SYLLABI AND SCHEME OF EXAMINATIONS FOR M.Sc. BIOINFORMATICS

(Based on Curriculum and Credit Framework for PG Programs under NEP)

WITH EFFECT FROM THE SESSION 2024-25

MAHARSHI DAYANAND UNIVERSITY
ROHTAK (HARYANA)

Director
Centre for Bioinformatics
Maharshi Dayanand University
Rohtak (Haryana)

Structure for 2 year Post Graduate Program

	Semester	Discipline-Specific Courses (DSC)	Skill Enhancement Courses (SEC) / Vocational Courses (VOC)/ Internship	Research thesis/project	Total Credits
	First-year of 2 Year PG program (NHEQF Level 6)				
	I	DSC 1 @ 4 credits	SEC1/VOC 1/Internship 1 @ 4 credits	---	24
		DSC 2 @ 4 credits			
		DSC 3 @ 4 credits			
		DSC 4 @ 4 credits			
		DSC 5 @ 4 credits			
	II	DSC 6 @ 4 credits	SEC2/VOC2/Internship 2 @ 4 credits	---	24
		DSC 7 @ 4 credits			
		DSC 8 @ 4 credits			
		DSC 9 @ 4 credits			
		DSC 10 @ 4 credits			
Students who exit after the first year on completion of 48 credits will be awarded a PG Diploma in the concerned discipline					
Second year of two-year PG program (NHEQF Level 6.5) (STUDENT SHOULD SELECT ANY ONE OPTION FOR THE SECOND YEAR OF 2 YEAR PG PROGRAM)					
Only Course Work					
Option 1	III	DSC 11 @ 4 credits	SEC 3/Internship 3/ Project Work 1 @ 4 credits	---	24
		DSC 12 @ 4 credits			
		DSC 13 @ 4 credits			
		DSC 14 @ 4 credits			
		DSC 15 @ 4 credits			
	IV	DSC 16 @ 4 credits	SEC4/Internship 4/ Project Work 2 @ 4 credits	---	24
		DSC 17 @ 4 credits			
		DSC18 @ 4 credits			
		DSC19 @ 4 credits			
		DSC20 @ 4 credits			
Coursework and Research					
Option 2	III	DSC 11 @ 4 credits	SEC 3/Internship 3 @ 4 credits	---	24
		DSC 12 @ 4 credits			
		DSC 13 @ 4 credits			
		DSC 14 @ 4 credits			
		DSC 15 @ 4 credits			
	IV	--	SEC4/Internship 4 @ 4 credits	Research thesis/project @20 credits	24

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Only Research (only for the students who have completed 4 Years Bachelor's Program)					
	Semester	**Discipline-Specific Courses (DSC)**	**Skill Enhancement Courses (SEC) / Vocational Courses (VOC)/ Internship**	**Research thesis/project**	**Total Credits**
Option 3	**III**	--	**SEC3/Internship 3 @ 4 credits**	**20 credits***	**24**
	IV	--	**SEC4/Internship 4 @ 4 credits**	**20 credits****	**24**

Note:

*The students who opted for Option 3 should submit a project report/synopsis of at least 50 pages comprising a Literature survey, identification of the Research Problem, Plan of work, methodology, as well as practical work (if any) at the end of 3rd semester and the same will be evaluated by internal and external examiners.

**The students should continue the research work in the 4th semester based on the project work/synopsis submitted at the end of the 3rd semester. The final thesis/project report will be evaluated by the internal and external examiners.

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Structure for 1 year Post Graduate Programme (2nd year of 2 Year PG Program)

	Semester	Discipline-Specific Courses (DSC)	Skill Enhancement Courses (SEC) / Vocational Courses (VOC)/Internship	Dissertation/ Project work	Total Credits
(STUDENT SHOULD SELECT ANY ONE OPTION)					
Only Course Work					
Option 1	**I (Semester III of 2-year PG Program)**	**DSC 11 @ 4 credits** **DSC 12 @ 4 credits** **DSC 13 @ 4 credits** **DSC 14 @ 4 credits** **DSC 15 @ 4 credits**	**SEC 3/Internship 3/ Project Work 1 @ 4 credits**	---	**24**
	II (Semester IV of 2-year PG Program)	**DSC 16 @ 4 credits** **DSC 17 @ 4 credits** **DSC18 @ 4 credits** **DSC19 @ 4 credits** **DSC20 @ 4 credits**	**SEC4/Internship 4/ Project Work 2 @ 4 credits**	---	**24**
Coursework and Research					
Option 2	**I (Semester III of 2-year PG Program)**	**DSC 11 @ 4 credits** **DSC 12 @ 4 credits** **DSC 13 @ 4 credits** **DSC 14 @ 4 credits** **DSC 15 @ 4 credits**	**SEC 3/Internship 3 @ 4 credits**	---	**24**
	II (Semester IV of 2 year PG Program)	--	**SEC4/Internship 4 @ 4 credits**	**Dissertation/ Project work @ 20 credits**	**24**

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Type of Course	Nomenclature of Course	Course Code	Credits Distribution			Total Credits	Workload (Hours)			Total Workload (Hours)	Marks				Total Marks
											Theory		Practical		
			L	T	P		L	T	P		External	Internal	External	Internal	
Semester I (Session 2024-25)															
DSC 1 @ 4 credits	Cell & Molecular Biology	24BIN201DS01	4	0	0	4	4	0	0	4	70	30			100
DSC 2 @ 4 credits	Biochemistry	24BIN201DS02	4	0	0	4	4	0	0	4	70	30			100
DSC 3 @ 4 credits	Microbiology and Genetics	24BIN201DS03	4	0	0	4	4	0	0	4	70	30			100
DSC 4 @ 4 credits	Basic Bioinformatics & Biostatistics	24BIN201DS04	4	0	0	4	4	0	0	4	70	30			100
DSC 5 @ 4 credits	Laboratory Course I (24BIN201DS01, 24BIN201DS02, 24BIN201DS03)	24BIN201DS05	0	0	4	4	0	0	8	8				100	100
SEC 1 @ 4 credits	Developing Skills in Computers for Biology	24BIN201SE01	0	0	4	4	0	0	8	8				100	100
Semester II (Session 2024-25)															
DSC 6 @ 4 credits	Immunology & Genetic Engineering	24BIN202DS01	4	0	0	4	4	0	0	4	70	30			100
DSC 7 @ 4 credits	Computational Biology	24BIN202DS02	4	0	0	4	4	0	0	4	70	30			100
DSC 8 @ 4 credits	Advanced Bioinformatics	24BIN202DS03	4	0	0	4	4	0	0	4	70	30			100
DSC 9 @ 4 credits	Genomics and Proteomics	24BIN202DS04	4	0	0	4	4	0	0	4	70	30			100
DSC 10 @ 4 credits	Laboratory Course II (25BIN202DS01, 25BIN201DS02)	24BIN202DS05	0	0	4	4	0	0	8	8				100	100
SEC 2 @ 4 credits	Developing Skills in-omics Biology	25BIN202SE01	0	0	4	4	0	0	8	8				100	100

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Type of Course	Nomenclature of Course	Course Code	Credits Distribution			Total Credits	Workload (Hours)			Total Workload (Hours)	Marks				Total Marks
			L	T	P		L	T	P		Theory		Practical		
											External	Internal	External	Internal	
Semester III (Session 2025-26) OPTION 1															
DSC 11 @ 4 credits	Molecular Modelling & Drug Designing	25BIN203DS01	4	0	0	4	4	0	0	4	70	30			100
DSC 12 @ 4 credits	Data Mining & Machine Learning	25BIN203DS02	4	0	0	4	4	0	0	4	70	30			100
DSC 13 @ 4 credits	Programming in C	25BIN203DS03	4	0	0	4	4	0	0	4	70	30			100
DSC 14 @ 4 credits	Programming in PERL, Python and HTML	25BIN203DS04	4	0	0	4	4	0	0	4	70	30			100
DSC 15 @ 4 credits	Laboratory Course III (25BIN203DS01, 25BIN203DS02)	25BIN203DS05	0	0	4	4	0	0	8	8				100	100
SEC 3 @ 4 credits	Developing Programming Skills	25BIN203SE01	0	0	4	4	0	0	8	8				100	100
Semester IV (Session 2025-26)															
DSC 16 @ 4 credits	Systems Biology	25BIN204DS01	4	0	0	4	4	0	0	4	70	30			100
DSC 17 @ 4 credits	Big Data & Cloud Computing	25BIN204DS02	4	0	0	4	4	0	0	4	70	30			100
DSC 18 @ 4 credits	Protein Bioinformatics	25BIN204DS03	4	0	0	4	4	0	0	4	70	30			100
DSC 19 @ 4 credits	Principles of Phylogenomics	25BIN204DS04	4	0	0	4	4	0	0	4	70	30			100
DSC 20 @ 4 credits	Communication Skills for Science and Technology	25BIN204DS05	4	0	0	4	4	0	0	4	70	30			100
Internship 4	Internship	25BIN204IN01	0	0	4	4	0	0	8	8			70	30	100

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@ 4 credits																

Type of Course	Nomenclature of Course	Course Code	Credits Distribution			Total Credits	Workload (Hours)			Total Workload (Hours)	Marks				
											Theory		Practical		Total Marks
			L	T	P		L	T	P		External	Internal	External	Internal	
Semester III (Session 2025-26) OPTION 2															
DSC 11 @ 4 credits	Molecular Modelling & Drug Designing	25BIN203DS01	4	0	0	4	4	0	0	4	70	30			100
DSC 12 @ 4 credits	Data Mining & Machine Learning	25BIN203DS02	4	0	0	4	4	0	0	4	70	30			100
DSC 13 @ 4 credits	Programming in C	25BIN203DS03	4	0	0	4	4	0	0	4	70	30			100
DSC 14 @ 4 credits	Programming in PERL, Python and HTML	25BIN203DS04	4	0	0	4	4	0	0	4	70	30			100
DSC 15 @ 4 credits	Laboratory Course III (25BIN203DS01, 25BIN203DS02)	25BIN203DS05	0	0	4	4	0	0	8	8				100	100
SEC 3 @ 4 credits	Developing Programming Skills	25BIN203SE01	0	0	4	4	0	0	8	8				100	100
Semester IV (Session 2025-26)															
Internship 4@ 4 credits	Internship	25BIN204IN01	0	0	4	4	0	0	8	8			70	30	100
Research thesis / project @20 credits	Dissertation / Project work	25BIN204PD01	0	0	20	20	0	0	40	40	-	-	350	150	500

Note: Preference to option 2 will be provided to the students who have passed all the papers of previous semesters (with minimum 75% marks).

