CBCS PATTERN FOR MICROBIOLOGY

B.Sc BIOINFORMATICS (CBCS) REVISED SYLLABUS – 2020-21

YEAR	SEMESTER	PAPER	TITLE	MARKS	CREDICTS
I	I	BIOINFO T: I	CELL BIOLOGY, MICROBIOLOGY AND VIROLOGY.	100	
		BIOINFO P: I	CELL BIOLOGY, MICROBIOLOGY AND VIROLOGY.	50	
	II	BIOINFO T: II	BIOMOLECULES, PROTEINS – STRUCTURE AND FUNCTIONS	100	
		BIOINFO P: II	BIOMOLECULES, PROTEINS – STRUCTURE AND FUNCTIONS	50	
II	III	BIOINFO T: III	BASIC OF COMPUTER, MATHEMATICS AND BIOSTATISTICS	100	
		BIOINFO P: III	BASIC OF COMPUTER, MATHEMATICS AND BIOSTATISTICS	50	
		BIOINFO T: IV	BIOINFO T IV: GENOMICS AND PROTEOMICS	100	
		BIOINFO P: IV	BIOINFO T IV: GENOMICS AND PROTEOMICS	50	
	IV	BIOINFO T: V	BIOINFO T V: MOLECULAR BIOLOGY	100	
		BIOINFO P: V	BIOINFO T V: MOLECULAR BIOLOGY	50	
III	V	**A – PAIR**			
		BIOINFO T: A1	PROGRAMMING IN C LONGUAGE	100	
		BIOINFO P: A1	PROGRAMMING IN C LONGUAGE	50	

		BIOINFO T: A2	GENETIC ENGINEERING	100	
		BIOINFO P: A2	GENETIC ENGINEERING	50	
		B – PAIR			
		BIOINFO T: B1	CHEMOINFORMATICS	100	
		BIOINFO P: B1	CHEMOINFORMATICS	50	
		BIOINFO T: B2	VISUAL BASIC AND NET BANKING	100	
		BIOINFO P: B2	VISUAL BASIC AND NET BANKING	50	
		C – PAIR			
		BIOINFO T: C1	TRUCTURAL BIOINFORMATICS AND DRUG DESIGN	100	
		BIOINFO P: C1	TRUCTURAL BIOINFORMATICS AND DRUG DESIGN	50	
		BIOINFO T: C2	BIODIVERSITY INFORMATICS & PROGRAMING IN PERL	100	
		BIOINFO P: C2	BIODIVERSITY INFORMATICS & PROGRAMING IN PERL	50	

CBCS PATTERN FOR BIOINFORMATICS

B.Sc BIOINFORMATICS (CBCS) REVISED SYLLABUS – 2020-21

BIOINFO T: I CELL BIOLOGY, MICROBIOLOGY AND VIROLOGY.

TOTAL HOURS: 50 **CREDITS: 4**

UNIT-I: No. of hours: 08

Cell Biology:

1.1 Cell as a basic unit of life.

1.2 Cell organization of prokaryotic and eukaryotic cells.

1.3 Structural and functional capitalization of cell:– Mitochondria, Chloroplast, Lysosomes, Golgi bodies, Plasma membrane, Cytoskeleton, Cell wall and Nucleus.

UNIT-II: No. of hours: 12

2.1 Cell cycle, cell division - mitosis and meiosis.
2.2 Chromosome structure, gene, gene number, gene clusters and Pseudogene.
2.3 Polytene and lampbrush chromosomes.
2.4 Packing of DNA, supercoiled DNA, nucleosome.
2.5 Inverted repeats, repetitive DNA sequence, satellite DNA.

2.6 Cell trafficking.

UNIT-III: No. of hours: 10

Microbiology:

3.1. Structure, classification and general characteristics of Bacteria (including ribotyping), Micoplasma, Protozoa, archea and yeast, fungi. Association of bacteria.
3.2. Methods in microbiology: Pure culture techniques, principles of microbial nutrition, construction of culture media, enrichment culture techniques for isolation of chemoautotrophs, chemoheterotrophs and photosynthetic microorganisms.

3.3. Sterilization-Application of sterilization methods in biotechnology, Various sterilization methods, Microbial contamination control and Sterility testing.

3.4. Microbial growth: The definition of growth, mathematical expression of growth, growth curve, measurement of growth and growth yield, synchronous growth, continuous culture.

UNIT-IV: **No. of hours: 10**

4.1 Staining Techniques - Simple and Differential staining techniques.

4.2 Principles of microscopy - Bright field and Electron microscopy (SEM and TEM).

4.3 Microbial growth: Principles of growth, Kinetics of growth, Methods of measuring growth:

4.4 Direct methods: viable plate counts, membrane filtration. Indirect methods: Metabolic activity – measurements of DNA, Protein, Microscopic counts, electronic counters, most probable number;

UNIT-V: **No. of hours: 10**

Virology:

5.1 Classification and General properties of plant, animal and bacterial viruses, Bacteriophages - lytic cycle & lysogeny.

5.2 Structure of viruses, assembly of viral membrane.

5.3 Life cycle and replication of viruses: RNA-negative strand (VSV), positive strand (Polio), segmented [Influenza], Retrovirus- RSV and HIV, DNA- adenovirus and SV-40.

5.4 Cultivation in cell culture, chick embryo and animal inoculation.

5.5 Persistent chronic and acute viral infections.

5.6 Mechanism of interferon and antiviral therapy.

5.7 Host virus interactions; plant and animal.

BIOINFO P: I CELL BIOLOGY, MICROBIOLOGY AND VIROLOGY.

