Sant Gadge Baba Amravati

University Amravati

M.Sc.

Bioinformatics

Programme

Objective:

1. The program aims to utilize and understand biological databases to gather, store, retrieve, manage, analyze and integrate biological data for generating new knowledge.
2. The program aims to impart extensive understanding and learning of theoretical concepts in Life Sciences.
3. Each semester includes at least one core course in life sciences along with computational biology in each semester.
4. Basic practical methodology is incorporated as practical sessions in Laboratory courses in each semester.
5. Developing and implementing computational logic, learning programming languages, algorithms and software for progressive life science solutions.
6. Better understanding of dynamic biological processes and their understanding at molecular level enabled through and correlated using internet and Bioinformatics.
7. To develop skilled bioinformatics professionals who have life science background and who are simultaneously proficient in pharmacogenomics, Drug delivery System and Parasitology.
8. To introduce new age concepts of big data in the 'omics' era and their analysis.

Programme Specific Outcomes (PSO):

1. Students undertaking the course shall have fundamental knowledge in theoretical Biochemistry, Cell Biology, Molecular Biology, genomic, computational biology and Genetics.
2. They will possess basic biochemistry and computational biology practical skills and its application in research and industry.
3. Students undertaking the course shall have fundamental knowledge in theoretical Cell Biology, Biochemistry, Mathematics, Statistics, Parasitology and database management, possess basic practical skills in these fields and its application in research and industry.
4. Students will learn on various aspects in Biotechnology and have hands on skills in Molecular Techniques.
5. Students will learn basic mathematical and statistical concepts and learn to apply them in aiding life science research and analysis.
6. As beginners the students will learn to use a computer, internet, scope and applications of bioinformatics.
7. Students will later learn to use the vast array of biological databases and their resources. Knowledge in life sciences would be the key and tools, methodologies and softwares used in bioinformatics will give them a comprehensive edge in data analysis.

8. Differential skills on basis of bioinformatics and computational biology proficiency would be later validated through academic supervision and systematically guided according to their skill.
9. Students as a part of curriculum will learn many programming languages from basic C, HTML etc. to PERL, PYTHON, R Programming, etc.
10. Students will be able to use free software, operating systems, work in command line environments and extensively work in databases, their creation and management. This will be ideal for job opportunities for them in IT enabled services as well.
11. Drug discovery strategies from life science point of view and the concerted computational approach are learned, evaluated and practiced through experimental sessions and thoroughly learned.
12. Students learn Genomics and Proteomics as primary subjects in their quest for biological repositories of information where in they will find their data which they will later analyze using next generation techniques for prediction of function and annotation.
13. Students also learn basics of data mining, machine learning, and artificial neural networks as a part of curriculum in bioinformatics which can be considered as a stepping stone in comprehending industry demands and hype surrounding big data analysis.

Employability Skills:

After completion of Programme in Bioinformatics the student/s would be placed in

1. Post-Doctoral fellow.
2. Data Scientist
3. Drug delivery system analyst
4. Pharmacogenomics industry
5. As a Computational Biologist.
6. Biotechnology industry as a biomolecular engineer
7. Senior Software Engineer
8. Bioinformatics Engineer
9. Bioinformatics Analyst
10. Parasitic informatician
11. As an academician
12. As a computer programmer.
13. As expert in genomics and proteomics industries.
14. As a primer designer.

Scheme of Teaching, Learning & Examination leading to the Degree in Master of Science in the Programme Bioinformatics
(Two year- Four Semester Degree Programme- C.B.C.S.)
(M.Sc. Part II) Semester III

S. No.	Subject	Subject Code	Teaching & Learning Scheme							Duration of Exam Hours	Examination & Evaluation Scheme						
			Teaching Periods Per Week				Credits				Theory		Practical		Total Marks	Minimum Passing	
			L	T	P	Total	L/T	Practical	Total		Theory+ MCQ External	Theory Internal	Internal	External		Marks	Grade
1	DSC-VII Proteomics		3	-	-	3	3	-	3	3	80	20	-	-	100	40	P
2	AEC- III Wet lab techniques		-	1	-	1	1	-	1	1	-	-	25	-	25	40	P
3	DSC-VIII System Biology		4	-	-	4	4	-	4	3	80	20	-	-	100	40	P
4	DSC –IX Bio-programming I		4	-	-	4	4	-	4	3	80	20	-	-	100	40	P
5	DSC- X Parasite Bioinformatics		4	-	-	4	4	-	4	3	80	20	-	-	100	40	P
6	Lab- 5Practical Based on DSC VII&VIII		-	-	6	6	-	3	3	*	-	-	-	100	100	50	P
7	Lab- 6 Practical Based on DSC IX& DSC-X		-	-	6	6	-	3	3	*	-	-	-	100	100	50	P
8	# Internship/ Field Work/ Work Experience @																
9	**Open elective/ GIC/ Open skill/ MOOC***																
Total						28			22						625		

L: Lecture, T: Tutorial, P: Practical

Student may complete their Internship/ Field Work/ Work experience in First or Second or Third semester of Master of Science in the Programme, according to their convenience; @ denotes Non-Examination credits.

Note: Internship/ Apprenticeship/ Field Work Experience (during vacations of semester I to III. This will carry 2 credits for learning of 60 hours or 3 Credits for learning of 90 hours. Its credits and grades will be reflected in final semester IV credit grade report.

-OEC (Optional) can be studied during semester I to IV

Part B

Syllabus Prescribed for 2022 Year **PG. Programme**

Programme **M.Sc. Bioinformatics**

Semester III

Code of the Course Subject	**Title of the Course/ Subject**	**No. of periods/ week**
DSC VII	**Proteomics**	**03**

Cos :

This course will introduce the concepts of Proteomics – its principles and techniques which play a significant role in modern systems biology and related areas. Proteomics deals with the qualitative and quantitative analysis of the proteins that express in a biological system. This course introduces the basics of evolution of proteomics as an area, the experimental aspects of tools and techniques in addressing systems level applications. As a result of this course, the students will have strong foundations and first hand scientific understanding of current trends in Proteomics.

