

YENEPOYA

(DEEMED TO BE UNIVERSITY)
Recognized under Sec 3(A) of the UGC Act 1956
Accredited by NAAC with 'A' Grade

REGULATIONS AND CURRICULUM GOVERNING

MASTER OF SCIENCE (MSC.) IN COMPUTATIONAL BIOLOGY & BIOINFORMATICS (BY RESEARCH) PROGRAM

(Effective from Academic Year 2023-24)

Name of the Constituent Unit/Centre: Yenepoya Research Centre



YENEPOYA
(DEEMED TO BE UNIVERSITY)

Deralakatte, Mangalore, Karnataka.

NOTIFICATION FROM THE UNIVERSITY

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Part–A

General Introduction and Programme Outcomes

1. Preamble

The broad goal of teaching and training of postgraduate students in MSc. Computational Biology and bioinformatics (By Research) (Formerly MSc Computational Biology) is to enable students to acquire sound knowledge in the bioinformatics and biological data analytics and develop competent practical skills to contribute effectively in the fields of academics and research.

Yenepoya Research Centre (YRC) has established several research facilities and has accumulated expertise in the frontier areas of multidisciplinary sciences, such as, Computational biology, Bioinformatics, Genomics, Proteomics, Metabolomics, Molecular biology, Microbiology, Biotechnology and Nanobiotechnology. The MSc. courses are envisaged under the centre's vision of knowledge dissemination in the interdisciplinary areas for competency in research, academics and industry. Towards this vision, the centre has already established human resources and expertise needed to offer the postgraduate courses.

Master of Science (MSc) in Computational Biology and Bioinformatics (By Research) is a post-graduation programme under the Faculty of Science, of Yenepoya (Deemed to be University), Mangalore.

The students pursuing this programme shall develop an in-depth understanding of various data analytics platforms and their implementation in the field of modern biology. The interdisciplinary research and academic setting at the Yenepoya Research Centre offer additional advantage for the students to take courses from other postgraduate departments as part of the choice-based credit system. The curriculum relies on learning by real time experience using the different computational programs and biological data sets of high quality. The

programme is designed to inculcate research mind set to solve real life complex problems and offer simple and effective solutions.

Biological / Biomedical data analysis requires divergent expertise with adequate awareness on future perspectives. The students will experience world-class quality education with experienced faculty, cutting-edge technology and resources acquiring knowledge, skill and right attitude. The course curriculum is designed in consultation with eminent scientists, professionals, and industrial experts to help the students to learn advanced topics in computational biology and bioinformatics that will make them competent to grab the opportunities.

2. Introduction to MSc in Computational Biology and Bioinformatics (by Research)

Bioinformatics has experienced a significant boom in India over the past decade. The country has emerged as a major contributor in the field of bioinformatics, with a growing number of research institutes, academic programs, and industry collaborations focused on this area. With a growing biotechnology sector and strong IT infrastructure, India has become home to various initiatives and programs to promote bioinformatics research and development with Government and industry collaborations. This growth has resulted in a flourishing bioinformatics community, an increasing number of career opportunities for bioinformatics graduates and an increasing demand for skilled bioinformatics professionals in both academia and industry, both in India and abroad.

The MSc in Computational Biology and Bioinformatics (by Research) is a postgraduate degree programme offered in YRC, by Yenepoya (Deemed to be University), Mangalore that integrates principles from biology, computer science, and statistics to analyze and interpret biological data using computational methods. This interdisciplinary field focuses on developing and applying computational algorithms, tools, and models to understand complex biological systems and solve biological problems. The curriculum of the programme covers a wide range of topics including molecular biology, genetics, genomics, proteomics, algorithms, statistics,

data mining, machine learning, and programming languages. Students will learn how to integrate computational techniques with biological knowledge to analyze large-scale biological datasets, model biological processes, and make predictions. This research oriented will provide access to well- equipped laboratories and computational resources. Students can utilize advanced technologies, software tools, and high-performance computing infrastructure for data analysis, modelling, and simulations. This research-oriented programme is designed to provide students with hands-on training and an opportunity to apply computational methods to real-world biological problems. Working with experienced research faculty and industry professionals, the students will gain practical skills and experience to independently address biological data analysis.

The MSc Computational Biology and Bioinformatics (by Research) spans two years of study involving a strong foundation in both biological sciences and computational methods. It combines theoretical coursework, practical training, and research projects to equip students with the necessary attitude, skills and knowledge for a career in this rapidly growing field. The graduates of this programme will have diverse career opportunities to work in academia, research institutes, pharmaceutical companies,

biotechnology industries, government agencies, and other industries. Job roles may include bioinformatics analyst, computational biologist, data scientist, research scientist, or scientific software developer. Some students also pursue further studies at the doctoral level.

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3. Goals and Objectives

The overall goal of the MSc programme in Computational Biology and Bioinformatics(by Research) is to provide students with a strong foundation in bioinformatics, advanced research skills, and a deep understanding of the integration of biology and computational methods. The programme has been designed to provide students with in- depth knowledge, practical skills, and research experience in the field of bioinformatics. Here are the key goals and objectives of such a programme:

Advanced Knowledge in Bioinformatics: The programme aims to provide students with a comprehensive understanding of bioinformatics, including its underlying principles,

methodologies, and applications. Students will learn about biological databases, algorithms, statistical analysis, data mining, machine learning, and computational modelling techniques used in bioinformatics research.

Critical Thinking and Problem – Solving: The programme fosters critical thinking skills and problem-solving abilities in the context of bioinformatics. Students will learn to identify and address complex biological problems using computational approaches. They develop the ability to evaluate and apply appropriate bioinformatics techniques and tools to analyze biological data and generate meaningful insights.

Integration of Biology and Computational Methods: The programme aims to bridge the gap between biological sciences and computational methods. Students will learn to integrate biological knowledge with computational techniques to gain a deeper understanding of biological systems and processes. They will explore the use of computational models to simulate biological phenomena and make predictions.

Research Skills: The programme focuses on developing research skills necessary for independent investigation in bioinformatics. Students will learn how to formulate research questions, design experiments, collect and analyze biological data, interpret results, and draw meaningful conclusions. They gain proficiency in using computational tools, software packages, and programming languages commonly used in bioinformatics research.

Hands-on Research Experience: A significant objective of the programme is to provide students with hands-on research experience. Students will engage in research projects under the guidance of experienced faculty members as research mentors, allowing them to apply bioinformatics techniques to real-world problems. They gain practical experience in experimental design, data analysis, and scientific communication.

Collaboration and Interdisciplinary Skills: The programme aims to develop students' interdisciplinary skills, fostering effective communication, teamwork, and collaboration. Students will learn to work in multidisciplinary research environments with researchers from diverse backgrounds, including biologists, computer scientists, statisticians, mathematicians, and contributors to collaborative research projects.

Ethical and Responsible Conduct: The programme emphasizes the importance of ethical and responsible conduct in bioinformatics research. Students will learn about the ethical considerations associated with handling biological data, maintaining data privacy and security,

and complying with regulatory guidelines. They develop an understanding of the ethical implications of their research and learn to conduct research with integrity.

