ADMISSION & EXAMINATION BYE-LAWS

FOR

MASTER OF SCIENCE

Computational & System Biology and Bioinformatics

M.Sc. (CSB)
Program Code: 582

CHOICE BASED CREDIT SYSTEM (CBCS)

DEPARTMENT OF COMPUTER SCIENCE & ENGINEERING
School of Engineering Sciences & Technology
JAMIA HAMDARD
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1. **Date of approval of present syllabus: 14.12.2021**

2. PROGRAM LEARNING OUTCOMES (PLOs)

PLO1: Communication Skills: The students will be able to demonstrate English language proficiency to perform effectively in the professional and personal life by being able to comprehend and write effectively and efficiently.

PLO2: Domain knowledge: The students will be able to understand the theoretical foundations and the limits of computing in Bioinformatics.

PLO3: Technical skills: The students will be to design, develop and evaluate new computer based systems for novel applications which meet the desired needs of industry and society.

PLO4: Knowledge inter-disciplinary in nature: The students will be exposed to acquires sufficient knowledge of the interdisciplinary subjects and use them in developing advanced computing techniques and tools in the field of biology.

PLO5: Positive attitude: The students will be able to inculcate a positive attitude through various courses.

PLO6: Critical thinking and problem-solving skills: The students will be able to apply the fundamentals of computer science in various biological related problems to come up with feasible solutions.

PLO7: Dynamism and team building skills: The students will be able to develop required skills to work efficiently on multidisciplinary projects and teams to accomplish a common goal.

PLO8: Professional ethics and social values: The students will develop an understanding of work ethics and will have the ability to carry out any task with professional ethics and without deviating from social values

PLO9: Self-awareness and emotional intelligence: The students will identify their strengths and talents and learn to establish a balance at the time of crisis.

PLO10: Entrepreneurship and Innovative qualities: The students will acquire entrepreneurship and innovative qualities through various learning programs.

PLO11: Responsibility towards society and environment: The students will realize their social responsibilities. The students are expected to learn tools and techniques for designing and integrating technology-based solutions for real world problems and drive scientific and societal advancement through technological innovation.

PLO12: Lifelong learning: The students are expected to engage in lifelong learning for the advancement of technology and its adaptation in multi-disciplinary environments.

ADMISSION RULES

MASTER OF SCIENCE

Computational & System Biology and Bioinformatics

M.Sc(CSB) offered by the Department of Computer Science & Engineering and coordinated by BIF centre and SPER.

OBJECTIVE

To prepare highly skilled professionals with a strong conceptual, theoretical& practical proficiency and research ability in the field of Computer Science & Engineering and related emerging areas; such as Data Sciences, Big Data Analytics, Healthcare and Bioinformatics

3. THE PROGRAM

Highlights of the program are described in the following table:

a.	*Name of the Program*	M. Sc (CSB)
b.	*Nature*	Regular and Full Time
c.	*Duration*	Two Years (4 Semesters)
d.	*Total number of credits*	100
e.	*Medium of Instruction and English Examinations*	English
f.	*Eligibility Criteria*	A minimum of 55% marks in Bachelor's degree program in bioinformatics, or any branch of basic/applied Sciences or Technology, including Life Sciences, Medicine, Pharmacy, Engineering and Computer Science and allied disciplines.
g.	*Selection procedure*	As per the merit of the qualifying examination
h.	*Total Seats*	7-8 candidates; inclusive of seats reserved for NRI / sponsored candidates; additional seats are available for Foreign Nationals.
i	*Period of Completion*	Not more than 04 years (8 Semesters)
j	*Commencement of the Program*	July of every academic session

4. PROGRAM STRUCTURE

Semester-wise course structure, guidelines for teaching, practical and associated assessment of the program is described in the following tables:

Course Type	Abbreviation
Program Core	PC
Discipline Elective	DE
Generic Elective	GE
Computer Science	CS
System biology	SB
Skill Enhancement Elective	SE
Laboratory	LAB
Dissertation	DISS

Course Type	Subject Area	Credits
Program Core (PC)	Computer Science (CS) courses including algorithms, data analysis, programming etc	30
	System biology (SB) courses related to, Immunology, Pharmacy	30
	Project Work, Seminar and/or Internship in Industry or elsewhere.	24
Discipline Specific Elective: (DSE)	Discipline Specific Elective: (DSE) courses relevant to chosen specialization/branch	8
Generic Elective (GE)	Generic Elective (GE) courses relevant to chosen specialization/branch	8
Total		100

L-T-P stands for number of contact hours as Lecture-Tutorial-Practical in a week.

1st Semester

Course Code	**Course Title**	**Course Type**	**Marks**			**L-T-P**	**Credits**
			Internal Assessment	**Semester Exam**	**Total**		
MCSB 101	Introduction of Bioinformatics, Biological Data & Databases	SB	25	75	100	3-1-0	4
MCSB 102	Biology for Bioinformatics	SB	25	75	100	3-1-0	4
MCSB 103	Programming in Perl	CS	25	75	100	3-1-0	4
MCSB 104	Essential Mathematics & Biostatistics	CS	25	75	100	3-1-0	4
	Discipline Specific Elective: (DSE) – I	DE	25	75	100	3-1-0	4
MCSB 105	Lab – I (Based on MCSB 101)	LAB	25	75	100	0-0-4	2
MCSB 106	Lab – II (Perl Lab)	LAB	25	75	100	0-0-4	2
	Skill Enhancement Course (SEC) - I	SE	-	-	-	2-0-0	-
Total					**800**	**17-5-8**	**24**

2nd Semester

Course Code	Course Title	Course Type	Marks			L-T-P	Credits
			Internal Assessment	Semester Exam	Total		
MCSB 201	Structural Bioinformatics & drug Design	SB	25	75	100	3-1-0	4
MCSB 202	Advanced Algorithm for Bioinformatics	CS	25	75	100	3-1-0	4
MCSB 203	Big Data Analysis for Bioinformatics Data	CS	25	75	100	3-1-0	4
MCSB 204	Chemoinformatics ,Chemogenomics and Immunoinformatics.	SB	25	75	100	3-1-0	4
	Discipline Specific Elective: (DSE) – II	PE	25	75	100	3-1-0	4
	Generic Elective - I	GE	25	75	100	3-1-0	4
MCSB 205	Lab III (Drug Design lab, based on 201)	LAB	25	75	100	0-0-4	2
MCSB 206	Lab IV(Big Data lab)	LAB	25	75	100	0-0-4	2
Total					**800**	**18-6-8**	**28**

Students be encouraged to go to Industrial Training/Internship for at least 2-3 months during semester break.

3rd Semester

Course Code	**Course Title**	**Course Type**	**Marks**			**L-T-P**	**Credits**
			Internal Assessment	**Semester Exam**	**Total**		
MCSB 301	NGS Data analysis – Microarray, RNA Seq, Single Cell sequencing	SB	25	75	100	3-1-0	4
MCSB 302	Programming in R and Python	CS	25	75	100	3-1-0	4
MCSB 303	System Biology	SB	25	75	100	3-1-0	4
MCSB 304	Data Modelling and Visualization	CS	25	75	100	3-1-0	4
	Generic Elective - II	GE	25	75	100	3-1-0	4
MCSB 305	Lab V (R and Python Lab)	LAB	25	75	100	0-0-4	2
MCSB 306	Lab VI (NGS lab)	LAB	25	75	100	0-0-4	2
MCSB 307	Minor project @ #	PROJ	25	75	100	0-0-4	4
	Skill Enhancement Course (SEC)-II	SE	-	-	-	2-0-0	-
Total					**800**	**17-5-12**	**28**

4th Semester

Course Code	Course Title	Course Type	Marks			L-T-P	Credits
			Internal Assessment	Semester Exam	Total		
MCSB 401	Project/ Dissertation@ #	DISS	300	200	500	0-0-40	20
Total						**0-0-40**	**20**

@ *Dissertation/Mini Project shall be based on latest research topics in the field of Bioinformatics, Computer Sciences.*

\# *Students are required to get approval of their title of Dissertation/Mini Project by Dissertation Assessment & Evaluation committee constituted by HOD. Supervisor of respective students must be member of the above committee. Students are required to give at least three presentations/seminars for progress monitoring & assessment purpose to their respective supervisors. Viva-voce will be held only after the submission of completion report duly signed by the supervisor of the respective student. A plagiarism report duly signed by the students are mandatory to submit in compliance with UGC (Promotion of Academic Integrity and Prevention of Plagiarism in Higher Educational Institutions) Regulations, 2017 (or any such regulations notified time to time) by competent authority.*

Discipline Specific Elective: (DSE)

Course Code	**Course Title**	**Marks**			**L-T-P**	**Credits**
		Internal Assessment	**Semester Exam**	**Total**		
Discipline Specific Elective: (DSE) – I						
MCSB DSE11	Database Management system	25	75	100	3-1-0	4
MCSB DSE 12	Fundamentals of Computing	25	75	100	3-1-0	4
MCSB DSE 13	Advance Bioinformatics Applications	25	75	100	3-1-0	4
Discipline Specific Elective: (DSE) – II						
MCSB DSE 21	Evolutionary bioinformatics	25	75	100	3-1-0	4
MCSB DSE 22	Proteomics & Metabolomics	25	75	100	3-1-0	4
MCSB DSE 23	Comparative and Functional Genomics	25	75	100	3-1-0	4

ENERIC ELECTIVE (GE)

Course Code	**Course Title**	**Marks**			**L-T-P**	**Credits**
		Internal Assessment	**Semester Exam**	**Total**		
Generic Elective – I						
MCSB GE 11	Research Methodology	25	75	100	3-1-0	4
MCSB GE 12	Computational Neuroscience & Neuroinformatics	25	75	100	3-1-0	4
MCSB GE 13	Programming in Java	25	75	100	3-1-0	4
Generic Elective – II						
MCSB GE 21	Soft Computing Techniques	25	75	100	3-1-0	4
MCSB GE 22	Artificial Intelligence and Machine Learning	25	75	100	3-1-0	4
MCSB GE 23	Bioinformatics tools and development	25	75	100	3-1-0	4

Skill Enhancement Course (SEC)

Course Code	Course Title	L-T-P
Skill Enhancement Course (SEC) – I		
MCSB SEC 11	Software Engineering	2-0-0
MCSB SEC 12	We based programming	2-0-0
MCSB SEC 13	Intellectual Property Rights	2-0-0
Skill Enhancement Course (SEC) – II		
MCSB SEC 21	Neural Networks and Deep Learning	2-0-0
MCSB SEC 22	Programming in C++	2-0-0
MCSB SEC 23	Cloud computing	2-0-0

5. EXAMINATION RULES

1. MODE OF CURRICULUM DELIVERY

Mode of curriculum delivery includes classroom teaching, assignments, test, lab work, presentations, participation in relevant events and regularity.

2. ATTENDANCE

a. All students are supposed to attend every lecture and practical classes. However, the attendance requirement for appearing in the examination shall be a minimum of 75% of the classes held.
b. Each one-period teaching shall account for one attendance unit.
c. The concerned teacher will take a roll call in every scheduled class, maintains and consolidate the attendance record, which would be submitted to the Head of the Department at the conclusion of the semester.
d. Attendance on account of participation (with prior permission from the Head of the Department) in the co-curricular/extra-curricular activities can be granted by the Dean on receipt of certificates or recommendations of the respective activity issued by the Head of the Department.
e. Attendance records displayed on the Notice Board from time to time, in respect of short attendance, shall be deemed to be a proper notification and no individual notice shall be sent to the students/local guardian.
f. In case a student is found to be continuously absent from the classes without information for a period of 30 days, the concerned teacher shall report it to the Head of the Department.
g. Head of the Department may recommend for striking off the name of a student from rolls, after ensuring **'one month continuous absence'**, from all the concerned teachers.
h. A student, whose name has been struck off on account of long absence may apply to the Dean for readmission within 15 days of the notice of striking off the name. The readmission shall be effected on payments of prescribed readmission fees.
i. A student with less than 75% attendance in a subject shall not be allowed to appear in that subject in the semester examination. The Head of the Department shall recommend all such cases to the Dean of the School.
j. The Dean, on the recommendation of the Head of the Department, may consider the relaxation of attendance up to 10% on account of sickness and /or any other valid reason. No application for relaxation of attendance (duly certified by a Registered Medical Practitioner/Public hospital or a competent authority) will be entertained after 15 days from the recovery from illness etc.

3. INTERNAL ASSESSMENT

a. Internal assessment, to be made by concerned teachers, will be based on minor tests, quizzes, presentation, programming test, demonstrations and assignments.

b. There will be three (3) Internal Assessment (Unit Tests) with a total of 20 marks ,and the best two (2) performances out of the three Unit tests of Internal Assessment will becounted. Other modes of assessment shall account for remaining 5 marks.

c. Dates for unit test will be announced at the beginning of the semester, by the examination coordinator.

d. The teacher concerned shall maintain a regular record of the marks obtained by students in unit tests and display the same in due course.

e. The concerned teachers shall submit the compiled internal assessment marks to the Head of the Department, on the conclusion of teaching of the current semester.

f. The Head shall display a copy of the compiled sheet, of internal assessment marks of all the papers, before forwarding it to the Controller of Examination, i.e. at the conclusion of the semester.

g. A promoted candidate, who has to reappear in the examination of a paper, will retain internal assessment marks.

h. In the case of re-admission, the candidates shall have to go through the internal assessment process afresh and shall retain nothing of the previous year.

4. SEMESTER EXAMINATIONS

Prescriptions for conducting semester examinations of theory and lab papers, those shall be conducted after the conclusion of each of the semesters, are presented in the following table:

S.N.	**Classification**	**Theory**	**Lab**
1.	Mode	Written Only	Written, Demo, Programming and viva- voce etc.
2.	Duration	03 Hours	04 Hours
3.	Total Marks	75 (Seventy Five Only)	75 (Seventy Five Only)

5. DISSERTATION/INDUSTRIAL PROJECT

a. Each student of the final semester will have to go for a Dissertation/Industrial Project work either in the industry or in the Department under the guidance of one or two faculty members.

b. Period of completion of Dissertation/Industrial Project work shall be full one semester.

c. There shall normally be two supervisors-one internal and one *external (in the case of industry project form the place where the student is pursuing project-work).*

d. All the students, who are pursuing the Dissertation/Industrial project work, shall be continuously in touch with the internal supervisor.

e. ***There shall be a mid-term evaluation of the progress*** and the internal supervisors will conduct it. However, an internal supervisor may ask the student to submit a confidential progress-report from the external supervisor *(in the case of industry project).*

f. All the candidates shall submit ***Three (03)*** hard copies of the project reports that are duly approved and signed by internal as well as external *(if applicable)* supervisors.

g. An external examiner, appointed for the purpose, shall evaluate the project report.

h. The Head of the Department shall fix a date and time for viva-voce examinations, on receipt of the evaluation-report of the project reports from the external examiner.

i. Head of the Department shall forward the compiled total marks (awarded in internal assessment, project Report and Viva-voce Examination), in the project-semester of each of the candidate, to the Controller of Examination.