Unit-I : (Introduction to Proteomics)	Introduction to Proteomics: Scope and Application, Complexity of the problem: Post translational modification, Phosphorylation, Methods of studying proteins, protein-protein interactions (Y2H), Practical application of proteomics and current research technology, Protein databases.
Unit-II : (The Proteome and Proteome technology)	Introduction of proteome technologies; Expression proteomics (express profile); Protein separation technology - 2D-Gel Electrophoresis, liquid chromotagraphy, use of affinity chromatography in; X-ray diffraction, NMR, mass spectroscopy and its uses in protein identification; Forward and Reverse Proteomics, Protein microarray and it types.
Unit-III : (Computational Protein Structure Prediction)	Secondary structure: Basic principles on which the prediction methods of first, second and third generation are based; algorithms of Chou Fasman, GOR methods; concepts in measuring the accuracy of predictions (Q3, Segment overlap, Mathew's correlation coefficient etc.) Tertiary Structure: Theoretical basis of the methods for structure prediction, choice of appropriate prediction approach; basic principles and protocol of Homology Modeling; Databases of models; Basic principles for fold recognition, threading approaches, basic principles of ab-initio structure prediction and the broad approaches, Structure Validation methods
Unit-IV : (Comparative Proteomics)	Protein structure comparison and classification: classes, folds; the concepts in 3D structure comparison, purpose of structure comparison, algorithms such as FSSP database, VAST and DALI. Visualization of structures using Rasmol or SPDBViewer or CHIME, Basic concepts in molecular modeling, different types of computer representations of molecules, Concepts of force fields: representations of atoms and atomic interactions, Protein Sequence alignment and it tools, Genomics and Proteomics

Unit-V : (Advance Proteomics)	Molecular force field model, molecular dynamics, MD simulation, gromacs software, hydrogen bonds, Protein structure minimization, Protein structure comparison and its algorithms.

Suggested Reading:

2. Azuaje F., Dopazo J., (2005) "Data analysis and visualization in genomics and proteomics" John Wiley and Sons
3. Dubitzky W. Granzow M. Berrar D (2007) "Fundamentals of data mining in genomics and proteomics"
4. Gu Jenny, Bourne P. (2009) "Structural bioinformatics" Wiley- Blackwell
5. Kraj A, Silberring J, (2008) "Proteomics: introduction to methods and applications" John Wiley & Sons
6. Liebler D.C, (2002), "Introduction to proteomics: tools for the new biology" Humana Press
7. Mishra N.C., (2010), "Introduction to Proteomics: Principles and Applications" John Wiley and Sons
8. Pennington S.R., Dunn M. J. (2001), "Proteomics: from protein sequence to function" BIOS
9. Reinders J, Sickmann A., (2009) "Proteomics: methods and protocols" Humana Press
10. Suhai S. (2000) "Genomics and proteomics: functional and computational aspects" Springer
11. Veetstra T.D., Yates J.R. (2006) "Proteomics for biological discovery" John Wiley and Sons
12. Polanski A., Kimmel M. (2007) "Bioinformatics" Springer Verlag Berlin Heibel berg

Learning Outcome

After successfully completing this course, you will have the following competences:

1. Practical and theoretical knowledge in proteomics.
2. Knowledge about common workflows for the large-scale analysis of proteins.
3. Fundamental knowledge about quantification of proteomes.
4. Understanding how to identify proteins from mass spectrometry data.
5. Able to evaluate MS/MS data including de novo sequencing.
6. Insight into the analysis of post-translational modifications and protein-protein interactions.
7. On-hands experience with in-gel digestions, LC-ESI and MALDI mass spectrometry and protein identification.

Part B		
Syllabus Prescribed for 2022 Year		**PG. Programme**
Programme		**M.Sc. Bioinformatics**
Semester III		
Code of the Course Subject	**Title of the Course/ Subject**	**No. of periods/ week**
AEC III	**Wet lab techniques**	**03**
Cos : 10. To familiarize the student with emerging field of biotechnology i.e. Recombinant DNA Technology as well as to create understanding and expertise in wet lab techniques in genetic Engineering.		
Unit I	PCR or Polymerase Chain Reaction, Components, primer, types of PCR, PCR reactions. Purification and analysis of proteins, protein chemistry, chromatography, immunology and spectroscopic methods.	
Suggested Reading:		
11. Wilson K, Goulding KH. (2018) Principles and Techniques of Biochemistry and Molecular Biology, Eight Edition , Edited by Hofmann A, Clokie S. Cambridge University Press		

12. Plummer DT. (2017) An Introduction to Practical Biochemistry. 3rd Edition McGraw Hill Education
13. Philips, R. Kondev J, Theriot J, Garcia H. (2012). Physical Biology of the Cell. 2nd Edition Garland Science.

Learning Outcome:
After completion of this course the student will able to understand the techniques, protocol and analytical tools required for the walk of Bioinformatics.

Part B

Syllabus Prescribed for 2022 Year **PG. Programme**

Programme **M.Sc. Bioinformatics**

Semester III

Code of the Course Subject	**Title of the Course/ Subject**	**No. of periods/ week**
DSC VIII	**System Biology**	**04**

Cos :

This course would be able to introduce the student to contemporary Systems Biology focused on mammalian cells, their constituents and their functions. Biology is moving from molecular to modular. As our knowledge of our genome and gene expression deepens and we develop lists of molecules (proteins, lipids, ions) involved in cellular processes, we need to understand how these molecules interact with each other to form modules that act as discrete functional systems. These systems underlie core subcellular processes such as signal transduction, transcription, motility and electrical excitability. In turn these processes come together to exhibit cellular behaviors such as secretion, proliferation and action potentials.

Unit-I : (Introduction to System Biology)	System Biology – Introduction, biological networks, analysis of biological networks; Need for system analysis in Biology, System Biology approaches, Dynamic Analysis, Organization of living cells, Components vs. Systems,. Systems Biology Markup Language (SBML)
Unit-II : (System Kinetics)	Biochemical Reaction Kinetics – Rate equation approach, elementary reactions, complex reaction, Michaelis-Menten equation for EK, Stochastic Modelling and Simulation, Ki and Km values of enzyme, Enzyme assay and its types.
Unit-III : (Reconstruction of Biochemical Networks)	Metabolic network modeling, Metabolic network simulation, Flux balance analysis, Regulation of metabolic networks, Signaling Networks, Applications of a reconstruction, KEGG, Reactome, Brenda databases; Cell designer software.

Unit IV : (Introduction to Synthetic Biology)	Synthetic Biology - Introduction, Emergence of Synthetic biology, Tools in Synthetic biology. Genetic engineering, Biosensors and its applications, Synthetic Life: Synthia; E-cell and V-cell Simulations and Applications. ethical concerns in the field of synthetic biology;
Unit V : (Introduction to R programming)	R programming – Introduction and preliminaries, Simple manipulation, Objects and Modules, Orders, Arrays, Lists, Reading data from files, Loops and conditions, Functions creation, Packages.

