



AMRITA
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Program

M. Sc. (Master of Science) in Bioinformatics

Faculty of Sciences

[Revised 2017-2018]

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Programme Outcome

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

Programme Specific Outcome

The postgraduate program in Bioinformatics (MSc Bioinformatics) offers science graduates a conceptual understanding of the objectives and limitations of both computer and biological sciences disciplines, along with the knowledge to make use of computational tools for acquisition, storage, analysis and visualization of biological data. This way the program essentially aims to be a solid stepping stone for a career either in academia or in industries involved in the R&D of biomedicine, environment, food, beverage, etc. The first two semesters, along with the basics of bioinformatics and programming concepts, focus on introductory courses on cell and molecular biology, evolution, chemistry, mathematics and statistics to bring uniformity in foundation across students from diverse disciplines, such as biology, physics, chemistry, computer science, engineering, etc. The third semester deals with critically advanced areas of bioinformatics such as comparative evolutionary genomics, mathematical modelling of biomolecules, mass spectrometry and proteomics, computer-aided drug-design, along with two electives to be selected from a list of cutting-edge topics, e.g. systems biology, next generation sequencing data analysis, computational neuroscience, metagenomics and microbiome, big data solutions in bioinformatics, etc. Each of these subjects individually has the capacity to lead the students toward their excellence in academic or industrial research and product development. The specific interest of every student is further nourished through the final dissertation semester in the student's selected area of research, either under the supervision of in-house faculty members or in high-quality research labs outside in India or abroad, thereby making the candidate ready for the world in the field of bioinformatics.

Curriculum Structure

| Semester 1 | | | |
|----------------------|--------------------|---|----------------|
| Sl.No | Course Code | Course Name | Credits |
| 1 | BIF410 | INTRODUCTION TO BIOINFORMATICS | 3 |
| 2 | BIF413 | PROGRAMMING CONCEPTS | 3 |
| 3 | BIO421 | CELL BIOLOGY | 3 |
| 4 | BIO425 | MOLECULAR BIOLOGY FOR BIOINFORMATICS | 3 |
| 5 | BIO410 | ENERGY AND INTERACTION IN BIOLOGICAL MODELING | 3 |
| 6 | BIF402 | DATABASE DESIGN AND IMPLEMENTATION FOR BIOINFORMATICS | 3 |
| 7 | BIF487 | PROGRAMMING FOR BIOINFORMATICS -LAB | 1 |
| 8 | BIF486 | BIOINFORMATICS TOOLS-LAB | 1 |
| 9 | BIF488 | DATABASE DESIGN FOR BIOINFORMATICS -LAB | 1 |
| 10 | SSD401 | CULTURAL EDUCATION | 1 |
| 11 | SSD401 | SOFTSKILLS | 1 |
| Total Credits | | | 23 |

| Semester 2 | | | |
|-------------------|--------------------|--|----------------|
| Sl.No | Course Code | Course Name | Credits |
| 1 | BIF409 | STRUCTURAL BIOINFORMATICS | 4 |
| 2 | BIF417 | MOLECULAR SEQUENCE ANALYSIS | 4 |
| 3 | BIF418 | MATHEMATICS FOR BIOINFORMATICS | 4 |
| 4 | BIF419 | STATISTICAL METHODS FOR BIOINFORMATICS | 3 |
| 5 | BIF415 | MACHINE LEARNING AND DATA MINING | 3 |
| 6 | BIO413 | MOLECULAR AND CELLULAR BIOPHYSICS | 2 |
| 7 | BIF416 | PROGRAMMING USING PERL | 3 |

| | | | |
|----------------------|--------|---------------------------------|-----------|
| 8 | BIO488 | CELL AND MOLECULAR BIOLOGY -LAB | 2 |
| 9 | BIF489 | PROGRAMMING USING PERL -LAB | 1 |
| 10 | AVP401 | AMRITA VALUES PROGRAMME | 1 |
| 11 | SSD402 | SOFT SKILLS - II | 1 |
| Total Credits | | | 28 |

| Semester 3 | | | |
|----------------------|-------------|--|-----------|
| Sl.No | Course Code | Course Name | Credits |
| 1 | BIO513 | EVOLUTION AND COMPARATIVE GENOMICS | 3 |
| 2 | BIO518 | MATHEMATICAL MODELING OF BIOLOGICAL SYSTEMS | 2 |
| 3 | BIO527 | MASS SPECTROMETRY AND PROTEOMICS | 3 |
| 4 | BIF519 | ADVANCED PROGRAMMING FOR BIOINFORMATICS | 4 |
| 5 | BIF520 | OBJECT ORIENTED PROGRAMMING LANGUAGE | 4 |
| 6 | BIF515 | COMPUTER-AIDED DRUG DESIGN AND PHARMACOINFORMATICS | 3 |
| 7 | BIF591 | ADVANCED PROGRAMMING -LAB | 1 |
| 8 | BIF592 | OBJECT ORIENTED PROGRAMMING-LAB | 1 |
| 9 | SSD501 | SOFTSKILLS III | 1 |
| 10 | | ELECTIVE I | 2 |
| 11 | | ELECTIVE II | 2 |
| 12 | | OPEN ELECTIVE | 2 |
| Total Credits | | | 28 |

| Elective | | | |
|-----------------|--------|------------------------------------|---|
| 1 | BIF551 | SYSTEMS BIOLOGY | 2 |
| 2 | BIF561 | COMPUTATIONAL NEUROSCIENCE | 2 |
| 3 | BIF562 | NEUROBIOLOGY AND ELECTROPHYSIOLOGY | 2 |

| | | | |
|---|--------|-----------------------------------|---|
| 4 | BIF563 | NEXT GENERATION SEQUENCE ANALYSIS | 2 |
| 5 | BIF564 | METAGENOMICS & MICROBIOME | 2 |
| 6 | BIF565 | BIOINFORMATICS & BIGDATA | 2 |
| 7 | BIF566 | CAREER DEVELOPMENT & BUSINESS | 2 |

| Semester 4 | | | |
|----------------------|--------------------|---------------------|----------------|
| | Course Code | Course Name | Credits |
| 1 | BIF 599 | Dissertation/Thesis | 10 |
| Total Credits | | | 10 |

| | |
|--|-----------|
| TOTAL CREDITS FOR THE PROGRAMME | 89 |
|--|-----------|

Course Objectives, Course Outcomes, Syllabus

SEMESTER -1

BIF410 INTRODUCTION TO BIOINFORMATICS CREDITS 3**Learning objective:**

To introduce to the field of bioinformatics via an array of publicly available tools and resources.

SYLLABUS:

Biological Data Acquisition: The form of biological information. Retrieval methods for DNA sequence, protein sequence and protein structure information; Databases – Format and Annotation: Conventions for database indexing and specification of search terms, Common sequence file formats. Annotated sequence databases - primary sequence databases, protein sequence and structure databases; Organism specific databases; Data – Access, Retrieval and Submission: Standard search engines; Data retrieval tools – Entrez, DBGET and SRS; Submission of (new and revised) data; Sequence Similarity Searches: Local versus global. Scoring matrices. Dynamic programming algorithms, Needleman-wunsch and Smith-waterman. Heuristic Methods of sequence alignment, BLAST and PSI BLAST. Multiple Sequence Alignment and software tools for pairwise and multiple sequence alignment; ORF finding;

REFERENCE:

1. Bioinformatics: Databases and Systems, by Stanley I. Letovsky
2. Bioinformatics Databases: Design, Implementation, and Usage (Chapman & Hall/ CRC Mathematical Biology & Medicine), by SorinDraghici
3. Data base annotation in molecular biology, principles and practices, Arthur M.Lesk
4. Current topics in computational molecular biology, Tao, Jiang, Ying Xu, Michael Q.Zang

Course outcome:

Students should be able to apply basic bioinformatic tools for various needs in biotechnology and microbiology programs, such as finding gene/protein homologs, designing primers, identifying mutations, etc.

BIF413 PROGRAMMING CONCEPTS CREDITS 3**Learning outcomes:**

To introduce concepts of programming with a basic language and widely used programming language C

SYLLABUS:

Introduction – Programming languages – Problem solving Technique Programming concepts, Flow charts, Compilers, Interpreters, Linkers Data types & Variables, Operators, Control constructs, Arrays, Matrices, Loops, Functions, Structures, Pointers, File handling, Logical Operations, Internet Programming, String Handling

REFERENCE:

1. YeshwantKanetkar, Let us C, 8th Edition, BPB publications

Course outcome:

By the end of the course the students get to know the

1. Basic concepts of computers and programming language C
2. Write programs to make computations easier

BIO421**CELL BIOLOGY****CREDITS 3****Learning objectives:**

The course involves understanding the concepts of protein sorting, apoptosis and circadian rhythms. The course also includes the communication between different cells by understanding various such signaling pathways and their role in Cancer, Cell death and other pathological conditions in addition to the applications of stem cells. Students will gain in-depth knowledge in the fields of cell biology and stem cell biology.

