Central University of Himachal Pradesh
(Established under Central Universities Act 2009
PO BOX: 21, DHARAMSHALA, DISTRICT KANGRA – 176215, HIMACHAL PRADESH
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List of the courses to be offered in Center of CBB (M.Sc. CBB) during monsoon semester of academic session 2019-2020

S.N.	Course Code	Course Name	Credits
		M. Sc. CBB Semester - I	
1	CBB 402	Modern Biology	2
2	CBB 403	Introduction to Statistics and Probability	2
3	CBB-431	Bioanalytical Techniques	2
4	CBB-418	Biomolecules	2
5	CBB 405	Basics of Bioinformatics	2
6	CBB 414	Practical course on Bioinformatics tools	2
7	CBB 411	Introduction PERL programming	2
8	CBB 413	Practical course on PERL	2
9		Skill Development	2
10		Human Making	2
		Total	**20**
		M. Sc. CBB Semester - III	
1	CBB 518	Elements of Systems Biology	4
2	CBB515	Computer Aided Drug Discovery	4
3	CBB-516	Molecular Evolution and Biodiversity	4
4	CBB 526	Next generation sequencing: methods and data analysis	2
5	CBB 525	Enzyme Kinetics	2
6	CBB 422	Basics of Microbiology and Immunology	2
7	CBB 428	Practical course on CADD	2
		Total	**20**

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SEMESTER I

Course Code: CBB 402
Course Name: Modern Biology
Instructor Name: Dr P. Aparoy
Credits Equivalent: 2 Credits (One credit is equivalent to 10 hours of lectures / organised classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives: The course is designed to:

- Introduce students the principles of modern biology
- Describe mechanisms that regulate biological systems, including: replication, transcription and translation.
- Acquaint the role of bioinformatics in evolution

Attendance Requirement:
Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student may not be permitted to appear in examination.

Evaluation Criteria:

1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment : 25%
   a) Class Test 10%
   b) Class Room Participation 10%
   c) Attendance 5%

Course Contents:

UNIT -I: Cellular and Molecular Basis of Life (4 Hours)

1. Cell structure and function
2. Molecular composition and organization of cell
3. Interactions/ Bonds important in biological systems
4. Genetic basis of heredity and variations

UNIT -II: Structure and Function of Proteins (4 Hours)

1. Importance of proteins in biological system
2. Structure of amino acids and their classification
3. Structure of proteins
4. Enzymes, their classification and kinetics

UNIT -III: Structure and Function of Nucleic Acids (4 Hours)

1. Structures of DNA
2. Structure of RNA
3. Organization of the nucleic acids
4. Organelle genomes

UNIT -IV: Central Dogma of Biology (4 Hours)

1. DNA replication in prokaryotes
2. DNA replication in eukaryotes
3. Transcription
4. Translation

UNIT -V Gene Regulation and Developmental Biology (4 Hours)

1. Gene regulation in prokaryotes
2. Gene regulation in Eukaryotes
3. Introduction to Developmental biology
4. Gametogenesis, Fertilization, Organogenesis and Cell differentiation

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SEMESTER I

Course Code: CBB 403

Course Name: Introduction to Statistics and Probability

Instructor Name : Dr P. Aparoy

Credits Equivalent: 2
2 Credits (One credit is equivalent to 10 hours of lectures / organized classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives:
CBB-403 will introduce the students to the concepts and methods of statistics, covering topics such as data organization, data presentation, data analysis, probability, estimation and hypothesis testing.

Attendance Requirement:
Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student may not be permitted to appear in examination.

Evaluation Criteria:
1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment : 25%
    a) Class test: 10%
    b) Class room participation: 10%
    c) Attendance: 5%

Course Contents:

Unit-I: Frequency Distributions and Graphs (2 Hrs)

- Introduction to Statistics; Frequency Distributions; Dot Plots; Bar Charts or Bar Graphs; Histograms; Frequency Polygons; Stem-and-Leaf Displays or Plots; Time Series Graphs; Pie Graphs or Pie Charts; Pareto Charts

Unit-II: Numerical Measures (4Hrs)

- Measures of Central tendency:
  Mean, Median, Mode - Notation and Formulae, Mean, Median and Mode for grouped data, relative merits of Mean, Median and Mode
- Measures of Dispersion:
  Range, Semi-interquartile range, Standard Deviation and Variance; Empirical Rule: The normal curve, Percentile and Quartile, Detecting Outliers

Unit-III: Correlation and Regression (4 Hrs)

- Introduction to correlation; A numerical Index to Correlation; Pearson Product-Moment Correlation Coefficient; Interpretation of Correlation Coefficient: Explained and Unexplained Variation; Spearman Rank Correlation
- Introduction to Regression; Criterion for the Line of Best Fit; Another Measure of Ability to Predict: The Standard Error of Estimate

Unit-IV: Probability (5 Hrs)

- Introduction and Basic Concepts of Probability; Probability of Simple and Combined Events; Various Laws of Probability; Bayes' Theorem; Random Variables and their Distribution; Binomial Distribution; Normal Distribution; Interpreting Scores in Terms of *z* Score; Sampling Distribution; Central Limit Theorem

Unit-V: Introduction to Statistical Inference (5 Hrs)

- Principles of Hypothesis Testing; One and Two tailed tests; *z*-test; *t*-test; Chi-Square test; ANOVA

