

(For Candidates admitted from the academic year 2022 onwards)

HOLY CROSS COLLEGE (AUTONOMOUS)

TIRUCHIRAPPALLI-620 002

SCHOOL OF LIFE SCIENCES

LEARNING OUTCOMES-BASED CURRICULUM FRAMEWORK (LOCF)

M. Sc. BIOINFORMATICS (INTEGRATED)

Programme Outcomes (POs)

PO 1 - Demonstrate ability and attitude to acquire knowledge and skills in the advancing global scenario to apply them effectively and ethically for professional and social development.

PO2 - Involve in research and innovative endeavors and share their findings for the wellbeing of the society.

PO3 - Work effectively in teams and take up leadership in multi-cultural milieu.

PO4 - Act with moral, ethical and social values in any situation.

PO5- Excel as empowered woman to empower women.

PO6 - Participate in activities towards environmental sustainability goals as responsible citizens.

PO7 - Pursue higher studies in the related fields of Science, Humanities and Management.

PO8 - Develop knowledge to utilize the microbes, plants and animals for human welfare, societal behavior, disease diagnosis, system regulations and ancestry study.

PO9 - Originate into a taxonomist, horticulturist, quality analyst, drug designer and scientist.

Programme Specific Outcomes (PSO)

PSO 1 – Students will get the opportunity to learn about new developments in the field and gain current information on both theoretical and applied biology.

PSO 2 – Students will be able to broaden their knowledge in the rapidly developing, multidisciplinary fields of the life sciences, such as molecular biology, computational biology, drug discovery, all of which provide a wealth of opportunities for better career options.

PSO 3 – Develop new tools and database that needs for further bioinformatics research with expertise in filed programming.

(For Candidates admitted from the academic year 2022-23 onwards)
UG COURSE PATTERN – B. Sc. BIOINFORMATICS (INTEGRATED)

Semester	Part	Course	Title of the Paper	Code	Hrs/ Week	Credit	Marks	
I	I	Language	Tamil paper I/ Hindi paper I / French paper 1	U22TL1GEN01	3	3	100	
	II	English	English Paper 1	U22EL2GEN01	3	3	100	
	III	Major Core 1	Fundamentals of Biological Systems	I22BI1MCT01	4	4	100	
	III	Major Core 2	Basics of Computer And Bioinformatics	I22BI1MCT02	4	4	100	
	III	Major Core 3	Main Practical I- Fundamentals of Biological Systems & Basics of Computer And Bioinformatics	I22BI1MCP03	5	3	100	
	III	Allied 1	Chemistry- I	U22CH1ALT01	4	2	100	
	III	Allied 2	Chemistry paper II	U22CH1ALP02	4	2	100	
	IV	EVS	Environmental studies	U22RE1EST01	2	1	100	
	IV	Value Education	Bible/Catechism/Ethics	U22VE2LVE01/ U22VE2LVB01/ U22VE2LVC01	1		-	
	VI	Extra credit	Internship/Field Work/Field Project- 30 hours. Extra Credit	U22EX1INT01	-	2	100	
VI	Service Oriented Course				-	-	-	
					Total	30	22+2	900
Semester	Part	Course	Title of the Paper	Code	Hrs/ Week	Credit	Marks	
II	I	Language	Tamil paper II/ Hindi paper II / French paper II	U22TL2GEN02	3	3	100	
	II	English	English Paper II	U22EL2GEN02	3	3	100	
	III	Major Core 4	Molecular Biology	I22BI2MCT04	4	4	100	
	III	Major Core 5	Computational Biology	I22BI2MCT05	5	4	100	
	III	Major Core 6	Main Practical II- Computational Biology and Molecular Biology	I22BI2MCP06	4	3	100	
	III	Allied 3	Molecular Genetics	U22ZO2ALT01	4	2	100	
	III	Major Skill	Web designing (Lab cum	I22BI2SBT01/ I22BI2SBT02	2	1	100	

		Based Elective 1	Theory)/Computer Literacy for Biologists				
	IV	Skill Based Course 1	Soft Skill Development	U22SS2SBC01	2	1	100
	IV	Skill Based Course 2	Rural Enrichment and Sustainable Development	U22RE2SBC02	2	1	100
	IV	Value Education	Bible Studies /Catechism / Ethics	U22VE2LVE01/ U22VE2LVB01/ U22VE2LVC01	1	1	100
	VI	Extension Activities	RESCAPES	U22EX2RES01		1	100
	VI	Extra Credit	Online Course	U22EX2ONC01	-	1	100
	VI	Summer Internship/Field Work/Field Project (30 hours – Extra Credit)		U22EX2INT02	-	2	100
	VI	Service Oriented Course		-	-	-	-
				Total	30	23+4	1200

Major Elective Courses offered

Semester	Part	Course	Title of the Paper	Code	Hrs/Week	Credit	Marks
IV	IV	Major Elective 1	Computer aided drug Design	I22BI4MET01	4	3	100

Non Major Elective Courses offered

Semester	Part	Course	Title of the Paper	Code	Hrs/Week	Credit	Marks
III	IV	Non Major Elective	Medical Informatics	I22BI3NMT01	2	2	100
IV	IV	Non Major Elective	Bioprogramming	I22BI4NMT02	2	2	100

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester I (B.Sc.)

Course Title	MAJOR CORE 1 – FUNDAMENTALS OF BIOLOGICAL SYSTEMS
Code	I22BI1MCT01
Course Type	Theory
Semester	I
Hours/Week	4
Credits	4
Marks	100

CONSPECTUS

This course develops an exhaustive acquaintance with the structural, functional, and molecular aspects of the cell and biomolecules and fundamentals of genetics, Microbiology, and Immunology.

COURSE OBJECTIVES

1. To relate the structural and functional properties of prokaryotic and eukaryotic cells.
2. Elucidate and demonstrate the structure and functions of atom, molecules, and chemical bonds.
3. Illustrate the principles of genetics and the mechanism of cell division during meiosis and mitosis.
4. Explain the classification and characteristic features of microorganism.
5. Reason out the mechanism of Immune system and their types

UNIT – I

12 hrs

Biology of Cells:

- 1.1 Cell as unit of life, structure of prokaryotic and eukaryotic cells. Cell Organelles. Differences and similarities in plant and animal cells.
- 1.2 Cell transport across plasma membrane, mechanisms of transport, Cell Cycle: Mitosis, Meiosis. Cell Energetics and respiration.
- 1.3 Regulation of cell cycle by hormones, Protein kinases, Oncogenes, Tumor suppressor genes and programmed cell death.

Extra Reading (Key words): Red hot mitochondria.

UNIT – II

12 hrs

Bio Molecules of Life:

- 2.1 Basics of Biomolecules - Structure and functions of Atoms, Molecules and Chemical bonds. Biomolecule structures – Carbohydrates, Lipids, and Nucleic acids. Water - Properties and its importance in Biosystems.
- 2.2 Amino Acids: Classification – essential and non-essential, non-protein amino acids; structure, stereochemistry, chemical reactions of amino acids due to carbonyl and amino groups.
- 2.3 Structural organization of proteins- primary, secondary, tertiary and quaternary structures. The Ramachandran Plot, Structure prediction by crystallography. Folding pathways. Domains, Motifs and their importance.

Extra Reading (Key words): Metabolism

UNIT – III

12 hrs

Fundamentals of Genetics:

3.1 History of genetics – Basic principles of heredity – Mendelian genetics: Mendel's experiments – Principle of segregation – Principle of independent assortment – Pedigree analysis and its application

3.2 Human chromosomes: Structure and chemical nature, Linkage and crossing over. Variation in chromosomal structure, Special chromosomal forms, Variation in chromosomal number – Deletion, Duplication, Inversion, Translocation.

3.3 Cell Division: Mitosis and Meiosis - Karyotyping and chromosomal banding–molecular cytogenetics: FISH, Fiber FISH and m-FISH.

Extra Reading/Key words: Epigenome

UNIT – IV

12 hrs

Microbiology:

4.1 Whittaker's classification and characteristic features of Microorganisms - Virus, bacteria, algae, fungi and protozoa – Microbial association. Scope of microbiology.

4.2 Methods in microbial culture – sterilization, inoculation and incubation; preparation of pure culture and maintenance.

4.3 Nutritional requirements, types of culture media, culture and growth characteristics. Current methods of microbial identification

Extra reading/Keywords: Symbiosis of prokaryotic cell and origin of eukaryotic cell

UNIT – V

12 hrs

Immunology:

5.1 Immune System- Cells of immune system. Lymphoid organs - Primary and secondary - structure and functions. Types of Immunity – Innate, acquired, passive, active, primary, secondary, humoral and cell mediated.

5.2 Antigens – Types, structure, immunogenicity- factors affecting immunogenicity antibody specificity, antigen specific receptor of antibodies. Haptens and Study of antigenicity.

5.3 Immunoglobulins– Structure, types, distribution and biological functions. Genetic control of Ig synthesis. Expression of heavy and light chain gene, antibody diversity, Ig class switching, somatic mutation. Molecules belonging to Ig super family. Antigen -Antibody interaction.

Extra Reading (Key words): CBC (Complete blood count) and T cell cloning.

Note: Texts given in the Extra reading /Key words must be tested only through assignment and Seminars.

PRESCRIBED TEXTBOOKS

1. Derobertis, Saez, And Derobertis 2017, Cell and molecular Biology - Eight Edition, ISBN- 978-8184734508
2. Kuby, J, 2003, Immunology. freeman & Company, New York .

SUGGESTED REFERENCE BOOKS

1. Branden, C and Tooze. J, (1991), Introduction to Protein Structure, Garland Publishing Inc., New York.
2. Rastogi, S.C., (1993), Biochemistry, Tata McGraw Hill Publishing Company Limited, New Delhi.
3. Mukherji, S. and Ghosh, A.K.,(1996), Plant Physiology : Tata McGraw Hill Publishing Company Limited, New Delhi.
4. Roderic D. M. Page, Edward C.(1998), Holmes Molecular evolution, A phylogenetic approach, Blackwell Science Inc.

