CENTRE FOR BIOINFORMATICS
M. D. UNIVERSITY, ROHTAK

CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Credit Matrix for M.Sc. - Bioinformatics Program

SEMESTER	CORE COURSES (C)	Discipline Specific COURSES (D)	OPEN ELECTIVE COURSES (E)	FUNDAMENTAL COURSE (F)	DISSERTATION (C)	TOTAL
I	28	-	-	-	-	28
II	20	4	3	2	-	29
III	12	12	3	-	-	27
IV	8	-	-	-	20	28
TOTAL	68	16	6	2	20	112

SCHEME OF EXAMINATION – M.Sc. (Bioinformatics)

General information:

Note 1 : The Criteria for award of **internal assessment** of 20% marks shall be as under:

A) One class test	:	10 marks.
B) Assignment & Presentation	:	5 marks
C) Attendance	:	5 marks
Less than 65%	:	0 marks
Upto 70%	:	2 marks
Upto 75%	:	3 marks
Upto 80%	:	4 marks
Above 80%	:	5 marks

Note 2: Core: these are core courses in every semester and the students have tocompulsorily study these courses to complete the requirement of the program.

Discipline Specific: This course has to be chosen by the student from the given program electivepapers of the respective semester and the lab course –during 2nd and 3rd semester.

The syllabus of each hard core and soft core paper will be divided into **four** units of **two** questions each. In all 9 questions are to be set. Question number 1 is compulsory and to be set covering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting at least one from each unit.

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Note 3 : The syllabus of each fundamental course paper will be divided into **two** units of **two** questions each. In all 5 questions are to be set. Question number 1 is compulsory and to be set covering entire syllabus. 4 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 2 other questions *i.e.*, selecting at least one from each unit.

Note 4 : Open Elective: The students are required to have one open elective paper in 2ndand 3rd Semester of their choice from any other M.Sc. course/Department in the M.D. university Campus.

The syllabus of each open elective paper will be divided into three units of **two** questions each. In all 7 questions are to be set. Question number 1 is compulsory and to be set covering entire syllabus. 6 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting at least one from each unit.

Note 5: The minimum pass marks for passing the examination shall be as under:

i. 40% in each theory paper including internal assessment.
ii. 40% in each practical examination/viva-voice including internal assessment.

Note 6: Optional papers can be offered subject to availability of requisite resources/ faculty.

Note 7: In the 4thsemester, the student will carry out dissertation work and the report will has tobe submitted by 30th June. The evaluation of the dissertation will be done by external examiner (approved by VC from the panel approved in PGBOS) and the internal examiner.

Program Specific Outcomes

The student post-graduating from M.Sc. Bioinformatics program will be able to:

PSO1 Bridge the Biologist-Computational Interface Gap of recent scientific researches.
PSO2 Serve the global scientific society with tools and techniques of Bioinformatics.
PSO3 Work as skilled manpower in the field of Bioinformatics and IT as a whole and Computer Aided Drug Design, in particular.
PSO4 Become an entrepreneur in the most recent and demanding sector of Bioinformatics.
PSO5 Become a part of Mission-skill India by disseminating the knowledge of Bioinformatics to next generation.

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SCHEME OF EXAMINATION – M.Sc. (Bioinformatics)

S.No.	Course Code	Nomenclature of course	Credit			Total credit	Hours	Maximum marks
			L	T	P			
1st Semester								
1	16BIN21C1	Cell & Molecular Biology	**4**	**0**	**0**	4	4	80+20
2	16BIN21C2	Biochemistry	**4**	**0**	**0**	4	4	80+20
3	16BIN21C3	Microbiology and Genetics	**4**	**0**	**0**	4	4	80+20
4	16BIN21C4	Basic Bioinformatics	**4**	**0**	**0**	4	4	80+20
5	16BIN21C5	Biostatistics & Mathematics	**4**	**0**	**0**	4	4	80+20
6	16BIN21CL1	Lab course I*	**0**	**0**	**4**	4	8	100
7	16BIN21CL2	Lab course II*	**0**	**0**	**4**	4	8	100
		Total	**20**	**0**	**8**	**28**	**36**	

* Lab course I pertains to 16BIN21C1and 16BIN21C2; Lab course II pertains to 16BIN21C3, 16BIN21C4 and16BIN21C5.

