

## Syllabus of B.Sc. (Bioinformatics)

Subject- Bioinformatics (as one subject)

B.Sc. I Year *wef. 2014-15*

### Semester I

Paper I: Basic of Bioinformatics 85 marks  
Practicals 50 marks

### Semester II

Paper II: Mathematics I 85 marks  
Practicals 50 marks

B.Sc. II Year

Semester III *Wef. 2015-16*

Paper III: Structural Bioinformatics 85 marks  
Practicals 50 marks

### Semester IV

Paper IV: Mathematics II 85 marks  
Practicals 50 marks

B.Sc. III Year *wef. 2016-17*

### Semester V

Paper I: Computer graphics, Machine learning and Bioperl 85 marks  
Practicals 50 marks

### Semester VI

Paper I: Informatics in omics and application 85 marks  
Practicals 50 marks

15 marks CCE as per higher education norms in each semester.  
Practicals based on theory are to be designed by the concerned teacher.

*Minimum Passing marks will be 28/85*

*[Signature]*  
*30/7/14*

*[Signature]*  
*30/7/14*

*Hamendra*  
*30/7/14*  
*[Signature]*  
*30/7/14*

**Session 2014-15**

**B.Sc. Part - I Semester - I**

wef. 2014 - 15

**Paper I - Basics of Bioinformatics**

**Max. Marks-85**

**Unit I Introduction to bioinformatics**

Introduction to bioinformatics, history of bioinformatics, Scope of bioinformatics  
Bioinformatics- a multidisciplinary approach and its relation with molecular  
biology. Bioinformatics in India-The flourishing future  
Applications of Bioinformatics

**Unit II Biological Database and its Types**

General Introduction of Biological Databases;  
Nucleic acid databases (GenBank, DDBJ, and EMBL).  
Protein databases (Primary, Composite, and Secondary).  
Specialized Genome databases: (SGD, TIGR, and ACeDB).  
Structure classification databases (CATH, SCOP, and PDBsum)  
Structure database (PDB)

**Unit III Data storage and retrieval and Interoperability**

Flat files, relational, object oriented databases and controlled vocabularies. File Format  
(Genbank, DDBJ, FASTA, PDB, SwissProt).  
Introduction to Metadata and search; Indices, Boolean, Fuzzy, Neighboring search.

**Unit IV Sequence Alignments and Visualization**

Introduction to Sequences, alignments and Dynamic Programming;  
Local alignment and Global alignment (algorithm and example),  
Pairwise alignment (BLAST and FASTA Algorithm and Tool) and multiple  
sequence alignment (ClustalW algorithm and tool). Methods for presenting large quantities  
of biological data: sequence viewers (Artemis, SeqVISTA), 3D structure viewers (Rasmol,  
Ligand Explorer SPDBv, Chime, Cn3D, PyMol), Anatomical visualization.

**Unit V Gene Expression and Representation of patterns and relationship**

General introduction to Gene expression in prokaryotes and eukaryotes, transcription factors  
binding sites. SNP, EST, STS.  
Introduction to Regular Expression, Hierarchies, and Graphical models (including Marcov  
chain and Bayes notes).

*[Signature]*  
30/7/14

*[Signature]*  
30/7/14

*[Signature]*  
30/7/14

**B.Sc. Part - I  
Semester - II**

**Session 2014-15**

**Paper II –Mathematics I**

**Max. marks-85**

**Unit I**

Sets, Types of Sets, Subsets, Complement of Sets, union and Intersection of Sets, Difference of Sets, Demorgan's Law, Cartesian product of Sets.

Basics of Probability, addition and multiplication law of probability, conditional Probability, Permutation and Combination.

**Unit II**

Introduction to data, data types and Source. Population and sample. Classification and Presentation of Data. Quality of data, private and public data sources. Measure of central tendency and dispersion: Mean, median, mode, range, standard deviation, Quartile deviation, variance

**Unit III**

Correlation and Regression: Definition, its Types, classification Karl-Pearson's correlation, Spearman's Rank correlation, Regression equation and fitting

**Unit IV**

Probability Distribution: Basics of Binomial, Poisson and Normal distributions and their application in biology. Random Variable; Discrete and Continuous Probability Distribution, Probability mass function, probability Density function, Mathematical Expectation.