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OPTION 3

Type of Course	Nomenclature of Course	Course Code	Credits Distribution			Total Credits	Workload (Hours)			Total Workload (Hours)	Marks				Total Marks
											Theory		Practical		
			L	T	P		L	T	P		External	Internal	External	Internal	
Semester III (Session 2025-26)															
Internship 3 @ 4 credits	Internship	25BIN203IN01	0	0	4	4	0	0	8	8			70	30	100
Research thesis /Project @20 credits	Dissertation / Project work	25BIN203PD01	0	0	20	20	0	0	40	40	-	-	350	150	500
Semester IV (Session 2025-26)															
Internship 4@ 4 credits	Internship	25BIN204IN01	0	0	4	4	0	0	8	8			70	30	100
Research thesis /Project @20 credits	Dissertation / Project work	25BIN204PD01	0	0	20	20	0	0	40	40	-	-	350	150	500

Here: L: Lecture; T: Tutorial; P: Practical

In each semester, the students can also opt any one paper of equivalent credit from online platform/SWAYAM course in lieu of core papers

** This component will be covered by seminar/presentation

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Semester I

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Cell & Molecular Biology	**Course Code**	24BIN201DS01
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Structural organization and function of intracellular organelles
2. Organization of genes and chromosomes
3. Cell division and cell cycle
4. Cell division and cell cycle
5. RNA synthesis and processing
6. Control of gene expression at transcription and translation level

Course Outcomes:

Students completing this course will be able to:

1. Define the basic structure and function of cell membrane and other intracellular organelles.
2. Describe the organization of genes and chromosomes in prokaryotes and eukaryotes.
3. Describe the cellular process of DNA replication, repair and recombination.
4. Explain the RNA synthesis and processing.
5. Explain the control points of gene expression at transcriptional and translational level.

Unit - I

Membrane structure and function: Structure of model membrane, lipid bilayer and membrane protein diffusion, osmosis, ion channels, active transport, membrane pumps, mechanism of sorting and regulation of intracellular transport, electrical properties of membranes. **Structural organization and function of intracellular organelles:** Cell wall, nucleus, mitochondria, Golgi bodies, lysosomes, endoplasmic reticulum, peroxisomes, plastids, vacuoles, chloroplast, structure & function of cytoskeleton and its role in motility.

Unit - II

Organization of genes and chromosomes: Operon, unique and repetitive DNA, interrupted genes, gene families, structure of chromatin and chromosomes, heterochromatin, euchromatin, transposons. **Cell division and cell cycle:** Mitosis and meiosis, their regulation, steps in cell cycle, regulation and control of cell cycle.

Unit - III

DNA replication, repair and recombination: Unit of replication, enzymes involved, replication origin and replication fork, fidelity of replication, extrachromosomal replicons, DNA damage and repair mechanisms, homologous and site-specific recombination. **RNA synthesis and processing: T**ranscription factors and machinery, formation of initiationcomplex, transcription activator and repressor, RNA polymerases, capping, elongation, and termination, RNA processing, RNA editing, splicing, and polyadenylation, structure and function of different types of RNA, RNA transport).

Unit - IV

Protein synthesis and processing (Ribosome, formation of initiation complex, initiation factors and their regulation, elongation and elongation factors, termination, genetic code, amino-acylation of tRNA, tRNA-identity, aminoacyl tRNA synthetase, and translational proof-reading, translational inhibitors, Post- translational modification of proteins.

Control of gene expression at transcription and translation level: Regulating the expression of phages, viruses, prokaryotic and eukaryotic genes, role of chromatin in gene expression and gene silencing.

References:

1. Cell and molecular biology-Concept and experiment. 2nd edn., Harris,D(Ed.), Karp, G.1999. John wiley & sons, sons, New York.
2. Principles of cell and molecular biology. 2nd edn., Mclaughlin,S., Trost,K., Mac Elree,E.(eds)., Kleinsmith,L.J.& Kish, V.M., 1995. Harper Collins Publisher, New York.
3. Cell and Molecular Biology. 8th edn., De Robertis, E.D.P. and De Roberts, E, M.F.1995. B.I.Waverly Pvt. Ltd., New Delhi.
4. Lewin, B. (2008). Genes-IX. Jones and Barlett Publishers, Inc., USA.
5. Burton E.Tropp (2008) Molecular biology: Genes to Proteins. Jones and Barlett Publishers, Inc., USA Bartlet, 4th edition
6. Watson J.D et al (2004) Molecular biology of the gene. Pearson education, 5th edition
7. Darnell J.E, Lodish F.H and Baltimore D (1986) Molecular cell Biology. Scientific American Books
8. Freifelder, D.C. (2008). Molecular Biology. Narosa Publishing House, New Delhi, 2nd ed.
9. Brown T. A (2006) Genome 3. Garland Science; 3 edition

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Biochemistry	**Course Code**	24BIN201DS02
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Principles of biophysical chemistry
2. Stabilizing interactions
3. Bioenergetics
4. Principles of catalysis
5. Conformation of proteins
6. Metabolism of carbohydrates, lipids, amino acids nucleotides and vitamins

Course Outcomes:

Students completing this course will be able to:

1. Define the the basic structure of atoms, molecules and chemical bonds along with the composition, structure and function of biomolecules.
2. Describe the basic principles of biophysical chemistry.
3. Analyze the energy flow in biological system at cellular level (Glycolysis, oxidative phosphorylation, etc.).
4. Explain the process of signal transduction and concepts of metabolic engineering.
5. Explain the metabolism of carbohydrates, lipids, amino acids nucleotides and vitamins.

Unit - I

Principles of biophysical chemistry (pH, buffer, Principles of thermodynamics, Water as biological solvent) Stablizing interactions (Van der Waals, electrostatic, hydrogen bonding, hydrophobic interaction, etc.). Acid base balance and their importance in clinical biochemistry

Carbohydrates: Classification, structure, occurrence and biological functions. Physicochemical properties of monosaccharides, oligosaccharides. Glycoproteins and proteoglycans.

Carbohydrate Metabolism: Reactions and energetics of glycolysis. Alcoholic and lactic fermentations, Reactions and energetics of TCA cycle, gluconeogenesis, glycogenesis and glycogenolysis. Reactions and physiological significance of HMP pathway.

Unit - II

Lipid: Classification, structure, occurrence and biological functions of lipids. Nomenclature and properties of fatty acids and triglycerides.

Lipid metabolism: Transport and mobilization of lipids, oxidation of saturated fatty acids (α-, β-, ω-), oxidation of unsaturated and odd-chain fatty acids, role of carnitine intransport of fatty acid, energetics of β-oxidation scheme, metabolism of ketone bodies and its biological significance. Biosynthesis of saturated and unsaturated fatty acids. Biosynthesis of triglycerides, phospholipids, Sphingolipids, cholesterol and prostaglandins.

Unit - III

Amino acids: Physicochemical and structural properties of amino acids, Titration curve, isoelectric point.
Proteins: Classification, structure, peptide bond, Conformation of proteins (Ramachandran plot, secondary, tertiary and quaternary structure; domains; motif and folds. Properties and biological functions of proteins. Amino acid sequencing techniques.
Amino acid metabolism: General reactions of amino acid metabolism- Transamination, Deamination and Oxidative decarboxylation. Biosynthesis and degradation of amino acids and their regulation. Urea cycle and its regulation

Unit - IV

Nucleic acids: properties of DNA in solution, Composition of RNA and DNA, generalized structure plan of nucleic acids, features of A, B, H and Z DNA, Structure and roles of different types of DNAs and RNAs
Nucleic acid Metabolism: Sources of atoms in purine and pyrimidine molecules, biosynthesis and degradation of purines and pyrimidines, regulation of purine and pyrimidine biosynthesis, structure and regulation of ribonucleotide reductase. Biosynthesis of ribonucleotides, deoxyribonucleotides and polynucleotides. Inhibitors of nucleic acid biosynthesis.
Porphyrin Metabolism: Biosynthesis and degradation of porphyrins.

