



**MAHATMA GANDHI UNIVERSITY**  
*of*  
**MEDICAL SCIENCES & TECHNOLOGY**  
JAIPUR

# **Syllabus**

**M. Sc. Bioinformatics**

**(2 Years Post Graduate Degree Course)**

## **NOTICE**

1. Amendments made by the court of the management of the university in rules/regulations of Graduate Medical Courses shall automatically apply to the rules/ regulations of the Mahatma Gandhi University of Medical Sciences and Technology.
2. The university reserves the right to make changes in the syllabus /books/ guidelines, fee-structure or any other information at any time without prior notice. the decision of the university shall be binding on all.
3. The jurisdiction of all court cases Shall be Jaipur Bench of Honorable Rajasthan High Court only.

**Rules and Regulations of  
M. Sc. Bioinformatics  
(2 Years Post Graduate Degree Course, Full Time)**

## **INTRODUCTION**

Biology is increasingly a field dominated by high-throughput methods, yielding large data sets which require data analysis using both public domain/commercial software as well as new algorithms to be implemented in a programming language. Previous generations of biologists painstakingly isolated proteins using techniques from biochemistry, collaborating protein chemists then determined the 3dimensional structure by X-ray diffraction, binding sites and protein function were determined, genetic screens were employed, etc. While this work is and will remain critical for biology, there has been a paradigm shift, from the older model, which can be summarized as *many experiments, one gene*, to the newer model of *one experiment, many genes*.

Along with this paradigm shift, newer computational techniques, going well-beyond classical bio statistics, have become necessary. Some buzzwords: profile, hidden Markov model, neural network, support vector machine, Monte Carlo, etc. The new fields of *bio informatics* and *computational molecular biology* have seen an influx of mathematicians, computer scientists, physicists, chemists, statisticians working on problems.

Bio informatics is a rapidly maturing field at the confluence of biology, mathematics and computer science. It strives to better understand the molecules essential for life, by harnessing the power and speed of computers. Mathematical models and software are developed by computational biologists, who must have good skills in math and computer science. However, the working (experimental) biologist is generally a user of "black box" bio informatics software and databases, with little knowledge of the underlying algorithms. While there's no need for the working biologist to be able to be able to develop sophisticated mathematical models or design and implement novel algorithms, there is a need to understand the broad ideas of algorithms underlying the tools the biologist uses. As a working professional in the medical and life sciences, this knowledge is important to understand the scope, applicability, and limitations of certain tools -- and, who knows, you may become turned on by the idea of ferreting out biological insights by applying mathematics and computer science, and so choose to pursue further courses to become a computational biologist.

This introductory course requires that you have a basic understanding of molecular biology, genetics, and use of Internet, but does not require that you have any background in mathematics or programming -- nevertheless, if you have had a course in probability theory and statistics, then you'll understand more easily some of the approaches. Nevertheless, the class will be self-contained, and I will not assume that anyone has had any math beyond calculus.

### **Objectives of The Course:**

- To broadly understand the type of mathematical and algorithmic reasoning that lies behind various important bio informatics tools,
- To gain some working knowledge in using certain biological databases and on-line bio informatics algorithms.

## **JOB OPPORTUNITIES**

There are multiple job opportunities available to Bio informatics graduates. The following is just a sample of jobs in various practice settings:

The course is suitable for anyone who has a good biology or mathematics base and is keen on research and pure sciences. It is a field of immense possibility for growth. The career, being a mix of both science and technology, gives you a number of options for fields that you can branch into after. Due to the need for both advancements in the medical field, this course has job opportunities in every corner. Several companies abroad have very high pay for Bio informatics graduates, especially laboratories. In India, since it, a growing field, the pay you receive is always steadily rising.

Academically, the course has a lot of scope in the case of masters as well as specializations. It also makes the candidate eligible for a PhD. and is hence, a very respectable course to pursue. This is a field that provides useful information to several other fields and is thus, very much in demand.

### **Listed here are a few popular careers in the field of Bioinformatics**

1. Bio information Analyst -Development of algorithms and software to determine the cure for diseases by studying their pathology. It also involves analyzing complex life forms, as well as other biological data.
2. Team Leader-Heads a research group of Bioinformatics graduates as well as organizes the process of both study and analysis.
3. Research Associate-Performs tasks related to research, study and innovation in the field of Bio informatics.
4. Bio Statistician- Deals with the collection, study and interpretation of data using the methods of statistics to come up with results in the field of bio informatics.
5. Computational Biologist-Study of biological systems using biological data that has been analyzed with the use of the software.
6. Bio informatics Software Developer-Helps with the creation and handling of software that is used to process and analyze biological data.
7. Pharmaceutical Research Statistician, Clinical Trials Coordinator, Data Manager-Provides data management services in order to meet customer needs. Manages projects, staff, and timelines.
8. Information Technology System Analyst, Project Manager, Data Manager-Works with software vendors to design clinical software, provides training to end-user staff, assists with system installations, provides system support.
9. Medical Software Companies Software Designer Software Tester-Designs and develops databases, performs various software testing, assists clients with system installations.

**Expectation From the Future Post Graduates Of Bioinformatics in the Industry:** On completion of this course, the students will be able to:

- How to determine the location of genes in a genome.
- How to assign putative function to computationally determined open reading frames.
- How to determine the likely secondary and tertiary structure of a protein, given the 1dimensional amino-acid sequence.

- How to compute the likely secondary structure, given an RNA nucleotide sequence.
- How to determine the signal portion and cleavage site of a signal peptide. □ Evaluate knowledge of practice relevant to Bio information management.
- Use formal research as a tool to evaluate and develop practice.
- Identify his/her professional learning and developmental needs.

### **1. TITLE OF THE COURSE:**

The title of the course shall be “**M. Sc. Bioinformatics**”

### **2. DURATION OF THE COURSE/ PERIOD OF THE TRAINING**

The duration of certified study of the M. Sc. Bioinformatics course shall extend over a period of 2 (two) academic years (**1720** hours of Theory and **480** hours of Practical Classes) and **550 hours** (last Four months) of project work. The student, upon successful completion of the course will be awarded M. Sc. Bioinformatics from MGUMST.

**Total hours – 2750.**

### **3. ELIGIBILITY FOR ADMISSION**

1. B. Sc. Bioinformatics or Pass in any health science undergraduate program of 3- and 4-years duration or equivalent with minimum aggregate of **50%** for general category and **45%** marks for reserved category candidates marks in any science group or allied health/Health administration. A candidate also must have passed in English (CORE or selective or functional) as a subject of studies in the qualifying examination.
2. Candidates will be required to produce evidence of their passing graduation latest by the day of personal interview.
3. Candidates with relevant work experience are encouraged to apply. Working professionals will be considered for admission only after submitting NOC from their employer.

