



INSTITUTE OF SCIENCE, TECHNOLOGY & ADVANCED STUDIES (VISTAS)
(Deemed to be University Estd. u/s 3 of the UGC Act, 1956)
PALLAVARAM - CHENNAI

ACCREDITED BY NAAC WITH 'A' GRADE

Marching Beyond 25 Years Successfully

M.Sc.Bioinformatics

Curriculum and Syllabus

Regulations 2021

(Based on Choice Based Credit System (CBCS))

and

Learning Outcomes based Curriculum Framework (LOCF))

Effective from the Academic year

2021-2022

Department of Bioinformatics

School of Life Sciences

Vision

The Vision of Department of Bioinformatics is to provide the best education and training for students to prepare them for professional research careers in biological sciences as well as software industry. The Department plans to produce eminent scientists in the field of Bioinformatics.

Mission

To facilitate, conduct and organize research work by teams comprised of core groups leading to inventions and to cooperate to meet this end and also to work acquiring the patents of such inventions. With its strong commitment to education, the department expects its graduates to have acquired solid subject knowledge and laboratory skills in the field of Bioinformatics upon their graduation. In addition, with our innovative curriculum, the graduates are also expected to possess all-round competence in IT technology, information gathering and synthesis, critical thinking, efficient oral and written communication, and teamwork spirit and capability so that their career prospects go beyond the field of life sciences.

PROGRAM EDUCATIONAL OBJECTIVES (PEO)

PEO-1: Describe the basis of biology, computer science and information technology and develop as a key expertise in applications of bioinformatics.

PEO-2: An extra-ordinary ability to gain practical knowledge and keen in developing a successful career in academia, R&D institutes and industrial sector.

PEO-3: Possess a high-level knowledge in comparing and analyze the best programming language, database and software to implement and support the critical biological challenges.

PEO-4: Promoting the bioinformatics hardcore research and support the experimental scientist in the hypothesis and mechanism related to biology.

PEO-5: Will address the increasing need for skilled computer expert in maintaining and analyze the biological resource and big data and contribute globally.

PROGRAM OUTCOME (PO)

PO-1: Life Sciences knowledge: Successful candidates will acquire current/recent specific knowledge in the respective discipline with proficiency in practical skills and leadership skills for a successful career.

PO-2: Problem analysis: Successful candidates will be able to analyse, design standards, resolve and troubleshoot problems in implementation or standardization of Life sciences protocols.

PO-3: Design/development of solutions: Successful candidates will develop creative and cognitive thinking and cooperate with each other to solve problems in the field of Life sciences.

PO-4: Conduct investigations of Practical problems: Successful candidates will acquire capabilities to plan and design protocols and utilize practical skills

PO-5: Conduct investigations of experimental problems: To validate hypothesis by executing experimental techniques independently coupled with the ability to assimilate, analyse, interpret and accurately evaluate subsequent data.

PO-6: Modern tool usage: Successful candidates will effectively be able to manage resources and time using ICT and other computer enabled devices.

PO-7: Ethics: Successful candidates will be aware of their role and responsibility in handling and

use of microbes including genetically modified microorganisms.

PO-8: Communication: Successful candidates will have the ability to understand and communicate all ideas and concepts effectively.

PO-9: Environment sustainability: Successful candidates will get adequate knowledge to use information and implement solutions for environmental protection, safeguards and remediation.

PROGRAMME SPECIFIC OUTCOME (PSO)

The M.Sc. programme Bioinformatics at VISTAS has documented measurable outcomes that are based on the needs of the programme's stakeholders. The programme specific outcomes that the department presently adapts to are as follows:

PSO-1: The syllabus addresses the need to introduce students to new tools and application in bioinformatics.

PSO-2: The PG course helps every candidate to analysis the software for data studies and comparisons and provides tools for modelling, visualizing, exploring and interpreting data.

PSO-3: To access the wealth of data to answer questions relevant to the average biologist, and is highly hands-on.

PSO-4: The main goal of the M.sc Bioinformatics to convert multitude of complex data into useful information and knowledge.

PSO-5: The course is intended to describe not only with the programming languages but it covers the proteomics, genomics, cell and molecular biology, genetic engineering, biochemical pathways etc., relevant to the improvement and development of mankind and industrial application purposes.

Board of Studies Members

M.Sc. BIOINFORMATICS

S.No	Name with Designation	Role
1.	Dr. Radha Mahendran, Professor & Head, Department of Bioinformatics, VISTAS, Chennai	Chairman
2.	Dr.J. Suganya Assistant Professor, Department of / Bioinformatics, VISTAS, Chennai	Internal Member
3.	Dr. D. Velmurugan, Professor, Dept of Crystallography and Biophysics, University of Madras, Guindy, Chennai	Academic Expert
4.	Dr. P. Gautam, Professor, Centre for Biotechnology.	Academic Expert
5.	Dr.M.N Ponnusamy, Emeritus Professor, Dept of Crystallography and Biophysics, University of Madras, Guindy, Chennai	Academic Expert
6.	Dr.M.Menaga, Managing Director, BioNeem Tech, Sipcot IT park, Siruseri Chennai	Industrial Expert
7.	Mr. Aganl Vincent Paul	Alumni
8.	Ms. Abinaya.B	Alumni
9.	Ms. Jyotsna.A	Student

VISTAS

VELS INSTITUTE OF SCIENCE, TECHNOLOGY AND ADVANCED STUDIES (VISTAS)

CHENNAI - 600 117

REGULATIONS 2021

CHOICE BASED CREDIT SYSTEM/LOCF

1. DURATION OF THE PROGRAMME:

1.1. Two years (four semesters)

1.2. Each academic year shall be divided into two semesters. The odd semesters shall consist of the period from July to November of each year and the even semesters from January to May of each year.

1.3 There shall be not less than 90 working days for each semester.

2. ELIGIBILITY FOR ADMISSION:

2.1. A candidate with a Bachelor's Degree in Science in the disciplinary of Genetics, Biochemistry, Biotechnology, Physics, Chemistry, Computer Science, Botany, Zoology, Microbiology, Mathematics, Statistics, Nutrition, Foodservice and Management & Dietetics, Agriculture, B.E./B. Tech (Biotech), B. V.Sc, MBBS, BDS, B. Pharm, BPT & BCA from the University, or an examination of some other University, accepted by the Syndicate as equivalent thereto, shall be permitted to appear and qualify for the M.Sc. Bioinformatics Degree examination of this University after a course of two academic years in an affiliated college of this University.

3. MEDIUM OF INSTRUCTION:

The medium of instruction for all PG programmes is English.

4. CREDIT REQUIRMENTS AND ELIGIBILITY FOR AWARD OF DEGREE:

A Candidate shall be eligible for the award of Master Degree only if he/she has undergone the prescribed course of study in VISTAS for a period of not less than two academic years and passed the examinations of all the prescribed courses of four Semesters earning a minimum of 90 credits as per the distribution given in for Part I and also fulfilled such other conditions as have been prescribed there of.

5. COURSE:

Each course / subject is to be designed under lectures / tutorials / laboratory or field work / seminar

/ practical training / Assignments / Term paper or Report writing etc., to meet effective teaching and learning needs.

6. COURSE OF STUDY AND CREDITS:

The Course Components and Credit Distribution shall consist Part I

The PG programme consists of a number of courses. The term ‘course’ is applied to indicate a logical part of the subject matter of the programme and is invariably equivalent to the subject matter of a ‘paper’ in the conventional sense. The following are the various categories of courses suggested for the PG programmes.

Part I – Core courses i.e. major courses that compulsorily required for each of the programme of study (CC), Ability Enhancement Course (AHC) and Discipline Specific Elective Course (DSE) .

For each course, credit is assigned based on the following:

Contact hour per week		CREDITS
1 Lecture hour	-	1 Credit
1 Tutorial hour	-	1 Credit
2 Practical hours	-	1 Credit

(Laboratory / Seminar / Project Work / etc.)

7. REQUIREMENTS FOR PROCEEDING TO SUBSEQUENT SEMESTER:

- 7.1. **Eligibility:** Students shall be eligible to go to subsequent semester only if they earn sufficient attendance as prescribed therefor by the Board of Management from time to time.
- 7.2. **Attendance:** All Students must earn 75% and above of attendance for appearing for the University Examination. (Theory/Practical)
- 7.3. **Condonation of shortage of attendance:** If a Student fails to earn the minimum attendance (Percentage stipulated), the HODs shall condone the shortage of attendance on medical grounds up to a maximum limit of 10% (i.e. between 65% and above and less than 75%) after paying the prescribed fee towards the condonation of shortage of attendance. The students with attendance of less than 65 and more than 50% shall be condoned by VC on the recommendation of HODs on genuine grounds, will be permitted to appear for the regular examination on payment of the prescribed condonation fee.

7.4. Detained students for want of attendance:

Students who have earned less than 50% of attendance shall be permitted to proceed to the next semester and to complete the Program of study. Such Students shall have to repeat the semester, which they have missed by rejoining after completion of final semester of the course, by paying the fee for the break of study as prescribed by the University from time to time.

7.5. Transfer of Students and Credits:

The strength of the credits system is that it permits inter Institutional transfer of students. By providing mobility, it enables individual students to develop their capabilities fully by permitting them to move from one Institution to another in accordance with their aptitude and abilities.

7.5.1. Transfer of Students is permitted from one Institution to another Institution for the same program with same nomenclature, provided, there is a vacancy in the respective program of Study in the Institution where the transfer is requested.

7.5.2. The marks obtained in the courses will be converted into appropriate grades as per the University norms.

7.5.3. The transfer students are not eligible for Ranking, Prizes and Medals.

7.5.4. Students who want to go to foreign Universities upto two semesters or Project Work with the prior approval of the Departmental / University Committee are allowed to transfer of their credits. Marks obtain in the courses will be converted into Grades as per the University norms and the students are eligible to get CGPA and Classification.

8. EXAMINATION AND EVALUATION

8.1. EXAMINATION:

- i) There shall be examinations at the end of each semester, for odd semesters in the month of October / November, for even semesters in April / May. A candidate who does not pass the examination in any course(s) shall be permitted to appear in such failed courses in the subsequent examinations to be held in October / November or April / May.
- ii) A candidate should get registered for the first semester examination. If registration is not possible owing to shortage of attendance beyond condonation limit / regulations prescribed OR belated joining OR on medical grounds, the candidates are permitted to move to the next semester. Such candidates shall re-do the missed semester after completion of the programme.

- iii) The results of all the examinations will be published through University Website. In the case of passed out candidates, their arrear results, will be published through University Website.

8.2 To Register for all subjects:

Students shall be permitted to proceed from the First Semester up to Final Semester irrespective of their failure in any of the Semester Examination, except for the shortage of attendance programs. For this purpose, Students shall register for all the arrear subjects of earlier semesters along with the current (subsequent) Semester Subjects.

8.3. Marks for Continuous Internal Assessment (CIA) Examinations and End Semester Examinations (ESE) for PART I.

8.3.1 There shall be no passing minimum for Continuous Internal Assessment (CIA) Examinations.

8.3.2 For End Semester examination, passing minimum shall be 40% (Forty Percentage) of the maximum marks prescribed for the Course/Practical/Project and Viva-Voce.