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4. Programme Educational Objectives

i. To provide a strong foundation in fundamental concepts, tools and resources in Computational Biology and Bioinformatics.

ii. To provide a sound foundation in biological data analytics

iii. To develop programming skills in languages such as Python and R: both theory and lab.

iv. To provide a strong foundation for high-throughput data analysis.

v. To introduce algorithms for analysis of biological data.

vi. To provide a foundation for machine learning

vii. To impart training in molecular modelling and simulations, structural biology, statistical and bioinformatic modelling and systems biology.

viii. To equip students with practical experience and prepare them for a career in either academia or industry

5. Programme Outcomes (PO)

Upon completion of the MSc. Computational Biology and Bioinformatics (By Research) programme, the students should be able to

PO1: Demonstrate the key concepts of molecular biology, genomics, proteomics, metabolomics and basics of programming languages (K)

PO2: Apply the acquired knowledge and skills in machine learning & artificial intelligence in nucleotide sequence data analysis and computer-aided drug designing. (S, A)

PO3: Make use of essentials of research methodology and biostatistics while implementing a research project. (K, S, A)

PO4: Interpret biological data sets using selected programming languages by effectively handling the machine generated and laboratory experimental data, and processing of biomedical images relevant to the biological science sector. (K, S, A)

PO5: Formulate research projects using robust research tools to produce new

knowledge. (K, S, A)

PO6: Take part in interdisciplinary scientific collaborations and discussions withexpertsoftherelatedfields(K,S,A)

K=Knowledge,S=Skill,A=Attitude

6. Learning Outcomes

i. Demonstrate proficiency in the core concepts of computational biology including database search, curation, database design and implementation, and basic mathematics and statistics.

ii. Demonstrate ability to apply skills in a real-life professional set-up through an industrial or academic internship in computational biology.

iii. Be able to effectively communicate scientific information in written and oralform and learn ethical considerations in scientific research.

7. Course learning outcomes:

In the MSc Computational Biology and Bioinformatics (by Research) programme, diverse courses are designed covering various aspects of computational biology as well as multi-omics technologies. Thus, each course has its own set of unique outcomes. The learning outcomes include knowledge in the core theoretical aspects as well as practical applications of the knowledge in the discipline. The outcomes from each course are defined so that the students satisfying the course and programme outcomes will be competitive in the current life sciences job market as well as in academia. Additionally, the elective courses and the supplementary courses on soft skills will broaden the multi-disciplinary knowledge of the student and will prepare the student for a successful career in the industry as well as in academia.

8. Teaching methods:

To ensure that the students are imparted with the knowledge and skills in the domain of Bioinformatics and Computational biology, a combination of both traditional learning as well as modern methods will be employed. These methods include:

Lectures using audiovisual mode (PowerPoint presentations)
Practical hands-on training of the theoretical aspects Seminars

and group discussions by the students

Peer-teaching methods

Research internships/Projects

9. Competencies of MSc. Computational Biology and Bioinformatics (by Research) graduate:

Knowledge:

- The graduates must be well-versed with the basic theoretical concepts and framework in the domains of Bioinformatics, Biostatistics, and Multi-Omics methodologies.
- Thegraduatesmustbefamiliarwiththefrequently-usedtoolsandtechniquesinthese disciplines.
- The graduates are expected to have at least a limited working knowledge of two or more computer programming languages.
- It is desirable for the graduates to be familiar with the state of the art in the above-mentioned fields.
- The graduates are expected to be familiar with the research methodologies and best practices employed in the academic research.
- The graduates are expected to be familiar with the basic concepts of research ethics and intellectual property.

Skills:

- Discipline-based skills: The graduates are expected to perform basic-level bioinformatics operations (sequence-search, homology modelling, interpretation of genomics, proteomics and metabolomics data etc.)
- Critical thinking skills: The graduates are expected to be familiar with different critical thinking methodologies that are required to perform research.
- Communication skills: The graduates are expected to effectively communicate their ideas/arguments to a wider audience, including those who are not familiar with the discipline.

This includes general communication skills as well as the ability of the graduate to clearly communicate the concepts associated with the computational biology discipline.

- Personality traits: Graduates are expected to develop basic personality traits that enable them to develop strong interpersonal relationships, such as time management, emotional intelligence, stress management, etc.
- Problem-solving skills: Graduates are expected to have the problem-solving skills that will be required in their careers in different domains including academia as well as industry.
- Research skills: The graduates are expected to leverage the critical thinking skills to effectively perform research projects in the computational biology domain.

Attitudes:

- Curiosity/Inquisitiveness: The graduates are expected to nurture their curiosity and apply it in the context of computational biology and bioinformatics.
- Teamwork: The graduates are expected to effectively collaborate and work as a team with other individuals, including those who are not familiar with the computational biology discipline.
- Ethics: The graduates must have the strong moral and ethical foundation to be responsible citizens of the country.
- Leadership: The graduates are expected to have basic leadership traits that will
  Enable them to successfully lead a team during the course of their careers.

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10. Qualification Descriptors:

At the end of two years:

i. Knowledge and skills for genomics involve applying computational tools, developing pipelines for next-generation sequencing (NGS) data analysis, and gaining insights into genomic information from DNA sequences.

ii. Performing data analysis requires proficiency in using computational tools like GraphPad Prism, R, and Python for statistical analysis, data manipulation, and scripting in bioinformatics.

iii. Investigating proteomics and mass spectrometry requires understanding the basics of computational proteomics, utilization of proteomic data analysis tools, and applying mass spectrometry for protein identification and characterization.

iv. Knowledge of basic sequence and structure-based bioinformatics concepts and techniques. Apply the techniques pertaining to sequence-search & identification and the techniques pertaining to the protein structure modelling,.

v. Exploring metabolomics and data analysis involves defining metabolites and metabolomics, analyzing metabolomics data using computational tools, and applying analytical methodologies for identifying potential drug metabolites.

vi. Applying artificial intelligence and machine learning involves understanding AI architectures, applying machine learning concepts for data analysis and prediction, and developing AI and ML models using Python or appropriate software.

vii. Understanding and applying statistical concepts involve defining population and sample, calculating appropriate sample size, estimating measures of central tendencies and dispersion, explaining basic concepts in probability theory, and constructing statistical hypotheses for biological data analysis.

viii. Performingdataanalysisusingcomputationaltoolsincludesusingdifferenttoolssuch as GraphPad Prism, R, and Python for statistical analysis, data manipulation, and scripting in bioinformatics.

ix. To be familiar with biomedical informatics and health applications, one shouldinvolve utilizing informatics tools for biomedical data analysis and visualization, applying image processing algorithms for medical decision-making, and gaining an understanding of different areas within health informatics.

11. Opportunities and Employability:

The MSc.Computational Biology and Bioinformatics (by Research) programme opens up a multitude of exciting opportunities and offers excellent employability prospects. In today's data-driven world, where the integration of biology and computer science is crucial, this programme equips students with the necessary skills to excel in the field. Graduates have a wide range of career options available to them, including positions in academic research institutions, pharmaceutical companies, biotechnology firms, healthcare organizations, and government agencies.

The programme's focus on cutting-edge genomic technologies and next-generation sequencing analysis (NGS) prepares students to tackle the challenges of deciphering genetic information and understanding its implications for various biological processes.

Furthermore, the emphasis on mass spectrometry-based proteomics analysis provides students with the expertise to analyze complex protein data and contribute to advancements in protein identification and characterization. With the increasing availability of large-scale biological datasets, the integration of big data using artificial intelligence (AI) and machine learning (ML) techniques is in high demand. Graduates of this programme are well-versed in these technologies, enabling them to tackle complex data analysis problems and derive meaningful insights.

Proficiency in programming languages like Python and R further enhances their capabilities in data manipulation and modeling, essential skills in the field of bioinformatics.

