	2	2	3
CO 4	3	3	3	2	3	3	1	1	3	3	3	2	3
CO 5	3	3	3	3	3	3	1	1	3	3	3	3	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI 600 086

M.Sc. DEGREE BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023 -2024)

SUMMER INTERNSHIP

CODE: 23BI/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 2023 -2024)

APPLIED BIOINFORMATICS

CODE: 23BI/PC/AB44

CREDITS : 4
L T P : 4 1 0
TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- to explore the potentials of dietary supplements with the impact on genome, proteome and metabolome.
- to examine factors that affect drug response and the application of pharmacogenetics to drug development and drug treatment
- to empower the trait screening and marker-assisted backcrossing for the improvement of genetic merit of plant breed.
- to be aware of biodiversity importance and utilize software for identification and accessing the biodiversity databases.
- to instill knowledge on the major steps in cancer development and progression and their relationship to disease mechanisms and therapeutic strategies

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	apply the nutritional information to genomics and vice versa	K1
CO2	emphasise the application of bioinformatics and biological databases for the development of personalized medicine.	K2
CO3	imbibe the genome technologies to change breeding, monitor and protect the wild plant population	K3
CO4	evaluate the red data books, biodiversity registers and to interpret their morphological and molecular characterization	K4
CO5	describe the major clinical-translational areas of research in cancer biology and the goals of biomedical research in these areas	K5, K6

CL – Cognitive Level
K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Nutrigenomics** 1.1. Introduction-Background & Preventive Health. Applications -Nutrigenomics & gut health-prebiotics and probiotics. Nutrition linked to genes and phenotypes. 1.2. Role of folate, choline, and vitamins B2, B6 and B12, in gene regulation. Databases -SGMD, Barleybase and others. 1.3 Tools-Use of BioConductor, Booly.	K1 K2-K3 K4-K6	13	1-5
2	**Pharmacogenomics** 2.1. Introduction to Pharmacogenomics, Application and Challenges in Pharmacogenomics, Genetic Variation, Types of Variants, SNPs, Insertion/Deletions. 2.2. Databases - Pharmacogenomics Knowledge Base (PharmGKB), GWAS (Genome Wide Association study). 2.3. Personalised medicine - The use of AI in personalised medicine. Database-PreMedKb	K1-K2 K4-K6 K3-K6	13	1-5
3	**Agrigenomics** 3.1. Genomics application in Agriculture- The advantages and outcomes. Wheat genomics program. Seed saving techniques. 3.2. Genomic breeding, genetic engineering of plants. Development of high performance plants- Case study. 3.3. Databases of interest -Integbio, NARO- (RAP-DB), Tools- Parentage Testing, Marker assisted backcrossing.	K1-K3 K3-K4 K5-K6	13	1-5
4	**Biodiversity Informatics** 4.1. Concepts of Biodiversity, Major drivers of biodiversity change; biodiversity management approaches, Endangered animals, Endemism and Red data books- Biodiversity registers 4.2. Software for identification of Accessing existing biodiversity databases on the WWW- Delta, MicroIS, AVIS, ICTV 4.3. UNEP/GEF biodiversity data management project (BDM). – CBD and bioethics– General agreement on trade and traffics.	K1-K3 K3-K4 K4-K6	13	1-5
5	**Cancer Genomics** 5.1. Carcinogenesis - chemical and physical carcinogenesis, molecular pathways in carcinogenesis, Apoptosis and cancer. Mutagens, genetic variants. 5.2. Databases and tools to analyse cancer data- TCGA, Bioportal, GTEX, HPA, Reactome, UALCAN, Oncomine, KM plotter, COSMIC. Kaplan meier survival plots. Analysing Big Data of Cancer Genomics. 5.3. Application of next generation sequencing technologies in diagnosis and prediction of cancer genes. Identification of Methylation sites, Expression profiles, pathway analysis.	K1-K2 K2-K3 K3-K6	13	1-5

BOOKS FOR STUDY

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

Rapley R and Harbron S. *Molecular analysis and Genome discovery*. John Willey, 2004.

Lynnette R. Ferguson, Nutrigenomics and Nutrigenetics in Functional Foods and Personalized Nutrition, CRC Press, 2016.

KJ Gaston, Biodiversity – An introduction, 2nd ed., Wiley-Blackwell, 2003.

Graham Dellaire, Jason N. Berman, Robert J. Arceci, Cancer Genomics: From Bench to Personalized Medicine, 1st ed., Academic Press, 2013.

BOOKS FOR REFERENCE

Bryce Mendelsohn, Jeanette McCarthy, Precision Medicine: A Guide to Genomics in Clinical Practice (INTERNAL MEDICINE), Paperback,McGraw-Hill Education

Raffaele De Caterina, J. Alfredo Martinez, Marin Kohlmeier, Principles of Nutrigenetics and Nutrigenomics: Fundamentals of Individualized Nutrition, Academic Press Inc., 2019.

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

JOURNALS

The Pharmacogenomics Journal
American Journal of Pharmacogenomics
Pharmacogenomics and Personalized Medicine
Agronomy Journal
Lifestyle genomics
Nutrigenomics- Frontiers in Nutrition
Cancer 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
http://www.emolecules.com/info/molecular-informatics
https://www.illumina.com/areas-of-interest/agrigenomics.html
https://center-forward.org/genomics-agricultural-innovation/
http://www.pmjournal.ir/
https://www.cbioportal.org/

PATTERN OF ASSESSMENT

Continuous Assessment: Total Marks: 50 Duration: 90 minutes

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: Total Marks: 50

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination Total Marks: 100 Duration: 3 hours

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs)
to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/AB44												
	Course Title: APPLIED BIOINFORMATICS												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	2	3	2	2	3	2	1	3	3	3	2	3
CO 2	3	3	3	2	3	3	2	1	3	3	3	3	3
CO 3	3	3	3	3	3	2	2	1	3	3	2	2	3
CO 4	3	3	2	3	3	3	3	2	3	3	2	3	3
CO 5	3	3	3	3	3	3	3	3	3	3	3	3	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI – 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2023–2024)

BIG DATA ANALYSIS

CODE: 23BI/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 the current decade
- to understand the various aspects of data science and applying them in health care
- to obtain adequate knowledge of machine learning approaches
- to be aware of fundamentals and the use of computing power of clusters in accessing the sheer size of biological big data
- to create a general pipeline for complex data models and control analysis in a step-by-step fashion

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	collect meaningful values out of big biological data	K1
CO2	describe the big data landscape including examples of real world big data problems	K2
CO3	identify what are and what are not big data problems and be able to recast big data problems as data science questions	K3
CO4	apply the skills of hadoop and spark technology to solve the data science questions	K4
CO5	create pipelines for data analysis and reusable methods	K5, K6

CL – Cognitive Level
K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Introduction to Big data** 1.1. Big data -characteristics, data structures and data repositories, Example of Big Data. 1.2. Machine and People Generated Data and Advantages. Characteristics of big data – 6 V's 1.3. Getting value out of big data using a 5-step process to structure your analysis.	K1 K2-K3 K4-K6	12	1-5

