

Central University of Punjab, Bathinda



M.Sc. Life Sciences (Bioinformatics)

Session: 2020-2022

Department of Computational Sciences

School of Basic and Applied Sciences

PROGRAMME OUTCOMES (M.Sc. Life Sciences (Bioinformatics))

Student graduating after successful completion of this course shall be able to

- Critically analyse current issues and trends influencing the field of Life Sciences and Bioinformatics.
- Competent to carry out understanding complex information from the concurrent scientific literature, identify the knowledge lacunae, shortlist attainable objectives, design comprehensive methodology and carry out the unsupervised research.
- Shall have scientific temperament.
- Establish professional relationships and development of Professional competencies
- Develop understanding and reflections on higher education policies and practices.

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Course Structure of the Programme

SEMESTER I							
S. No.	Course Code	Course Title	Course Type				
				L	T	P	Cr
1	LBI.508	Basics of Biochemistry	CF	2	0	0	2
2	LBI.509	Concepts of Genetics	CF	2	0	0	2
3	LBI.511	Sequence Analysis	CC	3	0	0	3
4	LBI.510	Mathematics for Biologists	CC	4	0	0	4
Choose any one of these courses							
5	LBI.506	Chemical Biology	DE	4	0	0	4
6	CCC.522	Statistical Mechanics	DE	4	0	0	4
7	LBI.532	Maths for Machine Learning	DE	4	0	0	4
Choose any one (theory and related lab) of these courses							
8	CCC.508	Scientific Programming	DE	4	0	0	4
9	CCC.515	Scientific Programming (Practical)	SBE	0	0	8	4
10	LBI.515	Programming 1	DE	4	0	0	4
11	LBI.516	Programming-I Lab	SBE	0	0	8	4
12	XXX	Interdisciplinary Course	IDC	2	0	0	2
Interdisciplinary course offered for other departments							
	CCC.516	Chemistry without test tube	IDC	2	0	0	2
Total				21	0	8	25

SEMESTER II							
S. No.	Course Code	Course Title	Course Type				
				L	T	P	Cr
1	LBI.512	Biological Databases and Management Systems	CC	4	0	0	4
2	CCC.525	Computational Methods	CC	4	0	0	4
3	CCC.528	Computational Methods Lab (Practical)	SBC	0	0	8	4
4	LBI.517	Practicals in Biological Databases and management Systems	SBC	0	0	8	4
5	XXX	Interdisciplinary Course	IDC	2	0	0	2
Interdisciplinary course offered for other departments							
	CCC.516	Chemistry without test tube	IDC	2	0	0	2
Choose any one (theory and related lab) of these courses							
6	LBI.527	Biomolecular Structure Modelling	DE	4	0	0	4
7	LBI.533	Practicals in Biomolecular Structure Modeling	DE	0	0	8	4
8	LBI.530	Programming II	DE	4	0	0	4
9	LBI.531	Practicals in Programming II	DE	0	0	8	4
Total				14	0	24	26

SEMESTER III							
S. No.	Course Code	Course Title	Course Type				
				L	T	P	Cr
1	CCC.554	Fundamentals of Molecular Simulations	CC	4	0	0	4
2	CCC.555	Molecular Simulations Lab (Practical)	SBC	0	0	8	4
3	LBI.521	Essentials of Immunology	CF	2	0	0	2
4	LBI.599	M.Sc. Project-I	SBE	0	0	0	4
Choose any one (theory and related lab) of these courses							
5	LBI.557	Data Mining and Machine learning	DE	4	0	0	4
6	LBI.558	Practicals in Data Mining and Machine learning	SBE	0	0	6	3
7	LBI.561	Genomic Data Analysis	DE	4	0	0	4
8	LBI.562	Genomic Data Analysis Lab	SBE	0	0	6	3
Choose any one of these courses/MOOC							
9	LBI.563	Complex Algorithms in Bioinformatics	DE	2	0	0	2
10	LBI.576	Computational Genomics and Proteomics	DE	2	0	0	2
11	CCC.559	Introduction to Molecular Docking	VAC	1	0	0	1
Total				13	0	14	24

SEMESTER IV							
S. No.	Course Code	Course Title	Course Type				
				L	T	P	Cr
Choose any two of these courses							
1	LBI.571	Systems Biology	DE	4	0	0	4
2	LBI.524	Molecular Evolution	DE	4	0	0	4
3	LBI.573	Cheminformatics	DE	4	0	0	4
4	LBI.572	Enriching Course for Bioinformatics - I	DEC	2	0	0	2
5	LBI.575	Enriching Course for Bioinformatics - II	DEC	2	0	0	2
6	LBI.574	Bioinformatics for Transcriptomics and Metabolomics	VAC	1	0	0	1
7	LBI.599	M. Sc. Project-II	SBE	0	0	0	8
Total				13	0	0	21
Grand Total				96 Credits			

Mode of Transaction: Lecture, Laboratory based Practical, Seminar, Group discussion, Team teaching, Self-learning.

Evaluation Criteria for Theory Courses

A. Continuous Assessment: [25 Marks]

- i. Surprise Test (minimum three) - Based on Objective Type Tests (10 Marks)
- ii. Term paper (10 Marks)
- iii. Assignment(s) (5 Marks)

B. Mid Semester Test-1: Based on Subjective Type Test [25 Marks]

C. End Semester Test-2: Based on Subjective Type Test [25 Marks]

D. End-Term Exam: Based on Objective Type Tests [25 Marks]

*Every student has to take up 2 ID courses of 2 credits each (Total 04 credits) from other disciplines in any two semesters of the program.

CC: Core Course, VAC: Value Added Course, EP: Elective Project, SEC: Skill Enhancement Course, IDE: Interdisciplinary Elective, DE: Discipline Elective, CF: Compulsory Foundation, SBC: Skill Based Core; SBE: Skill Based Elective, VAC: Value Added Courses

SEMESTER- I

Course Title: Basics of Biochemistry

L	T	P	Cr
2	0	0	2

Course Code: LBI.508

Total Hours: 30

Learning Outcomes: The outcomes of the subject is to ensure that a student comprehends the following:

- The structures and purposes of basic components of prokaryotic and eukaryotic cells, especially macromolecules, membranes, and organelles.
- The energy metabolism by cellular components in cells and the process of mitotic cell division.
- Influences of changes or losses in cell function; including the responses to environmental or physiological changes, or alterations of cell function brought about by mutation.

Course Content

Unit 1

8 Hours

Principles of biophysical chemistry Thermodynamics, Colligative properties, Stabilizing interactions: Van der Waals, Electrostatic, Hydrogen bonding, Hydrophobic interaction, etc.

Unit 2

7 Hours

Composition, structure, function and metabolism of Carbohydrates, Lipids.

Unit 3

7 Hours

Composition, structure, function and metabolism of Amino Acids and Nucleotides.

Unit 4

8 Hours

Enzymology: Classification, Principles of catalysis, Mechanism of enzyme catalysis, Enzyme kinetics, Enzyme regulation, Isozymes.

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

- Berg, J.M., Tymoczko, J.L. and Stryer, L. (2010). *Biochemistry*. W.H. Freeman & Company. USA.
- Brown, T.A. (2006). *Gene Cloning and DNA analysis: In Introduction*. Blackwell Publishing Professional. USA.

3. Haynie, D.T. (2007). *Biological thermodynamics*. Cambridge University. UK.
4. Mathews, C.K., Van Holde, K.E. and Ahern, K.G. (2000). *Biochemistry*. Oxford University Press Inc. New York.
5. Nelson, D. and Cox, M.M. (2013). *Lehninger Principles of Biochemistry*. BI publications Pvt. Ltd. Chennai, India.
6. Ochiai, E. (2008). *Bioinorganic chemistry: A survey*. Academic Press. Elsevier, India.
7. Randall, D. J., Burggren, W. and French, K. (2001). *Eckert animal physiology*. W.H. Freeman & Company. USA.
8. Raven, P.H., Johnson, G.B. and Mason, K.A. (2007). *Biology*. Mcgraw-Hill. USA.
9. Shukla AN (2009). *Elements of enzymology*. Discovery Publishing. New Delhi, India.
10. Voet, D. and Voet, J.G. (2014). *Principles of biochemistry*. CBS Publishers & Distributors. New Delhi, India.

Course Title: Concepts of Genetics

Course Code: LBI.509

Total Hours: 30

L	T	P	Cr
2	0	0	2

Learning Outcomes: At the end of the course, the students will be able to:

- gain a deep knowledge about the structures and organisation of nucleic acids
- learn DNA replication, Inheritance patterns

Course Content

Unit 1

8 Hours

Introduction and scope of genetics, DNA as genetic material: Double helical structure, Structure of DNA and RNA, Different types of DNA molecules, forces stabilizing nucleic acid structure, super coiled DNA, properties of DNA, denaturation and renaturation of DNA and Cot curves. DNA replication: Basic mechanism of DNA replication.

Unit 2

7 Hours

Cell division and Cell cycle: Mitosis, Meiosis Concepts of Linkage analysis and gene mapping: Coupling and repulsion phase linkage, Crossing over and recombination. Population genetics: Application of Mendel's laws to

populations, Hardy-Weinberg principle, inbreeding depression and heterosis, inheritance of quantitative traits.

Unit 3

7 Hours

Gene Interaction: Sex determination and Sex linked inheritance, Sex determination in humans, *Drosophila* and other animals, Sex determination in plants, Sex linked genes and dosage compensation.

Unit 4

8 Hours

Chloroplast and Mitochondrial inheritance, Yeast, *Chlamydomonas/Neurospora* Chromosomal aberrations: Types of changes—deletions, duplications, inversions, translocations, Change in chromosome number: trisomy and polyploidy.