The programme also emphasizes computer-aided drug design (CADD), a critical area for thediscovery and development of new therapeutics. Graduates are equipped with the knowledge and tools to contribute to the design and optimization of drugs, offering promising opportunities in pharmaceutical research and development.

Additionally, the acquisition of skills in health informatics enables graduates to work on projects involving healthcare data analysis, contributing to the improvement of patient care and disease management. The programme also covers metabolomics, allowing students to identify potential drug compounds and contribute to the field of personalized medicine.

The multidisciplinary research methodology taught in this programme empowers graduates to approach complex biological problems from various perspectives, fostering innovation and collaboration.

Finally, the hands-on experience gained through research projects in a real-world setting ensures that graduates are ready to tackle the practical challenges they will encounter in their professional careers.

PartB:

General Regulations

2. Title of the programme:

Master of Science (MSc.) in Computational Biology & Bioinformatics (By Research)

3. Eligibility for admission:

Bachelor's degree in any branch of science/engineering/medicine with a minimum of 50% marks in aggregate. The selection of candidates shall be on a merit basis.

4. Duration of the programme:

Two years with four semesters.

5. Course pattern:

Choice-based credit System with 4 semesters

Total Credits: 96credits

Core courses: 54 credits, Open

selective: 6 credits,

Research Project:36credits

[1credit=1houroftheory/weekor2hoursofLaboratoryorpractical/week).

6. Type of Courses:

Core course: a course that should compulsorily be studied by a candidate as a requirement

Open Elective: Generally, a course which can be chosen from a pool of courses and which may be very specific or specialized or advanced or supportive to the discipline/ subject of study or which provides an extended scope or which enables an exposure to some other discipline or subject or domain or nurtures the candidate's proficiency skill. The open elective courses shall be offered in the second and third semesters only.

The list of open elective courses offered shall be displayed on the University website.

A student shall not take the courses offered by the department in which she/he is enrolled.

Students can opt for SWAYAM and other online courses of required credit as open electives

Registration for the open elective courses shall be at least one week prior to the commencement of the course.

7. Semesters:

An academic year shall consist of two semesters;

Odd Semester 1st&3rd	July/August to December/January
Even semester 2nd& 4th	January/February to June/July

8. Attendance:

- Each course (theory, practical, etc.) shall be treated as an independent unit for the purpose of attendance.

- A student shall attend a minimum of 80% of the total instruction hours in a course including tutorials and seminars in each semester to be eligible for appearing the university examinations

9. Assessment of a Course:

Evaluation for a course shall be done on a continuous internal assessments basis(CIA) followed by one semester end university examination (SEE) for each course. The weightage of CIA shall be 50% and SEE shall be 50%.

8.1Registering for examination: The candidates having ≥80% attendance in each of the courses and secured a minimum of 50% in CIA can only be qualified to appear for the SEE. The candidate shall register for all the courses of the semester when he/she appears for the examination of that semester for the first time.

8.2.Scheme of Examinations:

8.2.1. Internal Assessment: Internal assessment marks shall be the basis of seminars, class tests, and assignments. CIA for practical courses shall be based on the quality of the records/reports and performance in practical sessions. The CIA marks shall be communicated to the Controller of Examinations before the commencement of the University examinations.

Components of CIA	Details	Weightage
Sessional Tests	Average of the two tests	60%
Seminar/assignments	One Seminar/Assignment relevant to the core courses	30%
Quiz/Viva-voce/ others	Course-specific activities to assess the skills and attitude	10%

8.2.2 Semester End Examination:

There shall be examinations at the end of each semester for all the courses including theory and practical. The SEE durations shall be three hours. Research projects shall be assessed based on the dissertation reports and viva voce examination.

- Pattern of question paper for semester-end examination-Theory

Sl. No.	Questions and Criteria	No. of questionsX marks	Max marks
1	Questions to define or explain (related to understanding) (5outof7 questions)	5X2	10
2	Problems/concepts(related to Reasoning) (4 out of 5 questions)	4X5	20
3	Descriptive problems/questions(related to applications) (2 out of 3 questions)	2X10	20
4	TOTAL		50

- PatternforPracticalexamination(25 marks)

Sl. No	Questions and Criteria	No. of questions X marks	Max marks
1	Major: Apply complex computational tool to perform the analysis and report	1X10	10
2	Minor: Apply simple computational tool To perform the analysis and report	1X5	05
3	Class records	-	05
4	Viva	-	05
	TOTAL	-	25

8.2.3. Valuation of answer scripts/practical: Each theory course shall be evaluated by one internal and one external examiner. There shall be a third evaluation if the difference is more than 15%.

Practical examination shall be jointly conducted and evaluated by one internal examiner and

one external examiner.

8.2.4. Valuation of Project: The CIA marks (200) shall be allotted by the supervisor based on the work progress, attendance and attitude of the candidate.

SEE shall be based on the dissertation and the viva voce. Dissertation shall be evaluated by an external and internal examiner on the following criteria;

Sl.No	Key Criteria for Dissertation	Max marks
1	Outline of the work and adequacy of the methodology	20
2	Rationale of the study and contribution to skill enhancement	20
3	Appropriateness of data analysis tools applied	30
4	Quality of data interpretations and reporting style	30
TOTAL		100

Viva-voce: Viva voce shall be conducted by a Common Viva-Board consisting of internal examiner and one external expert as approved by the Controller of Examinations. Viva duration shall be of maximum one hour (40 minutes for presentation and 20 minutes for Q/A session).

Sl. No	Key Criteria for Viva	Max marks
1	Justification on the work done and its relevance	30
2	Knowledge on the subject	30
3	Communication skills, clarity of presentation and Overall attitude	40
TOTAL		100

10. Letter Grades

The results of successful candidates at the end of each semester shall be declared in terms of

Grade Point Average (GPA) and alpha sign grade. The results at the end of the fourth semester shall be classified on the basis of the Cumulative Grade Point Average (CGPA) obtained in all the four semesters and the corresponding overall alpha-sign grade. The letter grade as described below shall be adopted.

Letter Grade	Grade Point	Range of marks
O(Outstanding)	10	95-100
A+(Excellent)	9	85-94
A(Very Good)	8	75-84
B+ (Good)	7	65-74
B(Average)	6	55-64
P(Pass)	5	50-54
F (Fail)	0	Lessthan50
Ab(Absent)	0	-

11. Calculation of Cumulative Grade Point Average (CGPA):

The Cumulative Grade Point Average (CGPA) at the end of the fourth semester shall be calculated as the weighted average of the semester GPW. The CGPA is obtained by dividing the total of GPW of all four semesters by the total credits for the programme. The following is the sample illustration of computing semester grade point averages (GPA), cumulative grade point average (CGPA) and the letter grades assigned.

CGPARange	Letter Grade
9.50-10.00	O(Outstanding)
8.50–9.49	A+ (Excellent)
7.50-8.49	A(Very Good)
6.5–7.49	B+ (Good)
5.50–6.49	B(Average)
5.00–5.49	P(Pass)

<5.00	F (Fail)

12. Marks qualifying for a pass

i. A candidate shall be declared to have passed the PG programme if he/she secures at least a CGPA of 5.0 (Course letter Grade P) in the aggregate of both internal assessment and semester end examination marks.

ii. For each course the total of 100% is determined from the CIA evaluation and the SEE weighted at 50% and aggregate of CIA and SEE at 50% as minimum for pass.

iii. The candidates who pass all the semester examinations in the first attempt in two years are eligible for ranks provided they secure at least a CGPA of 7.0 (at least letter Grade B).

iv. The results of the candidates who have passed the fourth semester examination but not passed the lower semester examinations shall be declared as NCL (Not Completed Lower semester examinations). Such candidates shall be eligible for the degree only after completion of all the lower semester examinations.

v. A candidate who passes the semester examinations in parts is eligible for only CGPA and letter Grade but not for ranking.

vi. Carry over shall be allowed for candidate who failed in not more than two courses in a semester. Candidate who fails in any of the unit/project work/Project Report/ dissertation shall reappear in that unit/project work/Project Report/ dissertation and pass the examination subsequently.

