



KARNATAKA STATE AKKAMAHADEVI WOMEN'S UNIVERSITY, VIJAYAPURA

POSTGRADUATE PROGRAM IN BIOINFORMATICS (M.Sc. BIOINFORMATICS)

Programme Outcome

- PO1. Provide education that helps to understand the fundamental and advanced concepts in the relevant field and prepare the students to communicate it effectively.
- PO2. Instigate confidence to develop hypothesis, design experiments and interpret the results.
- PO3. Prompt the students to work individually and synergistically.
- PO4. Enable students to think independently and critically.
- PO5. Make the students competent to identify their field of interest and find suitable employment in Industry and academia.

Programme Specific Outcome

The postgraduate program in Bioinformatics (MSc Bioinformatics) offers science graduates a conceptual understanding of the objectives and limitations of both computer and biological sciences disciplines, along with the knowledge to make use of computational tools for acquisition, storage, analysis and visualization of biological data. This way the program essentially aims to be a solid stepping stone for a career either in academia or in industries involved in the R&D of biomedicine, environment, food, beverage, etc. The first two semesters, along with the

basics of bioinformatics and programming concepts, focus on introductory courses on cell and molecular biology, microbiology, immunology, biochemistry, biophysics, perl, python, bioinstrumentation, statistics, R-programming, genomics and proteomics to bring uniformity in foundation across students from diverse disciplines, such as biology, physics, chemistry, computer science, engineering, etc. The third semester deals with critically advanced areas of bioinformatics such as systems biology, drug designing, genetic engineering, protein engineering, artificial intelligence, image processing, sequence analysis, medical bioinformatics, along with entrepreneurship and start-up enlighten them with cutting-edge topics, e.g. systems biology, next generation sequencing data analysis, computational neuroscience, metagenomics and microbiome, big data solutions in bioinformatics, etc. Each of these subjects individually has the capacity to lead the students toward their excellence in academic or industrial research and product development. The specific interest of every student is further nourished through the final dissertation semester in the student's selected area of research, either under the supervision of in-house faculty members or in high-quality research labs outside in India, thereby making the candidate ready for the world in the field of bioinformatics.

M.Sc(Bioinformatics) I Semester Syllabus Under CBCS(w.e.f. 2022-23 and onwards)										
Course Code	Subject Title	Credits	Teaching Scheme Hrs/week			Examination				Total Marks
			Lecture	Tutorial	Practical	Continuous Assessment		Semester End Examination (C3)		
						C1	C2	Exam. Duration (Hrs)	Theory/ Practical	
BI- HCT-1.1	Cell and Molecular Biology	04	4	0	0	15	15	3	70	100
BI- HCP-1.2	Practical-I: Cell and Molecular Biology	02	--	0	4	15	15	4	70	100
BI- HCT-1.3	Biochemistry and Biophysics	04	4	0	0	15	15	3	70	100
BI- HCP-1.4	Practical-II: Biochemistry and Biophysics	02	--	0	4	15	15	4	70	100
BI- HCT-1.5	Fundamentals, Computers and C-Programming	04	4	0	0	15	15	3	70	100
BI- HCP-1.6	Practical-III: Fundamentals, Computers and C-Programming	02	--	0	4	15	15	4	70	100
BI- SCT-1.7	Elective soft-core 1.7.1: Biostatics and R- Programming 1.7.2: Structural Bioinformatics 1.7.3: Bio- instrumentation	04	04	--	--	15	15	3	70	100
BI- SCP-1.8	Practical IV: Based on soft core paper	02	--	0	4	15	15	4	70	100
BI-OE-1.9	Open Elective Basics of Bioinformatics	04	04	--	--	15	15	3	70	100
Total Credits		28	20							900

BI- Bioinformatics, HCT- Hard core theory, HCP- Hard core practical, SCT- soft-core theory, SCP- Soft core practical, OE- Open elective

M.Sc (Bioinformatics) II Semester Syllabus Under CBCS(w.e.f. 2022-23 and onwards)										
Course Code	Subject Title	Credits	Teaching Scheme Hrs/week			Examination				Total Marks
			Lecture	Tutorial	Practical	Continuous Assessment		Semester End Examination (C3)		
						C1	C2	Exam. Duration (Hrs)	Theory/ Practical	
BI- HCT-2.1	Microbiology and Immunology	04	4	0	0	15	15	3	70	100
BI- HCP-2.2	Practical-I: Microbiology and Immunology	02	--	0	4	15	15	4	70	100
BI- HCT-2.3	Perl and Python	04	4	0	0	15	15	3	70	100
BI- HCP-2.4	Practical-II: Perl and Python	02	--	0	4	15	15	4	70	100
BI- HCT-2.5	Genomics and Proteomics	04	4	0	0	15	15	3	70	100
BI- HCP-2.6	Practical-III: Genomics and Proteomics	02	--	0	4	15	15	4	70	100
BI- SCT-2.7	Elective soft-core 2.7.1: Biological data Analytics 2.7.2: Image Processing 2.7.3:CGI	04	04	--	--	15	15	3	70	100
BI- SCP-2.8	Practical IV: Based on soft core paper	02	--	0	4	15	15	4	70	100
BI-OE-2.9	Open Elective Bioinformatics for Life Science	04	04	--	--	15	15	3	70	100
	Total Credits	28	20							900

BI- Bioinformatics, HCT- Hard core theory, HCP- Hard core practical, SCT- soft-core theory, SCP- Soft core practical, OE- Open elective

M.Sc (Bioinformatics) III Semester Syllabus Under CBCS (w.e.f. 2022-23 and onwards)										
Course Code	Subject Title	Credits	Teaching Scheme Hrs/week			Examination				Total Marks
			Lecture	Tutorial	Practical	Continuous Assessment		Semester End Examination (C3)		
						C1	C2	Exam. Duratio n (Hrs)	Theory/ Practical	
BI- HCT-3.1	System Biology and Drug Designing	04	4	0	0	15	15	3	70	100
BI- HCP-3.2	Practical-I: System Biology and Drug Designing	02	--	0	4	15	15	4	70	100
BI- HCT-3.3	Genetic Engineering and Protein Engineering	04	4	0	0	15	15	3	70	100
BI- HCP-3.4	Practical-II: Genetic Engineering and Protein Engineering	02	--	0	4	15	15	4	70	100
BI- SCT-3.5	Elective soft-core 3.5.1: Artificial Intelligence 3.5.2: Sequence Analysis 3.5.3: Biomolecular Modeling and Simulation	04	04	--	--	15	15	3	70	100
BI- SCP-3.6	Practical IV: Based on soft core paper	02	--	0	4	15	15	4	70	100
#BI-ESS-3.7	Entrepreneurship and Start-up Studies *	02	---	--	4	15	15	4	70**	100
BI-OE-3.8	Open Elective Medical Bioinformatics	04	04	--	--	15	15	4	70	100
	Total Credits	24	16							800

#ESS- Entrepreneurship and Start-up Studies * Entrepreneurship and Startup Studies Report is mandatory in 3rd Semester, **In C3 evaluation 70 marks is been distributed as 50 marks for report submission and 20 marks for presentation and Viva-Voce

M.Sc (Bioinformatics) IV Semester Syllabus Under CBCS (w.e.f. 2022-23 and onwards)										
Course Code	Subject Title	Credits	Teaching Scheme Hrs/week			Examination				Total Marks
			Lecture	Tutorial	Practical	Continuous Assessment		Semester End Examination (C3)		
						C1	C2	Exam. Duratio n (Hrs)	Theory/ Practical	
BI- HCT-4.1	Medical informatics	04	4	0	0	15	15	3	70	100
BI- HCP-4.2	Practical-I: Medical informatics	02	--	0	4	15	15	4	70	100
BI- SCT-4.3	Elective soft-core 4.3.1: Research Methodology, IPR and Bioethics 4.3.2: Data mining and Machine learning 4.3.3: High Throughput Technologies	04	04	--	--	15	15	3	70	100
BI- SCP-4.4	Practical II: Based on soft core paper	02	--	0	4	15	15	4	70	100
*BI-HCPW-4.5	Project Work	06	---	--	6	15	15	4	** 120	150
BI-OE-4.6	Open Elective Applied Bioinformatics	04	04	--	--	15	15	4	70	100
	Total Credits	22	12		14					650

Total Credits for All four Semester: 102 credits and Marks: 3250

*HCPW- Hard Core Project Work

**** Dissertation shall be evaluated for 70 Marks, Presentation and Viva Voce carries 50 Marks**

MSc(Bioinformatics) I Semester syllabus under CBCS (w.e.f. 2022-23 and onwards)			
Course Code	Course Name	Course Objectives	Course Learning Outcomes
BI. HCT-1.1	Cell and Molecular Biology	<ul style="list-style-type: none"> To provide the knowledge about cell, cell division, DNA replication, Transcription, translation, cell communication, cell signaling, mutations, etc. these concepts will helpful to understand the biology in molecular level and it is essential for bioinformatics. 	<ul style="list-style-type: none"> Students completing this course will have understanding of complete basics of cell and molecular biology it will helps in understanding the concepts of bioinformatics in further semester.
BI. HCP-1.2	Cell and Molecular Biology lab	<ul style="list-style-type: none"> From this lab students will learn the different experiments of cell and molecular biology such as chromatography, mitosis and meiosis, isolation of DNA's, etc. 	<ul style="list-style-type: none"> Students will get hands on experiments to study the different cellular and molecular biology techniques. They will understand chemical preparations and types of isolations and analysis.
BI. HCT-1.3	Biochemistry and Biophysics	<ul style="list-style-type: none"> This course will provide the information regarding concepts of biophysics (Newton's laws of motion, Thermodynamics laws, Conservation laws), Biochemistry (Nucleic acids, amino acids, protein structures, protein purification and sequencing techniques). 	<ul style="list-style-type: none"> Students will understand the concept of biophysics how physics works in biology. Students will get clear idea about biomolecules structure and function. They understand protein structure, motifs, folding and flexibility, protein purification and sequencing techniques.
BI. HCP-1.4	Biochemistry and Biophysics lab	<ul style="list-style-type: none"> This lab will provide hands on experiments of biochemical and Biophysical techniques 	<ul style="list-style-type: none"> Student will able to do experiments of qualitative and quantitative analysis of carbohydrates, proteins, amino acids, nucleic acids. They can able to handle bioinstrumentation like thin layer chromatography, column chromatography, HPLC, AGE, PAGE.
BI. HCT-1.5	Fundamentals of Computers and C-Programming	<ul style="list-style-type: none"> To provide the knowledge about computer system, working processor of computer, operating systems. To introduce the students about basic 	<ul style="list-style-type: none"> Students will able to understand working with computer system. Students will understand about programming languages and concepts of C.

		programming languages like c in the field of bioinformatics.	<ul style="list-style-type: none"> • They will gain the knowledge how to write the programs of C. • Students will get idea about how the biological problems can be solving by writing the programs.
BI. HCP-1.6	Fundamentals, Computers and C-Programming lab	<ul style="list-style-type: none"> • This lab will provide the knowledge on basic operating of computer. • This lab will aid in understanding and learning the basics of C programs and how to write some biological programs using C. 	<ul style="list-style-type: none"> • Students will able to understand working with computer system. • Students will understand how to write the C basic programs, flowcharts and algorithms. • Students will get idea about how the biological problems can be solving by writing the programs.
BI. SCT-1.7	1.7.1: Biostatistics and R-Programming	<ul style="list-style-type: none"> • To introduce the statistics in bioinformatics, basic concepts of statistics used to analyze the biological data. • Introducing R programming for management of the biological data analysis. 	<ul style="list-style-type: none"> • Students will understand the role of statistics in biology and different types of methods like classification, tabulation, Measures of central tendencies, measures of dispersion, bivariate statistical methods, time variables and concept of probability. • Students get idea about how to analyses the biological data by different types of statistical methods and graphs using R-programming.
	1.7.2: Structural Bioinformatics	<ul style="list-style-type: none"> • To provide knowledge about structural aspects of biomolecules such as nucleic acids and proteins and also explains the methods to predict the structure 	<ul style="list-style-type: none"> • Students will understand the structural features of proteins and nucleic acids and proteins. • Students will also understand the molecular interactions and methods to predict the structures of biomolecules
	1.7.3: Bio- instrumentation	<ul style="list-style-type: none"> • This course provides the knowledge about Chromatographic techniques and Mass spectrometry, Electrophoresis, Flowcytometry, Microscopy, Spectroscopy, Omics technologies. 	<ul style="list-style-type: none"> • Students will get clear idea about bio-instruments such as Chromatographic techniques and Mass spectrometry, Electrophoresis, Flowcytometry, Microscopy, Spectroscopy, Omics technologies.
BI. SCP-1.8	1.8.1: Biostatistics and R-Programming lab	<ul style="list-style-type: none"> • This lab will help the student to produce diagrammatical and graphical representation of data and different statistical problems can be solved with example problems.’ • Use of R-software and writing R programs based on our requirement data analysis like measures of central tendency, dispersion, probability and correlation and regression 	<ul style="list-style-type: none"> • Students will understand how the biological data can be represented through diagrammatically and graphically. • Understand how to use R- programming in solving and analyzing biological data.

		analysis.	
	1.8.2: Structural Bioinformatics lab	<ul style="list-style-type: none"> This lab will help the students to understand how to work with Structural prediction software's and databases 	<ul style="list-style-type: none"> From this lab students will able to handle variety of tools, databases and software's of Structure prediction of proteins and nucleic acids and molecular interaction.
	1.8.3: Bio- instrumentation lab	<ul style="list-style-type: none"> This lap will provide hands on training of Column chromatography, Estimation of Nucleic Acid and Protein through spectrophotometer, Electrophoresis of DNA and Protein, Observation of Cell Morphology and Cell division under inverted microscope, Demonstration of Conventional and Real time PCR for gene amplification, etc 	<ul style="list-style-type: none"> From this lab students will able to hand all the bio-instruments and students will get hands on training of Column chromatography, Estimation of Nucleic Acid and Protein through spectrophotometer, Electrophoresis of DNA and Protein, Observation of Cell Morphology and Cell division under inverted microscope, Demonstration of Conventional and Real time PCR for gene amplification, etc
BI-OE1.9	BI-OE1.9 Basics of Bioinformatics	<ul style="list-style-type: none"> This course will educate the beginners of non bioinformatics students, to understand the basic concepts of Bioinformatics, theoretical applications and overview of Bioinformatics 	<ul style="list-style-type: none"> Students will understand the basic concepts of Bioinformatics such as databases, tools, sequence analysis, general bioinformatics application.

