DR. BABASAHEB AMBEDKAR MARATHWADA UNIVERSITY

CIRCULAR NO. SU/Sci./B.Sc. Syllabi/6/2016

It is hereby inform to all concerned that, on the recommendations of the Committees/Ad-hoc Boards the Hon'ble Vice-Chancellor has accepted the following revised syllabi in his emergency powers under Section-14[7] of the Maharashtra Universities Act, 1994 on behalf of the Academic Council as mentioned against their names under the Faculty of Science :-

Sr. No.	B.Sc. III Year Revised Syllabi		Semester
[1]	B.Sc. Automobile Technology	[Degree Course],	V & VI
[2]	B.Sc. Workshop Technology	[Degree Course],	V & VI
[3]	B.Sc. Refrigeration & Air Conditioning	[Degree Course],	V & VI
[4]	B.Sc. Bioinformatics	[Degree Course].	V & VI
[5]	B.Sc. Biotechnology	[Optional],	V & VI
[6]	B.Sc. Horticulture	[Optional],	V & VI
[7]	B.Sc. Dry Land Agriculture	[Optional],	V & VI
[8]	B.Sc. Sericulture	[Optional],	V & VI

This is effective from the **Academic Year 2016-2017** and onwards as appended herewith.

These **syllabi are also available on the University Website www.bamu.ac.in**

All concerned are requested to note the contents of this circular and bring the notice to the students, teachers and staff for their information and necessary action.

University Campus,
Aurangabad-431 004.
REF.NO.SU/B.Sc./2016/3849-68

Date:- 23-06-2016.

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Director,
Board of College and
University Development.

Copy forwarded with compliments to :-

1] The Principals, affiliated concerned Colleges, Dr. Babasaheb Ambedkar Marathwada University.

Copy to :-

1] The Controller of Examinations,
2] The Section Officer, [B.Sc. Unit],
3] The Section Officer, [B.C.S. Unit],
4] The Programmer [Computer Unit-1] Examinations,
5] The Programmer [Computer Unit-2] Examinations,
6] The In-Charge, E-Suvidha Kendra, [Professional Unit], Rajarshi Shahu Maharaj Pariksha Bhavan, Dr. Babasaheb Ambedkar Marathwada University,
7] The Record Keeper,
Dr. Babasaheb Ambedkar Marathwada University.

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DR. BABASAHEB AMBEDKAR MARATHWADA UNIVERSITY, AURANGABAD

Revised Syllabus of

B.Sc. Third Year Bioinformatics

Semester- V to VI

Three Year Degree Course

(Effective from 2016-2017)

DR. BABASAHEB AMBEDKAR MARATHWADA UNIVERSITY,
AURANGABAD.
B.Sc. Bioinformatics T.Y. (V & VI Semester)
(SEMESTER PATTERN)

Semester-V				
Class	**Paper No.**	**Paper Title**	**Lectures**	**Marks**
B.Sc. III	XXV	RDT & Molecular Genetics	45	50
	XXVI	Immunology	45	50
	XXVII	Gene expression & Flow processing	45	50
	XXVIII	Bioinformatics methods	45	50
	XXIX	Introduction to LINUX	45	50
	XXX	Introduction to PERL & Julia	45	50
	LC-XIII	LINUX		50
	LC-XIV	Programming in PERL & Julia		50
	LC-XV	Project based on wet lab techniques		50
			Total	450

Semester-VI				
Class	**Paper No.**	**Paper Title**	**Lectures**	**Marks**
B.Sc. III	XXXI	Introduction to Python & R	45	50
	XXXII	Genomes to drug and vaccine	45	50
	XXXIII	Algorithms for bioinformatics	45	50
	XXXIV	Structural Bioinformatics	45	50
	XXXV	Object oriented and relational database	45	50
	LC-XVI	Introduction to python & R		50
	LC-XVII	Seminars on emerging area of bioinformatics		50
	LC-XVIII	Major Project		100
			Total	450

