SARDAR PATEL UNIVERSITY
Vallabh Vidyanagar, Gujarat
(Reaccredited with ‘A’ Grade by NAAC (CGPA 3.25)
Syllabus with effect from the Academic Year 2021-2022

Master Degree in Bioinformatics
M.Sc. (Bioinformatics) Semester II

Course Code	**PT02CBIC51**	Title of the Course	**Basic & Advanced Sequence Analysis**
Total Credits of the Course	4	Hours per Week	4

OBJECTIVES OF THE COURSE

- To provide an integrative approach to the understanding of both theory and practice of bioinformatics
- To apply biological concepts at different levels to study gene/protein analysis, and the proteins implicated in diseases
- To understand the evolution of the life
- To understand various sequencing technology and their concepts

Unit	**Description in Detail**	**Weightage (%)**
I	**BASIC SEQUENCE ANALYSIS:** Basic concepts of sequence similarity, identity and homology, definitions of homologues, orthologues, and paralogues **Scoring matrices:** PAM and BLOSUM series, matrix derivation methods and principles. Database Searches:Keyword-based Entrez and SRS; Sequence-based: BLAST & FASTA	25%
II	**PAIRWISE SEQUENCE ALIGNMENT:** Basic concepts of sequence alignment, Needleman and Wunsch, Smith and Waterman algorithms.Multiple sequence alignments (MSA):basic concepts of various approaches for MSA (e.g. progressive, hierarchical etc.). Algorithm of CLUSTALW and PileUp and use of HMM-based Algorithm for MSA.Basic concept and definition of sequence patterns, motifs and profiles, various types of pattern representations.	25%
III	**NEXT GENERATION SEQUENCE ANALYSIS:** Next-Generation DNA Sequencing:-Illumina (Solexa) sequencing, Roche 454 sequencing,Ion torrent: Proton / PGM sequencing, SOLiD sequencing**.** The Sequence Read Archive (SRA), sequence analysis methods ,Genome assembly, ChIP-seq analysis,RNA sequencing, RNA-Seq analysis (Transcriptome assembly)	25%
IV	**TAXONOMY AND PHYLOGENY:** Basic concepts in systematics, taxonomy and phylogeny; molecular evolution; nature of data used in Taxonomy and Phylogeny, Definition and description of phylogenetic trees and various types of trees, Phylogenetic analysis algorithms	25%

	such as maximum Parsimony, UPGMA, Transformed Distance, Neighbors-Relation, Neighbor-Joining,.	

Basic Text & Reference Books:-

1. Bioinformatics: Sequence and Genome Analysis by Mount D., Cold Spring Harbor Laboratory Press, New York. 2004
2. Bioinformatics- a Practical Guide to the Analysis of Genes and Proteins by Baxevanis, A.D. and Francis Ouellellette, B.F., Wiley India Pvt Ltd. 2009

Teaching-Learning Methodology	• Regular class room teaching will be done with following tools: a) Conventional black board and chalk. b) ICT tools such as projectors, smart boards, etc will also be used for better explanation of scientific components. • Appropriate reference materials will also provided to the students as and when required from departmental library resources.

COURSE LEARNING OUTCOMES

On Successful completion of the course, the student will be able to

- Better understanding of the bioinformatics concepts
- Applications of the gene and protein sequence analysis
- Apprehending the different databases in bioinformatics
- Perform a complete analysis of the genes and protein
- Compare and identify the differences in sequences

References		
Sr. No.	Details of the Evaluation	Weightage
1.	Internal Written Examination (As per CBCS R.6.8.3)	15%
2.	Internal Continuous Assessment in the form of Viva-voce, Quizzes, Seminars, Assignments, Attendance (As per CBCS R.6.8.3)	15%
3.	University Examination	70%

On-line resources to be used if available as reference material
On-line Resources:

https://genomevolution.org/
https://nptel.ac.in/courses/102/106/102106065/
https://nptel.ac.in/courses/102/104/102104056/
https://cnx.org/contents/24nI-KJ8@24.18:EmlvXoDL@7/Taxonomy-and-phylogeny

Master Degree in Bioinformatics
M.Sc. (Bioinformatics) Semester II

Course Code	**PT02CBIC52**	Title of the Course	**Principles of Mathematics & Biostatistics**
Total Credits of the Course	4	Hours per Week	4