SYLLABUS:

Tools of cell biology. Ultra structure of prokaryotic and eukaryotic cells, organelles structure marker and function, Endoplasmic reticulum, Golgi complex, Types of vesicles - transport and their functions, Lysosomes. Nucleus - Internal organization, Nuclear pore complex, Nucleosomes Chromatin. Mitochondrial Genome, Structure and Function – Oxidative Metabolism in the Mitochondrion – The Role of Mitochondria in the formation of ATP – Translocation of Protons and the Establishment of a proton-motive force – The Machinery for ATP formation – Peroxisomes. Genome studies of Mitochondria. Chloroplast structure and function – An overview of photosynthetic Metabolism, Cytoskeleton – components of Cytoskeleton, Microtubules, Intermediate filaments – Microfilaments, Protein trafficking, Cell- to -Cell Signaling: Ligand-Receptor interaction studies, GPCR, Receptor Tyrosine Kinase, Signal transduction through Ion channels, Intracellular signaling in Development and Disease, Recent advances in Prokaryotic Signalling, Transport across Cell Membranes, Protein Sorting: Organelle Biogenesis and Protein secretion, Stem Cell Biology, Cancer, Regulation of Cell Death; Apoptosis, Circadian Rhythms,

REFERENCE:

1. “Molecular Cell Biology” 5th Edition by Harvey Lodish, Arnold Berk, Paul Matsudaira, Chris Kaiser, Monty Krieger, Matthew Scott, Lawrence Zipursky and James Darnell. W.H Freeman and Company.
2. The Cell A Molecular Approach-Cooper-Hausman
3. Molecular Biology of the Cell- Bruce Alberts et al.

Course outcome:

After completion of the course the students will

1. Understand how the proteins synthesized in the cytosol are transported to different organelles
2. Understanding G protein signaling, receptor tyrosine kinase signaling and various other signaling mechanisms involved during the development of an organism which involves discussion of scientific articles.
3. Understand the role of circadian rhythms and apoptosis and their regulation in different pathological and physiological conditions.
4. Understand the basic concepts of stem cell biology with emphasis on the use of stem cell therapy to treat various disease conditions.

BIO425**MOLECULAR BIOLOGY FOR BIOINFORMATICS****CREDITS****3****Learning objective:**

Basic knowledge in general molecular biology. This course will help them understand and appreciate other subjects like rDNA Technology, Plant Biotechnology, Immunology etc.

SYLLABUS:

Tools of molecular biology, Structure of Nucleic acids and proteins, DNA-Protein interactions, Transcription in prokaryotes, Control of prokaryotic transcription, Transcription in Eukaryotes, Post transcriptional events, Transcriptional regulation, Translation and translational regulation, post translational modification, RNA and Protein export and its regulation. DNA Replication and enzymology, DNA damage and repair. Noncoding RNA, transposons. Introduction to Genomics; Metagenomics, whole genome sequencing, Genome wide association studies, Proteomics, Metabolomics. Evidence for DNA as genetic material. Gene transfer in microorganisms – conjugation, transformation, and transduction - protoplasmic fusion. The genomes of bacteria, viruses, plasmids. , Introduction to the methods of DNA sequencing, Sequence by Synthesis, Pyrosequencing, Sequencing by ligation

REFERENCE:

1. The Cell A Molecular Approach-Cooper-Hausman
2. Molecular biology by Rober F. Weaver

TEXT BOOKS

1. Molecular biology of Genes by James Watson
2. Molecular biology by David Freifelder
3. Molecular Biology of the Cell- Bruce Alberts et al.

Course outcome:

1. Students get introduced to the history of molecular biology and all the classic experiments that established DNA as the genetic material, methods in molecular biology.
2. DNA replication, damage and repair, transcription in prokaryotes and eukaryotes, transcriptional regulation, translation and translational regulation, systems biology, bioinformatics tools in molecular biology.
3. This will enable them to understand the way all living cell grows, divides and regulates their biological functions.

BIO410 ENERGY AND INTERACTION IN BIOLOGICAL MODELING CREDITS**3****Learning objective:**

A student who completes this course is expected to; identify the different classes of biomolecules, their chemical structures and functions. The course is also intended to assist the student in understanding the biochemical processes of the cell that can be applied in the domains of bioinformatics and drug discovery.

A student who completes this course is expected to; identify the different classes of biomolecules, their chemical structures and functions. The course is also intended to assist the student in understanding the biochemical processes of the cell that can be applied in the domains of bioinformatics and drug discovery.

SYLLABUS:

Basic Concepts of Organic Chemistry: Principles of Chemical Bonding, Structure and Properties of

Basic Concepts of Organic Chemistry: Principles of Chemical Bonding, hybridization Structure and Properties of water, Acids and Bases, Buffers; Mechanism of Organic Reactions: Chemistry of carbonyl compounds [Reactions with alcohols, amines, etc.], Oxidation-Reduction reactions, Keto-enol Tautomerism, important functional groups in biochemistry, Non-covalent interactions, Amino Acids and Proteins: Introduction, Classification optical isomerism, chemical properties, Acid-base properties- Peptide bond formation and properties. Levels of protein structure (brief mention of primary, secondary, tertiary & quaternary structures), Denaturation of proteins. Ramachandran plot. Determination of Primary Structure - sequencing strategies N-terminal and C-terminal sequencing, protein identification using MASCOT database. Enzymes: Introduction, Carbohydrates: Carbohydrates: Introduction, Sources, Classification. Reactions of carbohydrates, Isomerism of carbohydrates, Fischer projections, Haworth structures, pyranose and furanose structures, Anomers, Epimers, Chair and boat conformations, R and S configuration. Structure and functions of sugars, homo and heteropolysaccharides, glycoconjugates, glycoproteins, Lipids: Introduction, sources, Nomenclature, Classification. Properties & Functions. Steroids: Structure of steroid nucleus, biological role of cholesterol, fat soluble vitamins., Purines & Pyrimidines: Structures of purine and pyrimidine bases, keto-enol tautomerism, nucleosides, nucleotides, RNA, & DNA (differences), base pairing schemes, types of RNA: mRNA, rRNA , tRNA, Secondary structure of DNA, Watson and Crick model. Denaturation of DNA. Hyperchromic shift. Structure Activity Relationships. Introduction to Molecular Docking,

REFERENCE:

1. Fundamentals of Biochemistry- 3rd Edition - Voet&Voet –Wiley
2. Organic Chemistry – 8th Edition- Graham Solomons and Craig B. Fryhle- John Wiley and Sons

Course outcome:

1. To understand the concepts of basic Chemistry including principles of chemical bonding, hybridization, shape of water and ammonia. Acids, bases, buffers, Preparation of buffers, Non-covalent interactions and general types of reactions involved in biochemistry.
2. Identify and write the chemical structure of Amino acids and depict their ionization behavior, Peptide bond formation; describe the Primary, Secondary, Tertiary and Quaternary structure of proteins and their functions.
3. Analyze the structure and properties of Carbohydrates, Monosaccharide, Disaccharides and polysaccharides, Glycoconjugates.
4. Identify and analyze the classification, Structure and properties of lipids including Storage lipids, Membrane lipids, Steroids etc.
5. Identify and know the chemical structure of nucleotides including their components, describe primary, secondary structure of DNA and RNA.

BIF402 DATABASE DESIGN AND IMPLEMENTATION FOR BIOINFORMATICS

CREDITS 3

Learning objective:

To introduce concepts of database management system and make use of this in storing and retrieving biological data

SYLLABUS:

Introduction to DBMS: Basic Concepts - Data Abstraction - Data models and data independence. Instances and Schemas. Components of a DBMS and overall structure of a DBMS- Life Cycle of a DBMS application- Database terminology. Data Modeling: Basic concepts- Types of data models- Conceptual, physical and logical database models- E-R data model and Object-oriented data model. Components of ER Model- ER Modeling symbols. Entity and entity sets- Relations and relationship sets- E-R Diagrams- Reducing E-R Diagrams into tables. Relational DBMS Model: Basic concepts, Attributes and domains- Intention and extensions of a relation- concept of integrity and referential constraints- Relational Query Languages (Relational algebra and relational calculus (Tuple and domain relational calculus). Relational Database Design: Notion of normalized relations- Normalization using Functional Dependency- First Normal form- Second Normal Form- Third Normal form- BCNF. SQL: Structure of a SQL query- DDL and DML, TCL- SQL queries and sub queries- Tables, views and indexes- Aggregate functions- Set Operations, predicates and joins, Set Membership- Tuple variables- Set comparison- Database modifications using SQL. . PL/SQL: Basic Concepts-SQL within PL/SQL- Cursors -Concept of stored procedures and functions-packages- Triggers.

REFERENCES

1. Database Management Systems : Raghu Ramakrishnan
2. ORACLE PL/SQL Programming – Scott Urman BPB Publications.
3. Database Systems Concepts – Henry F Korth, Abraham Silberschatz.
4. Database Management Systems – Alexis Leon, Mathews Leon – Leon, Vikas Publications
5. Oracle 9i The Complete Reference – Kevin Loney, George Koch - Oracle Press

Course Outcome:

Students learn to

1. Use Oracle to create and design databases
2. Use PL/SQL programming in building platforms for storing and retrieving biological data

BIF487 PROGRAMMING FOR BIOINFORMATICS -LAB CREDITS

1

Learning Objective:

To introduce a hand on session on the concepts of programming with a basic language and widely used programming language C

SYLLABUS:

Introduction to computer programming- use of editors, compilation, debugging, Basic C programs, String Manipulation, File Management, Control and loops, Programs using if conditions; switch case, loops, arrays, functions, files, command line arguments, string manipulations.