5. Dan Graur and Wen-Hsiung Li, (2000), Fundamentals of Molecular evolution, II ed., Sinauer Associates, INC.
6. Bruce Alberts, Alexander Johnson, Julian Lewis, Martin Raff, Keith Roberts, Peter Walter, (2002), Molecular Biology of The Cell, IV edition, Garland Publishing Newyork.
7. J.M. Berg, J.L. Tymoczko and L. Stryer (2002), Biochemistry, 5th Edition W.H. Freeman.
8. Roitt, I., (2002), Essential Immunology. VI edition, Elsevier Science
9. Friefelder, D (2003) . Essentials of Molecular Biology, IV Edition., Jones and Bartlett Publication inc.
10. Krishnamurthy K.V., (2003) An Advanced Textbook on Biodiversity – Principles and Practice, Oxford & IBH Publishing Co. Pvt. Ltd., New Delhi.
11. Geoffrey M. Cooper, Robert E. Hausman, (2007). The Cell A Molecular Approach, Sinauer Associates, Inc.

Note: Learners are advised to use latest edition of books.

COURSE OUTCOMES

CO No.	COURSE OUTCOMES	Cognitive Level (K1-K6)
CO-1	Elucidate and demonstrate the structure and cellular functions of prokaryotic and eukaryotic cells.	K1
CO-2	To comprehend the structure and functions of biomolecules and associate the interaction of biomolecules in the process of biological system	K2
CO-3	Outline the fundamentals of genetics and their principles and applications.	K3
CO-4	To predict the classification and characteristic features of microorganism and discuss the current methods of microbial identification	K4

(K1=Remember, K2=Understand, K3=Apply, K4=Analyze, K5=Evaluate, K6=Create)

PO – CO MAPPING

CO/PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9
CO 1	3	1	-	-	1	1	2	2	3
CO 2	2	2	1	1	3	3	3	3	2
CO 3	3	3	2	2	2	2	3	3	3
CO 4	2	2	1	1	2	2	2	3	2

PSO – CO MAPPING

CO/PO	PSO1	PSO2	PSO3
CO1	1	1	3
CO2	3	1	2
CO3	3	2	1
CO4	3	3	2

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester I (B. Sc.)

Course Title	MAJOR CORE 2 – BASICS OF COMPUTER AND BIOINFORMATICS
Code	I22BI1MCT02
Course Type	Theory
Semester	I
Hours/Week	4
Credits	4
Marks	100

CONSPECTUS

This course covers the foundational principles in computer science and bioinformatics. It includes computer basics, operating systems, software development, web design, and an introduction to bioinformatics, databases, and genomic data analysis.

COURSE OBJECTIVES

1. To outline the learners with fundamentals and characteristics of computers.
2. To interpret the different types of operating system and software's and their application in bioinformatics
3. Explore the different biological database available in bioinformatics
4. Analysis and examine the structural features of proteins and nucleic acid from various database.
5. To examine structural bioinformatics, conformational analysis of proteins and nucleic acids.

UNIT – I

12 hrs

Introduction to Computers:

1.1 Introduction to Computers, Characteristics of Computers, Evolution of Computers - Computer Generations – Classification of Computers

1.2 Basic Computer organization – Hardware – Input and output devices – CPU –memory, Computer Software –Types of Software – Software Development Steps.

1.3 Internet Evolution - Basic Internet Terminology, Getting connected to Internet Applications – Internet usage - Browsers – Internet Explorer, Mozilla , Search engines , Email ,

Extra Reading (Key words): Internet resources for Life Sciences.

UNIT – II

12 hrs

Operating Systems and Softwares:

2.1 Operating systems - Different types of operating system - Windows , macOS, Linux Operating system (vi editor, few basic commands like directory creation, deletion, permission setting etc).

2.2 Software - system software, application software, compiler, interpreter, assembler, linker databases. Spreadsheets and presentation software, computer viruses and protection.

2.3 Web page design tools, CGI, bin scripts, linking, text formatting, adding images, tables, frames, web pages. Programming languages, Need for Programming in Life Sciences.

Extra Reading (Key words): Database management systems

UNIT – III

12 hrs

Overview of Bioinformatics:

3.1 History of Bioinformatics, Milestones in Bioinformatics, Scope, Goals and application. Human Genome Project and its outcomes.

3.2 Introduction to database – Database models – Database languages – Types of databases: Flat file, Relational databases and Object-oriented databases.

3.3 Introduction to single letter code of amino acids, symbols used in nucleotides, data retrieval- Entrez and SRS. Sequence Submission Methods and Tools - Sequin, Sakura, Bankit.

Sequence file formats: GenBank, ALN/ClustalW2, FASTA, PIR,

Extra Reading (Key words): Bioinformatics Programmes in India

UNIT – IV

12 hrs

Biological Databases:

4.1 Sequence Database-Nucleotide Sequence Database- Genbank, DDBJ, EMBL. Sequence motifs Databases: Prosite and Pfam

4.2 Protein Sequence Database- Uniprotkb, Swissprot, TrEMBL, PIR. Literature Databases: PubMed, PLoS, Biomed Central.

4.3 Genome database – GDB, Genomes On Line Database (GOLD), MGD, OMIM, TAIR. Viral genome database – ICTVdb, Microbial Genome Database – MBGD, NCBI - Microbial Genomes

Extra Reading (Key words): Applications of biological databases

UNIT – V

12 hrs

Structure and derived database:

5.1 Nucleotide structure database- NDB, Protein structure database – PDB, Molecular Modeling Database - MMDB

5.2 Structure classification databases-SCOP, CATH, PDBsum, Microarray databases - GEO, Array express

5.3 Chemical Structure database – PubChem, Drug bank. Cambridge structural database (CSD)– statistics, flat file format. KEGG pathway database, BRENDA enzyme database.

Extra Reading (Key words): ChEMBL

Note: Texts given in the Extra reading /Key words must be tested only through assignment and Seminars.

PRESCRIBED TEXT BOOKS

- Rajaraman V, Fundamentals of Computers, 6th Edition, Prentice Hall India Pvt., Limited, 2003. (Unit-I P.No, 1-81, 191-218, 249-264)
- Jin Xiong, Essential Bioinformatics, Cambridge University Press, 2006. (Unit-III P.No 1-8)

SUGGESTED REFERENCE BOOKS

- Andreas D. Baxevanis, B.F. Francis Ouellette, Bioinformatics A practical guide to the analysis of genes and proteins, Wiley Interscience, 2000
- Lesk, A.M., Introduction to Bioinformatics; Oxford University Press, UK, Fourth edition. (2014)
- Gibas C, Jambeck P, Developing Bioinformatics Computer Skill, 1st Edition, O'Reilly, 2001
- Higgins D, Taylor W(Eds), Bioinformatics- Sequence, structure and databanks, Oxford

University Press, New Delhi (2000).

- Durbin R, S.R. Eddy S.R, Krogh A, Mitchison G, Biological Sequence Analysis, Cambridge Univ. Press, Cambridge, UK 1998.
- Gautham N, Bioinformatics: databases and algorithms, , Narosa, Publications New Delhi, 2006.

Note: Learners are advised to use latest edition of books.

COURSE OUTCOMES

CO No.	COURSE OUTCOMES	Cognitive Level (K1-K5)
CO-1	Distinguish the intersection of life and information sciences, information theory Recognize the basic structure of a computer and concepts of Internet.	K1
CO-2	Build an extensive knowledge in operating systems and web page designing this will be helpful for their research work.	K2
CO-3	Articulate the basics of bioinformatics and its sequence submission methods.	K3
CO-4	Students will be able to categorize the biological database and analyse its information.	K4
CO-5	Predict and validate the function and structure of a protein.	K5

(K1=Remember, K2=Understand, K3=Apply, K4=Analyze, K5=Evaluate, K6=Create)

PO – CO MAPPING

CO/PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9
CO 1	2	2	1	-	-	-	-	-	-
CO 2	3	3	1	-	-	-	-	-	-
CO 3	2	2	1	-	-	-	-	-	2
CO 4	2	2	1	-	-	-	-	-	2
CO5	2	2	1	-	-	-	-	-	2

PSO – CO MAPPING

CO/PO	PSO1	PSO2	PSO3
CO1	1	1	1
CO2	3	2	3
CO3	2	2	3
CO4	1	2	2

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester I (B. Sc.)

Course Title	MAJOR CORE 3 – FUNDAMENTALS OF BIOLOGICAL SYSTEM AND BASICS OF COMPUTER AND BIOINFORMATICS
Code	I22BI1MCP03
Course Type	PRACTICAL
Semester	I
Hours/Week	5
Credits	3
Marks	100

CONSPECTUS

This course emphasizes the basics of computers and its operations. It also highlight the basic technique in the estimation of biomolecules, imparts specific skills on performing microbial isolation and identification approaches.

COURSE OBJECTIVES

1. To learn about the bioinformatics databases, databanks, data format and data retrieval from the online sources.
2. To learn the various Linux commands in Terminal.
3. To list out the various Windows commands in Command Prompt.
4. To differentiate structural and functional variations between prokaryotic and eukaryotic cells.
5. To compare and contrast the different stages of mitosis and meiosis.
6. To perform the isolation, identification and examination of microbes.

FUNDAMENTALS OF BIOLOGICAL SYSTEMS

1. Identification of plant, fungi, bacteria and animal cells
2. Study of mitosis and meiosis from permanent slides.
3. Identification of bacteria – Simple & Gram's staining
4. Isolation of microorganism using serial dilution, spread plate, pour plate and streak plate methods
5. Preparation of serum sample from whole blood.
6. Preparation of Pedigree chart of some common phenotypic characters of human and study on patterns of inheritance.
7. Identification of inactivated X chromosome as Barr body

BIOINFORMATICS DATABASE

1. Nucleotide Sequence databases – Genbank, EMBL, DDBJ
2. Windows commands
help, path, prompt, dir, cls, echo, xcopy, del, md, cd, rd, ren, more, path, sort, tree, dir, nd, chkdsk, ver, mem

Linux commands – pwd, ls, cd, mkdir & rmdir, rm, touch, cp, mv

a) Working with the files and directories related commands

date, who, man, cal, clear, echo, finger, cat, cp, ls, mv, rm, wc, chmod, pwd, mkdir, chdir, rmdir, ;. &&.

b) Pipes and Filters

sort, head, tail, grep, more, nl, cut, cmp, diff

3. Chemical Structure database – PubChem, Drugbank

4. Protein sequence databases – PIR, Swiss-Prot

5. Secondary database - Prosite, Prints, Blocks, Profiles, Pfam

6. Structure classification databases - SCOP, CATH,

7. Protein structure database – PDB, PDBsum

8. Literature database – PUBMED, OMIM, BioMed Central, Public Library of Sciences (PloS) and CiteXplore bibliographic databases

9. Genome database – ICTV, NCBI – Viral genome

10. Enzyme catalysis database - KEGG, BRENDA

(For The Candidates Admitted From 2022 Onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester II (B. Sc.)