References:

1. Biochemical calculations (1976) by Irwin H. Seghal (John Wiley and Sons Inc.).
2. Biochemistry (2004) by Voet Donald Voet, Judith G. (J Wiley and Sons.).
3. Physical biochemistry (1982) by D. Freifilder (W.H. Freeman and Company).
4. Lehninger's principles of biochemistry by D. L. Nelson and M. M. Cox (W. H. Freeman).
5. Biochemistry (1995) by Lubert Stryer (W.H. Freeman).
6. Biochemistry (1998) by Geoffrey L. Zubay (Wm.C. Brown).
7. Biochemistry (2006) by Reginald H. Garrett , Charles M. Grisham (Brooks/Cole)
8. Complex carbohydrate (1975) by Nathan Sharon (Addison-Wesley Pub. Co., Advanced Book Program).
9. A biologist's guide to principles and techniques in practical biochemistry (1986) by Keith Wilson, Kenneth H. Goulding (ELBS).
10. An introduction to practical biochemistry (2004) by Plummer D.T. (Tata McGraw Hill Publishers Co. Ltd., New Delhi).

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Microbiology and Genetics	**Course Code**	24BIN201DS03
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Classification of prokaryotes
2. Microbial growth
3. Mendelian principles
4. Extra chromosomal inheritance
5. Structural and numerical alterations of chromosomes

Course Outcomes:

Students completing this course will be able to:

1. Explain the history of microbiology and chronological events of microbiology development in 18th and 19th century.
2. Outline the phylogeny of prokaryotes.
3. Explain the effect of chemicals and other environmental factors on microbial growth.
4. Explore different mendelian and non-mendelian inheritance patterns.
5. Explain the extra-chromosomal inheritance and identify about structural and numerical chromosomal aberrations.

Unit - I

Development of microbiology in the 18th and 19th century. Morphology, structure and function of prokaryotic and eukaryotic cell. Archaea. Classification of prokaryotes – Basic principles and techniques used in bacterial classification. Viruses – morphology, classification and replication of plant, animal and bacterial viruses.

Unit - II

Evolutionary relationship among prokaryotes. Phylogenetic and numerical taxonomy. Use of DNA and r-RNA sequencing in classifications.

Microbial growth: Effect of chemicals and other environmental factors on growth. EMP,HMP, ED, TCA pathways, Aerobic and anaerobic respiration. Fermentative metabolism.

Unit - III

Mendelian principles: Dominance, segregation, independent assortment. Concept of gene:Allele, multiple alleles, pseudoallele, complementation tests.

Extensions of Mendelian principles: Codominance, incomplete dominance, geneinteractions, pleiotropy, genomic imprinting, penetrance and expressivity, phenocopy, linkage and crossing over, sex linkage, sex limited and sex influenced characters.

Unit - IV

Extra chromosomal inheritance: Inheritance of Mitochondrial and chloroplast genes,maternal inheritance.

Structural and numerical alterations of chromosomes: Deletion, duplication, inversion, translocation, ploidy and their genetic implications.

Recombination: Homologous and non-homologous recombination including transposition.

References:

1. Prescott, L.M., Harley, J.P. and Klein, D.A. (1999) Microbiology. W.C.B.Oxford.
2. Brock, T.D. (1990) Microbiology: A text book of Industrial Microbiology. 2nd edition, Sameur Association.
3. Tortora, G.J., Funke, B.R. and Case, (1996) Microbiology: An introduction, Benjamin Cummings.
4. Atlas, R.M. (1998) Microbiology: Fundamental and applications. 2nd edition, Macmillan Publishing Company, New York.
5. Pelezar, M.J., Chan, E.G.S. and Krieg, N.R. (1998) Microbiology.
6. Heritage, J., Evance, E.G.V. and Killington, R.A. (1999) Microbiology in action. Cambridge University Press.
7. Lim, D.V. (1989) Microbiology, West Publishing Company, New York.
8. Polasaa, H. Microbial gene technology. South Asian Publishers. New Delhi
9. Snustad, D.P. and Simmons, M.J. (2010).Principles of Genetics. John Wiley and Sons, Inc., New York.
10. Klug, W. S., & Cummings, M. R. (2006). Concepts of genetics. Upper Saddle River, NJ: Pearson Education.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Basic Bioinformatics & Biostatistics	**Course Code**	24BIN201DS04
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Computers and Operating system
2. Biological databases
3. Specialized genomic resources
4. Measures of central tendency and dispersal
5. Parametric and non-parametric statistics

Course Outcomes:

Students completing this course will be able to:

1. Understand the working of computers and different Operating systems.
2. Access the world of Bioinformatics, different types of biological data and databases.
3. Explain & differentiate between measures of central tendency & measures of dispersion.
4. Describe & solve questions based on Normal, Binomial and Possion distributions.
5. Analyze in detail with reference to genetics following techniques & solve questions based on them: X^2 -test, t-test, ANOVA.

Unit - I

Introduction to computer architecture; Generation of computers; Operating system- Overview; GUI and CLI; Windows; Unix; Linux (Red Hat/Ubuntu).

Unit - II

Introduction to bioinformatics and Omics science; Biological databases – primary, secondary; Sequence and structural; Protein and Gene Information Resources – PIR, SWISSPROT, PDB, GenBank, DDBJ. Specialized bioinformatics resources.

Unit - III

Measures of central tendency and dispersal; probability distributions (Binomial, Poisson and normal); Sampling distribution; Difference between parametric and non-parametric statistics; Confidence Interval; Errors.

Unit - IV

Levels of significance; Regression and Correlation; t-test; Analysis of variance; X2 test; Basic introduction to Multivariate statistics, etc.

References:

1. Mount, D. W. (2004). Sequence and genome analysis. Bioinformatics: Cold Spring Harbour Laboratory Press: Cold Spring Harbour, 2.
2. Selzer, P. M., Marhöfer, R. J., & Rohwer, A. (2008). Applied bioinformatics. An introduction–Springer, Verlag, Berlin, Heidelberg, Germany, 260.
3. Rastogi S. C. (2014) Bioinformatics: Methods and Applications - Genomics, Proteomics and Drug Discovery: PHI Learning.
4. Jones, N. C., Pevzner, P. A., & Pevzner, P. (2004). An introduction to bioinformatics algorithms. MIT press.
5. Miller, W. (2006). An Introduction to Bioinformatics Algorithms.Biostatistics: A foundation for analysis in the health sciences (2004) by Wayne W. Daniel (John Wiley).
6. Introductory statistics (2006) by Prem S. Mann (John Wiley)
7. Biostatistics (1996) P.N. Arora, P.K. Malhotra, Himalaya Publishing House, Mumbai.
8. Introduction to Biostatistics (1972) Sokal & Rohit – Toppan Co. Japan
9. Rastogi V.B (2009) Fundamentals of Biostatistics. ANE Books Publishers
10. Pagano M and Gauvreau K (2001) Principles of Biostatistics. Duxbury Pr; 2Stu Sol edition.
11. Glantz S. A (2005) Primer of Biostatistics. McGraw-Hill Medical; 6 edition

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Lab course I*	**Course Code**	24BIN201DS05
Hours/Week	8	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Course Objectives:

This course aims to introduce:

1. Basic tools of cell and molecular biology
2. Qunatitative and qualitative techniques in biochemistry
3. Differtn microbiological tools & techniques.

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Course Outcomes:

Students completing this course will be able to:

1. Develop lab etiquettes, observational skills and make discoveries in the laboratory.
2. Prepare samples and standards for analysis.
3. Operate a variety of wet lab instruments from start-up to shut-down to get meaningful results
4. Come to lab prepared to start work and plan to make most of your laboratory experience.

Cell & Molecular Biology

1. Study of permanent slides of mitosis or meiosis (cell cycle)
2. Genomic DNA isolation from blood cell.
3. Isolation and purification of plasmid DNA.
4. Separation and visualization of DNA using gel-electrophoresis.
5. Perform PCR.
6. Perform gradient PCR.
7. Perform restriction digestion.
8. Perform RFLP method by restriction digestion of DNA analysis of digested fragments on agrose gel.

Biochemistry

1. Principle working and application of basic instruments of biochemistry.
2. Biurate assay for the estimation of proteins
3. Folin Lowry's for the estimation of proteins
4. Quanitative estimation of carbohydrates by anthrone method.
5. Quanitative estimation of DNA by diphenyamine reaction.
6. Qualitative analysis of carbohydrates, proteins, lipids.

Microbiology

1. Principle, working and application of basic instrument in microbiology.
2. Prepare nutrient broth & nutrient agar plate & sterilize.
3. Isolate mixed culture from soil sample.
4. Isolate pure culture from mix culture using streak plate method.
5. Enrichment of pure culture from subculture.
6. Perform Gram staining.
7. Perform Capsule staining.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Developing skills in Computers for Biology	**Course Code**	24BIN201SE01
Hours/Week	8	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Course Objectives:

This course aims to introduce:

1. Use of computers for biostatistical analysis
2. Use of MS excel for calculations
4. Various Biological databases
5. Computational tools

Course Outcomes:

Students completing this course will be able to:

1. Access different biological databases for retrieval of information from them and analyze the sequence information using different available computational tools.
2. Analyze the large amount of Statistical data for basic statistical estimation and perform hypothesis testing.