REFERENCES

1. YeshwantKanetkar, Let us C, 8th Edition, BPB publications
2. Brian W. Kernighan, Dennis M. Ritchie. The C Programming Language, 2nd Edition, Prentice Hall PTR; 2 edition (April 1, 1988) [<http://books.cat-v.org/computer-science/c-programming-language/The.C.Programming.Language.2nd.Edition.pdf>]

Course outcome:

Students who complete the course would be able to

1. Understand basic programming concepts
2. Write and execute programs which could be used to understand and solve biological systems.
3. Manage large file based data.

BIF486

BIOINFORMATICS TOOLS -LAB

CREDIT 1

Learning Objectives:

To offer hands-on lessons on an array of publicly available tools and resources.

SYLLABUS:

Introduction to Matlab, Matrix calculations, Functions. ENTREZ, NCBI, Genomic databases, Organism specific databases, BLAST, FASTA, Phylip, Pymol, Prosite. Exploring NCBI Resources, 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), Literature Databases (PubMed, PubMedCentral, OMIM, Books, Citation Matcher), research at NCBI, education, FTP site. 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.

REFERENCE:

1. <http://vlab.amrita.edu/>
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.

BIF488

DATABASE DESIGN FOR BIOINFORMATICS -LAB

CREDIT 1

Learning objective:

To introduce a hands on session on database management system and make use of this in storing and retrieving biological data

SYLLABUS:

SQL, Creating databases and tables, Database administration, Function, Procedure, Trigger, Data processing in WEKA, Classification algorithms: decision tree classification, naive Bayesian classification, a brief introduction to other classifiers, Clustering algorithms: methods to cluster continuous data, methods to cluster categorical data, file processing in database environment, E-R models,

REFERENCES

1. ORACLE PL/SQL Programming – Scott Urman BPB Publications
2. Data Mining: Concepts and Techniques (The Morgan Kaufmann Series in Data Management Systems) -- by Jiawei Han, MichelineKamber;
3. Insight into Data Mining – Theory and Practice - K.P.Soman, ShyamDiwakar, V.Ajay, PHI, 2006.
4. Database Management Systems : Raghu Ramakrishnan
5. Oracle 9i The Complete Reference – Kevin Loney, George Koch - Oracle Press

Course outcome:

Students should be able to

1. Create and design databases using Oracle database management system
2. Built platforms for storing and retrieving biological data

SSD401

SOFT SKILLS

CREDIT 1

SYLLABUS:

Presentation Skills Speech techniques, content, purpose, strengths and weaknesses. Develop good listening and feedback skills

Resume Writing Purpose of Resumes, Resume Formats, Parts of the Resume

Group Discussion Type of GDs, Roles one could play, PESTLE analysis,

Interview Skills Types of Interviews, Behavioral interviews, STAR, HR questions

Course outcomes:

1. Become aware of personal speech habits and characteristics, Develop speech preparation and presentation techniques, audience awareness and self-awareness, Cultivate poise and self-confidence
2. Resume
3. Understand the key skills and behaviours required to facilitate a group discussion, speak with confidence, exhibit leadership skills and make the group achieve the goals.
4. Competent to answer Behavioral and HR questions.

SEMESTER -2

BIF409 **STRUCTURAL BIOINFORMATICS** **CREDITS**
4

Learning objective:

The course gives an idea about the aspect of computation in structural biology and how to use these computations in solving problems and understanding structure.

SYLLABUS:

Fundamentals of protein, DNA, RNA structure, macromolecular structure determination, X ray crystallography, NMR spectroscopy, Electron microscopy, Structure formats, molecular visualization, Protein structure evolution and SCOP database, CATH domain structure database, identifying structural domains in protein, prediction of protein - protein interaction from phylogenetic analysis, structure comparison and alignment, structural bioinformatics in drug discovery, CASP and CAFASP experiments, homology modeling, fold recognition methods, AB INITIO methods. Secondary structure prediction.

REFERENCE:

1. Structural bioinformatics, Philip E Bourne, Helge Weissig
2. Protein Bioinformatics : An Algorithmic Approach to Sequence and Structure Analysis by Ingvar Eidhammer, et al;

Course outcome:

A student who completes this course is expected to;

1. Know the structure of the different biological molecules
2. Its acquisition
3. Its storage
4. Prediction of unknown structures.

BIF417 **MOLECULAR SEQUENCE ANALYSIS** **CREDITS 4**

Learning Objective:

To introduce to the field of sequence analysis to extract features and functions and thus depict structure and evolution from genetic material

SYLLABUS:

Sequence Similarity Searches: Local versus global. Distance metrics. Similarity and homology. Scoring matrices. Dynamic programming algorithms, LCS, Dotplot, Needleman-wunsch and Smith-waterman, Gotoh algorithm. Heuristic Methods of sequence alignment, FASTA, BLAST and PSI BLAST. Multiple Sequence Alignment and software tools for pairwise and multiple sequence alignment; Phylogenetic Analysis: Comparative genomics, orthologs, paralogs. Methods of phylogenetic analysis: UPGMA, WPGMA, neighbor joining method, Fitch/Margoliash method, Character Based Methods. RNA secondary structure prediction algorithm: Nussinov algorithm, Genome Analysis: Whole genome analysis, existing software tools; Genome Annotation and Gene Prediction;

REFERENCE:

1. Bioinformatics: Databases and Systems, by Stanley I. Letovsky
2. Bioinformatics Databases: Design, Implementation, and Usage (Chapman & Hall/ CRC Mathematical Biology & Medicine), by Sorin Draghici

Course outcome:

Students should be able

1. Compare sequences,
2. Identify features, structures and mutations to reveal evolutionary relations

BIF418 MATHEMATICS FOR BIOINFORMATICS**CREDITS 4****Learning Objective:**

The course gives a brief idea into the basic concepts of matrix, calculus and trigonometric calculations required to model different biological systems

SYLLABUS:

Quantities and units, Numbers and equations, basic calculus, Limits of a function; Derivative of a function at a point, geometrical significance of derivative, rules for differentiation, differentiation of trigonometric, exponential and logarithmic functions, differentiation of inverse algebraic and inverse trigonometric functions, chain rule, differentiation of implicit functions and logarithmic differentiation; Physical aspects of derivatives; Higher order derivatives - maxima and minima; Applications of derivative - example from energy minimization, Integration: Anti-derivatives, finding function from its derivative; Definite integral as the limit of the Sum, properties of definite integrals; Fundamental theorem of integral calculus; Integration of Elementary Functions - standard integrals; Methods of integration - integration by substitution, integration by parts; Integration of trigonometric functions; Applications – Area under a curve, volume of bounded region; linear systems, differentiation, integration, differential equations, Continuity and Derivability, Concept of continuity (continuous and discontinuous functions), trigonometry, continuous and discrete models, ordinary differential equations, linear algebra – matrices and determinants, matrix operations, Matrices – why matrices needed; Linear equations & Matrices - row/column operations, Gauss elimination, decomposition, inverse; Determinant - properties of determinants, Cramer's rule, determinant to transpose and inverse; Matrices and sequence matching in bioinformatics (substitution matrices). Gauss-Jordan elimination, solutions of linear systems, description of orthogonality, basic optimization theory, linear programming, simplex method, basics of nonlinear programming. - Properties of Determinants, Minors and Cofactors, Multiplication of Determinants, Adjoint, Reciprocal, Symmetric Determinants, Cramer's rule, Different types of matrices, Matrix Operations, Transpose of a matrix, Adjoint of a square matrix, Inverse of a matrix, Eigen values and eigen vector The concept of a Vector, Vector addition and subtraction, Products of two vectors. Dot product and Cross product, Products of three vectors- scalar triple product and vector triple product, Gradient, Divergence and Curl.

REFERENCE:

1. Advanced Engineering Mathematics, Erwin Kreyszig, John Wiley & Sons, 01-Jan-2007 - 236 pages
2. Mathematics for Biological Scientists, Mike Aitken, Bill Broadhurst, Stephen Hladky, Garland

Course outcomes:

Students who complete this course will know how to use

1. Matrix to solve the biological systems like sequence alignment or gene expression
2. Calculus to calculate the rate of change of substrate or to find the area under the curve in enzyme kinetics.
3. Distance calculation to predict protein structure

BIF419 STATISTICAL METHODS FOR BIOINFORMATICS CREDIT 3

Learning objective:

Biostatistics is a course offered to 1st semester M.Sc., (BI). We have considered distributions relating to a single characteristics. How far the two variables, corresponding to two characteristics, tend to move together in same or opposite directions. The theory of probability is a study of Statistical or Random experiments. Using these figures, it might be possible to estimate the possible level of prices at some future data so that some policy measures can be suggested to tackle the problems. Average is a value which is typical or representative of a set of data

