

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2015-2016)

BIOCHEMISTRY

CODE: 15BI/PC/BC14

CREDITS: 4

L T P: 4 1 0

TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE

- To introduce the basic concepts of the structure of biomolecules
- To understand the importance of structural studies in bioinformatics
- To comprehend the basics of metabolism and enzyme kinetics

Unit 1

Introduction

(10 hrs.)

- 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

Central Metabolic Biochemistry

(15 hrs.)

- 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- B- Oxidation and Biosynthesis of Fatty Acids, Xenobiotics and General Detoxification Methods in the Body

Unit 3

Protein Structure

(20 hrs.)

- 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. Domains, Motifs and their importance
- 3.3 Basic structure of Carbohydrates, Lipids, Nucleic acids

Unit 4

Enzymes

(10 hrs.)

- 4.1 Enzyme Action Mechanisms
- 4.2 Enzyme Kinetics – Introduction, Basic Enzyme Kinetics, Michaelis - Menten Equation, significance of V max and Km, Line Weaver-Burk Plot
- 4.3 Competitive and Non-Competitive Inhibition, Feedback inhibition. Enzyme Regulation. Allosteric Modulation

Unit 5

Bioenergetics

(10 hrs.)

- 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, Worth Publishing, UK. 2012.

Thomas. E. Creighton, Proteins, W. H. Freeman, New York.2012.

BOOKS FOR REFERENCE

Champe, Pamela C, Richard A. Harvey and Denise R. Ferrier. *Lippincott's Illustrated Reviews: Biochemistry*, India: J.P. Brothers Medical, 2013.

Garrett, H. Reginald and Grisham, M. Charles. *Biochemistry*. USA: Thomson – Brooks/Cole, 2012.

Jeremy, M. Berg. *Biochemistry*, New York: W.H. Freeman, 2010.

Lubert and Stryer. *Biochemistry*, New York: W.H. Freeman, 2012.

Segal, I. H. *Enzyme Kinetics*, New York: John Wiley, 1993.

Voet, D. and Voet, G. *Biochemistry*, New York: John Wiley, 2012.

JOURNALS

Journal of Biochemistry
Indian Journal of Clinical Biochemistry
Biochemistry

WEB RESOURCES

www.themedicalbiochemistrypage.org

www.biochemistry.org

PATTERN OF EVALUATION

Continuous Assessment:

Total Marks: 50

Duration: 90 mins.

Section A – $10 \times 1 = 10$ Marks (All questions to be answered)

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

Section C – $1 \times 20 = 20$ Marks (1 out of 2 to be answered)

Third Component:

List of Evaluation modes

Assignment

Open book test

Case study

Clinical implications of metabolic pathways

Diagnostic applications of biochemicals

End Semester Examination:

Total Marks: 100

Duration: 3 hours

Section A – $20 \times 1 = 20$ Marks (All questions to be answered)

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

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

STELLAMARISCOLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS
(Effective from the academic year 2015-2016)
BIOPHYSICS

CODE:15BI/PC/BP14

CREDITS: 4

L T P: 4 1 0

TOTAL TEACHING HOURS: 65

OBJECTIVES OF THE COURSE:

- To provide 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 functions
- To understand the behavior and properties of biological macromolecules

Unit 1

Introduction (15 hrs.)

- 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 Orbital, Molecular Orbital – Hybrid Orbital – Valency
- 1.3 Thermodynamics Systems – Laws of Thermodynamics – Statement and Applications – Concepts of Entropy and Enthalpy

Unit 2

Spectroscopy (10 hrs.)

- 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

Nuclear Magnetic Resonance (10 hrs.)

- 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

Mass Spectrometry (15 hrs.)

- 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

Crystallography and Microscopy (15 hrs.)

- 5.1 Elementary Description of Crystallography – 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, Serdyuk, Nathan R. Zaccai and Joseph Zaccai. *Methods in Molecular Physics*. UK: Cambridge University Press, 2007.

Kensal E. VanHolde, Johnson Curtis W. and Ho Shing P. *Principles of Physical Biochemistry*, USA: Prentice Hall International Inc., 2005.

Narayanan P. *Introductory Biophysics* Mumbai, India: New Age Publishing Co., 2005

BOOKS FOR REFERENCE:

Bengt Nolting. *Methods in Modern Biophysics*. Germany: Springer, 2004.

Banwell C.N. *Fundamentals of Molecular Spectroscopy*. New Delhi: Tata McGraw-Hill Publishing Company Lt, 1994.

C.R.Cantor and P.Schimmel. *Biophysical Chemistry*. New York, USA: W.H. Freeman and Company, 1985.

D.Freifelder. *Physical Biochemistry*. New York, USA: W. H. Freeman and Company, 1982.