Suggested Reading:

11. B. O. Palsson "System Biology – Properties of Reconstructed Networks" Cambridge University Press
12. Olaf Wolkenhauer. (2010) "System Biology – Dynamic Pathway Modeling"
13. Andres Kriete, Roland Eils (2006) "Computational systems biology" Academic Press
14. Andrzej K. Konopka (2007) "Systems biology: principles, methods, and concepts" CRC Press/Taylor & Francis
15. Lilia Alberghina (2008) "Systems biology: definitions and perspectives" 2 Edition, Springer
16. Uri Alon (2007) "An introduction to systems biology: design principles of biological circuits" Chapman & Hall/CRC
17. W. N. Venables, D. M. Smith; "An Introduction to R (Version 2.8.1.)", R developer Core team.Bergman N. H. (2007),"Comparative genomics" Volume 2, Humana Press
18. Cantor C.R., Smith C.L., (1993) "Genomics: the science and technology behind the Human Genome Project" John Wiley and Sons
19. Choudhuri S., Carlson D. B. (2008), "Genomics: fundamentals and applications" Informa Healthcare
20. Clark M (2000), "Comparative genomics" Springer

Learning Outcome:

1. Describe the principles of systems biology
2. Describe key cellular processes like transcription, translation, signaling and protein secretion in a quantitative fashion
3. Use matrix notation to describe the stoichiometry of metabolic networks
4. Describe metabolic network reconstruction based on biochemical and genomic information
5. Describe how genome-scale metabolic models (GEMs) can be used for analysis of cellular physiology
6. Describe how constraints and objective functions are underlying principles of flux balance analysis
7. Describe the use of genome-scale metabolic models in research on human disease
8. Describe how meta-omics data can be analyzed
9. Describe the principles of RNAseq
10. Describe the principles of proteomics
11. Describe the principles of metabolomics

Part B

Syllabus Prescribed for 2022 Year PG. Programme

Programme M.Sc. Bioinformatics

Semester III

Code of the Course Subject	Title of the Course/ Subject	No. of periods/ week
DSC IX	**Bio-Programming – I**	**04**

Cos :

9. Student would know about the properties of DNA, RNA, and proteins, the relationships amongthese molecules, and some biological questions that have puzzled researchers.
10. Student would know how to convert a biological question into a computational problem that can besolved using computers.
11. Student would know how to read and understand solutions to computational problems, which willbe formalized as a series of tasks (an algorithm).
12. Student would learn about general approachesfor solving computational problems, and will be able to apply these approaches to newproblems encounter.

Unit-I : (Introduction to PERL)	Introduction to PERL, History and uses, PERL Basics, Data types, Basic Operators, Control Statements: if, if else, if elsif else, Loops: do, while, until, for, foreach, labels, lists, Arrays and associative arrays.
Unit-II : (Introduction to PERL)	Pattern matching: Regular expressions, Subroutines and functions: structure and invocations, scope Files and I\O: file handles, opening, closing, reading and writing, formats, manipulating files, Perl Modules: CPAN, Bioperl, obtaining and installing, Object oriented PERL
Unit-III : (Introduction to ODBC)	DBM Databases and DBM Hashes, Design of DBI, DBI Methods, DBI Environment Variables, DBD Interface Modules, Fixed Length Random-Access Databases, Variable-Length Databases, Win32 Database Interface, Perl Graphics, Using the GD.pm graphics lib
Unit-IV : (Introduction to HTML and CGI)	Basics structure of HTML, Basics HTML TAGS, URL Encoding, CGI Environment Variables, Handling forms, Accessing form Input, Extra Path Information, CGI.pm Module, Passing Parameters via CGI, Less Typing, Sever Side Includes, Debugging CGI programs, Stepping through programs, Breakpoints, Line Action
Unit-V : (HTML References Tags)	HTML Tag List, HTML Attributes, Global Attributes, Browser Support, Events, Colors, Canvas, Audio/Video, Doctypes, Character Sets, URL Encode, Lang Codes, Messages, Methods.

Suggested Reading:

8. Arun Jagota (2004) “Perl for Bioinformatics” Arun Jagota

9. D. Curtis Jamison (2003) “Perl programming for biologists” Wiley- IEEE
10. D. Curtis Jamison (2008) “Perl Programming For Bioinformatics & Biologists” Wiley-India
11. James D. Tisdall (2003) “Mastering Perl for bioinformatics” O’Reilly Media, Inc
12. Jules J Berman (2008) “Perl: The Programming Language” Jones & Bartlett Learning
13. Randal L. Schwartz, Tom Phoenix, Brian D. Foy (2008) “Learning Perl” O’Reilly Media, Inc
14. Vittal R. Srinivas (2005) “Bioinformatics: A Modern Approach” PHI Learning Pvt. Ltd

Learning Outcome:

1. Basic Applications of Computer; Components of ComputerSystem.
2. Concept of Internet; WWW and Web Browsers; SearchEngines
3. Data analysis by different computational techniques
4. Concepts of computer programming languages like C, JAVAhelps in solving different complex problem in biology or dataanalysis
5. Writing scripting for different data analysis
6. Command line scripting in DOS and LINUX
7. Writing script in R programming to solve biological problem.

Part B

Syllabus Prescribed for 2022 Year **PG. Programme**

Programme **M.Sc. Bioinformatics**

Semester III

Code of the Course Subject	**Title of the Course/ Subject**	**No. of periods/ week**
DSCX	**Parasite Bioinformatics**	**04**

Cos :

1. General concept of parasitology.
2. Knowledge of some parasitic diseases that could be transmitted between animals andman (Zoonotic diseases).
3. Knowledge how to protect man and domestic animals from parasites and theirtreatment.
4. Basic knowledge of parasitism, the different biological inter-relationships and the hostparasite relationships.
5. Knowledge of different parasitic examples from all phyla (Protozoa & Metazoa), theirmorphology, biology, life cycles, diagnosis, treatment & control.
6. Dissemination of health awareness of these parasitic diseases.

Unit-I : (Introduction to Parasitic Diseases)	Biology of Parasites - Life Cycle, Infectivity, Demographic distribution of strains (Malaria, Leishmaniasis, Trypanosoma, Filariasis), Role of bioinformatics in Diseases monitoring.
Unit-II : (Introduction to Parasitic Diseases)	Parasite Genome and Proteome Databases (AnoBase, ENSEMBL, PlasmoDB), Vectors of parasites – Biology of vectors; Giardiasis , Sleeping sickness, Chagas disease, Parasite-specific genes/ gene products (e.g. house-keeping genes, genes essential for survival), Resistant Genes.
Unit-III : (Techniques to study Parasitic Diseases)	Full Genome Comparison, Gene Prediction, Signal sequence prediction, Protein sequence comparison and analysis, Protein structure comparison and analysis, Micro Array and Proteomics Data Analysis, Structural genomics of parasites.
Unit-IV : (Introduction to Host-parasite interaction)	Host-parasite interaction: Recognition and entry processes of different pathogens like bacteria and viruses into animal and plant host cells; alteration of host cell behavior by pathogens, virus-induced cell transformation, pathogen-induced diseases in animals and plants; cell-cell fusion in both normal and abnormal cells.
Unit-V : (Introduction to Host-parasite interaction)	Host-Parasite and Host-Vector-Parasite Interactions, Pathway databases (KEGG, BioCyc, Pathguide, REACTOME), Multi-Drug Resistance - Mechanism of MDR: genomic, molecular, cellular, Identification of genes responsible for MDR, Approaches to novel drug discovery for parasite, Challenges and opportunities in vaccine development, Plant Parasites and diseases - Disease resistance genes of plants, Plant-pathogen interactions.

