

GITAM UNIVERSITY

(Declared as Deemed to be University U/S 3 of UGC Act, 1956)



**REGULATIONS & SYLLABUS
OF
M.Sc. (Bioinformatics)
(w.e.f admitted batch 2010 -11)**

Gandhi Nagar Campus, Rushikonda
VISAKHAPATNAM – 530 045
Website: www.gitam.edu

REGULATIONS

(w.e.f. admitted batch 2010-11)

1.0 ADMISSIONS

- 1.1 Admissions into M.Sc. (Bioinformatics) programme of GITAM University are governed by GITAM University admission regulations.

2.0 ELIGIBILITY CRITERIA

- 2.1 A pass in any B.Sc. degree are equivalent with any two of the following subjects: Biochemistry, Biotechnology, Microbiology, Bioinformatics, Chemistry, Medical Lab Technology, Genetics, Home science, Food and Nutrition, Zoology, Botany, Agriculture, Aqua Culture, Veterinary Sciences, Environmental Science, Physics, Computer Sciences and Mathematics.

- 2.2 Admissions into M.Sc. will be based on the following:

- (i) Score obtained in GAT (PG), if conducted.
- (ii) Performance in Qualifying Examination / Interview.

The actual weightage to be given to the above items will be decided by the authorities before the commencement of the academic year.

3.0 STRUCTURE OF THE M.Sc. PROGRAMME

- 3.1 The Programme of instruction consists of:

- (i) A core programme imparting to the student specialization of the stream concerned.
- (ii) Carry out a project approved by the Department and submit a report.

- 3.2 Each academic year consists of two semesters. M Sc programme has a curriculum and Name of the Course content (syllabi) for the Name of the Courses recommended by the Board of Studies concerned and approved by Academic Council.

- 3.3 Project Dissertation has to be submitted by each student individually.

4.0 CREDIT BASED SYSTEM

- 4.1 Each Name of the Course is assigned certain number of credits which will depend upon the number of contact hours (lectures & tutorials) per week.

- 4.2 In general, credits are assigned to the Name of the Courses based on the following contact hours per week per semester.

One credit for each Lecture / Tutorial hour.

One credit for two hours of Practicals.

Two credits for three (or more) hours of Practicals.

- 4.3 The curriculum of M.Sc. programme is designed to have a total of 80 - 100 credits for the award of M Sc degree. A student is deemed to have successfully completed a particular semester's programme of study when he / she earns all the credits of that semester i.e., he / she has no 'F' grade in any Name of the Course of that semester.

5.0 MEDIUM OF INSTRUCTION

The medium of instruction (including examinations and project reports) shall be English.

6.0 REGISTRATION

Every student has to register himself/herself for each semester individually at the time specified by the Institute / University.

7.0 CONTINUOUS ASSESSMENT AND EXAMINATIONS

7.1 The assessment of the student's performance in each Name of the Course will be based on continuous internal evaluation and semester-end examination. The marks for each of the component of assessment are fixed as shown in the Table 1.

Table 1: Assessment Procedure

| S.No. | Component of assessment | Marks allotted | Type of Assessment | Scheme of Examination |
|-------|----------------------------|----------------|--------------------------|---|
| 1 | Theory | 30 | Continuous evaluation | (i) Two mid semester examinations are to be conducted for 10 marks each. (ii) 5 marks are allocated for quiz. (iii) 5 marks are allocated for assignments. |
| | | 70 | Semester-end examination | The semester-end examination question paper in theory Name of the Courses will be for a maximum of 70 marks. |
| | Total | 100 | | |
| 2 | Practicals | 100 | Continuous evaluation | (i) One examination for a maximum of 20 marks will be conducted by the teacher handling the lab Name of the Course during mid of the semester (ii) One examination for a maximum of 70 marks will be scheduled at the end of the semester by the Head of the Department concerned. HoD will appoint one examiner from the department not connected with the conduct of regular lab, in addition to the teacher who handled the lab Name of the Course in the semester. (iii) 10 marks are allocated regular performance in the lab. |
| 3 | Project work (IV semester) | 200 | Project evaluation | (i) 150 marks are allocated for evaluation of the project work dissertation submitted by the candidate. (ii) 50 marks are allocated for the presentation of the project work & viva-voce at the end of |

| | | | | |
|---|------------|----|-----------|---|
| | | | | the semester, for which HoD of the department concerned shall appoint two examiners. |
| 4 | Viva -Voce | 50 | Viva-voce | 50 marks are allocated for comprehensive viva to be conducted at the end of the each semester. HoD of the department concerned shall appoint two examiners. |

8.0 REAPPEARANCE

- 8.1 A Student who has secured 'F' Grade in any theory Name of the Course / Practicals of any semester shall have to reappear for the semester end examination of that Name of the Course / Practicals along with his / her juniors.
- 8.2 A student who has secured 'F' Grade in Project work shall have to improve his report and reappear for viva – voce Examination of project work at the time of special examination to be conducted in the summer vacation after the last academic year.

9.0 SPECIAL EXAMINATION

- 9.1 A student who has completed the stipulated period of study for the degree programme concerned and still having failure grade ('F') in not more than 5 Name of the Courses (Theory / Practicals), may be permitted to appear for the special examination, which shall be conducted in the summer vacation at the end of the last academic year.
- 9.2 A student having 'F' Grade in more than 5 Name of the Courses (Theory/practicals) shall not be permitted to appear for the special examination.

10.0 ATTENDANCE REQUIREMENTS

- 10.1 A student whose attendance is less than 75% in all the Name of the Courses put together in any semester will not be permitted to attend the end - semester examination and he/she will not be allowed to register for subsequent semester of study. He /She has to repeat the semester along with his / her juniors.
- 10.2 However, the Vice Chancellor on the recommendation of the Principal / Director of the University college / Institute may condone the shortage of attendance to the students whose attendance is between 66% and 74% on genuine medical grounds and on payment of prescribed fee.

11.0 GRADING SYSTEM

- 11.1 Based on the student performance during a given semester, a final letter grade will be awarded at the end of the semester in each Name of the Course. The letter grades and the corresponding grade points are as given in Table 2.

Table 2: Grades & Grade Points

| Grade | Grade points | Absolute Marks |
|-------|--------------|----------------|
| O | 10 | 90 and above |
| A+ | 9 | 80 – 89 |
| A | 8 | 70 – 79 |
| B+ | 7 | 60 – 69 |
| B | 6 | 50 – 59 |
| C | 5 | 40 – 49 |
| F | Failed, 0 | Less than 40 |

- 11.2 A student who earns a minimum of 5 grade points (C grade) in a Name of the Course is declared to have successfully completed the Name of the Course, and is deemed to have earned the credits assigned to that Name of the Course. However, a minimum of 28 marks is to be secured at the semester end examination of theory Name of the Courses in order to pass in the theory Name of the Course.

12.0 GRADE POINT AVERAGE

- 12.1 A Grade Point Average (GPA) for the semester will be calculated according to the formula:

$$\text{GPA} = \frac{\Sigma [C \times G]}{\Sigma C}$$

Where

C = number of credits for the Name of the Course,

G = grade points obtained by the student in the Name of the Course.