13. Maximum period for completion of the Programme

A candidate shall complete the four semesters (two years) programme within four years from the date of admission. Students who wish to take career break can re-enrol themselves. The period of reentry should not be more than three consecutive years.

14. Courses and Scheme

Course name	Course type	Hrs/ Week	Exam hrs	CIA marks	SEE Marks	Max Marks	Credits
SEMESTER-1							
Informatics in Biology	T	4	3	50	50	100	4
Biostatistics	T	4	3	50	50	100	4
Python Programming	T	4	3	50	50	100	4
Artificial Intelligence and Machine learning	T	4	3	50	50	100	4
Cell and Molecular Biology	T	2	3	25	25	50	2
Bioinformatics and Biostatistics	P	4	3	25	25	50	2
Python Programming	P	4	3	25	25	50	2
Artificial Intelligence and Machine Learning	P	4	3	25	25	50	2
Total		30	-	300	300	600	**24**
SEMESTER-2							
Genomics and NGS analysis	T	4	3	50	50	100	4
Proteomics and drug design	T	4	3	50	50	100	4
Computational Metabolomics	T	4	3	50	50	100	4
Programming in R	P	6	3	25	25	50	3
Genomics and NGS analysis	P	4	3	25	25	50	2
Metabolomics	P	4	3	25	25	50	2
Proteomics and drug design	P	4	3	25	25	50	2
Open Elective	OE	3	3	50	50	100	3
Total		30	-	300	300	600	**24**
SEMESTER-3							
Research Methodology	T	4	3	50	50	100	4
Scientific Communication	T	3	3	50	50	100	3
Biomedical Informatics	P	4	3	25	25	50	2
Open Elective		3	3	50	50	100	3
Research Project–Phase1	Pr	24	1	125	125	250	12

Total		38	-	300	300	600	24
SEMESTER-4							
Research Project–Phase2	Pr	Full time	1	200	200	400	**24**

T-TheoryP-practical, OE-Open Elective, Pr -Project

PARTC Syllabus

FIRSTSEMESTER

COURSE NAME: BIOSTATISTICS (Credits4:56Hrs)

COURSE OUTCOME

CO1: Define population and sample, calculate an appropriate sample size, and estimate various measures of central tendencies and dispersion

CO2: Explain the basic concepts in probability theory and apply probability theories in biological data analysis

CO3: Describe various statistical tests, construct statistical hypotheses and apply proper statistical tests for biological data analysis

CO4: Differentiate between various association analysis and construct linear and non- linear models with biological data

COURSE CONTENTS

Unit1:

- Basic concepts of statistical mathematics: Matrices, Basic calculus: Differentiation and integration, Types of variables, population and sample, Accuracy and Precision
- Random sampling techniques
- Measures of centrality and measures of dispersion
- Descriptive statistics–central tendency and dispersion

Unit2:

- Probability
- Basic concepts of set theory
- Random variable
- Sample space and events,
- independent and mutually exclusive events,
- expected value
- additive and multiplicative rules
- conditional probability
- Bayes' theorem
- Probability distributions: Binomial, Poisson, Normal
- Skewness and Kurtosis

Unit3:

- Inferential statistics
- Hypothesis testing: null/alternative hypotheses

- Types of errors
- Size and power
- Parametric tests
- t-test: paired and independent
- Z-test
- ANOVA
- Non-parametric tests: Chi-square, Kruskal-Wallis test, Mann-Whitney U, and Wilcoxon signed-rank

Unit4:

- Organising and understanding multivariate data
- Visualisation of multivariate data
- Confusion matrix
- ROC analysis
- Covariance and covariance matrix
- Correlation coefficient and its significance
- Regression model
- Fitting linear regression
- PCA
- Eigenvalues and Eigenvectors
- HCA
- Survival Analysis

Books for reference:

1. M. Harris, G. Taylor &J. Taylor (2007), Maths & Stats for the life and medical sciences, Scion Publishing Ltd.

2. John Still well(2018), Elements of Mathematics from Euclid to Godel Princeton, University Press.
3. MendenhallR.J.Beaver&B.M.Beaver(2017), Introduction to Probability and Statistics, Cengage Learning Products.
4. IssacR.(1995), The Pleasures of Probability, Springer,Verlag.

COURSE NAME: INFORMATICS IN BIOLOGY (Credits:4:56hrs)Theory

COURSE OUTCOME

CO1: Explain the structure and functions of cells and subcellular processes

CO2: Outline the applications of computers and programming languages in biology

CO3: Illustrate basic concepts of Bioinformatics

CO4: Relate the usefulness of different biological databases for research and development

COURSE CONTENT

Unit1:

- Definition and properties of life
- Cellular nature of life
- Cell: the structural and functional unit of life
- Cell theory
- Types of cells
- Molecular architecture and components of cell
- Biomolecules and their properties
- Cellular metabolism/biochemical functions
- Development and differentiation
- Cell division-mitosis, meiosis

Unit2:

- Overview of a computing system. Different operating systems
- Modern Computing Paradigms: Workstations to Cloud Computing

- Computer Networking and Internet
- Network classification
- Introduction to Programming- High-level and Low-level programming
- Compilers and interpreters
- Popular programming languages

Unit3:

- Definition and overview of Bioinformatics
- History of Bioinformatics
- Scope of Bioinformatics
- Goals of Bioinformatics analysis
- Biological data
- Data retrieval system
- Different File formats (GenBank, FASTA etc.)

Unit4:

- Biological databases- structure and applications
- Types of biological databases
- Nucleotide sequence databases-Primary and Secondary nucleotide sequence databases
- Protein sequence and structured databases
- Small molecules databases

Books for Reference:

1. Karp G. (2016), *Cell and Molecular Biology: Concepts and Experiments*, John Wiley & Sons.
2. Kuriyan J., Konforti B., & Wemmer D. (2012), *The Molecules of Life: Physical and Chemical Principles*, Garland Science.

3. Pradip K. Sinha & Priti Sinha, *Information Technology (Theory and Practice)*, PHI Learning Pvt. Ltd.
4. Mount D. W. (2004), *Sequence and Genome Analysis. Bioinformatics*, Cold Spring Harbour Laboratory Press: Cold Spring Harbour.
5. Rastogi S. C., Mendiratta N., & Rastogi P. (2013), *Bioinformatics: Methods and Applications (Genomics, Proteomics and Drug Discovery)*, PHI Learning Pvt. Ltd.
6. Choudhuri S., & Kotewicz M. (2016), *Bioinformatics for Beginners: Genes, Genomes, Molecular Evolution, Databases and Analytical Tools*, Elsevier.