TOTAL HOURS: 30 **CREDITS: 2**

1. Microbiology Good Laboratory Practices and Biosafety.
2. Preparation of culture media for cultivation of bacteria
3. Preparation of culture media for cultivation of fungi
4. Sterilization of medium using Autoclave
5. Sterilization of glassware using Hot Air Oven
6. Light compound microscope and its handling
7. Study of mitosis on onion root tips
8. Study of meiosis on onion buds
9. Isolation and separation of cell organelles from plant cell.
10. Study of growth curve of *E.coli*

SUGGESTED READING:

- Pelczar, M.J., Chan, E.C.S. and Kreig, N.R. (1993). Microbiology. 5th Edition, Tata Mc Graw Hill Publishing Co., Ltd., New Delhi.

- Dube, R.C. and Maheswari, D.K. (2000) General Microbiology. S Chand, New Delhi. Edition), Himalaya Publishing House, Mumbai.

- Power, C.B. and Daginawala, H.F. (1986). General Microbiology Vol I & II

- Prescott, M.J., Harley, J.P. and Klein, D.A. (2010). Microbiology. 5th Edition, WCB Mc GrawHill, New York.

- Reddy, S.M. and Reddy, S.R. (1998). Microbiology □ Practical Manual, 3 rd Edition, Sri Padmavathi Publications, Hyderabad.

- Singh, R.P. (2007). General Microbiology. Kalyani Publishers, New Delhi.
- Stanier, R.Y., Adelberg, E.A. and Ingram, J.L. (1991). General Microbiology, 5th Ed., Prentice Hall of India Pvt. Ltd., New Delhi.
- Microbiology Edited by Prescott
- Jaya Babu (2006). Practical Manual on Microbial Metabolisms and General Microbiology. Kalyani Publishers, New Delhi.
- Gopal Reddy *et al.*, Laboratory Experiments in Microbiology

B.Sc BIOINFORMATICS (CBCS) REVISED SYLLABUS – 2020-21

BIOINFO T: II BIOMOLECULES, PROTEINS – STRUCTURE AND FUNCTIONS

TOTAL HOURS: 48 **CREDITS: 4**

UNIT-I **No. of hours: 8**

Classification, Structures and Carbohydrate Metabolism:

1.1 Classification, characteristics and functions of monosaccharides, disaccharides - polysaccharides.

1.2 Epimers, isomers, anomers, chiral carbon atom, chair and boat form, glucopyranose and fructopyranose.

1.3 General scheme of metabolism, historical and experimental details in derivation of a metabolic pathway.

1.4 Glycolysis - aerobic and anaerobic, regulation of glycolysis.

1.5 Krebs cycle and its regulation;

1.6 Hexose monophosphate shunt.

UNIT-II **No. of hours: 10**

Amino Acids and Proteins:

Amino Acids:

2.1 Chemical structure and general properties of amino acids, pI of amino acids, acid base concepts.

2.2 Henderson and Hasselbaclh equation.

2.3 General metabolism scheme of amino acids and Urea cycle.

Proteins:

2.4 Classification- size, shape, degree of association, complexity. Classification of proteins according to biological functions (Enzymes, transport, storage, contractile, structural, defense and regulatory)

2.5 Structure of peptide bond - restricted rotation, cis - trans bending, Ramchandran plot. Peptides.

UNIT-III No. of hours: 10

Protein structure:

3.1 Secondary structure - alpha helix and beta pleated structure, triple helix (collagen) and Super secondary structures.

3.2 Tertiary structure - forces stabilizing tertiary structure, unfolding/refolding experiment.

3.3 prediction of secondary and tertiary structure.

3.4 Dynamics of protein folding, role of molecular chaperones in protein folding, Lysosomal and membrane proteins.

3.5 Quaternary structure - forces stabilizing quaternary structure.

3.6 Structure function relationship - myoglobin and hemoglobin.

3.7 Techniques for studying primary sequence of proteins, experimental methods, end group analysis, finger printing and sequenators.

UNIT- IV No. of hours: 10

4.1 Chemical synthesis of peptides, solid phase automated synthesis.

4.2 Prediction of conformation from amino acid sequence.

4.3 Zymogens and their conversion into active proteins

4.4 Protein evolution - phylogenic tree, convergent and divergent trees, sequence analysis, comparison matrix, Dot matrix and substitution matrix.

4.5 Protein turnover: Ubiquitination, proteasome and protein degradation.

UNIT-V No. of hours: 10

5.1 Concept of prosthetic group, apoenzyme, holoenzyme, enzyme. Coenzyme.

5.2 Vitamins as coenzymes: sources, requirements, functions and deficiency symptoms of water soluble vitamins. Structure and biochemical role, Assay of vitamins.

5.3 Cofactors: Role of trace elements, their bound forms in biological systems and in enzyme structure and function.

BIOINFO P: II BIOMOLECULES, PROTEINS – STRUCTURE AND FUNCTIONS

TOTAL HOURS: 48 **CREDITS: 2**

1. Qualitative Analysis of Carbohydrates.

2. Qualitative Analysis of Aminoacids.

3. Colorimetric estimation DNA by diphenylamine method.
4. Estimation of RNA by Orcinol method.

5. Colorimetric estimation of proteins by Biuret / Lowry method.

6. Estimation of reducing sugar-Anthrone method.

7. Estimation of sugar by titration method–Benedict's method.

8. Determination of pKa and pI values of amino acids.

9. Assay of amylase activity

10. Effect of temperature / pH on enzyme activity

11. demonstration of immobilization of enzyme activity.