**MSc (Bioinformatics) II Semester syllabus under CBCS
(w.e.f. 2022-23 and onwards)**

Course Code	Course Name	Course Objectives	Course Learning Outcomes
BI. HCT-2.1	Microbiology and Immunology	<ul style="list-style-type: none"> This course provides the knowledge about Immunology concepts like introduction to antibodies, generation of antibodies, immune cells, etc. It provides the knowledge about microbiology concepts. 	<ul style="list-style-type: none"> Students will get basic knowledge of microbiology and techniques. Students get basic knowledge about immunology: immune cells, introduction to antibodies and generation of antibody, etc.
BI. HCP-2.2	Microbiology and Immunology lab	<ul style="list-style-type: none"> This lab will provide hands on experiments of microbiology and immunology experiments. 	<ul style="list-style-type: none"> Students will perform basic microbiological lab techniques This lab helps the students to get hands on training to do immunology experiments.
BI. HCT-2.3	Perl and Python	<ul style="list-style-type: none"> This course provides the introduction and working of Perl and python programming in bioinformatics. 	<ul style="list-style-type: none"> Students can understand the concepts of Perl and python language and they can use the programming in bioinformatics work.
BI. HCP-2.4	Perl and Python lab	<ul style="list-style-type: none"> Aim of this lab to give knowledge about how to write basic perl and python programs and how to work with bioperl and biopython. 	<ul style="list-style-type: none"> From this lab students can learn how to work with perl and bioperl as well as python and biopython platforms and writing programs according to the bioinformatics requirements.
BI. HCT-2.5	Genomics and Proteomics	<ul style="list-style-type: none"> The goal of the course is to determine how all the genes in a genome act and how their products interact to produce a functional organism. The different methods of sequencing, microarrays, protein fingerprints and the role of bioinformatics tools applied to analyse and interpret the protein-protein interactions in different cell types will be detailed. 	<ul style="list-style-type: none"> Students can acquire the knowledge of genomics: the study of genes, genomes, sequencing methods, gene expression analysis methods, etc Students can understand the proteomics: the study of proteome analysis methods, protein interaction analysis, etc.

BI. HCP-2.6	Genomics and Proteomics lab	<ul style="list-style-type: none"> This lab will help the students to understand how to work with genomics and proteomics data analysis and its basic techniques 	<ul style="list-style-type: none"> From this lab students will be able to handle a variety of tools, databases and software's of genomics and proteomics. Some of the experimental techniques can also be performed.
BI. SCT-2.7	2.7.1: Biological data Analytics	<ul style="list-style-type: none"> This course provides knowledge about data analysis of biological data using different biological databases and techniques 	<ul style="list-style-type: none"> Students are going to be able to understand about big data analysis of biological data and problems. They will learn data analyzing techniques, such as sequence alignment and analysis, gene prediction, phylogenetic analysis and protein data and structure analysis, etc.
	2.7.2: Image Processing	<ul style="list-style-type: none"> This course introduces the image processing concepts like Digital images, image pre-processing, segmentation, Image enhancement in different domains, morphology, etc. 	<ul style="list-style-type: none"> Students will get knowledge about image processing concepts and students can work on that.
	2.7.3: CGI	<ul style="list-style-type: none"> This course introduces about CGI concepts in different programming languages. 	<ul style="list-style-type: none"> Students will get knowledge about CGI concepts in different programming languages and how to work on it.
BI. SCP-2.8	2.8.1: Biological data Analytics lab	<ul style="list-style-type: none"> This lab will provide immense knowledge about biological data analysis with a variety of tools. 	<ul style="list-style-type: none"> Students can get to understand how to analyse the biological data using a variety of biological databases
	2.8.2: Image Processing lab	<ul style="list-style-type: none"> This lab provides how to do image processing using MATLAB. 	<ul style="list-style-type: none"> By this lab students can work with MATLAB based image processing practicals.
	2.8.3: CGI lab	<ul style="list-style-type: none"> This lab provides Uses of CGI, pm Module and Passing Parameters via CGI, Debugging CGI programs 	<ul style="list-style-type: none"> Students can write the programs related to CGI concepts
BI-OE-2.9	Open Elective Bioinformatics for Life Science	<ul style="list-style-type: none"> The main objective of this course is to introduce general concepts of Bioinformatics to the life science department students of KSAWU. 	<ul style="list-style-type: none"> The outcome of the course is that students from other departments gain the knowledge of how to utilize bioinformatics resources.

**M.Sc (Bioinformatics) III Semester syllabus under CBCS
(w.e.f. 2022-23 and onwards)**

Course Code	Course Name	Course Objectives	Course Learning Outcomes
BI. HCT-3.1	System Biology and Drug Designing	<ul style="list-style-type: none"> This course provides introduction to system biology, system biology networking, simulation of pathways and different databases and tools for pathway prediction. It also provides the information regarding drug discovery: basics, technology and strategies and also provides the different types of tools and software's for drug discovery. Pharmacogenomics concept. 	<ul style="list-style-type: none"> Students will understand the system biology: networks and pathways, simulation of pathways, pathway databases. Students will understand the Drug Designing techniques and approaches. They will learn the drug designing process and software's.
BI. HCP-3.2	System Biology and Drug Designing lab	<ul style="list-style-type: none"> This lab will help the students to understand how to work with system biology databases and tools. The lab will also provide the step-by-step strategies of discovering the drug using variety of tools and software's. 	<ul style="list-style-type: none"> Students can learn how to work with system biology practical's like analyzing the networks, designing pathways, etc. From this lab students will be able to access the chemical databases and draw the chemical compounds. Understand how to analyse the target protein and be able to study the binding sites. Students can perform docking to study the interaction between protein and ligand molecule, so on.
BI. HCT-3.3	Genetic Engineering and Protein Engineering	The aim of this course is to provide introduction, methods and various techniques of genetic and protein engineering concepts.	Students will gain knowledge on genetic engineering concepts and technologies as well as protein engineering concepts and technologies.
BI. HCP-3.4	Genetic Engineering and Protein Engineering lab	This lab aim is to give hands on training of genetic and protein engineering techniques.	Student will get expertise in Genetic engineering and protein engineering practical techniques.

BI. SCT-3.5	3.5.1: Artificial Intelligence and Image Processing	<ul style="list-style-type: none"> Aim of the course is to give basics of artificial intelligence, methods and application of artificial Intelligence. This course introduces the image processing concepts like Digital images, image pre- processing, segmentation, Image enhancement in different domains, morphology, etc. 	<ul style="list-style-type: none"> Students will get knowledge of concept of artificial intelligence in biology. Students will get knowledge about image processing concepts and students can work on that.
	3.5.2: Sequence Analysis	<ul style="list-style-type: none"> Aim of the course to introduce the methods of Sequence analyses and their applications in Bioinformatics 	<ul style="list-style-type: none"> Students will be trained to perform genomic evolutionary analyses as well as structure modeling from protein sequences, etc.
	3.5.3: Biomolecular Modeling and Simulation	<p>To introduce the basic concepts and techniques involved in molecular modeling and molecular dynamics approach also explains about drug discovery process.</p> <p>□</p>	<ul style="list-style-type: none"> Students will gain knowledge on modern approaches used in molecular modeling and dynamics concepts. Students can also understand the drug discovery process.
BI. SCP-3.6	3.6.1: Artificial Intelligence and Image Processing lab	<ul style="list-style-type: none"> This lab provides working with artificial intelligence using programmes and tools. This lab provides how to do image processing using MATLAB. 	<ul style="list-style-type: none"> Student will get knowledge on artificial intelligence working with basic practicals. By this lab students can work with MATLAB based image processing practicals.
	3.6.2: Sequence Analysis lab	<ul style="list-style-type: none"> To make the students familiarized with the techniques used in Bioinformatics sequence analysis and their applications 	<ul style="list-style-type: none"> Students can understand the information's available in Bioinformatics databases and their applications in research
	3.6.3: Biomolecular Modeling and Simulation lab	<ul style="list-style-type: none"> To make the students familiarized with the Bioinformatics databases and their applications 	<ul style="list-style-type: none"> Students will understand the information's available in Bioinformatics databases and their applications in research
#BI-SCP-3.7	Entrepreneurship and Start-up Studies *	<ul style="list-style-type: none"> Objective of this course is to develop business idea among the students, making a business plan, visiting industry, presenting a business at the 	<ul style="list-style-type: none"> Student will acquaint on thinking innovative ideas and transforming into a business plan. Students will get familiar on making complete

		end of the course	business plan.
BI. OET-3.8	Open Elective Medical Bioinformatics	This course will educate the beginners of bioinformatics students, to understand the basic concepts of Medical Bioinformatics, theoretical applications and overview of medical Bioinformatics	<ul style="list-style-type: none"> Students will understand the basic concepts of Medical Bioinformatics such as databases, tools, general medical bioinformatics application.

MSc(Bioinformatics) IV Semester syllabus under CBCS (w.e.f 2022-23 and onwards)			
Course Code	Course Name	Course Objectives	Course Learning Outcomes
BI. HCT-4.1	Medical informatics	<ul style="list-style-type: none"> This course provides the information regarding medical informatics, medical standards, medical data storage and automation, Health informatics, Recent trends in medical informatics 	<ul style="list-style-type: none"> Students can able to understand medical informatics, medical standards, medical data storage and automation, Health informatics, Recent trends in medical informatics
BI. HCP-4.2	Medical informatics lab	<ul style="list-style-type: none"> This lab provides how to work with medical bioinformatics aspect and how to analyse the data with different working producer using tools and databases. 	<ul style="list-style-type: none"> From this lab students will understand how to analyze the medical data and how to study the disease mechanism. Students will understand analyzing the human genome and variant analysis, etc.
BI. SCT-4.3	4.3.1: Research Methodology, IPR and bioethics	<ul style="list-style-type: none"> To give an overview of the research methodology and explain the technique of defining a research problem To explain carrying out a literature search, its review, developing theoretical and conceptual frameworks and writing a review. To explain various research designs and their characteristics. To explain the details of sampling designs, measurement and scaling techniques and also different methods of data collections. 	<ul style="list-style-type: none"> Students can understand the basics of how to design, conduct research, analyze and communicate the results to research community. Students can learn various forms of the intellectual property, its relevance and business impact in the changing global business environment.