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Reading

1. Anthony, J.F., Miller, J.A., Suzuki, D.T., Richard, R.C., Gilbert, W.M. (1998). *An introduction to Genetic Analysis*. W.H. Freeman publication, USA.
2. Atherly, A.G., Girton, J.R., McDonald, J.F. (1999). *The science of Genetics*. Saundern College publication.
3. Snusted, D.P., Simmons, M. J. (2010). *Principles of Genetics*. John Wiley & Sons, New York.
4. Gupta, P.K. (2009). *Genetics*. Rastogi publications, Meerut, India.
5. Gupta, P.K (2008). *Cytology, Genetics and Evolution*. Rastogi publications, Meerut, India.
6. Jocelyn, E.K., Elliott, S.G., Stephen, T.K. (2009). *Lewin's Genes X*. Jones & Bartlett Publishers, USA.
7. Schaum, W.D. (2000). *Theory & problems in Genetics by Stansfield, out line series* McGrahill, USA.
8. Tamarin, R.H. (1996). *Principles of Genetics, International edtn*. McGrawhill, USA.

Course Title: Sequence Analysis

Course Code: LBI.511

Total Hours: 45

L	T	P	Cr
3	0	0	3

Learning Outcomes: The outcomes of the subject is to ensure that a student can apply the knowledge of the following

- Data storage formats
- Pairwise alignments
- Sequence patterns and profiling
- Multiple sequence alignment

Course Content

Unit 1

13 Hours

Basic concepts of sequence similarity, identity and homology, homologues, orthologues, paralogues and xenologues Pairwise sequence alignments: basic concepts of sequence alignment, Needleman and Wunsch, Smith and Waterman algorithms for pairwise alignments, gap penalties

Unit 2

10 Hours

Scoring matrices: basic concept of a scoring matrix, PAM and BLOSUM series Tools such as BLAST (various versions of it) and FASTA

Unit 3

12 Hours

Multiple sequence alignments (MSA): basic concepts of various approaches for MSA (e.g. progressive, hierarchical etc.). Algorithm of CLUSTALW (including interpretation of results), concept of dendrogram and its interpretation.

Unit 4

10 Hours

Sequence patterns and profiles: Basic concept and definition of sequence patterns, motifs and profiles, profile-based database searches using PSI-BLAST, analysis and interpretation of profile-based searches.

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Reading

1. A.D. Baxevanis *et. al.*, Current Protocols in Bioinformatics, (2005) Wiley Publishers
2. David W.Mount Bioinformatics (2001) Cold Spring Harbor Laboratory Press, ISBN 0-87969-608-7
3. Computational Molecular Biology by P. A. Pevzner, Prentice Hall of India Ltd, (2004) ISBN81-203-2550-8
4. D.E.Krane and M.L.Raymer Fundamental concepts of Bioinformatics (2003) Pearson Education ISBN 81-297-0044-1
5. N.Gautham Bioinformatics Narosa publications. (2006) ISBN-13: 9781842653005

Course Title: Mathematics for Biologists

Course Code: LBI.510

L	T	P	Cr
4	0	0	4

Total Hours: 60

Learning Outcomes: At the end of the course, the students will be able to:

- Identify and describe the basic mathematical techniques that are commonly used by chemist.
- Develop skills in vectors, matrices, differential calculus, integral calculus and probability.
- Apply the principles to a number of simple problems that have analytical solutions.
- Design different methods to problems related to chemistry.

Course Content**Unit-1****15 Hours**

Vectors in 2D, 3D and in general, circles, transformation of coordinates, polar coordinates, parametric equations, and the solid analytic geometry of vectors, lines, planes, spherical coordinate.

Unit-2**15 Hours**

Functions, limits, derivative, physical significance, basic rules of differentiation, maxima and minima, exact and inexact differentials, partial differentiation.

Unit-3**15 Hours**

Addition and multiplication; inverse, adjoint and transpose of matrices, matrix equation, Introduction to vector spaces, matrix eigen values and eigen vectors, diagonalization, determinants (examples from Huckel theory).

Unit-4**15 Hours**

Basic rules for integration, integration by parts, partial fraction and substitution, definite integrals, evaluation of definite.

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested readings

1. The chemistry Mathematics Book, E.Steiner, Oxford University Press (2008).
2. Mathematical for Physical Chemistry : F. Daniels, Mc. Graw Hill (1959).
3. Chemical Mathematics D.M. Hirst, Longman (1979).
4. Basic Mathematics for Chemists, Tebbutt, Wiley (1994).
5. G. Arfken, H. Weber and F. Harris, *Mathematical Methods for*

Physicists (Elsevier Academic Press, Massachusetts, USA) 2012.

Course Title: Chemical Biology

Course Code: LBI.506

Total Hours: 60

L	T	P	Cr
4	0	0	4

Learning Outcomes: On completion of the course, students will be able to:

- Understand the importance of various atomic models.
- Identify the nature of values in of hybridization.
- Understand the chemical kinetics
- Critically analyse the nuances of solid state.

Course Content

Unit 1

15 Hours

Atomic structure and chemical bonding: Bohr model, spectrum of hydrogen atom, quantum numbers; Wave-particle duality, de Broglie hypothesis; Uncertainty principle; shapes of s, p and d orbitals; Electronic configurations of elements (up to atomic number 30); Aufbau principle; Pauli's exclusion principle and Hund's rule; Orbital overlap and covalent bond; Hybridisation involving s and p orbitals only.

Unit 2

15 Hours

Concept of atoms and molecules; Mole concept; Chemical formulae; Concentration in terms of mole fraction, molarity, molality and normality. Chemical equilibrium: Law of mass action; Equilibrium constant, Le Chatelier's principle (effect of concentration, temperature and pressure); Significance of ΔG and ΔG_0 in chemical equilibrium

Unit 3

15 Hours

Chemical kinetics: Rates of chemical reactions; Order of reactions; Rate constant; First order reactions; Temperature dependence of rate constant (Arrhenius equation).

Unit 4

15 Hours

Solid state: Classification of solids, crystalline state, seven crystal systems (cell parameters a, b, c, α , β , γ), close packed structure of solids (cubic), packing in fcc, bcc and hcp lattices;

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested readings:

1. Physical Chemistry by A. J. Mee, James Clare Speakman, Heinemann Educational Publishers (1993)
2. Physical Chemistry by P.W. Atkins, Oxford University Press; (2014)

Course Title: Statistical Mechanics

Course Code: CCC.522

Total Hours: 60

L	T	P	Cr
4	0	0	4

Learning Outcomes: At the end of the course, the students will be able to:

- apply the classical laws of thermodynamics and their application, mathematical review of classical mechanics
- learn the postulates of statistical mechanics, Liouville's Theorem, and statistical interpretation of thermodynamics
- identify the microcanonical, canonical, grand canonical and isobaric-isothermal ensembles, partition function, elementary probability theory, distributions and fluctuations
- learn the methods of statistical mechanics and their use to develop the statistics for Bose-Einstein, Fermi-Dirac and photon gases
- the principles and techniques from statistical mechanics to a range of modern day research based problems.

Course Content

Unit 1

16 Hours

Mathematical Review of Classical Mechanics: Lagrangian Formulation, Hamiltonian Formulation, Poisson Brackets and Canonical Transformations; Classical approach to Ensembles: Ensembles and Phase Space, Liouville's Theorem, Equilibrium Statistical Mechanics and its ensembles; Partition Function: Review of rotational, vibrational and translational partition functions. Application of partition functions to specific heat of solids and chemical equilibrium. Real gases.

Unit 2

16 Hours

Elementary Probability Theory, Distributions and Averages, Cumulants and Fluctuations, The Central Limit Theorem; Distributions & Fluctuations: Theory of Ensembles, Classical and Quantum, Equivalence of Ensembles, Fluctuations of Macroscopic Observable

Unit 3

14 Hours

Basic Thermodynamics: Review of Concepts, The Laws of Thermodynamics, Legendre Transforms, The Maxwell Relations, The Gibbs-Duhem Equation and Extensive Functions, Intensive Function

Unit 4

14 Hours

Bose-Einstein distribution: Einstein condensation. Thermodynamic properties of ideal BE gas. Fermi-Dirac distribution: Degenerate Fermi gas. Electron in metals. Magnetic susceptibility.

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. Kerson Huang, Statistical Mechanics, Wiley (2008).
2. R. K. Pathria and P. D. Beale, Statistical mechanics, Elsevier (2011).

3. D. A. Mcquarrie, Statistical Mechanics, University Science Books (2011).
4. D. Chandler, Introduction to Statistical Mechanics, Oxford University Press (1987).

Course Title: Maths for Machine Learning

Course Code: LBI.532

Total Hours: 60

L	T	P	Cr
4	0	0	4

Learning Outcomes: Upon successfully completing this course, students will be able to

- Apply mathematics to create novel solution in datamining and machine learning.
- Identify/characterize/define a machine learning problem
- Design a program to calssify, find regression and cluster entities
- Create automated machine dependent solutions
- optimize real world problems

Course Content

Unit 1

15 Hours

Symmetric matrices and positive definite matrices (real eigenvalues and orthogonal eigenvectors, tests for $x'Ax > 0$, applications); Linear transformations and change of basis (connected to the Singular Value Decomposition - orthonormal bases that diagonalize A

Unit 2

15 Hours

The Statistical Theory of Machine Learning: Classification, Regression, Aggregation;

Unit 3

15 Hours

Empirical Risk Minimization, Regularization; Suprema of Empirical Processes Algorithms and Convexity: Boosting;

Unit 4

15 Hours

Kernel Methods Convex Optimization Online Learning: Online Convex Optimization; Partial Information Bandit Problems; Blackwell's Approachability

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. Steiner, E. The Chemistry Mathematics, 2008, Oxford University Press.
2. Doggett, G. and Sucliffe, B.T. Mathematics for Chemistry, 1995, Longman.
3. Daniels, F. Mathematical Preparation for Physical Chemistry, 2003, McGraw Hill.
4. Hirst, D.M. Chemical Mathematics, Longman.