6. EXAMINATION

a. The performance of a student in a semester shall be evaluated through continuous class assessment and end semester examination. The continuous assessment shall be based on class tests, assignments/ tutorials, quizzes/ viva voce and attendance. The end semester examination shall be comprised of written papers, practical and viva voce, inspection of certified course work in classes and laboratories, project work, design reports or by means of any combination of these methods.

b. The marks obtained in a subject shall consist of marks allotted in end semester theory paper, practical examination and sessional work.

c. The minimum pass marks in each subject including sessional marks (Theory, Practical or Project etc.) shall be 40%.

7. PROMOTION SCHEME

a. A student will be required to clear minimum **40% of his/her papers** in a semester/annual examination to be eligible **for promotion to the next semester/year**. A student may appear in the supplementary examination after each semester/annual examination and can have a choice to appear in the backlog papers in the supplementary examination or in the subsequent regular semester/annual

b. examination with a prescribed fee. A students detained due to shortage of attendance will repeat his/her paper in the subsequent semester concerned (even/odd).

c. A **detained** Student is not allowed to re-appear in the internal assessment (Unit test). His/her old internal assessment marks will remain same.

A student who cleared all the papers of a semester/annual examination of a programme /course will be eligible for improvement examination as per university rule.

8. THE GRADING SYSTEM

As per University Rule

9. CALCULATION OF SGPA AND CGPA OF A STUDENT IN A SEMESTER

As per University Rule

After having passed all the FOUR semesters, the students shall be eligible for the award of **Master of Science (Computational & System Biology and Bioinformatics),** degree of JAMIA HAMDARD.

10. CLASSIFICATION OF SUCCESSFUL CANDIDATES

The result of successful candidates, who fulfill the criteria for the award of **Master of Science (Computational & System Biology and Bioinformatics),** shall be classified at the end of last semester, on the basis of his/her final CGPA (to be calculated as per university rule).

NAME OF THE SCHOOL

School of Enigeering Sciences and Technology

Vision Statement (School Level): To become the best institution in the national and international map in terms of quality of teaching and research, technical knowledge and academics in the field Computer Science & Engineering, Electronics & Communication Engineering, Bioinformatics with sincere honesty adding values in the core aspect of students' life.

Mission Statements (3 to 4) (School Level):

MS1: To offer state-of-the-art undergraduate, postgraduate and doctoral programs in Computer Science & Engineering, Electronics and Communication Engineering & Engineering and Bioinformatics.

MS 2: To provide one of the best working environments to motivate faculty and students to work towards vision of the Department.

MS 3: To develop association with industry, other Universities/Institute/Research Laboratories and work in collaboration with them.

MS 4: To use our expertise in all the relevant disciplines for helping society in solving its real life problem.

MS 5: To develop entrepreneurship skills in the students so that they can become problem solver and innovative developer and contribute to the society by providing employment to others.

NAME OF THE DEPARTMENT/CENTRE

Department of Computer Sciences and Engineering

Vision Statement (Department/Centre Level): To become the best institution in the national and international map in terms of quality of teaching and research, technical knowledge and academics in the field Computer Science & Engineering, Electronics & Communication Engineering, Bioinformatics with sincere honesty adding values in the core aspect of students' life.

Mission Statements (3 to 4) (Department/Centre Level):

MS1: To offer state-of-the-art undergraduate, postgraduate and doctoral programs in Computer Science & Engineering, Electronics and Communication Engineering & Engineering and Bioinformatics.

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Name of the Academic Program …Master Of Science (Computational & System Biology and Bioinformatics)

QUALIFICATION DESCRIPTORS (QDs)

Upon the completion of Academic Programme (Kindly fill name of programme), students will be able to:

QD-1**:** have better understanding of subject that can lead to successful designing of new softwares with Good efficiency and low cost for mass acceptibility.

QD-2 have profesional ethics, leadership and profesional communication among diversified group which leads to achieve targeted goal.

QD-3 : To apply "systems" approach such as, mathematical modeling or networks, to understand complex biological systems.

QD-4 To investigate a problem by finding gaps, designing experiments, carrying out relevant lab experiments and analyzing results.

QD-5 to communicate properly the concepts and its applicability.

Mapping Qualification Descriptors (QDs) with Mission Statements (MS)

	MS-1	**MS-2**	**MS-3**	**MS-4**	**MS-5**
QD-1*	1	1	2	3	3
QD-2	1	3	3	1	1
QD-3	1	3	3	3	2
QD-4	2	3	3	3	2
QD-5	2	3	1	1	3

Write '3' in the box for 'High-level'mapping, 2 for 'Medium-level'mapping, 1 for 'Low-level'mapping.

NAME OF THE SCHOOL / DEPARTMENT / CENTRE

SEST, Department of Computer Science and Engineering

Name of the Academic Program … Master Of Science (Computational & System Biology and Bioinformatics)

PROGRAM LEARNING OUTCOMES (PLOs) (12)

After completing this Course, the students should be able to …………

PLO1: Communication Skills: The students will be able to demonstrate English language proficiency to perform effectively in the professional and personal life by being able to comprehend and write effectively and efficiently.

PLO2: Domain knowledge: The students will be able to understand the theoretical foundations and the limits of computing in Bioinformatics.

PLO3: Technical skills: The students will be to design, develop and evaluate new computer based systems for novel applications which meet the desired needs of industry and society.

PLO4: Knowledge inter-disciplinary in nature: The students will be exposed to acquires sufficient knowledge of the interdisciplinary subjects and use them in developing advanced computing techniques and tools in the field of biology.

PLO5: Positive attitude: The students will be able to inculcate a positive attitude through various courses.

PLO6: Critical thinking and problem-solving skills: The students will be able to apply the fundamentals of computer science in various biological related problems to come up with feasible solutions.

PLO7: Dynamism and team building skills: The students will be able to develop required skills to work efficiently on multidisciplinary projects and teams to accomplish a common goal.

PLO8: Professional ethics and social values: The students will develop an understanding of work ethics and will have the ability to carry out any task with professional ethics and without deviating from social values

PLO9: Self-awareness and emotional intelligence: The students will identify their strengths and talents and learn to establish a balance at the time of crisis.

PLO10: Entrepreneurship and Innovative qualities: The students will acquire entrepreneurship and innovative qualities through various learning programs.

PLO11: Responsibility towards society and environment: The students will realize their social responsibilities. The students are expected to learn tools and techniques for designing and integrating technology-based solutions for real world problems and drive scientific and societal advancement through technological innovation.

PLO12: Lifelong learning: The students are expected to engage in lifelong learning for the advancement of technology and its adaptation in multi-disciplinary environments.

PROGRAM SPECIFIC OUTCOMES (PSOs)
(In case of specializations in each academic program, 2 to 4)
After completing this Course, the students should be able to …………
PSO1: have better understanding of subject that can lead to successful designing of new softwares with Good efficiency and low cost for mass acceptibility.

PSO2 have profesional ethics, leadership and profesional communication among diversified group which leads to achieve targeted goal.

PSO3 : To apply “systems” approach such as, mathematical modeling or networks, to understand complex biological systems.

PSO4: To investigate a problem by finding gaps, designing experiments, carrying out relevant lab experiments and analyzing results.

PSO5: to communicate properly the concepts and its applicability.

Mapping of Program Learning Outcomes (PLOs)
With Qualification Descriptors (QDs)

	QD-1	QD-2	QD-3	QD-4	QD-5
PLO-1		3		3	1
PLO-2	3		3	3	2
PLO-3	1		3	3	
PLO-4	3	3	3	3	
PLO-5		2	1		3
PLO-6	1		3	3	
PLO-7	2	3			3
PLO-8		2	2	1	3
PLO-9		2	2		3
PLO-10	2		2	3	1
PLO-11	2	1			2
PLO-12	1		3	3	1
PSO1	3	3	1	1	1
PSO2		3			1
PSO3	1		3	1	
PSO4		1		3	1
PSO5	1	2		3	3

Write ‘3’ in the box for ‘High-level’ mapping, 2 for ‘Medium-level’ mapping, 1 for ‘Low-level’ mapping.

Name of the Academic Program Master Of Science (Computational & System Biology and Bioinformatics)

Course Code: …MCSB 101
Title of the Course: …… Introduction of Bioinformatics, Biological Data & Databases
L-T-P 3-1-0. (L=Lecture hours, T=Tutorial hours, P=Practical hours)
Credits…4

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to
CLO1: apply basic bioinformatics tools for various need in biotechnology and microbiology programs (Cognitive level: Apply)
CLO2: Explain about the methods to characterise and manage the different types of Biological data. (Cognitive level: Understand)
CLO3: To get introduced to the basic concepts of Bioinformatics and its significance in Biological data analysis. (Cognitive level: Understand)
CLO4: Introduction to the basics of sequence alignment and analysis. (Cognitive level: Analyze)
CLO5: Classify different types of Biological Databases. (Cognitive level: Evaluate)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO 1	**PLO 2**	**PLO 3**	**PLO 4**	**PLO 5**	**PLO 6**	**PLO 7**	**PLO 8**	**PLO 9**	**PLO 10**	**PLO 11**	**PLO 12**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CLO 1		2							2		1	**3**	**3**				
CLO 2	1	2	2					1				**3**			**3**	**3**	**3**
CLO 3			3	3				1		1		**3**	**2**			**3**	
CLO 4				3	1		1				1	**3**			**2**		**3**
CLO 5						3						**3**	**2**	**1**		**3**	

Detailed Syllabus

UNIT 1 **10 Hours**

Introduction to Bioinformatics: Introduction and branches of Bioinformatics. Aim, scope and research areas of Bioinformatics. Overview of Available Bioinformatics Resources on the Web, Protein and Genome; Information Resources and Analysis Tools; Established Techniques and Methods; Sequence File Formats FASTA, GenBank, FASTQ, GTF and Structured File Formats.

UNIT 2 **10 Hours**

Biological Databases: Introduction of Biological databases and its type. Classification format of biological databases. Biological database retrieval system. Protein Sequence and Structural Databases, Nucleotide Sequence Databases, Gene Expression Database; Biological database and datasets; Overview of Bioinformatics resources on web (NCBI/EBI/EXPASY etc.). Nature of biological data and formats; Biological literature databases, PubMed. Nucleic acid sequence databases, GenBank/EMBL/DDBJ/ RefSeq/dbSTS/dbEST; Protein sequence databases, Uniprot, PIR, UniProtKB, UniRef, UniParc, Proteomes, NextProt ;Derived databases: InterPro and constituent databases, Recent derived databases; RNA sequence databases, SRA, GEO, TCGA, ENA, miRBase, lncRNAdb, MIT/ICBP siRNA database Species and Biodiversity databases / resources, NCBI Taxonomy database, GBIF, Sahyadri ; Specialized Databases: Pfam, SCOP, GO, Metabolic Pathways.

UNIT 3 **10 Hours**

Methods of Sequence Analysis: Pairwise and multiple sequence alignment for DNA and protein sequences. Local and global sequence similarity. Pairwise sequence alignment methods; Heuristic Methods; BLAST and its variants, Statistics of Sequence Alignment Score; E-Value, P-Value, scoring matrix, PAM, BLOSUM, Gap Penalty, Gonnet and Lookup tables; Multiple Sequence Alignments; ClustalW, Hidden Markov Models, HMM Based Multiple-Sequence Alignment, Sequence logos, consensus & patterns, Basic concept of sequence profiles, Derivation of profiles; applications - Gribskov's Profile Analysis method

Application tools: Primer designing.

UNIT 4 **10 Hours**

Tools for molecular mapping: QTL, minisatellites, SNP's.

Mapping techniques: JoinMap, MapQTL, LOD Score method for estimating recombination frequency.

Genome analysis and Gene identification: Sequencing, Assembly, Annotation, Sequencing pipelines and databases.

Comparative genomics: Homologs, Paralogs and orthologs; Synteny; Comparative genomics of *Arabidopsis* and *Brassica rapa* / Chimpanzees and human.

UNIT 5 **10 Hours**

Phylogenetic Analysis: Methods of Phylogeny, Software for Phylogenetic Analyses, Consistency of Molecular Phylogenetic Prediction. Distance and Character Based Methods and Software, Computing Tools for Phylogenetic Analysis, Distances, CLUSTALW, MUSCLE, DALIGN, T-Coffee, MAFFT, GROWTREE, PAUP, PHYLIP and MEGA; Construction and Visualization Phylogenetic Tree; and Application of Phyolgenetic Analysis.

REFERENCE BOOKS:

1.Bioinformatics:DatabasesandSystems,byStanleyI.Letovsky
2.BioinformaticsDatabases:Design,Implementation,andUsage(Chapman&Hall/CRC MathematicalBiology&Medicine),bySorinDraghici
3.Databaseannotationinmolecularbiology,principlesandpractices,ArthurM.Lesk
4.Currenttopicsincomputationalmolecularbiology,Tao,Jiang,YingXu,MichaelQ.Zang

Teaching-Learning Strategies in brief

- For teaching, ICT tools have been used.
- Also, white board teaching had been done for explaining and clarifying many concepts and numericals
- Cooperative leaning is encouraged via participation in active discussions.

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25. End semester exam of 75 Marks is conducted.
- Assignments were provided.
- Quizes had been conducted too.