Course Objectives:	**OBJECTIVES OF THE COURSE** • To enhance the skills in mathematics those are essential for learning Bioinformatics • To understand and implement various mathematical techniques being applied in analyzing information of biological data • To understand statistical methods in its several forms is the basis of biological research • To introduce the various statistical techniques useful for handling quantitative data

Unit	Description in Detail	Weightage (%)
I	**MATRICES AND LINEAR ALGEBRA** Matrices:- Properties of Determinants, Minors and Cofactors, Multiplication of Determinants, Adjoint, Reciprocal, Symmetric Determinants, Cramer’s rule, Different types of matrices, Matrix Operations, Transpose of a matrix, Adjoint of a square matrix, Inverse of a matrix, Eigen values and eigen vector Linear Algebra: - Definition of vector space, Subspaces, Linear independence and Bases.	25%
II	**CALCULUS: DIFFERENTIAL CALCULUS**: Derivative of a function, Concept of limit, Continuity, Differentiation, Maxima and Minima of a function, Introduction to Partial Differentiation, Integral Calculus: The Idea of the Integral, The Definite Integrals, Indefinite Integrals. Numerical Methods: Solution of algebraic and transcendental equations: Bisection method, Method of false position / Regula-falsi method, Newton-Raphson method.	25%
III	**NUMERICAL DESCRIPTIVE TECHNIQUES:** Measures of central tendency: mean, median, mode, relation between mean, median and mode. Partition values: quartiles, deciles, percentiles; Measures of dispersion: Absolute and Relative Measures, Moments, skewness and kurtosis Correlation and Regression: Principles of least squares, scatter diagram, correlation, covariance, correlation coefficient, properties of correlation coefficient, regression, properties of linear regression, rank correlation, multiple correlation	25%

IV	**PROBABILITY THEORY** Concept of probability: sample space and events, independent events, mutually exclusive events. axioms of probability, conditional probability, Baye's theorem, Introduction to Markov Chain Model. Sampling Distribution of Sample Mean and Sample Proportion, Standard Error Probability Distribution:Bernoulli trials, binomial distribution, normal distributions, Poisson distribution, Test of Hypothesis of Small and Large Samples- Standard Normal distribution, Chi-square distribution, Student's t distribution, F distribution, Analysis of Variance	25%

Teaching-Learning Methodology	• Regular class room teaching will be done with following tools: a. Conventional black board and chalk. b. ICT tools such as projectors, smart boards, etc will also be used for better explanation of scientific components. • Appropriate reference materials will also provided to the students as and when required from departmental library resources.

Evaluation Pattern

Sr. No.	Details of the Evaluation	Weightage
1.	Internal Written Examination (As per CBCS R.6.8.3)	15%
2.	Internal Continuous Assessment in the form of, Viva-voce, Quizzes, Seminars, Assignments, Attendance (As per CBCS R.6.8.3)	15%
3.	University Examination	70%

Course Outcomes: Having completed this course, the learner will be able to

1.	Understand the importance of mathematics for research based problems
2.	Apply the different statistical tests for the research
3.	Learn to solve aptitude based problems in competitive exams
4.	Gain skills on solving the population genetics equations Apply the regression and correlation techniques to interpret biological problems

Suggested References:

Sr. No.	References
1.	Algebra by Serge A. Lang, Pearson Education. 2003
2.	Introduction to Calculus & Analysis, Vol I and II by Richard Courant & Fritz John, Springer publisher.1999
3.	Biostatistics (9 Ed.) by Wayne W. Daniel, Wiley 2004
4.	Schaum’s Outlines - Introduction to Probability and Statistics by Seymour Lipschutz and John Schiller., TATA McGraw-Hill edition. 1998

On-line resources to be used if available as reference material

On-line Resources:--
https://courses.lumenlearning.com/
https://en.wikipedia.org/wiki/Differential_calculus
https://www.studocu.com/
https://en.wikipedia.org/wiki/Probability_theory

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Master Degree in bioinformatics
M. Sc. (Bioinformatics) Semester II

Course Code	**PT02CBIC53**	Title of the Course	Databases in Life Sciences
Total Credits of the Course	4	Hours per Week	4