- 12.2 Semester Grade Point Average (SGPA) is awarded to those candidates who pass in all the Name of the Courses of the semester.
- 12.3 To arrive at Cumulative Grade Point Average (CGPA), a similar formula is used considering the student's performance in all the Name of the Courses taken in all the semesters completed up to the particular point of time.
- 12.4 The requirement of CGPA for a student to be declared to have passed on successful completion of the M Sc programme and for the declaration of the class is as shown in Table 3.

Table 3: CGPA required for award of Degree

| | |
|---------------------|--------------|
| Distinction | $\geq 8.0^*$ |
| First Class | ≥ 7.0 |
| Second Class | ≥ 6.0 |
| Pass | ≥ 5.0 |

* In addition to the required CGPA of 8.0, the student must have necessarily passed all the Name of the Courses of every semester in **first attempt**.

13.0 ELIGIBILITY FOR AWARD OF THE M.Sc. DEGREE

- 13.1 **Duration of the programme:**
A student is ordinarily expected to complete the M.Sc. programme in four semesters of two years. However a student may complete the programme in not more than four years including study period.
- 13.2 However the above regulation may be relaxed by the Vice Chancellor in individual cases for cogent and sufficient reasons.
- 13.3 A student shall be eligible for award of the M.Sc. degree if he / she fulfils all the following conditions.
- Registered and successfully completed all the Name of the Courses and projects.
 - Successfully acquired the minimum required credits as specified in the curriculum corresponding to the branch of his/her study within the stipulated time.
 - Has no dues to the Institute, hostels, Libraries, NCC / NSS etc, and
 - No disciplinary action is pending against him / her.
- 13.4 The degree shall be awarded after approval by the Academic Council.

RULES

1. With regard to the conduct of the end-semester examination in any of the practical Name of the Courses of the programme, the Head of the Department concerned shall appoint one examiner from the department not connected with the conduct of regular laboratory work, in addition to the teacher who handled the laboratory work during the semester.
2. In respect of all theory examinations, the paper setting shall be done by an external paper setter having a minimum of three years of teaching experience. The panel of paper setters for each Name of the Course is to be prepared by the Board of Studies of the department concerned and approved by the Academic Council. The paper setters are to be appointed by the Vice Chancellor on the basis of recommendation of Director of Evaluation / Controller of Examinations.
3. The theory papers of end-semester examination will be evaluated by two examiners. The examiners may be internal or external. The average of the two evaluations shall be considered for the award of grade in that Name of the Course.
4. If the difference of marks awarded by the two examiners of theory Name of the Course exceeds 14 marks, the paper will have to be referred to third examiner for evaluation. The average of the two nearest evaluations of the three shall be considered for the award of the grade in that Name of the Course.
5. Panel of examiners of evaluation for each Name of the Course is to be prepared by the Board of Studies of the department concerned and approved by the Academic Council.
6. The examiner for evaluation should possess post graduate qualification and a minimum of three years teaching experience.
7. The appointment of examiners for evaluation of theory papers will be done by the Vice Chancellor on the basis of recommendation of Director of Evaluation / Controller of Examinations from a panel of examiners approved by the Academic Council
8. Project work shall be evaluated by two examiners at the semester end examination. One examiner shall be internal and the other be external. The Vice Chancellor can permit appointment of second examiner to be internal when an external examiner is not available.

SYLLABUS
M.Sc. (Bioinformatics)
Programme Code: SPRBI 200700
FIRST SEMESTER

| Sl. No. | Course Code | Name of the Course | Scheme of Instruction | | Scheme of Examination | | | Credits to be awarded |
|---------------|-------------|--|-----------------------|-----|-----------------------|---------------|-----|-----------------------|
| | | | Hours per week | | Duration in Hrs. | Maximum Marks | | |
| | | | L/T | D/P | | S | C | |
| 1 | SPRBI 101 | Molecular Biology | 4 | --- | 3 | 70 | 30 | 4 |
| 2 | SPRBI 102 | Basic Mathematics and Biostatistics-I | 4 | --- | 3 | 70 | 30 | 4 |
| 3 | SPRBI 103 | Biomolecules and Bioenergetics | 4 | --- | 3 | 70 | 30 | 4 |
| 4 | SPRBI 104 | Computers Basics and programming in BioC | 4 | --- | 3 | 70 | 30 | 4 |
| 5 | SPRBI 111 | Molecular Biology Lab | --- | 12 | 6 | -- | 100 | 2 |
| 6 | SPRBI 112 | 'C' programming Lab | --- | 12 | 6 | -- | 100 | 2 |
| 7 | SPRBI 113 | Viva voce | --- | | - | 50 | - | 1 |
| Total: | | | | | | 650 | | 21 |

S- Semester End Examination C- Continuous Evaluation

M.Sc. (Bioinformatics)
SECOND SEMESTER

| Sl. No. | Course Code | Name of the Course | Scheme of Instruction | | Scheme of Examination | | | Credits to be awarded |
|---------------|-------------|---|-----------------------|-----|-----------------------|---------------|-----|-----------------------|
| | | | Hours per week | | Duration in Hrs. | Maximum Marks | | |
| | | | L/T | D/P | | S | C | |
| 1 | SPRBI 201 | Basic Mathematics and Biostatistics-II | 4 | --- | 3 | 70 | 30 | 4 |
| 2 | SPRBI 202 | Database management systems & Biological databases | 4 | --- | 3 | 70 | 30 | 4 |
| 3 | SPRBI 203 | Biological Sequence analysis | 4 | --- | 3 | 70 | 30 | 4 |
| 4 | SPRBI 204 | BioC++ and Data Structures | 4 | --- | 3 | 70 | 30 | 4 |
| 5 | SPRBI 211 | DBMS & Biological Databases Lab | --- | 12 | 6 | -- | 100 | 2 |
| 6 | SPRBI 212 | C ++ programming & Biological Sequence Analysis Lab | --- | 12 | 6 | -- | 100 | 2 |
| 7 | SPRBI 213 | Viva voce | --- | | - | 50 | -- | 1 |
| Total: | | | | | | 650 | | 21 |

S- Semester End Examination C- Continuous Evaluation

**M.Sc. (Bioinformatics)
THIRD SEMESTER**

| Sl. No. | Course Code | Name of the Course | Scheme of Instruction | | Scheme of Examination | | | Credits to be awarded |
|---------------|-------------|------------------------------------|-----------------------|-----|-----------------------|---------------|-----|-----------------------|
| | | | Hours per week | | Duration in Hrs. | Maximum Marks | | |
| | | | L/T | D/P | | S | C | |
| 1 | SPRBI 301 | Molecular Modeling | 4 | --- | 3 | 70 | 30 | 4 |
| 2 | SPRBI 302 | Biocomputing (BioPerl & BioJava) | 4 | --- | 3 | 70 | 30 | 4 |
| 3 | SPRBI 303 | Genomics | 4 | --- | 3 | 70 | 30 | 4 |
| 4 | SPRBI 304 | Proteomics | 4 | --- | 3 | 70 | 30 | 4 |
| 5 | SPRBI 311 | Molecular Modeling and BioPerl Lab | --- | 12 | 6 | -- | 100 | 2 |
| 6 | SPRBI 312 | Genomics & Proteomics Lab | --- | 12 | 6 | -- | 100 | 2 |
| 7 | SPRBI 313 | Viva voce | --- | | - | 50 | -- | 1 |
| Total: | | | | | | 650 | | 21 |