8.3.3 In the aggregate (CIA and ESE) the passing minimum shall be of 40%.

8.3.4. He / She shall be declared to have passed the whole examination, if he/she passes in all the courses wherever prescribed in the curriculum by earning 90 CREDITS in Part I.

9. Question Paper Pattern for End Semester Examination

Maximum marks: 100

Section A: $10 \times 3 = 30$

Each question carries 3 marks (Any 10 out of 12)

Section B: $5 \times 8 = 40$

Each question carries 8 marks (Any 5 out of 8)

Section C: $2 \times 15 = 30$

Each question carries 15 marks (Answer all either or pattern)

10. SUPPLEMENTARY EXAMINATION: Supplementary Examinations are conducted for the students who appeared in the final semester examinations. Eligible criteria for appearing in the Supplementary Examinations are as follows:

10.1. Eligibility: A Student who is having a maximum of two arrear papers is eligible to appear for the Supplementary Examination.

10.2. Non-eligibility for those completed the program: Students who have completed their Program duration but having arrears are not eligible to appear for Supplementary Examinations.

11. RETOTALLING, REVALUATION AND PHOTOCOPY OF THE ANSWER SCRIPTS:

11.1. Re-totalling: All PG Students who appeared for their Semester Examinations are eligible for applying for re-totalling of their answer scripts.

11.2. Revaluation: All current batch Students who have appeared for their Semester Examinations are eligible for Revaluation of their answer scripts. Passed out candidates are not eligible for Revaluation.

11.3. Photocopy of the answer scripts: Students who have applied for revaluation can download their answer scripts from the University Website after fifteen days from the date of publication of the results.

12. The examination and evaluation for MOOCs will be as per the requirements of the regulatory bodies and will be specified at the beginning of the Semester and notified by the university NPTEL-SWAYAM Coordinator (SPOC).

13. CLASSIFICATION OF SUCCESSFUL STUDENTS

13.1. PART I CORE SUBJECTS, ALLIED, ELECTIVES COURSES AND PROJECT: Successful Students passing the Examinations for the Part I courses and securing the marks

a) CGPA 9.00 to 10.00 shall be declared to have passed the examination in **First class with Outstanding**.

b) CGPA 7.50 to 8.99 shall be declared to have passed the examination in **First class with distinction**.

c) CGPA 6.00 to 7.49 shall be declared to have passed the examination in **First Class**.

d) CGPA 5.00 to 5.99 in the aggregate shall be declared to have passed the examination in the **SECOND** Class.

e) CGPA 4.00 to 4.99 shall be declared to have passed the examination in the **THIRD** Class.

14. MARKS AND GRADES:

The following table shows the marks, grade points, letter grades and classification to indicate the performance of the Student:

14.1. Computation of Grade Point Average (GPA) in a Semester, Cumulative Grade Point Average (CGPA) and Classification

GPA for a Semester: = $\sum_i C_i G_i \div \sum_i C_i$ That is, GPA is the sum of the multiplication of grade points by the credits of the courses divided by the sum of the credits of the courses in a semester.

Where, C_i = Credits earned for course i in any semester,

G_i = Grade Points obtained for course i in any semester

n = Semester in which such courses were credited.

CGPA for the entire programme: = $\sum_n \sum_i C_{ni} G_{ni} \div \sum_n \sum_i C_{ni}$ That is, CGPA is the sum of the multiplication of grade points by the credits of the entire programme divided by the sum of the credits of the courses of the entire programme

The Students who have passed in the first appearance and within the prescribed semester of the UG Programme (Major, Allied and Elective courses only) are eligible.

Grade Conversion Table – PG			
Range of Marks	Grade Points	Letter Grade	Description
90 – 100	10	O	Outstanding
82 – 89	9	A+	Excellent
75 – 81	8	A	Very Good
67 – 74	7	B+	Good
60 – 66	6	B	Above Average
50 – 59	5	C	Average
40 – 49	4	D	Minimum for pass
0 – 39	0	RA	Reappear
		AAA	Absent

14.2. Letter Grade and Class CGPA

Overall Performance – UG		
CGPA	GRADE	CLASS

4.00 - 4.99	D	Third Class
5.00 - 5.99	C	Second Class
6.00 - 6.69	B	First Class
6.70 - 7.49	B+	
7.50 - 8.19	A	First Class with Distinction*
8.20 - 8.99	A+	
9.00 - 10.00	O	First Class - Outstanding*

15. RANKING

- Students who pass all the examinations prescribed for the Program in the FIRST APPEARANCE ITSELF ALONE are eligible for Ranking / Distinction.
- In the case of Students who pass all the examinations prescribed for the Program with a break in the First Appearance are only eligible for Classification.
- Students qualifying during the extended period shall not be eligible for RANKING.

16. MAXIMUM PERIOD FOR COMPLETION OF THE PROGRAMS TO QUALIFY FOR A DEGREE

16.1. A Student who for whatever reasons is not able to complete the programs within the normal period (N) or the Minimum duration prescribed for the programme, may be allowed two years period beyond the normal period to clear the backlog to be qualified for the degree. (Time Span = N + 2 years for the completion of programme)

16.2. In exceptional cases like major accidents and child birth an extension of one year considered beyond maximum span of time (Time Span= N + 2 + 1 years for the completion of programme).

17. REVISION OF REGULATIONS, CURRICULUM AND SYLLABI

The University may from time to time revise, amend or change the Regulations, Curriculum, Syllabus and Scheme of examinations through the Academic Council with the approval of the Board of Management.

COURSES OF STUDY AND SCHEME OF ASSESSMENT

(MINIMUM CREDITS TO BE EARNED: 90)

M.Sc Bioinformatics Course Components

Component	I Sem	II Sem	III Sem	IV Sem	Total Credits
Core Courses	12	14	12	20	58
Ability Enhancement Courses (AEC)	-	-	-	-	-
Discipline Specific Elective (DSE)	12	10	8	-	30
Generic Elective (GEC)	-	-	2	-	2
Total Credits	24	24	22	20	90

M.Sc. BIOINFORMATICS COURSE

COURSES OF STUDY AND SCHEME OF ASSESSMENT

(MINIMUM CREDITS TO BE EARNED: 90)

M.Sc Bioinformatics Course Components

UGC DOCUMENT ON LOCF BIOINFORMATICS

Learning Outcomes based Curriculum Framework

(LOCF)

for

M.Sc BIOINFORMATICS

Postgraduate Programme

2021

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1. Introduction:

In the increasingly globalized society, it is important that the younger generation especially the students are equipped with knowledge, skills, mindsets and behaviors which may enable them to perform their duties in a manner so that they become important contributors to the development of the society. This will also help them to fully utilize their educational training for learning a decent living so that the overall standard of their families and surroundings improve leading to development of welfare human societies. To achieve this goal, it is imperative that their educational training is improved such that it incorporates the use of newer technologies, use of newer assessment tools for mid-course corrections to make sure that they become competitive individuals to shoulder newer social responsibilities and are capable of undertaking novel innovations in their areas of expertise. In the face of the developing knowledge society, they are well aware about the resources of self-development using on-line resources of learning which is going to be a major component of learning in the future. The learning should also be a continuous process so that the students are able to re-skill themselves so as to make themselves relevant to the changing needs of the society. In the face of this need, the educational curricula, teaching learning processes, training, assessment methods all need to be improved or even re-invented.

2. Learning Outcomes based approach to Curriculum Planning: (LOCF)

Learning Outcome based approach to curriculum planning (LOCF) is almost a paradigm shift in the whole gamut of higher education such that it is based on first and foremost identifying the outcomes of the learning required for a particular subject of study, and then planning all components of higher education so as to achieve these outcomes. The learning outcomes are the focal point of the reference to which all planning and evaluation of the end learning is compared and further modifications are made to fully optimize the education of the individuals in a particular subject. For the subject of bio science the outcomes are defined in terms of the understanding and knowledge of the students in biology and computer application in biology and the practical skills the students are required to have to be competitive biologist. So, that they are able to play their role as Biologist.

2.1 Nature and extent of the M.Sc. Programme:

The undergraduate programme in Bioinformatics is the first level of college or university degree in the country as in several other parts of the world. After obtaining this degree, a Bioinformatician may enter into the job market or opt for undertaking further higher studies in the subject. After graduation the students may join industry, academia, public health and play their role as

bioinformatician in a useful manner contributing their role in the development of the welfare society. Thus the undergraduate level degree in Biocomputing must prepare the students for all these objectives. Thus the LOCF curriculum developed has a very wide range covering all aspects of bioinformatics with reasonable depth of knowledge and skills so to as to diversify them in various specialties of the subject and play their role professionally as expected of them. It is also imperative that bioinformatician are evaluated in a manner appropriate to assess their proper development as bioinformatician. The current LOCF in Biocomputing has been designed in keeping all these important points in mind.

2.2 Aims of Postgraduate's degree programme in Bioinformatics

In Bioinformatics apart from getting a job in the IT sector, candidates with the right skill set and knowledge can apply to pharmaceutical companies, biomedical organizations, biotech research centres, agricultural companies and even NGOs that need bioinformationists in India & abroad. Several Indian companies have already started offering good employment opportunities for Biocomputing candidates. A broad range of course will be studied to establish a basic understanding and appreciation of the issues and problems of computational biology. The course includes an applied component, which gives an introduction to programming for biological data and use in a range of web-based Biocomputing utilities. Biocomputing is supposed to be an enigmatic field in areas like software development, bio-database design and maintenance, sequence assembly, proteomics, clinical pharmacologist, sequence analysis, and bio-analytics there is option to become an academician too after completing the studies. Job opportunities in this field are available with research institutions, and with pharmaceutical companies, chemical industries, agriculture and allied industries working to expand the realm of information.

3. Postgraduate attributes in Life Science:

Broaden the outlook and attitude, develop the current skills and abilities, and learn

- New one to do extremely well in studies and career, grow into responsible global citizens. Contour the academic career of the students, make them employable, enhance
- To shape one's life and also that of colleagues and peers. Demonstrate behavioral attributes for the enhancement of soft skills, socialistic
- Research insight and support the participation in co-curricular and extracurricular activities. Instill skills and abilities to develop a positive approach and be self-contained
- Approach and leadership qualities for successful career and nurture responsible human being.

- Provide highly skilled and knowledgeable human resources for agricultural Sector, food industry, dairy industry, medical and paramedical field, pharmaceutical and research institutes

4. Qualification Descriptors: The following may serve as the important qualification descriptors for a PG degree in Bioinformatics:

1. Knowledge of the diverse places where biological science is involved.
2. Understanding of diverse biological processes.
3. Advanced skills and safety issues related to handling of Microbes, Animals and Plants Good laboratory practices etc.
4. Advanced skills in working with microbes such as pilot scale culturing, downstream processes, diagnostics etc.
5. Generation of new knowledge through research projects
6. Ability to participate in team work through biological projects.
7. Ability to present and articulate their knowledge of biology.
8. Knowledge of recent developments in the area of biology.
9. Analysis of data collected through study and projects / dissertations / reviews / research surveys.
10. Ability to innovate so as to generate new knowledge.
11. Awareness how some biology leads may be developed into enterprise.
12. Awareness of requirements for fruition of a biology-related enterprise.
13. Ability to acquire intellectual property rights.