COURSENAME:BIOINFORMATICSANDBIOSTATISTICS

Credits2:56HrsPRACTICAL

COURSE OUTCOME

CO 1: Identify databases for retrieving biological data such as nucleotide and amino acid sequences

CO 2: Perform statistical analysis of biological data using different computational tools (GraphPad Prism and R)

COURSE CONTENT

This course includes hands on practical trainings on the topics as detailed in Theory courses Biostatistics and Informatics in Biology.

COURSENAME: PYTHONPROGRAMMING (Credits 4:56 Hrs) Theory

COURSE OUTCOME

CO1: Develop basic Python programming skills

CO2: Demonstrate the use of control structures for a task

CO3: Utilize different functions available in Python packages for data analysis

CO4: Apply Object-Oriented Programs and file handling for performing a wide range of operations

COURSE CONTENT

Unit1:

- Introduction to Python
- Overview of the Python language
- Uniqueness and features
- Basic Python syntax
- Comments
- Basic data types of Python
- Input/output and Control Structures
- Python operators
- Arithmetic operators
- String data processing
- String values and String special operators

Unit2:

- Python basic control structures
- if, if-else, elif – general format and multi-way branching
- For-/while-loops- general format
- examples based on processing natural number sequences

- Break
- continue and pass
- Concept of recursion
- Loop coding techniques

Unit3:

- Functions: Built-in functions and user-defined functions
- Tuples and dictionaries
- Creating module
- Python Packages (Data analysis and Visualisation) -basics of NumPy
- Matplotlib
- Biopython
- Pandas
- Python web framework-Django and Flask

Unit4:

- Object-Oriented Programming(OOP)using python
- Basics of OOP
- Properties and Methods
- Working with classes and Instances
- Inheritance
- Encapsulation
- Exception handling
- Working with files- txt/CSV files

Books for Reference:

1. TimJ.S., WayneB.(2015), Python Programming for Biology, Bioinformatics, and Beyond, Cambridge University Press.
2. Mark S. (2018), Programming in Python 3: A complete Introduction to the Python Language, 2nd Edition, Pearson Education.
3. DawsonM.(2010),PythonProgrammingfortheAbsoluteBeginner,3rdEdition, Cengage Learning.
4. Beazley, D. M. (2009), Python Essential Reference, Pearson Education.
5. TimJ.S., WayneB.(2015), Python Programming for Biology, Bioinformatics, and Beyond, Cambridge University Press.

COURSE NAME: PYTHON PROGRAMMING (Credits2:56Hrs)Practical

COURSE OUTCOME

CO 1: Make use of Python language to process biological sequences (nucleotideand amino acids)

CO 2: Develop Python scripts for analysis of biological data to provide meaningful information

COURSE CONTENT

This course includes hands-on practical training on the topics as detailed in the Theory course on Python Programming

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COURSE NAME: ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING

COURSE OUTCOME

CO1: Demonstrate architectures and working of AI

CO2: Develop the basic concepts of Machine Learning to perform actions such as predictions, estimations, and recommendations

CO3: Construct neural networks using Python or any other appropriate software

CO4: Make use of neural networks for image processing

COURSE CONTENT

Unit1:

- Introduction to Artificial Intelligence(AI)
- Overview and branches of AI
- Machine learning as a subset of AI
- Types of learning(supervised ,semi-supervised, unsupervised and transfer learning)
- Supervised learning(linear regression,Logistic regression, KNN and SVM)
- Unsupervised learning(k-means clustering)
- Concepts of learning

Unit2:

- Introduction to Machine Learning(ML)
- Major ML approaches
- Major ML problem categories
- Classification
- Regression and Clustering
- LearningProcess(labels,training,testing,under-fittingandover-fitting)
- Performance measures for ML models (accuracy, sensitivity, specificity, precision, f1 score, AUCand ROC)
- Cross-validation

Unit3:

- Artificial Neural Networks(ANNS)
- Evolution of ANNs
- Comparison of human brain and ANN
- Learning Process (Feature extraction, Labelling, Training, and Testing)
- Perceptron (artificial neurons, Linear and non-linear problem spaces, Bias, Learning as adjusting weights, Gradient descent for percept, Limitations of perceptron)
- Feedforward and feedback networks
- Self-organizing networks

Unit4:

- Basic concepts of image processing
- Concept of image filtering
- Transforms
- Enhancement
- Restoration
- Feature Extraction and reconstruction
- Convolution Neural Networks(CNNS) –basics and architecture
- CNN for deep learning

Books for Reference:

1. Mitchell T.M.(2013), Machine learning, McGraw-Hill, InternationalStudentEdition.
2. AlpaydinE.(2020),"Introduction to Machine Learning", MIT Press.
3. Kulkarni, P. & Joshi P. (2015), Artificial intelligence: building intelligent systems, PHI Learning Pvt. Ltd.
4. Heaton,J.(2013).Artificial Intelligence for Humans, Volume1:FundamentalAlgorithms. CreateSpace Independent Publishing Platform.

COURSE NAME: ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING

Credits2:56Hrs) Practical

COURSE OUTCOME

CO 1: Develop artificial intelligence and machine-learning models for analysing biological data

CO 2: Apply appropriate algorithms for generating Artificial Intelligence and Machine learning models

COURSE CONTENT

This course includes hands on practical trainings on the topics as detailed in Theory course on ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING

COURSENAME:CELLANDMOLECULARBIOLOGY(Credits2:28Hrs)

Theory

COURSE OUTCOME

CO1: Explain the basic principles of genetics

CO2: Illustrate central dogma of molecular biology

CO3: Explain the concept of biological pathways (Immune response, metabolic and disease pathways)

COURSE CONTENT

Unit1:

- Genes and inheritance

- Gene regulation
- Genotype and phenotype
- Genestructure and regulation
- Evolution at the molecular level
- Mutations Epigenetics
- Genetic basis of disease

Unit2:

- Transcription and its regulation, RNA polymerase, transcription factors
- Posttranscriptional modification
- Genetic Code, triplet code, incorporation of novel amino acids
- Translation–initiation, elongation, termination of protein synthesis
- Posttranslational modifications of proteins

Unit3:

- Biological Pathways, cycles, and networks
- Gene regulatory and protein interaction/signalling networks
- Homeostasis and feedback/forward loops
- Network modules/ topology
- Metabolic pathways and pathways of immune response

Books for Reference:

1. KarpG.(2016),Cell and Molecular Biology: Concepts and Experiments,John Wiley&Sons.
2. Russell P.J.(2004).Cell and Molecular Biology. Cengage Learning India Private Ltd.
3. Hausman R.E.,& Cooper G.M.(2004).The Cell: a molecular approach.ASM, Washington, DC.

4. Jogd and S.N.(2009).Gene Biotechnology. Himalaya Publishing house.
5. Nelson D.L., Lehninger A.L., & Cox M.M. (2008), Lehninger principles of Biochemistry, Macmillan.