Suggested Reading:

1. Bush, A. O., Fernandez, J. C., Esch, G.W. & Seed, R. J., "Parasitism", Cambridge University Press, 2001.
2. Melville, S.E., "Parasite genomics protocols", New Jersey. Humana Press, 2004.
3. Latey, A.N, Pune, "A modern textbook of Parasitology", Narendra prakashan, 1991.
4. Wyler, D.J. "Modern parasite biology: cellular immunological and molecular aspects", Ed., 1990.

Learning Outcome:

1. Identify parasitism, parasites and their examples.
2. Describe parasitic diseases and modes of diagnosis.
3. Trace control of parasitic infections.
4. Understand host-parasite relationship.

Sant Gadge Baba Amravati University, Amravati

Syllabus Prescribed for 2022 Year **PG Programme**
Programme: M. Sc. Bioinformatics

Semester 1 Code of the Course/Subject	**Title of the Course/Subject** (Laboratory/Practical/practicum/hands-on/Activity)	**(No. of Periods/Week)**

Practical V	Practical Based on DSC VII&VIII	**06**

CO:

1. Fundamentals of Computer, Basic Applications of Computer; Components of Computer System.
2. Concept of Computing, Data and Information
3. Basics of Operating System; Popular Operating Systems(Windows, Linux, DOS);
4. Data structure and its relevance to biological science
5. Communication using the Internet: Basic of Computer networks; LAN, MAN, WAN;
6. Concept of Internet; WWW and Web Browsers; Search Engines; Understanding URL
7. Design & Structure of biological databases
8. Introduction to PERL as scripting language; variables; Array; Initialization and manipulation
9. Arithmetic and logical operators; Conditional statement and Loops; Regular Expressions; Function and subroutines
10. Application of PERL in Bioinformatics; concatenating DNA fragments; DNA to RNA; Reading protein Files; Finding motifs; ORFs; DNA to protein

*** List of Practical/Laboratory Experiments/Activities etc.**

1	Microbial Database
2	MLVA
3	HBMMD
4	DSMZ
5	RIDOM
6	GPMS

Proteomics

1	Protein Sequence Databases
2	Protein Structure Databases
3	Protein Sequence Analysis by BioEdit
4	Advanced Visualization Software and 3D representations
5	Coordinate generations and inter-conversions
6	Secondary Structure Prediction
7	GORIV
8	Online Secondary structure prediction tools
9	Fold Recognition, ab initio (Rosetta Server)
10	Homology based comparative protein modeling
11	Energy minimizations
12	Validation of models
a.	WHATIF
b.	PROSA
c.	PROCHECK
d.	VERIFY 3D
e.	RAMPAGE
f.	Protein Structure Alignment
g.	Protein Structure Comparison
h.	Modeller9v7

i.	Geno-3D
j.	Discovery Studio Server
	Learning Outcome: 1. Bioinformatics – an Overview, Definition and History.Information Networks –Internet inBioinformatics, Evolution of Bioinformatics – Scope –Potentials of Bioinformatics, Human Genome Project 2. Introduction to Biological Databases: NCBI, EMBL, PIR,SWISS-Prot, PubChem 3. Compound, KEGG-Pathway, ChEMBL, BindingDB.Analysis of Three Dimensional Structures of Proteins,RCSB-PDB. Primary and Secondary database 4. Various file formats for bio-molecular sequences: genbank,fasta, gcg, msf, nbrf-pir etc. 5. Basic concepts of sequence similarity, identity andhomology, definitions of homologues, orthologues,paralogues. 6. Scoring matrices: basic concept of a scoring matrix, PAMand BLOSUM series

Sant Gadge Baba Amravati University, Amravati

Syllabus Prescribed for 2022 Year **PG Programme**
Programme: M. Sc. Bioinformatics

Semester 1 Code of the Course/Subject	**Title of the Course/Subject** (Laboratory/Practical/practicum/hands-on/Activity)	**(No. of Periods/Week)**
Practical VI	Practical based on DSC IX& DSC- X	**06**

CO:

1. Identify parasitism, parasites and their examples
2. Describe parasitic diseases and modes of diagnosis. Trace control of parasitic infections.
3. Understand host-parasite relationship.

*** List of Practical/Laboratory Experiments/Activities etc.**

1.	Exercise in Structured Programming: 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 stat Functions, Formats, Directory Access & Manipulation, Process Management, Formatting Data, System Information
2.	Exercise in Regular Expressions: Uses of Regular Expressions, Patterns, Single-Character Patterns, Grouping Patterns (Sequence, Multipliers, Parentheses as memory, Alternation) Anchoring Patterns, Precedence, Matching Operators, Ignoring Case, Different Delimiter, Variable Interpolation, Special Read-Only Variables, Substitutions, Split and Join Functions, Dynamic Programming, Approximate String Matching
3.	Exercise in CGI: URL Encoding, CGI Environment Variables, Handling forms, Accessing form Input, Extra Path Information, CGI.pm Module, Passing Parameters via CGI, Less Typing, Sever Side Includes, Debugging CGI programs, Stepping through programs, Breakpoints, Line Action
4.	Exercise in CPAN Database Modules: DBM Databases and DBM Hashes, Design of DBI, DBI Methods, DBI Environment Variables, DBD Interface Modules, Fixed Length Random-Access Databases, Variable-Length Databases, Win32 Database Interface, Perl Graphics, Using the GD.pm graphics library

5.	Exercise in Bioperl: Installing Bioperl, General Bioperl Classes, Sequences (Bio::SeqClass, Sequence Manipulation), features and Location Classes (Extracting CDS), Alignments (AlignIO), Analysis (Blast, Genscan),Databases (Database Classes, Accessing a local database), Implementing REBASE
6.	Exercise in HTML: Basics structure of HTML, Formatting text with HTML, Adding local and remote links, Adding graphics, creating lists in HTML, Creating tables in HTML, Frames, and Forms.
7.	Parasite Bioinformatics
a	ICTV database
b	Parasite Genome and Proteome Databases.
8.	Genome Comparison
9.	Gene Prediction (Parasite)
10.	Signal sequence prediction (Parasite)
11.	Protein sequence comparison and analysis
12.	Protein structure comparison and analysis (from parasite genome)
	Learning Outcome: 1. Right use of microscopes. 2. Identification and description of parasites. 3. Using computers and internet. 4. Characterize methods of resistance and appropriate treatment 5. or each disease. 6. Conducting documentary about some parasites throughout theKingdom.