5. Barrante, J. R. Applied Mathematics for Physical Chemistry, 2008, Prentice Hall.
6. Tebbutt P. Basic Mathematics for Chemists, 1998, John Wiley

Course Title: Scientific Programming

Course Code: CCC.508

Total Hours: 60

L	T	P	Cr
4	0	0	4

Learning Outcomes: At the end of the course, the students will be able to:

- Identify and describe the basic art of scientific programming related to Fortran 95/2003.
- Concepts related to variables, I/O, arrays, procedures, modules, pointers and parallel programming.
- Develop skills to write programs related to standard problems and as well as to chemistry.

Course Content

Unit 1

15 Hours

Introduction to Computers and Fortran language: History and evolution of Fortran language, Basic elements of Fortran: Character sets, structure of statements, Structure of a Fortran Program, compiling, linking and executing the Fortran program.

Unit 2

15 Hours

Constants and variables, assignment statements and arithmetic calculations, intrinsic functions, Program design and branching structures, loop and character manipulation.

Unit 3

15 Hours

Basic I/O concepts, Formatted READ and WRITE statements, Introduction to Files and File Processing, Introduction to Arrays and procedures, Additional features of arrays and procedures- 2-D and multidimensional arrays, allocatable arrays in procedures, derived data types.

Pointers and dynamic data structures- using pointers in assignment statements, with arrays, as components of derived data types and in procedures, Introduction to object oriented programming in Fortran.

Unit 4

15 Hours

What is parallel programming, Why use parallel programming, Parallel Architecture, Open MP & MPI, Models of Parallel Computation, Parallel Program Design, Shared Memory & Message Passing, Algorithms, Merging & Sorting.

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. Chapman, Fortran 95/2003 for Scientists and Wngineers, McGraw-Hill International Edition, New York (2006).
2. V. Rajaraman, Computer Programming in Fortran 90 and 95, PHI Learning Pvt. Ltd, New Delhi (1997).
3. W. H. Press, S. A. Teukolsky, W. H. Vetterling, B. P. Flannery, Fortran Numerical Recipes Volume 2 (Fortran 90), Cambridge University Press (1996).
4. Parallel Programming in C with MPI and OpenMP by M J Quinn (2003).
5. Introduction to Parallel Computing by Ananth Grama, George Karypis, Vipin Kumar, and Anshul Gupta (2003).

Course Title: Scientific Programming (Practical)

Course Code: CCC.515

Total Lecture: 120

L	T	P	Cr
0	0	8	4

Learning Outcomes: The students, after completion of this course, will be able to:

- Identify/characterize/define a computational problem
- Design a fortran program to solve the problem
- Create pseudo executable code
- Read most of the basic fortran code

Course Content

1. Structure of a Fortran Program, compiling, linking and executing the Fortran programs. Constants and variables, assignment statements and arithmetic calculations, intrinsic functions, Program design and branching structures, loop and character manipulation.
2. Basic I/O concepts, Formatted READ and WRITE statements, Introduction to Files and File Processing, Introduction to Arrays and procedures, Additional features of arrays and procedures- 2-D and multidimensional arrays, allocatable attays in procedures, derived data types.
3. Pointers and dynamic data structures-using pointers in assignment statements, with arrays, as components of derived data types and in procedures, Introduction to object oriented programming in Fortran.

Matrix summation, subtraction and multiplication, Matrix inversion and solution of simultaneous equation, Gaussian elimination.

4. Parallel Program Design, Shared Memory & Message Passing, Algorithms.

Transactional Modes: Laboratory based practicals; Problem solving; Self-learning.

Suggested Readings

1. Chapman, Fortran 95/2003 for Scientists and Wngineers, McGraw-Hill International Edition, New York (2006).

2. V. Rajaraman, Computer Programming in Fortran 90 and 95, PHI Learning Pvt. Ltd, New Delhi (1997).

3. W. H. Press, S. A. Teukolsky, W. H. Vetterling, B. P. Flannery, Fortran Numerical Recipes Volume 2 (Fortran 90), Cambridge University Press (1996).

4. Parallel Programming in C with MPI and OpenMP by M J Quinn

5. Introduction to Parallel Computing by Ananth Grama, George Karypis, Vipin Kumar, and Anshul Gupta.

Course Title: Programming I

Course Code: LBI.515

Total Lecture: 60

L	T	P	Cr
4	0	0	4

Learning Outcomes: Upon successfully completing this course, students will be able to “do something useful with Python”.

- Identify/characterize/define a problem
- Design a program to solve the problem
- Create pseudo executable code
- Read most of the basic Python code

Course Content

Unit1

15 Hours

Introduction, gitHub, Functions, Booleans and Modules, Sequences, Iteration and String Formatting, Dictionaries, Sets, and Files

Unit 2

15 Hours

Exceptions, Testing, Comprehensions, Advanced Argument Passing, Lambda -functions as objects

Unit 3

15 Hours

Object Oriented Programming, More OO -- Properties, Special methods

Unit 4

15 Hours

Iterators, Iterables, and Generators, Decorators, Context Managers, Regular Expressions, and Wrap Up

Transactional Modes: Laboratory based practicals; Problem solving; Self-learning.

Suggested Readings

- Core Python Programming (<http://corepython.com/>): Only available as a dead trees version, but if you like to have book to hold in your hands anyway, this is the best textbook style introduction out there. It starts from the beginning, but gets into the full language. Published in 2009, but still in print, with updated appendixes available for new language features. In the third edition, "the contents have been cleaned up and retrofitted w/Python 3 examples paired w/their 2.x friends."
- Dive Into Python 3 (<http://www.diveinto.org/python3/>): This book offers an introduction to Python aimed at the student who has experience programming in another language.
- Python for You and Me (<http://pymbook.readthedocs.org/en/latest/>): Simple and clear. This is a great book for absolute newcomers, or to keep as a quick reference as you get used to the language. The latest version is Python 3.
- Think Python (<http://greenteapress.com/thinkpython/>): Methodical and complete. This book offers a very "computer science"-style introduction to Python. It is really an intro to Python in the service of Computer Science, though, so while helpful for the absolute newcomer, it isn't quite as "pythonic" as it might be.
- Python 101 (<http://www.blog.pythonlibrary.org/2014/06/03/python-101-book-published-today/>) Available as a reasonably priced ebook. This is a new one from a popular Blogger about Python. Lots of practical examples. Also available as a Kindle book: <http://www.amazon.com/Python-101-Michael-Driscoll-ebook/dp/B00KQTFHNK>
- Problem Solving with Algorithms and Data Structures (<http://interactivepython.org/runestone/static/pythonds/index.html>(Links to an external site.)Links to an external site.)

- Python Course (http://www.python-course.eu/python3_course.php(Links to an external site.)Links to an external site.)

References for getting better, once you know the basics

- Python Essential Reference (<http://www.dabeaz.com/per.html>): The definitive reference for both Python and much of the standard library.
- Hitchhikers Guide to Python (<http://docs.python-guide.org/en/latest>): Under active development, and still somewhat incomplete, but there is good stuff.
- Writing Idiomatic Python (<https://www.jeffknupp.com/writing-idiomatic-python-ebook>): Focused on not just getting the code to work, but how to write it in a really "Pythonic" way.
- Fluent Python (<http://shop.oreilly.com/product/0636920032519.do>): All python3, and focused on getting the advanced details right. Good place to go once you've got the basics down.
- Python 3 Object Oriented Programming (<https://www.packtpub.com/application-development/python-3-object-oriented-programming> (Links to an external site.)Links to an external site.): Nice book specifically about Object Oriented programming structure, and how to do it in Python. From local Author and founder of the Puget Sound Programming Python (PuPPy) meetup group, Dusty Phillips.

Course Title: Programming I Lab
Course Code: LBI.516
Total Hours: 120

L	T	P	Cr
0	0	8	4

Learning Outcomes: Upon successfully completing this course, students will be able to “do something useful with Python”.

- Identify/characterize/define a problem
- Design a program to solve the problem
- Create executable code
- Read most Python code
- Write basic unit tests

Course Content

1. Working with Data. A detailed tour of how to represent and work with data in Python. Covers tuples, lists, dictionaries, and sets. Students will also learn how to effectively use Python's very powerful list processing

primitives such as list comprehensions. Finally, this section covers critical aspects of Python's underlying object model including variables, reference counting, copying, and type checking.

2. Program Organization, Functions, and Modules. More information about how to organize larger programs into functions and modules. A major focus of this section is on how to design functions that are reliable and can be easily reused across files. Also covers exception handling, script writing, and some useful standard library modules.
3. Classes and Objects. An introduction to object-oriented programming in Python. Describes how to create new objects, overload operators, and utilize Python special methods. Also covers basic principles of object oriented programming including inheritance and composition.
4. Inside the Python Object System. A detailed look at how objects are implemented in Python. Major topics include object representation, attribute binding, inheritance, memory management, and special properties of classes including properties, slots, and private attributes.

Transactional Modes: Laboratory based practicals; Problem solving; Self-learning.