5. Programme Learning Outcome

- (i) A advanced and systematic or coherent understanding of the academic field of Science, its different learning areas and applications, and its linkages with related disciplinary areas/subjects.
- (ii) The skills and knowledge gained has intrinsic beauty, which also leads to proficiency in analytical reasoning. This can be utilized in modeling and solving real life problems.
- (iii) Procedural knowledge that creates different types of professionals related to the disciplinary including professionals engaged in research and development, teaching and government/public service
- (iv) Skills in areas related to one's specialization area within the disciplinary and current and emerging developments in the field of Science

- (v) Demonstrate relevant generic skills and global competencies such as (i) problem solving skills that are required to solve different types of problems with well-defined solutions, and tackle open-ended problems that may cross disciplinary-area boundaries;
- (vi) Communication skills involving the ability to listen carefully, to read texts and research papers analytically and to present complex information in a concise manner to different groups/audiences
- (vii) Analytical skills involving paying attention to detail and ability to construct logical arguments using correct technical language
- (viii) ICT skills
- (ix) Personal skills such as the ability to work both independently and in a group.

6. Teaching learning Process: The teaching-learning process should be aimed at systematic exposition of basic concepts so as to acquire knowledge of respective discipline in a canonical manner. Students have great freedom of choice of subjects which they can study. The various components of teaching learning process are summarized in the following.

1. The most common method of imparting knowledge is through lectures. There are diverse modes of delivering lectures such as through blackboard, power point presentation and other technology aided means. A judicious mix of these means is a key aspect of teaching-learning process.
2. Assimilating ideas, deepening understanding, and gaining mastery of new concepts all take time, commitment, and intelligent effort. To reinforce learning, to monitor progress, and to provide a regular pattern of study, tutorials are essential requirements. During these tutorials, difficulties faced by the students in understanding the lectures, are dealt with.
3. Necessary and sufficient infrastructural facilities for the, laboratories and libraries equipped with adequate modern and modular furniture and other requirements. Modern and updated laboratory equipments needed for the undergraduate laboratories and reference and text books for the libraries
4. Home assignments at regular intervals and project work involving applications of theory are necessary to assimilate basic concepts of the respective discipline. Hence, it is incumbent on the part of a learner to complete open-ended projects assigned by the teacher.
5. The teaching-learning process needs to be further supported by other activities devoted to subject-specific and interdisciplinary skills, summer and winter internships in their discipline. During these internships it is expected that a learner will interact with experts and write a report on a topic provided to the learner.

6. Institute visit by a learner is also a part of learning process. During such visits a learner has access to knowledge by attending academic activities such as seminars, colloquia, library consultation and discussion with faculty members. These activities provide guidance and direction for further study.
7. Special attempts should be made by the institution to develop problem-solving skills and design of laboratory experiments for demonstration at the UG level. For this purpose a mentor system may be evolved where 3-4 students may be assigned to each faculty member.

M.Sc. BIOINFORMATICS COURSE
COURSES OF STUDY AND SCHEME OF ASSESSMENT

(MINIMUM CREDITS TO BE EARNED: 90)

SEMESTER I

Code No.	Course	Hours/Week			Maximum Marks			
		Lecture	Tutorial	Practical	Credits	CA	SEE	Total
CORE 1	Introduction To Bioinformatics	4	0	0	4	40	60	100
CORE 2	Computer Programming in C and C++	4	0	0	4	40	60	100
CORE	Practical 1 - Biological Databank and Sequence Analysis –	0	0	4	2	40	60	100
CORE	Practical 2 – Bio programming in C and C++ -	0	0	4	2	40	60	100
DSE 1	Genomics and Transcriptomics	4	0	0	4	40	60	100
DSE 2	Proteomics: Principles and Techniques	4	0	0	4	40	60	100
DSE 3	Enzymes And Metabolisms	4	0	0	4	40	60	100
Total		20	0	8	24			

CA - Continuous Assessment

SEE - Semester End Examination

SEMESTER II

Code No.	Course	Hours/Week			Maximum Marks			
		Lecture	Tutorial	Practical	Credits	CA	SEE	Total
CORE 3	Programming in VB and RDBMS	4	0	0	4	40	60	100
CORE 4	Programming in Perl and Bioperl	4	0	0	4	40	60	100
CORE	Practical 3 - Programming in VB and RDBMS	0	0	4	2	40	60	100
CORE	Practical 4 - Programming in Perl and Bioperl	0	0	4	2	40	60	100
CORE	Mini Project	0	0	4	2	40	60	100
DSE 4	Plant Bioinformatics	4	0	0	4	40	60	100
DSE 5	Concepts in Artificial Intelligence	3	0	0	3	40	60	100
DSE 6	Molecular Evolution and Phylogeny	3	0	0	3	40	60	100
Total		18	0	12	24			
CA - Continuous Assessment				SEE - Semester End Examination				

SEMESTER III

Code No.	Course	Hours/Week			Maximum Marks			
		Lecture	Tutorial	Practical	Credits	CA	SEE	Total
CORE 5	Computer Aided Drug Designing	4	0	0	4	40	60	100
CORE 6	Advanced Programming in Java	4	0	0	4	40	60	100
CORE	Practical 5 - Computer Aided Drug Designing –	0	0	4	2	40	60	100
CORE	Practical 6 - Programming In Java And BioJava -	0	0	4	2	40	60	100
DSE 7	Python for Bioinformatics	4	0	0	4	40	60	100
DSE 8	Recent Technologies in OMICS Sciences	4	0	0	4	40	60	100
GE	Generic Elective I	2	0	0	2	40	60	100
Total		18	0	8	22			

CA - Continuous Assessment

SEE - Semester End Examination

UGC Recommended Generic Electives

1. Consumer Affairs
2. Disaster Management
3. Universal Human Values

SEMESTER IV

Code No.	Course	Hours/Week			Maximum Marks			
		Lecture	Tutorial	Practical	Credits	CA	SEE	Total
CORE 7	Operating Systems	4	0	0	4	40	60	100
CORE 8	Clinical Research	4	0	0	4	40	60	100
CORE	Main Project	0	0	22	12	40	60	100
Total		8	0	22	20			

List of DSE courses is specified after the curriculum:

- **DSE 1** - Genomics and Transcriptomics
- **DSE 2** - Proteomics: Principles and Techniques
- **DSE 3** - Enzymes and Metabolism
- **DSE 4** - Plant Bioinformatics
- **DSE 5** - Concepts in Artificial Intelligence
- **DSE 6** - Molecular Evolution and Phylogeny
- **DSE 7** - Python for Bioinformatics
- **DSE 8** - Recent Technologies in OMICS Sciences

Syllabus Core

Course

Course Objective: This course will enable the students to understand the nature of biological data and need for biological databases and also to explore major biomolecular sequence databases (organization and contents); search and retrieve data from the databases using their respective search engines. To understand and appreciate the need and significance of sequence analysis and the bioinformatics approaches, algorithms for sequence analysis, the application of methods for analysis of the biomolecular sequence data

UNIT I INTRODUCTION TO COMPUTERS 15

Basics of computing: Introduction to operating systems – WINDOWS, UNIX, LINUX; Advantages of security installation; Use of internet; Graphics – visualization techniques; softwares and hardwares; Computer networking – LAN, WAN, MODEM, Optical vs electronic networking, firewalls; Ethernet and TCP/IP family of protocols.

UNIT II INTRODUCTION TO BIOLOGICAL DATABASES 10

Nucleotide databases (Genbank, EMBL, DDBJ); Protein databases (Swiss-Prot, Tr-EMBL, PIR_PSD, Expsy); Derived Databases (Prosite, PRODOM, Pfam, PRINTS) Specialized Genome databases: (NCBI, EBI, TIGR, SANGER).

UNIT III BIOLOGICAL DATABASES II 10

Sequence submission Methods and tools (Sequin, Sakura, Bankit); Sequence retrieval systems (Entrez& SRS); Sequence File Formats and Conversion tools; Metabolic Pathway database (KEGG, EMP, EcoCyc, BioCyc and MetaCyc); Specialized database (IMGT, Rebase, COG, LIGAND, BRENDA); Structural database (CATH, SCOP, and PDBsum).

UNIT IV SEQUENCE ANALYSIS 12

Analysis of protein and nucleic acid sequences, multiple alignment programs, Development of programs for analysis of nucleic acid sequences, Pair wise Sequence Alignment - Similarity, Identity and Homology, Global Alignment, Local Alignment; database search methods-Multiple Sequence Alignment - Multiple alignment programs, Development of programs for analysis of

Nucleic acid sequences, Conversion of various file formats; Phylogenetic Analysis - Concept of dendrograms; Strings and Evolutionary trees.

UNIT V STRUCTURAL ANALYSIS

13

Analysis of structures and correctness of structures, Submission of data to PDB: atomic coordinates and electron density maps; Anatomy of Proteins - Ramachandran plot, Secondary structures, Motifs, Domains, Tertiary and quaternary structures; Calculation of conformational energy for bio-macromolecules; Methods for Prediction of Secondary and Tertiary structures of Proteins.

Total: 60 Hours

COURSE OUTCOMES:

CO-1: To understand the basics of computer, internet and computer networking softwares.

CO-2: To acquire the concepts of different biological databases

CO-3: To study the sequence file formats and retrieval system.

CO-4: To analyze the evolutionary relationship and alignment.

CO-5: To study the structures of protein and their function site.

Text Book:

1. Baxevanis A.D., Davison D.B., Page R. D. M. & Petsko G.A. Current Protocols in Bioinformatics. New York, John Wiley & Sons Inc., 2004. ISBN: 0555015254 Syllabus draft: April 26, 2010.

Reference Books:

1. Korf Ian, Yandell Mark, Bedell Joseph. BLAST: an essential guide to the basic local alignment search tool. Shroff Publishers and Distributors Pvt. Ltd., 2003. ISBN: 8173665125.
2. Lesk, A.M. "Introduction to Bioinformatics", 1st Edition, Oxford University Press, Oxford, UK , 2002 . ISBN: 90421

Course Objective: This course will enable the students to conceptualize and formulate logic and flow for the implementation of a computational task and develop codes using the structured programming approach of 'C' & C++ programming language and also to develop and implement programs to analyze biological data.

UNIT I C PROGRAMMING 10

Concept of variables and constants, structure of a C program. Operators & Expressions: Arithmetic, Unary, Logical, Bit-wise, Assignment & Conditional Operators, Library Functions, Control Statements: while, do While, for statements, Nested loops, if.. else, switch, break, continue and go to statements, Comma operator.

UNIT II FUNCTION, STRING, POINTERS 13

Functions: Defining & Accessing : Passing arguments, Function Prototype, Recursion, Use of Library Functions, Storage Classes: Automatic, External and Static Variables (Register), Arrays: Defining & Processing, Passing to a function, Multidimensional Arrays. String: Operations of Strings (String handling through built-in & UDF: Length, Compare Concatenate, Reverse, Copy, Character Search using array) Pointers: Declarations, Passing to a function, Operations on Pointers, Pointers & Arrays, Array of Pointer, Pointer Arithmetic, Array accessing through pointers, Pointer to structure, Pointer to functions, Function returning pointers, Dynamic Memory Allocations.