SUGGESTED READING:

- Berg JM, Tymoczko JL and Stryer L (2011) Biochemistry, W.H.Freeman and Company Caldwell, D.R. (1995). Microbial Physiology and Metabolism, W.C. Brown Publications, Iowa, USA.
- Lehninger, A.L., Nelson, D.L. and Cox, M.M. (1993). Principles of Biochemistry, 2 nd Edition, CBS Publishers and Distributors, New Delhi.
- Sashidhara Rao, B. and Deshpande, V. (2007). Experimental Biochemistry: A student Companion. I.K. International Pvt. Ltd.
- Tymoczko JL, Berg JM and Stryer L (2012) Biochemistry: A short course, 2nd ed., W.H.Freeman
- Voet,D. and Voet J.G (2004) Biochemistry 3rd edition, John Wiley and Sons

White, D. (1995). The Physiology and Biochemistry of Prokaryotes, Oxford University Press, New York.

B.Sc BIOINFORMATICS (CBCS) REVISED SYLLABUS – 2020

BIOINFO T: III BASIC OF COMPUTER, MATHEMATICS AND BIOSTATISTICS

TOTAL HOURS: 50 **CREDITS: 4**

UNIT-I No. of hours: 10

Introduction to Computers:

1.1 History and development of computers; generations of computers; (I, II, III, IV and V),

1.2 classifications of computers; analog computers, digital computers, mainframe computers, mini frame computers, microcomputers, fundamentals of logical concepts.

1.3 Digital Computers:- Basic principle of operation of digital computers, structure of digital computers; arithmetic unit, central unit, memory unit, Input unit and output unit.

1.4 Computer Coding:- Number system, decimal number system, binary number system, binary to decimal conversion, Binary arithmetic, octal number system, hexadecimal number system.

UNIT-II No. of hours: 10

2.1 Languages and flow charts and Operating Systems:-Machine level languages, assembly level languages, and high level languages.

2.2 Input and Output devices :-Punched card reader, paper tape reader, magnetic tape, floppy disk, magnetic disk,optimal scanner, voice data, entry terminal, teleprocessing terminal, visual display unit, modern input devices, Output devices; CRT, printer, plotter.

2.3 Memory: - Primary memory or main memory; magnetic core memory, semi-conductor memory, RMA, ROM, PROM, EPROM, EEPROM. Secondary memory or auxillary memory or storage devices; Hard disk, discket, magnetic tape, ZIP, devices, digital tape, CD-ROM, DVD, virtual, memory, catche memory.

2.4 Operating Systems:- DOS, windows 98/XP/VISTA,UNIX/LINUX, Mac OS, VMS.

UNIT-III No. of hours: 10

Modern Computers:

3.1 Workstations, parallel processing computers, supercomputers.

3.2 Internet and related programmes: - WWW, HTML, HTTP, telnet, FTP, computer domain.

3.3 Introduction to Biostatistics: Applications and uses, sample variable, statistical sampling, population, primary and secondary data, screening and representation of data.

3.4 frequency distribution, bar diagram, histogram. Pie diagram, cumulative frequency curves.

3.5 Mean, median, mode, Comparision between mean, median and mode.

3.6 Measures of dispersion: range, variation, standard deviation, coefficient of variation, symmetry, probability distribution.

UNIT-IV **No. of hours: 10**

Basic Mathematics:

4.1 Sets:- Finite set, infinite set, null or void set, subset, Intervals; closed and open, universal set, operations of set. Relations and functions.

4.2 Matrices:-Types of matrices, properties of matrices, addition, substraction of matrices, matrix, multiplication, elementary transformation, inverse of matrices.

4.3 Determinants: - Definition, properties associated with determinants. Trignometry and Derivatives.

4.4 Introduction Of Databases:-Concept of data, data models, data representation, mining, various types of databases, biological data and data analysis. Related programs; Oracle, SQL, VB, Database management System (DBMS). Introduction to protein and nucleic acid databases.

UNIT-V **No. of hours: 10**

5.1 Basic principles of probability theory, Bayes theorem

5.2 Normal distribution, statistical inference –Types of errors and levels of significance.

5.3 Comparison of variance (F-test), small sample test, t-test for comparison of means, chi square test.

5.4 Analysis of variance–one way and two way, multiple comprises. Correlation and Linear regression. Sequence Analysis: Introduction to hidden Markov models.

BIOINFO P: III BASIC OF COMPUTER, MATHEMATICS AND BIOSTATISTICS

TOTAL HOURS: 30 **CREDITS: 2**

1. Use of software for sequence analysis of nucleotides and proteins.
2. Problem related to t – test and chi^2 test.
3. Use of Internet/software for sequence analysis of nucleotides and proteins:
4. Studies of public domain data bases for nucleic acid and protein sequences.
5. Determination of protein structure (PDB).
6. Genome sequence analysis
7. Problems related to measures of central tendency, dispersion, t-test and chi

   Square test.

8. Computer basic knowledge; hardware, connection cables, typing, Windows 98/XP, Internet browsers, search engines.
9. LAN connections, setting up the IP address, network security.
10. Internet surfing and searching information, downloading and installing software. Hands on session with Microsoft Word, Microsoft Excel (Spreadsheet Application).
11. Hands on session with Microsoft Access (Database related applications).

SUGGESTED READINGS:

1. Daniel, 2006, Biostatistics, Eighth Edition. John Wisley and sons.

2. Durbin, Eddy, Krogh, Mithison, Biological sequence analysis.

3. T.A.AttwoodandD.J.parry–smith, 2001, Introduction of Bioinformatics.

4. A.D.Baxevaris,1998, Bioinformatics: A practical guide to the analysis of Genes and proteins,(Edited) B.F.Publication.

5. David W, 2005, Bio-informatics; sequence and Genome Analysis, 2ndEdition By Mount CB Spublishers.

B.Sc BIOINFORMATICS (CBCS) REVISED SYLLABUS – 2020-21

BIOINFO T: IV GENOMICS AND PROTEOMICS

TOTAL HOURS: 45 **CREDITS: 4**

UNIT-I No. of hours: 10

1.1 Genomics: Nucleotide sequence Databases, its Analysis and Identification.

1.2 Goals of the Human Genome Project, cloning vectors, concept of maps, physical maps, shotgun libraries, DNA polymorphism, nucleotides, DNA sequences.

