



# **St. PETER'S UNIVERSITY**

**St. Peter's Institute of Higher Education and Research**

**(Declared Under Section 3 of the UGC Act, 1956)**

**AVADI, CHENNAI – 600 054**

**TAMIL NADU**

**B.Sc. (BIO INFORMATICS)**

**Code No. - 323**

**(Effective From 2009 – 2010)**

**(Distance Education)**

**St. PETER'S INSTITUTE OF DISTANCE EDUCATION**

**Recognized by Distance Education Council and**

**Joint Committee of UGC – AICTE - DEC, New Delhi**

**(Ref. F. No. DEC/SPU/CHN/TN/Recog/09/14 dated 02.04.2009 and**

**Ref.F.No.DEC/Recog/2009/3169 dated 09.09.2009)**

**St. PETER'S UNIVERSITY**  
**St. PETER'S INSTITUTE OF DISTANCE EDUCATION**  
Chennai – 600 054.

**Code No. – 323**  
**B.Sc. (BIO INFORMATICS)**  
(Distance Education)

**Regulations and Syllabi**  
(Effective from 2009 – 2010)

**1. Eligibility:** Candidates who have passed the Higher Secondary Examination conducted by the Government of Tamilnadu with Mathematics as one of the subjects, or any other examination recognized as equivalent thereto are eligible for admission to Three Year B.Sc Programme in Bio Informatics.

**2. Duration:** Three Years.

**3. Medium:** English is the medium of instruction and examination.

**4. Methodology:** The methodology of distance education includes the supply of self-instructional study materials in print format and in CD, face-to-face instruction for theory and practicals for a limited period during week ends and on holidays, provision of virtual class in phased manner, dissemination of information over e-mail, Student – Support Service at various centres of the University, Continuous Assessment and End Assessment conducted by the University at various parts of India.

**5. Weightage for Continuous and End Assessment:** There is no weightage for Continuous Assessment unless the ratio is specifically mentioned in the scheme of Examinations. The End Assessment (EA) has 100% weightage.

**6. Credit System:** Credit system be followed with 36 credits for each Year and each credit is equivalent to 25 hours of effective study provided in the Time Table of the formal system.

## 7. Scheme of Examinations

### First Year

Code No.	Course Title	Credit	Marks	
			EA	Total
	<b>Theory</b>			
<b>109UTMT01</b>	<b>Tamil – I</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>109UHIT01</b>	<b>(or) Hindi – I</b>			
<b>109UEHT02</b>	<b>English - I</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>109UBIT03</b>	<b>Numerical Methods &amp; Biostatistics</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>109UBIT04</b>	<b>Bioinformatics Algorithms</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>109UBIT05</b>	<b>Allied – I Molecular Biology and Genetics</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>109UBIP01</b>	<b>Practical – I Molecular Biology and Genetics Lab</b>	<b>6</b>	<b>100</b>	<b>100</b>
	<b>Total</b>	<b>36</b>	<b>600</b>	<b>600</b>

### Second Year

Code No.	Course Title	Credit	Marks	
			EA	Total
	<b>Theory</b>			
<b>209UTMT01</b>	<b>Tamil – II</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>209UHIT01</b>	<b>(or) Hindi – II</b>			
<b>209UEHT02</b>	<b>English - II</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>209UBIT03</b>	<b>Graph Theory and System Biology</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>209UBIT04</b>	<b>Python for Bioinformatics</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>209UBIT05</b>	<b>Allied – II PERL Programming</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>209UBIP01</b>	<b>Practical – II Python for Bioinformatics Lab</b>	<b>6</b>	<b>100</b>	<b>100</b>
	<b>Total</b>	<b>36</b>	<b>600</b>	<b>600</b>

### Third Year

Code No.	Course Title	Credit	Marks	
	<b>Theory</b>		<b>EA</b>	<b>Total</b>
<b>309UBIT01</b>	<b>Medical Informatics</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>309UBIT02</b>	<b>Enzyme Engineering</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>309UBIT03</b>	<b>Microarray and Image Processing</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>309UBIT04</b>	<b>Web Programming for Bioinformatics</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>309UBIP01</b>	<b>Practical – III Medical Informatics Lab</b>	<b>6</b>	<b>100</b>	<b>100</b>
<b>309UBIP02</b>	<b>Practical – IV Enzyme Engineering &amp; Web Programming Lab</b>	<b>6</b>	<b>100</b>	<b>100</b>
	<b>Total</b>	<b>36</b>	<b>600</b>	<b>600</b>