### **4. MEDIUM OF THE COURSE**

English shall be the medium of instruction for all the subjects of study and for examination of the course.

### **5. CURRICULUM**

The curriculum and the syllabus for the course shall be as prescribed by the academic Council from time to time.

### **6. SELECTION PROCEDURE**

1. Admission to M. Sc. Bioinformatics course shall be made on the basis of eligibility criteria set by university and interview to be conducted for the purpose.
2. Successful candidates on the basis of 12<sup>th</sup> percentage will be called for the University combined entrance examination followed by interview & shall have face an interview board. The interview board will include the Principal of Institute of Health Informatics and Head of the Institution, whose recommendations shall be final for the selection of the students.
3. During subsequent counseling (s) the seat will be allotted as per the merit of the candidate depending on the availability of seats on that particular day.
4. Candidate who fails to attend the Entrance Examination on the notified date(s) will forfeit the claim for admission and placement in the waiting list except permitted by the competent authority under special circumstances.
5. The name of the student(s) who remain(s) absent from classes for more than 15 days without information at a stretch after joining the said course will be struck off from the college rolls without giving any prior notice.

## **7. ENROLLMENT**

Every candidate who is admitted to M. Sc. Bioinformatics degree course in Mahatma Gandhi Institute of Health Informatics shall be required to get himself/herself enrolled with the Mahatma Gandhi University of Medical Sciences & Technology (MGUMST) after paying the prescribed eligibility and enrolment fees.

A candidate shall deposit enrolment fees along with tuition fees at the time of his/her admission to the course. Such a candidate who fails to submit, through the college Principal, duly filled enrolment form along with original documents including migration certificate required for enrolment within two months of his/her admission or up to November 30 of the year of admission whichever is later, he/she will have to pay late fee prescribed by the University

## **8. COMMENCEMENT OF THE COURSE**

The course shall commence from the 1 August of every academic year.

## **9. ATTENDANCE**

No candidate shall be permitted to appear for any one of the parts of M. Sc. Bioinformatics degree course examinations, unless he/ she has attended the course in the subject for the prescribed period in an affiliated Institution recognized by this University and produces the necessary certificate of study, attendance, satisfactory conduct and progress from the Head of the Institution.

- \* A candidate is required to put in a minimum of **75%** of attendance in both theory classes and practical's separately before appearance to the examination. This relaxation in attendance includes for medical & any other reasons approved by the head of the Institution.

- \* A candidate lacking in the prescribed attendance and progress in any one of the subjects in theory and practical in the first appearance shall not be permitted for admission to the entire examination.

## **10. SCHEME OF EXAMINATION**

The students will be Assessed/ Evaluated as under: -

A candidate shall be declared to have passed the examination if he or she obtains the following qualifying marks:

**50%** marks in the university examination and **50%** marks in internal assessment evaluated by the department.

Practical examination and 50% aggregate in practical and 50% internal evaluation marks evaluated by the department.

### **10.1 Internal Assessment (carrying 30% weightage)**

Internal assessments will be conducted in every year. Internal assessments will consist of departmental examinations, departmental posting evaluations / seminars and 05 (five) case studies/project reports. The objective is to allow students to have hands on experience. It would also help students to develop and formulate the data collection process and data analysis.

### **10.2 University Examination (Carrying 70 % weightage)**

- a) Each theory paper examination shall be of 3 hours duration and of maximum marks 70.
- b) There will be six question papers of theory in first year and shall be in accordance with the different subjects/area covered during First year course.
- c) There will be Five question paper of theory in accordance with the different subjects/area covered during Second year course.
- d) For the First- and Second-year examinations, the university will appoint internal and external examiners, one of the external examiners will be invited from the other recognized university. question papers shall be set by these examiners (appointed by the university) covering their respective areas of syllabus. The answer book shall be evaluated by the concerned examiners.
- e) The Paper setter shall set the questions within the prescribed course of study of the concerned paper. There will be a set pattern of question papers duly approved by Academic Council. Model question paper is annexed with this document.
- f) Passing mark - A candidate will have to obtain at least 50% marks in each Theory paper to pass.
- g) Revaluation of answer books is not permitted. However, scrutiny of answer books is allowed as per MGUMST rules. There will be no grace marks awarded.
- h) University examination shall be conducted twice in a year, that is main and supplementary examination
- i) Answer books will be evaluated by both external and internal examiners. It will be decided by the President as to which paper to be assigned to which examiner for evaluation.
- j) If a student fails in any year examination expect second year, she/he will be allowed to write supplementary exam after every 06 months. However, if a student fails in three and more papers, she/ he will not be promoted to next year. Consolidated score sheet of internal assessment will be submitted by the college to MGUMST within 15 days of conclusion of second year.

### 10.3 Practical

#### Examination format.

First year – 200 Marks (100 External + 100 Internal)

Second year – 400 Marks (200 External + 200 Internal)

Dissertation – 200 Marks (100 External + 100 Internal)

It shall be left on the examiners – Internals and the Externals, as the case may be, to examine and evaluate the students in the way they wish and award the marks without giving any specific details. The total marks obtained by the candidate in the Project assignment and viva shall be the aggregate of the marks awarded by all the examiners put together as one figure.

**A student shall be required to obtain a minimum of 50% pass mark in the Dissertation examination. A candidate who fails to obtain 50% marks shall be declared failed.**

### 10.4 Dissertation

1. All students will be required to write a dissertation involving primary research in his/her area of interest.
2. The dissertation includes a critical review of literature pertaining to the specific area of interest data analysis and analysis of the selected problem.
3. One faculty member will be assigned as a guide to each student in consonance with university/council norms.
4. Synopsis/protocol of the dissertation shall be submitted by the student after three months of admission of course.
5. Dissertation duly completed and signed by guide shall be submitted at least three months before the final year exam.
6. The dissertation will be examined by two examiners appointed by the university.
7. Student shall be allowed to appear for the university examinations only after the acceptance of the dissertation by the examiners.

### 10.5 Distinction

A student scoring more than 75% marks in any paper will be awarded distinction in that paper.

### 10.6 Evaluation weightage

The final evaluation for each subject shall be based on internal assessment components (30 percent weight) and University Examination (70 percent weight) conducted by the University.

