FACULTY OF SCIENCE

SYLLABI

FOR

M.Sc. BIOINFORMATICS
(SEMESTER SYSTEM)

1ST TO 4TH SEMESTER

EXAMINATIONS 2017-2018

--:O:--
# OUTLINES OF TESTS, SYLLABI AND COURSES OF READING FOR M. Sc. BIOINFORMATICS

## Semester – I (Session: 2017-2018)

<table>
<thead>
<tr>
<th>Paper Code</th>
<th>Lectures/week (Th+Prac)</th>
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<th>Theory</th>
<th>Practical</th>
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<tbody>
<tr>
<td>MBIN-8001</td>
<td>6+3</td>
<td>Basic Biology</td>
<td>75 (60+15)</td>
<td>MBIN-8051 25 (20+5)</td>
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<td>OR</td>
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<tr>
<td>MBIN-8002</td>
<td>6+3</td>
<td>Mathematics</td>
<td>75 (60+15)</td>
<td>MBIN-8052 25 (20+5)</td>
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<tr>
<td>MBIN-8003</td>
<td>6+3</td>
<td>Fundamentals of Modern Biology</td>
<td>75 (60+15)</td>
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<tr>
<td>MBIN-8004</td>
<td>6+3</td>
<td>Macromolecular Biochemistry</td>
<td>75 (60+15)</td>
<td>MBIN-8054 25 (20+5)</td>
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<tr>
<td>MBIN-8005</td>
<td>6+3</td>
<td>Computer Programming and Concepts of Computing</td>
<td>75 (60+15)</td>
<td>MBIN-8055 25 (20+5)</td>
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<tr>
<td>MBIN-8006</td>
<td>6+3</td>
<td>Introduction to Database Systems</td>
<td>75 (60+15)</td>
<td>MBIN-8056 25 (20+5)</td>
</tr>
</tbody>
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**Total Marks (Semester – I)** 375 125

## Semester – II (Session: 2017-2018)

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<tr>
<td>MBIN-8007</td>
<td>6+3</td>
<td>Statistics and Probability</td>
<td>75 (60+15)</td>
<td>MBIN-8057 25 (20+5)</td>
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<tr>
<td>MBIN-8008</td>
<td>6+3</td>
<td>Sequence Bioinformatics and Software Tools</td>
<td>75 (60+15)</td>
<td>MBIN-8058 25 (20+5)</td>
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<tr>
<td>MBIN-8009</td>
<td>6+3</td>
<td>Programming Languages in Bioinformatics-I</td>
<td>75 (60+15)</td>
<td>MBIN-8059 25 (20+5)</td>
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<tr>
<td>MBIN-8010</td>
<td>6+3</td>
<td>Immunology &amp; Cell Biology</td>
<td>75 (60+15)</td>
<td>MBIN-8060 25 (20+5)</td>
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<td>MBIN-8011</td>
<td>6+3</td>
<td>Metabolic Pathway Analysis</td>
<td>75 (60+15)</td>
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**Total Marks (Semester – II)** 375 125
### Semester – III (Session: 2017-2018)

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<tr>
<td>MBIN-8012</td>
<td>6+3</td>
<td>Elements of System Biology</td>
<td>75 (60+15)</td>
<td>MBIN-8062 25 (20+5)</td>
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<td>MBIN-8013</td>
<td>6+3</td>
<td>Programming Languages in Bioinformatics-II</td>
<td>75 (60+15)</td>
<td>MBIN-8063 25 (20+5)</td>
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<td>MBIN-8014</td>
<td>6+3</td>
<td>Structural Biology</td>
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<td>MBIN-8015</td>
<td>6+3</td>
<td>Genomics and Proteomics-I</td>
<td>75 (60+15)</td>
<td>MBIN-8065 25 (20+5)</td>
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<td>MBIN-8016</td>
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<td>Applications of Computational Biology</td>
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<td><strong>Total Marks (Semester – III)</strong></td>
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<td><strong>375</strong></td>
<td><strong>125</strong></td>
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### Semester – IV (Session: 2017-2018)

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<tr>
<td>MBIN-8017</td>
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<td>Genomics and Proteomics-II</td>
<td>75 (60+15)</td>
<td>MBIN-8067 25 (20+5)</td>
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<tr>
<td>MBIN-8018</td>
<td>6+3</td>
<td>Molecular Modeling &amp; Pharmacoinformatics</td>
<td>75 (60+15)</td>
<td>MBIN-8068 25 (20+5)</td>
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<tr>
<td>MBIN-8019</td>
<td>6+3</td>
<td>Informatics in Biodiversity &amp; Bioethics</td>
<td>75 (60+15)</td>
<td>MBIN-8069 25 (20+5)</td>
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<td>MBIN-8020</td>
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<td>Expression Bioinformatics</td>
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<tr>
<td>MBIN-8021</td>
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<td>Project Work</td>
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<td><strong>Total Marks (Semester – IV)</strong></td>
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<td><strong>275</strong></td>
<td><strong>225</strong></td>
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Total Marks (Semester – IV): 275+150=500

Grand Total: Semester (I + II + III + IV) = 500 + 500 + 500 + 500 = 2000
Objective
It introduces the students of Non-medical background to the concepts of biological sciences which are integral understanding and application of Bioinformatics.

Note 1
1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. Seven Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT - I
INTRODUCTION TO LIFE SCIENCES:
• Basic characteristics of life. Classification: 5 kingdom classification of life: Monera, Protista, Fungi, Plantae, And Animalia.
• Cell as a basic unit of living systems. The cell theory. Detailed classification of cell types within an organism. Structure of prokaryotic and eukaryotic cells; Membrane structure and function and various cell organelles.
• The structure of the four classes of macromolecules-nucleic acids, carbohydrates, lipids and proteins and their role in the cell.

