[44] SEAT No._____ (44) **SARDAR PATEL UNIVERSITY**
External Examination
Class- T.Y. B. Sc. VI Semester
Date: - 02-04-2018, Day: - Monday
Time: - 10:00 am to 01:00 pm

Course: - US06CGEN04

Subject: Genetics
Bioinformatics

Title: - Bioinformatics
Total Marks: 70

[10]

Q1. Multiple choice questions (**All are compulsory**).

(1) It is a simple type of Database based on ordering and indexing.
   a) Flat file indexing system
   b) Object oriented database
   c) RDMS
   d) None

(2) _____ compares protein sequence against protein databases.
   a) blastp.   b) blastn.   c) blastx.   d) tblastx.

(3) The optimal alignment of two similar sequences is usually that _____ number of matches and _____ the number of gaps.
   a) Minimize, maximize.
   b) Maximize, minimize.
   c) Degrade, upgrade.
   d) Upgrade, degrade.

(4) Lalign is a tool for
   a) Alignment
   b) Structure identification
   c) Drug design
   d) Sequence identification

(5) Which is a repository for the 3-dimensional structure data for large biomolecules?
   a) NCBI   b) EMBL   c) Swiss-Prot.   d) PDB.

(6) The Central Processing Unit (CPU) consists of:
   a) Input, output and processing
   b) Control unit, primary storage & secondary storage
   c) Control unit, arithmetic-logic unit, primary storage
   d) Control unit, processing, and primary storage

(7) Secondary database is
   a) Data collected from scientist
   b) modified data of primary database
   c) Data collected from public
   d) none

(8) In PowerPoint, each page is called
   a) A worksheet   b) A text page   c) A slide   d) A presentation

(9) The alignment search uses only conserved region in the sequences
   a) Local alignment
   b) Global alignment
   c) Pairwise alignment
   d) Multiple alignment

(10) Which of the following units is having the biggest capacity:
   a) Byte   b) Kilobyte   c) Gigabyte   d) Megabyte

[20]

Q2. Answer the following questions in short. (**Attempt any 10**) (each carry 2 marks)
   (1) Enlist any 4 databases that contain sequence information.
   (2) How freeware software differ from shareware software?
   (3) Differentiate between EMBL and TrEMBL.
   (4) Differentiate between pairwise & multiple sequence alignment.
   (5) Give the abbreviation for following: BLAST; OMIM; EMBL; SCOP
   (6) Enlist any 4 useful websites linked with Bioinformatics.
   (7) Discuss the importance of search engine.
   (8) Give the important features of Swiss-Prot.
   (9) Diagrammatically explain the structure of Eukaryotic gene.

P.T

(P.T.O.)

(1)

(10) Enlist any 4 databases of NCBI.

(11) What is Unix Operating system?

(12) What are biological databases? Explain with an example.

Q3. (a) Discuss the basic structural organization of computer. [5]

(b) Explain different generations of computer with examples. [5]

OR

Q3. Explain MS OFFICE and its various applications in detail [10]

Q4. (a) Find the alignment score for the following sequences [04]

ATTGCATGGAAACT

ATCGGATTGACACT

Given: --- Match score: 2 & Mismatch score: -1

(b) Discuss the basic concept and scope in Bioinformatics [06]

OR

Q4. Explain NCBI database with its important features, databases and applications. [10]

Q5. (a) Write a short note on Phylogenetic analysis. [5]

(b) Describe BLAST, its type & importance. [5]

OR

Q5. What is a pairwise sequence alignment? Discuss any one tool for it. [10]

Q6. What is gene structure prediction? Elaborate any two methods in detail. [10]

OR

Q6. Describe any two tools used in protein structure prediction. [10]

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