1. Explore different protein and nucleotide sequence databases
2. Swiss-Prot, search sequences for
    a. human MAP kinase inhibitor.
    b. human catalase.
    c. synechocystis cytochrome P450.
    d. coli DNA polymerase.
    e. HIV CCR5 receptor
    f. cholera dehydrogenase.
3. Visit to the web page of NCBI and use advanced search options to find protein sequences for 'human kinase' modified or added in last 30 days in Genbank.
4. Using Enterz. search DNA sequences for mouse fas antigen with annotated exons or introns.
5. Working in Linux (Ubuntu) environment and exploring the bioinformatics freewares.
6. Study MS-excel.
7. Construct cumulative frequency distribution table and plot diff. graphs.
8. Calculate mean, median and mode using ms-excel and other available online tools.
9. Calculate mean deviation through mean using ms-excel.
10. Calculate standard deviation using ms-excel.
11. Determine Karl Pearson's coff. of correlation using ms-excel.
12. Use one way ANOVA to compare more than two graphs.
13. Calculate normal distribution using statistical calculator.
14. Calculate chi-square using online statistical calculator.
15. Fitting a normal distribution to the data and testing its goodness of fit.

Semester II

V

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Immunology & Genetic Engg	**Course Code**	24BIN202DS01
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Innate and adaptive immune system
2. Antibody diversity
3. Humoral and cell mediated immune responses
4. Different separation methods
5. Protein sequencing methods

Course Outcomes:

Students completing this course will be able to:

1. Outline the innate and adaptive immune system and explain the role of cells and molecules involved in immune system.
2. Explain the genetic and molecular basis of immune reactions.
3. Apply the methods of vaccine development and monoclonal antibody generation.
4. Discuss the basic principle and applications of genetic engineering.
5. Explain the method of cloning and expression of genes in prokaryotic and eukaryotic hosts.

Unit - I

Innate and adaptive immune system Cells and molecules involved in innate and adaptive immunity, antigens, antigenicity and immunogenicity. B and T cell epitopes, structure and function of antibody molecules.

Generation of antibody diversity, monoclonal antibodies, antibody engineering, antigen-antibody interactions, MHC molecules, antigen processing and presentation, activation and differentiation of B and T cells, B and T cell receptors

Unit - II

Humoral and cell mediated immune responses, primary and secondary immune modulation, the complement system, Toll-like receptors, cell-mediated effector functions, inflammation, hypersensitivity and autoimmunity.

Immune response during bacterial (tuberculosis), parasitic (malaria) and viral (HIV) infections, congenital and acquired immunodeficiencies, vaccines.

Unit - III

Isolation and purification of RNA , DNA (genomic and plasmid) and proteins, different separation methods. One and two dimensional gel electrophoresis, Isoelectric focusing. Molecular cloning of DNA or RNA fragments in bacterial and eukaryotic systems. Expression of recombinant proteins using bacterial, animal and plant vectors. Isolation of specific nucleic acid sequences. Generation of genomic and cDNA libraries in plasmid, phage, cosmid, BAC and YAC vectors.

Unit - IV

In vitro mutagenesis and deletion techniques, gene knock out in bacterial and eukaryoticorganisms. Protein sequencing methods, detection of post translation modification of proteins. DNA sequencing methods, strategies for genome sequencing.

Methods for analysis of gene expression at RNA and protein level, large scale expression, such as micro array based techniques, RFLP, RAPD and AFLP techniques.

References:

1. Benjamin E. (1996), Immunology – A short course 3rd Edition, John Wiley, New York
2. Kuby J. (1997), Immunology, 3rd Edition, W.H. Freeman & Co., New York
3. Roitt, I.M. (1997), Essential Immunology, 9th Edition, Oxford Black Well Science, London
4. Tizard I.R. (1995), Immunology – An introduction, 4th Edition, Philadephia Sauders College press.
5. Gene cloning and DNA analysis – An Introduction (2006) 5th edition, T.A. Brown, Blackwell publisher.
6. Essential genes (2006), Benzamin Lewin, Pearson education international.
7. Genome-3 (2007) T.A Brown. Garland science, Taylor & Francis, NewYork.
8. Principles of gene manipulation and Genomics (2006) 7th edition, S.B Primose and R.M Twyman, Blackwell publishing.
9. Molecular Biotechnology-Principles and Applications of Recombinant DNA (2003) 3rd edition, Bernard R Glick and Jack J pasternak. ASM press, Washington.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Computational Biology	**Course Code**	24BIN202DS02
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Algorithms in Computing
2. Combinatorial Pattern Matching
3. Genetic Algorithm
4. Hidden Markov Models
5. Artificial Neural Networks
6. Clustering and Trees

Course Outcomes:

Students completing this course will be able to:

1. Explain various algorithms for computing and analyze the algorithm using different types of notations.
2. Explain the concept of Genetic algorithm, Optimization & its applications in bioinformatics.
3. Explain the concept of machine learning in terms of HMM, ANN, SVM.
4. Describe Clustering techniques and tree construction techniques.

Unit - I

Introduction: Algorithms in Computing; Analyzing algorithms-Asymptotic notation, Standardnotations, Big 'O' notations; Algorithm design techniques.
Exhaustive Search- Restriction Mapping, Finding Motifs;
Greedy Algorithms- Genome Rearrangements, Sorting by Reversals, Finding Motifs.
Divide-and-Conquer Algorithms- Divide-and-Conquer Approach to Sorting, Space-EfficientSequence Alignment, Block Alignment;

Unit - II

Combinatorial Pattern Matching- Hash Tables, Repeat Finding, Exact Pattern Matching;Expectation and Maximation (EM) with forward and backward algorithms, discriminative learning.
Genetic Algorithm: Basic Concepts, Reproduction, Cross over, Mutation, Fitness Value,Optimization using GAs; Applications in bioinformatics

Unit - III

Hidden Markov Models: Markov processes and Markov Models, Hidden Markov Models,Parameter estimation for HMMs, Optimal model construction, Applications of HMMs **Artificial Neural Networks**: Historic evolution – Perceptron, NN Architecture, supervisedand unsupervised learning, Back Propagation Algorithm, Training and Testing, Self-organizing Feature Map and Radial Basis Function Network; Overview of Support Vector Machines, Bayesian network

Unit - IV

Clustering and Trees: Hierarchical Clustering, k-Means Clustering, Evolutionary Trees,Distance-Based Tree Reconstruction, Reconstructing Trees from Additive Matrices, CharacterBased Tree Reconstruction, Small and large Parsimony Problem.

References:

1. Pachter, L., & Sturmfels, B. (Eds.). (2005). Algebraic statistics for computational biology (Vol. 13). Cambridge university press.
2. Waterman, M. S. (1995). *Introduction to computational biology: maps, sequences and genomes*. CRC Press.
3. TL, W. J. (Ed.). (2003). *Computational biology and genome informatics*. World Scientific.
4. Aluru, S. (Ed.). (2005). *Handbook of computational molecular biology*. CRC Press.
5. Jin, Y., & Wang, L. (Eds.). (2008). *Fuzzy systems in bioinformatics and computational biology* (Vol. 242). Springer.
6. Fenyö, D. (Ed.). (2010). *Computational biology*. Humana Press.
7. Arabnia, H. R. (Ed.). (2010). *Advances in computational biology* (Vol. 680). Springer Science & Business Media.
8. Haubold, B., & Wiehe, T. (2006). *Introduction to computational biology: an evolutionary approach*. Springer Science & Business Media.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Advanced Bioinformatics	**Course Code**	24BIN202DS03
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Note: examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:
DNA sequence analysis
Pharmacogenomics
Analysis packages

Course Outcomes:

Students completing this course will be able to:

1. Access and explain the tools and techniques of analyzing DNA and protein sequences.
2. Perform Secondary database searching.
3. Discuss the basic principles and applications of pharmacogenomics.
4. Utilize the different analysis packages available for different computational jobs.

Unit - I

DNA sequence analysis: Pair wise alignment techniques, Global and local alignments; Algorithms; Scoring Matrices, Gap penalties and Statistical significance. tools of sequence alignment: FASTA; BLAST and its variations; Multiple sequence alignment; Tools – CLUSTAL; MUSCLE; T-Coffee.

Unit – II

Protein sequence analysis: BLAST-P; PROSITE; Pfam; CATH; SCOP
Secondary database searching, building search protocol.

Computer aided drug design – Basic principles, protein modeling and design.

Unit - III

Pharmacogenomics: Introduction, applications, Genome for medicine, current and future perspectives.

Metagenomics: Introduction; concepts; Applications in clinical research; environmental research; etc.

Phylogenomics: Basic principle and applications.

Unit - IV

Analysis packages – Commercial databases and packages, GPL software for Bioinformatics, web-based analysis tools. System modeling and metabolomics – concepts and principles.

References:

1. Mount, D. W. (2004). Sequence and genome analysis. Bioinformatics: Cold Spring Harbour Laboratory Press: Cold Spring Harbour, 2.
2. Selzer, P. M., Marhöfer, R. J., & Rohwer, A. (2008). Applied bioinformatics. An introduction–Springer, Verlag, Berlin, Heidelberg, Germany, 260.
3. Rastogi S. C. (2014) Bioinformatics: Methods and Applications - Genomics, Proteomics and Drug Discovery: PHI Learning.
4. Jones, N. C., Pevzner, P. A., & Pevzner, P. (2004). An introduction to bioinformatics algorithms. MIT press.
5. Miller, W. (2006). An Introduction to Bioinformatics Algorithms.Biostatistics: A foundation for analysis in the health sciences (2004) by Wayne W. Daniel (John Wiley).
6. Priti Sinha, Pradeep Sinha (2003) Computer Fundamentals (With CD) 6th Edition 6th Edition, BPB Publications

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Genomics & Proteomics	**Course Code**	24BIN202DS04
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Introduction to the concept of Genome
2. Comparative genomics
3. Epigenetics
4. Proteomics
5. Metabolomics

Course Outcomes:

Students completing this course will be able to:

1. Explain the concept of genomes, genomics and their networks (in context to HGP).
2. Discuss about comparative genomics, epigenome and epigenetics.
3. Apply learnt proteomics technique for structure prediction and drug discovery process.
4. Define the concept of metabolomics and access the various metabolic pathway databases.