Course Title	MAJOR CORE 4 – MOLECULAR BIOLOGY
Total Hours	60
Hours/Week	4
Code	I22BI2MCT04
Course Type	Theory
Credits	4
Marks	100

CONSPECTUS

This course focus on the exhaustive acquaintance with the structural, functional and molecular aspects of the genetic material and their mechanisms relating to their research applications.

COURSE OBJECTIVES

1. Demonstrate the structure and cellular functions of DNA & chromosome
2. Outline and examine the mechanism of DNA replication and the function of chromosomes in replication
3. Criticize and relate to the concept of processing of prokaryotic & eukaryotic RNA synthesis
4. Comprehend the mechanism of protein synthesis
5. Critically assess and predict the mechanism of gene regulation and recombination

UNIT – I

12 hrs

DNA Structure:

- 1.1. The beginning of Molecular Biology; DNA: A carrier of genetic information, Chemical structure of DNA and Base composition, biologically important nucleotides.
- 1.2. Watson - Crick Model, Supercoiled DNA, structure of different types of nucleic acids, hydrolysis of nucleic acids.
- 1.3. Conformation of nucleic acids: A, B, Z-DNA, t-RNA, micro-RNA. Stability of nucleic acid structure.

Extra Reading/Key words: One gene -one protein hypothesis & Central dogma of cell

UNIT – II

12 hrs

Replication:

- 2.1. Replication-Types of DNA replication. Unit of replication, enzymes involved, replication origin and replication fork.
- 2.2. DNA damage, DNA repair mechanisms. DNA mutations – types and detection of mutations.
- 2.3. RNA binding proteins, Ribonucleoproteins, RNA-protein recognition and interactions.

Extra Reading/Key words: Mutation Fog

UNIT – III

12 hrs

Transcription:

- 3.1. Prokaryotic and eukaryotic - Regulatory signal elements: promoter, motifs.

3.2. Transcription factors and transcription activators and repressors, capping, elongation and termination.

3.3. RNA processing, RNA editing, splicing, polyadenylation.

Extra Reading/Key words: Types of RNA and Overlapping genes

UNIT – IV

12 hrs

Translation

4.1. Ribosome, genetic code formation of initiation complex, initiation factors and their regulation

4.2. Elongation and elongation factors, Termination, amino acylation of tRNA

4.3. translational proof-reading, translational inhibitors, post- translational modification.

Extra Reading/Key words: Cell-free protein synthesis in protein therapeutics

UNIT – V

12 hrs

Gene Regulation:

5.1. Gene Regulation-Types, Operon concept - Lac, Trp and Ara operons

5.2. Insertional elements and Transposons - Plant, Bacterial and Animal, Structure- organization and transposition.

5.3. Recombination and its types - Holiday junction - Rec A and other recombinases.

Extra Reading/Key words: Transposable elements in clinical applications.

Note: Texts given in the Extra reading /Key words must be tested only through assignment and Seminars.

PRESCRIBED TEXT BOOKS

1. De Robertis DP (2017) Cell and Molecular Biology, 8th Edition, Lippincott Williams and Williams.

2. Ajoy Paul. Textbook of Cell and Molecular Biology (2015). Books & Allied Ltd Publishers. ISBN-10: 8187134747.

3. Freifelder, D. (2015), Essentials of molecular Biology, fourth edition, Jones and Bartlett Publications Inc.

SUGGESTED REFERENCE BOOKS

1. Gerald Karp, (2013), Cell Biology, VII edition International Student Version, Wiley publication.

2. Harvey Lodish, Arnold Berk, Chris A. Kaiser, Monty Krieger, Anthony Bretscher, Hidde Ploegh, Angelika Amon, Matthew P. Scott, (2012), Molecular Cell Biology, VII edition, W.H. Freeman and Company, New York.

3. David P Clark, (2009) Molecular Biology. (Understanding the genetic revolution), Elsevier Academic Press.

4. Geoffrey M. Cooper, Robert E. Hausman (2007), The Cell - A Molecular Approach, Sinauer Associates, Inc.

5. James D Watson, Tania A. Baker, Stephen P. Bell, Alexander Gann, Michael Levine and Richard Losick, Benjamin Cummings (2004). Molecular Biology of the Gene, Fifth Edition

6. Lodish, Harvey, Arnold, Matsudaira, Paul, Kaiser, Chris A., Krieger, Monty Scott, Matthew P., Zipursky, Lawrence, Darnell, James (2004), Molecular Cell Biology, W.H. Freeman and Company.

Note: Learners are advised to use latest edition of books.

COURSE OUTCOMES

CO No.	COURSE OUTCOMES	Cognitive Level (K1 – K6)
CO-1	Construct a model depicting the structure and function of chromosome	K1
CO-2	Describe the mechanism of replication in relation to the structure, function and numerical alterations of chromosomes in prokaryotes and eukaryotes	K2
CO-3	Reason out the mechanism of construction, damage of DNA and interactions	K3
CO-4	Examine in detail the factors affecting the regulation of RNA and protein synthesis and their properties	K4

(K1=Remember, K2=Understand, K3=Apply, K4=Analyze, K5=Evaluate, K6=Create)

PO – CO MAPPING

CO/PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9
CO 1	2	3	3	1	1	2	3	3	3
CO 2	2	2	-	-	2	1	3	2	3
CO 3	3	3	1	1	3	2	3	3	2
CO 4	2	3	1	-	2	1	2	3	3

PSO – CO MAPPING

CO/PO	PSO1	PSO2	PSO3
CO1	2	1	1
CO2	3	2	2
CO3	2	2	3
CO4	3	3	2

(For The Candidates Admitted From 2022 Onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester II (B. Sc.)

Course Title	MAJOR CORE 5 – COMPUTATIONAL BIOLOGY
Code	I22BI2MCT05
Course Type	Theory
Semester	II
Total Hours	75
Hours/Week	5
Credits	4
Marks	100

CONSPECTUS

Computational Biology is an interdisciplinary subject integrating the fields of computer science, molecular cell biology, biochemistry and statistics. It gives an exposure to the students in the basic knowledge about how to store, analyse and interpret biological data.

COURSE OBJECTIVES

1. Aims at providing an elementary knowledge in Bioinformatics and Biological Information on the web.
2. Apply the knowledge of computational biology for analysing the Sequence.
3. Analysis with most basic and useful computational programs for phylogenetic analysis.
4. Analysis the structural features of protein using computational tools.
5. Evaluate the essential features of the interdisciplinary field of science for better understanding of biological data.

UNIT – I

15 hrs

Introduction to computational biology and sequence alignment:

- 1.1 Introduction to Computational Biology: nature and scope of computational biology. Introduction to sequence: Maximum Gilbert, Sanger Sequencing, Next generation sequencing.
- 1.2 Sequencing alignment: Introduction to sequence alignment, alignment definition, basic concepts of sequence similarity, identity and homology, definitions of homologues, orthologues, paralogues and xenologues.
- 1.3 Phylogenetics: history and philosophy of phylogenetics, concept of homology, molecular phylogenetics, gene evolution. Phylogenetic trees - basic definitions, gene phylogeny Vs species phylogeny.

Extra Reading /Key words: Computational methods for sequence alignment

UNIT – II

15 hrs

Sequence Alignment Methods:

- 2.1: Sequence analysis of biological data: significance of sequence alignment, Alignment algorithm - dot plot, dynamic programming, k-tupel method.
- 2.2: Pairwise Sequence alignment: local and global alignment, Needleman- Wunsch algorithm, Smith-Waterman algorithm.

2.3: Scoring matrices: PAM matrices, BLOSUM matrices, Comparison between PAM and BLOSUM matrices, application of substitution matrices. Sequence similarity search tool FASTA and BLAST programs.

Extra Reading /Key words: Statistical methods and scoring functions.

UNIT – III

15 hrs

Multiple Sequence Alignment:

3.1: Multiple sequence alignment: Introduction to multiple sequence alignment, methods of multiple sequence alignment, Progressive method, iterative method, genetic algorithm, application of multiple sequence alignment.

3.2: Phylogenetic tree – Definition, terminology, Properties. Types of Trees. Stages of Phylogenetic analysis.

3.3: Methods for phylogenetic tree construction, distance matrix methods, UPGMA, NJ, Maximum Parsimony, Maximum likelihood, Tree evaluation (Bootstrap), lineage sorting, Problems and errors in phylogenetic reconstruction.

Extra Reading /Key words: Significance of ancestral nodes in evolution

Unit – IV

15 hrs

Protein Structure Prediction:

4.1 Protein Structure – Primary structure, Secondary Structure, Tertiary structure. Protein structure visualization tools – RasMol, Swiss PDB Viewer, PYMOL

4.2 Secondary Structure Prediction – RNA secondary structure prediction, Protein secondary structure prediction - Chou-Fasman, Garnier-Orguthorpe – Robson (GOR) methods.

4.3 Protein Tertiary Structure -Predicting 3D structure – comparative (homology) modeling, threading (fold recognition) and ab initio methods. CASP.

Extra Reading /Key words: Tools and software packages used in protein structure prediction

Unit –V

15 hrs

Gene Prediction:

5.1: Introduction to Gene Prediction, Categories of gene prediction programs: Gene prediction in prokaryotes, conventional determination of open reading frames.

5.2: Gene Prediction using Markov Models and Hidden Markov Models, Gene Prediction in Eukaryotes, content and signal methods, Analysis and prediction of regulatory regions.

5.3: Gene Prediction tools: Similarity based and ab-initio prediction- GENSCAN, GRAIL, FGENES-SMART. Prediction using Neural Networks, homology based gene prediction programs.

Extra Reading /Key words: Tools used for gene prediction

Note: Texts given in the Extra reading /Key words must be tested only through assignment and Seminars.