UNIT	CONTENT	CL	Hrs	CO
2	**Big data in healthcare** 2.1 Data Science in Biomedicine and Healthcare. Sequence Processing, Medical Image Analysis, Natural Language Processing. 2.2 Network Modeling and Probabilistic Modeling. Concepts of Hadoop and spark, The Hadoop Distributed File System: A Storage System for Big Data, YARN: A Resource Manager For Hadoop. 2.3 MapReduce: Simple Programming for Big Results. Introduction to Spark for big data analysis. Pyspark in Solving big data.	K1-K2 K4-K6 K3-K6	15	1-5
3	**Biological data analysis** 3.1 ChIPseq - Introduction and biological theories on ChIPseq analysis. DNA fragment evaluation. Peak identification. Two condition comparison. Saturation analysis. Motif finding and related theories. 3.2 ATAC sequencing, Bisulfite sequencing for big biological data. 3.3 Integrating Multiomics big data. Seqware, distmap, read annotation pipelines.	K1-K3 K3-K4 K5-K6	13	1-5
4	**Computer clusters** 4.1 Introduction to essential computing, Distributed computing systems. An oversimplified, but useful, view of a computing cluster, Essential Unix/Linux Terminal Knowledge, Clusters, parallel, supercomputers, workstations, HPC. 4.2 Cluster computing and the job scheduler, High performance computer clustering (HPCC), learning about the resources on HPCC 4.3 Cloud computing - Cloud Primer, Cloud Foundations, Cloud Security and Migration. Cloud services – AWS or Google cloud.	K1-K3 K3-K4 K4-K6	12	1-5
5	**Workflows and pipelines** 5.1 Introduction to Snake make and next flow- installation, rules, directives: input, output, shell, script, target files, best-practices of bioinformatics pipeline development. 5.2 History of containers, Containers vs. virtual machines. Docker -Concept of and the difference between Docker & Singularity containers 5.3 Git and version control - github learning lab, git cheat sheet and best practices, REST- API.	K1-K2 K2-K3 K3-K6	13	1-5

BOOKS FOR STUDY

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

BOOKS FOR REFERENCE

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

WEB SOURCES

https://hevodata.com/learn/top-21-hadoop-big-data-tools/
https://www.cloudxlab.com
https://www.abinitio.com

JOURNALS

BMC: Big data Analytics
Journal of Bigdata, Springer
Big Data Research, Elseiver

PATTERN OF ASSESSMENT

Continuous Assessment: Total Marks: 50 Duration: 90 minutes

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs)
to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/BD44												
	Course Title: BIG DATA ANALYSIS												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	2	3	2	2	3	3	3	3	2	1	3	3	3
CO 2	3	3	3	1	2	3	2	2	3	2	2	3	3
CO 3	3	3	3	2	2	2	3	1	3	1	1	3	3
CO 4	3	3	2	1	2	3	2	3	3	3	3	3	3
CO 5	3	3	3	3	3	3	3	2	2	3	3	3	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023 -2024)

SYSTEMS BIOLOGY

CODE: 23BI/PC/SM44 **CREDITS: 4**

L T P : 4 1 0

TOTAL TEACHING HOURS: 65

OBJECTIVE OF THE COURSE

- to introduce the basic concepts of systems biology
- to train the students in designing a new organism through modelling network concept and manipulating them for biological applications
- to investigate the effects and regulation of gene expression in different temporal and spatial environments
- to simulate and interpret the complex cell organelle interactions and their relations with different biological entities
- to construct novel biological parts or devices and to redesign the existing natural biological systems.

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	understand the principles of integrative analysis methods for biological system analysis and interactions.	K1
CO2	appreciate the model behaviour concepts	K2
CO3	model gene expressions and integrate them with other omics	K3
CO4	simulate the cell environments and model a cell	K4
CO5	develop synthetic biology applications for omics	K5, K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
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	K1- K3 K2– K4 K5- K6	15	1-5
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	K1, K2 K3, K4 K5, K6	10	1-5
3	**Modeling of Gene Expression** 3.1. Modeling of Gene Expression-Modules of Gene Expression – Promoter Identification - General Promoter Structure 3.2. Sequence Based Prediction of Promoter Representation of Gene 3.3. Network as Directed and Undirected Graphs, Bayesian Networks- Boolean Networks- Gene Expression Modeling with Stochastic Equations	K1, K2 K3, K4 K5, K6	15	1-5
4	**Integrating Networks** 4.1. Computer Simulation of the whole Cell. Human Erythrocyte Model and its applications. Software for Modeling, ECELL, VCELL and GROMOS. 4.2. Simulation of cellular subsystems, network of metabolites and enzymes 4.3. Signal transduction networks, Gene 5 regulatory networks, metabolic pathways: databases such as KEGG, EMP, MetaCyc, AraCyc.	K1, K2 K3, K4 K5, K6	12	1-5
5	**Introduction to Synthetic Biology** 5.1. General concepts and enabling technologies. Biological Parts. Modularity and Standardization. 5.2. Part repositories DNA synthesis and assembly. Genome Editing. Controlling Gene Expression and Protein Production. 5.3. Gene synthesis and genetic engineering. Optogenetics. Gene therapy, Microbiome engineering, synthetic biosystems.	K1, K2 K3, K4 K5, K6	13	1-5

BOOKS FOR STUDY

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

Andres Kriete and Roland Eils. *Computational Systems Biology*. Uk: Elsevier, 2005.

BOOKS FOR REFERENCE

Uri Alon. *An Introduction To Systems Biology: Design Principles Of Biological Circuits*. London: Chapman & Hall/Crc, Taylor And Francis Group, 2006.

Choi And Sangdun. *Introduction To Systems Biology*. Usa: Humana Press, 2007.

Edda Klipp, Wolfram Liebermeister, Christoph Wierling, Axel Kowald, Hans Lehrach, Ralf Herwig. *Systems Biology: A Textbook*. Uk: Wiley- Vch.Edinburgh, 2009.

Zoltan Szallasi, Joerg Stelling, Vipul Periwal. *Systems Modeling In Cellular Biology*. USA: Mit Press, 2006.

Najarian, K., Najarian, S., Gharibzadeh, S., & Eichelberger, C. N. (2009). Systems biology and bioinformatics: a computational approach. CRC Press

JOURNALS

Current Synthetic and Systems Biology
Journal of Computer Science & Systems Biology
Eurasip Journal on Bioinformatics and Systems Biology
BMC Systems Biology

WEB RESOURCES

http://Sysbio.Med.Harvard.Edu/
www.Systemsbiology.Org
www.Systemsbiology.Ucsd.Edu/
www.Sysbio.Org/

PATTERN OF ASSESSMENT

Continuous Assessment: Total Marks: 50 Duration: 90 minutes

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs)
to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PC/SM44												
	Course Title: SYSTEMS BIOLOGY												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	3	3	2	2	2	2	1	3	2	2	2	3
CO 2	3	3	2	2	3	2	1	1	2	2	3	2	3
CO 3	3	3	3	2	3	1	1	2	3	3	2	2	3
CO 4	3	3	2	2	2	1	1	1	3	2	3	3	2
CO 5	3	3	3	2	2	2	1	1	3	2	2	3	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2023 -2024)

DISSERTATION

CODE: 23BI/PC/DS45 **CREDITS: 5**

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 beforethe 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 examinerswould 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**

Rubrics for Evaluation	**Marks**	**Cognitive Level**
Documentation	10	K1
Formulating topic statement	15	K2
Explaining the conceptual framework	15	K3
Textual analysis	25	K4
Research arguments	15	K5
Research conclusions & Viva	20	K6

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2023-2024)

CELL BIOLOGY AND GENETICS

CODE: 23BI/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
- to gain the fundamentals of human genetics and hereditary
- to comprehend the cellular components underlying the cell division and inheritance of gene traits

COURSE LEARNING OUTCOMES

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

COs	DESCRIPTION	CL
CO1	relate the functions and the key mechanisms of cells at the molecular level to integrate the chemical and biological points	K1, K2
CO2	illustrate the structural organization of genes and the control of gene expression	K3
CO3	explore prokaryotic and eukaryotic protein synthesis mechanisms and demarcate their working in various healthcare issues	K4
CO4	conceptualize mechanisms of signal transduction, cell cycle and cell death in the critical analysis of research problems	K5
CO5	compile the concepts of cell and molecular biology to offer precise solutions to complications in cancer	K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**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	K1, K2 K3-K4 K5-K6	15	CO 1-5

