।। सा विद्या या विमुक्तये ।।

स्वामी रामानंद तीर्थ मराठवाडा विद्यापीठ, नांदेड

"ज्ञानतीर्थ" परिसर, विष्णुपूरी, नांदेड - ४३१६०६ (महाराष्ट्र)

SWAMI RAMANAND TEERTH MARATHWADA UNIVERSITY NANDED

"Dnyanteerth", Vishnupuri, Nanded - 431606 Maharashtra State (INDIA)

Established on 17th September 1994 – Recognized by the UGC U/s 2(f) and 12(B), NAAC Re-accredited with 'A' Grade

ACADEMIC (1-BOARD OF STUDIES) SECTION

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संलग्नित महाविद्यालयांतील विज्ञान व तंत्रज्ञान विद्याशाखेतील पदवी स्तरावरील तृतीय वर्षाचे CBCS Pattern नुसारचे अभ्यासक्रम शैक्षणिक वर्ष २०२१–२२ पासून लागू करण्याबाबत.

प रि प त्र क

या परिपत्रकान्वये सर्व संबंधितांना कळविण्यात येते की, मा. विद्याशाखेने **दिनांक ३१ मे २०२१ रोजीच्या बैठकीतील केलेल्या शिफारशीप्रमाणे व दिनांक १२ जून २०२१ रोजी संपन्न झालेल्या ५१ व्या मा. विद्या परिषद बैठकीतील विषय क्र. २६/५१–२०२१**च्या ठरावानुसार प्रस्तुत विद्यापीठाच्या **संलग्नित महाविद्यालयांतील विज्ञान व तंत्रज्ञान विद्याशाखेतील पदवी स्तरावरील तृतीय वर्षाचे** खालील विषयांचे **C.B.C.S. (Choice Based Credit System) Pattern** नुसारचे अभ्यासक्रम शैक्षणिक वर्ष २०२१–२२ पासून लागू करण्यात येत आहेत.

1. B.Sc.-III Year-Biophysics
2. B.Sc.-III Year-Bioinformatics
3. B.Sc.-III Year-Biotechnology
4. B.Sc.-III Year-Biotechnology (Vocational)
5. B.Sc.-III Year-Botany
6. B.Sc.-III Year-Horticulture
7. B.Sc.-III Year-Agro Chemical Fertilizers
8. B.Sc.-III Year-Analytical Chemistry
9. B.Sc.-III Year-Biochemistry
10. B.Sc.-III Year-Chemistry
11. B.Sc.-III Year-Dyes & Drugs Chemistry
12. B.Sc.-III Year-Industrial Chemistry
13. B.C.A. (Bachelor of Computer Application)-III Year
14. B.I.T. (Bachelor of Information Technology)-III Year
15. B.Sc.-III Year-Computer Science
16. B.Sc.-III Year-Network Technology
17. B.Sc.-III Year-Computer Application (Optional)
18. B.Sc.-III Year-Computer Science (Optional)
19. B.Sc.-III Year-Information Technology (Optional)
20. B.Sc.-III Year-Software Engineering
21. B.Sc.-III Year-Dairy Science
22. B.Sc.-III Year-Electronics
23. B.Sc.-III Year-Environmental Science
24. B.Sc.-III Year-Fishery Science
25. B.Sc.-III Year-Geology
26. B. A./B.Sc.-III Year-Mathematics
27. B.Sc.-III Year-Microbiology
28. B.Sc.-III year Agricultural Microbiology
29. B.Sc.-III Year-Physics
30. B. A./B.Sc.-III Year Statistics
31. B.Sc.-III Year-Zoology

सदरील परिपत्रक व अभ्यासक्रम प्रस्तुत विद्यापीठाच्या **www.srtmun.ac.in** या संकेतस्थळावर उपलब्ध आहेत. तरी सदरील बाब ही सर्व संबंधितांच्या निदर्शनास आणून द्यावी, ही विनंती.

'ज्ञानतीर्थ' परिसर,
विष्णुपुरी, नांदेड – ४३१ ६०६.
जा.क्र.: शैक्षणिक–१/परिपत्रक/पदवी–सीबीसीएस अभ्यासक्रम/२०२१–२२/७५

दिनांक : १२.०७.२०२१.