B.Sc. Bioinformatics T.Y. (V & VI semester) syllabus

Semester-V	Semester- VI
Paper-XXV- RDT & Molecular Genetics	Paper-XXXI - Introduction to Python & R
Paper-XXVI-Immunology	Paper-XXXII- Genomes to drug and vaccine
Paper-XXVII- Gene Expression & Flow processing	Paper-XXXIII- Algorithms for bioinformatics
Paper-XXVIII- Bioinformatics methods	Paper-XXXIV- Structural bioinformatics
Paper-XXIX- Introduction to LINUX	Paper-XXXV- Object oriented and relational databases
Paper-XXX- Introduction to PERL & Julia	LC-XVI- Programming in Python & R
LC-XIII-LINUX	LC-XVII- Seminar on emerging area of bioinformatics
LC-XIV-Programming in PERL and Julia	LC-XVIII- Major Project
LC-XV-Project based on wet lab techniques (Microbial, Biotechnological, Molecular, Cell Biology, Genomics)	

Semester V

Paper-XXV- RDT & Molecular Genetics

Unit I

History of molecular biotechnology, Recombinant DNA technology, Manipulation of gene expression in prokaryotes, Recombinant protein production in eukaryotic cells.

Unit II

Production of therapeutic agents, vaccines, commercial products by recombinant microorganisms, Bioremediation, Microbial insecticides.

Unit III

Methodology and applications of genetic engineering of plants, Transgenic animals, Human molecular genetics, gene therapy, Legal and patent issues in RDT.

Unit IV

Early concepts of inheritance, Sex determination, Linkage, recombination and genetic mapping in eukaryotes, Somatic cell genetics, Structural and numerical changes in chromosomes, recombination in bacteria, fungi and viruses, tetrad analysis.

Unit V

Inheritance of quantitative traits, Concepts in population genetics, Genes and behaviour, Genetics and evolution, An overview of some recent discoveries in the field of genetics.

References:

1. Genetic Engineering, 200 by Nicholl.
2. Principals of Gene Manipulations, 1994 by Old and Primrose, Blackwell Scientific Publications.
3. Klug WS & Cummings MR. 2003 Concepts of Genetics. Peterson Education.
4. Lewin B. 2008. Genes IX. Jones & Bartlett Publication.

Paper-XXVI-Immunology

Unit I

Innate and adaptive immunity in vertebrates, Antigen processing and presentation, Contemporary challenges to the immune system, Infectious diseases, Autoimmune diseases, Categories of vaccines, Immunoglobulin classes and subclasses, CDR and LDR regions and sequence numbering.

Unit II

Immunogenetics & immunogenomics, Hybridoma technology: applications, Humanization of antibodies by design, BCR,TCR,MHC, MHC polymorphism its causes and supertype, concept of epitope, Affinity Maturation, Recognition of Antigen by B cells, Neutralizing Antibody.

Unit III

Reverse vaccinology, Rational Vaccine design, Evolution and escape due to variations, Immunoinformatics databases & tools: IMGT & IEDB, BciPep, Epitome, CED, AgAbDb.

Unit IV

Specificity, characterization, Ag-Ab: Sequential and conformational epitopes, MHC- peptide, HLA: nomenclature, HLA-peptide interactions & matrices.

Unit V

B-cell epitope predictions using sequence-based approaches, B-cell epitope predictions using structure-based approaches, T-cell epitope prediction methods, Vaccine design: Pipeline & workflows, Prediction of immunogenicity.

References:

1. Flower Darren R. Bioinformatics for Vaccinology Publisher: UK, John Wiley & Son Inc. 2008. ISBN: 9780470027110.
2. Flower Darren R. Immunoinformatics: Predicting Immunogenicity In Silico Publisher: New Jersey,Humana Press. 2007. ISBN: 9781603271189.
3. Kindt, Thomas J.,Osborne Barbara A.Goldsby Richard A. Kuby Immunology 6th Edition. Publisher:New York, W. H. Freeman. 2007. ISBN: 9780716785903.
4. Lund Ole , Nielsen Morten , Lundegaard Claus, Kesmir Can, Brunak SÃ¸ren. Immunological Bioinformatics. Publishesr: London, MIT PRess 2005 ISBN: 0262122804.
5. Foundation Novartis.Immunoinformatics: Bioinformatic Strategies for Better Understanding of Immune Function. Publisher: Chichester,John Wiley & Sons Inc. 2003. ISBN: 0470853565.