P. Gunning , A. R. Kirby, V. J. Morris. *Atomic Force Microscopy*. London: Imperial College Press, 2009.

Leach A.R, *Molecular Dynamics Simulation*. New York, USA: John Wiley and Sons, 2001.

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

D.Sherwood. *Crystals, X-rays and Proteins*. London, UK: Longman Group Lts, 1976.

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2015 -2016)

PROGRAMMING IN C++

CODE: 15BI/PC/CP14

CREDITS : 4

L T P : 312

TOTAL TEACHING HOURS: 78

OBJECTIVES OF THE COURSE

- To familiarize students with the programming language
- To gain knowledge of C++ programming language
- To enable the application of C++ program in real time programs

Unit 1

Introduction to Programming language (10 hrs.)

- 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

Functions and variables (12 hrs.)

- 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

Overview of classes (15 hrs.)

- 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
String manipulation (15 hrs.)

- 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
Introduction to files (13 hrs.)

- 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

E. Balagurusamy. *Object Oriented Programming with C++*. New Delhi: Tata McGraw-Hill, 2013.

Hubbard, John. *Programming with C++, Schaum's Outline Series*. New Delhi: Tata McGraw Hill, 2003.

BOOKS FOR REFERENCE:

Bjarne, Stroustrup. *The C++ Programming Language*. India: Addison Wesley, 2013.

Brain, W. Kernighan and Dennis. M. Ritchie. *The C Programming Language*. USA: Prentice Hall, 1988.

Sanjeev Sofat. *Object Oriented Programming Using C++*, India : Cyber Tech. Publication, 2009.

JOURNALS

C/C++ Users Journal

International Journal of Computer Applications

Computer Methods and Programs in Biomedicine

Science of Computer Programming

WEB RESOURCES

<http://www.cplusplus.com/doc/tutorial/>

<http://www.cprogramming.com/>

<http://www.stroustrup.com/4th.html>

PATTERN OF EVALUATION

Continuous Assessment:

Total Marks: 50

Duration: 90 mins.

Theory:

Section A – 15 x 1 = 15 Marks (All questions to be answered)

Section B – 5 x 2 = 10 Marks (2 out of 4 to be answered)

Practical:

Section C – 2 x 12.5 = 25 Marks

Third Component:

List of Evaluation modes

Seminars

Assignments

Problem solving

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

Questions 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

Find the missing statements in a given programme

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M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2015 -2016)

DATABASE MANAGEMENT SYSTEMS

CODE : 15BI/PC/DB14

CREDITS : 4

L T P : 312

TOTAL TEACHING HOURS : 78

OBJECTIVES OF THE COURSE

- To introduce the basic concepts of Relational Database Management System and Client Server Environment
- To train the students in Designing databases and manipulating them for Biological applications through Oracle

Unit 1

Introduction to Database Systems and Linux (10 hrs.)

- 1.1 Introduction to File and Database systems- Database System Structure, Data Models. Introduction to Network Models – ER Model. Relational Model
- 1.2 Introduction to Linux Operating System, Properties of Linux, Desktop Environment, Linux Basics Commands
- 1.3 Working With Files, Text Editors, I/O Redirections, Pipes, Filters, and Wildcards. Changing Access Rights

Unit 2

SQL Definition and Normalization (12 hrs.)

- 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

Files and RDBMS (16 hrs.)

- 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

Data Definition and Manipulation Language (15 hrs.)

- 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

Constraints and MySQL (12 hrs.)

- 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, Data types and Commands

TEXT BOOKS

Ramakrishnan Raghu and Gehrke Johannes. *Database Management Systems*, USA: McGraw–Hill, 2003.

BOOKS FOR REFERENCE

George Koch and Kevin Loney. *Oracle 8 - The Complete Reference*, USA: Tata McGraw – Hill, 2000.

Kyte, Thomas. *Expert Oracle Database Architecture- 9i and 10g Programming Techniques and Solutions*. USA: Berkeley press, 2006.

Michael Abbey and Michael J. Correy. *Oracle 8i - A Beginners Guide*. USA :McGraw-Hill, 1999.

JOURNALS

International Journal of Database Management Systems

Journal of Database Management

Journal of Advanced Database Management & Systems

International Journal of Intelligent Information and Database Systems

International Journal of Computer Science and Information

WEB RESOURCES

www.oracle.com/technetwork/oem/db-mgmt/db-mgmt-093445.html

<http://education-portal.com/academy/lesson/what-is-a-database-management-system-purpose-and-function.html>

www.odbms.org/

http://www.comptechdoc.org/os/linux/usersguide/linux_ugbasics.html

<http://www.dummies.com/how-to/content/common-linux-commands.html>

PATTERN OF EVALUATION

Continuous Assessment:

Total Marks: 50

Duration: 90 mins.