स्वाक्षरित
सहा.कुलसचिव
शैक्षणिक (१–अभ्यासमंडळ) विभाग

प्रत माहिती व पुढील कार्यवाहीस्तव :
१) मा. कुलसचिव यांचे कार्यालय, प्रस्तुत विद्यापीठ.
२) मा. संचालक, परीक्षा व मूल्यमापन मंडळ यांचे कार्यालय, प्रस्तुत विद्यापीठ.
३) प्राचार्य, सर्व संबंधित संलग्नित महाविद्यालये, प्रस्तुत विद्यापीठ.
४) साहाय्यक कुलसचिव, पदव्युत्तर विभाग, प्रस्तुत विद्यापीठ.
५) उपकुलसचिव, पात्रता विभाग, प्रस्तुत विद्यापीठ.
६) सिस्टम एक्सपर्ट, शैक्षणिक विभाग, प्रस्तुत विद्यापीठ.
७) अधीक्षक, परिक्षा विभाग विज्ञान व तंत्रज्ञान विद्याशाखा प्रस्तुत विद्यापीठ.

Swami Ramanand Teerth Marathwada University, Nanded.

Choice Based Credit System (CBCS) Course Structure

Faculty of Science and Technology

B.Sc. Bioinformatics Third Year Effective from June 2021

Semester	Code	Title of the course	Hr/ Week	Type of course	Credit	Marks		Total
						ESA	CIA	
Vth		Environmental studies	4					
	CCBI-1E	Genetic engineering	4	CC	4	75	25	100
	CCBI-2E	Computational structural biology	4	CC	4	75	25	100
	CCBI-3E	Chemoinformatics	4	CC	4	75	25	100
	DSEBI-4E (Select any one)	(I) Programming in java (II) Biodiversity, agriculture, ecosystem and environment	4	DSE	4	75	25	100
	Lab course IX	Practical based on CCBI 1E + 2E	4	PR	4	100		100
	Lab course X	Practical based on CCBI 3E + DSEBT 4E	4	PR	4	100		100
				Total	24	500	100	600
Semester	**Code**	**Title of the course**	**Hr/ Week**	**Type of course**	**Credit**	**Marks**		**Total**
						ESA	**CIA**	
VIth	CCBI-1F	Concept of genomics	4	CC	4	75	25	100
	CCBI-2F	Concept of proteomics	4	CC	4	75	25	100
	CCBI-3F	Metabolomics	4	CC	4	75	25	100
	DSEBI-4F (Select any one)	(I) Programming with PHP (II) Drug and molecular modeling	4	DSE	4	75	25	100
	Lab course XI	Practical based on CCBI 1F + 2F	3 + 3	PR	4	100		100
	Lab course XII	Practical based on CCBI 3F + DSEBI-4F	3 + 3	PR	4	100		100
	Lab course XIII	Dissertation/ Project work/ Review writing	3	PR	2	50		50
				Total	26	550	100	650
CC- Core course, DSE- Discipline specific elective, ACE-Ability enhancement course, ESA-End semester assessment, CIA-Continuous internal assessment, PR-Practical, SEC-Skill enhancement course								
Total credits (Sem I + II + III+ IV + V +VI) = 24+24+26+26+24+26 = 150								

CCBI-1E Genetic Engineering

Maximum Marks : 75 **Hours : 45** **Credits: 4**

Salientfeatures: This course will help to understand concept genetic engineering and applications of r-DNA technology.

Utility of course: To understand basics of Genetic engineering techniques

Learning Objective: to improve the knowledge of genomic techniques

Prerequisites: Basic knowledge of biology and Genetic Engineering

Unit 1:- Principles of Gene Cloning

Essential tools for Gene cloning: Endonucleases: types & properties, DNA Ligases, Plasmids, Antibiotic résistance markers. **Vectors:** Plasmids (pBR322, pUC18/19), Bacteriophages (λ Phage, M13 Phage), Cosmids, Artificial Chromosomes, Ti plasmid. **Methods of Gene Transfer** - vector based and direct transfer of DNA. Gene Cloning Strategies. Markers and reporter genes in gene cloning.