Scheme of Teaching, Learning & Examination leading to the Degree in Master of Science in the Programme Bioinformatics

(Two year- Four Semester Degree Programme- C.B.C.S.)
(M.Sc. Part II) Semester IV

S. No.	Subject	Subject Code	Teaching & Learning Scheme							Duration of Exam Hours	Examination & Evaluation Scheme						
			Teaching Periods Per Week				Credits				Theory		Practical		Total Marks	Minimum Passing	
			L	T	P	Total	L/T	Practical	Total		Theory+ MCQ External	Theory Internal	Internal	External		Marks	Grade
1	DSC-XI Bio-programming II		3	-	-	3	3	-	3	3	80	20	-	-	100	40	P
2	AEC- IVR-programming		-	1	-	1	1	-	1	1	-	-	25	-	25	40	P
3	DSC-XII Chemo-informatics		4	-	-	4	4	-	4	3	80	20	-	-	100	40	P
4	DSC -XIII Molecular Modeling and Drug Designing		4	-	-	4	4	-	4	3	80	20	-	-	100	40	P
5	DSC- XIV Research Methodology, IPR and Bioethics.		4	-	-	4	4	-	4	3	80	20	-	-	100	40	P
6	SEC-II- Python		2	-	-	2	2	-	2	2					50	20	P
7	Lab- 7Practical Based on DSC XI, XII, XIII & XIV		-	-	6	6	-	3	3	*	-	-	-	100	100	50	P
8	Lab-8Practical Based on Project		-	-	6	6	-	3	3	*	-	-	-	100	100	50	P
9	# Internship/ Field Work/ Work Experience @																
10	**Open elective/ GIC/ Open skill/ MOOC* Pharmacogenomics**	**OEC-II**	4	-	-	4	4	-	4	3	80	20	-	-	100	40	P
Total						30			24						675		

L: Lecture, T: Tutorial, P: Practical

Student may complete their Internship/ Field Work/ Work experience in First or Second or Third semester of Master of Science in the Programme, according to their convenience; @ denotes Non-Examination credits.

Note: Internship/ Apprenticeship/ Field Work Experience (during vacations of semester I to III. This will carry 2 credits for learning of 60 hours or 3 Credits for learning of 90 hours. Its credits and grades will be reflected in final semester IV credit grade report.

-OEC (Optional) can be studied during semester I to IV

Part B

Syllabus Prescribed for 2022 Year **PG. Programme**

Programme **M.Sc. Bioinformatics**

Semester IV

Code of the Course Subject	**Title of the Course/ Subject**	**No. of periods/ week**
DSC XI	**Bio-programming II**	**03**

Cos :

11. To facilitate the students in gaining programming skills.
12. To enable the students to design and execute Java, C++ and Perl scripts
13. To interpolate biological demands through programming

Unit I : (Introduction to Java)	Basics of JAVA, History, an overview of JAVA, Object Oriented Programming, Data types- Variables and Arrays, the simple types, floating point types, Operators, Control statements, Class fundamentals, Declaring objects, Assigning object reference variables, Introducing methods, Constructors, Garbage collection, using objects as parameters, Argument passing, Retaining objects, Recursion, Introducing Access control, Understanding static; Nested and inner classes, exploring the string class, Using command line arguments.
Unit II : (Introduction to Java)	Inheritance: Basics, Member access and inheritance. Using super: to call super class constructors, Creating a multilevel hierarchy. The object class Packages and Interfaces: Packages, Defining a package, Understanding class path, Access protection: Importing packages, Defining an interface, Implementing interfaces, Applying interfaces, Variables in interfaces, Exception Handling: Fundamentals, Exception types, Uncaught exceptions, Using try and catch, Displaying a description of an exception. Multiple catch clauses, Nested statements, throw, throws; Java's built in exceptions, Creating own exception subclasses, Using exceptions
Unit III : (Introduction to Unix & Linux**)**	Introduction to Unix & Linux, History of Unix & Linux, Basic Concepts of Operating Systems, Kernel, shell and file system structure, Basic Concepts of Linux, Basic Commands of Linux, Advanced Linux Commands, Installation of Linux, Interactive Installation, Kickstart Installation, Network based Installation, Startup and Shutdown scripts, Boot Sequence,Kernel Initialization
Unit IV : (Introduction to Unix & Linux**)**	The UNIX Filesystem and Shell Intro: The Shell - Executing commands and command options, Interactive features: job control, history; The UNIX file system, File Utilities (cp, mv, rm, etc.), comm, cmp, diff, Editors: vi, emacs; Processes and Filters: Process Utilities (ps, kill, wait, sleep); Filters: cat, head, tail, sort, uniq; Regular Expressions and Sed: Regular expressions, grep, fgrep, egrep, Sed
Unit V : (Introduction to Bio-Java)	Installing Bio-Java, Symbols, Basic Sequence Manipulation (DNA to RNA, Reverse Complement, motif as regular expression), Translation (DNA to Protein, Codon to amino acid, Six frame translation), Proteomics (Calculate the mass and pI of a peptide), Sequence I/O (File Formats conversions), Locations and Features (Point Location, Range Location, Feature modifications), BLAST and FASTA (Blast and FastA Parser, extract information from parsed results), User Interfaces.

Suggested Reading:

14. Benjamin, Cummings and Booch, G. (1994) "Object Oriented Design and Applications"; Second edition, Addison Wesley Publishers.
15. Horstmann, C.S. (2000) "Computing Concepts with Java 2 Essentials"; Second Edition, John Wiley Publishers
16. Naughton, P. and Schildt, H. (1999) "Java-2: The complete Reference"; Third Edition, McGraw Hill Publishers.
17. Bal H, Hujol J, (2007) "Java for bioinformatics and biomedical application" Springer Japan
18. Lindsey C. S., Tolliver J.S., Lindblad T, (2005) "JavaTech: an introduction to scientific and technical computing with JAVA" Cambridge University Press

19. Srinivas V.R. (2005) “Bioinformatics: A modern Approach” PHI learning Pvt. Ltd

Learning Outcome:

1. Learn the basics of programing
2. Relate the necessity for programming in biology
3. Handling biological concepts with C++ and Perl scripts
4. Apply programing to analyze genomic sequences
5. Understand Bio-Perl and their application in bioinformatics to handle the complex data

Part B

Syllabus Prescribed for 2022 Year **PG. Programme**

Programme **M.Sc. Bioinformatics**

Semester IV

Code of the Course Subject	**Title of the Course/ Subject**	**No. of periods/ week**
AEC IV	**R-programming**	**01**

Cos :

Understand the basics of Fundamentals of R.
Understands the loading, retrieval techniques of data.
Understand how data is analysed and visualized using statistic functions.
6.

Unit I R-Programming	Introduction to R: What is R? – Why R? – Advantages of R over Other Programming Languages - R Studio: R command Prompt, R script file, comments – Handling Packages in R: Installing a R Package, Few commands to get started: installed. packages(), package Description(), help(), find. package(), library() - Input and Output – Entering Data from keyboard – Printing fewer digits or more digits – Special Values functions : NA, Inf and –inf. R Data Types: Vectors, Lists, Matrices, Arrays, Factors, Data Frame – R - Variables: Variable assignment, Data types of Variable, Finding Variable ls(), Deleting Variables – R Operators: Arithmetic Operators, Relational Operators, Logical Operator, Assignment Operators, Miscellaneous Operators - R Decision Making: if statement, if – else statement, if – else if statement, switch statement – R Loops: repeat loop, while loop, for loop – Loop control statement: break statement, next statement.