Reference Books

- Murray Spiegel, John Schiller, R. Alu Srinivasan, Debasree Goswami. (2017). Probability and Statistics, McGraw Hill Education; 3 edition
- Roger E. Kirk (2007) Statistics: An Introduction, Cengage Learning; 5th edition
- Neil A. Weiss (2012) Introductory Statistics , 9th edition

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SEMESTER I

Course Code: CBB431
Course Name : Bioanalytical Techniques
Course Instructor: Mr. Satpal

Credits Equivalent: **2 Credits**

2 Credits (One credit is equivalent to 10 hours of lectures / organized classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives: The course is designed to:

- Introduce students about the techniques used to study biochemical analysis of cellular structures and macromolecules
- Acquaintstudentstothebasicprinciplesofva riousimmunochemic altechniques
- Tou n derstandthetech niq uestomonitorhowthestructureanddynamicsofbiom oleculesenablesspecificbiologicalfunctions

Attendance Requirement :
Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75 % attendance is a must failing which a student may not be permitted to appear in examination.

Evalua tion Criteria :

1. MidTermExaminatio n :25%
2. EndTermExamination:50%
3. Continuous InternalAssessmen t:25%
    a. Assignment:10%
    b. ClassTest:5%
    c. Presentation:10%

Course Contents:

UNIT-1: Introduction to Centrifugation and Microscopy

- Basic principles of centrifugation and types of centrifuges
- Preparative and Analytical Centrifugation
- Light Microscope
- Stereomicroscope

UNIT-II : Mass Spectrometric Techniques

- lntroduction , Ionisation
- Mass analyzers, Detectors
- Structural Information by tandem mass spectrometry
- Analyzing protein complexes

UNIT-III: ElectrophoreticTechniques

- Introduction ,Electrophoresis of proteins
- Electrophoresis of proteins
- Electrophoresis of nucleic acids
- Electrophoresis of nucleicacids and capillaryelectrophoresis

UNIT-IV: Chromatographic Techniques

- Principle of chromatography
- Liquidchromatography and highperformance liquidchromatography
- Adsorption , Partition and Ion Exchangechrolnatography.
- Molecular exclusion, gasliquid and thinlayerchromatography

UNIT-V: Spectroscopic Techniques

- Introduction to Spectroscopic Techniques
- X-Ray Spectroscopy; applications
- Nuclear magnetic resonance spectroscopy; applications
- Circular Dichromism and Electron spin spectroscopy; application

Prescribed Text and Reference Books:

1 BiochemistryandMolecularBiology, 7th edition, Keith Wilson and John Walker

2) Fundamentals of Bioanalytical Techniques and Instrumentation, Ghosal & Srivastava,2009, published by Ashoke K.Ghosh.

3) Introduction to Biophysical Methods for Protein and Nucleic Acid Research, Jay A. Glasel, Murray P.Deutscher and Murray P. Deutscher, ISBN: 978-0-12-286230-4

4).Biophysical Techniques, Iain Campbell, 368pages, 16 February 2012.

Sr.No.	Journals articles (specific articles, Complete reference)
1	Spectroscopic Methods in Biochemistry -Principles and Applications,© Jorg H. Kleinschmidt WS 2000/ 2001
2	A review of chromatographic methods for the assessment of phospholipids in biological samples,2005; Brianna L Peterson and Brian S. Cummings, BIOMEDICAL CHROMATOGRAPHY, Biomed. Chromatogr. 20: 227-243 (2006)
3	An Introduction to Mass Spectrometry, 1998,Scott E. Van Bramer

Relevant Websites

Sr.No.	Web address	Salient Features
1	Journal of Biochemical and Biophysical Methods (http://www.sciencedirect.com/science/journal/0165022X)	Methodological aspects of biochemistry, biophysics, molecular genetics and cellular biology

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SEMESTER I

Course Code: CBB-418
Course Name: Biomolecules
Course Instructor: Mr. Satpal

Credits Equivalent: 2 Credits (One credit is equivalent to 10 hours of lectures / organized classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives: The course is designed to:

- Introduce students about the structure and function of Biomolecules.
- Study various forces responsible for their molecular structures.
- Study their role in body metabolism.

Attendance Requirement:
Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student may not be permitted to appear in examination

Evaluation Criteria:

1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment: 25%
    a) Presentation 10%
    b) Class Participation 10%
    c) Attendance 5%

Course Contents:

Unit-1: Water and its Property (4 Hours)

- Physiochemical properties of water
- Dissociation and Association constant, pI, pKa

- Ionization of water-Weak acids and Weak bases, Buffering in biological system
- Hesselberg-Henderson equation

.Unit-2: Carbohydrates (4 Hours)

- Structure and function of -Monosaccharides- disaccharides- oligosaccharides
- Structure and Biological functions of Homo and Heteropolysaccharides
- Biosynthesis and Degradation of Glucose and Glycogen
- Glycolipids and Peptidoglycans

Units-3: Proteins (4 Hours)

- Amino acid Structure and function
- Structural organization of proteins- Primary, Secondary , Tertiary and Quaternary,
- Ramachandran plot and super secondary structure
- Forces stabilizing protein structure and shape, Protein denaturation and folding

Units-4: Lipids (4 Hours)

- Lipids Classification- structure and properties
- Fatty acids- saturated and unsaturated fatty acids
- Phospholipids, Glycoplipids, Sphingolipids and Cholesterol
- Structure and biological role of prostaglandins, thromboxanes and leukotrienes

Units-5: Nucleic Acids (4 Hours)

- Structure and Function: Physical and Chemical properties of Nucleic acids
- Double helical model of DNA and Forces responsible for A, B and Z- DNA
- DNA denaturation and renaturation- hypochromicity- Tm
- Application of DNA microarray

Text Book:

1. Nelson.D.L, Cox. M. M. Lehninger's Principle of Biochemistry. 4th ed. Freeman, 2004
2. Murray. R.K, Granner.D.K, Mayes. P. A, Rodwell. V. W. Harper's Biochemistry. 27th ed. McGraw Hill, 2006.