Theory:

Section A – 15 x 1 = 15 Marks (All questions to be answered)

Section B – 5 x 2 = 10 Marks (2 out of 4 to be answered)

Practical:

Section C – 2 x 12.5 = 25 Marks

Third Component:

List of Evaluation modes

Seminars

Group discussion

Assignments

Problem solving

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 (2 out of 3 to be answered)

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

(Effective from the academic year 2015 - 2016)

BIOINFORMATICS

CODE : 15BI/PC/BI24

CREDITS : 4

L T P : 4 1 0

TOTAL TEACHING HOURS : 65

OBJECTIVES OF THE COURSE

- To provide an integrative approach to the understanding of 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

Introduction to Biological Databases (12hrs.)

- 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

Introduction to Sequence Alignment (14 hrs.)

- 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

Basic Local Alignment Search Tool (15 hrs.)

- 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
Multiple Sequence Alignment (12 hrs.)

- 4.1 Definition of Multiple Sequence Alignment
- 4.2 Databases of Multiple Sequence Alignment Programs- BLOCKS, PRINTS
- 4.3 Integrated Multiple Sequence Alignment Resources: InterPro, iProClass

Unit 5
Evolutionary Analysis (12 hrs.)

- 5.1 Introduction to Evolutionary Analysis, Bootstrap, Tree Construction Methods
- 5.2 Neighbor-Joining Method, Unweighted Pair Group Method with Arithmetic Mean (UPGMA)
- 5.3 Maximum Parsimony Method and Maximum-Likelihood Method

TEXT BOOKS

Baxevanis, Andreas, D. and Francis B.F. Ouellette, *Bioinformatics-A Practical Guide to the Analysis of Genes and Proteins*. New York: John Wiley, 2004.

David W. Mount. *Bioinformatics Sequence and Genome Analysis*. New Delhi: CBS Publishers, 2003.

Pevsner, Jonathan. *Bioinformatics and Functional, Genomics*. USA: John Wiley, 2009.

BOOKS FOR REFERENCE:

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

Chen and Yi-Ping Phoebe. *Bioinformatics Technologies*. Germany: Springer, 2005.

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

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

Lesk, Arthur M. *Introduction to Bioinformatics*. UK: Oxford University Press, 2014.

JOURNALS

BMC Bioinformatics
Bioinformatics
Journal of Bioinformatics and Computational Biology
Journal of Biomedical Informatics
Journal of Integrative Bioinformatics

WEB RESOURCES

<http://bioinformaticsweb.net/tools.html>

<https://www.bits.vib.be/index.php/training/122-basic-bioinformatics>

<http://bioinformaticssoftwareandtools.co.in/>

<http://www.genscript.com/tools.html>

PATTERN OF EVALUATION

Continuous Assessment:

Total Marks: 50

Duration: 90 mins.

- a) Section A – 10 x 1 = 10 Marks (All questions to be answered)
- b) Section B – 2 x 10 = 20 Marks (2 out of 4 to be answered)
- c) Section C – 1x 20 = 20 Marks (1 out of 2 to be answered)

Third Component:

List of Evaluation modes

Assignment

Open book test

Seminars

Quiz

End Semester Examination:

Total Marks: 100

Duration: 3 hrs.

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 2015 -2016)

MOLECULAR BIOLOGY

CODE: 15BI/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 enable the understanding of the process and regulation of cell division
- To analyse the involvement of molecules in life processes

Unit 1

Gene Organisation (15 hrs.)

- 1.1 DNA Structure and Organisation of the Genome and Genetic Rearrangements
- 1.2 Organisation of Eukaryotic Genomes - Coding Sequences. Repetitive Sequences in Eukaryotic Genomes, Replication in Prokaryotes
- 1.3 Genetic Rearrangements – Transposable Elements

Unit 2

Transcription (15 hrs.)

- 2.1 Transcription: Eukaryotes and Prokaryotes
- 2.2 Regulation: Transcriptional Control: By Regulatory Proteins, Steroid Hormone Receptors - Heat Shock Genes- Homeotic Genes
- 2.3 Mechanisms Modifying Transcriptional Control By Regulatory Proteins – DNA Methylation And Genetic Control, Histone Modification, Post Transcriptional Regulation

Unit 3

Translation (12 hrs.)

- 3.1 Translational Regulation. Post translational Regulation; Regulation in Prokaryotes
- 3.2 Specialised Mechanisms Regulating rRNA Genes
- 3.3 Genetic Control of Vertebrate Immune System

Unit 4

Organelle Genome (10 hrs.)

