Chhattisgarh Swami Vivekanand Technical University, Bhilai

Scheme of Teaching and Examination

M.Tech. (Biomedical Engineering and Bioinfomatics)

3rd Semester

S. N.	Board of Study	Sub Code	Subject Name	Periods Per Week			Scheme of Examination			Total Marks	Credit L+(T+P)/2
							Theory /Practical				
				L	T	P	ESE	CT	TA		
1	Biomedical Engg.	590311 (17)	Machine Learning for Bioinformatics	3	1	-	100	20	20	140	4
2	Refer Table- 3 **Elective-III**			3	1	-	100	20	20	140	4
3	Biomedical Engg.	590321 (17)	Project Work	-	-	28	100	-	100	200	14
4	Biomedical Engg.	590322 (17)	Seminar on Industrial Training and Dissertation	-	-	3	-		20	20	2
Total				**6**	**2**	**31**	**300**	**40**	**160**	**500**	**24**

L-Lecture, **T**- Tutorial, **P**- Practical, **ESE**- End Semester Examination, **CT**- Class Test, **TA**- Teacher's Assessment

Refer Table- 3 (**Elective -III)**			
S. N.	**Board of Study**	**Sub Code**	**Subject Name**
1	Biomedical Engg.	590331(17)	Protein Engineering & Design
2	Biomedical Engg.	590332(17)	Virtual Instrumentation in BME
3	Biomedical Engg.	590333(17)	Cell Physiology and Bio Potential
4	Biomedical Engg.	590334(17)	Genomics and Proteomics
5	Biomedical Engg.	590335(17)	Biological sequence Analysis

Chhattisgarh Swami Vivekanad Technical University, Bhilai

Semester: M. Tech-III Branch: Biomedical Engineering and Bioinfomatics
Subject: Machine Learning For Bioinformatics Code: 590311(17)
Total Theory Period: 40Total Tutorial Period 12
Total Marks in End Semester Exam: 100
Minimum of class test to be conducted: 02

Unit- I

Introduction: Machine-Learning Foundations: The Probabilistic Framework, Bayesian modelling, The Cox Jaynes axioms,Bayesian inference & induction, Model structures: graphical models & other tricks - Probabilistic Modeling & Inference: Examples - The simplest sequence models, Statistical mechanics Machine Learning Algorithms, Dynamic programming Gradient descent, EM/GEM algorithms, Markov chain Monte, Carlo methods Simulated annealing, Evolutionary & genetic algorithms. Learning algorithms: miscellaneous aspects.

Unit- II

SVM: introduction, architecture, kernel, ROC, feature selection, sensitivity, specificity, accuracy implementation, SVM applications in sequence analysis, structure prediction, drug design, SVM light - LIBSVM , Weka, R.

Unit- III

Neural Networks: Introduction, Universal approximation properties, Priors & likelihoods - Learning algorithms: back-propagation Neural Networks: Applications, Sequence encoding & output interpretation, Sequence correlations & neural networks, Prediction of protein secondary structure, Prediction of signal peptides & their cleavage sites, Applications for DNA & RNA nucleotide sequences, Prediction performance evaluation, Different performance measures, Perceptron's and Multilayer Perceptron's, Neural Networks in Drug Design.

Unit- IV

Hidden Markov Models: The Theory - Introduction -Prior information & initialization - Likelihood & basic algorithms Learning algorithms - Applications of HMMs: general aspects, Protein applications - DNA & RNA applications - Advantages & limitations of HMMs – tools.

Unit- V

Probabilistic Graphical Models in Bioinformatics, Markov Models & DNA symmetries, Markov Models & gene finders, Hybrid models & neural network parameterization of graphical models, The single-model case, -directional recurrent neural networks for protein secondary structure prediction.

Texts & Reference:

1. Pierre Baldi and SørenBrunak, "Bioinformatics: The Machine Learning Approach", MIT Press, 1998.
2. David W Mount, "Bioinformatics: Sequence and Genome Analysis", 2nd Edition, CBS Publishers, 2004.
3. Zupan J., Gasteiger J., "Neural Networks in Chemistry and Drug Design", Wiley-VCH, 2000.

Chhattisgarh Swami Vivekanada Technical University, Bhilai

Semester: M. Tech-III Branch: Biomedical Engineering and Bioinfomatics
Subject: Protein Engineering & Design Code: 590331(17)
Total Theory Period: 40Total Tutorial Period 12
Total Marks in End Semester Exam: 100
Minimum of class test to be conducted: 02

Unit- I

Aminoacids(thestudentsshouldbethoroughwiththreeandsinglelettercodes)andtheirmolecularproperties(size,solubility,charge,pKa),Chemicalreactivity inrelationtopost-translationalmodification(involvingamino,carboxyl,hydroxyl,thiol,imidazolegroups)andpeptidesynthesis.