S.No.	Course Code	Nomenclature of course	Credit			Total credit	Hours	Maximum marks
			L	T	P			
2nd Semester								
8	16BIN22C1	Immunology & Genetic Engg.	**4**	**0**	**0**	4	4	80+20
9	16BIN22C2	Programming in C	**4**	**0**	**0**	4	4	80+20
10	16BIN22C3	Computational Biology	**4**	**0**	**0**	4	4	80+20
11	16BIN22D1 or 16BIN22D2	Genomics & Proteomics[#] Or Protein Bioinformatics[#]	**4**	**0**	**0**	4	4	80+20
12		OPEN ELECTVE[!]	**3**	**0**	**0**	3	3	80+20
13		Fundamentals of computer and networking or a paper to be chosen from the basket of foundation electives provided by the University	**2**	**0**	**0**	2	2	40+10
14	16BIN22CL1	Lab course III*	**0**	**0**	**4**	4	8	100
15	16BIN22CL2	Lab course IV*	**0**	**0**	**4**	4	8	100
		Total	**21**	**0**	**8**	**29**	**37**	

One course to be opted out of soft core (D) courses.

! Open elective (E): To be chosen from pool of E courses of University. Students of M.Sc. (Bioinformatics) notto opt for 16BIN22E1 (Introduction to Bioinformatics)

* Lab course III pertains to 16BIN22C1 and 16BIN22C2; Lab course IV pertains to 16BIN22C3,16BIN22D1/16BIN22D2

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S.No.	Course Code	Nomenclature of course	Credit			Total credit	Hours	Maximum marks
			L	T	P			
3rd Semester								
16	17BIN23C1	Database Management Systems	**4**	**0**	**0**	4	4	80+20
17	17BIN23C2	Molecular Modelling & Drug Designing	**4**	**0**	**0**	4	4	80+20
18	17BIN23DA1 or 17BIN23DA2	Programming in PERL and HTML[#] Or Systems Biology[#]	**4**	**0**	**0**	4	4	80+20
19	17BIN23DB1 or 17BIN23DB2	Big Data and Cloud Computing[#] or Datamining & Machine Learning[#]	**4**	**0**	**0**	4	4	80+20
20		OPEN ELECTVE[!]	**3**	**0**	**0**	3	3	
21	17BIN23CL	Lab course V*	**0**	**0**	**4**	4	8	100
22	17BIN23DL	Lab course VI*	**0**	**0**	**4**	4	8	100
		Total	**19**	**0**	**8**	**27**	**35**	

Two courses to be opted out of soft core (D) courses.

! Open elective (E): To be chosen from pool of E courses of University.

* Lab course V pertains to 17BIN23C1 and 17BIN23C2

*Lab course VI pertains to 17BIN23DA1/17BIN23DA2/17BIN23DB1/17BIN23DB2.

S.No.	Course Code	Nomenclature of course	Credit			Total credit	Hours	Maximum marks
			L	T	P			
4th Semester								
23	17BIN24C1	Principles of phylogenomics	**2**	**0**	**2**	4	4	80+20
24	17BIN24C2	Communication Skills in Science & Technology	**2**	**0**	**2**	4	4	80+20
25	17BIN24C3	Dissertation	**20**	**0**	**0**	20	40	300
		Total Credits	**24**	**0**	**4**	**28**	**48**	
		Cumulative program credit	**84**	**0**	**28**	**112**	**156**	

SEMESTER-I

CENTRE FOR BIOINFORMATICS
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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Cell & Molecular Biology **Credit: 4 0 0**

Course Code: 16BIN21C1 **MM. Th 80+ IA 20** **Time: 3 Hours**

Students completing this course will be able to:

CO1 Define the basic structure and function of cell membrane and other intracellular organelles.