Paper-XXVII- Gene Expression & Flow processing

Unit I

Prokaryotic gene expression, operons -positive & negative regulation, sigma factors Initiation, elongation and termination of transcription -template & enzyme properties.

Unit II

Eukaryotic RNA polymerase I, II & III transcribed genes, promoter & regulatory sequences, transcription factors.

Unit III

Techniques -foot printing, Reporter genes, Organization of globin, immunoglobulin, HLA, rRNA and 5 sRNA genes.

Unit IV

Processing of RNA and Proteins -Transport and Stability, Stress & hormones regulated gene expression.

Unit V

Organization of human genome. RFLP, Fingerprinting, RAPDs, Micro arrays, ESTs.

References:

1. Gene VII; Benjamin Lewin

2. Recombinant DNA technology; Watson

3. Molecular Biology; Watson

4. General Biochemistry; Lehninger, Nicolson and Cox

Paper-XXVIII- Bioinformatics methods

Unit I

Nature of pairwise sequence alignment and database searching, Optimum sequence alignments methods, Principles, algorithms and methods of pairwise sequence alignment, statistical significance of pairwise sequence alignments.

Unit II

Introduction to multiple sequence alignments and its importance, MSA methods and its significance, CLUSTALW2, MUSCLE, Concepts of phylogeny, homology, analogy, orthology and paralogy, phylogenetic data analysis , tree building methods , tree evaluation & interpretation methods, PHYLIP.

Unit III

Concept of molecular modeling, in silico methods of molecular modelling, software for homology modeling , computer and graphic representation of simple molecules and peptides , use of structural databases in molecular modelling.

Unit IV

Concepts of geometry optimization and energy minimization , introduction of molecular dynamic simulation and monte carlo simulation. concepts and applications of macromolecular docking.

Unit V

Motif searching, protein-protein interactions, cis-element predictions.

References:

1. Andreas D. Bazavanis and B.F. Francis (Eds.) Bioinformatics: A Practical Guide to Analysis of Genes and Proteins, Wiley Interscience Publishers.
2. Thomas Lengauer (Eds.) Bioinformatics – Genomes to Drugs, Vol. I: Basic Technologies, Wiley-WCH publishers.
3. Jay A. Glasel and Murray P. Deutscher (Eds.) Introduction to Biophysical Methods for Protein and Nucleic Acid Research, Academic Press.
4. T.K. Attwood and DJ Parry Smith Introduction to Bioinformatics, Pearson education, Asia.

Paper-XXIX- Introduction to LINUX

Unit I

Basics of LINUX, need of LINUX, History, Difference Between Linux and Windows, Difference Between Linux and Unix, GNU , Usage, Career Options, Interesting Facts about Linux, Why Linux is Virus proof, Various Linux Distributions, Pros and Cons.

Unit-II

GNU/LINUX OS Installation, Basic System configuration and Administration, OS Installation, Root in LINUX, Who/why/what is root, Basic commands: mkdir, touch, ls, pwd, cd, chmod, df, du, dd, adduser, sort, passwd, rm/rmdir, date, tar, gzip, top .

Unit-III

Editors, Vi Editor, Understanding Files and Directories in Linux, File Structure and hierarchy, File Permissions, LVM overview, Schedulers: cron, at, User Administration, Software Installation In Linux: RPM, make.

Unit -IV

Linux Boot process:Boot Loaders (LILO and GRUB), System Initialization, inittab, rc.sysinit, rc, LVM (Logical Volume Manager), TCP/IP Network Management: route, ifconfig, ping, netstat, Driver/Module Installation and Removal: modprobe, rmmod, insmod ,lsmod, modinfo.

Unit -V

Log Monitoring and rotating, OpenSSH - The GNU/Linux Secure Shell, sudo and su - Giving users SuperUser Privileges, Various Linux Administrations, Linux Hardening, Linux Scripting using bash: awk, sed, grep, while, for, echo, variables, functions, information over open source projects: lynis(Unix-based auditing tool, rootkit hunter.