#### WEIGHTAGE DISTRIBUTION

Item	Weight (%)
<b>1.Internal assessment</b>	
Class participation/presentation, assignments, study records	<b>10.00%</b>
Assignment, quizzes and summer training report	<b>10.00%</b>



Departmental Postings, case studies, project reports	<b>10.00%</b>
<b>2.University exam</b>	<b>70.00%</b>
<b>Total</b>	<b>100%</b>

YEAR WISE EVALUATION MARKS DISTRIBUTION									
Year	Paper	Theory			Practical			Total	Totals
		IA	UE	Pass Marks	Internal	External	Pass Marks		
<b>First year</b>	I	30	70	50 % in each IA & UE	----	----	50 % in each IA & UE	100	<b>800</b>
	II	30	70		----	----		100	
	III	30	70		50	50		200	
	IV	30	70		---	---		100	
	V	30	70		50	50		200	
	VI	30	70		----	----		100	
<b>Second year</b>	I	30	70	50 % in each IA & UE	50	50	50 % in each IA & UE	200	<b>1100</b>
	II	30	70		50	50		200	
	III	30	70		50	50		200	
	IV	30	70		50	50		200	
	V	30	70		---	----		100	
	<b>Dissertation VI (Viva-Voce)</b>	-	-			100		100	
<b>GRAND TOTAL</b>	<b>11</b>	<b>330</b>	<b>770</b>		<b>400</b>	<b>400</b>		<b>1900</b>	

## 11. Result:

Result – Division: Successful candidates will be categorized as under.

1	Those securing 50% and above but less than 60% in the aggregate marks of First and Second year taken together (Aggregate marks)	Pass
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2	Those securing 60% and above but less than 75% in the aggregate marks of First and Second year taken together (Aggregate marks)	Pass with First Division
3	Those securing 75% and above in the aggregate marks of First, marks of First and Second year taken together (Aggregate marks)	Pass with Honors

## 12. Promotion to 2<sup>nd</sup> year of the program

- A candidate if failed in one or two subjects in in first year of the M. Sc. Bioinformatics program can be promoted in second year.
- A candidate can take any number of attempts with condition that maximum period allowed to complete the M. Sc. Bioinformatics Shall be 4 years.
- Results of the candidates successful at the final year examination will be declared only after clearing back paper subjects of first and/or second year if any by him.

## 13. Supplementary examination.

University examination shall be conducted in every six months, that is main and supplementary examination.

## 14. Authority to issue transcript

**The Controller of Examination of the University shall be the authority for issuing transcript after receiving the described fee from the candidate**

## 15. Nomenclature of Papers

	<b>M. Sc. Bioinformatics First year</b>
Paper Ist	Cell Biology, Microbiology and Virology
Paper IInd	Bio-molecules
Paper IIIrd	Basic of computer, Mathematics and Bio statistics
Paper IVth	Molecular Biology
Paper Vth	Genomics and Proteomics
Paper VIth	Immunology
	<b>M. Sc. Bioinformatics Second Year</b>
Paper Ist	Genetic Engineering
Paper IInd	Advances in Structural Bioinformatics
Paper IIIrd	Drug designing
Paper IVth	Programming in Perl
Paper Vth	Research & its Application
<b>Dissertation</b>	

## 16. COURSE OUTLINE

Duration	02 Years
Working Days	6 Days in A Week
Working Hours	36 Hours in A Week

### Course Outline

#### M. Sc. Bioinformatics (First Year)

**Duration: 960 Hours (Theory) Practical: 320 Hours (Practical)**

#### **PAPER I - Cell Biology, Microbiology and Virology (160Hrs..)**

##### **Unit- I (40Hrs..)**

Cell as a basic unit of life., Cell organization of prokaryotic and eukaryotic cells.,Structural and functional capitalization of cell:–Mitochondria, Chloroplast, Lysosomes, Golgi bodies,Plasma membrane, Cytoskeleton, Cell wall and Nucleus.

##### **Unit- II (40Hrs..)**

Cell cycle, cell division - mitosis and meiosis. Chromosome structure, gene, gene number, gene clusters and Pseudo gene,Polytene and lamp brush chromosomes,Packing of DNA, supercoiled DNA nucleosome ,Inverted repeats, repetitive DNA sequence, satellite DNA,Cell trafficking.

##### **Unit- III ( 40Hrs.)**

Structure, classification and general characteristics of Bacteria,(including ribotyping) ,Mycoplasma, Protozoa, Archea and yeast,Fungi. Association of bacteria.,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., Sterilization-Application of sterilization methods in biotechnology, Various sterilization methods, Microbial contamination control and Sterility testing. Microbial growth: The definition of growth, mathematical,expression of growth, growth curve, measurement of growth and growth yield, synchronous growth, continuous culture.

##### **Unit- IV ( 40Hrs.)**

Classification and General properties of plant, animal and bacterial viruses, Bacteriophages - lytic cycle & lysogeny. Structure of viruses, assembly of viral membrane., Life cycle and replication of viruses: RNA-negative strand (VSV), positive strand (Polio), segmented [Influenza], Retrovirus- RSV and HIV, DNA- adenovirus and SV-40. Cultivation in cell culture, chick embryo and animal inoculation. Persistent chronic and acute viral infections. Mechanism of interferon and antiviral therapy. Host virus interactions; plant and animal.

## **PAPER II : Biomolecules (160 Hours)**

### **Unit- I ( 40Hrs.)**

Classification, Structures and Carbohydrate Metabolism, Classification, characteristics and functions of monosaccharides, disaccharides – polysaccharides, Epimers, isomers, anomers, chiral carbon atom, chair and boat form, glucopyranose and fructopyranose, General scheme of metabolism, historical and experimental details in derivation of a metabolic pathway, Glycolysis - aerobic and anaerobic, regulation of glycolysis, Krebs cycle and its regulation, Hexose monophosphate shunt.

### **Unit-II ( 40Hrs.)**

Amino Acids and Proteins Chemical structure and general properties of amino acids, pI of amino acids, acid base concepts, Henderson and Hasselbalch equation, General metabolism scheme of amino acids and Urea cycle Proteins Classification- size, shape, degree of association, complexity. Classification of proteins according to biological functions (Enzymes, transport, storage, contractile, structural, defense and regulatory). Protein structure , Secondary structure - alpha helix and beta pleated structure, triple helix (collagen) and Super secondary structures, Tertiary structure - forces stabilizing tertiary structure, unfolding/refolding experiment, prediction of secondary and tertiary structure, Dynamics of protein folding, role of molecular chaperones in protein folding, Lysosomal and membrane proteins. Quaternary structure - forces stabilizing quaternary structure, Structure function relationship - myoglobin and hemoglobin, Techniques for studying primary sequence of proteins, experimental methods, end group analysis, finger printing and sequenators.

### **Unit- III ( 40Hrs.)**

Lipids Definition and classification of lipids. Fatty acids – general formula, nomenclature and chemical properties Structure, function and properties of simple, complex, acylglycerols, phosphoglycerides, sphingolipids, waxes, terpenes, steroids and prostaglandins, Beta oxidation - pathway and regulation, Role of acyl carnitine in fatty acyl transport. Synthesis of fatty acid - structure and composition of fatty acid synthetase complex, pathway and regulation. synthesis of triacyl glycerides, Ketone bodies - formation and utilisation.