Name of the Academic Program Master Of Science (Computational & System Biology and Bioinformatics)
Course Code: …MCSB 102
Title of the Course: ……Biology for Bioinformatics
L-T-P 3-1-0. (L=Lecture hours, T=Tutorial hours, P=Practical hours)
Credits…4

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to
CLO1: comprehend the cell organelle, cell membrane (Cognitive level: Understand)
CLO2: signal transduction and its implications. (Cognitive level: Evaluate)
CLO3: Understand cell cycle and its relevance. (Cognitive level: Understand)
CLO4: Understand the basics of techniques to study cells. (Cognitive level: Understand)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO 1	**PLO 2**	**PLO 3**	**PLO 4**	**PLO 5**	**PLO 6**	**PLO 7**	**PLO 8**	**PLO 9**	**PLO 10**	**PLO 11**	**PLO 12**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CLO1		2							2			**3**	**3**				
CLO2	1	2	2					1			1	**3**			**3**	**3**	**3**
CLO3			3	3				1		1		**3**	**2**			**3**	
CLO4	1			3	1	3	1					**3**			**2**		**3**

Detailed Syllabus:

UNIT 1 **10 Hours**

Nucleic acid: Composition, Primary and Secondary structures, Circular DNA

UNIT 2 **10 Hours**

Genome organization: Prokaryotic and eukaryotic genomes – C value paradox, repetitive and non-repetitive DNA., transposons and retroposons; Exons and introns organization of interrupted genes, one gene-many proteins concept; Gene numbers essential genes and total gene number, gene clusters, pseudogenes; Gene families globin and rDNA gene families; Organelle genome – mitochondrial and chloroplast

Packaging of genome – Bacterial genome as nucleoid; Eukaryotic genome nucleosomes, chromatin, solenoids, loops, domains, scaffolds, chromosomes

UNIT 3 **9 Hours**

DNA Replication- Details of prokaryotic and eukaryotic DNA replication: DNA polymerases, initiation, elongation and termination of replication; multiple origins of replication, Regulation of replication

DNA damage, repair and recombination- DNA damaging agents physical and chemical, types of DNA damages; DNA repair systems in prokaryotes and eukaryotes Single step repair, Base excision repair, Nucleotide excision repair, Mismatch repair, Recombination repair; Recombination - homologous and non-homologous recombination

UNIT 4 **9 Hours**

Gene Expression - Transcription: Details of prokaryotic and eukaryotic transcription: RNA polymerase, promoters, initiation, elongation and termination of transcription; regulation of transcription, operons

Processing of transcripts - 5’ capping, 3’ polyadenylation, splicing and editing, self- splicing

Translation: Details of prokaryotic and eukaryotic translation: Protein synthesis machinery, initiation, elongation and termination, Genetic code, accuracy of translation, regulation, Post-translational modifications of proteins .

UNIT 5 **10 Hours**

Recombinant DNA technology: Enzymes, cloning strategies, vectors, screening for recombinants .

Small non-coding RNAs – micro-RNA, small nuclear RNA, small nucleolar RNA, si- RNA, piwi-RNA and Genome editing.

REFERENCEBOOKS:

1.“MolecularCellBiology”5thEditionbyHarveyLodish,ArnoldBerk,PaulMatsudaira,Chris Kaiser,MontyKrieger,MatthewScott,LawrenceZipurskyandJamesDarnell.W.HFreeman andCompany.
2.TheCellAMolecularApproach-Cooper-Hausman
3.MolecularBiologyoftheCell-BruceAlbertsetal.

Teaching-Learning Strategies in brief

- For teaching, ICT tools have been used.
- Also, white board teaching had been done for explaining and clarifying many concepts and numericals
- Cooperative leaning is encouraged via participation in active discussions.

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25. End semester exam of 75 Marks is conducted.
- Assignments were provided.
- Quizes had been conducted too.

Name of the Academic Program Master Of Science (Computational & System Biology and Bioinformatics)
Course Code: …MCSB 103
Title of the Course: …… **Programming in Perl**
L-T-P 3-1-0. (L=Lecture hours, T=Tutorial hours, P=Practical hours)
Credits…4

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to …………

CLO1: Create programs using regular expressions and scalar operators to parse, analyze and error-check files, user input and other data. (Cogntive Level: Create)

CLO2: Create programs which generate files and/or manipulate files and their attributes. (Cogntive Level: Create)

CLO3: Create programs which selectively access portions of files rather than entire (Cogntive Level: Create)

CLO4: Review the items needed as background for this course. (Cognitive Level: Understand)

CLO5: connect various applications. (Cognitive level: Evaluate)

Mapping of Course Learning Outcomes (CLOs)with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO 1	**PLO 2**	**PLO 3**	**PLO 4**	**PLO 5**	**PLO 6**	**PLO 7**	**PLO 8**	**PLO 9**	**PLO 10**	**PLO 11**	**PLO 12**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CLO1		3	3			2		3		3		**1**	**3**		**1**		**2**
CLO2		3	3			3			1			**2**		**1**		**1**	
CLO3		3	3		1	3		2						**1**	**1**		**1**
CLO4		3	3			1		2		1					**2**		**2**
CLO5		3	3	3		1		1			1	**2**				**1**	**1**

Each Course Learning Outcome (CLOs) may be mapped with one or more Program Learning Outcomes (PLOs). Write '3' in the box for 'High-level' mapping, 2 for 'Medium-level'mapping, 1 for 'Low-level'mapping. Map with PSOs wherever applicable.

Detailed Syllabus:

UNIT1 **9 Hours**

Concepts of flowcharting, algorithm development, pseudo codes etc.

UNIT 2 **10 Hours**

Introduction: Use of Perl in Bioinformatics, history of Perl, Availability, Support, Basic Concepts,Scalar Data: Numbers, Strings, Scalar Operators, Scalar Variables, Scalar Functions

UNIT 3 **9Hours**

Basic I/O, Array operators and Functions, Scalar and List Context , Control Structures: Statement Blocks

UNIT 4 **10 Hours**

Hash Functions, Hash Slices, Regular Expressions,Subroutines, Miscellaneous Control Structures

UNIT 5 **10 Hours**

File handles and File Tests, Directory Handles, File and Directory Manipulation, Process Management: Using system and exec, Using Backquotes

Reference Books:

1.Wall, Larry, Tom Christiansen, bryan d foy, and Jon Orwant. "Programming Perl: Unmatched power for text processing and scripting, edition 4", Sebastopol, CA: O'Reilly Media, 2012.
2.Swartz, Randal L., brian d foy, and Tom Phoenix, "Lerning Perl: Making Easy Things Easy and Hard Things Possible, Edition 7", 2016
3.Beginning Perl (first edition) by Simon Cozens free on-line at: http://www.perl.org/books/beginning-perl
4.http://perldoc.perl.org

Teaching-Learning Strategies in brief

- For teaching, ICT tools have been used.
- Also, white board teaching had been done for explaining and clarifying many concepts and numericals
- Cooperative leaning is encouraged via participation in active discussions.

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25.
- End semester exam for final evaluation of 75 marks is conducted.
- Assignments were provided.
- Quizes had been conducted too.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB -104
Title of the Course: Essential Mathematics & Biostatistics
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:
CLO1: Understand the concept of set theory, trigonometry function & series expansion. (Cognitive Level: Understand)
CLO2: Apply the basic knowledge of vector algebra & matrices to solve the basic computational problems. (Cognitive Level: Apply)
CLO3: Discuss the fundamentals of differential calculus, integral calculus, differential equations, Fourier series & Laplace transform and use to analyse the computational problems. (Cognitive Level: Analyze)

CLO4: Explain basics of statistics, probability theory & probability distributions (continous & discrete), and apply in Bioinformatics. (Cognitive Level: Analyze)

CLO5: Describe regression, correlation and statistical tests, and analyse data sets. (Cognitive Level: Understand)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO10**	**PLO11**	**PLO12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1	1			3	1	3						1	1				
CLO2		1		3	1	3			2		1	1		1			1
CLO3	1		2	3	1	3		1		1		1		1	1	1	
CLO4		1		3	1	3			1		1	1	1				
CLO5			1	3	1	3	1					1			1		

Each Course Outcome (CO) may be mapped with one or more Program Outcomes (POs). Write '3' in the box for 'High-level'mapping, 2 for 'Medium-level'mapping, 1 for 'Low'-level'mapping.

Unit-1: Set Theory, Trigonometry, Vector & Matrices:- (10 H)
Introduction to Set Theory, Trigonometry - Trigonometric Functions, Series Expansion, Inverse, General Values, Graphs, Taylor series Vector Algebra, Basic Computations, Matrices.

Unit-2: Calculus:- (10H)

Limits, Continuity, Analysis, Differentiation (1D & Partial), Reimann Integration, Definite Integrals.

Unit-3: **Ordinary & Partial Differential Equation & Integral transform:–(10H)**

1st Order & 2nd Order Ordinary Differential Equations. Self-Adjoint Equations, Method of Separation of Variables Fourier Series, Fourier Transform, Laplace Transform

Unit-4 Probability Theory & Statistics:- (10H)
Introduction to theory of Probability, Conditional Probability, Bayesian Rules, Overview of applications of statistics in Bioinformatics, Introduction to principles of statistical sampling from a population, Frequency Distributions and Statistical Measures: mean, mode, median, variance, standard deviation, coefficient of variation, measures of skewness and kurtosis, Computation of these measurements for the given data, Regression, correlation, fitting regression line

Unit-5 Distributions & Hypothesis Testing:- (10H)
Random variable, Distributions of random variables, Binomial, Poisson, Geometric, Normal and extreme value distribution, Test of significance viz. Z test, t test, paired t test, chi^2 test of goodness of fit

Reference Books:

1. Isaev Alexander. Introduction to Mathematical Methods in Bioinformatics. Publisher: Berlin; New York: Springer, 2004. ISBN: 3540219730
2. Raman K. V. & Pal Sourav. Mathematics in Chemistry. New Delhi, Vikas Publishing House Pvt Ltd., 2004. ISBN: 8125912886
3. Jones D.S., Sleeman B.D. Differential Equations and Mathematical Biology, Publisher: Chapman & Hall. 2003. ISBN:1584882964
4. Bracewell Ronald. The Fourier transform and it's applications 3rd edition. Publisher: New Delhi : McGraw Hill, 2000. ISBN: 0073039381.
5. Stephenson G., Radmore P. M. Advanced Mathematical Methods for Engineering and Science Students, Cambridge University Press, 1990.
6. Arfken George. Mathematical methods for physicists. Publisher: Orlando: Academic Press 1985. ISBN: 0120598205.

Teaching-Learning Strategies in brief

- Build positive environment in the classroom.
- Provide concrete basic and advanced knowledge of the subject.
- Solve problems based on the basic & advanced concepts of the subject.
- Encourage to the students to ask more & more questions.
- Motivate to the students to develop critical & strategic thinking

Assessment methods and weightages in brief

- By taking two sessional examinations.
- By giving assignments.
- By conducting class tests.
- By taking semester examination.

- **Internal assessment = 25 marks & Semester Examination =75 marks is conducted**

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB -201
Title of the Course: Structural Bioinformatics & drug Design
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to …………

CLO1: understand the drug stereochemistry drug design and molecular modeling in drug design. (Cognitive level: Understand)

CLO2: Draw the 3D structure of cyclic peptide and generate its smiles notation and physiochemical properties. (Cognitive level: Create)

CLO3: Analyze the docking studies of protein with its suitable inhibitors. (Cognitive level: analyze)

CLO4: Convert the SMILES into MOL2 format. (Cognitive level:

Mapping of Course Learning Outcomes (CLOs)with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO 1	**PLO 2**	**PLO 3**	**PLO 4**	**PLO 5**	**PLO 6**	**PLO 7**	**PLO 8**	**PLO 9**	**PLO 10**	**PLO 11**	**PLO 12**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CLO1		3	3		2	2		3		3		**1**	**3**		**1**		**2**
CLO2	1	3	3			3			1			**2**		**1**		**1**	
CLO3		3	3	1		3		2			2			**1**	**1**		**1**
CLO4		3	3			1		2		1					**2**		**2**

Detailed Syllabus

UNIT 1 10 Hours

Fundamentals of macromolecular structure: Functional significance of structure, principles of protein structure: secondary structures, motifs, domains, tertiary and quaternary structures. Relationship between sequence and 3D structure of a protein. Structural implications of the peptide bond; rigid planar peptide unit; cis and trans configuration; conformations of a pair of linked peptide units; Ramachandran plot and Protein Data Bank. Conformations of biomacromolecules, Thermodynamics of protein folding, Sequence Motif Databases, Pfam, PROSITE, Protein Structure Classification; SCOP, CATH, Other Relevant Databases, KEGG, Fold Recognition, Prediction of binding pockets on protein structures, Structure-based function Prediction, Prediction of RNA structures.

UNIT 2 **10 Hours**

Protein Structure Alignments: Structure Superposition, RMSD, Different Structure Alignment Algorithms, DALI, and TM- align.

Protein Structure Visualization Tools: (PyMOL, Chimera, VMD), Protein Structure Comparison Tools and Methods, Protein Structural Alignment (Dali, CE, TM-Align), Protein Structure

Classification and Databases (PDB, CATH, SCOPE, CDD), Drug design software, Enzyme kinetics and inhibition. Rational approaches to lead discovery based on traditional medicine, Random screening, Non-random screening, serendipitous drug discovery. Pharmacophore, Lock-Key principle and induced fit

UNIT 3 **10 Hours**

Structure Prediction: Protein Secondary Structure Prediction, Chou-Fasman, GOR Method, Artificial Neural Networks, Protein Secondary Structure Prediction Tools and Severs (DSSP, STRIDE, Jpred, Psipredetc), Protein Tertiary Structure Prediction, Homology Modelling, Refinement of the homology model, Structure Validation Strategies, Comparison of various strategies in homology modelling, Prediction of protein structures by threading, Energy Minimization methods and Conformational Analysis, global conformational minima determination.

UNIT 4 **10 Hours**

Drug Design: Introduction to drug discovery, Current approaches and philosophies in drug design, Molecular Modelling and virtual screening techniques, lead identification, Concept of pharmacophore mapping and pharmacophore-based Screening, Analysis of the receptor, Docking: Rigid docking, flexible docking, manual docking, docking based screening, Scoring Functions, Binding energy calculations De novo drug design., Drug likeness screening, ADMET properties.

UNIT 5 **10 Hours**

Quantitative Structure Activity Relationship (QSAR): SAR versus QSAR, QSAR methodology, Quantum-chemical descriptors, COMFA and COMSIA. Molecular mechanisms of diseases and drug action. Pharmacokinetics: Models and Applications, Drug–receptor interactions. Pharmacodynamics, Biomolecular interactions and binding thermodynamics, Biochemical and cell-based assays. Molecular recognition and specificity. Future developments.