References:

1. Moving from Windows to Linux, Second Edition by Chuck Easttom.

2. Linux in a Nutshell, O' Reilly Publication.

3. Linux Administration Handbook by Evi Nemeth.

4. An introduction to Linux for bioinformatics 2016 by Paul Thothard

Paper-XXX- Introduction to PERL & Julia

Unit I

History of Perl, Perl in Bioinformatics: Basic concepts, Scalar data, Arrays and list data, Control structures, Hashes. Regular expressions: Concepts about regular expressions, simple uses of regular expressions, patterns, matching operator, substitutions, the split and join functions.

Unit II

Subroutines: System and user functions, the local operator, variable-length parameter lists, lexical variables, Filehandles and file tests: Opening and closing a filehandle, using pathnames and filenames, die, using Filehandles.

Unit III

Other data transformation: Finding a substring, extracting and replacing a substring. Formatting data: Sorting, Transliteration CGI programming: The CGI.pm Module, CGI program in context, simple CGI programs, passing parameters via CGI, Perl and the Web.

Unit IV BioPerl and Julia

Bioperl: Introduction, Installation procedures, Architecture, Uses of Bioperl and other tutorials on Bioperl

Julia::Getting started some introductory words, installation, paths, and various bits of magic, The REPL-Using the REPL; Julia as a calculator; getting help, Arrays and tuples, Types-Storing data – Arrays and tuples; the core of Julia and scientific programming, Controlling the flow Functions- a quick introduction to types, the way to organize your code and the secret to making your programs fast, loops and decisions; ifs and elses, functions and methods; multiple dispatch Dictionaries and sets-storing data in dictionaries and sets, Strings and characters working with strings,

Unit V

Julia:: Working with text file-reading data from text files; elementary file processing, Working with dates and times- working with date and time functions, Plotting -Plotting; an introduction to some of the plotting packages, Metaprogramming-metaprogramming, expressions and macros , Modules and packages-how Julia code is organized, and should be developed, DataFrames-data frames; organizing data in tables

References:

1. Harshawardhan P Bal, "Perl Programming for Bioinformatics", Tata McGraw Hill, 2003.
2. James Tisdall, "Mastering Perl for Bioinformatics", O'Reilly, 2010.
3. James Lee, "Beginning Perl", Apress, 2004.
4. Curtis Jamison D., "Perl Programming for Bioinformatics & Biologists", John Wiley & Sons, INC., 2004.
5. Michael Moorhouse, Paul Barry, "Bioinformatics Biocomputing and Perl", Wiley, 2004.
6.Getting started with Julia Programming by Ivo Balbaert
7. Mastering Julia by Malcolm Sherrington

LC-XIII-LINUX

1. Study of Basic commands of Linux.
2. Study of Advance commands of Linux.
3. Study of current directory according to the following arguments:
   a. Suffix to be replaced
   b. Replacement suffix
4. Shell scripting using general-purpose utilities.
5. Shell programming using filters (including grep, egrep, fgrep).
6. Write a shell script to validate the entered date. (eg. Date format is : dd-mm-yyyy)
7. Write a shell script to check entered string is palindrome or not.

C-XIV-Programming in PERL, Bioperl and Julia

1. Basic arithmetic operations using loop, array and decision making statement.
2. chop, chomp based simple Perl program
3. Program based on control structures- dowhile, foreach and with control flow statements-redo, next, goto etc.
4. Subroutines
5. Retrieving sequence file and searching for a pattern
6. Comparing files. Combining and extracting data from different files using modules
7. MSA using Perl and conserved domain identification and hast table creation
8. Blast usingBioperl

9. CGI- Perl Programs for developing MSA.

10. Number with Julia, String, Types, Function, Methods ,Control flow

11. Arrays, 2-D Arrays, Dictionaries

LC-XV-Project based on wet lab techniques

Project will be based on any one of the techniques mentioned below

- Microbial
- Biotechnological
- Molecular
- Cell Biology
- Genomics

Semester VI

Paper-XXXI - Introduction to Python & R

Unit I

Python program structure- builtin types- basic statements, Functions basics- scope rules- argument passing- Odds and Ends- Function Gotchas.