Unit 2:- Techniques in Molecular Biology

Denaturation & Renaturation of DNA, Tm, GC content from Tm. Renaturation kinetics of DNA. Complexity of DNA. **Electrophoresis:** Agarose Gel Electrophoresis. **Blotting techniques**: Southern, Northern, Western Blotting and applications. **PCR:** Mechanism, types and applications. DNA Micro array principle & applications. **DNA Sequencing:** Sanger's and Maxam Gilbert's Method. Automated DNA sequencing.

Unit 3:- Library construction

Library construction: Genomic library, cDNA library. Nucleic Acid Probe. Chemical Synthesis of DNA. Autoradiography of DNA. **Screening of library** -Probe based direct and indirect methods.

Unit 4:- Applications of r-DNA technology

Agricultural applications (i) BT -Cotton, (ii) Transgenic maize, (iii) Golden rice etc. **Protein engineering:** Improvement in properties of proteins and enzymes.

Pharmaceutical Applications: (i) Recombinant hormones (ii) Vaccines (iii) Blood Clotting factors (v) Tissue Plasminogen Activator (vi) Erythropoietin (v) Human growth hormone. Concept of gene therapy.

Reference books:

1. Principles of Genome analysis and Genomics - Old & Primrose -Black well
2. Molecular biology of Gene – J .D Watson
3. From Genes to Clones - Winnacker - Panima
4. Molecular Biotechnology –Glick-ASM
5. ABC of Gene cloing - Wong-Springer
6. Genomes 3 - T.A.Brown -Garland Science
7. Gene cloning and DNA Analysis - T.A. Brown - Wiley- Blackwell
8. Text book of Biotechnology – U Satyanarayan –Book & Allied

Practical : Based on Syllabus

CCBI-2E Computational Structural Biology

Maximum Marks : 75 **Hours : 45** **Credits: 4**

Salient features: To understand basic Advance structural Biology

Utility of course: To uncover structure of biomolecules through computational approach & applied Bioinformatics

Learning Objective: to improve the knowledge of computational approach & applied Bioinformatics (Visualization and Manipulation of Protein Structures, Basics of Protein Structure Modeling — Structure validation & refinement).

Prerequisites: basic knowledge about Biomolecules, structural database and Molecular visualization tools

Unit 1: Structural data. Databases and structure analysis. Exploring the Database & searches on PDB and CSD, WHATIF.

Unit 2: Molecular visualization tools

Visualization of tertiary structures, quaternary structures, architectures and topologies of proteins and DNA using molecular visualization softwares such as RasMol, Cn3D, Chime, PyMOL etc.

Unit 3: Methods for prediction of secondary structure of proteins:

Prediction of secondary structures of proteins using at least 5 different methods with analysis and interpretation of the results. Comparison of the performance of the different methods for various classes of proteins.

Unit 4: Methods for prediction of tertiary structure of proteins

Methods for prediction tertiary structure of proteins along with analysis and interpretation of results.

Homology modeling: InsightII, Discovery Studio, SWISSMODEL, SWISSPDB Viewer.

Fold recognition methods: PHYRE, TOPITS, GenThreader (or other equivalent methods)

References:

1. Cesareni Giovanni, Gimona Mario, Sudol Marius, Yaffe Michael (Editors). Modular Protein Domains. Publisher: Weinheim Wiley-VCH. 2005. ISBN: 352730813X.

2. Höltje Hans-Dieter, Sippl Wolfgang, Rognan Didier, Folkers Gerd. Molecular Modeling: Basic Principles and Applications. Publisher: New York, Wiley -VCH. 2003. ISBN: 3527305890.

3. Webster David (Editor). Protein Structure Pre diction: Methods and Protocols
(Methods in Molecular Biology) Volume 143. Publisher: New J ersey Humana Press. 2000. ISBN: 0896036375.

4. Sternberg Michael J . E. Protein Structure Prediction: A Practical Approach. Publisher: USA, Oxford University Press. 1997. ISBN: 0199634953.