- 4.1 Mitochondrion Genome – Organisation and Function
- 4.2 Transcription and Translation in Mitochondria
- 4.3 Chloroplast Genome – Organisation and Function

Unit 5

Cell Cycle

(13 hrs.)

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 and Paul Matsudaira. *Molecular Cell Biology*. USA: W.H. Freeman, 2008.

Wolfe, Stephen L. *Molecular and Cellular Biology*. USA: Wadsworth, 2005.

BOOKS FOR REFERENCE

Cooper, Geoffrey M. and Robert E. Hausman. *The Cell, A Molecular Approach*. USA: Sinauer Associates, 2004.

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

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

Journals

Journal of Molecular Biology
Molecular Biology

Web Resources

www.cellbio.com

www.molbiolcell.org

www.sciencedirect.com

PATTERN OF EVALUATION

Continuous Assessment Test:

Total Marks: 50

Duration: 90 mins.

Section A – 10 x 1 = 10 Marks (All questions to be answered)

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

Section C – 1 x 20 = 20 Marks (1 out of 2 to be answered)

Third Component:
List of Evaluation modes

Assignment
Test
Seminars

End Semester Examination:

Total Marks: 100

Duration: 3 Hours

Section A – $20 \times 1 = 20$ Marks (All questions to be answered)

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

Section C – $2 \times 20 = 40$ 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 2015 -2016)
MOLECULAR BIOLOGY PRACTICAL

CODE: 15BI/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 (10 hrs.)

- 2.1 Extraction of DNA from Onion, Extraction of RNA from Yeast
- 2.2 Estimation of DNA and RNA
- 2.3 Estimation of Proteins by Lowry's Method

Unit 3 (7 hrs.)

- 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 (7 hrs.)

- 4.1 Isolation of Plasmid DNA (Demo)
- 4.2 Amplification of DNA by PCR

Unit 5 (7 hrs.)

- 5.1 Electrophoretic Techniques: Agarose Gel Electrophoresis, SDS PAGE (Demo)
- 5.2 Southern Blotting (Demo)

BOOKS FOR REFERENCE:

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

Sadasivam, S. and Manickam, A. *Biochemical Methods*. India: New Age International, 2009.

Wilson, K; Walker, J. *Principles and techniques of Biochemistry and Molecular Biology*. USA: Cold Spring Harbor Laboratory Press, 2010.

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 2015 -2016)

BIOINFORMATICS PRACTICAL

CODE: 15BI/PC/P222

CREDITS : 2
L T P : 0 0 3
TOTAL HOURS : 39

OBJECTIVE OF THE COURSE

- To provide practical experience of the various databases and tools involved in Bioinformatics

Unit 1 **(8 hrs.)**

Nucleotide Databases

- 1.1 Primary Nucleotide Sequence Databases: NCBI, EMBL, GenBank, DDBJ
- 1.2 Database of Essential Genes

Unit 2 **(8 hrs.)**

BLAST

- 2.1 Basic Local Alignment Search Tool (BLAST)

Unit 3 **(8 hrs.)**

Protein Sequence Databases

- 3.1 Protein Sequence Databases – PIR, PRF/SEQDB, RefSeq, Swiss-Prot, TrEMBL
- 3.1 Protein Structure Databases – PDB, CSD, NDB
- 3.2 Protein Structural Classification Databases – CATH, SCOP

Unit 4 **(7 hrs.)**

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 (IMG, Rebase, COG, LIGAND, BRENDA)

Unit 5 **(8 hrs.)**

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. *Bioinformatics- A Practical Guide to the Analysis of Genes and Proteins*. New York: John Wiley, 2004.

David W.Mount. *Bioinformatics Sequence and Genome Analysis*. New Delhi: CBS Publishers, 2003.

Lesk, Arthur M., *Introduction to Bioinformatics*. UK: Oxford University Press, 2014.

PATTERN OF EVALUATION

End Semester Examination

Total Marks: 100

Duration: 3 Hours

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

Interpretation of results

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 2015 -2016)
ALGORITHMS FOR BIOINFORMATICS

CODE: 15BI/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

Introduction

(10 hrs.)

- 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

Restriction Mapping

(10 hrs.)

- 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

Sequence Alignment

(15 hrs.)

- 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
Clustering and Evolutionary Trees (15 hrs.)

- 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
Pattern Matching (15 hrs.)

- 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. *An Introduction to Bioinformatics Algorithms*. USA: MIT press, 2011.

Pavel A. Pevzner. *Computational Molecular Biology- An algorithmic approach*. USA: MIT press, 2004.

BOOKS FOR REFERENCE

Alfred V. Aho, John E. Hopcroft and Jefferey D.Ullman. *Data Structures and Algorithms*. London: Addison Wesley, 1983.