SYLLABUS

Describing Data: Introduction to the practice of data analysis. Topics include descriptive statistics such as mean, median, range, inter-quartile range and standard deviation as well as basic descriptive plots such as histogram, barplot, dotplot, scatterplot and pairwise scatterplot, Basic Probability: Introduction to probability concepts such as experiments, trials, outcomes, events and sample spaces. Initial focus is on simple probability spaces (coin flips and dice rolls) to give students a concrete understanding of the concepts, Probability Theory: Concept of probability: sample space and events, independent events, mutually exclusive events. axioms of probability, conditional probability, additional and multiplication theorem of probability, Bayes theorem, Introduction to Markov Chain Model. Meaning and objective of sampling, Sampling Error, Types of Sampling, Sampling Distribution, Sampling Distribution of Sample Mean and Sample Proportion, Standard Error Probability Distribution: Bernoulli trials, binomial distribution, normal distributions, Poisson distribution, & The Central Limit Theorem: From the simple notion of probability distributions developed in UNIT 2, the ideas are generalized to continuous distributions with the primary focus on the normal probability distribution culminating in a thorough discussion of the Central Limit Theorem and it's utility to data analysts, Introduction To Inference: Basic introduction to statistical inference focusing on one- and two- sample problems. This unit includes discussion of the z- and t-test, F-test, chi-square test as a well as nonparametric methods including Wilcoxon Rank Sum and Kolmogorov-Smirnov tests, Anova: Introduction to the analysis of grouped data. Focus is on one- and two-way designs and their analysis. Additional topics in repeated measures designs for advanced students. Correlation and Regression: Principles of least squares, scatter diagram, correlation, covariance, correlation coefficient, properties of correlation coefficient, regression, properties of linear regression, rank correlation, and multiple correlation. Regression: Introduction to regression analysis. Topics include multiple regression, model selection, and special fitting techniques such as robust estimation, local regression and regression splines. Multivariate Methods: Introduction to multivariate methods useful to bioinformatics including k-means clustering and principal components analysis. Bioinformatics Applications: Introduction to the analysis of bioinformatics data. Topics include end-to-end analysis of microarray gene expression data including data quality considerations, RNA degradation in Affymetrics Chips, 2-color CDNA arrays, data normalization and summarization and differential expression testing and annotation.

REFERENCE:

1. Introduction to the Practice of Statistics by Moore and McCabe
2. Course Manuals: S-PLUS Command Line Essentials, The Analysis of Microarrays

Course outcome:

- 1: To understand the concepts.
- 2: To find r , ρ and study the nature of correlation and regression. Identify the different axiomatic approach.
- 3: To study and solve problems related to connectives under different situations.
- 4: To study the need of statistical approach Identify the different axiomatic approach.
- 5: To get a single value that describes the whole data and to study the variability of observation
- 6: To understand the basic concepts of pmf and pdf

BIF415 MACHINE LEARNING AND DATA MINING CREDITS
3**Learning Objective:**

The course gives an idea of the different algorithms to be used to train and test systems along with mining relevant data from a system.

SYLLABUS:

What is Data Mining? Motivating Challenges; The origins of data mining; Data Mining Tasks. Types of Data; Data Quality. Data Preprocessing; Measures of Similarity and Dissimilarity, Machine learning, Hypothesis, Version space, MAP, Maximum likelihood. Classification: Preliminaries; General approach to solving a classification problem; Decision tree induction; Rule-based classifier; Nearest-neighbor classifier, SVM. Association Analysis: Problem Definition; Frequent Itemset generation; Rule Generation; Compact representation of frequent itemsets; Alternative methods for generating frequent item-sets, Neural Networks, Cluster Analysis: Overview, K-means, Agglomerative hierarchical clustering, DBSCAN, Overview of Cluster Evaluation, Further Topics in Data Mining: Multidimensional analysis and descriptive mining of complex data objects; Spatial data mining; Multimedia data mining; Text mining; Mining the WWW. Outlier analysis, data mining applications; Additional themes on Data mining; Social impact of Data mining; Trends in Data mining. Data warehouse – Difference between Operational DBs and Data warehouses – Multidimensional Data Model – Data warehouse Architecture – Data warehouse Implementation – Knowledge Discovery from Databases(KDD) Process – Data Processing for Data Mining – Data Cleaning, Integration, Transformation, Reduction – Data Mining Primitives – Data Mining Query Language - Natural language processing – BioNLP - Document clustering – Suffix Tree Clustering – LINGO - Basics of Deep Learning – Artificial Neural Networks - Bio-Entity Recognition -

REFERENCE:

1. Data Mining: Concepts and Techniques (The Morgan Kaufmann Series in Data Management Systems) -- by Jiawei Han, MichelineKamber;
2. Insight into Data Mining – Theory and Practice - K.P.Soman, ShyamDiwakar, V.Ajay, PHI, 2006.

Course outcome:

1. To understand the concept of machine learning.
2. Learn the different classification and clustering algorithms
3. To mine data from databases

BIO413 **MOLECULAR AND CELLULAR BIOPHYSICS** **CREDITS**
2

Learning Objective:

The course in molecular and cellular biophysics is meant to introduce biophysics as a course in biosciences applying the theoretical language of physics to aid functional understanding of molecular and cellular processes.

SYLLABUS:

Biophysics, branches in biophysics, Molecular structure in biological systems: states and forces, hydration, movement, structure formation, self-assembly, mechanical properties, energetics. Membrane transport and diffusion, Famous laws in biophysics, Timing and role in cell biology, Neuronal biophysics – action potential, HH equation, cable theory, ion channels, Biomechanics, Biophysical techniques.

REFERENCE:

1. Daniel Goldfarb, Biophysics demystified, McGraw Hill, 2011.
2. Meyer B. Jackson, Molecular and cellular biophysics, Cambridge University Press, 2006, ISBN: 978-0-521-62470-1.
3. Christof Koch, Biophysics of Computation, Oxford University Press: New York, New York, 1999.

Course outcome:

1. To understand physical laws underlying biological systems
2. To understand timing and role in biological systems
3. To understand Neuronal biophysics

BIF416 **PROGRAMMING USING PERL** **CREDITS**
3

Learning outcome:

This course introduces the concept of PERL programming language with string analysis along with the introduction of modules and BioPERL

SYLLABUS:

Why Perl is used for bioinformatics applications, Scalars, Arrays and its operations, Hashes, Regular expressions, string manipulation, File management, Command line arguments, sub routines, Packages, Modules, etc

REFERENCE:

1. Randal L. Schwartz, Tom Phoenix, brian d foy Learning Perl, 5th Edition, O'Reilly Media
2. David Till, Teach Yourself Perl 5 in 21 days
3. James Tisdall, Beginning Perl for Bioinformatics, O Reilly Publications
4. Rex A Dawyer, Genomic Perl, Cambridge University Press

Course outcome:

Students are expected to learn

1. Array manipulations
2. String manipulation
3. Use and function of modules
4. BioPERL

BIO488 CELL AND MOLECULAR BIOLOGY -LAB CREDITS**2.****Learning objective:**

"The course should enable the students to • Isolate plasmid DNA and genomic DNA • Undertake as well as understand principle behind Gel Electrophoresis • Prepare Competent bacterial Cells • Comprehend how to undertake PCR and restriction digestion of DNA • Undertake lignin staining in plant cross sections • Use microscope effectively and also grasp the basics of animal cell culture "

SYLLABUS:

Isolation of plasmid DNA and genomic DNA; Protein extraction and purification by affinity chromatography and analysis by SDS-PAGE. Polymerase chain reaction (PCR). Microscopic observation of different types of cells: bacteria, animal cell, plant cell, fungi. Cell viability test by Trypan Blue. Image analysis (SDS-PAGE, cell morphology, tissue section) by ImageJ. Basics of animal cell culture.

REFERENCES:

1. Sambrook, J., Russell, D. W., & Russell, D. W. (2001). Molecular cloning: a laboratory manual (3-volume set).
2. Amrita University Virtual Lab.
3. Freshney, R. I. (2005). Culture of specific cell types. John Wiley & Sons, Inc.

Course outcome:

The students should be able to

- Isolate plasmid DNA and genomic DNA
- Undertake Gel Electrophoresis
- Prepare Competent bacterial Cells
- Undertake PCR and restriction digestion of DNA •
- Undertake lignin staining and appreciate the significance of the in plants
- Know the basics of animal cell culture"

BIF489 PROGRAMMING USING PERL -LAB CREDIT 1**Learning Objective:**

This course introduces a hands on experience on the concept of PERL programming language with string analysis along with the introduction of modules and BioPERL

SYLLABUS:

File management programs using Perl in Linux, running external programs, pattern matching, string manipulation, built in data types & modules in Perl, system calls, etc.

REFERENCE:

1. James Tisdall, Beginning Perl for Bioinformatics, O Reilly Publications
2. Rex A Dawyer, Genomic Perl, Cambridge University Press

Course outcome:

Students are expected to have a practical experience on

1. Array manipulations
2. String manipulation
3. Use and function of modules
4. BioPERL

AMRITA VALUE PROGRAM

SD 402

SOFT SKILLS II

CREDITS:1

Learning objectives:

The objective of this course to give students training and experiences that will allow them to be successful in their second year and beyond. There are two components in this course. Verbal skills that equips you with vocabulary skills, Essential Grammar, write Cover letter and SOPs

SYLLABUS:

Cover Letter Skills, key words, action words, S V Agreement Subject, Pronoun, Verb, To write grammatically correct sentences, Modifier Adjectives and Adverbs, Clauses Noun, clause, Relative clauses etc, Punctuation Punctuation marks, Tenses Time, Tenses, Reading and Comprehension Language, pronunciation, SOP

Course outcome:

1. They will be able to write a Cover Letter
2. To write grammatically correct sentences
3. Enrichment of vocabulary and knowledge, and fluency

SEMESTER -3

BIF513 EVOLUTION AND COMPARATIVE GENOMICS

CREDITS

3

Learning objective:

To understand the importance and ways of comparing different parts of the genomes of eukaryotes and prokaryotes in connection to evolution of gene regulations, protein functions, metabolic networks, etc.