Suggested Readings

- The Python Tutorial (<https://docs.python.org/3/tutorial/>): This is the official tutorial from the Python website. No more authoritative source is available.
- Code Academy Python Track (<http://www.codecademy.com/tracks/python>): Often cited as a great resource, this site offers an entertaining and engaging approach and in-browser work.
- Learn Python the Hard Way (<http://learnpythonthehardway.org/book/>): Solid and gradual. This course offers a great foundation for folks who have never programmed in any language before. [Python 2]

SEMESTER II

Course Title: Biological Database and Management System

Course Code: LBI.512

Total Lecture: 60

L	T	P	Cr
4	0	0	4

Learning Outcomes: Upon successfully completing this course, students will be able to apply principles of DBMS to create novel solution in bioinformatics.

- Identify/characterize/define and solve a data collection, sorting and management problem
- Design an approach to create a Relational DBMS
- Create non-redundant databases

Course Content

Unit 1

15 Hours

Biological Databases: Nucleotide Sequence Databases, GenBank, DDBJ, EMBL, Sequence Flatfile and submission process, Protein sequence databases, UniProt, Mapping databases, Genomic databases, PDBsum, PDB, SCOP, CATH, Pathway and molecular interaction databases.

Unit 2

15 Hours

Database planning and Design concepts General Database Planning and Design – Document or forms – preparation and architecture Entity-Relational ship Model- entities, Attributes, keys, tables design, relationships, roles and dependencies.

Unit 3

15 Hours

Relational DB Introduction to relational DB and transactions. SQL-statements-Data Definition-Manipulation-control-Objects, - Views, sequences and Synonyms. Working with code and forms- Front end development-query sublanguage-modifying relations in SQL.

Unit 4

15 Hours

Internals of RDBMS Physical data structures, query optimization. Join algorithm staisca and cost base optimization. Transaction processing.concurrency control and recovery management. Transaction model properities, state serizability, lock base protocols, two phase locking.

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1 Abraham Silberschatz, Henry F.Korth and S.Sudhashan (2005) Database system concepts. 5 Ed McGraw Hill Publications.

2 Elmasri Ramez and Novathe Shamkant, “ Fundamentals of Database systems” (2007) Benjamin cummings Publishing Company. ISBN-10: 0321369572.

3 P. Ramakrishnan Rao: Database Management system, (2003) 3EdMcGraw Hill Publications. 9780071230575

- 4 Jim Gray and A.Reuter “ Transaction processing : Concepts and Techniques” Morgan Kaufmann Press.(1997) ISBN- 10: 1558601902
- 5 V.K .Jain. Database Management system (2002) Dreamtech Press ISBN 8177222279
- 6 Date C.J. “ Introduction to database management” (2009) Vol1, Vol2, Vol3 addison Wesley.
- 7 Ullman, JD “ Principles of Database systems” (1992) Galgottia publication
- 8 James Martin Principles of Database Management systems” (1985) PHI.
6. Introduction to NCBI Taxonomic Browser
7. DDL & DML: Creating and working with databases, creating tables, dropping tables, primary and secondary keys, data validation, simple queries using MySQL, cursors, stored procedures.
8. DTD and XML schema- simple DTD and creation of data in XML.

Course Title: Computational Methods

Course Code: CCC.525

Total Hours: 60

L	T	P	Cr
4	0	0	4

Learning Outcomes: At the end of the course, the students will be able to solve:

- the large scale systems of linear, non-linear and simultaneous equations
- the matrix and determinants, interpolations, polynomial and spline interpolation
- the numerical differentiation and integration
- complex curve fitting methods, explicit schemes to solve differential equations
- the simple optimisation, vectorisation.

Course Content

Unit 1

15 Hours

Linear and Non –Linear equations: Solution of Algebra and transcendental equations, Bisection, Falsi position and Newton-Rhapson methods-Basic principles-Formulae-algorithms.

Simultaneous equations: Solutions of simultaneous linear equations-Guass elimination and Gauss Seidel iterative methods-Basic principles-Formulae-Algorithms, Pivotal Condensation.

Unit 2

15 Hours

Matrix and Determinants: Matrix Inversion, Eigen-values, Eigen-vector,

Diagonalization of Real Symmetric Matrix by Jacobi's Method.

Unit 3

16 Hours

Interpolations: Concept of linear interpolation-Finite differences-Newton's and Lagrange's interpolation formulae-principles and Algorithms

Numerical differentiation and integration:

Numerical differentiation-algorithm for evaluation of first order derivatives using formulae based on Taylor's series, Numerical integration-Trapezoidal Rule, Simpson's 1/3 Rule, Weddle's Rule, Gauss Quadrature Formulae-Algorithms. Error in numerical Integration.

Curve Fit: least square, straight line and polynomial fits.

Unit 4

14 Hours

Numerical Solution of differential Equations: Picards Method, Taylor's Series Method, Euler's Method, Modified Euler's Method, Runge-Kutta Method, Predictor-Corrector Method.

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. V. Rajaraman, Computer Oriented Numerical Methods, PHI, 1993.
2. E. Balaguruswamy, Numerical Methods, Tata McGraw Hill, 2017.
3. F. Acton, Numerical Methods that Work, Harper and Row, 1997.
4. S. D. Conte and C.D. Boor, Elementary Numerical Analysis, McGraw Hill, 2005.
5. S. S. Shastri, Introductory Methods of Numerical Analysis, PHI, 2012.

Course Title: Computational Methods lab

Course Code: CCC.528

Total Hours: 120

L	T	P	Cr
0	0	8	4

Learning Outcomes: At the end of the course, the students will be able to:

- learn computer code for the large scale systems of transcendental and polynomial equations
- understand numerical strategies to write a computer code for the solution of matrix and determinants, interpolations, polynomial and spline interpolation
- learn the computer code for numerical differentiation and integration, differential equations, complex curve fitting, and simple optimisation

Course Content

Jacobi Method of Matrix Diagonalization, Solution of transcendental or polynomial equations by the Newton Raphson method, Linear curve fitting and calculation of linear correlation coefficient, Matrix summation, subtraction and multiplication, Matrix inversion and solution of simultaneous equation, Gaussian elimination, Finding Eigen values and eigenvectors, Matrix factorizations Curve Fitting – Polynomial curve fitting

on the fly, Least squares curve fitting, General nonlinear fits, Lagrange interpolation based on given input data, Numerical integration using the Simpson's method, Numerical integration using the Gaussian quadrature method, Solution of first order differential equations using the Rung-Kutta method, Numerical first order differentiation of a given function, Fast Fourier Transform, Monte Carlo integration.

Transactional Modes: Laboratory based practicals; Problem solving; Self-learning.

Suggested Readings

1. Y.Kirani Singh and B.B.Chaudhuri, MATLAB Programming, Prentice-Hall India, 2007
2. Rudra Pratap, Getting Started with Matlab 7, Oxford, Indian University Edition, 2006
3. E. Balaguruswamy, Numerical Methods, Tata McGraw Hill (2017).
4. V. Rajaraman, Computer oriented numerical methods, PHI Learning Pvt. Ltd., (2018).

Course Title: Practical in Biological Database and Management System

Course Code: LBI.517

Total Lecture: 120

L	T	P	Cr
0	0	8	4

Learning Outcomes: Upon successfully completing this course, students will be able to apply principles of DBMS to create novel solution in bioinformatics.

- Identify/characterize/define and solve a data collection, sorting and management problem
- Design an approach to create a Relational DBMS
- Create non-redundant databases

Course Content

1. Data Definition, Table Creation, Constraints,
2. Insert, Select Commands, Update & Delete Commands.
3. Nested Queries & Join Queries
4. Views
5. High level programming language extensions (Control structures, Procedures and Functions).
6. Front end tools
7. Forms
8. Triggers
9. Menu Design
10. Reports.

Transactional Modes: Laboratory based practicals; Problem solving; Self-learning.

Suggested Readings

1 Abraham Silberschatz, Henry F.Korth and S.Sudhashan (2005) Database system concepts. 5 Ed McGraw Hill Publications.

2 Elmasri Ramez and Novathe Shamkant, “ Fundamentals of Database systems” (2007) Benjamin cummings Publishing Company. ISBN-10: 0321369572.

3 P. Ramakrishnan Rao: Database Management system, (2003) 3EdMcGraw Hill Publications. 9780071230575

4 Jim Gray and A.Reuter “ Transaction processing : Concepts and Techniques” Morgan Kaufmann Press.(1997) ISBN- 10: 1558601902

5 V.K .Jain. Database Management system (2002) Dreamtech Press ISBN 8177222279

6 Date C.J. “ Introduction to database management” (2009) Vol1, Vol2, Vol3 addison Wesley.

7 Ullman, JD “ Principles of Database systems” (1992) Galgottia publication

8 James Martin Principles of Database Management systems” (1985) PHI.

Course Title: Biomolecular Structure Modelling

Course Code: LBI.527

Total Hours: 60

Learning Outcomes: On completion of the course the student should be able to:

- describe different types of protein–ligand interactions and characterise binding pockets
- use different search methods to find compounds with specific properties in large compound databases
- set up, perform and evaluate different virtual screening methods using large datasets
- account for and set up molecular dynamics simulations and free energy calculations

Course Content

Unit 1

15 Hours

Basics of Biomolecules: Principles of protein and nucleic acid structure: Primary, Secondary, Tertiary structure and Qaternary structure.

Protein secondary structure: Introduction, Hydrogen bond, Defining a secondary structure element, Methods for predicting secondary structure

Unit 2

15 Hours

Protein tertiary structure modeling: Basic concepts, Protein folding and Energetics, Comparative modeling, Threading, Ab initio modeling, Modeling protein sidechains, CASP: A blind protein structure prediction competition, CAPRI, Protein Structure Initiative (PSI).