Clark, John and Derek Allan Holton. *A First Look at Graph Theory*. Singapore: Singapore Publishers, 1995.

Horowitz, Ellis, and Sartag Sahni. *Fundamentals of Computer Algorithms*. New Delhi: Galgotia Publications, 1994.

Jeffrey J. McConnell. *Analysis of Algorithm*. New Delhi: Narosa Publishing House, 2002.

Thomas H. Cormen, Charles E. Leiserson and Ronald L. Rivest. *Introduction to Algorithms*. New Delhi: Prentice Hall of India, 1990.

JOURNALS

Algorithms for Molecular Biology

Journal of Computational Intelligence in Bioinformatics

International Journal of Bioinformatics Research and Applications

Developments in Bioinformatic Algorithms

WEB RESOURCES

http://www.comp.nus.edu.sg/~ksung/algo_in_bioinfo/

<http://bioinformaticsalgorithms.com/>

http://bix.ucsd.edu/bioalgorithms/presentations/Ch08_GraphsDNAseq.pdf

<http://www.ait-budapest.com/advanced-algorithms-for-bioinformatics>

PATTERN OF EVALUATION

Continuous Assessment:

Total Marks: 50

Duration: 90 mins.

Section A: $5 \times 10 = 50$ (7 questions to be set)

Third Component:

List of Evaluation modes

Seminars

Assignments

Problem solving

End Semester Examination

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

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2015 -2016)

GENOMICS AND PROTEOMICS

CODE: 15BI/PC/GP34

CREDITS : 4

L T P : 3 1 2

TOTAL CONTACT HOURS: 78

OBJECTIVES OF THE COURSE

- To provide an insight into the complete genome sequences of a few organisms as well as the Human genome through Comparative and Functional genomics
- To develop an understanding of the entire protein complement of a cell through analytical approaches, Data mining and other software tools

Unit 1

Genomics (16 hrs.)

- 1.1 Rates and patterns of Nucleotide substitution, Causes of variation in Substitution rates, Positive Selection
- 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

Comparative Genomics (16 hrs.)

- 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 Software's – MZEF & HEXON, ORF analysis, ORF finder, Application of Genome Analysis, Human Diseases, Response to Drugs, Genome

Unit 3

Functional Genomics (15 hrs.)

- 3.1 Gene Expression Analysis by Micro Arrays, SAGE, Applications of Microarrays in Medicine
- 3.2 Strategies for Generating ESTs and Full Length Inserts; EST Clustering and Assembly, EST databases (DB-EST, UNIGene); Statistical Analysis of EST Data
- 3.3 The Human Genome Project and Medicine, KEGG and Metabolic Pathways, Pathway Regulatory Networks

Unit 4

Proteomics

(16 hrs.)

- 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

Application of Proteomics

(15 hrs.)

- 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 Lesk M. *Introduction to Genomics*. New York: Oxford university press, 2008.

Brown, T. A. *Genomes -3*. USA: John Wiley and Sons inc., 2006.

Daniel C. Leibler. *Introduction to Proteomics: Tools for New Biology*. USA: Humana Press, 2002.

Srivastava Sudhir. *Informatics in Proteomics*. USA: Taylor & Francis Group, 2005.

BOOKS FOR REFERENCE

Brown P. O and Botstein D. *Exploring the new world of the genome with DNA microarrays*. USA: Nat. Genet, 1999.

Collado Vides Julio and Ralf Hofstadter. *Gene Regulation and Metabolism – Post Genomic Computational Approaches*. India: Ane Books, 2004.

Dale, Jeremy W and Malcolm von Schantz. *From Genes to Genomes – Concepts and Applications of DNA Technology*. USA: John Wiley and Sons, 2012.

Griffiths, A.J.F, Miller, J.H, Suzuki, D.T. Lewontin, R. C. and Gelbart, W.M. *An Introduction to Genetic Analysis*. USA: W.H. Freeman, 1996.

Golemis and Erica. *Protein-Protein Interaction*. USA: CSHL, 2005.

End Semester Examination:

Total Marks: 100

Duration: (3 hrs.)

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 ORFs, 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 2015 -2016)

MOLECULAR MODELING AND COMPUTER AIDED DRUG DESIGNING

CODE: 15BI/PC/MC34

CREDITS : 4

L T P : 3 1 2

TOTAL TEACHING HOURS : 78

OBJECTIVES OF THE COURSE

- To provide a theoretical background to the various methods of molecular modelling
- 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

Introduction (15 hrs.)

- 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

Energy Minimization and Computer Simulation Methods (16 hrs.)

- 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

Molecular Dynamics Simulation, Monte Carlo Simulation Methods (15 hrs.)