SYLLABUS:

Algorithms and tools for Whole Genome Comparisons; Introduction to the CoGe system for Comparative Genomics, Polyploidies within plant genomes; Conserved Non-coding sequences; Post-polyploidy Fractionation mechanisms; Transposons and Epigenetic mechanisms in plant genomes; Repetitive elements within genomes

REFERENCE:

1. Wendell J Ed., Plant Genome Diversity.

Course outcome:

Students should be able to understand and perform genome-level comparative studies of molecular sequences isolated from multiple individuals within and across species.

BIF518 MATHEMATICAL MODELING OF BIOLOGICAL SYSTEMS

CREDITS 2

Learning objective:

The course introduces mathematical modeling from a biology perspective.

SYLLABUS:

Mathematical models in biology – Introduction, types of models, levels of modeling, specificity of modeling in biology, Some standard models – unlimited growth, limited growth, constraints with respects to a substrate, competition selection, Lotka-Volterra models. Oscillations and rhythms in biological systems-glycolysis, intracellular calcium, cellular cycles, Modeling Neuronal behavior.

REFERENCE:

1. Mathematical models in biophysics, Riznichenko Galina Yur'evna, Book Online, Biophysical society.
2. Biophysics of Computation, Christof Koch, Oxford University Press: New York, New York, 1999.

TEXT BOOKS

1. Calculus: for the social, managerial and life sciences – Laurence D. Hoffmann, McGraw Hill, 1980
2. Methods in Neuronal Modeling: From Ions to Networks,ed. Christof Koch and IdanSegev, 2nd edition. MIT Press, Cambridge, MA, 1998.

Course outcome:

At the end of the course, students are expected to 1. Understand modeling biological systems 2. Use different modeling tools used to understand computational sciences with focus on data from biology such as population growth, epidemic spread etc...

BIO527 MASS SPECTROMETRY AND PROTEOMICS CREDITS
3**Learning objective:**

The main aim of this course is to provide in-depth knowledge of concepts and techniques within the field of mass spectrometry and proteomics.

SYLLABUS:

History of mass spectrometry, Basics of MS instrumentation, Ionization Sources: Electrospray (ESI), Matrix assisted laser desorption and ionization (MALDI), Mass analyzers: Quadrupole, Ion traps (Linear trap, 3D trap, Orbitrap, Ion Cyclotron Resonance), Time-of Flight, Hybrid analyzers, Ion mobility mass spectrometers, Detectors: Electron multiplier, Microchannel plate, Photomultiplier tube. Fundamental parameters of mass spectrometers: Mass accuracy, Resolution, Sensitivity.

Understanding mass spectra: Peptide and protein data interpretation, Tandem mass spectrometry, Fragmentation techniques: Collision induced dissociation (CID), Electron transfer dissociation (ETD), Electron capture dissociation (ECD), Sequential Window Acquisition of all Theoretical Mass Spectra (SWATH), In-source decay (ISD), Post-source decay (PSD),

History of proteomics, Protein and peptide separation techniques: Electrophoresis, Liquid chromatography, MudPIT, Peptide mass finger printing, Data dependent and data independent MS/MS, Database search algorithms, Proteomic work-flows, Protein identification, analysis and validation.

Posttranslational modification analysis: Phosphorylation, Glycosylation, Quantitative proteomics: Absolute and relative quantitation through stable isotope labeling (AQUA, SILAC, iTRAQ, ICAT), DIGE, Label-free quantitation: Spectral count, Peak area.

REFERENCE:

1. Bioinformatics and Functional Genomics – Jonathan Pevsner - 2nd edition, Wiley-Blackwell, 2009. ISBN-10: 0471210048
2. Introduction to Proteomics: Tools for the New Biology. Daniel C. Liebler, Humana Press Inc., 2002. ISBN-10: 0896039919
3. Principles of Proteomics. R.M Twyman (2004). (BIOS Scientific publishers). ISBN-10: 1859962734
4. Discovering Genomics, Proteomics and Bioinformatics, 2nd Edition. Campbell AM & Heyer LJ, Benjamin Cummings 2007; CSH Press, NY. ISBN-10: 8131715590

Course outcome:

1: Familiarization of basic concept of mass spectrometers used for bimolecular characterization and understand the major physical components and performance parameters of mass spectrometers

- 2: Able to apply the advanced knowledge acquired to interpret mass spectrometric data
- 3: Perceive multiple work-flows for large scale protein identification and protein structural characterization
- 4: Learn to apply multiple proteomic strategies to quantitate biomolecules

BIF519 ADVANCED PROGRAMMING FOR BIOINFORMATICS CREDITS

4

Learning objective:

The objective of this course is to provide complete understanding on webservers and how it can be made use in storing and accessing biological data

SYLLABUS:

Client - Server Technology, Web servers, Web browsers, HTML forms, Scripting Languages, Form variables, actions, methods & data retrieval from the web, CGI Programming and its alternatives, accessing form values in the server side, file management in the web, Perl DBI Programming, Creating images dynamically using GD in Perl, XML, Using BioPerl to access public databases and different types of files, Regular expressions, string manipulations, data retrieval and manipulation - Parallel programming/ Computing – MapReduce , Interfaces with other languages: C, Java, Perl, Python, XML, etc. –Formatting Data: sorting, Transliteration Database manipulation Databases and DBM Hashes, Opening and closing, DBM Hashes, Fixed-Length Random –Access Databases, Variable-Length (Text) Databases, Win32 Databases Interfaces

REFERENCE:

1. James Tisdall, Mastering Perl for Bioinformatics, Oreilly Publications
2. Gibas&Jambeck, Developing Bioinformatics Computer Skills, Oreilly Publications

Course outcome:

Students are expected to learn t 1. The aspect of client-server technology. 2. HTML with CGI programming embedded 3. To use Bioperl to retrieve data from public databases

BIF520 OBJECT ORIENTED PROGRAMMING LANGUAGE CREDIT 4

Learning objective:

The course introduces the object oriented concepts like the encapsulation, Inheritance and polymorphism.

SYLLABUS:

Java packages, data types, string manipulation, file management, Applet programming, Graphics in Java using Applets & Java Server Pages, Socket Overview, JAVA and the net, The networking classes and interfaces, InetAddress: Factory methods, Introspection, TCP/IP server sockets - DataGrams: Datagram packet, Datagram server and client - Introduction to JDBC. Type of JDBC connectivity - Accessing relational database from Java programs - Establishing database connections - Developing Biological Applications using BioJava.

REFERENCE:

1. Gary Cornell, Cay Horstmann, Core Java™ 2, Volume I--Fundamentals, 7th Edition, Prentice Hall of India
2. H. Schildt, (2001), “The Complete Reference – Java 2”, Fourth Edition, Tata McGraw Hill
3. Dietel nad Dietel (2001), “Java: How to program Java 2”, Second Edition, Pearson Education

Course outcome:

The student who complete the course knows

1. The concepts of encapsulation, Inheritance and polymorphism.
2. To create frames and applets
3. To create Server Pages with JDBC connections
4. Basics of BioJava

BIF515 COMPUTER-AIDED DRUG DESIGN AND PHARMACOINFORMATICS CREDITS 3

Learning objective:

This course introduces the concept of pharmacology with information technology for enhancing the process of drug discovery

SYLLABUS:

Computer-aided Drug Design: Concepts and Principles in CADD - 2D and 3D QSAR - Docking and protein-ligand structural recognition techniques - Virtual Screening - Molecular Dynamics - Pharmacophore generation - Advanced concepts in Structural Bioinformatics - Homology modeling: concepts, principles and application - Proteome-based technology

Introduction: Classification of drugs, Major sources of drugs, Common filters for drugs design, Molecular descriptors, Structure activity relationship, Pharmacophore and pharmacophoric graph, Machine learning approach in designing filters; Targets of drug design: Protein as the target, structural and sequence analysis, Nucleus as target, coding and noncoding RNA, SNP analysis, other important targets; Molecular modeling and simulation in drug designing: QM and MM modeling, computation of weak interaction, docking, MD simulation based docking; Pharmacokinetics: One-compartment model, Two-compartment model, Multi-compartment models, Pharmacokinetic parameters, Absorption, Distribution, Metabolism, Excretion, Multiple doses, Salt factor, Bioavailability, Clinical case studies; Pharmacodynamics: Drug receptor action, Direct physiological action, Drug-drug interaction, Polymorphism and drug metabolism, Drug potency and efficacy, Agonists and antagonists, Receptor effector coupling, Spare receptors, Therapeutic index; Types of drug design: Structure based, ligand based, fragment based, metabolites and their importance in drug design; Pharmacogenomics: SNPs analysis, Statistical methods, Gene-gene interaction, Gene – environment interaction, Gene silencing techniques; Pharmacoinformatics: Chemogenomics, chemoinformatics, immunoinformatics, cancer informatics, neuroinformatics, toxicoinformatics, Tools used in pharmacoinformatics, Case studies and applied pharmacoinformatics.

REFERENCE:

1. Malone, P.M., Kier, K.L., Srtanovich, J.E. Drug Information-A Guide for Pharmacists. McGraw-Hill, 2006.
2. Krishnan Namboori P K and Deepak O M. Computational Drug Design and Delivery systems-principles and applications, Springer. 2012.
3. Prasad V. Bharatam, Modeling and Informatics in Drug Design, John Wiley & Sons Inc.2007.

