

DEPARTMENT OF COMPUTER SCIENCE

FACULTY OF NATURAL SCIENCES, JAMIA MILLIA ISLAMIA, NEW DELHI-110025

TEL.: +91-11-26980014 (DIRECT), +91-11-26981717 EXTN 3450/ 3452

PhD (Computer Science / Bioinformatics) Entrance Test, 2018

Syllabus for Part-B

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|----------------------------------|---|-----------------|
| Multiple-Choice Questions | (Compulsory Component: 50 Questions) | 50 Marks |
| | (For Computer Science and Bioinformatics Both) | |
| Subjective Questions | (Elective Component: 5 Questions out of 10) | 50 Marks |

----- (COMPULSORY COMPONENT) -----

- Set, Relation, Function, Pigeonhole Principle, Inclusion-Exclusion Principle, Partial and Total Ordering, Lattice, Elementary Counting Techniques, Recurrence Equations.
- Mathematical Logic, Preposition, Connectives, Truth tables; Well-formed formulas, Tautology, Contradiction, Equivalence of Formulas, Duality, Normal Forms, Theory of inference, Predicate Calculus.
- Measuring Central Tendency and Dispersion of Data, Correlation Analysis, Regression Analysis, Analysis of Variance, Hypothesis Testing, Probability and Distributions - Sample Space and Events, Types of Events, Addition and Multiplication Rules, Conditional Probability and Bayes Theorem.
- Logic Gates, Boolean Functions, Combinational and Sequential Circuits, Number System, Integer/Real Data Representation, Instruction Formats, Addressing Modes, Memory Organization, I/O Organization. Von-Neumann Architecture, Number System, Complements, Binary Arithmetic, Numeric and Character Data Representation, Memory and I/O Devices.
- Operating Systems and its Types, OS Structure, Components and Services. Memory Management – Swapping, Memory Allocation, Paging and Segmentation; IPC, Deadlocks and Security.
- Network Fundamentals, LAN, MAN, WAN, Network Topologies, Reference Models: OSI and TCP/IP Models, Transmission Media.
- Programming in C: Identifiers, Variables and Constants, Data Types, Operators, Control Structures, Structured Data Types: Array, Struct, Union, String, Enum, and Pointers. File Handling in C.
- OOP using C++: Class, Object, Inheritance, Polymorphism, and Overloading; Constructors and Destructors; Virtual Functions, Templates and Exception Handling.
- Linear Data Structures: Array, Linked-Lists, Stack, Queue. Non-Linear Data Structures: Tree and Graph, Hashing and Tables. File Structures: Fields, Records and Files; Sequential, Direct, Index-Sequential and Relative Files, Inverted Lists and Multi-Lists. Linear Data Structures: Array, Linked-Lists, Stack, Queue. Non-Linear Data Structures: Tree and Graph.
- Asymptotic Notations for Complexity, Best, Average and Worst Case Analyses, Searching and Sorting, Design Techniques: Divide-and-Conquer Approach, Dynamic Programming, Greedy Techniques.
- DBMS and Types; Database Concepts, Data Models, ER Diagram, Design of Relational Database, Functional Dependency, Database Decomposition and Normalization, Relational Algebra and Structured Query Language.

----- ELECTIVE COMPONENT (Section EC: COMPUTER SCIENCE) -----

1. Relational Database Management System, ER and EER Models, Database Constraints, Database Decomposition and Normalization, Relational Algebra and SQL, Query Processing and Optimization, Transaction Management, Serializability and Recoverability, Concurrency Control

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Techniques, Deadlock, Time Stamping, Database Recovery Techniques.

2. System Development Life Cycle, Software Process Models. Software Metrics, Software Design: System Design, Detailed Design, Function-Oriented Design, Object-Oriented Design, User-Interface Design. Design Level Metrics. Software Testing and Quality Assurance, Testing Metrics, Software Quality and Reliability, Risk Management, Software Re-engineering, Software Architecture.
3. Arrays and Matrices: Single and Multi-Dimensional Arrays, Matrix Representation using 2D Arrays, Diagonal, Tri-diagonal, Lower Triangular, Upper Triangular, and Sparse Matrices. Linked Lists: Singly, Doubly, and Circular Linked Lists. Stack and Queue, Priority Queue. Binary Tree, Binary Search Tree, AVL Tree, B and B+ Tree. Graph Representation and Traversals, Spanning Tree, Skip List and Hashing.
4. Computer Networks, OSI and TCP/IP Model, TCP and UDP, IP, Datagram, Addressing, Subnetting and Masking; ARP, RARP, ICMP, IGMP. Client-Server Model: BOOTP and DHCP. Domain Name System (DNS), Internet and Intranet, Internet Services: E-mail, World Wide Web (WWW) etc. Asynchronous Transmission Mode (ATM): Architecture, Switching, Layers, and Applications.
5. Analysis and Design of Algorithms, Asymptotic Notations, Master Theorem, Searching Techniques: Linear and Binary Search. Sorting Techniques. Divide and Conquer Approach - Strassen's Matrix Multiplication, Dynamic Programming and Optimization - Binomial Coefficient Finding, Chained Matrix Multiplication, Longest Common Subsequence Problem, and Travelling Salesman Problem. Greedy Techniques - Prim's, Kruskal's, and Dijkstra's Algorithms, Huffman Code. Backtracking Algorithms for n-Queens, Sum-of-Subsets, Graph Coloring, and 0-1 Knapsack Problems. Branch and Bound Methods for 0-1 Knapsack and Travelling Salesman Problems.