- 3.1 Molecular Dynamics Using Simple Model, Molecular Dynamics with Continuous Potentials
- 3.2 Molecular Dynamics at Constant Temperature and Pressure, Incorporating Solvent effects into Molecular Dynamics, Conformational Changes From Molecular Dynamics Simulation
- 3.3 Introduction to Monte Carlo Simulation of Molecules, Calculation of Chemical Potential-Simulating Phase Equilibria by Gibbs Ensemble Monte Carlo Method

Unit 4

Molecular docking (16 hrs.)

- 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

Computer Aided Drug Design (16 hrs.)

- 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, Auto dock

TEXT BOOKS

Andrew R. Leach. *Molecular Modeling: Principles and Applications*. USA: Prentice Hall, 2007.

Daan Frenkel and Berend Smit. *Understanding Molecular Simulation: From Algorithms to applications*. USA: Academic Press, 2002.

N. Claude Cohen. *Guidebook on Molecular Modelling In Drug Design*. California: Academic Press, 2006.

BOOKS FOR REFERENCE

Alan Hinchliffe. *Molecular Modelling for Beginners*. USA: John Wiley & Sons, 2008.

Charifson P S. *Practical Application of Computer Aided Drug Design*. New York: Dekker, 1997.

JOURNALS

Journal of Molecular Modeling

Journal of Molecular Graphics and Modelling

Journal of Computer-Aided Molecular Design

Current Computer Aided-Drug Design

WEB RESOURCES

<http://accessengineeringlibrary.com/browse/computer-aided-drug-design-and-delivery-systems>

<http://www.southernresearch.org/life-sciences/lead-discovery-and-optimization/medicinal-chemistry/computational-chemistry>

<http://www.ch.ic.ac.uk/local/organic/mod/>

http://www.chemcomp.com/MOE-Molecular_Modeling_and_Simulations.htm

PATTERN OF EVALUATION

Continuous Assessment:

Total Marks: 50

Duration: 90 mins.

Theory:

Section A – 1 x 15 = 15 Marks (ALL questions to be answered)

Section B – 2 x 5 = 10 Marks (2 out of 4 to be answered)

Practical:

Section C – 25 Marks

Third Component:

List of Evaluation modes

Assignment

Seminars

Quiz

End Semester Examination:

Total Marks: 100

Duration: 3 hrs.

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 (protein, compound, etc.)	-	15 marks
Interaction of molecules-Docking	-	15 marks
Homology modeling	-	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 2015 -2016)

PERL

CODE : 15BI/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 facilitate the writing of Perl programs that support research in biology
- To learn the usage of CGI and HTML for web page designing

Unit 1

Introduction to Perl Programming (15 hrs.)

- 1.1 Introduction to Perl 5, Variable Types, Data Types, Statements and Declarations, Default Variables
- 1.2 Expressions, Statements, Operators in Perl, Operator Precedence, String Operators, Control Structures
- 1.3 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 2

Associative Array and Perl Functions (15 hrs.)

- 2.1 Subroutines- Defining Subroutines, Returning Values, Using Arguments.
- 2.2 Associative Arrays (Hashes)
- 2.3 Perl functions –abs, atan2, chr, cos, eval, exists, grep, index, int, join, keys, lc, lcfirst, length, pack, rand

Unit 3

File Handling (16 hrs.)

- 3.1 Working with Filehandle. An Overview of Filehandle, Typical Way of Opening a Perl File Handlers, Opening a Perl File Handle Reference in Normal Scalar Variable
- 3.2 Use Perl IO::File to Open a File Handle, Open the Standard Input and Standard Output, Use Sysopen () to Open the File
- 3.3 Array of Arrays - Hashes, Associative Hashes

Unit 4

File Handling and Bioperl (16 hrs.)

- 4.1 Opening File Handle Reading, Writing and Reading an Array to a Text File, Closing File Handle
- 4.2 Writing and Reading a Hash to a Text File. Packages, Random Number Generation, Signals, Command Line Argument, Standard Modules

4.3 Introduction to Bioperl: Installation Procedures, Architecture, Uses of Bioperl.
Translating DNA into Proteins, Reading DNA From Files in FASTA Format

Unit 5

Common Gateway Interface (16 hrs.)

- 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
- 5.3 Starting an HTML Document, Displaying Images, HTML Form, Text Fields, Text Areas, Check Boxes, Scrolling Lists, Radio Buttons, Password Fields, Pop up Menus

TEXT BOOKS

Conrod Bessant, Ian Shadforth and Darren Oakley. *Building Bioinformatics Solutions with Perl, R and MySQL*. New York: Oxford University Press, 2014.

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

Guelich, Scott, Shishir Gundavaram and Gunther Birznieks. *CGI Programming with Perl*. USA: O'Reilly and Associates, 2012.

