STELLA MARIS COLLEGE
(AUTONOMOUS), CHENNAI - TAMILNADU

TRUTH   CHARITY

M.Sc. Degree
BIOINFORMATICS
(CHOICE BASED CREDIT SYSTEM)

SYLLABUS
(Effective from the academic year 2011 – 2012)

M.Sc. DEGREE : BIOINFORMATICS

COURSES OF STUDY

(Effective from the academic year 2011 - 2012)

CHOICE BASED CREDIT SYSTEM

Subject Code	Title of Course	Credits	Lecture Hours	Tutorial Hours	Practical Hours	Exam Hours	Continuous Assessment	End Semester	Maximum Marks
			Total Teaching Hours						
Semester - I									
11BI/PC/BC14	Biochemistry	4	4	1	0	3	50	50	100
11BI/PC/DB14	Database Management Systems	4	3	1	2	3	50	50	100
11BI/PC/CP14	C++ for Bioinformatics	4	3	1	2	3	50	50	100
11BI/PC/BP14	Biophysics	4	4	1	0	3	50	50	100
11BI/PE/BS14	Biostatistics	4	4	0	0	3	50	50	100
OR									
11BI/PE/CG14	Cell Biology and Genetics	4	4	0	0	3	50	50	100
11BI/PA/WA12	Welfare of the Aged	2	2	0	0	-	50	-	100
Semester - II									
11BI/PC/MB24	Molecular Biology	4	4	1	0	3	50	50	100
11BI/PC/P122	Molecular Biology - Pratical	2	0	0	3	3	50	50	100
11BI/PC/BI24	Basic Bioinformatics	4	4	1	0	3	50	50	100
11BI/PC/P222	Basic Bioinformatics - Practical	2	0	0	3	3	50	50	100
11BI/PE/RM24	Research Methodology and Scientific Communication	4	4	0	0	3	50	50	100
11BI/PK/SS22	Soft Skills	2	2	0	0	-	50	-	100
Semester - III									
11BI/PC/GP34	Genomics and Proteomics	4	3	1	2	3	50	50	100
11BI/PC/PL34	Perl	4	3	1	2	3	50	50	100
11BI/PC/AB34	Algorithms for Bioinformatics	4	4	1	0	3	50	50	100
11BI/PC/MC34	Molecular Modeling and Computer Aided Drug Designing	4	3	1	2	3	50	50	100
11BI/PN/SI 32	Summer Internship	2	-	-	-	-	50	-	100
Semester - IV									
11BI/PC/RB44	Recent Advances in Bioinformatics	4	4	1	0	3	50	50	100
11BI/PC/DM44	Data Mining and Machine Learning	4	4	1	0	3	50	50	100
11BI/PC/DS48	Dissertation	8	-	-	12	-	50	50	100
11BI/PE/CR44	Introduction to Clinical Research Management	4	4	0	0	3	50	50	100
Offered to Other Departments									
11BI/PE/CI24	Cheminformatics	4	4	0	0	3	50	50	100
11BI/PE/IM34	Immunoinformatics and Pharmacology	4	4	0	0	3	50	50	100

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M.Sc. DEGREE : BIOINFORMATICS

COURSES OF STUDY

(Effective from the academic year 2011 - 2012)

CHOICE BASED CREDIT SYSTEM

Subject Code	Title of Course	Credits	Total Teaching Hours			Exam Hours	Continuous Assessment	End Semester	Maximum Marks
			Lecture Hours	Tutorial Hours	Practical Hours				
Independent Study Courses									
11BI/PI/PT24	Python	4	-	-	-	3	-	50	100
11BI/PI/SB24	Systems Biology	4	-	-	-	3	-	50	100

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SYLLABUS
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BIOCHEMISTRY

CODE:11BI/PC/BC14   **CREDITS : 4**
L T P : 4 1 0
TOTAL TEACHING HOURS : 65

OBJECTIVES OF THE COURSE
  ➢ To understand the concepts of the structure of biomolecules.
  ➢ To understand the importance of structural studies in bioinformatics and
  ➢ To understand the basics of metabolism and enzyme kinetics.

Unit   1   **(10 hrs)**
Introduction
1.1   Basics of Structural Biology. Distinctive properties of living systems.
1.2   Biomolecules - definition and structural organisation of complex biomolecules.
1.3   Water – Properties and its importance in biosystems.

Unit   2   **(15 hrs)**
Central Metabolic Biochemistry
2.1   Carbohydrate metabolism – Glycolysis, glycogen metabolism, TCA cycle, HMP shunt.
2.2   Protein metabolism – oxidative deamination, Transamination and Urea Cycle.
2.3   Fatty acid metabolism- β- oxidation and Biosynthesis of fatty acids. Xenobiotics and general detoxification methods in the body.

Unit   3   **(20 hrs)**
Protein Structure
3.1   Amino acid properties, four levels of protein structure. Physical interactions - physical and chemical properties.
3.2   Conformational properties of polypeptide chains – three-dimensional conformations, Local restrictions on flexibility, The Ramachandran Plot, Regular conformations of polypeptides-α -helix, β –sheet, other regular conformations. Folding pathways. Stereochemistry, Visualization tools, Domains, Motifs and their importance.
3.3   Basic structure of Carbohydrates, Lipids, Nucleic acids

Unit 4   **(10 hrs)**
      Enzymes
      4.1   Enzyme action Mechanisms.
      4.2   Enzyme Kinetics – Introduction, Basic enzyme kinetics, Michaelis-Menten Equation, significance of Vmax and Km, Lineweaver-Burk plot.
      4.3   Competitive and non-competitive Inhibition, Feedback inhibition. Enzyme regulation. Allosteric modulation.

Unit 5   **(10 hrs)**
      Bioenergetics
      5.1   Review of Chemical Equilibria and Keq. Relationship between equilibria and free energy.
      5.2   Relationship between free energy, heat, and entropy. ATP as the "energy currency" of the cell   oxidizing and reducing agents in cells, and how they are "recycled".
      5.3   The respiratory chain, oxidative phosphorylation, chemi-osmotic theory. Signal transduction and relay of signals

TEXT BOOKS
    Albert, L. Lehninger et al**,** Biochemistry*,* (5th Edition)**,** UK: Worth Publishing, 2007.
    Thomas. E. Creighton, Proteins, (2nd Edition), New York: W. H. Freeman and Company, 2005.

REFERENCE BOOKS
    Champe, Pamela C, Richard A. Harvey and Denise R. Ferrier, Lippincott's Illustrated Reviews: Biochemistry, India: Indian Ed. J.P. Brothers Medical Publishers, 2005.
    Garrett, H. Reginald and Grisham, M. Charles, Biochemistry, (3rd Edition)**,** U.S.A: Thomson – Brooks/Cole, 2005.
    Jeremy, M. Berg, Biochemistry, (5th Ed.), New York: W.H. Freeman, 2001.
    Lubert, Stryer, Biochemistry, (5th Ed.). New York: H. Freeman, 2005.
    Segal, I. H., Enzyme Kinetics, New York: John Wiley and Sons Inc., 1975.
    Voet, D. and Voet, G., Biochemistry (2nd Ed.), New York: John Wiley and Sons Inc., 2000.

PATTERN OF EVALUATION (End Semester Examination.)

Total Marks: 100   Duration: 3 Hours

    Section A – 20 x   1 = 20 Marks (All questions to be answered)

    Section B –   4 x 10 = 40 Marks (4 out of 7 to be answered)

    Section C –   2 x 20 = 40 Marks (2 out of 4 to be answered)

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SYLLABUS
(Effective from the academic year 2011 -2012)

DATABASE MANAGEMENT SYSTEMS

CODE : 11BI/PC/DB14   **CREDITS : 4**
                                                                    L T P : 3 1 2
                                                                    TOTAL TEACHING HOURS :78

OBJECTIVES OF THE COURSE
➢ To introduce the basic concepts of Relational Database Management System and Client Server Environment.
➢ To be trained in Designing databases and manipulating them for Biological applications through Oracle.

Unit   1   **(15 hrs)**
Introduction to Database Systems
1.1   Introduction to File and Database systems- Database system structure, Data Models.
1.2   Introduction to Network and Hierarchical Models – ER model.
1.3   Relational Model – Relational Algebra and Calculus.

Unit   2   **(15 hrs)**
SQL definition and Normalization
2.1   SQL – Data definition- Queries in SQL- Updates- Views – Integrity and Security.
2.2   Relational Database design – Functional dependences and Normalization for Relational Databases (up to BCNF).
2.3   Query forms.

Unit   3   **(16 hrs)**
 Files and RDBMS
3.1   Record storage and Primary file organization- Secondary storage Devices- Operations on Files- Heap File- Sorted Files- Hashing Techniques – Index Structure for files –Different types of Indexes- B-Tree - B+Tree – Query Processing.
3.2   Multimedia Databases - Basic Concepts and Applications. Indexing and Hashing.Text databases.
3.3   Overview of RDBMs, Advantages of RDBMs over DBMs. Data Mining.

Unit 4   **(16 hrs)**
   Data Definition and Manipulation Language
   4.1   Data Definition Language, Data Manipulation Language, Transaction
           Control & Data Control Language Grant & Revoke Privilege Command.
   4.2   Set operators, Joins-Kinds of Joins, Table   aliases, Sub queries, Multiple
           & correlated Sub queries.
   4.3   Functions-Single Row, Date, Character, Numeric, Conversion, Group
           functions.

Unit 5   **(16 hrs)**
   Constraints and MySQL
   5.1   Constraints-Domain, Equity, Referential Integrity Constraints.
   5.2   Locks -Types of Locks, Table Partitions, Synonym.
   5.3   Introduction to PL/SQL, Introduction, MySQL as an RDBMS Tool,
           Datatypes and Commands.

TEXT BOOKS

   Ramakrishnan Raghu and Gehrke Johannes, <u>Database Management Systems,</u> USA:
   McGraw –Hill Co, 2003.

REFERENCE BOOKS

   George Koch and Kevin Loney**,** <u>Oracle 8 - The Complete Reference,</u> USA: Tata
   McGraw – Hill Co, 1998.

   Kyte, Thomas, <u>Expert Oracle Database Architecture- 9i and 10g Programming</u>
   <u>Techniques and Solutions.</u> USA: Apress, Berkeley, CA, 2006.

   Michael Abbey and Michael J. Correy, <u>Oracle 8i - A Beginners Guide,</u> USA:
   McGraw-Hill Co., 1999.

PATTERN OF EVALUATION (End Semester Examination.)
Total Marks: 100   Duration: 3 Hours

The question paper pattern: theory and practical
Theory:
     Section A – 30 x   1 = 30 Marks (All questions to be answered)
     Section B – 10 x 2 = 20 Marks (2 out of 4 to be answered)
Practical:
     Section C –   2 x 25 = 50 Marks

Question comprising the following:
Display the output for the given query,
Error finding,
Output of the given programme,
Find the missing statements in a given programme.