Suggested Reading:

1. Dixon & Webb. Enzymes. 3rd ed. Longmans, 1979.
2. Berg.J.M, Tymoczko.J.L, Stryer, L. Biochemistry. 6 th ed. Freeman, 2006.
3. Adams. R.L, Knowler.J.Leader. D.P. Biochemistry of Nucleic Acids. Cambridge Univ. Press, 1998.

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SEMESTER I

Course Code: CBB 405
Course Name: Basics of Bioinformatics
Credits: 2
Credits Equivalent: 2 Credits (One credit is equivalent to 10 hours of lectures / organized classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)
Attendance Requirement:
Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student may not be permitted to appear in examination

Evaluation Criteria:
1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment: 25%
    a) Presentation 10%
    b) Class Participation 10%
    c) Attendance 5%

Course Contents:

UNIT - I: Introduction and Historical Background

- What is Bioinformatics, introduction.
- Historical developments and evolution of Bioinformatics.
- Importance of Bioinformatics in Life Sciences

UNIT - II: Biological Databases
- Introduction
- Primary and Secondary Databases
- Nucleotide Sequence Databases
- Protein Sequence Databases (Swissprot, Uniprot)

- SCOP, CATH and FSSP
- Information retrieval from databases

UNIT - III: Assessing Pair wise Sequence Similarity

- Types of alignment: Local and Global
- Scoring matrices
- BLAST – Types and how it works
- Comparing FASTA and BLAST

UNIT - IV: Sequence alignment: Local and global

- Needleman Wunsch and Smith Waterman algorithms
- Exercises on pair wise alignment

UNIT - V: Phylogenetic Analysis

- Concepts in Molecular Evolution
- Phylogenetic Trees and Dendrograms
- How to Construct a tree
- Methods in Phylogenetic reconstructions

Suggested Reading:

1. Bioinformatics: Sequence and Genome Analysis by David W. Mount.
2. Introduction to Bioinformatics by Arthur M Lesk.
3. Introduction to Bioinformatics by T K Attwood, D J Perry-Smith and Samiron Phukan.

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SEMESTER I

Course Code: CBB 411

Course Name: Introduction to PERL Programming

Course Instructor: Dr. Vikram Singh

Credits Equivalent: 2 Credits

(One credit is equivalent to 10 hours of lectures / organised classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives: Programming skills constitute the core part of the MSc curriculum on Computational Biology and Bioinformatics.

This course is designed to

1. Help students in developing logical skills.
2. Introduce them the basic syntax of PERL programming.

Co-requisite: CBB 413–Practical Course on PERL

Attendance Requirements:

Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student will not be permitted to appear in examination.

Evaluation Criteria:

1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment: 25%
    a) Class participation 5%
    b) Attendance 5%
    c) Class test 10%
    d) Assignment 5%

Course Contents

Unit 1: Introduction to programming and PERL data types (5 hours)

Introduction to programming languages, Machine level v/s high level languages.
Introduction to PERL, #!, Basic input/output variables. Usage of 'use strict' and 'use warning' pragma.
Scalar variables: Numeric and String operators.
Single and double quoted strings, backslash interpolation, substr function.
Lists and Arrays: Accessing elements of an array, Special array indices, Scalar and List context.
Array functions: push, pop, shift, unshift, join, split, splice, sort.
Hashes: Accessing elements of a hash.
Hash functions: keys, values, exists, defined, delete, each.

Unit 2: Control structures (4 hours)

Decision Making (Branching) Structures – if and if-else statements, Nested if-else statement, else-if ladder.
Looping Structures – for, for each, while, do-while, until and do-until statements, next, last, continue, exit, redo statements.

Unit 3: Input methods, File Operations and Randomization (3 hours)

Input from standard input, Input from the diamond operator. Chop and chomp operators.
To read, write, append, open and close files. Using pathnames and filenames.Usage of die function.
Generating random numbers and their applications in Biology.

Unit 4: Regular Expressions (4hours)

Matching with regular expressions. Matching with m//. Binding operator =~
Pattern matching, substitution operator, transliteration operator.
Regexp basics, modifiers, quantifiers, metacharacters.

Unit 5: References, Subroutines and Introduction to BioPERL (4 hours)

References, Two dimensional arrays in PERL.
Global and local variables. Subroutines – (i) Pass by Value, (ii) Pass by reference.
Writing modules, Creating and using BioPERL objects.