Reference Books:

1. Gasteiger Johann, Engel Thomas. Chemoinformatics: A Textbook. Publisher: Wiley-VCH; 1st edition. 2003. ISBN: 3527306811.
2. Leach Andrew R., Valerie J. Gillet. An introduction to chemoinformatics. Publisher: Kluwer academic, 2003. ISBN: 1402013477.
3. Gasteiger Johann, Handbook of Chemoinformatics: From Data to Knowledge (4 Volumes). Publisher: Wiley-VCH. 2003. ISBN:3527306803.
4. Muthukumarasamy Karthikeyan, Renu Vyas. Practical Chemoinformatics. Publisher:
5. Springer. 2014. ISBN: 9788132217794
6. Bajorath Jürgen. Chemoinformatics and computational chemical biology. Publisher: Humana Press. 2011. ISBN: 9781607618386

Teaching-Learning Strategies in brief

- Build positive environment in the classroom.
- Provide concrete basic and advanced knowledge of the subject.

- Solve problems based on the basic & advanced concepts of the subject.
- Encourage to the students to ask more & more questions.
- Motivate to the students to develop critical & strategic thinking

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25. End semester exam of 75 Marks is conducted.
- By giving assignments.
- By conducting class tests.
- By taking semester examination.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB -202
Title of the Course: Advanced algorithms for Bioinformatics
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:
CLO1: Able to apply algorithmic principles to address problems in biology. (Cognitive level: APPLY)
CLO2: Use various methods from computational biology to implement their algorithmic versions. (Cognitive level: implement)
CLO3: Analyze problems in biology and able to design new protocols and algorithms for biological data analysis. (Cognitive level: analyse)
CLO4: Able to analyze the algorithms in computational biology and identify their limiting factors to propose new design principles. (Cognitive level: Analyze)

CLO5: Assessment of biological complexity through algorithmic principles. (Cognitive level: Evaluate)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO 1	**PLO 2**	**PLO 3**	**PLO 4**	**PLO 5**	**PLO 6**	**PLO 7**	**PLO 8**	**PLO 9**	**PLO 10**	**PLO 11**	**PLO 12**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CLO1		3	3	1		2		3		3		**1**	**2**				**2**
CLO2		3	3		2	3					2			**2**		**1**	
CLO3	3	3	3	1		3		2	1	2				**1**	**1**	**1**	**1**
CLO4	3	3	3			1		2		1	2	**2**		**1**			**2**
CLO5	3	1	2		2	2	1		1				**1**		**2**		

Detailed Syllabus

UNIT I –INTRODUCTION (10hours)

:An overview of Algorithms, Sequence and String search algorithms with mathematical formulations for similarity and distance scoring systems with their algorithmic implementations.
Complexity of DNA problems and their simulatory solutions. Genome assembly algorithms, their computational implications and applications.

UNIT II- GRAPH ALGORITHMS (9 hours)

:Graph algorithms in bioinformatics and their applications to fragment assembly, Eulerian and Hamiltonian Cycle Problem, Interval graph algorithm, shortest superstring problem and its mapping with traveling salesman problem.

UNIT III- Motif and Regulatory element's Algorithms: (9 hours)

s:Algorithms for finding regulatory motifs in genomic sequences through profiles and consensus approaches. Brute Force Motif Search, Median String Search algorithms and their refinements. Algorithms for Sequencing by hybridization (SBH), use of spectrum approach to solve SBH problem.

UNIT IV- Gene prediction: (11 hours)

Algorithmic approaches for Contig assembly to super- contigs. Computational challenges for gene prediction, popular algorithms and their implementations for gene prediction. Exon chaining and Spliced Alignment Problems.

Brute Force and branch and bound algorithms:Brute Force and branch and bound algorithms for Partial Digest Problem, restriction mapping, partial digest and double digest problems and their solutions through multiset and homometric sets.

UNIT V- MSA advancedments (9 hours)

:Progresssive and iterative refinements of MSA algorithms, Barton-Sternberg Iterative Refinement Algorithm, STAR and TREE alignment approaches, Greedy and Entropy approach for MSA.

Reference Books:

1. Computational Molecular Biology: An algorithmic approach (2004), P.A. Pevzner, PHI.
2. An Introduction to Bioinformatics Algorithms (2004) N.C. Jones and P.A. PevznerAne Books.
3. Algorithms in Bioinformatics (2004), G. Benson and R. Page (Eds): Springer Verlag. 4. Bioinformatics Algorithms: Techniques and Applications, I.I. Mandoiu and A Zelikovsky, Wiley Interscience Press.
5. Biological Sequence Analysis: Probabistic models of proteins and nucleic acids (1998) Durbin R., et al, Cambridge University press.

Teaching-Learning Strategies in brief

For teaching, ICT tools have been used.

White board teaching had been done for explaining and clarifying many concepts and numericals

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25.
- End semester exam of 75 Marks is conducted.
- By giving assignments.
- By conducting class tests.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB -203
Title of the Course: Big Data Analysis for Bioinformatics Data
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO1: Understand Big Data and its analytics.(Cognitive Level:

CLO2: Analyze the Big Data framework like Hadoop and NOSQL to efficiently store and process Big Data to generate analytics. (Cognitive Level:

CLO3: Design of Algorithms to solve Data Intensive Problems using Map Reduce Paradigm. (Cognitive Level:

CLO4: Design and Implementation of Big Data Analytics using pig and spark to solve data intensive problems and to generate analytics. (Cognitive Level:

CLO5: Implement Big Data Activities using Hive. (Cognitive Level: Create)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO10**	**PLO11**	**PLO12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1			3		3	3		2	2	1	1	1	2		2	1	1
CLO2	1	3	3	1		3		2		2	1			2	2	1	1
CLO3		3	3	3	2		2			1		1	2			2	2
CLO4			3		3	3		2			1			1		2	
CLO5	2	3		2		3	2	2		1		2	2		1		1

Detailed Syllabus

UNIT – 1 ESSENTIALS OF BIG DATA AND ANALYTICS: 9 Hours

Data, Characteristics of data and Types of digital data, Sources of data, Working with unstructured data, Evolution and Definition of big data, Characteristics and Need of big data, Challenges of big data; Overview of business intelligence, Data science and Analytics, Meaning and Characteristics of big data analytics, Need of big data analytics, Classification of analytics, Challenges to big data analytics, Importance of big data analytics, Basic terminologies in big data environment.

UNIT – 2 HADOOP : 10 Hours

Introducing Hadoop, Need of Hadoop, limitations of RDBMS, RDBMS versus Hadoop, Distributed computing challenges, History of Hadoop , Hadoop overview, Use case of Hadoop, Hadoop distributors, HDFS (Hadoop Distributed File System) , Processing data with Hadoop, Managing resources and applications with Hadoop YARN (Yet another Resource Negotiator), Interacting with Hadoop Ecosystem.

UNIT – 3 MAPREDUCE PROGRAMMING 10Hours

Introduction , Mapper, Reducer, Combiner, Partitioner, Searching, Sorting, Compression, Real time applications using MapReduce, Data serialization and Working with common serialization formats, Big data serialization formats.

UNIT – 4 HIVE: 9 Hours

Introduction to Hive, Hive architecture, Hive data types, Hive file format, Hive Query Language (HQL), User-Defined Function (UDF) in Hive

UNIT – 5 PIG 9 Hours

The anatomy of Pig , Pig on Hadoop, Pig Philosophy, Use case for Pig; ETL Processing , Pig Latin overview , Data types in Pig , Running Pig , Execution modes of Pig, HDFS commands, Relational operators, Piggy Bank , Word count example using Pig.

References:

1. Seema Acharya, Subhashini Chellappan, “Big Data Analytics”, 1st Edition, Wiley, 2015
2. Boris lublinsky, Kevin t. Smith, Alexey Yakubovich, “Professional Hadoop Solutions”, 1st Edition, Wrox, 2013.
3. Chris Eaton, Dirk Deroos et. al., “Understanding Big data”, Indian Edition, McGraw Hill, 2015.
4. Tom White, “HADOOP: The definitive Guide”, 3rd Edition, O Reilly, 2012.
5. Vignesh Prajapati, “Big Data Analytics with R and Hadoop”, 1st Edition, Packet Publishing Limited, 2013.

Teaching-Learning Strategies in brief

For teaching, ICT tools have been used.

White board teaching had been done for explaining and clarifying many concepts and numericals

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25. End semester exam of 75 Marks is conducted.
- By giving assignments.
- By conducting class tests.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB -204
Title of the Course: Chemoinformatics ,Chemogenomics and Immunoinformatics
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO 1 explain the role of immune cells and their mechanism in body defense mechanism. (Cognitive Level: Evaluate)

CLO2 apply the knowledge of immune associated mechanisms in medical biotechnology research. (Cognitive Level: Apply)

CLO3 adopt immunological techniques for industrial uses.. (Cognitive Level: Analyze)

CLO 4 manipulate the structure of chemical compounds. (Cognitive Level: Evaluate)

CLO 5 format the structure in various formats(Cognitive Level: Create)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO10	PLO 11	PLO 12	PSO1	PSO2	PSO3	PSO4	PSO5
CLO1	1	3	3	3	3	3		2	2	1	1	1	2		2	1	1
CLO2		3	3		3	3	2	2		2	1				2	1	1
CLO3	2	3	3	3					2	1		1	2	1		2	2
CLO4	1	3	3		3	3		2			1	1	2			2	
CLO5	3	3		3		3	2	2	1			2	2		1		1

Detailed Syllabus

UNIT 1 **10 Hours**

Chemoinformatics: Basic concepts of Cheminformatics, Application of and modern prospective of Cheminformatics. Manipulations in 2D and 3D structures of chemical compounds, representation of chemical reactions, molecular descriptors, calculations of physical and chemical data, calculation of structural deciphers. In silico representation of chemical information (SMILES, IchI, SDF, MOL, PDB, PDBQT, etc)**,** Computer-oriented chemical compounds nomenclature, Computer-Assisted structure elucidation. Molecular drawing and interactive visualization, Chemical name and formula searching. Pharmaceutical Chemistry.

UNIT 2 10 Hours

Molecular Structures: Cheminformatics Databases, Chemical Database Design, Bio Catalysts Database, The MOS Database, The Failed Reaction Database, Protecting Groups Database, Solid- Phase Synthesis Database, Compound Databases (ZINC, PubChem, ChEMBL, DrugBank, etc.).Chemistry & Information technology, chemical data collation, retrieval, analysis & interpretation, hypothesis generation & validation, development of structure activity/property relationships, artificial intelligence techniques in chemistry.Building molecules on a computer, quantum and molecular mechanics methods for geometry optimization, Simulation methods for molecules and materials. Representation of reactions: SMARTS, SMIRKS, Matrices. Searching chemical structures - Exact (Canonicalizing SMILES: Morgan, CANGEN), Substructure, Superstructure and Similarity search (Tanimoto, Euclidean and Tversky index), Clustering small molecules - Hierarchical and non-hierarchical methods, 3D pharmacophore-based searching: Common Pharmacophore features, building hypotheses and searching databases (5)

UNIT 3 9 Hours

Personalized Medicine: Computational Chemistry in drug design, Role of Pharmacogenomics in Drug Discovery & Therapeutics. Pharmacogenetics: Biomarkers, Promise of Personalized Medicine. Genetic drug response profiles, Effect of drug on gene expression, Pharmacogenetics, Drug Metabolism. Pharmacogenomics of drug transporters-OATP, OAT, OCT, OCTN, PepT, MRP, MDR, ABC transporter. Interethnic Differences in drug response. Drug metabolism.

UNIT 4 9 Hours

Combinatorial Chemistry: Combinatorial chemistry technologies & libraries, Solution phase synthesis, High-Throughput Synthesis and Screening, Target-oriented synthesis: Designing organic synthesis, Retrosynthetic analysis, disconnection approach, linear and convergent synthesis. Diversity-oriented synthesis: concept of forward-synthetic analysis, appendage diversity, skeletal diversity, stereo-chemical diversity, complexity and diversity. Asymmetric Synthesis: Use of chiral auxiliaries, chiron approach. Principles and use of enzymes in the synthesis of industrially important sugar / fatty acid esters, sugar nucleotide derivatives.

UNIT 5 10 Hours

Immunoinformatics overview, Reverse vaccinology, Rational Vaccine design, Evolution and escape due to variations. Immunoinformatics databases & tools. Molecular interactions, Epitope prediction algorithms:

Reference Books

 1. Flower Darren R. Bioinformatics for Vaccinology Publisher: UK, John Wiley & SonsInc. Latest Edition.
 2. Flower Darren R. Immunoinformatics: Predicting Immunogenicity In Silico
3. Gasteiger Johann, Engel Thomas. Chemoinformatics: A Textbook. Publisher: Wiley-VCH;1st edition. 2003. ISBN: 3527306811.
4. Leach Andrew R., Valerie J. Gillet. An introduction to chemoinformatics. Publisher: Kluweracademic, 2003. ISBN: 1402013477.
5. Gasteiger Johann, Handbook of Chemoinformatics: From Data to Knowledge (4 Volumes).Publisher: Wiley-VCH. 2003. ISBN:3527306803.
6. Muthukumarasamy Karthikeyan, Renu Vyas. Practical Chemoinformatics.

Publisher:

7. Springer. 2014. ISBN: 9788132217794
8. Bajorath Jürgen. Chemoinformatics and computational chemical biology. Publisher: HumanaPress. 2011. ISBN: 9781607618386

Teaching-Learning Strategies in brief

For teaching, ICT tools have been used.

Also, white board teaching had been done for explaining and clarifying many concepts and numericals.

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25. End semester exam of 75 Marks is conducted.
- By giving assignments.
- By conducting class tests.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB -301
Title of the Course: NGS Data analysis – Microarray, RNA Seq, Single Cell sequencing
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

CLO1: Understand the different platforms for first and second generation sequencing .(Cognitive LEVEL: Understand)
CLO2: Understand the advantage and disadvantage of different types of first and second generation sequencing (Cognitive Level: Understand)
CLO3: Understand the different types of high throughput sequencing. (Cognitive Level: Remember)
CLO4: Understand the basics of NGS data analysis - assembly and mapping. (Cognitive Level: Analyse)
CLO5: Understand the ethics involved in sequencing projects. (Cognitive Level: Understand)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO10**	**PLO11**	**PLO12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1	1	3	3			2				1			2		2	1	1
CLO2		3	3		1	2	1		1						2	1	1
CLO3				3		3				2		2	2			2	2
CLO4	2					1	1	2			1	2	2	1		2	
CLO5		1		3		1				1		2	2	3	1		1

Detailed Syllabus

UNIT I: **9 Hours**

History & evolution of sequencing: First-generation technologies – Sanger dideoxy sequencing, Maxam-Gilbert sequencing. Technologies used in Human Genome Project. Shotgun sequencing. Advantages and disadvantages of first generation sequencing. Next (second)-generation sequencing – difference between first and next generation sequencing, NGS platforms – Roche 454, ABI SOLiD, Ion torrent, Illumina. Advantages and disadvantages of second generation sequencing.