UNIT III STRUCTURES AND FILES 12

Structures: Defining & Processing, Passing to a function, Unions (Array within structure, Array of structure, Nesting of structure, Passing structure and its pointer to UDF, Introduction to Unions and its Utilities) Data Files: Open, Close, Create, Process Unformatted Data Files. (Formatted Console I/O functions, Unformatted Console I/O functions, Modes Of Files, Use Of fopen(), fclose(), fgetc(), fputc(), fgets(), fprintf(), fscanf(), fread(),fwrite(), Command Line Arguments). Documentation, debugging, C Processors, Macros. Examples illustrating structured

program development methodology and use of a block structured algorithmic language to solve specific problems.

UNIT IV INTRODUCTION TO OBJECT ORIENTED PROGRAM 10

Introduction to object oriented programming, user defined types, polymorphism, and encapsulation. Getting started with C++ - syntax, data-type, variables, strings, functions, exceptions and statements, namespaces and exceptions, operators. Flow control, functions, recursion. Arrays and pointers, structures.

UNIT V ABSTRACTION MECHANISMS, INHERITANCE 10

Abstraction Mechanisms: Classes, private, public, constructors, destructors, member functions, static members, references etc. Class hierarchy, derived classes. Inheritance: simple inheritance, polymorphism, object slicing, base initialization, virtual functions.

Total: 60 Hours

COURSE OUTCOMES:

- CO-1: To understand the basics of C program and their operators using Conditional statements and loops.
- CO-2: To utilize the concepts of operators and in build functions to program the control structures and decision-making concept
- CO-3: To design the array, structure, pointers, files and unions in the programming.
- CO-4: To choose the OOPS concepts and to utilize the constructors and operators
- CO-5: To discuss the concepts of files and inheritance

Text Book:

Balagurusamy E. Programming In ANSI C. Publisher: New Delhi Tata McGraw Hill Publishing Company Ltd. 2007. ISBN: 9780070648227

Reference Books:

1. Kanetkar Yashavant. Let Us C 9th Edition. Publisher: New Delhi BPB Publications. 2009. ISBN: 9788183331630.
2. Jonassen Inge, Kim Junhyong. Algorithms in Bioinformatics: 4th International Workshop, WABI 2004 Bergen, Norway, September 2004 Proceedings. Publisher: New York Springer. 2004. ISBN: 3540230181.
3. Kernighan Brian W. Ritchie Dennis M. The C Programming Language 2nd Edition. Publisher: USA, Prentice-Hall, Inc. 1988. ISBN: 0876925964

Course Objective: This course will enable the students to understand the nature of biological data and need for biological databases and also to explore major biomolecular sequence databases (organization and contents); search and retrieve data from the databases using their respective search engines. To understand and appreciate the need and significance of sequence analysis and the bioinformatics approaches, algorithms for sequence analysis, the application of methods for analysis of the biomolecular sequence data

1. Biological Databanks, Sequence Databases, Structure Databases, Specialized Databases.	02
2. Data retrieval tools and methods.	02
3. Database file formats.	02
4. Molecular visualization.	02
5. Gene structure and function prediction (using GenScan, Gene Mark).	02
6. Sequence similarity searching (NCBI BLAST).	02
7. Protein sequence analysis (ExPASy proteomics tools).	02
8. Multiple sequence alignment (Clustal).	02
9. Molecular phylogeny (PHYLP).	02
10. Analysis of protein and nucleic acids sequences.	03
11. Sequence analysis using EMBOSS or GCG Wisconsin Package.	03
12. Development of programs in the analysis of nucleic acid sequences – such as protein coding regions in prokaryotes.	03
13. Programs to calculate potential energy of regular structures such as Collagen triple helix, DNA double helix, and their visualization in wire and stick model as well as space filling model.	03

Total:30 Hours

COURSE OUTCOMES:

CO-1: Explore the basics and databases for information retrieval and data analysis

CO-2: Adapt the knowledge on genetic structure and introns and coding regions for the benefits of human studies.

CO-3: To learn the sequence similarity with different sequences and their alignment.

CO-4: To analyze the evolutionary relationship and alignment.

CO-5: To study the structures of protein and their function site.

Text Book:

1. Epstein Richard J. Human molecular biology: an introduction to the molecular basis of health and disease. Publisher: Cambridge, UK ; Cambridge University Press, 2003.ISBN: 052164481X.

Reference Books:

1. Korf Ian, Yandell Mark, Bedell Joseph. BLAST: an essential guide to the basic local alignment search tool. Shroff Publishers and Distributors Pvt. Ltd., 2003. ISBN: 8173665125.
2. Baxevanis Andreas D. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, 3rd Edition. Publisher: New York, John Wiley & Sons, Inc. 2002, ISBN: 9814126756
3. Lesk, A.M. "Introduction to Bioinformatics:", 1st Edition, Oxford University Press, Oxford, UK , 2002.ISBN: 9042112221
4. Teresa Attwood, Parry-Smith David J. Introduction to Bioinformatics. Publisher: Pearson Education (Singapore) Pte.Ltd., 2001. ISBN:8178085070
5. Mount David W.. Bioinformatics: Sequence and Genome Analysis. Publisher: Cold Spring Harbor Laboratory Press; 1st edition 2001. ISBN: 0879695978
6. Gibas Cynthia, Jambeck Per. Developing Bioinformatics Computer Skills. Publisher: Shroff Publishers and distributors O'Reilly Media, Inc., 2001. ISBN: 8173662428

Course Objectives: This course will enable the students to conceptualize and formulate logic and flow for the implementation of a computational task and develop codes using the structured programming approach of 'C' & c++programming language and also to develop and implement programs to analyze biological data.

- | | |
|---|---|
| 1. Operators and Expressions, Branching and Looping in C. | 3 |
| 2. Classes and Objects in C++. | 3 |
| 3. Program to demonstrate Inheritance in C++. | 3 |
| 4. Translate DNA sequence to Protein in C & C++. | 5 |
| 5. Comparing two Sequences. | 3 |
| 6. Calculate the true length of a Sequence. | 3 |
| 7. Function Blocks: a. Handling default reference arguments b. Handling inline and overloaded function C++. | 5 |
| 8. Arrays and String as objects: Insertion, Deletion, reversal sorting of elements into a single in C++. | 5 |

Total: 30 Hours

COURSE OUTCOMES:

CO-1: To understand the basics of C program and their operators using Conditional statements and loops.

CO-2: To utilize the concepts of operators and in build functions to program the control structures and decision-making concept

CO-3: To design the array, structure, pointers, files and unions in the programming.

CO-4: To choose the OOPS concepts and to utilize the constructors and operators

CO-5: To discuss the concepts of files and inheritance

Text Book:

Balagurusamy E. Programming In ANSI C. Publisher: New Delhi Tata McGraw Hill Publishing Company Ltd 2007. ISBN: 9780070648227

Reference Books:

1. Kanetkar Yashavant. Let Us C 9th Edition. Publisher: New Delhi BPB Publications. 2009. ISBN: 9788183331630.
2. Jonassen Inge, Kim Junhyong. Algorithms in Bioinformatics: 4th International Workshop, WABI Bergen, Norway, September 2004 Proceedings. Publisher: New York Springer. 2004. ISBN: 3540230181.

Course Objective: Identify the differences between the procedural languages and event – driven languages. Define and modify the properties and methods associated with an object. To load, modify, and save changes made to forms and projects in the Visual Basic Environment. Make clear understand on RDBMS concepts and Database languages such as Oracle and PL/SQL.

UNIT I Introduction to Visual Basic 12

Introduction to Visual Basic: IDE, working with forms, developing an application, variables, datatypes and modules, procedures and control structures, arrays in VB. Working with VB Controls: Creating and using controls, working with control arrays - ODBC and Data Access Objects.

UNIT II User Interfaces 12

Menus Events and Dialog Boxes: Menu and Events definition, Event model in VB, Menu Interfaces, Mouse Events, Dialog Boxes: Definition, Types of Dialog Boxes, Applying dialog. Graphics, MDI and FlexGrid: Graphics for application, Multiple Document Interface and Using the FlexGrid Control

UNIT III VB Classes and Objects 12

Classes: Definition, advantages of classes, class methods. Objects: Definition and methodology. Introduction to VB Classes and Objects, Creating various forms, Objects and projects. Working with objects, Classes and class modules, Creating VB objects.

UNIT IV Introduction to DBMS 12

Advantages and Components of a Database Management Systems - Feasibility Study - Class Diagrams - Data Types - Events - Normal Forms - Integrity - Converting Class Diagrams to Normalized Tables - Data Dictionary. Query Basics - Computation Using Queries - Subtotals and GROUP BY Command - Queries with Multiple Tables Subqueries – Joins, Testing Queries.

UNIT V Introduction to ORACLE 12

ORACLE - Introduction to Oracle, Data definition languages - Data Manipulation language, Data Control Language, Data types in Oracle. Constraints in Oracle, Data and String

Functions, Union and Intersect operator, Sub queries, Introduction to PL / SQL, Simple PL / SQL programs.

Total: 60 Hours

COURSE OUTCOMES:

- CO-1: To build the fundamentals of visual basic
- CO-2: To utilize the concepts of user interface
- CO-3: To utilize the VB classes and objects
- CO-4: To design the DBMS and role in database creation
- CO-5: To design the ORACLE and its connectivity

Text Books:

1. Steven Holzner, "Visual Basic 6 Programming: Black Book", Dreamtech Press, 2000.
2. C. J. Date, A. Kannan, "Database Systems", Pearson Education Publication, 2006

References Books:

1. Noel Jerke, "Visual Basic 6: The Complete Reference", Tata McGraw Hill, 1999.
2. Kevin Loney, George Kuch, "Oracle – The complete Reference", Tata McGraw Hill Publication, 2005
3. C. J. Date, "Database Systems", Addison Wesley Publication, 1990.

Course Objective: To learn the fundamentals of the Perl programming language and how it can be used to write data reporting and systems administration applications. To discover how to use of the DBI.pm module and related DBD (driver) files with Perl to build database-driven applications.

UNIT I Introduction to Perl. 10

Introduction:- Scalar Data- Numbers, Strings, Scalar Variables, Output with print, Getting User Input, The chomp operator, undef Value, defined function, The if and while control structures, Lists and Arrays:- Accessing elements of an array, Special Array indices, List Literals, List Assignment, Subroutines:- Defining a subroutine, Invoking a subroutine, Return values, Arguments, Private variables in subroutines, the return operator.

UNIT II Expressions 15

Input and Output:- Input from Standard Input, Input from the diamond operator, Invocation arguments, Output to Standard Output, Filehandles, Opening a Filehandle, Hashes:- Hash Element Access, Hash Functions, Regular Expressions, Matching with Regular Expressions:- Matches with m//, Option Modifiers, Anchors, The Binding operator, =~, Interpolating into Patterns, The match Variables, General Quantifiers. Processing Text with Regular Expressions:- Substitutions with s///, The split Operator, The join Function, m// in List context, More Powerful Regular Expressions.