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SYLLABUS
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C++ FOR BIOINFORMATICS

CODE: 11BI/PC/CP14 **CREDITS : 4**
L T P : 3 1 2
TOTAL TEACHING HOURS : 78

OBJECTIVES OF THE COURSE
  ➢ This course will help you to become familiar with the programming
    language.
  ➢ It will help in gaining knowledge of C++ programming language.
  ➢ The application of C++ program will help you to do practical oriented
    programs.

Unit   1   **(15 hrs)**
Introduction to Programming language
1.1   Introduction to Programming, Choice of Language: Machine/Assembly
      Language.
1.2   Higher Level Languages, Data: Simple, Compound, Code: Syntax and
      Semantics.
1.3   Introduction to Programming in C++: C++ Characteristics, Object-
      Oriented Terminology, Object-Oriented Paradigm, Abstract Data Types.

Unit   2   **(15 hrs)**
Functions and variables
2.1   Tokens, Expressions and Control Structures: Tokens, keywords,
      Identifiers and constants, Basic data types, User defined data types,
      Derived data types.
2.2   Functions and Variables: Functions: Declaration and Definition.
2.3   Variables: Definition, Declaration, and Scope, Dynamic Creation and
      Derived Data, Arrays and Strings in C++.

Unit   3   **(16 hrs)**
Overview of classes
3.1   Classes in C++: Defining Classes in C++, Classes and Encapsulation,
      Member Functions.
3.2   Instantiating and Using Classes, Using Constructors, Destructors, Friend
      Function. Inheritance:
3.3   Overview of Inheritance, Constructor and Destructor Calls
      Polymorphism: Overview of Polymorphism.

Unit   4   **(16 hrs)**

String manipulation

4.1   Input and Output in C++ Programs: Standard Streams, Manipulators, Unformatted Input and Output, File Input and Output, Formatted console I/O operations

4.2   Exceptions: Exceptions, Inheritance and Exceptions, Exception Hierarchies.

4.3   Operator Overloading String manipulation: Creating String objects, Manipulating string, Relational operators. String characteristics, Comparing and swapping.

Unit   5   **(16 hrs)**

Introduction to files

5.1   Working with files: Opening and closing a file, Classes for file stream operations

5.2   Detecting end of file, More about open (): file mode, Updating file, Error handling, Command line arguments.

5.3   Pointers: Pointers, Pointers to objects, Pointers to derived classes, Virtual functions, References.

TEXT BOOKS

Balagurusamy, E., Object Oriented Programmig with C++, New Delhi: Tata McGraw-Hill Publishing Co. Ltd., 2007.

Hubbard, John, Programming with C++, Schaum's Outline Series, Tata McGraw Hill International Editions, 2000.

REFERENCE BOOKS

Bjarne, Stroustrup, The C++ Programming Language, Addison Wesley Pub. Co., 2000.

Brain, W. Kernighan and Dennis. M. Ritchie, The C Programming Language, USA: Prentice Hall, 1988. (also available online).

E-book: Bruce Eckel, Thinking in C++: Introduction to Standard C++, Volume-1, 2nd Edition., 2000.

Sanjeev Sofat, Object Oriented Programming Using C++, New Delhi: Cyber Tech. Publication, 2002.

PATTERN OF EVALUATION (End Semester Examination – 3 Hrs.)

Total Marks: 100   Duration: 3 Hours

Theory:

Section A – 30 x   1 = 30 Marks (All questions to be answered)
Section B – 10 x 2 = 20 Marks (2 out of 4 to be answered)

Practical:
Section C –   2 x 25 = 50 Marks

Question comprising the following.

Error finding,
Output of the given programme,
Write a C++ program such as:
   a) Palindrome, multiplication,
   b) To find the area, circumference of a circle,
   c) Average of three marks,
   d) Armstrong no, Leap year,
   e) Find the sum of the digits of the number
   f) Using functions,
   g) Using classes, constructor and destructor etc
Find the missing statements in a given programme.

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SYLLABUS
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BIOPHYSICS

CODE: 11BI/PC/BP14   **CREDITS: 4**
                                                          L T P: 4 1 0
                                          TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE
  ➢ To give a basic understanding about the forces that determine the structure
     of biological macromolecules.
  ➢ To provide knowledge about the techniques used in studying biological
     structure and function.
  ➢ To understand the behavior and properties of biological macromolecules.

Unit   1   **(15 hrs)**
Introduction
1.1   Atoms, Molecules and Chemical bonds.
1.2   Bohr model of the atom – atomic spectra. De Broglie theory of matter
        waves – Schrödinger wave equation – interpretation of wave function –
        atomic orbitals – molecular orbitals – hybrid orbitals –valency.
1.3   Thermodynamics systems – laws of thermodynamics – statement and
        applications – concepts of entropy and enthalpy.

Unit   2   **(10 hrs)**
Spectroscopy
2.1   Visible, UV and IR spectroscopy.
2.2   Raman spectroscopy –'fingerprinting' using Raman spectra –
        complementarity of Raman and IR spectroscopy.
2.3   Fluorescence spectroscopy – principles and applications only for all.

Unit   3   **(10 hrs)**
Nuclear Magnetic Resonance
3.1   The phenomenon, Spin-spin interaction.
3.2   Relaxation and Nuclear Overhauser Effect, Chemical shift, measuring the
        spectrum, one dimensional NMR Two dimensional.
3.3   NMR application to Macromolecules.

Unit   4   **(15 hrs)**
   Mass Spectrometry
   4.1   Mass Spectrometry for protein and peptide analysis.
   4.2   MALDI-TOF Analyzer, Tandem Mass Analyzer, The Ion Trap Mass
           Analyzer, Q-TOF Instrument.
   4.3   Protein identification by Peptide Mass Fingerprinting, Peptide Sequence
           Analysis by TMS and Protein Identification by TMS data.

Unit   5   **(15 hrs)**
   Crystallography and Microscopy
   5.1   Elementary description of crystallography – small and macro molecule
           crystal growth, data collection, structure solution, refinement and
           interpretation – concept of resolution.
   5.2   AFM: Atomic Force Microscopy basic principle and application.
   5.3   CFM: Chemical Force Microscopy basic principles and applications.

TEXT BOOKS

Igor N. Serdyuk, Nathan R. Zaccai and Joseph Zaccai, <u>Methods in Molecular Physics</u>**,**
UK: Cambridge University Press, 2007.

Kensal E.van Holde, Johnson Curtis W. and Ho Shing P., <u>Principles of Physical
Biochemistry</u>**,** USA: Prentice Hall International Inc, 2004.

Narayanan P.<u>Introductory Biophysics,</u> Mumbai: New Age Publishing Co., Mumbai,
1999.

REFERENCE BOOKS

Banwell C.N., <u>Fundamentals of Molecular Spectroscopy,</u> New Delhi: Tata McGraw-
Hill Publishing Company Ltd., 1983.

Bengt Nolting, <u>Methods in Modern Biophysics</u>, Germany: Springer, 2004.

Cantor, C.R., and P.Schimmel, <u>Biophysical Chemistry, Vol.I, II and III</u> , New York,
USA: W.H.Freeman and Company, 1985.

Freifelder, D., <u>Physical Biochemistry,</u> New York, USA: W.H.Freeman and
Company, 1982.

Gunning, A.P., A. R. Kirby , V. J. Morris, <u>Atomic ForceMicroscopy,</u>   London:
Imperial College Press, 2004.

Leach A.R (1996) <u>Molecular Dynamics Simulation,</u> New York, USA: John Wiley
and Sons, 1996.

Sears F.W, Zemansky M.W and Young H.D. <u>College Physics</u>, Massachusetts, USA: Addison Wesley Publishing Company, 1985.

Sherwood, D., <u>Crystals, X-rays and Proteins,</u> London, UK: Longman Group Lts., 1976.

PATTERN OF EVALUATION (End Semester Examination.)

Total Marks: 100   Duration: 3 Hours

SECTION A - 20 x 1 = 20 Marks (All questions to be answered)

SECTION B - 4 x 10 = 40 Marks (4 out of 7 to be answered)

SECTION C - 2 x 20 = 40 (2 out of 4 to be answered)

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SYLLABUS
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BIOSTATISTICS

CODE: 11BI/PE/BS14   **CREDITS : 4**
                                                                   L T P : 4 0 0
                                                   TOTAL TEACHING HOURS : 52

OBJECTIVES OF THE COURSE
  ➢ To understand statistical methods in its several forms is the basis of biological research.
  ➢ To introduce the various statistical techniques useful for handling quantitative data.

Unit   1   **(10 hrs)**
Introduction to Biostatistics
1.1   Scope, collection, classification and tabulation, Graphical representation of data- measures of location and dispersion -Diagrammatic and Graphical Presentation of data, Types of data, Significance and uses of diagrammatic representation-limitations. Frequency distribution: Discrete and continuous frequency distribution.
1.2   Measures of Central Tendency-Mean-Median- Mode-Geometric mean-Harmonic mean for raw data- Discrete series and   Continuous series.
1.3   Measures of dispersion- Quartile deviation, Mean Deviation, Standard Deviation- Coefficient of variation, Range

Unit   2   **(10 hrs)**
Correlation and Regression
2.1   Skewness, Kurtosis, Moments, Correlation analysis, Types of correlation-Simple, Linear and Nonlinear- Pearson's Coefficient Correlation -Rank Correlation.
2.2   Coefficient-Regression analysis- Definition-Uses-Types of Regression
2.3   Regression Equation of X on Y- Regression Equation Y on X-Assumptions

Unit   3   **(10 hrs)**
Probability
3.1   Rules of probability, Apriori Probability, Posterior Probability, Axiomatic Probability, Theorems of probability, Addition and Multiplication Theorem- Conditional Probability and Bayes Theorem.
3.2   Application of Biostatistics in Bioinformatics
3.3   Probability distributions: Binomial distribution, Poisson distribution, Normal distribution.

Unit 4 (12hrs)

Sampling Techniques

4.1 Sampling techniques, Basis of Statistical Inference

4.2 Sampling Distribution, Standard error, testing of hypotheses, Null Hypothesis: Type I and Type II errors.

4.3 Test of significance for large and small samples based on Normal, t, F distributions with regard to mean, variance, proportions and correlation coefficient.

Unit 5 (10 hrs)

Application and Testing

5.1 χ^2 test of goodness of fit, contingency tables, χ^2 test for independence of two attributes, Analysis of Variance (ANOVA).

5.2 Stochastic Processes- Markov process-Semi Markov process- Markov Chains- Hidden Markov models.

5.3 Population Genetics: Hardy–Weinberg principle

TEXT BOOKS

Jae K.Lee, Statistical Bioinformatics for Biomedical and Life Science Researchers, USA: John Wiley & Sons Publications, 2010.