S- Semester End Examination C- Continuous Evaluation

**M.Sc. (Bioinformatics)
FOURTH SEMESTER**

| Sl. No. | Course Code | Name of the Course | Scheme of Instruction | | Scheme of Examination | | | Credits to be awarded |
|-----------------|--------------|---|-----------------------|-----|-----------------------|---------------|-----|-----------------------|
| | | | Hours per week | | Duration in Hrs. | Maximum Marks | | |
| | | | L/T | D/P | | S | C | |
| 1 | SPRBI 401 | Drug Designing , Bioethics and IPR | 4 | --- | 3 | 70 | 30 | 4 |
| 2 (Elective) | SPRBI 402(a) | Systems Biology | 4 | --- | 3 | 70 | 30 | 4 |
| | SPRBI 402(b) | Machine learning and implementation of Algorithms | | | | | | |
| | SPRBI 402(C) | Immuniinformatics | | | | | | |
| 3 | SPRBI 411 | Drug Designing Lab | --- | 12 | 6 | -- | 100 | 2 |
| 4 | SPRBI 412 | Viva voce | --- | -- | -- | 50 | -- | 1 |
| 5 | SPRBI 413 | Project & Seminar | --- | | - | 50 | 150 | 6 |
| Total: | | | | | | 550 | | 17 |

S- Semester End Examination C- Continuous Evaluation

Total Credits: 80

M.Sc. (Bioinformatics) I Semester

SPRBI 101 : Molecular Biology

UNIT - I

Structure and properties of purine and pyrimidine bases, nucleosides, nucleotides, chemical synthesis of oligonucleotides, physicochemical properties of nucleic acids, two-dimensional structure of DNA, Different forms of DNA – A, B and Z, circular and super coiling DNA, Types of RNA, structure of t-RNA, sequencing of DNA, DNA methylation, DNA damage by physical and chemical agents.

UNIT - II

Models and strategies of DNA replication. – semiconservative, discontinuous and rolling circle model, origin and directions of replication, Enzymes involved in DNA replication in prokaryotes and eukaryotes, inhibitors of DNA replication. DNA repair mechanisms. Models of general recombination, transposition of DNA- transposable elements and retroposons.

UNIT - III

Principles of transcription, prokaryotic and eukaryotic RNA polymerases, promoters, initiation of transcription, chain elongation and termination. Transcription factors, posttranscriptional processing of pre-mRNA, Processing of rRNA and tRNA, RNA editing.

UNIT - IV

General features of genetic code, structural components of prokaryotic and eukaryotic ribosomes, protein synthesis in prokaryotes and eukaryotes, inhibitors of protein synthesis, post translational modifications and protein targeting.

Unit - V

Prokaryotic gene regulation: Structure and function of Lac, Ara, Trp and His operons, Phase variation in Salmonella, Lytic and Lysogenic phases of Bacteriophage λ life cycle, Sporulation in *Bacillus subtilis*.

Eukaryotic gene regulation: Interaction of eukaryotic transcriptional factors with DNA - helix-turn-helix motif, zinc finger motif, leucine zipper, helix-loop-helix motif. Steroid hormone induced gene expression. Development and differentiation in Drosophila- role of homeoboxes

Text Books:

- Molecular Biology of the gene, Watson, J.D., Fifth Edition, Pearson Education International.
- Molecular Cell Biology, Lodish, H., Scott, M.P., Matsudaira, P., Darnell, J., Zipursky, L., Kaiser, C.A., Berk, A. and Krieger, M., Fifth Edition, W.H. Freeman and Co.
- Molecular Cell Biology of the Cell, Alberts, B., Johnson, A., Lewis, J., Raff, M., Roberts, K. and Walter, P. Fourth Edition, Garland Science, Taylor and Francis Group.
- Genes VIII, Lewin, B. Eighth Edition, Pearson Education International.

M.Sc. (Bioinformatics) I Semester

SPRBI 102: Basic Mathematics and Biostatistics - I

UNIT - I

Algebra; Logarithms, Quadratic equations, Simple problems on cubic equations, Solution of a system of linear equations using determinants.

UNIT - II

Trigonometry and Analytical Geometry: Trigonometric ratios – Simple problems – introductions to complex numbers and De Moivre's theorem, Cartesian coordinates in two dimensions – Distance formula, Straight line, Slope of a line, Intercepts of a line, Equation of a line, Intersection of two lines, Angle between two lines, - Introduction to Circle, ellipse and parabola.

UNIT - III

Limits - differentiation of Elementary Functions; Integrations – integrations as antiderivative, integration of simple functions; Definite and Indefinite integrals,

UNIT - IV

Graphical techniques, Measures of central tendency – mean, median, and mode; measures of dispersion – Range, Standard Deviation, And Variance; Coefficient of variation, quartiles and percentiles.

UNIT - V

Basic notions of set theory, Definitions of Permutations and combinations, probability of an event and properties of probability, Conditional probability, independent events, Bayes theorem, Discrete and continuous random variables.

Text Books:

- Calculus, Vol. I and II; Narayanan, S. and Manicavachaagam Pillai, T.S., First Edition, Vishwanathan Printers and Publishers.
- Engineering mathematics, Veerarajan, T, Third Edition, Tata McGraw Hill Publishing Co. Ltd.
- Trigonometry, Algebra and Calculus, Veerarajan, T., Third Edition, Tata McGraw Hill Publishing Co. Ltd.
- Biostatistics, Arora, P.N. and Malhan, P.K., First Edition, Himalaya Publishing House.

Reference Books:

- Text Book of Integral Calculus, Sharma, A.K., First Edition, Discovery Publishing House.
- Higher Engineering Mathematics, Grewal, B.S., Thirty seventh Edition, Khanna Publishers.
- A foundation for analysis in health sciences In Biostatistics, Daniel, W. W. (Editor), Sixth Edition, John Wiley.
- Statistical methods in the Biological and Health Sciences, Milton, J.S., Second Edition, McGraw Hill Publishers.
- Fundamentals of Biostatistics, Rosner, B., Sixth Edition, Duxbury Press.
- Statistical methods in Biology, Bailey, N.T.J., Third Edition, Oxford University Press.

Note: The emphasis will be on concepts and problem solving rather than rigor.