Unit 3

15 Hours

Introduction to drug designing, ADMET, drug metabolism, toxicity and pharmacokinetics, Identification and validation strategies. Drug Target classification, Design and development of combinatorial libraries for new lead generation.

Unit 4

15 Hours

Concept of Pharmacophore, Functional group considered as pharmacophore, Ehrlich's magnetic bullet, Fischer's Lock and Key, Structure-based drug design-'de novo' design methodologies 3D-database searching techniques, docking. QSAR

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning

Suggested Readings

1. Grant, Guy H.; Richards, W. Graham Computational chemistry Oxford: Oxford Univ. Press, 1995
2. Schneider, Gisbert; Baringhaus, Karl-Heinz; Kubinyi, Hugo Molecular design : concepts and applications Weinheim: Wiley-VCH, c2008
3. Andrew R. Leach Molecular Modelling Principles and applications. (2001) II ed . Prentice Hall.
4. Lednicer, D. "Strategies for Organic Drug Discovery Synthesis and Design"; (1998) Wiley International Publishers.
5. Gordon, E.M. and Kerwin, J.F "Combinatorial chemistry and molecular diversity in drug discovery" (1998) Wiley-Liss Publishers.

Course Title: Practicals in Biomolecular Structure Modelling

Course Code: LBI.533

Total Hours: 120

L	T	P	Cr
0	0	8	4

Learning Outcomes: On completion of the course the student should be able to:

- Identify different types of protein-ligand interactions and characterise

binding pockets

- Apply different search methods to find compounds with specific properties in large compound databases
- Evaluate different virtual screening methods using large datasets
- Devise and set up molecular dynamics simulations and free energy calculations

Course Content

The following experiments should be conducted by the students:

A. Molecular Recognition

1. Prediction of Protein-ligand interaction sites
2. Prediction of Protein-protein interaction sites
3. Prediction of Protein-membrane interaction sites
4. Prediction of Protein-nucleic acid interaction sites

B. Docking

1. Protein Ligand Docking using
 - (i) Autodock
 - (ii) Vina
 - (iii) Dock
2. Protein-protein docking by HADDOCK or other similar methods

C. Modelling macromolecular structure

1. Homology modeling
2. *ab-initio* structure modeling

Transactional Modes: Laboratory based practicals; Problem solving; Self-learning.

Suggested Readings

1. *Grant, Guy H.; Richards, W. Graham* Computational chemistry Oxford: Oxford Univ. Press, 1995
2. *Schneider, Gisbert; Baringhaus, Karl-Heinz; Kubinyi, Hugo* Molecular design : concepts and applications Weinheim: Wiley-VCH, c2008

Course Title: Programming II

Course Code: LBI.530

Total Hours: 60

L	T	P	Cr
4	0	0	4

Learning Outcomes: Upon successfully completing this course, students will be able to “do something useful with Python”.

- Identify/characterize/define a numerical problem
- Design a program to solve the data parsing problem
- Create Time code
- Read most of the basic Python code

Course Content

Unit 1**12 Hours**

Intro to OOP- Define Classes- Create Objects- Understand methods and attributes- Work with `self`

Unit 2**12 Hours**

Advanced OOP concepts - Work with class and static methods- Inheritance and polymorphism

Unit 3**15 Hours**

File handling- Work with JSON, CSV or XML files- Python pickle- Functional programming- List comprehensions- Iterators and Generators

Unit 4**21 Hours**

Solving $Ax = b$ for square systems by elimination (pivots, multipliers, back substitution, invertibility of A , factorization into $A = LU$), Complete solution to $Ax = b$ (column space containing b , rank of A , nullspace of A and special solutions to $Ax = 0$ from row reduced R); Basis and dimension (bases for the four fundamental subspaces); Least squares solutions (closest line by understanding projections); Orthogonalization by Gram-Schmidt (factorization into $A = QR$)

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Reading

- Core Python Programming (<http://corepython.com/>): Only available as a dead trees version, but if you like to have book to hold in your hands anyway, this is the best textbook style introduction out there. It starts from the beginning, but gets into the full language. Published in 2009, but still in print, with updated appendixes available for new language features. In the third edition, "the contents have been cleaned up and retrofitted w/Python 3 examples paired w/their 2.x friends."
- Dive Into Python 3 (<http://www.diveinto.org/python3/>): This book offers an introduction to Python aimed at the student who has experience programming in another language.
- Python for You and Me (<http://pymbook.readthedocs.org/en/latest/>): Simple and clear. This is a great book for absolute newcomers, or to keep as a quick reference as you get used to the language. The latest version is Python 3.

- Think Python (<http://greenteapress.com/thinkpython/>): Methodical and complete. This book offers a very "computer science"-style introduction to Python. It is really an intro to Python in the service of Computer Science, though, so while helpful for the absolute newcomer, it isn't quite as "pythonic" as it might be.
- Python 101 (<http://www.blog.pythonlibrary.org/2014/06/03/python-101-book-published-today/>) Available as a reasonably priced ebook. This is a new one from a popular Blogger about Python. Lots of practical examples. Also available as a Kindle book: <http://www.amazon.com/Python-101-Michael-Driscoll-ebook/dp/B00KQTFHNK>
- Problem Solving with Algorithms and Data Structures (<http://interactivepython.org/runestone/static/pythonds/index.html> (Links to an external site.))Links to an external site.)
- Python Course (http://www.python-course.eu/python3_course.php (Links to an external site.))Links to an external site.)

References for getting better, once you know the basics

- Python Essential Reference (<http://www.dabeaz.com/per.html>): The definitive reference for both Python and much of the standard library.
- Hitchhikers Guide to Python (<http://docs.python-guide.org/en/latest>): Under active development, and still somewhat incomplete, but there is good stuff.
- Writing Idiomatic Python (<https://www.jeffknupp.com/writing-idiomatic-python-ebook>): Focused on not just getting the code to work, but how to write it in a really "Pythonic" way.
- Fluent Python (<http://shop.oreilly.com/product/0636920032519.do>): All python3, and focused on getting the advanced details right. Good place to go once you've got the basics down.
- Python 3 Object Oriented Programming (<https://www.packtpub.com/application-development/python-3-object-oriented-programming> (Links to an external site.))Links to an external site.): Nice book specifically about Object Oriented programming structure, and how to do it in Python. From local Author and founder of the Puget Sound Programming Python (PuPPy) meetup group, Dusty Phillips.

Course Title: Practicals in Programming II
Course Code: LBI.531
Total Lecture: 120

L	T	P	Cr
0	0	8	4

Learning Outcomes: Upon successfully completing this course, students will be able to “do something useful with Python”.

- Identify/characterize/define a numerical problem
- Design a program to solve the data parsing problem
- Create Time series code
- Read most of the advanced Python code

Course Content

- Introduction to Numpy and Pandas
- Visualizations with Matplotlib and Seaborn
- Statistical analysis to understand our data
- Data cleaning and normalization.
- Advanced Pandas models
- Hierarchical indexing
- Data Wrangling and transformations
- Advanced visualizations
- Introduction to Machine Learning
- Intro to Regressions- Linear and logistic regression using Scikit Learn
- Intro to Classification- Classification with K nearest Neighbours- Decision Trees and Random Forest

Transactional Modes: Laboratory based practicals; Problem solving; Self-learning.

Suggested Readings

- Core Python Programming (<http://corepython.com/>): Only available as a dead trees version, but if you like to have book to hold in your hands anyway, this is the best textbook style introduction out there. It starts from the beginning, but gets into the full language. Published in 2009, but still in print, with updated appendixes available for new language features. In the third edition, "the contents have been cleaned up and retrofitted w/Python 3 examples paired w/their 2.x friends."
- Dive Into Python 3 (<http://www.diveinto.org/python3/>): This book offers an introduction to Python aimed at the student who has experience programming in another language.
- Python for You and Me (<http://pymbook.readthedocs.org/en/latest/>): Simple and clear. This is a great book for absolute newcomers, or to keep as a quick reference as you get used to the language. The latest version is Python 3.
- Think Python (<http://greenteapress.com/thinkpython/>): Methodical and complete. This book offers a very "computer science"-style introduction to Python. It is really an intro to Python in the service of

Computer Science, though, so while helpful for the absolute newcomer, it isn't quite as "pythonic" as it might be.

- Python 101 (<http://www.blog.pythonlibrary.org/2014/06/03/python-101-book-published-today/>) Available as a reasonably priced ebook. This is a new one from a popular Blogger about Python. Lots of practical examples. Also available as a Kindle book: <http://www.amazon.com/Python-101-Michael-Driscoll-ebook/dp/BOOKQTFHNK>
- Problem Solving with Algorithms and Data Structures (<http://interactivepython.org/runestone/static/pythonds/index.html>) (Links to an external site.)
- Python Course (http://www.python-course.eu/python3_course.php) (Links to an external site.)

References for getting better, once you know the basics

- Python Essential Reference (<http://www.dabeaz.com/per.html>): The definitive reference for both Python and much of the standard library.
- Hitchhikers Guide to Python (<http://docs.python-guide.org/en/latest>): Under active development, and still somewhat incomplete, but there is good stuff.
- Writing Idiomatic Python (<https://www.jeffknupp.com/writing-idiomatic-python-ebook>): Focused on not just getting the code to work, but how to write it in a really "Pythonic" way.
- Fluent Python (<http://shop.oreilly.com/product/0636920032519.do>): All python3, and focused on getting the advanced details right. Good place to go once you've got the basics down.
- Python 3 Object Oriented Programming (<https://www.packtpub.com/application-development/python-3-object-oriented-programming>) (Links to an external site.): Nice book specifically about Object Oriented programming structure, and how to do it in Python. From local Author and founder of the Puget Sound Programming Python (PuPPy) meetup group, Dusty Phillips.