Rao P. S. S. Sundar, Introduction To Biostatistics And Research Methods, India: Prentice Hall, 2009.

Veer Bala Rastogi, Fundamentals of Biostatistics, New Delhi: Ane Books Pvt Ltd, 2010.

REFERENCE BOOKS

Antonisamy, B., Solomon Christopher, P. Prasanna Samuel, Biostatistics: principles and practice, India: Tata McGraw Hill Pub. Co., 2010.

Bernard Rosner, Fundamentals of Biostatistics, USA: Duxbury Press, 2010.

Liqiang Ni, An introduction to Biostatistics, University of Central Florida, 2009.

Martin Gollery, Handbook of hidden Markov models in bioinformatics, USA: CRC Press, 2008.

Papoulis, Athanasios and S. Unnikrishnan Pillai, Probability, Random Variables and Stochastic Processes, (4th Ed.), India: Tata McGraw Hill Pub. Co., 2002.

Richard, J., Sundar P. S. S. Rao, An Introduction To Biostatistics: A Manual For Students In Health Sciences, 3rd Edn, India: Prentice Hall, 2004.

PATTERN OF EVALUATION (End Semester Examination – 3 Hrs.)

Section A: $10 \times 10 = 100$ (12 questions to be set).

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SYLLABUS
(Effective from the academic year 2011 - 2012)

CELL BIOLOGY AND GENETICS

CODE: 11BI/PE/ CG14   **CREDITS : 4**
                                                                                  L T P : 4 0 0
                                                                                  TOTAL TEACHING HOURS : 52

OBJECTIVES OF THE COURSE
  ➢ To understand the structure and function of the basic unit of life – the Cell and all its components in both Prokaryotic and Eukaryotic cells.
  ➢ To understand the basic concepts of Genetics.

Unit   1   **(10 hrs)**
Prokaryotic and Eukaryotic cells
1.1   Characteristics, Similarities and differences
1.2   Bacteria Cells - Structure, organisation, transport, Virus - Structure, Viral Infective cycles, origin and significance, Viroids and Prions.
1.3   Chromosomes - Structure and function of chromosomes, Centromeres and telomeres, Mitosis and Meiosis.

Unit   2   **(12 hrs)**
Organelles
2.1   Structure and function of Mitochondria, Plastids (i.e.: chloroplasts), Endoplasmic Reticulum Golgi bodies, Lysosomes and Peroxisomes.
2.2   DNA -Structure – conformations, Histones and Non-Histones, Nuclear matrix and Lamins; Nuclear envelope, Pore complexes, transport through the envelope.
2.3   RNA.- Ribosomes – Structure, Assembly of polypeptides on Ribosomes, Post-translational modifications. Protein synthesis in prokaryotes.

Unit   3   **(12 hrs)**
Cytoskeleton
3.1   Structure of the Cell Wall.
3.2   Structure and Role of Microtubules and Microfilaments in cells - Cell-cell interactions- Cell Adhesion, tight junctions and plasmodesmata.
3.3   Introduction to Membranes - Structure, Function, and Communication: Roles of membranes in eukaryotic cells; Membrane structure and composition,   The Plasma Membrane - Fluid Mosaic Model; organization of membranes in the cells

Unit   4   **(10 hrs)**

Multiple alleles

4.1   Human blood groups (A, B, AB, O, M, N and H) and Rh factor -
        Inheritance and significance

4.2   Gene Linkage and Recombination**:**   Coupling and repulsion hypothesis
        Linkage in *Drosophila* Cytological proof of crossing over - Example –
        Drosophila

4.3   Mapping: Locating genes along a chromosome: Two - point and three -
        point crosses

Unit   5   **(8 hrs)**

Karyotyping

5.1   Sex Determination and Sex Chromosomes

5.2   Chromosomal mechanisms of sex determination and Karyotyping.

5.3   Sex determination in Human - Barr body - Importance of Y Chromosome
        - Klinefelters' and Turners' Syndromes Inter –sexuality Linked
        Inheritance: Colour blindness and Haemophilia Y - linked genes.

TEXT BOOKS

Klug, William, S. and Michael R. Cummings Concepts of Genetics, New Jersey,
USA: Prentice Hall International, Inc., 1997..

Purvis, William K, David Sadava, Craig Heller and Gordan H. Orians, Life: The
Science of Biology, CA. USA: Sinauer Inc., 1999.

REFERENCE BOOKS

Darnell, James, Harvey Lodish and David Baltimore, Molecular and Cell
Biology, New York: Scientific American Books, Distributed by W.H. Freeman &
Co.. 1998.

Karp, Gerald, Cell and Molecular Biology- Concepts and Experiments, USA: John
Wiley and Sons, Inc., 1996.

Karp, Gerald and Nancy L. Puritt, Cell and Molecular Biology- Concepts and
Experiments, USA: John Wiley and Sons, Inc., 1998.

Lodish Harvey, Arnold Berk, Paul Matsudaira, Chris A. Kaiser, Monte Krieger,
Mathew P. Scott, S. Lawrence Zipursky and James Darnell, Molecular Cell Biology,
New York: W.H. Freeman and Co., 2004.

Burns, George W., and Botto, Paul J., The Science of Genetics, (6th ed), New York:
Macmillan Publishing Company, 1989.

Lewin, Benjamin, Genes IX, Oxford.UK: Oxford University Press, 2007.

Roitte, Ivan M., Brostoff, Jonathan and Male, David K., <u>Immunology</u> (2nd ed), Philadelphia: J.B. Lippincott Company, 1990.

Watson, James, D., et al, <u>Molecular Biology of the Gene</u> (4th ed), California, USA: The Benjamin Cummings Publishing Company Inc., 1987.

PATTERN OF EVALUATION (End Semester Examination.)

Total Marks: 100   Duration: 3 Hours

    Section A – 20 x   1 = 20 Marks (All questions to be answered)

    Section B –   4 x 10 = 40 Marks (4 out of 7 to be answered)

    Section C –   2 x 20 = 40 Marks (2 out of 4 to be answered)

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SYLLABUS
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MOLECULAR BIOLOGY

CODE: 11BI/PC/MB24   CREDITS : 4
                                                                        L T P : 4 1 0
                                                        TOTAL TEACHING HOURS : 65

OBJECTIVES OF THE COURSE
  ➢   To understand the structure and function of the genetic material.
  ➢   To understand the process and regulation of cell division.
  ➢   To have a basic understanding of the regulation of transcription and
       translation.

Unit   1   **(15 hrs)**
DNA
1.1   Types of DNA sequences, genomic DNA, cDNA
1.2   DNA Structure and Replication: Eukaryotes and Prokaryotes
1.3   Transcription and Translation: Eukaryotes and Prokaryotes.

Unit   2   **(15 hrs)**
Regulation
2.1   Transcriptional and Translational Regulation in Eukaryotes
2.2   Regulatory Proteins - Steroid hormone receptors - Heat shock genes-
       homeotic genes. Mechanisms modifying Transcriptional Control by
       regulatory proteins –DNA methylation and Genetic control, histone
       modification and Genetic regulation
2.3   Specialised mechanisms regulating rRNA genes. Post transcriptional
       Regulation; Translational Regulation. Post translational Regulation;
       Regulation in Prokaryotes

Unit   3   **(12 hrs)**
Gene Organisation
3.1   Organisation of the Genome and Genetic Rearrangements.
3.2   Organisation of Eukaryotic genomes - coding sequences. Repetitive
       sequences in Eukaryotic genomes Genetic rearrangements – transposable
       elements.
3.3   Genetic control of vertebrate Immune system

Unit   4   **(10 hrs)**
Organelle Genome
4.1   Mitochondrion and Chloroplast genomes – organisation and function.
4.2   Transcription and Translation in Mitochondria.
4.3   Folding and assembly of Rubisco.

Unit   5   **(13 hrs)**
      Cell Cycle
      5.1   Cell Cycle, Cell Cycle Regulation
      5.2   Mitosis and Meiosis.
      5.3   Cancer: Characteristics, genetic basis, initiation and progression.

TEXT BOOKS

Harvey Lodish; Arnold Berk; Chris A. Kaiser; Monty Krieger; Matthew P. Scott; Anthony Bretscher; Hidde Ploegh; Paul Matsudaira, (2008), Molecular Cell Biology, W.H.freeman, USA

Wolfe, Stephen L., (2005), Molecular and Cellular Biology, Wadsworth, Inc. CA., USA

REFERENCE BOOKS

Cooper, Geoffrey M. and Robert E. Hausman, The Cell, A Molecular Approach (3rd. Ed.), MA, USA: Sinauer Associates, Inc., 2004.

Darnell, James, Harvey Lodish and David Baltimore, Molecular and Cell   Biology, NY, USA: Scientific American Books, Distributed by W.H. Freeman and Co., 2004.

Karp, Gerald, Cell and Molecular Biology - Concepts and Experiments, USA: John Wiley and Sons, 1996.

PATTERN OF EVALUATION (End Semester Examination.)

Total Marks: 100   Duration: 3 Hours

Section A – 20 x   1 = 20 Marks (All questions to be answered)

Section B –   4 x 10 = 40 Marks (4 out of 7 to be answered)

Section C –   2 x 20 = 40 Marks (2 out of 4 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE : BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011 -2012)

MOLECULAR BIOLOGY - PRACTICAL

CODE: 11BI/PC/P122   **CREDITS : 2**
                                                                             L T P : 0 0 3
                                                                             TOTAL HOURS : 39

OBJECTIVE OF THE COURSE:
  ➢ To provide practical experience of the various techniques involved in
     Molecular Biology and Biochemistry.

Unit   1   **(8 hrs)**
    1.1   Cell Fraction and Extraction of cell organelles.
    1.2   Isolation of sub-cellular organelles and particles –Mitochondria and
           Chloroplast

Unit   2   **(8hrs)**
    2.1   Extraction of DNA from liver, Extraction of RNA from onion
    2.2   Estimation of DNA and RNA
    2.3   Estimation of proteins by Lowry's method.

Unit   3   **(8hrs)**
    3.1   Estimation of mitochondria by assessing the marker enzyme
    3.2   Denaturing proteins and identification of amino acids by Thin layer
           chromatography.

Unit   4   **(7hrs)**
    4.1   Isolation of plasmid DNA(Demo)
    4.2   Amplification of DNA by PCR.

Unit   5   **(8hrs)**
    5.1   Electrophoretic techniques: SDS PAGE and Agarose gel electrophoresis
    5.2   Southern blotting.

REFERENCE BOOKS

Wilson, K; Walker, J (Editors) Principles and techniques of Biochemistry and Molecular Biology, 6th edition, CUP UK, 2005.