UNIT III Control Structures and Files. 15

Control Structures:- The unless Control Structure, The until Control Structure, Expression Modifiers, The Naked Block Control Structure, The elsif Clause, Autoincrement and Autodecrement, The for Control Structure, Loop Controls, Logical Operators, File Tests:- File Test Operators, The stat and lstat functions, The localtime function, Bitwise Operators, Using the Special Underscore Filehandle, Strings and Sorting:- Finding a Substring with index, Manipulating a Substring with substr, Formatting Data with sprintf, Advanced Sorting, Perl Modules:- Finding Modules, Installing Modules, Using Simple Modules.

UNIT IV Introduction to Bioperl . 10

Bioperl:- Introduction, 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

UNIT V Common Gateway Interface (CGI)

10

Common Gateway Interface:- Web Servers and Browsers, HTML tags, table, frames, form elements, GET, POST & HEAD Method, 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

Total: 60 Hours

COURSE OUTCOMES:

- CO-1: To build the essentials of Perl using subroutines.
- CO-2: To utilize the concepts of expressions with modifiers.
- CO-3: To understand the perception of control structures.
- CO-4: To develop perl program using procedures and functions to solve the biological problems.
- CO-5: To create the perl script for research project purpose and database creation with CGI.

Text Book:

1. Martin C Brown, "Perl the Complete Reference", Tata McGraw Hill, 2001

References Books:

1. Erick Storm, "Perl CGI Programming", BPB Publication, 1998.
2. Steven Holzner, "Perl: Black Book", Second Edition, Dreamtech Publication, 2007.
3. Ed Peschko & Michele Dewolf, "Perl Developer's Guide", Tata McGraw Hill, 2000.

Course Objective: Identify the differences between the procedural languages and event – driven languages. Define and modify the properties and methods associated with an object. To load, modify, and save changes made to forms and projects in the Visual Basic Environment. Make clear understand on RDBMS concepts and Database languages such as Oracle and PL/SQL.

VB

1. Creating Simple application forms in Visual Basic. 02
 - a) Creating a form for simple Arithmetic Calculations
 - b) Creating a form for simple Biological applications
2. Creating application forms using Variables, Data Types and Control structures. 02
 - a) Creating Factorial Calculator
 - b) Creating GC – Content Calculator
3. Creating application forms using different types of “Objects” in VB. 02
 - a) Creating form to find,
 - i) Leap Year,
 - ii) Currency Exchange,
 - iii) Octal, Decimal, Hexadecimal Calculation
 - iv) Scroll Bar
 - b) Creating form to find
 - i) The Complement of given sequence
 - ii) The reverse of given sequence
 - iii) The frequency of Nucleotides.
4. Creating application forms using Menus, Mouse Events. 02
5. Creating applications forms using Graphics in VB. 02

Oracle, PL/SQL

- 1.a) Creation of student information records containing Roll number, Name, Subject Code Marks etc.,
- b) Finding the total and average marks, result for each student table.

- | | |
|---|----|
| c) Record Manipulations such as Deletion, Modification, Addition and Counting the Record. | 02 |
| 2. Creating table that demonstrates simple biological applications | 02 |
| 3. Creating table to demonstrate applications with biological sequences. | 03 |

Database Creation using VB with RDBMS

- | | |
|--|----|
| 1. Create a database that demonstrates “Library Information System” with VB forms and Query language.(User Interface with VB) | 03 |
| 2. Create a database that stores and retrieves simple biological applications. (User Interface with VB). | 03 |
| 3. Create a database for “Railway Reservation System”. (User Interface with VB) | 03 |
| 4. Create a database that stores and retrieves biological sequences and to find the similarities between two sequences. (User Interface with VB) | 04 |

Total: 30 Hours

COURSE OUTCOMES:

CO-1: To build the fundamentals of visual basic

CO-2: To utilize the concepts of user interface

CO-3: To utilize the VB classes and objects

CO-4: To design the DBMS and role in database creation

CO-5: To design the ORACLE and its connectivity

Text Books:

1. Steven Holzner, “Visual Basic 6 Programming: Black Book”, Dreamtech Press, 2000.
2. C. J. Date, A. Kannan, “Database Systems”, Pearson Education Publication, 2006

References Books:

1. Noel Jerke, “Visual Basic 6: The Complete Reference”, Tata McGraw Hill, 1999.
2. Kevin Loney, George Kuch, “Oracle – The complete Reference”, Tata McGraw Hill Publication, 2005
3. C. J. Date, “Database Systems”, Addison Wesley Publication, 1990.

Course Objective: To learn the fundamentals of the Perl programming language and how it can be used to write data reporting and systems administration applications. To discover how to use of the DBI.pm module and related DBD (driver) files with Perl to build database-driven applications.

1. Write a Perl program to find the length of the given sequence? 02
2. Write a Perl program to reverse and concatenation of the given sequence? 02
3. Write a Perl program to complement and reverse complement of DNA sequence? 02
4. Write a Perl program to calculate GC content in the given DNA sequence? 02
5. Write a Perl program to translate DNA into Protein Sequence? 02
6. Operators and Expressions. 02
7. Branching and Looping. 02
8. Formatting Data. 02
9. Sort an Array of Strings in Reverse Order. 02
10. Splitting DNA sequence into Pieces by Using split (). 02
11. How do I read or write Fasta files using Bioperl? 02
12. Comparing two Sequences. 02
13. How do I calculate the true length of a Sequence? 02
14. How can I parse a PDB file using Bioperl? 02
15. Translating DNA sequence into Protein Sequence . 02

Total: 30 Hours

COURSE OUTCOMES:

CO-1: To build the essentials of Perl using subroutines.

CO-2: To utilize the concepts of expressions with modifiers.

CO-3: To understand the perception of control structures.

CO-4: To develop perl program using procedures and functions to solve the biological problems.

CO-5: To create the perl script for research project purpose and database creation with CGI.

Text Book:

1. Martin C Brown, "Perl The Complete Reference", Tata McGraw Hill, 2001

References Books:

1. Erick Storm, "Perl CGI Programming", BPB Publication, 1998.
2. Steven Holzner, "Perl: Black Book", Second Edition, Dreamtech Publication, 2007.

COURSE OBJECTIVES:

- For the benefit of the students, it has been mandatory to attend a minimum of two months mini project Programme during semester1 vacation
- Student should go for mini project Programme in any bioinformatics industries or laboratories and learn their laboratory techniques by hands on training.
- After the mini project Programme, student should submit detailed reports about the project work in printed format.
- Evaluation is based on work done, quality of report, performance in viva-voce, presentation etc.
- The report will be evaluated by duly appointed teaching faculty from head of department.

Course Objective: This course will enable the students to understand the critical relationship among biomolecular structure, function and force field models. To utilize basic modeling techniques to explore biological phenomena at the molecular level. To emphasize Modelling drug/receptor interactions in detail by molecular mechanics, molecular dynamics simulations and homology modeling.

UNIT I Molecular Modeling and Mechanics 10

Basic Concepts of Molecular Structure: Bond Length, Bond Angle, Torsion Angle, Non-Covalent Interactions and force field parametrisation and transferability – Molecular Structure and Internal Energy – Energy Minimization, Derivative and Non-Derivative Methods, Local and Global Minima.

UNIT II Quantum Mechanics 10

Introduction to Computational Quantum Mechanics: One Electron Atom, Poly Electronic Atoms and Molecules, Hartree Fock Equations, Molecular Properties calculation using Ab initio and Semi Empirical Methods, Density Functional Theory, Moller and Plesset Perturbation Theory.

UNIT III Molecular Modeling and Docking 13

Molecular Modeling in Drug Discovery, Sequence Analysis, Secondary structure prediction, Tertiary Structure prediction- Homology Modeling, Threading and ab-initio methods, Structure validation, Molecular Docking – Introduction, Approaches (Simulation and Shape complementarity approach), Molecular Docking Algorithm, Docking Optimization- Scoring functions, Molecular Docking Application.

UNIT IV Pharmacophore 12

Pharmacophore – Historical Perspective and Features, Viewpoint of Pharmacophore, Pharmacophore modeling- Molecular alignments, handling flexibility, alignment techniques, scoring and optimization, conformational expansion, validation and usage, Applications of pharmacophore model in medicinal chemistry.

UNIT V Molecular Dynamics 10

Molecular Dynamics- Introduction, MD using simple models, MD with continuous potentials, setting up and running a molecular dynamics simulation, Constraint Dynamics,

Monte Carlo Simulation Methods- Monte Carlo simulation of molecules, Simulation Analysis.

Total: 60 Hours

COURSE OUTCOMES:

CO-1: To understand the fundamentals of molecular mechanics and its structure.

CO-2: To analyze the concept of computational quantum mechanics using energy theory.

CO-3: To apply the basic principles, models, and theory of molecular docking in drug designing.

CO-4: To design the model using molecular ligand system and their pharmacophore prediction.

CO-5: To learn the various methods of dynamic approaches in the *Insilco* docking studies.

Text Book:

1. Andrew R. Leach. Molecular Modelling: Principles and Applications, second edition. Pearson Education EMA, January 2001 ISBN 0-582-38210-6

References Books:

1. D. C. Rapaport, The Art of Molecular Dynamics Simulation, 2004, ISBN 0-521-82568-7
2. M. P. Allen, D. J. Tildesley, Computer simulation of liquids, 1989, Oxford University Press, ISBN 0-19-855645-4.
3. R. J. Sadus, Molecular Simulation of Fluids: Theory, Algorithms and Object-Oriented, 2002, ISBN 0-444-51082-6
4. J.M.Haile, Molecular Dynamics Simulation Elementary Methods, John Wiley and Sons, 1997.
5. Satya Prakash Gupta, QSAR and Molecular Modeling, Springer - Anamaya Publishers, 2008.
6. Guy H. Grant and W. Graham Richards. Computational Chemistry Oxford Chemistry Primers, 29 1995. 9780198557401

Course Objectives: Understand fundamentals of programming such as variables, conditional and iterative execution, methods, etc. Understand fundamentals of object-oriented programming in Java, including defining classes, invoking methods, using class libraries, etc. Be aware of the important topics and principles of software development. Have the ability to write a computer program to solve specified problems.

UNIT I Fundamental of Java 10

Java features – Java Platform – Java Fundamentals – Expressions, Operators – Arithmetic – Logical - Comparison – Bitwise operators, Control Structures – Looping : while, do while, for, Branching: if, if else, elseif ladder, nested if, Classes, Packages and Interfaces – Exception Handling.

UNIT II Java for WWW 10

Introduction to Java Scripts, Objects in Java Script, and Dynamic HTML with Java Script. XML: Document type definition, XML Schemas, Document Object model, Presenting XML, Using XML Processors: DOM and SAX Review of Applets, Class, Event Handling, AWT Programming.

UNIT III Introduction to Swing 10

JApplet, Handling Swing Controls like Icons – Labels – Buttons – Text Boxes – Combo – Boxes – Tabbed Pains – Scroll Pains – Trees – Tables Differences between AWT Controls & Swing Controls Developing a Home page using Applet & Swing. Java Beans: Introduction to Java Beans, Advantages of Java Beans, JDK Introspection, Using Bound properties, Bean Info Interface, Constrained properties Persistence, Customizers, and Java Beans API.