UNIT	CONTENT	CL	Hrs	CO
2	**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 Nonhistones, Nuclear matrix and Lamins; Nuclear envelope, Pore complexes, transport through the envelope 2.3. RNA- Types, Ribosomes – Structure, Assembly of polypeptides on Ribosomes	K1, K2 K3-K4 K5-K6	10	CO 1-5
3	**Cytoskeleton** 3.1. Structure of the Cell Wall, Structure and Role of Microtubules and Microfilaments in cells -cell-cell interactions- cell adhesion, tight junctions and plasmodesmata 3.2. Introduction to Membranes - Structure, Function, and Communication: Roles of membranes in eukaryotic cells; Membrane structure and composition 3.3. The Plasma Membrane - Fluid Mosaic Model	K1, K2 K3-K4 K5-K6	15	CO 1-5
4	**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	K1, K2 K3-K4 K5-K6	12	CO 1-5
5	**Cell Cycle and Karyotyping** 5.1. Chromosomes- Structure and function, Centromeres and Telomeres, 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	K1, K2 K3-K4 K5-K6	13	CO 1-5

BOOKS FOR STUDY

Harvey Lodish, Arnold Berk, Chris A. Kaiser, Monty Krieger, Anthony Bretscher, Hidde Ploegh. Molecular Cell Biology., W. H. Freeman-Macmillan Learning, New York, 8th ed., 2016.

Peter Snustad and Michael J. Simmons, Principles of Genetics, Wiley Publications, USA, 7th ed., 2015.

Klug, William, S., Michael R. Cummings. Concepts of Genetics. Pearson Publications, USA, 12th ed., 2009.

BOOKS FOR REFERENCES

Watson, James, D. Molecular Biology of the Gene. Pearson Publications, USA, 7th ed., 2013.

Hartwell L, Hood L, Goldberg M, Ann E. Reynolds, Lee Silver, Genetics: From Genes to Genomes, McGraw-Hill Education, UK, 4th ed., 2010.

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: **Total Marks: 50** **Duration: 90 minutes**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
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Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
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	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs) to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PE/CG15												
	Course Title: CELL BIOLOGY AND GENETICS												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	3	3	2	2	2	2	1	1	2	2	2	1
CO 2	3	3	3	2	2	2	1	1	1	2	2	1	1
CO 3	3	3	3	3	3	2	2	2	2	1	2	2	2
CO 4	3	3	3	3	3	2	2	2	2	1	1	2	2
CO 5	3	3	3	3	3	2	3	2	1	2	2	1	1

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2023-2024)

BIOMATHEMATICS AND BIOSTATISTICS

CODE: 23BI/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
- to interpret the statistical measures reported in the scientific researches

COURSE LEARNING OUTCOMES

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

COs	DESCRIPTION	CL
CO1	list the importance of mathematics for research based problems	K1
CO2	explain the different statistical tests for the research	K2
CO3	analyse and solve aptitude based problems in competitive exams	K3, K4
CO4	evaluate the equations and problems related to population genetics	K5
CO5	propose the regression and correlation techniques to interpret drug activity based on qsar	K6

CL – Cognitive Level
K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Set Theory and Vectors** 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. Vectors Additions, Subtraction, Dot, Cross, Magnitude, Scalar Triple Product.	K1, K2 K3-K4 K5-K6	15	1-5
2	**Matrices, Relations and Functions** 2.1. Matrix, Basic Operations, Transpose, Square matrices, Non Singular Matrices. 2.2. Inverse of a Matrix, Determinants, Elementary Applications. 2.3. Relations and Functions - Linear Function, Polynomials and Differences	K1, K2 K3-K4 K5-K6	10	1-5
3	**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 Coefficient, Permutations, Combinations, Identities Applications.	K1, K2 K3-K4 K5-K6	15	1-5
4	**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. 4.2. Frequency distribution: Discrete and continuous frequency distribution. Mean-Median- Mode. 4.3. Measures of dispersion- Standard Deviation, Coefficient of variation, Range	K1, K2 K3-K4 K5-K6	12	1-5
5	**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 Equations. 5.3. Chi - χ^2 test, t-test, Analysis of Variance (ANOVA), Population Genetics: Hardy-Weinberg principle.	K1, K2 K3-K4 K5-K6	13	1-5

BOOKS FOR STUDY

Lipschutz S. and Lipson, M.L. Discrete Mathematics, McGraw Hill Book Company, UK, 3rd ed., 2017.

Veer Bala Rastogi, Fundamentals of Biostatistics, Ane Books Pvt Ltd, India, 1st ed., 2009.

Jae K.Lee, Statistical Bioinformatics for Biomedical and Life Science Researchers, John Wiley & Sons Publications, USA, 1st ed., 2010

Rao P. S. S. Sundar, Introduction to Biostatistics and Research Methods, Prentice Hall, India, New Delhi, 5th ed., 2012.

Narayanan S., Manicavachagam Pillay, T.K., Ancillary Mathematics- Book II, India**:** S. Viswanathan Printers and Publishers, India, 1st ed., 2009.

BOOKS FOR REFERENCE

Vittal, P.R. Allied Mathematics**,** Margham Publishers, India, 3rd ed., 2012.

Papoulis, Athanasios and S. Unnikrishnan Pillai, Probability, Random Variables and Stochastic Processes, Tata McGraw Hill Pub. Co. UK, 4th ed., 2017.

J. Richard, Sundar P. S. S. Rao, An Introduction to Biostatistics: A Manual for Students in Health Sciences, Prentice Hall, India, New Delhi, 3rd ed., 2004

Bernard Rosner, Fundamentals of Biostatistics, Duxbury Press, USA, 8th ed., 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 minutes**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs)
to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PE/BS15												
	Course Title: BIOMATHEMATICS AND BIOSTATISTICS												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	3	3	2	2	1	1	1	3	2	1	1	2
CO 2	3	3	3	3	3	3	1	1	3	2	1	2	2
CO 3	3	3	3	3	3	3	2	1	3	1	1	2	2
CO 4	3	3	3	3	3	3	2	2	3	2	3	2	3
CO 5	3	3	3	3	3	3	2	2	3	3	3	3	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023-2024)

RESEARCH METHODOLOGY, BIOETHICS AND IPR

CODE: 23BI/PE/RM15 **CREDITS: 5**

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
- to comprehend the importance of intellectual property rights and bioethics to perceive in the field of research
- to decipher the regulations, national, international protocols relative to research and materials.