UNIT - II
INTRODUCTION TO MICROORGANISMS:
• An introduction to microbial cell biology and cell architecture: Modern classification based on 3 domains of life: Archaeabacteria, Eubacteria and Eukaryota.
• Salient features of gram positive and gram negative bacteria and archaebacteria. Pathogenic and beneficial microorganisms.
UNIT - III

INTRODUCTION TO GENETICS AND ORIGIN OF LIFE:


REFERENCE BOOKS:


MBIN-8051 Basic Biology: Practical Course

Max. Marks: 25(20+5)

1. Preparation of different types of stains
2. Different types of staining techniques
3. Study of normal and abnormal karyotypes
4. Estimation of DNA and Protein: Spectrophotometric way
6. Examination of various stages of mitosis and meiosis
7. To study cell structure from onion leaf peels, Hydrilla, Spirogyra, Amoeba, Paramecium and Euglena
MBIN-8002 MATHEMATICS

Max. Marks: 75
Theory : 60
Int. Ass. : 15

Objective
The objective is to introduce students about basic Mathematics including real members, set theory, Calculus, Matrices and Vectors, Differential Equations. These techniques are useful in solving Bioinformatics Problems.

Note 1
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4. The candidates will be required to attempt 5 questions in all by selecting one question compulsory from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT - I

REAL NUMBERS:
Different kinds of number- Integers, Rational and Irrational, Surds and their properties, Fractional indices, Complex Numbers, Extending the Real Number System, Operations with complex numbers.

SETS: Set, Relation and function, Product of sets, Relations, Functions (Polynomials, Trigonometric, Logarithmic, Exponential), Graphical Representation of functions, Concept of A.P., G.P., Binomial Theorem, Expanding \((x+y)^n\) € IN.

UNIT - II

LIMIT: Limits of functions.
CALCULUS: Differentiation of algebraic, logarithmic and trigonometric functions, Increasing and decreasing functions, Maxima and Minima.
Integration: Finding a function from its derivatives, Definite Integral.

UNIT - III

MATRICES AND VECTORS: Matrix algebra, Determinants, Applications, Elementary Mathematical logic and Basic concepts of Boolean algebra; Elementary computing system Binary, Octal and Hexadecimal system.
REFERENCE BOOKS:

MBIN-8052 Mathematics: Practical Course

Max. Marks: 25(20+5)

1. Finding roots of Equation (Polynomials or transcendental) using bisection method. (2-3 practical).
2. Curve tracing (Using Maxima and Minima, symmetry along X-axis, Y-axis, Y=X, Y=-X, point of intersection with X-axis and Y-axis, f(|x|), f(|f(x)|)) (2-3 practical).
5. Relations (Graphical Representation of relation from set A to set B and set A to set B) (1 practical).
6. Functions (Graph of standard functions, modulus, greatest integer, exponential, log\(e\), signum, sin, cos, tan, cot, sec, cosec) (2-3 practical).
7. Increasing and decreasing (polynomial functions), Wavy curve method. (2 practical).
8. Plotting of irrational numbers \(\sqrt{2}, \sqrt{3}, \sqrt{5}\), etc. on number line. (1 practical).
9. Aragand plane (plotting of complex numbers). (1 practical)
Objective
The Contents are related to the fundamental of molecular biology and their application in recombinant DNA technology.

Note 1

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5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT - I
DNA Structure & synthesis: Structure of components of DNA, mode of DNA replication, enzymes involved in DNA replication, DNA Polymerase in Prokaryotes and Eukaryotes, origin of replication, replication fork, initiation, elongation and termination of DNA replication, telomerase and replication of ends of eukaryotic chromosomes.
Transcription: Transcription in prokaryotes, Initiation, elongation, termination of transcription in eukaryotes, transcriptional factors.

UNIT - II
Processing of RNA: Types of RNA, RNA splicing, splicosome machinery, Splicing pathways, alternative splicing, exon shuffling, RNA editing.
Regulation of gene expression in prokaryotes: Lac, tryp operon, eukaryotic gene expression.
Translation: The cracking of Genetic Code, basic features of Genetic code, the ‘Wobble hypothesis’, frame shifting, structure of t-RNA, ribosomes in prokaryotes & eukaryotes, post translation modifications.

UNIT - III
Tools of recombinant DNA technology: Restriction enzymes, DNA ligase, modifying enzymes. Plasmid vectors, phage vectors, phagemids, cosmids, shuttle vectors, BACs & YACs. Expression vectors versus cloning vectors.
Gene cloning: DNA libraries –Genomic and cDNA. Cloning strategies, Screening of libraries from clones, identification of desired recombinants by alpha complementation, insertional inactivation, complementation of mutant phenotype, immuno screening, colony hybridization.
Polymerase Chain Reaction & Its Applications: Principle, components, applications, site-directed mutagenesis.
Fusion proteins for protein expression. Creation of in frame fusion like His-tags and GST-tags for protein purification in *E.coli*.

REFERENCE BOOKS:


MBIN-8053

**Fundamentals of Modern Biology: Practical Course**

Max. Marks: 25(20+5)

1. Preparation of media, cotton plugging and sterilisation techniques
2. Experiments on isolation, spread plates, pour plates, selective media, differential media, staining (simple, differential, Gram, endospore, capsule staining), count of microbes (standard plate count)
3. Isolation of chromosomal DNA from bacteria
4. Isolation of plasmid DNA from bacteria by alkaline lysis method
5. Restriction digestion of plasmid DNA
6. DNA agarose gel electrophoresis
7. Polymerase chain reaction
Objective
This paper includes the details about the Bio-molecules i.e. carbohydrates, nucleic acids and proteins alongwith their structure.