M.Sc. (Bioinformatics) I Semester
SPRBI 103: Biomolecules and Bioenergetics

UNIT – I

Principles of bioenergetics- free energy, enthalpy and entropy. Free energy changes in biological transformations in living systems. Redox potential. Phosphate group transfer potential and ATP, high energy compounds, oxidation and reduction reactions and enzymes, Mitochondrial electron transport system-organization of components and importance. Substrate level phosphorylation, oxidative phosphorylation, mechanism and theories of oxidative phosphorylation. Respiratory chain inhibitors and uncouplers of oxidative phosphorylation.

UNIT - II

Classification, chemical properties, structural and functional roles of carbohydrates and lipids. Glycolysis, TCA cycle, β -oxidation of fatty acids. Biosignaling- Molecular mechanism of signal transduction, secondary messenger – cAMP, cGMP, IP₃, Diacylglycerol and nitric oxide.

UNIT - III

Amino acids- classification, structure and physiochemical properties. Chemical synthesis of peptides. Proteins – classification, purification and Characterization. Structural organization, sequence determination, 2D and 3D-Conformation and Ramachandran plots. Protein folding, Protein degradation-ubiquitin pathway. General catabolic reactions of amino acids, urea cycle.

UNIT - IV

Enzymes – Classification, Assay, Nature and Mapping of active site, Factors affecting enzyme activity, Kinetics of single substrate enzyme catalyzed reactions- Michaelis and Menten equation, Line weaver – Burk, Edaie –Hofstee and Hanes plots, V_{max}, K_m, K_{cat}, specificity constant (K_{cat}/K_m) and their significance, Kinetics of multisubstrate reactions – classification with examples.

UNIT –V

Nature of enzyme catalysis- acid-base, covalent and metal ion catalysis. Mechanism of action of serine proteases, carboxy peptidase and ribonuclease. Enzyme inhibition- competitive, non-competitive and uncompetitive inhibition, Irreversible inhibition. Enzyme regulation-allosteric and covalent modification and zymogen activation, Multienzyme complexes, Ribozyme, abzyme.

Text Books:

- Understanding Enzymes, Palmer, T, First Edition, Harvard publishing.
- Biochemistry by Stryer, L., Fourth Edition, Freeman W.H. and CO.
- Text book of Biochemistry, West and Todd, Fourth Edition. Oxford and IBH.
- Principles of Biochemistry, Nelson Cox, Fourth Edition. Freeman.
- Biochemistry, Voet and Voet, Third Edition, John Wiley and Sons.

M.Sc. (Bioinformatics) I Semester

SPRBI 104: Computers Basics and Programming in BioC

UNIT - I

Introduction to computers: Anatomy of digital computer; Memory units: RAM, ROM, types of RAM, introduction to auxiliary memory; Definition and functions of operating systems. Simple examples of algorithms and flowcharts.

UNIT - II

Basic of C: Introduction to C, Historical development of C, Features of C, Character Set, Constants, Variables, Data types and Key words, Operators, Operator – Precedence and Associativity, Typecasting, Basic I/O functions.

UNIT - III

Control structures: If statement, if-else statement, nested if-else, Switch Statement, Break statement, Continue statement, go to statement. Loops: for loop, while loop, do-while loop. Functions: Need of functions, function parameters, Passing values between functions. Calling Convention, function declaration and prototypes, calling function by value and by reference, Recursion.

UNIT - IV

Arrays: Introduction to arrays, Initialization of arrays, passing array elements to a function, pointers and arrays, two dimensional array.

Strings: What are strings, array of string, and standard library string functions.

UNIT -V

Structures and Unions: What is a structure, Declaration of structure members and structure variables, how structure elements are stored, initialization of structure, Nested structure, Array of structures, Union, Difference between Union and structure.

File handling: Introduction-File Structure-File handling functions-File types - Unbuffered and Buffered files-files Error Handling-Low level file I/O Redirection and Piping, function I/O.

Text Books:

- Let us C, Yashwant K., Fourth Edition, BPB publications.
- The C programming language, Ritchie, D.M., Second Edition, Prentice Hall Publishers.
- Computer Fundamentals and Applications, Balaguruswamy, E., Second Edition, Tata McGraw-Hill Publishing Co. Ltd.

Reference books:

- Fundamentals of Information technology, Alexis Leon and Mathews Leon, First Edition, Vikas Publishing House Pvt. Ltd.
- Programming with C, Venugopal, K.R., Sudeep R.P., Second Edition, Tata McGraw Hill.
- Introduction to Computers, Norton, P., Sixth Edition, Tata McGraw Hill..

**M.Sc. (Bioinformatics) I Semester
SPRBI 111: Molecular Biology Lab**

1. Isolation of plasmid
2. Isolation of DNA.
3. Isolation of RNA.
4. Determination of T_m of DNA.
5. Restriction digestion of λ -DNA and separation by agarose gel electrophoresis.
6. Ligation of DNA fragments.
7. Amplification of DNA by PCR.
8. Southern blotting technique.
9. RFLP analysis.
10. RAPD analysis.
11. Bacterial transformation.
12. DNA Finger printing.
13. Enzyme kinetics- P^H
14. Amylase activity

**M.Sc. (Bioinformatics) I Semester
SPRBI 112: 'C' Programming Lab**

1. Write a program to find the Factorial of a given number using Recursion.
2. Write a program to find out max & min elements with their positions in a given array and then sort the above array.
3. Write a program to find whether the given string is Palindrome or not.
4. Given an array of strings write a program to sort the string in Dictionary Order.
5. Write a C program to calculate variance of the given data.
6. Write a C program to calculate correlation coefficient of the given data.
7. Write a C program to calculate regression lines of the given data.
8. Program to translate m-RNA sequence to protein sequence.
9. Write a program to count no of bases in given DNA sequence.
10. Write a C program to calculate the melting temperature of polynucleotide using its sequence as input.

M.Sc. (Bioinformatics) II Semester
(New syllabus w.e.f. admitted batch 2010-11)

SPRBI 201: Basic Mathematics and Biostatistics - II

UNIT – I

Concepts of hypothesis and testing – Sampling techniques, Confidence interval for a population mean of the sample, The t-distribution, Confidence interval for the difference between two population means, Confidence interval for the variance of a normally distributed population, Confidence interval for the ratio of the variances of two normally distributed populations.

UNIT – II

Introduction to multivariate analysis – Correlation, rank correlation, linear regression, chi – square test for goodness of fit, ANOVA.

UNIT – III

Probability density and mass functions and distribution functions – Binomial poisson and normal distribution, exponential distribution Parametric estimation using maximum likelihood and Bayesian methods (MAP estimates), Hidden Markov models, Parametric estimation for HMMs (Baum-Welch and Viterbi training).

UNIT - IV

Matrices: Different types of matrices-Addition, Subtraction and Multiplication of matrices, Transpose of a matrix, Singular matrix and Inverse of a matrix.

Vectors: The concept of a vector – Dot product, Cross product, Angle between two vectors, Scalar triple product, Divergence, Curl, Equation of a normal.

UNIT –V

Partial differentiation, Differential equations: First order ordinary differential equations, Laplace transform – Definition, Properties, transform of derivatives – introduction to fourier series and transforms, derivate as a rate of change and maxima and minima problems.