Sambrook, J ; Russel, DW, Molecular Cloning, 3rd edition , USA: Cold Spring Harbor Laboratory Press, 2001.

Sadasivam, S; Manickam, A., Biochemical Methods, 2nd edition, India: New Age International Pvt Ltd, 1996.

PATTERN OF EVALUATION (End Semester Examination.)
Total Marks: 100   Duration: 3 Hours

Spotters 4 in number each carrying 6 marks totaling 24 marks

Any two experiments each carrying 30 marks each—10 marks for procedure, 10 marks for the result and 10 marks for the conduct of the experiment

Viva – 10 marks

Record - 6 marks

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011 - 2012)

BASIC BIOINFORMATICS

CODE : 11BI/PC/BI24   CREDITS : 4
                                                                    L T P : 4 1 0
                                                      TOTAL TEACHING HOURS : 65

OBJECTIVES OF THE COURSE
➢ To give an integrative approach to understanding both theory and practice of bioinformatics.
➢ To apply biological concepts at different levels to study gene / protein analysis, and the proteins implicated in diseases.

Unit   1   **(12 hrs)**
Introduction to biological Databases
1.1   Type of databases, Public Biological Databases – NCBI, EBI, CMBI, OMIM. Primary nucleotide sequence databases: EMBL, GenBank, DDBJ.
1.2   Secondary nucleotide sequence databases: UniGene, SGD. Sequence submission Methods and tools (Sequin, Sakura, Bankit).
1.3   Sequence retrieval systems (Entrez & SRS); Sequence File Formats and Conversion tools. Finding scientific articles, using Pubmed.

Unit   2   **(14 hrs)**
Introduction to sequence alignment
2.1   Protein Alignment, Homology, Similarity, Identity, Gaps
2.2   Pairwise alignments: Dot Plots, Scoring matrix-PAM, BLOSUM, Gap penalty
2.3   Dynamics programming - Alignment Algorithms: Global Sequence Alignment: Needleman-Wunsch Algorithm. Local Sequence Alignment: Smith –Waterman Algorithm. Rapid, Heuristic versions of Smith Waterman: FASTA and BLAST - Statistics of sequence alignment score: E-Value, P-Value

Unit   3   **(15 hrs)**
Basic Local Alignment Search Tool
3.1   BLAST Search Steps, Search Strategy, General concepts.
3.2   BLAST Algorithm: Local Alignment Search Statistics and E Value. Raw Scores and Bit Scores, Relation between E and P Values. Gapped Alignments in BLAST, Evaluation of results.
3.3   Advanced BLAST Searching-Specialised BLAST sites: - Organism Specific BLAST Sites, Ensemble BLAST, TIGR BLAST, PSI-BLAST.

Unit 4 (12 hrs)

Multiple Sequence Alignment

4.1   Definition of Multiple Sequence Alignment. Databases of Multiple Sequence Alignment Programs- BLOCKS, PRINTS.

4.2   Integrated Multiple Sequence Alignment Resources: InterPro, iProClass .

Unit 5 (12 hrs)

Evolutionary Analysis

5.1   Introduction to Evolutionary Analysis, Bootstrap, Tree construction methods:

5.2   Neighbor-Joining method, Unweighted Pair Group Method with Arithmetic Mean (UPGMA), Maximum parsimony Method and Maximum-likelihood Method.

TEXTBOOKS

Baxevanis, Andreas, D. and Francis B.F. Ouellette, (2nd. Ed), Bioinformatics- A Practical Guide to the Analysis of Genes and Proteins, New York: John Wiley and Sons, 2001.

David W.Mount, (2003), Bioinformatics Sequence and Genome Analysis, New Delhi: CBS Publishers & Distributors, 2003.

Pevsner, Jonathan, Bioinformatics and Genomics Functional, New Jersey, USA: John Wiley & Sons Inc. 2003.

REFERENCE BOOKS

Baldi, P. and Brunak, S., Bioinformatics: Machine Learning Approach, USA: MIT Press, 2003.

Chen, Yi-Ping Phoebe (Ed), Bioinformatics Technologies, Springer, Berlin Heidelberg, Germany, 2005.

Durbin, R., S. Eddy, A. Krogh and G. Mitchison, Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids, (Reprint), USA: Cambridge University Press, 2005.

Higgins, Des and Willie Taylor, Bioinformatics –Sequence, Structure and Databanks – Practical Approach; Oxford University Press, 2001.

Lesk, Arthur M., Introduction to Bioinformatics, UK: Oxford University Press, 2005.

PATTERN OF EVALUATION (End Semester Examination.)

Total Marks: 100   Duration: 3 Hours

SECTION A - 30 x 1 = 30 Marks (All questions to be answered)

SECTION B - 3 x 10 = 30 Marks (3 out of 5 to be answered)

SECTION C - 2 x 20 = 40 (2 out of 4 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011 -2012)

BASIC BIOINFORMATICS - PRACTICAL

CODE: 11BI/PC/P222 **CREDITS : 2**
 L T P : 0 0 3
 TOTAL HOURS : 39

OBJECTIVES OF THE COURSE
> ➢ To provide practical experience of the various tools involved in Bioinformatics.

Unit 1 **(8hrs)**
 Nucleotide Databases
 1.1 Primary nucleotide sequence databases: NCBI, EMBL, GenBank, DDBJ
 1.2 Database of Essential Genes

Unit 2 **(8hrs)**
 BLAST
 2.1 Basic Local Alignment Search Tool (BLAST)

Unit 3 **(8hrs)**
 Protein Sequence Databases
 3.1 Protein Sequence Databases – PIR, PRF/SEQDB, RefSeq, Swiss-Prot,
  TrEMBL.
 3.2 Protein Structure Databases – PDB, CSD, NDB.
 3.3 Protein Structural Classification Databases – CATH, SCOP

Unit 4 **(7hrs)**
 Visualization tools
 4.1 Protein Family Databases –Pfam, ProDom, TIGRFAM
 4.2 Protein visualization tools- Cn3D, Jmol, Rasmol, Weblab Swiss PDB Viewer.
 4.3 Specialized database (IMGT, Rebase, COG, LIGAND, BRENDA).

Unit 5 **(8hrs)**
 Multiple sequence alignment and Evolutionary tool
 5.1 Multiple Sequence Alignment tools: Clustal W and Clustal X.
 5.2 Phylogenetic Tree construction tool: MEGA

TEXT BOOKS

Baxevanis, Andreas, D. and Francis B.F. Ouellette, (2nd. Ed), <u>Bioinformatics- A Practical Guide to the Analysis of Genes and Proteins</u>, New York: John Wiley and Sons, 2001.

David W.Mount, <u>Bioinformatics Sequence and Genome Analysis,</u> New Delhi: CBS Publishers & Distributors, 2003.

Lesk, Arthur M., <u>Introduction to Bioinformatics</u>, UK: Oxford University Press, 2005.

PATTERN OF EVALUATION (End Semester Examination.)
Total Marks: 100   Duration: 3 Hours

Five out of six questions to be answered (5 X 20=100)

Viva – voce would be part of the practical.

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011 -2012)

RESEARCH METHODOLOGY AND SCIENTIFIC COMMUNICATION

CODE:11BI/PE/RM24   **CREDITS : 4**
L T P : 4 0 0
TOTAL TEACHING HOURS : 52

OBJECTIVES OF THE COURSE
  ➢ To describe and express the role and importance of research in basic and applied sciences.
  ➢ To write research proposals / projects and apply for grants in the field of Bioinformatics.

Unit   1   **(10 hrs)**
Introduction
1.1   Principles and practice of research
1.2   Literature review
1.3   Action plan and pilot study undertaking a research project.

Unit   2   **(12 hrs)**
Types of Data
2.1   Data collection, sampling. Sources of Data Primary, Secondary and Tertiary sources.
2.2   Classification and presentation of data.
2.3   Documents, Types of Documents, Archives, chronologies. Electronic Sources of data: Internet, Websites, Data sets.

Unit   3   **(10 hrs)**
Scientific Communication
3.1   Format of thesis Presentation of the results, tabulations and figures
3.2   Writing project proposals, writing grant proposals, writing reports, Presentation of project

Unit   4   **(10 hrs)**
Paper Critiquing
4.1   Editing and proof reading a thesis
4.2   Paper critiquing
4.3   Bibliography and end matters, common errors in scientific writing

Unit 5   **(10 hrs)**

    Bioethics

5.1   Bioethics- Introduction. Intellectual Property Rights (IPR) and patents, TRIPS

5.2   Ethical, Legal, Social Issues (ELSI)

5.3   Case studies on patents (Basmati, Turmeric and Neem).

TEXT BOOKS

Beauchamp, T.L., and Childress, J.F. <u>Principles of Biomedical Ethics</u>, 4th edition, Oxford University Press India, 1994.

Gopalan, R. <u>Thesis Writing</u>, Chennai: Vijay Nicole Imprints Private Limited, 2005.

Gurumani, N., <u>Research Methodology for Biological Sciences,</u> Chennai: MJP, 2006.

Raman, A., <u>A Handbook on Research Processes</u>, Chennai: S. Viswanathan Pvt. Ltd., 2003.

PATTERN OF EVALUATION (End Semester Examination.)

Total Marks: 100   Duration: 3 Hours

Section A – 20 x   1 = 20 Marks (All questions to be answered)

Section B –   4 x 10 = 40 Marks (4 out of 7 to be answered)

Section C –   2 x 20 = 40 Marks (2 out of 4 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE : BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011 - 2012)

SOFT SKILLS

CODE : 11BI/PK/SS22 **CREDITS : 2**
  L T P : 2 0 0
  TOTAL TEACHING HOURS : 26

OBJECTIVES OF THE COURSE
- ➢ To empower and create opportunities for self development.
- ➢ To instill confidence and face challenges.

Unit 1 (6 hrs)
Behavioural Traits
1.1 Self Awareness
1.2 Communication Skills – Verbal and Non Verbal
1.3 Leadership Qualities
1.4 Etiquette and mannerisms
1.5 Experiential Learning – Based on activities

Unit 2 (5 hrs)
Team Work
2.1 Interpersonal Skills
2.2 People Management
2.3 Creative Thinking
2.4 Critical Thinking
2.5 Experiential Learning – Based on activities

Unit 3 (5 hrs)
Time Management
3.1 Importance of time management
3.2 Planning and Prioritizing
3.3 Organizing skills
3.4 Action Plan
3.5 Experiential Learning – Based on activities

Unit 4 (5 hrs)
Conflict Resolution
4.1 Reasons for conflict
4.2 Consequences of conflict
4.3 Managing emotions
4.4 Methods of resolving conflicts
4.5 Experiential Learning – Based on activities

Unit   5   **(5 hrs)**
        Career Mapping
        5.1   Goal setting
        5.2   Career Planning
        5.3   Resume writing
        5.4   Handling Interviews
        5.5   Experiential Learning – Based on activities

BOOKS FOR REFERENCE

Khera, Shiv, (2002), <u>You Can Win</u>**,** Macmillan India Ltd., Delhi.