4. Tagelsir Mohamed Gasmelseid, Pharmacoinformatics and Drug Discovery Technologies: Theories and Applications, IGI-Global, 2012
5. Advanced Concepts in Structural Bioinformatics: Structural Bioinformatics: Philip E. Bourne (Editor), Helge Weissig (Editor). ISBN: 978-0-471-20199-1
6. Protein Structure Prediction: A Practical Approach (The Practical Approach Series , No 170) by Michael J. E. Sternberg
7. Computer-aided Drug Design: Practical Application of Computer-Aided Drug Design (Hardcover) by Charifson (Author)
8. Computer-Aided Drug Design. Methods and Applications. Edited by Thomas J. Perun and C. L. Propst Marcel Dekker
9. CADD virtual lab

Course outcome:

The student who complete the course knows

1. Basics of drugs , the rules that govern drug behavior and its classification
2. Identify the drug targets and understand the mode of action

BIF591 ADVANCED PROGRAMMING -LAB CREDIT 1

Learning objective:

This lab course introduces the concept of markup languages and create a web platforms to store retrieve and analyze data

SYLLABUS:

HTML forms; Using CGI.pm module to create dynamic HTML pages, accessing databases - local and NCBI, running blast programs, data retrieval using XML files, using Perl DBI, using GD for graphics in the web, etc. String Manipulation; File Management; Creating User interfaces for Biological Applications; Developing Applets with Java 2D graphics; Modules and Packages in Python; Classes in Python; Bio-python and its applications.

REFERENCE:

1. James Tisdall, Mastering Perl for Bioinformatics, Oreilly Publications
2. Gibas&Jambeck, Developing Bioinformatics Computer Skills, Oreilly Publications
3. Alan Gauld (2000) Learn To program Using Python Addison –Wesley

Course outcome:

Students are expected to learn

1. Create HTML pages
2. Create forms and validate with CGI programming
3. Use DBI connection to create databases from web pages

BIF592 OBJECT ORIENTED PROGRAMMING LAB CREDIT 1

Learning objective:

The course introduces the object-oriented concepts like the encapsulation, Inheritance and polymorphism.

Syllabus:

String Manipulation; File Management; Creating User interfaces for Biological Applications; Developing Applets with Java 2D graphics; Connecting to databases using JDBC – Exception handling in Java.

REFERENCE

1. Gary Cornell, Cay Horstmann, Core Java™ 2, Volume 2, Advanced Features, 7th Edition, Prentice Hall of India

Course outcome:

1. Introduce the basic concept of object oriented programming language with JAVA.
2. Understand string manipualtions and file handling.
3. Understanding frames, applets and web servers.

ELECTIVE I **CREDITS 2**

ELECTIVE II **CREDITS 2**

OPEN ELECTIVE **CREDITS 2**

SSD501 **Soft Skills III** **Credits:1**

Learning Objective:

This course is designed to help the student discover their skills in problem solving and reasoning. These skills can effectively help them in clearing the aptitude tests conducted by companies and help them in clearing various competitive exams like CAT, MAT, RRB, SSC NET etc., This course will teach student how to be confident and prepared with the knowledge of problem solving and reasoning skills. The key learning topics focus on making students to develop more math skills that can help them get better jobs. Applicants will also learn how to develop skills for critical thinking and analytical reasoning. This Course is a complete tool to help you launch your formal preparation for Quantitative section in various aptitude tests like the CAT, GRE and GMAT.

SYLLABUS:

Geometry: 1 D & 2 D: Lines, Angles, Pythagoras Theorem, Triangle & its types, Similar, Congruent, Quadrilateral, Other polygons & Circles. **Mensuration:** 3D: Cuboid, Cube, Cylinder, Cone, Sphere, Frustum etc. **Cubes:** N cuts, N+1 pieces, Painting a cube, Dice, Different views of the same dice. **Alpha Numeric Puzzles:** No: series, letter series, coding & decoding, odd man out, symbols & notation. **Logical Connectivities & Binary Logic;** Conditions: If, Whenever, Wherever, Unless,

Only if, If and only if. **Basic of Non Verbal Reasoning:** Clock wise, Anticlock wise, 1 step, Angles. **Clocks:** Angle, Minute hand & Hour hand speed, Time, Relative speed, Gain/ Loose. **Calendars:** Leap year, Non leap year, Odd days. **Data Interpretation:** Bar chart, Pie chart, Line graph, Table method, Data reasoning. **Syllogism:** All, Some, Some not, No, statements, conclusion. **Net papers solving:** Aptitude questions

Course Outcome:

- To discover the patterns, find lengths, angles, areas, Study the polygons & its properties.
- Process of finding out Volume, LSA, CSA & TSA and many real life applications
- To find the number of cubes after division, Questions related to SA painting etc
- To find the missing letter/number, Analogy, Odd man out, Symbols based questions
- To find the exact conclusion from given statements
- To find the next pattern or odd man out
- To find the angle between the hands, to find the time when the angle is given
- To find the exact day of the week when the date is given
- Understanding the given data and to answer the questions based on that data, Percentage change
- Deductive reasoning
- Solving Aptitude question

ELECTIVES

BIF551

SYSTEMS BIOLOGY

CREDITS 2

Learning objective:

This course provides systems level understanding of the biological systems with the application of different tools and file formats

SYLLABUS:

System Biology - Concepts and working principles of System Biology - Practical applications of System Biology in Life Sciences - Introduction to System Biology platforms Proprietary system Biology platform. Microarray data analysis - Microarray analysis platforms - Introduction to Concepts and principles of Microarray technology - Application of Microarrays in Life Sciences. Different Markup languages used in systems biology. Modeling biological systems: Metabolism, Cell Signaling, Aging, Evolution Introduction to NGS technology

REFERENCE:

1. System Biology: Computational Systems Biology (Hardcover) by Andres Kriete (Editor), Roland Eils (Editor)
2. Stochastic Modelling for Systems Biology. ISBN-10 1-58488-540-8 and ISBN-13 978-158488-540-5
3. Microarray Data Analysis: Gene Expression Data Analysis. A Beginner's Guide By: Helen Causton (Imperial College), J Quackenbush and Alvis Brazma (The European Bioinformatics Institute)
4. A Practical Approach to Microarray Data Analysis (Hardcover) by Daniel P. Berrar (Editor), Werner Dubitzky (Editor), Martin Granzow (Editor)

Course outcome:

1. Practical applications of System Biology in Life Sciences

2. Analysis of microarray in different platforms 3. Use of different markup languages for systemic modeling

BIF561 **COMPUTATIONAL NEUROSCIENCE** **CREDITS**
2

Learning objective:

This course deals with the study of structure and function of nervous system and how information is transmitted from one part to the other with emphasis on physiology, development, anatomy etc.

SYLLABUS:

Systems theory for the analysis of neurons and neural circuits, as well as to cable theory, passive and active compartmental modeling, numerical integration methods, models of plasticity and learning, models of brain systems, and their relationship to artificial neural networks, Modeling using NEURON, different types of neural codes.

REFERENCE:

1. Biophysics of Computation, Christof Koch, Oxford University Press: New York, New York, 1999.

Course outcome:

1. To understand the basics of neuroscience
2. The role of neurotransmitter in information transmittion
3. To have a deeper understanding on the sensory motor systems

BIF562 **NEUROBIOLOGY AND ELECTROPHYSIOLOGY**
CREDITS 2

Learning Objective:

The course deals with understanding the functioning of neuron , its physiological properties and the methods of recording data

SYLLABUS:

Neurons and glia, Action potentials, Synapses, Sensory and Motor functions, Plasticity, Neurobiology of Vision, Attention and Language, Learning and memory systems, Patch clamping technique, Voltage and current clamp.

REFERENCE:

1. Kandel, Eric R., James H. Schwartz, and Thomas M. Jessell. Principles of Neural Science. 4th ed. New York: McGraw-Hill, 2000. ISBN: 0-8385-7701-6.

Course outcome:

1. To understand basics of neuron and the information flow
2. Role of plasticity
3. To have a deeper understanding on the electrophysiological techniques

BIF563 **NEXT-GENERATION SEQUENCING ANALYSIS** **CREDITS**
2

Learning outcome:

Offers an overview of multiple automated pipelines involving an array of tools to analyze data from different next-generation sequencing platforms.

SYLLABUS

Overview of Next Generation Sequencing (NGS), Functional Genomics, and course goals. Basics into the linux and shell scripting. QC and preprocessing of NGS data. fastX and fastQC tools for data filtering, read trimming, adapter clipping. Creating pipelines to automate processing and mapping of data. Mapping NGS data, Overview of read alignment methods. Post-processing of mapped data – making bed and bedgraph files. Organizing and prioritizing pipeline output. Common ChIP-seq analyses: Determining reads in peaks, peak location relative to genes. MEME: Identification of motifs under discreet peaks. MAST: mapping motifs back to genomes. FIMO: determine occurrences of motif in selected sequence. Introduction to RNA-seq and alignment considerations: Tophat and cufflinks vs. Trinity vs. STAR. Alignment of RNA-seq data. Differential gene expression analysis. Gene ontology and gene set enrichment analysis

REFERENCE:

1. Xinkun Wang(2016) ,Next-Generation Sequencing Data Analysis ,CRC Press
2. Alexander Zelikovsky and Ion Mandoiu (2016), Computational Methods for Next Generation Sequencing Data Analysis, Wiley publication

Course outcome:

On completion, the students should be able to use at least one pipeline comprising of publicly available tools to perform analysis of next generation sequencing data.