		<ul style="list-style-type: none"> • To explain various forms of the intellectual property, its relevance and business impact in the changing global business environment. • To discuss leading International Instruments concerning Intellectual Property Rights 	
	4.3.2: Data mining and Machine learning	<ul style="list-style-type: none"> • This course focuses on machine learning algorithms for analyzing biological data. The course will introduce the main topics in this area, such as analysis of protein/DNA sequences, protein structures, molecular graphs, and so on. The main focus is on the role of deep learning and data mining in computational biology and bioinformatics. 	<ul style="list-style-type: none"> • Students will be knowledgeable about the fundamental bioinformatics tasks like sequence and structure analysis and evolution, biological networks, and machine learning methods in bioinformatics • Students able to understand the key algorithms for the main tasks • Students able to implement and apply the techniques to real world datasets.
	4.3.3: High Throughput Technologies	<ul style="list-style-type: none"> • The course is aimed to critically apprise the students with the concepts and tools that contribute towards understanding scientific research data analyses. Biological interpretations after the structured statistical, computational and mathematical analyses are explained thoroughly after the technical aspects of the technology involved. 	<ul style="list-style-type: none"> • Demonstrate the ability to understand the high throughput processes and characteristics of such high throughput biological experiments. • Evaluate the concepts of sequencing, transcriptomics and other 'omics' methods applied and deduce logical interpretations from the data analysis. • Apply theoretical knowledge of the technologies involved to create knowledge-base for solving tactical problems in the various assignments in the subject. • Describe the biological analytical models generated with conceptual approaches with bioinformatics and statistical approaches applied to the high throughput data. • Critically assess the data characteristics, experimental design for efficient progress

			in high throughput biology.
BI. SCP-4.4	4.3.1: Research Methodology, IPR and Bioethics lab	<ul style="list-style-type: none"> This lab gives information regarding research methodology application by using tools and techniques. It helps the students to work in research field. 	<ul style="list-style-type: none">
	4.3.2: Data mining and Machine learning lab	<ul style="list-style-type: none"> To learn various mining techniques used to analyses huge biological data to find the hidden patterns. 	<ul style="list-style-type: none"> Able to handle the huge heterogeneous biological data sets by applying different mining algorithms and techniques.
	4.3.3: High Throughput Technologies lab	This lab aimed to provide the high throughput data analysis by using various biological tools and software's.	Students will get hands on training to analysis sequencing and gene expression data by using various tools and software's.
BI-HCPW-4.5	Project Work	To enable the students to have hands-on research experience and write a comprehensive report and present and defend the same.	<ul style="list-style-type: none"> At the end of the course students will be acquainted on carrying out the independent research, familiar with research processes, writing the thesis, and presentation.
BI. OET-4.6	Open Elective Applied Bioinformatics	This course aim is to give clear idea about how to analyse the sequences such as alignment methods, similarity search tools, phylogenetic analysis method and software's	<ul style="list-style-type: none"> Students can clearly understand the sequence analysis like sequence alignment methods, sequence similarity search tools. Students can able to analyses the phylogenetic relationship. They can get clear idea about comparative genome analysis concept.

M.Sc. Bioinformatics CBCS Course Syllabus

I Semester

BI. HCT-1.1 Cell and Molecular Biology

Total: 60 hrs

Unit I

Concept of Macromolecular assembly and structure and function of cell organelles. chemical organization of cell, comparison of cells, Cell division-mitosis and meiosis, eukaryotic cell cycle and its regulation. Cellular Physiology – electron transport system in mitochondria and chloroplast.

Organization of prokaryotic and eukaryotic genomes, components of eukaryotic chromatin and chromosome structure, DNA super coiling, Gene expression in prokaryotes- Lac operon, Gal operon- role of promoters, Arabinose operon- positive control and trp operon – attenuation control. Gene expression in eukaryotes. Role of histones, histone acetyltransferases and histone deacetylases, transcription factors, NFkB, DNA binding protein motifs.

20 hrs

Unit II

DNA replication- prokaryotic and eukaryotic DNA replication, mechanism of replication. Enzymes and necessary proteins in DNA replication. Telomeres, telomerase and end replication. Role of telomerase in aging and cancer.

Transcription-prokaryotic and eukaryotic transcription- RNA polymerases- general and specific transcription factors- regulation- Transcription termination; post transcriptional modification. Translation: prokaryotic ad eukaryotic translation and regulation.

16 hrs

Unit III

Mutations - Introduction and Types of Gene mutations, Base substitution, Frame shift mutation (insertion, deletion, missense, nonsense mutation). Mutagens - Physical and chemical, Reverse mutation in bacteria, DNA damage and repair mechanism (Mismatch repair photoreactivation, excision and SOS repair). Beneficial and harmful effects of mutations. Transposable elements.

8 hrs

Unit IV

Cell Communication – Membrane Transport Principles, Active Transport, Ion Channel; Protein Sorting- An Overview Of Targeting Proteins To Mitochondria, Nucleus, Endoplasmic Reticulum, Lysosome And Plasma Membrane. Cell-Cell Communication.

Cell signaling mechanism, K⁺ channel, cell signaling through receptors and messengers, cell signaling through growth factors, Apoptosis, Necrosis and Autophagy.

16 hrs

BI. HCP-1.2 Lab based on BI. HCT-1.1

Cell biology

1. Paper chromatography/Thin Layer chromatography of chlorophyll pigments
2. Mitosis and Meiosis
3. Chromosomal analysis and Karyotyping
4. Bacterial Growth curve study
5. Human Bar Body study
6. Study of mutants of *Drosophila*
7. Study of polytene chromosome

Molecular biology

1. Quantitative estimation of DNA and RNA.
2. Isolation & purification of genomic DNA from bacteria
3. Isolation & purification of plasmid DNA.
4. Agarose gel electrophoresis of chromosomal & plasmid DNA.
5. Restriction digestion of chromosomal & plasmid DNA
6. Isolation of DNA fragments from agarose gel.
7. Transformation studies

References:

1. Karp, G. (2005) "Cell and Molecular Biology: Concepts and Experiments"; Fourth Edition, Wiley Publishing Co. USA.
2. Lodish, H., Scott, M.P., Matsudaira, P., Darnell, J., Zipursky, L., Kaiser, C.A., Berk, A. and Krieger, M. (2003) "Molecular Cell Biology"; Fifth Edition, W. H. Freeman and Co., New York.
3. De Robertes and DE Robertes (2002) "Cell and Molecular Biology". Saunders College, Philadelphia, USA.
4. Brown, T.A.(Ed). 1998. Molecular Biology I: Recombinant DNA. Academic press, New York.
5. Brown, T.A.(Ed). 1998. Molecular Biology II: Gene Analysis, Academic press, New York.
6. Watson, J.D. *et al.* 1987. Molecular Biology of the Genes, 4th ed. The Benjamin Cunnings Pub. Inc., California.
7. Lewin, B. 1997. Gene VI. John Wiley and Sons, New York.
8. Freifelder and G.M. Malacinski. 1996. Essentials of Molecular Biology Panim, New Delhi.

BI. HCT-1.3 Biochemistry and Biophysics

Total: 60 hrs

Unit I

Nucleic Acids: Structure Of Nucleic Acids: Structures of Purines and Pyrimidines, Structure of DNA; Type of DNA and their structures, A, B and Z DNA, Supercoiled DNA, T_m and C_{ot} Curve for Dissociation of DNA. Motifs of DNA - Promoters, Enhancers and Attenuators.

DNA Protein Interaction: Recognition of DNA in Prokaryotes and Eukaryotes. Interaction of Specific Proteins with references to Trp-Repressors, CAP Proteins, Zinc Finger Proteins, Lac-Repressors, Phage Repressor and Cro Protein.

15 hrs

Unit II

Amino Acids: General Properties, Classification of Amino Acids; Based On Polarity, Based On Functional Groups, Essential and Non-Essential Amino Acids, Acid Base Properties, Stereo Chemistry. Non Standard Amino Acids.

Proteins: Salient Features of Peptide Bond; Conformation and its properties, Structural Hierarchy of the Protein, Primary, Secondary, Tertiary and Quaternary Structures with Examples.

15 hrs

Unit III

Motifs of Proteins: Alpha Structures: Coiled Coil, Four Helix Bundles, and Globin Motifs with Examples, Beta Structures: Up And Down Beta Barrel, Greek Key Motif, and Jelly Roll Motifs with Examples Alpha/Beta Structures: Horse Shoe Motifs, TIM Barrel Motifs, Rosmann Fold, Beta Alpha Beta Motifs with Examples and Other Motifs.

Folding And Flexibility: Concept of Protein Folding; Christian Anfinsen Reaction on Bovine Pancreatic RNase, Lavinthal Paradox, Thermodynamics Of Protein Folding, Steps Involved In Protein Folding, Structure And Molecular Mechanism Of Chaperon Mediated Protein Folding.

15 hrs

Unit IV

Mechanics: Newton's Law of Motion- Mechanics of Particle- Work Energy Principle- Relational Dynamics- Static and Dynamic Equilibrium – Conservation Laws. Thermodynamics- Concept of Temperatures- Thermodynamic Equilibrium; Zeroth Law- Conservation of Energy; First Law- Concept of Entropy; Second Law- Absolute Law of Temperature; Third Law of Thermodynamics.

15 hrs

BI. HCP-1.4 Lab based on BI. HCT-1.3

1. Qualitative and Quantitative Analysis of Carbohydrates.
2. Qualitative and Quantitative Analysis of Proteins.
3. Qualitative and Quantitative Analysis of Amino Acids.
4. Qualitative Analysis of Nucleic Acids.
5. Study of Protein Motifs.
6. Bioinstrumentation - Thin layer chromatography, Column chromatography, HPLC, AGE, PAGE.

References

1. Resnick, R., Halliday, D And Walker (2001) "Fundamentals Of Physics". Sixth Edition, John Wiley And Sons, USA
2. Tipler, P. A (1999) "Physics for Engineers and Scientists: Fourth Edition, W.H. Freeman And Company, USA
3. Essentials of Immunology by Riott I .M. 1998. ELBS, Blackwell Scientific Publishers, London.
4. Immunology 2 nd Edition by Kuby J. 1994. W.H. Freeman and Co. New York.
5. Immunology - Understanding of Immune System by Claus D. Elgert. 1996. Wiley - Liss, New York.
6. Fundamentals of Immunology by William Paul.
7. Cellular and Molecular Immunology. 3rd Edition by Abbas.
8. Immunobiology: The Immune System in Health and Disease. 3rd Edition by Travers.
9. Immunology- A short Course. 2 nd Edition by Benjamin.
10. Manual of Clinical Laboratory and Immunology 6th Edition. 2002 by Noel R. Rose, Chief Editor: Robert G. Hamilton and Barbara Detrick (Eds.) , ASM Publications.

BI. HCT-1.5 Fundamentals, Computers and C-Programming

Total: 60 hrs

Unit I

Generations of Computer, Computer Organization, Basics of operating system DOS, Windows, Unix, Linux Application Software. Storage devices (RAM, ROM, Hard Drives etc). Communication Technology- Networking- LAN, WAN And MAN, Internet- Wireless Communication- Internet, Network Topologies- Types And Application, Internet Technologies: Web Services- Www, URL, DNS- Servers E Mail Server, WEB Servers, Browsers- IP Addressing.

16 hrs

C-Programming

Unit II

Introduction: History Of C Language, The Character Set – Alphabets, Digits And Special Symbols, Constants – Primary & Secondary Constants, Variables, Standard C Keywords, Data Types – Int, Float, Double, Char. C Instructions: Type Declaration Instruction, Arithmetic Instruction, Input/ Output Instruction, Control Instructions. Hierarchy of Operations, Priority, Operators Like Int to Float, Float to Int, Double to Int, etc., Type Conversions, Structure of a C Program

Operators: Arithmetic, Relational, Logical, Assignment, Increment and Decrement, Conditional, Bitwise, Special Operators. Decision-Making, Branching And Looping: *If*, Multiple Statements Within *If*, *If-Else*, Nested *If-Else* Statement, Use of Logical Operators Like *&&*, *||* And *!* Conditional Operator *While*, *Do*, *Do-While* and *For* Loop Control Structures, Nesting of Loops *Break* And *Continue* Statements, *Switch*, Case Control Structure, *Goto* Control.

18 hrs

Unit III

Pointers and Arrays Functions: Declaration, Initialization, Accessing elements of an Array, reading & entering data into an Array, Pointers and 2D And 3D Arrays, Accessing Address of a Variable, Declaring and Initializing Pointers, Accessing variables through Pointers, Pointer expression. Functions: Need for User Defined Functions, Multifunction Program, C Function Forms, Return Values and their types, Calling a Function, Handling of Non Integer Functions, Nesting of Functions, Function with Arrays,

12 hrs

Unit IV

Strings: Declaring and Initialization of Strings, Reading Strings From Terminal, Writing Strings to Screen, Arithmetic operations on Characters, Putting Strings together, Comparison of two Strings, Strings-Handling Functions, Table of Strings.

Structures and Unions: Structure Initialization and Giving Values to Members, Arrays of Structures, Arrays within Structures, Structures within Structures, Structures and Functions. Size of the Structures, Unions and Case Studies.

14 hrs

BI. HCP-1.6 Lab based on BI. HCT-1.5

C-Programming

1. Flow Charts, Algorithm Keywords Identifiers, Variables Constants, Scope of Life of Variables- Local and Global variables. Data types, Expressions, Operators- Arithmetic Operators, Logical Operators, Relational, Conditional, Bitwise Operators- Input/ Output Library Functions.
2. Declaration Statements, Control Statement: If Statement, If...Else Statement, Nesting of If...Else statement, Switch Statement- Iteration Statements- Arrays: Multiple Dimensional Arrays, Array Declaration and Initialization of Arrays.
3. Functions: User Defined and Library Functions- File Handling: Opening A File, Closing A File Reading and Writing into a File, Appending a File, Pointers

References:

1. Balaguruswamy, E. (1985) "Computer Fundamentals And Applications ", Second Edition, Tata Mcgraw Hill Publishing Co Ltd., India.
2. The C Programming Language B.W. Kjernighan and D.M.Ritchie 2nd ed. Prentice Hall, India
3. Yashavant Kanetkar, 2002. Let Us C, 4th Ed, BPB Publications, New Delhi.
4. Yashavant Kanetkar, 1998. Graphics Under C, BPB Publications, New Delhi.
5. Schildt, Herbert, 2000. C: The Complete Reference, 4th Ed. Tata Mc Graw – Hill Publishing Co. Ltd., New Delhi.
6. Rajaraman, V. 1994, Computer Programming In C. Printice-Hall Of India Pvt. Ltd., New Delhi.
7. Sudha G Purohit et al, Statistics using R , Narosa publishing house, New Delhi
8. Lafore, R. (2002) "Object Oriented Programming Using C++", Fourth Edition, Sams Publishers.

