UNIVRSITY OF ALLAHABAD
COMBINED RESEARCH ENTRANCE TEST 2012
CRET 2012

SYLLABUS:Bio-Informatics

Note: For Level 1 B and Level 2 tests
Level 1 B:
There will be 50 multiple choice objective type questions covering ENTIRE syllabus 3 marks will awarded for correct answer and 1 mark will be deducted for each wrong answer.
Duration 1=30 Hours (90 minutes).

Level 2: There will be in all 14 Questions divided into 3 Parts.
There will be three sections
   A. In Section-A there will be 10 Short answer (50 words) type questions covering entire syllabus (all compulsory) total marks of this Part will be 100 i.e. 10X10.
   B. In Section-B there will be 03 Medium answer (200words) type questions with internal choice/s considering specializations (all compulsory) total marks of this Part will be 60 i.e. 20X3.
   C. In Section-C there will be 01 Long answer (400 words) type question on research methodology and research aptitude with internal choice/s total marks of this Part will be 40.
Duration 3 Hours
Total marks shall be 200

Carbohydrates: monosaccharides, oligosaccharides polysaccharides, proteoglycans and glycoproteins; Lipids; fatty acids, acylglycerols; phospholipids, sphingolipids, cholesterol and their biological importance;

Proteins: amino acids and peptides; protein structure, function and evolutionary relationships; protein—protein interactions; protein folding; **Nucleic acid:** bases, nucleotides, RNA and DNA, different structural forms of DNA; denaturation, renaturation and hybridization of DNA; Protein and Nucleic Acid Electrophoresis techniques.

Enzymes: Nomenclature and classification; units of enzyme activity; coenzymes and metal cofactors; temperature and pH effects; Michaelis–Menten kinetics, inhibitors and activators; active site and catalytic mechanisms; Isoenzymes; Metabolic systems multienzyme complexes and multifunctional enzymes; Oxidation of glucose in cells; high energy bond, glycolysis, citric acid cycle and oxidative phosphorylation.

BIO–STATISTICS
Calculus; Limits, Complete Differentials, Partial differentials of function, Integration: Definite and nondefinite integral, Logarithms, Ordinary differential equations (first order), Partial differential equations–example from biology, Vector–Addition, subtraction, dot cross, scalar triple product, divergence, curl of a vector, equation of normal; Matrix algebra: Addition, subtraction, multiplication, transpose inverse, and conjugate of matrix, Boolean logic; Additional subtraction, multiplication and division using binary, octal and hexadecimal systems, introduction to principles of statistical sampling from a population. Random sampling;

Frequency distributions and associated statistical measures; Probability Distribution; Correlation and regression analysis; Multivariate analysis: Hypothesis testing; Markov Models; Cluster Analysis – Nearest neighbour search, Search using stem numbers, Search using text signatures; Phylogenetic Analysis Tools; Maximum Likelihood, Parsimony methods.

IMMUNOLOGY: Overview of immune system, innate and acquired immune system: Structure and function of antibody molecule and TCR: Genetics of antibody diversity; MHC I & II, Polymorphism; Characteristics of B Cell and T Cell antigens; MHC Peptide interaction; Affinity maturation; Autoimmunity and molecular mimicry; Ligand– receptor interaction in the light of protein structure in immune system; Use of bioinformatics in immunology and vaccine development.

BIOLOGICAL DATABASES, DATA MINING
Data warehousing, data capture, data analysis, Introduction to Nucleic Acid and Protein Sequence Data Banks: Nucleic acid sequence data banks: Genbank, EMBL nucleotide sequence data bank, AIDS Virus sequence data bank, rRNA data bank, Protein sequence data banks; NBRF–PIR, SWISSPROT, Signal peptide data bank; Database Similarity Searches; BLAST, FASTA, PSI–BLAST algorithms: Pair wise sequence alignment – NEEDLEMAN and Wunsch, Smith Waterman algorithms; Multiple sequence alignments – CLUSTAL PRAS: Patterns motifs and Profiles in sequences: Derivation and searching; Derived Databases of patterns, motifs and profiles: Prosite, Blocks, Prints–S, Pfam etc.; Primer Design.

SEQUENCE ANALYSIS
Analysis of protein and nucleic acid sequences, multiple alignment programs, Development of programs for analysis of nucleic acid sequences. Use of GCG package. Conversion of various file formats. Use of Molecular Package(s), programs of calculate potential energy of regular structures and their visualization. Use of curve, NUPARM, NEW helix etc.

MOLECULAR MODELLING
Concepts of Molecular Modeling. Molecular structure and internal energy, Application of molecular graphics. Energy minimization of small molecules, Empirical representation of molecular energies. Use of Force Fields and MM methods. Local and global energy minima. Techniques in MD and Monte Carlo. Simulation for conformational analysis *Ab initio*, DFT and semi–empirical methods, Design of ligands, Drug–receptor interactions. Classical SAR/QSAR, 2D and 3D data searching. Protein quaternary structure modeling. Interaction networks and systems biology.

GENOMICS AND PROTEOMICS
Genomics – Genome sequencing technology. Whole genome analysis, Comparative genomics – Paralogs and orthologs, Phylogenetic profiling. Pathway analysis, Repeat analysis, Human genetic disorders, Candidate gene identification, Linkage analysis, Genotyping analysis, Concepts of Pharmacogenomics

Proteomics – Introduction to basic Proteomics technology, Bio–informatics in Proteomics. Gene to Protein Function: a Roundtrip, Analysis of Proteomes. Analysis of 2–D gels. Protein to Disease and Vice Versa, Human Genome and science after Genome era.

Genome Technology: high throughout sequencing and assembly.

Microarray and genome wide expression analysis: transcriptomes, proteome: Genomics in medicine, disease monitoring, profile for therapeutic molecular targeting. Diagnostics drug discovery and genomics. Pharmacogenomics and its application. SNPs and their applications. Proteomics in medicine and its application. Patenting and data generation from patent literature for commercial benefits. IPR and bioinformatics. Bioinformatics patents.

MICROARRAY TECHNOLOGY: Introduction to basic microarray technology, Bioinformatics in microarrays. Getting started – target selection, Customized microarray design, Image processing and quantification. Normalization and filtering. Exploratory statistical analysis. Public Microarray data resources.

BIOTECHNOLOGY
Molecular Biology of Pro and Eukaryotes, Plant and Animal Cloning and Expression Vectors, Hybrid Vectors, Homologous and Heterologous Expression, Industrial Biotechnology, Tools of Genetic Engineering, Recombinant DNA Technology Transgenetics. Molecular Farming, Organ, Tissue and Cell Culture techniques. Nanobiotechnology
Nanomedicine PCR technique, GFP. Molecular Genetics.

BIOPHYSICAL METHODS
TREES and GRAPHS
COMPUTER AIDED DRUG DESIGNING