Course Objectives:	**OBJECTIVES OF THE COURSE** • To introduce the basic concepts of Relational Database Management System and Client / Server Environment • To be trained in designing databases and manipulating them for biological applications

Unit	Description in Detail	Weightage (%)
I	**DATABASE MANAGEMENT:** database as a collection of one or more related tables, popular database systems. Relation databases - Tables, Queries, Forms, and Reports; Understanding the importance of each database component. Creating a table, Understanding tables and relationships between them – Data types, Primary key, foreign key; Data validation.	25%
II	**INTRODUCTION TO SQL:** structure of an SQL expression - select from, and where, clauses, the rename operation, string operations. Set operations, aggregate functions, using group by clause, null values, nested sub-queries, in and not in predicates; Creating IVews with create IVew,.SQL DDL: Domain types, Schema definition - create table, drop table, alter table. Modification of databases - delete, insert, update; transactions – commit, rollback. Integrity: Domain constraints, referential integrity, foreign key; Assertions, triggers.	25%
III	**BIOLOGICAL DATA MANAGEMENT:** Data cleaning, preprocessing and normalization. Database System Architecture and Information retrieval: Centralized and Client-Server Architecture. The formats of common public repositories - NCBI, ENSEMBL; federation techniques between different types of data; methods of data transfer - BioPax, MLs, and others.	25%

IV	**BIOINFORMATICS DATABASE TECHNOLOGIES** : Enterprise solutions - Oracle, IBM; open source solutions - BioPerl, BioJava, BioSQL.Sequence Retrieval System (SRS).	25%

Teaching-Learning Methodology	• Regular class room teaching will be done with following tools: a. Conventional black board and chalk. b. ICT tools such as projectors, smart boards, etc will also be used for better explanation of scientific components. • Appropriate reference materials will also provided to the students as and when required from departmental library resources.

Evaluation Pattern

Sr. No.	Details of the Evaluation	Weightage
1.	Internal Written Examination (As per CBCS R.6.8.3)	15%
2.	Internal Continuous Assessment in the form of, Viva-voce, Quizzes, Seminars, Assignments, Attendance (As per CBCS R.6.8.3)	15%
3.	University Examination	70%

Course Outcomes: Having completed this course, the learner will be able to

1.	Understand data models and schemas in DBIS
2.	Skills to Create, update, retrieve and Manage data
3.	Handle files and databases
4.	Gain efficient skills on Atomicity, Consistency, Isolation, and Durability Clear understanding and usage of SQLanguage

Suggested References:

Sr. No.	References
1.	Database System Concepts (4th Ed.) by Silberschatz, A., Korth, H.F. and Sudarshan, S., 2002, McGraw Hill Publishers.

2.	An Introduction to Database Systems (7th Ed.) by Date, C.J., Addison Wesley Publishers. 2000
3.	Fundamentals of Database Systems (4th Ed.) by Elmasri and Navathe, Addison Wesley Publishers. 2004
4.	National Center for Integratvie Biomedical Informatics (NCIBI)

On-line resources to be used if available as reference material
On-line Resources:-- https://www.javatpoint.com/dbms-tutorial

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Master Degree in Bioinformatics
M.Sc. (bioinfomatics) Semester II

Course Code	**PT02CBIC54**	Title of the Course	**Experimental Methods-III**
Total Credits of the Course	04	Hours per Week	4hr

Course Content		
Unit	Description	Weigh tage* (%)
1.	**Exercises Based on Biosequence Analysis** 1. Sequence Analysis Packages: EMBOSS, NCBI ToolKit, SMS 2. Database search engines: Entrez, SRS, DBGET 3. Pairwise alignment: a. Search tools against Databases: i. BLAST ii. FASTA 4. Multiple sequence alignment: a. Clustal b. Dialign c. Multalign 5. Sequence patterns and profiles: a. generation of sequence profiles i. PSI-BLAST b. derivation of and searching sequence patterns: i. MeMe, ii. PHI-BLAST iii. SCanProsite iv. PRATT 6. Protein motif and domain analysis: a. MEME/MAST b. eMotif c. InterproScan d. ProSite e. ProDom f. Pfam 7. Phylogenetic analysis – MEGA, PAUP, PHYLIP **Exercises based on statistics**	100

Basic R:-

1. Obtaining R
2. Generating R codes,
3. Scripts,
4. Text editors for R,
5. Graphical User Interfaces (GUIs) for R,
6. Introduction of Packages