Practical : Based on Syllabus

CCBI-3E Chemoinformatics

Maximum Marks : 75 **Hours : 45** **Credits: 4**

Salient features: This subject will help to understand the basic concept of chemoinformatics.

Utility of course: To understand the chemoinformatics for drug designing.

Learning Objective: to improve the knowledge of chemical structure representation and chemoinformatics tools for drug discovery.

Prerequisites: Basic knowledge about chemical entities, chemical databases and drug.

Unit 1: Introduction

Chemoinformatics definition, scope of chemoinformatics, history of chemoinformatics, why to use informatics methods in chemistry?

Unit 2: Representations of chemical compounds

Introduction, **Computer representations of chemical structures:** Graph theoretic representations, Linear notations, Connection tables, Canonical representations of molecular structures.

2D structure databases. Reaction databases. The representation of patents and patent databases.

Representations of 3D molecular structures: Experimental 3D databases, 3D database Searching.

Unit 3: Molecular Descriptors

Introduction, **Descriptors calculated from the 2D Structure:** Simple counts, Physicochemical properties, Molar refractivity. **Structure searching**: Substructure Searching, Screening Methods, Similarity searching.

Unit 4: Drug and Drug -Targets

Drug: Definition, Drug–likeness, and compound filters, rule of five. **Lead Compound:** Definition, Natural and synthetic resources of lead compounds. **Drug targets:** Enzymes, receptors, carrier proteins, structural proteins, nucleic acids, etc.

Unit 5: Chemoinformatics tools for drug discovery

Combinatorial synthesis and combinatorial library. QSAR. 3D Pharmacophores. **Screening Methods:** High-throughput screening, Virtual Screening, Protein-ligand docking.

The Prediction of ADMET Properties, Toxicity Prediction.

Reference Books:

1. Handbook of Chemoinformatics, volume 1, by J ohn Gastiger, Thomas Engel, WILEYVCH pub 2003.
2. An Introduction to Chemoinformatics, by Andrew R. Leach & Valerie j. Gillet, Springer
3. Instant Notes in Me dicinal Chemistry, by G. Patrick, BIOS Scientific pub. 2001

Practical : Based on Syllabus

DSEBI-4E Elective (I) Programming in JAVA

Maximum Marks : 75 **Hours : 45** **Credits: 4**

Salient features: Understanding the basic concepts and techniques of java programming and develop skills of using recent software

Utility of course: the subject will help in skill ed in programming language.

Learning Objective: To enhance the knowledge of programming.

Prerequisites: Basic knowledge about programming.

Unit 1: An Introduction and overview of Java

A short history of java, Features of java, Comparison of Java and C++, Java Tools and Editors (Appletviewer, Jar, Jdb). JavaEnvironment. Types of Comments, Built In Data Types, Variables and Constants (Final Keyword Related to variables), Operators, Memory Allocation U sing new Operator., Output using println() method, Control Statements, Arrays, Simple J ava Program.

Unit 2: Objects and Classes

Defining Your Own Classes, methods and objects, using this keyword, constructors, types of constructors, constructor overloading , static variables and methods, access specifiers (private, protected and public), packages - creating, accessing and using packages, Garbage collection, finalize() method.

Unit 3: Inheritance and Interfaces

Inheritance Basics and Types of Inheritance, use e xtends keyword, Super class, Subclass and use of Super Keyword, Method Overriding, Use of final keyword related to method and class, Use of Abstract class, Defining and Implementing Interfaces, interface variables and interface methods.

Unit 4: Exception H andling

Dealing Errors, types of exception, exceptions handling using try and catch, using throws keyword, uses finally block.

Unit 5: Strings, Streams and Files

String class and String Buffer Class, Stream classes, Byte Stream classes, Character Stream Classes, Using the File class, Creation of files, Reading/Writing characters and bytes, Handling primitive data types.

Unit 6: Applet Programming with Graphical User Interface

Applet Life Cycle, Applet HTML Tags, Passing parameters to Applet, Repaint() method, User Interface Components with AWT in applet, Buttons and Labels, Checkboxes and Radio Buttons, Lists and Combo Boxes, Dialogs (Message, confirmation, input (like file selection).

