

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"><tr><td></td><td>A</td><td>B</td><td>C</td><td>D</td><td>E</td><td>F</td></tr><tr><td>A</td><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><td>B</td><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><td>C</td><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><td>D</td><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><td>E</td><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><td>F</td><td>7.4</td><td>7.2</td><td>6.2</td><td>6.4</td><td>1.8</td><td>0</td></tr></table> Handwritten notes: A tree diagram showing a root node branching into two main clades. The left clade contains nodes A, B, and C, with A and B being sister taxa. The right clade contains nodes D, E, and F, with D and E being sister taxa. The root node is labeled with a '1' and a '0'.		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																																													
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																																													
	Build a rooted tree from the distance matrix using UPGMA Algorithm.																																																		