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	better understanding of the research methods	K1
CO2	design an action plan of research	K2
CO3	acquire skills of writing a research manuscript	K3
CO4	application of statistical study in research	K4
CO5	understand the ethics in writing research work	K5, K6

CL – Cognitive Level

K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Types of Data and research problem identification** 1.1. Data Collection, Sources of Data- Primary, Secondary and Tertiary Sources, Sampling Methods- Probability and non-probability methods, Sample size and Sampling error. 1.2. Definition of Research, Types of research, Research Methodology, Principles and Practice of Research, Identifying The Research Problem. 1.3. Research Design: Exploratory, Descriptive and Experimental Research Design.	K1- K3 K2– K4 K5- K6	15	1-5
2	**Scientific Communication** 2.1. Literature Review - Its Relevance and Importance in Directing Research. Citations – Types of Citations, Bibliography and End Matters, Editing and Proofreading. 2.2. Action Plan, Design and Pilot Study undertaking a Research Project, Writing a Research grant Proposal, Format of thesis. 2.3. Scholarly Communication: IMRaD concepts for papers, and Poster and Oral Presentation, the Purpose and the Methods of Paper Critiquing.	K1, K2 K3, K4 K5, K6	12	1-5
3	**Writing well** 3.1. Writing for non- native audiences, usage of simple sentences, untangle long noun phrases, make complete sentences, Use of punctuations- comma, colon, semicolon, dash and periods, Creating non-textual information- acquiring, processing and printing illustrations. 3.2. Concepts of mind maps. Use of Encyclopedias, Research Guides, Handbook etc., Academic Databases for Computer Science Discipline, Use of tools / techniques for Research: methods to search required information effectively. 3.3. Reference Management Software like Zotero/ Mendeley, Software for paper formatting like LaTeX/MS Office, Software for detection of Plagiarism.	K1, K2 K3, K4 K5, K6	13	1-5
4	**Bioethics** 4.1. Bioethics – Definition – Bioethics of IPR, Ethical Issues in Biotechnology, Animal Models. 4.2. Ethical issues related to embryonic stem cells, Genetic testing and screening, human clinical trials and drug testing, Ethical Clearance 4.3. Ethics in Scientific Writing, Plagiarism and Common Errors in Scientific Writing. Misconduct in science.	K1, K2 K3, K4 K5, K6	12	1-5

UNIT	CONTENT	CL	Hrs	CO
5	**Intellectual Property Rights** 5.1. Introduction of IPR, General Agreement on Trade and Tariff (GATT) and World Trade Organizations. Establishment and functions of GATT, World Trade Organization (WTO) and World International Property Organization (WIPO). 5.2. WTO Summits, Role of Integrated Business Solution Center (IBSC) and Review Committee on Genetic Manipulation (RCGM), Production of Plant variety and farmers right act. 5.3. TRIPS, Different types of intellectual property rights (IPR), Patents, Trade mark, Trade secret, Copyright, Geographical distribution on biological diversity, Obligations, Production of Traditional Knowledge, Impact of GM Crops and GM Foods. Case studies on Patents (Basmati, Turmeric and Neem).	K1, K2 K3, K4 K5, K6	13	1-5

BOOKS FOR STUDY

Gopalan, R. Thesis Writing. India: Vijay Nicole Imprints Private Limited, 2005.
Gurumani, N. Research Methodology for Biological Sciences. India MJ Publishers, 2010.
Ahuja VK., Intellectual Property Rights in India, 1st ed., Lexis Nexis publisher 2015.

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
Radhakrishnan R and Balasubramanian S., Intellectual Property Rights, Excel Books Publishers, 2008

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: **Total Marks: 50** **Duration: 90 minutes**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs) to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PE/RM15												
	Course Title: RESEARCH METHODOLOGY, BIOETHICS AND IPR												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	3	1	3	1	3	2	3	2	1	3	3	2
CO 2	3	3	2	2	1	1	2	2	2	2	2	2	2
CO 3	3	3	3	3	1	2	1	2	3	1	2	1	2
CO 4	3	3	3	3	2	3	1	1	2	2	3	3	3
CO 5	3	3	2	3	2	1	1	1	1	1	1	1	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023-2024)

IMMUNOINFORMATICS

CODE: 23BI/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
- to familiarize the structure of antigen and antibodies and its function
- to analyse the immune data by integrating genomics and proteomics approach
- to understand the application of information technology to immunology

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	grasp the functions of the immune system	K1,K2
CO2	understand the application of information technology to immunology	K2,K3
CO3	study informatics-based approaches for prediction of epitopes and immuno-diagnostic tools	K3,K4
CO4	comprehend knowledge about computer aided vaccine design and reverse vaccinology	K4,K5
CO5	analyse the immunological data to find computational solutions available for immunological research	K5,K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**Immune System** 1.1. Introduction to Immune System - Adaptive and Innate Immunity. 1.2. Cells and organs of the Immune System, Soluble Mediators of Immunity, Cell and Antibody mediated immunity. 1.3. Immune Responses - Inflammation, Immunopathology, Auto immune diseases,Vaccines	K1-K3 K2-K4 K5-K6	10	1-5
2	**Antigens and Antibodies** 2.1. Antigen types – Epitope, Affinity Maturation, Epitope mapping 2.2. Immunoglobulin classes and subclasses, Structure and Function. 2.3. Major Histocompatibility Complex (MHC) its Polymorphism, Causes for Polymorphism, MHC Supertypes, Human Leucocyte Antigen (HLA) – Types and Polymorphisms.	K1-K3 K2-K4 K5-K6	15	1-5
3	**Computational Immunology** 3.1. Computational Immunology - Databases in Immunology, dbMHC-MHC databaseat NCBI 3.2. B-cell and T-cell Epitope Prediction, T-cell epitope databases, B-cell epitope databases, SYFPEITHI MHC-presented epitopes, IEDB 3.3. IMGT International ImMunoGeneTics Information system, HLA Nomenclature and the IMGT/HLA Sequence Database	K1-K3 K2-K4 K5-K6	10	1-5
4	**Vaccine Design** 4.1. From immunome to Vaccine – Prediction of immunogenicity, Vaccine design tools. 4.2. Reverse Vaccinology and Immunoinformatics, Peptides with AntimicrobialActivity or Antibiotic Peptides. 4.3. Functional Prospecting of Genes and Transcripts, Future of Computational Modeling and Prediction Systems in Clinical Immunology	K1-K3 K2-K4 K5-K6	15	1-5
5	**Viral Bioinformatics** 5.1. Viral Bioinformatics - Computational Views of Hosts and Pathogens using VIDA. 5.2. Virus- human protein interaction databases. Virus- NCBI. GISAID database. 5.3. Virus mint, Virus host database. Viral zone- Expasy	K1-K3 K2-K4 K5-K6	15	1-5

BOOKS FOR STUDY

Darren R. Flower. *Bioinformatics forImmunomics (Immunomics Reviews).* New York: Springer-Verlag, 2010.

Abul K. Abbas, Andrew H. H. Lichtman, and Shiv Pillai. *Cellular and Molecular Immunology* USA: Elsevier, 2017.

Andrew R. Leach, Valerie J. Gillet. *An Introduction to Chemoinformatics*.UK: Springer, 2007.

BOOKS FOR REFERENCE

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

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

Bunin, Barry A. Dordrecht. *Chemoinformatics: Theory, Practice, and Products*.UK: Springer, 2010.

WEB SOURCES

http://www.imgt.org/Immunoinformatics.html
http://rsob.royalsocietypublishing.org/content/3/1/120139
http://cheminformatics.org/
http://www.emolecules.com/info/molecular-informatics

JOURNALS

Immunoinformatics
BMC Genomics
Journal of Computational Biology
Immunology
Journal of Computational Biology

PATTERN OF ASSESSMENT

Continuous Assessment: Total Marks: 50 Duration: 90 minutes

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs)
to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PE/IM15												
	Course Title: IMMUNOINFORMATICS												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	3	3	3	2	2	1	2	1	2	2	1	1	3
CO 2	3	3	3	2	2	3	2	1	3	2	1	1	3
CO 3	3	3	3	3	3	3	2	1	3	3	3	2	3
CO 4	3	3	3	2	3	3	3	3	3	3	3	2	3
CO 5	3	3	3	3	3	3	3	2	3	3	3	2	3

High Correlation: 3

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023-2024)

CLINICAL RESEARCH MANAGEMENT

CODE: 23BI/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
- to compare different medical approaches and the effectiveness on groups of population
- to provide high quality data by reducing the error rate and improving the significance of research analysis

