



Name: ..... Roll No.: .....

Branch: ..... Signature of Invigilator: .....

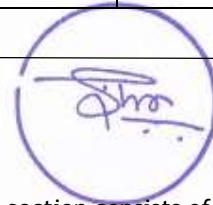
Semester: VIth

Date: 05/05/2022 (MORNING)

Subject with Code: BE316 BIOINFORMATICS ALGORITHMS

Marks Obtained	Section A (30)	Section B (20)	Total Marks (50)

INSTRUCTION TO CANDIDATE



1. The booklet (question paper cum answer sheet) consists of two sections. First section consists of MCQs of 30 marks. Candidates may mark the correct answer in the space provided / may also write answers in the answer sheet provided. The Second section of question paper consists of subjective questions of 20 marks. The candidates may write the answers for these questions in the answer sheets provided with the question booklet.
2. The booklet will be distributed to the candidates before 05 minutes of the examination. Candidates should write their roll no. in each page of the booklet.
3. Place the Student ID card, Registration Slip and No Dues Clearance (if applicable) on your desk. All the entries on the cover page must be filled at the specified space.
4. Carrying or using of mobile phone / any electronic gadgets (except regular scientific calculator)/chits are strictly prohibited inside the examination hall as it comes under the category of unfair means.
5. No candidate should be allowed to enter the examination hall later than 10 minutes after the commencement of examination. Candidates are not allowed to go out of the examination hall/room during the first 30 minutes and last 10 minutes of the examination.
6. Write on both side of the leaf and use pens with same ink.
7. The medium of examination is English. Answer book written in language other than English is liable to be rejected.
8. All attached sheets such as graph papers, drawing sheets etc. should be properly folded to the size of the answer book and tagged with the answer book by the candidate at least 05 minutes before the end of examination.
9. The door of examination hall will be closed 10 minutes before the end of examination. Do not leave the examination hall until the invigilators instruct you to do so.
10. Always maintain the highest level of integrity. Remember you are a BITian.
11. Candidates need to submit the question paper cum answer sheets before leaving the examination hall.

**Birla Institute of Technology, Mesra**  
**BE 316 Bioinformatics Algorithm**  
**Open Elective**

**Time: 2 hrs.**  
**Total marks: 50**

**Multiple Choice Question**

**1\*30=30**

1. In ER model, dashed ellipses are used to denote
  - a. Multivalued attributes
  - b. Derived attributes
  - c. Single attributes
  - d. Weak attributes
2. Which of the following allows us to uniquely identify the entity in entity set?
  - a. Key
  - b. Domain
  - c. Tuple
  - d. Row
3. Which type of data can be stored in the database?
  - a. Image oriented data
  - b. Text, files containing data
  - c. Data in the form of audio or video
  - d. All of the above
4. A distributed database has advantage over centralized database on what point
  - a. Software cost
  - b. Software complexity
  - c. Slow response
  - d. Modular growth
5. Genomics deal with
  - a. Genome data
  - b. Gene data
  - c. Gene Ontology data
  - d. All
6. Fasta format is
  - a. Protein sequence file format
  - b. Protein structure file format
  - c. Sequence file format
  - d. Nucleotide file format
7. Secondary database example
  - a. NCBI
  - b. PDB
  - c. SCOP
  - d. DDBJ

8. What is the best time complexity of bubble sort?
  - a.  $N^2$
  - b.  $N \log N$
  - c.  $N$
  - d.  $(N \log N)^2$
9. If the number of records to be sorted is small, then ..... sorting can be efficient.
  - a. Merge
  - b. Heap
  - c. Selection
  - d. Bubble
10. Which of the following sorting algorithm is of divide and conquer type?
  - a. Bubble sort
  - b. Insertion sort
  - c. Merge sort
  - d. Selection sort
11. Which of the following is not the required condition for a binary search algorithm?
  - a. The list must be sorted
  - b. There should be direct access to the middle element in any sublist
  - c. There must be a mechanism to delete and/or insert elements in the list.
  - d. Number values should only be present
12. What is motif?
  - a. Protein structure
  - b. Protein sequence
  - c. Conserved sequence
  - d. Pattern
13. Say the correct consequences
  - a. Chromosome , DNA, Gene
  - b. DNA, chromosome, gene
  - c. Chromosome , gene, DNA
  - d. None
14. MEME software represents the result of .....
  - a. Domain
  - b. Motif
  - c. Motif logo
  - d. Domain structure
15. Two main measures for the efficiency of an algorithm are
  - a. Processor and memory
  - b. Complexity and capacity
  - c. Time and space
  - d. Data and space
16. What is the type of the algorithm used in solving the 8 Queens problem?
  - a. Greedy
  - b. Dynamic
  - c. Branch and Bound
  - d. Backtracking
17. \_\_\_\_\_ is the maximum number of steps that can executed for the given parameters

- a. Average case
  - b. Worst case
  - c. Time complexity
  - d. Best case
18. Which of the following properties are necessary for an Algorithm?
- a. Definiteness
  - b. Correctness
  - c. Effectiveness
  - d. A and C
19. In a protein sequence alignment, \_\_\_\_\_ refers to the percentage of matches of the same amino acid residues between two aligned sequences.
- a. sequence identity
  - b. sequence homology
  - c. sequence similarity
  - d. sequence non homology
20. \_\_\_\_\_ alignment does not assume that the two sequences in question have similarity over the entire length.
- a. Local
  - b. Global
  - c. Heuristic
  - d. Clustal
21. All are sequence alignment tool except
- a. Rasmol
  - b. BLAST
  - c. FASTA
  - d. ClustalW
22. BLAST stands for .....
23. Which databank works only for protein
- a. NCBI
  - b. GEO
  - c. OMIM
  - d. PDB
24. Blosum matrix is used for
- a. Pairwise sequence alignment
  - b. Multiple sequence alignment
  - c. Structure alignment
  - d. All
25. DML is provided for \_\_\_\_\_.
- a. Description of logical structure of database
  - b. Addition of new structures in the database system
  - c. Manipulation & processing of database
  - d. Definition of physical structure of database system
26. BLASTX program stands for
- a. Translate protein sequence
  - b. Translate DNA database
  - c. Translate input sequence
  - d. None

27. Which of the following is generally used for performing tasks like creating the structure of the relations, deleting relation?
- DML (Data Manipulation Language)
  - Query
  - Relational Schema
  - DDL (Data Definition Language)
28. What do you mean by one to many relationships?
- One class may have many teachers
  - One teacher can have many classes
  - Many classes may have many teachers
  - Many teachers may have many classes
29. In general, a file is basically a collection of all related\_\_\_\_\_.
- Rows & Columns
  - Fields
  - Database
  - Records
30. ANN stands for
- Artificial New Network
  - Arbitrary New Network
  - Artificial New Network
  - Artificial Neural network

**Descriptive Question**

**4\*5=20**

- Consider an array with values {5, 1, 6, 2, 4, 3}, do bubble sorting with diagram. Write advantages of bubble sort.
- With proper diagram define different tier of database architecture.
- Do the steps of performing local alignment (Smith Waterman) for following two sequences with match=2, mismatch=0 and gap=0. ABCDEF and AACDF
- What do you mean genome rearrangement? State with example. What are the factors involved in genome rearrangement?