

SEAT No. _____

[82/A-44]

() SARDAR PATEL UNIVERSITY

External Examination

Class- S.Y. B. Sc. IV Semester

Date: - 11-04-2017, Day: - Tuesday,

Time: - 02:00 pm to 05:00 pm

Course: - US04CBNF01

Subject: Bioinformatics Title: - Bioinformatics Sequence Analysis

Total Marks: 70

- Q1. Multiple choice questions (All are compulsory). [10]
- (1) _____ is a database similarity search tool.
a) BLAST b) CLUSTAL W c) CLUSTAL X d) RASMOL
 - (2) Continuous set of spaces in the sequence
a) Match b) Gaps c) Mismatch d) None of the above
 - (3) Smith and Watermann algorithm is used for
a) Local alignment b) Global alignment c) Structure prediction d) All
 - (4) The _____ tool compares translated nucleotide query sequence against protein databases.
a) blastp b) tblastn c) blastx d) tblastx
 - (5) Which alignment is useful to detect the highly conserved regions?
a) Local b) Global c) Pairwise sequence d) Multiple sequence.
 - (6) The ClustalW uses step for multiple alignment is :
a) guide tree formation b) the order they are entered into the program
c) the percent identity d) the organisms they come from
 - (7) The imino acid found in the protein is
a) Proline b) Glycine c) Valine d) Aspartic acid
 - (8) Which of the following pairs of amino acids is basic in nature?
a) histidine b) alanine c) leucine d) glutamatic acid
 - (9) Sequence alignment helps scientists
a) to trace out evolutionary relationships b) to infer the functions of newly synthesized genes
c) to predict new members of gene families d) all of these
 - (10) The _____ the E-value, the more significant the hit.
a) lower b) higher c) average d) superior
- Q2. Answer the following questions in short. (Any ten) [20]
- (1) Differentiate local and global alignment.
 - (2) Give the biological significance of Gaps.
 - (3) Enlist different types of Edit operations used in sequence alignment
 - (4) Give the abbreviation for: BLAST, NCBI, PAM, BLOSUM.
 - (5) Differentiate between Needleman Wunch and Smith Watermann algorithm.
 - (6) Align the sequence i) ATCGCCCAATTCT ii) ATCGCCAAAATTC
Given match score: 5 and mismatch score: -2
 - (7) Give the name of all polar amino acids along with its codes.
 - (8) Give different types of bonds present in protein structure.
 - (9) How Clustal W tool is used? Give different steps.
 - (10) Explain the utility of BLAST.
 - (11) Differentiate PAM and BLOSUM.
 - (12) Diagrammatically show α helix and β sheets.

P.T.O

Q3. What is Sequence alignment? Explain in detail about its types and importance [10]

OR

Q3. Discuss local alignment. Explain any one tool in detail for it. [10]

Q4. (i) What is progressive method? Explain the algorithm. [05]

(ii) Elaborate different types of BLAST. [05]

OR

Q4. Explain scoring matrix and its types with example. [10]

Q5. Explain DP algorithm and its type with an example. [10]

OR

Q5. Use Needleman/Wunsch algorithm for aligning following sequences [10]

G A A T T C A G T T A (sequence #1)

G G A T C G A (sequence #2)

so M = 11 and N = 7 (the length of sequence #1 and sequence #2, respectively)

GIVEN: Match score : +1 , Mismatch : 0, Gap penalty: 0

Find score and all possible alignments.

Q6. What are proteins? Discuss its properties and structure in detail. [10]

OR

Q6. Explain Chou Fasman method in detail for protein structure prediction [10]

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