R Objects and data structures:

1. Variable classes,
2. Vectors and matrices,
3. Data frames and lists,
4. Data sets included in R packages,
5. Summarizing and exploring data

Manipulating objects in R:

1. Mathematical operations (recycling rules, propagation of names, dimensional attributes, NA handling)
2. Basic matrix computation (element-wise multiplication,
3. matrix multiplication, outer product,
4. transpose, eigenvalues, eigenvectors),
5. Textual operations
6. Basic graphics

Hypothesis testing and data handling:

1. Parametric and nonparametric tests,
2. Chi-square test,
3. t-tests, ANOVA,
4. Correlation and regression,
5. Principal component Analysis

sTeaching-Learning Methodology	Practical sessions will be conducted in a suitably equipped laboratory either individually or in groups depending on the nature of exercise as well as availability of infrastructure

Evaluation Pattern		
Sr. No.	Details of the Evaluation	Weightage
1.	Internal Practical Examination (As per CBCS R.6.8.3)	30%

2.	University Practical Examination	70%

PRACTICAL OUTCOMES

- Better understanding of the bioinformatics concepts with available analysis tools
- Use of bioinformatics and biological databases to problem solving in real research problems
- Perform a complete analysis of the genes and protein
- Understand the evolutionary concepts related to biological query

List of Practical’s

- Primary Nucleotide Sequence Databases: NCBI, EMBL, DDBJ
- Basic Local Alignment Search Tool (BLAST)
- Protein Sequence Databases – PIR, RefSeq, Swiss-Prot
- Protein Structure Databases – PDB
- Protein Family Databases –Pfam, TIGRFAM
- Protein Visualization Tools- Rasmol, Swiss PDB Viewer
- Specialized Database -IMGT
- Multiple Sequence Alignment Tools: Clustal W
- Phylogenetic Tree Construction Tool: MEGA
- Introduction to Linux commands and Different Platforms and Applications
- Different file formats – FASTQ, SAM, BAM, GFF, Databases and tools – UCSC genome, Galaxy, SRA, NCBI refseq, ENA, FastQC, Bowtie

Master Degree in bioinformatics
M.Sc. (Bioinformatics) Semester II

Course Code	**PT02CBIC55**	Title of the Course	Experimental methods -IV
Total Credits of the Course	06	Hours per Week	4hr

Course Content

Unit	Description	Weightage * (%)
1.	**Part-1** **Data Definition Language (DDL) statements:** Creating database, Selecting database, Deleting database, Creating table, Modifying Table, Deleting table **Data Manipulation statements:** a) Inserting, updating and deleting records b) RetrieIVng Records c) RetrieIVng specific rows and columns d) Use of MySQL operators – Arithmetic operators, Comparison e) Operators, Logical operators f) Math functions, Aggregate functions g) String operations h) Limiting, Sorting and grouping query results i) Handling null values j) Renaming or aliasing table and column names k) Using subqueries l) Using Joins – joining a table to itself, joining multiple tables m) Use of Indexes n) Security Management o) Granting and Revoking rights on tables	100
	Part-2 **JSP:** 1. Setting Up a Servlet and JSP EnIVronment 2. Two Types of Syntax 3. Scripting Elements 4. JSP Configuration 5. Standard JSP Actions 6. Web Application 7. Servlets and HTTP Servlets	

8. GET and POST
9. HTTP Response Codes
10. JSP in XML Syntax

XML:

1. Write a XML code to IVew a simple XML file.
2. Write a Perl script for parsing XML file.
3. Write a XML file for storing a database.
4. Display the CD catalog formatted with the CSS file.
5. Write a code to record a Nucleotide Sequence encoded in XML
6. Sample DTD for representing protein data.
7. Sample instance document adhering to the protein DTD**.**

or

Based on Fundamental of Algorithms

1. Balanced Search Trees: Operations and Applications
2. Binary Search Tree Basics,
3. Red-Black Trees
4. Insertion in a Red-Black Tree
5. Big-Oh Notation
6. Graph Representations
7. Graph Search
8. Dijkstra's Shortest-Path Algorithm

Teaching-Learning Methodology	Practical sessions will be conducted in a suitably equipped laboratory either individually or in groups depending on the nature of exercise as well as availability of infrastructure