### **Unit- IV ( 40Hrs.)**

Enzymes and Nucleic acids, Classification of enzymes, IUB system, enzyme substrate complex, active site of enzymes, stereo specificity and ES complex formation, Effect of temperature and pH and substrate concentration on reaction rate, Activation energy, transition state theory, enzyme activity. Michaelis-Menten equation, significance of Vmax and Km, Enzyme inhibition, types of inhibitors and mode of action, Chemical modification of enzymes, Structure and functions of Ribonuclease, trypsin, chymotrypsin,

Enzyme regulation, feedback control, product inhibition, Structure of nucleoside, nucleotide. De novo and salvage pathways of nucleotide synthesis. Experimental evidence for nucleic acids as genetic material, Secondary structure of DNA, Watson and Crick model of DNA.

A, B and Z forms of DNA, Tm and its relation to GC content, Chemical and enzymatic degradation of nucleic acids.

### **PAPER III: Basic of Computer, Mathematics and Biostatistics (160 Hours)**

#### **Unit- I (40Hrs.)**

Introduction to Computers, History and development of computers; generations of computers; (I, II, III, IV and V), classifications of computers; analog computers, digital computers, mainframe computers, miniframe computers, microcomputers, fundamentals of logical concepts. Digital Computers:- Basic principle of operation of digital computers, structure of digital computers; arithmetic unit, central unit, memory unit, Input unit and output unit, Computer Coding:- Number system, decimal number system, binary number system, binary to decimal conversion, Binary arithmetic, octal number system, hexadecimal number system.

#### **Unit-II ( 40Hrs.)**

Languages and flow charts and Operating Systems:- Machine level languages, assembly level languages, high level languages, Input and Output devices :- Punched card reader, paper tape reader, magnetic tape, floppy disk, magnetic disk, optical scanner, voice data, entry terminal, teleprocessing terminal, visual display, unit, modern input devices, Output devices; CRT, printer, plotter. Memory: - Primary memory or main memory; magnetic core memory, semi-conductor memory, RMA, ROM, PROM, EPROM, EEPROM. Secondary memory or auxiliary memory or storage devices; Hard disk, diskette, magnetic tape, ZIP, devices, digital tape, CD-ROM, DVD, virtual, memory, cache memory. Operating Systems:- DOS, windows 98/XP/VISTA, UNIX/LINUX, Mac OS, VMS.

#### **Unit- III ( 40Hrs.)**

Modern Computers, Workstations, parallel processing computers, supercomputers, Internet and related programmes: - WWW, HTML, HTTP, telnet, FTP, computer domain, Introduction to Biostatistics: Applications and uses, sample variable, statistical sampling, population, primary and secondary data, screening and representation of data, frequency distribution, bar diagram, histogram. Pie diagram, cumulative frequency curves, Mean, median, mode, Comparison between mean, median and mode, Measures of dispersion: range, variation, standard deviation, coefficient of variation, symmetry, probability distribution.

#### **Unit- IV ( 40Hrs.)**

Basic Mathematics, Sets:- Finite set, infinite set, null or void set, subset, Intervals; closed and open, universal set, operations of set. Relations and functions. Matrices:- Types of matrices,

properties of matrices, addition, subtraction of matrices, matrix, multiplication, elementary transformation, inverse of matrices. Determinants: - Definition, properties associated with determinants. Trigonometry and Derivatives. 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.

## **Paper IV: Molecular biology (160 Hours)**

### **Unit- I (40Hrs.)**

Genome Organization of bacterial genome, Structure of eukaryotic Chromosomes, Role of nuclear matrix in chromosome organization and function, matrix binding proteins, heterochromatin and euchromatin, molecular components, DNA reassociation kinetics (Cot curve analysis), repetitive and unique sequences, kinetics and sequence complexities, Satellite DNA, DNA melting and buoyant density, packing and organization of chromatin, nucleosome phasing, DNase I hypersensitive regions, DNA methylation & Imprinting, Mutation:-Nonsense, missense and point mutations, intragenic and intergenic suppression, frameshift mutations, physical, chemical and biological mutagens.

### **Unit-II ( 40Hrs.)**

DNA Replication, Repair & Recombination ,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, Gene stability and DNA repair, DNA repair enzymes, photoreactivation, nucleotide excision repair, mismatch correction, SOS repair, 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.

### **Unit- III ( 40Hrs.)**

Prokaryotic & Eukaryotic Transcription, 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, Operon concept, Regulation of transcription of lac, trp, ara, his, and gal operons, transcriptional control in lambda phage, Transcript processing, Processing of tRNA and rRNA, 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. 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- IV ( 40Hrs.)**

Translation & Transport ,The translation machinery, ribosomes, composition and assembly. Universal genetic code, degeneracy of codons, termination codons, isoaccepting tRNA, wobble hypothesis, Mechanism of initiation, elongation and termination, Co- and post-translational

modifications, genetic code in mitochondria, Protein synthesis. Transport of proteins and molecular Chaperones, protein stability, protein turnover and degradation.

## **Paper V: Genomics and Proteomics (160 Hours)**

### **Unit- I ( 40Hrs.)**

Genomics: Nucleotide sequence Databases, its Analysis and Identification, Goals of the Human Genome Project, cloning vectors, concept of maps, physical maps, shotgun libraries, DNA polymorphism, nucleotides, DNA sequences, Sequence databases: GeneBank, EMBL Nucleotide sequence databank, DNA Data Bank of Japan (DDBJ), database formats. Recombinant DNA technology, restriction enzymes, resource for restriction enzyme (REBASE), similarity search. Polymerase chain reaction, primer selection for PCR, BLASTn, application of BioEdit. Genome information and special features, coding sequences (CDS), untranslated regions (UTR's), cDNA library, expressed sequence tags (EST), Approach to gene identification; masking repetitive DNA, database search, codon-bias detection, detecting functional sites in the DNA. Internet resources for gene identification, detection of functional sites, gene expression.

### **Unit-II ( 40Hrs.)**

Gene expression: - Introduction, Basic steps for gene expression. Microarray:- Concept of microarrays; spotted arrays, oligonucleotide arrays, designing the experiment, Two-color microarray experiments. Clustering gene expression profiles; Agglomerative, Hierarchical, Nearest neighbour (Single-linkage), complete linkage, average-linkage, weighed pair-group average, k-means clustering, self-organizing maps (SOM) clustering. Tools for microarray analysis; soft-finder, xCluster, MADAM, SAGE, Microarray design, microarray experimentation, fabrication computational analysis of Microarray data, Applications of microarray technology. Proteomics:- Protein sequence information, composition and properties, physicochemical properties based on sequence, sequence comparison, Primary databases, Secondary databases. Pair-wise sequence alignment, gaps, gap-penalties, scoring matrices, PAM250, BLOSUM62, local and global sequence alignment, multiple sequence alignment, useful programs, ClustalW, BLASTp.