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	evaluate critical global regulatory and health care issues that challenge and influence biopharmaceutical product development	K1,K2
CO2	understand the drug development process and its importance in clinical trials	K2,K3
CO3	forecast the resources necessary for regulatory submission and comprehend regulatory Affairs procedure in clinical research	K3,K4
CO4	understand the basic statistical principles, concepts, and methods for clinical data analysis and reporting	K4,K5
CO5	demonstrate advanced critical thinking skills necessary to enhance employment opportunities or advance within the biopharmaceutical industry	K5,K6

CL – Cognitive Level

K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Clinical Research** 1.1. History of drug development - Pharmaco-epidemiology. 1.2. Issues in Clinical Trials. Nuremberg Code, Declaration of Helsinki, InternationalConference of Harmonization and Good Clinical Practice. 1.3. Clinical trials – History of clinical trials. Stages of Clinical trials.	K1-K3 K2-K4 K5-K6	10	1-5
2	**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.	K1-K3 K2-K4 K5-K6	10	1-5
3	**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 DrugApproval Activities, PMS.	K1-K3 K2-K4 K5-K6	15	1-5
4	**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 andMisconduct, Roles and Responsibilities of Clinical Research Professionals.	K1-K3 K2-K4 K5-K6	15	1-5
5	**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	K1-K3 K2-K4 K5-K6	15	1-5

BOOKS FOR STUDY

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

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

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

BOOKS FOR REFERENCE

Russ B. Altman, David Flockhart, David B. *Goldstein Principles of Pharmacogenetics and Pharmacogenomics.* UK: John Wiley, 2012.
Martin M. Zdanowicz. *Concepts in Pharmacogenomics*. UK: Mc Graw Hill, 2010.

JOURNALS

Journal of Clinical Research
BioethicsPerspectives 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 minutes**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
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	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
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	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs) to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PE/CR15												
	Course Title: BASICS OF CLINICAL RESEARCH MANAGEMENT												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	2	3	3	3	3	2	3	3	1	2	2	2	1
CO 2	2	3	3	2	2	2	3	3	1	2	2	1	1
CO 3	2	2	3	2	2	2	3	2	2	1	2	2	2
CO 4	2	2	3	3	2	3	2	2	2	1	1	2	2
CO 5	2	2	2	3	2	2	2	2	1	2	2	1	1

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023-2024)

STRUCTURAL BIOINFORMATICS

CODE: 23BI/PE/SB15

CREDITS: 5
L T P : 4 1 0
TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- to develop new ways for analysing biological macromolecular data in order to address biological problems and discover new information
- to understand the factors that influence and determine the function of biological macromolecules
- to create general-purpose methods for manipulating information about biological macromolecules and the application of these methods to solve problems in biology
- to impart the importance of indeterminate protein structure data analysis to gain useful information in the view of research context.
- to discern the subcellular location of protein and to create the 3D protein map for further prediction of novel information about its regulation.

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	recognize the fundamental structural and functional concepts of DNA and RNA molecules	K1
CO2	demonstrate the relativity and mechanisms of DNA molecules with protein molecules	K2
CO3	utilise the knowledge on the structure and properties of protein molecules and identify them computationally using variety of tools	K3
CO4	infer the functions, similarity, structural properties and their interactions in complex with other biological molecules using bioinformatics tools and databases	K4
CO5	measure the importance of peptides to proteins in the body functions and apply for solving biological problems	K5, K6

CL – Cognitive Level
K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Molecular Structures – An Introduction** 1.1. Introduction to Molecular structures including genes and gene products: protein, DNA, and RNA structure. structure representation, comparison of structures, visualisation, and modeling 1.2. DNA sequence and structures- complementarity, Chargaff's rule, other base pairs in sequence, reverse complementarity, palindromic sequences. 1.3. RNA sequences, types and structures – mRNA, tRNA, rRNA, miRNA, siRNA, circRNA, lncRNA, sg RNAs.	K1- K3 K2– K4 K5- K6	12	1-5
2	**Nucleic acids** 2.1. DNA – chromosome structure and architecture, Intron-exon boundary, histones, euchromatin, heterochromatin, CpG islands, methylated DNA structures. 2.2. Computational Structure prediction –RNA Structure determination methods, RNA structural refinement, predicting targets for inhibitory RNAs, Reading frames; Codon Usage analysis. 2.3. Translational and transcriptional signals, Splice site identification, Gene prediction methods and RNA fold analysis.	K1, K2 K3, K4 K5, K6	13	1-5
3	**Proteins** 3.1. Protein sequences and structure fundamentals, Amino acids – types, single letter codes, essential and non-essential amino acids. 3.2. Protein sequence analysis-Compositional analysis, Hydrophobicity profiles, Amphiphilicity detection, Moment analysis, Transmembrane prediction methods, Protein function prediction, motifs and domains, predicting binding site geometry and evolution. 3.3. Patterns and fingerprints. Point based and surface based binding site matching, Pattern based search using MeMe and PRATT); Motif-based search using ScanProsite and eMOTIF; Profile-based database searches using PSI-BLAST and HMMer.	K1, K2 K3, K4 K5, K6	15	1-5
4	**Structural Properties of Proteins** 4.1. Prediction of Coiled coils, Low complexity, non-globular, and disordered regions, Contact prediction, Alternative splicing 4.2. Target selection for diseases, Identification of Extreme environments, Functionally important residues, Local sequence motifs, Exons and domains, Mutations and their effect on structures. 4.3. Protein-protein interactions, Protein evolution, Structure-function relationships in proteins	K1, K2 K3, K4 K5, K6	12	1-5

UNIT	CONTENT	CL	Hrs	CO
5	**Peptides and Proteogenomics** 5.1. Peptide modelling - Signal peptides, natural peptides, Proteome - peptide repositories – PRIDE DB, peptide modeling, epitope and antibody structures. 5.2. Peptide- protein docking, Databases and tools for identifying protein- peptide interactions, network analysis, Tools and softwares to predict protein-protein and protein-peptide interactions. 5.3. Proteogenomics overview, Phenotype- Genotype, Gene expression, Proteogenomics approach to unravel proteoforms, Sequence centric proteogenomics, ProTIGY.	K1, K2 K3, K4 K5, K6	13	1-5

BOOKS FOR STUDY

Jenny Gu, Philip E. Bourne, Structural Bioinformatics, 2nd Ed., 2009.

Thomas E. Creighton, Proteins: Structures and Molecular properties, 2nd ed., WH Freeman Publications, 1992.

Akos Vegvari, Proteogenomics (Advances in Experimental Medicine and Biology), 1st ed., Springer Publications, 2016.

Stephen Neidle, Mark Sanderson, Principles of Nucleic acid Structure, 2nd ed., Academic Press, 2021.