Holzner and Steven. *Perl Black Book*. India: Dream Tech Press, 2006.

Tisdall James D. *Beginning Perl for Bioinformatics*. USA: O'Reilly and Associates, 2000.

Tisdall James D. *Beginning Perl for Bioinformatics*. USA: O'Reilly and Associates, 2003.

BOOKS FOR REFERENCE

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

Larry Wall, Tom Christiansen and Jon Orwant. *Programming Perl*. New Delhi: O'Reilly-Shroff Publishers, 2012.

Randall. L. Schwartz and Tom Phoenix. *Learning Perl*. New Delhi: O'Reilly -Shroff Publishers, 2008.

Shishir Gundavaram. *CGI programming on the World Wide Web*. USA: O'Reilly and Associates, 2012.

JOURNALS

The Perl Journal

Computer Science & Perl Programming

Perl Programming for Biologists
Science of Computer Programming
Programming and Computer Software

WEB RESOURCES

<https://www.perl.org/>

<http://www.cs.cf.ac.uk/Dave/PERL/>

<http://www.comp.leeds.ac.uk/Perl/basic.html>

http://www.tutorialspoint.com/perl/perl_introduction.htm

PATTERN OF EVALUATION

Continuous Assessment:

Total Marks: 50

Duration: 90 mins.

Theory:

Section A – 1 x 15 = 15 Marks (ALL questions to be answered)

Section B – 2 x 5 = 10 Marks (2 out of 4 to be answered)

Practical:

Section C – 25 Marks

Third Component:

List of Evaluation modes

Program writing

Quiz

Assignments

End Semester Examination:

Total Marks: 100

Duration: 3 hrs.

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, Open reading frame, reading a PDB file etc.),

Output of the given programme.

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086

M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2015 - 2016)

SUMMER INTERNSHIP

CODE: 15BI/PN/SI32

CREDITS : 2

OBJECTIVES OF THE COURSE

- To enable students to gain experiential learning in the field in Bioinformatics
- To acquire hands – on training in Bioinformatics Software's

The Summer Internship program is for a minimum period of three weeks. The students are expected to have regular attendance in their respective Institute and submit an report to the Department reporting the experiments they have observed/conducted. The students are expected to give a seminar presentation in the third semester of the work they have observed/conducted.

Guidelines for Evaluation

The maximum marks for the Summer Internship is 50 and is divided into the following:

- a) Log Book (20 Marks)
- b) Seminar presentation (15 Marks)
- c) Attendance (15 Marks)

STELLA MARIS COLLEGE (AUTONOMOUS), CHENNAI - 600 086
M.Sc. DEGREE: BIOINFORMATICS

SYLLABUS

(Effective from the academic year 2015 -2016)

ADVANCES IN BIOINFORMATICS

CODE: 15BI/PC/BA44

CREDITS : 4

L T P : 4 1 0

TOTAL TEACHING HOURS : 65

OBJECTIVES OF THE COURSE

- 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 design and also how to handle the microarray data
- To provide a better understanding of R package and its applications in bioinformatics

Unit 1

Pharmacogenomics (10 hrs.)

- 1.1 Definition of Pharmacogenomics and Toxicogenomics – Case Study in Alzheimer’s Diseases
- 1.2 Safety Metabolisms Pharmacology – Exploitory Toxicology
- 1.3 Preclinical Toxicology, Pharmacokinetics and Metabolism

Unit 2

Cheminformatics (11 hrs.)

- 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

Next Generation Sequencing (15 hrs.)

- 3.1 Introduction to Next-generation sequencing. History and Future of DNA Sequencing
- 3.2 Workflow Different Platforms Applications
- 3.3 Run Types and Data Analysis

Unit 4

Microarray Analysis (15 hrs.)

- 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

R programming

(14 hrs.)

5.1 Introduction to R, 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. *The R Book*. USA: John Wiley, 2012.

Ole Lund. *Immunological Bioinformatics*. USA: MIT press, 2005

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

BOOKS FOR REFERENE

Darren Flower. *Bioinformatics for Immunomics (Immunomics Reviews)* USA: Springer, 2010.

Gentleman R, Carey V.J, Huber W, Irizarry, RA, and Dudoit, S. *Bioinformatics and Computational Biology Solutions Using R and Bioconductor*. New York: Springer, 2008.