### **Unit- III ( 40Hrs.)**

Proteomics classification; Tools and techniques in proteomics; 2-D gel electrophoresis, gel filtration, PAGE, isoelectric focusing, affinity chromatography, HPLC, ICAT, fixing and spot visualization, Mass spectroscopy for protein analysis, MALDI-TOF Electrospray ionization (ESI), Tandem mass spectroscopy (MS/MS) analysis; tryptic digestion and peptide fingerprinting (PMF). Protein Micro array in protein expression, profiling and diagnostics, drug target discovery. Database searching, 3-dimensional structure determination by X-ray and NMR. Phylogenetic analysis:- Evolution, elements of phylogeny, methods of phylogenetic analysis, Phylogenetic tree of life, comparison of genetic sequence of organisms, phylogenetic analysis tools-Phylip, ClustalW.

### **Unit- IV (40Hrs.)**

Applications of Bioinformatics in various fields ,Environment, biotechnology, molecular biology, neurobiology, agriculture, drug designing, biomedical genome medicines, medical microbiology.

## Paper VI - Immunology (160Hrs.)

### Unit- I (40Hrs.)

Immunology – fundamentals and anatomy of immune system Immunity – Innate and acquired immunity. Components of innate and acquired immunity. Antigen, Haptens, adjuvants, mitogens. Antibodies – structure, functions. The anatomy of the immune response: - Cells and organs of immune system. Regulation of immune response: - Humoral and Cell mediated response.

### Unit-II ( 40Hrs.)

Immunity to infection Antigen processing and presentation, MHC, complement system. Bacterial, viral, protozoal and parasitic infections with reference to (Diphtheria, influenza virus, malaria and helminthes) with specific representative examples of each group. Vaccines – Active and passive immunization, DNA vaccines, multivalent subunit vaccines, synthetic peptide vaccines.

### Unit- III ( 40Hrs.)

Clinical immunology and immunodeficiency diseases Hypersensitivity: - Type I, II, III, and IV reactions. Autoimmunity – organ specific and systemic autoimmune diseases. Treatment of autoimmune diseases. Transplantation and tumor immunology: - Graft rejection, tissue typing, immuno suppressive therapy and clinical transplantation. Tumor antigens, cancer immuno therapy. Immunodeficiency diseases: - Phagocytic, humoral, cell mediated deficiencies and SCID. AIDS- causes, syndrome, diagnostic tools, treatment and development of vaccine.

### Unit- IV (40Hrs.)

Immunotechnology Antigen antibody interactions – Principles, types and applications of agglutination, precipitation, complement fixation, viral neutralization, immunodiffusion, immunoelectrophoresis, ELISA and RIA Monoclonal antibodies – Hybridoma technology and various cellular technologies. Automation in immunological techniques – auto analyzers used in immunology, FACS

### Lab Course – I (80Hrs.)

#### Name of the Practical's

- 1 Computer basic knowledge; hardware, connection cables, typing, Windows 98/XP, Internet browsers, search engines.
- 2 LAN connections, setting up the IP address, network security.
- 3 Internet surfing and searching information, downloading and installing software. 4 Hands on session with Microsoft Word, Microsoft Excel (Spreadsheet Application).
- 5 Hands on session with Microsoft Access (Database related applications).
- 6 Measures of Central Tendency and Dispersion
- 7 Statistical Analysis using EXCEL. (Descriptive statistics and graphical presentation.)
- 8 Calculation of Mean, Mode and Median using spreadsheet application.
- 9 Sketching of pmf/pdf of Binomial, Poisson and Normal distributions.
- 10 Correlation and Regression Analysis.
- 11 Simple random sampling and stratified sampling.



## **Lab Course – II ( 80Hrs.)**

### **Name of the Practicals**

1. Understanding PubMed database.
- 2 Analysis of protein sequence from protein database.
- 3 Analysis of gene sequence from nucleotide database.
- 4 Getting and analysis of primary protein structure.
- 5 Secondary structure analysis of protein.
- 6 Tertiary protein structure analysis using Rasmol.
- 7 Introduction of various bibliographic databases.
- 8 Getting the gene sequences by exploring and querying the nucleic acid databases. 9 Understanding of Kyto Encyclopedia of Genes and Genome (KEGG) database for biological pathways, metabolism, cellular process, genetic information processing.
- 10 Database retrieval system- SRS of EBI and DBGet.
- 38
- 11 Investigation of molecular interactions using the program KineMage.

## **Lab Course – III ( 80Hrs.)**

### **Name of the Practicals**

- 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.
- 11 Phylogenetic analysis of protein and nucleic acid by using MEGA-4.
- 12 Similarity search using the Blast and interpretation of the results. 13 Quaternary structural analysis.

## **Lab Course – IV ( 80Hrs.)**

### **Name of the Practicals**

- 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.  
39  
12 AWT- Control and event handling

## **M. Sc. Bioinformatics Second Year**

**Duration: 760 Hours (Theory) Practical: 160 Hours (Practical)**

**Dissertation: 550 Hours**

### **Paper I Genetic Engineering (160Hrs.)**

#### **Unit- I (40Hrs.)**

DNA & basics of recombinant DNA technology Structure of DNA: A-,B-,Z-, and triplex DNA, Measurement of properties, spectrophotometric, CD, AFM, and electron microscope analysis of DNA structure. 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. Labeling of DNA: Nick translation, random priming, radioactive and non-radioactive probes, use of Klenow enzyme, T4 DNA polymerase, bacterial alkaline phosphatase, polynucleotide kinase. Hybridization techniques: Northern, Southern and Colony hybridization, Fluorescence *in situ* hybridization, Restriction maps and mapping techniques, DNA fingerprinting, chromosome walking & chromosome jumping. DNA-Protein interactions: - Electro mobility shift assay, DNase I footprinting, methyl interference assay.

#### **Unit-II ( 40Hrs.)**

Cloning vectors Gene Cloning Vectors: Plasmids, bacteriophages, Cloning in M13 mp vectors, phagemids, Lambda vectors. Insertion and replacement vectors, EMBL,  $\lambda$ DASH,  $\lambda$ gt10/11,  $\lambda$ ZAP etc. Cosmid vectors. Artificial chromosome vectors (YACs, BACs), Animal Virus derived vectors- SV-40, vaccinia/baculo & retroviral vectors. Expression vectors; pMal, GST, pET-based vectors. Protein purification; His-tag, GSTtag, MBP-tag etc. Restriction proteases, intein-based vectors. Inclusion bodies, methodologies to reduce formation of inclusion bodies. Baculovirus and pichia vectors system.

