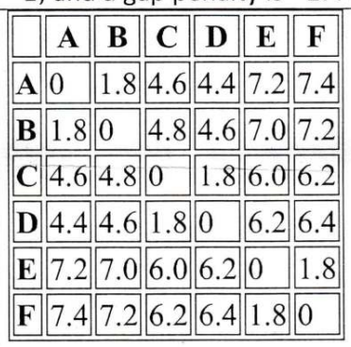
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ClassTest 2

CSE115 (Introduction to Biology and Chemistry for Computation)

Time: 50 minutes Marks: 15

1.	You are given two biological sequences, `GATTACA` and `GCATGCU`. Your task is to align these sequences in a way that considers every character from start to end. Use the following scoring scheme to guide your work: a match scores `+1`, a mismatch scores `−1`, and a gap penalty is `−2`. Perform the algorithm with description.	8
2.	 Build a rotated tree from the distance matrix using UPGMA Algorithm.	7

	A	B	C	D	E	F
A	0	1.8	4.6	4.4	7.2	7.4
B	1.8	0	4.8	4.6	7.0	7.2
C	4.6	4.8	0	1.8	6.0	6.2
D	4.4	4.6	1.8	0	6.2	6.4
E	7.2	7.0	6.0	6.2	0	1.8
F	7.4	7.2	6.2	6.4	1.8	0

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