1.3 Sequence databases: GeneBank, EMBL Nucleotide sequence databank, DNA Data Bank of Japan (DDBJ), database formats.

UNIT-II No. of hours: 10

2.1 Recombinant DNA technology, restriction enzymes, resource for restriction enzyme (REBASE), similarity search. Polymerase chain reaction, primer selection for PCR, BLASTn, application of BioEdit.

2.2 Genome information and special features, coding sequences (CDS), untranslated regions (UTR's), cDNA library, expressed sequence tags (EST).

2.3 Approach to gene identification; masking repetitive DNA, database search, codon-bias detection, detecting functional sites in the DNA.

2.4 Internet resources for gene identification, detection of functional sites, gene expression.

UNIT-III No. of hours: 10

Gene experience, DNA microarray and Proteomics:

3.1 Gene experience: - Introduction, Basic steps for gene expression.

3.2 Microarray:- Concept of microarrays; spotted arrays, oligonucleotide arrays, designing the experiment, Two-color microarray experiments.

3.3 Proteomics:-Protein sequence information, composition and properties, physicochemical properties based on sequence, sequence comparison,

3.4 Prmary databases, Secondary databases.

3.5 Pair-wise sequence alignment, gaps, gap-penalties, scoring matrices, PAM250,BLOSUM62, local and global sequence alignment, multiple sequence alignment, useful programs, ClustalW, BLASTp.

UNIT-IV **No. of hours: 10**

4.1 Proteomics classification; Tools and techniques in proteomics; 2-D gel electrophoresis, gel filtration, PAGE, isoelectrick focusing, affinity chromatography, HPLC, ICAT, fixing and spot visualization, Mass spectroscopy for protein analysis, MALDI-TOF, Electrospray ionization (EST), Tandem mass spectroscopy (MS/MS) analysis; tryptic digestion and peptide fingerprinting (PMF).

4.2 Protein Micro array in protein expression, profiling and diagnostics, drug target discovery.

4.3 Database searching, 3-dimensional structure determination by X-ray and NMR.

4.4 Phylogenetic analysis:-Evolution, elements of phylogeny, methods of phylogenetic analysis, Phylogenetic tree of life, comparison of genetic sequence of organisms, phylogenetic analysis tools-Phylip, Clustal W.

UNIT-V **No. of hours: 5**

Applications of Bioinformatics in various fields:

5.1 Environment, biotechnology, molecular biology, neurobiology, agriculture, drug designing, biomedical genome medicines, medical microbiology.

BIOINFO P: IV BIOINFO T IV: GENOMICS AND PROTEOMICS

TOTAL HOURS: 45 **CREDITS: 4**

1. Introduction of National Center for Biotechnology Information (NCBI).
2. Introduction of biological search engine- Entrez
3. Introduction to literature database at NCBI and querying the PUBMED central database using the ENTREZ search engine
4. Analysis of 3D structure of protein using RasMol through command line.
5. Analysis of 3D structure of protein and nucleic acid using Cn3D.
6. Pair-wise sequence alignment by using ClustalW.
7. Multiple sequence alignment by using ClustalW.
8. Introduction of BioEdit. Effect of insertion INDEL from given amino acid using
9. Pairwise and Multiple sequence alignment using BioEdit.
10. Phylogenetic analysis using web tool.

SUGGESTED READINGS:

1. Daniel, 2006, Biostatistics, Eighth Edition. John Wisley and sons.

2. Durbin, Eddy, Krogh, Mithison, Biological sequence analysis.

3. T.A.AttwoodandD.J.parry–smith, 2001, Introduction of Bioinformatics.

4. A.D.Baxevaris,1998, Bioinformatics:Apracticalguidetotheanalysisof

Genes and proteins,(Edited) B.F.Publication.

5. David W, 2005, Bio-informatics;sequenceandGenomeAnalysis,2ndEdition

By Mount CB Spublishers.

B.Sc BIOINFORMATICS (CBCS) REVISED SYLLABUS – 2020-21

BIOINFO T: V MOLECULAR BIOLOGY

TOTAL HOURS: 50 **CREDITS: 4**

UNIT-I **No. of hours: 10**

Genome Organization:

1.1 Organization of bacterial genome, Structure of eukaryotic chromosomes.

1.2 Role of nuclear matrix in chromosome organization and function, matrix binding proteins, heterochromatin and euchromatin, molecular components.

1.3 DNA reassociation kinetics (Cot curve analysis), repetitive and unique sequences, kinetics and sequence complexities.

1.4 Satellite DNA, DNA melting and buoyant density, packing and organization of chromatin, nucleosome phasing, DNase I hypersensitive regions, DNA methylation & Imprinting.

UNIT-II **No. of hours: 10**

2.1 Mutation:-Nonsense, missense and point mutations, intragenic and intergenic suppression, frameshift mutations, physical, chemical and biological mutagens.

2.2 Concepts of replication initiation, elongation and termination in prokaryotes and eukaryotes, enzymes and accessory proteins involved in DNA replication, Fidelity in replication, replication of single stranded circular DNA.

2.3 Gene stability and DNA repair, DNA repair enzymes, photoreactivation, nucleotide excision repair, mismatch correction, SOS repair.