Text Books:

- Engineering mathematics, Veerarajan, T, Third Edition, Tata McGraw Hill Publishing Co. Ltd. .
- Biostatistics, Arora, P.N. and Malhan, P.K., First Edition, Himalaya Publishing House.
- Statistical methods in Bioinformatics, Warren, J., Gregory, E. and Grant, R., First Edition, Springer-Verlag, Berlin.

Reference Books:

- Text Book of Integral Calculus, Sharma, A.K., First Edition, Discovery Publishing House.
- Higher Engineering Mathematics, Grewal, B.S., Thirty seventh Edition, Khanna Publishers.
- Biological sequence analysis, Durbin, Eddy, Krogh and Mitchison, Eight Edition, Cambridge University Press.
- A foundation for analysis in health sciences In Biostatistics, Daniel, W. W. (Editor), Sixth Edition, John Wiley.
- Statistical methods in the Biological and Health Sciences, Milton, J.S., Second Edition, McGraw Hill Publishers.
- Fundamentals of Biostatistics, Rosner, B., Sixth Edition, Duxbury Press.
- Statistical methods in Biology, Bailey, N.T.J., Third Edition, Oxford University Press.

Note: The emphasis will be on concepts and problem solving rather than rigor.

M.Sc. (Bioinformatics) II Semester
(New syllabus w.e.f. admitted batch 2010-11)

SPRBI 202: Database management systems and Biological databases

UNIT - I

Types of databases. Data abstraction. Data models (ER, Hierarchical and Network). Relational database design. Indexing and hashing. Multimedia databases – concepts and applications. Distributed databases.

UNIT – II

SQL: Data definition, data manipulation and control statements. Database objects, tables, views, sequences and synonyms. Application development using Visual Basic as front end: variables, procedures and controlling program executors, forms, standard controls.

UNIT - III

Concepts regarding nature and type of data available in biological databases: Biological literature databases, biodiversity information databases, microbiological databases – (eukaryotic, bacterial and viral), cell type databases, toxicology databases, spectroscopic databases, protein and nucleic acid sequence databases, genome databases.

UNIT - IV

Concepts regarding nature and type of data available in structural databases (macromolecular and small molecule), metabolic pathways databases, signal transduction pathways databases, molecular interaction databases, gene expression databases.

UNIT - V

Tools for searching databases. BLAST & FASTA for searching databases, different types of BLAST & FASTA. Significance of BLAST & FASTA.

Text books:

- Database system Concepts, Silberschatz, A., Korth, H.F. and Sudarshan, S., Fourth Edition, McGraw Hill Publishers.
- An introduction to Database systems, Date, C.J., Seventh Edition, Addison Wesley Publishers.
- Fundamentals of Database systems, Elmasri and Navathe, Fourth Edition, Addison Wesley Publishers.
- Principles of Database systems, Ullman, J. D., Second Edition, Galgotia Publications.
- Introduction to Bioinformatics, Attwood, T.K. and Parry, D.J., Second Edition, Addison Wesley Longam Limited.

Reference books:

- Bioinformatics: Sequence and Genome Analysis, Mount, D., First Edition, Cold Spring Harbor Laboratory Press.
- Bioinformatics: sequence, structure and databanks, Higgins, D. and Taylor, W., First Edition Oxford University Press, Oxford.
- Nucleic Acids Research (Journal) – January database issue of every year (free and open access at <http://nar.oxforduniversitypress.org>)
- Bioinformatics – a practical guide to the analysis of Genes and Proteins, Baxevanis, A.D. and Francis Ouellette, B.F., First Edition, John Wiley & Sons.

M.Sc. (Bioinformatics) II Semester
(New syllabus w.e.f. admitted batch 2010-11)

SPRBI 203: Biological Sequence Analysis

UNIT -I

Edit distance, Similarity score matrices (PAM, BLOSUM), Pairwise sequence alignment-Dot plot matrix - repeat matches, palindromic sequences, Dynamic programming – Needleman-Wunsch algorithm for global alignment, Smith-waterman algorithm for local alignment., Pairwise alignment with gap penalty functions, Linear space algorithm.

UNIT -II

Multiple sequence alignment: sum-of-pairs scoring scheme, entropy based scoring schemes, multidimensional dynamic programming, progressive alignment, profile alignment Hidden Markov Models in pairwise sequence alignment, profile HMMs for sequence families, multiple sequence alignment by profile HMM training.

UNIT –III

Molecular phylogenetics: Introduction to phylogeny, Phylogenetic trees and Sequence graphs, Phylogenetic tree construction methods - Distance based methods - Clustering based methods (UPGMA and Neighbor Joining), optimal criterion method (FM and Minimum Evolution methods) and character based methods. traditional parsimony methods - Exhaustive, Branch and Bound, and heuristic. Maximum Likelihood method, Tree evaluation methods - Bootstrap.

UNIT -IV

Probabilistic models of evolution – Jukes cantor model and Kimura model. Using the likelihood for inference. Combined multiple sequence alignment and phylogeny – Sankoff and Cedergren method.

UNIT -V

Prediction of RNA secondary structure: Nussinov folding algorithm, energy minimization, covariance models.

Text Books:

- Biological sequence analysis, Durbin, Eddy, Krogh and Mitchison, Eighth Edition, Cambridge University Press.
- Essential Bioinformatics, Jin xiong, Cambridge University Press.

Reference Books

- Bioinformatics: Sequence and Genome Analysis, Mount, D., First Edition, Cold Spring Harbor Laboratory Press.
- Introduction to Bioinformatics, Lesk, A.M., First Edition, Oxford University Press.

M.Sc. (Bioinformatics) II Semester
(New syllabus w.e.f. admitted batch 2010-11)

SPRBI 204: BioC++ and Data structures

UNIT - I

Introduction to C++, A Simple C++ Program, Stream Bases I/O, Reference Variables, and Decision Making And Branching – If Statement, If-else Statement, Nested If-else, break Statement, Switch Statement, continue Statement, go to Statement , Decision Making and Looping – For, While, Do-While, structures, Function Definition, User Defined And Library Function, function Declaration and prototypes, calling function, Inline Functions, Function / Operator Over loading, Default Arguments, Runtime Memory Management.

UNIT – II

A Simple Program Using Class Access, Specifiers. Accessing Class Members, Defining Member Functions, Memory Allocation for Objects, Static Data Members, Static Member Functions, Friendly Functions. Base Class, Derived Class, Single, Multiple, Multilevel, Hierarchical, Hybrid Inheritance, Need for Virtual Functions, Virtual Base Classes, Pure Virtual Functions, Virtual Destructors. Generic Classes, Function Template, Class Template.

UNIT - III

Constructors, Parameterized Constructor, Copy Constructor, Multiple Constructors in a Class, Constructors with Default Arguments, Dynamic Constructors, Destructors. Scope Resolution Operator.

UNIT - IV

LISTS, STACKS & QUEUES: Abstract Data Types, Representation & implementation of ADT list, Representation, Implementation and applications of ADT stack and Queue, Singly Linked List, Doubly linked list, Circular linked lists.

