ACADEMIC (1-BOARD OF STUDIES) SECTION

प्रस्तुत विद्यापीठाच्या उप–केंद्र, लातूर येथील संकुलातील विज्ञान व तंत्रज्ञान विद्याशाखेतील पदव्युत्तर स्तरावरील प्रथम वर्षाचे CBCS Pattern नुसारचे अभ्यासक्रम शैक्षणिक वर्ष २०१९–२० पासून लागू करण्याबाबत.

प रि प त्र क

या परिपत्रकान्वये सर्व संबंधितांना कळविण्यात येते की, **दिनांक ०८ जून २०१९ रोजी संपन्न झालेल्या ४४व्या मा. विद्या परिषद बैठकीतील ऐनवेळचा विषय क्र.११/४४–२०१९** च्या ठरावानुसार प्रस्तुत विद्यापीठाच्या **प्रस्तुत विद्यापीठाच्या उप–केंद्र, लातूर येथील संकुलातील विज्ञान व तंत्रज्ञान विद्याशाखेतील पदव्युत्तर स्तरावरील प्रथम वर्षाचे** खालील विषयांचे **C.B.C.S. (Choice Based Credit System) Pattern** नुसारचे अभ्यासक्रम शैक्षणिक वर्ष २०१९–२० पासून लागू करण्यात येत आहेत.

1. Bioinformatics
2. Computer Science

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

'ज्ञानतीर्थ' परिसर,
विष्णुपुरी, नांदेड – ४३१ ६०६.
जा.क्र.: शैक्षणिक–१/परिपत्रक/उप–केंद्र, लातूर संकुले/ पदव्युत्तर–
सीबीसीएस अभ्यासक्रम/२०१९–२०/४६६
दिनांक : ११.०७.२०१९.

स्वाक्षरित/–
उपकुलसचिव
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) मा. संचालक, सर्व संबंधित संकुले, स्वा.रा.ती.म. विद्यापीठ उप–केंद्र, औसा रोड, पेठ, लातूर.
४) साहाय्यक कुलसचिव, पदव्युत्तर विभाग, प्रस्तुत विद्यापीठ.
५) उपकुलसचिव, पात्रता विभाग, प्रस्तुत विद्यापीठ.
६) सिस्टम एक्सपर्ट, शैक्षणिक विभाग, प्रस्तुत विद्यापीठ.

Swami Ramanand Teerth Marathwada University Nanded
(NAAC Re-accredited with 'A' Grade)

School of Technology
Sub Centre, Latur

Syllabus of

M.Sc. Bioinformatics (2 years)

(Revised CBCS pattern)

Introduced from Academic Year 2019-20

School of Technology,
SRTMUN Sub-Centre, Latur

M.Sc. Bioinformatics

M.Sc. Bioinformatics (2years) degree builds the student on higher studies in Life Science and to become competent in the current race and development of new computational technologies. The duration of the study is of four semesters, which is normally completed in two years. The primary goal of this M.Sc. program is to increase the understanding of life science . What sets it apart from others is its approach and focus on developing and applying computationally intensive techniques to achieve higher goals in life science. Major inputs given in the curriculum are from the field of Structure analysis,Functional genomics,Structural genomics, Microarray,Genetic algorithm, Artificial neural network,Metabolic engineering

CBCSpattern and CGPA system

The School newly introduces its M.Sc. Bioinformatics program as per CBCS(Choice based credit system) pattern, in which choice, is given to the students under open electives and subject electives. The students can choose open electives from the same course or from other course of the same school or from other courses of other schools.

The Evaluation of performances of students for the course under Choice based Credit system (CBCS) is based on CGPA (Cumulative Grade Point Average) formulae. A Cumulative Grade Point Average is the mean Grade Point Average (GPA) from all academic terms within a given academic year, whereas the GPA may only refer to one term.

Eligibility and Fees

The eligibility of a candidate to take admission to M.Sc. (Bioinformatics) 2 years program is B.Sc. with any one subject from Physics, Chemistry, Botany, Agriculture, life science .More details on admission procedure and fee structure can be seen from the prospectus of the University.