BIF564

METAGENOMICS AND MICROBIOME

CREDITS

2

Learning Objective:

Includes studies of microbial species populations from different environmental habitats and host organs, such as soil, gut, etc. with respect to their genomic diversity at family, genus, species, sub-species and clonal levels.

SYLLABUS:

Introduction to metagenomics, microbiome, species populations, habitat, Vectors, host organisms. Taxonomic divisions, analysis methods for 16s RNA, impact of bacterial diversity (microbiome) to human health, types of sequencing methods: 16S RNA and DNA, practice analysis of 16s sequencing data using different platform, Types of Metagenomics Sequencing Methods, Typical Metagenomics Pipeline. Analysis and interpretation of 16S rRNA sequencing

REFERENCE:

1. Diana Marco (2010), Metagenomics: Theory, Methods and Applications
2. Frans J. de Bruijn (2011), Handbook of Molecular Microbial Ecology I, Wiley Online Books
3. Frans J. de Bruijn (2011), Handbook of Molecular Microbial Ecology II, Wiley Online Books

Course outcome:

Students successfully completing this course should have a reasonable understanding of population and genomic diversity of microbiota in different organs, especially in the human gut.

Learning Objective:

Considers a data science approach on how to collect, store, analyze and visualize very large set of biological data.

SYLLABUS:

Introduction of databases and tools. Measure of data: 4V's (volume, velocity, variety, and veracity). Types of Digital Data, Introduction to Big Data, Big Data Analytics, History of Hadoop, Apache Hadoop, Analysing Data with Hadoop, Hadoop Streaming, Hadoop Echo System, The Design of HDFS, HDFS Concepts, Command Line Interface, Hadoop file system interfaces. Types of big data in bioinformatics, Micro array data analysis, Gene–gene network analysis, Pathway analysis, Disease network analysis, Evolutionary data analysis, Protein-Protein interaction analysis, sequence analysis. Tissue level expression analysis with RNA-sequencing, Understanding whole genome sequencing and whole exome sequencing. Graphical visualization tools like Cytoscape

REFERENCE:

1. Anand Rajaraman and Jeffrey David Ulman, “Mining of Massive Datasets”, Cambridge University Press, 2012.
2. Glen J. Myat, “Making Sense of Data”, John Wiley & Sons, 2007
3. Gregg Hartvigsen, A Primer in Biological Data Analysis Using R, Columbia University Press, 2014

Course outcome:

This course should enable the students to have insights on how to map large scale biological data from diverse sources in an interactive and meaningful way in the framework of a comprehensive database.

Learning Objective:

Guides through the steps toward success in a biotech/bioinformatics industry job or as a startup entrepreneur.

SYLLABUS:

Job Search Considerations and searching, Key steps involved in job searching, Identifying job interest, Creating a Compelling Marketing Campaign: Resume, covering letter, pitch and online profile, In Depth Research on job, Four Stages of Networking, Different types of interviews and how to get ready for an interview. Motivation strategies, Troubleshooting job search strategies, Effective negotiation, Social media based job search, Career advancement with job success, Startups. Career success in the area of biotechnology and bioinformatics. How to emerge as a startup entrepreneur in the biotech arena. Legal aspects of startups.

REFERENCE:

1. Dee, Phil(2006). Building a Successful Career in Scientific Research
2. GYSBERS, Norman C; MOORE, Earl J, (1987). Career Counseling Skills and Techniques For Practitioners

Course outcome:

Students taking this course should have a clear overview of important scientific, administrative, marketing and legal aspects of a biotech company.

SEMESTER – 4**BIF599****DISSERTATION/THESIS****CREDIT 10**

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Evaluation Scheme and Grading System**CREDIT SYSTEM OF EVALUATION*****Introduction**

Amrita School of Biotechnology follows a credit-based system for evaluation under a semester pattern. This allows flexibility on courses, time frame, teaching and learning, evaluation procedures and mobility.

Academic year and Semesters

An academic year (July to June) consists of two semesters and possibly a summer term. Each semester has a minimum of 80-85 teaching days and about 8-10 days for the end semester examinations.

Credit based Academic System

A credit-based system is a systematic way of describing an educational programme by attaching credits to its components. Credit is a way of quantifying the knowledge content. When enough credits are accrued or earned, the programme is completed successfully.

Credit system makes educational programmes easy to understand and compare both nationally and internationally. It facilitates mobility, academic flexibility and universality and helps universities to organize as well as reorganize their study programmes quickly. It can be used across a variety of programmes and modes of delivery.

Programme

An educational programme specializing in a specific area covers many knowledge segments. An example is the B.Sc. programme in Biotechnology.

Allotment of Credits

Credits are allocated to the knowledge segments giving due importance to their weightings.

The sum of the credits allotted to the knowledge segments decides the programme credits. The programme is successfully completed from the academic angle, once the specified programme credits have been earned.

Example: (For a B.Sc. Biotechnology Programme)

| Knowledge Segment | Category | Credits |
|--|----------|---------|
| Language, Cultural Education & Soft Skills | S | 17 |
| Mathematics, Physics & Chemistry | M | 20 |
| Core Lifesciences | C | 67 |
| Laboratory Courses | L | 16 |
| Project/Dissertation Thesis | P | 7 |
| Total Credits for programme completion | | 127 |

Under each knowledge component, the credits are again distributed among the identified courses. The number of courses and the credits allocated to each, could vary. However, the student need to get only the minimum credits in each of the components as mentioned in the example and a prescribed minimum total number of credits for successfully completing the academic programme. Additional credits taken will be an added advantage from the professional angle, but not from the academic requirements.

Course Credits

Each course, except for a few special courses, has a certain number of credits assigned to it depending on the lectures, tutorials, laboratory works and contact hours in a week. Lectures (L) and Tutorials (T) will have one credit per each contact hour in a week. Laboratory and Practical (P) classes carry one credit for two / three contact hours in a week. Projects, fieldwork etc are given a specific number of credits without any direct reference to the hours spent.

Example:

a) A Course on Plant Biology

Number of Lecture hours per week – 3 Credits: 3
 Number of Tutorial hours per week – 1 Credits: 1
 Total credits for the course 3 + 1 = 4

b) A Laboratory Course on Microbiology:

Number of Laboratory hours per week -3 Credits: 2

These are normally indicated in the curriculum, as follows:

| Category | Course Code | Course Title | Hours per week | | | Credits |
|----------|-------------|------------------|----------------|---|----|---------|
| | | | L | T | P | |
| C | BIO223 | Plant Biology | 3 | 1 | 0 | 4 |
| L | MIC281 | Microbiology Lab | 0 | 3 | 0 | 2 |
| P | BIO399 | Project | 5 | 5 | 20 | 7 |

Curriculum

Curriculum is the framework of an academic programme. In the credit based system, curriculum will specify the category, course code, course title, course delivery (Lectures / Tutorials / Lab / Project) and the credits. Curriculum is presented semester-wise for convenience and will take into account all the knowledge segments and their assigned credits. The total credits to be earned for programme completion will be specified clearly. Our curriculum has the following credit allocations among the knowledge segments:

B.Sc. Biotechnology

| Knowledge Segments | Category Admissions | 2016 Admissions onwards |
|--|---------------------|-------------------------|
| Language, Cultural Education & Soft Skills | S | 17 |
| Mathematics, Physics & Chemistry | M | 20 |
| Core Lifesciences | C | 67 |

| | | |
|---|---|-----|
| Laboratory Courses | L | 16 |
| Project/Dissertation Thesis | P | 7 |
| Total credits needed for programme completion | | 127 |

B.Sc. Microbiology

| Knowledge Segments | Category | 2016 |
|---|------------|--------------------|
| | Admissions | Admissions onwards |
| Language, Cultural Education & Soft Skills | S | 17 |
| Mathematics, Physics & Chemistry | M | 20 |
| Core Lifesciences | C | 66 |
| Laboratory Courses | L | 18 |
| Project/Dissertation Thesis | P | 7 |
| Total credits needed for programme completion | | 128 |

For the **M.Sc. programmes**, a total of 76 credits (Biotechnology), 76 Credits (Microbiology), 79 credits (Bioinformatics) have to be earned. 10 credits of project work have to be earned additionally for the successful completion of the programme.

Credit System Flexibility

Credit system allows flexibility on the selection of courses and time frame for completion of the programme. It also provides a good blend of teaching and learning, ensuring credible evaluation procedures and student mobility. The credit system is evolved around the teacher and the taught.

The prominent features of the credit system cover continuous evaluation of students' performance through well-planned assessment procedures and the flexibility to allow a student to progress at a pace suited to his / her individual ability and convenience, subject to certain conditions. While a prescribed minimum number of credits are to be earned for the award of degree, a minimum level of performance is necessary for progressing with the studies.

Class Advisors and Counsellors

Each class will have one/two class counsellor(s) to help and guide the students in the academic process, solve their problems, if there is any, as also to provide counselling and guidance for the needy. They will also monitor the progress of the students in their studies and report the same to their parents periodically.

Checks and Controls in the Credit System

To achieve purposeful flexibility, a good system control is needed. Hence there are specific rules and procedures to be adhered to in the credit system. Certain courses in each knowledge segment are identified as core courses and others as electives. There is mandatory registration and credit earnings requirements for core courses. Electives are free to be chosen from those offered, for registration. While it is mandatory to register for the elective courses, failure to earn credits in them does not necessarily mean repeating the courses. Another elective course may be permitted as a replacement course.