UNIT IV Introduction to Servlets 15

Lifecycle of a Servlet, JSDK the Servlet API, The javax.servelet Package, Reading Servlet parameters, Reading Initialization parameters. The javax. servelet HTTP package, Handling Http Request & Responses, Using Cookies- Session Tracking, Security Issues Introduction to JSP, The Problem with Servlet. The Anatomy of a JSP Page, JSP Processing. JSP Application. Design with MVC Setting Up and JSP Environment: Installing the Java Software Development Kit, Tomcat Server & Testing Tomcat

Biojava: Introduction to Biojava, Installing Biojava, Symbols and Symbol Lists, Sequence and Features, Sequence I/O Basics, viewing molecule structures through BioJava. JSP Application Development: Generating Dynamic Content, Using Scripting Elements Implicit JSP Objects, Conditional Processing – Displaying Values Using an Expression to Set an Attribute, Declaring Variables and Methods Error Handling and Debugging Sharing Data between JSP pages, Requests, and Users Passing Control and Date between Pages – Sharing Session and Application Data – Memory Usage Considerations.

Total: 60 Hours

COURSE OUTCOMES:

CO-1: To understands the fundamentals of Java and OOP technology.

CO-2: To identify classes, objects, members of a class and relationships among them needed for a specific problem

CO-3: To write Java application programs using array and String.

CO-4: To demonstrate the concepts of errors, File handling using Multithreaded Programming

CO-5: To write Java programs to utilizing the java applet code and graphics Programming.

Text Book:

1. E Balagurusamy, “Programming with Java: A Primer”, Fourth Edition, Tata McGraw Hill, 2010

References Books:

1. P. Naughton and H.Schildt- Java2 (The Complete Reference) - Third Edn.TMH 1999.
2. Deital & Deital, “How to Program Java”, Pearson Education, 1999.
3. Cays Horstmann, Gary Cornell, “Core Java 2: Advanced Features”, Sun Micro System, 2007

Course Objective:

This course will enable the students to understand the critical relationship among Biomolecular structure, function and force field models. To utilize basic modeling techniques to explore biological phenomena at the molecular level. To emphasize Modelling drug/receptor interactions in detail by molecular mechanics, molecular dynamics simulations and homology modeling.

1.	Small molecule building, using ISIS Draw and CHEM SKETCH.	02
2.	Homology Modeling using SPDBV	02
3.	Homology Modeling using Modeller.	03
4.	Model structure refinement using SPDBV	03
5.	Model validation using What Check and Pro Check	03
6.	Docking using Hex.	02
7.	Docking using AUTODOCK	03
8.	Molecular dynamics using AMBER	03
9.	Docking using ARGUSLAB.	05
10.	Virtual screening using NCI database.	04

Total: 30 Hours**COURSE OUTCOMES:**

CO-1: To design the small molecules using softwares.

CO-2: Able to model the protein structure with the help of modelling softwares.

CO-3: To analyse and validate the structure of protein.

CO-4: To demonstrate the concepts of molecular docking and dynamics using softwares.

CO-5: To perform and handled large sets of compounds using screening method.

Text Book:

1. Andrew R. Leach. Molecular Modelling: Principles and Applications, second edition. Pearson Education EMA, January 2001 ISBN 0-582-38210-6

References Books:

1. D. C. Rapaport, The Art of Molecular Dynamics Simulation, 2004, ISBN 0-521-82568-7
2. M. P. Allen, D. J. Tildesley, Computer simulation of liquids, 1989, Oxford University Press, ISBN 0-19-855645-4.
3. R. J. Sadus, Molecular Simulation of Fluids: Theory, Algorithms and Object-Oriented, 2002, ISBN 0-444-51082-6
4. J.M.Haile, Molecular Dynamics Simulation Elementary Methods, John Wiley 1997.

Course Objective: Understand fundamentals of programming such as variables, conditional and iterative execution, methods, etc. Understand fundamentals of object-oriented programming in Java, including defining classes, invoking methods, using class libraries, etc. Be aware of the important topics and principles of software development. Have the ability to write a computer program to solve specified problems

1) Operators and Expressions, Branching and Looping.	02
2) Classes and Objects.	02
3) Packages.	02
4) Formatting Data.	02
5) Sort an Array of Strings in Reverse Order.	02
6) Implementing Case Differences Ignorance.	02
7) Splitting DNA sequence into Pieces by Using split().	02
8) Applet Example.	02
9) Drawing Circle, rectangle using Java Graphics	02
10) How do I read or write Fasta files using Biojava?	02
11) Comparing two Sequences.	02
12) How do I calculate the true length of a Sequence?	02
13) How can I parse a PDB file using Biojava?	03
14) Creating web page using JSP.	03

Total: 30 Hours

COURSE OUTCOMES:

CO-1: To understands the fundamentals of Java and OOP technology.

CO-2: To identify classes, objects, members of a class and relationships among them needed for a specific problem

CO-3: To write Java application programs using array and String.

CO-4: To demonstrate the concepts of errors, File handling using Multithreaded Programming

CO-5: To write Java programs to utilizing the java applet code and graphics Programming.

Text Book:

1. E Balagurusamy, "Programming with Java: A Primer", Fourth Edition, Tata McGraw Hill, 2010

References Books:

1. P. Naughton and H.Schildt- Java2 (The Complete Reference) - Third Edn.TMH 1999.
2. Deital & Deital, "How to Program Java", Pearson Education, 1999.

Course Objectives: Aims to give clear view of operating system structure, Processing and its memory. Also to make the student to clear understand on OS memory management system and its implementations on computer programming structures.

UNIT I Operating Systems Introduction 12

Introduction - Views- Goals - types of operating systems – Operating System Structure – Components of Operating System - Operating System services - system calls and system programs, Development of Operating Systems, Uses of Operating Systems, Types of Operating Systems, .

UNIT II Process Management and Process Scheduling 12

Process management - Process concepts - process scheduling - operation on process Inter process communication - CPU Scheduling: Scheduling criteria – Scheduling algorithms – Multiple- processor scheduling – Real time scheduling – Algorithm Evaluation. Case study: Process scheduling in Linux.

UNIT III Storage Management 12

Memory Management - Single and multiple partitioned allocation – paging - segmentation - internal & External Fragmentation. Non-Contiguous Allocation: Paging and Segmentation Schemes - Implementation - Hardware-Protection - Sharing – Fragmentation. Virtual Memory Management - Demand paging and Page Replacement Algorithms, Information management - File concept - Access methods - Directory structure - allocation methods - free space management - disk scheduling.

UNIT IV File System 12

File-System Interface: File concept – Access methods – Directory structure – File system mounting – Protection. File-System Implementation: Directory implementation – Allocation methods – Free-space management – efficiency and performance – recovery – log-structured file systems. Case studies: File system in Linux – file system in Windows.

UNIT V I / O Systems 12

I/O Systems – I/O Hardware – Application I/O interface – kernel I/O subsystem – streams – performance. Mass-Storage Structure: Disk scheduling – Disk management – Swap-space management – RAID – disk attachment – stable storage – tertiary storage.

Total: 60 Hours

COURSE OUTCOMES:

CO-1: To build the basics of operating system and services

CO-2: To choose the suitable methods for process management and scheduling

CO-3: To utilize the storage management and virtual memory management

CO-4: To discuss the file system and its protection.

CO-5: To list the use of I/O systems.

Text Books:

1. Andrew S. Tanenbaum, "Modern Operating Systems", Second Edition, Pearson Education, 2004

References Books :

1. Davis Rajkumar, "Operating System: A Systematic View", Pearson Education, 2007
2. H. M. Deitel, "Operating System", Second Edition, Pearson Education, 1990.
3. Harvery M. Deitel, Paul J. Deitel, "Operating System", Third Education, Pearson Education, 2004

Course Objective:

This course will enable the students to understand the key concepts of research in responsible to the conduct of research and able to conduct research that conforms to the highest standards for the protection of human research subjects.

UNIT I Introduction to Clinical Research 12

Introduction to clinical research, History of clinical research, Clinical Research Degree, Clinical Research Training and an overview of the common research designs. Safety-Sponsor, Local site investigators, Institutional review boards (IRBs), Regulatory agencies. Economics - Sponsor, Investigators, Subjects, Participation as labor. Participating in a clinical trial - Locating trials, Steps for volunteers, Research. an overview of key trial activities in clinical research, clinical research and media.

UNIT II Introduction to Clinical Trails 12

Introduction to clinical trials, Trials of drugs, Trials of devices. History - Development, Modern trials. Types - different phases of clinical trials,. Trial design - Active comparator studies, Master protocol, Clinical trial protocol, Design features, Placebo groups, Duration. Administration – Marketing, Information technology. Ethical aspects - Conflicts of interest and unfavorable studies. Ethical principles that govern clinical trials.

UNIT III Good Clinical Research Practice (GCPR) 12

Introduction to Good clinical research practice – Background, Objectives, Scope, Overview of the clinical research process, Key trial activities include -Development of the trial protocol, . Development of standard operating procedures (SOPs), Development of support systems and tools, Generation and approval of trial-related documents, Selection of trial sites and the selection of properly qualified, trained, and experienced investigators and study personnel, Ethics committee review and approval of the protocol, Review by regulatory authorities. Enrollment of subjects into the study: recruitment, eligibility, and informed consent

UNIT IV WHO Principles 12

WHO principles of GCPR- Principle 1: Ethical Conduct, Principle 2: Protocol, Principle 3: Risk Identification, Principle 4: Benefit-Risk Assessment, Principle 5: Review by Iec/Irb, Principle 6: Protocol Compliance, Principle 7: Informed Consent, Principle 8: Continuing

Review/ Ongoing Benefit-Risk Assessment, Principle 9: Investigator Qualifications, Principle 10: Staff Qualifications, Principle 11: Records. Principle 12: Confidentiality/Privacy, Principle 13: Good Manufacturing Practice, Principle 14: Quality Systems

UNIT V Presentation Skills

12

Continuing review, investigator and staff qualifications, records confidentiality, Ethical conduct, protocol, risk identification, benefit risk assessment, review, protocol compliance, and informed consent GMP, and quality systems. 6 main Elements of Presentation skills - Be Prepared, Give of Yourself, Stay Relaxed, Use Natural Humor, Plan Your Body & Hand Positions, Pay attention to all details How to present research result (Presentation).

Total: 60 Hours

COURSE OUTCOMES:

CO-1: To understand the basic concepts of clinical research and their trial techniques for the good research.

CO-2: To acquire the knowledge about the clinical research and ethics for novel research.

CO-3: To acquire the knowledge of good clinical research program.

CO-4: To must able to recognize the concepts of GPCR rules.

CO-5: To learn how to present the data and research result.