Features of CBCS pattern

[1]   Master Degree would be of 100 Credits

[2]   Each semester shall consists of four theory courses and two practical courses and one foundation Course or seminar

[3]   Four theory courses = 16 Credits

[4]   two practical courses= 8 Credits

[5]   one foundation course /seminar=1 credit

[6]   Total credits per semester= 25

[7]   Total Credits of Four Semesters= 100

[8]   Total marks per semester= 625

[9]   Total marks for Master Degree program =2500

[10] One Credit = 25 marks , Two Credits = 50 Marks

[11] Four Credits = 100 Marks

[12] Each Theory Course/Practical course = 100 Marks

Internal Exam evaluation	External Exam evaluation
50 Marks = 2 Credits	50 Marks = 2 Credits

[13] Break up of internal marks evaluation for each Theory course (choose any two)

Home Assignments /Seminar / Mini Project/ E – Content Development / Examination/ Skill based activity or Concerned Teacher can adopt any other internal evaluation method as per requirement of course.	Total Marks 50 Marks = 2 Credits

[14] Practical Course = 100 Marks

Internal Exam evaluation	External Exam evaluation
50 Marks = 2 Credit	50 Marks = 2 Credits

[15] Break up of internal exam marks for Practical

Internal Exam (choose at least one from following)	Total Marks
Record Book */Experiments / Mini Project/ E – Content Development / Examination/ Skill based activity / Concern Teacher can adopt any other internal evaluation method as per requirement of course.	50 marks = 2 Credits

* Compulsory

Passing rules: As per the CGPA system of the University

Outline of M.Sc. Bioinformatics Syllabus (As per CBCS Pattern)

Sr. No	Course category	Course Code	Course Title	Internal credits	External credits	Total credits
First Semester						
1.	**Core**	BIM1-1	Mathematics for Bioinformatics	2	2	4
2	**Subjects**	BIM1-2	Matlab	2	2	4
3		BIM1-3	Practical Lab I (based on BIM1-2	2	2	4
Choose any one from BIM1-4 A and 1-4 B						
4	**Subject Elective**	BIM1-4 A	Biological Databases and sequence analysis	2	2	4
5		BIM1-4 B	Unix and C Programming	2	2	4
6		BIM1-5	Practical Lab II A / Lab II B	2	2	4
7	**Open Elective**	BIM1-6	Introduction to Bioinformatics / Inter school/Intra school / MOOC * (NPTEL / SWAYAM)	2	2	4
8	**Foundation course**	BIM1-7	Skill based activity **Genome analysis and annotation**	1	-	1
						25
Second Semester						
1	**Core**	BIM2-1	Structural Bioinformatics	2	2	4
2	**Subjects**	BIM2-2	Chemo informatics	2	2	4
3		BIM2-3	Practical Lab III	2	2	4
Choose any one from BIM2-4 A and 2-4 B						
4	**Elective Subjects**	BIM2-4 A	Genomics, Transcriptomics Proteomics	2	2	4
5		BIM2-4 B	Introduction to Database System	2	2	4
6		BIM2-5	Practical Lab IVA / Lab IV B	2	2	4
7	**Open Elective**	BIM2-6	Perl Programming and Python / Inter school /Intra school / MOOC * (NPTEL / SWAYAM)	2	2	4
8	**Foundation course**	BIM2-7	Skill based activity **Database designing using Oracle**	1	-	1
						25

Sr. No	Course category	Course Code	Paper Title	Internal credits	External credits	Total credits
Third Semester						
1.	**Core Subjects**	BIM3-1	Immunology and Immuno informatics	2	2	4
2		BIM3-2	Comparative Genomics	2	2	4
3		BIM3-3	Java Programming	2	2	4
4		BIM3-4	Practical Lab V	2	2	4
Choose any one from BIM3-5 A and BIM3-5 B						
5	**Elective subjects**	BIM3-5 A	Metabolic Engineering and Systems Biology	2	2	4
6		BIM3-5 B	Statistics and R	2	2	4
7		BIM3-6	Practical Lab VI A / Lab VI B	2	2	4
8	**Seminar**	BIM3-7	Seminar	1	-	1
						25
Fourth Semester						
1	**Core Subjects**	BIM4-1	Web Technology	2	2	4
2		BIM4-2	Modern Drug Design	2	2	4
3		BIM4-3	Project	-	4	4
4		BIM4-4	Practical Lab VII	2	2	4
Choose any one from BIM4-5 A and 4-5 B						
5	**Elective Subjects**	BIM4-5 A	Plant Genomics	2	2	4
6		BIM4-5 B	Advanced Molecular Phylogenetics	2	2	4
7		BIM4-6	Practical Lab VIII	2	2	4
8	**Seminar**	BIM4-7	Seminar*	1	-	1
						25

* Excluding syllabus

Note:

1. **MOOC (NPTEL / SWAYAM) course opts by the student should be excluding syllabus.**
2. **Student must provide the MOOC (NPTEL / SWAYAM) course certificate before theory examination of the concern semester.**
3. **Student must register the MOOC (NPTEL / SWAYAM) course within the semester or previous semester registration is permissible for next semester credit transfer.**

BIM1-1 Mathematics for Bioinformatics
Objectives :- This course will enable the students to:
achieve skills in mathematics that are essential for application in bioinformatics

Unit I Sets, Types of Sets, Subsets, Complement of Sets, union and Intersection of Sets, Difference of Sets, Demorgan's Law, Cartesian product of Sets. Basics of Probability, Permutation and Combination.