**8. Passing Requirements:** The minimum pass mark (raw score) be 40% in End Assessment.

**9. Grading System:** Grading System on a 10 Point Scale be followed with 1 mark = 0.1 and the conversion of the Grade point as given below.

$$\begin{aligned}
 \text{Overall Grade Point Average (OGPA)} &= \frac{\text{Sum of Weighted Grade Points}}{\text{Total Credits}} \\
 &= \frac{\sum(EA) C}{\sum C}
 \end{aligned}$$

**The Overall Grade:** The Overall Grade and Classification of candidates be arrived at from the Overall Grade Point Average as stipulated in the following conversion Table.

<b>Grade</b>	<b>Over all Grade Point Average(OGPA)</b>	<b>Over all weighted Average marks</b>	<b>Classification</b>
0	9.0 to 10.0	90 to 100	First Class
A	8.0 to 8.9	80 to 89	First Class
B	7.0 to 7.9	70 to 79	First Class
C	6.0 to 6.9	60 to 69	First Class
D	5.0 to 5.9	50 to 59	Second Class
E	4.0 to 4.9	40 to 49	Third class
<b>F</b>	0.0 to 3.9	0 to 39	<b>Reappearance</b>

The Grade Sheets of all candidates provide particulars such as (1) Overall weighted Average Marks and (2) Overall Grade.

**10. Pattern of the Question Paper:** The question paper for the End Assessment will be set for three hours and for the maximum of 100 marks with following divisions and details.

**Part A:** 10 questions (with equal distribution to all the units in the syllabus). Each question carries 2 marks.

**Part B:** 5 questions with either or type (with equal distribution to all the units in the syllabus).

Each question carries 16 marks.

The total marks scored by the candidates will be reduced to the maximum prescribed in the Regulations.

## **11. Syllabus**

## **109UBIT03 - NUMERICAL METHODS AND BIostatISTICS**

### **Unit I: Iterative Methods and Solution of Simultaneous Equations**

Introduction, Newton's relations, Evaluation of polynomials, Solution of quadratic equation, Bisection method, Newton-Raphson method, Existence of solutions, Gauss-Seidel iteration method, Gauss-Jordan method, Gauss-Jordan Matrix inverse, Eigenvalues and Eigenvectors.

### **Unit II: Interpolation and Numerical Integration**

Introduction, linear interpolation, polynomial interpolation, Difference tables, Gregory-Newton interpolation, Trapezoidal rule, Simpson's rule, Newton's Three-eighths rule, Gaussian Quadrature

### **Unit III: Solution of Differential Equations**

Introduction, Euler's Method, Taylor's Method, Runge-Kutta Methods, Predictor Corrector Methods, Automatic Error Monitoring and Stability of solution

### **Unit IV: Distributions**

Frequency Distribution: Sampling, frequency distribution, measure of central tendency: mean, median and mode, measure of dispersion, moments: arithmetic mean, variance, skewness and kurtosis, Probability Distribution: probability, binomial distribution, Poisson distribution

### **Unit V: Curve Fitting and Correlation**

Linear least square fit, nonlinear fit, polynomial fit, coefficient of correlation, multiple correlation, partial correlation, rank correlation

### **Text Books**

1. E.Balagurusamy, "Computer Oriented Statistical and Numerical Methods", MacMillan series, Madurai (1988).
2. V.Rajaraman, Computer oriented numerical methods, Prentice-Hall publications, 2007.

### **Reference book**

1. M.K.Jain, S.R.K.Iyengar and R.K.Jain, Numerical methods for scientific and engineering computation, Third Edition, New Age International (1993)

## **109UBIT04 - BIOINFORMATICS ALGORITHMS**

### **Unit I**

Algorithms and Complexity: What is an algorithm-Biological algorithm versus computer algorithms-The change problem-Correct versus Incorrect algorithms-Recursive algorithm- Towers of Hanoi problem- Big O notation- Algorithm design techniques.

### **Unit II**

Exhaustive Search: Molecular Biology Primer- Branch and Bound Algorithm- Greedy Algorithm- Restriction Mapping- Impractical restriction mapping Algorithm- A practical restriction mapping Algorithm- Profiles-The motif finding problem-Search Trees.