UNIT II: **9 Hours**

Third-generation sequencing: PacBio, Oxford nanopore. Advantages and disadvantages of third generation sequencing. Comparison of output, accuracy and types of errors of first, second and third generation sequencing technologies. Introduction to NGS technologies: DNA-seq, RNA-seq, ChIP-seq, Hi-C, Metagenomics, Single cell sequencing.

UNIT III: **10 Hours**

Preparation for sequencing: Different sample preparation methods for different type of NGS (DNASeq, RNASeq, ChIPSeq, Metagenomics, Single cell), Adaptors, Index, Barcode. Library preparation methods - Bridge amplification, Emulsion PCR. Sequencing methods – sequencing by synthesis, ion semiconductor, SMRT, nanopore.

UNIT IV: **10 Hours**

NGS Data formats & Pre-processing: Data formats overview – FASTQ, subreads, nanopore data, single cell data. Single-end, Paired-end, Mate-pair. NGS Data sources – NCBI SRA, EBI-ENA, DDBJ-SRA, GEO; Retrieving data from data sources - SRA toolkit; Aspera connect. Sequence quality measures – Phred quality score. Quality check – tool – FASTQC, Pre-processing: Trimmomatic, Fastx-toolkit.

UNIT V: **10 Hours**

Introduction to NGS Data Analysis: Assembly (overview) – principles, output file formats – contigs, scaffolds, assembly quality assessment – N50, total length, no. of contigs/scaffolds; Mapping (overview) – Principles, tools – BWA, Bowtie, SAMtools, output file formats – BAM, SAM, mapping alignment assessment – no. of reads mapped, concordant reads; Visualisation tools – IGV

Reference:

1. Dr. Michal Janitz. (2008), Next Generation Genome Sequencing: Towards Personalized Medicine, Wiley.

2. Stuart M Brown. (2013), Next-Generation DNA Sequencing Informatics, Cold Spring Harbor Laboratory Press. 3. Sara El-Metwally, Osama M. Ouda & Mohamed Helmy. (2014), Next Generation Sequencing Technologies and Challenges in Sequence Assembly, Springer, New York, NY.

4. Gaurav Sablok, Sunil Kumar, Saneyoshi Ueno, Jimmy Kuo & Claudio Varotto. (20I5), Advances in the Understanding of Biological Sciences Using Next Generation Sequencing (NGS) Approaches, Springer International Publishing.

5. Xinkun Wang. (2016), Next-generation sequencing data analysis, CRC Press.

6. Urszula Demkow and Rafał Płoski. (2016), Clinical Applications for Next Generation Sequencing, Academic Press.

7. Masoudi-Nejad, Ali, Narimani, Zahra, Hosseinkhan & Nazanin. (2013), Next Generation Sequencing and Sequence Assembly - Methodologies and Algorithms, Springer, New York. 8. Ion Măndoiu & Alexander Zelikovsky. (2016), Computational Methods for Next Generation Sequencing Data Analysis, Wiley.

9. Jerzy K. Kulski (2016), Next Generation Sequencing - Advances, Applications and Challenges, InTech

10. Emmanuel A. Kornyo. (2017), A Guide to Bioethics, CRC Press.

11. Richard McCombie W, Elaine R. Mardis, James A. Knowles & John D. McPherson. (2019), Next-Generation Sequencing in Medicine, Cold Spring Harbor Laboratory Press.

12. Wing-Kin Sung. (2020), Algorithms for Next-Generation Sequencing, Chapman and Hall/

Teaching-Learning Strategies in brief

- Build positive environment in the classroom.
- Provide concrete basic and advanced knowledge of the subject.
- Solve problems based on the basic & advanced concepts of the subject.
- Encourage to the students to ask more & more questions.
- Motivate to the students to develop critical & strategic thinking

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25. End semester exam of 75 Marks is conducted.
- Assessments through Sessional, Assignments, Quizzes etc.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB -302
Title of the Course: Programming in R and Python
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO 1 Explain and use basic concepts in programming. (Cognitive Level: Evaluate)
CLO 2 Construct and execute basic programs in Python and R (Cognitive Level: Create)
CLO 3 Design and implement basic algorithms in Python and R (Cognitive Level: Create)
CLO 4 Use external libraries with Python and R-packages. (Cognitive Level: Apply)
CLO 5 Graphically visualise data and results of statistical calculations. (Cognitive Level: Analyze)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO 10	PLO 11	PLO 12	PSO1	PSO2	PSO3	PSO4	PSO5
CLO1		3	3			2		1		1			2		2	1	1
CLO2		3	3			2	1		2		1				2	1	1
CLO3		3	3	3	1	3		1		1		2	2	1		2	2
CLO4		3	3			2			1			2	2	1		2	
CLO5		3	3	3		2	1			1		2	2		1		1

Each Course Outcome (CO) may be mapped with one or more Program Outcomes (POs). Write '3' in the box for 'High-level'mapping, 2 for 'Medium-level'mapping, 1 for 'Low'-level'mapping.

Detailed Syllabus

Unit 1: R Basics **10 Hours**
Basic operations in R, Math operations in R, Vector , working with null values, Import & Export files in R, Data-frame, Joins, One-way and Two way tables, Vectors, Matrices
Unit II: Python Basics **10 Hours**
Objects and Functions, Identifiers, Variables and Datatypes, Operators, Python Flow, Function Arguments, Recursive functions ,Lambda, Exception Handling , Iterators, Generators and Decoders.

Unit III: Mathematics for Data science **10 Hours**

Probability, Statistics, Linear Algebra, Gradient Descent, Calculus for data science, ANOVA, Hypothesis testing.

Unit IV: Numpy and Pandas Numpy: **10 Hours**

Arrays, Vectorization, Boolean Indexing, Matrix multiplication, Tuple, Join/Merge data, Unicode strings etc. Pandas: Data Structure, Data frame, Reading data, Handling missing data.

Unit V: Exploratory Data Analysis **9 Hours**

Data Visualization using GGPLOT2 and Matplotlib, Data Pre-processing, Data Transformation, Data Reduction, Feature Extraction. Univariate and Multi-variate analysis.

Reference Books:

1. Business Analytics (The science of data driven decision making) Kumar
2. https://dataflair.training/blogs/data-- manipulationinr/ U Dinesh
3. Machine Learning For Dummies, John Paul Mueller, Luca Massaron
4. Python for Dummies, Aahz Maruch and Stef Maruch
5. Introduction to Machine Learning with Python Muller Andreas

Teaching-Learning Strategies in brief

- For teaching, ICT tools have been used.
- white board teaching had been done for explaining and clarifying many concepts and numericals.

Assessment methods and weightages in brief

- Internal Assessment: 25 Marks
- Semester Exam: 75 Marks
- Assessments through Sessional, Assignments, Quizzes etc.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB -303
Title of the Course: System Biology
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO 1: have a system-level understanding of the biological systems. (Cognitive Level: Understand)
CLO 2: to develop and analyse the properties of in silico models of gene-gene interactions (Cognitive LEVEL: Analyse)
CLO 3: to develop and analyse the properties of in silico models of protein-protein interactions.(Cognitive Level: Analyse)
CLO 4: understand the concepts of networks and graphs. (Cognitive Level: Understand)
CLO5: read, understand and interpret published articles in mathematical modelling and network biology. (Cognitive Level: Create)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO 10	PLO 11	PLO 12	PSO1	PSO2	PSO3	PSO4	PSO5
CLO1	1	3	3		1	2	1				1		2		2	1	1
CLO2	1	3	3	2		2	1	2	1		1	2	1	1	2	1	1
CLO3	1	3	3	2		3	1	2	1		1	2	2			2	2
CLO4		3	3		1	2		2		2		2	2	1		2	
CLO5	2	3		3		2			2		1	2	2		1		1

Detailed Syllabus

Unit-I 10Hours

Networks and graph theory: Basic properties of biological networks: Degree, average degree and degree distribution. Adjacency matrix, weighted and unweighted networks, Bipartite network, Paths and distances.

Unit-II 9 Hours

Random Networks: Erdos-Renyi model, Small-world effect, clustering coefficient. Scale-free networks: Power laws, Hubs, ultra-small property, degree exponent, The Barabasi-Albert Model. Degree correlations: assortativity and disassortativity.

Unit-III **9 Hours** Biological networks: Complex Biological Systems, Types of Biological networks, Intracellular networks: Gene-regulatory network, Protein-interaction network, Metabolic networks and Signalling network; Inter-cellular networks: Neuronal networks, Network motifs, Computational medicine.

Unit-IV **9 Hours** Modularity: Motifs and sub-graphs, Feed-forward loops, Single-input modules: LIFO, FIFO. Dense overlapping regulons (DORs). Optimal gene design circuits: fitness function and optimal expression of a protein in bacteria, Robustness of complex systems.

Unit-V **10 Hours** Constraint-based modelling – Metabolic reconstruction, Flux Balance Analysis (FBA): Translating biochemical networks into linear algebra, Stoichiometric matrix, Elementary mode, Extreme pathways, Objective function, Optimization using linear programming. Genome-scale cellular models: Virtual Erythrocytes, Global human metabolic model (Recon 3D).

References:

1.Networks: An Introduction by M.E.J. Newman, Oxford University Press, 2010.

2. Introduction to Systems Biology: Design Principles of Biological Circuits by Uri Alon, Chapman & Hall/CRC, 2007.

3. An Introduction to Systems Biology: Design Principles of Biological Circuits by Uri Alon Published byChapman & Hall/CRC Mathematical and Computational Biology.

Teaching-Learning Strategies in brief

- For teaching, ICT tools have been used.
- Also, white board teaching had been done for explaining and clarifying many concepts and numericals
- Cooperative leaning is encouraged via participation in active discussions.

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25. End semester exam of 75 Marks is conducted.
- Assignments were provided.
- Quizes had been conducted too.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB -304
Title of the Course: Data Modelling and Visualization
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO1: Use effectively the various visualization structures (like tables, spatial data, tree and network etc.)(Cognitive Level: Remember)
CLO2: Evaluate information visualization systems and other forms of visual presentation for their effectiveness. (Cognitive Level: Evaluate)
CLO3: Design and build data visualization systems.((Cognitive Level: Create)
CLO4: Understand the key techniques and theory behind data visualization and modelling. ((Cognitive Level: Understand)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO 10**	**PLO 11**	**PLO 12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1	1	3	3		1	2	1				1		2		2	1	1
CLO2		3	3	2		2		2	1					1	2	1	1
CLO3	1	3	3			3	1				1	2	2			2	2
CLO4		3	3		1	2		2		2		2	2	1		2	
CLO5	2	3		3		2			2		1	2	2		1		1

Each Course Outcome (CO) may be mapped with one or more Program Outcomes (POs). Write ‘3’ in the box for ‘High-level’mapping, 2 for ‘Medium-level’mapping, 1 for ‘Low’-level’mapping.

Detailed Syllabus

UNIT - I Data-Analytic Thinking 6 Hours

Knowing your data, Data preprocessing,Storytelling with data

UNIT - II Data Modeling 11 Hours

Linear regression ,Logistic regression,K-nearest neighbors,K-means clustering, Performance measure, Implementation of some modeling algorithms using R

UNIT - III Data Visualization 11Hours

Value of Visualization – What is Visualization and Why do it: External representation – Interactivity – Difficulty in Validation. Data Abstraction: Dataset types – Attribute types – Semantics. Task Abstraction – Analyze, Produce, Search, Query. Four levels of validation – Validation approaches – Validation examples. Marks and Channels

UNIT - IV Rules of thumb 10Hours

Categorical regions – Spatial axis orientation – Spatial layout density. Arrange spatial data: Geometry – Scalar fields – Vector fields – Tensor fields. Arrange networks and trees: Connections, Matrix views – Containment. Map color: Color theory, Color maps and other channels.

UNIT - V Manipulate view 10 Hours

Change view over time – Select elements – Changing viewpoint – Reducing attributes. Facet into multiple views: Juxtapose and Coordinate views – Partition into views – Static and Dynamic layers – Reduce items and attributes: Filter – Aggregate. Focus and context: Elide – Superimpose – Distort – Case studies.

Reference Books:

1. Tamara Munzner, Visualization Analysis and Design, A K Peters Visualization Series, CRC Press, 2014.
2. Scott Murray, Interactive Data Visualization for the Web, O’Reilly, 2013.
3. Alberto Cairo, The Functional Art: An Introduction to Information Graphics and Visualization, New Riders, 2012
4. Nathan Yau, Visualize This: The FlowingData Guide to Design, Visualization and Statistics, John Wiley & Sons, 2011.

Teaching-Learning Strategies in brief

- For teaching, ICT tools have been used.
- Also, white board teaching had been done for explaining and clarifying many concepts and numericals
- Cooperative leaning is encouraged via participation in active discussions.

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25.
- End semester exam of 75 Marks is conducted.
- Assignments were provided.
- Quizes had been conducted too.

Discipline Specific Elective: (DSE) – I

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB DSE11
Title of the Course: Database Management System
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO1: Differentiate database systems from file systems by enumerating the features provided by database systems and describe each in both function and benefit. (Cognitive Level: Understand)

CLO2: Demonstrate an understanding of the relational data model. ((Cognitive Level: Understand)

CLO3: Transform an information model into a relational database schema and to use a data definition language and/or utilities to implement the schema using a DBMS. (Cognitive Level: Evaluate)

CLO4: Formulate, using relational algebra, solutions to a broad range of query problems. (Cognitive Level: Create)

CLO5: Formulate, using SQL, solutions to a broad range of query and data update problems. (Cognitive Level: Create)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO10**	**PLO11**	**PLO12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1	3	3	3	3	3	3		2	2	1	1	1	2		2	1	1
CLO2	3	3	3	3	3	3	2	2	2	2	1	1			2	1	1
CLO3	3	3	3	3	3				2	1		1	2			2	2
CLO4	3	3	3		3	3	2	2			1	1	2			2	
CLO5	3	3		3	3	3	2	2	1			2	2		1		1

Detailed Syllabus

Unit – I

Introduction to DBMS **8 Hours**

Basics of File Processing Systems and Database Systems, Difference between traditional file system and DBMS, Responsibilities of Database Administrator, Three level Architecture of Database System, Physical and Logical data independence.