Text Books:

1. Schwartz *et al.*(2011), Learning PERL. O'Reilly
2. James Tisdall(2001), Beginning PERL for Bioinformatics. O'Reilly
3. James Tisdall(2007), Mastering PERL for Bioinformatics. O'Reilly

Additional Readings:

4. Christiansen*et al.*(2012), Programming PERL. O'Reilly

Following is a tentative list of programs that students are supposed learn coding themselves

1 Learning mathematical operators
   a. WAP to print the "hello world".
   b. WAP for the addition of two numbers
   c. WAP using other mathematical operators (-,*,/,% etc.)
2. Learning string operators
   a. WAP to describe the usage of \t, \n etc.
   b. WAP to illustrate the usage of a concatenation string operator
   c. WAP to demonstrate the usage of repetition string operator
   d. WAP to demonstrate the usage of length, reverse etc. operators
3. To calculate area and volume of basic objects
   a. WAP to calculate area of circle
   b. WAP to calculate volume of sphere
   c. WAP to calculate area and volume of square
   d. WAP to calculate area and volume of rectangle
   e. WAP to calculate area and volume of cube
4. To transcribe DNA into RNA using substitution operator and transliteration operator
5. To calculate the reverse complement of DNA sequence
6. To calculate the values in a series in iterative manner
   a. $1^2, 2^2, 3^2, 4^2, 5^2$….
   b. …
7. To calculate the sum of first n-terms of a given algebraic series
   a. $(1+x^2+x^3+------+x^n)$
   b. …
8. To calculate the factorial of a given number
9. To generate first n terms of Fibonacci series
10. To find which term is greater using ASCII code
11. To find out triplets of given DNA sequence using substr
12. To count the percentage of nucleotides in a given DNA sequence
13. To translate a DNA sequence into an amino acid sequence in all six reading frames
14. To map genetic code using hash.
15. To translate a given RNA sequence into its corresponding peptide.

16 Programs to print various 2-dimensional patterns using "only one" for loop
   a. for obtaining right triangle pattern
   b. for obtaining inverted right triangle pattern

   c. for the matrix patterns 11111

22222
33333
44444
55555

d. WAP to get the result $1+1^2=2$
$2+2^2=6$
$3+3^2=12$

$n+n^2=$_

17. To check if the given number is prime or not.
18. To check if the given string is palindrome or not
19. To print 2-dimentionsional pattern using “nested” for loop
    a. WAP to create a following matrix
        i. 12345
           12345
           12345

        ii. 1234
            2345
            3456
            4567

    b. WAP to create following pattern

        i. *
           **
           ***
           ****

        ii. ****
            ****
            ****
            ****

        iii. Equilateral triangle

20. To create a random DNA sequence using rand operator
21. To simulate DNA mutation i.e. insertion and deletion
    a. WAP to randomly remove a nucleotide from a DNA sequence
    b. WAP to randomly insert a nucleotide into a DNA sequence
22. To generate two random DNA sequences and find out the percentage identity between them
23. To read DNA sequence from a file and WAP to write DNA sequence into a file
24. Finding patterns in the DNA and protein sequences using various metacharacters (^,.,?,*,+,{},(),$,\,|)
25. Writing subroutines (Call by value)
    a. Addition

    b. Multiplication
    c. Subtraction etc.
    d. Factorial of given number
    e. Fibonacci series
26. Referencing and dereferencing of
    a. Scalar
    b. Array
27. Writing subroutine (Call by reference)
28. To construct and use a 2-D array
29. To design a simple module and use it in a program

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SEMESTER I

Course Code: CBB 413

Course Name: Practical course on PERL

Instructor: Dr. Vikram Singh

Credits Equivalent: 2 Credits
(One credit is equivalent to 20 hours of lectures / organised classroom activity / contact hours; 10 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 30 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives: This course is designed to give students an opportunity for implementing the theoretical understanding of PERL programming (learned in the course CBB 411) into the PERL scripts.
Upon successful completion of this course students will be able to apply the knowledge of PERL programming to develop the applications in Computational Biology and Bioinformatics.

Pre-/Co-requisite: CBB 411 -- Introduction to PERL Programming

Attendance Requirements:

Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student will not be permitted to appear in examination.

Evaluation Criteria:
1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment: 25%
    a) Class Test 10%
    b) Assignments 5%
    c) Home work 10%

Course Contents

Unit 1: Understanding PERL data types (Scalar, Array, Hash) and usage of mathematical and string operators. (8 hours)

- Using Mathematical operators (Addition, Subtraction, Multiplication, Division, Modulus operators)
- Using String operators (Concatenation, Repetition operators)
- To calculate Area and Volume of basic objects (circle, sphere, parallelogram cube etc.).
- Finding reverse complement of a DNA sequence.
- Transcription, Reverse Transcription.

Unit 2: Learning Control Structure (10hours)

- Counting nucleotides in the given DNA sequence.
- Translating a DNA sequence into an amino acid sequence in all six reading frames.
- To check if a given number is even, odd or prime. To generate first *n* terms of Fibonacci series.
- To calculate the factorial of a given number.
- Finding sum of first n terms of a given algebraic series.
- To check if the given number or string is palindrome.

Unit 3: Input Methods, File Operations and Randomization(6hours)

- Reading and writing DNA and/or protein data from/into a file.
- Generating random DNA, random protein sequence.
- Simulating DNA mutation.
- Finding % identity between two random DNA sequences.

Unit 4: Regular Expressions(8 hours)

- Finding simple motifs in DNA or protein sequences.
- Using regular expressions to find complex patterns in the DNA and protein sequences.
- Parsing FASTA files
- Parsing Genbank files.

Unit 5: References, Subroutines and introduction to BioPERL(8hours)

- Referencing and dereferencing of scalars and arrays
- Reading and writing a 2-dimensionl matrix in PERL
- Writing subroutines (pass by value and pass by reference) for the programs of units 1 and 2.
- Writing PERL modules

- Learning the usage of CPAN
- Creating simple BioPERL objects.