PRESCRIBED TEXT BOOKS

1. Lesk, A.M., Introduction to Bioinformatics; Oxford University Press, UK, Fourth edition. 2014.
2. Mount D., Bioinformatics: Sequence and Genome Analysis. Cold Spring Harbor Laboratory Press, New York. 2004.
3. Teresa K. Attwood, David J. Parry-Smith. Introduction to Bioinformatics. Pearson Education. 1999.

SUGGESTED REFERENCE BOOKS

1. Rastogi, SC., Mendiratta, N., Rastogi, P. (2013). Bioinformatics: Methods And Applications: (Genomics, Proteomics and Drug Discovery). PHI Learning Pvt. Ltd.
2. Michael Gromiha M, (2010). Protein Bioinformatics - From Sequence to Function, Elsevier India Pvt. Ltd, New Delhi.
3. Jin Xiong, Essential Bioinformatics, Cambridge University Press, 2006, ISBN 9780511806087, Unit I-V.
4. Gautham, N. (2006). Bioinformatics: Databases and Algorithms. Alpha Science Int'l Ltd.
5. Attwood T.K, parry-Smith D.J.(2005) ” Introduction to Bioinformatics”, Pearson Education, 1st Edition, 11th Reprint.
6. Baxeavanis and B.F. (1998). Ouellette. Bioinformatics: A practical Guide to the Analysis of Genes and Proteins, Wiley- Interscience, Hoboken, NJ.

Note: Learners are advised to use latest edition of books.

COURSE OUTCOMES

CO No.	COURSE OUTCOMES	Cognitive Level(K1-K6)
CO-1	Understand the tools and techniques used in biological data analysis.	K1, K2
CO-2	Analyse protein sequence and identify the various computational tool for alignment.	K3
CO-3	Correlate the information in database and predict the evolutionary significance.	K4
CO-4	Analysis the different method for protein structure prediction.	K3

(K1=Remember, K2=Understand, K3=Apply, K4=Analyze, K5=Evaluate, K6=Create)

PO – CO MAPPING

CO/PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9
CO 1	3	2	1	-	-	-	-	-	1
CO 2	3	3	1	-	-	-	-	-	-
CO 3	2	3	2	1	-	-	-	-	2
CO 4	2	2	3	2	-	-	-	2	-

PSO – CO MAPPING

CO/PO	PSO1	PSO2	PSO3
CO1	3	1	2
CO2	2	2	3
CO3	3	2	2
CO4	3	3	2

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester II (B. Sc.)

Course Title	MAJOR CORE 6 MAIN PRACTICAL II – COMPUTATIONAL BIOLOGY & MOLECULAR BIOLOGY
Code	I22BI2MCP06
Course Type	PRACTICAL
Semester	II
Hours/Week	4
Credits	3
Marks	100

CONSPECTUS

The primary goal of this bioinformatics laboratory course is to investigate bioinformatics resources. Allows for the practical application of theoretical concepts.

COURSE OBJECTIVES

1. Analysis the significance of sequence similarity.
2. To learn computer-based evolutionary analysis of biological sequences

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

1. Pairwise alignment (i). Global alignment (II). Local alignment
2. Dot matrix analysis using Dot matcher
3. Database searching i) BLAST ii) FASTA
4. Protein structure prediction
 - a. Primary feature computing by PROTPARAM
 - b. Secondary structure by SOPMA, J-Pred, PSIPRED
5. Sequence Alignment - Clustal W, T-Coffee, DIALIGN. Clustal Omega, MEGA.
6. To perform the prediction of gene location for a given sequence using GENEMARK/GENSCAN.
7. Protein tertiary structure prediction- SWISS MODEL.

MOLECULAR CELL BIOLOGY

1. Estimation of DNA (DPA method).
2. Estimation of RNA (Orcinol method)
3. Isolation of genomic DNA from plant
4. Isolation of genomic DNA from bacterium (E. coli)
5. Separation of DNA by AGE

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester II (B. Sc.)

Course Title	MAJOR SKILL BASED ELECTIVE 1 - WEB DESIGNING (Theory Cum Lab)
Total Hours	30
Hours/Week	2
Code	I22BI2SBT01
Course Type	Theory Cum Lab
Credits	1
Marks	100

CONSPECTUS

The student will learn the basics of web development. In addition, students will learn the significance of various scripting language, their control and other related aspects.

COURSE OBJECTIVES

1. Learn the language of the web: HTML and CSS.
2. Develop basic programming skills using Javascript.
3. Apply fundamental design principles to the presentation of concepts, knowledge, goods, and services on websites.
4. Analyze the basic programming principles to construct a websites.

UNIT – I

6 hrs

Introduction to Web Programming:

- 1.1 Introduction to web development, Creating a website, Web Page Uploads, Web Hosting Service.
- 1.2 Web Page Example, HTML tags, Structural elements.
- 1.3 History of HTML, HTML Governing Bodies, Differences Between Old HTML and HTML5, HTML Attributes, body Elements.

Extra Reading/Key words: Adobe dreamweaver

UNIT – II

6 hrs

Cascading Style Sheets:

- 2.1 Introduction to Cascading Style, CSS overview, CSS rules, CSS Syntax and Style.
- 2.2 Class Selectors, ID selectors, span and div Elements, Cascading.
- 2.3 CSS properties, Color Properties, RGB values for color, Font properties, Text properties, Border properties.

Extra Reading/Key words: SASS

UNIT – III

6 hrs

Links and Images:

- 3.1 <a> Element, Relative URLs, index.html File, Web Design, Navigation Within a Web Page, CSS for Links, a Element Additional Details, Bitmap Image Formats: GIF, JPEG, PNG
- 3.2 img Element, Vector Graphics, Positioning Images, Shortcut Icon, iframe Element, Sprites.
- 3.3 Audio, Background Images, Web Fonts, Video, CSS Image.

Extra Reading/Key words: Media types

UNIT – IV

6 hrs

JavaScript:

4.1 Introduction to JavaScript, History of JavaScript, Buttons, Functions, Variables, Identifiers.

4.2 Assignment Statements and Objects, Document Object Model, Event-Handler Attribute, Arithmetic Operators, Math Object Methods, Parsing Numbers: parseInt, parseFloat.

4.3 Controls, Text control, Email Address Generator Web Page, Accessing a Form's Control Values, window Object, if Statement: if by itself, if Statement: else and else if Clauses.

Extra Reading/Key words : Unit testing tools

UNIT – V

6 hrs

Practical:

1. Create a webpage using HTML
2. Generate Time Table of your class using HTML table tag.
3. Design your own profile page with educational details, Achievement and Hobbies.
4. Create a webpage using HTML and CSS
5. Generate a HTML form and validate using JavaScript
6. Write a JavaScript program to calculate multiplication and division of two numbers for users input.
7. Write a JavaScript program to determine whether a given year is a leap year.

Note: Texts given in the Extra reading /Key words must be tested only through Assignment and Seminars.

PRESCRIBED TEXT BOOKS

1. John Dean (2019), Web Programming with HTML5, CSS, and JavaScript, ISBN 9781284091793

SUGGESTED REFERENCE BOOKS:

1. Ralph Moseley and Savaliya M.T, 2011. Developing Web Applications, Wiley-India Private Limited, 2011.
2. Robert W. Sebesta 2013. Programming the World Wide Web, 7th edition, Pearson Education.
3. Kogent Learning Solutions Inc., Web Technologies Black Book, Dreamtech Press, 2009
4. Joel Sklar 2015, Principles of Web Design, Cengage Learning, 6th Edition.

Note: Learners are advised to use latest edition of books.

COURSE OUTCOMES

CO No.	COURSE OUTCOMES	Cognitive Level (K1 – K6)
CO-1	Understand the concepts of Web design, and the requirements of effective web.design.	K1
CO-2	Summarize the role of different scripting language in web design.	K2
CO-3	Custom the JavaScript to develop the dynamic web pages.	K3
CO-4	Develop web pages using the HTML and CSS features with different layouts as per need of applications.	K4

(K1=Remember, K2=Understand, K3=Apply, K4=Analyze, K5=Evaluate, K6=Create)

PO – CO MAPPING

CO/PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9
CO 1	2	3	2	1	1	-	-	-	-
CO 2	2	2	2	-	-	1	2	-	-
CO 3	3	3	1	1	1	-	-	-	-
CO 4	2	3	1	-	2	1	-	-	-

PSO – CO MAPPING

CO/PO	PSO1	PSO2	PSO3
CO1	3	1	2
CO2	1	3	-
CO3	2	-	-
CO4	3	1	-

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester II (B. Sc.)

Course Title	MAJOR SKILL BASED ELECTIVE-1 COMPUTER LITERACY FOR BIOLOGISTS
Total Hours Code	30
Hours/Week	2
Code	I22BI2SBT02
Course Type	Theory
Credits	1
Max Marks	100

CONSPECTUS

The course is designed to aim at imparting a basic knowledge on computer in day today life and to use the computer for basic purposes of preparing their personnel/business letters, viewing information on Internet (the web), sending mails, using internet banking services etc.

COURSE OBJECTIVES

1. To provide hands-on use of Microsoft Office 2013 applications Word, Excel, Access and PowerPoint. Completion of the assignments will result in MS Office applications knowledge and skills.
2. To understand the recent application domains of internet in everyday life.
3. To exhibit knowledge to secure corrupted systems, protect personal data, and secure computer networks in an Organization.
4. To equip students with modern and more current developments in the Banking Sector; precisely the application of the internet, computers and other electronically-based gadgets that facilitate the operations and practices of banking, locally and in international transactions.
5. To determine and analyze software vulnerabilities and security solutions to reduce the risk of exploitation

UNIT – I

6 hrs

Office Packages:

- 1.1. MS- Word: Creation of Documents (letters, Bio- data, etc). Creation of Tables, Formatting Tables (Time table, Calendar, etc) Working with Mail Merge (Circular letters).
- 1.2. MS – Excel: Creation of Worksheet (Mark Sheet, Pay Slip, PF Contribution list, etc). Excel Function.Creating charts (Line, Pie, Bar, etc).
- 1.3. MS- Power Point: Creation of Presentations (Duplicate and New slides, Layouts, View, Slide show, etc.). Working with objects (Movie, Sound, Word, Excel, etc.) Working with Transition and Animation effects (Text, Object, Pictures)

Extra Reading/Key words: Units of Data Storage.