**Unit V**

Matrices, Types of Matrices, Addition of matrices, Subtraction of matrices and Product of matrices. Properties of Matrix Multiplication. Transpose of Matrix, Symmetric and Skew-symmetric Matrices, Inverse of Matrix

  
Three handwritten signatures and dates are present at the bottom of the page. The first signature is on the left, followed by the date '30/7/14' and another signature below it. The second signature is in the middle, followed by the date '30-7-14'. The third signature is on the right, followed by the date '30/7/14'.

wef. 2015-16

**B.Sc. Part - II**  
**Semester - III**  
**Paper III –Structural Bioinformatics**

**Max. marks-85**

**Unit I**

Fundamentals of X-ray diffraction, NMR spectroscopy of macromolecules  
Protein Structure: Primary, Secondary, Super Secondary, Domains, Tertiary, Quaternary, Ramachandran plot.

**Unit II**

Protein secondary structure classification databases: HSSP, FSSP, CATH, SCOP.  
Protein secondary structure prediction methods: GOR, Chou-Fasman, PHD, PSI- PRED, J-Pred.

**Unit III**

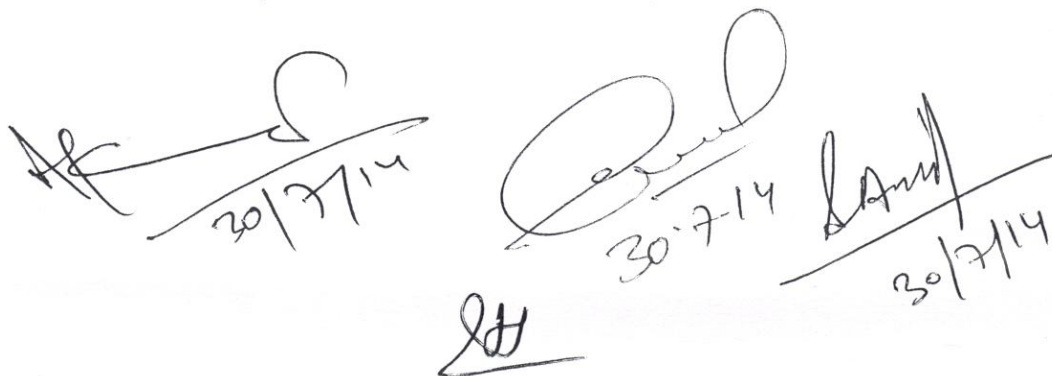
Protein Tertiary structure prediction methods: Homology Modeling, Threading and Fold Recognition, Ab- initio Method.  
Protein folding and Forces that stabilize molecular structures in Folding,  
Molecular Dynamics of Protein, Molecular Docking of Protein, Small molecule and Nucleotide, Concepts of Force Field

**Unit IV**

Motif and Domain: Motif databases and analysis tools.  
Domain databases (CDD, SMART, ProDom) and Analysis tools.  
HMM (Hidden Markov Model): Introduction to HMM, its application in Sequence alignment and Structure prediction, HMM based Softwares (HMMER and HMMSTR)

**Unit V**

Structural features of RNA: Primary, Secondary, Tertiary.  
Introduction to RNA Secondary structure prediction, Methods for RNA Secondary structure prediction, Limitation of RNA Secondary structure prediction

Three handwritten signatures with dates are present at the bottom of the page. The first signature is on the left, the second is in the middle, and the third is on the right. All three dates are 30/7/14.

**B.Sc. Part - II  
Semester - IV**

**Session 2015-16**

**Paper IV- Mathematics II**

**Max. marks-85**

**Unit I**

Law of Indices, trigonometric ratios, Inverse trigonometric functions.  
Binomial theorem.

**Unit II**

Sequences and series AP, GP, HP, Logarithmic and Exponential Series.

**Unit III**

Basics of Functions and Limits, Elementary Differentiation and Integration  
Fourier transform, Laplace transform and other standard transform.

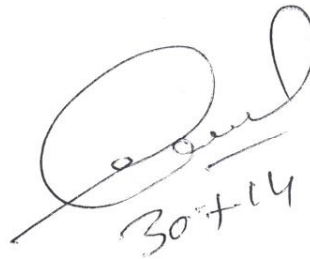
**Unit IV**

Coordinate geometry: Distance between two points, section formula, Locus of points.  
Equation of lines, Circle, Ellipse, Parabola, Hyperbola

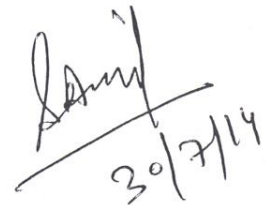
**Unit V**

Vector: Addition, subtraction, dot product, cross product, scalar triple product,  
Vector differentiation and vector integration, gradient, divergence, curl of a vector, equation  
of normal

Handwritten signature and date: 30/7/14

Handwritten signature and date: 30/7/14

Handwritten signature

Handwritten signature and date: 30/7/14

Syllabus of B.Sc.  
Bioinformatics (Sem. V & VI)  
Effective during 2016-17  
session.