Note 1
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Note 2
External system of examination will be followed.

UNIT – I

UNIT--II
Protein folding: Levinthal paradox, theory and experimentation; determinants of protein folding; Folding/misfolding pathways.
Binding of small molecules by polymer: identical and independent sites model, nearest interaction and statistical weight, cooperative binding and excluded binding. The random walk, Helix coil transitions in proteins, Boltzmann distribution, concept of statistical thermodynamics, Negative entropy and third law of thermodynamics, partition function application in biological systems.

UNIT - III
REFERENCE BOOKS:


MBIN-8054: MACROMOLECULAR BIOCHEMISTRY: PRACTICAL COURSE
Max. Marks: 25(20+5)

1. Building Amino Acids and numbering them
2. Exploring peptide conformations
3. Measuring Torsion angle
4. The alpha helix: build a peptide of 10 amino acids.
5. The (anti-) parallel beta sheet
6. Study protein structure (use Chitenase) using Rasmol, Raswin (PDB)
   Preparation of buffers
7. Determination of pI value of casein by variation of pH
8. Determination of pK values of glycine.

MBIN-8005: COMPUTER PROGRAMMING AND CONCEPTS OF COMPUTING
Max. Marks: 75
Theory : 60
Int. Ass. : 15

Objective
This paper covers computer fundamentals, programming concepts based on ‘C’ Language, arrays, structure and Unions, Pointers and File handling.

Note 1
1. Sixty (60) hrs. of teaching for each paper is mandatory.
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3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.
UNIT - I

**Computer Fundamentals:** Block Structure of a computer, characteristics of computers, classification of computers.

**Number System:** Bit, byte, binary, decimal, hexadecimal and octal systems, conversion from one system to the other. Character codes (ASCII, EBDIC, BCD, Excess-3 Grey).

**Introduction to Programming:** Algorithms, Flow Charts, Basic constructs of Programming Languages, Types of programming languages.

**Introduction to ‘C’ Language:** Character Set, Constants, Variables, Identifiers, Keywords, Data Types, Operators and Expressions, Assignment statement, Basic Input/Output statement. Simple ’C’ Programs.

UNIT - II

**Control Structures:**
Decision making statements, if statement, if-else statement, nested if, Switch-Case, Looping statements: While, do-while, for loop, Nested loops, infinite Loops, Break and Continue statements.

**Arrays:**
One dimensional arrays: Array manipulation; Searching, Insertion, Deletion of an element from an array; Finding the largest/ smallest in an array.

**Functions:**
Library functions, user defined functions, function declaration, function definition, function call. Passing arguments to a function: call by reference; call by value, recursive functions.

**Structures and Unions:**
Structure variables, initialization, structure assignment, nested structure, structures and functions, Unions.

UNIT - III

**Pointers:**
Address operators, pointer type declaration, pointer assignment, pointer initialization, pointer arithmetic, function and pointers, pointer arrays.

**Data and File handing:**
Various file operations: Creation, deletion, Reading and writing operations on Text and data files.

REFERENCE BOOKS:

4. C in a Nutshell by Peter Prinz Published by O'Reilly, (2005)
Learn programming in 'C' language:

1. Write a program to find whether a number entered is even or odd, prime or non prime.
2. Write a program to find factorial of a number.
3. Write a program to print Fibonacci Series for first 'n' numbers.
4. Program to swap two numbers using third variable using functions.
5. Write a program to print the following output using for loops:
   
   1
   22
   333
   4444
   55555
   666666

6. Write a program to read and write 2D array.
7. Write a program to find largest/smallest element in an array.
8. Program to add, subtract and multiply two matrices.
9. To find the length of a string without using library functions.
10. To check whether a string entered is a palindrome or not.
11. Program to illustrate how a student data is entered and displayed using structure.
12. Write a program to show how pointer to pointer operates.

Objective
Since Bioinformatics relies highly on Biological database an introduction to Database System and Programming is necessary for better understanding the architecture of databases.

Note 1
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4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.
UNIT – I

Database System Concepts and-Architecture: Data Models, Schemas, and Instances, DBMS Architecture and Data Independence


UNIT – II

SQL: Client Server Technology, data types, creating tables, insertion, deletion, altering the contents of table, renaming and destroying tables, data constraints. Basic Queries in SQL, nested queries and set comparisons, joins. Concept of Views in SQL, granting and revoking permissions, revoking privileges given.

UNIT – III

Introduction to PL/SQL, processing a PL/SQL block, what is a cursor, error handling in PL/SQL. Stored Procedures and functions. Database triggers.

Introduction to application development using visual basic: Working with code and forms. Various events and working with event handlers. Variables, procedures, and functions. Standard control, object browsing. Connecting to MS-Access using VB and accessing data.

REFERENCE BOOKS:

2. Introduction to Database Systems by C.J. Date, Publisher: Addison Wesley; 3rd edition (2003)

MBIN-8056: INTRODUCTION TO DATABASE SYSTEMS: PRACTICAL COURSE
Max. Marks: 25(20+5)

Create the student table based on following:

Table instance chart
Column name - Roll no, name, date of Admission, Marks.
Data type - varchar2, Date, number
Length- 4, 25, date, 3