Reference Books:

1. Complete reference Java by Herbert Schildt (5th editio n)
2. Java 2 programming black books, Steven Horlzner
3. Programming with Java , A primer ,Forth edition , By E. Balagurusamy
4. Java servlet Programming by Jason Hunter, O'Reilly
5. Core Java Volume -I-Fundamentals, Eighth Edition, Cay S. Horstmann, Gary Cornell,
6. Prentice Hall, Sun Microsystems Press.
7. Core Java Volume -II-Advanced Features, Eighth Edition, Cay S. Horstmann, Gary Cornell, Prentice Hall, Sun Microsystems Press.

Practical : Based on Syllabus

DSEBI-4E Elective (II) Biodiversity, Agriculture, Ecosystem andEnvironment

Maximum Marks : 75 **Hours : 45** **Credits: 4**

Unit 1: Biodiversity

Biodiversity: status, scope, types, monitoring and documentation. Major drivers of biodiversity change. Biodiversity management approaches. Uses of biodiversity. Loss of biodiversity. Metadatabases. Virtual libraries. Special interest networks. Biodiversity application software.

Unit 2: Agriculture

Crops: Comparative genomes of plant and model plants. Insect resistance. Improve nutritional quality. Grow drought resistant crops in poorer soils. Biodiversity of Indian medicinal plants. **Ecosystem:** Ecosystem structure, ecosystem function, energy flow and mineral cycling (C, N, P), primary production and decomposition, structure and function of some Indian ecosystems.

Unit 3: Conservation Biology

Principles of conservation, major approaches to management, Indian case studies on conservation/management strategy (Project Tiger, Biosphere reserves)

Unit 41: Environment

Waste cleanup: Superbugs and their concept, microbes and climate change, alternative energy sources and fuel cells. Biotechnological applications of microbes, Antibiotic resistance, Forensic analysis of microbes, The reality of bioweapon, Metagenomics.

Reference Books:

1. Tandon, P., Abrol, Y.P. and Kumaria, S. (2007). Biodiversity and itsSignificance. I. K. Internati onal Publishing House Pvt. Ltd, New Delhi.
2. Singh, J.S., Singh, S.P. and Gupta, S.R. (2006). Ecology, Environment andResource Conservation. Anamaya Publishers, New Delhi.

Practical : Based on Syllabus

CCBI-1F Concept of Genomics

Maximum Marks : 75 **Hours : 45** **Credits: 4**

Salient featur es: To introduce with basic Genomics and bioinformatics tools and methods to help student in order to conduct advanced rese arch in genomics.

Utility of course: To understand complex biological systems and computational research

Learning Objective: To enhance the knowledge of genomics

Prerequisites : Basic knowledge of genome and genomics databases

Unit 1: Introduction.
Genomics definition, History - Early sequencing efforts, DNA sequencing technology developed, Complete genomes, The "omics" revolution, C -Value paradox, Human Genome Project.

Unit 2: Genome Analysis
Sequencing - Shotgun sequencing, High -throughput sequencing, Illumina (Solexa) sequencing
Ion Torrent Assembly- Assembly approaches, Finishing. Annotation. Genome databases

Unit 3: Introduction to Research Areas of Genomics
Functional genomics, Structural genomics, comparative genomics Epigenomics, Metagenomics, Pharmacogenomics. **Study systems** - Viruses and bacteriophages genomics, Cyanobacteria genomics, Human genomics.

Unit 4: Applications of genomics
Biomarker discovery, gene expression, transfection, epigenetics, agriculture, Pharmaceuticals, genomic medicine, Synthetic biology and bioengineering, etc.

Reference Books:

1. Principles of Genome analysis and Genomics -Primrose and Twyman - Blackwell Publishing
2. Principles of Proteomics -R.M Twyman -BIOS advanced text
3. Functional Genomics -Stephen Hunt, Livesey - Oxford
4. Genetic Programming -W. Banzhaf, Nordin, Keller, Francone - Elsevier Bioinformatics: sequence and genome analysis by David Mount, cold springer harbour press, 2004.
5. Comparative genomics: empirical and analytical approaches to gene order dynamics, map alignment and the evolution of gene families by Sankoff, D. & Nadeau, J .H., Netherlands, Kluwer Academic Publishers, 2000.