Unit - I

Genomics: Introduction to the concept of genome, gene networks: basic concepts,Prediction of genes, promoters, splice sites, regulatory regions: basic principles, application of methods genome projects. Human Genome Project. Large scale genome sequencing strategies, Genome assembly and annotation. Genome databases of Plants, animals and pathogens, Metagenomics: Concept and applications.

Unit - II

Comparative genomics: Basic concepts and applications, whole genome alignments:understanding the significance; Artemis, BLAST2, MegaBlast algorithms, PipMaker, AVID, Vista, MUMmer, applications of suffix tree in comparative genomics, synteny and gene order comparisons Comparative genomics databases: COG, VOG.

Epigenetics: DNA microarray: database and basic tools, Gene Expression Omnibus (GEO),ArrayExpress, SAGE databases: understanding of microarray data, normalizing microarray data, detecting differential gene expression, correlation of gene expression data to biological process and computational analysis tools (especially clustering approaches).

Unit - III

Proteomics: Concept of proteome, protein array, Methods of protein analysis: PAGE (Native,SDS), Mass Spectrometry, X-ray crystallography, nuclear magnetic resonance (NMR), Deriving function from sequence, Proteomics in drug discovery and toxicology.

Unit - IV

Metabolomics: Introduction to metabolomics, technology in metabolomics, structure andevolution of biological networks, Importance of metabolic engineering, Metabolic pathway databases (EcoCyc, MetaCyc, LIGAND, ENZYME, BRENDA, KEGG).

References:

1. Selzer, P. M., Marhöfer, R. J., & Rohwer, A. (2008). Applied bioinformatics. An introduction–Springer, Verlag, Berlin, Heidelberg, Germany, 260.
2. Mount, D. W. (2004). Sequence and genome analysis. Bioinformatics: Cold Spring Harbour Laboratory Press: Cold Spring Harbour, 2.
3. Jones, N. C., Pevzner, P. A., & Pevzner, P. (2004). An introduction to bioinformatics algorithms. MIT press
4. Pennington, S. R., & Dunn, M. J. (2001). Proteomics: from protein sequence to function. Garland Science.
5. Marko-Varga, G. (Ed.). (2014). Genomics and Proteomics for Clinical Discovery and Development (Vol. 6). Springer.
6. Akay, M. (Ed.). (2006). Genomics and proteomics engineering in medicine and biology (Vol. 24). John Wiley & Sons.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Lab course II*	**Course Code**	24BIN202DS05
Hours/Week	8	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Course Objectives:

This course aims to introduce:

1. Computational tools to analyze the protein, RNA or DNA sequences.
2. Computational tools to perform MSA
3. Gene Predictions
4. 3D structure visualization tools of proteins

Course Outcomes:

Students completing this course will be able to:

1. Use computational methods to help execute a biological research plan.
2. Perform computational analyses of biological datasets and relate the results to core principles in biology.
3. Access different structure visualization tools to analyze the pdb files in detail.
4. Explore the data in various interaction databases.

Immunology & Genetic Engg.

1. To ampilfy the given sample of DNA.
2. To separate DNA using agarose gel electrophosis.
3. To perform Gradient PCR to estimate annealing temperature
4. To perform RFLP/AFLP of given DNA sample.
3. To learn technique of radial immuno diffusion.
4. To learn the technique of ouchterlony double diffusion.
5. To learn the technique of immuno electrophorosis.
6. To learn the technique of ELISA.

Computational Biology

1. Exploit the available online and standalone tools based on HMM and ANN to analyze the protein, RNA or DNA sequences.
   Generating multiple sequence alignment using clustal OMEGA.
2. Development of Phylogenetic trees using MEGA.
3. Development of Phylogenetic trees using Phylip.
4. Clustering of sequences at different levels of identity.
5. Gene Predictions in prokaryotes and eukaryotes using different tools.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Developing skills in –omics biology	**Course Code**	24BIN202SE01
Hours/Week	8	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Course Objectives:

This course aims to introduce:

1. Computational tools to analyze the protein, RNA or DNA sequences.
2. Computational tools to perform MSA
3. Gene Predictions
4. 3D structure visualization tools of proteins

Course Outcomes:

Students completing this course will be able to:

1. Use computational methods to help execute a biological research plan.
2. Perform computational analyses of biological datasets and relate the results to core principles in biology.
3. Access different structure visualization tools to analyze the pdb files in detail.
4. Explore the data in various interaction databases.

1. To study BLAST and its different variants.
2. Solve queries related to FASTA and BLAST.
   a. Download sequence with accession no = NP-013658 from NCBI and perform BLAST
   b. change E value to 0.01 and change word size from 3-2 and show change word.
   c. reset E value to 10 and substitution matrix from BIOSUM 62 -BLOSUM 45 and show how result differ.
   d. reset the substitution matrix to 62, run same search with or without low complexity filter ON and show how result differ.
3. Perform MSA by using different tools
   a. Clustal omega.
   b. T-coffee
   c. M view
   d. MUSCLE
   e. MAFFT
   f. kalign
4. Retrieve structure of proteins from PDB and visualize the structure in RASMOL or any other visualization tool.
5. Genome annotation using Blast2GO
6. Functional annotation using tools, such as InterProScan
7. Gene annotation using Gene Ontology (GO) mapping

Semester III

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Molecular Modelling & Drug Designing	**Course Code**	25BIN203DS01
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:
1. Molecular Mechanics
2. Potential Energy Surface
3. Molecular Dynamics Simulation
4. Drug design
5. Structure Activity Relationship

Course Outcomes:

Students completing this course will be able to:
1. Explain the basic principles of molecular mechanics.
2. Describe the concept of QSAR methods and their applications in drug design.
3. Discuss the basic concepts and methods of molecular dynamic simulations.
4. Explain and perform molecular docking and virtual screening.

Unit - I

Molecular Mechanics: Introduction, The Morse Potential, The Harmonic Oscillator Model for Molecules, Two atoms connected by a bond, Poly atomic Molecules, Energy due to Stretch, Bend, Stretch-Bend, Torsional strain, van der Waals and Dipole-Diploe interactions. Types of Potentials: Lennard-Jones, Truncated Lennard-jones, Exponential-6, Ionic and Polar potentials. Types of Force Fields: AMBER, CHARMM, Merck Molecular Force Field, Consistent Force Field, MM2, MM3 and MM4 force fields.

Unit - II

Potential Energy Surface: Convergence Criteria, Characterizing Stationary Points, Search forTransition States. Optimization: multivariable Optimization Algorithms, level Sets, Level Curves, Gradients, Optimization Criteria, Unidirectional Search, Finding Minimum Point, Gradient based Methods-Steepest Descent and Conjugate Gradient Methods

Molecular Dynamics Simulation: Introduction, Radial distribution functions, Pair Correlation function, Newtonian dynamics, Integrators- Leapfrog and Verlet algorithm, Potential truncation and shifted-force potentials, Implicit and explicit Solvation models, Periodic boundary conditions, Temperature and pressure control in molecular dynamics simulations.

Unit - III

Drug design: Drug discovery process. Target identification and validation, lead optimization andvalidation. Methods and Tools in Computer-aided molecular Design, Analog Based drug design: Pharmacophores (3D database searching, conformation searches, deriving and using 3D Pharmacophore) and QSAR. Structure based drug design: Docking, *De Novo* Drug Design (Fragment Placements, Connection Methods, Sequential Grow), Virtual screening.

Unit - IV

Structure Activity Relationship: Introduction to QSAR, QSPR, Various Descriptors used in QSARs:Electronics; Topology; Quantum Chemical based Descriptors. Regression Analysis, The Significance and Validity of QSAR Regression Equations, Partial Least Squares (PLS) Analysis, Multi Linear Regression Analysis.

References:

1. Leach, A. R., & Gillet, V. J. (2007). An introduction to chemoinformatics. Springer.
2. Mannhold, R., Kubinyi, H., & Folkers, G. (2005). Chemoinformatics in drug discovery (Vol. 23). T. I. Oprea (Ed.). Weinheim:: Wiley-VCH.
3. Varnek, A., & Tropsha, A. (Eds.). (2008). Chemoinformatics approaches to virtual screening. Royal Society of Chemistry.
4. Mannhold, R., Kubinyi, H., & Folkers, G. (2006). Chemoinformatics in drug discovery (Vol. 23). John Wiley & Sons.
5. Vinter, J. G., & Gardner, M. (Eds.). (1994). Molecular modelling and drug design. Macmillan International Higher Education.
6. Solomon, K. A. (2019). Molecular modelling and drug design. MJP Publisher.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Datamining & Machine Learning	**Course Code**	25BIN203DS02
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Database Models
2. Datamining concepts
3. Machine learning concepts.
4. Classification and Prediction
5. Clustering Methods

Course Outcomes:

Students completing this course will be able to:

1. Classify datamining systems
2. Explain major issues in data mining.
3. Describe concept of association rule mining and single dimensional boolean association rules.
4. Explain supervised learning concepts.
5. Explain unsupervised learning concepts

Unit - I

Introduction to Data Mining: Relational Databases, Data Warehouses, Transactional Databases, Advance Database Systems and Applications, Data Mining Functionalities, Classification of Data Mining Systems, Major issues in Data Mining.