UNIT-III **No. of hours: 10**

3.1 Recombination:- homologous and non-homologous recombination, site specific recombination, Holliday structure, resolution, chi sequences in prokaryotes, gene targeting, gene disruption, FLP/FRT and Cre/Lox recombination RecA and other recombinases.

3.2 Prokaryotic Transcription & Regulation: Promoters, Regulatory elements, Transcription unit, constitutive and inducible promoter, operators, Initiation, Attenuation, Termination, Rho-dependent and independent termination, Anti-termination, Transcriptional regulation, positive and negative regulation.

UNIT – IV **No. of hours: 10**

4.1 Operon concept, Regulation of transcription of lac, trp, ara, his, and gal operons, transcriptional control in lambda phage, Transcript processing.

4.2 Processing of t RNA.

4.3 Eucaryotic transcription and regulation: RNA polymerase structure and assembly, RNA polymerase I, II, III, Eukaryotic promoters and enhancers, General Transcription factors, TATA binding proteins (TBP) and TBP associated factors (TAF), Activators and repressors, transcription initiation, elongation and termination, activation and repression.

4.4 Transcriptional and post-transcriptional gene silencing, expression and processing of heterogeneous nuclear RNA, tRNA, rRNA, 5'-Cap formation,3'-end processing and polyadenylation, Splicing, RNA editing, Nuclear export of mRNA, mRNA stability, catalytic RNA.

UNIT – V **No. of hours: 10**

5.1 The translation machinery, ribosomes, composition and assembly.

5.2 Universal genetic code, degeneracy of codons, termination codons, isoaccepting tRNA, wobble hypothesis.

5.3 Mechanism of initiation, elongation and termination, Co- and post-translational modifications, genetic code in mitochondria.

5.4 Protein synthesis. Transport of proteins and molecular chaperones.

5.5 Protein stability, protein turnover and degradation.

BIOINFO P V: MOLECULAR BIOLOGY

TOTAL HOURS: 48 **CREDITS: 2**

1. Study of different types of DNA and RNA using micrographs and model / schematic Representations.
2. Study of semi-conservative replication of DNA through micrographs / schematic representations
3. Isolation of genomic DNA from *E. coli*
4. Estimation of DNA using UV spectrophotometer.
5. Resolution and visualization of DNA by Agarose Gel Electrophoresis.
6. Resolution and visualization of proteins by Polyacrylamide Gel Electrophoresis (SDS - PAGE).
7. Problems related to DNA and RNA characteristics, Transcription and Translation.
8. Induction of mutations in bacteria by UV light.
9. Instrumentation in molecular biology - Ultra centrifuge, Transilluminator, PCR

SUGGESTED READING:

- Freifelder, D. (1990). Microbial Genetics. Narosa Publishing House, New Delhi.

  Freifelder, D. (1997). Essentials of Molecular Biology. Narosa Publishing House, New Delhi.
- Glick, B.P. and Pasternack, J. (1998). Molecular Biotechnology, ASM Press, Washington D.C., USA.
- Lewin, B. (2000). Genes VIII. Oxford University Press, England.
- Maloy, S.R., Cronan, J.E. and Freifelder, D. (1994). Microbial Genetics, Jones and Bartlett Publishers, London.
- Ram Reddy, S., Venkateshwarlu, K. and Krishna Reddy, V. (2007) A text Book of Molecular Biotechnology. Himalaya Publishers, Hyderabad.
- Sinnot E.W., L.C. Dunn and T. Dobzhansky. (1958). Principles of Genetics. 5 th Edition. McGraw Hill, New York.

- Smith, J.E. (1996). Biotechnology, Cambridge University Press.
- Snyder, L. and Champness, W. (1997). Molecular Genetics of Bacteria. ASM press,
- Strickberger, M.W. (1967). Genetics. Oxford & IBH, New Delhi.
- Verma, P.S. and Agarwal, V.K. (2004). Cell Biology, Genetics, Molecular Biology, Evolution and Ecology. S. Chand & Co. Ltd., New Delhi.

Vth SEMEISTER PAPERS

THERE WILL BE THREE PAIRS OF EACH DOMAIN OF CORE COURSE.

STUDENT HAS TO CHOOSE ONE PAIR FROM EACH DOMAIN.

ELECTIVE THEORY

A – PAIR

B.Sc BIOINFORMATICS (CBCS) REVISED SYLLABUS – 2020-21

BIOINFO T: A1 PROGRAMMING IN C LONGUAGE

TOTAL HOURS: 40 **CREDITS: 4**

UNIT – I **No.of Hours: 8**

1.1 History of C

1.2 Characteristics of C

1.3 Program Structure, Constants.

1.4 Data types, Variables, Keywords, Console Input/output Statements, Compilation and Execution.

UNIT – II **No.of Hours: 8**

Operators, Branching & Looping Statements:

2.1Arithmetic Unary Assignment Relational & Logical Conditional

2.2 If Statement, Nested if, Statement else-if.

2.3 Ladder switch, Statement Looping.

2.4 Concepts for loop while loop do-while loop Jump Statements.

UNIT – III **No.of Hours: 8**

Arrays & Functions:

3.1 Array Concepts Rules & Restrictions.

3.2 Single & Multi Dimensional Arrays

3.3 Types of Functions, Functions and Arrays Function.

3.4 Prototyping, Scope of Variables Built-in Functions.

UNIT – IV **No.of Hours: 8**

4.1 String Functions, String Manipulation.

4.2 Pointer Concepts, Pointers and Functions Pointers and Arrays, 4.3 Array of Pointers, Static Initialization, Pointers and Structures, Illegal indirection.