Text Book:

1. Glasser, Stephen P. Essentials of Clinical Research springer 2014 ISBN 9783319054704

References Books:

1. John I. Gallin. Principles and Practice of Clinical Research (Third Edition). Elsevier Inc 2012. ISBN: 978-0-12-382167-6
2. Gupta SK. Basic Principles of Clinical Research and Methodology. Institute of Clinical research.2007 ISBN 9788184480863
3. Friedman, L.M., Furberg, C.D., DeMets, D., Reboussin, D.M., Granger, C.B. Fundamentals of Clinical Trials springer 2015 ISBN 978-3-319-18539-2.
4. Dr. Arun Bhatt, Clinical Trials And Good Clinical Practice In India Career Publication ISBN10: 8188513210

- Student should do research on their own interest or research guide interest on any biotechnology topic for 6 month in the university or any industries or laboratories.
- The candidates shall undertake the major project work in the Sixth Semester either in the Department concerned or in industries, institutes or any other organizations and the project report shall be submitted at the end of the Sixth semester.
- In case the candidate undertakes the project work outside the Department, the Staff concerned within the Department shall be the Main guide and the Staff/scientist under whom the work is carried out will be the Co-guide. The candidate shall bring the attendance certificate from the place of project work carried out.
- After the research, he/she should submit the detailed reports about the research in a dissertation and should present in an external examiner.
- Evaluation is based on work done, quality of report, performance in viva-voce, presentation etc.
- The report will be evaluated by duly appointed teaching faculty from head of department.

**DISCIPLINE
SPECIFIC ELECTIVE**

Course Objective: The course intends to give advanced theoretical knowledge on genomic organization and Genomic methods like microarray and transcriptome analysis

UNIT I Organization and Structure of Genomes 10

General organization and structure of genomes of viruses, prokaryotes, eukaryotes, and organelles (chloroplast, mitochondrion)

UNIT II Genome Mapping and Sequencing 10

Isolation and cloning of genomic DNA, Genome mapping (genetic and physical), STS assembly, ESTs, RAPDs, RFLPs, AFLPs, SSLPs, SNPs, linkage analysis, Restriction mapping, FISH, Chromosome painting, microsatellites, Gene finding, annotation, ORF and functional prediction, Chain termination and chemical degradation sequencing methods, Whole genome shot-gun sequencing.

UNIT III Large Scale Genomics/ Functional Genomics Analyses 15

Genome-wide association (GWA) analysis; Comparative Genomic Hybridization (CGH); Serial Analysis of Gene Expression (SAGE); Massively parallel Signature Sequencing (MPSS); Analysis of alteration in gene expression by Differential Display and Suppression Subtractive Hybridization. Introduction to Next Generation Sequencing (NGS) technologies for genome sequencing.

UNIT IV Microarray Technology and Analysis 10

Designing and producing microarrays; cDNA microarray technology; oligonucleotide arrays and designs; Sample preparation, labeling, hybridization, generation and analysis of microarray data.

UNIT V High-Throughput Transcriptomics Analysis 15

Gene Expression analysis by cDNA and oligonucleotide arrays; Methylome analysis using microarray; ChIP-on-Chip; Bioinformatics analysis of large-scale microarray data for comparative transcriptomics: Data normalization; Cluster analysis; Significance Analysis of Microarrays (SAM); Gene Ontology and Pathway analysis.

Total: 60 Hours

COURSE OUTCOMES:

CO-1: To understand the basics of genome structure and its organelles.

CO-2: To perform a range of practical techniques including DNA extraction and

sequencing, RT-PCR, reporter gene assay, metabolomics and genetic mapping.

CO-3: To design and analyse gene expression technique using Next Generation Sequencing (NGS) technologies.

CO-4: To gain knowledge on Microarray technology.

CO-5: To obtain and analyse information and data relating to specific genes using general and plant-specific databases, proteomics and metabolomics online portals, next generation sequencing tools and next generation mapping portals.

Text Books:

1. S.P. Hunt and F. J. Livesey, Functional Genomics.2000.
2. S. B. Primose. Principles of Genome Analysis.1998.

Reference Books:

1. C. R. Cantor and C. L. Smith. Genomics_ The Science and Technology behind the Human Genome Project,1999.
2. N. K. Spur, B. D. Young, and S. P. Bryant ICRF Handbook of Genome Analysis Volume 1 & 2. 1998.

Course Objective: To acquaint the student with Proteome organization, identification, expression and applications of proteomics analysis. And its applications

UNIT-I An Introduction to proteomics 10

Protein structure and function-Amino acids and their properties-Amino acids form polypeptides-Protein structure – four levels of organization-Cellular functions performed by proteins.

UNIT-II An overview of systems biology 10

Emergence of systems biology-. Evolution from protein chemistry to proteomics-Evolution of proteomics from protein chemistry-Promises of proteomics-Techniques commonly used for proteome analysis.

UNIT-III Analysis of Proteomes I 10

Analysis of proteomes - Two-dimensional polyacrylamide gel electrophoresis, Sample Preparation, Solubilization, Reduction, Resolution, Reproducibility of 2-DE Detecting proteins in polyacrylamide gels, Image analysis of 2-DE gels.

UNIT -IV Analysis of Proteomes II 15

Mass spectrometry based methods for protein identification- De novo sequencing using mass spectrometric data- Correlative mass spectrometric based identification strategies, 2-DE gel electrophoresis coupled with mass spectrometry, Micro array techniques- Types of microarrays, designing a microarray experiment, Microarray Technology in Treating Disease.

UNIT-V Applications of Genomics and Proteomics Analysis 15

Analysis of Genomes – Human, Mouse, Plasmodium falsiparum, Saccharomyces cerevisiae, Mycobacterium tuberculosis. Application of proteome analysis- drug development and toxicology, Pharmaceutical Applications, Proteomics in drug Discovery in human, phage antibodies as tools, Glycobiology and Proteomics in plant genetics and breeding.

Total: 60 Hours

COURSE OUTCOMES:

CO-1: To understand the basics of genome structure and its organelles.

CO-2: To perform a range of practical techniques including DNA extraction and sequencing, RT-PCR, reporter gene assay, metabolomics and genetic mapping.

CO-3: To design and analyse gene expression technique using Next Generation Sequencing (NGS) technologies.

CO-4: To gain knowledge on Microarray technology.

CO-5: To obtain and analyse information and data relating to specific genes using general and plant-specific databases, proteomics and metabolomics online portals, next generation sequencing tools and next generation mapping portals.

Text Books:

1. S. B. Primrose and R.M. Twyman - Principles of Genome Analysis and Genomics, 7th Edition, Blackwell Publishing, 2006.
2. S. Sahai - Genomics and Proteomics, Functional and Computational Aspects, Plenum Publication, 1999.

Reference Books:

1. Andrezej K Konopka and James C. Crabbe, Compact Hand Book - Computational Biology, Marcel Dekker, USA, 2004.
2. Pennington & Dunn - Proteomics from Protein Sequence to Function, 1st edition, Academic Press, San Diego, 1996.

Digestion and absorption of proteins. General aspects of amino acids metabolism; deamination, transamination, transmethylation, transpeptidation, and decarboxylation. Metabolism of ammonia: urea cycle and its regulation, Nitrogen balance, biosynthesis of non-essential amino acids. Metabolic breakdown of individual amino acids. Clinical correlations of protein metabolism. Integration of metabolism.

Total: 60 hours

COURSE OUTCOMES:

- CO-1: To Describe the structure, functions and the mechanism of action of enzymes. Learning kinetics of enzyme catalysed reactions and enzyme inhibitions and regulatory process. Ability to perform immobilization of enzymes. Exposure of wide applications of enzymes and future potential.
- CO-2: To Understand the fundamental energetics of biochemical processes, chemical logic of metabolic pathways. Knowing in detail about concepts to illustrate how enzymes and redox carriers and the oxidative phosphorylation machinery occur
- CO-3: To describe the Metabolism of carbohydrates and its regulation
- CO-4: To gain knowledge on Metabolism of lipid and its regulation
- CO-5: To obtain and analyse the metabolism of amino acids and their role in maintaining the body function.

Text Book:

1. Shanmughavel P, "Principles of Bioinformatics", Pointer Publishers, Jaipur, India. 2005.

Reference Books:

1. C. K. Mathews, K. E. Van Holde, & K.G. Ahern, "Biochemistry", Third Edition, Prentice Hall, 1999.
2. Cesareni Giovanni, Gimona Mario, Sudol Marius, Yaffe Michael (Editors). Modular Protein Domains. Publisher: Weinheim Wiley-VCH. 2005.

PPNEMA, MaizeGDB, TAIR database, CCPMT, Blast2GO, SSR locator Bioinformatics Tools for Inferring Functional Information from Plant Microarray Data – Agbase, Kyoto Encyclopedia of Genes and Genomes (KEGG), Ensembl, Entrez

Total: 60 Hours

COURSE OUTCOMES:

- CO-1: Acquire knowledge on fundamentals of plant cells and its functions to incorporate in developing plant databases
- CO-2: Originate the chances to understand the classification of plant kingdom and to access through computer-aided learning
- CO-3: Adapt the knowledge on plant genetics and design experimental techniques for the agricultural, industrial benefits from plants
- CO-4: Explore the basics and databases for information retrieval and data analysis
- CO-5: Utilize and assess the plant genomics data to predict novel traits

Text Book:

- 1. Khalid Rehman Hakeem, Adeel Malik, Fazilet Vardar-Sukan. by Plant Bioinformatics.

References Books:

- 1. Molecular Plant Taxonomy: Methods and Protocols (Methods in Molecular Biology, 1115) Softcover reprint of the original 1st ed. 2014.
- 2. David Edward, Plant Bioinformatics Methods and Protocols .

Course Objective: This Course mainly focuses more on machine learning, deep learning, probabilistic programming, multiagent systems, and includes sections where the AI's utility function is uncertain, rather than certain.

Unit I Introduction 9

What Is AI- the Foundations of Artificial Intelligence- The History of Artificial Intelligence- Intelligent Agents-How Agents Should Act, Structure of Intelligent Agents, Environments

Unit II Search Method 9

Solving Problems by Searching- Problem-Solving Agents, Formulating Problems, Search Strategies, Avoiding Repeated States, Constraint Satisfaction Search- Informed Search Methods- Best-First Search- Heuristic Functions- Memory Bounded Search- Iterative Improvement Algorithms- Game Playing- Introduction, Games as Search Problems, Perfect Decisions in Two-Person Games, Imperfect Decisions, Alpha-Beta Pruning, Games That Include An Element of Chance.

Unit III Logical Reasoning Systems 9

Variations, Using First Order Logic-Introduction to Logical Reasoning system Indexing, Retrieval and Unification- Logical Programming Systems- Theorem Provers- Forward-Chaining Production Systems- Frame Systems and Semantic Networks.

Unit IV Reasoning Under Uncertainty 9

Uncertainty- Acting under Uncertainty- Basic Probability Notation- The Axioms of Probability, Bayes' Rule and its Use- Probabilistic Reasoning Systems- Representing Knowledge in an Uncertain Domain the Semantics of Belief Networks- Inference in Belief Networks, Inference in Multiply Connected

Belief Networks- Non monotonic reasoning- Dealing with ignorance- Dempster Shafer theory- Dealing with vagueness- Fuzzy logic and fuzzy sets.

Unit V Planning and Learning 9

Planning A Simple Planning Agent- From Problem Solving to Planning, Planning in Situation Calculus, Basic Representations for planning, A Partial-Order Planning Example, A Partial-Order Planning Algorithm- Learning- A General Model of Learning Agents, Inductive Learning, Learning Decision Trees- Neural Networks- Bayesian Methods for Learning Belief

Networks- Genetic Algorithms and Evolutionary Programming- Knowledge in Learning- Explanation-Based Learning.