1) After the table student add, modify, and drop any column of your own choice.
2) Write a Query to display the ename concatenated with job separated by 'comma' and 'space' and name the column employee and title.
3) Write a Query to display the ename sales, and commission for all employees, who earn commission sort date in descending order of salary and commission.
4) Give an example of
   a) Self join
   b) Equi join
   c) Non equi join
   d) Outer join
5) Create a query to display the employee number and ename of employees who earn more than the average salary. Sort the result in ascending order of salary.
6) Explain the concept of view by taking an example or writing a Query in SQL
   Write a Query to
   a) Create a user with password.
   b) Grant system privileges to the user.
   c) Create a manager role and then allows the manager to create tables and views.
   d) Change the password
   e) Grant query or privileges to the user on employee table.
   f) Grant privileges to update specific column to user and roles.
   g) Revoke the privileges given to user on employee table.
7) Write a program in pl/sql to explain following:
   a) Cursor
   b) Exception handling
   c) Procedures and functions
   d) Triggers
8) Design Employee Information system Demonstrating the use of database connectivity with oracle or Access
9) Design an application illustrating the use of event handling.
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Total Marks (Semester – II): 375 + 125 = 500
Objective
To introduce students about descriptive statistics and their interpretation. The concepts of Probability, distributions, correlation, Regression, Estimation and Testing of parametric and non-parametric hypotheses are also discussed.

Note 1
1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. Seven Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT - I
Nature of Data and methods of compilation: Measurement scales, Attribute and variable, Discrete and continuous variables. Collection, Compilation and Tabulation of data.
Representation of data: Histogram, Frequency Polygon, Frequency Curve, Ogives.
Measures of central tendency: Mean, Median, Mode and their properties.
Measuring variability of data: Range, Quartile deviation and Standard deviation, Sample and Population variance. Deciles and Percentiles. Skewness and Kurtosis, Box and Whisker plot.

UNIT - II
Correlation & Regression Analysis: Scatter diagram. Karl Pearson’s and Spearman’s rank correlation coefficient. Linear Regression and its properties.

UNIT - III
Hypothesis testing: The basic idea of significance test. Null and alternative hypothesis, Type-I and Type-II errors. Tests of hypothesis for the parameters of a normal distribution (two sample problems also). Chi-square test of goodness of fit. One way and two way Analysis of Variance (ANOVA).
Non-Parametric tests: Sign test, Wilcoxon signed rank test, Mann-whitney test.

REFERENCE BOOKS:


MBIN-8057 STATISTICS AND PROBABILITY PRACTICAL COURSE
Max. Marks: 25(20+5)

These entire practical will also be done on software’s like SPSS or SYSTAT. If these are not available then write programs for all these practicals in C language.

1. Graphical representation of data and measures of central tendency: mean, median, mode.
3. Measures of Skewness and Kurtosis
4. Correlation coefficient, regression lines.
5. Problems related to Binomial, Poisson and Normal distributions.
6. Z-test (one sample and two sample problems)
7. t-test (one sample and two sample problems)
8. F-test and Chi-square test.
9. One way ANOVA and two way ANOVA.
10. Non-parametric tests (sign test, Wilcoxon signed rank test and Mann-whitney test).
MBIN-8008: SEQUENCE BIOINFORMATICS AND SOFTWARE TOOLS

Max. Marks: 75
Theory : 60
Int. Ass. : 15

Objective
In this paper, sequence analysis of proteins and genes using various computational tools which are important to study conservation in different species and establish phylogeny & homology is covered.

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5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT-I

Sequence Databases: Primary and secondary databases. Introduction to nucleotide sequence databases (DDBJ, EMBL, Genbank), RefSeq at NCBI and Protein sequence databases (SWISSPROT, PIR, UNIPROT).
Introduction to nucleotide and protein sequence data formats: FASTA, Genbank flatfile.
Sequence Retrieval: GQuery.

UNIT - II

Sequence Alignment:
Dotplot, advantages and disadvantages.
Pairwise alignment: Local and Global alignment; Needleman and Wunsch algorithm, Smith Waterman algorithm; PAM & BLOSSUM matrices.
Multiple Sequence Alignment: Definition of Consensus, Motifs, Fingerprints, Singature, Pattern & Profile Formation (PSSM). PROSITE Data base for Profile and Pattern. Application of multiple seq. alignment, use of Clustal W and Clustal X for multiple seq alignment.

Methods For Similarity Searching:
Notion of homology: Orthologues, Paralogues, Analogues. Understanding, Identity, Homology & Similarity with reference to evolutionary relationships.
Similarity search: BLAST: concepts & algorithm, applications and significance, Salient features of various BLAST versions: BLASTp, BLASTn, BLASTx, tBLASTn, tBLASTx, PSI and PHI BLAST. FASTA & its algorithm.
UNIT - III

Phylogenetic Analysis:
Evolutionary change in nucleotide sequence’s rates & patterns of nucleotide substitution.

Terminology of phylogenetic trees: Branches, nodes, internal nodes, rooted & unrooted trees, Phylogram, Cladogram.

Phylogenetic estimation: Distance based methods (UPGA & NJ) and character based methods(Maximum Parsimony & Maximum Likelihood).

Computer tools for phylogenetic analysis: PAUP, PHYLIP, Bootstrapping evaluation method.

REFERENCE BOOKS:

MBIN-8058: SEQUENCE BIOINFORMATICS AND SOFTWARE TOOLS:
PRACTICAL COURSE

Max. Marks: 25(20+5)
1. GQuery
2. EMBL
3. Genbank
4. SWISSPROT/ TrEMBL
5. UniProt
6. Using BLAST & Interpretation of its results
7. Multiple sequence alignment using ClustalW
8. Phylogenetic analysis using tree view or other software
Objective
The students will be taught computational programming that would help in developing databases and Bioinformatics tools for sequence and structure prediction.

Note 1
1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. **Seven** Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT - I
The genesis of JAVA: Why JAVA is important to the internet. The continuing revolution. An overview of JAVA, Object Oriented Programming, Data types- Variables and Arrays, the simple types, Floating point types. Operators, Control statements.