4.4 Defining New Data types, Unions Type Casting Enumerated, Data types Static Variables, Type Definition.

UNIT – V **No. of Hours: 8**

5.1 Null pointers, pointers and settings

5.2 Pointer and two – dimensional arrays

5.3 Function philosophy

5.4 Function basics, Function prototypes

5.5 Storage classes and visibility

BIOINFO P: A1 PROGRAMMING IN C LONGUAGE

TOTAL HOURS: 48 **CREDITS: 2**

1 Find prime number between 1 to 50.

2 Write a program which uses switch & break case statements.

3 Find out length of given string.

4 Find area of rectangle using constructor

5 Write a program of insertion sort.

6 Write a program which implements stack operation.

7 Multithreading using get property.

8 Multithreading using sleep property.

9 Write a program which implements mouse listener and mouse motion listener.

10 Creating a frame window in an applet.

11 Draw line , rectangle, oval in an applet.

SUGGESTED READING:

1. The C Programming Language is written by Brian W. Kernighan and Dennis M. Ritchie.
2. C: The Complete Reference is written by Herbert Schildt.
3. Programming in ANSI C is written by E Balagurusamy.
4. Let Us C is written by Yashavant Kanetkar
5. Head First C is written by David Griffiths.

B.Sc BIOINFORMATICS (CBCS) REVISED SYLLABUS - 2020

BIOINFO T: A2 GENETIC ENGINEERING

TOTAL HOURS: 50 **CREDITS: 4**

UNIT – I No.of Hours: 10

1.1 Restriction analysis: Types of restriction enzyme, Type I, II and III, restriction modification systems, type II restriction endonucleases and properties, isoschizomers and neoschizomers, mcr/mrr genotypes, Cohesive and blunt end ligation, linkers, adaptors, homopolymeric tailing.

1.2 Labeling of DNA: Nick translation, random priming, radioactive and non-radioactive probes, use of Klenow enzyme, T4 DNA polymerase, bacterial alkaline phosphatase, polynucleotide kinase.

UNIT – II No.of Hours: 10

2.1 Gene Cloning Vectors: Plasmids, bacteriophages, Cloning in M13 mp vectors, phagemids, Lambda vectors. Cosmid vectors. Artificial chromosome vectors (YACs, BACs),

2.2 Animal Virus derived vectors- SV-40, vaccinia/bacculo & retroviral vectors.

2.3 Hybridization techniques: Northern, Southern and Colony hybridization, Fluorescence *in situ* hybridization.

2.4 DNA fingerprinting, chromosome walking & chromosome jumping.

UNIT – III No.of Hours: 10

3.1 Insertion of Foreign DNA into Host Cells: Transformation, Transfection.

3.2 Chemical and physical methods, liposomes, microinjection, macroinjection, electroporation, biolistics, somatic cell fusion, gene transfer by pronuclear microinjection.

3.3 Plant transformation technology: Basis of tumor formation, hairy root, features of Ti and Ri plasmids, mechanism of DNA transfer, role of virulence genes, use of Ti and Ri as vectors.

3.4 Cloning and expression in yeasts (Saccharomyces, Pichia etc.). Animal and plants cells.

UNIT – IV No.of Hours: 10

4.1 Methods of selection and screening, cDNA and genomic cloning, expression cloning, jumping and hopping libraries.

4.2 south western and far western cloning, yeast two hybrid system, phage display,

4.3 Construction of cDNA libraries in plasmids and screening methodologies, Construction of cDNA and genomic DNA libraries in lambda vector.

4.4 Principles in maximizing gene expression, Site-directed mutagenesis.

UNIT – V **No.of Hours: 10**

5.1 PCR - Primer design, Fidelity of thermostable enzymes, DNA polymerases, multiplex, nested, reverse transcriptase, real time PCR, touchdown PCR, hot start PCR, colony PCR, cloning of PCR products, T-vectors, proof reading enzymes, PCR in gene recombination, deletion, addition, overlap extension, and SOEing, site specific mutagenesis.

5.2 Applications:

PCR in molecular diagnostics, viral and bacterial detection, PCR based mutagenesis.

Sequencing methods: Enzymatic DNA sequencing, Chemical sequencing of DNA, principle of automated DNA sequencing, RNA sequencing.

Applications of recombinant DNA technology in medicine, agriculture, veterinary sciences.

5.3 **Gene Therapy:**

Creation of knockout mice, disease model, somatic and germ-line therapy in vivo and ex-vivo, suicide gene therapy, gene replacement, gene targeting.

BIOINFO T A2: GENETIC ENGINEERING

TOTAL HOURS: 40 **CREDITS: 2**

1. Isolation of Plasmid DNA from E.coli
2. Transformation in Bacteria using plasmid.
3. Restriction digestion of DNA and its electrophoretic separation.
4. Ligation of DNA molecules and their testing using electrophoresis.
5. Activity of DNAase and RNAse on DNA and RNA.
6. Isolation of Plasmid DNA.
7. Demonstration of PCR.
8. Electrophoretic separation of DNA fragments on agarose gel
9. Demonstration of southern blotting technique.
10. Demonstration of SDS – PAGE.

B – PAIR

B.Sc BIOINFORMATICS (CBCS) REVISED SYLLABUS – 2020-21

BIOINFO T: B1 CHEMOINFORMATICS

TOTAL HOURS: 50 **CREDITS: 4**

UNIT – I No. of Hours: 10

Alkanes, Alkenes and alkynes, Alkyl halides: rearrangement reactions of alkyl carbocation, Grignard reactions, nucleophilic substitution reactions;

Alcohols: esterification, dehydration and oxidation, reaction with sodium, phosphorus halides, ZnCl2/conc.- HCl, conversion of alcohols into aldehydes and ketones;

Aldehydes and Ketones: oxidation, reduction reactions,

Carboxylic acids: formation of esters, acid chlorides and amides, ester hydrolysis.