Total: 45 Hours

COURSE OUTCOMES:

CO-1: To compare AI with human intelligence and traditional information processing.

CO-2: To design AI functions and components involved in intelligent systems such as computer games, expert systems, semantic web, information retrieval, machine translation, mobile robots, decision support systems, and intelligent tutoring systems.

CO-3: To analyze the structures and algorithms of a selection of techniques related to searching, reasoning, machine learning, and language processing.

CO-4: To apply the basic principles, models, and algorithms of AI to recognize, model, and solve problems in the analysis and design of information systems.

CO-5: To discuss the core concepts and algorithms of advanced AI, including informed searching, CSP, logic, uncertain knowledge and reasoning.

Text Books:

1. Stuart Russel and Peter Norvig, “Artificial Intelligence- A Modern Approach”, Prentice Hall, 1995.
2. George F Luger, “Artificial Intelligence”, Pearson Education, 4th Edition, 2001.

References Books:

1. Engene Charniak and Drew Mc Dermott, “Introduction to Artificial Intelligence”, Addison Wesley, 2000.
2. Nils J. Nilsson, “Principles of Artificial Intelligence”, Narosa Publishing House, 2000.

Course Objective:

This course make us to understand DNA can be extracted and sequenced from a diverse range of biological samples, providing a vast amount of information about evolution and ecology. The analysis of DNA sequences contributes to evolutionary biology at all levels, from dating the origin of the biological kingdoms to untangling family relationships.

Unit I Evolution of life 9

History of evolution of life on earth: Chemical basis of evolution, Evolution of DNA, RNA and proteins, origin of the genetic code. Hardy-Weinberg equilibrium; Evolutionary changes by mutation, gene flow, genetic drift and natural selection.

Unit II Homology in molecular evolution 9

The concept of homology in molecular evolution. Role of transitions and transversions; chromosomal deletions and insertions in evolution. Role of repetitive DNA, transposable elements and junk DNA in evolution.

Unit III Theory of molecular evolution 9

Neutral theory (Kimura) and nearly neutral theory (Ohta) of molecular evolution (Kimura). Phylogenetic tree. Reconstruction of phylogenetic trees using distance matrix methods, the Maximum Parsimony method, and Maximum likelihood and Bayesian inference. Selection at the molecular level.

Unit IV Concept of the Molecular Clock 9

The concept of the Molecular Clock. Calibration. Limitation of molecular clock models. Human molecular clock: deducing evolutionary histories through mitochondrial DNA and Y chromosome.

Unit V Evolution of the genome 9

Evolution of the genome: Human Genome Project, ENCODE, Genome 10 K, Genome duplication (Ohno's hypothesis), Gene duplication, Exon Shuffling, Concerted evolution.

Total: 45 Hours

COURSE OUTCOMES:

CO-1: To understand the funadamentals of evolution in life.

CO-2: To analyze the concept of homology between the species and their predictions related

to molecular evolution.

CO-3: To apply the basic principles, models, and theory of molecular evolution in life.

CO-4: To design the model using molecular clock system.

CO-5: To discuss the core concepts and advanced technique to find the evolution of human genome through hypothesis.

Text Book:

1. Lindelle Bromham,. An Introduction to Molecular Evolution and Phylogenetics- IIInd Edition

References Books:

1. Wen Hsiung-Li, Molecular Evolution , Sinauer Associates, Sunderland, MA. ISBN 0878934634. 1997,
2. Ridley .M ,Evolution (3rd Edition) ,Blackwell Science. 2004, ISBN 1-4051-0345-1997

Course Objective: Read and understand the Python syntax. Be familiar with Python's fundamentals and develop simple applications. Apply the principles and techniques of object-oriented programming. Use sophisticated techniques and Python modules that are particularly useful for bioinformatics programming. Build new Python software tools for life science research. Summarize text patterns using regular expressions.

UNIT I Introduction to Python 12

Introduction to Python, History of Python, Python Features, Python Development Tools, Writing Python Program, Values and Variables:- Numeric Values, Variables and Assignment, Identifiers, Control codes within Structure, Controlling the print Function

UNIT II Expression 12

Expressions and Arithmetic:- Operator Precedence and Associativity, Comments, Errors (Syntax, Run-time errors, Logic Errors), Arithmetic Examples, Conditional Execution - Simple if Statement, if/else statement, Compound Boolean Expressions, Nested Conditionals, Multi-way Decision Statements, Conditional Expressions.

UNIT III Conditional Execution 12

Conditional Execution:- What is conditional statement in Python, Simple if Statement, if/else statement, nested if condition, else – if ladder, Compound Boolean Expressions, Nested Conditionals, Multi-way Decision Statements, Conditional Expressions.

UNIT IV Iteration 12

Iteration:- While Statement, For Statement, Nested Loops, the break statement, the continue statement, Infinite Loops, Computing Square roots, Drawing a Tree, Using Functions – mathematical functions – time Functions, reading the files from existing database using Python.

UNIT V Sequence Analysis through Python 12

Sequence Alignment:- Alphabets, Matching Sequences – Perfect Matches – Insertions and Deletions – Rearrangements – Global Versus Local Alignments – Sequence Length, Simple Alignment (Direct Alignment), Statistics:- Simple Statistics, Distributions, Normalizations, Multivariate Statistics, Probabilities, Odds.

Total: 60 hours

COURSE OUTCOMES:

CO-1: To understand why Python is a useful scripting language for developers.

CO-2: To learn how to design object-oriented programs with Python classes.

CO-3: To learn how to use indexing and slicing to access data in Python programs.

CO-4: To learn how to write functions and pass arguments in Python.

CO-5: To learn how to use exception handling in Python applications for error handling

Text Book:

1. Jason Kinser, "Python for Bioinformatics", Jones and Bartlett Publishers, Sudbury, Massachusetts 2009

References Books:

1. Richard L., Halterman, "Learning to Program With Python", 2011
2. Kent D. Lee, "Python Programming Fundamentals: Second Edition", Springer, 2010
3. Cody Jackson, "Learning to Program Using Python", Second Edition, 2013
4. Mark Lutz, "Learning Python", Third Edition, O'Reilly, 2007

Course Objective: This course will enable the students to understand the knowledge in large scale microarray data, Next Generation Sequencing Technology, and its applications.

UNIT I Micro Array Singenomics 12

Designing and producing microarrays; types of microarrays; cDNA microarray technology; oligonucleotide arrays; Sample preparation, labeling, hybridization, generation of microarray data. Gene Expression analysis by cDNA and oligonucleotide arrays; ChIP-on-Chip; Bioinformatic analysis of large-scale microarray data for comparative transcriptomics

UNIT II Next Generation Sequencing Technologies 12

Introduction to Next Generation Sequencing (NGS) technologies; Principles of NGS by Roche/454, Illumina, Life Technologies, Pacific Biosciences, Ion Torrent technologies; Applications of NGS to disease diagnosis and personalized medicine.

UNIT III Protein Micro Arrays 12

Types of protein arrays; Protein microarray fabrication; Experimental analysis of proteins arrays. Data acquisition and processing; Applications of protein microarray types.

UNIT IV 2D-Gel Electrophoresis of Proteins 12

Sample preparation, First-dimension IEF with IPG; Second dimensional separation of proteins; Image analysis of 2-DE gels; Protein expression profiling and comparative proteomics of complex proteomes using 2-DE.

UNIT V Mass-Spectrometry 12

Basics of Mass-spectrometry (MS) and bimolecular analysis; Common ionization methods for peptide/protein analysis (MALDI and ESI); Principles of Time of Flight (TOF), Ion Trap (IT), Quadrupole (Q), Fourier Transform-Ion cyclotron Resonance (FT-ICR), and Orbitrap mass analyzers; Collision-Induced Dissociation (CID) of peptides; Analysis of complex protein mixtures using Nano-liquid chromatography (Nano-LC) coupled to Mass-spectrometry analysis; Analysis of metabolites using Gas-chromatography coupled to Mass-spectrometry; Massspectrometry analysis of Post-Translational Modifications of proteins (Phosphorylation and glycosylation). Accurate quantitation of peptides and small molecules using SRM/MRM approach.

COURSE OUTCOMES:

CO-1: To understand the basic of Microarray and chip technology

CO-2: To attain the knowledge about Next Generation sequencing

CO-3: To learn the Experimental techniques of protein microarray.

CO-4: To analyze the protein expression profiling by 2D gel Method.

CO-5: To acquire the knowledge of spectrometric techniques.

Text Books:

1. Schena M. (2000) DNA Microarrays _ A Practical Approach. Oxford University Press.
2. Rinaldis E. D. and Lahm A (2007) DNA Microarrays. Horizon bioscience.

References Books:

1. Muller H. J. and Roder T. (2006) Microarrays. Elsevier Academic Press
2. Causton H. C., Quackenbush J., and Brazma A. (2004) A Beginner's Guide _ Microarray. Gene Expression Data Analysis. Blackwell Publishing.
3. Schena M. (2005) Protein Microarrays. Jones and Bartlett Publishers

7. Assessment Methods:

It is important that the students of PG Bioinformatics program achieve the desired results in terms of the learning outcomes to be professionally sound and competitive in a global society. Achieving the desired learning outcomes is also imperative in terms of job employment leading to a happy and prosperous individual further leading to a happy and prosperous family and thereby a happy and prosperous society or nation. The assessments tasks are pivotal to get an authentic feedback for the teaching learning process and for mid-course corrections and further improvements in future. The assessment tasks are carried out at various stages of the duration of the PG Bioinformatics programme like Mid-term assessments, End-term assessments, Semester examinations, Regular assessments, viva-voce etc.

The assessment tasks are listed below:

- **Multiple Choice Questions (MCQ)** are one of the predominant form of assessment Tasks. This task is used during all kinds of term and semester examinations.
- **Short-Answer Questions** during term and semester examinations are used to assess the ability of the student to convey his thoughts in a coherent way where prioritization of the information in terms of their significance is tested.
- **Surprise Quizzes** are regularly used during continuous assessment while the teaching learning process is continuing which prepares the student to quickly recall information or quickly analyses a problem and come up with proper solutions.
- **Visual/Pictorial Quizzes** are used to sharpen the comprehension of the students after looking at all the components of a system.
- **Impromptu Opinions** on Biocomputing problems are sought from student during regular teaching learning which helps them to think quickly in a given context. This helps build their ability to come up with solutions to problems which the students might not have confronted previously.
- **Problem Solving** question are generally given during the laboratory work.
- **Data Interpretation** is also another assessment task which is used to develop analytical skills of the students. This assessment is used during laboratory work as well as during conduction of project work.
- **Paper/ Project presentations** are used to assess the articulation skills of the student. These are carried out both during the duration of the teaching learning processes as well as during end-Semester examinations.

- **Report Writing** is used to assess the keenness of the students for details related to Biocomputing while visiting laboratories/industries as students invariably are required to submit a report after such visits.
- **Assignment Writing** is used to assess the writing abilities of the students during midterm vacations.
- **Viva-voce** during the laboratory working hours and during laboratory examination are used to assess the over-all knowledge and intelligence of the students.