Mishra, Rajiv K., (2004), <u>Personality Development : Transform Yourself</u>**,** Rupa and Co., New Delhi.

Newstrom, John W. and Scannell, Edward E., (1980), <u>Games Trainers Play: Experiential Learning</u>**,** Tata McGraw Hill, New Delhi.

NO END SEMESTER EXAM

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE : BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011 -2012)

GENOMICS AND PROTEOMICS

CODE: 11BI/PC/GP34   **CREDITS : 4**
                                                             L T P : 3 1 2
                                TOTAL CONTACT HOURS : 78

OBJECTIVES OF THE COURSE
- ➢ To give an insight into the complete genome sequences of a few organisms as well as the Human genome through Comparative and Functional genomics.
- ➢ To study the entire protein complement of a cell through analytical approaches, Data mining and other software tools.

Unit 1   **(16 hrs)**
Genomics
1.1   Rates and patterns of Nucleotide substitution, Causes of variation in substitution rates, Positive Selection, Non-random usage of synonymous codons
1.2   Molecular Clocks, Local Clocks, Understanding a Genome sequence, Locating the genes in a Genome Sequence, Gene location by sequence inspection, Experimental techniques for gene location, Determining the functions of individual genes
1.3   Computer analysis of a gene function, Assigning gene function by experimental analysis, Detailed studies of a protein coded by an unknown gene.

Unit 2   **(16hrs)**
Comparative Genomics
2.1   Comparative Genomics, Viral genomes, Variations at the level of individual nucleotides, Duplications, Comparisons at the chromosome level: synteny, Genomes of chimpanzees and humans, Genome sequencing projects
2.2   Phylogenetic analysis: Relationship of phylogenetic analysis to sequence alignment, Genome complexity and phylogenetic analysis , Maximum parsimony method, Distance methods, Reliability of phylogenetic predictions.
2.3   Gene prediction softwares – MZEF & HEXON, ORF analysis, ORF finder, Application of Genome Analysis, Human diseases, response to drugs, genome.

Unit 3   **(15hrs)**

Functional Genomics

3.1   Gene expression analysis by micro arrays, SAGE, Applications of microarrays in medicine

3.2   Strategies for generating EST's and full length inserts; EST clustering and assembly, EST databases (DBEST, UNIGene,); Statistical analysis of EST data.

3.3   The Human Genome Project and medicine, KEGG and metabolic pathways, Pathway regulatory networks.

Unit 4   **(16 hrs)**

Proteomics

4.1   Tools of Proteomics - Database, mass spectrometry, software for matching MS data with specific protein sequences (de novo sequence interpretation)

4.2   Analytical protein and peptide separations - Complex protein and peptide mixtures. Protein separation before digestion: 1D and 2D-SDS-PAGE

4.3   Preparative IEF, HPLC, Protein separations after digestion: Tandem LC approaches for peptide analysis, Protein Digestion Techniques Screening Methods - (Yeast two-hybrid and other mammalian screen methods) Protein interaction networks and protein pathways

Unit 5   **(15 hrs)**

Application of Proteomics.

5.1   Identifying Protein-Protein Interactions and Protein Complexes

5.2   Mapping Protein Modifications.

5.3   Restriction enzymes and proteolytic enzyme digestion.

TEXT BOOKS

Arthur M Lesk, <u>Introduction to Genomics</u>**,** New York: Oxford university press, 2007.

Brown, T. A., <u>Genomes -2,</u> NY, USA: John Wiley and Sons inc. 20002.

Daniel C. Leibler, <u>Introduction to Proteomics: Tools for New Biology</u>**,** Totowa, NY, USA Humana Press, 2002.

Srivastava Sudhir, <u>Informatics in Proteomics</u>, New York, USA: Taylor & Francis Group, 2005.

REFERENCE BOOKS AND ARTICLES

Brown P. O., Botstein D., <u>Exploring the new world of the genome with DNA microarrays</u>, Nat. Genet, 1999.

Collado-Vides, Julio and Ralf Hofstadter, <u>Gene Regulation and Metabolism – Post Genomic Computational Approaches</u>, India: Ane Books, 2004.

Dale, Jeremy W. and Malcolm von Schantz, <u>From Genes to Genomes – Concepts and Applications of DNA Technology</u>, NY, USA: John Wiley and Sons, 2002.

Golemis, Erica (Ed.), <u>Protein-Protein Interaction</u>, NY, USA: CSHL, 2002.

Griffiths, A.J.F, Miller, J.H, Suzuki, D.T. Lewontin, R. C. and Gelbart, W.M., <u>An Introduction to Genetic Analysis</u>, (6 Ed.), NY, USA: W.H. Freeman, 1996.

Hunt Stephen, P. and Livesey, Fredrick J., <u>Functional Genomics -A Practical Approach</u>, Great Britain: Oxford University Press, 2000.

Lesk, Arthur, M., <u>Introduction to Protein Science: Architecture, Function and Genomics</u>, UK: OUP, 2004.

Mount, David, W., <u>Bioinformatics: Sequence and Genome Analysis</u>, NY, USA: Cold Spring Harbor Lab, 2001.

Pennington, S, (Editor), M. J. Dunn (Editor); <u>Proteomics: From Proteins Sequence to Function</u>, Germany: Springer Publications, 2001.

Palzkill, Timothy; <u>Proteomics</u>, USA: Kluwer Academic Publishers, 2002.

PATTERN OF EVALUATION (End Semester Examination.)
Total Marks: 100   Duration: 3 Hours

The question paper pattern: theory and practical

Theory:
   Section A – 1 x 20 = 20 Marks (ALL questions to be answered)

   Section B – 3 x 10 = 30 Marks (3 out of 5 to be answered)

Practical:
   Section C –   50 Marks

The **practical** exam would have the following pattern:
Database search (Literature, Sequence similarity etc.) -		15 marks
Mapping of genomes, finding ORF's, etc.	-	15 marks
Gene Prediction, etc.	-	15 marks
Viva – voce	-	5 marks
Total		**50 marks**

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE : BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011 -2012)

PERL

CODE : 11BI/PC/PL34   CREDITS : 4
                                                                                    L T P : 3 1 2
                                                        TOTAL TEACHING HOURS : 78

OBJECTIVES OF THE COURSE
> ➢ To introduce the technique of programming in Perl.
> ➢ To write Perl programs that support research in biology.
> ➢ To adapt and use Perl programs written by others.
> ➢ To learn the usage of CGI and HTML for web page designing.

Unit 1 (16 hrs)
Introduction to Linux
1.1   Introduction to LINUX operating system, Properties of Linux, Desktop Environment, Linux basics commands.
1.2   Working with files, Text editors, I/O redirections, Pipes, Filters, and Wildcards.
1.3   File System Security, Changing access rights

Unit 2 (15 hrs)
Introduction to Perl Programming
2.1   Introduction to Perl 5, variable types, data types, statements and declarations, Default variables.
2.2   Expressions, Statements, Operators in Perl, operator precedence, string operators, control structures,
2.3   Creating Regular expressions-characters, character classes, alternative match patterns, quantifiers, assertions, back references, modifiers and translator operations, matching words, extracting substrings, Perl I/O.

Unit 3 (15 hrs)
Associative array and Perl functions
3.1   Subroutines- Defining Subroutines, Returning Values, Using Arguments.
3.2   Associative Arrays (Hashes).
3.3   Perl functions –abs, atan2, chr, cos, eval, exists, grep, index, int, join, keys, lc, lcfirst, length, pack, rand.

Unit   4   **(16 hrs)**
   File handling
   4.1   Working with Filehandle An Overview of Filehandle, Opening Filehandle
           Reading, writing and reading an array to a text file,Closing Filehandle .
   4.2   Writing and reading a hash to a text file. Packages, random number
           generation, perl debugging,
   4.3   Environment variables, signals, command line argument, standard
           modules.
   4.4   Introduction to Bioperl: Installation procedures, Architecture, Uses of
           bioperl.Translating DNA into proteins, Reading DNA from files in
           FASTA format.

Unit   5   **(16 hrs)**
   Common gateway interface
   5.1   CGI programming with CGI .pm, Calling CGI program, Perl for CGI,
           environmental variables, advantages and drawbacks of CGI, CGI
           applications.
   5.2   Creating HTML controls, Reading Data from HTML controls, using Perl
           scripts, starting an HTML document, displaying images, HTML form, text
           fields, text areas, check boxes, scrolling lists, radio buttons, password
           fields, popup menus

TEXT BOOKS

   Conrod Bessant, Ian Shadforth, Darren Oakley, Building Bioinformatics Solutions
   with Perl, R and MySQL, New York: Oxford University Press, 2009.

   Ellen Siever, Weber, Stephen Figgins, Robert, Arnold Robbins, Linux in a
   Nutshell-A Desktop Quick Reference, 5th edition, O'Reilly and Associates, 2006.

   Guelich, Scott, Shishir Gundavaram and Gunther Birznieks, CGI Programming
   with Perl, (2nd. Ed). USA: O'Reilly and Associates, 2000.

   Holzner, Steven, (2006), Perl Black Book, (2nd. Edition), New Delhi: Dream Tech
   Press, 2006.

   Tisdall, James. D., Beginning Perl for Bioinformatics (1st Ed), USA: O'Reilly
   and Associates, 2000.

   Tisdall, James. D., Mastering Perl for Bioinformatics (1st Ed), USA: O'Reilly and
   Associates, 2003.

REFERENCE BOOKS:

Bradley M. Kuhn, Neil A. Smyth, Picking Up Perl (2nd Edition**,** Free Software Foundation (available online free), 2005.

Elizabeth Castro, Perl and CGI for the World Wide Web, Addison- Wesley Pub Co., 1998.

Jacqueline, D. Hamilton, CGI Programming 101**,** Cgi101.Com Web-learning**:** www.CGI101.com., 2004.

Larry Wall, Tom Christiansen & Jon Orwant, (2000), Programming Perl, (3rd Ed), New Delhi. O'Reilly-Shroff Publishers and Distributors Pvt. Ltd., 2000.

Randall. L. Schwartz & Tom Phoenix, Learning Perl, (3rd Ed), New Delhi: O'Reilly - Shroff Publishers and Distributors Pvt. Ltd. 2000.

Shishir Gundavaram, CGI programming on the World Wide Web, (1st Ed), USA: O'Reilly and Associates, 1996.