Text Books:

Schwartz *et al.* (2011), Learning PERL. O'Reilly

James Tisdall (2001), Beginning PERL for Bioinformatics. O'Reilly

James Tisdall (2007), Mastering PERL for Bioinformatics. O'Reilly

Additional Readings:

20. Christiansen *et al.* (2012), Programming PERL. O'Reilly

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SEMESTER III

Course Code: CBB 518
Course Name: Elements of Systems Biology
Instructor Name: Dr Vikram Singh
Credits Equivalent: 4 Credits

(One credit is equivalent to 10 hours of lectures / organised classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives: This course will be centered on (i) the theoretical and practical aspects of modeling in systems biology – both deterministic and stochastic and (ii) the study of biological networks. Students will become acquainted with the key concepts and computational approaches of both these fields.

"Systems Biology" finds its major application in the research field known as "Synthetic Biology" (aiming to design and realize modified or new biological parts). Students will also become familiar with necessary mathematical and computational concepts of Synthetic Biology.

Students having prior knowledge of any programming language will be encouraged to write their own codes for simulating and analyzing model biological systems.

Attendance Requirement:
Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student may not be permitted to appear in examination

Evaluation Criteria:
1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment: 25%
    a. Attendance: 5%
    b. Class-room participation: 5%
    c. Class test: 5%
    d. Presentation and assignment: 10%

Course Contents

Unit 1: Introductory interdisciplinary concepts (8 hours)

- Definition and scope of systems and synthetic biology. Introduction to biological complexity -- Self organization, Emergence, Chaos, Robustness.
- First-order systems: Fixed points and stability, Population growth.
- Bifurcations (with examples) in first order systems: Saddle node, Pitch fork, Transcritical.
- Basic notion of bifurcations in second order systems: Period doubling, Hopf.

Unit 2: Deterministic modelling in systems biology (8 hours)

- Chemical kinetics, Michaelis-Menten kinetics, Hill equations
- Feedback in gene regulation: positive, negative, mutual inhibition
- Deterministic methods of systems modelling (Euler and RK4), with numerical applications on

  a) Simple examples of autocatalysis, linear degradation etc.

  b) Examples from natural systems: Predator-Prey, p53-mdm2.

  c) Examples from synthetic systems: Brusselator, Repressilator.

Unit 3: Stochastic modelling in systems biology (8 hours)

- Introduction to noise in biological systems. Intrinsic vs. extrinsic noise. System behavior and role of noise.
- Stochastic Methods for modelling biological systems (Master equation, Gillespie's stochastic simulation algorithm)
- Application of Gillepsie's SSA on Brusselator, Predator-Prey and other simple examples.

Unit 4: Design principles of biological networks (8 hours)

- Introduction to networks: Hamiltonian path vs. Eulerian path; Basic terminology; Topology of genetic, metabolic and ecological networks.
- Network models: Erdös-Renyi, Small-world, Scale-free.
- Global Properties: Average path length, network diameter, centrality measures, clustering coefficients etc. Modular and hierarchical networks.
- Local Properties: Regulatory motifs and graphlets in networks. Motifs in TRNs: discussion on FFL, SIM and other motifs.

UNIT 5: Analysis of biological networks (8 Hours)

- Elementary graph algorithms: Breadth-first search, Depth-first search, Topological sort, Strongly connected components. Growing a minimum spanning tree.
- Finding shortest path: Single source shortest path, All pairs shortest paths
- Network clustering: Clique based clustering, Center based clustering
- Basics of flux balance analysis.

Text Books:

21. **Steven H. Strogatz (1994),** Nonlinear Dynamics and Chaos: With Applications to Physics, Biology, Chemistry, and Engineering. Perseus Books, Massachusetts.
22. **Szallasi *et al.* (2010),** System Modelling in Cellular Biology. MIT Press.
23. **Junker and Schreiber (2008),** Analysis of Biological Networks. Wiley-Interscience, New Jersy.

Additional Readings:

2 **Uri Alon (2006),** an Introduction to the Systems Biology. Chapman and Hall.
3 **Mark Newman (2010),** Networks: An Introduction. Oxford University Press.
4 **Klipp *et al.* (2009),** Systems Biology in Practice. Wiley-VCH.
5 **BO Palsson (2006),** Systems Biology. Cambridge University Press.
6 **Press *et al.* (2007),**Numerical Recipies in C. Cambridge University Press.
7 **Singh and Dhar (2015),** Systems and Synthetic Biology, Springer

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SEMESTER III

Course Code: CBB 515
Course Name: Computer Aided Drug Discovery
Course Instructor: Dr P. Aparoy
Credits Equivalent: 4 Credits (One credit is equivalent to 10 hours of lectures / organised classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)
Course Objectives:
This course will be centred on**:**

- When to use CADD methods in your research (and when not to).
- Which methods are best to use to solve your particular research problems.
- Structure Based and Ligand based drug design approaches and examples.
- Role of Scaffold Hopping in modern drug discovery

Attendance Requirement:
Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student may not be permitted to appear in examination.
Evaluation Criteria:

1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment : 25%
    a) Class room participation 5 %
    b) Assignments 5 %
    c) Class test 10 %
    d) Presentations 5 %

Course contents:
Unit –I: Introduction to Drug Discovery and Proteins **(5 classes)**

- Introduction : Drug Discovery process
- Differences between traditional and computational drug discovery
- Proteins: Amino acids; Levels of Protein Structure
- Anfinsen's experiment and dogma

Unit –II: Introduction to Molecular Modelling (**10 classes**)