Introducing classes: Class fundamentals, Declaring objects, Assigning object reference variables, Introducing methods, Constructors, The this keyword. Garbage collection, using objects as parameters, Argument passing, Retaining objects, Recursion, Introducing Access control, Understanding static. Nested and inner classes, exploring the string class, Using command line arguments.

Inheritance: Basics, Member access and inheritance. Using super: to call super class constructors, Creating a multilevel hierarchy, Method overriding, Dynamic method dispatch, Using abstract classes, Using final with inheritance, Using final to prevent overriding, Using final to prevent inheritance, The object class.

UNIT - II
Packages and Interfaces: Packages, Defining a package, Understanding class path, Access protection: Importing packages, Defining an interface. Implementing interfaces, Applying interfaces, Variables in interfaces.

UNIT - III

Multithreaded programming: The Java thread model. Thread priorities, Synchronization, Messaging, The thread class and the runnable interface. The main thread: creating a thread, Implementing runnable, extended thread, Choosing an approach, creating multiple threads. Using is alive () and join(), Thread priorities; Synchronization :Using synchronized methods, the synchronized statement, Inter-thread communication, Deadlock, Suspending resuming and stopping threads, Using multithreading.

I/O Applets: I/O basics - Streams, Byte streams and character streams. The predefined streams; Reading console Input : reading characters, reading strings, Writing files, Applets, Fundamentals, The transient and volatile modifiers, Using instance of, Native methods, Problems with native methods.

REFERENCE BOOKS:


MBIN-8059: PROGRAMMING LANGUAGE IN BIOINFORMATICS – 1:
PRACTICAL COURSE

Max. Marks: 25(20+5)

1. Write a program to compute the area of a circle.
2. Write a program to illustrate how objects are created in a class in Java.
3. Write a program to demonstrate method overloading.
4. Write a program to show how a factorial can be computed by use of a recursive method.
5. Program to show how to inherit a subclass from a super-class using keyword extends.
6. Write a program to illustrate method overriding.
7. Write a program to demonstrate multiple catch statements.
8. Write a program that creates multiple threads.
9. To create an applet that sets the foreground and background colors and displays a message when an applet starts up.
10. Create a child frame window from within an applet.

MBIN-8010: IMMUNOLOGY AND CELL BIOLOGY

Marks : 75
THEORY : 60
INT. ASS. : 15

Objective
Cells & immune system involve interaction of various bio-molecules resulting in normal functions or various pathophysiological conditions. So the students are exposed to the underlying concepts and phenomena of Cell Biology & Immunology.
Note 1
1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. Seven Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT I
Thymus derived lymphocytes (T cells) and their classification, Antigen presenting cells (APC)., Macrophages, Dendritic cells, Natural killer cells and lymphocyte activated killer cells, langerhans cells; Eosonophils, neutrophils and mast cells, their origin and functions, mechanisms of phagocytosis.

UNIT II
Immunotechniques: Immunofluorescence, ELISA, immunoblotting, monoclonal antibodies

UNIT III
Nutrient Transport: Transport of nutrients, ions and macromolecules across membranes.
Protein Targeting: The secretory pathway – translocation across the ER, ER-Golgi transport by vesicular budding and fusion; Protein targeting to the mitochondria.
Cell Cycle and Its Regulation: Signal transduction: Mechanism, GPCR, Ras-MAPK, PI3K, JAK-STAT.

RECOMMENDED BOOKS:
2. E. Benjamin and S. Leskowitz, Immunology: A Short Course, Wiley Liss, NY,
7. The Elements of Immunology by Fahim Halim Khan, Pearson Education 2009.

MBIN-8060: IMMUNOLOGY AND CELL BIOLOGY: PRACTICAL COURSE
Max. Marks: 25(20+5)

1. Immunodiffusion
2. Immunoprecipitation
3. Gel electrophoresis
4. Spectrophotometry
5. TLC, DLC
6. Microtomy
7. ELISA

MBIN-8011: METABOLIC PATHWAY ANALYSIS
Max. Marks: 75
Theory : 60
Int. Ass. : 15

Objective
This paper introduces students to the concepts of enzyme kinetics, metabolism, databases, its related flux of metabolites.

Note 1
1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. Seven Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT - I
Introduction to metabolism: Catabolism, Anabolism, Characteristics of metabolic pathways, thermodynamics of phosphate compounds and metabolic control.
Fueling reactions: Glycolysis, Fermentation, Metabolism of hexoses, TCA cycle and oxidative phosphorylation, Glycogen breakdown, Bioenergetics of these metabolic pathways.

UNIT - II
Regulation of Metabolic Pathways at Enzyme Level – Regulation of enzyme activity, overview of enzyme kinetics, allosteric enzymes, feedback inhibition. Aspartate transcarbamylase, holoenzymes, coenzymes rates of enzymatic reactions.
Chemical Kinetics: Elementary reactions, rates of reactions. Transition state theory.

UNIT – III


REFERENCE BOOKS:

MBIN-8061 METABOLIC PATHWAY ANALYSIS: PRACTICAL COURSE  
Max. Marks: 25(20+5)

1. Principles of the Ecocyc database: Eschericia coli K12
2. Principles of the MetaCyc database
3. Using the Plantcyc, the Enzymology Database
4. Using the LIGAND database (KEGG)
5. Using the KEGG to study metabolic pathways
6. BRENDA
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Total Marks (Semester – III): 375 + 125 = 500
Objective
This paper deals with study of principles, properties and concepts of System Biology alongwith the various tools to analyze the systems.

Note 1
1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. Seven Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT - I
Introduction: System biology in biology & modeling, system level understanding of biological systems, Properties of models-Robustness, Redundancy, Control, Modular Design, Model Assignment, system state, steady states, variables, parameters & constants, Model behavior, process classification, purpose & adequateness of models, advantages of computational modeling, model development, aspects of biological systems & corresponding models.