UNIT - V

Sorting- Heapsort, Quicksort, Mergesort , Sorting lower bounds , Radix sort, Bucket sort, Hashing, Binary Search Trees, Red-Black Trees, B-Trees, Binomial Heaps, Data Structures for Union-Find

Text Books:

- Object Oriented Programming with C++, Balagurusamy, E., Third Edition, Tata McGraw-Hill.
- Mastering C++, Venugopal, K.R., Rajkumar, T., Ravishankar, First Edition, Tata McGraw-Hill Publishing Co. Ltd.
- Fundamentals of Data Structures, Horowitz E. and Sahani, S., First Edition, Galgotia Booksourve Pvt. Ltd.
- Object Oriented Programming using C++, Lafore, R., Fourth Edition, Sams Publishers.

M.Sc. (Bioinformatics) II Semester
SPRBI 211 : DBMS and Biological Databases Lab

- 1 Use of SQL: Database design for biological data. Data manipulation. Queries, views and forms.
- 2 Databases: PubMed, PubMed Central, Public Library of Sciences. NCBI, EBI, ExPASy.
- 3 Sequence and structure databases: organization of data, contents and formats of database entries, retrieval of data using text-based search tools, sources of data, method for deposition of data to databases. Genbank, EMBL, DDBJ, SWISS-PROT, TrEMBL, PIR-PSD, TIGR, SANGER, COG, EST, STS GSS. PDB, NDB, CCSD.
- 4 Derived databases: sources of primary data, methods for deriving the secondary data, organization, formats, interpretation: Prosite, PRODOM, Pfam, PRINTS, CATH, SCOP, DSSP, FSSP, DALI, Others – KEGG.
- 5 Bioinformatics resources at the species level: ICTV database, Viral genomes at NCBI, VBRC, VBCa, PBRC and subviral RNA database, treebase.
- 6 Use of BLAST for searching sequence databases.
- 7 Structural alignment

M.Sc. (Bioinformatics) II Semester
SPRBI : 212 C++ Programming & Biological Sequence Analysis Lab

- 1 Write a C++ program for the following experiments:
 - a. Classes
 - b. Constructors
 - c. Inheritance
 - d. Polymorphism
- 2 Sequence alignment using Needleman-Wunsch method.
- 3 Effect of scoring matrices and gap penalties on sequence alignment.
- 4 Multiple sequence alignment.
- 5 Use of HMM profiles.
- 6 Phylogenetic tree construction using parsimony for protein sequences.
- 7 Phylogenetic tree construction using parsimony for nucleic acid sequences.
- 8 Phylogenetic tree construction using UPGMA.
- 9 Phylogenetic tree construction using neighbor joining.
- 10 Displaying phylogenetic information.
- 11 RNA secondary structure prediction.

M.Sc. (Bioinformatics) III Semester

SPRBI 301: Molecular Modeling

UNIT - I

Concepts of computational chemistry. Molecular mechanics: general features of force fields - bond stretching & bending, torsional angle, out of plane bending, cross terms, non-bonded interactions, point charges, calculation of atomic charges, polarization, Vander Waals interactions, hydrogen bond interactions.

UNIT - II

Quantum mechanics: Hamiltonian operators, Overview of Schrödinger's wave equation, Born Oppenheimer approximation, Application of Hartree-Fock equations to molecular systems, Molecular graphics.

UNIT - III

Energy minimization: statement of the problem, line minimization and energy minimization, Simulation methods: Time averages, ensemble averages, Molecular dynamics methods, Monte Carlo methods, Differences between MD and MC, Simulated Annealing procedure. Initial configuration.

UNIT - IV

Protein structure comparison and alignment- introduction to graph theory - Planar Graphs, Euler's Formula, Distance matrices, Structural alignment methods (CE, VAST, DALI, SSAP, TM-align).

UNIT -V

Comparative modeling of proteins: Homology modeling – Superimposition, Template selection, Backbone modeling, loop building (Search/generation), Side chain generation, and Model evaluation and validation. Fold recognition methods - Threading-Bowie-Luthy-Eisenberg, Profile-Profile alignment, combined modeling approaches. Abinitio method - Anfinsen Thermodynamic Hypothesis.

Text books:

- Molecular modeling: principles and applications, Andrew R. L., Second Edition, Prentice Hall.
- Structural bioinformatics, Bourne, P.E. and Weissig, H., Second Edition.

Reference Books:

- Bioinformatics: Sequence and Genome Analysis, Mount, D., First Edition, Cold Spring Harbor Laboratory Press.
- Introduction to Protein Architecture, Lesk, A.M., First Edition, Oxford University Press.
- Introduction of Molecular Crystallography, Mepherson, A., First Edition, John Wiley Publications.
- Proteins: structure and molecular properties, Creighton, T.E., Second Edition, Freeman W.H. and Company.

M.Sc. (Bioinformatics) III Semester

SPRBI 302: Biocomputing (BioPerl and BioJava)

UNIT - I

Unix/Linux- Basics, Filesystems, Essential Commands and Text Editors.

UNIT - II

Perl - Introduction, Data Types -Lists/Arrays and Hash, Scalar Functions, Quoting Basics, Functions/Subroutines, Operators and Control Structures, Data Types: Boolean, Pattern Matching and Regular Expressions, File Handling and File Manipulation, Error Handling, Variable Scope, Mathematical Functions, Special Variables, References, Aggregate data structures, Using Modules.

UNIT - III

BioPerl Modules- Sequences and Strings, Motifs and Loops, flow control, String operators and Writing files, Subroutines-Scoping, Arguments, Command line arguments, Passing data to subroutines, Modules and Libraries, Debugging, CPAN – Comprehensive PERL archive network) Data Structures and Algorithms for Biology Restriction Maps and Restriction Enzyme Data, Working and Analyzing with GenBank and BLAST data Subroutines, Text and String Processing.

UNIT - IV

Introduction - java, applications, “hello world” two ways, Variables and Operators, Control Structures, Objects, Arrays. Applet Class, basic HTML, the applet HTML tag, TCP/IP, UDP, servers, clients.

UNIT - V

Setup, Alphabets and Symbols, Basic Sequence Manipulation, Translation, Proteomics, Sequence I/O, Annotations, Locations and Features, BLAST and FASTA, Counts and Distributions, Weight Matrices and Dynamic Programming, User Interfaces, Genetic Algorithms.

Text books:

- Beginning Perl for Bioinformatics, Tisdall, J.D., First Edition O'Reilly Publishers.
- Programming Perl, Wall, W., Christiansen, T. and Orwant, J., Third Edition, O'Reilly Publishers.
- Java-2: The complete Reference, Naughton, P. and Schildt, H., Third Edition, McGraw Hill Publishers.

Reference Books:

- Computing Concepts with Java 2 Essentials”; Horstmann, C.S., Second Edition, John Wiley Publishers.
- Object Oriented Design and Applications, Benjamin, Cummings and Booch, G., Second Edition, Addison Wesley Publishers.