-----ELECTIVE COMPONENT (Section EC: BIOINFORMATICS)-----

1. Genome Evolution and Phylogenetics, DNA Sequencing, The Human Genome Project, Genomic Variations. Structural Genomics Technology: Genome Annotation, SNPs and TOGA, RAPD, AFLP and RFLP Analyses, DNA and RNA Fingerprinting, Functional Genomics. Metabolic Reconstruction: Metabolic Pathway, Metabolic Regulation, Genome-Proteome Connection, Interaction Networks. Proteomics: Protein Function and Expression, 2D-gel Electrophoresis, Amino Acid Sequencing. Protein-Protein Interaction: Protein-Ligand Interaction, Large Molecular Complexes, Phage Display, Protein Chips. Microarray: cDNA Microarrays, Oligonucleotide Microarray Chips, Cancer and Genomic Microarrays, DNA Microarrays and Analysis of Metabolic Control. Cancer and Genomic Microarrays.
2. Systems Biology, Biological Systems, Measurement Technologies and Experimental Methods, System Structure Identification. System Behavior Analysis Methods, System Control, Modular Design, Structural Stability. Modeling Genetic Networks: Gene Regulatory Network, Biochemical Processes, Transcription, Exons & Introns, Splicing, Translation, Post Translation Modification. Boolean, Differential Equation, Stochastic, and Kinetic Logic Models. Genetic Algorithms, Generative Models. Reverse Engineering and Data Mining from Gene Expression Data. Automated Reverse Engineering of Metabolic Pathways by Means of Genetic Programming: Representation of Chemical Reaction Networks, Repertoire of Functions, Repertoire of Terminals, Constrained Syntactic Structure, Fitness Measures.
3. Computer-Aided Drug Design, Molecular Modeling, Prediction of Tertiary Structures of Proteins, Minimization of Peptide Energy, Ramachandran Plot, Torsional Space Minimization, Molecular Dynamics. Molecular Visualization Tools: Visualization of Tertiary and Quaternary Structures, Architectures and Topologies of Proteins and DNA. Drug design: Drug discovery process, Target Identification and Validation, Lead Optimization and Validation. Structure Activity Relationship - QSARs and QSPRs. Quantum Chemical Based Descriptors. Structure-Based Drug Design and Ligand-Based Drug Design: Docking, Lock and Key Hypothesis, Ligand Docking, High Throughput Screening, Virtual Screening, Protein-Ligand Docking, Protein-Protein Docking, Energy Minimization.

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Biomolecular Simulations Techniques

Computational Methods for Data Analysis, Pair-Wise Alignment, Statistical Analysis of Alignment Score, Local vs. Global Alignment, Multiple Sequence Analysis. Scoring Matrices: Derivation and Comparison of PAM and BLOSUM Matrices. Protein Secondary Structure Predictions.

4. Phylogenetic Analysis: Phylogenetic Trees, Phenotypic and Molecular Phylogeny. Cladogram, Similarities and Distances. Orthologs, Paralogs and Xenologs. Tree Evaluation. Markov Chains and Hidden Markov Model (HMM), Pairwise Alignment using HMMS, Profiles, and HMMER. Structure Analysis: Covariance Models, SCFG-Based RNA Profiles. Protein Folding Problem, Protein Structure Alignment and Analysis.

5. Modern Biology Experimental Techniques, Separation of Proteins, Chromatography, Gel Filtration, HPLC, Reverse Phase HPLC, Electrophoresis. Characterization of Proteins: Amino Acid Composition Analysis, N-terminal Analysis, Peptide Mapping, Sequencing Strategies. Spectroscopy: UV/Visible Spectrometry, Fluorescence, Circular Dichroism, IR, FTIR and Raman Spectroscopies, Dynamic Light Scattering, Laser Spectroscopy, Surface Plasmon Resonance, Differential Scanning Calorimetry, Isothermal Calorimetry. Methods for Protein Structure Determination: NMR Data Analysis, NOESY and COESY, SAXS, X-ray Crystallography, Protein Crystallization and X-ray Diffraction, DNA Sequencing Methods. Methods for Analysis of Gene Expression at RNA and Protein Level, Large-Scale Expression Analysis. Protein Engineering. Microscopy Techniques.

NOTE : Candidates will have to choose their area of PhD as either Computer Science or Bioinformatics. The Multiple choice question (MCQ) Compulsory paper will be common for Computer Science and Bioinformatics both. For the Elective Component, if they opt Computer Science then they will have to opt Section EC: Computer Science of Elective Paper and attempt any five questions out of 10 from it and if they opt Bioinformatics then they will have to opt Section EC: Bioinformatics of Elective Paper and attempt any five questions out of 10 from it.