SECOND SEMESTER

COURSENAME: GENOMICS AND NGS ANALYSIS (Credits 4:56Hrs)

Theory

COURSE OUTCOME

CO1: Analyse DNA sequence data using basic computational genomic tools

CO2: Illustrate different sequence alignment tools and their relevance in data analysis

CO3: Develop Pipelines for NGS data analysis

CO4: Construct RNA-Seq Pipeline

COURSE CONTENT

Unit1:

- Genes and genomes
- Gene/genome database
- NGS–shotgun sequencing
- De-novo and re-sequencing
- Assembly and annotation
- ORF

- Transcriptional
- Translational and splicing signals
- Gene finding
- Gene function prediction
- Transcription factor binding site identification

Unit2:

- Sequence alignment, Pair-wise, multiple, global, local alignment
- Scoring matrices
- Homology
- Clustering and phylogeny
- Phylogenetic tree
- Different types of phylogenetic trees and Tree Construction methods
- RNA structure prediction
- Gene expression databases
- Gene regulation network analysis
- Comparative genomics
- Population and personal genomics in medicine

Unit3:

- Next-generation sequence analyses
- Data format
- Quality control
- Mapping–short-read alignment
- Short/longreads

- Denovo alignment
- Indexing
- Analysis pipelines
- Whole-genome sequencing
- Read depth and seq coverage
- Variant calls
- Indels
- Structural variations

Unit4:

- NGS analysis of cancer samples–DNA-seq
- RNA-seq and Methyl-seq
- ChIP-seq analyses–DNA/RNA protein interaction
- Expressed sequence tags and sequence polymorphisms
- Exome sequencing
- Small RNA-seq

Books for Reference:

1. PevsnerJ.(2009).Bioinformatics and Functional Genomics.JohnWiley & Sons
2. RastogiS.C., MendirattaN.,&RastogiP.(2013). Bioinformatics: Methods and Applications: (Genomics, Proteomics and Drug Discovery). PHI Learning Pvt. Ltd.
3. WangX.(2016),"Next-generation sequencing data analysis", CRC Press.
4. Sablok G., Kumar S., Ueno S., Kuo J., & Varotto C. (Eds.) (2015), "Advances in the understanding of biological sciences using next generation sequencing (NGS) approaches", Springer International Publishing.
5. Mandoiu I., & Zelikovsky A. (2016), "Computational methods for next generation sequencing data analysis", John Wiley & Sons.

COURSE NAME: GENOMICS AND NGS ANALYSIS (Credits 2:56Hrs)

Practical

COURSE OUTCOME

CO1: Make use of appropriate tools for Genomics and NGS data analysis tools

COURSE CONTENT

This course includes practicals from topics as detailed in the theory course GENOMICSAND

NGSANALYSIS

COURSE NAME: PROTEOMICS AND DRUG DESIGN (Credits 4:56Hrs)

Theory

COURSE OUTCOME

CO1: Explain the basics concepts of Computational Proteomics

CO2: List different protein databases and tools

CO3: Illustrate the applications of Mass-spectrometry in Proteomics

CO4: Make use of molecular docking and dynamics for *insilico* drug discovery

COURSE CONTENT

Unit1:

- Protein-Basics
- Types of proteins and examples
- Primary structure-basic structure of amino acids
- Classification of Amino Acids
- Primary, secondary, tertiary, and quaternary structures of proteins
- Protein stability, folding and denaturation
- Active site and allosteric site of protein
- Protein sequence and functional analyses
- BLAST
- Scoring matrix

- Pairwise and multiple alignments
- Motifs and domains

Unit2:

- Protein visualization tools (Pymol, Swiss PDB Viewer)
- Protein databases (UniProtKB, Interpro, PDB, PIR, SCOP, CATH, ProDom, Pfam, AlphaFold)
- Protein structure prediction
- Basics of NMR and X-ray crystallographic concepts
- Computationalapproachforproteinstructureprediction(ChouFasmanmethod, Homology modelling, Ab initio prediction and Threading)
- Protein-protein interaction
- PPI databases
- Protein signaling network analysis

Unit3:

- Proteins and proteomics
- Mass-spectrometry–different mass analyzers
- Label-free quantitative proteomics
- Ion and spectral counts
- Exploratory and quantitative proteomics–SILAC
- iTRAQ
- TMT
- 18Olabelling
- Differential Proteomics
- Post-translational modifications

- Un-targeted proteomics
- Clinicalproteomics
- Proteogenomics

Unit4:

- Molecular Concept of Disease
- Types of diseases
- Molecular targets
- Molecular and chemical properties of drugs (Lipinski's rule of five)
- Ligands and leads
- Drug discovery pipeline
- Molecular docking
- Structure-based & ligand based approaches
- QSAR
- ADMET
- Concept of Molecular Dynamics
- VMD and NAMD
- Atomic interactions, force field, salvation boundary conditions
- Quantum Mechanics methods

Books for Reference:

1. Orengo C., Jones, D.T.,& Thornton, J.M.(2003).Bioinformatics: Genes, proteins and computers. Garland Science.
2. Palzkill T.(2002).Kluwer. Proteomics. Springer.
3. DeHoffmann,E.,& Stroobant,V.(2007). Mass spectrometry: principles and applications. John Wiley & Sons.
4. BourneP & WeissigH(2003).Structural Bioinformatics, John Wiley & Sons, Inc

COURSE NAME: PROTEOMICSANDDRUGDESIGN(Credits2:56Hrs)

Practical

COURSE OUTCOME

CO1: Make use of appropriate tools for proteomic data analysis

CO2: Utilize appropriate molecular docking and dynamics for in silico drug design

This course includes practicals from topics as detailed in theory course PROTEOMICS AND DRUG DESIGN CB-CC-203

COURSE NAME: COMPUTATIONAL METABOLOMICS (Credits 4:42Hrs)

Theory

COURSE OUTCOME

CO1: Define Metabolites and metabolomics

CO2: Explain about various types of platforms used in metabolomics

CO3: Identify the metabolites from the metabolomics data using computational tools

CO4: Outline different analytical methodologies used in metabolomics

COURSE CONTENT

Unit1:

- Metabolites and metabolomics
- Extraction, derivatisation, and GC-MS quantification
- General workflow including quenching and sample preparation

- Different solvent systems for metabolite extraction
- Workflow for Lipidomics

Unit2:

- LC optimisations and modes of data acquisition: Positive and negative polarities
- Gradient selection
- Types of columns
- Column and pore size
- Data acquisition quality
- QA/QC

Unit3:

- Data analysis-Data repositories
- Introduction to Peak Detection
- Retention time alignment; identification of molecular features and metabolites
- Structural confirmation of metabolites
- Data analysis tools (MZmine, MS2compound)
- Metabolic pathways and inborn errors of metabolism
- Statistical methods most applied for analysis of metabolomics data (PCA, PLS, PLS-DA)

Unit4:

- Analytical methodologies
- Case studies on measurement methods to carry out basic experimental design for a given biological and biomedical problem and outline their applications
- Targeted vs. untargeted metabolomics
- Integrative analysis of the metabolome with genomics, transcriptomics and proteomics

data

- Comparative analysis between various metabolite repositories and databases

Books for Reference:

1. Fan T. W. M., Andrew N. and Richard M. (2012). The Handbook of Metabolomics. Humana Press.

2. Lindon J. C., Nicholson J. K., Holmes E. (2007). The Handbook of Metabonomics and Metabolomics. Elsevier.

3. Shuzhao Li (Ed.). (2020). Computational Methods and Data Analysis for Metabolomics. Humana, New York.

4. Wehrens R., & Salek R. (Eds.). (2019). Metabolomics: Practical Guide to Design and Analysis. CRC Press.

COURSE NAME: METABOLOMICS (Credits:2:56Hrs)

Practical

COURSE OUTCOME

CO 1: Identify the key metabolites form the given metabolomic data set using analytical tools

COURSE CONTENT

This course includes practicals from topics as detailed in theory course on COMPUTATIONAL METABOLOMICS.