Certain courses are pre-requisites for advanced courses. For example, Molecular Biology could be a pre-requisite for Genetic Engineering. This means that the student cannot take Genetic Engineering unless he/she has completed Molecular Biology. Here the term completion means that the student has registered for the course, done all assignments and tests, attended the class with 75% or more attendance and has written the end semester examination. The student need not have to earn credits (i.e., pass the course) for fulfilling the pre-requisite needs.

How to go about with the credit system?

The first step, in the credit based system, is the registration for the various courses. For first semester, registration is done at the beginning of the semester. In the subsequent semesters (2nd semester onwards), registration will be done at the end of the previous semester. The students have to enroll for the courses, earlier registered, at the start of the semester.

During enrolment, one can drop the earlier registered courses or add new courses, with the approval of the faculty advisor / Counsellor and the concurrence of the Dean of the School.

All students will have to register before a specified date. However for valid reasons, late registration with a fine will be permitted up to a specified date. These dates will be announced well in advance.

Registration

Students will be made aware of all information on the courses being offered in that semester. There will be an on-line registration procedure. The students have to enter the details of the courses they want to register for. In the first few semesters there may not be much of a choice to decide on. As one progresses, the flexibility will become more evident. Students have to consult the faculty members who have been identified as their advisors, for advice and assistance in registration.

Minimum and Maximum credits for which one can register in a semester is specified in the relevant curricula. Any deviations will need the approval from the Dean, School of Biotechnology.

A student is permitted to register / enroll for courses only if he / she has:

- a) Paid all fees and has no dues to the university
- b) Has maintained a progress, as required by the university
- c) Has completed any pre-requisite courses prescribed
- d) Has no disciplinary action pending against him / her

Conduct of Courses

Credit system encourages learning. Apart from regular class lectures, students will be given major assignments which will form a part of the course and will also be considered for evaluation. Seminars, design and other assignments, technical paper writing, quizzes etc. could also be a part of the course being conducted.

The teacher offering the course will evaluate the performance of the students at regular intervals and in the end semester examination. A class committee comprising all teachers handling all the courses for the class, the class advisor and students' representatives will monitor the conduct of all the courses of a class.

A course committee comprising all teachers / mentors offering a course in all the campuses will decide on the course plan, evaluation procedure and any midway correction to be taken. Decisions taken by this committee will be informed to all students who have registered for the course. The class / course committees without students' representative will finalise the grades and results for the class / course.

It is mandatory for the students to appear for the end semester examination / supplementary examination for the completion of the course.

If the Project work is not satisfactory, the student will be asked to continue the project till he / she completes it satisfactorily.

Attendance

- Additionally, a 5% weightage is given to attendance above the total weightage
- All students are required to attend 100% of the classes.
- Leave of absence could be applied for in the form provided in the School website/Store and will be granted by Counsellor only in genuine cases.
- Two types of leave are permitted, namely, Duty Leave and Other leaves
- All leaves except Duty leave put together, as sanctioned by the Counsellor should not exceed 25% of the total classes, for eligibility to appear for the end semester examination.

• Marks for attendance

- i) 5 marks for 96-100% attendance
- ii) 4 marks

for 91-95% attendance iii) 3 marks for 86-90%

attendance iv) 2 marks for 80-85% attendance v)

0 mark for 75-79% attendance

vi) 'FA' for < 75% attendance

Students representing the University events either within the campus or outside the campus will be marked as present (OD). However, students should submit an OD form approved by Chairperson/Dean prior to attending the event. OD form submitted after the event will not be entertained and the student will be marked absent.

Grading System

| 2015 Admissions onwards | | |
|-------------------------|-------|--|
| Grade Point | Grade | Rating |
| O | 10 | Outstanding |
| A+ | 9.5 | Excellent |
| A | 9 | Very Good |
| B+ | 8 | Good |
| B | 7 | Above Average |
| C | 6 | Average |
| P | 5 | Pass |
| F | 0 | Failed |
| FA | 0 | Failed due to lack of Attendance |
| I | - | Incomplete (Awarded only for Laboratory project courses) |
| W | - | Withheld |

If the student secures 'F' grade in any of the courses, he/she can reappear for the supplementary exam.

If the student secures 'FA' grade in any of the courses, he/she has to re-register(redo) for the course when it is being offered next.

A student who has been awarded 'I' grade in the laboratory courses shall take up additional laboratory sessions during the first two months of the next semester and earn a pass grade, which will be reflected in the next semester's grade sheet.

If a student is absent for the end semester examination, he/she will be allowed to reappear on proper evidence for his/her absence.

Grade Point Average (SGPA)

Based on the credits for which the student has registered and the grades awarded, Semester Grade Point Average [SGPA] and Cumulative Grade Point Average [CGPA] are calculated.

$$SGPA = \frac{\sum (C_i \times GP_i)}{\sum C_i}$$

where C_i is the number of credits for i th course in that semester and GP_i is the grade points earned by the student for that course.

Cumulative Grade Point Average (CGPA)

The overall performance of a student at any stage of the M.Tech. program is evaluated by the Cumulative Grade Point Average (CGPA) upto that point of time.

$$CGPA = \frac{\sum (C_i \times GP_i)}{\sum C_i}$$

where C_i is the number of credits for i th course in any semester and GP_i is the grade points earned by the student for that course. The summation is over all the courses registered by the student and evaluated during all the semesters up to that point of time, including the failed courses. The CGPA is rounded off to two decimals. The ranking of the students in a batch at any intermediate or final stage is based on CGPA.

Grade Sheet

Grade sheet issued to the student at the end of the semester will contain the following information.

1. Name, Roll No., Grade Sheet No., Semester, Branch, Month and year of Examination.
2. Course Code, Course Title, Credits and Grade Obtained, Grade Points Earned for the courses registered.
3. Credits registered and earned during the semester.
4. Cumulative Credits earned and Grade Points.
5. SGPA.
6. CGPA.

Revaluation of Answer Papers

An aggrieved student can request for revaluation of answer script of the end semester examination, through a well laid out procedure. There will be revaluation fee for each paper. If the revaluation leads to a better grade, the revised grade will be awarded to the

student and in such cases the revaluation fee will be refunded in full. Revaluation is allowed only for lecture-based courses.

Course Completion

A student is said to have successfully completed a course and earned the corresponding credits, if he / she has;

- Registered for the course.
- Put in 75% or more attendance in the course.
- Written the periodical tests and end semester examination.
- Obtained a pass grade D or above in the course.
- No disciplinary proceedings against him / her.

REMEDIAL MEASURES

Supplementary Examination

- Students with 'F' Grade may take the supplementary examination in a course up to a maximum of three additional attempts (excluding main end semester examination) carrying the previous internal assessment marks earned by them.
- Students failing to pass the course after two additional attempt shall henceforth appear for the supplementary examination for the entire 100 marks and the internal assessment marks earned by them in their regular registration shall not be considered.
- Grade Rule for supplementary examination: Supplementary exams will be evaluated against the most recent grade rule (whenever the course was offered recently during a regular semester)
- Fee for the supplementary examination will be Rs.300/ - per paper during the regular duration of the program, after which the student shall pay Rs.1000 per attempt.

Re-registration/Redo

A student who has not secured a pass grade in a course in the initial registration can register for the same course when offered next along with the junior batch. Students with FA grade are also permitted to register. Two chances of re-registration is allowed per course apart from the regular registration.

Contact Courses

Students in the final semester with one or two arrears with F grade(s) can register for the contact course, if offered. The contact course will run for 45 / 60 hours of contact classes depending on the credit load of the course. Students with FA grade in a given course cannot register for the course under this option.

Runtime Re-do Course

Students with F / FA grade in course can register for a runtime re-do course, if available, on the condition that the total number of credits registered in the semester shall not exceed 28 credits. Runtime re-do courses are run concurrently with a regular semester and would last a full semester.

Discipline

Every student is required to observe strict discipline and decorous behaviour both inside and outside the campus and should not indulge in any activity which may bring down the prestige of Amrita Vishwa Vidyapeetham.

A disciplinary action committee will deal with any act of indiscipline or misbehaviour, unfair practice in the class / university examination etc., and its decision on the action to be taken shall be final. Serious acts of indiscipline may even attract penalty leading to expulsion from the University.

Award of the Degree

A student will be declared eligible for the award of the Degree, if he / she has:

- Registered and earned the credits for all the core courses and project work.
- Earned the minimum required number of credits for the branch of study as specified in the curriculum.
- Earned the specified number of credits in all categories.
- No disciplinary action pending against him / her.
- There are no outstanding dues against him / her.

Classification of successful candidates

A student shall be considered to have successfully completed the programme, if he/she has

-

- a) registered and successfully completed all the core courses and projects.
- b) earned the required minimum number of credits as specified in the curriculum corresponding to the branch of his/her study, within the stipulated time.
- c) Earned the specified number of credits in all the categories of courses.

Candidates, who have successfully completed the programme, shall be classified as follows:

- a) Candidates securing a CGPA of 8.00 and above – DISTINCTION. b) Candidates securing a CGPA between 6.50 and 7.99 – FIRST CLASS and the same be mentioned in the Degree Certificate’.
- c) If the programme is completed after six(B.Sc.)/four(M.Sc.) semesters of study, the candidates securing a CGPA of 6.50 and above shall be classified to have completed the programme, only with FIRST CLASS.

