

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.	<table border="1"><thead><tr><th></th><th>A</th><th>B</th><th>C</th><th>D</th><th>E</th><th>F</th></tr></thead><tbody><tr><th>A</th><td>0</td><td>1.8</td><td>4.6</td><td>4.4</td><td>7.2</td><td>7.4</td></tr><tr><th>B</th><td>1.8</td><td>0</td><td>4.8</td><td>4.6</td><td>7.0</td><td>7.2</td></tr><tr><th>C</th><td>4.6</td><td>4.8</td><td>0</td><td>1.8</td><td>6.0</td><td>6.2</td></tr><tr><th>D</th><td>4.4</td><td>4.6</td><td>1.8</td><td>0</td><td>6.2</td><td>6.4</td></tr><tr><th>E</th><td>7.2</td><td>7.0</td><td>6.0</td><td>6.2</td><td>0</td><td>1.8</td></tr><tr><th>F</th><td>7.4</td><td>7.2</td><td>6.2</td><td>6.4</td><td>1.8</td><td>0</td></tr></tbody></table> Handwritten notes: A tree diagram showing a root node branching into two main clusters. The left cluster contains nodes A, B, and C, while the right cluster contains nodes D, E, and F. The root node is labeled with a distance of 14. The left cluster is labeled with a distance of 10, and the right cluster is labeled with a distance of 6. The nodes A, B, and C are labeled with distances of 4, 4.8, and 4.6 respectively. The nodes D, E, and F are labeled with distances of 6.2, 6.0, and 6.4 respectively.		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	7
	A	B	C	D	E	F																																													
A	0	1.8	4.6	4.4	7.2	7.4																																													
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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																																													
Build a rooted tree from the distance matrix using UPGMA Algorithm.																																																			