Suggested Reading:

8. Sandip Rakshit, R Programming for Beginners, McGraw Hill Education (India), 2017, ISBN : 978-93-5260-455-5.
9. Seema Acharya, Data Analytics using R, McGrawHill Education (India), 2018, ISBN: 978-93-5260-524-8.
10. Tutorials Point (I) simply easy learning, Online Tutorial Library (2018), R Programming, Retrieved from https://www.tutorialspoint.com/r/r_tutorial.pdf.
11. Andrie de Vries, Joris Meys, R for Dummies A Wiley Brand, 2nd Edition, John Wiley and Sons, Inc, 2015, ISBN: 978-1-119-05580-8.

Learning Outcome:

12. Install, Code and Use R Programming Language in R Studio IDE to perform basic tasks on Vectors, Matrices and Data frames.
13. Describe key terminologies, concepts and techniques employed in StatisticalAnalysis.
14. Define, Calculate, Implement Probability and Probability Distributions to solve awide variety of problems.
15. Conduct and Interpret a variety of Hypothesis Tests to aid Decision Making.
16. Understand, Analyse, Interpret Correlation and Regression to analyse the underlying relationships between different variables.

Part B

Syllabus Prescribed for 2022 Year **PG. Programme**

Programme **M.Sc. Bioinformatics**

Semester IV

Code of the Course Subject	**Title of the Course/ Subject**	**No. of periods/ week**
DSC XII	**Chemo-informatics**	**04**

Cos :

2. Have the knowledge of the basic ligand/structure based approaches.
3. Understand the basic algorithms used in the established software to carry out the most common CADD project.
4. Understand the importance of proper use of various parameters in cheminformatics application programs.
5. Practical use of various computational tools available for computer aided drug design including 2D/3D structural database.

Unit-I : (Introduction to Chemo-informatics)	Chemo-informatics: Introduction, scope and application, Basics of Chemo-informatics, Current Chemo-informatics resources for synthetic polymers, pigments. Primary, secondary and tertiary sources of chemical information, Databases: Chemical Structure Databases (PubChem, Binding database, Drugbank), Database search methods: chemical indexing, proximity searching, 2D and 3D structure and substructure searching. Drawing the Chemical Structure: 2D & 3D drawing tools (ACD Chemsketch) Structure optimization.
Unit-II : (Introduction to Chemo-informatics)	Introduction to quantum methods, combinatorial chemistry (library design, synthesis), spectroscopic methods and analytical techniques, Representation of Molecules and Chemical Reactions: Different types of Notations, SMILES Coding, Structure of Mol files and Sd files (Molecular converter, SMILES Translator). Similarity search of the molecule (Zinc Database).
Unit-III : (Introduction to Chemo-informatics)	Analysis and use of chemical reaction information, chemical property information, spectroscopic information, analytical chemistry information, chemical safety information, QSAR- Data Analysis, Structure-Activity Relationships, 2D QSAR, 3D QSAR, QSPR, Statistical methods used in QSAR, Lead Identification, Molecular Descriptor Analysis.
Unit-IV : (Introduction to Chemo-informatics)	Target Identification: Molecular Modeling and Structure Elucidation: Homology Modelling (Modeller 9v7, PROCHECK), Visualization and validation of the Molecule (Rasmol, Pymol Discovery studio), Applications of Chemo- informatics in Drug Research - Chemical Libraries, Virtual Screening, Prediction of Pharmacological Properties.
Unit-V : (Introduction to Chemo-informatics)	Drug Discovery: Structure based drug designing, Docking Studies (Target Selection, Active site analysis, Ligand preparation and conformational analysis, Rigid and flexible docking, Structure based design of lead compounds, Library docking), Pharmacophore - Based Drug Design, Pharmacophore Modeling (Identification of pharmacophore features, Building 2D/3D pharmacophore hypothesis), Toxicity Analysis-Pharmacological Properties (Absorption, Distribution and Toxicity), Global Properties (Oral Bioavailability and Drug-Likeness) (ADME, OSIRIS, and MOLINSPIRATION)

Suggested Reading:

1. Bajorath J (2004), “Chemoinformatics: Concepts, Methods and Tools for Drug Discovery” Humana Press
2. Leach A, Gillet V, “An Introduction to Chemoinformatics” Revised edition, Springer

3. Gasteiger J. Engel T. “A textbook of Chemoinformatics” Wiley- VCH GmbH & Co. KGaA
4. Bunin B. Siesel B. Guillermo M. “Chemoinformatics: Theory, practice & products”, Springer
5. Lavine B. (2005), “Chemometrics and chemoinformatics” American Chemical Society
6. Casteiger J. and Engel T (2003) “Chemoinformatics” Wiley-VCH
7. Bunin Barry A. SieselBrian,MoralesGuillermo,Bajorath Jürgen. Chemoinformatics: Theory, Practice, & Products Publisher:New York, Springer. 2006. ISBN: 1402050003.
8. Gasteiger Johann, Engel Thomas. Chemoinformatics: A Textbook. Publisher: WileyVCH; 1st edition. 2003. ISBN: 3527306811.
9. Leach Andrew R., Valerie J. Gillet. An introduction to chemoinformatics. Publisher: Kluwer academic, 2003. ISBN: 1402013477.
10. Gasteiger Johann, Handbook of Chemoinformatics: From Data to Knowledge (4 Volumes), 2003. Publisher: Wiley-VCH. ISBN: 3527306803.

Learning Outcome:

- To impart knowledge on chemical databases, various advanced techniques and tools like docking, QSAR studies etc employed in computational drug discovery
- Introduction about the basic concepts of cheminformatics
- Explain about various approaches used in the design of pharmacophores
- Describe about the concepts of SAR & QSAR
- Explain various techniques used in virtual screening
- Describe about various techniques used in Structure Based Drug Design

Part B

Syllabus Prescribed for 2022 Year **PG. Programme**

Programme **M.Sc. Bioinformatics**

Semester IV

Code of the Course Subject	**Title of the Course/ Subject**	**No. of periods/ week**
DSC XIII	**Molecular Modeling and Drug Design**	**04**

Cos :

15. A Molecular Modeling and Drug Design is structure-based drug design and the biophysical aspects of macromolecule and small molecule interactions.
16. A working knowledge of the molecular modeling tools and databases used to produce models that facilitate the understanding of macromolecular interactions.
17. The skills required for working in the pharmaceutical industry and for further study in the areas of molecular structure and interaction.