CO2 Describe the organization of genes and chromosomes in prokaryotes and eukaryotes.

CO3 Describe the cellular process of DNA replication, repair and recombination.

CO4 Explain the control points of gene expression at transcriptional and translational level.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

UNIT I

Membrane structure and function: Structure of model membrane, lipid bilayer andmembrane 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, interruptedgenes, 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 expressionof phages, viruses, prokaryotic and eukaryotic genes, role of chromatin in gene expression and gene silencing.

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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Biochemistry **Credit: 4 0 0**

Course Code: 16BIN21C2 **MM. Th 80+ IA 20** **Time: 3 Hours**

Students completing this course will be able to:

CO1 Define the the basic structure of atoms, molecules and chemical bonds along with the composition, structure and function of biomolecules.
CO2 Describe the basic principles of biophysical chemistry.
CO3 Analyze the energy flow in biological system at cellular level (Glycolysis, oxidative phosphorylation, etc.).
CO4 Explain the process of signal transduction and concepts of metabolic engineering.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

UNIT I

Principles of biophysical chemistry: pH, buffer, reaction kinetics, thermodynamics,colligative properties.

Structure of atoms, molecules and chemical bonds. Composition, structure and function of biomolecules (carbohydrates, lipids, proteins, nucleic acids and vitamins).

UNIT II

Stabilizing interactions: Van der Waals, electrostatic, hydrogen bonding, hydrophobicinteraction, etc.

Bioenergetics: Glycolysis, oxidative phosphorylation, coupled reaction, group transfer,biological energy transducers.

UNIT III

Principles of catalysis: Enzymes and enzyme kinetics, enzyme regulation, mechanism ofenzyme catalysis. Measurement of enzyme activity. Cofactors: their structure and role; ribozymes, isozymes, abzymes.

Conformation of proteins: Ramachandran plot, secondary structure, domains, motif andfolds. Conformation of nucleic acids (helix (A, B, Z), t-RNA, micro-RNA. Stability of proteins and nucleic acids.

UNIT IV

Metabolism: Metabolism of carbohydrates, lipids, amino acids nucleotides and vitamins.Mitochondrial electron transport chain and oxidative phosphorylation. Compartmentation of metabolic pathways.

Signal transduction; Metabolic engineering concepts.

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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Microbiology & Genetics **Credit: 4 0 0**

Course Code: 16BIN21C3 **MM. Th 80+ IA 20** **Time: 3 Hours**

Students completing this course will be able to:

CO1 Explain the history of microbiology and chronological events of microbiology development in 18th and 19th century.
CO2 Outline the phylogeny of prokaryotes.
CO3 Explore different mendelian and non-mendelian inheritance patterns.
CO4 Explain the extra-chromosomal inheritance and identify about structural and numerical chromosomal aberrations.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

UNIT I

Development of microbiology in the 18th and 19th century. Morphology, structure and function of prokaryotic and eukaryotic cell. Archea. 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.

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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Basic Bioinformatics **Credit: 4 0 0**

Course Code: 16BIN21C4 **MM. Th 80+ IA 20** **Time: 3 Hours**

Students completing this course will be able to:

- **CO1** Access the world of Bioinformatics, different types of biological data and databases.
- **CO2** Access and explain the tools and techniques of analyzing DNA and protein sequences.
- **CO3** Discuss the basic principles and applications of pharmacogenomics.
- **CO4** Utilize the different analysis packages available for different computational jobs.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

UNIT I

Introduction: Biological databases – primary, secondary and structural, Protein and GeneInformation Resources – PIR, SWISSPROT, PDB, GenBank, DDBJ. Specialized genomic resources.

UNIT II

DNA sequence analysis: cDNA libraries and EST, EST analysis, pair wise alignmenttechniques, database searching, multiple sequence alignment, tools of sequence alignment. Global and local alignments, matrices, gap penalties and statistical significance.

UNIT-III

Secondary database searching, building search protocol, computer aided drug design – basic principles, protein modeling and design.