UNIT – II

6 hrs

Smart devices and online transactions:

- 2.1. Smart devices - Smart phone, Tablet PC, Smart TV, Smart Camera, Smart Watch and Smart

Oven.

- 2.2. Operating system for Smart phones- Apple iOS, Android, Windows 10, Benefits of Smart Phones.
- 2.3. E-Commerce and M-Commerce: Components of E-Commerce- types, and benefits of each (B2B, B2C, C2B, C2C). Applications of M-Commerce- Mobile ticketing, mobile money transfer, mobile banking, mobile marketing and advertising. Payment methods in M-Commerce- Premium rate telephone numbers, Direct mobile dealing, Macro, Micro payment services and mobile wallets.

Extra Reading/Key words: Google play for Android Phones.

UNIT – III

6 hrs

Social networking and cyber security

- 3.1 Social Networking Sites: Characteristics of Social Networking Website-
- 3.2 Social Networking Services (Facebook, SnapChat, Instagram, Whatsapp, Pinterest, LinkedIn and Twitter) Advantages and Disadvantages of Social Network.
- 3.3 Cyber law: Evolution and Historical events in cyber law. Case studies- Article taken from Media. Building blocks of cyber law (Netizens, Cyber space and Technology). Cyber Crime, Electronic and Digital devices, Intellectual Property, Data Protection and Privacy. Merits and Demerits of Cyber crime.

Extra Reading/Key words: How to stay out of trouble from Social Network.

UNIT – IV

6 hrs

Application of computer literacy

- 4.1. Computer Literacy for Banking Scheme and Applications:
- 4.2. Banking products-ATM card, Banking Instruments-Cheque, Demand Draft (DD), Banking Services Delivery Channels.
- 4.3. Know Your Customer (KYC), Opening of bank account and documents required, Types of bank accounts. Bank's services including remittances, loan, mobile banking, Overdraft, Pension etc.

Extra Reading/Key words: Social Security Schemes-Atal Pension Yojana (APY)

UNIT – V

6 hrs

Policies & Laws:

- 5.1 Government, federal, state, city, local and other public datasets- Data APIs, Hubs, Marketplaces, Platforms, Portals, and Search Engines.
- 5.2 Enigma, National Government Statistical Web Sites
- 5.3 Open Data Census, Socrata OpenData- provides easy access to government, NGO, and other public domain datasets. Census India, Open Government Data (OGD) Platform, India. Competitive exams: IIT-JAM, JEST, TIFR GS, JNU EE, NEST, BINC, GATE, CSIR.

Extra Reading/Key words: Applications of IECT

Note: Texts given in the Extra reading /Key words must be tested only through Assignment and Seminars.

PRESCRIBED TEXT BOOKS

1. Stefano Allesina and Madlen Wilmes (2019). Computing Skills for Biologists: A Toolbox. Princeton University Press.

SUGGESTED REFERENCE BOOKS

1. Bittu Kumar (2017) Mastering Ms-Office, ISBN: 9350578786, V&S Publishers

WEBSITE REFERENCES

1. https://www.webopedia.com/DidYouKnow/Hardware_Software/mobile-operating-systems-mobile-os-explained.html<https://makeawebsitehub.com/social-media-sites/>
2. https://www.tutorialspoint.com/information_security_cyber_law/information_security_cyber_law_tutorial.pdf
3. https://www.tutorialspoint.com/information_security_cyber_law/information_security_cyber_law_tutorial.pdf
4. <https://www.irjet.net/archives/V4/i6/IRJET-V4I6303.pdf>

Note: Learners are advised to use latest edition of books.

COURSE OUTCOMES

CO No.	COURSE OUTCOMES	Cognitive Level (K1 – K6)
CO-1	Describe the usage of computers and why computers are essential components in business and society.	K1
CO-2	Utilize the Internet Web resources and evaluate on-line e-business system.	K2
CO-3	Apply the categories of programs, system software and applications. Organize and work with files and folders.	K3
CO-4	Critically assess the social and ethical implications of computer technology in their daily life.	K4

(K1=Remember, K2=Understand, K3=Apply, K4=Analyze, K5=Evaluate, K6=Create)

PO – CO MAPPING

CO/PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9
CO 1	2	3	3	1	1	1	3	3	2
CO 2	2	2	-	-	2	1	3	2	3
CO 3	3	3	1	1	3	2	3	3	2
CO 4	2	3	1	-	2	1	2	3	3

PSO – CO MAPPING

CO/PO	PSO1	PSO2	PSO3
CO1	3	1	1
CO2	3	2	1
CO3	2	1	3
CO4	3	3	2

(For candidates admitted from the academic year 2022-23 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester III (B. Sc.)

Course Title	MAJOR CORE 7- PROGRAMMING IN C AND C++
Total Hours	75
Hours/Week	5
Code	I22BI3MCT07
Course Type	Theory
Credits	4
Marks	100

CONSPECTUS

To study fundamentals of programming techniques viz., sequence of execution, Selection of blocks to be executed, repetition of execution etc with the help of C programming language.

COURSE OBJECTIVES:

1. Understand the basics structure of C programming.
2. Compute the essential characters and operators used in writing arithmetical program.
3. Study the utility of incorporating decision making statements in C program.
4. Constructs and executes program with arrays and strings.
5. Examines the variations in user-defined functions while constructing programs.

UNIT – I

15 hrs

Introduction to C:

1.1 Overview of C - 'C' History and Background - C program structure - Sample Program, Basic structure of C programs – Programming style – Executing C Program.

1.2 C tokens – Keywords and Identifiers, Constants, Variables – Declaration of variables, Datatypes, Defining symbolic constants.

1.3 Operators – Introduction, Arithmetic, Relational, Logical, Assignment, Increment and decrement, Conditional operators.

Extra Reading (Key words): Special Operator.

UNIT – II

15 hrs

Conditional statements:

2.1 Decision Making and Branching - Introduction - Decision Making with If Statement – Simple If – If-Else Statement – Nesting of If-Else – The Else-if ladder – The Switch statement – The Goto statement.

2.2 Decision Making and Looping - Introduction – The While Statement – The Do statement - The For statement – Jumps in loops.

2.3 Arrays in C - One Dimensional Array, Two Dimensional Array; String Handling in Array - Declaration of String Variable, Printing of a string, Concatenation of a String, Comparison of the String.

Extra Reading (Key words): Control flow statements, Modular programming

UNIT – III

15 hrs

Functions:

3.1 Introduction – User defined function – Elements of user defined function – Definition of function – Function calls – Function declaration – Nesting of function -Recursion

3.2 Pointers – Accessing the address of a variable – Declaring pointer variables – Initialization of pointer variables-pointer expression – Array of pointers

3.3 File operation – defining - opening – Closing. Input,output operations on files. Linked lists – Types of linked lists – creating linked lists – Application of linked lists.

Extra Reading (Key words): Data abstraction

UNIT – IV

15 hrs

Introduction to C++

4.1 Object oriented programming paradigm – Basic concept of Object oriented programming – Objects, Classes, Data abstraction, Inheritance, Polymorphism, Dynamic programming, Message Passing. Application of object oriented programming.

4.2 Structure of C++ program - Tokens – Keywords, Identifiers vs Constants. Operators in C++

4.3 Control Structure – if statement, switch statement, do-while statement, while statement, for statement.

Extra Reading (Key words): Storage management

UNIT – V

15 hrs

Function, classes and inheritance

5.1 Function – function prototyping, call by reference – inline function- function overloading- Friend and inline function.

5.2 Classes – Specifying classes – creating object. Defining member function – outside the class definition – Inside the class definition. Arrays within the class, Arrays of Objects, Friendly function

5.3 Inheritance – defining derived classes - Single inheritance – making private member inheritable – Multilevel inheritance, Multiple inheritance, Hierarchical inheritance, Hybrid inheritance.

Extra Reading (Key words): Polymorphism encapsulation

Note: Texts given in the Extra reading /Key words must be tested only through Assignment and Seminars.

PRESCRIBED TEXT BOOKS

1. Programming in ANSI C, E. Balagurusamy, Tata McGraw Hill Publishing Company Ltd, New Delhi, 3rd Edition.

SUGGESTED REFERENCE BOOKS

1. Parthasarathy S (2008). Essentials of Programming in C for Life Sciences, Ane Books India, New Delhi. First Edition, ISBN 978-81-8052-261-1; Second Edition, 2011, ISBN 978-93-8116-208-8.
2. "C Made easy", Herbert Schildt (1987), Computer Science Series, McGraw-Hill International Editions.
3. The Complete Reference C", Herbert Schildt (1995), Tata MC Graw Hill, Fourth Edition.
4. Deitel & Deitel (2001). C++ How to Program – Pearson Education/Prentice Hall of India (chapters: 1, 6) (Text book)
5. Balagurusamy, E. (2003), Object Oriented Programming with C++, PHI. (Text book)

6. Balaguruswami E, (2013), 6th Edition, Object Oriented Programming with 'C++', Tata Mac Graw Hill.
7. Bhawe, O.M.P, Patekar, S. A. (2004). Object Oriented Programming with C++, Pearson Education, Singapore PvtLtd.

Web reference

Note: Learners are advised to use latest edition of books.

COURSE OUTCOMES:

CO No.	Course Outcomes	Cognitive Level (K1 – K6)
CO-1	Relate with the basic structure of C programming.	K1
CO-2	Study on their essentials functions employed in execution of a program.	K2
CO-3	Introduction of various types of operators introduced in different programs to perform mathematical functions.	K3
CO-4	Understand the rule of using branching and looping in programs.	K4
CO-5	Differentiate the usage between various forms of arrays.	K5

(K1=Remember, K2=Understand, K3=Apply, K4=Analyze, K5=Evaluate, K6=Create)

PO – CO MAPPING

CO/PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9
CO 1	3	3	1	1	1	1	3	3	3
CO 2	3	3	2	2	2	2	3	3	3
CO 3	3	3	2	2	2	2	3	3	3
CO 4	2	3	3	2	2	2	2	3	3
CO5	1	2	2	2	1	2	1	3	3

PSO – CO MAPPING

CO/PO	PSO1	PSO2	PSO3
CO1	2	3	2
CO2	3	3	3
CO3	3	2	3
CO4	2	3	3
CO5	3	2	2

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester III (B. Sc.)