Unit-I : (Concepts in Molecular Modeling)	Introduction; Coordinate System; potential energy surfaces molecular graphics; Computer hardware and software; Mathematical concepts – introduction of molecular mechanics & quantum mechanics
Unit-II : (Molecular Mechanics)	Features of molecular mechanics, force fields; Bond structure and bending angles – electrostatic, Vander Waals and non-bonded interactions, hydrogen bonding in molecular mechanics; Derivatives of molecular mechanics energy function; Calculating thermodynamic properties using force field; Transferability of force field parameters, treatment of delocalized pi system; Force field for metals and inorganic systems – Application of energy minimization
Unit-III : (Molecular Dynamics Simulation Methods)	Molecular Dynamics using simple models; Molecular Dynamics with continuous potentials and at constant temperature and pressure; Time-dependent properties; Solvent effects in Molecular Dynamics; Conformational changes from

	Molecular Dynamics simulation. Introduction, Newton's equation of motion, equilibrium point, radial distribution function, pair correlation functions, MD methodology, periodic box, algorithm for time dependence; leapfrog algorithm, Verlet algorithm, Boltzman velocity, time steps, duration of the MD run. Ligand protein interactions using Gromacs.
Unit-IV : (Molecular Modeling in Drug Discovery)	Deriving and using 3D pharmacophore; Molecular Docking; Structure based methods to identify lead compounds; de novo ligand design; Applications of 3D Database Searching and Docking, Finding new drug targets to treat diseases – Pharmacophore identification - Structure based drug design - Molecular Simulations
Unit-V : (Structure Activity Relationship)	QSARs and QSPRs, QSAR Methodology, Various Descriptors used in QSARs: Electronic; Topology; Quantum Chemical based Descriptors. Use of Genetic Algorithms, Neural Networks and Principle Components Analysis in the QSAR equations

Suggested Reading:

21. Andrew R. Leach (2001) "Molecular Modeling – Principles and Applications"; Second Edition, Prentice Hall, USA
22. Fenniri, H. (2000) "Combinatorial Chemistry – A practical approach", Oxford University Press, UK.
23. Gordon, E.M. and Kerwin, J.F. (1998) "Combinatorial chemistry and molecular diversity in drug discovery"; Wiley-Liss Publishers
24. Lednicer, D. (1998) "Strategies for Organic Drug Discovery Synthesis and Design"; Wiley International Publishers
25. Swatz, M.E. (2000) "Analytical techniques in Combinatorial Chemistry"; Marcel Dekker Publishers

Learning Outcome:

This course will be able to demonstrate:

1. An understanding of the general concepts of macromolecule interactions.
2. A solid grounding in the mathematics that underpin the methods used.
3. A working knowledge of the methods and tools used in molecular modelling.
4. Knowledge of the experimental techniques that support molecular models.
5. Strong skills in the critical analysis and synthesis of scientific information.
6. The ability to conduct independent research, place findings in context and suggest new research ideas.
7. How to conduct an independent research project and how to report research data in formats suitable for publication.

Part B

Syllabus Prescribed for 2022 Year **PG. Programme**

Programme **M.Sc. Bioinformatics**

Semester IV

Code of the Course Subject	**Title of the Course/ Subject**	**No. of periods/ week**
DSC XIV	**Research Methodology, IPR and Bioethics**	**04**

Cos :

13. Identify an appropriate research problem in their interesting domain.
14. Understand ethical issues Understand the Preparation of a research project thesis report.
15. Understand the Preparation of a research project thesis report
16. Understand the law of patent and copyrights.
17. Understand the Adequate knowledge on IPR

Unit I : (Research Methodology)	Research and Technical Writing: What is research? The process of research – various types of research – research methodology – Hypothesis – research writing – basic principles; publication process – peer review - Journal impact factors – popular journals in Computational Biology & Bioinformatics (brief overview of their scope), Professional Societies in the field – their role in research and knowledge dissemination, Open Access Publications, Concept of ethics – its application in Scientific Research and Academics, Solving ethical conflicts, moral reasoning & ethical theories, responsibilities and rights.
Unit II : (Intellectual Property Rights)	General principles of Intellectual property rights (IPR); Patents and methods; application of patents; Legal implications; International treaties for protection of IP – Bern, Paris, TRIPS, WIPO treaties, Biodiversity convention, etc
Unit III : (Intellectual Property Rights)	Nature of Intellectual Property: Patents, Designs, Trademarks and Copyright. Process of Patenting and Development: technological research, innovation, patenting, development; International cooperation on Intellectual Property, Procedure for grants of patents, Patenting under PCT; Scope of Patent Rights; Licensing and transfer of technology. Patent information and databases, Geographical Indications
Unit IV : (Bioethics)	The legal and socioeconomic impacts of biotechnology; public education of the process of the processes of biotechnology involved in generating new forms of life for informed decision making; Biosafety regulation and national and international guidelines; rDNA guidelines; Experimental protocol approval; levels of containment
Unit V : (Bioethics)	Environmental aspects of biotechnology applications; Use of genetically modified organisms and their release in environment; Special procedures for rDNA-based product production; Biodiversity and farmers rights; Beneficial applications and development of research focus to the need of the poor; Identification of directions for yield effect in agriculture, aquaculture, etc; Bioremediation

Suggested Reading:

15. Sasson, A. (1988) “Biotechnologies and Development”, UNESCO Publications
16. Sasson, A. (1993) “Biotechnologies in developing countries present and future”; UNESCO Publishers
17. Singh, K. “Intellectual Property Rights on Biotechnology”; BCIL, New Delhi
18. Halbert, (2007) “Resisting Intellectual Property” Taylor & Francis Ltd
19. Ramappa T., “Intellectual Property Rights Under WTO”, S. Chand

Learning Outcome:

1. Understand the research problem and research process.
2. Understand research ethics .
3. Prepare a well-structured research paper and scientific presentations
4. Explore on various IPR components and process of filing.
5. Understand the adequate knowledge on patent and rights.

Part B

Syllabus Prescribed for 2022 Year **PG. Programme**

Programme **M.Sc. Bioinformatics**

Semester IV

Code of the Course Subject	**Title of the Course/ Subject**	**No. of periods/ week**
SEC II	**Python**	**01**

Cos :

1. Identify/characterize/define a problem
2. Design a program to solve the problem
3. Create executable code
4. Read most Python code

Unit I	General Introduction to Python and the class. Using the command interpreter and development environment., Python differences. Introduction to git and GitHub, Basic data types. Functions: definition and use, arguments, block structure, scope, recursion, Modules and import Conditionals and Boolean expressions Sequences: Strings, Tuples, Lists, Iteration, looping and control flow. String methods and formatting, Dictionaries, Sets and Mutability. List and Dict Comprehensions, Advanced Argument passing, Lambda, Multiple inheritance, Properties, Special methods, Emulating built-in types, Iterators and Generators, Decorators, Context Managers, Regular expression.

Suggested Reading:

8. Jake VanderPlas, “Python Data Science Handbook: Essential Tools for Working with Data”, 1st Edition, O'Reilly Media, 2016. ISBN-13: 978-1491912058
9. AurelienGeron, “Hands-On Machine Learning with Scikit-Learn and TensorFlow: Concepts, Tools, and Techniques to Build Intelligent Systems”, 2nd Edition, O’Reilly Media, 2019. ISBN – 13: 978-9352139057.
10. Wesley J Chun, “Core Python Applications Programming”, 3rd Edition, Pearson Education India, 2015. ISBN-13: 978-9332555365
11. Miguel Grinberg, “Flask Web Development: Developing Web Applications with Python”, 2nd Edition, O'Reilly Media, 2018. ISBN-13: 978-1491991732.