Unit- II

Primarystructure:peptidemapping,peptidesequencing-automatedEdmanmethodandMassSpectrometry.High-throughputproteinsequencingsetupSecondarystructure:Alpha,betaandloopstructuresandmethodstodetermineSuper-secondarystructure:Alpha-turn-alpha,beta-turn-beta(hairpin),beta-sheets,alpha-beta-alpha,topologydiagrams,upanddown&TIMbarrelstructuresnucleotidebindingfolds,sitesTertiarystructure:Domains,denaturationanddenaturation,proteinfoldingpathways,overviewofmethodstodetermine3Dstructures,Interactionwithelectromagneticradiation(radio,micro,infrared,visible,ultraviolet,X-ray)andelucidationofproteinstructure.Quaternaryassociations:Modularnature,formationofcomplexes.

Unit- III

Overviewofproteinstructure,PDB,structurebasedclassification,databases,visualizationtools,structurealignment,domain architecturedatabases,protein-ligand interactions.Covalent,Ionic,Hydrogen,Coordinate,hydrophobicandVanderwallsinteractionsinproteinstructure.

Unit- IV

BioinformaticsApproaches:Secondarystructurepredictionanddeterminationofmotifs,profiles,patterns,fingerprints,supersecondarystructures,predictionofsubstratebindingsites,tertiarystructure,quaternarystructure,methodstodetermine tertiaryandquaternarystructure,posttranslationalmodification.

Unit-V

Methodsofproteinisolation,purificationandquantification;largescalesynthesisofengineeredproteins,designandsynthesisofpeptides;methodsofdetectionandanalysisofproteins.Proteindatabaseanalysis, methodstoalterprimarystructure of proteins,examples of engineeredproteins,proteindesign,principlesandexamples.Advantagesandpurpose,overviewofmethods,underlyingprincipleswithspecificexamples:thermalstabilityT4-lysozyme,recombinantinsulintoreduceaggregationandinactivation,*denovo*proteindesign.

Unit- VI

DNA-bindingproteins:prokaryotictranscriptionfactors,Helix-turn-HelixmotifinDNAbinding,Trprepressor,Eukaryotictranscriptionfactors, Znfingers,helix-turnhelixmotifsin home domain,Leucinezippers,Membraneproteins:Generalcharacteristics,Trans-membranesegments,prediction,bacteriorhodopsinandPhotosyntheticreactioncenter.Immunoglobulin's:IgGLightchainandheavychainarchitecture,abzymesandEnzymes:Serineproteases,understandingcatalyticdesignbyengineeringtrypsin,chymotrypsinandelastase,substrate-assistedcatalysisothercommercialapplications.

Texts& Reference:

1. MoodyP.C.EandA.JWilkinson.ProteinEngineering,IRLPress,OxfordUniversityPress.
2. ProteinSciencebyArthurMLesk,OxfordUniversityPress.
3. ProteinStructurebyCreighton,OxfordUniversityPress.
4. IntroductionofproteinstructurebyBrandenCandToozeR.,Garland.

Chhattisgarh Swami Vivekanad Technical University, Bhilai

Semester: M. Tech-III Branch: Biomedical Engineering and Bioinfomatics
Subject: Virtual Instrumentation in BME Code: 590332(17)
Total Theory Period: 40Total Tutorial Period 12
Total Marks in End Semester Exam: 100
Minimum of class test to be conducted: 02

Unit- I

Introduction: Overview of medical instruments, advantages of virtual instrument on hardware instrument, Architecture, educational Laboratory Virtual Instrumentation Suite (ELVIS) and its building blocks, Graphical programming languages.

Unit- II

Data Acquisition (DAQ) Fundamentals: PC-Based DAQ System: Basic hardware architecture of PC, PC Sound card, common communication ports and protocols available in PC, review on sensors and signal conditioning, DAQ hardware, Specifications of Data acquisition systems: Analog input: sampling rate, multiplexing, resolution, relative accuracy, noise, Analog output, Triggers, Real-Time system integration, Digital I/O. Timing I/O, Software Multichannel analog DAQ system, Set up for data acquisition, universal DAQ card, Use of timer-counter and analog outputs on the universal DAQ card.

Unit- III

Application Development Software (LabVIEW): LabVIEW application development for virtual instrumentation (VI), Creating a virtual instrument in LabVIEW, Dataflow programming concepts, Sub VIs and modular code creation, Arrays and File I/O , Textual Math Integration with LabVIEW, Interfacing external instruments to a PC.

Unit- IV

Programming Environment in Virtual Instrumentation: Data formulation, Wave form generators, Acquiring data and its graphical representation, File formats, Simulating a DAQ device, Using counter and digital I/O, Measuring analoginput, Generating analog output, Types of scopes.