Pharmacogenomics: introduction, applications, Genome for medicine, current and futureperspectives.

UNIT-IV

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

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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Biostatistics & Mathematics Credit: 4 0 0

Course Code: 16BIN21C5 MM. Th 80+ IA 20 Time: 3 Hours

Students completing this course will be able to:

CO1 Explain & differentiate between measures of central tendency & measures of dispersion.
CO2 Describe & solve questions based on Normal, Binomial and Possion distributions.
CO3 Utilize the Matrix algebra, Geometric & Arthmetic progression
CO4 Analyze in detail with reference to genetics following techniques & solve questions based on them: X^2 -test, t-test, ANOVA.
CO5 Compute solution of equations by Bisection, Iteration and Newton Raphson method along with numerical differentiation.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

UNIT I

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 II

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

UNIT III

Coordinate geometry with basic concepts of 2D and 3D geometry, Vector algebra – Addition and subtraction of vectors, Dot and cross product, Scalar triple product.

UNIT IV

Matrix algebra: basic definitions, matrix operations, transpose of a matrix, inverse of matrix, eigen values, Boolean algebra. Geometric and Arithmetic Progression.

Solution of equation by bisection method, Iteration method, Newton Raphson method, numerical differentiation.

Course Title: Lab Course I **Credit: 0 0 4**

Course Code: 16BIN21CL1 **MM. 100** **Time: 8 Hours**

Students completing this course will be able to:

CO1 Develop lab etiquettes, observational skills and make discoveries in the laboratory.
CO2 Prepare samples and standards for analysis.
CO3 Operate a variety of wet lab instruments from start-up to shut-down to get meaningful results
CO4 Come to lab prepared to start work and plan to make most of your laboratory experience.

Practical exercises pertaining to 16BIN21C1 and 16BIN21C2.

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, lipds.

Course Title: Lab Course II **Credit: 0 0 4**

Course Code: 16BIN21CL2 **MM. 100** **Time: 8 Hours**

Students completing this course will be able to:

CO1	Identify and demonstrate proper safety procedures concerning laboratory safety.
CO2	Identify the parts and function of the microscope
CO3	Grow and identify the microbial cultures using different growth mediums.
CO4	Access different biological databases for retrieval of information from them and analyze the sequence information using different available computational tools.
CO5	Analyze the large amount of Statistical data for basic statistical estimation and perform hypothesis testing.

Practical exercises pertaining to 16BIN21C3, 16BIN21C4 and 16BIN21C5.

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.

Biostatistics and Mathematics

1. Study ms-excel.
2. Construct cumulative frequency distribution table and plot diff. graphs.
3. Calculate mean, median and mode using ms-excel and other available online tools.
4. Calculate mean deviation through mean using ms-excel .
5. Calculate standard deviation using ms-excel.
6. Determine karl pearson's coff. of correlation using ms-excel.
7. Use one way ANOVA to compare more than two graphs.
8. Calculate normal distribution using statistical calculator.
9. Calculate chi-square using online statistical calculator.
10. Fitting a normal distribution to the data and testing its goodness of fit.

Basic Bioinformatics

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. Go 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. 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 substition matrix to 62, run same search with or without low complexity filter ON and show how result differ.
6. Perform MSA by using different tools
    a. clustal omega.
    b. T-coffee
    c. M view
    D. MUSCLE
    E. MAFFT
    F. kalign
7. Retrieve struture of proteins from PDB and visualize the structure in RASMOL or any other visualization tool.

SEMESTER-II

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Course Title: Immunology & Genetic Engineering Credit: 4 0 0

Course Code: 16BIN22C1 MM. Th 80+ IA 20 Time: 3 Hours

Students completing this course will be able to:

CO1	Outline the innate and adaptive immune system and explain the role of cells and molecules involved in immune system.
CO2	Explain the genetic and molecular basis of immune reactions.
CO3	Apply the methods of vaccine development and monoclonal antibody generation.
CO4	Discuss the basic principle and applications of genetic engineering.
CO5	Explain the method of cloning and expression of genes in prokaryotic and eukaryotic hosts.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

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.