M.Sc. (Bioinformatics) III Semester

SPRBI 303 : Genomics

UNIT - I

Genome organization, DNA sequencing - Combinatorial approaches to genome sequencing – shot gun method, Hierarchical method, High throughput sequencing method. Fragment and map assembly, Research tools for genome assembly - Phred, Phrap, Consed.

UNIT - II

Genome databases: Viral databases, pathogen databases, bacterial databases, fungal databases, human databases, plant databases. Genome browsers.

UNIT - III

Structural Genomics: Gene and genome annotation (identifying fine structure of genes – exons, introns, promoters, enhancers, DNA motifs, splice sites, transcriptional and translational factors , finding repetitive elements – CpG islands etc.)

UNIT - IV

Functional Genomics: cDNA, EST, SAGE, MPSS and RNA expression. Predicting function of gene, DNA microarrays- design, visualization of data, analysis (clustering of microarray data through K-means technique), computation analysis tools for correlation of gene expression data to biological processes, algorithmic approaches to clustering gene expression data and applications – Methods and tools for identification of disease associated genes in molecular diagnostics (molecular markers).

UNIT - V

Comparative genomics: Introduction and overview of genome comparison (homology, paralogy, synteny – gene order), genome alignment, genome rearrangements - sorting by reversals, break point graphs, interleaving graphs and hurdles, duality theorem for genomic distance, genome duplications, Various tools in comparative genomics (MuMmer, BLAST2).

Text Books:

- Bioinformatics, Andrzej Polanski and Marek Kimmel, First Edition, Springer Publications.
- Bioinformatics and Functional Genomics, Pevsner, J., John Wiley and Sons.
- Principles of genome analysis and Genomics, Primrose, S.B. and Twyman, R.M., Third Edition, Blackwell Publishing Company.
- Essential Bioinformatics, Jin xiong, Cambridge University Press.

Reference Books

- Bioinformatics: Sequence and Genome Analysis, Mount, D., First Edition, Cold Spring Harbor Laboratory Press.
- Introduction to Bioinformatics, Lesk, A.M., First Edition, Oxford University Press.
- Essentials of Genomics and Bioinformatics, Sensen, C.W., First Edition, Wiley-VCH Publishers.

M.Sc. (Bioinformatics) III Semester

SPRBI 304: Proteomics

UNIT - I

Basic methods for studying proteomics - Proteome - Isolation of proteins, Purification of proteins - Principles of electrophoresis - Capillary electrophoresis, SDS PAGE, Principles of chromatography - Gel chromatography, ion exchange chromatography, affinity chromatography, Protein digestions techniques.

UNIT – II

Structure prediction Tools:

X-ray crystallography technique, Nuclear Magnetic Resonance (NMR), Mass spectroscopy (MS) – Electron Spray Ionization (ESI) - Matrix Assisted Laser Desorption Ionization (MALDI) – Time of Flight(TOF) in determining the structure of protein.

UNIT – III

Insilico Tools:

Primary sequence analysis, Secondary structure prediction (Chou-Fasman, GOR, Neural Network) Conformational properties of Proteins.

UNIT- IV

Functional Proteomics:

Wet bench and insilico tools for protein-protein interactions. Predicting function of the protein - Motifs, Domains, Profiles; Protein sequence to structure to function relationship.

UNIT - V

Comparative proteomics:

Introduction and overview of proteome comparison, 2D gel and Microarray - techniques – Acquisition and analysis of data, Tools for correlation of protein expression data to biological processes, Applications of proteomics.

Text books

- Keith Wilson - Biochemical techniques
- Introduction to Bioinformatics by Arthur M. Lesk
- Mass spectrometry, principles and applications by I. Howe, D.H.Williams, and R.D. Bowen 2nd edition, McGraw Hill, London, 1981.
- Introduction to Proteomics - Tools for the new biology by Daniel .C.Liebler Humana press 2002.

M.Sc. (Bioinformatics) III Semester
SPRBI 311 : Molecular modeling and BioPerl Lab

1. Generating 3D representations from 2D descriptions of small molecules.
2. Use of molecular mechanics for geometry optimization of a small molecule.
3. Evaluate energy of a small molecule using a: CNDO b: ab initio using 631G basis set.
4. Align, superimpose and compare structures of protein using protein modeling softwares.
5. Polypeptide conformational analysis using Monte-Carlo and Molecular Dynamics methods.
6. Secondary structure prediction Servers: PHD, PSIPRED
7. Prediction of transmembrane helices.
8. Use Perl/BioPerl to convert sequence information between different formats for alignment and for accessing a local database.
9. Use Perl/BioPerl to convert DNA sequence information to amino acid sequence.
10. Use of BioJava for creating web-interface.

M.Sc. (Bioinformatics) III Semester
SPRBI 312 : Genomics and Proteomics lab

1. Genomic databases and characterization of genomes.
2. To predict/ORF for genomic/DNA sequences of the prokaryotic and eukaryotic origin.
3. SNP analysis
4. Contig and Genome assembly.
5. Functional annotation.
 - predicting function of protein using protein – protein interaction pipelines.
 - predicting function of protein various pipelines

M.Sc. (Bioinformatics) IV Semester
SPRBI 401 : Drug Designing, Bioethics and IPR

UNIT- I

What are drugs, Drug discovery methods, requirements of a drug: binding, delivery (absorption, distribution), stability (metabolisation, elimination), toxicity and synthesizability, Applications of drug discovery.

UNIT - II

First and Second generation of drug designing: QSAR, Fundamentals of QSAR-objectives, expressions of biological activity, QSAR parameters related to chemical structure, Analysis of results - correlative methods, and Regression analysis., MFA, 3-D QSAR, QSAR descriptors, Finding new drug targets to treat diseases.

UNIT - III

Rational drug designing – Target identification, lead identification, lead optimization, Toxicology studies, Preclinical trials, Clinical trails, FDA registration.

UNIT - IV

CADD - Computer aided drug design, Pharmacophore properties, Ligand based drug design and structure based drug design, Denovo ligand design, Virtual screening, Limitations of CADD. **Molecular Docking** – Docking problem, Principles and methods of docking: Rigid body and flexible docking and 3-D database search approaches.

UNIT - V

Bioethics and Intellectual property rights (IPR) -The legal and socioeconomic impacts of biotechnology; public education of the process of the processes of biotechnology involved in generating new forms of life for informed decision making. General principles of Intellectual property rights (IPR); Patents and methods, application of patents; Legal implications and copy rights; International treaties for protection of IP – Bem, Paris, TRIPS, WIPO, Treaties, Biodiversity convention, Bioremediation, farmers and industrial rights.

Text books:

- Jeff Hasty, Joel Pradines, Milos Dolnik, and J. J. Collins Advances in Drug discovery techniques by Alan L. Harvey.
- Structure based drug design, Penelope W Codding.
- Biotechnologies and Development, Sasson, A., UNESCO Publications
- Intellectual Property Rights on Biotechnology, Singh, K., BCIL, New Delhi.