- Force Field
- Intermolecular interactions
- Energy minimization; Local and global minima
- Types of energy minimization methods

Unit –III: Structure Based Drug Design **(10 classes)**

- Protein Structure Prediction; Homology modelling
- Docking and its applications : Various search algorithms and scoring functions
- *De novo* drug design methods
- Virtual screening and its applications
- Molecular Dynamics

Unit –IV: Ligand Based Drug Design **(10 classes)**

- QSAR
- Pharmacophore Modelling
- Pseudoreceptor Modelling
- Scaffold Hopping

Unit –V: Clinical Trials and Drug Discovery **(5 classes)**

- Success stories of CADD
- Clinical trials

Reference books:

- Andrew Leach (2009) Molecular Modelling: Principles and Applications, Pearson Education (ISBN-13: 9788131728604).
- Kenneth M. Merz, Dagmar Ringe, Charles H. Reynolds (2010) Drug Design: Structure- and Ligand-Based Approaches, Cambridge University Press (ISBN-13: 9780521887236)
- Lipkowitz, KB, Boyd, DB, Eds (1997) Reviews in Computational Chemistry; John Wiley & Sons, Inc.: Hoboken, NJ, USA (ISBN: 9780471192480)

Additional Readings

1. David L. Nelson, Michael M. Cox (2017) Lehninger Principles of Biochemistry 7th Edition, WH Freeman publisher

2. Laurie AT, Jackson RM. Methods for the prediction of protein-ligand binding sites for structure-based drug design and virtual ligand screening. Curr Protein Pept Sci. 2006 Oct; 7(5):395-406. Review. PubMed PMID: 17073692.
3. Krieger E, Nabuurs SB, Vriend G. Homology modeling. Methods Biochem Anal. 2003;44:509-23. Review. PubMed PMID: 12647402.
4. Dias R, de Azevedo WF Jr. Molecular docking algorithms. Curr Drug Targets. 2008 Dec;9(12):1040-7. Review. PubMed PMID: 19128213.
5. Oda A, Tsuchida K, Takakura T, Yamaotsu N, Hirono S. Comparison of consensus scoring strategies for evaluating computational models of protein-ligand complexes. J Chem Inf Model. 2006 Jan-Feb;46(1):380-91. PubMed PMID: 16426072.
6. Warren GL, Andrews CW, Capelli AM, Clarke B, LaLonde J, Lambert MH, Lindvall M, Nevins N, Semus SF, Senger S, Tedesco G, Wall ID, Woolven JM, Peishoff CE, Head MS. A critical assessment of docking programs and scoring functions. J Med Chem. 2006 Oct 5;49(20):5912-31. PubMed PMID: 17004707.
7. Bissantz C, Kuhn B, Stahl M. A medicinal chemist's guide to molecular interactions. J Med Chem 53 (2010) 5061-5084.
8. Sun H. Pharmacophore-based virtual screening. Curr Med Chem. 2008;15(10):1018-24. Review. PubMed PMID: 18393859.
9. Hans-Joachim Böhm, Alexander Flohr, Martin Stahl, Scaffold hopping, Drug Discovery Today: Technologies, Dec 2004; 1 (3) :217–24.

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SEMESTER III

Course Code: CBB 516

Course Name: Molecular Evolution and Biodiversity

Course Instructor:

Credits Equivalent: 4 Credits (One credit is equivalent to 10 hours of lectures / organized classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives: The course is designed to:

- Make students familiar with laws of genetics.
- Understand mechanism behind the process of molecular evolution.
- Study various techniques which are used to study genetic patterns and evolutionary history.
- Study genetic processes that result in biodiversity.

Attendance Requirement:

Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student may not be permitted to appear in examination

Evaluation Criteria:

1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment: 25%

a) Presentation 10%

b) Class Participation 10%

c) Attendance 5%

Course Content:

UNIT I: INTRODUCTION TO MOLECULAR EVOLUTION (8 hours)

Introduction to Molecular evolution: Meaning and importance of Molecular evolution, heredity and variation, Variations- nature and types, Evolution of new genes

Mendelian laws of inheritance

Exceptions in Mendel‘s laws:

Organization and structure of gene, evolution of Genetic code, Molecular clock

UNIT II: HISTORY AND DEVELOPMENT OF EVOLUTIONARY THEORY (8 Hours)

Neodarwinism: spontaneous mutation controversy, Natural selection and modes of selection:

Stabilizing and dispersing selections

Speciation and evolutionary forces involved in speciation

Levels of selection, Kin selection theory, Molecular phylogeny

UNIT III: EVOLUTION AT MOLECULAR LEVEL (8 Hours)

Mutation and its types: Point mutation, Gene duplication, Chromosomal rearrangement, polyploidy and aneuploidy

DNA Damage and Repair: Types of DNA Repair: Base Excision Repair Nucleotide Excision Repair, Mismatch Repair, Double Strand Break Repair

Recombination: Homologous recombination and Site specific recombination

UNIT IV: MOLECULAR EVOLUTION IN BACTERIAL PATHOGENS (8 Hours)

Molecular epidemiology of pathogenic bacteria, Bacterial structure in relation to pathogenicity, Colonization and invasion by pathogens

Endosymbiosis and lateral gene transfer, Transposition, Retropostion and Junk DNA

Strategies of genome evolution, gene acquisition

UNIT V: BIODIVERSITY (8 hours)

Biodiversity: Genetic, species and ecosystem diversity. Biodiversity at global and national levels.