Unit II Measure of central tendency and dispersion: Mean, median, mode, range, standard deviation, variance

Unit III Correlation and Regression: Types, Karl-Pearson's correlation, Spearman's Rank correlation, Regression equation and fitting

Unit IV Probability Distribution: Basics of Binomial, Poisson and Normal distributions and their application in biology. Random Variable; Discrete and Continuous Probability Distribution, Probability mass function, probability Density function, Mathematical Expectation.

Unit V Matrices, Types of Matrices, Addition of matrices, Subtraction of matrices and Product of matrices. Properties of Matrix Multiplication. Transpose of Matrix, Symmetric and Skew-symmetric Matrices, Inverse of Matrix

Out come :- students will learn the applications of mathematics in Bioinformatics

BIM1-2 Matlab
Objectives :- This course will enable the students to:
achieve skills in MATLAB that are essential for application in bioinformatics

Unit I . Practicing MATLAB environment with simple exercises to familiarize Command Window, History, Workspace, Current Directory, Figure window, Edit window, Shortcuts, Help files.

Unit II Data types, Constants and Variables, Character constants, operators, Assignment statements.

Unit III . Control Structures: For loops, While, If control structures, Switch, Break, Continue statements. 4. Input-Output functions, Reading and Storing Data.

Unit IV Vectors and Matrices, commands to operate on vectors and matrices,

Unit V matrix Manipulations.

Out come :- Students will learn the applications of MATLAB in bioinformatics

References
1. R.K.Bansal, A.K.Goel, M.K.Sharma, "MATLAB and its Applications in Engineering", Pearson Education, 2012
1. Amos Gilat, "MATLAB-An Introduction with Applications", Wiley India, 2009.
2. Stephen.J.Chapman, "Programming in MATLAB for Engineers", Cengage Learning, 2011.

BIM1-3 Matlab
Objectives:- to learn the practical applications of MATLAB in Bioinformatics

1. Practicing MATLAB environment with simple exercises to familiarize
Command Window, History, Workspace, Current Directory, Figure window,
Edit window, Shortcuts, Help files.
2. Data types, Constants and Variables, Character constants, operators,
Assignment statements.
3. Control Structures: For loops, While, If control structures, Switch, Break,
Continue statements.
4. Input-Output functions, Reading and Storing Data.
5. Vectors and Matrices, commands to operate on vectors and matrices, matrix
Manipulations.
6. Arithmetic operations on Matrices, Relational operations on Matrices, Logical
operations on Matrices.
7. Polynomial Evaluation, Roots of Polynomial, Arithmetic operations on
Polynomials.
8. Graphics: 2D plots, Printing labels, Grid & Axes box, Text in plot, Bar and Pie
chart.

Outcome:- The students will learn the different Matlab tools

BIM1-4 A   Biological Databases and sequence analysis

Objectives:
This course will enable the students to: understand the nature of biological data and need for biological databases• to understand and explore major biomolecular sequence databases (organization and• contents); search and retrieve data from the databases using their respective search engines understand and appreciate the need and significance of sequence analysis and the• bioinformatics approaches for the same understand algorithms for sequence analysis• understand the application of methods for analysis of the biomolecular sequence data•

Unit I   Nature of biological data •   Overview of Bioinformatics resources on the web   o NCBI/EBI/EXPASY etc Biological Databases: Nucleic acid sequence databases

Unit II   o GenBank/EMBL/DDBJ   Biological Databases: Protein sequence databases o UniProtKB Overview of concepts in sequence analysis • Pairwise sequence alignment algorithms

Unit III o Needleman & Wunsch o Smith & waterman Scoring matrices for Nucleic acids and proteins   o MDM o BLOSUM o CSW Database Similarity Searches

Unit IV • o BLAST o FASTA Multiple sequence alignment o PRAS o CLUSTALW Derived databases