Course Title	MAJOR CORE 8 - PRACTICAL – PROGRAMMING IN C AND C++
Total Hours	75
Hours/Week	5
Code	I22BI3MCP08
Course Type	Practical
Credits	4
Marks	100

CONSPECTUS

This course makes the students to understand the system development work and to perform variety of tasks related to Life Sciences using C programming and C++.

COMPUTER PROGRAMMING IN C

1. Calculation of pH of a given solution for a given H⁺ ion Concentration
2. To determined the average molecular weight of a given double stranded DNA of length
3. Computing the rpm value for a given RCF value and the maximum radius in cm of a centrifuge.
4. Calculate sedimentation time (in hrs. & mins.) using clearing factor and sedimentation coefficient
5. Computing the sedimentation time of a molecule of known sedimentation coefficient s in an aqueous medium at 20° C with a rotor at specified rpm and known r_{\max} and r_{\min} values.
6. Computing the percentage of A+T and G+C content of a given DNA sequence.
7. Confirming the palindrome nature of a sequence.
8. Converting the DNA sequence into a mRNA sequence by simply converting the nucleotide base T to U.
9. Computing base composition of a given nucleotide sequence. Read the sequence from a data file.
10. Convert the given Fahrenheit value to centigrade scale (or vice versa)

COMPUTING PROGRAMMING IN C++

1.
 - a. Calculate Body Mass Index (BMI) value.
 - b. Calculate pH of the solution using H⁺ ion.
 - c. Calculate Average Molecular Weight of DNA.
 - d. Check the Palindrome of a given sequence.
2. Compute multiplication & Division of two numbers using inline functions.
3. Compute Simple Interest using Default Arguments.
4. Compute Volume of Cube, Cylinder & Rectangular Box using function overloading.
5. Define a class to represent a gene sequence data and include the following members:
Data members: Name of the gene id, length, A,T,G,C content

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester III (B. Sc.)

Course Title	MAJOR SKILL BASED ELECTIVE 2- PUBLIC SPEAKING AND SCIENTIFIC WRITING
Code	I22BI3SBT03
Course Type	Theory
Semester	III
Hours/Week	2
Credits	1
Marks	100

CONSPECTUS

This course aims to display different types of speeches to face the public. Also demystify the writing process and teach the fundamentals of effective scientific writing.

COURSE OBJECTIVES

1. To understand of the process of preparing an effective public speech
2. To acquire skills for informative speech, persuasive speech, crisis speech
3. To demonstrate important aspect of literature survey before writing an article
4. To provide an ideal knowledge for dissertation & thesis writing
5. To explain the process of writing and publishing research articles

UNIT – I

6 hrs

Introduction to speaking skill:

- 1.1 The process of preparing a speech – Audiences Analysis. Developing confidence, practice speeches, Presentation Skills. Ethics of public speaking.
- 1.2 Selecting a Topic and Purpose - Organizing the Speech, Types of Organizational Arrangements, Outlining the Speech.
- 1.3 Adapting to audiences - evaluation techniques and listener needs.

Extra Reading/Key words: Ethical Speaker.

UNIT – II

6 hrs

Types of public speeches:

- 2.1 Speech – Introductory, informative, persuasive, crisis and special occasion speeches.
- 2.2 Tools - Sensory aids in public speaking, managing speech anxiety.
- 2.3 Enhancement - Improving listening and note-taking skills, the four stages of listening and the different types of listening

Extra Reading/Key words: Speech anxiety symptoms.

UNIT – III

6 hrs

Literature analysis:

- 3.1 Subject analysis - literature survey, data collection, utilizing library for research writing
- 3.2 On line tools – Google scholar, Data Analysis and Evaluation.
- 3.3 Hypothesis - framing and objective of the study.

Extra Reading/Key words: Literature Database.

UNIT – IV

6 hrs

Dissertation & thesis writing:

4.1 Dissertation - Abstract, Contents, Objective & scope of the study.

4.2 Parts of Thesis - Introduction, review of literature, results, discussion

4.3 Thesis - Summary and Conclusion, Reference.

Extra Reading/Key words: Computational advances in Dissertation writing.

UNIT – V

6 hrs

Research paper writing:

5.1 Manuscript Structure – authors, title, abstract, keywords, introduction, materials and methods, results & discussion, acknowledgement, declarations.

5.2 Reference writing, abbreviations, appendix, plagiarism, ethics, copyrights, language.

5.3 Journals and Publications- e-journals, national & international journals, impact factor, citations, h-index, i10 and i20 index. Submitting an article, revising, editing, proof reading – publication.

Extra Reading/Key words: Types of publications.

Note: Texts given in the Extra reading /Key words must be tested only through assignment and Seminars.

PRESCRIBED TEXT BOOKS

• Sinha, S.C. , Dhiman, A.K., (2002). Research Methodology, Ess Publications.

• Kothari, C.R., (1990). Research Methodology: Methods and Techniques. New Age International. 418p.

SUGGESTED REFERENCE BOOKS

• Chris Anderson., (2016). TED talks: the official TED guide to public speaking. Publisher: Headline Publishing Group, London.

• Lucas, S., Simeon, L., & Wattam, J., (2008). The art of public speaking. Toronto: McGraw-Hill Ryerson.

• Garg, B.L., Karadia, R., Agarwal, F. and Agarwal, U.K., (2002). An introduction to Research Methodology, RBSA Publishers.

Note: Learners are advised to use latest edition of books.

COURSE OUTCOMES

CO No.	COURSE OUTCOMES	Cognitive Level (K1-K6)
CO-1	Validate knowledge of public speaking principles and concepts	K1
CO-2	Apply methods of organizing a speech through an outline	K3
CO-3	Able to carry out literature survey for effective writing using online tools.	K3
CO-4	Categorize knowledge about dissertation and thesis writing, towards a quote and paraphrase sources and avoid plagiarism.	K4
CO-5	Appraise the process of writing and publishing research articles	K5

(K1=Remember, K2=Understand, K3=Apply, K4=Analyze, K5=Evaluate, K6= Create)

PO – CO MAPPING

CO/PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9
CO 1	3	2	3	1	3	1	2	-	1
CO 2	3	2	3	1	3	1	2	-	1
CO 3	2	3	2	2	2	2	1	1	2
CO 4	2	2	3	3	2	3	3	1	1
CO5	2	1	2	1	3	2	2	1	1

PSO – CO MAPPING

CO/PO	PSO1	PSO2	PSO3
CO1	2	2	1
CO2	2	2	2
CO3	3	2	1
CO4	3	3	2
CO5	3	2	2

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester III (B. Sc.)

Course Title	MAJOR ELECTIVE 3 – MEDICAL INFORMATICS
Total Hours	30
Hours/Week	2
Code	I22BI3NMT01
Course Type	Theory
Credits	2
Marks	100

CONSPECTUS

Medical documentation and electronic patient records. Image capturing, analysis and processing techniques. Medical terminology and standards. Modelling, simulation, and visualisation as tools for diagnosis and therapy. Medical knowledge representation and decision support. User interfaces in health care. Telemedicine

COURSE OBJECTIVES

1. Understand the basic concept of medical informatics and account for the challenges in deploying and using advanced data analysis and information systems in health care practice.
2. Analyze how practices within health care can be supported by computerized tools.
3. Describe how the requirements of different stakeholders within health care (e.g. physicians, nurses, lab analysts) can be studied and fulfilled to overcome their problems virtually.
4. Learn potential benefits of medical informatics and to determine the problems in health care practice are appropriate to address, including ethical and safety positions, by using computerized methods for visualization and analysis
5. Apply the informatics tools and technology and describe the challenges in designing advanced data analysis and information systems for health care practice

UNIT – I

6 hrs

Introduction to medical informatics:

- 1.1 Introduction - Computer based medical informatics retrieval
 - 1.2 Database and information system in health care, Big Data in hospitals;
 - 1.3 Basic medical imaging - acquisition, diagnostic display, enhancement and analysis
- Medical Informatics - Branches

Extra Reading/Key words: Biomonitoring drugs

UNIT – II

6 hrs

Medical data storage and automation:

- 2.1 Health care Data - Representation: Relational-Hierarchical and network Approach, Data modelling for patient database development.
- 2.2 Biomedical statistics - Introduction, Computer processing of biosignals,
- 2.3 Medical imaging - Advanced imaging, diagnostic image processing

Extra Reading/Key words: PACS Architecture

UNIT – III

6 hrs

COMPUTERIZED PATIENT RECORDS

3.1 Medical standard organization - JCI, Computer based patient records

3.2 Tracking history by computer - Barcoding, Computerized prescription for Patients.

3.3 Automated clinical laboratories - Automated methods in hematology, cytology and histology, Computer assisted medical imaging,

Extra Reading/Key words: Nuclear medicine

UNIT – IV

6 hrs

Cybersecurity in health care:

4.1 Informatics in Patient Care Settings - Health data storage and exchange – Telemedicine

4.2 Clinical imaging - Automated staffing and workload systems - Quality assurance. Social, ethical and legal Issues,

4.3 Computer processing of medical image - Introduction, Clinical software development. Medical startups, Intellectual property Right Protection.

Extra Reading/Key words: CPG Resources

UNIT – V

6 hrs

Recent advances in medical informatics:

5.1 Virtual reality - applications in medicine,- Virtual endoscopy

5.2 Computer assisted medicine - Surgery, Computer assisted medical education. Virtual hospital- e-health services, Telemedicine.

5.3. Errors - Technologies to Decrease Medication Errors

Extra Reading/Key words: National Institute for Health and Clinical Excellence

Note: Texts given in the Extra reading /Key words must be tested only through Assignment and Seminars.

PRESCRIBED TEXT BOOKS

1. Edward H. Shortliffe, James J. Cimino, Michael F. Chiang, Biomedical Informatics- Computer Applications in Health Care and Biomedicine, 5th edition , 2021.
2. Joseph Tan (2008) (McMaster University, Canada), Medical Informatics: Concepts, Methodologies, Tools, and Applications (4 Volumes).