BOOKS FOR REFERENCE:

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

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

JOURNALS

Journal of Structural Biology

BMC Structural Biology

Computational and Structural Biotechnology Journal

Journal of Molecular Biology

WEB RESOURCES

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

https://bio.tools/bioinfo3d

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

PATTERN OF ASSESSMENT

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

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

Mapping of Course Outcomes (COs) to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PE/SB15												
	Course Title: STRUCTURAL BIOINFORMATICS												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	2	2	3	2	3	3	1	1	1	2	3	2	1
CO 2	3	3	2	3	3	2	1	2	1	2	3	2	1
CO 3	3	3	3	3	2	2	2	2	1	2	2	1	2
CO 4	3	2	2	3	2	2	1	2	2	2	2	2	2
CO 5	3	3	3	2	3	2	1	1	2	2	3	1	2

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023-2024)

ALGORITHMS FOR BIOINFORMATICS

CODE: 23BI/PE/AL15 **CREDITS: 5**

L T P : 4 1 0

TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- to provide students with the basic knowledge of algorithms, computational biology and their advances in biology.
- to facilitate the students to attain skills in solving biological problems with algorithms, computational biology, sequence matching and learn its various biomedical applications.
- to develop skills to analyse algorithms related to bioinformatics
- to enable students with a particular focus on algorithms and data structures for search, comparisons, and motif discovery in strings.
- to instigate problem-solving skills through sorting and searching, algorithm design paradigms, and graph algorithms in the field of biological applications

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	understand the working of bioinformatics algorithms	K1
CO2	describe the divide-and-conquer paradigm and explain when an algorithmic design situation calls for it.	K2
CO3	apply the algorithms and design techniques to solve problems	K3
CO4	employ the important algorithmic design paradigms and methods of biomedical data analysis.	K4
CO5	solve current biological research problems using computational approaches	K5, K6

CL – Cognitive Level

K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Introduction** 1.1. Algorithms and Complexity. Definition, Biological Algorithms versus Computer Algorithms, Fast versus Slow Algorithms. 1.2. Algorithm Design Techniques Exhaustive Search Branch-and-Bound Algorithms Greedy Algorithms. Dynamic Programming algorithm. 1.3. Divide-and-Conquer Algorithms Machine Learning Randomised Algorithms, Big-O Notation.	K1-K4 K2-K5 K3-K6	10	1-5
2	**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	K1-K4 K2-K5 K3-K6	15	1-5
3	**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	K1-K4 K2-K5 K3-K6	15	1-5
4	**Clustering and Evolutionary Analysis** 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. 4.3 Evolutionary Trees and Hierarchical Clustering Character-Based Tree Reconstruction	K1-K4 K2-K5 K3-K6	10	1-5
5	**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. Hidden Markov Models, BLAST: Comparing a Sequence against a Database.	K1-K4 K2-K5 K3-K6	15	1-5

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

Miguel Rocha, Pedro G. Ferreira, Bioinformatics Algorithms: Design and Implementation in Python, Academic Press, 1st ed. 2018.

Thomas H. Cormen, Charles E. Leiserson and Ronald L. Rivest. Introduction to Algorithms. New Delhi: Prentice Hall of India, 3rd ed. 2009.

Jeffrey J. McConnell. Analysis of Algorithm. New Delhi: Narosa Publishing House, 2007.

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.

JOURNALS

Algorithms for Molecular Biology

Journal of Computational Intelligence in Bioinformatics

International Journal of Bioinformatics Research and Applications

BMC Bioinformatics

Bioinformatics Algorithms

WEB SOURCES

https://www.comp.nus.edu.sg/~ksung/algo_in_bioinfo/

https://www.bioinformaticsalgorithms.org/

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

https://compeau.cbd.cmu.edu/online-education/bioinformatics-algorithms-an-active-learning-approach/

https://www.bioalgorithms.info/

PATTERN OF ASSESSMENT

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

Sections	Cognitive levels	Marks	Pattern
A	K1, K2, K3	20	2 X 10 =20 (2 out of 3 questions to be answered - Open choice) Answers in about 1000 words
B	K4, K5, K6	30	3 X 10 = 30 (3 out of 4 questions to be answered - Open choice) Answers in about 1000 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs, open book tests/ Tests/ Assignment/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3-CO4	20
	K5 - K6	CO5	10
	Total		50

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

Sections	Cognitive levels	Mark allocation	Pattern
A	K1, K2, K3	50	5 X 10 =50 (5 out of 6 questions to be answered - Open choice) Answers in about 1000 words
B	K4, K5, K6	50	5 X 10 =50 (5 out of 6 questions to be answered - Open choice) Answers in about 1000 words
	Total	100	

Mapping of Course Outcomes (COs)
to Programme Outcomes (POs) and Programme Specific Outcomes (PSOs)

Semester	**Subject Code:** 23BI/PE/AL15												
	Course Title: ALGORITHMS FOR BIOINFORMATICS												
Course Outcomes (COs)	**Programme Outcomes (POs)**								**Programme Specific Outcomes (PSOs)**				
	PO 1	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CO 1	2	3	3	2	2	1	1	1	2	3	2	1	3
CO 2	2	3	3	2	2	1	1	1	2	3	2	2	3
CO 3	1	3	3	1	3	2	1	1	3	2	1	2	3
CO 4	3	2	3	2	2	3	2	1	3	3	2	2	3
CO 5	3	2	3	2	2	3	2	2	3	3	3	3	3

High Correlation: 3 Moderate Correlation: 2 Low Correlation: 1

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI – 600 086

Postgraduate Elective Course offered by the Department of Bioinformatics for M.A. / M.Sc./ M. Com Degree Programmes

SYLLABUS

(Effective from the academic year 2023–2024)

INTRODUCTION TO BIOINFORMATICS

CODE: 23BI/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
- to construct the phylogenetic trees to study the evolutionary concepts
- to implement the fundamental tools to predict the important sites of genes and proteins

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	better understanding of the bioinformatics concepts	K1
CO2	emphasis the application of bioinformatics and biological databases to problem solving in real research problems	K2
CO3	understand the evolutionary concepts related to biological query	K3
CO4	perform a complete analysis of the genes and protein	K4
CO5	analyse the importance of protein structure and functions of enzymes in restriction mapping.	K5, K6

CL – Cognitive Level

K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create

UNIT	CONTENT	CL	Hrs	CO
1	**Introduction to Bioinformatics**			
	1.1 Introduction to Bioinformatics, Classification of biological databases, Biological data formats, Application of Bioinformatics in various fields	K1-K4	8	1-5
	1.2 Introduction to single letter code of amino acids, symbols used in nucleotides	K2-K3		
	1.3 Data retrieval systems- Entrez and SRS	K3-K6		

UNIT	CONTENT	CL	Hrs	CO
2	**Sequence and Structure analysis**			
	2.1 Introduction to Sequence alignment. BLAST, Multiple sequence alignment	K1-K4	8	1-5
	2.2 Structural Databases – PDB and other online tools	K4-K6		
	2.3 Visualizing tools – Rasmol, Pymol	K3-K6		
3	**Phylogenetic analysis**			
	3.1 Evolutionary analysis: distances, Cladistic and Phenetic methods	K1-K3	8	1-5
	3.2 Clustering Methods. Rooted and unrooted tree representation	K3-K6		
	3.3 Bootstrapping strategies, Tools for Phylogenetic tree construction	K4-K6		
4	**Genomics**			
	4.1 Genome - Gene finding methods	K1-K3	7	1-5
	4.2 Gene prediction tools	K3-K4		
	4.3 Repeat Sequence finder	K4-K6		
5	**Proteomics**			
	5.1 Proteomics - Protein structure – levels of organisation	K1-K3	8	1-5
	5.2 Protein separation techniques – SDS-PAGE	K4-K6		
	5.3 Restriction Enzymes and Mapping	K2-K3		

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 SOURCES

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: **Total Marks: 50** **Duration: 90 minutes**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI – 600 086

Postgraduate Elective Course offered by the Department of Bioinformatics for M.A. / M.Sc./ M. Com Degree Programmes

SYLLABUS

(Effective from the academic year 2023–2024)

APPLICATIONS OF BIOINFORMATICS

CODE: 23BI/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 access the fundamental biological databases and their retrieval, submission systems.
- to understand the basics of pharmacogenomics in the context of variability in drug response
- to recognize the application of information technology in immunology
- to introduce the basic concepts of using chemical structure databases