Murrell P. *R Graphics*. USA: Chapman & Hall/CRC, 2011

JOURNALS

Pharmacogenomics and Personalized Medicine

Pharmacogenetics and Genomics

Chemoinformatics: Concepts, Methods, and Tools for Drug Discovery

International Journal of Chemoinformatics and Chemical Engineering

Immunology

The R Journal

WEB RESOURCES

<http://ghr.nlm.nih.gov/handbook/genomicresearch/pharmacogenomics>

<http://cheminformatics.org/>

<http://omicsonline.com/immunoinformatics.php>

<http://cran.r-project.org/doc/Rnews/>

<http://www.r-project.org/>

<http://www.ebi.ac.uk/training/online/course/ebi-next-generation-sequencing-practical-course/what-you-will-learn/what-next-generation-dna->

PATTERN OF EVALUATION

Continuous Assessment:

Total Marks: 50

Duration: 90 mins.

Section A – 10 x 1 = 10 Marks (All questions to be answered)

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

Section C – 1 x 20 = 20 Marks (1 out of 2 to be answered)

Third Component:

List of Evaluation modes

Assignment

Case study

Seminars

Quiz

End Semester Examination:

Total Marks: 100

Duration: 3 hrs.

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 2015-2016)

BASICS OF CLINICAL RESEARCH MANAGEMENT

CODE : 15BI/PC/CR44

CREDITS : 4

L T P : 4 1 0

TOTAL PRACTICAL HOURS : 65

OBJECTIVES OF THE COURSE:

- To provide an overview of clinical research.
- To understand the various aspects of clinical research management
- To be conversant with the regulations in clinical management

Unit 1

Drug Development Processes (14 hrs.)

- 1.1 History of Drug Development. Discovery and Selection of Compounds for Human Investigation - Pharmacology-Epidemiology
- 1.2 Pharmacokinetics and Pharmacodynamics - Toxicological Requirements
- 1.3 Clinical Trials – History of Clinical Trials-Stages of Clinical Trials

Unit 2

Clinical Research (15 hrs.)

- 2.1 Issues in Clinical Trials. Nuremberg Code, Declaration of Helsinki, International Conference of Harmonisation and Good Clinical Practice
- 2.2 Role of Ethics Committees and Institutional Review Boards- Special Populations; Women Elderly and Children
- 2.3 Designing of Protocol, SOP CRF, e-CRF, ICF

Unit 3

Regulations in Clinical Research (12 hrs.)

- 3.1 Evolution and History of Regulations in Clinical Research, Patents US Regulatory Structure, IND, NDA, ANDA
- 3.2 FDA Audits and Inspections EU Regulatory Affairs, Organization and Function, INDIAN Regulatory System, Schedule Y- Rules and Regulations
- 3.3 Post Drug Approval Activities, PMS

Unit 4

Clinical Research Management (12 hrs.)

- 4.1 Preparation of a Successful Clinical Study
- 4.2 Study Management, Project management Documentation
- 4.3 Monitoring, Audits, Inspections and Pharmacovigilance

Unit 5

Biostatistics and Data Management

(12 hrs.)

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. *Clinical Research What It Is and How It Works*. UK: Jones Barlett Publishers, 2006.

Richard K. Rondel, Sheila A. Varley, Colin F. Webb. *Clinical Data Management*. UK: John Wiley, 2013.

Steven Piantadosi. *Clinical Trails A Methodologic Perspective*. UK: John Wiley, 2005.

BOOKS FOR REFERENCE

Martin M. Zdanowicz. *Concepts in Pharmacogenomics*. UK: Mc Graw Hill, 2010.

Russ B. Altman, David Flockhart, David B. Goldstein *Principles of Pharmacogenetics and Pharmacogenomics*. UK: John Wiley, 2012.

JOURNALS

Journal of Clinical Research & Bioethics

Perspectives in Clinical Research

Asian Journal of Pharmaceutical and Clinical Research

WEB RESOURCES

<http://hub.ucsf.edu/clinical-study-management>

http://icmr.nic.in/ethical_guidelines

<http://www.niaaa.nih.gov/research/guidelines-and-resources/clinical-trial-regulations-policies-and-guidance>

<http://www.fda.gov/ScienceResearch/SpecialTopics/RunningClinicalTrials/ucm155713.html>

PATTERN OF EVALUATION

Continuous Assessment:

Total Marks: 50

Duration: 90 mins.

Section A – 10 x 1 = 10 Marks (All questions to be answered)

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

Section C – 1 x 20 = 20 Marks (1 out of 2 to be answered)

Third Component:

List of Evaluation modes

Seminars

Quiz

Group discussion

Assignments

Case studies.

End Semester Examination

Total Marks: 100

Duration: 3 hrs.

Section A – $20 \times 1 = 20$ Marks (All questions to be answered)

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

Section C – $2 \times 20 = 40$ 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 2015 -2016)
DISSERTATION

CODE: 15BI/PC/DS49

CREDITS: 9
L T P :0 0 12

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 | Chapterization, 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.