UNIT – II No. of Hours: 10

Amines: basicity of substituted anilines and aliphatic amines, preparation from nitro compounds, reaction with nitrous acid, azo coupling reaction of diazonium salts of aromatic amines. Introduction to cheminformatics, Evolution of cheminformatics, History of chemical information science, Use of cheminformatics, Prospectus of cheminformatics, History of medicinal chemistry.

UNIT – III No. of Hours: 10

Prodrugs and soft drugs, Drug targets , Drug solubility, Natural resources of lead compounds, Pharmacokinetics & drug metabolism.

Biological testing and bioassays, Preclinical testing and clinical trial, Synthesis,

Patenting and manufacture, Complexes and chelating agents,

Molecular modeling using computer.

UNIT – IV No. of Hours: 10

Combinatorial chemistry technologies & libraries. Solution phase synthesis, High-throughput synthesis and screening.

Combinatorial libraries, Analytical methods, Biopanning.

Peptide display libraries:- Design and construction, Chemical literature, Chemical information searches, Chemical information sources, Chemical name and formula searching, Analytical chemistry (Constitutional Chemistry), Chemical history, Biography, Directories, and industry sources.

UNIT – V **No. of Hours: 10**

Chemical Database Design. Bio Catalysts Database, The MOS Database, The Failed Reaction Database, Protecting Groups Database, Solid-Phase Synthesis Database Database concepts, structured query language, Design of chemical database, data abstraction, bio Catalysts Database, Reaction database, Failed reaction Database, Sequence Database, Spectra Database,

Toxicology Database

BIOINFO P: B1 CHEMOINFORMATICS

TOTAL HOURS: 40 **CREDITS: 2**

1. Model building of nucleic acid, protein and organic molecules using the ISIS draw.
2. Model building of nucleic acid, protein and organic molecules using the chemsketch
3. Introduction to PDB.
4. Downloading and analysis of the pdb file of the biomolecules.
5. Analysis of Secondary and tertiary structure of protein using visualizing software like Rasmol.
6. Analysis of quaternary structure of protein using visualizing software liken Rasmol.
7. Analysis of the secondary structure of protein using web tool.
8. Three dimensional structure prediction by using the homology modeling technique using SPDBV.
9. Energy calculation of the biomolecules using molecular mechanics and quantum mechanics. (Argus lab).
10. Calculate PI/MW of protein.

B.Sc BIOINFORMATICS (CBCS) REVISED SYLLABUS – 2020-21

BIOINFO T: B2 VISUAL BASIC AND NET BANKING

TOTAL HOURS: 50 **CREDITS: 4**

UNIT – I No.of Hours: 08

1.1 Event driven programming, History of VB.Net, Features of VB.Net, Architecture of VB.Net [.Net server, framework,services etc.].

1.2 Net Framework: framework components, classes, CLR, VB.Net IDE, VB.Net: Variables, Keywords, constants, Data types, Conditional statements, looping statements, case control statements.

UNIT – II No.of Hours: 08

Activex controls, Forms, Controls & properties Text Boxes, Labels, Command Button, Radio Button, Option Buttons, Check Boxes, List Box ,ComboBox,Scoroll Bar, Progress Bar, Group Box, Calendar, Date Time Picker, Picture Box, Image List, Rich Text Box, Popup/Content Menus, List View Control , Tree View Box.

UNIT – III No.of Hours: 08

The array class collections, lists, string class, jagged array, array list String class and function. OOP using .net Classes Objects, constructor, destructor Methods, properties, delegates, assemblies, namespaces.

UNIT – IV No.of Hours: 08

Inheritance, Single, multiple, multilevel inheritance, Polymorphism-constructor overloading, method overloading, overriding, File operation-read, write, delete, Exception - type of errors, structured and unstructured exception.

Tracing errors: breakpoint, watch, quick watch, locals and autos.

UNIT – V No.of Hours: 08

Components of ADO.Net, Features of ADO.Net, Datasets, Data table, Datarow, datacolumn, Datareader, ADO.Net programming.

BIOINFO P: B2 VISUAL BASIC AND NET BANKING

TOTAL HOURS: 40 **CREDITS: 2**

1. Molecular Docking of protein and ligand by HEX.
2. Protein Structure Prediction (Homology Modeling) using SPDBV.
3. Model Building and Energy minimization using Sybyl7.3.
4. Model Building and Energy minimization using SPARTAN.
5. Model Building and Energy minimization Gaussian.
6. Quantum chemical (QM) and molecular mechanics (MM) practical using SPARTAN.
7. Quantum chemical (QM) and molecular mechanics (MM) practical using Gaussian.
8. Molecular dynamics (MD) simulation using Gromacs.
9. Molecular dynamics (MD) simulation using Sybyl.
10. Molecular dynamics (MD) simulation using AMBER.

C – PAIR

B.Sc BIOINFORMATICS (CBCS) REVISED SYLLABUS – 2020-21

BIOINFO T: C1 TRUCTURAL BIOINFORMATICS AND DRUG DESIGN

TOTAL HOURS: 50 **CREDITS: 4**

UNIT – I No. of Hours: 10

1.1. Nucleic acid structures, RNA folding, RNA loops, conformational study.

1.2. Protein-protein interactions, protein ligand interactions. DNA-binding proteins, RNA-binding proteins.

1.3. Ramachandran plot, Strutural databases:- Protein Data bank (PDB), Nucleic Acid Data Bank (NDB),Molecular modeling Data Bank (MMDB).

1.4. Protein identification and characterization:- AACompIdent, TagIdent, PepIdent and MultiIdent, PROSEARCH, PepSea, PepMAPPER, FindPept.