Primitives and System Architectures: Data Mining Primitives, Data Mining Query Language, Designing Graphical User, Interfaces Based on a Data Mining Query Language, Architectures of Data Mining Systems.

Unit - II

Concept Description and Association Rules: Concept Description, Characterization and comparison, Data Generalization and Summarization-Based Characterization, Analytical Characterization, Mining Class Comparisons, Mining Association Rules in Large Databases, Association Rule Mining, Mining Single Dimensional Boolean Association Rules from Transactional Databases.

Unit - III

Introduction to Machine Learning Methods: supervised learning, Unsupervised learning, Semi-supervised learning, Reinforcement learning; Batch learning, Online learning; Instance based learning: Model based learning

Unit - IV

Supervised Learning: Classification and Regression, Generalization, Overfitting, and Underfitting Supervised Machine Learning Algorithms: k-Nearest Neighbours, Decision Trees, Kernelized Support Vector Machines, Neural Networks

Unsupervised Learning: K means clustering, Hierarchical clustering, Density based clustering

References:

1. Silberschatz, A., Korth, H. F., & Sudarshan, S. (1997). Database system concepts (Vol. 5). New York: McGraw-Hill.
2. Codd, E. F. (1990). The relational model for database management: version 2. Addison-Wesley Longman Publishing Co., Inc.
3. Dean, J. (2014). Big data, data mining, and machine learning: value creation for business leaders and practitioners. John Wiley & Sons.
4. Hsu, H. H. (Ed.). (2006). Advanced data mining technologies in bioinformatics. IGI Global.
5. Wang, J. T., Zaki, M. J., Toivonen, H. T., & Shasha, D. (2005). Introduction to data mining in bioinformatics. In Data Mining in Bioinformatics (pp. 3-8). Springer, London.
6. Yang, Z. R. (2010). Machine learning approaches to bioinformatics (Vol. 4). World scientific.
7. Zhang, Y. Q., & Rajapakse, J. C. (Eds.). (2009). Machine learning in bioinformatics (Vol. 4, p. 0470397411). New York: Wiley.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Programming in C	**Course Code**	25BIN203DS03
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Programming logic
2. Structured programming concepts
3. Data structures
4. Macro programming in C
5. File and exception handling in C.

Course Outcomes:

Students completing this course will be able to:

1. Develop algorithms and problem solving techniques.
2. Compile C programs and execute them.
3. Discuss the concept of structured programming.
4. Explain the concept of file handling and exception handling in C.

Unit - I

Programming logic: Algorithm development, Techniques or problem solving, Flow-charting, Step-wise refinement, Algorithms for searching, sorting (exchange and insertion), merging of ordered lists, Programming.

Unit - II

Arithmetic Expressions, Assignment statement, Logical expression, Sequencing, Alteration and iteration; ring processing; Sub programs, Recursion, Files and pointers; Structured programming concepts; Top down Design, Development of efficient program; program correctness; Debugging and testing of programs

Unit - III

Programming in C: Data structures - Representation of integers, characters, real Data types: constants and variables; Pointers, pointers to functions.

Unit - IV

Macro programming in C: Graphs, data structure - linked list, stack, queue, binary trees, and threaded binary trees.

File and exception handling in C.

References:

1. Kelley, A., & Pohl, I. (1994). *A book on C; Programming in C.* Benjamin-Cummings Publishing Co., Inc..
2. Kernighan, B. W., & Ritchie, D. M. (2006). *The C programming language.*
3. Ritchie, D. M., Kernighan, B. W., & Lesk, M. E. (1988). The C programming language. Englewood Cliffs: Prentice Hall.
4. Kanetkar, Y. P. (2016). Let us C. BPB publications.
5. Kanetkar, Y. P. (2002). Pointers in C.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Programming in PERL, Python and HTML	**Course Code**	25BIN203DS04
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. PERL BASICS
2. ADVANCED PERL AND BIOPERL
3. Python programming language
4. Programming concepts in Python
5. HTML, XML & PHP

Course Outcomes:

Students completing this course will be able to:

1. Perform the programming in PERL language.
2. Solve various biological issues like pattern matching and array handling using PERL with a real-world example.
3. Perform programming in Python
4. Execute advance programming in Python
5. Compute the code for web-site creation and compare different hosting languages (HTML, XML)
6. Demonstrate the web-site creation and hosting using languages like PHP.

Unit - I

PERL: Strings, Numbers, and Variables. Variable Interpolation, Basic Input and Output, File handles, Making Decisions, Conditional Blocks, Loops, Combining Loops with Input, Standard Input and Output, Finding the Length of a Sequence File.

Pattern Matching, Extracting Patterns, Arrays, Arrays and Lists, Split and Join, Hashes, A Real-World Example, BioPERL; Applications

Unit - II

PYTHON: History, Features, Setting up path, Working with Python, Basic Syntax, Variable and Data Types, Operator

Conditional Statements: If, If- else, Nested if-else

Looping: For, While, Nested loops

Control Statements: Break, Continue, Pass

String Manipulation: Accessing Strings, Basic Operations, String slices, Function and Methods

Lists, Tuples, Sets, Dictionaries

Unit - III

PYTHON Functions: Defining a function, Calling a function, Types of functions, Function Arguments, Anonymous functions, Global and local variables

Modules: Importing module, Math module, Random module, Packages, Composition

Input-Output: Printing on screen, Reading data from keyboard, Opening and closing file, Reading and writing files, Functions

Exception Handling: Exception, Exception Handling, Except clause, Try ? finally clause, User Defined Exceptions.

scikit-learn; Essential Libraries: NumPy, SciPy, matplotlib, pandas, mglearn

Advanced Python: Regular Expressions, Object Oriented Programming using Databases and SQL

Unit - IV

Creation, hosting and maintenance of web-site using HTML, XML. Creation, hosting and maintenance of web-site using PHP: Introduction, PHP Advanced, Forms, MYSQL database

References:

1. Foy, B. (2007). *Mastering Perl*. O'Reilly Media, Inc..
2. Quigley, E. (2014). Perl by example. Pearson Education.
3. Tiago Antao (2022) Bioinformatics with Python Cookbook, Third Edition. Packt Publishing.
4. Martin Jones (2013) PYTHON FOR BIOLOGISTS: A complete programming course for beginners. http://pythonforbiologists.com/
5. Ohwofosirai, D. (2013). Learn Web Design With Html Examples and Screen Shots: Html Tutorial Guide. Ohwofosirai Desmond.
6. Duckett, J. (2008). Beginning Web programming with HTML, XHTML, and CSS. John Wiley & Sons.
7. Fraley, R. C. (2004). How to conduct behavioral research over the Internet: A beginner's guide to HTML and CGI/Perl. New York, NY: Guilford Press.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Lab course III*	**Course Code**	25BIN203DS05
Hours/Week	8	**Credits**	4
Max. Marks.	100 (External assessment:70; Internal assessment: 30)	**Time**	3 Hours

Course Objectives:

This course aims to introduce:

1. Tools and Techniques of molecular modeling and small molecule designing
2. Tools of molecular docking simulations.
3. Enegry minimization concepts
4. Data Mining of Biological data sets
5. Machine learning concepts

Course Outcomes:

Students completing this course will be able to:

1. Understand concepts of molecular modeling of small molecules and proteins.
2. Perform molecular docking of protein-ligand and protein-protein.
3. Perform different structural analyses of protein structures, including energy minimization.
4. Perform data mining using available softwares.
5. Build classification and regression models using ML techniques.

Molecular Modelling & Drug Designing

1. Generate a 3D-model of a protein using SWISS-MODEL; ROSETTA; ALPHA-FOLD.
2. Evaluate the 3D-model of a given protein for structural stability parameters.
3. Retrieve a pdb file of a protein structure and perform energy minimization using Chimera.
4. Retrieve a compound from pubchem (pdb format) and minimize its structure using Chimera.
5. Perform docking of a given ligand against given protein (using HEX and PATCHDOCK).
6. Alnalysis of docked complex using LIGPLOT.
7. Generate structures of five drugs using Chemsketch.
8. Perform protein protein docking using HEX.
9. Root mean square deviation energy calculation using Chimera.
10. Convert the files from one format to another using Open Babel.

Datamining & Machine Learning

1. Preprocessing of the biological data (Understanding Data, Removing Attributes, Applying filters)
2. Classification of Data using different ML tools (Setting Test Data, selecting classifiers and visualization of results)
3. Building Regression models using different ML tools
4. Clustering of biological data (Building clusters, Examining output and visualizing clusters)
5. Study of Association rules for biological data analysis
6. Feature Selection and feature Extraction.