SEMESTER III

Course Title: Fundamental of Molecular Simulations

Course Code: CCC.554

Total Hours: 60

L	T	P	Cr
4	0	0	4

Learning Outcomes: At the end of the course, the students will be able to:

- learn the modelling of small to large molecular environments
- understand various force field for biomolecular simulation in details
- learn different methods for simulating large systems
- gain the knowledge about different molecular simulation techniques
- understand the dynamics of the structural transitions

Course Content

Unit 1**15 Hours**

Biomolecular Modeling and Structure - molecular modeling today: overview of problems, tools, and solution analysis, minitutorials in protein and nucleic acid structure. Techniques for Conformational Sampling- Monte Carlo, global optimization, etc.

Unit 2**15 Hours**

Molecular Mechanics: general features, bond stretching, angle bending, improper torsions, out of plane bending, cross terms, non-bonded interactions, Ramachandran diagram point charges, calculation of atomic charges, polarization, van der waals interactions, hydrogen bond interactions, Water models, Force field, all atoms force field and united atom force field.

Unit 3**15 Hours**

Energy minimization: Steepest descent, conjugate gradient – Derivatives, First order steepest decent and conjugate gradients. Second order derivatives Newton-Raphson, Minima, maxima saddle points and convergence criteria.-non derivatives minimization methods, the simplex, sequential univariate, Newton's equation of motion, equilibrium point, radial distribution function, pair correlation functions, MD methodology, periodic box, Solvent access, Equilibration, cut-offs.

Unit 4**15 Hours**

Simulation methods : algorithm for time dependence; leapfrog algorithm, Verlet algorithm, Boltzmann velocity, time steps, duration of the MD run, Starting structure, analysis of MD job, uses in drug designing, ligand protein interactions. Various methods of MD, Monte Carlo, systematic and random search methods. Differences between MD and MC, Energy, Pressure, Temperature, Temperature dynamics, simulation softwares. Various methods of MD, Monte Carlo, systematic and random search methods.

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. Andrew R. Leach Molecular Modelling Principles and applications . (2001) II ed . Prentice Hall.
2. Fenniri, H. "Combinatorial Chemistry – A practical approach", (2000) Oxford University Press, UK.
3. Lednicer, D. "Strategies for Organic Drug Discovery Synthesis and Design"; (1998) Wiley International Publishers.

1. Gordon, E.M. and Kerwin, J.F “Combinatorial chemistry and molecular diversity in drug discovery” (1998) Wiley-Liss Publishers.

Course Title: Molecular Simulations Lab

Course Code: CCC.555

Total Hours: 120

L	T	P	Cr
0	0	8	4

Learning Outcomes: At the end of the course, the students will be able to:

- learn the basics of Linux environment
- use the remote computing as a tool for high performance computation
- use different energy minimization techniques
- create molecular model from scratch, and high definition images using various graphics tools
- gain the practical in-hand experience of various modeling and classical simulation tools
- learn the use of different insilico techniques for biomolecular simulations

which will enhance their employability in their further potential carrers in academia and industry

Course Content

1. Advanced Visualization Software and 3D representations with VMD and Rasmol.
2. Coordinate generations and inter-conversions.
3. Secondary Structure Prediction.
4. Fold Recognition, *ab initio method*.
5. Homology based comparative protein modeling.
6. Energy minimizations and optimization.
7. Validation of models.
 - a. WHATIF
 - b. PROSA
 - c. PROCHECK
 - d. VERIFY 3D
2. Protein Structure Alignment.
3. Modeller
4. Structure based Drug Design
 - a. Molecular Docking
 - b. De Novo Ligand Design
 - c. Virtual Screening
5. Ligand based Drug Design
 - a. Pharmacophore Identification
 - b. QSAR
6. Molecular Dynamics with Gromacs
7. Binding Site Identification

Transactional Modes: Laboratory based practicals; Problem solving; Self-learning.

Suggested Readings:

1. Andrew R. Leach Molecular Modelling Principles and applications . (2001) II ed . Prentice Hall.
2. Fenniri, H. “Combinatorial Chemistry – A practical approach”,(2000) Oxford University Press, UK.
3. Lednicer, D. “Strategies for Organic Drug Discovery Synthesis and Design”; (1998) Wiley International Publishers.
4. Gordon, E.M. and Kerwin, J.F “Combinatorial chemistry and molecular diversity in drug discovery” (1998) Wiley-Liss Publishers.

Course Title: Essentials of Immunology**Course Code: CCC.521****Total Hours: 30**

L	T	P	Cr
2	0	0	2

Learning Outcomes: By the end of the course, students will have gained a fundamental understanding of immune system and to understand the concept of immune-based diseases as either a deficiency of components or excess activity as hypersensitivity. It is a fundamental subject, necessary for gaining insights into the application possibilities of immuno-informatics ranging from sub-cellular to large systems. The outcomes of the subject is to ensure that a student condensed the following

- Antigenicity
- Mechanisms of Antibody diversity
- MHC and HLA systems
- Inflammation and autoimmunity

Course Content**Unit: 1****8 Hours**

Immune system: The cells and organs of immune system. Recognition of self and nonself, Humoral immunity-immunoglobulins, basic structure, classes and subclasses, structural and functional relationships, nature of antigen, antigen-antibody reaction

Unit: 2**8 Hours**

Molecular mechanisms of antibody diversity and Cellular immunity: Organization of genes coding for constant and variable regions of heavy chains and light chains. Mechanisms of antibody diversity, class switching. Complement system, their structure, functions and mechanisms of activation by classical, alternative

Unit: 3**6 Hours**

Structure and functions of Major Histocompatibility Complex (MHC) and Human Leukocyte Antigen (HLA) system, polymorphism, distribution, variation and their functions. Organization and rearrangement of T-cell receptor genes (TCR).

Unit: 4**8 Hours**

Immune System in Health and Diseases: Inflammation, hypersensitivity and autoimmunity, Immunity to microbes, immunity to tumors, AIDS and immunodeficiencies, hybridoma technology and vaccine development associated challenges for chronic and infectious diseases.

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings:

1. Kindt, T.J., Osborne, B.A. and Goldsby, R.A. (2007). *Kuby Immunology*. W.H. Freeman, USA.
2. Abbas. (2008). *Cellular and Molecular Immunology*. CBS Publishers & Distributors, India.
3. Charles, A. and Janeway, J.R. (1994). *Immunobiology: The immune system in health and disease*. Blackwell Publishing, USA.
4. Delves, P.J., Roitt, I.M. and Seamus, J.M. (2006). *Roitt's essential immunology (Series-Essentials)*. Blackwell Publishers, USA.
5. Elgert, K.D. (2009). *Immunology: Understanding the immune system*. Wiley-Blackwell, USA.
6. Paul, W.E. (1993). *Fundamental immunology*. Raven Press, SD, USA.
7. Sawhney, S.K. and Randhir, S. (2005). *Introductory practical biochemistry*. Alpha Science International Ltd. New Delhi, India.
8. Tizard. (2008). *Immunology: An Introduction*. Cengage Learning, Thompson, USA.

Course Title: M.Sc. Project I**Course Code: LBI.599****Invested Hours: 120**

L	T	P	Cr
0	0	0	4

Course Objective and Learning Outcomes: The objective of project part I would be to ensure that the student learns the nuances of the scientific research. Herein the student shall have to carry out the experiments to achieve the objectives as mentioned in the synopsis. The data collected as a

result of experiments must be meticulously analyzed in light of established scientific knowledge to arrive at cogent conclusions.

The Evaluation criteria shall be multifaceted as detailed below:

S.No.	Criteria	Marks allotted
Continuous Assessment		
1.	Review of literature and Bibliography	10
2.	Identification of gaps in knowledge	10
3.	Objective formulation	15
4.	Methodology	15
5.	Continuous evaluation of student by guide	30
Research Presentation		
6.	Presentation	20
	Total	100*

The final presentation shall be evaluated by a three membered committee consisting of

- a. HOD/OHOD of the department
- b. VC nominee
- c. Supervisor (and Co-supervisor if applicable)

***Evaluation Criteria:**

S or Satisfactory: ≥ 60

U or Unsatisfactory: < 60

Transactional Modes: Laboratory based practicals; Problem solving; Self-learning.

Course Title: Data Mining and Machine learning

Course Code: LBI.557

Total Lecture: 60

L	T	P	Cr
4	0	0	4

Learning Outcomes: On completion of the course the student should be able to:

- learn the data cleaning, cross-validation, and application of regression analysis
- gain knowledge about distance matrices, various methods of clustering as well as dimensionality reduction
- apply several techniques for information retrieval and text mining

Course Content

Unit 1

8 Hours

Introduction: Overview of Machine Learning field with intro to statistics Data Cleaning, imputation, cross-validation, and interpreting results Probability and Statistics Regression

Unit 2**14 Hours**

Unsupervised Methods: Clustering: Distance Metrics, K-Means, leader, Jarvis-Patrick, hierarchical clustering; (The students should note that the correlation of gene expression data to biological process and computational analysis tools involves many clustering techniques) Clustering: Self-organized maps, EM-algorithm; Dimensionality Reduction: PCA, LDA, Sammon's

Unit 3**20 Hours**

Supervised Methods: Classification: K-NN, naïve Bayes, decision trees, boosting and bagging; Classification: Ensemble methods, random Forests; Support vector machines Neural networks; Introduction to Deep learning

Unit 4**18 Hours**

Application Areas: Information retrieval and text mining, and n-grams; Recommendation systems; Outlier detection

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. Data Mining: Concepts and Techniques, Third Edition by Han, Kamber, and Pei, 2011.
2. Pattern Recognition and Machine Learning by Christopher Bishop; 2007.
3. Applied Predictive Modeling by Max Kuhn and Kjell Johnson; 2013.
4. An Introduction to Statistical Learning and Applications in R by James, Witten, Hastie, Tibshirani; 2014.
5. Python for Data Analysis by Wes McKinney; 2013.