UNIT – II
Modeling Tools: Modeling & visualization: Gepasi, E-cell, virtual cell, Py BIOS, SBW, JDesigner, cell designer, Petri Nets, STOCKS2, Genetic programming,
Model Exchange Languages: Introduction to System Biology Mark Up Language, MathML.

UNIT – III
Computer Simulation of the Cell: Human erythrocyte model & its applications, Mycoplasm genitalium as a model virtual cell.

REFERENCE BOOKS:
5) Discovering Genomics, Proteomics and Bioinformatics, 2/E by A. Malcolm Campbell and Laurie J. Heyer, Publisher: Benjamin Cummings, (2003).
6) Foundations of System Biology using cell illustrator and pathway databases, Nagasaki & Saito, Springer 2009

**MBIN-8062: ELEMENTS OF SYSTEM BIOLOGY: PRACTICAL COURSE**

Max. Marks: 25(20+5)

1) Building a simple model building in E-cell
2) Understanding Gepasi models.
3) Understanding MATLAB.
4) Understanding V-Cell
5) Understanding system biology models.

**MBIN-8013: PROGRAMMING LANGUAGE IN BIOINFORMATICS-II**

Max. Marks: 75
Theory : 60
Int. Ass. : 15

**Objective**

*PERL Programming is important to the development of biological databases. This paper also deals with details of XML.*

**Note 1**

1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. Seven Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

**Note 2**

External system of examination will be followed.

**UNIT-I**

**Programming in PERL**

Writing Perl scripts; arithmetic/string/logic operators; reading/translating/comparing parts of strings; Control statements; Input from command (ARGV, ARGC); directory/file handling (creating/appending/deleting/moving files, listing of files); creating internal/external subroutines; pattern matching; how to read/write from databases.

**PERL Scripts for Bioinformatics**

Role of Perl in Bioinformatics; Scripts for reading DNA/protein sequences from FASTA files; Calculate amino acid and dipeptide composition; Computing frequency of nucleotides from DNA sequence; Searching restriction sites; Understanding BioPerl; Calling BioPerl subroutines in Perl scripts;
UNIT- II

Introduction to XML
What is XML; Comparison of XML with HTML, XHTML, SGML, RSS, MathML, WAP; XML syntax/elements/attributes; Fundamentals of XML; Write simple XML files; Viewing XML in browser; Creating Well-Formed XML Documents; Creating Valid XML Documents; Fundamentals of XML Namespaces.

UNIT- III

XML, Bioinformatics and PERL
XML major features (data sharing, separate data from HTML, data transport, platform change); Displaying XML with CSS; XML tree; Validating XML codes; Working with XML parsers; Processing of XML documents; Processing of XML documents using Perl; Using XML for Biological Data Exchange; Evaluating XML Usage in Bioinformatics; Solving bioinformatics problems using Perl and XML

REFERENCE BOOKS:
2. SAMS Teach Yourself Perl in 21 days by Laura Lemay, 2nd edition, Pearson Education, 2002
4. Teach yourself XML in 21 days by Techmedia, 2000
5. Mastering XML by Techmedia, 2002

MBIN-8063 Programming Languages in Bioinformatics-II: Practical Course

Maximum Marks 25 (20+5)

PERL:
1. Script to illustrate the use of Arithmetical/String/logical operators.
2. Write a script that illustrates the concept of all the control structures.
3. Script to calculate number of charge and polar residues in a protein
4. Write a script for searching restriction sites in a DNA sequence
5. Write a script that reads a sequence from a FASTA/EMBL/PIR formatted file.

XML:
6. Write a XML code to view a simple XML file.
7. Write a Perl script for parsing XML file.
8. Write a XML file for storing a database.
9. Display the CD catalog formatted with the CSS file.
10. Write a code to record a Nucleotide Sequence encoded in XML
11. Sample DTD for representing protein data.
12. Sample instance document adhering to the protein DTD.
Objective
Various tools are discussed to study properties of molecules for better understanding their structure and functions.

Note 1
1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. Seven Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT – I
Microscopy: Light Microscopy and its applications, bright field, dark field, fluorescence, phase contrast microscopy.
Electron microscopy: SEM, TEM – general design, resolution, electron sources, TEM grids, electron lenses and their biological applications.
Confocal Microscopy

UNIT – II
Mass Spectroscopy: Principles, equipment used in MS analysis, MS/MS, LC/MS, GC/MS. Use of MS in structure determination – MS & Microheterogeneity in proteins, confirmation and analysis of peptide synthesis, peptide mapping, Post translational modifications analysis of proteins. Determination of protein disulphide patterns. Protein sequencing by MS. Introduction to DNA component analysis by MS.

UNIT – III
Three dimensional structure determinations of Macromolecules:
The protein folding problem, folding transition states, structure of native state.
Structure determination by NMR: principle, physical basis, chemical shift, spin coupling, NOE, COSY, Sequential assignment & structural elucidation.
Crystallization of Biomacromolecules: Physical basis, crystallization methods. X-ray diffraction of crystals, calculation of electron density, maps.
Comparison of X-ray crystallography & NMR.
Structural Databases: The Protein database, finding a protein structure in the database.

REFERENCE BOOKS:

MBIN-8064: STRUCTURAL BIOLOGY: PRACTICAL COURSE

Max. Marks: 25(20+5)

1. Use and care of Light Microscope
2. Exploring protein database
   a) PDB database for X-ray & NMR data.
   b) SCOP
   c) CATH
3. Databases for Mass Spectroscopy
4. RasMol
5. Demonstration of MS, NMR and fluorescence instruments.