### **Unit III**

Graph Algorithms: Introduction to Graphs- Directed Graphs-Undirected graphs-weighted and unweighted graphs- NP- Complete problem-Eulerian cycle-Hamiltonean cycle-Graphs and genetics- Shortest Superstring Problem-DNA array sequencing technique- Sequencing by Hybridization-SBH as a Hamiltonian path problem

### **Unit IV**

Combinatorial Pattern matching: Repeat finding-Hash tables- Exact pattern matching-Suffix trees-Heuristic similarity search Algorithms- Approximate Pattern matching-BLAST

### **Unit V**

Evolutionary trees-Distance based tree Reconstruction- Character based Tree Reconstruction. Reconstructing trees from additive matrices-Evolutionary trees and Hierarchical clustering

### **Textbook:**

1. Neil Jones & Pavel Pevzner An Introduction to Bioinformatics Algorithms, MIT Press, 2004.

### **Reference**

1. M. Waterman, "Introduction to Computational Biology: Maps, Sequences & Genomes", CRC Press, 1995.

## **109UBIT05 - MOLECULAR BIOLOGY AND GENETICS**

### **Unit I: Concepts of Genetics**

Science of genetics – objectives, terminologies, methods, Mendelian genetics, Linkage, crossing over and Mapping , Genetics of Bacteria and Bacteriophages,

### **Unit II: Application of genetics**

DNA mutation- types, repair and transposition, Genetics of populations, Genetics and evolution, Genetics and diseases: Cancer, HIV-AIDS

### **Unit III: Chromosome organization and replication**

DNA structure and chromosome organization,. DNA Replication Mechanism of DNA synthesis, Enzymes, origin and termination of replication, other replicative structures, Eukaryotic DNA replication. Different tools and techniques in molecular biology: Cloning, construction of DNA libraries, PCR

### **Unit III: Transcription**

Transcription: Central dogma, Prokaryotic and eukaryotic transcription, post-transcriptional modification - RNA splicing, ribozyme. RNA editing.

### **Unit IV: Translation**

Translation: Process of translation in prokaryotes and eukaryotes, post-translational modifications, inhibitors of protein synthesis.

### **Unit V: Regulation of gene expression**

Regulation of Gene Expression: Control in Bacteria and phages – Inducible and catabolite repression (Lac operon), Repressible and Attenuation ( Trp operon), Lytic and Lysogenic cycles in Phage  $\lambda$ . Control in Eukaryotes: Cis and trans regulatory elements, Chromatin in gene regulation, transcriptional control, translational control, RNA interference in medical applications

### **Text books**

1. David R Hyde, Genetic and Molecular Biology, Tata McGraw Hill Publications, New Delhi, 2010
2. David Friefelder, Molecular Biology, Narosa Publ. House. 2000

## **109UBIP01 - MOLECULAR BIOLOGY AND GENETICS LAB**

1. Exercises and problems in Mendelian Genetics
2. Exercises and problems in Linkage and mapping
3. Isolation of plasmid DNA
4. Isolation of genomic DNA – from bacteria, chloroplast and human samples
5. Spectrophotometric determination of Nucleic acid purity and concentration
6. Restriction enzyme digestion of DNA
7. Cloning: Preparation and transformation of competent E.coli cells
8. Agarose gel electrophoresis
9. Invitro amplification of DNA using PCR

## **209UBIT03 - GRAPH THEORY AND SYSTEM BIOLOGY**

### **UNIT I: Graph Theory**

Graphs-Graphs as models-connected graphs-k-connected graphs-2 connected graphsconnectivity of digraphs-k-connected and k-edge-connected graphs.

### **UNIT II: Basics of systems Biology**

Introduction - Basic concepts in system Biology - Metabolic Networks- Transcriptional Regulatory Networks- Signaling Networks.

### **UNIT III: Modeling algorithms**

Kinetic Modeling - Cellular Network reconstruction and Static Modeling - Construction and verification and verification of kinetic models- introduction to DBsolve - Enzyme Kinetics modeling.

### **UNIT IV: Modeling and simulation algorithms**

Kinetic Models of Biochemical Pathways -Modeling Biochemical network - Kinetic Models of Excitable Membranes and Synaptic Interactions, Stochastic Simulation of Cell Signaling Pathways

### **UNIT V: Software's application in systems Biology**

Statistical tools for gene expression analysis and system Biology- Software for modeling and simulation-The ERATO system biology work Bench, Cytoscape, Gepasi, and Cell Designer.