Unit- V

Analysis Tools and Medical Applications in Virtual Instrumentation: Realization of Fourier transform and Fast Fourier Transform (FFT), Wavelet transform, Correlation (Windowing and filtering) tools in LabVIEW, VI based temperature monitor, VI based cardiac monitor (ECG), Bio-bench-A virtual instrument application for data acquisition and analysis of physiological signals, ECG signal processing, Bio-Informatics and NI LabVIEW technology in drug discovery process.

Texts & Reference:

1. Olansen, Jon B. and Eric Roscow, Virtual Bio Instrumentation: Biomedical, Clinical, and Healthcare Applications in LabVIEW, Published by Prentice Hall, 2002.
2. Hall T. Martin, Meg L. Martin, LabVIEW for Automotive, Telecommunications, Semiconductor, Biomedical and Other Applications (National Instruments Virtual

Instrumentation Series), Prentice Hall PTR.

3. Gary Jonson, “Labview Graphical Programming”, Second Edition, McGraw Hill, New York, Fourth edition 2006.
4. Lisa K wells & Jeffrey Travis, “Labview for everyone”, Prentice Hall Inc, New Jersey, First edition 1997.
5. Gupta S J, Gu.pta P, “PC interfacing for Data Acquisition & Process Control”, Instrument Society of America, Second Edition, 1994.

Chhattisgarh Swami Vivekanad Technical University, Bhilai

Semester: M. Tech-III Branch: Biomedical Engineering and Bioinfomatics
Subject: Cell Physiology and BiopotentialCode: 590333(17)
Total Theory Period: 40Total Tutorial Period 12
Total Marks in End Semester Exam: 100
Minimum of class test to be conducted: 02

Unit- I
Fundamental Physicochemical Concepts: Introduction: Homeostasis and Cellular Physiology, Diffusion and Permeability, Osmotic Pressure and Water Movement, Electrical Consequences of Ionic gradients

Unit- II
Ion Channels and Excitable Membranes: Ion Channels, Passive Electrical Properties of Membranes, Generation and Propagation of the Action Potential, Ion Channel Diversity.

Unit- III
Solute Transport: Electrochemical Potential Energy and Transport Processes, Passive Solute Transport, Active Transport.

Unit- IV
Physiology of Synaptic Transmission, Synaptic Physiology.

Unit-V
Molecular Motors and Muscle Contraction, Molecular Motors and the Mechanism of Muscle Contraction
Excitation-Contraction Coupling in Muscle, Mechanics of Muscle Contraction.

Texts & Reference:

1. Nicholas Sperelaki , Cell Physiology Source Book: A Molecular Approach.

2. Mordecai P. Blaustein, Mordecai P. Blaustein, Kao Joseph P. Y., Donald R. Matteson, Cellular Physiology

Chhattisgarh Swami Vivekanad Technical University, Bhilai

Semester: M. Tech-III Branch: Biomedical Engineering and Bioinfomatics
Subject: Genomics and ProteomicsCode: 590334(17)
Total Theory Period: 40Total Tutorial Period 12
Total Marks in End Semester Exam: 100
Minimum of class test to be conducted: 02

Unit- I

Introduction: Introduction to Genomics & Proteomics. Structure, Organization and features of Prokaryotic &Eukaryotic genomes.C-values of eukaryotic genomes-coding, non-coding and repetitive sequences.Organization of genome with in nucleus, mitochondria and chloroplast. Genome mapping: Genetic and physical mapping. Polymorphisms.Molecular markers–RFLP, AFLP, RAPD, SCAR, SNP, ISSR, and Protein markers– Allozymes and Isozymes, Telomerase.FISH– DNA amplification markers and Cancer bio markers. Genome sequences data bases and *Genomean* notation and Gene Ontology.

Unit- II

Genome Sequencing: Recent developments and next generation sequencing, ultra-high-through put DNA Sequencing using Micro array technology. Genome sequencing projects on *H.Influenzae, E.coli, Orizasativum*and Neem. Human-genome project.Raw genome sequence data, Gene variation and associated diseases, diagnostic genes and drug targets.Genotyping-DNA Chips.Comparative and Functional Genomics: Studies with model systems such as Yeast, Drosophila, C.*elegans*, and Arabidopsis. Approach estoanalyze global gene expression–transcript me, Serial Analysis of Gene Expression (SAGE), Expressed Sequence Tags (ESTs), Massively Parallel Signature Sequencing (MPSS), micro array and its applications, gene tagging.

Unit- III

Genome annotation: Extrinsic, Intrinsic (Signals and Content), Conservative in formation used in gene prediction. Frame works for Information integration–Ex on chaining. Generative models: Hidden Morkov Models, Discriminative learning and Combiners. Evaluation of Gene prediction methods–Basic tools, Systematic evaluation and Community experiments (GASP, EGASP and NGASP). Functional annotation of Proteins: Introduction, Protein sequence data bases, UniProt, UniProt KB–Sequence curation, Sequence annotation, Functional annotation, annotation of protein structure, post-translational modification, protein-protein interactions and pathways, annotation of human sequences and diseases in UniProt and UniProt KB. Protein family classification for functional annotation–Protein signature methods and Databases, Inter Pro, Inter Pro Scan for sequence classification and functional annotation.Annotation from Genes and Protein to Genome and Proteome.