MBIN-8015: GENOMICS AND PROTEOMICS - I

Max. Marks: 75
  Theory : 60
  Int. Ass. : 15

Objective
The fundamentals of genomics and proteomics dealing with gene/protein structural elements and the forces responsible for their structure are covered.

Note 1
1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. Seven Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT – I

UNIT – II
Introduction to proteomics: The proteome, analysis of proteomes- 2D-PAGE. Sample preparation, solubilization, reduction, resolution, reproducibility of 2D-PAGE. Mass

**UNIT – III**

**Genomic DNA Sequencing Strategies:** Shotgun & Hierarchical (clone contig) strategies, principles of next generation DNA sequencing- Solexa, 454, Ion Torrent, ABI. Quality check: FASTQC.

**DNA Sequencing Strategies:** Maxam and Gilbert method, Sanger method, Pyrosequencing, Sequencing error verification: Base calling and Phred Score

**Sequence assembly and analysis:** De novo and reference based genome assembly.

**Proteomic Strategies:** Protein isolation, methods of solubilization, stabilization. Solubility of proteins: effects of salt concentration, organic solvents, effects of pH. SDS-PAGE, Native PAGE, determination of covalent structures (Edman degradation).

Post translational modifications: glycosylation, phosphorylation, lipid attachment, disulphide bond formation.

**REFERENCE BOOKS:**
1. Introduction to Genomics by Arthur Lesk. Published by Oxford University Press, 2007.
5. Recent advances in Bioinformatics, edited by Irfan A. Khan, Aditya khanum-ukaaz publications (2002).
8. S.R. Pennington (editor), M. J. Dunn - Proteomics - from protein structure to function, Viva Publisher (2003).

**MBIN-8065: GENOMICS AND PROTEOMICS - I: PRACTICAL COURSE**

Max. Marks: 25(20+5)

1. Detection of open reading frames in given sequences using ORF finder at NCBI
2. Softwares for gene identification on the web
   a) GenScan
   b) Glimmer
   c) JIGSAW Gene Prediction
3. Softwares for splice site predictions on the web
   a) NetGene2
   b) GeneSplicer
4. Proteomics 2D PAGE Database
5. Native PAGE
6. SDS PAGE
7. RAST
8. Genome Sequence assembly software: Velvet
**Objective**
This paper covers use of computational biology in predicting patterns/structures of genomic and proteomic elements.

**Note 1**
1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. **Seven** Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

**Note 2**
External system of examination will be followed.

**UNIT – I**
**Genome Annotation:** Introduction to the genome sequencing projects (Goals of Genome Sequencing Projects)-the first bacterial genome, eukaryotic genome, traditional routes of gene identification: Functional and Positional Cloning and *in silico* methods, software programs for finding genes: ORF finders, Genemark, Glimmer, Genscan, Grai.

**UNIT – II**

**UNIT – III**
**Predictive Methods Using RNA Sequence:** RNA secondary structure thermodynamics, RNA secondary structure prediction, programs for prediction of RNA secondary structure: Mfold, RNA fold, S fold, Vienna RNA package.

**REFERENCE BOOKS:**
1. Transcription factor databases like Transfac.
2. Using PSORT
3. Using PROSITE
4. Using PFAM
5. Using interPRO
6. Using hydropathy plot
7. Using expasy
8. Repeat finder
9. Mfold
## OUTLINES OF COURSE FOR M.Sc. BIOINFORMATICS  
**Semester – IV (Session: 2016-2017)**

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<td>Genomics and Proteomics-II</td>
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<td>MBIN-8067 25 (20+5)</td>
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<td>MBIN-8018</td>
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<td>Molecular Modeling &amp; Pharmacoinformatics</td>
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Total Marks (Semester – IV): 275+75+150=500
Objective
This paper deals with proteomic and genomic sequence and structures in-silico tools. Also various servers will be discussed.

Note 1
1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. Seven Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT – I
Human Genome Project: History, milestones, background and organization of HGP, how the human genome was mapped, strategies in identifying human disease genes.
Single nucleotide polymorphisms: SNPs, SNP detection methods, SSCP, PCR based, DGGE, TGGE, dHPLC sequencing. SNP and disease, Polymorphism versus Mutations, SNP database - dbSNP.

UNIT - II
Proteomics Principles: Proteomics Automation and Analysis, Mass spectroscopy to characterize Proteins and protein complexes
Protein-Protein interaction methods: FRET, Yeast 2-hybrid system, bacterial 2-hybrid system, Co-immunoprecipitation, protein cross-linking, GST-pull down assays; Phage display, Applications of Phage Display.
Protein-protein interaction databases, genome-wide protein interaction studies, protein interaction databases-BIND, DIP,GRID and STRING database.
Predicting algorithms for pathways and interactions: Phylogenetic profiles, gene neighborhood, Gene fusion.

UNIT - III
Applications of Genomics and Proteomics: Web Based Servers and soft wares for genome analysis: Ensembl, UCSC genome browser, VISTA, NCBI genome.
Large genome alignments: Problems of complexity, repeats and size. MUMMER, BLASTZ, LAGAN, AVID.
Principles of Protein structure prediction:

**Protein structure predictions:** Fold Recognition (threading) and Homology Based

**Protein structure databases:** SCOP, CATH, PDB.

Analysis of membrane proteins, hydropathy plots. PSORT, PROSITE, PFAM

**REFERENCE BOOKS:**


**MBIN-8067: GENOMICS AND PROTEOMICS - II: PRACTICAL COURSE**

Max. Marks: 25(20+5)

1. Database of interacting proteins (DIP)
2. BIND
3. SNP databases at NCBI
4. Genscan & glimmer
5. DIALIGN
6. MAVID
7. UCSC and Ensemble Genome Browser

**MBIN-8018 MOLECULAR MODELING & PHARMACOINFORMATICS**

Max. Marks: 75

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**Objective**

*This paper covers the concepts of molecular modeling and drug design and aims at better understanding of the field of pharmacoinformatics.*

**Note 1**

1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. Seven Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.
Note 2

External system of examination will be followed.

