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NOIDA INSTITUTE OF ENGINEERING AND TECHNOLOGY, GREATER NOIDA

(An Autonomous Institute Affiliated to AKTU, Lucknow)

B.Tech.

SEM: III - THEORY EXAMINATION (2022 - 2023)

Subject: Bioinformatics

Time: 3 Hours

Max. Marks: 100

General Instructions:

IMP: Verify that you have received the question paper with the correct course, code, branch etc.

1. This Question paper comprises of three Sections -A, B, & C. It consists of Multiple Choice Questions (MCQ's) & Subjective type questions.
2. Maximum marks for each question are indicated on right -hand side of each question.
3. Illustrate your answers with neat sketches wherever necessary.
4. Assume suitable data if necessary.
5. Preferably, write the answers in sequential order.
6. No sheet should be left blank. Any written material after a blank sheet will not be evaluated/checked.

SECTION A

20

1. Attempt all parts:-

- | | | |
|------|---|---|
| 1-a. | Sequence retrieval tool of EMBL? (CO1) | 1 |
| | (a) BankIt | |
| | (b) Sakura | |
| | (c) SRS | |
| | (d) NCBI | |
| 1-b. | Which database contain the 3D structure of protein? (CO1) | 1 |
| | (a) GenBank | |
| | (b) DDBJ | |
| | (c) PDB | |
| | (d) EMBL | |
| 1-c. | The matrix used for the best local alignment of protein sequences is (CO2) | 1 |
| | (a) BLOSUM62 | |
| | (b) IUB | |
| | (c) BLOSUM80 | |

- (d) PAM20
- 1-d. Needleman-Wunch algorithm is used for (CO2) 1
- (a) Global alignment
 - (b) Multiple sequence alignment
 - (c) Both Global and Local
 - (d) None of the above
- 1 Which process hinders clarification of the deepest branchings in a phylogenetic tree that depicts the origins of the three domains? (CO3) 1
- (a) binary fission
 - (b) mitosis
 - (c) meiosis
 - (d) horizontal gene transfer
- 1 Which eukaryotic kingdom is polyphyletic and therefore not acceptable, based on cladistics? (CO3) 1
- (a) Plantae
 - (b) Fungi
 - (c) Animalia
 - (d) Protista
- 1-g. The term epigenetics was coined in year? (CO4) 1
- (a) 1945
 - (b) 1942
 - (c) 1966
 - (d) 1962
- 1-h. What is epistasis? (CO4) 1
- (a) Type of linkage
 - (b) Masking or modifying gene effect
 - (c) upper portion of chromosome
 - (d) Group of genes
- 1-i. HMMs stands for (CO5) 1
- (a) Hidden Markov Models
 - (b) High Molecular Model
 - (c) Hidden Magnetic Models

(d) Hidden Markov Models

- 1-j. What term is used to signify a preparation that appears identical to the preparation of an active drug but which has no biological activity? (CO5) 1
- (a) Dummy drug
- (b) Peptidomimetic
- (c) Placebo
- (d) Gazebo

2. Attempt all parts:-

- 2.a. Why secondary biological databases are also known as derived databases? (CO1) 2
- 2.b. What are various steps involved in smith-waterman algorithm? (CO2) 2
- 2.c. Explain the term Phylogenetic analysis? (CO3) 2
- 2.d. Discuss the role of epigenetics in transcription regulation? (CO4) 2
- 2.e. What do you mean by Regression? (CO5) 2

SECTION B

30

3. Answer any five of the following:-

- 3-a. How Webcutter 2.0 can be used for the restriction analysis of various DNA sequences? (CO1) 6
- 3-b. What are biodiversity databases? Explain. (CO1) 6
- 3-c. What are the various conditions taken under consideration during pairwise sequence alignment? How they effect the sequence alignment? (CO2) 6
- 3-d. Different versions of Blast tool has their own importance. Comment on this statement. (CO2) 6
- 3.e. Explain the phylogenetic tree terminologies? Give the details. (CO3) 6
- 3.f. What is computational epigenetics? Explain the significance of computational epigenetics in detail. (CO4) 6
- 3.g. Write a short note on Artificial Neural Network algorithms? How this algorithm works? (CO5) 6

SECTION C

50

4. Answer any one of the following:-

- 4 Explain SWISSPROT/UNIPROT, PIR (protein information resource) in detail. (CO1) 10
- 4 Explain various applications of patent databases in different fields? (CO1) 10

5. Answer any one of the following:-

- 5-a. Discuss multiple sequence alignment in detail. What are the different methods of sequence alignment? Explain in detail. (CO2) 10
- 5-b. How local alignment is different from global alignment? Explain with the help of suitable examples. (CO2) 10

6. Answer any one of the following:-

- 6 What are the advantages and disadvantages of Unweighted Pair Group Method with Arithmetic Mean? Explain in detail. (CO3) 10
- 6 Discuss various steps involved in Fitch-Margoliash Method of phylogenetic tree construction by giving suitable example. (CO3) 10

7. Answer any one of the following:-

- 7 How genetical disorders can be identified using epigenetics? How these type of disorders can be treated with genome editing technology? (CO4) 10
- 7 Describe the various methodologies for the identification of genetic variations? What is the importance of finding genetic variations? (CO4) 10

8. Answer any one of the following:-

- 8 Discuss the significance of molecular modelling in drug designing? Give the details of various methods of molecular modelling in bioinformatics? (CO5) 10
- 8 Describe the classical and semi-classical calculations in Machine learning? What are the major difference between classical and semi-classical calculations? (CO5) 10