Unit V Prosite o BLOCKS o Pfam/Prodom o Recent derived database (To be decided by faculty member) Biological databases: structural databases o PDB o NDB

References
1. Baxevanis A.D., Davison D.B., Page R. D. M. & Petsko G.A. Current Protocols in Bioinformatics. New York, John Wiley & Sons Inc., 2004. ISBN: 0555015254
2. Korf Ian, Yandell Mark, Bedell Joseph. BLAST: an essential guide to the basic local alignment search tool. Shroff Publishers and Distributors Pvt. Ltd., 2003. ISBN: 8173665125.
3. Baxevanis Andreas D. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, 3rd Edition. Publisher: New York, John Wiley & Sons, Inc. 2002, ISBN: 9814126756
4. Teresa Attwood, Parry-Smith David J. Introduction to Bioinformatics. Publisher:

Pearson Education (Singapore) Pte.Ltd., 2001. ISBN:8178085070.
5. Mount David W.. Bioinformatics: Sequence and Genome Analysis. Publisher: Cold
Spring Harbor Laboratory Press; 1st edition 2001. ISBN: 08

Outcome :- students will get knowledge about the various biological database

BIM1-4 B   Unix and C Programming

Objectives: This course will enable the students to: make effective use of advanced Linux/Unix commands•
perform advanced tasks in parallel computing environment•

Unit I Using Vim, g-Vim editor

Unit II Advanced Unix commands

Unit III Grep, SED, AWK

Unit IV Shell scripting

Unit V Configuring services in Unix

Package management in Red hat like systems (RHEL, fedora etc.)

Outcome :- students will learn the UNIX commands

References
Neil Matthew, Stones Richard. Beginning Linux Programming 3rd Edition.
Publisher:• New Delhi Wiley Dreamtech India Pvt. Ltd. 2004. ISBN: 8126504846.

BIM1-5 Biological Databases and sequence analysis/Unix and C Programming
Objectives :- to learn the practical applications of sequence analysis in bioinformatics

1. Knowledge of different biological database
2. Protein and gene sequence data bases
3. (NCBI, DDBJ, EMBL, SWISS PROT, PIR)
4. Structure databases
5. (MMDB, PDB, FSSP, CATH, SCOP)
6. Pathway Databases
7. (KEGG, BRENDA, METACYC, ECOCYC)
8. Bibliographic database
9. (PUBMED, MEDLINE)
10. Sequence retrieval from biological database
11. Analysis of protein sequence using Expasy
12. Sequence similarity searching of nucleotide and protein sequences
13. Finding homologous sequences
14. Multiple sequence alignment
15. Dynamic programming method- local and global alignment
16. Gene prediction methods

    Unix
    a. Using Vim, g-Vim editor (2 assignments)
    b. Advanced Unix commands (3 assignments)
    c. Grep, SED, AWK (6 assignments)

      d. Shell scripting (2 assignments)
      e. Configuring services in Unix (2 assignments)
      f. Package management in Red hat like systems (RHEL, fedora etc.) (2 assignments

C programming
1. Interconverting the sequence from one databank format to the other eg.
2. GenBank format to FASTA format, FASTA to PIR format etc.
3. Determining the base composition in a nucleic acid sequence and amino acid
4. composition in a protein sequence.
5. Generating the complimentary sequence of a DNA sequence
6. Pattern search algorithms
7. Search for a specific oligonucleotide pattern (eg. GAACATCC) in a given
8. DNA sequence.
9. Find the position where a specific sequence say "GGTCCCGAC" will
10. hybridize a given DNA sequence.
11. Find the restriction enzyme cleavage sites eg. where PVUZ, ECORI etc. will
12. cut the DNA.
13. Locate palindromic sequence stretches in a DNA sequence.
14. Count the number of Open Reading frames (ORF's) in a DNA sequence.
15. Calculate the codon usage in a nucleic acid sequence.
16. Translate a DNA sequence into protein sequence in the forward and reverse
17. frames.
18. Implementation of the Needleman-Wunsch algorithm for pair wise alignment
19. and testing alignment score with randomized pairs of sequences also.
20. Numerical Techniques (4 assignments)
21. Basic Formalism, Methods for Solving Equations, Finding Eigen values &
    Eigenvectors

Outcome :- students will learn the sequence analysis tools and its applications in bioinformatics

BIM1-6 Introduction to Bioinformatics / Inter school/Intra school / MOOC * (NPTEL / SWAYAM)

Objective:- To understand the Definition and scope of Computational Biology and Bioinformatics.