COURSENAME:PROGRAMMINGINR (Credits:3:84Hrs)

Practical

COURSE OUTCOME

CO1: Explain concepts of data analysis using R programming

CO2: Make use of R packages for statistical analysis

CO3: Develop R scripts for data analysis

COURSE CONTENT

Unit1:

- Introduction and Features of R
- Significances of R. Rstudio
- Basic datatypes. Operators
- Data Structures. Control Statements
- Functions-Built-in and user-defined functions
- Data management using R
- File handling in R

Unit2:

- Statistics using R
- Basic statistical operations (mean, median, range, minima, maxima, variance, standard deviation, correlation coefficient, and covariance

Unit3:

- Basic graphics functions in R
- Packages in R
- Bioconductor Packages (biological sequence data handling
- Applications of R in Computational Biology (Sequence alignment, Phylogenetic tree

construction and Computational gene finding

Books for Reference:

1. Gentleman R. (2008), "R Programming for Bioinformatics", CRC Press.
2. Vries A., Meys J. (2012), "R Programming for Dummies", Wiley India.
3. Keen K. J. (2010), Graphics for Statistics and Data Analysis with R, CRC Press.
4. Nina Zumel, John Mount. (2014), Practical Data Science with R, Manning Publications.

COURSE TYPE: OPEN ELECTIVE

Credits 3

Students can enrol for any three-credit course either through SWAYAM or offered by other departments.

COURSE NAME:RESEARCH METHODOLOGY (Credits3:42Hrs)

COURSE OUTCOME

CO1: Illustrate research designs and its applications

CO2: Contrast among different experimental designs based on applications

CO3: List regulatory bodies and their role in promoting ethical practices in research

CO4: Outlined different forms of Intellectual Property Rights and their importance in research

COURSE CONTENT

Unit1:

- Definition of Research and Objectives
- General Characteristics of Research
- Types of Research
- Research Approach: Qualitative and Quantitative
- Significance of Research
- Research and Scientific Methods
- Important Research designs: Experimental (randomized, non-randomized, single blind and double blind)
- Observational research design (cross-sectional, prospective, retrospective, and case control)

Unit2:

- Concept and Identification of Research Problem
- Understanding lacunae in research
- Defining a research problem
- Literature review
- Typesofresearch articles
- Search tools (Databases, PubMed, Google Scholar, Keyword search)
- Basis of systematic review(filtering criteria)
- Research Questions and Hypothesis: Basis and characteristics for a good hypothesis

Unit3:

- ICMR Guidelines: National Ethical Guidelines for Biomedical and Health Research Involving Human Participants

- Declaration of Helsinki Ethical Principles for Medical Research Involving Human Subjects
- CPCSEA guidelines for use of animals in research
- Central Drugs Standard Control Organization (CDSCO)
- National Guidelines for Stem Cell Research (ICMR and DBT)
- DBT Guidelines for Biosafety
- GLP guidelines (OECD)

Unit4:

- Definitions of different forms of IP
- Patent, designs, trademarks, copyright, trade secrets: IPR- intellectual property rights and patent law
- Commercialization
- Trade-related aspects of intellectual property rights(TRIPS)
- Inventions and patents key differences
- Understanding the inventorship
- Ownership and rights, Royalty, Novelty
- Inventive step and industrial applicability
- Introduction to patent specifications; provisional and complete specifications
- Patent filing procedure
- Patent-granting organisations
- Geographical indications in patent
- Copyright and Plagiarism
- Entrepreneurship ecosystem in India; Start-up India and other initiatives

Books for Reference:

1. Grey D E(2014).Doing research in the real world. SAGE.
2. Popper K(2002).The logic of scientific discovery. Routledge Classics.
3. Quinn GP, Keough MJ (2002). Experimental design and data analysis for biologists. Cambridge University Press.
4. Singh YK (2006). Fundamentals of research methodology and statistics. New Age International Publishers.

COURSE NAME: BIOMEDICAL INFORMATICS (Credits2:56Hrs)

Practical

COURSE OUTCOME

CO1: Define the scope of biomedical informatics

CO2: Make use of informatics tools to perform biomedical data analysis, including data visualisation

CO3: Illustrated different areas of health informatics

CO4: Apply image processing tools/algorithms for extracting features from medical images that can aid in decision-making in health care

COURSE CONTENT

Unit1:

- Biomedical informatics–basics
- Electronic medical records
- Communication technology and health data integration
- Big data in medical informatics
- Biomedical information retrieval–text and image-based

- Natural language processing
- Visualization

Unit2:

- Problem-solving and decision-making
- Probabilistic clinical reasoning
- Areas of health informatics–neuroinformatics, public health informatics

Unit3:

- Predicting clinical outcome
- Real-time prediction
- Tracking epidemics
- Biomedical imaging information
- Radiology image analysis
- Neuro-image processing

Books for Reference:

1. Shortliffe E. H., Cimino J. J. (2014). Biomedical Informatics. Springer.
2. Sullivan F., Wyatt J. C. (2006). ABC of Health Informatics. Blackwell Publishing.
3. Verma A., Singh A. (2013). Principles of Biomedical Informatics. Elsevier Inc.
4. Shortliffe E. H., Shortliffe E. H., Cimino J. J., & Cimino J. J. (2014). Biomedical Informatics: Computer Applications in Health Care and Biomedicine. Springer.

COURSE NAME: SCIENTIFIC COMMUNICATION (Credits4:56Hrs)

COURSE OUTCOME

CO1: Explain the research and good laboratory practices

CO2: List advanced software tools for the maintenance of scientific records

CO3: Extend their communication skills and provide them a platform to overcome their shortcomings and strengthen them to face the competitive world

CO4: Outline about innovations, entrepreneurship, startup companies, and product development

COURSE CONTENT

Unit1:

- The review of literature–Approaches to research
- Use of the search engines such as PubMed, Scopus, and ScienceDirect, etc.
- Planning the research-Development of hypothesis and research ideas
- Designing research work or projects
- Selecting methods of data collection
- Organising the research notes and logbooks-Interpretation of results
- Ethics and integrity in research
- Learning Good Laboratory Practices (GLP)

Unit2:

- Writing research and review paper
- Documenting the paper
- Drafting and revising
- Preparing the final draft

- Essentials of manuscript communication to journals
- Powerpoint presentation
- Presenting the scientific findings in front of scientific peers
- Presenting the oral poster presentation in symposium and conference
- Attending the webinars, TED talks, podcasts etc.

Unit3:

- Learning and utilisation of advanced software such as EndNote, Adobe Photoshop, Origin Lab, Sigma Plot, and Graph Pad Prism etc.
- Development of quality figures for publications, research proposals, and presentations-Introduction to Microsoft Offices (Word, Excel and PowerPoint)
- Creative writing and publishing
- How to write a research proposal

Unit4:

- Building a motivated research collaboration among the researchers and expertise in the similar research field
- Social interaction–Developing self in work and career
- Management in health,mindfulnessandtime
- Prepare and attend the research job interview-Preparation of resume
- Do and Don’ts-Innovation and entrepreneurship
- Industrial visits
- Conducting research-based projects
- Developing start-up companies

Books for Reference:

1. Bell, Judith, Waters, and Stephen (2014). Doing Your Research Project: A Guide for First-Time Researchers. McGraw-Hill Open University Press.
2. Boffito, Daria C., Patience, Gregory S., Patience, and Paul A. (2015). Communicate Science: Papers, Presentations, and Posters Effectively. Academic Press.
3. Specht, J. (2017). Personality Development Across the Lifespan. Academic Press.
4. Victoria E., and McMillan (2011). Writing Papers in the Biological Sciences. Bedford St. Martin's Macmillan.