SUGGESTED REFERENCE BOOKS

1. Ana D. Cleveland, Donald B. Cleveland, (2009), Health Informatics for Medical Librarians
2. William R. Hersh, Robert E. Hoyt, (2018), Health Informatics - Practical Guide Seventh Edition
3. Edward H. Shortliffe, James J. Cimino, Michael F. Chiang, (2021), Biomedical Informatics Computer Applications in Health Care and Biomedicine

Note: Learners are advised to use latest edition of books.

COURSE OUTCOMES

CO No.	COURSE OUTCOMES	Cognitive Level
CO-1	Explain the structure of medical Informatics and functional capabilities of hospital informatics.	K1
CO-2	Analyze the needs of software and computers in medical imaging and automation clinical practices.	K2
CO-3	Apply the tools and software to fulfill the needs of medical standards.	K3
CO-4	Explain the importance of health care informatics	K4
CO-5	Evaluate the recent trends, virtual hospitability and various ICT applications in medical informatics.	K5

(K1=Remember, K2=Understand, K3=Apply, K4=Analyze, K5=Evaluate, K6=Create)

PO – CO MAPPING

CO/PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9
CO 1	3	2	3	1	3	1	2	-	1
CO 2	3	2	3	1	3	1	2	-	1
CO 3	2	3	2	2	2	2	1	1	2
CO 4	2	2	3	3	2	3	3	1	1
CO5	2	1	2	1	3	2	2	1	2

PSO – CO MAPPING

CO/PO	PSO1	PSO2	PSO3
CO1	2	2	1
CO2	2	2	2
CO3	3	2	1
CO4	3	3	2
CO5	3	2	2

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester IV (B. Sc.)

Course Title	MAJOR CORE 9 - PROGRAMMING IN PERL AND PYTHON
Code	I22BI4MCT09
Course Type	Theory
Semester	IV
Hours/Week	5
Credits	4
Marks	100

CONSPECTUS

This course provides a concise exploration of Perl and Python programming for bioinformatics. Covering key programming fundamentals, regular expressions, and file handling, it emphasizes practical applications in sequence analysis.

COURSE OBJECTIVES

1. Understand the basic concepts of PERL programming.
2. Apply BioPERL for file manipulation, pattern matching, and understand BioPERL modules for bioinformatics applications.
3. Gain proficiency in Python programming, covering data types, control flow, functions, and file handling.
4. Acquire skills in utilizing Python for string manipulation, subroutines, and working with special variables.
5. Develop expertise in regular expressions in Python, encompassing simple uses, pattern matching, and advanced concepts like quantifiers and metacharacters.

UNIT – I

15 hrs

Programming in PERL:

- 1.1 Programming in PERL: Introduction and Features
- 1.2 Creating a PERL program, Literals and variables- strings, List, Arrays, Hash,
- 1.3 Basic Operators and Control Structures.

Extra reading/Keywords: perl applications

UNIT – II

15 hrs

PERL regular expressions and file handling:

- 2.1 Creating Regular Expressions-Characters, Character Classes, Alternative Match Patterns, Quantifiers, Assertions, Back References, Modifiers and Translator Operations, Matching Words, Extracting Substrings,
- 2.2 File Handling - Overview of Filehandle - Typical Way of Opening a Perl File Handlers - Opening a Perl File Handle Reference in Normal Scalar Variable
- 2.3 Use Perl IO::File to Open a File Handle, Open the Standard Input and Standard Output, Use Sysopen () to Open the File.

Extra Reading (Key words): File permissions and ownership

UNIT – III

15 hrs

Python overview & Functions

3.1 Introduction- Python interpreter and interactive mode, values and data types, variables, expressions, statements, tuple assignment, precedence of operators, comments, modules and functions, function definition and use, flow of execution, parameters and arguments

3.2 Control flow, functions, conditionals- boolean values and operators, if, if-else, if-elif-else, iteration-state, while, for, break, continue, pass

3.3 Fruitful functions- return values, parameters, local and global scope, function composition, recursion.

Extra reading/Keywords: Python recursion, modular programming.

UNIT – IV

15 hrs

Arrays:

4.1 Strings- string slices, immutability, string functions and methods, string module, Lists as arrays.

4.2 Subroutines function in python- function definition, calling a function, passing parameters, local variables, returning values,

4.3 Special variables and its types, file handle special variables, local and global special variables.

Extra reading/Keywords: Software development using programming

UNIT – V

15 hrs

Introduction to Bio scripting:

5.1. BioPERL: Introduction to BioPERL, BioPERL objects, Searching and matching sequences in PERL, BLAST parsing, Handling PDB files

5.2 Biopython: Parsing DNA Data Files: FASTA Files – Genbank Files, Sequence Alignment: Alphabets, Matching Sequence

5.3 Sequence retrieval, Alignments, Simple Alignments, Numerical Sequence Alignment, Clustering: K-means clustering.

Extra reading/Keywords: Debugging and object-oriented programming

Note: Texts given in the Extra reading /Key words must be tested only through assignment and Seminars.

PRESCRIBED TEXT BOOKS

1. Chang, J., Chapman, B., Friedberg, I., Hamelryck, T., De Hoon, M., Cock, P., & Talevich, E. (2017), Biopython Tutorial and Cookbook. Update, 15-19.
2. Timothy, A. B. (2015), Exploring Python. Mc-Graw Hill Education (India) Private Ltd.
3. DSVGK, K. (2014), Basics in PERL and BioPERL: A programming guide. GRIN Verlag.
4. Christiansen, T., & Torkington, N. (2003), Perl Cookbook: Solutions & Examples for Perl Programmers. "O'Reilly Media, Inc."

SUGGESTED REFERENCE BOOKS

1. Michael Moorhouse (2004), Paul Barry, Bioinformatics Biocomputing and Perl, Wiley.
2. Curtis Jamison D (2003), Perl Programming for Biologists, John Wiley & Sons, INC..
3. James Tisdall, Beginning Perl for Bioinformatics, O'Reilly, 2001.
4. Matrin C Brown (2001), The Complete Reference PERL, 2nd Edn, Tata McGraw Hill, New Delhi.

WEBSITE REFERENCES

1. <http://bioperl.org>
2. <https://www.tutorialspoint.com/perl/index.htm>
3. www.perlmonks.org/?node_id=585436
4. <https://www.tutorialspoint.com/index.htm>

Note: Learners are advised to use latest edition of books.

COURSE OUTCOMES

CO No.	COURSE OUTCOMES	Cognitive Level (K1-K6)
CO-1	Gain knowledge of Perl and Python programming fundamentals.	K1
CO-2	Effectively use regular expressions for searching, matching, and extracting information from strings.	K2
CO-3	Apply Python programming concepts in solving problems, utilizing control flow structures, and implementing functions.	K3
CO-4	Analyze and implement advanced perl and Python concepts related to file handling, arrays, and special variables.	K4
CO-5	Evaluate the role of Perl and Python in bioinformatics sequencing, demonstrating a deep understanding of their applications in the field.	K5

(K1=Remember, K2=Understand, K3=Apply, K4=Analyze, K5=Evaluate, K6=Create)

PO – CO MAPPING

CO/PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9
CO 1	2	2	3	-	-	-	-	1	1
CO 2	3	2	-	-	-	-	2	2	1
CO 3	2	2	3	2	2	2	2	2	2
CO 4	2	2	2	2	2	2	2	2	2
CO 5	3	3	2	3	3	3	2	3	3

PSO – CO MAPPING

CO/PO	PSO1	PSO2	PSO3
CO1	3	2	2
CO2	2	2	2
CO3	3	2	2
CO4	2	3	2
CO5	3	2	3

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester IV (B. Sc.)

Course Title	MAJOR CORE 10 – MAIN PRACTICAL IV – PROGRAMMING IN PERL & PYTHON
Hours/Week	4
Code	I22BI4MCT10
Course Type	Practical
Credits	4
Marks	100

CONSPECTUS

This course provides a comprehensive overview of essential concepts and practical skills for manipulating biological sequences using the Perl and Python programming language.

COURSE OBJECTIVES

1. Gain proficiency in reading and manipulating biological sequences, including DNA, RNA, and proteins, using perl and python programming.
2. Develop skills in pattern matching using regular expressions to identify specific sequences or motifs within biological data.
3. Learn to analyze nucleotide sequences by counting nucleotides and calculating GC percentages.
4. Acquire knowledge of file handling basics for reading and writing sequence data.
5. Apply programming skills to solve real-world bioinformatics problems, including finding restriction sites and working with PDB and UniProt files

PROGRAMS IN PERL

1. Program to read a protein sequence from a file.
2. Program to find Reverse Compliment of a sequence
3. Program to transcribe a DNA sequence from file
4. Program to translate mRNA sequence to protein sequence.
5. Program to find whether a particular pattern is found in a protein or not.
6. Program to count the number of Nucleotides in a sequence and to find out the GC Percentage
7. Program to convert DNA sequence to protein sequence.
8. Program to concatenate two strings of DNA using subroutine.
9. Program to append ATGC to a DNA sequence using subroutines
10. Program to convert DNA to RNA
11. Program for determining frequency of nucleotide in a sequence file
12. Program to find the percentage of hydrophobic amino acids in a sequence

PROGRAMS IN PYTHON:

1. Program to count the number of nucleotides in a sequence.
2. Program to print the number of unknown characters in the sequence.
3. Program to read protein sequence from a file.
4. Program to find out the GC percentage in a sequence.
5. Program to transcribe a DNA sequence
6. Program to find Reverse Compliment of a sequence
7. Program to translate mRNA sequence to protein sequence

8. Program to find restriction site in a sequence using control structures.
9. Program to find whether a particular pattern is found in a protein or not.
10. Program that takes the protein sequence from the PDB (download the FASTA file manually), and writes a corresponding UniProt file.
11. Program to parse sequence from FASTA and Genbank file formats.
12. Program to perform complement and reverse complement operations on given sequences.

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester IV (B. Sc.)

Course Title	MAJOR ELECTIVE – COMPUTER AIDED DRUG DESIGN
Hours/Week	4
Total Hours	60
Code	I22BI4MET01
Course Type	Theory
Credits	3
Marks	100

CONSPECTUS

The course explains the drug discovery process by employing computational methods and algorithms.