Unit I Major Bioinformatics Resources: NCBI, EBI, ExPaSy. Pairwise sequence alignments: Sequence similarity, identity, and homology.

Unit II Global and local alignment, Dot plots for sequence comparison, Dynamic programming, BLAST and PSI-Blast, Application of Blast tool, Concept of Scoring matrix (PAM and BLOSUM).

Unit III Multiple sequence alignments: Progressive Alignment Algorithm (ClustalW), Application of multiple sequence alignment.

Unit IV Computational gene prediction methods, analysis of codon usage bias, computational prediction and analysis of regulatory sites

Unit V Schematic representations and structure visualization of proteins structure, Protein DataBank.

Outcome :- students will know the scope of the bioinformatics for the future technologies

References
1. Claverie, J.M. and Notredame C. 2003 Bioinformatics for Dummies. Wiley Editor.
2. Letovsky, S.I. 1999 Bioinformatics. Kluwer Academic Publishers.
3. Baldi, P. and Brunak, S. 2001 Bioinformatics: The machine learning approach, The MIT Press
4. Setubal, J. and Meidanis, J. 1996 Introduction to Computational Molecular Biology. PWS Publishing Co., Boston.
5. Lesk, A.M. 2005, 2nd edition, Introduction to Bioinformatics. Oxford University Press.
6. Fogel, G.B. and Corne, D.W., Evolutionary Computation in Bioinformatics.
7. Mount, D.W., Bioinformatics: 2001, Sequence and Genome Analysis. CSHL Press.
8. Durbin R., Eddy S., Krogh A. and Mithchison G. 2007 Biological Sequence Analysis, Cambridge

BIM1-7 Skill based activity
Genome analysis and annotation

SEMESTER II

BIM2-1 Structural Bioinformatics

Objectives: This course will enable the students to: understand the levels of structural organization of macromolecules and experimental• methods of structure determination know the approaches for structure analysis• acquire knowledge of various algorithms• & methods of structure prediction understand the principles of macromolecular interactions•

Unit I Macromolecular Structure (14)• Protein - Primary, Secondary, Supersecondary, Tertiary and Quaternary structure, Potential energy maps,

Unit II Ramachandran map, Nucleic acid – DNA and RNA, Carbohydrates o Co-ordinate systems Overview of experimental techniques to study macromolecular structures

Unit III Methods to study 3D structure: X-ray, NMR, Cryo-electronmicroscopy o Validation using Procheck, ProsaII Principles of protein folding and methods to study protein folding

Unit IV Macromolecular interactions (
Protein – Protein Protein – Nucleic acids Protein - carbohydrates Structure of Ribosome
Prediction of protein structure

Unit V secondary structure prediction methods First, second and third generation methods♣ o Tertiary structure prediction Homology modeling, fold recognition and ab initio methods♣

Outcome :- students will learn the different aspects of Structural bioinformatics

Referenecs
1. Forbes Burkowski. Structural bioinformatics: An algorithmic approach. Publisher: CRC• Press, 2009. ISBN: 9781584886839.
2. Drenth Jan. Principles of Protein X-Ray Crystallography. Publisher: Netherlands,• Springer Science. 2007. ISBN: 9780387333342.
3. Bourne Philip E., Weissig Helge. Structural Bioinformatics (Methods of Biochemical• Analysis, V. 44), 2003. Publisher: Wiley-Liss. ISBN: 0471202002. Höltje Hans-Dieter, Sippl Wolfgang, Rognan Didier, Folkers Gerd.
4. Molecular• Modeling: Basic Principles and Applications. Publisher: New York, Wiley-VCH. 2003. ISBN: 3527305890.
5. Leach, Andrew. Molecular Modelling: Principles and Applications. Publisher: Prentice• Hall. 2001. ISBN: 0582239338.
6. Friesner Richard A. Computational Methods for Protein Folding:advances in Chemical• Physics Volume 120 Kindle Edition. Publisher: New York, John Wiley & Sons. 2002. ISBN: 0471209554.
7. Heilmeyer L., Friedrich P. Protein Modules in Cellular Signalling. Publisher:• Amsterdam, IOS Press. 2001. ISBN: 1586031805.
8. Rhodes Gale.Crystallography Made Crystal Clear, Third Edition: A Guide for Users of• Macromolecular Models. Publisher: USA, Academic Press 2000 ISBN: 0125870728.
9. Branden ,Tooze John. Introduction to Protein Structure. Publisher: New York, Garland• Publishing Inc. 1999. ISBN: 0815323050.
10. Hill H.A.O. Sadler P.J., A.J. Ed. Metal Sites in Proteins and Models Redox Centres• Publisher: New York, Springer 1999. ISBN: 3540655564.
11. Sternberg Michael J. E. Protein Structure Prediction: A Practical Approach. Publisher:• USA, Oxford University Press. 1997. ISBN: 0199634953.
12. Fasman G.D.Prediction of Protein Structure and the Principles of Protein Conformation.
13. Publisher: New York, Plenum Press. 1989 ISBN: 0306431319.