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Course Title: Programming in C **Credit: 4 0 0**

Course Code: 16BIN22C2 MM. Th 80+ IA 20 **Time: 3 Hours**

Students completing this course will be able to:

CO1 Develop algorithms and problem solving techniques.
CO2 Compile C programs and execute them.
CO3 Discuss the concept of structured programming.
CO4 Explain the concept of file handling and exception handling in C.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

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,threaded binary trees.
File and exception handling in C.

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Course Title: Computational Biology **Credit: 4 0 0**

Course Code: 16BIN22C3 **MM. Th 80+ IA 20** **Time: 3 Hours**

Students completing this course will be able to:

CO1 Explain various algorithms for computing and analyze the algorithm using different types of notations.
CO2 Explain the concept of Genetic algorithm, Optimization & its applications in bioinformatics.
CO3 Explain the concept of machine learning in terms of HMM, ANN, SVM.
CO4 Describe Clustering techniques and tree construction techniques.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

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.

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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Genomics & Proteomics **Credit: 4 0 0**

Course Code: 16BIN22D1 MM. Th 80+ IA 20 **Time: 3 Hours**

Students completing this course will be able to:

CO1 Explain the concept of genomes, genomics and their networks (in context to HGP).
CO2 Discuss about comparative genomics, epigenome and epigenetics.
CO3 Apply learnt proteomics technique for structure prediction and drug discovery process.
CO4 Define the concept of metabolomics and access the various metabolic pathway databases.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

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).

CENTRE FOR BIOINFORMATICS
M. D. UNIVERSITY, ROHTAK

CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Protein Bioinformatics **Credit: 4 0 0**

Course Code: 16BIN22D2 MM. Th 80+ IA 20 **Time: 3 Hours**

Students completing this course will be able to:

- **CO1** Apply different methods to study 3 dimensional structure of proteins (X-ray crystallography; NMR; Mass Spectrophotometry)
- **CO2** Describe and use different visualization methods and tools for protein 3D structures.
- **CO3** Explain the concept and significance of protein-protein interaction (PPI).
- **CO4** Discuss the methods of analyzing protein sequence (Compositional, moment analysis, etc)

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

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 interactionscreening, 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; Amphiphilicitydetection; Moment analysis; Transmembrane prediction methods; Secondary structure prediction methods

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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Lab Course III **Credit: 0 0 4**

Course Code: 16BIN22CL1 **MM. 100** **Time: 8 Hours**

Students completing this course will be able to:

CO1 Understand advanced laboratory concepts of Immunology by completing protocols and experiments

CO2 Obtain and interpret experimental immunological data.

CO3 Read, understand and trace the execution of programs written in C language.

CO4 Write and execute the C code for a given algorithm.

CO5 Choose the loops and decision making statements to solve the problem.

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15 or more practical exercises pertaining to 16BIN22C1 and 16BIN22C2.

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.

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.

Course Title: Lab Course IV **Credit: 0 0 4**

Course Code: 16BIN22CL2 **MM. 100** **Time: 8 Hours**

Students completing this course will be able to:

CO1 Use computational methods to help execute a biological research plan.

CO2 Perform computational analyses of biological datasets and relate the results to core principles in biology.

CO3 Access different structure visualization tools to analyze the pdb files in detail.

CO4 Explore the data in various interaction databases.

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15 or more practical exercises pertaining to 16BIN22C3 and 16BIN22D1/16BIN22D2.

Computational Biology

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

Genomics & Proteomics#

1. Predict gene from a given DNA sequence using Genescan.
2. Analyse the pathway involved in tuberculosis using pathway databases.
3. Study process of glycolosis the pathway using Metacyc.
4. Retrieve & classify the enzyme using BRENDA.
5. Predict probable promotor regions a given gene sequence.
6. Compare genome of human and mice using pipmaker and vista.
7. Generate homology models of protein using modeller and swiss-model
9. Visualization of given protein PDB files using SPDB viewer, RasMol, Chimera etc.