UNIT – II **No. of Hours: 10**

Molecular modeling:-Introduction, force field, quantum chemistry, Schrödinger equation, potential energy functions.

various approximations; LCAO, HF, semi-empirical calculations; single point calculations, full-geometry optimization methods, ZDO, MNDO, CNDO, NDDO, AM1, PM3, RM1.

Molecular mechanics:-Definition, balls and springs, force fields, bond-stretching, bond-bending, dihedral motions, out of plane angle potential, non-bonded interaction, coulomb interactions, conformational search, united atoms and cut-offs.

UNIT – III **No. of Hours: 10**

Antibacterial antibiotics; narrow spectrum and broad spectrum antibiotics.

Recent advances in pharmaceutical Biotechnology: synthetic vaccines, DNA vaccines, edible vaccines.

Policies in drug designing:- Quality assurance: ISO, WHO, certification, Good manufacturing practices, GMP, GLP, Government regulations, policies, Food and drug administration. IPR

Bioinformatics in drug development, Chemo informatics and Pharmaco informatics.

Applications of Drug Discovery and In-Silico Drug Designing, Area influencing drug discovery; Molecular Biology, pharmaco genomics and pharmaco proteomics.

UNIT – IV **No. of Hours: 10**

Introduction, Structure-based drug designing approaches: - Target Identification and Validation, homology modeling and protein folding, receptor mapping, active site analysis and pharmacophore mapping, Grid maps.

UNIT –V **No. of Hours: 10**

Introduction, Ligand-based drug designing approaches: Lead Designing, combinatorial chemistry, High Throughput Screening (HTS), QSAR, Database generation and Chemical libraries, ADME property.

Introduction to docking methods to generate new structure; Tools and Molecular docking programs: AutoDock, Dock, HEX.

BIOINFO P: C1 TRUCTURAL BIOINFORMATICS AND DRUG DESIGN

TOTAL HOURS: 40 **CREDITS: 2**

1. Accept three numbers & find out the largest & lowest among these.
2. Calculate compound interest of given principal amount for given time period with given rate of interest. Use appropriate controls.
3. Implement a standard calculator.
4. Accept 10 elements in array & perform binary search.
5. Demonstrate string class method & properties.
6. List box & combo box demonstration with differences in properties.
7. Simple class & object based programs.
8. Calculate difference between two dates use proper User Defined data type.
9. Demonstrate simple polymorphism.
10. Connect your application to Ms-Access/SQL server database using ADO.Net classes.
11. Implement read and write operation of file.
12. Design different application using SQL/MS-Access and ADO.Net.

B.Sc BIOINFORMATICS (CBCS) REVISED SYLLABUS – 2020-21

BIOINFO T: C2 BIODIVERSITY INFORMATICS & PROGRAMING IN PERL

TOTAL HOURS: 50 **CREDITS: 4**

UNIT – I No. of Hours: 10

Introducing biodiversity informatics: - Global patterns of distribution of biodiversity, biomes, Composition and distribution of biodiversity in India.

Taxonomic Database Working Group (TDWG) standards, compatibility and interoperatability, taxonomically intelligent systems.

Identification of plants and animals: Floral and faunal survey techniques, inventorying and monitoring of species and the use of diversity indices to assess habitats.

UNIT – II No. of Hours: 10

Identification of plants and animals: Floral and faunal survey techniques, inventorying and monitoring of species and the use of diversity indices to assess habitats.

Software used to discover phylogenies, use and status of specimen data, species distribution, example software projects for compiling data.

Ex-situ conservation: Protected Area Network of India, Assessing the status of species, Threats from invasive alien species.

UNIT – III No. of Hours: 10

The Organization of DNA ,The Organization of Proteins , In Silico, Limits to Computation

Getting started with perl:- A Low and Long Learning Curve.

Perl's Benefits, Installing Perl on Your Computer, How to Run Perl Programs, Text Editors and Finding Help.

The art of programming:-Individual Approaches to programming, Edit-Run-Revise (and Save), An Environment of Programs, Programming Strategies.

UNIT – IV No. of Hours: 10

The Programming Process, sequences and strings:- Representing Sequence Data, A Program to Store a DNA Sequence , Concatenating DNA Fragments.

Transcription: DNA to RNA, Using the Perl Documentation, Calculating the Reverse Complement in Perl, Proteins, Files, and Arrays , Reading Proteins in Files, Arrays Scalar and List Context.

Motifs and Loops:-Flow Control , Code Layout, Finding Motifs, Counting Nucleotides, Exploding Strings into Arrays, Operating on Strings Writing to Files.

UNIT – V **No. of Hours: 10**

Subroutines and Bugs: - Subroutines, Scoping and Subroutines , Command-Line Arguments and Arrays, Passing Data to Subroutines, Modules and Libraries of Subroutines, Fixing Bugs In Your Code.

Mutations and Randomization: - Random Number Generators, A Program Using Randomization, A Program to Simulate DNA Mutation, Generating Random DNA, Analyzing DNA.

The genetic code:-Hashes, Data Structures and Algorithms for Biology, The Genetic Code, Translating DNA into Proteins, Reading DNA from Files in FASTA Format, Reading Frames.

BIOINFO P: C2 BIODIVERSITY INFORMATICS & PROGRAMING IN PERL

TOTAL HOURS: 40 **CREDITS: 2**

1. Understanding various functions of perl.
2. Installing perl on your PC.
3. Create perl script.
4. Write a program to store protein sequence.
5. Write a program to store DNA sequence.
6. Write a program to store RNA sequence.
7. Use perl to concatenation of DNA
8. Use perl to concatenation of protein sequence.
9. Perl script for to simulate DNA mutation.