BI. SCT-1.7.1 Biostatistics and R- Programming

Total: 60 hrs

Unit I

Organization and collection of data - Data units population vs sample-Standardization of terms variables-Levels of measurement –Dealing with response and non response

Classification (Objectives and Methods-Quantitative and qualitative) Tabulation-Graphical and Diagrammatical representation-Spatial Data Analysis-summarization.

Measures of central tendencies-Arithmetic mean, Median, Mode, Percentages, Proportion, Harmonic mean, Geometric mean, Rates, Ratios, Percentiles, Indicators and Indices.

16 hrs

Unit II

Measures of Dispersion-Range, Standard deviation, standard errors and co-efficient of variation and uses, normal distributions, skewness and kurtosis.

Bivariate statistical methods-Pearson's correlation coefficient-specific measures-Measures of association- Spearman rank correlation coefficient-contingency coefficient.

Regression-Linear regression-Logistic regression-Prediction-Applications in Bioinformatics-validity & Reliability.

14 hrs

Unit III

Time variable-Survival Analysis-Life table-Life expectancy measures-Time series Data analysis- Chi-square test, t-test, F-test and Z-test, ANOVA and its types.

Concept of probability-A priori & posterior Probabilities - Laws of probability-Additive multiplicative and complementary probabilities conditional probability.

14 hrs

R-language

Unit IV

Introduction to R, R as statistical software and language, R as calculator, graphics with R. Getting data into R and R objectives, extracting subsets of data-frames by value, sorting data, merging data, exporting data, simple functions (t-apply, s-apply, summary and table). Basic plotting tools, revisiting the plot functions, loops, functions and if statements. ANOVA and test of significances. Management of biological data with R.

16 hrs

BI. SCP-1.8 Lab based on BI. SCT-1.7.1

1. Diagrammatical and graphical representation of data.
2. Examples on measures of central tendency.
3. Examples on measures of dispersion.
4. Corelation and regression. Examples on pearson correlation coefficient spearman rank coefficient, regression coefficient and equations
5. Time series analysis: examples on methods of finding measuring trend seasonal and cyclic variations
6. R- Software: Based on theory discuss all concept using R software, exercises the statistical problems with R.
7. Descriptive statistics in R- Diagrammatic and Graphical representation of data with R, measure of central tendency and dispersion, with example using R software.
8. Using R - Probability and probability distribution and Correlation and regression analysis.

References:

1. Statistics concepts and Applications Author: Harry Frank & Steven.c.Athoen
Puplications: Cambridge University Press
2. Introduction to Statistics Author: Hog and Caraig Puplications: Wiley Eastern
3. Mathematical Statistics Author: S.C.Gupta and V.K.Kapoor Publications:
Sultan Chand pulications
4. Basic Statistics Author: Dunn.O.J Publications: John Wiley & Sons
5. Principles of Statistics Author: Khan and khanamm Publications: Himalaya Publications
6. Robert G., 2008. "R-programming in Bioinformatics" CRC press, Taylor and
Francis Group, USA.
7. Own J., Robert M., and Andrew R. 2014. Introduction to scientific and simulation
using R. CRC press, Taylor and Francis Group, USA.

BI. SCT-1.7.2 Structural Bioinformatics

Total: 60 hrs

Unit I

Structural features of Biomolecules; techniques used to determine the structure of Biomolecules; methods for single crystal X-ray diffraction of macromolecules: molecular replacement method and direct method- Fiber diffraction; analysis of structures and correctness of structures; submission of data to PDB: atomic coordinates and electron density maps

Proteins: Principles and Analysis of proteins; Hierarchical organization of protein structure- Primary, Secondary, motif, domains, Tertiary, Quaternary structure, internal co-ordinates of Proteins- Theory, Derivation and significance of Ramachandran Plot.

18 hrs

Unit II

Structure of Nucleic Acids: DNA and RNA; Base pairing- Watson crick and Hoogestein; Types of DNA A,B,Z and their geometrical as well as structural features, DNA bending; Types of RNA and geometrical parameters of each and their composition, Structure of ribosome.

Molecular Interactions: Protein-Protein interaction, Structural Analysis of domain interactions, Protein- DNA interactions, Types of interactions of DNA with proteins and small molecules.

16 hrs

Unit III

Methods for prediction of secondary and tertiary structures of proteins- knowledge- based structure prediction; fold recognition; ab initio methods for structure prediction, comparative protein modeling.

Methods for comparison of 3D structure of proteins; methods to predict three dimensional structures of nucleic acids, rRNA; electrostatic energy surface generation.

16 hrs

Unit IV

Molecular mechanics and molecular dynamics of oligopeptides, proteins, nucleotides and small molecules- mechanism of dynamics of bio- macromolecules, simulation of molecular mechanics and dynamics, simulations of free energy changes; force fields. Molecular interactions of protein –protein, protein-DNA, protein-carbohydrate and DNA- small molecules.

10 hrs

BI. SCP-1.8 Lab based on BI. SCT-1.7.2

Practicals are designed based on the **BI. SCT-1.7.2 syllabus**

Reference

1. Andrew R. Leach (2001) "Molecular Modelling- Principles And Applications"; Secod Edition, Prentice Hall, USA.
2. Creighton, T.E. (1983) "Proteins: Structure And Molecular Properties:: Second Edition, W.H. Freeman And Company, New York, USA
3. Protein Structure, stability and folding Ed. K.P. Murphy (2001) Humana Press.
4. Introduction to protein architecture Arthur M. Lesk (2001) Oxford University Press.
5. Introduction of Macromolecular Crystallography – A. Mcpherson (2003) John Wiley Publications.
6. Introduction to protein structure, Branden, Carl and Tooze, John Garland Publ. Inc., 1991
7. Introduction to bioinformatics-attwood and parrysmith, pearson education.
8. Bioinformatics-A Beginner's guide by gena-michelclaverie,johnwiley&sons.
9. Structural bioinformatics by Philip.e.bourne and helgeweissing, wiley.
10. Structure and mechanism in protein science-Fresh W H freeman and co.

BI. SCT-1.7.3 Bio- instrumentation

Total: 60 hrs

Unit I - Chromatographic Techniques and Mass spectrometry

Introduction to chromatography, Planar chromatography (paper and thin layer chromatography), Column chromatography, Ion exchange chromatography, Gel-exclusion chromatography, Affinity chromatography, High performance liquid chromatography (HPLC), Mass spectrometry, Gas chromatography mass spectrometry (GC-MS), Liquid chromatography mass spectrometry (LC-MS).

15 hrs

Unit II - Electrophoresis

Introduction to electrophoresis, sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE), Discontinuous gel electrophoresis, Agarose gel electrophoresis, Pulsed field gel electrophoresis, 2- Dimensional Electrophoresis, Capillary electrophoresis, Immunoelectrophoresis.

10 hrs

Unit III – Flowcytometry

Introduction, basic components of a flow cytometer, sample preparation, limitations of the flow cytometer.

Microscopy

Principle, design and application of light microscope, phase contrast microscope, fluorescence microscope, scanning electron microscope, transmission electron microscope, scanning tunneling microscope, atomic force microscope, confocal microscope,

15 hrs

Unit IV – Spectroscopy

Nuclear Magnetic Resonance Spectroscopy, Ultraviolet-Visible Absorption Spectrometry, Fluorescence Spectrometry, X-Ray Crystallography, Infrared Spectroscopy, Atomic absorption spectrometry, plasma emission spectroscopy and Electron spin resonance spectroscopy

Omics technologies:

Conventional PCR, Real Time PCR, Sequencing Technologies (DNA and Protein) Microarray etc.

20 hrs

BI. SCP-1.8. Lab based on BI. SCT-1.7.3

Practicals are designed based on the **BI. SCT-1.7.3 syllabus**

Practicals:

1. Column Chromatography
2. Estimation of Nucleic Acid and Protein through spectrophotometer
3. Electrophoresis of DNA and Protein
4. Observation of Cell Morphology and Cell division under inverted microscope
5. Demonstration of Conventional and Real time PCR for gene amplification

REFERENCES

1. Biochemistry Laboratory: Modern theory and techniques, 2nd Edition - Rodney Boyer.
2. Bioinstrumentation. Student edition. John Wiley and Sons, Ltd - John G Webster.
3. Bioinstrumentation: Tools for understanding life, Published by National Association of Biology Teachers - James, Dennis and Lange.
4. Instrumental method of chemical analysis -Shrama BK
5. Instrumental methods of analysis- DA Skoog
6. An introduction to practical Biochemistry -Plummer
7. Instrumentation - Chatwal and Anand
8. Modern experimental Biology - Boyer

BI-OE-1.9 Basic Bioinformatics

Total: 60 hrs

Unit I

Data generation; Generation of large scale molecular biology data. (Through Genome sequencing, Protein sequencing, Gel electrophoresis, NMR Spectroscopy, X-Ray Diffraction, and microarray). Applications of Bioinformatics.

DNA and protein sequences, genome and transcriptome, open reading frames, gene structure in prokaryotes and eukaryotes, coding and non-coding genes, extracting, collecting and storing sequences; various file formats for bio-molecular sequences: GenBank, FASTA, GCG, MSF, NBRF-PIR.

20 hrs

Unit II

Introduction to data types and Source. Population and sample, Classification and Presentation of Data. Quality of data, private and public data sources. General Introduction of Biological Databases; Nucleic acid databases (NCBI, DDBJ, and EMBL). Protein databases (Primary, Composite, and Secondary). Specialized Genome databases: (SGD, TIGR, and ACeDB). Structure databases (CATH, SCOP, and PDBsum)

Flat files, relational, object oriented databases and controlled vocabularies. File Format (Genbank, DDBJ, FASTA, PDB, SwissProt). Introduction to Metadata and search; Indices, Boolean, Fuzzy, Neighboring search. The challenges of data exchange and integration. Ontologies, interchange languages and standardization efforts.

20hrs

Unit III

Introduction to Sequences, alignments and Dynamic Programming; Local alignment and Global alignment (algorithm and example), Pairwise alignment (BLAST and FASTA Algorithm) and multiple sequence alignment (Clustal W algorithm). Methods for presenting large quantities of biological data: sequence viewers (Artemis, SeqVISTA), 3D structure viewers (Rasmol, SPDBv, Chime, Cn3D, PyMol), Anatomical visualization.

10hrs

Unit IV

General introduction to Gene expression in prokaryotes and eukaryotes, transcription factors binding sites. SNP, EST, STS. Introduction to Regular Expression, Hierarchies, and Graphical models (including Markov chain and Bayes notes). Genetic variability and connections to clinical data.

Molecular structures – visualizing and graphical representations. Calculation of geometric parameters (bond distance, bond angle, dihedral angle). Identifying intramolecular and inter molecular interactions from crystal structures (using GUI).

10hrs

REFERENCES

1. N. Gautham; Bioinformatics: Databases and Algorithms; Alpha Science, 2006.
2. D. W. Mount; Bioinformatics Sequence and Genome Analysis; Cold Spring Laboratory Press, 2001.
3. F. J Burkowski; Structural Bioinformatics An Algorithmic Approach; CRC Press, 2009.
4. A. M Lesk; Introduction to Bioinformatics; Oxford University Press, 2002.
5. J. Bedell, I. Korf and M. Yandell; BLAST; O'Reilly Press, 2003.
6. J. M. Keith; Bioinformatics Vol. 1, Data, sequence analysis & evolution; Humana Press, 2008.
7. R. Durbin; Biological sequence analysis; Cambridge University Press, 1998.
8. R. M. Holmes; A cell biologists' guide to modeling and bioinformatics; Wiley Interscience, 2007.

II Semester

BI. HCT-2.1 Microbiology and Immunology

Unit-I:

Biodiversity: Introduction to microbial biodiversity – distribution, abundance, ecological niche. Three domains of life. Major groups of micro-organisms: General characteristics of Archaea, Eubacteria, Mycoplasma, Rickettsiae and Chlamydias. Bacterial classification based on 16S rRNA, cellular metabolism and fatty acids. The International Committee on Systematic Bacteriology (ICSB). Construction and analysis of phylogenetic tree.