ELECTIVE PAPERS

M.Sc. (Bioinformatics) IV Semester SPRBI 402(a): Systems Biology

UNIT - I

Introduction, basics and applications of systems biology. Systems Microbiology: System Structure Identification, System Behavior Analysis, System Control, System Design, Measurement for Systems Biology

The cells as a well stirred bioreactor, Michaelis Menten kinetics, a genetic switch in Lambda phage, synthetic genetic switches, stability analysis, Modeling *E.coli* chemotaxis, Genetic oscillators.

UNIT - II

Cell systems biology: computational cell biology, computer simulation of the cell, modeling approaches: differential equation, dynamic systems theory, dealing with uncertainty, computational modeling.

Importance of diffusion and gradients for cellular regulation, local excitation, global inhibition model, Rapid Pole-to-pole oscillations in *E. coli*, Models for Eukaryotic gradient sensing.

UNIT - III

Developmental Systems Biology: System structure identification, Network Structure Identification: Bottom-Up Approach, Top-Down Approach, Parameter Identification

Building and organism starting from a single cell, Quorum sensing, *Drosophila* development, Whole cell simulation, Virtual erythrocytes, pathological analysis, fermentation analysis, flux balance analysis, minimal gene complement.

UNIT - IV

Metabolic systems biology: system behavior analysis, Simulation, Analysis Methods: bifurcation analysis, metabolic control analysis, and sensitivity analysis. Robustness of biological systems, Complex Engineering Systems

UNIT - V

Classification of metabolic pathways, metabolic pathway databases – KEGG, EMP, Malarial parasite metabolic pathways, EcoCyc and MetaCyc, Boehringer-Mannheim biochemical pathways.

References books:

- Foundations of Systems Biology, Hiroaki Kitano, First Edition, The MIT Press.
- Molecular Cell Biology of the Cell, Alberts, B., Johnson, A., Lewis, J., Raff, M., Roberts, K and Walter, P, Fourth Edition, Taylor and Francis Group.
- Noise-based switches and amplifiers for gene expression, Jeff Hasty, Joel Pradines, Milos Dolnik, and Collins, J. J. (2000). PNAS, USA 97: 2075-2080.
- Construction of a genetic toggle switch in *Escherichia coli*, Gardner, T. S., Charles R., Cantor and Collins, J. J. (2000) Nature 403, 339-342.

M.Sc. (Bioinformatics) IV Semester
SPRBI 402(b): Machine learning and implementation of Algorithms

UNIT – I

Definition, goals and applications of machine learning. Training data, concept representation, function approximation. Representing concepts as decision trees. Recursive induction of decision trees. Searching for simple trees and computational complexity. Active learning with ensembles

UNIT – II

Experimental Evaluation of Learning Algorithms: Measuring the accuracy of learned hypotheses. Comparing learning algorithms: cross-validation, learning curves, and statistical hypothesis testing. Artificial Neural Networks.

UNIT – III

Bayesian Learning and Instance-Based Learning: Probability theory and Bayes rule. Naive Bayes learning algorithm. Parameter smoothing. Generative vs. discriminative training. Logistic regression. Bayes nets and Markov nets for representing dependencies. Constructing explicit generalizations versus comparing to past specific examples. k-Nearest-neighbor algorithm. Case-based learning.

UNIT – IV

Graph Algorithms: Graphs and digraphs. Shortest path problems. Complexity. Bellman's optimality principle. Dijkstra's algorithm. Shortest spanning trees. Kruskal's greedy algorithm. Prim's algorithm for shortest spanning trees. Networks. Flow augmenting paths. Ford-fulkerson algorithm for maximum flow. assignment problems. bipartite matching.

UNIT – V

Text Processing: Pattern matching algorithms- Brute force, the Boyer-Moore algorithm, the KMP algorithm, tries- standard tries, compressed tries, suffix tries, text compression- Huffman coding algorithm.

Text books

- Fundamentals of Data Structures, Horowitz E. and Sahani, S., First Edition, Galgotia Booksource Pvt. Ltd.
- Data structures and program design in C++, Robert L.Kruse and Alexander J.Rybe, Prentice hall

M.Sc. (Bioinformatics) IV Semester SPRBI 402(c): Immunoinformatics

Unit – I

Basics of the Immune System: Innate & Adaptive Immunity, Cells of the Immune System, Antigens, Antibodies-Immunoglobulin Classes & Subclasses.

Unit – II

Membrane Receptors for Antigen: BCR, TCR, Major Histocompatibility Complex- MHC Polymorphism, Causes & Supertypes of MHC; Antigen Processing & Presentation: The Cytosolic & Endocytic Pathway, Epitopes-Affinity Maturation, Recognition of Antigen by B Cells, Neutralizing Antibody.

Unit – III

Immunoinformatics-Principles and its Uses; Databases, Tools and Web Resources for Immunoinformatics: The International ImMunoGeneTics information system (IMGT), AntigenDB, The Immune Epitope Database (IEDB), The Immuno Polymorphism Database (IPD).

Unit – IV

Epitope Mapping & Prediction: B-cell epitope prediction methods, T-cell epitope prediction methods; Role of Immunogenomics & Immunoproteomics in Vaccine Development, Peptide Modeling.

Unit – V

Computational Vaccinology: Concept, Application & Workflow; Computer Aided Selection of Vaccine Antigens; Vaccine candidate design, Reverse Vaccinology, Vaccinomics role in Bioinformatics.

Text Books

- Flower Darren R. Bioinformatics for Vaccinology Publisher: UK, John Wiley & Sons Inc.
- Flower Darren R. Immunoinformatics: Predicting Immunogenicity In Silico Publisher: New Jersey, Humana Press.
- Kindt, Thomas J., Osborne Barbara A., Goldsby Richard A. Kuby Immunology 6th Edition. Publisher: New York, W. H. Freeman.
- Lund Ole , Nielsen Morten , Lundegaard Claus, Kesmir Can, Brunak SÅ,ren. Immunological Bioinformatics. Publishesr: London, MIT Press

Reference Books

- Foundation Novartis. Immunoinformatics: Bioinformatic Strategies for Better Understanding of Immune Function. Publisher: Chichester, John Wiley & Sons Inc.
- Roitt Ivan, Delves Peter. Roitt's Essential Immunology 10th Edition. Publisher: Canada, Blackwell.
- Ellis Ronald W. Vaccines: New Approaches to Immunological Problems. Publisher: Stoneham, Butterworth-Heinemann

**M.Sc. (Bioinformatics) IV Semester
SPRBI 411: Drug Design lab**

1. QSAR.
2. 3D-QSAR.
3. Evaluation of synthesizability and ease of formulation.
4. Virtual Screening.
5. ADMET
6. Structure Based Drug Designing.
7. Docking: Online servers and Standaloon packages.

**M.Sc. (Bioinformatics) IV Semester
SPRBI 412: Viva-Voce**

**M.Sc. (Bioinformatics) IV Semester
SPRBI 413: Project work and Seminar**