Practical : Based on Syllabus

CCBI-2F Concept of Proteomics

Maximum Marks : 75 **Hours : 45** **Credits: 4**

Salient features: To introduce with basic proteomics and bioinformatics tools and methods to help student in order to conduct advanced research in proteomics.
Utility of course: To understand complex biological systems and computational research
Learning Objective: To enhance the knowledge of proteomics
Prerequisites : Basic knowledge of genome , proteome and genomics databases

Unit 1: Introduction.

Definition, Proteome, Different protein functions, What Is Proteomics?; Why Proteomics?; Applications of proteomics, **Protein Structure Basics -** Amino Acids, Peptide bond, Hierarchy, Determination of Protein Three -Dimensional Structure, Protein Structure Database.

Unit 2: Protein synthesis and Modifications
Translation overview, **Post translational modifications** - Protein processing in Endoplasmic Reticulum and Golgi apparatus, role of chaperons, The modifications such as proteolytic cleavage; formation of disulfide bonds; addition of phosphoryl, methyl, acetyl, or other groups onto certain amino acid residues; attachment of oligosaccharides or prosthetic groups to create mature proteins.

Unit 3: Protein separation and Identification
Extracting proteins from biological samples, **Protein Separations -** 1D- and 2D SDS - PAGE, Isoelectric Focusing (IEF), HPLC (reverse phase (RP), size exclusion, ion exchange, or affinity chromatography), identification using MS, MALDI-TOF etc.

Unit 4: Protein Analysis
Protein-protein interactions, Protein array, protein structure prediction Tools and servers.

Reference Books:

1. Principles of Genome analysis and Genomics -Primrose and Twyman - Blackwell Publishing
2. Introduction to proteomics: tools for the new biology by Liebler, D.C. & Yates, J .R.III, Humana Press
3. Protein Science -Arthur M. Lesk - Oxford
4. Proteomics: from protein sequence to function by Pennington, S. R. & Dunn,
5. M. J .: Viva Books Introduction to proteomics: tools for the new biology by Liebler, D.C. & Yates, J .R.III, New York. Humana Press, 2002.

Practical : Based on S yllabus

CCBI-3F Metabolomics

Maximum Marks : 75 **Hours : 45** **Credits: 4**

Salient features: To understand basic metabolomics

Utility of course: To uncover Biological pathway through computational approach & applied Bioinformatics

Learning Objective: to improve the knowledge of computational metabolomics, Metabolite separation and Detection , etc

Prerequisites : basic knowledge about Biomolecules , biological pathways database

Unit 1: Introduction to Metabolomics

Definition and concepts of metabolom, metabolites, catabolism, anabolism, metabolism, metabonomics. **Applications -**medical diagnosis, biomarker discovery, agriculture, toxicity assessment/toxicology, nutrigenomics etc.

Unit 2: Metabolic Pathways

Major Metabolic Pathways: Gluconeogenesis, Pentose phosphate pathway, Glycogen synthesis (Glycogenesis) and degradation (Glycogenolysis), Fatty acid synthesis, Amino acid catabolism, Purine nucleotide synthesis

Unit 3: Metabolite separation and Detection Methods

Separation -Gas chromatography, HPLC. **Detection -** Mass spectrometry (MS), MALDI, Nuclear magnetic resonance (NMR) spectroscopy. Statistical methods- XCMS, MZmine, MetAlign etc.

Unit 4: Computational metabolomics

Full Genome Annotation through knowledge of Metabolic Pathways Organism Specific Metabolic Pathways, Comparison of Metabolic Pathways

Reference Books:

1. Fundamentals of Bi ochemistry (2nd edition) by D., Voet, Voet, J .G. & Pratt,

C. W. J ohn Wiley & Sons, 2006.

2. Lehninger Principles of Biochemistry (4th edition) by D. L. Nelson & M. M. Cox, W. H. Freema n & Co, 2005.
3. Gene regulation and metabolism: postgenomic computational approaches. By Collado-Vides, J . & Hofestadt, R. Cambridge, The MIT Press, 2002.