COURSE OBJECTIVES

1. To classify different types of Biological Databases.
2. To articulate the various tools and methodologies used in multiple sequence alignment, phylogenetic analysis and genetic diversity analysis observed in biological sequences.
3. To correlate the various computational methods and tools used for protein secondary structure prediction and genome analysis.
4. To relate the numerous approaches in prediction of protein three dimensional structure.
5. To compute the complex interactions within biological systems and modelling the biological systems through conceptual and mathematical approaches towards drug designing.

UNIT – I

12 hrs

Overview of Bioinformatics:

- 1.1 Databases – types – relational databases – object oriented databases
- 1.2 Introduction to Biological Database – Primary databases – secondary databases – specialized databases. Nucleotide Sequence Databases- Genbank, DDBJ, EMBL.
- 1.3 Human genome project – Background, Goals, Main conclusion of Human genome project, Human genome variation – SNPs and HapMap Project.

Extra reading/Keywords: Newly developed databases.

UNIT – II

12 hrs

Databases:

- 2.1 Protein Sequence Databases- Swissprot, TrEMBL. Protein Structure Database- PDB.
- 2.2 Derived databases- Prosite, Pfam. Literature Databases- Pubmed,.
- 2.3 Chemical databases- Pubchem, Drug bank

Extra Reading/Key words: KEGG.

UNIT – III

12 hrs

Sequence analysis:

- 3.1 Sequence alignment methods- pairwise sequence alignments – BLAST, FASTA.
- 3.2 Multiple sequence alignment – steps -tools for multiple sequence alignment.
- 3.3 Phylogenetic Analysis - construction, rooted and un-rooted tree representation - Tools.

Extra reading/Keywords: UPGMA method.

UNIT – IV

12 hrs

Drug discovery:

4.1 Drugs – definition - historical evolution – classification of drugs - nomenclature of drugs - General idea regarding the milestones in drug research. Sources of Drugs.

4.2 Drug discovery phases-preclinical phase studies – clinical development – FDA review – Post market monitoring.

4.3 ADMET prediction - ADMET parameters and their role, ADMET prediction methods and tools.

Extra reading/Keywords: Drugs discovered by CADD

UNIT – V

12 hrs

Computer – aided drug design:

5.1 CADD - concepts and principles – applications – success – limitations - Database resources for cadd - therapeutic target information - PDB, chemical information – pubchem – drug bank.

5.2 Drug design – structure based drug design – modelling - molecular docking – virtual screening.

5.3 Ligand based drug design – pharmacophore - QSAR.

Extra reading/Keywords: Software for molecular docking and dynamics.

Note: Texts given in the Extra reading /Key words must be tested only through assignment and Seminars

PRESCRIBED TEXT BOOKS

1. Baxevanis., & B.F., Ouellette., (2009). *Bioinformatics: A practical Guide to the Analysis of Genes and Proteins*, Wiley- Interscience, Hoboken, NJ.
2. Attwood, T.K., & Parry Smith, D.J., (2004). *Introduction to Bioinformatics*, 1st Edition, Pearson Education Ltd, New Delhi.
3. Jin Xiong, *Essential Bioinformatics.*, (2006). Cambridge University Press, ISBN 9780511806087.

SUGGESTED REFERENCE BOOKS

1. Arthur M. Lesk., (2003). *Introduction to Bioinformatics*, Oxford University Press, New Delhi.
2. David, W., Mount., (2001). *Bioinformatics Sequence and Genome Analysis*. Cold Spring Harbor Laboratory Press.
3. Higgins, D., and Taylor, W., (2000). (Eds), *Bioinformatics- Sequence, structure and databanks*, Oxford University Press, New Delhi.
4. Jeffrey *et al.*, (2000). *Structural genomics and its importance for gene function analysis*. Nature Biotechnology. 18:283 – 287.

WEBSITE REFERENCE

1. <https://personal.utdallas.edu/~son051000/comp/EdelmiroMoman.pdf>
2. <https://www.profacgen.com/pharmacophore>.
3. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6030848/>
4. <https://www.biologicscorp.com/blog/protein-structure-prediction-methods>

Note: Learners are advised to use latest edition of books.

COURSE OUTCOMES

CO No.	COURSE OUTCOMES	Cognitive Level (K1-K6)
CO-1	Explore the various applications of BLAST and FASTA in understanding differences in evolutionary patterns.	K1
CO-2	Exemplify the biomaterial cite and their uses in the pharmaceutical industry primes to novel drug development.	K2
CO-3	Transform the key concepts of 'omics approaches in the direction of the targeted drug development, analyzing biological data, protein Visualization Tools such as Rasmol and Swiss pdb.	K3
CO-4	Categorize evolution tree, cladogram, retrieve the biological information accessed through various information resources to identify the disorders and its mode of insertion.	K4
CO-5	Compute the docking, and molecular simulation, to critique the Computer-Aided Drug Designing concerning the human care.	K5

(K1=Remember, K2=Understand, K3=Apply, K4=Analyze, K5=Evaluate, K6=Create)

PO – CO MAPPING

CO/PO	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9
CO1	1	1	-	-	-	1	1	1	1
CO2	1	1	1	-	2	1	1	2	1
CO3	1	2	2	1	2	2	1	2	2
CO4	2	2	3	1	2	2	2	3	3
CO5	3	3	3	2	3	3	3	3	3

PSO – CO MAPPING

CO/PSO	PSO1	PSO2	PSO3
CO1	2	3	1
CO2	2	3	1
CO3	3	3	2
CO4	2	2	2
CO5	3	2	3

(For the candidates admitted from 2022 onwards)
M.Sc. BIOINFORMATICS (INTEGRATED) – Semester IV (B. Sc.)

Course Title	NME – BIOPROGRAMMING
Code	I22BI4NMT02
Course Type	Theory cum Lab
Semester	IV
Hours/Week	2
Credits	2
Marks	100

CONPECTUS

This course explores the intersection of biology and programming, providing students with the skills and knowledge to use coding for solving biological problems

COURSE OBJECTIVES

1. To outline the learners with fundamentals and characteristics of computers.
2. To interpret the different types of operating system and software's for their applications.
3. To Understand and apply fundamental programming concepts, such as variables, data types, loops and conditionals.
4. To gain an appreciation of how computational methods and programming can be applied to solve biological problems and advance biological research.
5. To acquire fundamental programming skills, with a focus on languages commonly used in bioinformatics and computational biology, such as Perl and Python.

UNIT – I

6 hrs

Introduction to Computers:

- 1.1 Computers - Characteristics of Computers –
- 1.2 Evolution of Computers - Basic Computer organization
- 1.3 Hardware – Input and output devices – CPU – memory – Software

Extra Reading /Key words: User Interface

UNIT – II

6 hrs

Operating systems:

- 2.1 Introduction to operating Systems
- 2.2 Windows Commands, UNIX / Linux - basic commands
- 2.3 General purpose, file handling, vi editor & environment.

Extra Reading /Key words: Kernel

UNIT – III

6 hrs

Programming:

- 3.1 Basic Programming Concepts – Variables – Constant – condition – loops. Need for Programming in Life Sciences
- 3.2 Commonly used programming languages – C - C++ - PERL - Python.
- 3.3 Introduction to BioPERL: FILE Handling- Input/Output operator - open() and close() commands – Exception handling, the debugger, and the Perl symbol table.

Extra Reading /Key words: PHP, MATLAB

UNIT – IV**6 hrs**

1. Windows commands - date, time, help, cls, copy, del, dir, md, cd, find.
2. Python programs - Hello world program, User Input and Greeting, Arithmetic Operations
3. List Operations

UNIT – V**6 hrs**

1. Hello world program
2. Perl script that calculates the square of a given number.
3. Perl script that prompts the user for their name and then generates greetings.
4. Perl script generates a random number.
5. Perl script for addition of two numbers.

Note: Texts given in the Extra reading / Key words must be tested only through assignment and Seminars.

PRESCRIBED TEXT BOOKS

1. Peter Norton (2006), *Introduction to Computers 6th Edition*, Tata McGraw-Hill Pub. Co.Ltd., New Delhi, .
2. Pradip Dey, Manas Ghosh(2006)., *Computer Fundamentals and Programming in C*, Oxford University Press, New Delhi, 2006.
3. Simon Cozens, Peter Wainwright (2000), *Beginning Perl*, Wrox Press

SUGGESTED REFERENCE BOOKS

1. S.Parthasarathy, *Essentials of Computer Programming in C for Life Sciences*, 2nd Edition, Ane Books, New Delhi, 2011.
2. Michael Moorhouse, Paul Barry, *Bioinformatics Biocomputing and Perl*, Wiley, 2004.
3. D. Curtis Jamison, *Perl Programming for Biologists*, John Wiley & Sons, INC., 2003.
4. James Tisdall, *Beginning Perl for Bioinformatics*, O'Reilly, 2001.

Note: Learners are advised to use latest edition of books.

WEBSITE REFERENCES

1. https://www.tutorialspoint.com/perl/perl_introduction.htm
2. <https://www.geeksforgeeks.org/perl-vs-c-c/>
3. <https://edu.gcfglobal.org/en/computerbasics/understanding-operating-systems/1/>
4. <https://www.python.org/about/gettingstarted/>

COURSE OUTCOMES

CO No.	COURSE OUTCOMES	Cognitive Level (K1-K6)
CO-1	Recognize the basic structure of a computer and concepts of hardware and software	K1
CO-2	Demonstrate the basics of Operating Systems and its applications.	K2
CO-3	Apply basic problem-solving skills and create simple algorithms to solve common computational tasks.	K3
CO-4	Categorize the key concepts of bio programming languages	K4
CO-5	Handle errors and debug code effectively to identify and fix issues.	K5

(K1=Remember, K2=Understand, K3=Apply, K4=Analyze, K5=Evaluate, K6=Create)

PO – CO MAPPING

CO/PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9
CO 1	3	2	-	-	-	-	2	-	2
CO 2	3	2	-	-	-	-	2	-	-
CO 3	2	2	2	-	-	-	2	-	-
CO 4	3	2	1	-	-	-	2	1	2
CO 5	2	2	1	-	-	-	2	1	2

PSO – CO MAPPING

CO/PO	PSO1	PSO2	PSO3
CO1	1	3	2
CO2	2	2	1
CO3	1	2	2
CO4	2	2	2
CO5	2	2	3