PATTERN OF EVALUATION (End Semester Examination.)
Total Marks: 100   Duration: 3 Hours

Theory:

Section A – 30 x   1 = 30 Marks (All questions to be answered)

Section B – 10 x 2 = 20 Marks (2 out of 4 to be answered)

Practical:

Section C –   2 x 25 = 50 Marks

Question comprising the following:

Complete a programme,
Write a Perl program related to Bioinformatics (transcription, translation, finding motifs/repeats/restriction enzyme etc.),
Output of the given programme.

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE : BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011 -2012)

ALGORITHMS FOR BIOINFORMATICS

CODE: 11BI/PC/AB34   CREDITS : 4
                                                          L T P : 4 1 0
                                            TOTAL TEACHING HOURS :65

OBJECTIVES OF THE COURSE
  ➢   To develop a quantitative understanding of how living things are built.
  ➢   To raise the awareness of the impact of algorithms on the efficiency of the
      system.
  ➢   To develop skills to analyze algorithms related to Bioinformatics.

Unit   1   **(10hrs)**
Introduction
1.1.   Algorithms and Complexity. Definition. Biological Algorithms versus
       Computer Algorithms. Fast versus Slow Algorithms Big-O Notation.
1.2.   Algorithm Design Techniques Exhaustive Search Branch-and-Bound
       Algorithms Greedy Algorithms
1.3.   Dynamic Programming Divide-and-Conquer Algorithms Machine
       Learning Randomized Algorithms

Unit   2   **(10hrs)**
Restriction Mapping
2.1   Impractical Restriction Mapping Algorithms, A Practical Restriction
       Mapping Algorithm.
2.2   Regulatory Motifs in DNA Sequences Profiles: The Motif Finding
       Problem Search Trees.
2.3   Finding a Median String. String matching algorithm.

Unit   3   **(15 hrs)**
Sequence Alignment
3.1   Longest Common Subsequences - Global Sequence Alignment- Local
       Sequence Alignment
3.2   Graph Algorithms- Graphs and Genetics- DNA Sequencing Shortest
       Superstring Problem.
3.3   DNA Arrays as an Alternative Sequencing Technique. Sequencing by
       Hybridization.

Unit   4   **(15hrs)**
       Clustering and Evolutionary Trees
       4.1   Gene Expression Analysis. Hierarchical Clustering -k-Means Clustering-
                 Clustering and Corrupted Cliques.
       4.2   Evolutionary Trees - Distance-Based Tree Reconstruction
                 Reconstructing Trees from Additive Matrices. Evolutionary Trees and
                 Hierarchical Clustering Character-Based Tree Reconstruction.
       4.3   Secondary Structure Prediction methods, Artificial Neural Networks.

Unit   5   **(15 hrs)**
       Pattern Matching
       5.1   Combinatorial Pattern Matching. - Identical, Similar and Distant Repeats
                 Finding methods. Exact Pattern Matching
       5.2   Keyword Trees and Suffix Trees. Heuristic Similarity Search
                 Algorithms
       5.3   BLAST: Comparing a Sequence against a Database.

TEXT BOOKS

Neil C Jones and Pavel A. Pevzner, <u>An Introdcution to Bioinformatics Algorithms,</u> USA: MIT press, 2004.

Pavel A.Ppevzner, <u>Computational Molecular Biology- An algorithmic approach</u>, USA: MIT press, 2000.

REFERENCE BOOKS

Alfred V. Aho, John E. Hopcroft and Jefferey D.Ullman, <u>Data Structures and Algorithms</u>, London: Addison Wesley Pub. Co. 1983.

Clark, John and Derek Allan Holton, <u>A First Look at Graph Theory,</u> Singapore: Allied Publishers Ltd., in association with World Scientific, 1995.

Jeffrey J. McConnell, <u>Analysis of Algorithm,</u> New Delhi: Narosa Publishing House, 2002.

Horowitz, Ellis, and Sartag Sahni, <u>Fundamentals of Computer Algorithms,</u> New Delhi: Galgotia Publications (P) Ltd., 1994.

Thomas H. Cormen, Charles E. Leiserson and Ronald L. Rivest, <u>Introduction to Algorithms,</u> New Delhi: Prentice Hall of India Pvt. Ltd., 1990.

PATTERN OF EVALUATION (End Semester Examination – 3 Hrs.)

   Section A: 10×10 = 100 (12 questions to be set)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2011 -2012)

MOLECULAR MODELING AND COMPUTER AIDED DRUG DESIGNING

CODE: 11BI/PC/MC34   **CREDITS : 4**
                                                                 L T P : 3 1 2
                                                                 TOTAL TEACHING HOURS : 78

OBJECTIVES OF THE COURSE
  ➢ To provide some of the theoretical background to the various methods
    available to a molecular modeller.
  ➢ To introduce the techniques used in molecular modelling.
  ➢ To illustrate how these techniques can be used to study physical, chemical and
    biological phenomena of bio molecules.

Unit   1   **(15 hrs)**
Introduction
1.1   Concepts in molecular modelling**:** Basic principles – molecular
       representations Coordinate Systems-Potential Energy Surfaces
1.2   Features of molecular mechanics, force fields– atom-atom pair potentials –
       bond length and bond angle and torsion angle potential
1.3   Non- bonded interactions-Van der Waals and electrostatic potential –
       hydrogen bonding terms.

Unit   2   **(16hrs)**
Energy Minimisation and Computer Simulation Methods
2.1   Energy Minimisation-Introduction- Derivative and Non-derivative Energy
       Minimization Methods**.**
2.2   Calculation of Simple Thermodynamic Properties, Practical aspects of
       Computer Simulation, Boundaries, Monitoring the equilibration, long –
       range forces
2.3   Analyzing the Results of Simulation and Estimating Errors

Unit   3   **(16hrs)**
Molecular Dynamics Simulation and Monte Carlo Simulation Methods
3.1   Molecular Dynamics Using Simple Model
3.2   Molecular Dynamics with Continuous Potentials,
3.3   Molecular Dynamics at constant temperature and pressure, Incorporating
       Solvent effects into Molecular Dynamics, conformational changes from
       Molecular Dynamics simulation

3.4   Monte Carlo Simulation Methods-Introduction-Monte Carlo Simulation of Molecules

3.5   Calculation of Chemical Potential-Simulating Phase Equilibria by Gibbs Ensemble Monte Carlo Method

Unit   4   **(16 hrs)**

Molecular docking

4.1   Molecular docking. Structure based drug design – de novo approach

4.2   Molecular Descriptors-Quantitative structure-activity relationship – concept, and properties of organic molecules- various descriptors used in the QSAR, multiple linear regression and its applications to drug design.

4.3   3D pharmacophore-derivation and matching Importance of molecular modeling in drug discovery.

Unit   5   **(15 hrs)**

Computer Aided Drug Design

5.1   Insilco modeling and CADD: Molecular modeling using computers CADD,

5.2   Protein-ligand docking in drug design-Active site prediction-Target discovery-Target validation-Lead optimization.

5.3   Modeller, What-if web interface.

TEXT BOOKS

Andrew R. Leach, <u>Molecular Modeling: Principles and Applications</u>, USA: Prentice Hall, 2001.

Claude Cohen, N., <u>Guidebook on Molecular Modelling In Drug Design,</u> California: Academic Press, San Diego, 2006.

Daan Frenkel, Berend Smit, <u>Understanding Molecular Simulation</u>, Second edition, From Algorithms to applications, USA: Academic Press, 2002.

REFERENCE BOOKS

Alan Hinchliffe, <u>Molecular Modelling for Beginners,</u> USA: John Wiley & Sons, 2003.

Charifson P.S., <u>Practical Application of Computer Aided Drug Design,</u> New York: Dekker, 1997.

PATTERN OF EVALUATION (End Semester Examination)

Total Marks: 100   Duration: 3 Hours

SECTION A - 20 x 1 = 20 Marks (All questions to be answered)

SECTION B - 4 x 10 = 40 Marks (4 out of 7 to be answered)

SECTION C - 2 x 20 = 40 (2 out of 4 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE : BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011 -2012)

RECENT ADVANCES IN BIOINFORMATICS

CODE: 11BI/PC/RB44   **CREDITS : 4**
                                                          L T P : 4 1 0
                                                          TOTAL TEACHING HOURS : 65

OBJECTIVES OF THE COURSES
  ➢ To develop a quantitative understanding of how Pharmacogenomics plays a major role and the impact of cheminformatics packages available for drawing molecular structure.
  ➢ To provide awareness about immunoinformatics tools available for vaccine deisgn and also how to handle the microarray data.
  ➢ To provide a better understanding of R package and its applications in bioinformatics.

Unit   1   **(10 hrs)**
Pharmacogenomics
1.1   Definition of Pharmacogenomics & Toxicogenomics – case study in Alzheimer's diseases –
1.2   Safety metabolisms pharmacology – Exploitary Toxicology
1.3   Preclinical Toxicology, Pharmacokinetics & Metabolism.

Unit   2   **(11 hrs)**
Cheminformatics
2.1   2D and 3D Molecular Structures. Chemical Structure Drawing Packages.
2.2   Molecular Descriptors and Fingerprints.Molecular Similarity (or Diversity).
2.3   Searching for Chemicals on the Internet (PubChem, eMolecules). SMILES.

Unit   3   **(15 hrs)**
Immunoinformatics
3.1   Bioinformatics strategies for better understanding of immune function
3.2   Future of computational modeling and prediction systems in clinical immunology
3.3   Role of Immunoinformatics in personalized medicine. From immunome to vaccine- epitope mapping, vaccine design tools

Unit   4   (15 hrs)
Micro array Analysis
4.1   DNA Microarray: The Technical Foundations, Importance and definition
        Designing a MicroArray Experiment: The Basic steps
4.2   Types of Microarray, NCBI and Microarray Data Management, GEO
        (Gene Expression Omnibus), MAML.
4.3   The Promise of Microarray Technology in Treating Disease. Microarray
        Data, Preprocessing the Data, Measuring Dissimilarity of Expression
        Pattern, Distance Motifs and Dissimilarity measures, Visualizing
        Microarray Data.

Unit   5   (14 hrs)
R programming
5.1.   Introduction, Installing R
5.2   R as a deluxe calculator, creating objects and assigning values.
5.3   Graphics; simple plotting, advanced plotting, using color in plots, using
        subscripts and superscripts in graph labels, interactive graphics, saving
        graphical output, loops.

TEXT BOOK

Crawley, M.J. (2007). The R Book. USA: Wiley and sons, 2007.

Ole Lund, (2005) Immunological Bioinformatics, USA: MIT press. 2005.

Rammensee, Immunoinformatics- Bioinformatics Strategies for Better Understanding
of Immune, Function, USA: Wiley and sons, 2003.

Robert Gentleman, R Programming for Bioinformatics, ISBN-13: 978-1420063677,
2005.

REFERENCE BOOKS

Boca Raton.Venables, W.N., Smith, D.M., and the R Development Core Team.An
Introduction to R. Notes on R: A Programming Environment for Data Analysis and
Graphics. Version 2.6.1., 2007.