COURSENAME: OPENELECTIVE (Credit3)

Student can enroll for any three credit course either through SWAYAM or offered by other departments.

COURSE NAME:RESEARCH PROJECT PHASEI (Credits:12)

COURSE OUTCOME

CO1: Experiment with research problem using acquired domain knowledge and skills

CO2: Build research project management skills (teamwork, communication, analytical reasoning) and report writing

SHORT-TERMPROJECT

The student will complete an individual short-term project within this semester including literature review, research design, and carry-out research work by preparing short research report. The short-term project work must utilize computational skills that are learned in the previous semesters.

Students are encouraged to complete their project in collaboration with an outside organization

in order to gain experience with different work culture. Every month, students must submit a work progress report and also keep a lab note with daily updates.

EVALUATION CRITERIA	EVALUATIONCOMPONENTS
1. PROJECT MANAGEMENT	• Lab Notebook • Work Progress Reports
2.PROJECT REPORTING : Originality	• Project report • Plagiarism verification report
3.TECHNICALWORK	• Meeting the Objectives • Update with relevant literature • Application of data analysis tools • Data interpretation • Demonstration of Results
4.COMMUNICATION SKILLS	• Presentation skills • Communication with the team members (feedback from the team members) • Scientific report writing

FourthSemester

COURSE NAME: RESEARCH PROJECT PHASEII (Credits:24)

Students can opt for internal or external organization for taking up the research project. Students should submit monthly progress report and maintain a log book. The data and the outcome of the project can be prepared as a manuscript and submitted to the supervisor. The final project report shall include the following sections Introduction, review of literature, materials and

methods, results, discussion, conclusion and references. At the end of the programme, the students are expected to submit a thesis and defend their dissertation during a presentation in the presence of a panel of examiners. An open presentation and/or poster session is arranged where students present their results and get feedback from peers and faculties of the institute.

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PartD: CO-PO mapping

Sem	Course	COs	PO1	PO2	PO3	PO4	PO5	PO6
I	Biostatistics	CO1	Slight	Slight	Substantial	Moderate	Substantial	Moderate
		CO2	Slight	Slight	Substantial	Moderate	Substantial	Moderate
		CO3	Slight	Slight	Substantial	Moderate	Substantial	Moderate
		CO4	Slight	Slight	Substantial	Moderate	Substantial	Moderate
	Bioinformatics and Biostatistics (P)	CO1	Substantial	Moderate	Substantial	Substantial	Substantial	Moderate
		CO2	Substantial	Moderate	Substantial	Substantial	Substantial	Moderate
	Python Programming	CO1	Substantial	Substantial	Slight	Substantial	Moderate	Moderate
		CO2	Substantial	Substantial	Slight	Substantial	Moderate	Moderate
		CO3	Substantial	Substantial	Slight	Substantial	Moderate	Moderate
		CO4	Substantial	Substantial	Slight	Substantial	Moderate	Moderate
	Python Programming(P)	CO1	Substantial	Substantial	Slight	Substantial	Moderate	Moderate
		CO2	Substantial	Substantial	Slight	Substantial	Moderate	Moderate
	Artificial Intelligence and Machine Learning	CO1	Moderate	Substantial	Slight	Slight	Moderate	Substantial
		CO2	Moderate	Substantial	Slight	Slight	Moderate	Substantial
		CO3	Moderate	Substantial	Slight	Slight	Moderate	Substantial
		CO4	Moderate	Substantial	Slight	Slight	Moderate	Substantial
	Artificial Intelligence and Machine Learning (P)	CO1	Moderate	Substantial	Slight	Slight	Moderate	Substantial
		CO2	Moderate	Substantial	Slight	Slight	Moderate	Substantial
	Informatics in Biology	CO1	Moderate	Slight	Slight	Substantial	Substantial	Moderate
		CO2	Moderate	Slight	Slight	Substantial	Substantial	Moderate
		CO3	Moderate	Slight	Slight	Substantial	Substantial	Moderate
		CO4	Moderate	Slight	Slight	Substantial	Substantial	Moderate
		CO1	Substantial	Slight	Slight	Slight	Moderate	Moderate

	Cell and Molecular Biology	CO2	Substantial	Slight	Slight	Slight	Moderate	Moderate
		CO3	Substantial	Slight	Slight	Slight	Moderate	Moderate

II	Genomics and NGS analysis	CO1	Substantial	Moderate	Slight	Moderate	Slight	Substantial
		CO2	Substantial	Moderate	Slight	Moderate	Slight	Substantial
		CO3	Substantial	Moderate	Slight	Moderate	Slight	Substantial
		CO4	Substantial	Moderate	Slight	Moderate	Slight	Substantial
	Genomics and NGS analysis(P)	CO1	Substantial	Moderate	Slight	Moderate	Slight	Substantial
	Proteomics and Drug Design	CO1	Substantial	Slight	Slight	Moderate	Slight	Moderate
		CO2	Substantial	Slight	Slight	Moderate	Slight	Moderate
		CO3	Substantial	Slight	Slight	Moderate	Slight	Moderate
		CO4	Substantial	Slight	Slight	Moderate	Slight	Moderate
	Proteomics and Drug Design(P)	CO1	Substantial	Slight	Slight	Moderate	Slight	Moderate
		CO2	Substantial	Slight	Slight	Moderate	Slight	Moderate
	Computational Metabolomics	CO1	Substantial	Slight	Slight	Moderate	Slight	Moderate
		CO2	Substantial	Slight	Slight	Moderate	Slight	Moderate
		CO3	Substantial	Slight	Slight	Moderate	Slight	Moderate
		CO4	Substantial	Slight	Slight	Moderate	Slight	Moderate
	Metabolomics(P)	CO1	Substantial	Slight	Slight	Moderate	Slight	Moderate
	Programming in R(P)	CO1	Slight	Moderate	Substantial	Moderate	Substantial	Substantial
		CO2	Slight	Moderate	Substantial	Moderate	Substantial	Substantial
		CO3	Slight	Moderate	Substantial	Moderate	Substantial	Substantial
III	Research Methodology	CO1	Slight	Slight	Substantial	Moderate	Substantial	Moderate
		CO2	Slight	Slight	Substantial	Moderate	Substantial	Moderate
		CO3	Slight	Slight	Substantial	Moderate	Substantial	Moderate
		CO4	Slight	Slight	Substantial	Moderate	Substantial	Moderate
	Biomedical Informatics(P)	CO1	Slight	Substantial	Slight	Moderate	Moderate	Substantial
		CO2	Slight	Substantial	Slight	Moderate	Moderate	Substantial
		CO3	Slight	Substantial	Slight	Moderate	Moderate	Substantial
		CO4	Slight	Substantial	Slight	Moderate	Moderate	Substantial

	Scientific Communication	CO1	Slight	Slight	Moderate	Moderate	Moderate	Substantial
		CO2	Slight	Slight	Moderate	Moderate	Moderate	Substantial
		CO3	Slight	Slight	Moderate	Moderate	Moderate	Substantial
		CO4	Slight	Slight	Moderate	Moderate	Moderate	Substantial
	Research Project Phase I	CO1	Moderate	Moderate	Substantial	Substantial	Substantial	Substantial
		CO2	Moderate	Moderate	Substantial	Substantial	Substantial	Substantial
IV	Research Project Phase II	CO1	Moderate	Moderate	Substantial	Substantial	Substantial	Substantial