Evaluation Pattern		
Sr. No.	Details of the Evaluation	Weightage
1.	Internal Practical Examination (As per CBCS R.6.8.3)	30%
2.	University Practical Examination	70%

Course Outcomes: Having completed this course, the learner will be able to	
1.	Relate the necessity for statistical programming in biology

2.	Handling biological concepts with R scripts
3.	Apply programing to analyse genomic sequences
4.	Development of package with R programming skills
5.	Perform genomic data analysis

List of Practical's

- SQL – Data Definition- Queries in SQL- Updates- Views – Integrity and Security
- Relational Database design – Functional dependences and Normalization for Relational Databases (up to BCNF) and Query search
- Introduction to R, Installing R, Loops
- R as a Deluxe Calculator, Creating Objects and Assigning Values
- Graphics: Simple Plotting, Advanced Plotting, Using Color in Plots, Using
- Subscripts and Superscripts in Graph Labels, Interactive Graphics, Saving
- Graphical Output, Loops

Master Degree in bioinformatics
M.Sc. (Bioinformatics) Semester II

Course Code	**PT02CBIC56**	Title of the Course	Comprehensive Viva
Total Credits of the Course	01	Hours per Week	1hr

Course Objectives:	The objective of the viva is to 1. To check the in-depth knowledge gain by the students throughout the semester

Course Content		
Unit	Description	Weightage* (%)
1.	Evaluation of knowledge gained from three core, one elective and two practical by conducting comprehensive viva	50

Teaching-Learning Methodology	Internal Continuous Assessment in the form of Viva-voce

Evaluation Pattern		
Sr. No.	Details of the Evaluation	Weightage
1.	University Examination	100

Course Outcomes: Having completed this course, the learner will be able to	
1.	Will be able to defend the questions related to core and elective papers studied during semester-I

Suggested References:	
Sr. No.	References
	NIL
On-line resources to be used if available as reference material	
On-line Resources: ---	

Master Degree in bioinformatics
M.Sc. (Bioinformatics) Semester II

Course Code	**PT02EBIC51**	Title of the Course	**Web Application Development in Bioinformatics**
Total Credits of the Course	4	Hours per Week	4

Course Objectives:	**OBJECTIVES OF THE COURSE** • To provide an insight to Data mining • To introduce the techniques used in data mining • To understand these techniques in collecting and sorting of data

Unit	Description in Detail	Weightage (%)
I	**NETWORK BASICS :** Communication Technology – Networking Elements: Networking Hardware, advantages of computer networking, Introduction to the concept of protocol, Network topology, Networking serIVces: Types of Networks – LANs, WANs & MANs, Intranet–Wireless communication – Internet serIVces, Uses of Internet, Function of network connecting deIVces	25%
II	**XML:** Comparison of XML with HTML, XHTML, SGML, RSS, MathML, WAP; XML syntax/elements/attributes; Fundamentals of XML; Write simple XML files; IVewing XML in browser; Creating Well-Formed XML Documents; Creating Valid XML Documents; Fundamentals of XML Namespaces.	25%
III	**JAVA SERVLETS AND JAVA SEVER PAGES (JSP) - I** Introduction to Java servlets, The servlet life cycle, Using generic servlets and HTTP servlets, Introduction to Java Server Pages, JSP Architecture and life cycle,Developing simple JSP pages, Introduction to security in servlets/JSP enIVronment Case studies related to bioinformatics	25%
IV	**JAVA SERVLETS AND JAVA SEVER PAGES (JSP) - II** JSP directives,JSP scripting elements,JSP action elements,JSP implicit objects,Introduction to internationalization Case studies related to bioinformatics	25%

Teaching-Learning Methodology	• Regular class room teaching will be done with following tools: a. Conventional black board and chalk. b. ICT tools such as projectors, smart boards, etc will also be

	used for better explanation of scientific components. • Appropriate reference materials will also provided to the students as and when required from departmental library resources.