Protein Bioinformatics#

1. Study 3D structure of varoius molecules using rasmol or any other structure visualization tool like swiss pdb viewer.
3. Using CHIMERA for interactive visualization and analysis of molecular structures.
4. Use interpro for finding matches against collection of protein signature database.
5. Predict secondary structure of protein using Jpred.
6. Find transmembrane region within in a protein.
7. Generate homology models of protein using modeller and swiss-model

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SEMESTER-III

CENTRE FOR BIOINFORMATICS
M. D. UNIVERSITY, ROHTAK

CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Database Management System Credit: 4 0 0

Course Code: 17BIN23C1 MM. Th 80+ IA 20 Time: 3 Hours

Students completing this course will be able to:

CO1 Discuss, Design and apply different data models.
CO2 Plan the Data security in DBMS.
CO3 Utilize the methods of data updation, curation and retrieval through structured query language (SQL)
CO4 Demonstrate ORACLE programming and its use for DBMS.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

UNIT I

Data Abstraction; Data Models; Instances and Schemes; E-R Model - Entity and entity sets; Relations and relationship sets; E-R diagrams; Reducing E-R Diagrams to tables; Network Data Model: Basic concepts; Hierarchical Data Model: Basic Concepts.

UNIT-II

Multimedia Databases - Basic Concepts and Applications; Indexing and Hashing; Basic concepts (ISAM, B+ Tree indexed files, B Tree indexed files, Static Hash functions, Dynamic Hash functions); Text Databases; Introduction to Distributed Database Processing, Data Security.

UNIT-III

MySQL/MS-Access - Select Statements; Data Definition Statements; Data Manipulation Statements; Data Control Statements; Other Database Objects (Views Sequences, Synonyms); Introduction to Application Development using Visual Basic; Working with Code and Forms; Variables.

UNIT-IV

Procedures and Controlling Program Executor; Standard Controls; Data Access Using Data Control; Connecting to Oracle Database using Visual Basic.

CENTRE FOR BIOINFORMATICS
M. D. UNIVERSITY, ROHTAK

CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Molecular Modeling & Drug Designing **Credit: 4 0 0**

Course Code: 17BIN23C2 **MM. Th 80+ IA 20** **Time: 3 Hours**

Students completing this course will be able to:

CO1 Explain the basic principles of molecular mechanics.
CO2 Describe the concept of QSAR methods and their applications in drug design.
CO3 Discuss the basic concepts and methods of molecular dynamic simulations.
CO4 Explain and perform molecular docking and virtual screening.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

UNIT I

Molecular Mechanics: Introduction, The Morse Potential, The Harmonic Oscillator Model forMolecules, 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 Correlationfunction, 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.

CENTRE FOR BIOINFORMATICS
M. D. UNIVERSITY, ROHTAK

CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Programming in PERL & HTML **Credit: 4 0 0**

Course Code: 17BIN23DA1 **MM. Th 80+ IA 20** **Time: 3 Hours**

Students completing this course will be able to:

CO1 Perform the programming in PERL language.
CO2 Solve various biological issues like pattern matching and array handling using PERL with a real world example.
CO3 Compute the code for web-site creation and compare different hosting languages (HTML, XML, ASP and JSP)
CO4 Demonstrate the web-site creation and hosting using languages like PHP, PERL and CGI.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

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.

UNIT-II

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

UNIT-III

Creation, hosting and maintenance of web-site using HTML, XML, ASP, JSP.

UNIT-IV

Creation, hosting and maintenance of web-site PHP, PERL and CGI.

CENTRE FOR BIOINFORMATICS
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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Systems Biology Credit: 4 0 0

Course Code: 17BIN23DA2 MM. Th 80+ IA 20 Time: 3 Hours

Students completing this course will be able to:

CO1 Discuss and explain the concept of systems biology and biological networks.

CO2 Explain the principles and levels of simulations of biological pathways upto Whole Cell Simulation and access different pathway databases.