General structure of prokaryotic cell. Growth kinetics in batch cultures. Genetic recombination in bacteria: Conjugation, Transformation and Transduction; Construction of genetic maps in bacteria. General characteristics and classification of plant and animal viruses; Structure and replication of Bacteriophage (T4 and λ), Viroids & Prions.

20hrs

Unit II

Techniques in Microbiology: Aseptic techniques in microbiology- different methods of sterilization. Techniques for isolation of microorganisms- serial dilution, streak plate, spread plate and pour plate methods.

Staining techniques (simple staining, differential staining). Structural staining- cell wall, capsule and endospore staining.

10hrs

Immunology

Unit III

Introduction and Antibodies: Innate and acquired immunity, active and passive immunity, natural and artificial immunity and humoral. Lymphoid system- primary or secondary organ. Cells- Lymphocytes, mononuclear, phagocytes, antigen presenting, polymorphs, mast cells, cluster designation (CD) and antigen specific receptors – Principles and its uses.

15hrs

Unit IV

Antibody generation: structure and function –clonal selection theory-different types of immunoglobulins, effectors, receptors and antibody diversity. Complement system activation, pathways and biological effects. Major Histochemical molecules/peptide complexes Structure and Function and production of MHC Locus in Mice and Human. T-lymphocytes and cytokine network, receptors, production from TH1 and TH2 CD4+ T- cells.

15hrs

BI. HCP-2.2. Lab based on BI. HCT-2.1

Practicals:

1. Study the parts and usage of a Compound Microscope
2. Sterilization Techniques – Moist heat and dry heat methods
3. Study of cultural colony characters- Size, shape, color etc.
4. Staining-Principles and techniques
 - i) Simple staining
 - ii) Grams staining
 - iii) Negative staining
 - iv) Motility test
5. Immuno-diffusion - Rocket immunoelectrophoresis, Agarose Gel Immunodiffusion, RIA, ELISA.

REFERENCES

1. Microbiology: Pelczar M J
2. Microbiology: Prescott L M, Harley J P and Klein D A
3. Textbook of Microbiology - Ananthanarayan
4. General microbiology - Powar & Dagainawala
5. Textbook of Microbiology - R C Dubey.
6. Practical Microbiology R.C Dubey, D.K Maheshwari, S Chand and Company, New Delhi.
7. Microbiology Laboratory Manual - Cappuccino, Sherman, Pearson Education
8. Essentials of Immunology by Riott I .M. 1998. ELBS, Blackwell Scientific Publishers, London.
9. Immunology 2 nd Edition by Kuby J. 1994. W.H. Freeman and Co. New York.
10. Immunology - Understanding of Immune System by Claus D. Elgert. 1996. Wiley -Liss, New York.
11. Fundamentals of Immunology by William Paul.
12. Cellular and Molecular Immunology. 3rd Edition by Abbas.
13. Immunobiology: The Immune System in Health and Disease. 3rd Edition by Travers.
14. Immunology- A short Course. 2 nd Edition by Benjamin.
15. Manual of Clinical Laboratory and Immunology 6th Edition. 2002 by Noel R. Rose, Chief Editor: Robert G. Hamilton and Barbara Detrick (Eds.) , ASM Publications.

BI. HCT-2.3 Perl and Python

Total: 60 hrs

Perl

Unit I

Getting Started with Perl: Overview, perl benefits, Command interpretations, commands, scalar strings, values, numbers and variables, assignments, scalar operations, and functions, statements and blocks, array variables, literal representation of arrays, array operations and functions, scalar and list context, hash variables, literal representation of hash variables, hash functions, using hashes for genetic code, gene expression data using hashes.

Operators – arithmetic operators, bitwise operators, string operators, file test operators, conditional and logical operators (true and false), logical operators, binding operators, loops, i/o functions.

15 hrs

Unit II

Programming with PERL – Representing sequence data, a program to store a DNA sequence, concatenation of strings, transcription, translation, flow control, finding motifs, counting nucleosides, conversion of sequences into FASTA format.

Subroutines, advantages of subroutines, scoping and subroutines, arguments, passing data to subroutines, modules and libraries of subroutines, concept about file handling, open and closing of file handle, opening and closing a directory handle, directory manipulations, Perl debugger, regular expressions and pattern matching, simple uses of regular expressions, matching operators, substitutions, split and join function.

10 hrs

Python

Unit III

Working with Python, An interpreter for python, Relational operators, Logical operators, Bitwise operators, Variables and assignment Statements, Keywords, Script mode.

Control structures, if-else conditional statement, Looping statements, Nested loops, break, continue and pass, Debugging, Scope of variables, Strings, String manipulations, Regular Expressions, Built-in Functions, I/O Functions, Function Definition and Call, Importing user defined modules, Command-line arguments, Mutable and Immutable objects, Recursion.

10 hrs

Unit IV

Advanced Concepts: Lists, Accessing lists, Working with lists, Operations, related Functions and Methods, Tuples, Accessing tuples, Working with tuples, Operations, related Functions and Methods, Dictionary, Working with dictionary, Accessing values in dictionaries, Working with dictionaries, Operations, related Functions and Methods.

Files and Exceptions: File Handling, Writing structures to a file, Errors and Exceptions, Handling exceptions using try-except, File processing examples.

Biopython: Working with sequences, parsing sequence file formats, connecting with biological databases, sequence objectives, sequence input and outputs, accessing biological database resources.

25hrs

BI. HCP-2.4 Lab based on BI. HCT-2.3

1. Basic operators and control flow, basic perl data types, references, matrices, complex/nested data structures, scope(my, local, our), function/subroutines, system and user function, the local operator, variable –length parameter lists, notes on lexical variable, file handle and file tests, stat and isstat functions, formats, directory access & manipulation, process management, formatting data, system information.
2. Uses of regular expressions, patterns, single-character patterns, grouping patterns (sequence, multipliers, parentheses as memory, alternation) anchoring patterns, precedence, matching operators, ignoring case, different delimiters, variable interpolation, special read-only variables, substitutions split and join functions, dynamic programming, approximate string matching.

Bioperl

3. Installing bioperl, general bioperl classes sequences (Bio::seq class, sequence manipulation), features and location classes (extracting CDS), alignments (AlignIO), analysis (BLAST, GenScan), Databases (database classes, accessing a local database), implementing REBASE.

Python

1. Programming to store a DNA sequence, concatenation, reverse complement.
2. Writing sequence files (converting between sequence file formats, converting a file of sequences to their reverse complements)
3. Getting your sequence record objects as formatted strings
4. Sequence alignment using python programming

References:

1. Perl CookBook – T.Christainsen and N.Torkington 2nd ed. 2003 O’Reilly
<http://zoic.org/tranining/nohtml/perldb.pdf> <http://doc.bioperl.org/>
2. Programming Perl – Larry Wall, Tom Christiansen & John Orwant 3ed 2000- O’ Reilly
3. James Tisdall. D. 2002. Beginning Perl for Bioinformatics, O’Reilly, Shroff Publishers and Distributors Pvt. Ltd., New Delhi.
4. Schwartz, R.T. and Tomphoenix. 2004. Learning Perl, O’Reilly, Shroff Publishers and Distributors Pvt. Ltd., New Delhi.
5. Richard L., Halterman, 2011 Learning to

BI. HCT-2.5 Genomics and Proteomics

Total: 60 hrs

Genomics

Unit I

Introduction – Genomes, Omics and its importance, general features, C-value paradox, structural and comparative genomics, transcriptomics, proteomics and metabolomics, Genome structure predictions of prokaryotes and eukaryotes. Integrated genomic maps, gene expression profiling.

Functional genomics of microbes, plants and animals: Sequencing technologies - shotgun approach, sanger sequencing, pyro-sequencing, de-novo sequencing of whole genomes, assembly of sequence reads, concept of base calling; annotation and other methods of genome alignments; EST, STS and SNPs sequence analysis.

20 hrs

Unit II

Transcriptome analysis methods: Serial Analysis of Gene Expression (SAGE) and its application. Databases of expressed sequence tag (ESTs) and data mining.

Micro arrays protocol and its application - gene expression analysis; DNA array for global expression profile; Types of DNA array, Array database; Applications of DNA microarray – analysis of gene expression, differential gene expression under different conditions and during development of organisms.

Comparative genomics- Comparative genomics, steps involved in comparative genomics, Implications of comparative genomics.

20 hrs

Proteomics

Unit III

Definition and scope: methods of proteome analysis, 2D-PAGE, DIGE, Mass spectrometry and analysis (ESI, MALDI TOF and hybrid), LC-MS, Tandem Mass spectrometry, Peptide mass finger printing – MASCOT, SALSA. Multidimensional chromatography and MuDPIT.

10 hrs

Unit IV

Protein interaction analysis: Principle, strategy and applications of tandem affinity purification (TAP), Yeast two hybrid (Y2H) systems and analysis of selective interacting domains in proteome mapping, protein structure determination and structural proteomic tools, concepts of protein engineering, proteomic databases (PRIDE, NEXTPRO), Shotgun proteomics approach for isolation and study of whole cell interactome, and interactome analysis.

10 hrs

BI. HCP-2.6. Lab based on BI. HCT-2.5

Practicals:

1. TM-HMM
2. Plasmid construction
3. Gene tool
4. Pept tool
5. Split tree
6. Detection of recombination event in viral genome using RDP software
7. Protein scope- protein structure viewer and Propred.
8. Comparative proteomics analysis 2D-PAGE gel profile to study differentially expressed proteins.
9. Mass spectrometry data analysis - Peptide mass finger printing using MASCOT.
10. Study of databases - EcoCyc, MetaCyc and BioCyc, PantherDB, Reactome, Biocarta, StringDB, PRIDE, NEXTPRO.
11. Mathematical modeling and simulating of Biochemical network
12. Import and simulate models from different databases
13. To Import and simulate a model from the repository

REFERENCES

1. Genomics: The Science and Technology Behind the Human
2. Genome Project (2000). Edited by C.Cantor and C.L.Smith, Wiley -Interscience, New York.
3. Genome Analysis – A practical Approach (1995) by J.M. Davies, Oxford University Press, Oxford.
4. Genome Mapping – A Practical Approach (1997) by P.H. Dear, Oxford University Press, Oxford.
5. Genome Analysis – A Practical Approach (1990). Edited by K.E Davies, IRL Press, Oxford.
6. The Human Genome (1992) by T. Strachan. BIOS Scientific Publishers Limited, Oxford.
7. Proteine Research: New Frontiers in Functional Genomics (1997).Edited by M.R. Wilkins, K.L. Williams, R.D.Appel and D.F.
8. Expression Genetics: Acclerated and High Throughput Methods (1999) Edited by M.McClelland and A. Pardee, Eaton Publishing, MA.

BI. SCT-2.7.1 Biological data Analytics

Total: 60 hrs

Unit – I

Introduction to Bioinformatics: History of Bioinformatics, Role of Bioinformatics in biological sciences, scope of bioinformatics. Introduction to Database: Types of database. Biological Database: Need of biological database, Sequence and Structure database – (GenBank, ENA, DDBJ, PIR, Uniprot and PDB), Protein Structure Visualization tools.

Sequence Alignment and Motif, Domain Prediction Pairwise Alignment: Dot Matrix Method, Dynamic programming - (Local and Global Alignment). Scoring Matrices: Amino acid scoring matrices, PSSM, PAM, BLOSUM. Database Similarity Searching: BLAST and FASTA, BLAST variants. BLAST output format.

Multiple Sequence Alignment, Introduction to Phylogenetic: Phylogenetic Basics, Terminologies. Phylogenetic Tree construction Methods: Distant based method - (UPGMA, NJ) Character Based Method – (MP and ML), Phylogenetic Tree Evaluation: Bootstrapping.

24 hrs

Unit - II

Gene and Promoter Prediction and Phylogenetic Gene Prediction methods: Conventional determination of Open Reading Frames (ORF), Markov model and HMM., Promoter and Regulatory Element Prediction.

Protein Structure Prediction and Molecular Dynamics Globular Proteins: Ab-initio, Homology Based, Neural networks method. Transmembrane Proteins: Prediction of Helical membrane, β -barrel membrane proteins. Introduction to Homology modeling: Model refinement, model evaluation, homology model databases. Threading and fold recognition, CASP.

16 hrs

Unit - III

Introduction of Molecular Modeling: Coordinate system, potential energy. Steps in Molecular Modeling: introduction to Quantum Mechanics, introduction to Molecular mechanics. Force Filed: Types of force fields: Amber force field, CHARMM force field. Introduction about molecular dynamics (GROMACS).

10 hrs

Unit IV

Drug Discovery Introduction: Drug Discovery Process, Molecular Modeling in Drug Discovery, Molecular Docking, Quantitative Structure-Activity Relationship (QSAR). Docking and Virtual Screening: Using different docking algorithms, Optimization of docking algorithms based on different target. Ligand - Receptor Interactions: Docking software's (AUTODOCK, LEAD IT), Post docking analysis. Pharmacokinetics: Absorption, Distribution, Metabolism, Excretion and Toxicity of drugs.