7. Evaluation(Testing) of developed models/classifiers.
8. Scoring of developed models/classifiers.
9. Implementation of Neural Networks, SVM, Random forest, and other ML methods on biological data set.
10. Exploring freely available online tools for data mining and machine learning.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Developing programming skills	**Course Code**	25BIN203SE01
Hours/Week	8	**Credits**	4
Max. Marks.	100 (External assessment:70; Internal assessment: 30)	**Time**	3 Hours

Course Objectives:

This course aims to introduce:

1. Different programming data structures and syntax in C language
2. Different programming data structures and syntax in PERL.
3. Different programming data structures and syntax in PYTHON
4. Development of web pages using PHP and HTML

Course Outcomes:

Students completing this course will be able to:

1. Read, understand and trace the execution of programs written in C language.
2. Write and execute the C code for a given algorithm.
3. Choose the loops and decision making statements to solve the problem.
4. Create and Execute PERL and PYTHON programs to unravel biological issues
5. Use PHP and HTML to create web pages with advanced interactivity

Programming in C

1. WAP to perform arithmetic operations (Addition, Subtraction, Multiplication, Division) on two numbers.
2. WAP to calculate gross salary of an employee [using formula: gross_sal = basic_sal+hra+da].
3. WAP to calculate area of circle.
4. WAP to evaluate marks of student for 3 subjects, calculate percentage and display their grades. Marks grades CASE -1: 90-100 A CASE -2: 80-89 B CASE -3: 65-79 C CASE -4: Otherwise D
5. WAP to determine sum of odd series from 1 to N.
6. WAP to calculate factorial of a number.
7. WAP to print Fibonacci series up to N. [E.g. - 0 1 1 2 3 5..........]
8. WAP to identify whether given number is prime or not.
9. WAP to identify whether given number is even or odd.
10. WAP to print whether given year is leap year or not.
11. WAP to check whether the 5 digit number is palindrome or not [A palindrome number or numeral palindrome is a number that remains the same when its digits are reversed. Like 16461, for example, it is "symmetrical".].
12. WAP to find the sum of the digits of a number.
13. WAP to input 3 sides of triangle and identify the type of triangle.
14. WAP to input 5 digit numbers and find the sum of the first and last digit.
15. WAP to check whether the number is power of 2 or not.
16. WAP to find out GCD of two numbers.
17. WAP to check whether given number is perfect power of any natural number.
18. WAP to convert Fahrenheit to centigrade.
19. Programs related to arrays, functions, recursion, file handling, pointers etc.

Programming in PERL, HTML

WAP in PERL to-

1. perform arithmetic operations..
2. calculate area/perimeter
3. convert temp f-c.
4. add element in array.
5. delete element from array.
6. length of array.
7. reverse the array.
8. Sort, shift, unshift, pop, push or splice the array.
9. use all command of array in an program.
10. find index no. of last element in array.
11. join elements of array.
12. concatenate two arrays in to one array.
13. concatenate two scalar values.
14. find index no. of string.
15. find index no. of pattern in string.
16. use r-index command.
17. sum of all elements of array.
18. find sum of even no. in array.
19. cut substring from a string.
20. convert DNA to RNA.
21. match pattern in sequence.
22. squeeze space in seqence.
23. use split command.
24. create hash.
25. maintain hash.
26. open a file in read mode.
27. find complementary of a DNA sequence in file.
28. find occurance of ploy T.
29. distance between TATA & GC Box.
30. presence of GTGT at end of sequence.
31. whether sequence in array is in fasta format.
32. print fibonacci series.
33. print table of any no.
34. print odd no. up to 10.
35. print even no. up to 20.
36. **Develop webpages using HTML and PHP**.

Programming in PYTHON

1. Display of Python list in the given order
2. Concatenate two lists index-wise in Python
3. Given a Python list. Turn every item of a list into its square using Python
4. Concatenate two lists in the given order using Python
5. Given a two Python list. Iterate both lists simultaneously such that list1 should display item in original order and list2 in reverse order
6. Remove empty strings from the list of strings
7. Add a given item after an item in the given Python List
8. Given a Python list, find a value in the list, and if it is present, replace it with another given value. Only update the first occurrence of a value.

Semester IV

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Systems Biology	**Course Code**	25BIN204DS01
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Systems Biology Networks
2. Simulation of pathways
3. Networks and Motifs
4. Signaling & Experimental methods in systems biology
5. Design of Circuits and Databases

Course Outcomes:

Students completing this course will be able to:

1. Discuss and explain the concept of systems biology and biological networks.
2. Explain the principles and levels of simulations of biological pathways upto Whole Cell Simulation and access different pathway databases.
3. Understand the signaling and experimental methods in systems biology.
4. Design and demonstrate the circuits in network biology.

Unit - I

Introduction: Systems Biology Networks- basics of computer networks, Biological uses andIntegration. Micro array – definition, Applications of Micro Arrays in systems biology. Selforganizing maps and Connectivity maps - definition and its uses. Networks and Pathways – Types and methods. Metabolic networks.

Unit - II

Simulation of pathways: Whole cell: Principle and levels of simulation – Virtual Erythrocytes.Pathological analysis. Flux Balance Analysis. Biochemical metabolic pathways, Metabolomics and enzymes. Interconnection of pathways, metabolic regulation. Translating biochemical networks into linear algebra. Cellular models. **Networks and Motifs**: Gene Networks: basic concepts, computational models. Lambda receptor andlac operon as an example. – all types of networks and its uses.

Unit - III

Signaling & Experimental methods in systems biology: slow and auto–regulation The coherent FFL-temporal order, FIFO, DOR, Global, Development, memory and irreversibilitysignaling networks and neuron circuits-robust adapation–any model.

Unit - IV

Design of Circuits and Databases: Introduction- databases KEGG, EMP, MetaCyc, AraCyc etc.,Expression databases and various databases related to systems biology. Optional design of gene circuits I- cost and benefit: gene circuits II- selection of regulation. Stochasticity in gene expression.

References:

1. Kitano, H. (2001). Foundations of systems biology. The MIT Press Cambridge, Massachusetts London, England.
2. Klipp, E., Herwig, R., Kowald, A., Wierling, C., & Lehrach, H. (2005). *Systems*

biology in practice: concepts, implementation and application. John Wiley & Sons.

3. Wilkinson, D. J. (2018). *Stochastic modelling for systems biology*. CRC press.
4. Soyer, O. S. (Ed.). (2012). *Evolutionary systems biology* (Vol. 751). Springer Science & Business Media.
5. Voit, E. (2017). *A first course in systems biology*. Garland Science.
6. Klipp, E., Liebermeister, W., Wierling, C., & Kowald, A. (2016). *Systems biology: a textbook*. John Wiley & Sons.
7. Choi, S. (Ed.). (2007). *Introduction to systems biology*. New Jersey:: Humana press.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Big Data and Cloud Computing	**Course Code**	25BIN204DS02
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA)	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Big Data
2. Big Data analytics
3. Cloud Computing
4. Next generation Cloud Applications in Bioinformatics.

Course Outcomes:

Students completing this course will be able to:

1. Explain the concept of big data and its characteristics.
2. Utilize different methods of big data analytics.
3. Identify the challenges in handling big data.
4. Assess different bioinformatics cloud for big data manipulation.

Unit - I

Big Data: Introduction to big data concept; Characteristics of big data; Big data in bioinformatics; Challenges in big data handling; Challenges of Conventional Systems: Web Data, Evolution Of Analytic Scalability.

Unit - II

Big Data analytics I: Regression Modeling; Multivariate Analysis; Bayesian Modeling; Inference and Bayesian Networks; Support Vector and Kernel Methods; Analysis of Time Series: Linear Systems Analysis; Nonlinear Dynamics; Rule Induction; Neural Networks: Learning And Generalization; Competitive Learning; Principal Component Analysis and Neural Networks; Fuzzy Logic: Extracting Fuzzy Models from Data; Fuzzy Decision Trees; Stochastic Search Methods.

Unit - III

Big Data analytics II: Database Design, Sample Application RDBMS Design, Sample Design, Application Code, Creating Database, Loading Schema, Data Structures, Setting Connections, Population of database, Application Features. Integrating Cassandra with Hadoop - Hadoop, MapReduce, Cassandra Hadoop Source Package, Outputting Data to Cassandra, PIG, HIVE.

Unit - IV

Cloud Computing: Cloud computing definition, private, public and hybrid cloud; Cloud types; IaaS,PaaS, SaaS. Benefits and challenges of cloud computing, public vs private clouds, role of virtualization in enabling the cloud; Benefits and challenges to Cloud architecture. Bioinformatics clouds for big data manipulations. Next generation Cloud Applications in Bioinformatics.

References:

1. Catlett, C., Gentzsch, W., & Grandinetti, L. (Eds.). (2013). *Cloud computing and big data* (Vol. 23). IOS Press.
2. Ma, Z. (Ed.). (2016). *Managing big data in cloud computing environments*. IGI Global.
3. Kannan, R. (Ed.). (2016). *Managing and processing big data in cloud computing.*

IGI Global.

4. Mishra, B. S. P., Das, H., Dehuri, S., & Jagadev, A. K. (Eds.). (2018). *Cloud Computing for Optimization: Foundations, Applications, and Challenges*. Springer International Publishing.
5. Wang, B., Li, R., & Perrizo, W. (Eds.). (2015). *Big data analytics in bioinformatics and healthcare*. Medical Information Science Reference.
6. Lytras, M. D., & Papadopoulou, P. (Eds.). (2017). *Applying big data analytics in bioinformatics and medicine*. IGI Global.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Protein Bioinformatics	**Course Code**	25BIN204DS03
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Methods to study 3D structure
2. Molecular visualization tools
3. Macromolecular interactions
4. Protein sequence analysis
5. Secondary structure prediction methods

Course Outcomes:

Students completing this course will be able to:

1. Apply different methods to study 3 dimensional structure of proteins (X-ray crystallography; NMR; Mass Spectrophotometry)
2. Describe and use different visualization methods and tools for protein 3D structures.
3. Explain the concept and significance of protein-protein interaction (PPI).
4. Discuss the methods of analyzing protein sequence (Compositional, moment analysis, etc)

Unit - I

Methods to study 3D structure: Overview of macromolecular x-ray crystallography, Principles of crystallography, Mass spectrometry, NMR, Co-ordinate systems, Fitting and refinement, Validation, Analysis of 3D structures, Principles of protein folding and methods to study protein folding, Structure of Ribosome.