CO3 Understand the signaling and experimental methods in systems biology.

CO4 Design and demonstrate the circuits in network biology.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

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.

CENTRE FOR BIOINFORMATICS
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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Big Data and Cloud Computing **Credit: 4 0 0**

Course Code: 17BIN23DB1 **MM. Th 80+ IA 20** **Time: 3 Hours**

Students completing this course will be able to:

CO1 Explain the concept of big data and its characteristics.
CO2 Utilize different methods of big data analytics.
CO3 Identify the challenges in handling big data.
CO4 Assess different bioinformatics cloud for big data manipulation.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

UNIT I

Big Data: Introduction to big data concept; Characteristics of big data; Big data inbioinformatics; 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 andBayesian 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 ApplicationCassandra 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.

CENTRE FOR BIOINFORMATICS
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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Datamining & Machine Learning **Credit: 4 0 0**

Course Code: 17BIN23DB2 **MM. Th 80+ IA 20** **Time: 3 Hours**

Students completing this course will be able to:

- **CO1** Classify datamining systems & explain major issues in data mining.
- **CO2** Describe concept of association rule mining and single dimensional boolean association rules.
- **CO3** Explain concept of classification and prediction with an emphasis on comparison of classification methods.
- **CO4** Explain and compare different clustering methods.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

UNIT I

Introduction: Importance of Data Mining, Relational Databases, Data Warehouses, TransactionalDatabases, 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

Classification and Prediction: Classification and Prediction, Issues: Data preparation for classificationand Prediction, Comparing classification Methods, Classification by Decision Tree Induction: Decision Trees and Decision Tress induction

UNIT IV

Clustering Methods: Clustering Analysis, Types data in clustering analysis: Scaled variable, Binaryvariables, Variables of Mixed Types, Partitioning Methods: K-means and K-Medoids, Model-Based Methods, Data Mining Applications: Data mining for Biomedical and DNA Data Analysis

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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Lab Course V **Credit: 0 0 4**

Course Code: 17BIN23CL **MM. 100** **Time: 8 Hours**

Students completing this course will be able to:

CO1 Model an application's data requirements using conceptual modeling tools like ER diagrams and design database schemas based on the conceptual model.

CO2 Write SQL commands to create, populate, update and query tables in a relational DBMS.

CO3 Well skilled in theoretical and practical aspects of molecular modeling, particularly in Docking studies.

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15 or more Practical exercises pertaining to 17BIN23C1 and 17BIN23C2.

MMDD

1. Retrieve a pdb file of a protein structure and perform energy minimization using chimera and then perform docking.
2. Retrieve a compound from pubchem (pdb format) and minimize its structure using Chimera.
3. Perform docking of valporic acid against voltage gated sodium channel (using HEX and PATCHDOCK).
4. Generate structures of five drugs using Chemsketch.
5. Perform protein protein docking using HEX.
7. Root mean square deviation energy calculation using Chimera.
8. Convert the files from one format to another using open Babel.

DBMS

1. To study Data Definition language Statatements.
2. To study Data Manipulation Statatements.
3. Study of SELECT command with different clauses.
4. Study of SINGLE ROW functions (character, numeric, Data functions).
5. Study of GROUP functions (avg, count, max, min, Sum).
6. Study of various type of SET OPERATORS (Union, Intersect, Minus).
7. Study of various type of Integrity Constraints.
8. Study of Various type of JOINS.
9. To study Views and Indices.

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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Lab Course VI Credit: 0 0 4

Course Code: 17BIN23DL MM. 100 Time: 8 Hours

Students completing this course will be able to:

CO1 Use PHP and HTML to create web pages with advanced interactivity

Or

Explain basic concepts, models, and statistical measures to characterize the properties of general networks, as well as using the software tool Cytoscape to analyze empirical networks.

CO2 Create and Execute PERL programs to unravel biological issues.

Or

Access and retrieve the data from different interaction databases like KEGG, STRINGS etc.