UNIT - I

Concepts In Molecular Modeling: coordinate system, potential energy surface, molecular graphics, molecular surface.

Force fields: Empirical potential energy, molecular mechanics force field methods, energy minimization methods, conformational analysis & genetic algorithm.

UNIT – II

Introduction To Drug Designing & QSAR: Drug designing- Different approaches to drug designing, basic principle of similarity & complementarity, high throughput vs rational drug designing, target identification & validation, active site of a target, scoring & lead optimization.

Basic Concepts In QSAR: Objective of QSAR, development of HANSCH QSAR equation, QSAR descriptors.

UNIT – III


REFERENCE BOOKS:
3. Drug design by V. Kothekar, (Dhrub publications), (2006)
4. Chemoinformatics by Johann Gasteiger, Thomas Engel (Eds.) 2002 (WILEY-VCH GmbH & Co. KGaA)

MBIN-8068: MOLECULAR MODELING & PHARMACOINFORMATICS:
PRACTICAL COURSE

Max. Marks: 25(20+5)

Visualization Software’s
1. SPDBv
2. Pymol
3. VMD
4. Discovery Studio Visualizer

Ligand Building & Docking Software’s
1. LigBuilder
2. AUTODOCK
3. HEX

Protein Modeling Tool
1. Modeller
Objective
The role of Bioinformatics in study of biodiversity would be covered alongwith the importance and implications of bioethics.

Note 1
1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. Seven Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsorily from each unit and one of their choice.
5. The questions (2-7) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.

UNIT – I
Biodiversity and Speciation: Ecological Biodiversity & levels of biodiversity (genetic Species & Ecosystem diversity). Species diversity (alpha, beta and gamma diversity), Speciation & species concept, Microevolution: definition, change, mechanism. Speciation: Species, Causes, Reproductive isolation, Evidences of speciation, Co speciation. Macroevolution (Gradualism Model & Punctuated Equilibrium Model).


UNIT II
Vectors of parasites
Biology of vectors, Genome & Proteome Databases: Mosquito

UNIT – III

National Governance of Biosafety in India: Transnational Governance & Cartagene Protocol on Biosafety & its significance.
REFERENCES:
2. Bioinformatics and Molecular Evolution by Paul Higgs and Teresa Attwood (University of Manchester), Blackwell Publishing, (2005)
3. Fundamentals of Molecular Evolution by Dan Graur, University of Houston, and Wen-Hsiung Li, University of Chicago, Publication Date: August 1999

MBIN-8069: INFORMATICS IN BIODIVERSITY & BIOETHICS:
PRACTICAL COURSE
Max. Marks: 25(20+5)
1. Species 2000: indexing the world's known species
2. Tree of life: web project
3. ATCC: The Global Bio-resource Center,
4. NBII at http://www.nbii.gov/
5. SSU rRNA database
6. ViralZone database for viral taxonomy

MBIN-8020 EXPRESSION BIOINFORMATICS
Max. Marks: 50
Theory : 45
Int. Ass. : 05

Objective
The contents of the paper is designed to give students knowledge about microarray technology, its basic concepts and practical implications. Also, the role of biological databases and tools in microarray technology is made conversant to the students.

Note 1
1. Sixty (60) hrs. of teaching for each paper is mandatory.
2. Eight Questions will be set in all, uniformly distributed over the entire syllabus at least two questions from each unit.
3. Q.No.1 will be of objective type (containing 8 parts carrying 1½ mark each) covering the entire syllabus and will be compulsory.
4. The candidates will be required to attempt 5 questions in all by selecting one question compulsory from each unit and one of their choice.
5. The questions (2-8) may be divided into at least two parts.
6. Each question will carry 12 marks.

Note 2
External system of examination will be followed.
UNIT I
DNA Microarray: cDNA Microarray technology, oligonucleotide Microarray technology, Microarray databases, Applications of microarrays. Microarray experimentation.
An introduction to Microarray analysis.
Image processing; Normalizing expression measurements, Cluster analysis- Hierarchical clustering, k-means clustering, Self-organizing maps. CHIP-on-chip arrays.

UNIT II
Protein Microarray: Overview of Protein microarray technology, Comparison of protein and DNA micro array. Experimental strategy for making proteome library. Protein chips; Detection technology; Types of protein micro arrays: analytical microarrays, functional microarrays and reverse phase microarrays.
ESTs and EST databases-dbEST
Alternative splicing, Subtractive hybridization, Differential Display
Regulatory RNA and post transcriptional regulation: RNAi, snRNA anti-sense RNA, miRNA, SiRNA, piRNA, SnoRNA.

REFERENCE BOOKS:
4. Protein Microarray Technology by Dr. Dev Kambhampati Copyright © 2004 Wiley-VCH Verlag GmbH & Co. KGaA
5. Protein Microarrays By Mark Schena Published 2005 Jones & Bartlett Publishers
6. Protein Arrays: Methods and Protocols By Eric Fung Published 2004 Humana Press.

MBIN-8021: PROJECT WORK
Max. Marks: 150

Every student will submit a thesis report based on the work carried out under the guidance of Department/ University/ Research Institute/ Industry faculty, in the Bioinformatics or other related fields. The report will be evaluated in terms of quality of written work, experimental and performance in the viva-voce by internal and/or external examiner(s).

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