Practical: Based on Syllabus

DSEBI-4F Elective (I) Programming with PHP

Maximum Marks : 75 **Hours : 45** **Credits: 4**

Salient features: Understanding the basic concepts and techniques of PHP programming and develop skills of using recent software.

Utility of course: The subject will help in skilled in programming language.

Learning Objective: To enhance the knowledge of programming.

Prerequisites: Basic knowledge about programming.

Unit 1: Introduction to PHP; Environment setup, Basic Syntax, Defining variable and constant; PHP Operator types, Decision making: If…else, If…elseif; Loop types, Looping with HTML.

Unit 2: PHP Arrays: Creation of array in PHP, Accessing array, Performing different operation in array, Numeric array, Associative array, Multidimensional array; **PHP Strings:** Searching & Replacing string, Formatting string, String related library functions.

Unit 3: Expression Handling, PHP web concepts; HTML Form with PHP, Using HTML Forms, Identifying Browser & Platform, Display Images Randomly, Capturing Form Data, Dealing with Multivalue filed, Browser Redirection, GET and POST methods.

Unit 4: File I/O; PHP Functions: What is a function, Define a function, Call by value and Call by reference, Recursive function, File include, require function; PHP File uploading: Generating File uploaded form, Creating an upload script; PHP login examples: Facebook login, Paypal login, etc.; PHP and MySQL; PHP and AJAX;

Reference Books:

1. "PHP: A Beginner's Guide" by Vikram Vaswani
2. "PHP Programming For Beginners: The Simple Guide to Learning PHP Fast!" by Tim Warren
3. "Beginning PHP and MySQL From Novice to Professional" by W Jason Gilmore
4. "Learning PHP 5" by David Sklar

Practical: Based on Syllabus

DSEBI-4F Elective (II) Drug and Molecular Modeling

Maximum Marks : 75 **Hours : 45** **Credits: 4**

Salient features: This subject will help to understand the basic concept of Drug and Molecular Modelling.

Utility of course: To understand the drug designing.

Learning Objective: To improve the knowledge of Molecular Modelling and drug designing.

Prerequisites: Basic knowledge about protein stucture, chemical databases and drug.

Unit 1: Classification of drugs, routes of drug administration. Absorption & Distribution of drugs. Role of kidney in drug interaction with biomolecules. Binding of drugs to plasma proteins.

Unit 2: Drug receptors: Drug –receptor interaction, Drug action not mediated by receptors. Structural based drug design, mechanism of their action. Lipinski's rule of 5, Clinical trials

Unit 3: Effect of drug doses on the rate of metabolism - mechanisms and importance of Phase I and Phase II biotransformation. Role of cytochrome p450. Enzyme inhibition strategies, enzyme induction and pharmacological activity, LD50 and IC50.

Unit 4: Principles & mode of action cancer and HIV chemotherapy agents and target sites for cancer and HIV chemotherapeutic agents. antimetabolites, antibod ies, plantibodies, radiation therapy and alkylating agents. PubChem database. Quantitative Structure Activity Relationship (QSAR). Types of descriptors

Reference Books:

1. Singh.H and Kapoor. V.K, 2002. Organic pharmaceutical chemistry. Vallabh prakashan pub lishers. New Delhi
2. Andrew, R., 1998. Molecular modeling: principles and application. Leach. Harlow.
3. Andrew, R., 1997. Molecular modeling: Basic principles and applications. Hans- X.
4. Leach A. R., "Molecular Modeling - Principles and applications", Prentice Hall, 2ndedition, 1996.
5. Paul S Charifson, "Practical application of CADD", Informa Health Care, 1997. PerunT.J . and C.L. Propst, "Computer Aided Drug Design", Informa Health Care, 1992.
6. Rastogi et al, "Bioinformatics – Genomics, proteomics, and drug disco very", PHI Publishing, 2008.

Practical: Based on Syllabus