Course Title: Practicals in Data mining and Machine learning

Course Code: LBI.558

Total Lecture: 90

L	T	P	Cr
0	0	6	3

Learning Outcomes: On completion of this module, students should be able to:

- learn the issues involved in dealing with large amount of data
- deal with the principles of a number of machine learning algorithms
- implement and apply different machine learning algorithms on large data sets
- know how to analyse large data sets
- familiar with potential applications of different algorithms

- critically analyse and evaluate a research area

Course Content

Basics of Data Mining: dimensionality reduction
 Support Vector Machines: common kernel functions; implementation of kernels; non-parametric SVM-based clustering; regression; multiclass SVM
 Decision Trees and Decision Support Systems: classification tree algorithms (e.g., survival trees, clustering trees, linear splits, class prior, binary splits);
 Neural Networks: basic principles of self-organisation and supervised learning; representation aspects of neural networks, neural circuits, neurons; learning and neural coding

Transactional Modes: Laboratory based practicals; Problem solving; Self-learning.

Suggested Readings:

1. Leskovec, J & Rajaraman, A. & Ullman, J (2014). *Mining of Massive Datasets*.
2. Bishop, C. (2007). *Pattern Recognition and Machine Learning*.

Course Title: Genomic Data Analysis

Course Code: LBI.561

Total Lecture: 60

L	T	P	Cr
4	0	0	4

Learning Outcomes: On completion of this module, students should be able to:

- the issues involved in dealing with large amount of data
- analyse genome and transcriptome data including read mapping

Course Content

Unit 1

15 Hours

Methods for large-scale sequencing and its different applications. Read mapping and NGS data types, Assembly of raw sequence data to complete genomes. Mapping of raw sequence data to existing reference genomes.

Unit 2

15 Hours

Principles for annotation of genes and other biological information, annotation system, the problems with automatic annotation. human genomics and functional annotation.

Unit 3

15 Hours

Bioinformatic aspects on different methods to study the function, variation and evolution using large-scale sequencing of the genome.

Unit 4

15 Hours

Comparative analysis of gene expression data, Bioinformatic aspects of metagenomics

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. Richard C. Deonier, Simon Tavaré , Michael S. Waterman (2005) Computational Genome Analysis: An Introduction. Springer Science & Business Media.
2. Ju Han Kim (2018) Genome Data Analysis. Springer Verlag, Singapore
3. Peter N. Robinson, Rosario Michael Piro, Marten Jager (2017) Computational Exome and Genome Analysis. Chapman and Hall/CRC

Course Title: Genetic Data Analysis Lab

Course Code: LBI.562

Total Lecture: 90

L	T	P	Cr
0	0	6	3

Learning Outcomes: On completion of the course the student should be able to:

- Gain a advanced practical knowledge of big data analysis
- Emphasizes best practices such as quality control and differential display analysis

Course Content

- Vector Screening
- Raw read quality assessment
- Reference sequence indexing
- Reference based mapping
- Mapping quality assessment
- Mapping data visualization
- Heat map preparation

Transactional Modes: Laboratory based practicals; Problem solving; Self-learning.

Suggested Readings

1. Web source <https://landing.varstation.com/varstation-genomic-analysis>
2. Web source <https://www.expasy.org/genomics>
3. Melinda Mills, Nicola Barban, Felix C. Tropf (2020). An Introduction to Statistical Genetic Data Analysis. MIT Press

Course Title: Complex Algorithms in Bioinformatics

Course Code: LBI.563

L	T	P	Cr
2	0	0	2

Total Lecture: 30

Learning Outcomes: On completion of this module, students should be able to:

- The issues involved in dealing with large amount of data
- Gain a depp knowledge about the principles of a number of optimization algorithms
- Know how to apply HMM

Course Content

Unit 1

8 Hours

TSP; Weight matrices: Sequence weighting, pseudo count correction for low counts.

Unit 2

8 Hours

Monte Cralo, Gibbs sampling, and Psi-Blast.

Unit 3

8 Hours

Hidden Markov Models: Model construction, Viterbi decoding, and posterior decoding, and Baum Welsh HMM learning

Unit 4

6 Hours

Genetic Algorithm: Real world problems of optimization; BCO; ACO;

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. Mastering Algorithms with Perl; Oreilly
2. Algorithms by Robert Sedgewick
3. Art of Computer Programming, Volume 1: Fundamental Algorithms by Donald Ervin Knuth

Course Title: Computational Genomics and Proteomics

Course Code: LBI.576

Total Lecture: 30

L	T	P	Cr
2	0	0	2

Learning Outcomes: At the end of the course, the students will be able to:

- learn the importance of DNA-Protein Interactions During Transcription
- gain a deep knowledge about the role of bioinformatics-OMIM database, integrated genomic maps, gene expression profiling
- apply probabilistic modeling techniques for the building of transcriptional regulatory networks which will help them to use the techniques of computational proteomics in their further potential careers in academia and industry.

Course Content

Unit 1**7 Hours**

The Importance of DNA-Protein Interactions During Transcription. Initiation-Regulation of Transcription, Synthesis and Processing of the Proteome, The Role of tRNA in Protein Synthesis, The Role of the Ribosome in Protein Synthesis, Post-translational Processing of Proteins, Protein Degradation.

Unit 2**8 Hours**

Role of bioinformatics-OMIM database, integrated genomic maps, gene expression profiling; identification of SNPs, SNP database (DbSNP)

Unit 3**8 Hours**

DNA microarray: database and basic tools, Gene Expression Omnibus (GEO), ArrayExpress, SAGE databases, understanding of microarray data, normalizing microarray data, detecting differential gene expression,

Unit 4**7 Hours**

Only for yeasts: building predictive models of transcriptional regulatory networks using probabilistic modeling techniques.

Extra Reading Topics (Not in evaluatory content)

Genomes, Transcriptomes and Proteomes, The Human Genome and its Importance, Structure of the Eukaryotic and Prokaryotic Genome, the Repetitive DNA Content of Genomes. Mechanism of Genetic Action, Gene-protein relations, Genetic fine structure, Mutational sites Complementation, How Genomes Function, Accessing the Genome, Inside the Nucleus, Chromatin Modifications and Genome Expression, Assembly of the Transcription Initiation Complex, Metagenomics

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. Sándor Suhai (2002). Genomics and Proteomics. Springer US
2. CAMPBELL (2007). Discovering Genomics, Proteomics and Bioinformatics. Pearson Education
3. Richard P. Grant (2004). Computational Genomics: Theory and Application. Horizon Bioscience

Course Title: Introduction to Molecular Docking

Course Code: CCC.559

Total Lecture: 15

L	T	P	Cr
1	0	0	1

Learning Outcomes: At the end of the course, the students will be able to:

- demonstrate various force field for biomolecular modeling
- execute various molecular docking methods
- identify the dynamics of structural transitions which will help them to develop the molecular docking techniques in their further potential

careers in academia and industry.

Course Content

Unit 1 **3 Hours**

Biomolecular structure and molecular recognition,

Unit 2 **4 Hours**

3D structure determination and molecular modeling,

Unit 3 **4 Hours**

Protein structure prediction, force fields for molecular dynamics simulation,

Unit 4 **4 Hours**

Different molecular docking methods, software's used in molecular docking.

Transactional Modes: Lectures; Tutorials; Problem solving; Self-learning.

Suggested Readings

1. Schneider, Gisbert; Baringhaus, Karl-Heinz; Kubinyi, Hugo Molecular design : concepts and applications Weinheim: Wiley-VCH, c2008
2. Andrew R. Leach Molecular Modelling Principles and applications . (2001) II ed . Prentice Hall.
3. Lednicer, D. "Strategies for Organic Drug Discovery Synthesis and Design"; (1998) Wiley International Publishers.
4. http://autodock.scripps.edu/faqs-help/manual/autodock-4-2-user-guide/AutoDock4.2_UserGuide.pdf

SEMESTER IV

Course Title: Systems Biology

Course Code: LBI.571

Total Hours: 60

L	T	P	Cr
4	0	0	4

Learning Outcomes: At the end of the course, the students will be able to:

- identify the optimal structure for analyzing deep sequencing data
- discuss the main features of biological networks.
- use mathematical modelling to discuss relevant issues in Biology
- prepare a presentation based on a research paper in Systems Biology

Course Content

Unit 1**15 Hours**

Transcription networks, basic concepts, Auto-regulation, a network motif, the feed forward loop network motif

Unit 2**15 Hours**

Temporal programs and the global structure of transcription networks, Network motifs in developmental, signal-transduction and neuronal networks

Unit 3**15 Hours**

Robustness of protein circuits, the example of bacterial chemotaxis, Robust patterning in development

Unit 4**15 Hours**

Kinetic proofreading, optimal gene circuit design; Rules for gene regulation based on error minimization, Simplicity in biology

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. An Introduction to Systems Biology: Design Principles of Biological Circuits by Uri Alon, Chapman & Hall, ISBN 1-58488-642-0.
2. Hake, S. and Wilt, F. (2003). Principles of Developmental Biology. W.W. Norton and Company, New York, USA.
3. Hall, B.K. and Hallgrimsson, B. (2007). Strickberger's Evolution. Jones and Bartlett Publishers, India.
4. Lewin, R. (2004). Human Evolution - An Illustrated Introduction. Wiley-Blackwell, USA.