Unit – II

Introduction to various Database Models **10 Hours**

Entity Relationship Model and its importance, Introduction to various Symbols used In ERD (Entity: Types of Entities, week Entity, Composite Entity, Strong Entity, Attribute: Types of Attribute, Relationship: Type of relationship, Connectivity, Cardinality), Conversion of ER diagram to tables, Comparative study of Network, Hierarchical and Relational Models, Codd's 12 Rules, Comparison of Object Oriented Database and Object Relational Database.

Unit – **III** **11 Hours**

Normalization in DBMS

Normalization and its various forms(1NF, 2NF, 3NF and BCNF), Functional Dependencies, Multi-valued Dependencies, Study of various Database Integrity like Domain, Entity, Referential Integrity Constraints.

Unit – IV **10 Hours**

SQL

Categories of SQL Statements, The CREATE Statement, The DROP Command, The ALTER Command, Integrity Constraints, DML Statements: The SELECT Statement, The INSERT Statement, The DELETE Statement, The UPDATE Statement, SQL Operators: Simple Selects Comparison Operators, IN and NOT IN Operators, BETWEEN Operator, The LIKE Operator Logical

Operators, IS NULL and IS NOT NULL, ANY, ALL, SQL FUNCTIONS, Joining Tables, SQL Subqueries, GROUP BY Clause, HAVING Clause

Unit-V

Advanced Database Concepts **9 Hours**

Emerging database technologies and applications: Spatial databases,Mobile databases, Multimedia databases, Genome data management, Overview of Data Warehouse, OLAP, Big data, biological big data, and big data analytics

Reference Books:

1. R. Elmasri & S.B. Navathe, Fundamentals of Database Systems, Pearson Education, 6th edition, 2010.
2. Silberschatz, H. Korth & S. Sudarshan, Database System Concepts, TMH, 5th Edition, 2010.
3. R. Ramakrishnan & J. Gehrke, Database Management Systems, 3rd edition, TMH, 2007.

Teaching-Learning Strategies in brief

- For teaching, ICT tools have been used.
- Also, white board teaching had been done for explaining and clarifying many concepts and numericals
- Cooperative leaning is encouraged via participation in active discussions.

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25.
- End semester exam of 75 Marks is conducted.
- Assignments were provided.
- Quizes had been conducted too

Name of the Academic Program Master Of Science (Computational & System Biology and Bioinformatics)
Course Code: … MCSB DSE 12
Title of the Course: …… Fundamentals of computing
L-T-P 3-1-0. (L=Lecture hours, T=Tutorial hours, P=Practical hours)
Credits…4

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to …………
CLO1: have an indepth knowledge of what is inside computer. (Cognitive Level: Remember)
CLO2: have how data is stored in memory and computation takes place. (Cognitive Level: Remember)
CLO3: understand how hardware interacts with operating system. (Cognitive Level: Understand)
CLO4: understand how networking takes place with the help of programming in linux. (Cognitive Level: Understand)
CLO5: connect various applications. (Cognitive Level: Create)

Mapping of Course Learning Outcomes (CLOs)with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO 1	**PLO 2**	**PLO 3**	**PLO 4**	**PLO 5**	**PLO 6**	**PLO 7**	**PLO 8**	**PLO 9**	**PLO 10**	**PLO 11**	**PLO 12**	**PSO 1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CLO1		3	2	1	1	2		3		3		**1**	**3**		**1**		**2**
CLO2	3		3		3	1	3		3			**2**		**3**		**1**	
CLO3				3		3		2	1	2	1			**2**	**2**		**1**
CLO4		3	3		3	1		2	2	1	1				**3**		**2**
CLO5	3						3				3	**3**				**3**	**2**

Each Course Learning Outcome (CLOs) may be mapped with one or more Program Learning Outcomes (PLOs). Write ‘3’ in the box for ‘High-level’ mapping, 2 for ‘Medium-level’mapping, 1 for ‘Low-level’mapping. Map with PSOs wherever applicable.

Detailed Syllabus:

UNIT 1 **9 Hours**

Computing Concepts: Basic Computing Systems, Layers of a Computing System, History of Computing, History of Computing Software, Stored-Program Concept and von Neumann Architecture. Fetch-Execute Cycle, RAM and ROM, Types of RAM and ROM, Secondary and Tertiary Storage Devices, Cache Memory, Memory Hierarchy, Input- Output Devices, Touch Screens.

UNIT 2 **11 Hours**

Data Representation and Number Systems: Binary Values and Computers, Data and Computers, Analog and Digital Data; Binary Representation. Number Systems: Binary, Octal, Decimal, and Hexadecimal. Conversions of Data from one Number System to another Number System. Representation of Numeric Data – Negatives and Real Data Representation. Representing Texts - ASCII and Unicode Character Sets. Binary Arithmetic – Addition and Subtraction of Numbers in Different NumberSystems.

UNIT 3 **11 Hours**

Operating Systems: Introduction and Examples of Operating Systems, Roles of Operating Systems:Memory, Process, and CPU Management. Batch Processing, Categories of Operating Systems:Timesharing, Multitasking, Multithreading, and Multiprogramming Operating Systems. Process Statesand Process Control Block.

UNIT 4 **11 Hours**

Computer Networks: Introduction to Computer Networks. Network Topologies, Types of Networks,Internet vs. Intranet, Switch, Bridge, and Routers. Firewalls, Network Protocols, TCP/IP, NetworkAddresses, Domain Name System, Internet services: E-mail, FTP, ISP, etc.

UNIT 5 **7 Hours**

Linux basic concepts & installations: Basic command, file transfer, cluster handling,

Reference Books:

1. Fundamental concepts of Bioinformatics – D E Krane and M L Raymer, Pearson Education.

2. Operating System Principles- by **Silberschatz , Galvin , Gagne**

3. Data Communications and Networking- Behrouz Forouzan. Tata Mc GrawHill.

4. **Fundamentals of Digital Circuits- Kumar A. Anand**.PHI

5. Linux in Easy Steps-Mike McGrath. Bpb publication.

Teaching-Learning Strategies in brief

- Build positive environment in the classroom.
- Provide concrete basic and advanced knowledge of the subject.
- Solve problems based on the basic & advanced concepts of the subject.
- Encourage to the students to ask more & more questions.
- Motivate to the students to develop critical & strategic thinking

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25. End semester exam of 75 Marks is conducted.
- By giving assignments.
- By conducting class tests.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB DSE 13
Title of the Course: Advance Bioinformatics Applications
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO1: Examine factors that affect drug response and the application of pharmacogenetics to drug development and drug treatment. (Cognitive Level: Understand)
CLO2: Emphasis the application of bioinformatics and biological databases to problem solving in real research problems. (Cognitive Level: Understand)
CLO3: familiar with the use of a wide variety of internet applications and biological database. (Cognitive Level: Understand)
CLO4: analyse the raw reads of sequences. (Cognitive Level: Analyze)
CLO5: Perform genomic data analysis. (Cognitive Level: Analyse

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO 10**	**PLO 11**	**PLO 12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1		3	3	1		2	1				1		2		2	1	1
CLO2		3	2	1	1	2		2	1					1	2	1	1
CLO3	2	2	3	3		2				1		2	2	1		2	2
CLO4			3		1	1	1		2		1		1			2	
CLO5	2	3		3		3		2		2	1		2	1	1		1

Detailed Syllabus

UNIT-I COMMERCIAL BIOINFORMATICS **10 Hours**
History of Bioinformatics – Goal of bioinformatics as a separate discipline – Survey of bioinformatics companies in India and abroad – Emerging branches of Bioinformatics: Genomics, Proteomics, Systems Biology, Chemoinformatics, and Synthetic biology.

UNIT- II GENOME ANALYSIS **9 Hours**
Sequence assembly and Finishing methods - Sequence assemblers – finishing and visualization programmes - Gene expression analysis - Data collection - Image processing - Measures of expression - Finding significant genes - Clustering approaches – SNP – Types - SNP discovery methods - databases and browsers - Applications of Bioinformatics in Gene Therapy.

UNIT -III PHARMACEUTICAL BIOINFORMATICS AND DRUG DISCOVERY 9 Hours

Scope of Pharmaceutical bioinformatics and drug discovery - Pharmacogenetics and individual medicine – Medical applications: Genetic basis of disease – Cancer – Drug discovery and testing – Personalized medicine - Genomics and proteomics in medicine, diagnostics, drug discovery and target finding.

UNIT -IV TRANSGENIC PLANTS AND ANIMALS 10 Hours

Transgenic plants and animals - Need for Transgenic plants and animals - Applications of transgenic animal technology - Ethical issues of transgenic plants, animals and other organisms.

UNIT-V BAR CODING 10 Hours

Bar Code of Life - Need for bar coding-Uses of bar coding - Applications of Bioinformatics in Biodiversit

Reference Books:

1. T. A. Brown, Genomes, 6th Edition, BIOS Scientific Publishers, Ltd., Oxford, UK, 2006.
2. Baxevanis D and Ouellette BFF, Bioinformatics: A practical guide to the analysis of genes and proteins (3rd Ed), John Wiley & Sons, Inc., 2005.
3. Jenson, O.N., in Proteomics. A Trends Guide (eds Black Stock, Co- and Mann), Elsevier Science, London, 1998.
4. S.R.Pennington and M.J.Dunn, Proteomics, Viva Books Pvt. Ltd., New Delhi, 2002.
5. R.C. Dubey, A Textbook of Biotechnology, S.Chand & Company, 1993.
6. Paul D. N. Hebert, Alina Cywinska, Shelley L. Ball and Jeremy R. deWaard, Biological identifications through DNA barcodes, Proc. Roy. Soc. (London) B, 270 (2003) 313 – 321.
7. Mark Y. Stoeckle and Paul D. N. Hebert, Barcode of Life, Scientific American, October 2008, 82 – 88.

Teaching-Learning Strategies in brief

- Build positive environment in the classroom.
- Provide concrete basic and advanced knowledge of the subject.
- Solve problems based on the basic & advanced concepts of the subject.
- Encourage to the students to ask more & more questions.
- Motivate to the students to develop critical & strategic thinking

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25. End semester exam of 75 Marks is conducted.
- By giving assignments.
- By conducting class tests.

Discipline Specific Elective: (DSE) – II

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB DSE 21
Title of the Course: Evolutionary bioinformatics
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)
COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO1: understand the molecular basis of the evolution of the genome. (Cognitive Level: Understand)
CLO2: to analyse the genomic data using phylogenetics. (Cognitive Level: Analyse)
CLO3: infer the evolutionary explanation of a biological phenomenon. (Cognitive Level: Analyse)
CLO4: Understand the need of evolutionary medicine. (Cognitive Level: Understand)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO 10**	**PLO 11**	**PLO 12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1		3	3	1		2				1			2	1	2	1	1
CLO2	2	3			1	2	1		1		1				2	1	1
CLO3		3	3	3		3		1				2	2			2	2
CLO4	1	3	3		1	2	1			1		2	2			2	

Detailed Syllabus

Unit 1 Evolution of DNA and proteins **9 Hours**
origin of the genetic code. Hardy-Weinberg equilibrium; Evolutionary changes by mutation, gene flow, natural selection and genetic drift.

Unit 2 molecular evolution **9Hours**
Role of transitions and transversions; chromosomal deletions and insertions in evolution. Role of pseudogenes, repetitive DNA, transposable elements and junk DNA in evolution.

Unit 3 Theories **10Hours**
Neutral theory (Kimura) and nearly neutral theory (Ohta) of molecular evolution. Phylogenetic tree. Reconstruction of phyogenetic trees using distance matrix methods, the Maximum Parsimony method, Maximum likelihood and Bayesian inference. Estimation of selection at the molecular level.

Unit 4 Molecular Clock **10 Hours**

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 5 Evolution of the genome: **10 Hours**

Human Genome Project, ENCODE, Genome duplication (Ohno's hypothesis), Exon Shuffling, Concerted evolution. Evolutionary Medicine.

Reference books:

1. An Introduction to Molecular Evolution and Phylogenetics by Lindell Bromham, 2016, Oxford University Press.
2. Molecular Evolution by Wen Hsiung-Li, 1997, Sinauer Associates, Sunderland, MA.
3. Molecular Evolution and Phylogenetics by Masatoshi Nei and Sudhir Kumar, 2000, Oxford University Press.
4. Neutral Theory of Molecular Evolution by Motoo Kimura, 1985, Cambridge University Press.
5. Bioinformatics and Molecular Evolution by Paul G. Higgs and Teresa K. Attwood, 2013, Willey-Blackwell.

Teaching-Learning Strategies in brief

- Build positive environment in the classroom.
- Provide concrete basic and advanced knowledge of the subject.
- Solve problems based on the basic & advanced concepts of the subject.
- Encourage to the students to ask more & more questions.
- Motivate to the students to develop critical & strategic thinking

Assessment methods and weightages in brief

- 2 sessionals has to be conducted for a total of 25. End semester exam of 75 Marks is conducted.
- By giving assignments.
- By conducting class tests.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB DSE 22
Title of the Course: Proteomics & Metabolomics
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO1: provide a system level understanding of complex interactions within biological systems and to model the biological systems employing computational and mathematical concepts. (Cognitive Level: Understand)
CLO2: Describe about various approaches used in the simulation of metabolic pathways Explain about gene regulatory networks. (Cognitive Level: Analyse)
CLO3: Describe about network motifs and their use in Biology. (Cognitive Level: Evaluate)
CLO4: understand the proteins enclosed by the genes with respect to structure, function, protein – protein interactions, techniques for separation and analysis, database and applications. (Cognitive Level: Understand)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO 10**	**PLO 11**	**PLO 12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1		3	3	1		2		2		1	1		2	1	2	1	1
CLO2	2	3	3	3	1	3	2		1						2	1	1
CLO3	2			3		3	1	2			1	2	2		1	2	2
CLO4	1	3	3		1	1	2			1		2	2	1		2	

Detailed Syllabus

UNIT -I INTRODUCTION 10 Hours

Proteomics introduction – Protein sequencing – Protein Digestion Techniques – Mass Spectrometers for Protein and Peptide Analysis – Protein Identification by Peptide Mass Fingerprinting – Software Tools for Peptide Mass Fingerprinting: Finding the Matches – Peptide Sequence Analysis and Protein Identification with Tandem Mass Spectrometry

UNIT -II PROTEOME DATABASES 10 Hours

Proteome databases – Comparative proteomics methods – 2D gel databases – Protein interaction data bases – Metabolic pathway databases – resources for interaction prediction – network and pathway visualization tools – Protein network analysis

UNIT- III FUNCTIONAL PROTEOMICS 10 Hours

Functional proteomics – protein phenotypes – Protein-Protein Interaction Mapping: Experimental – Yeast two-hybrid system – phage display – protein fragment complementation assays – Computational approach

UNIT -IV METABOLOME INFORMATICS 9Hours

Introduction to the ARM Database- The Genome-Based E-CELL Modeling (GEM) System- Large-Scale Simulation of Metabolism-Metabolomics and Medical Sciences

UNIT-V INTRODUCTION TO METABOLIC ENGINEERING 9Hours

Importance of metabolic engineering-comprehensive models for cellular reactions-material balances & data consistency- metabolic pathway synthesis.