10 hrs

References

1. David W Mount, "Bioinformatics sequence and Genome analysis", Second Edition, Cold Spring Harbor Laboratory Press, 2013.
2. Attwood T K, D J Parry-Smith, "Introduction to Bioinformatics", Pearson Education, 2005.
3. Neil C. Jones and Pavel A. Pevzner, "An Introduction to Bioinformatics Algorithms", MIT Press, 2005. 2. Steffen Schulze-Kremer, "Molecular Bioinformatics: Algorithms and Applications", Walter de Gruyter, 1996.

BI. SCT-2.7.2 Image Processing

Total: 60 hrs

Unit I

Digital Image and its properties: Basic concepts, Image digitization, Digital image properties.

Image Pre-Processing: Brightness and geometric transformations, local preprocessing.

16 hrs.

Unit II

Segmentation: Thresholding, Edge-based segmentation, Region based segmentation, Matching.

Image enhancement in the spatial domain: Background, Some basic gray level transformations, Histogram processing, Enhancement using arithmetic/logic operations, Basics of spatial filtering, Smoothing spatial filters, Sharpening spatial filters.

18 hrs

Unit III

Image enhancement in the frequency domain: Background, Introduction to the Fourier transform and the frequency domain, Smoothing, Frequency-Domain filters, Sharpening Frequency Domain filters, Homomorphic filtering.

16 hrs

Unit IV

Image compression: Fundamental, Image compression models, Elements of information theory, Error-Free Compression, Lossy compression.

Region identification, Contour-based shape representation and description Region based shape representation and description, Shape classes. Morphology: Basic morphological concepts, Morphology principles, Binary dilation and erosion, Gray-scale dilation and erosion, Morphological segmentation and watersheds.

10 hrs

REFERENCE BOOKS:

1. *Milan Sonka, Vaclav Hlavan and Roger Boyle*, "Image Processing, Analysis and Machine Vision", Thomson Learning, Brooks/Cole, 2nd Edition. 2001. [Chapters 2,4 (4.1 to 4.3), 5 (5.1 to 5.4), 6, 11 (11.1 to 11.4, 11.7)].
2. *Rafel C Gonzalez and Richard E Woods*, "Digital Image Processing", Pearson Education, 2nd Edition, 2003. [Chapters 3 (3.1 to 3.7), 4 (4.1 to 4.5), 8 (8.1 to 8.5)]
3. *Anil K Jain*, "Fundamentals of Digital Image Processing", 1997, Pearson Education / Prentice- Hall of India Pvt., Ltd.
4. *B. Chanda D Dutta Majumder*, "Digital Image Processing and Analysis", 2002, Prentice-Hall, India.

BI. SCP-2.8.2 Lab based on BI. SCT-2.7.2

PRACTICALS

MATLAB based practical image processing.

BI. SCT-2.7.3 CGI

Total: 60 hrs

Unit I

Introduction on CGI, Applications of CGI, Some Working CGI Applications, Internal Workings of CGI, Configuring the Server, Programming in CGI, CGI Considerations.

Input to the Common Gateway Interface: Using Environment Variables, Accessing Form Input, Extra Path Information, Other Languages Under UNIX.

16 hrs

Unit II

Other Languages Under Microsoft Windows, Other Languages on Macintosh Servers, Examining Environment Variables.

Output from the Common Gateway Interface, Forms and CGI,HTML Tags, Sending Data to the Server, Designing Applications Using Forms in Perl,

16 hrs

Unit III

Decoding Forms in Other Languages, Environment Variables, Including Boilerplates, File Statistics, Executing External Programs, Executing CGI Programs.

Common Gateway Interface:- Web Servers and Browsers, HTML tags, table, frames, form elements, GET, POST & HEAD Method, URL Encoding, Extra Path Information, CGI.pm Module, Passing Parameters via CGI, Less Typing, Server Side Includes, Debugging CGI programs, Stepping through programs, Breakpoints, Line Action

18 hrs

Unit-IV

Debugging CGI programs WEB DESIGNING & XML: HTML Specifications and Syntax, XML Basics, Style Sheets, XML Applications, Java Script.

10 hrs

BI. SCP-2.8.3 Lab based on BI. SCT-2.7.3

URL encoding, CGI environment variables, handling forms, accessing form input, extra path information, CGI.pm module, passing parameters via CGI, less typing, server side includes, debugging CGI programs, stepping through programs, breakpoints, line action

References:

Erick Storm, "Perl CGI Programming", BPB Publication, 1998

BI-OE-2.9 Bioinformatics for Life science

Total: 60 hrs

Unit I

Nature and scope of life science: Branches of life sciences, Characteristics of life, Levels of Organization, Origin of life, Biochemical evolution- evolution of Proteins and Nucleotide.

Cell Biology: The cell as basic unit of life- Prokaryotic cell and Eukaryotic cell, Cell Structure and Function- cell membrane, cell organelles, Cell Division; Mitosis & Meiosis.

Cell Energetics: Laws of Thermodynamics, Photosynthesis, Anaerobic & aerobic respiration, Structure and function of mitochondria, respiratory pathways: Glycolysis, Krebs's Cycle, Electron transport chain.

20 hrs

Unit II

Chromosome-Genome-Genes-Databases: Bio-molecules- DNA, RNA, Protein and amino acids, Chargaff's Rules, Codon bias, GC content. Central Dogma: Replication, Transcription, Translation, Post transcriptional & post translational modifications, RNA processing, RNA splicing and RNA editing. Sense/coding and anti-sense/template strands, Genetic code, wobble hypothesis. Introduction to DNA and Protein sequencing, Human Genome Project, Bioinformatics databases, Type of databases, Nucleotide sequence databases, Primary nucleotide sequence databases-EMBL, Gene Bank, DDBJ; Secondary nucleotide sequence databases.

15 hrs

Unit III

Proteins and Databases: Protein structure and function, Protein Primary structure, Amino acid residues, Secondary, Tertiary, Quaternary Structure of Protein, Protein sequence databases- SwissProt/ TrEMBL, PIR, Sequence motif databases -Pfam, PROSITE, Protein structure databases, Protein Data Bank-SCOP, CATH, KEGG, ChEMBL, Sequence, structure and function relationship.

10 hrs

Unit IV

Introduction to Computational Biology and Bioinformatics: Nature and scope of Computational Biology and Bioinformatics, Basic algorithms in Computational Biology, Introduction to sequence alignment (only general ideas, not algorithm) - Local and global, pair wise and multiple, BLAST.

Applications of Bioinformatics in various fields of life science: Environment, biotechnology, molecular biology, neurobiology, agriculture, drug designing, biomedical genome medicines, medical microbiology.

15 hrs

REFERENCES:

1. Becker, W. M., Kleinsmith, L. J., Hardin, J., & Raasch, J. (2003). The world of the cell (Vol. 6). San Francisco: Benjamin Cummings.
2. Berg, J. M., Tymoczko, J. L., & Stryer, L. (2002). Biochemistry, ; W. H.
3. Claverie, J., M., Notredame, C. (2003). Bioinformatics: A Beginner's Guide. Wiley India Pvt. Limited. Devasena, T. (2012). Cell Biology. Published by Oxford University Press.

4. Fall, C.P., Marland, E.S., Wagner, J.M., Tyson, J.J.(2002). *Computational Cell Biology*. Springer.
5. Hausman, R. E., & Cooper, G. M. (2004). *The cell: a molecular approach*.ASM, Washington, DC.
6. Karp, G. (2009). *Cell and Molecular Biology: Concepts and Experiments*. John Wiley & Sons.
7. Kuriyan, J., Konforti, B., & Wemmer, D. (2012). *The molecules of life: Physical and chemical principles*. Garland Science.
8. Lewin, B. (2011). *Lewin's genes X (Vol. 10)*. J. Krebs, S. T. Kilpatrick, & E. S. Goldstein (Eds.). Jones & Bartlett Learning.
9. Lodish, H. (2008). *Molecular cell biology*. Macmillan.
10. Mason, K. A., Losos, J. B., Singer, S. R., & Peter, H. Raven, and George B. Johnson.(2011). *Biology*.
11. Misener, S., Krawetz, S.A.(1999). *Bioinformatics Methods and Protocols*. Humana Press.
12. Moody, G. (2004). *Digital code of life: how bioinformatics is revolutionizing science, medicine, and business*. John Wiley& Sons.
13. Nelson, D. L., Lehninger, A. L., & Cox, M. M. (2008). *Lehninger principles of biochemistry*. Macmillan.
14. Old, R. W., & Primrose, S. B. (1981). *Principles of gene manipulation: an introduction to genetic engineering (Vol. 2)*. Univ of California Press.
15. Rastogi, S. C. (2005). *Cell biology*. New Age International.
16. Reece, J. B., Taylor, M. R., Simon, E. J., & Dickey, J. (2009). *Biology: concepts & connections (Vol. 3, p. 2)*. Pearson/Benjamin Cummings.
17. Wünschiers, R. (2004). *Computational Biology: Unix/Linux, data processing and programming*. Springer.
18. Zvelebil, M. J., & Baum, J. O. (2008). *Understanding bioinformatics*. Garland Science.

III Semester

BI.HCT-3.1 System Biology and Drug Designing

Total: 60 hrs

Unit I

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

6 hrs

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. Cellular models. Networks and Motifs: Gene Networks, Lambda receptor and Lac operon as an example.

Design of Circuits and Databases: Introduction- databases KEGG, PantherDB, Reactome, Biocarta, StringDB, Expression databases and various databases related to systems biology.

16 hrs

Unit III

Drug Discovery: Basics, technologies and strategies.

Historical perspective, objectives and strategies of drug discovery, animal models in drug discovery, management and regulatory issues, important parameters in drug discovery, process of drug discovery, computational techniques, areas influencing drug discovery, modeling, simulation and algorithms in drug discovery. Use of chemical databases in identifying drug targets, G-protein coupled receptors as drug targets.

Drug Designing techniques and approaches. Preclinical Pharmacology, Pharmacological screening of Candidate molecules, Clinical trials.

Target identification and Target validation - Molecular modelling and simulation.

20 hrs

Unit IV

Concept of lead, lead identification and lead optimization, Computer Aided Drug Design (CADD) Structure based drug design (SBDD) and Ligand Based Drug Design (LBDD); Specific activity relationship (SAR), Quantitative Structure Activity Relationship (QSAR) methods and applications. Combinatorial chemistry and virtual screening.

Pharmacogenomics: Hereditary basis for differences in population, Examples of pharmacogenetic traits. Enzymes involved in the metabolism of drugs. Pharmacological Technology.

Association between Genome data and drug response pattern. Analysis of variation among the population by polymorphism. Pharmacogenetic and Pharmacogenomics applications.

18 hrs

BI. HCP-3.2 Lab based on BI. HCT-3.1

1. Chemical databases
2. Pharmacophore identification
3. Protein structure database
4. Homology modelling
5. Binding site/active site identification
6. Computational Toxicity and druggability studies
7. Computational pharmacokinetics studies
8. Computed atlas of surface topography of protein (cast p).
9. Software - V-Life, Marvin sketch, Chems sketch, etc
10. Molecular Docking studies (Autodock)
11. QSAR studies
12. *In silico* Protein-protein interaction studies

References

1. Molecular Modelling, Principles and Applications, IInd Edition, A.R. Leach, 2001, Prentice Hall
2. Proteine Research: New Frontiers in Functional Genomics (1997). Edited by M.R. Wilkins, K.L. Williams, R.D.Appel and D.F. Hochstrasser, Springer – Verlag, New York.
3. Expression Genetics: Acclerated and High Throughput Methods (1999) Edited by M.McClelland and A. Pardee, Eaton Publishing, MA.
4. 2-D Proteome Analysis Protocols (1998). Edited by A.L. Link, Humana Press, Totowa, NJ.
5. Proteins and Proteomics. 2002. R.J. Simpson. Cold Spring Harbor Lab. Press. New York.

BI.HCT-3.3 Genetic Engineering and Protein Engineering

Total: 60 hrs

Unit I

Tools and methods for genetic engineering: Restriction endonucleases, DNA and RNA modifying enzymes – types and properties Introduction to cloning vectors pUC, BACs, YACs, shuttle vectors Overview of molecular cloning – primer design and PCR, gene cloning strategies and construction of cDNA and genomic libraries.

Preparation of competent cells, transformation and transfection techniques (chemical and physical methods). Selection, screening and analysis of recombinants using restriction mapping, blotting and sequencing methods. Autoradiography and autofluorography.

10 hrs

Unit II

Genome editing technologies: Transposable genetic elements, Recombinases, Cre and FLP recombinases and their mode of action, recombination mediated cassette exchange (RMCE), use of sitespecific recombinases in genome manipulation. Zinc Finger Nuclease (ZFN) technology, its uses and limitations. Transcription activator like effector nuclease (TALENs) design and applications. Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR) and CRISPR associated (Cas) systems in prokaryotes, application and types of CRISPR/Cas9 technology, uses in genome manipulation and biotechnology. Successful examples of using gene editing in gene therapy and crop improvement. Ethical issues in genome editing. Basic techniques involved in rDNA technology; Enzymes involved in RDT (Klenow fragment, Taq DNA, Ribonucleases, Alkaline phosphatase, Nuclease, T4 DNA ligase) Restriction enzymes.