BIM2-2 Chemo informatics

Objectives: This course will enable the students to: understand the fundamentals of chemoinformatics• appreciate complementary aspects of chemoinformatics and bioinformatics for design• of bioactive molecules. get hands-on experience in chemical structure representation, storage and analysis of• small molecular data.

Unit I   Introduction to Chemoinformatics: aims, scope. Role of Chemoinformatics in• pharmaceutical/chemical research (1) Chemical Structure representation: 1D, 2D and 3D structures (1)• Molecular file formats (SMILES, WLN, SDF, MOL) (1)• Molecular patterns- SMARTS, SMIRKS (1)• Fragment based Molecular Fingerprints (ChemAxon, Daylight, MDL and BCI• fingerprints- Daylight fingerprints).

Unit II (1) Molecular Descriptors (1D, 2D and 3D) and MACCS Keys (2)• Topological, electrotoplogical and shape indices. Molecular Similarity and Molecular Diversity Analysis. Similarity metrics:• Tanimoto Coefficient, Euclidean distance and Tversky Index (1)•   Chemical Databases – Design, Storage and Retrieval methods (1)•

Unit III   Molecular Database Screening: (Lipinski Rule: Drug/Lead like molecules) (1)•   Chemical Structure based Search techniques: Exact, Sub-structure and similar• structure searches.

Unit IV (2) Clustering and Statistical methods for Molecular Informatics (PLS, PCA, PCR,• kNN, ANN, Correlation and regression analysis) (2)

Unit V Modeling of small molecules (Generation of lowest energy conformations from• 2D structures) using Molecular Mechanics and Quantum mechanics method

Outcome :- students will learn the basics of Chemoinformatics

References:
1. Bunin Barry A. Siesel Brian,Morales Guillermo,Bajorath Jürgen. Chemoinformatics: Theory, Practice, & Products Publisher:New York, Springer. 2006. ISBN: 1402050003.
2. Gasteiger Johann, Engel Thomas. Chemoinformatics: A Textbook. Publisher: WileyVCH; 1st edition. 2003. ISBN: 3527306811
3. Leach Andrew R., Valerie J. Gillet. An introduction to chemoinformatics. Publisher:Kluwer academic , 2003. ISBN: 1402013477.
4. Gasteiger Johann, Handbook of Chemoinformatics: From Data to Knowledge (4• Volumes), 2003. Publisher: Wiley-VCH. ISBN:3527306803.

BIM2-3 Chemoinformatics

Objectives :- to learn the introduction and different file formats of chemical structure representation

1. Practical session for chemical structure representation and storage in special file
2. formats (SMILES,WLN, sd and mol). (1)
3. Importance of 3D structures and method of generation from 1D & 2D
4. representations. (1)
5. A brief introduction to building molecular databases with special emphasis on retrieval
6. using structure input. (1)
7. Substructure/Exact/similar structure based searching (1)
8. Property based search of molecular databases (1)
9. Quantitative Structure Activity/Property/Toxicity Relationship Studies (3)
10. Pharmacophore hypothesis and searching (2)
11. Docking studies (Rigid, Flexible & library based) (3)
12. Design and analysis of focused combinatorial library (2)

Outcome :- students will learn the chemoinformatics scope and different molecular file formats

BIM2-4 A Genomics, Transcriptomics Proteomics

Objectives :- To learn the genome ,transcriptome and proteome of different organism

Unit-I : (Introduction to Proteomics) Introduction to Proteomics: Scope and Application, Complexity of the problem: Post translational modification, Phosphorylation, Methods of studying proteins, establishing protein-protein interactions, Practical application of proteomics and current research technology, Protein databases