Genetic variations, genetic drift, factors that affect genetic variations

Threats to biodiversity, Conservation of biodiversity

Biogeographic classification of India

PRESCRIBED TEXT AND REFERENCE BOOKS:

1. John H.Gillespie. (2004), Population genetics: A concise guide, (2nd edn), John Hopkins

2. P.Higgs and T.Atwood. (2005), Bioinformatics and Molecular Evolution, John Wiley and Sons

3. Molecular Biology of the gene (2004), Watson, Baker, Bell, Gann, Levine and Losick,(5th edn)

Additional Readings:

4. Purves, Sadava, Orians and Heller, Life-The Science of Biology (7th edn)

5. Bebjamin and Pierce (2005), Genetics, A Conceptual Approach (2nd edn)

6. D.C.Reanney Hicks and Smith. (1973), Molecular Evolution, Frontiers of Biology

7. Richard B. Primack. (2002). Essentials of Conservation Biology (3rd edition)

8. Eldon John Gardner, Michael J. Simmons, D. Peter Snustad. Principles of Genetics (8th edition)

9. T. A. Brown. (2010). Gene Cloning and DNA Analysis: An Introduction (6th edition)

10. T.A. Brown (2002). Genomes 2, BIOS scientific Publishers

Journal Articles

11. Evolution of *Mycobacterium tuberculosis* (2013). *Adv Exp Med Biol.*; 783:81-91.

12. Genomic fluidity and pathogenic bacteria: applications in diagnostics, epidemiology and intervention (2008). *Nat Rev Microbiol.* 6(5): 387-94.

13. *Mycobacterium leprae*: genes, pseudogenes and genetic diversity (2011). *Future Microbiol* 6(1): 57–71. Doi: 10.2217/fmb.10.153

14. Studying Genomes Through the Aeons: Protein Families, Pseudogenes and Proteome Evolution (2002). *Journal of Molecular Biology*.

15. Horizontal Gene Transfers in prokaryotes show differential preferences for metabolic and translational genes (2009). *BMC Evolutionary Biology*.

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SEMESTER III

Course code: CBB 526

Course Name: Next generation sequencing: methods and data analysis

Credit Equivalent: 2 Credits (One credit is equivalent to 10 hours of lectures / organised classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher - led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives: The course is designed to:

- Introduce students to the fundamental of DNA and RNA sequencing
- Introduce to high throughput sequencing (HTS) technologies and algorithms involved.
- Applications of HTS in biology

Attendance Requirements:

Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student will not be permitted to appear in examination.

Evaluation Criteria:

1.Mid Term Examination: 25%

2.End Term Examination: 50%

3.Continuous Internal Assessment: 25%

(a) Assignment: 10%

(b) Class test: 5%

(c) Presentation: 10%

Course Contents:

Unit-I: First generation sequencing technologies (4 hours)

- Introduction
- Maxam-Gilbert sequencing
- Sanger sequencing
- Limitations of first generation technologies

Unit-II: High Throughput Sequencing Technologies (HTS) (10 hours)

- Introduction to HTS
- Overview of HTS platforms
- Future sequencing technology
- Comparison of available HTS techniques
- NGS file formats
- NGS databases

Unit-III: Genome sequence assembly (8 hours)

- Reference based genome assembly
- *De novo* genome sequence assembly
- Challenges in genome assembly
- Single-End reads and Pair-End reads in assembly
- Data preprocessing methods and sequence read correction methods
- Assembly errors and evaluation of assembly methods

Unit-IV: Assembly algorithms (8 hours)

- The overlap graph approach
- De Bruijin graph approach
- Classification of *De Novo* assembly algorithms
- Greedy algorithms
- Overlap Layout Consensus (OLC) algorithms
- De Bruijin Graph-Based algorithms
- Comparison of algorithms

Unit-V: Application of HTS (10 hours)

- Comparative genomics
- Functional genomics
- Diagnostic and exome sequencing
- RNA-seq (transcriptomics) and ChIP-seq
- Disease gene identification
- Metagenomics and Microbiome studies
- Microarray and Metabolomics

TEXT BOOKS:

1. Masoudi-Nejad, Ali, Zahra Narimani, and Nazanin Hosseinkhan. *Next generation sequencing and sequence assembly: methodologies and algorithms*. Vol. 4. Springer Science & Business Media, 2013.

Other References (Review articles)

1. Hert, D. G., Fredlake, C. P., & Barron, A. E. (2008). Advantages and limitations of next-generation sequencing technologies: a comparison of electrophoresis and non-electrophoresis methods. *Electrophoresis*, *29*(23), 4618-4626.

2. Wang, Z., Gerstein, M., & Snyder, M. (2009). RNA-Seq: a revolutionary tool for transcriptomics. *Nature reviews genetics*, *10*(1), 57.

3. Werner, T. (2010). Next generation sequencing in functional genomics. *Briefings in bioinformatics*, *11*(5), 499-511.

4. Prakash, T., & Taylor, T. D. (2012). Functional assignment of metagenomic data: challenges and applications. *Briefings in bioinformatics*, *13*(6), 711-727.

5. Metzker, M. L. (2010). Sequencing technologies—the next generation. *Nature reviews genetics*, *11*(1),

31.

6. Compeau, P. E., Pevzner, P. A., & Tesler, G. (2011). How to apply de Bruijn graphs to genome assembly. *Nature biotechnology*, *29*(11), 987.