Darren Flower, In Silico Immunology, USA: Springer, 2006.

Gentleman, R., Carey, V.J., Huber, W., Irizarry, R.A., and Dudoit, S.,eds. (2005),
Bioinformatics and Computational Biology Solutions Using R and Bioconductor,
New York: Springer, 2005.

Murrell, P., R Graphics. USA: Chapman & Hall/CRC, 2006.

http://cran.rproject.org/doc/manuals/R-intro.pdf.

PATTERN OF EVALUATION (End Semester Examination.)

Total Marks: 100   Duration: 3 Hours

    Section A – 20 x   1 = 20 Marks (All questions to be answered)

    Section B –   4 x 10 = 40 Marks (4 out of 7 to be answered)

    Section C –   2 x 20 = 40 Marks (2 out of 4 to be answered)

M.Sc. DEGREE : BIOINFORMATICS
SYLLABUS
(Effective from the academic year 2011 -2012)

DATA MINING AND MACHINE LEARNING

CODE : 11BI/PC/DM44   CREDITS : 4
                                                                                         L T P : 4 1 0
                                                                      TOTAL TEACHING HOURS : 65

OBJECTIVES OF THE COURSE
  ➢   To provide an insight to Data mining.
  ➢   To introduce the techniques used in data mining.
  ➢   To understand these techniques in collecting and sorting of data.

Unit   1   (10 hrs)
Data mining
1.1   Introduction: Classification of data, Relational databases. Data warehouses
        Transactional databases .Advanced database systems and advanced
        database applications.
1.2   Data mining functionalities. Concept /class description: characterization
        and discrimination. Association analysis.
1.3   Classification and prediction -Clustering analysis. Evolution and deviation
        analysis. Classification of data mining systems. Major issues in data
        mining.

Unit   2   (10 hrs)
Genetic Algorithm
2.1   Introduction to Genetic Algorithm, Features and anatomy of genetic
        algorithm, methodology
2.2   Cross over techniques, fitness function. Applications in bioinformatics.

Unit   3   (15 hrs)
Data Processing
3.1   Data Preprocessing. Data integration and transformation, Data reduction.
        Association rule mining.
3.2   The Apriori algorithm: Finding frequent item sets From association
        mining to correlation analysis
3.3   Classification and Prediction Classification by back propagation
        Association-based classification Other classification methods.

Unit 4   **(15 hrs)**

Clustering

4.1   Clustering – cluster analysis – Types of clustering methods- Types of data in clustering analysis

4.2   A categorization of major clustering methods. Hierarchical methods. Density Based clustering methods. Grid based methods. Outlier analysis.

4.3   Data Mining applications and trends in data mining – Data mining applications in biotechnology and bioinformatics

Unit 5   **(15 hrs)**

Neural networks and machine learning

5.1   Introduction to Neural networks, learning rules, Classification Analysis, learning algorithm and model evaluation.

5.2   SOM and SVM techniques in data mining

TEXT BOOK

Jiawei Han and Micheline Kamber, <u>Data Mining: Concepts and Techniques</u>, 2nd ed., USA: Morgan Kaufmann Publishers, 2006.

REFERENCE BOOK

Oliviero carugo and Frank Eisenhaber, <u>Data Ming techniques for life sciences</u>, Singapore: Humana Press, 2009.

PATTERN OF EVALUATION (End Semester Examination.)

Total Marks: 100   Duration: 3 Hours

Section A – 20 x 1 = 20 Marks (All questions to be answered)

Section B – 4 x 10 = 40 Marks (4 out of 7 to be answered)

Section C – 2 x 20 = 40 Marks (2 out of 4 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE : BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011 -2012)

DISSERTATION

CODE: 11BI/PC/DS48   **CREDITS: 8**

Dissertation : 50   **Viva : 50**

The Dissertation shall contain at least 50 pages and shall be typed with double spacing.

The format for the thesis is as follows:

1.   Cover page shall contain
        a) Title of the dissertation
        b) Name of the Candidate
        c) Department of Bioinformatics
                    Stella Maris College (Autonomous), Chennai – 86

        d) Month, Year

2.   The dissertation shall contain
        a) Contents page
        b) i. Certificate page
            ii. Acknowledgement page

        c) At least 5 Chapters including an introduction, Review of Literature, Materials and Methods, Result and Discussion and Summary
        d) List of figures / list of abbreviations (if needed) shall be given as an appendix
        e) Bibliography shall be given in alphabetical / chronological order at the end.

3.   Each candidate may prepare 3 hard copy and one soft copy of the thesis, one copy for her and submit 2 copies to the Head of the department 15 days before the commencement of the fourth semester examination.
4.   The candidate may be advised that the dissertation will be valued and given credit on the criteria of
        a) Motivation towards the chosen area / formulation of the problem
        b) Methodology and Analysis
        c) Capacity to interpret the results obtained

5.   The Controller of Examination is requested to arrange for the valuation of the Dissertation as well as the conduct of the Viva – Voce at the college where the candidates take examinations, within two weeks of the last date of examination for M.Sc. Degree. The panel of examiners will consist of an external examiner and the guide. The guidelines for the Viva-Voce examiners would be that a) They will satisfy themselves that this is a work of the candidate as certified by the department b) The thesis is in the given form and c) The candidate has clear understanding of the concepts, discussed in the thesis.

The Department should certify as follows :

This is to certify that the dissertation in the broad area _____ titled _____ is submitted by _____- at the elective level for the degree of Master of Science (Mathematics) during the year_____

        sd/   sd/

Head of the Department   Guide

6.   A) Guidelines for evaluation

The maximum mark for the dissertation is 100 divided into four components

i.	Style, format and neatness in presentation	15
ii	Chapterisation, logic and reasoning	10
iii	Methodology – Analysis and interpretation	25
iv	Viva	50

B) There will be double valuation for the dissertation by the guide and an external examiner who will conduct the viva – voce. The norms for evaluation will be same as applicable for theory papers.

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011-2012)

INTRODUCTION TO CLINICAL RESEARCH MANAGEMENT

CODE : 11BI/PE/CR44   CREDITS : 4
                                                                                      L T P : 4 0 0
                                                           TOTAL PRACTICAL HOURS : 52

OBJECTIVES OF THE COURSE
➢ To give a basic understanding about clinical research.
➢ To understand the various aspects of clinical research management.
➢ To be conversant with the regulations in clinical management.

Unit 1 (10 hrs)
Drug Development Processes
1.1   History of drug development. Discovery and selection of compounds for human investigation. Toxicological requirements. Pharmacokinetics and pharmacodynamics. Drug interactions.
1.2   Special populations; elderly, children, renal and hepatic insufficiency. Bioequivalence, formulation and stability testing. Phase I studies.
1.3   Clinical development programme planning. Statistical principles in determining sample size, randomisation and analysis.

Unit 2 (10 hrs)
Clinical Research
2.1   Good Clinical Practice and International Harmonisation. Case report form design.
2.2   Role of Ethics Committees and Institutional Review Boards. Informed consent. Data Management including electronic transmission of data.
2.3   Quality assurance; quality control, audit and regulatory inspection. Medical devices Clinical research in emerging markets Detecting and managing fraud.

Unit 3 (12 hrs)
Regulations in Clinical Research
3.1   Evolution and History of Regulations in Clinical Research, Patents US Regulatory Structure, IND, NDA, ANDA
3.2   Post Drug Approval Activities, PMS, FDA Audits and Inspections EURegulatory Affairs, EMEA Organization and Function, INDIAN Regulatory system, Schedule Y- Rules and Regulations

3.3   Clinical Research Methodology - Designing of Protocol, CRF, e-CRF, IB, ICF, SOP Pharmaco-epidemiology, BA/BE Studies Report writing, Publication

Unit   4   **(10 hrs)**
Clinical Research Management
4.1   Preparation of a successful clinical study
4.2   Study management, Project management Documentation,
4.3   Monitoring, Audits, Inspections and Pharmacovigilance

Unit   5   **(10 hrs)**
Biostatistics and Data Management
5.1   Importance of statistics in clinical research
5.2   Statistical considerations at the design, analysis and reporting stage.
5.3   Data validation, SAE reconciliation, query management

TEXT BOOKS

Lori A. Nesbitt, <u>Clinical Research What It Is and How It Works</u>, UK: Jones Barlett Publishers, 2004.

Richard K.Rondel, Sheila A. Varley, Colin F. Webb, <u>Clinical Data Management</u>", Second Edition, UK: John Wiley & Sons, 2002.

Steven Piantadosi, <u>Clinical Trails A Methodologic Perspective</u>, Second Edition, UK: John Wiley & Sons, 2005.

PATTERN OF EVALUATION (End Semester Examination.)
Total Marks: 100   Duration: 3 Hours

Section A – 20 x   1 = 20 Marks (All questions to be answered)

Section B –   4 x 10 = 40 Marks (4 out of 7 to be answered)

Section C –   2 x 20 = 40 Marks (2 out of 4 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

**Postgraduate Elective Course offered by the Department of Bioinformatics for
M.A. / M.Sc./ M.Com. Degree Programmes**

SYLLABUS
(Effective from the academic year 2011 -2012)

CHEMINFORMATICS

CODE: 11BI/PE/CI24   **CREDITS : 4**
                                                        L T P : 4 0 0
                                    TOTAL TEACHING HOURS : 52

OBJECTIVES OF THE COURSE
  ➢ To introduce the basic concepts of Chemical structure databases.
  ➢ To familiar with the cheminformatics tool available and its application.

Unit   1   **(10 hrs)**
   Introduction
   1.1   Databases: Chemical Structure Databases (PubChem, Binding database,
           Drugbank,).
   1.2   Drawing the Chemical Structure: 2D & 3D drawing tools (ACD
           Chemsketch).
   1.3   Structure optimization.

Unit   2   **(10 hrs)**
   Representation of Molecules
   2.1   Representation of Molecules and Chemical Reactions-
   2.2   Different types of Notations, SMILES Coding, Structure of Mol files and
           Sdf files(Molecular converter, SMILES Translator).
   2.3   Similarity search of the molecule.

Unit   3   **(12 hrs)**
   Drug Designing
   3.1   Drug Designing: Prediction of Properties of Compounds, QSAR- Data
           Analysis.
   3.2   Structure-Activity Relationships, Electronic properties, Lead
           Identification.
   3.3   Molecular Descriptor Analysis.

Unit   4   **(10 hrs)**
   Pharmacophore-Based Drug Design
   4.1   Pharmacophore-Based Drug Design. Structure Based drug design.
   4.2   Toxicity Analysis-Pharmacological Properties, Global Properties
   4.3   Oral Bioavailability and Drug-Likeness.