### **Text Books**

1. Bernhard Q. Palsson, Systems Biology Properties of reconstructed networks, Publisher- Cambridge University Press, 2009
2. Oleg Demin and Igor Goryanin, Kinetic Modelling in Systems Biology, Publisher- CRC Press, 2009.

### **Reference Books**

1. Hiroaki Kitano, Foundations of Systems Biology, MIT Press, 2001
2. Douglas B.West, Introduction to Graph Theory, Prentice-Hall India, 1996

## **209UBIT04 - PYTHON FOR BIOINFORMATICS**

### **Unit I: Introduction**

Strings- Lists- Dictionaries-Tuples- Files- Numeric type basic- Numbers in Action- Number extensions- Dynamic typing interlude- Shared References.

### **Unit II: Python in Statistics and Probability**

Simple Statistics – average - standard deviation – distributions – normalization – multivariate statistics - Probabilities- Decisions from Distributions – correlations

### **Unit III: Sequence Alignment using Python**

Alphabets – matching sequences- perfect matches- insertions and deletions- rearrangements- Global Vs. Local alignments- sequence length- simple alignment- direct alignment-statistical alignment, Brute Force alignment

### **Unit IV: Dynamic Programming using Python**

Dynamic programming algorithm-the scoring matrix, the arrow matrix- extracting the Aligned sequences-Efficient programming- Global Versus Local alignments in Dynamic Programming- How Dynamic Programming can provide a good alignment.

### **Unit V: Microarray analysis using Python**

Gene expression array files-Raw data-GEL files- TIFF headers-the image file directory-reading the data- Spot finding – Intensity variations – block location-the coarse grid- fine-tuning the spot locations- spot measurement.

### **Text Books**

1. Jason Kinser "Python for bioinformatics" First edition, Jones and Bartlett Publishers, 2009
2. Mark Lutz "Learning Python", Fourth Edition, O'REILLY Publication,2009

### **Reference book**

1. Alex Martelli, David Ascher, Python cookbook, O'Reilly, 2002.

## **209UBIT05 - PERL Programming**

### **Unit I**

Intoduction-History of Perl –Perl Benefits –Installing Perl-Running Perl Programs- Using Perl on Windows and UNIX - Data types – Operators – variables -Variable Interpolation

### **Unit II**

Perl Control Structures - Deciding If, If-else if- else, For loops ,While loops , Until -Lists-simple list , Accessing list values- Arrays - Array functions – Push and Pop , Shift and unshift – Hashes.

### **Unit III**

Subroutines – subroutines for calculation, Reference to subroutine, Passing arrays and hashes to subroutines. Regular Expression – Working with regular expression. File Handling – Writing to Files

### **Unit IV**

Modules – Types , Perl standard modules. Object oriented Perl – Working with objects. Perl and Databases – Perl and DBM

### **Unit V**

Perl for Bioinformatics – Sequences and Strings – Representing Sequence data, store a DNA sequence, concatenating DNA fragments, Transcription. Motifs – Finding motifs, counting nucleotides. Genbank – Files and libraries. Protein Data Bank – files and folders, PDB files. Blast – String matching and homology, blast output files

### **Text Books**

1. Simon Cozens and Peter Wainwright, Beginning Perl, Shroff publishers, Apress reprint 2005
2. James Tisdall, Beginning Perl for Bioinformatics, O'Reilly Publications, Fourth Indian reprint 2005.

## **209UBIP01 - PYTHON FOR BIOINFORMATICS LAB**

- 1.** Write a program to open the SWISSPROT sequence and find the length of the sequence.
- 2.** Write a program to retrieve the PDB file from RCSB.
- 3.** Write a program to open a file and read the X,Y and Z coordinates using PDB.
- 4.** Write a program to calculate the bond length between two atoms using PDB.
- 5.** Write a program to converting DNA sequences to Protein sequences.
- 6.** Write a program to draw the plot using GnuPlot to find the average and deviations of ten samples.
- 7.** Write a program to align two sequences using Direct Alignment method.
- 8.** Write a program to align two sequences using Brute Force method.
- 9.** Write a program to find scoring matrix
- 10.** Write a program to find arrow matrix.
- 11.** Write a program to open the file for reading in a binary format using the function ReadRawFile.
- 12.** Write a program to read the data using the function ReadGEL.