Unit II

Basics- Module files- import model- reloading- modules Gotchas- classes- Exceptions OOLS Built-in Tools- Common Tasks in Python.

Unit III

An Automated Complaint System- Interfacing with COM- Cheap Public Relations- A Tkinter-Based GUI Editor for Managing Form Data- Design Considerations- JPython- The Felicitous Union of Python and Java

Unit IV

Introduction and preliminaries of R, Simple manipulations; numbers and vectors, Objects, their modes and attributes, Ordered and unordered factors, Arrays and matrices, Lists and data frames, Reading data from files, Probability distributions.

Unit V

Grouping, loops and conditional execution, Writing your own functions, Statistical models in R, Graphical procedures, Packages, OS facilities, Applications of R in molecular biology data analysis.

References:

1. Cynthia Gibas, Per Jambeck, Developing Bioinformatics Computer Skills, O'Reilly, 2001.

2. Harvey M. Deitel, Python: How to Program, Prentice Hall, 2002.

3. Patrick O'Brien, Beginning Python for Bioinformatics, O'Reilly, 2002.

4. Alex Martelli, Python in a Nutshell, O'Reilly, 2006.

5. A Little Book of R for Bioinformatics by Avril Coghlan, 2014.

6. Learn R in a Day by Steven Murray.

Paper-XXXII- Genomes to drug and vaccine

Unit I

Genome Assembly, Genome Databases and related data resources (EST, STS, GSS, HSS etc.), Nature and types of data, Organization of data in databases, Genome Data , Tools for Genomic Data Mining.

Unit II

Basic Aspects of Genome Annotation, Database Search Engines: Special tools for searching genomic data, Prediction of ORFs and Genes, Identification of Disease Genes in the context of Human Genetics and Genetics of Model Animals.

Unit III

Identification of Drug Targets, Pharmacogenetics, The genetics of drug metabolism, the genetics of therapeutic targets; Interactions of small molecules and gene-based drug targets.

Unit IV

Protein Sequence Analysis and Prediction of epitomes on Genomic scale Interactions of epitomes with Antibodies, MHC molecules and TCR.

Unit V

Approaches for designing vaccines, Peptide/DNA vaccines, Polytope vaccines, Recombinant vaccines.

References:

Bio informatics from Genome to drugs (ed.) Vol., I &II ;Thomas Lengaure

Microcomputer in physiology : a practical approach ;P.J. Frasre

Paper-XXXIII- Algorithms for bioinformatics

Unit I

Introduction to Algorithms, Dynamic Programming, Sequence Alignment:Edit distance, LCS. PAM and BLOSUM Scoring Matrices. Global alignments: Needleman Wunsch Algorithm, Local Alignments: Smith Waterman Algorithm, Gap Penalties.

Unit II

Graph Algorithms, SBH and Eulerian Paths, De-novo Peptide Sequencing: Longest Paths and Space Efficient Alignment Algorithms. Fast LCS using Table Lookup.

Unit III

Exact Pattern Matching: KMP Algorithm, Keyword Trees, Aho-Corasick Algorithm. Clustering Basics: Hierarchical Clustering, Multiple Sequence Alignment: CLUSTAL, Center-based Clustering, Clustering via Cliques.

Unit IV

Evolutionary Trees and Ultrametrics, Additive distance trees, Perfect Phylogeny Problem, Small Parsimony Problem, Nearest Neighbor Interchange.

Unit V

Hidden Markov Models: Basics, Forward and Backward (Viterbi) Algorithms, Randomized algorithms and their applications.

References:

1. Neil C. Jones and Pavel A. Pevzner, "An Introduction to Bioinformatics Algorithms", MIT Press, 2005.
2. Gusfields D, "Algorithms on strings, trees and sequences: Computer Science and Computational Biology", Cambridge University Press, 1997.
3. Steffen Schulze-Kremer, "Molecular Bioinformatics: Algorithms and Applications", Walter de Gruyter, 1996.
4. Gary Benson, Roderic Page (Eds.), "Algorithms in Bioinformatics", Springer International Edition, 2004.
5. Richard Durbin, Sean R. Eddy, Anders Krogh, Graeme Mitchison. "Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acid", Cambridge University Press, 1999.