Unit- IV

Proteomics: Scope, Experimental methods for studying proteomics, methods of protein isolation, purification and quantification. Methods for large scale synthesis of proteins.Applications of peptides in biology. Analysis of proteome–High through put screening–Yeast two hybrid system and Protein chips, engineering novel proteins, Mass Spectroscopy based protein expression and post-translational modification analysis. Bioinformatics analysis clustering methods.Analysis of proteome functional information.

Unit- V Applications of Computational Tools towards Proteomics studies (to be discussed with appropriate case studies)–
Applicationsofproteomeanalysistodrugdevelopmentandtoxicity,phage antibodies astools forproteomics,glycoanalysisinproteomics,proteomics astoolsdiseasediagnosticsandplantgenetics.Chromatographicdataanalysis.Chromatogramsequencealignmentandediting.CGHandGenotypeArrayAnalysis.X-

Raydataandspectroscopicdataanalysis.2DPAGEimageanalysis.MSdataanalysis.

Texts& Reference:

1. PharmacogenomicsbyWernerKalow,UrsA.Meyer,RachelF.Tyndale,InformaHealthcare,2005.
2. StatisticalandComputationalPharmacogenomics(InterdisciplinaryStatistics) by Rongling Wu, Min Linen,Chapman&Hall/CRC, 2008.
3. GenesVIIIbyBenjaminLewis,JonesandBartlettPublisher,2006.
4. GenomicsandProteomicsbySándorSuhai,Springer,2000.
5. Moderngenomeannotation:theBioSapiensNetworkbyDmitrijFrishman,AlfonsoValencia,Springer,2008.

Discoveringgenomics,proteomicsandbioinformaticsbyA.MalcolmCampbell,

LaurieJ.Heyer,PublishedbyPearson/BenjaminCummings,2006.

Chhattisgarh Swami Vivekanad Technical University, Bhilai

Semester: M. Tech-III Branch: Biomedical Engineering and Bioinfomatics
Subject: Biological Sequence Analysis Code: 590335(17)
Total Theory Period: 40Total Tutorial Period 12
Total Marks in End Semester Exam: 100
Minimum of class test to be conducted: 02

Unit- I

Pairwise alignment techniques – Global alignment, Local alignment methods, Algorithm and statistics of global alignment, Algorithm and statistics of local alignment, Scoring matrices, Gap penalty, Dot matrix sequence comparison-Heuristic algorithms – FASTA and BLAST, Gapped BLAST & PSI BLAST, PHI-BLAST, E-value - Significance of sequence alignment.

Unit- II

Multiple sequence alignment – Goal of multiple sequence alignment to pairwise alignment, progressive methods-CLUSTAL W, PILEUP Iterative methods Position – Specific scoring matrices – Hidden Markov Models of multiple sequence alignment.

Unit- III

Predictive methods: Different secondary structure prediction methods – Chou fasman method, GOR method, Algorithm behind the methods - Tools used for secondary structure prediction - Tertiary structure prediction – homology modeling tool - Description on software packages - EMBOSS – programs and its usage.

Unit- IV

Markov chains, Hidden Markov Models for sequence Analysis –Building an HMM, Viterbi algorithms, Forward, Backward and EM algorithms, Applications of HMMs (HMMer, PFAM). Predictive methods using DNA sequences, Predictive methods using protein sequences- Prediction of RNA secondary structure- Expressed sequence tags (ESTs).

Unit- V

Mathematical basis for phylogenetic - Genetic algorithms - Multiple alignment - Construction of phylogenetic trees - Phylogenetic Analysis – building the data model, extraction of a phylogenetic data set, Tree building method, Distance methods, Character based method, phylogenetic software - Gene prediction methods, Genome analysis and annotation, Large–scale genome analysis and computational tools.

Texts& Reference:

1. Durbin R., Eddy S., Krogh A.&Mitchison G., "Biological Sequence Analysis: Probabilistic Models of Proteins & Nucleic Acids", Cambridge University Press, 1999.
2. Gusfield D., "Algorithms on Strings, Trees & Sequences: Computer Science & Computational Biology", Cambridge University Press, 1997.
3. Lesk A.M., "Introduction to Bioinformatics", Oxford University Press, 2002.
4. Pevzner P., "Computational Molecular Biology: An Algorithmic Approach", MIT Press, 2000.
5. Setubal J. &Meidanis J., "Introduction to Computational Molecular Biology", PWS Publishing Company, 1997.