Evaluation Pattern		
Sr. No.	Details of the Evaluation	Weightage
1.	Internal Written Examination (As per CBCS R.6.8.3)	15%
2.	Internal Continuous Assessment in the form of Viva-voce, Quizzes, Seminars, Assignments, Attendance (As per CBCS R.6.8.3)	15%
3.	University Examination	70%

Course Outcomes: Having completed this course, the learner will be able to	
1.	Gain insight into the field of Bioinformatics from theoretical models to finished software
2.	Understand how software design and methods can be integrated with existing tools to create productive information environment for bioinformatics practice
3.	Understand how open source can be powerful in creating web-based applications in Bioinformatics
4.	Understand important roles of programming languages and databases in Bioinformatics software development and service

Suggested References:	
Sr. No.	References
1.	Database System Concepts (4th Ed.) by Silberschatz, A., Korth, H.F. and Sudarshan, S., 2002, McGraw Hill Publishers.
2.	An Introduction to Database Systems (7th Ed.) by Date, C.J., Addison Wesley Publishers. 2000 XML for Bioinformatics ,Cerami, Ethan,Springer International Edition

On-line resources to be used if available as reference material
On-line Resources:-- https://www.w3schools.com/xml/xml_whatis.asp

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Master Degree in Bioinformatics
M.Sc (Bioinformatics) Semester II

Course Code	**PT02EBIC52**	Title of the Course	**Fundamentals of Algorithms**
Total Credits of the Course	4	Hours per Week	4

Course Objectives:	The objective of the paper is to • To develop a quantitative understanding of how living things are built • To raise the awareness of the impact of algorithms on the efficiency of the system • To develop skills to analyse algorithms related to Bioinformatics

Unit	Description in Detail	Weightage (%)
I	**LOGIC:** Logic operators AND, OR etc., Truth tables, Theory of inference and deduction, Mathematical Inductions. Matrix representation of graphs: Incidence matrix, adjacency matrices and their properties.	25%
II	**COMPUTING ALGORITHMS** Fundamentals: Models of Computation, Complexity Measures, Algorithms in Computing, Analyzing algorithms, Designing algorithms, Asymptotic notation, Standard notations, Big ‘O’ notations,.	25%
III	**SORTING, SEARCHING & STRINGS MATCHING** Sorting: Bubble-Sort, Merge-Sort, Heap-Sort, Quick-Sort, Radix-Sort, Median-Algorithms, Lower Bounds String Matching: Naïve algorithm, Boyer Moore algorithm	25%
IV	**GRAPHS** Representation of Graphs, Transitive Closure, Shortest Path Problems, Minimum Spanning Trees Trees : Binary tree and its uses, Spanning trees, Fundamental Circuits., Cutsets and related algorithms.	25%

Teaching-Learning Methodology	• Regular class room teaching will be done with following tools: a. Conventional black board and chalk. b. ICT tools such as projectors, smart boards, etc will also be used for better explanation of scientific components.

	• Appropriate reference materials will also provided to the students as and when required from departmental library resources.

Evaluation Pattern		
Sr. No.	Details of the Evaluation	Weightage
1.	Internal Written Examination (As per CBCS R.6.8.3)	15%
2.	Internal Continuous Assessment in the form of Viva-voce, Quizzes, Seminars, Assignments, Attendance (As per CBCS R.6.8.3)	15%
3.	University Examination	70%

Course Outcomes: Having completed this course, the learner will be able to	
1.	Know the main problems in the field of bioinformatics and computational molecular biology
2.	Analyse the correctness of algorithms and how it works
3.	Describe the divide-and-conquer paradigm and explain when an algorithmic design situation calls for it.
4.	Apply the algorithms and design techniques to solve problems
5.	Analyse the complexities of various problems in different domains.

Suggested References:	
Sr. No.	References
1.	Fundamentals of Algorithms by E. Horowitz and S. Sahani., Galgotia Book source Pvt. Ltd. 1999 1.
2.	Data Structures by Seymour Lipschutz., Tata Mc-Graw-Hill publication. 2007
3.	Introduction to Algorithms (3rd Ed.) by T .H. Cormen, C. E. Leiserson, R .L. Rviest., The MIT Press. 2007
4.	Higher Engineering Mathematics (37thEdition), B. S. Gerwal, , Khanna Publishers)
5.	Hans Schneider and George P Barker : Matrices and Linear algebra, Holt Rinehart, 1968.

On-line resources to be used if available as reference material
On-line Resources: https://www.tutorialspoint.com/ https://edu.gcfglobal.org/en/computer-science/algorithms/1/ https://www.geeksforgeeks.org/