References books:

1.M. Tomita, T. Nishioka, Metabolomics- The Frontier of Systems Biology, Springer Publications, 2003.
2. Gregory N. Stephanopoulos, Metabolic Engineering- Principles and Methodologies, Academic press, First Edition, 1998.
3. Baxevanis D and Ouellette BFF, Bioinformatics: A practical guide to the analysis of genes and proteins (2nd Edn.), John Wiley & Sons, Inc. 2002.
4. Brown TA, Genomes (2nd Edn.), BIOS Scientific Publishers, Oxford, UK, 2002.
5. Sensen CW, Essentials of Genomics and Bioinformatics, Wiley–VCH. 2002.

Teaching-Learning Strategies in brief

- Build positive environment in the classroom.
- Provide concrete basic and advanced knowledge of the subject.
- Solve problems based on the basic & advanced concepts of the subject.
- Encourage to the students to ask more & more questions.
- Motivate to the students to develop critical & strategic thinking

Assessment methods and weightages in brief

- By giving assignments.
- By conducting class tests.
- 2 sessionals has to be conducted for a total of 25. End semester exam of 75 Marks is conducted.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB DSE 23
Title of the Course: Comparative and Functional Genomics
L-T-P: 3-1-0
Credits: 04

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO1: elucidate complete genomes of species. (Cognitive Level: Understand)
CLO2 Understand why researchers have honed in on conserved DNA sequences between other vertebrates and humans. (Cognitive Level: Understand)
CLO3 Get familiarize with the tools and databases available for genomic analysis, with an appreciation of the quantitative concepts that form the basis of those tools. (Cognitive Level: Apply)
CLO4 Understand the concepts associated to Genomics and apply the same in various fields. (Cognitive Level: Understand)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO10**	**PLO11**	**PLO12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1		3	3	1		2				1			2	1	2	1	1
CLO2	2	3			1	2	1		1		1				2	1	1
CLO3		3	3	3		3		1				2	2			2	2
CLO4	1	3	3		1	2	1			1		2	2			2	

Detailed Syllabus

Unit 1Comparative genomics: **10 Hours**
Databases for genomics resources, Technologic principles of currently utilized methods within the field of functional genomics. Sequence alignment: global versus local, inferring gene function from relatedness to other genes, Finding Open Reading Frames, overall structure and organization of the genome in microorganisms, plants and animals. Extra-chromosomal elements: Mitochondrial genome, mitochondrial plasmids. Organization of nuclear and organellar genomes; Repetitive DNA-satellite DNAs and interspersed repeated DNAs, Transposable elements, LINES, SINES, Alu family and their application in genome Mapping**.**

Unit 2 Molecular Phylogenetics: 10 Hours
Fine structure of gene, split genes, pseudogenes, non-coding genes, overlapping genes and multi-gene families. Genome sequencing methods, Genome annotation at different levels, Comparative genome sequencing. Molecular Phylogenetics Origins, Applications of Molecular Phylogenetics. Phylogenomic comparisons, introduction to programs, Phylogenetic analyses: tree terminology and parsimony,

Phylogenetic analyses to determine relationships and interpret character evolution. Single gene disorders-conventional and contemporary methods. Candidate gene identification; Genetic polymorphism and disease susceptibility.

Unit 3 **Databases and Software for Genome Biology:** **10 Hours**

Gene Expression Analysis using Microarrays and RNA-Seq, Application of DNA microarrays for the analysis of gene expression, protein-DNA binding, chromatin structure, chromatin modifying complexes, and RNA polymerase occupancy. Error models and data normalization techniques for high-resolution array technologies. Clustering genes into sets and discovering gene set features that can be used for diagnostic purposes. Importance of chromatin structure in contemporary modelling, relationship between chromatin structure and transcriptional regulation.

Unit 4 **Functional Genomics-I:** **10 Hours**

Determining the Functions of Individual Genes, Pathway and GO annotation systems, Non-coding DNA, gene prediction methods and tools. Genome Evolution, Genome and Transcriptome Assembly Algorithms, Profile HMMs for Protein Family Modelling, Human Genome Project, Genomics and Personalized medicine**,** Sex-linked inheritance: Conceptual basis, sex influenced traits, mechanism of sex determination. Mutation variability across the genome**.** Mutation detection, diagnosis and therapy. Genes and Environment - heritability, penetrance and expressivity.

Unit 5 Functional Genomics-II: **10 Hours**

Integration of genomic, epigenetic and external effects in the context of understanding gene and genome function, Genome regulation: Introduction, levels of regulation, evidence and experimental designs/methodologies, role of genetic analysis in understanding gene function and regulation. Transcriptional control - DNA sequence elements and transcription factors**.** Mutation – Classification, mechanism, repair, role in genetic analysis and evolution. Post- transcriptional regulation – Alternative RNA

Reference

1.Hartl & Ruvolo. Genetics: Analysis of Genes and Genomes. Jones & Bartlett Learning Mount.

2.Bioinformatics sequence and Genome analysis. Cold Spring Harbor Laboratory Press Deonier, Tavaré, & Waterman. Computational Genome Analysis: An Introduction. Springer

Teaching-Learning Strategies in brief

- Build positive environment in the classroom.
- Provide concrete basic and advanced knowledge of the subject.
- Solve problems based on the basic & advanced concepts of the subject.
- Encourage to the students to ask more & more questions.
- Motivate to the students to develop critical & strategic thinking

Assessment methods and weightages in brief

1. Internal Assessment: 25 Marks
2. Semester Exam: 75 Marks
3. Assessments through Sessional, Assignments, Quizzes etc.

GENERIC ELECTIVE-I

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB GE 11

Title of the Course: Research Methodology
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO 1: Understand research problem formulation and analyze research related information. Follow research ethics. (Cognitive Level: Understand)

CLO2: Understand the functions of the literature review in research, carrying out a literature search. (Cognitive Level: Understand)

CLO3: Understand that today's world is controlled by Computer, Information Technology, but tomorrow world will be ruled by ideas, concept, and creativity. (Cognitive Level: Understand)

CLO4: Understand the art of interpretation and the art of writing research reports (Cognitive Level: Implement)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO10**	**PLO11**	**PLO12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1	3	3	1	1	1	3		1		1		1	2		2	1	1
CLO2	3	3	1	1		2				1	1	1		1	2	1	1
CLO3	3	3	1	2	1	2	1	1		1		1	2			2	2
CLO4	3	3	1	2		2				1		1	2	1		2	

Detailed Syllabus

UNIT I –RESEARCH FORMULATION AND DESIGN 10 Hours

Motivation and objectives – Research methods vs. Methodology. Types of research – Descriptive vs. Analytical, Applied vs. Fundamental, Quantitative vs. Qualitative, Conceptual vs. Empirical, concept of applied and basic research process, criteria of good research. Defining and formulating the research problem, selecting the problem, necessity of defining the problem, importance of literature review in defining a problem, literature review-primary and secondary sources, reviews, monograph, patents, research databases, web as a source, searching the web, critical literature review, identifying gap areas from literature and research database, development of working hypothesis.

UNIT II – DATA COLLECTION AND ANALYSIS 10 Hours

Accepts of method validation, observation and collection of data, methods of data collection, sampling methods, data processing and analysis strategies and tools,data analysis with statically package (Sigma STAT,SPSS for student t-test, ANOVA, etc.), hypothesis testing.

UNIT III – SOFT COMPUTING 9 Hours

Computer and its role in research, Use of statistical software SPSS, GRETL etcin research. Introduction to evolutionary algorithms - Fundamentals of Genetic algorithms, Simulated Annealing, Neural Network based optimization, Optimization of fuzzy systems.

UNIT IV –RESEARCH ETHICS, IPR AND SCHOLARY PUBLISHING 9Hours

Ethics-ethical issues, ethical committees (human & animal); IPR- intellectual property rights and patent law, commercialization, copy right, royalty, trade related aspects of intellectual property rights (TRIPS); scholarly publishing- IMRAD concept and design of research paper, citation and acknowledgement, plagiarism, reproducibility and accountability.

UNIT V –INTERPRETATION AND REPORT WRITING 10 Hours

Meaning of Interpretation, Technique of Interpretation, Precaution in Interpretation, Significance of Report Writing, Different Steps in Writing Report, Layout of the Research Report, Types of Reports, Oral Presentation, Mechanics of Writing a Research Report, Precautions for Writing Research Reports, Conclusions.

Reference Books

1. Garg, B.L., Karadia, R., Agarwal, F. and Agarwal, U.K., 2002.
2. An introduction to Research Methodology, RBSA Publishers. Kothari, C.R., 1990.
3. Research Methodology: Methods and Techniques. New Age International. 418p. Sinha, S.C. and Dhiman, A.K., 2002.
4. Research Methodology, Ess Ess Publications. 2 volumes. Trochim, W.M.K., 2005.
5. Research Methods: the concise knowledge base, Atomic Dog Publishing. 270p. Wadehra, B.L. 2000.
6. Law relating to patents, trade marks, copyright designs and geographical indications. Universal Law Publishing.

Teaching-Learning Strategies in brief

- Build positive environment in the classroom.
- Provide concrete basic and advanced knowledge of the subject.

- Solve problems based on the basic & advanced concepts of the subject.

Assessment methods and weightages in brief

1. Internal Assessment: 25 Marks
2. Semester Exam: 75 Marks
3. Assessments through Sessional, Assignments, Quizzes etc.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB GE 12
Title of the Course: Computational Neuroscience & Neuroinformatics
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO1: understand the working of neurons. (Cognitive Level: Understand)
CLO2:.analyse various diseases related to neurons and related genes. (Cognitive Level: Analyse)
CLO 3:. Understand the equilibrium maintained by the Brain over the body. (Cognitive Level: Understand)
CLO 4:. Understand purpose of various imaging techniques. (Cognitive Level: Understand)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	PLO2	PLO3	PLO4	PLO5	PLO6	PLO7	PLO8	PLO9	PLO 10	PLO 11	PLO 12	PSO1	PSO2	PSO3	PSO4	PSO5
CLO1		3	3	1		2		1	1	1			2	1	2	1	1
CLO2	2	2	1		1	2				1	1		1		2	1	1
CLO3	1	3		3		3	2	1	1	2	1	2				2	2
CLO4	1	3	1	1	1	2	1			1		2	2			2	

Detailed Syllabus

Unit 1 **10 Hours**

Neuroanatomy: Gross anatomy of adult brain, organization of the nervous system, subdivision of the nervous system, concept of CNS, ANS & PNS, meninges. The scalp, skull, meninges and cerebrospinal fluid, anatomy of the pituitary (normal & enlarged), vertebral column, cutaneous nerve supply of head and neck limb and trunk. Brain, spinal cord, cranial nerve, spinal nerve, autonomic nervous system.

Unit2 **10 Hours**

Neurophysiology: Neurons and glial cells, Resting Potential & Action potential, Propagation of Nerve Impulses, Degeneration & regeneration /repair of nerve fibers, Nerve growth factors. Synaptic & neuro-muscular transmission, Muscle tone, posture, Equilibrium & their regulation. Pain production, pathways and analgesics, head ach & referred pain. Vestibular apparatus & motion sickness. Integrative functions of thalamus, cerebellum, basal ganglia & Cerebral cortex. Blood brain barrier, Blood CSF barrier, Spit Brain, EEG.

Unit 3 **10 Hours**

Neurogenetic diseases: Autosomal (recessive and dominant) and X-linked neurological diseases – Neurodegenerative diseases, unstable mutation (repeat expansion) causing spinocerebellar ataxias, Huntington's disease, Myotonic dystrophy, Friedreich's ataxia, Fragile-X syndrome, etc., and molecular pathology. Metabolic defects causing neurological diseases (Tay-Sach's, Gaucher's diseases, etc). Complex genetic diseases, gene environment interactions,Pathogenetics of migraine, epilepsy, autism and schizophrenia.

Unit 4 **10 HOURS**

Neuroinformatics: Biophysics & Theoretical Neuroscience with Computational application; Elements of Neural network and computation, complexity and learning. Non-linear elements and networks, linear and polynomial threshold elements, network capacity, learning theory, the sample complexity of learning, perception training, learning complexity, the intractability of learning, model selection. Brain as electrical machine; Neuron & Nervous system Modeling; Essential Bioinformatics related to Neuroinformatics; Application of Neuroinformatics; Neuroinformatics related to Brain Disease/Disorder.

Unit 5 **9 Hours**

Neuroimaging – Neuroradiology: CT, MRI, Mylography; Interventional Radiology - PET (Positron Emission Tomography) – CVA, Epilepsy, etc., Single - Photon Emission Computed Tomography, MR Spectroscopy, Magnetic Source imaging.

References:

Teaching-Learning Strategies in brief

- For teaching, ICT tools have been used.
- Also, white board teaching had been done for explaining and clarifying many concepts and numericals.