#### **Unit- III ( 40Hrs.)**

Cloning methodologies Insertion of Foreign DNA into Host Cells: Transformation, Transfection. Chemical and physical methods, liposomes, microinjection, macroinjection, electroporation, biolistics, somatic cell fusion, gene transfer by pronuclear microinjection. 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. Cloning and expression in yeasts (*Saccharomyces*, *Pichia* etc.). Animal and plants cells. methods of selection and screening, cDNA and genomic cloning, expression cloning, jumping and hopping libraries, southwestern and far western cloning, yeast two hybrid system, phage display, Construction of cDNA libraries in plasmids and screening methodologies, Construction of cDNA and genomic DNA libraries in lambda vector. Principles in maximizing gene expression, Site-directed mutagenesis.

## **Unit- IV ( 40Hrs.)**

PCR and its applications 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, PCR in molecular diagnostics, viral and bacterial detection, PCR based mutagenesis. Applications:-Sequencing methods: Enzymatic DNA sequencing, Chemical sequencing of DNA, principle of automated DNA sequencing, RNA sequencing. Chemical Synthesis of oligonucleotides. Gene silencing techniques: Introduction to siRNA and siRNA technology, micro RNA, construction of siRNA vectors, principle and application of gene silencing. Gene knockouts and 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 Other applications: Transgenics, Genome projects and their implications, application in global gene expression analysis. Applications of recombinant DNA technology in medicine, agriculture, veterinary sciences

## **Paper II - Advances in Structural Bioinformatics (160Hrs.)**

### **Unit- I ( 40Hrs.)**

**Structural biology and structural databases** Nucleic acid structures, RNA folding, RNA loops, conformational study. various ribose ring conformations, ribose-ring puckering. protein-protein interactions, protein ligand interactions. DNA-binding proteins, RNA-binding proteins. Ramachandran plot, 3-dimensional structures of membrane proteins, importance of 310 helix and loops, biophysical aspects of proteins and nucleic acids. Structural databases:- Protein Data bank (PDB), Nucleic Acid Data Bank (NDB),Molecular modeling Data Bank (MMDB). Secondary structure, three-dimensional structure prediction, protein folding and functional sites, protein folding classes.

### **Unit-II ( 40Hrs.)**

Protein structure prediction Protein Structure Prediction:- Homology modeling, prediction of protein structure from sequences, functional sites. Protein folding problem, protein folding classes, protein identification and characterization:- AACompIdent, TagIdent, PepIdent and MultiIdent, PROSEARCH, PepSea, PepMAPPER, FindPept, Predicting transmembrane helices, Primary structure analysis and prediction,Secondary structure analysis and prediction, motifs, profiles, patterns and fingerprints search. Methods of sequence based protein prediction.

### **Unit- III ( 40Hrs.)**

Molecular Modeling and Molecular Mechanics 15 Molecular modeling:-Introduction, force field, quantum chemistry, Schrödinger equation, potential energy functions. energy minimization, local and global minima, saddle point, grid search. various approximations; LCAO, HF, semi-empirical calculations; single point calculations, full-geometry optimization methods, ZDO, MNDO, CNDO, NDDO, AM1, PM3, RM1. conformational search, Z-matrix, docking, molecular modeling packages. 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. Derivative methods:- First-order methods; Steepest descent, conjugate gradient, Second order methods; Newton-Raphson method.

#### **Unit- IV (40Hrs.)**

Molecular dynamics, Molecular dynamics: -Introduction, Newton's equation of motion, equilibrium point, radial distribution function, pair correlation functions, MD methodology, periodic box, algorithm for time dependence; leapfrog algorithm, Verlet algorithm, Boltzman velocity, time steps, duration of the MD run. Starting structure, analysis of MD job, uses in drug designing, ligand protein interactions.

### **Paper III - Drug Designing (160Hrs.)**

#### **Unit- I (40Hrs.)**

Pharmaceutical Biotechnology 15 Introduction: - Antibacterial antibiotics; narrow spectrum and broad spectrum antibiotics. Mechanism of action of antibiotic, antifungal antibiotics, antiviral agents, antitumor agents. Chemical disinfectants, antiseptics, preservatives. Sulfa drugs.

1.4 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

#### **Unit-II (40Hrs.)**

Introduction drug design and discovery, Introduction: - Natural product, Drugs; principles of drug Development. Bioinformatics in drug development, Chemoinformatics and Pharmacoinformatics. Applications of Drug Discovery and In-Silico Drug Designing,Area influencing drug discovery; Molecular Biology, pharmacogenomics and pharmacoproteomics.

#### **Unit- III (40Hrs.)**

Structure-based drug designing 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- IV (40Hrs.)**

Ligand-based drug designing and docking 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: Auto Dock, Dock, HEX.

### **Paper IV - Programming in Perl (160Hrs)**

#### **Unit- I (40Hrs.)**

Biology and Computer science 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

### **Unit-II s(40Hrs.)**

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

### **Unit- III ( 40Hrs.)**

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

### **Unit- IV ( 40Hrs.)**

Mutations, Randomization and The genetic code 1Mutations 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

### **PAPER V: Research & its applications (120 Hours)**

#### **Unit: I (40 Hours)**

Bio-statistics & Research Methodology

Introduction Introduction to Bio statistics & research methodology, Types of variables & scales of measurements, Measures of central tendency and dispersion, Rate, Ratio, Proportion, Incidence & Prevalence Sampling Random & non- random sampling, Various methods of sampling, Simple random sampling, Stratified, Systematic, Cluster, Multistage, Sampling & Non sampling errors, Methods of minimizing errors

#### **Unit : II (40 Hours)**

Basic probability distribution & Sampling distributions

Concept of probability distribution- Normal, Poisson & Binomial distribution-Parameters & Applications Concepts of sampling distribution-Standard Error & Confidence Interval Skewness & Kurtosis Tests of Significance Basics of Testing of Hypothesis- Null & Alternate Hypothesis- Level of significance (Parametric) & power of test-p Value-Tests of significance- test (Paired & Unpaired),Chi- Square test, Test of Proportion-

One-way analysis of variance- Repeated measures of analysis of variance- Test of significance (non-parametric)

#### **Unit : III (40 Hours)**

## Correlation & Regression

Simple correlation- Pearson's & Spearman's Testing the significance of correlation coefficient linear & multiple regression Sample size determination General concepts- Sample size for estimating the means & proportion Concept of multivariate analysis- Introduction to logistic regression & survival analysis Reliability & Validity evaluation of diagnostic tests Format of scientific document Structure of research protocol Structure of thesis/ research report- Formats of reporting in scientific journals - Systematic review – Metaanalysis

## Dissertation Submission and Viva-Voce

### Lab Course – I (80Hrs.)

#### Name of the Practicals

- 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 like 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.
- 11 Molecular Docking of protein and ligand by HEX.
- 12 Protein Structure Prediction (Homology Modeling) using SPDBV.
- 13 Model Building and Energy minimization using Sybyl7.3.
- 14 Model Building and Energy minimization using SPARTAN.
- 15 Model Building and Energy minimization Gaussian.
- 16 Quantum chemical (QM) and molecular mechanics (MM) practical using SPARTAN.
- 17 Quantum chemical (QM) and molecular mechanics (MM) practical using Gaussian.
- 18 Molecular dynamics (MD) simulation using Gromacs. 19 Molecular dynamics (MD) simulation using Sybyl.
- 20 Molecular dynamics (MD) simulation using AMBER.

