CENTRAL UNIVERSITY OF HIMACHAL PRADESH

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: **Genes and Chromosomes**   **(3 Hours)**
- Chromosomal Elements
- DNA Super coiling
- Structure of Chromosomes

UNIT-II: Bioinformatics in Exploring Evolution   (3 Hours)

- Role of Sequence Alignments in Exploring Evolution
- Role of Three-Dimensional Structure in Exploring Evolution
- Introduction to Evolutionary Trees

UNIT -III: DNA metabolism   (5 Hours)

- DNA replication
- DNA repair
- DNA recombination

UNIT -IV: RNA metabolism   (5 Hours)
- DNA dependent synthesis
- RNA dependent synthesis
- RNA processing

UNIT -V: Protein metabolism   (4 Hours)

- Genetic code
- Protein synthesis
- Post translational modification

Prescribed Text Books:

1. Nelson & Cox, Lehninger. (2017). Principles of Biochemistry 7th edition, W. H. Freeman Publications
2. Jeremy M. Berg, Lubert Stryer, John L. Tymoczko, Gregory J. Gatto. (2015). Biochemistry 8th edition, W. H. Freeman Publications
3. U. Satyanarayana, U. Chakrapani. (2017) Biochemistry : 5th edition. Elsevier Health Sciences

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

SEMESTER I

CourseCode:CBB431

CourseName : 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
- Acquaintstudentstothebasicprinciplesofvariousimmunochemicaltechniques
- Tounderstandthetechniquestomonitorhowthestructureanddynamicsofbiomoleculesenablesspecificbiologicalfunctions

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. MidTermExamination :25%
2. EndTermExamination:50%
3. Continuous InternalAssessment: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

- Introduction , 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

CENTRAL UNIVERSITY OF HIMACHAL PRADESH

[Established under the Central Universities Act 2009]
PO Box: 21, Dharamshala, District Kangra - 176215 (HP)
www.cuhimachal.ac.in

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.

SEMESTER I

Course Code: CBB 405

Course Name: Basics of Bioinformatics

Course Instructor: Ms. Neha Chaudhary

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.

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. $(1+x^2+x^3+\text{------}+x^n)$
- 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

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