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	examine factors that affect drug response and the application of pharmacogenetics to drug development and drug treatment	K1
CO2	apply the immunological data and to the sophisticated computational solutions available for immunological research	K2
CO3	emphasis the application of bioinformatics and biological databases to problem solving in real research problems	K3
CO4	investigate the immune cells types, activities and access the database for epitope prediction	K4
CO5	ability to interpret the 2D and 3D chemical structures and access them computationally.	K5, K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**Introduction to Bioinformatics**			
	1.1. Classification of biological data, and different data formats	K1-K2	7	1-5
	1.2. Introduction to single letter codes of amino acids, symbols used in nucleotides	K2-K3		
	1.3. Bioinformatics Perspectives on Human Diseases	K3-K6		
2	**Bioinformatics databases**			
	2.1. Overview of Biological Sequence Databases - NCBI, EMBI, DDBJ	K1-K3	8	1-5
	2.2. Sequence Retrieval Systems (Entrez & SRS), Sequence Submission Methods and Tools (Sequin, Sakura, Bankit)	K3-K4		
	2.3. Finding Scientific Articles Using PubMed, Identification of disease genes, OMIM database	K4-K6		
3	**Pharmacogenomics**			
	3.1. Introduction to Basic Concept of Pharmacogenomics, Application and Challenges in Pharmacogenomics, Personalized Medicine	K1-K3	8	1-5
	3.2. Genetic Variation, Types of Variants, SNPs, Insertion/Deletions	K3-K6		
	3.3. Databases - Pharmacogenomics Knowledge Base (PharmGKB)	K4-K6		
4	**Computational Immunology**			
	4.1. Introduction to Immune System - Adaptive and Innate Immunity, Cells of the Immune System	K1-K3	8	1-5
	4.2. Major Histocompatibility Complex (MHC) its Polymorphism, Principles of B-cell and T-cell Epitope Prediction	K3-K4		
	4.3. Databases in Immunology, IMGT immunoinformatics	K4-K6		
5	**Applications of Cheminformatics Tools in Drug Design**			
	5.1. Definition of drugs - 2D and 3D Molecular Structures	K1-K3	8	1-5
	5.2. Searching for Chemicals on the Internet (PubChem, eMolecules)	K4-K6		
	5.3. Chemical structure drawing tools	K2-K3		

BOOKS FOR STUDY

Darren R. Flower. Bioinformatics for Immunomics (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 Pharmacogenomics. 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 SOURCES

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

PATTERN OF ASSESSMENT

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

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	**Cognitive levels**	**Course Outcome**	**Marks allocation**
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	**Cognitive levels**	**Marks**	**Pattern**
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI – 600 086

Postgraduate Elective Course offered by the Department of Bioinformatics for M.A. / M.Sc./ M. Com Degree Programmes

SYLLABUS

(Effective from the academic year 2023–2024)

COMPUTER AIDED DRUG DESIGN

CODE: 23BI/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 know the guidelines and regulations imbibed by fda
- 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 (COs)

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

COs	DESCRIPTION	CL
CO1	identify the key elements in drug and explain new methodologies for drug design	K1
CO2	describe the role and importance of the various disciplines involved in the different phases of drug discovery and development	K2
CO3	review and evaluate preclinical and clinical pharmaceutical studies	K3
CO4	follow new ideas in utilizing main approaches of ligand screening methods	K4
CO5	examine the pharmacodynamic and pharmacokinetic properties for small molecules	K5, K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**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	K1-K2 K2-K3 K3-K6	7	1-5

UNIT	CONTENT	CL	Hrs	CO
2	**Regulations in Drug Discovery** 2.1. FDA regulations on Drug Development 2.2. Indian Regulatory Systems 2.3. Ethical Considerations and Special Populations	 K1-K3 K3 K4-K6	8	1-5
3	**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	 K1-K3 K3-K6 K4-K6	8	1-5
4	**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	 K1-K3 K3-K4 K3-K6	8	1-5
5	**Pharmacokinetics and Molecular Docking** 5.1. Pharmacokinetics - ADME Prediction 5.2. Pharmacodynamics 5.3. Molecular Docking - Scoring and evaluation	 K1-K3 K4-K6 K3-K6	8	1-5

BOOKS FOR STUDY

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

Charifson P S. Practical Application of Computer Aided Drug Design. New York:Dekker, 1997.

BOOKS FOR REFERENCE

Andrew R. Leach. Molecular Modeling: Principles and Applications. USA: Prentice Hall, 2007.

Daan Frenkel and Berend Smit. Understanding Molecular Simulation: From Algorithms to applications. USA: Academic Press, 2002.

Alan Hinchliffe. Molecular Modelling for Beginners. USA: John Wiley & Sons, 2008.

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

JOURNALS

Journal of Molecular Graphics and Modelling
Journal of Computer-Aided Molecular Design
Current Computer Aided-Drug Design

WEB SOURCES

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

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

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	5	5 X 1 =5 (All questions to be answered, Objective type)
B	K3, K4	10	5 X 2 =10 (Answers in about 50 words)
C	K4, K5	20	2 X 10 = 20 (Internal choice) Answers in about 600 words
D	K6	15	1 X 15 = 15 (1 out of 2 questions to be answered - Open choice) Answers in about 1200 words
	Total	50	

Other Components: **Total Marks: 50**

Categories of other components	Cognitive levels	Course Outcome	Marks allocation
Quiz/MCQs/open book tests/ Tests/ Assignment/ Mini projects/ Debate/ Seminar/ Weblems	K1 - K2	CO1-CO2	20
	K3 - K4	CO3- CO4	20
	K5 - K6	CO5	10
	Total		50

End semester examination **Total Marks: 100** **Duration: 3 hours**

Sections	Cognitive levels	Marks	Pattern
A	K1, K2	10	10 X 1 =10 (All questions to be answered, Objective type)
B	K3, K4	20	10 X 2 =20 (Answers in about 50 words)
C	K4, K5	40	4 X 10 = 40 (Internal choice) Answers in about 600 words
D	K6	30	2 X 15 = 30 (2 out of 4 questions to be answered - Open choice) Answers in about 1200 words
	Total	100	

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2023 -2024)

TRANSLATIONAL BIOINFORMATICS

CODE: 23BI/PI/TB24 **CREDITS : 4**

OBJECTIVES OF THE COURSE

- to develop a quantitative understanding of recent and emerging fields of bioinformatics
- to provide a platform for knowledge on imminent concepts to serve the present societal requirements
- to provide a better understanding of data and its applications in bioinformatics
- to impart a forum for disseminating the field of medical and biological image analysis
- to illustrate the information technology-driven efficiency to integrate real world context in public health informatics

COURSE LEARNING OUTCOMES (COs)

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

COs	DESCRIPTION	CL
CO1	apply knowledge of bioinformatics data exploration	K1, K2
CO2	analyse, interpret and appraise bioinformatics research data	K3
CO3	critically appraise the key concepts and conclusions from disease models	K4
CO4	infer functional association networks	K5
CO5	justify the use of genome scale networks in clinical settings	K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**Introduction** 1.1. Overview of bioinformatics and principle applications: Sequencing, Microarray, 'omics' fields, Systems biology, data mining. 1.2. Relationships to diseases and health. Data-driven Disease Biology. 1.3. Translational Bioinformatics: Past, Present, and Future.	K1-K3 K2-K4 K5-K6		1-5