Unit - II

Molecular visualization tools: Visualization of tertiary structures, quaternary structures,architectures and topologies of proteins and DNA using molecular visualization software such as RasMol, Cn3D, SPDBV, Chime, Mol4D, etc.

Unit - III

Macromolecular interactions: Protein-protein interaction (Two hybrid interaction screening, Immunoprecipitation). Tools for analysis Protein-protein interaction, Protein-protein interactions databases such as STRINGS, DIP, PPI server and tools for analysis of, protein-protein interactions. Nucleic acid-Protein interactions – Concept of epigenomics, nuclear receptors, orphan nuclear receptors.

Unit - IV

Protein sequence analysis: Compositional analysis; Hydrophobicity profiles; Amphiphilicity detection; Moment analysis; Transmembrane prediction methods; Secondary structure prediction methods

References:

1. Eidhammer, I., Jonassen, I., & Taylor, W. R. (2004). Protein Bioinformatics: An algorithmic approach to sequence and structure analysis (Vol. 1). Chichester: Wiley.
2. Lesk, A. M. (2001). Introduction to protein architecture: the structural biology of proteins. Oxford: Oxford University Press.

3. Gromiha, M. M. (2010). Protein bioinformatics: from sequence to function. academic press.
4. Jones, N. C., Pevzner, P. A., & Pevzner, P. (2004). An introduction to bioinformatics algorithms. MIT press.
5. Fu, H. (Ed.). (2004). Protein-protein interactions: methods and applications (Vol. 261). Springer Science & Business Media.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Principles of phylogenomics	**Course Code**	25BIN204DS04
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Concepts in Molecular Evolution
2. Phylogenetic trees and their comparison
3. Probabilistic models of evolution
4. Approaches for tree reconstruction
5. Applications of phylogeny analyses

Course Outcomes:

Students completing this course will be able to:

1. Explain the concept of molecular evolution and phylogenomics.
2. Perform and evaluate different methods of constructing phylogenetic tree.
3. Demonstrate the evaluation methods for reliability of phylogenetic tree and tree reconstruction approaches.
4. Apply comparative methods for detection of new species or organism.

Unit - I

Concepts in Molecular Evolution; Nature of data used in Taxonomy and Phylogeny: Morphological and molecular character data.

Phylogenetic trees and their comparison: Definition and description, various types of trees; Consensus (strict, semi-strict, Adams, majority rule, Nelson). Data partitioning and combination. Tree to tree distances, similarity

Unit - II

Probabilistic models and associated algorithms o Probabilistic models of evolution, Maximum likelihood algorithm; Phylogenetic analysis algorithms; Maximum Parsimony; Distance-based: UPGMA, Transformed Distance, Neighbors-Relation, Neighbor-Joining.

Unit - III

Approaches for tree reconstruction o Character optimization; delayed and accelerated transformation. o Reliability of trees. Bootstrap, jackknife, decay, randomization tests.

Unit - IV

Applications of phylogeny analyses o Comparison of Phylogenetic Trees obtained using DNA seq. Vs. protein seq. Vs. Full genomes. Need for addition of other properties towards total phylogenetic analysis.

Comparative methods for detection of species / organism relationships o Gene duplication, Horizontal transfer, Domain evolution.

References:

1. Jennings, W. B. (2016). *Phylogenomic data acquisition: principles and practice.* CRC Press.
2. DeSalle, R., Tessler, M., & Rosenfeld, J. (2020). *Phylogenomics: a primer.* CRC Press.

3. Selzer, P. M., Marhöfer, R. J., & Rohwer, A. (2008). Applied bioinformatics. An introduction–Springer, Verlag, Berlin, Heidelberg, Germany, 260.
4. Mount, D. W. (2004). Sequence and genome analysis. Bioinformatics: Cold Spring Harbour Laboratory Press: Cold Spring Harbour, 2.
5. Jones, N. C., Pevzner, P. A., & Pevzner, P. (2004). An introduction to bioinformatics algorithms. MIT press

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Communication Skills in Science & Technology	**Course Code**	25BIN204DS05
Hours/Week	4	**Credits**	4
Max. Marks.	100 (70 EA+30 IA	**Time**	3 Hours

Note: The examiner has to set a total of nine questions (two from each unit and one compulsory question consisting of short answer from all units. The candidate has to attempt one question each from each unit along the compulsory question (5 x 14 = 70 marks)

Course Objectives:

This course aims to introduce:

1. Basics of Technical Communication
2. Oral/visual Communication
3. Reports
4. Writing Journal Articles
5. Technical Proposal and Thesis Writing Methodology

Course Outcomes:

Students completing this course will be able to:

1. Explain the basic concepts of technical communication.
2. Use different types of oral and visual communications technique.
3. Compare the methods of informal and formal report writing in technical communications.
4. Utilize the learnt methods and rules of technical proposal and thesis writing.

Unit - I

Basics of Technical Communication: Introduction and Structure of Communication, TheProcess of Communication, Language as a Tool of Communication, Levels of communication, The Flow of Communication, Communication Networks, The Importance of Technical Communication.

Unit - II

Oral/visual Communication: Active Listening, Speech Structure, The Art of Delivery,Effective Presentation Strategies, Use of audio visual Aids, ICTs, Handling the Audience, Body Language, Conducting Meetings, Interviews, Group Discussion, Negotiation, Small Talk.

Unit - III

Reports: Informal and Formal: Characteristics of a Report, Types of Reports, The Importanceof Reports, Formats, Prewriting, Structure of Reports, Writing the Report, Revising, Editing and Proofreading.

Writing Journal Articles: Word choice and Syntax style, Number use, References, Plagiarism.

Unit - IV

Technical Proposal and Thesis Writing Methodology

References:

1. Ziman, J. M. (1987). *An introduction to science studies: The philosophical and social aspects of science and technology*. Cambridge University Press.
2. Lloyd, M., & Bor, R. (2009). *Communication skills for medicine E-book*. Elsevier Health Sciences.
3. Engeström, Y., & Middleton, D. (Eds.). (1998). *Cognition and communication at work*. Cambridge University Press.

4. Spektor-Levy, O., Eylon, B. S., & Scherz, Z. (2009). Teaching scientific communication skills in science studies: Does it make a difference?. *International journal of science and mathematics education*, *7*(5), 875-903.
5. Ammon, U. (Ed.). (2011). *The dominance of English as a language of science: Effects on other languages and language communities* (Vol. 84). Walter de Gruyter.
6. Tarango, J., & Machin-Mastromatteo, J. D. (2017). *The Role of Information Professionals in the Knowledge Economy: Skills, Profile and a Model for Supporting Scientific Production and Communication*. Chandos Publishing.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Internship	**Course Code**	25BIN204IN01
Hours/Week	8	**Credits**	4
Max. Marks.	100 (External assessment:70; Internal assessment: 30)	**Time**	3 Hours

Course Objectives:

This course aims to introduce:

11. Skills of applying theoretical knowedge into practical terms.
12. Learn the social application of Bioinformatics tools & techniques
13. Learn the commercial application of Bioinformatics tools & techniques

Course Outcomes:

Students completing this course will be able to:

1. Correlate the tools and techniques learnt during classroom teaching and their applications in context to society.
2. Identify the commercial applications of Bioinformatics tools & techniques
3. Understand the working environment of industry/commercial entitiy/research organization.

- Internships will require 120 hours (1 credit: 30 hrs of engagement) of involvement working with local industry, government or private organizations, business organizations and similar entities during summers.
- Intrnal evaluation will be done by the organization where Internship will be carried out.
- External evaluation will be based on Report writing; presentation and viva-voce carried out jointly by an Internal and an External examiner.

Name of the Program	M.Sc. Bioinformatics	**Program Code**	BINF2
Name of the Course	Dissertation	**Course Code**	25BIN204PD01
Hours/Week	40	**Credits**	20
Max. Marks.	500 (External assessment:350; Internal assessment: 150)	**Time**	3 Hours

Course Objectives:

This course aims to introduce:

1. Skills of applying theoretical knowedge into practical terms.
2. Concept of minor research project, prepare synopsis
3. Concept of executing a minor research project according to psynopsis, anlyse the results and present outcome.

Course Outcomes:

Students completing this course will be able to:

1. Correlate the tools and techniques learnt during classroom teaching and their applications in context to practical applications.
2. Perform text mining and prepapre synopsis.
3. Carry out a small project and anlyse the findings and present the outcome.

- Dissertation is a long piece of academic writing based on original research.
- Dissertation will require 40 hours/week (1 credit: 30 hrs of engagement) of involvement working with *in-house* research laboratories, under a recognized research supervisor.
- Intrnal evaluation will be done by the research supervisor of concerned student.
- External evaluation will be based on Dissertation writing; presentation and viva-voce carried out jointly by an Internal and an External examiner.