20 hrs

Unit III

Protein engineering – definition, applications; Features or characteristics of proteins that can be engineered (definition and methods of study) – affinity and specificity; Spectroscopic properties; Stability to changes in parameters as pH, temperature and amino acid sequence, aggregation propensities, etc. Protein engineering with unnatural amino acids and its applications.

Methods of measuring stability of a protein; Spectroscopic methods to study physicochemical properties of proteins: far-UV and near-UV CD; Fluorescence; UV absorbance; ORD; Hydrodynamic properties–viscosity, hydrogen-deuterium exchange; NMR spectroscopy.

15 hrs

Unit IV

Experimental methods of protein engineering: directed evolution like gene site saturation mutagenesis; Module shuffling; Guided protein recombination, etc., Optimization and high throughput screening methodologies like GigaMetrix, High throughput microplate screens etc., Application to devices with bacteriorhodopsin as an example; Engineering antibody affinity by yeast surface display; Applications to vaccines, Peptidomimetics and its use in drug discovery.

Computational approaches: Computational approaches to protein engineering: sequence and 3D structure analysis, Protein design, Directed evolution for protein engineering and its potential.

15 hrs

Suggested Readings

1. Recombinant DNA: Watson
2. Genetic engineering: Sandya Mitra
3. Brown TA, Genomes, 3rd ed. Garland Science 2006
10. Genetic Engineering of Animals, A.Puhler, 1993. VCH Publishes, Weinheim FRG.
11. Edited by T E Creighton, (1997), Protein Structure: a Practical Approach, 2nd Edition, Oxford university press.
2. Cleland and Craik, (2006), Protein Engineering, Principles and Practice, Vol 7, Springer Netherlands.
3. Mueller and Arndt, Protein Engineering Protocols, 1st Edition, Humana Press.
4. Ed. Robertson DE, Noel JP, (2004), Protein Engineering Methods in Enzymology, 388, Elsevier Academic Press.
5. J Kyte; (2006), Structure in Protein Chemistry, 2nd Edition, Garland publishers.

BI. HCP-3.4 Lab based on BI. HCT-3.3

Practicals

1. Isolation of genomic DNA from bacteria/plant/Animal.
2. Isolation of plasmid DNA from bacteria.
3. Restriction digestion analysis.
4. Ligation of restricted fragments.
5. Restriction mapping: Analysis of maps for suitable molecular biology experiment by using bioinformatics tools
6. Transformation of rDNA in E. coli by electroporation method.
7. PCR amplification study using thermal cycler and analysis of the products.
8. Competent cell preparation.
9. Preparation of competent cells in E.coli and yeast.
10. Western and southern blotting.
11. Protein electrophoresis-1D+2D

12. HPLC
13. FPLC
14. MALDI-TOF
15. LC-MS

BI.SCT-3.5.1 Artificial Intelligence and Image Processing in Life Science

Total: 60 hrs

Unit I

Introduction to Artificial Intelligence: Introduction to Artificial Intelligence, Problems, Approaches and tools for Artificial Intelligence. Introduction to search, Search algorithms, Heuristic search methods, Optimal search strategies. Use of graphs in Bioinformatics. Grammars, Languages and Automata. Current Techniques of Artificial Intelligence: Probabilistic approaches: Introduction to probability, Bayes' theorem, Bayesian networks and Markov networks.

Classification Methods: Linear Classifiers & Logistic Regression, Linear Classifiers, Overfitting & Regularization in Logistic Regression, Decision Trees, Preventing Overfitting in Decision Trees, Handling Missing Data, Clustering and retrieval of data, Nearest Neighbor Search, Clustering with kmeans, Hierarchical Clustering.

20hrs

Unit II

Agents– Problem formulation– uninformed search strategies – heuristics – informed search strategies – constraint satisfaction. Study of Ethical, legal and social issues associated with AI.

Supervised learning (parametric/non-parametric algorithms, support vector machines, kernels, neural networks, Unsupervised learning (clustering, dimensionality reduction, recommender systems, deep learning, Best practices in machine learning (bias/variance theory; innovation process in machine learning and AI, Support vector machines (SVMs), case studies and applications.

10hrs

Unit III

Genetic programming – Method, Applications, Guidelines and Bioinformatics applications. Boolean Networks, Bayesian Networks and Fuzzy Neural Networks with case studies. Learning from observation - Inductive learning – Decision trees – Explanation based learning – Statistical Learning methods - Reinforcement Learning

Digital Image and its properties: Basic concepts, Image digitization, Digital image properties. Image Pre-Processing: Brightness and geometric transformations, local preprocessing.

10hrs

Unit IV

Segmentation: Thresholding, Edge-based segmentation, Region based segmentation, Matching. Image enhancement in the spatial domain: Background, Some basic gray level transformations, Histogram processing, Enhancement using arithmetic/logic operations, Basics of spatial filtering, Smoothing spatial filters, Sharpening spatial filters. Image enhancement in the frequency domain: Background, Introduction to the Fourier transform and the frequency domain, Smoothing, Frequency-Domain filters, Sharpening Frequency Domain filters, Homomorphic filtering.

Image compression: Fundamental, Image compression models, Elements of information theory, Error-Free Compression, Lossy compression. Region identification, Contour-based shape representation and description Region based shape representation and description, Shape classes.

20hrs

BI. HCP-3.6.1 Practicals:

Artificial Neural Network exercises - Genetic Algorithm/Programs - Fuzzy Logic Programs - Feature selection/Extraction - Protein structure prediction - Classification – Clustering - Regression/Non-linear models

References

1. Artificial Intelligence: A Modern Approach (3rd Edition) by Stuart Russell and Peter Norvig (Dec 11, 2009)
2. Artificial Intelligence: Foundations of Computational Agents by David L. Poole and Alan K. Mackworth (Apr 19, 2010)
3. Machine Learning: An Algorithmic Perspective (Chapman & Hall/Crc Machine Learning & Pattern Recognition) by Stephen Marsland (Apr 1, 2009)
4. Intelligent Bioinformatics: The Application of Artificial Intelligence Techniques to Bioinformatics Problems by Edward Keedwell and Ajit Narayanan (Jun 20, 2005)
5. Gene Expression Programming: Mathematical Modeling by an Artificial Intelligence (Studies in Computational Intelligence) by Candida Ferreira (Jul 11, 2006)

BI.SCT-3.5.2 Sequence Analysis

Total: 60 hrs

Unit I

Sequence Analysis – Basic concepts of sequence similarity, identity and homology, definitions of homologues, orthologues, paralogues and xenologues Scoring matrices: basic concept of a scoring matrix, Matrices for nucleic acid and proteins sequences, PAM and BLOSUM series, matrix derivation methods and principles. Repeats: Tandem and Interspersed repeat finding, Motifs, consensus, position weight matrices.

Pairwise sequence alignment – Basic concepts of sequence alignment, gap penalties, Needleman and Wunsch, Smith and Waterman algorithms for pairwise alignments and application in Nucleic acid and protein sequences alignments. Multiple sequence alignments (MSA) – The need for MSA, basic concepts of various approaches for MSA (e.g. progressive, hierarchical etc.).

20hrs

Unit II

Algorithm of CLUSTALW and PileUp and application, concept of dendrogram and its interpretation, Use of HMMbased Algorithm for MSA (e.g. SAM method).

Comparative Genomics – Basic concepts, Applications of Comparative Genomics: Identifications of Protein coding genes, Regulatory Regions, virulence factors / pathogeneity islands; Reconstruction of metabolic pathways, Genome analysis tools : Artemis, Geneplot .

15hrs

Unit III

Sequence patterns and profiles – Basic concept and definition of sequence patterns, motifs and profiles, various types of pattern representations viz. consensus, regular expression (Prosite-type) and sequence profiles; profile-based database searches using PSI-BLAST, analysis and interpretation of profile-based searches.

Algorithms for derivation and searching sequence patterns – MEME, PHI-BLAST, SCanProsite and PRATT. Algorithms for generation of sequence profiles: Profile Analysis method of Gribskov, HMMer, PSI-BLAST.

15hrs

Unit IV

Molecular Phylogenetics – Phylogenetics Basics: Molecular Evolution and Molecular Phylogenetics, Terminology, Gene Phylogeny versus Species Phylogeny, Forms of Tree Representation; Phylogenetic Tree Construction Methods and Programs: Distance-Based Methods, Character-Based Methods, Phylogenetic Tree Evaluation, Phylogenetic Programs.

10hrs

Text Books:

1. Bioinformatics: Sequence and Genome Analysis by Mount D., Cold Spring Harbor Laboratory Press, New York. 2004

2. Bioinformatics- a Practical Guide to the Analysis of Genes and Proteins by Baxevanis, A.D. and Francis Ouellette, B.F., Wiley India Pvt Ltd. 2009

Reference Books:

a. Introduction to Bioinformatics (1st Edition) by Arthur M. Lesk, Oxford University Press, 2002

b. Bioinformatics in the Post-Genomic Era by Jeffrey Augen, Addison-Wesley Publisher, 2004

BI.SCT-3.5.3 Biomolecular Modeling and Simulation

Total: 60 hrs

Unit I

Computational Chemistry: concepts of computational chemistry-Born-Oppenheimer approximations, Application of Hartree-Fock equations to molecular systems, approximate molecular orbital theories, semi-empirical methods. Macro-molecular force fields, salvation, long range forces.

Molecular Mechanics: Introduction, The Morse Potential, The Harmonic Oscillator Model for Molecules, Comparison of Morse and Harmonic Potential, Two atoms connected by a bond, Poly atomic Molecules, Energy due to Stretch, Bend, Stretch-Bend, Torsional strain, van der Waals and Dipole Dipole 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.

20hrs

Unit II

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

10 hrs

Unit III

Energy minimization: Steepest descent, conjugate gradient – Derivatives, First order steepest decent and conjugate gradients. Second order derivatices Newton-Raphson, Minima, maxima saddle points and convergence criteria.-non derivatives minimization methods, the simplex, sequential univariate .

10 hrs

Unit IV

Simulation methods : Newton's equation of motion, equilibrium point, radial distribution function, pair correlation functions, MD methodology, periodic box, Solvent access, Equilibration, cutoffs, algorithm for time dependence; leapfrog algorithm, Verlet algorithm, Boltzmann velocity, time steps, duration of the MD run, Starting structure, analysis of MD job, uses in drug designing, ligand protein interactions. Various methods of MD, Monte Carlo, systematic and random search methods. Differences between MD and MC, Energy, Pressure, Temperature, Temperature dynamics, simulation software's. Various methods of MD, Monte Carlo, systematic and random search methods.

20 hrs

References

1. Computational Chemistry and Molecular Modeling-Principles and Applications by Ramachandran, Deepa and Namboori, 2008, Springer_Verlag. Reference for Unit 1 and 2.
2. Molecular Modeling Principles and Applications (2nd Ed.) by Andrew R. Leach, Prentice Hall, USA. 2001
3. Molecular Modelling for Beginners, (2nd Edition) by Alan Hinchliffe, John Wiley & Sons Ltd. 2008
4. Molecular Modeling and Simulation – An interdisciplinary Guide by Tamar Schlick, Springer-Verlag.

2000

5. Computational medicinal chemistry for drug discovery edited by Patrick Bultinck, Marcel Dekker Inc. 2004

BI. HCP-3.6.3 Lab based on BI. SCT-3.5.3

Practicals are designed based on the BI.SCT-3.5.3 Biomolecular Modeling and Simulation syllabus

BI. OET-3.8 Medical Bioinformatics

Total: 60 hrs

Unit I

Medical Informatics: Introduction – Medical Informatics, Bioinformatics, Health Informatics, Structure of Medical Informatics, Functional capabilities of Hospital Information System, On-line services and Off line services, Dialogue with the computer.

Medical Standards: Evolution of Medical Standards, IEEE 11073, HL7, DICOM, IRMA, LOINC, HIPPA, Electronics Patient Records, Healthcare Standard Organizations, JCAHO (Joint Commission on Accreditation of Healthcare Organization), JCIA (Joint Commission International Accreditation), Evidence Based Medicine, Bioethics.

20 hrs

Unit II

Medical Data Storage And Automation: Representation of Data, Data modeling Techniques, Relational Hierarchical and network Approach, Normalization techniques for Data handling - Plug-in Data Acquisition and Control Boards, Data Acquisition using Serial Interface, Medical Data formats, Signal, Image and Video Formats, Medical Databases, Automation in clinical laboratories, Intelligent Laboratory Information System, PACS.

15 hrs

Unit III

Health Informatics: Bioinformatics Databases, Bio-information technologies, Semantic web and Bioinformatics, Genome projects, Clinical informatics, Nursing informatics, Public health informatics, Education and Training.