UNIT	CONTENT	CL	Hrs	CO
2	**Biomedical Knowledge Integration** 2.1. Data, Molecules, and Diseases, Computational Causal Analytics, Transforming patient care. 2.2. Omics based approaches in diagnosis and treatment. Health informatics and the influence on the delivery of healthcare. 2.3. The electronic patient record and the importance of coding healthcare delivery consultations. The management of multi-dimensional and heterogeneous data sets.	K1-K3 K2-K4 K5-K6		1-5
3	**Biomedical Image Analysis** 3.1. Picture archive communication system (PACS) design and implementation; clinical PACS-based imaging informatics 3.2. Elemedicine/teleradiology; image content indexing, image data mining; grid computing in large-scale imaging informatics 3.3. Image-assisted diagnosis, surgery and therapy.	K1-K3 K2-K4 K5-K6		1-5
4	**Disease Informatics** 4.1. Small molecules and diseases. Cause and treatment of diseases. The Small Molecule Pathway Database (SMPDB). Toxin and Toxin-Target Database (T3DB), Poly Search and Metabolite Set Enrichment Analysis. 4.2. Protein interaction and diseases - molecular and genetic basis of diseases. Protein-DNA interaction disruptions 4.3. Protein misfolding problems. Network based approaches in complex diseases.	K1-K3 K2-K4 K5-K6		1-5
5	**Biological Knowledge Assembly and Interpretation** 5.1. Gene Set-Wise Differential Expression Analysis, Gene set enrichment analysis. 5.2. Differential coexpression analysis. Statistical inferences- p values, hyper parametric test, Bonferroni corrections, Benjamini Hochberg corrections. 5.3. False drug discovery rate.	K1-K3 K2-K4 K5-K6		1-5

BOOKS FOR STUDY

Arjen Hommersom, Peter JF Lucas, 2015. Foundations of Biomedical Knowledge representation: Methods and Applications, 1st ed., Springer Publications, 2015.

Vitali Sintchenko, Infectious Disease Informatics, 2010th ed., Springer Publications, 2009.

Hsinchun Chen, Daniel Zeng, Ping Yan, Infectious Disease Informatics: Syndromic Surveillance for Public Health and Bio-Defence. 2010th ed., Springer Publications, 2010.

Geoff Dougherty, Medical Image Processing: Techniques and Applications, 2011th ed., Springer Publications, 2011

BOOKS FOR REFERENCE

Maricel Kann (Ed), Fran Lewitter (Ed), PLOS Computational Biology: Translational Bioinformatics, 2016.

Trevor Hastie, Robert Tibshirani and Jerome Friedman, The Elements of Statistical Learning: Data Mining, Inference, and Prediction (Second Edition) 2009.

WEBSITE

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

PATTERN OF ASSESSMENT

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

Section	Cognitive Level and Allocation of Marks	Marks per Section	No of Questions to be answered	No. of Questions to be set
A	K1(10) K2(10)	20X1=20	10 K1 questions 10 K2 questions	10 K1 questions 10 K2 questions
B	K3(10)	10X2=20	10 K3 questions	10 K3 questions
C	K4(15) K5(15)	3X5=15 3X5=15	3 K4 questions 3 K5 questions	4 K4 questions 4 K5 questions
D	K6(30)	2X15=30	2 K6 questions	3 K6 questions
	Total	100	38	41

End semester examination Total Marks: 100 Duration: 3 hours

Section A - 10 X 1 =10 (All questions to be answered, Objective type)
Section B - 10 X 2 =20 (All questions to be answered, Answers in about 50 words)
Section C - 4 X 10 = 40 (Internal choice - Answers in about 600 words)
Section D - 2 X 15 = 30 (2 out of 4 questions to be answered, Answers in about 1200 words)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2023 -2024)

JAVA FOR BIOINFORMATICS

CODE: 23BI/PI/JV24 **CREDITS : 4**

OBJECTIVES OF THE COURSE (COs)

- to understand the concepts of object oriented programming.
- to learn about the control structures, class with attributes and methods used in java
- to understand the application of java in biological research
- to automate the tasks of parsing the different biological data formats, implement data structures and algorithms for common genomics and proteomics analysis
- to facilitate the code reuse for the standard implementation of external scripts and applications in biological data analysis.

COURSE LEARNING OUTCOMES

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

COs	DESCRIPTION	CL
CO1	understanding of the structure of the java programming language.	K1, K2
CO2	apply the basic principles of creating a java program.	K3,K4
CO3	differentiate various methods used in java	K4
CO4	comprehend the relevance of java in biological applications	K5
CO5	decipher the uses of biojava pipelines in bioinformatics	K6
CL – Cognitive Level **K1 – Remember | K2 – Understand | K3 – Apply | K4 – Analyse | K5 – Evaluate | K6 – Create**		

UNIT	CONTENT	CL	Hrs	CO
1	**Introduction to Java** 1.1. Java Basics: Importance and features of JAVA, Lexical elements of JAVA 1.2. Data types and Control structure, Program structure, Arrays 1.3. Command line input handling, OOPS, String Handling.	K1-K3 K2-K4 K5-K6		1-5
2	**File Handling** 2.1. Package, Exception Handling and File Handling: Package concept, working with util package	K1-K3		1-5

UNIT	CONTENT	CL	Hrs	CO
	2.2. Built-in Exceptions, Exception Handling, User Defined Exception 2.3. Streams in Java: FileInputStream, FileOutputStream, DataInputStream, DataOutputStream, Serialization.	K2-K4 K5-K6		
3	**JDBC and Applets** 3.1. JDBC, Steps to connect database, Classes and Methods for Database connectivity and Data Manipulation 3.2. Applets: Importance of applets, Steps to build an applet, Applet class methods, applet life cycle 3.3. Creation and execution of applets, Graphics class methods.	K1-K3 K2-K4 K5-K6		1-5
4	**Class and objects** 4.1. Defining a class and Creating objects – Accessing class members 4.2. Constructors – Method overloading – Static members – Nesting of Methods – this keyword – Command line input. 4.3. Inheritance: Defining inheritance and types of inheritance	K1-K3 K2-K4 K5-K6		1-5
5	**Biojava** 5.1. Concepts, Installation, Symbols &SymbolList, DNATools, MotifTools, RNATools, DNA to RNA conversion 5.2. Translation of DNA sequence to Protein sequence, proteomics classes: Calculate Mass and isoelectric point 5.3. Sequence I/O basics, Parsing, remote pdb file access	K1-K3 K2-K4 K5-K6		1-5

BOOKS FOR STUDY

E. Balagurusamy, "*Programming with Java*", India, Tata McGraw Hill, 5th Edition, 2014.

Sagayaraj, Denis, Karthick and Gajalakshmi, "*Java Programming for Core and advanced learners*", India, Universities Press Private Limited 2018.

Herbert Schildt. Java – A Beginner's Guide, 7th Edition, McGraw Hill, 2017.

Andreas Prlic, Andrew Yates, Spencer E. Bliven, et al., BioJava: on open-source framework for bioinformatics. Bioinformatics. 28(20): 2693-2695. https://www.biojava.org. 2012.

BOOKS FOR REFERENCE

Bert Bates , Kathy Sierra, "Head First Java: Your Brain on Java - A Learner's Guide1",1st Edition, O'Reilly Media, 2022.

Herbert Schildt , "Java: A Beginner's Guide*",* 8th Edition, McGraw Hill, 2020.

Joshua Bloch , "Effective Java*",* 3rd Edition, Addison-Wesley Professional, 2018.

Eric Freeman , Elisabeth Robson, "Head First Design Patterns: Building Extensible and Maintainable Object-Oriented Software*",* 2nd Edition, O'Reilly Media, 2020.

JOURNALS

Java Development Journal
Java World
Java Revisited
Journal of Bioinformatics and Computational Biology

WEB RESOURCES

https://nptel.ac.in/courses/106105191/
https://www.udacity.com/course/java-programming-basics--ud282

End semester examination Total Marks: 100 Duration: 3 hours

Section A - 10 X 1 =10 (All questions to be answered, Objective type)
Section B - 10 X 2 =20 (All questions to be answered, Answers in about 50 words)
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