### Lab Course – II ( 80Hrs.)

#### Name of the Practicals

- 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. 13 Understanding various functions of Perl 14 Installing Perl on your PC.
- 15 Create Perl script.
- 16 Write a program to store protein sequence.
- 17 Write a program to store DNA sequence.
- 18 Write a program to store RNA sequence.
- 19 Use Perl to concatenation of DNA
- 20 Use Perl to concatenation of protein sequence.
- 21 Perl script for to simulate DNA mutation.

**MODEL QUESTION PAPER**

M. Sc. Bioinformatics .....

CBM&V-I

**M. Sc. Bioinformatics  
Part I Main Examination (Month, year)  
Paper – I  
Cell Biology, Microbiology and Virology**

**Time: Three Hours  
Maximum Marks: 70**

Attempt all Questions  
All the parts of one question should be answered at one place.  
Only one Supplementary Copy along with one main answer book is allowed

**Q No. 1. Long Answer (Attempt any two) 2X15 = 30**

- A. what do you understand about cell origination? defined mitochondria.
- B. what do you understand cell division, define mitosis ?
- C. what are the methods Methods in microbiology? Define Pure culture techniques.

**Q No 2 . Short Essay (Attempt any Two) 2X10 = 20**

- A. Define DNA Structure?
- B. .Classification and general characteristics of bacteria . define micoplasma ?
- C. What is the sterilization ? explain application of sterilization.

**Q No 3 Short notes (Any four) 4X5 = 20**

- A. What is host virus interactions ?
- B. what is microbial growth and curve ?
- C. define characteristics of protozoa?
- D. What is anti viral therapy?
- E. What is cell trafficking ?



## MODEL QUESTION PAPER

MSc. BioInfo

BM-II

### M. Sc. Bioinformatics Part I Main Examination (Month , year)

#### Paper - II Bio-Molecules

**Time: Three Hours**  
**Maximum Marks: 70**

Attempt all Questions

All the parts of one question should be answered at one place.

Only one Supplementary Copy along with one main answer book is allowed

- Q 1. Long Answer (Attempt any two) 2x15 = 30**
- a Describe pharmacokinetics and drug metabolizing?
  - b Describe molecular modelling using computer tools?
  - c Describe chemoinformatics data base design ?
- Q 2. Short Essay (Attempt any Two) 2x10 = 20**
- a write down tools of chemical data base design ?
  - b Define sequence data base and its type ?
  - c Explain prodrugs and soft drug , drug targeted ?
- Q 3. Short notes (Any four) 4x5 = 20**
- A. What is bio logical data base ?
  - B. what is bio panning ?
  - C. What is drug solubility ?
  - D. what is structural data base ?
  - E. What is BLAST ?

**MODEL QUESTION PAPER**

M. Sc. Bioinformatics .....

BCMB-III

**M. Sc. Bioinformatics**  
**Part I Main Examination (Month , year)**  
**Paper - III**  
**Basic of computer, Mathematics and Bio statistics**  
**Time: Three Hours**  
**Maximum Marks: 70**  
Attempt all Questions

All the parts of one question should be answered at one place.  
Only one Supplementary Copy along with one main answer book is allowed

**Q No. 1 Long Answer (Attempt any two) 2X15 = 30**

- A. what is computer ? explain classification of computer .
- B. define memory and its type .
- C. define internet and related programs?

**Q No. 2 Short Essay (Attempt any Two) 2X10 = 20**

- A. What is DBMS and its software ..
- B. describe introduction of protein and nucleic acid and data base
- C. What is hardware? And describe its parts ?

**Q No. 3 Short notes (Any four) 4X5 = 20**

- A. Block diagram of computer ?
- B. What is cache memory ?
- C. Difference between data and inflammation?
- D. What is SQL?
- E. What is printer and plotter?

**MODEL QUESTION PAPER**

M. Sc. Bioinformatics .....

MB-IV

**M. Sc. Bioinformatics**  
**Part I Main Examination (Month , year)**  
**Paper - IV**  
**Molecular Biology**  
**Time: Three Hours**  
**Maximum Marks: 70**

Attempt all Questions

All the parts of one question should be answered at one place.  
Only one Supplementary Copy along with one main answer book is allowed

**Q No. 1 Long Answer (Attempt any two)**

**2X15 = 30**

- A. Describe ketone bodies lamination and utilization
- B. describe bacterial cell wall component
- C. describe de-novo and salvage pathway of nucleotide synthesis

**Q No. 2 Short Essay (Attempt any Two)**

**2X10 = 20**

- A. Explain Watson and crick model of DNA
- B. structure and function of ribonuclease
- C. Beta – oxidation – pathway .

**Q No. 3 Short notes (Any four)**

**4X5 = 20**

- A. Definition of lipids
- B. what Is activation energy
- C. .What is glycogenesis .
- D. What is epimers , ieomers .
- E. define glycolysis .

**MODEL QUESTION PAPER**

M. Sc. Bioinformatics .....

GP-V

**M. Sc. Bioinformatics**  
**Part I Main Examination (Month, year)**  
**Paper - V**  
**Genomics and Proteomics**  
**Time: Three Hours**  
**Maximum Marks: 70**

Attempt all Questions

All the parts of one question should be answered at one place.  
Only one Supplementary Copy along with one main answer  
book is allowed

**Q. No. 1 Long Answer (Attempt any two)**

**2X15 = 30**

- A. Explain structure of eukaryotic chromosomes?
- B. what is enzyme? Describe DNA repair enzymes?
- C. describe nuclear export of MRNA , MRNA stability ?

**Q. No. 2 Short Essay (Attempt any Two)**

**2X10 = 20**

- A. Describe of transportation of proteins
- B. describe processing of TRNA and MRNA?
- C. what is recombination? Describe its types?