Course Title: Molecular Evolution**Course Code: LBI.524****Total Hours: 90**

L	T	P	Cr
4	0	0	4

Learning Outcomes: After completing the course the student should be able to

- describe evolutionary processes that give rise to variation in sequences and genomes and how these influence the architecture of the genome, contents and variation in base composition
- explain and justify different models for sequence and genome evolution
- choose, apply and evaluate bioinformatics methods for studying genetic variation in and between species.

Course Content**Unit 1****15 Hours**

Comparison of DNA sequences to calculate gene distance; Convergent and divergent evolution; Mutation Vs. Substitution-Rate of Molecular Evolution. Jukes Cantor Correction and evolutionary distance

Unit 2

15 Hours

Hardy-Weinberg equilibrium – Heterozygosity, gene frequency and heterozygosity; Loss of heterozygosity-mutant alleles-theta as the measure

Unit 3

15 Hours

Molecular clock- Concepts and significance-molecular mechanisms of molecular clock- Neutral theory -gene family organization.

Unit 4

15 Hours

Paralogy and Orthology- coordination expression in evolution-genome: content, structure and evolution. Molecular evolution of recently diverged species - Databases of Molecular evolution.

Transactional Modes: Lectures; Tutorials; Problem solving; Self-learning

Suggested Readings

1. Darwin, C.R. (1911). On the origin of species by means of natural Selection, or preservation of favoured races in the struggle for life. Hurst Publishers, UK.
2. Dawkins, R. (1996). The Blind Watchmaker, W.W. Norton & Company Jones and Bartlett Publishers.
3. Futuyma, D.J. (2009). Evolution. Sinauer Associates Inc. USA
4. Bromham, L. (2016). An Introduction to Molecular Evolution and phylogenetics. OUP Oxford.

Course Title: Cheminformatics

Course Code: LBI.573

Total Hours: 60

L	T	P	Cr
4	0	0	4

Learning outcomes:

On successful completion of this module, students should be able to: the students will obtain some knowledge and will get training in

- Data organization and search in chemical databases;
- QSAR and pharmacophores modelling;
- Chemical data visualization and analysis
- Virtual screening tools and efficiency assessments

Course Content

Unit I:

15 Hours

Cheminformatics as a theoretical chemistry discipline: definition, main concepts and areas of application. Representing chemical structures on computer. Molecular graphs. Connectivity tables. Adjacency and distance matrices. Linear representations SMILES and SMIRKS. Hashed fingerprints. Exchange formats for chemical structures (MOL, SDF,...) and reactions (RXN et RDF). Chemical Databases. Different types of searching structures in the databases: exact match, sub-structural, super-structural and by similarity.

Unit 2

15 Hours

Molecular descriptors. Definition and main requirements. Different types of descriptors: constitutional, topological indices, geometry-based, surface-based, substructural fragments, lipophilicity, etc. Development and validation of QSAR/QSPR models. Data preparation. Statistical parameters assessing models performance. Cross-validation. Models applicability domain. Ensemble modeling.

Unit 3

15 Hours

Molecular Interaction Fields. 3D QSAR. Molecular fields' similarity
Pharmacophore approach Pharmacophore features. Ligand- and structure-based pharmacophores. Merged and shared pharmacophores. Pharmacophore-based virtual screening

Unit 4

15 Hours

Chemical Space concept. Graph-based chemical space: scaffolds, frameworks and R-groups. Scaffold tree approach. Descriptor-based chemical space: distance and similarity metrics. Data visualization: Generative Topographic Mapping. Network-like similarity graphs. Activity landscapes. Bioisosteres. Activity cliffs.
Virtual screening workflow. Drug-likeness filters and structural alerts. Parameters of screening efficiency.

Transactional Modes: Lectures; Tutorials; Problem solving; Self-learning.

Suggested Readings

- A. Leach, V. Gillet "An Introduction to Chemoinformatics", Springer, 2007
- "Tutorials in Chemoinformatics", A. Varnek, Ed. , WILEY, 2017

Course Title: Bioinformatics for Transcriptomics and Metabolomics

Course Code: LBI.574

Total Hours: 15

L	T	P	Cr
1	0	0	1

Learning Outcomes: On completion of the course the student should be able to:

- Identify to process the raw read file generated by illumina sequencing.
- carry out the reference base expression estimation analysis
- learn alignment QC, visualization and differential expression studies

Course Content

Unit I **4 Hours**
Introduction to NGS techniques: Illumina (Solexa) sequencing, Roche 454 sequencing,

Unit II **4 Hours**
Ion torrent: Proton/PGM sequencing, SOLiD sequencing; sequence formats and quality.

Unit III **4 Hours**
Alignment of Next-Gen sequences to reference sequences, RNA-Seq analysis- Transcriptome mapping and differential expression: tools and pipeline.

Unit IV **3 Hours**
Introduction to metabolomics.

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. Shawn E. Levy and Richard M. Myers, "Advancements in Next-Generation Sequencing". Annu. Rev. Genom. Hum. Genet. 2016. 17:16.1-16.21
2. Beginner's Handbook of Next Generation Sequencing, Genohub
3. Next Generation Sequencing Methods and Protocols. Head, Steven R., Ordoukhanian, Phillip, Salomon, Daniel R

Course Title: Enriching Course for Bioinformatics – I

Course Code: LBI.572

Total Hours: 30

Learning outcomes:

L	T	P	Cr
2	0	0	2

Course Content

Unit I: **8 Hours**

Unit of replication, enzymes involved, replication origin and replication fork, fidelity of replication, DNA damage and repair mechanisms, homologous and site-specific recombination

Unit II: **7 Hours**

Cell Signalling: Signalling through G-protein coupled receptors, signal transduction pathways

Unit III: **8 Hours**

Zygote formation, cleavage, blastula formation, embryonic fields, gastrulation and formation of germ layers in animals

Unit IV:**7 Hours**

Codominance, incomplete dominance, pleiotropy, sex linkage, sex limited and sex influenced characters

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. Anthony, J.F., Miller, J.A., Suzuki, D.T., Richard, R.C., Gilbert, W.M. (1998). An introduction to Genetic Analysis. W.H. Freeman publication, USA.
2. Scott, F. and Gilbert, S.F. (2010). Developmental Biology. Sinauer Associates, Inc. USA.
3. Slack, J.M.W. (2005). Essential Developmental Biology, Wiley-Blackwell, USA.
4. Alberts, B., Bray, D., Lewis, J., Raff, M., Roberts, K. and Watson, J.D. (2010). Molecular Biology of the cell. Garland publishers, Oxford.
5. Celis, J.E. (2006). Cell biology: A laboratory handbook, Vol 1, 2, 3. Academic Press, UK.
6. Gupta, P.K. (2008). Cytology, Genetics and Evolution. Rastogi publications, Meerut, India

Course Title: Enriching Course for Bioinformatics – II**Course Code: LBI.575****Total Hours: 30**

L	T	P	Cr
2	0	0	2

Learning outcomes:**Course Content****Unit I:****7 Hours**

Conformation of proteins (Ramachandran plot, secondary structure, domains, motif and folds), Stability of proteins and nucleic acids.

Unit II:**8 Hours**

regulating the expression of phages, viruses, prokaryotic and eukaryotic genes, role of chromatin in gene expression and gene silencing

Unit III:**8 Hours**

Respiration and photorespiration – Citric acid cycle; plant mitochondrial electron transport and ATP synthesis;

Unit IV:

7 Hours

Photosynthesis: - Light harvesting complexes; mechanisms of electron transport.

Transactional Modes: Lecture; Tutorial; Problem solving; Self-learning.

Suggested Readings

1. Berg, J.M., Tymoczko, J.L. and Stryer, L. (2010). Biochemistry. W.H. Freeman & Company. USA.
2. Brown, T.A. (2006). Gene Cloning and DNA analysis: In Introduction. Blackwell Publishing Professional. USA.
3. Haynie, D.T. (2007). Biological thermodynamics. Cambridge University. UK.
4. Mathews, C.K., Van Holde, K.E. and Ahern, K.G. (2000). Biochemistry. Oxford University Press Inc. New York.
5. Nelson, D. and Cox, M.M. (2013). Lehninger Principles of Biochemistry. BI publications Pvt. Ltd. Chennai, India.

Course Title: M.Sc. Project II

Course Code: LBI.599

Total Hours: 240

L	T	P	Cr
0	0	0	8

Course Objective and Learning Outcomes: The objective of project part II would be to ensure that the student learns the nuances of the scientific research. Herein the student shall have to carry out the experiments to achieve the objectives as mentioned in the synopsis. The data collected as a result of experiments must be meticulously analyzed in light of established scientific knowledge to arrive at cogent conclusions.

The Evaluation criteria shall be multifaceted as detailed below:

S.No.	Criteria	Marks allotted
Continuous Assessment		
1.	Research work and Report writing	40
2.	Continuous evaluation of student by guide	30
Research Presentation		
3.	Presentation and defense of research work	30
	Total	100*

The final presentation shall be evaluated by a three membered committee consisting of

- a. HOD/OHOD of the department
- b. VC nominee
- c. Supervisor (and Co-supervisor if applicable)

***Evaluation Criteria:**

S or Satisfactory: ≥ 60

U or Unsatisfactory: < 60

Transactional Modes: Laboratory based practicals; Problem solving; Self-learning.

IQAC