Unit-II : (The Proteome and Proteome technology) Introduction; Expression proteomics (express profile); Cell map proteomics; Protein separation technology - 2D-Gel Electrophoresis, liquid chromotagraphy, affinity chromatography (for cell map proteomics); X-ray diffraction, NMR, mass spectroscopy and its uses in protein identification; Forward and Reverse Proteomics Introduction to Genomics) Introduction to genomics- scope and application, Computational genomics, Organization of the prokaryotic and eukaryotic genomes, Genome maps and types, current sequencing technologies, partial sequencing, gene identification, gene prediction rules and software, Genome databases; Annotation of genome, Genome diversity: taxonomy and significance of genomes – bacteria, yeast, Caenorhabditis, Homo sapiens, Arabidopsis, etc. (Functional Genomics) Microarray - Gene Expression, methods for gene expression analysis; DNA array for global expression profile; Types of DNA array, Array databases; Applications of DNA microarray – analysis of gene expression, differential gene expression under different conditions and during development of organisms, Human Genome Project - Construction of physical maps; Basics of radiation hybrid maps; Sequencing of the entire human genome, annotation and analysis of genome sequences: sequence repeats, transposable elements, gene structure, Pseudogenes

Unit-III : (Computational Genome Analysis) Introduction to genome analysis, Gene analysis; gene order; chromosome rearrangement; compositional analysis; clustering of genes; composite genes; Basics of Single Nucleotide Polymorphisms, detection and its implications; dbSNP and other SNP related database, Gene Prediction method, Perdition of ORFs,

Unit IV Prediction of signal sequence (Promoter, Primers, Splice site, UTR etc); BLAST, PSI BLAST, PHI BLAST; Epitope prediction; Gene expression analysis; Genome annotation Unit-IV : (Comparative Genomics) Relevance of comparative genomics; orthologs and paralogs;

Unit V Comparative genomics of prokaryotes; Minimal genome; Vertical and horizontal gene transfer, Comparative genomics of organelles; Comparative genomics of eukaryotes, Differences and similarities in genomes of organisms; Evolution of prot

References:
. Baxevanis, A.D. and Francis Ouellellette, B.F. (1998) "Bioinformatics– a practical guide to the analysis of genes and proteins" John Wiley and Sons
2. Des Higgins, Willie R. Taylor, Willie Taylor (2000) "Bioinformatics: sequence, structure, and databanks : a practical approach" Oxford University Press
3. Mount, D. (2004) "Bioinformatics: Sequence and Genome Analysis"; Cold Spring Harbor Laboratory Press, New York. (ISBN 0-87969- 712-1)
4. Sharma, V. Munjal, A. and Shankar, A. (2008) "A text book of Bioinformatics" first edition, Rastogi Publication, Meerut – India.
 5. Stanley Letovsky (1999) "Bioinformatics: databases and systems" Springer
Outcome :- students will learn the Genome transcriptome and Proteome of an organism

BIM2-4 B Introduction to Database System

Objective :-To learn the basic of Database system

Unit I Independence, Database languages & Interfaces, View of Data, Data Models, Database Languages, Database, Users and Administrators, Database System Structure

Unit II : (Introduction Data models) ER Model: Keys, Constraints, Design Issues, Extended ER features, Reductions of ER Schema to Tables. Relational Model: Structure, Relational Algebra; Hierarchical Model, Network Model, Object Oriented Model

Unit-III : (Structured Query Language) Basic Structure, Set Operations, Aggregate Functions, Null Values, Nested Sub queries, Views, Integrity: Domain constraints, Joined Relations, Data-Definition Language, Embedded SQL, Dynamic SQL; Locking techniques, Granularity of Data Items – Database System Architecture and information retrieval: Centralized and Client-Server Architecture, Distributed DBMS, Data Mining, Data Integration, Data Warehousing

Unit IV : (Relational Database and Storage) Pitfalls in Relational Design Database, Functional dependencies, Decomposition Normal Forms – 1NF, 2NF, 3NF & Boyce- Codd NF, Overall Database Design Process, Multi-valued Dependencies,

Unit V : Data Storage – Ordered indices, Static Hashing, Dynamic Hashing - Transaction Management – Security and Authorization.

Outcome :- students will learn the Structural query language

References:
1. Date, C.J. (2000) "An introduction to Database systems"; Seventh Edition, Addison Wesley Publishers.

 2. Elmasri and Navathe (2004) "Fundamentals of Database systems" Fourth Edition, Addison Wesley Publishers.

 3. Silberschatz, A., Korth, H.F. and Sudarshan, S. (2002) "Database system Concepts"; Fourth Edition, McGraw Hill Publishers.

