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GIET UNIVERSITY, GUNUPUR – 765022
M. Sc. (First Semester) Examinations, March – 2023
22LSPC104 – Bioinformatics and Biostatistics
(Life science)

Time: 3 hrs

Maximum: 70 Marks

(The figures in the right hand margin indicate marks.)

PART – A**(2 x 10 = 20 Marks)****Q.1. Answer all questions**

	CO #	Blooms Level
a. What is the flat file? Write four examples of sequence flat file format.	CO ₁ -PO ₁	K ₁
b. What is PDBID? Give two examples	CO ₁ -PO ₁	K ₁
c. Write the difference between the Needleman-Wunch algorithm and the Smith-Waterman algorithm	CO ₁ -PO ₁	K ₁
d. Justify the given MSA is a P-fam QPILLL LR-LL- K-ILLL PPVLIL Assume that match= 1, Mismatch= -1 and gap= -1	CO ₂ -PO ₁	K ₁
e. If there are 5 OTU in an MSA how many rooted and unrooted phylogenetic tree are constructed	CO ₂ -PO ₁	K ₂
f. Convert the given molecular marker into MSA TCYGIFVL TCGIFVL SCYGIFVLSG ACGIFVLSG	CO ₂ -PO ₂	K ₁
g. Find the Hamming distance between two sequence ADVANCED and NEWDELHI	CO ₃ -PO ₂	K ₂
h. Find the mean and mode of the following data 3,5,7,2,5,1,3,5	CO ₃ -PO ₁	K ₁
i. What is the difference between negative and positive correlations?	CO ₃ -PO ₁	K ₁
j. Write the equation of regression X on Y and Y on X	CO ₃ -PO ₁	K ₂

PART – B**(10 x 5 = 50 Marks)**Answer ANY FIVE questions

	Marks	CO#	Blooms Level
2. a. Explain briefly on Genbank database	5	CO ₁ -PO ₁	K ₁
b. State the difference between global and local alignment	5	CO ₁ -PO ₁	K ₁
3.a. Find the optimal alignment and alignment score of two sequences AATTCGCGTA and TATCGCTACA by using dot matrix algorithm	7	CO ₁ -PO ₁	K ₂

- b. Explain the option of BLAST 3 CO₁-PO₁ K₁
4. a. Calculate PAM-I of the given MSA 7 CO₂-PO₂ K₂
- ACGCTAFKI
GCGCTAFKI
SCGCTAFKL
GCGCTGFKI
GCGCTLFKI
ASGCTAFKL
ACACTAFKL
- b. Find the hamming distance between the sequence HLIKLAAIWL and HLWKLAAIWA. Write the difference between hamming distance and Edit distance. 3 CO₂-PO₂ K₁
- 5.a. What is the secondary structure of a protein? Find the types of secondary structure information if a protein containing a total of 1800 residues and 810 of them are in helix, considering the residue Ala among residues due and 210 are in helix 5 CO₂-PO₂ K₂
- b. Explain briefly the homology modelling. Write the computational procedure for homology modelling by swiss model. How it is differ from threading modelling 5 CO₃-PO₁ K₂
6. a. Design a phylogenetic tree by using NJ Method 7 CO₃-PO₁ K₂
- A B C D E F
A 0
B 5 0
C 4 7 0
D 7 10 7 0
E 6 9 6 5 0
F 8 11 8 9 8 0
- b. Write the flowchart of phylogeny 3 K₁
- 7.a. Find the mean and median for the following data. 5 K₁
- 6, 15, 4, 10, 12, 11, 5, 3, 16
- b. Calculate the coefficient of correlation of the given data 5 CO₃-PO₁ K₂
- | Case | A | B | C | D | E | F | G | H |
|------|----|---|---|----|----|----|----|---|
| X-1 | 10 | 6 | 9 | 10 | 12 | 13 | 11 | 8 |
| X-2 | 9 | 4 | 6 | 9 | 11 | 13 | 9 | 4 |
8. a. 4. Calculate the mean deviation from mean for the following distribution. 5 CO₃-PO₁ K₂
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|---|---|---|----|---|----|---|
| X | 1 | 3 | 8 | 5 | 6 | 7 |
| F | 4 | 9 | 16 | 9 | 11 | 6 |
- b. Find the lines of regression X on Y and Yon X 5 CO₃-PO₂ K₂
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|---|---|---|---|---|---|
| X | 3 | 5 | 6 | 6 | 9 |
| Y | 2 | 3 | 4 | 6 | 5 |

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