## **309UBIT01 - MEDICAL INFORMATICS**

### **INIT I: Introduction**

Introduction- Hospital management and information system: functional area- pre-requisites integrated hospital information systems- health information system- and disaster management plan

### **UNITII: Knowledge based and Expert systems**

Artificial intelligence- expert systems- materials and methods- computer based patient Records computer assisted medical education, modern medical equipments (Digital X-ray etc.).

### **UNITIII: Modules**

Hospital Management and Information systems- structure and functions- computer assisted patient education, computer assisted patient surgery

### **UNIT IV: Computer assisted surgical techniques**

Three-dimensional imaging: limitations of endoscopy and imaging- benefits of virtual endoscopy- materials and methods- limitations- applications- merits and demerits- surgical simulation- virtual environment

### **UNIT V: Telecommunication based systems**

Tele-medicine- needs- materials and methods- Internet tele-medicine- controversial issues reliability- cost analysis- applications- tele-surgery- the Internet, Database of medical informatics

### **Text Books**

1. Mohan Bansal, Medical Informatics- a primer, Tata McGraw-Hill, 2003.
2. Charles P. Friedman, Jeremy C. (EDT) Wyatt, Evaluation Methods in Medical Informatics- Springer-Verlag, 1997.

### **Reference Books**

1. Hsinnchun Chen, Medical Informatics: Knowledge Management and Data Mining in Biomedicine, Springer, 2005.
2. F. T. De Dombal, Medical Informatics: The Essentials, Butterworth-Heinemann, 1996.

## **309UBIT02 - ENZYME ENGINEERING**

### **Unit I: Applications of Enzymes**

Classification of Enzymes; Purification and characterization of enzymes from natural sources Comparison of chemical and enzyme catalysis.

### **Unit II: Isolation of Enzymes:**

Extraction and Purification of Crude Enzyme extracts from plant, animal and microbial sources-some case studies; methods of characterization of enzymes; development of enzymatic assays.

### **Unit III: Mechanisms and Kinetics of Enzyme Action**

Mechanisms of Enzyme Action; Concept of active site and energetics of enzyme substrate complex formation; Specificity of enzyme action; Kinetics of single substrate reactions; turnover number; estimation of Michaelis-Menton parameters. Multi-substrate reaction mechanisms and kinetics.

### **UNIT IV: Enzyme Inhibition**

Types of Inhibition- kinetic models; Substrate and Product Inhibition; Allosteric regulation of enzymes; Deactivation kinetics.

### **Unit V: Enzyme Immobilization**

Physical and Chemical techniques for enzyme Immobilization - adsorption. Matrix entrapment, encapsulation. cross-linking. covalent binding - examples; Advantages and disadvantages of different Immobilization techniques. overview of applications of immobilized enzyme systems.

### **Text book**

1. Trevor palmer, Understanding Enzymes, East West Press, 2004

### **Reference**

1. Colin Ratledge and Bjorm Kristiansen , Basic Biotechnology, Third edition, Cambridge University Press, 2002

## **309UBIT03 - MICROARRAY AND IMAGE PROCESSING**

### **Unit I: DNA Microarray**

DNA array formats, DNA array readout methods, Gene expression profiling experiments: Problems, pitfalls, and solutions, Statistical analysis of array data: Inferring changes, Statistical analysis of array data: Dimensionality reduction, clustering, and regulatory regions

### **Unit II: Microarray Measurements to Analyses**

Generic Features of Microarray Technologies, Replicate Experiments, Reproducibility, and Noise, Prototypical Objectives and Questions in Microarray Analyses, Preprocessing: Filters and Normalization

### **Unit III: Genomic Data–Mining Techniques**

Hierarchy of Bioinformatics Algorithms Available in Functional Genomics, Data Reduction and Filtering, Self–Organizing Maps, Finding Genes That Split Sets, Phylogenetic–Type Trees, Relevance Networks, Determining the Significance of Findings, Genetic Networks

### **Unit IV: Image Analysis.**

Gridding, Segmentation, Intensity Extraction, Background Correction, Software, Foreground Intensity Extraction, Background Correction, Image Output File, Image Analysis for Affymetrix GeneChip™

### **Unit V: Quality Control**

Probe-Level Quality Control for Two-Color Arrays, Gene Level Quality Control for Two-Color Arrays, Array-Level Quality Control for Two-Color Arrays, Quality Control for GeneChip™ Arrays, Data Imputation.