Assessment methods and weightages in brief

- Internal Assessment: 25 Marks
- Semester Exam: 75 Marks
- Assessments through Sessional, Assignments, Quizzes etc.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB GE 13
Title of the Course: Programming in Java
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO1: Use the syntax and semantics of java programming language and basic concepts of OOP. (Cognitive Level: Implement)
CLO2:. Develop reusable programs using the concepts of inheritance, polymorphism, interfaces and packages. (Cognitive Level: Create)
CLO 3:. Apply the concepts of Multithreading and Exception handling to develop efficient and error free codes. (Cognitive Level: Apply)
CLO 4:. Design event driven GUI and web related applications which mimic the real word scenarios. (Cognitive Level: Create)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO 10**	**PLO 11**	**PLO 12**	**PSO1**	**PSO 2**	**PSO 3**	**PSO 4**	**PSO 5**
CLO1		3	3	1		2				1			2	1	2	1	1
CLO2	2	3			1	2	1		1		1				2	1	1
CLO3		3	3	3		3		1		1		2	2			2	2
CLO4	1	3	3		1	2	1			1		2	2			2	

Detailed Syllabus

Unit 1 **9 Hours**

Java Basics – Importance and features of java, Modifiers, Access Controls, Data types, Expressions, Declarations, Statements & Control Structures, Program Structures, String handling, Packages, Interfaces, Working with java util Package, Garbage Collection

Unit 2 **11 Hours**

Exception Handling, I/O & JDBC – Exception Handling: built in exception, creating your own exceptions, Input Stream & Output Stream: Streams, Byte and Character stream, Predefined streams, Reading and Writing from Console and Files, Buffered Reader & Writer, Serialization, Database: JDBC Basics

Unit 3 **10 Hours**

Multithreading and Communication – Java Thread Model: Life Cycle of Thread, Thread class, Runnable interface, Inter thread Communication, Suspending, Resuming and Stopping threads, Synchronization, Scheduling and Priority of Threads.

Unit 4 **10 Hours**

AWT & Event Handling – Creating User interface with AWT, Applets, Applet Life Cycle, Simple Graphics, Fonts and Colors, Events, Listeners, Components, Containers, Working with Layouts, Event Classes, Event Listener Interfaces, Adapter and Inner Classes

Unit 5 **9 Hours** BioJava – Installing BioJava, Symbols, Basic Sequence Manipulation (DNA to RNA, Reverse Complement, motif as regular expression), Translation (DNA to Protein, Codon to amino acid, Six frame translation), Proteomics (Calculate the mass and pI of a peptide), Sequence I/O (File Formats conversions), Locations and Features (PointLocation, RangeLocation, Feature modifications), BLAST and FASTA (Blast and FastA Parser, extract information from parsed results), Counts and Distributions, Weight Matrices and Dynamic Programming, User Interfaces.

Reference Books

1. Herbert Schildt, Java- A Beginners Guide (4th Ed.)., Tata Mc-Graw-Hill publication. 2007
2. Computing Concepts with Java 2 Essentials (2nd Ed.) by Horstmann, C.S., John Wiley Publishers. 2000
3. Object Oriented Design and Applications (2nd Ed.) by Benjamin, Cummings and Booch, G., Addison Wesley Publishers. 1994

Teaching-Learning Strategies in brief

- Build positive environment in the classroom.
- Provide concrete basic and advanced knowledge of the subject.
- Solve problems based on the basic & advanced concepts of the subject.
- Encourage to the students to ask more & more questions.
- Motivate to the students to develop critical & strategic thinking

Assessment methods and weightages in brief

1. Internal Assessment: 25 Marks
2. Semester Exam: 75 Marks
3. Assessments through Sessional, Assignments, Quizzes etc.

GENERIC ELECTIVE-II

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB GE 21
Title of the Course: Soft Computing Techniques
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)
COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO1: Develop intelligent systems leveraging the paradigm of soft computing techniques. (Cognitive Level: Create)
CLO2: Implement, evaluate and compare solutions by various soft computing approaches for finding the optimal solutions. (Cognitive Level: Evaluate)
CLO3: Recognize the feasibility of applying a soft computing methodology for a particular problem. (Cognitive Level: Understand)
CLO4: Design the methodology to solve optimization problems using fuzzy logic, genetic algorithms and neural networks. (Cognitive Level: Create)
CLO5: Design hybrid system to revise the principles of soft computing in various applications. (Cognitive Level: Create)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO10**	**PLO11**	**PLO12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1		3	3	1		2	1				1		2		2	1	1
CLO2	2	3	3	1	1	2		2	1					1	2	1	1
CLO3	2	2	3			3					1	1	2			2	2
CLO4			3		1	1	1			2		2	1	1		2	
CLO5	2	3		3		3		2	2	2	1	2	2	1	1		1

Detailed Syllabus

Unit –I Soft Computing 10 Hours
Introduction to soft computing, soft computing vs. hard computing, various types of soft computing techniques, applications of soft computing. Artificial Intelligence: Introduction, Various types of production systems, characteristics of production systems, breadth first search, depth first search techniques, other Search Techniques like hill Climbing, Best first Search, A* algorithm, AO* Algorithms

and various types of control strategies. Knowledge representation issues, Prepositional and predicate logic, monotonic and non monotonic reasoning, forward Reasoning, backward reasoning, Weak & Strong Slot & filler structures, NLP.

Unit –II Neural Network 10 Hours

Structure and Function of a single neuron: Biological neuron, artificial neuron, definition of ANN, Taxonomy of neural net, Difference b/w ANN and human brain, characteristic and applications of ANN, single layer network.

Unit – III Perceptron 10Hours

Perceptron training algorithm, Linear separability , Widrow & Hebb's learning rule/Delta rule, ADALINE, MADALINE, AI v/s ANN. Introduction of MLP, different activation functions, Error back propagation algorithm, derivation of BBPA, momentum, limitation, characteristics and application of EBPA. Counter propagation network: architecture , functioning & characteristics of counter Propagation network, Hop field/ Recurrent network, configuration, stability constraints, associative memory, and characteristics, limitations and applications. Hopfield v/s Boltzman machine. Adaptive Resonance Theory: Architecture, classifications, Implementation and training. Associative Memory.

Unit – IV Fuzzy Logic 10 Hours

Fuzzy set theory, Fuzzy set versus crisp set, Crisp relation & fuzzy relations, Fuzzy systems: crisp logic, fuzzy logic, introduction & features of membership functions. Fuzzy rule base system : Fuzzy propositions, formation, decomposition & aggregation of fuzzy Rules, fuzzy reasoning, fuzzy inference systems, fuzzy decision making & Applications of fuzzy logic.

Unit – V Genetic algorithm 10 Hours

Fundamental, basic concepts, working principle, encoding, fitness function, reproduction, Genetic modeling: Inheritance operator, cross over, inversion & deletion, mutation operator, Bitwise operator ,Generational Cycle, Convergence of GA, Applications & advances in GA, Differences & similarities between GA & other traditional methods.

References:

1. N.K.Bose, Ping Liang, Neural Network fundamental with Graph, Algorithms & Applications, TMH, 1st Edition, 1998.
2. Bart Kosko, Neural Network & Fuzzy System, PHI Publication, 1st Edition, 2009.
3. Rich E, Knight K, Artificial Intelligence, TMH, 3rd Edition, 2012.
4. George J Klir, Bo Yuan, Fuzzy sets & Fuzzy Logic,Theory & Applications, PHI Publication, 1st Edition, 2009.
5. Martin T Hagen, Neural Network Design, Nelson Candad, 2nd Edition, 2008.
6. S.N. Sivanandam & S.N. Deepa, Principles of Soft Computing, Wiley Publications, 2nd Edition, 2011.
7. S, Rajasekaran & G.A. Vijayalakshmi Pai, Neural Networks, Fuzzy Logic & Genetic Algorithms, Synthesis & applications, PHI Publication, 1st Edition, 2009.
8. Web references: www.myreaders.info/html/soft_computing.html

Teaching-Learning Strategies in brief

- Solve problems based on the basic & advanced concepts of the subject.
- Encourage to the students to ask more & more questions.
- Motivate to the students to develop critical & strategic thinking

Assessment methods and weightages in brief

1. Internal Assessment: 25 Marks
2. Semester Exam: 75 Marks
3. Assessments through Sessional, Assignments, Quizzes etc.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB GE 22
Title of the Course: Artificial Intelligence and Machine Learning
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)

COURSE LEARNING OUTCOMES (CLOs)

CLO1: Demonstrate fundamental understanding of the history of artificial intelligence (AI) and its foundations. . (Cognitive Level: Understand)

CLO2: Demonstrate awareness and a fundamental understanding of various applications of AI techniques in intelligent agents, expert systems, artificial neural networks and other machine learning models. . (Cognitive Level: Understand)

CLO3: Apply basic principles of AI in solutions that require problem solving, inference, perception, knowledge representation, and learning. . (Cognitive Level: Apply)

CLO4: Explain about the concepts of computational learning theory and dimensionality reduction. . (Cognitive Level: Analyse)

CLO5: Appreciate the underlying mathematical relationships within and across Machine Learning algorithms and the paradigms of supervised and un-supervised learning. . (Cognitive Level: Understand)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO10**	**PLO11**	**PLO12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1	1	3	3			2	2					1	2	1	2	1	1
CLO2		3	3		1	2		1		1	1				2	1	1
CLO3	1	3	3	3		3		1		1		2	2	1		2	2
CLO4		3	3			2	2		1			2	2			2	

Detailed Syllabus

Unit 1 **10 Hours**

Introduction – Definition – Future of Artificial Intelligence – Characteristics of Intelligent Agents – Typical Intelligent Agents – Problem Solving Approach to Typical AI Problems.

Unit 2 **10 Hours**

Problem Solving Methods – Search Strategies – Uninformed – Informed – Heuristics – Local Search Algorithms and Optimization Problems – Searching with Partial Observations – Constraint Satisfaction Problems – Constraint Propagation – Backtracking Search – Game Playing – Optimal Decisions in Games – Alpha – Beta Pruning – Stochastic Games.

UNIT 3 **10 Hours**

AI Applications – Language Models – Information Retrieval – Information Extraction – Natural Language Processing – Machine Translation – Speech Recognition – Robot – Hardware – Perception – Planning - Moving.

UNIT 4 **10 Hours**

Algorithmic models of learning, Learning classifiers, functions, relations, grammars, probabilistic models, value functions, behaviors and programs for experience. Bayesian, maximum some posterior, and minimum description length frameworks.

UNIT 5 **10 Hours**

Parameter Estimation, sufficient statistics, decision trees, neural networks, support vector machines, Bayesian networks, bag of words classifiers, N-gram models; Markov and Hidden Markov models, probabilistic relational models, association rules, nearest neighbor classifiers, locally weighted regression, ensemble classifiers.

Reference Books

1. Bishop, C. (2006). Pattern Recognition and Machine Learning. Berlin: Springer-Verlag.
2. S. Russell and P. Norvig, ―Artificial Intelligence: A Modern Approach‖, Prentice Hall, Third Edition, 2009.
3. Bratko, - Prolog: Programming for Artificial Intelligence, Fourth Edition, Addison-Wesley Educational Publishers Inc., 2011.

Teaching-Learning Strategies in brief

- For teaching, ICT tools have been used.
- Also, white board teaching had been done for explaining and clarifying many concepts and numericals.

Assessment methods and weightages in brief

- Internal Assessment: 25 Marks
- Semester Exam: 75 Marks
- Assessments through Sessional, Assignments, Quizzes etc.

Name of the Academic Program: M. Sc. (Computational & System Biology, and Bioinformatics)
Course Code: MCSB GE 23
Title of the Course: Bioinformatics tools and development
L-T-P: 3-1-0
Credits: 04
(L=Lecture hours, T=Tutorial hours, P=Practical hours)
COURSE LEARNING OUTCOMES (CLOs)

After completing this Course, the students should be able to:

CLO1: train how to use and development of the bioinformatics databases and tools. (Cognitive Level: Create)
CLO2: apply basic bioinformatic tools for DNA/RNA/protein sequence alignments. (Cognitive Level: Apply)
CLO3: find gene/protein homologs, design primers. (Cognitive Level: Apply)
CLO4: identify mutations, reconstructing phylogenetic trees, etc. (Cognitive Level: Analyse)

Mapping of Course learning Outcomes (CLOs) with Program Learning Outcomes (PLOs) and Program Specific Outcomes (PSOs)

	PLO1	**PLO2**	**PLO3**	**PLO4**	**PLO5**	**PLO6**	**PLO7**	**PLO8**	**PLO9**	**PLO10**	**PLO11**	**PLO12**	**PSO1**	**PSO2**	**PSO3**	**PSO4**	**PSO5**
CLO1		3	3	1		2	1				1		2		2	1	1
CLO2	2	3	3	1	1	2		2	1					1	2	1	1
CLO3	2	2	3			3					1	1	2			2	2
CLO4			3		1	1	1			2		2	1	1		2	

Detailed Syllabus

Unit 1 **10 Hours**

Introduction to Matlab, Matrix calculations, Functions. ENTREZ, NCBI, Genomic databases, Organism specific databases, BLAST, FASTA, Philipp, Prosite. Visualization: Chimera, Pymol, RasMol, Cn3D, discovery studio, Meastro Visulizer etc. Aligning nucleotide sequences; designing a degenerate primer of 20 bases from nucleotide

Unit 2 **9 Hours**

Alignment data and calculate the level of degeneracy of this primer.Exploring NCBI Resouces, GenBank; Molecular databases (sequence databases - nucleotides, proteins, structures, genes, expression, taxonomy; Marker databases – dbSNP, dbSTS, dbEST, Unigene), genomes and maps, tools (Entrez, BLAST, nucleotide sequence analysis, protein sequence analysis, 3-D structure display and similarity searching).

Unit 3 **9Hours**

Literature Databases (PubMed, PubMedCentral, OMIM, Books, Citation Matcher), research at NCBI, education, FTP site.

Unit 4 **10 Hours**

File format conversion: FmtSeq, ReadSeq, Sequence manipulation Suite.Mutation analysis tool: Dynamut, BioEdit etc.

Protein structures: Visualizing and analysis of inter atomic distances, H-bond calculations,secondary structure analysis and salt bridge analysis of protein structures using different software. Prediction of 3D structure of protein.

Unit 5 **10Hours**

Searching and retrieval of nucleotide sequences from GenBank database, Retrieval of protein sequences from "SWISS-PROT" database. Searching and retrieving the protein structure data using Entrez and protein viewing softwares. Database homology search of a nucleotide sequence using Blastn, Retrieval of related sequences in a given format.

Modeling solvers – Euler, Runge-Kutta, numerical integration.

References:

1. Jin Xiong: Essential Bioinformatics, Cambridge University Press Tramontano: Introduction to Bioinformatics, Chapman and Hall Series
2. https://www.ncbi.nlm.nih.gov/
3. https://www.rcsb.org/ Course outcome: Students should be able to apply basic bioinformatic tools for DNA/RNA/protein sequence alignments, finding gene/protein homologs, designing primers, identifying mutations, reconstructing phylogenetic trees, etc.

Teaching-Learning Strategies in brief

- Solve problems based on the basic & advanced concepts of the subject.
- Encourage to the students to ask more & more questions.
- Motivate to the students to develop critical & strategic thinking

Assessment methods and weightages in brief

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