**Q. No. 3 Short notes (Any four)**

**4X5 = 20**

- A. What is operon?
- B. what is catalytic RNA?
- C. What is biological data ?
- D. What is biological mutagen
- E. Differentiate between prokaryotic and eukaryotic cells

**MODEL QUESTION PAPER**

M. Sc. Bioinformatics .....

IM-VI

**M. Sc. Bioinformatics**

**Part I Main Examination (Month , year)**

**Paper - VI**

**Immunology**

**Time: Three Hours**

**Maximum Marks: 70**

Attempt all Questions

All the parts of one question should be answered at one place.

Only one Supplementary Copy along with one main answer book is allowed

**Q. No. 1 Long Answer (Attempt any two)**

**2X15 = 30**

- A. Define immunity and its type ?
- B. what is vaccines ? Define active and passive immunization ?
- C. What is hypersensitivity ? Describe its type .

**Q. No. 2 Short Essay (Attempt any Two)**

**2X10 = 20**

- A. Describe antigen and antibody interactions?
- B. what is hybridoma technology ? explain drug designing ?
- C. Explain AIDS syndrome,causes ,diagnostic tool,treatment ?

**Q. No. 3 Short notes (Any four)**

**4X5 = 20**

- A. What is Monoclonal antibodies ?
- B. what is autoimmunity ?
- C. What is specter data base ?
- D. What is ELISA ?
- E. Define DIVA vaccine ?

**MODEL QUESTION PAPER**

M. Sc. Bioinformatics .....

GE-I

**M. Sc. Bioinformatics**  
**Part II Main Examination (Month , year)**  
**Paper - I**

**Genetic Engineering**

**Time: Three Hours**

**Maximum Marks: 70**

Attempt all Questions

All the parts of one question should be answered at one place.

Only one Supplementary Copy along with one main answer book is allowed

**Q. NO. 1. Long Answer (Attempt any two)**

**2X15 = 30**

- A. Define nucleic acid structure ?
- B. Describe quantum chemistry of molecular modelling ?
- C. describe method of sequence based protein prediction ?

**Q. NO. 2. Short Essay (Attempt any Two)**

**2X10 = 20**

- A. Describe protein folding methods?
- B. what is RNA folding ? Explain it.
- C. define structural databases PDB,NDB,MMDB?

**Q. NO. 3. Short answers (Any four)**

**4X5 =**

**20**

- A. What is RNA loop?
- B. what is motifs ?
- C. What is Z-Matrix ?
- D. What is PDB ?
- E. Define 3-D structure of protein ?

**MODEL QUESTION PAPER**

M. Sc. Bioinformatics .....

ASB-III

**M. Sc. Bioinformatics**  
**Part II Main Examination (Month , year)**  
**Paper - II**  
**Advances in Structural Bioinformatics**

Attempt all Questions

All the parts of one question should be answered at one place.

Only one Supplementary Copy along with one main answer book is allowed

**Q. No. 1. Long Answer (Attempt any two) 2X15 = 30**

- A. Describe DNA finger printing?
- B. Describe gone cloning vectors?
- C. describe plant transformation technology?

**Q. No. 2. Short essay (Attempt any Two) 2X10 = 20**

- A. What is PCR and its application ?
- B. Application of recombination DNA technology in medicine?
- C. Application of genomic cloning ?

**Q. No. 3. Short Notes (Any four) 4X5 = 20**

- A. What is enzymatic DNA sequencing ?
- B. what is gene knockouts ?
- C. what is somatic cell fusion ?
- D. Define restriction maps ?
- E. What is cosmid vectors ?

**MODEL QUESTION PAPER**

M. Sc. Bioinformatics .....

DD-II

**M. Sc. Bioinformatics**  
**Part II Main Examination (Month , year)**  
**Paper - III**  
**Drug designing**  
**Time: Three Hours**  
**Maximum Marks: 70**

Attempt all Questions

All the parts of one question should be answered at one place.

Only one Supplementary Copy along with one main answer book is allowed

**Q. No. 1 Long Answer (Attempt any two) 2X15 = 30**

- A. Describe mechanism of action of antibiotics ?
- B. Describe molecular docking programme ?
- C. Describe mechanism of action of antitumor agents ?

**Q 2 .Short Essay (Attempt any Two) 2X10 = 20**

- A. Describe principle of Drug development?
- B. Define In-Silico organization of DNA? .
- C. define Subroutine and bugs ?

**Q 3 Short notes (Any four) 4X5 = 20**

- A. What is antiviral agents?
- B. what is GMP ?
- C. What is PERL?
- D. What is homology modelling ?
- E. Define

H



**MODEL QUESTION PAPER**

M. Sc. Bioinformatics .....

PP-IV

**M. Sc. Bioinformatics**  
**Part II Main Examination (Month , year)**  
**Paper - IV**  
**Programming in Pearl**  
**Time: Three Hours**  
**Maximum Marks: 70**  
Attempt all Questions

All the parts of one question should be answered at one place.

Only one Supplementary Copy along with one main answer book is allowed

**Q 1. Long Answer (Attempt any two) 2X15 = 30**

- A. Describe Data Structures and Algorithms for Biology?
- B. Describe Random Number Generators, A Program Using Randomization??
- C. Describe the Organization of Proteins In Silico?

**Q 2 Short essay (Attempt any Two) 2X10 = 20**

- A. What is Arrays Scalar and List Context in Perl?
- B. Write A Program to Store a DNA Sequence , Concatenating DNA Fragments  
Transcription: DNA to RNA?
- C. Calculate the Reverse Complement in Perl using the Perl Documentation?

**Q 3 . Short notes (Any four) 4X5 = 20**

- A. What is Subroutines and Bugs??
- B. What is Text Editors and Finding Help?
- C. What is Limits to Computation in Perl??
- D. What is sequences and strings??
- E. What is Perl& its Benefits?

**MODEL PAPER**

M. Sc. Bioinformatics .....

Res. & its Appl.-V

**M. Sc. Bioinformatics  
Part II Main Examination (Month , year)  
Paper – V**

**Research & its Applications**

**Time: Three Hours**

**Maximum Marks: 70**

Attempt all Questions

All the parts of one question should be answered at one place.

Only one Supplementary Copy along with one main answer book is allowed

**Q 1. Long Answer (Attempt any two) 2X15 = 30**

- A. Define Research. Explain research methodology
- B. Describe about types of variables & scales of measurements
- C. What do you understand about Clinical trials/ Interventional studies

**Q 2. Short Essay (Attempt any Two) 2X10 = 20**

- A. What is Biostatistics, Discuss in brief.
- B. What is Simple random sampling?
- C. Basics of Testing of Hypothesis

**Q 2. Short notes (Any four) 4X5 = 20**

- A. Significance of correlation coefficient
- B. Cohort studies
- C. Multivariate Analysis
- D. Reliability & Validity
- E. Meta-analysis