7. Reuter, J. A., Spacek, D. V., & Snyder, M. P. (2015). High-throughput sequencing technologies. *Molecular cell*, *58*(4), 586-597.

8. Cao, Y., Fanning, S., Proos, S., Jordan, K., & Srikumar, S. (2017). A review on the applications of next generation sequencing technologies as applied to food-related microbiome studies. *Frontiers in microbiology*, *8*, 1829.

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SEMESTER III

Course Code: CBB 525
Course Name: Enzyme Kinetics

Credits Equivalent: 2 Credits (One credit is equivalent to 10 hours of lectures / organised classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives: The course is designed to:

- Introduce students about the structure & function of enzymes
- Acquaint students to the basic principles of enzyme kinetics
- To understand the molecular mechanisms of enzyme catalysis
- To understand the enzyme inhibition and its types

Attendance Requirement:
Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student may not be permitted to appear in examination.

Evaluation Criteria:

1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment : 25%

a) Presentation 10%
b) Class Participation 10%
c) Attendance 5%

Course Contents:

UNIT -I: Introduction to Enzymes (4 Hours)

- Enzymes, Enzyme commission's system of classification and significance of EC number
- Mechanism of action of enzyme catalysis and factors affecting catalytic power and specificity
- Structure of Proteins
- Monomeric and Oligomeric Enzymes

UNIT -II: Introduction to bioenergetics, catalysis and kinetics (4 Hours)

- Concepts of bioenergetics
- Factors affecting rates of chemical reactions
- Kinetics of uncatalysed chemical reactions
- Kinetics of enzyme catalysed reactions

UNIT -III: Kinetics of Single substrate Enzyme Catalysed Reactions (4 Hours)

- Henri and Michaelis-Menten Equation; significance and its modification
- Lineweaver- Burk Plot, Eadie- Hofstee and Hanes Plot
- Eisenthal and Cornish- Bowden plot, Haldane relationship for reversible reactions
- Rapid Reaction Kinetics

UNIT -IV: Enzyme Inhibition (4 Hours)

- Reversible Inhibition: Competitive and Uncompetitive Inhibition
- Non-competitive Inhibition and Mixed Inhibition
- Partial Inhibition and Substrate Inhibition
- Allosteric Inhibition and Irreversible Inhibition

UNIT –V: Kinetics of Multi-Substrate Enzyme- Catalyzed Reactions (4 Hours)

- Ping-pong bi-bi, Random-order and Compulsory-order Mechanisms
- Steady State Kinetics
- Investigation of Reaction Mechanisms using Steady- State Methods
- Investigation of Reaction Mechanisms using Non Steady- State Methods

Prescribed Text Reference Books:

1).Understanding Enzymes,Trevor Palmer,Prentice Hall,4th Ed,1995
2. Biochemistry By Lubert Stryrer,3rd Ed.,1995,W.F. Freeman and Co., New York.
3. Enzyme Structure and Mechanisms, Alan Ferst,W.M. Freeman, New York,1985.

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SEMESTER III

Course Code: CBB 422
Course Name: Basics of Microbiology and Immunology

Credits Equivalent: 2
2 Credits (One credit is equivalent to 10 hours of lectures / organized classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives:
This introductory course will provide a broad overview of Immunology and basic concepts of Microbiology. The course will cover an introduction to the human immune system; bacteria & viruses and the diseases they cause.
As an introductory course, it emphasizes the description of molecular and cellular elements of the immune system, and their basic function This course is also designed to give the student insight into the fundamentals of microbiology with emphasis on its relation to human biology and disease.

Attendance Requirement:
Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student may not be permitted to appear in examination.

Evaluation Criteria:
1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment : 25%
a. Assignment: 10%
b. Presentation/Class room Participation: 10%
c. Attendance: 5%

Course Contents:
Unit I - Introduction to the Immune System (4 Hours)

- Overview of the Immune System
- Elements of Innate and Acquired Immunity
- Immunogens and Antigens
- Antibody Structure and Function

- Antigen-Antibody Interactions

Unit II - Antigen Recognition and B and T Cell Development (4 Hours)
- Biology of the B Lymphocyte
- Role of The MHC complex in The Immune Response
- Biology of the T Lymphocyte
- Activation and Function of T and B Cells

Unit III - The Immune System in Health And Disease (4 Hours)
- Cytokines
- Tolerance and Autoimmunity
- Immunodeficiency Disorders
- Transplantation

Unit IV – Bacteria (4 Hours)
- Bacterial Structure
- Mechanisms of Gene Transfer
- Mechanisms of Bacterial Pathogenesis
- Antibiotics and Resistance

Unit V – Viruses (4 Hours)
- Epidemiology and Control of Virus Infections
- Respiratory, Gastrointestinal and Sexually Transmitted Viruses
- Virus Diagnostic Methods

Reference Books:
4. Immunology: Janis Kuby, Cold W H Freeman & Co (Sd); 3rd edition (February 1997).
5. Microbiology: Lansing M. Prescott, McGraw-Hill Science/Engineering/Math; 8 edition (February 3, 2010)
6. Basic Immunology: Abul K. Abbas & Andrew H. Lichtman, 3rd Edition (January 29, 2010).

Further readings:
1. Color Atlas of Immunology, Gerd - Rudiger Burmester & Antonio Pezzutto, Thieme; 1 edition (December 2002).
2. Human Microbiology: Simon P. Hardy, Publisher: Taylor and Francis CRC ebook account; 1 edition (April 16, 2007).