## B.Sc. BIOINFORMATICS

III year

Semester-V

*Paper: Computer graphics, Machine learning and Bioperl*

2016-17

AK 16/5/16

Jyoti 16/5/16

MM: 85

### Unit I

**Color models:** CMY, HSV, RGB, Visualization techniques.

Graphics display devices, Raster and Random scan devices, color CRT monitors, LCD and LED.

### Unit II

**HMM (Hidden Markov Model):** Introduction to HMM, its application in Sequence alignment and Structure prediction, based Softwares (HMMER and HMMSTR)

**Artificial Neural Networks,** Genetic algorithm, Bayesian modeling, Monte Carlo Simulation Method, Markov Models and their application

### Unit III

**Perl basic:** Variables, Perl operations, A Program to store DNA sequence, Concatenating DNA fragment, Transcription: DNA to RNA, Subroutines, scoping and subroutines, command-line arguments and arrays passing data to subroutines, modules and libraries of subroutines, fixing bugs.

### Unit IV

**Random number generators** a program using randomization, a program to simulate DNA, Mutation, generating random DNA, analyzing DNA, Hashes, data structures and algorithms for biology, the genetic code,

### Unit V

**Translating DNA** into proteins reading DNA from files in FASTA format, reading frames, Regular expressions, restriction maps and restriction enzymes, Genbank files, Genbank libraries, separating sequence and annotation parsing, Annotations indexing, parsing PDB files, parsing BLAST files.

## Recommended Books:

1. Bioinformatics- Sequence and Genome analysis- David W. Mount
2. Molecular Modeling- Principles and application- Andrew R. Leach
3. Principles of Biochemistry- Lehninger
4. Biochemistry- Stryer
5. Bioinformatics from Genomes to Drugs- Thomas Lengauer

## *Practical*

MM: 50

1. Exercises on WINDOWS,LINUX
2. Internet search and graphics
3. Explore species 2000
4. Find out evolutionary relationship using Treeview/phylip package

### *Based on PERL language*

5. Write a program to store a DNA sequence
6. Write a program to concatenate DNA sequences
7. Write a program to find complementary and reverse complement of given DNA sequence
8. Write a program to demonstrate the use and types of different types of PERL variable.
9. Write a program that uses all arithmetic operators
10. Write a program using subroutines
11. Write a program to perform Transcription
12. Write a program to perform Translation
13. Write a program to read DNA file in FASTA format
14. Write a program to generate Random DNA sequence
15. Write a program to stimulate DNA mutation
16. Write a program to analyze DNA sequence
17. Write a program to parse GenBank file
18. Write a program to parse BLAST file & PDB file using PERL

AK  
16/5/16

AK  
16/5/16

# B.Sc. BIOINFORMATICS

III year

Semester-VI

*Paper - Informatics in omics and application*

2016-17

MM: 85

## Unit I

**Genomics:** Genome Annotation, Genome Assembly, Structural and Functional Genomics. Comparative Genomics

**Microarray:** technique, Design, Analysis, Drug target identification.

## Unit II

**System biology:** Introduction, Associated disciplines, Interactomics (PPI), Fluxomics, Biomics.

**Metagenomics:** Introduction, metagenome, shotgun metagenomics (pyrosequencing).

Tools in metagenomics, MEGAN, MG-RAST, and SEED.

**Application:** Gene survey, Environmental genomes, Microbial diversity.

**Phylogeny:** Introduction to Phylogenetic analysis, Concept of Phylogenetic Tree

## Unit III

**Metabolic pathway database** (KEGG pathway database), Concept of metabolome and metabolomics.

**Drug Discovery and design:** Target identification, Target Validation, Lead Identification, lead optimization, preclinical Pharmacology & Toxicology.

## Unit IV

**Cheminformatics:** Cheminformatics tools for drug discovery.

**Chemical Structure Representation** (SMILE & SMART).

**Chemical databases:** CSD, ACD, WDI, ChemBank, hazardous chemical database, PUBCHEM.

## Unit V

**Quantitative Structure Activity Relationship** (2D & 3D). Combinatorial libraries & their design. High throughput screening, virtual screening, Lipinski's rule of five.

AR

---

16/5/16

lyt

---

16/5/16



## *Practical*

MM: 50

1. Explore KEGG database
2. Explore Drug Bank database
3. Explore PubChem database
4. Explore MG-RAST and SEED.
5. Access to the latest curated data sets using SEED viewer
6. Generate a chemical structure using SMILE
7. Explore Primer 3 tool
8. Explore String Database
9. To generate chemical structures using MARVIN SKETCH
10. To explore different chemical databases.
11. To perform different stages of in silico drug discovery using different tools

AK 5  
16/5/16

Jyoti c  
16/5/16