 4. Ullman, J. D. (2001) "Principles of Database systems"; Second Edition, Galgotia Publication

BIM2-5   Genomics, Transcriptomics Proteomics/Introduction to Database System

Objective :- To learn the different databases and analysis tools of genomes

> **Genomics & Proteomics**
> 1 Introduction to genomics- scope and application,
> 2 Computational genomics,
> 3 Organization of the prokaryotic
> and eukaryotic genomes,
> 4 Genome maps and types, current
> 5 sequencing technologies, partial sequencing, gene
> identification,
> 6 gene prediction rules and software, Genome
> databases;

7 Annotation of genome, Genome diversity:
8 taxonomy and significance of genomes – bacteria,

Introduction to Database System
1 Database & Database users, Characteristics of Database,
2 Database System applications, Database System Versus
3 File Systems, Concepts and Architecture, Data Models,
4 Schemas & Instances, DBMS architecture and Data
5 Independence, Database languages & Interfaces, View of
6 Data, Data Models, Database Languages, Database, Users
and Administrators, Database System Structure
(Introduction Data models)
7 ER Model: Keys, Constraints, Design Issues, Extended ER
features, Reductions of ER Schema to Tables. Relational
Model: Structure, Relational Algebra; Hierarchical Model,
8 Network Model, Object Oriented Model
(Structured Query Language)
9 Basic Structure, Set Operations, Aggregate Functions, Null
Values, Nested Sub queries, Views, Integrity: Domain
constraints, Joined Relations, Data-Definition Language,
Embedded SQL, Dynamic SQL; Locking techniques,
Granularity of Data Items – Database System Architecture
and information retrieval: Centralized and Client-Server
10 Architecture, Distributed DBMS, Data Mining, Data
Integration, Data Warehousing
Outcome :- students will learn the basics of databases and their applications

BIM2-6 Perl Programming and Python / Inter school /Intra school / MOOC * (NPTEL / SWAYAM)

Practicals Objectives: This course will enable the students to: know basic concepts in programming•
develop Perl scripts to solve biological problems• Practicals/Tutorials: 45 sessions of 2 hours each (2
sessions/week)

Unit I Concepts of flowcharting, algorithm development, pseudo codes etc.• Introduction: What is Perl?
Why use Perl in Bioinformatics? History of Perl,• Availability, Support, Basic Concepts Scalar Data: What
Is Scalar Data? Numbers, Strings, Scalar Operators, Scalar• Variables, Scalar Operators and Functions

Unit II   Arrays and List Data: What Is a List or Array? Literal Representation, Variables,• Array Operators
and Functions, Scalar and List Context Control Structures: Statement Blocks• Hashes: What Is a Hash?
Hash Variables, Literal Representation of a Hash, Hash• Functions, Hash Slices Basic I/O•

Unit III Regular Expressions: Concepts About Regular Expressions, Simple Uses of Regular• Expressions,
Patterns, More on the Matching Operator, Substitutions,

Unit IV The split and join Functions Subroutines: System and User Functions, The local Operator,
Variable-length• Parameter Lists, Notes on Lexical Variables (6) Miscellaneous Control Structures:•

Unit V File handles and File Tests: What Is a File handle? Opening and Closing a File handle,• Using Pathnames and Filenames, A Slight Diversion: die, Using File handles, The -x File Tests, The stat Function Formats: What Is a Format? Defining a Format, Invoking a Format• Syllabus draft: BoS April 26, 2010 Dr.

Outcome:- The students will learn the basics of Perl programming
References:
 Moorhouse Michael, Barry Paul. Bioinformatics, Biocomputing and Perl: an• introduction to bioinformatics computing skills and practice. Publisher: John Wiley and Sons, 2004. ISBN:047085331X.

 Tisdall James D. Mastering Perl for bioinformatics. Publisher: Shroff Publishers and• distributors O'Reilly Media, Inc. 2003. ISBN: 8173666768. Bal, H.P.

 Perl programming for Bioinformatics. Publisher: Tata McGraw-Hill New• Delhi. 2003. 0070474478. Curtis Jamison D.. Perl programming for biologists. Publisher : John Wiley• & sons, inc., 2003 ISBN 0471430595. Tisdall James D. Beginning Perl for bioinformatics. Publisher: Shroff Publishers and• distributors O'Reilly Media, Inc. 2001 ISBN: 8173663955. Gibas Cynthia, Jambeck Per. Developing Bioinformatics Computer Skills. Publisher:• Shroff Publishers and distributors O'Reilly Media, Inc., 2001. ISBN: 8173662428 Schwartz Randal L., Phoeni•

BIM2-7 Skill based activity

Database designing using Oracle