### **Text books**

1. Pierre Baldi and g. Wesley Hatfield, DNA microarrays and gene expression From experiments to data analysis and modeling, Cambridge University press, New York, 2002
2. Richard M. Simon and Edward L. Korn, Design and Analysis of DNA Microarray Investigations, Springer Berlin Heidelberg New York. 2003
3. Isaac S. Kohane, Alvin Kho, Atul J. Butte, Microarrays for an Integrative Genomics, MIT Press, 2005.

### **Reference Book**

1. Mark Schena, Steen Knudsen, Guide to Analysis of DNA Microarray Data, 2nd Edition John Wiley & Sons, 2004

## **309UBIT04 - WEB PROGRAMMING FOR BIOINFORMATICS**

### **UNIT I: HTML**

Introduction – Web pages and html – overview of html – Working with text – formatting with html tags – physical and logical styles – setting fonts – headings – presenting and arranging text – working with images – graphic formats –using clip art - creating images – link and lists – creating hyperlinks - creating lists – creating a table.

### **UNIT II: Advanced HTML**

Working with frames – creating vertical and horizontal frames – working with style sheets – external and embedded style sheets –html document life cycle - advanced html – optimizing web page for internet explorer – embedding java script in html.

### **UNIT III: XML-I**

Introduction – xml – xml applications – xml document - life of an xml document – structuring data - examining the data - xmlizing the data – the advantages of xml format – attributes – empty tags - XSL

### **UNIT IV: XML -II**

Document type definition – document type declaration – validating against DTD – element declarations – entity declaration –internal general entities – external general entities – attribute declaration- declaring attributes in DTD's –declaring multiple attributes – attribute types – embedding non-xml data.

### **UNIT V: PERL AND CGI**

Introduction – Perl and CGI – setting up GCI on Unix – apache – starting apache server stopping apache server – writing CGI scripts – basic CGI – writing interactive CGI scripts.

### **Text Books**

1. Steven Holzner , HTML, Dreamtech press, Reprint Edition 2008.
2. Elliotte Rusty Harold, "XML Bible", Second Edition, IDG Books India (P) Ltd, 2003,

### **Reference Books**

1. Simon Cozens and Peter Wainwright, Beginning Perl, Shroff publishers, 2005
2. Reference book on HTML Complete, BPB publications, Second edition 2000.

### **309UBIP01 - MEDICAL INFORMATICS LAB**

1. Collect the patient data through internet.
2. Analysis the data
3. Collect the new forms of clinical information
4. Electronic Health Record analysis
5. Find the doctor using of information sources
6. How to apply Probability in health informatics data.
7. Use truth tables in medical informatics data
8. Apply predicate calculus in medical bioinformatics
9. Hospital Management and Information systems
10. Statistical hypothesis testing in Medical informatics

## **309UBIP02 - ENZYME ENGINEERING & WEB PROGRAMMING LAB**

1. Estimation of Acid Phosphatase from potato
2. Kinetic studies - Effect of pH on the activity of acid phosphatase
3. Kinetic studies - Effect of Temperature on the activity of acid phosphatase
4. Kinetic studies - Effect of substrate concentration on the activity of acid phosphatase
5. Kinetic studies - Effect of enzyme concentration on the activity of acid phosphatase
6. Estimation of Alkaline phosphatase from cucumber
7. Estimation of Urease from horse gram
8. Estimation of amylase from saliva
9. Estimation of serum SGPT (Kit method)
10. Estimation of serum SGOT (Kit method)
11. Isoenzyme analysis of Lactate Dehydrogenase
12. Enzyme immobilization- Entrapment in polyacrylamide gel

### **WEB PROGRAMMING LAB**

1. Working with HTML – A simple web page
2. Web page - Presenting and Arranging text.
3. Working with images.
4. Working with hyper link and lists.
5. Web page with tables.
6. Working with frames.
7. Creating simple web page using XML.
8. Usage of database in XML.
9. Working with XML and XSL
10. Web page with animations effects.
11. Web page with applet.
12. CGI scripting with Perl.

**Registrar**