Paper-XXXIV- Structural bioinformatics

Unit I

Define Bioinformatics and structural bioinformatics, fundamentals of protein structure, fundamentals of DNA & RNA structure, computational aspects of high throughput Crystallographic macromolecular structure determination, Macromolecular structure determination by NMR Spectroscopy, Electron Microscopy, Molecular visualization.

Unit II

PDB, NDB database, Comparative features-protein structure evolution and the SCOP databases, the CATH domain structure databases, structural quality assurance all-atom contacts; a new approach to structure validation, structure comparison and alignment.

Unit III

Secondary structure assignments, identifying structural domains in proteins, Inferring protein function from structure. Prediction of protein-protein interaction from evolutionary information, electrostatic interactions.

Unit IV

Principles and methods of docking and ligand design, structural bioinformatics in drug discovery, CASP and CAFASP experiments and their finding.

Unit V

Protein secondary structure prediction methods: Chau Fasman, GOR, 3D structure Prediction methods: homology, threading and ab initio.

References:

Structural Bioinformatics by Phillip E. Brurne & Helge Weissig, A John Wiely & Sons Publications.

Paper-XXXV- Object oriented and relational databases

Unit I
Introduction, Database System Concepts and Architecture, Entity-Relationship Model. EER and Object Modeling.

Unit II
Relational Model, Algebra, Calculus, ER- and EER-to-Relational Mapping, Relational languages SQL and QBE, RDBMS Systems: SQL server and MS Access.

Unit III
Object-oriented concepts, Object Modeling, Object-Oriented Databases, Object Database Languages, Object Database Design, Object-Relational and Extended Relational Database Systems.

Unit IV
Functional Dependencies, Normalization, Design Algorithms and Further Dependencies.

Unit V
Query Processing and Optimization, Transaction Processing, Concurrency Control, Recovery Security and Authorization.

References:

1. Database Management and Design by G. W. Hansen and J. V. Hansen, Prentice-Hall of India, Eastern Economy Edition, Latest Edition.
2. Database System Concepts by A. Silberschatz, H.F. Korth and S. Sudarshan, 3rd edition, McGraw-HilI, Latest International Edition.

LC-XVI- Introduction to Python & R

Python

1. String methods
2. Operators
3. Using a class from a module
4. Fetch a PDB entry from the RCSB Web server
5. Extracting the complete CDS from a GenBank entry
6. Import from Bio.Clustalw
7. Using a class from a module
8. Fetching enzymes referenced in a SwissProt entry and display related proteins

Introduction to R

1. Construct and execute basic programs in R using elementary programming techniques, e.g. import/export of data from file or Internet, assign and manipulate data structures, create user-defined functions, loops, condition statements and debugging.
2. Use R for statistical calculations
3. Implement and describe Monte Carlo techniques as well as perform simulation studies with analysis and evaluation of result
4. Graphically visualise data and results of statistical calculations
5. Use external R-packages in statistics and data mining

LC-XVII- Seminar on emerging area of bioinformatics

Students have to perform one project and one seminar in the semester any one of the following:

- Seminars on Applications of Bioinformatics in Biotechnology
- Seminars on Applications of Bioinformatics in Drug Designing
- Seminars on Applications of Bioinformatics in Agriculture
- Seminars on Applications of Bioinformatics in Human Health
- Seminars on Applications of Bioinformatics in Plant Breeding
- Seminars on Applications of Bioinformatics in Veterinary science
- Seminars on Applications of Bioinformatics in any recent field of science.

LC-XVIII- Major Project

Project should be based on the following topics

- Parasite bioinformatics
- Biodiversity informatics
- Microbial informatics
- Immunology bioinformatics
- Plant bioinformatics
- Molecular modelling
- Any recent advanced topic in the field of life sciences.