CO3 Develop and deploy cloud application using popular cloud platforms

Or

Develop the classifiers using SVM's or ANN's and evaluate their performances.

CO4 Explain and identify the techniques of big data analysis in cloud

Or

Enlist various algorithms used in information analysis of Data Mining Techniques

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15 ore more Practical exercises pertaining to 17BIN23DA1/ 17BIN23DA2/ 17BIN23DB1/ 17BIN23DB2.

DATA MINING AND MACHINE LEARNING

1. Create ER model and convert it into relational model and export into SQL using ERD plus.
2. Study concept of star schema, dimensional model creating star schema and generating its SQL code.
3. SQL: create, insert, select and all other related commands.
4. Preperation of data sets to perform machine learning using ANN or SVM.
5. Development of classifiers using different machine learning tools.

PERL and HTML

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 seqence.
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.

Development of webpages using HTML and PHP.

Systems Biology

1. Browse & search metabolic pathway databases
2. Understanding of Kyto Encyclopedia of Genes and Genome (KEGG) database for biological pathways, metabolism, cellular process, genetic information processing.
3. Structural and topological properties of biochemical networks
4. Explore Cytoscape network analysis software.

Big Data and Cloud Computing

1. Remote desktop, files sharing, remote file transfer,
2. Bioinformatics experiments on cloud storage
3. Experiments on network traffic management in simulated distributed environments installation and setting up of Hadoop.
4. Exercises on development using Hadoop

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SEMESTER-IV

CENTRE FOR BIOINFORMATICS
M. D. UNIVERSITY, ROHTAK

CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Principles of phylogenomics **Credit: 2 0 2**

Course Code: 17BIN24C1 MM. Th 80+ IA 20 **Time: 3 Hours**

Students completing this course will be able to:

- **CO1** Explain the concept of molecular evolution and phylogenomics.
- **CO2** Perform and evaluate different methods of constructing phylogenetic tree.
- **CO3** Demonstrate the evaluation methods for reliability of phylogenetic tree and tree reconstruction approaches.
- **CO4** Apply comparative methods for detection of new species or organism.

Note: l In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

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.

CENTRE FOR BIOINFORMATICS
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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Communication Skills for Science & Technology Credit: 2 0 2
Course Code: 17BIN24C2 MM. Th 80+ IA 20 Time: 3 Hours

Students completing this course will be able to:

CO1 Explain the basic concepts of technical communication.
CO2 Use different types of oral and visual communications technique.
CO3 Compare the methods of informal and formal report writing in technical communications.
CO4 Utilize the learnt methods and rules of technical proposal and thesis writing.

Note: In all 9 questions are to be set. Question number 1 is compulsory and to be setcovering entire syllabus. 8 Questions will be set with two questions from each unit. Students are required to attempt one compulsory question and 4 other questions *i.e.*, selecting atleast one from each unit.

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

CENTRE FOR BIOINFORMATICS
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CBCS-SCHEME OF EXAMINATION (M.Sc. -Bioinformatics)-2016-17 onwards

Course Title: Dissertation **Credit: 20 0 0**

Course Code: 17BIN24C3 **MM. 300** **Time: 3 Hours**

Students completing this course will be able to:

CO1 Find, analyse, evaluate, select and integrate information using various biological sources to plan his/her own studies, ultimately preparing them to develop research aptitude to carry on their independent studies in future.

CO2 Present and evaluate their results responsibly, critically and objectively.

CO3 Understand ethical standards for scientific research, uses them, following principles of scientific integrity.

CO4 Utilize the knowledge of learnt different freewares and commercial packages available in bioinformatics community.

The course is designed to result in the satisfactory completion and defense of the Masters dissertation.

This process includes

a) the conceptualization of the independent research that will comprise the dissertation,
b) the preparation of and satisfactory defense of the dissertation proposal,
c) the collection, analysis, and interpretation of data,
d) presentation of findings in the dissertation format, and
e) oral defense of the dissertation.

Dissertation activity must be completed within prescribed time frame for the semester.