Recent Trends In Medical Informatics: Medical Expert Systems, Virtual reality applications in medicine, Virtual Environment, Surgical simulation, Radiation therapy and planning, Telemedicine, virtual Hospitals, Smart Medical Homes, Personalized e-health services, Biometrics, GRID and Cloud Computing in Medicine.

15 hrs

Unit IV:

Clinical research: History, Evolution (Nuremberg code, Declaration of Helsinki, Belmont report, ICH GCP formation) and future of clinical research. Domains in clinical research: Clinical trial/operations, data management, pharmacovigilance, medical writing etc.

10 hrs

References:

1. R.D.Lele, "Computers in medicine progress in medical informatics", Tata McGraw Hill Publishing Ltd, 2005.
2. Mohan Bansal, "Medical informatics", Tata McGraw Hill Publishing Ltd, 2003.
3. Orpita Bosu and Simminder Kaur Thukral, "Bioinformatics Databases, Tools and Algorithms", Oxford University press, 2007.
4. Yi Ping Phoebe Chen, "Bioinformatics Technologies", Springer International Edition, New Delhi

IV Semester

BI.HCT-4.1 Medical informatics

Total: 60 hrs

Unit I

MEDICAL INFORMATICS: Introduction – Medical Informatics, Bioinformatics, Health Informatics, Structure of Medical Informatics, Functional capabilities of Hospital Information System, On-line services and Off line services, Dialogue with the computer.

MEDICAL STANDARDS: Evolution of Medical Standards, IEEE 11073, HL7, DICOM, IRMA, LOINC, HIPPA, Electronics Patient Records, Healthcare Standard Organizations, JCAHO (Joint Commission on Accreditation of Healthcare Organization), JCIA (Joint Commission International Accreditation), Evidence Based Medicine, Bioethics.

20 hrs

Unit II

MEDICAL DATA STORAGE AND AUTOMATION: Representation of Data, Data modeling Techniques, Relational Hierarchical and network Approach, Normalization techniques for Data handling - Plug-in Data Acquisition and Control Boards, Data Acquisition using Serial Interface, Medical Data formats, Signal, Image and Video Formats, Medical Databases, Automation in clinical laboratories, Intelligent Laboratory Information System, PACS.

15 hrs

Unit III

HEALTH INFORMATICS: Bioinformatics Databases, Bio-information technologies, Semantic web and Bioinformatics, Genome projects, Clinical informatics, Nursing informatics, Public health informatics, Education and Training.

Medical Expert Systems, Virtual reality applications in medicine, Virtual Environment, Surgical simulation, Radiation therapy and planning, Telemedicine, virtual Hospitals, Smart Medical Homes, Personalized e-health services, Biometrics, GRID and Cloud Computing in Medicine.

15 hrs

Unit IV:

Clinical research: History, Evolution (Nuremberg code, Declaration of Helsinki, Belmont report, ICH GCP formation) and future of clinical research. Domains in clinical research: Clinical trial/operations, data management, pharmacovigilance, medical writing etc.

10 hrs

REFERENCES:

5. R.D.Lele, "Computers in medicine progress in medical informatics", Tata McGraw Hill Publishing Ltd, 2005.
6. Mohan Bansal, "Medical informatics", Tata McGraw Hill Publishing Ltd, 2003.
7. Orpita Bosu and Simminder Kaur Thukral, "Bioinformatics Databases, Tools and Algorithms", Oxford University press, 2007.
8. Yi Ping Phoebe Chen, "Bioinformatics Technologies", Springer International Edition, New Delhi

BI. HCP-4.2 Lab based on BI.HCT-4.1

PRACTICAL

1. Study of different Medical data formats.
2. Study of disease mechanism using KEGG
3. Study of human genome and various gene locations using Ensembl.
4. Variant analysis in the genome of cancer patient.
5. Study of virtual hospital
6. Study on e-health care services

BI.SCT-4.3.1 Research Methodology, IPR and Bioethics

Total: 60 hrs

Unit I

Research: Definition, Importance and Meaning of Research, Objectives of research, Characteristics of Research, Types of Research. Steps in Research; Identification, Selection and Formulation of Research Problem, Research Questions, Research Design, Formulation of Hypothesis, Review of Literature. Problems encountered by researchers in India.

Scientific report writing: Introduction to Scientific papers and Journals, computer and internet application in Research. Preparation of Manuscript; Author instructions, Methodology, modes of paper communication, criteria for publication.

20 hrs

Unit II

Thesis writing: Abstract, Introduction, Review of Literature, Materials and Methods, Results and Discussion, Summary and Conclusion and References. Presentation of a scientific Paper / Document: Preparation of Oral Presentation and Poster Presentation for conferences. Use of Audio-Visual aids in Presentation.

Parametric Tests: Testing of significance Mean, Proportion, Variance and Correlation, Testing for Significance of Difference between Means, Proportions, Variances and Correlation Co efficient. Chi-square tests, ANOVA One way and two ways.

18 hrs

Unit III

Research Report: Types of Reports, Styles of reporting, Steps in drafting reports, editing the final draft, evaluating the final draft.

Introduction to IPR and Patents: Intellectual property, Protection of Intellectual property, World intellectual property organizations, Forms of protection- patent, copyright, trademark, trade secrets, geographical indications,. Criteria and procedure of patenting, patenting biological material. Patent procedure in India. Types of patenting, Patenting of biological materials with examples and case studies.

14 hrs

Unit IV

Plant breeder's right: UPOV, Breeders exemption, Plant variety protection in India. Farmer's right, advantages and disadvantages of PBR. Technology transfer Introduction, types of technology transfer and Indian scenario.

8 hrs

Reference Books:

1. Research Methodology, Method and Techniques by C.R. Kothari or by Santosh Gupta.
2. Research Methodology by Gurumani.

3. Introduction to Biotechnology by B. D. Singh..
4. Bandarkar, P.L. and Wilkinson T.S. (2000): Methodology and Techniques of Social Research, Himalaya Publishing House, Mumbai.
5. Batnagar, G.L. (1990): Research Methods and Measurements in Behavioral and Social Sciences, Agri. Cole Publishing Academy, New Delhi.
6. Mukherjee, R. (1989): The Quality of Life: Valuation in Social Research, Sage Publications, New Delhi.
7. Biju Dharmapalan (2012). Scientific Research Methodology. Narosa Publications, New Delhi
8. Kothari, C.R. (2000) Research Methodology- Methods and Techniques, 2nd edition, New age International (P) Ltd. Publishers, New Delhi,
9. Gupta, S.F., (2002). Statistical Methods, Sultana Chand and Sons, 31 Revises Edition,

BI.SCT-4.3.2 Data mining and Machine learning

Total: 60 hrs

Unit I

Introduction – Introduction, Importance of 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.

20 hrs

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.

16 hrs

Unit III

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

Clustering Methods – Clustering Analysis, Types data in clustering analysis: Scaled variable, Binary variables, Variables of Mixed Types.

16hrs

Unit IV

Partitioning Methods: K-means and K-Medoids, Model-Based Methods, Data Mining Applications: Data mining for Biomedical and DNA Data Analysis.

8 hrs

References:

1. Data Mining Concepts and Techniques – Jiawei Hen, Micheline Kambler, Academic Press Morgan Kaufman Publishers. 2006
2. Data Mining: Practical machine learning tools Techniques with java implementation by Ian H.Witten, Eibe Frank, 2005.
3. Machine Learning and data mining in pattern recognition in third International conference MLDM, by Petra Perner and Azriel Rosenfield, Springer.2003

BL.SCT-4.3.3 High Throughput Technologies

Total: 60 hrs

Unit I

High-throughput sequencing technology

Introduction to Omic's technologies, Next-generation sequencing; Genome Alignment, Genome Visualization, De Novo Assembly Genome Variation.

Quantitative transcriptomics: qRT-PCR; Advanced transcriptomics: gene expression microarrays, Next-generation sequencing in transcriptomics: RNA-seq experiments; Analysis of transcription factor binding sites.

14 hrs

Unit II

Information processing from Sequence data

Organizing high throughput data; Analysis of Genome, Transcriptome, Metagenome, miRNA and Epigenomics data; Multiple testing and false discovery rate; Quality control of raw reads: FASTQC and fastx toolkit; Read alignment to a reference genome: Bowtie and Tophat; Peak calling: MACS, USeq and SISR.

Statistical Modeling; Hierarchical Models and the basics of Bayesian Statistics; Exploratory Data Analysis for High throughput data; Analysis of Metagenomic Data; QIIME, PICRUST; High-Throughput Sequencing Data Informatics.

16 hrs

Unit-III

RNA sequencing and analysis

Introduction to R; Informatics for RNA-seq Analysis and ChIP-seq; Experiment design for ChIP-seq and RNA-seq; Small non-coding RNA analysis: R, Reaper; Exploratory Analysis of Biological Data using R; Pathway and Network Analysis of -omic Data; Microbiome projects; Proteogenomics

10 hrs

Unit IV

Gene Expression Analysis and Network Analysis

Microarray Expression Analysis - Quantification of expression and differential expression analysis and differential exon usage: R, DESeq, DEXSeq; Normalisation and experimental design models for microarray data. Metabolomics - Informatics and Statistics for Metabolomics; Expression and Differential Expression, Isoform Discovery and Alternate Expression, Regulatory Network Analysis

12 hrs

BI. SCP-4.4.1 Lab based on BI. SCT-4.3.1

NGS sequencing data analysis tools

- FastQC
- BWA
- Bowtie
- Fastx tool kit
- Samtools

Microarray Data analysis tools

- R and bioconductor

References:

- Data Mining Techniques for the Life Sciences Oliviero Carugo (Editor), Frank Eisenhaber (Editor) Humana Press; 2010 edition. ISBN-13: 978-1603272407.
- An Introduction To High Content Screening: Imaging Technology, Assay Development, and Data Analysis in Biology and Drug Discovery - Steven A. Haney (Editor), Douglas Bowman (Editor), Arijit Chakravarty (Editor). Wiley-Blackwell (31 December 2014). ISBN-13: 978-0470624562.
- High Throughput Screening: Methods and Protocols (Methods in Molecular Biology) 29 Nov 2011 - William P. Janzen (Editor), Paul Bernasconi (Editor) ISBN-13: 978-1617794919.
- RNA Bioinformatics (Methods in Molecular Biology) Hardcover – 22 Jan 2015 - Ernesto Picardi (Editor) ISBN-13: 978-1493922901.

BI-HCPW-4.5 Project Work

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.

BI-OE-4.6 Applied Bioinformatics

Total: 60 hrs

Unit I

Dynamic programming algorithm: Introduction to PAM and BLOSUM matrices; differences between distance and similarity matrices.

Global and local pairwise alignment methods – SmithWaterman and Needleman-Wunsch algorithms. Concepts behind multiple sequence alignment; Clustal-Omega, TCOFFEE. BLAST, sequence search, difference versions of BLAST, gapped BLAST and BLAT.

16hrs

Unit II

Basic concept and definition of sequence patterns, motifs and profiles, various types of pattern representations viz. consensus, regular expression (prosite-type) and profiles.

Use of Hidden Markov model (HMM) in assigning homology. Phylogeny: sequence evolution, distance matrices, phylogeny construction by UPGMA, Neighbour joining and parsimony methods, evolution model for nucleic acids.

Phylogenetic Analysis – Phylogenetics, Cladistics and Ontology; Phylogenetic Representations- Graphs, Trees and Cladograms; Classification and Ontologies; Steps In Phylogenetic Analysis Methods of Phylogenetic Analysis- Similarity And Distance Tables, Distance Matrix Method.

24hrs

Unit III

Protein secondary structure calculation – DSSP, membrane topology prediction, ligand-receptor interactions, composition of active sites in functional proteins, conformational change and activity, allostery, effects of point mutations on proteins structure and function.

10hrs

Unit IV

Gene Structure predictions – Exons, introns, ORFs, regulatory regions, prokaryotic gene prediction, eukaryotic gene prediction, gene structure prediction tools – GenScan, Genome Scan, GRAIL, GLIMMER, ORF finder.

10hrs

References:

1. A. M. Lesk; Introduction to Bioinformatics; Oxford University Press, 2002.
2. N. Gautham; Bioinformatics: Databases and Algorithms; Alpha Science, 2006.
3. D. W. Mount; Bioinformatics Sequence and Genome Analysis; Cold Spring Laboratory Press, 2001.
4. J. Bedell; I. Korf, M. Yandell; BLAST; O'Reilly Press, 2003.
5. F. J. Burkowski; Structural Bioinformatics An Algorithmic Approach; CRC Press, 2009. 6. J. M. Keith; Bioinformatics Vol. 1, Data, sequence analysis & evolution; Humana Press, 2008.
7. R. Durbin; Biological sequence analysis; Cambridge University Press, 1998.
8. R. M. Holmes; A cell biologists' guide to modeling and bioinformatics; Wiley Interscience, 2007.