Unit   5   **(10 hrs)**

       Applications of Cheminformatics tools

       5.1   Applications of Cheminformatics tools. ADME, OSIRIS, MOLINSPIRATION.

       5.2   JME Molecule Editor, Chemaxon

       5.3   Marvin Sketch.

TEXT BOOKS

Johann Gasteiger and Thomas Engel, <u>Chemoinformatics -A Textbook,</u> (2nd edition), Germany: Wiley-VCH, 2003.

Johann Gasteiger, <u>Handbook of Chemoinformatics,</u> From Data to Knowledge, (2nd edition), Germany: Wiley-VCH, Germany, 2003.

REFERENCE BOOKS

Andrew R. Leach, Valerie J. Gillet, <u>An Introduction to Chemoinformatics,</u> (2nd edition), UK: Springer, 2007.

Bunin, Barry A. Dordrecht, <u>Chemoinformatics: Theory, Practice, and Products,</u> (2nd edition), UK: Springer, 2007.

Bajorath, Juergen,Totowa, N.J., <u>Chemoinformatics: Concepts, Methods, and Tools for Drug Discovery,</u>(3rd edition), New York, USA: Humana Press, 2004.

Ekins, Sean, edition, Hoboken, N.J, <u>Computer Applications in Pharmaceutical Research and Development,</u>(2nd edition), Germany: Wiley, 2006.

PATTERN OF EVALUATION (End Semester Examination.)

Total Marks: 100   Duration: 3 Hours

Section A – 20 x   1 = 20 Marks (All questions to be answered)

Section B –   4 x 10 = 40 Marks (4 out of 7 to be answered)

Section C –   2 x 20 = 40 Marks (2 out of 4 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

Postgraduate Elective Course offered by the Department of Bioinformatics for
M.A. / M.Sc./ M.Com. Degree Programmes

SYLLABUS
(Effective from the academic year 2011 - 2012)

IMMUNOINFORMATICS AND PHARMACOLOGY

CODE:11BI/PE/IM34   CREDITS : 4
                                                               L T P : 4 0 0
                                                    TOTAL TEACHING HOURS : 52

OBJECTIVES OF THE COURSE
  ➢ To understand the application of information technology to immunology.
  ➢ To apply the immunological data and to the sophisticated computational
    solutions available for immunological research.

Unit   1   (6 hrs)
       Immune System
       1.1   Adaptive and innate immunity
       1.2   Cells of the immune system, soluble mediators of immunity, Antigens,
              Immune responses
       1.3   Inflammation, Immunopathology

Unit   2   (10 hrs)
       Major Histocompatibility Complex
       2.1   Insights from MHC bound peptides.
       2.2   Generating data for databases.
       2.3   The peptide repertoire of HLA molecules

Unit   3   (12 hrs)
       Vaccine
       3.1   From immunome to vaccine.
       3.2   Epitope mapping Vaccine design tools
       3.3   The future of computational modelling and prediction systems in clinical
              immunology.

Unit   4   (12 hrs)
       Immunogenetics
       4.1   From Immunogenetics to immunomics.
       4.2   Functional prospecting of genes and transcripts
       4.3   IMGT International ImMunoGeneTics information system.HLA
              nomenclature and the IMGT/HLA Sequence Database.

Unit   5   **(12 hrs)**
     Viral Bioinformatics

     5.1   Viral Bioinformatics. Computational views of hosts and pathogens using VIDA

     5.2   Drug Discovery: Introduction. Conventional drug design approaches, irrational vs. rational, Lipinski rule-pharamcophore kinetics and dynamics-ADME properties

     5.3   Applications of computer based drug discovery.

TEXT BOOKS

Articles published by Novartis Foundation Symposium in Immunoinformatics: <u>Bioinformatics Strategies for Better Understanding of Immune Function</u>, John Wiley and Sons, Ltd. UK, 2003.

<u>Immunoinformatics: Predicting Immunogenicity In Silico</u> (Methods in Molecular Biology) by Darren R. Flower, 2007.

<u>Immunoinformatics</u> (Immunomics Reviews:) by Christian Schönbach, Shoba Ranganathan, and Vladimir Brusic 2007.

PATTERN OF EVALUATION (End Semester Examination.)
Total Marks: 100   Duration: 3 Hours

    Section A – 20 x   1 = 20 Marks (All questions to be answered)

    Section B –   4 x 10 = 40 Marks (4 out of 7 to be answered)

    Section C –   2 x 20 = 40 Marks (2 out of 4 to be answered)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011 -2012)

PYTHON

CODE: 11BI/PI/PT24   **CREDITS: 4**

OBJECTIVES OF THE COURSE
 ➢ This course will help you gaining knowledge of Python with the programming
   language.
 ➢ The application of Python program will help you to do practical oriented
   programs.

Unit   1
   Introduction
   1.1   Introduction to Python language, Use of Third-Party Software, Object-
           Oriented Programming
   1.2   The environment
   1.3   Biopython

Unit   2
   NumPy and SciPy
   2.1   Introduction to NumPy and SciPy, Basic Array Manipulations,
   2.2   Basic Math: Equal or copy, Comparisons, Slicing, Sorting and Shaping,
           Statistical Methods, Array Conversion
   2.3   Introduction to SciPy

Unit   3
   Parsing DNA Data Files
   3.1   FASTA Files, Genbank Files: File overview, Parsing the DNA, Gene and
           Protein Information
   3.2   Gene Locations Splices, Extracting all Gene Locations, Coding DNA,
           Proteins, Extracting Translations

Unit   4
   Sequence Alignment
   4.1   Matching Sequences: Perfect Matches, Insertions and deletions
   4.2   Rearrangements, Global Versus Local Alignments, Sequence Length
   4.3   Clustering: K-means Clustering

Unit   5
   Text Mining
   5.1   An introduction to Text Mining, Collecting Bioinformatics Textual Data,
           Creating Dictionaries
   5.2   Document Analysis: Text Mining ten Documents, Word Frequency,
           Indicative Words, Document Classification

TEXT BOOKS

Jason Kinser, <u>Python for Bioinformatics</u>, Jones and Barlett Publishers, Massachusetts, 2009.

Mitchell L Model, <u>Bioinformatics Programming Using Python</u>**,** O'Reilly Media Publication. CA, 2009.

REFERENCE BOOKS

Mark Lutz, <u>Learning Python, Fourth Edition</u>, O'Reilly Media Publication. CA, 2009.

Martin C Brown, <u>Python: The Complete Reference</u>, McGraw-Hill/Osborne Media, 2001.

PATTERN OF EVALUATION (End Semester Examination – 3 Hrs.)

The duration of the examination will be 3 hrs. – 1 hr theory and 2 hrs practical.

Theory:
    Section A – 30 x   1 = 30 Marks (All questions to be answered)
    Section B – 10 x 2 = 20 Marks (2 out of 4 to be answered)

Practical:
    Section C –   2 x 25 = 50 Marks

Question comprising the following:

Complete a programme,
Write a Python program related to Bioinformatics (transcription, finding motifs/repeats/restriction enzyme etc.),
Output of the given programme.

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2011 -2012)

SYSTEMS BIOLOGY

CODE: 11BI/PI/SB24   **CREDITS : 4**

OBJECTIVES OF THE COURSE
- ➢ To introduce the basic concepts of Systems biology.
- ➢ To train the students in designing a new organism through modelling network concept and manipulating them for biological Applications.

Unit   1
Introduction
1.1   Introduction – Systems Biology is a Living Science
1.2   Properties of models-Model behaviour- Model development
1.3   Typical Aspects of Biological Systems and Corresponding Models
1.4   Systems Biology is Data Integration.

Unit   2
Standard Models and Approaches in Systems Biology
2.1   Standard Models and Approaches in Systems Biology
2.2   Enzyme Kinetics and Thermodynamics-Metabolic Networks-
2.3   Systems Equations-Signal Transduction-Function and
2.4   Structure of Intra- and Intercellular Communication-Receptor-Ligand Interactions.

Unit   3
Modeling of Gene Expression
3.1   Modeling of Gene Expression-Modules of Gene Expression – Promoter
3.2   Identification- General Promoter Structure- Sequence-based Prediction of Promoter.
3.3   Approaches that Incorporate Additional Information-Representation of Gene Network as Directed and Undirected Graphs.
3.4   Bayesian Networks-Boolean Networks- Gene Expression Modeling with Stochastic Equations.

Unit   4

Analysis of Gene Expression Data

4.1   Analysis of Gene Expression Data- Introduction-Data Capture-DNA Array Platforms

4.2   Image Analysis and Data Quality Control-Grid Finding- Quantification of Signal Intensities- Signal Validity- Pre-processing-Global Measures.

4.3   Linear Model Approaches- Nonlinear and Spatial Effects-Other Approaches.

4.4   Fold-change Analysis.

Unit   5

Clustering Algorithms

5.1   Clustering Algorithms-Hierarchical Clustering- Self-organizing Maps (SOMs).

5.2   K-means- Validation of Gene Expression Data-Cluster Validation.

5.3   Principal Component Analysis-Functional Categorization- Classification Methods. Experimental Planning in the Systems Biology Phase of Biological Research.

5.4   Publication in the Era of Systems Biology- Systems Biology and Text Mining.

5.5   Systems Biology in Medicine, Drug Development, in Food Production and Biotechnology, Ecology, Nanotechnology.

5.6   Guiding the Design of New Organisms -Computational Limitations-Potential Dangers.

TEXT BOOKS

E. Klipp, R. Herwig, A. Kowald, C. Wierling, H. Lehrach , Systems Biology in Practice-Concepts, Implementation and Application, (1 st edition) WILEY-VCH Verlag GmbH & Co.KGaA, Germany, 2005.

Andres Kriete and Roland Eils, Computational Systems Biology,(3rd   edition) Elsevier, United Kingdom, 2005.

REFERENCE BOOKS

Uri Alon, An introduction to Systems Biology: Design Principles of Biological Circuits, (1 st edition),Chapman&Hall/CRC, Taylor and Francis Group, London, 2006.

Choi, Sangdun, Introduction to Systems Biology, (1 st edition) Humana   Press, New York City, USA, 2007.

Edda Klipp, Wolfram Liebermeister, Christoph Wierling, Axel Kowald, Hans Lehrach, Ralf Herwig, Systems Biology: A Textbook, (4th edition) Edinburgh.UK: Wiley-VCH, 2009.

Zoltan Szallasi, Joerg Stelling, Vipul Periwal, <u>Systems Modeling in Cellular Biology</u>,(1 st edition), USA: MIT Press, 2006.

PATTERN OF EVALUATION (End Semester Examination.)
Total Marks: 100   Duration: 3 Hours

Section A – 20 x   1 = 20 Marks (All questions to be answered)

Section B –   4 x 10 = 40 Marks (4 out of 7 to be answered)

Section C –   2 x 20 = 40 Marks (2 out of 4 to be answered)