Learning Outcome:
Problem solving and programming capability.

Part B

Syllabus Prescribed for 2022 Year **PG. Programme**

Programme **M.Sc. Bioinformatics**

Semester IV

Code of the Course Subject	**Title of the Course/ Subject**	**No. of periods/ week**
OEC II	**Language for Bioinformatics**	**04**

Cos :

3. Able to apply design principles to develop web based applications specially for biological data analysis Familiarity CO-2
4. To understand working on world wide web through implementations Familiarity and Assessment CO-3
5. Use various methods from computational biology to implement their programmatic versions Assessment CO-4
6. Able to design new web pages and web sites Assessment and Usage CO-5
7. Able to developed programs to describe and analyze problems in biology

Unit-I: (Language)	Introduction to Internet and World Wide Web. An overview of scripting languages, with applications towards biological data and sequence analysis. Complexity of DNA problems and their computational implications and applications. Introduction

	to HTML, DHTML, XML. accessing different objects of the HTML page, Dynamic page generation, Cascading Style Sheets (CSS).
Unit-II: (Language)	JAVASCRIPT: Document object model, Elements of the document object model, basic principles of JS, object based programming using JavaScript; data types and structures, array and string handling, function implementations, XML: DTD, XML schemas, XML document structure, retrieving data from database in XML format; various bio based versions of XML.
Unit III: (Language)	PHP: PHP beginning to advanced level, data types, array and string handling, mathematical expressions and functions in PHP, PHP programming (implementation of object model), Database connectivity using PHP.
Unit-VI :(Language)	Programming basics, Sequences and Strings: Storing a DNA sequence, Concatenation, Transcription, Translation, Arrays and Scalar list, Strings to Array, Operations on Strings, Subroutines and Command line arguments
Unit-V :(Language)	Calling modules, Hashes, Data Structures in Perl, Reading files and writing output formats, Regular expressions and Perl Operations, Parsing genbank, PDB, BLAST, and other file formats, Object-oriented programming, Complex Data Structures, Relational Databases.

Suggested Reading:

4. Beginning Perl for Bioinformatics By James Tisdall, O'Reilly Media (2001)
5. Mastering Perl for Bioinformatics By James Tisdall, O'Reilly Media (2003)
6. Python For Bioinformatics By Sebastian Bassi, Chapman and Hall (2010)
7. HTML the complete reference, 2004, TMH.
8. Beginning PHP and Professional PHP, 2009, Wrox, Wiley Dreamtech.
9. JavaScript: The complete Reference, 2004, TMH.

Learning Outcome:

1. Students will demonstrate the ability to identify, formulate and solve computer systemsengineering problems.
2. Students will demonstrate the ability to design and experiment both in hardware andsoftware, analyze and interpret data.
3. Students will demonstrate an ability to analyze the given problems and design solutions,as per the needs and specifications.
4. Students will develop confidence for self education and ability for lifelong learning
5. Students will be capable of participating and succeeding in competitive examinations.

Sant Gadge Baba Amravati University, Amravati

Syllabus Prescribed for 2022 Year **PG Programme**
Programme: M. Sc. Bioinformatics

Semester 1 Code of the Course/Subject	**Title of the Course/Subject** (Laboratory/Practical/practicum/hands-on/Activity)	**(No. of Periods/Week)**
Practical VII	Practical Based on DSC XI, XII, XIII & XIV	**12**

CO:

1. To develop logical understanding of the subject.
2. To create the ability to model, solve and interpret Molecular Modelling, Drug Design, Chemo-informatics , Bio- Programming and Research Methodology, IPR and Bioethics problems.
3. To provide an overview of functions of complex variable which helps in solvingmany biological problems

*** List of Practical/Laboratory Experiments/Activities etc.**

Molecular Modeling, Drug Design, Chemo-informatics , Bio- Programming –II and Research Methodology, IPR and Bioethics

1	Binding site identification
2	Pharmacophore identification
3	Rigid body docking using Autodock and ADT
4	Molecular dynamics simulations using Gromacs
5	Visual Molecular Dynamics (VMD)
6	Advance Visualization with (Discovery Studio)
7	Receptor and Ligand Optimization

8	Conformational Analysis
9	Chemo-informatics Software
a.	AMBER
b.	ArgusLab 3.0
c.	BABEL
d.	Chemos
e.	VEGA
f.	PubChem
g.	ChemSketch
10	Chemo-informatics databases
11	Chemical structure representation
12	Smiles - Simplified Molecular Input Line Entry System
13	Molecular Dimension Limited (MDL) file format for chemical connectivity
14	Chemical Structure similarity
15	Fingerprints and search for substructure similarity using expasy
16	Generation of 3D structures from 2D representations
17	3D structure similarity
18	Elements of molecular descriptors
19	Writing Pseudo Codes
20	Working with Objects, Arrays, Conditionals and Loops
21	Creating Classes and Applications in Java
22	Managing Simple Events and Interactivity
23	Creating User Interfaces with AWT, Modifiers
24	Packages and Interfaces, Exception, Multithreading
25	Streams and I/O, Using Native Methods and Libraries
26	Java Programming Tools, Working with Data Structures
27	Sequence Analysis Packages - EMBOSS, NCBI Tool Kit
28	Analysis of Biological Sequences
a.	Basic Blast
b.	Specialized Blast

Learning Outcome:

1. Research, inquiry and analytical thinking abilities
2. The capability and motivation for intellectual development
3. Ethical, social and professional understanding
4. Effective research communication
5. Teamwork, collaborative and management skills
6. be able to describe the process of drug discovery and development
7. be able to discuss the challenges faced in each step of the drug discoveryprocess
8. have gained a basic knowledge of computational methods used in drugdiscovery

Sant Gadge Baba Amravati University, Amravati

Syllabus Prescribed for 2022 Year **PG Programme**
Programme: M. Sc. Bioinformatics

Semester 1 Code of the Course/Subject	**Title of the Course/Subject** (Laboratory/Practical/practicum/hands-on/Activity)	**(No. of Periods/Week)**
Practical VII	Practical Based on Project Work	**06**

CO:

1. Identify and discuss the role and importance of research in the bioinformatics.
2. Identify and discuss the issues and concepts salient to the research process.
3. Identify and discuss the complex issues inherent in selecting a research problem, selecting an appropriate research design, and implementing a research project.
4. Identify and discuss the concepts and procedures of sampling, data collection, analysis and reporting.

Learning Outcome:

1. Explain key research concepts and issues
2. Read, comprehend, and explain research articles in their academic discipline.
3. Able to formulate new research problem.