CENG 465
Introduction to Bioinformatics

Spring 2021-2022

Assignment #1
Written Assignment

Problem 1 (50 Points): Given the following dynamic programming score table constructed using the Smith-Waterman local alignment algorithm, find the match score, mismatch penalty, and gap penalty parameters. Show your reasoning. Also, show the best local alignment of the two sequences both on the table as a traceback of cells and as an alignment of two sequences written over two lines with gaps and matches/mismatches. What is the score of the local alignment? Verify that the score on the table and the score of the alignment you have written are the same. Assume that there is a single match score which is positive and single gap and mismatch penalties which are negative. In other words, a single match score is used for all types of matches. Similarly, a single mismatch penalty is used for all types of mismatches. Linear gap model is used.

	-	M	I	M	A	G	E	D	I	L
-	0	0	0	0	0	0	0	0	0	0
G	0	0	0	0	0	7	3	0	0	0
A	0	0	0	0	7	3	1	0	0	0
M	0	7	3	7	3	1	0	0	0	0
A	0	3	1	3	14	10	6	2	0	0
E	0	0	0	0	10	8	17	13	9	5
D	0	0	0	0	6	4	13	24	20	16
K	0	0	0	0	2	0	9	20	18	14

Problem 2 (50 Points): Fill in the dynamic programming score table using the Needleman-Wunsch dynamic programming global alignment algorithm to globally align the two sequences given below. Use the BLOSUM62 matrix given below as the scoring matrix. Use the linear gap model with a gap penalty of -4. Show the best alignment of these two sequences. Also, show the alignment path on the partial scores table.

	-	M	C	G	M	G	C	M	E	L
-	**0**	**-4**	**-8**	**-12**	**-16**	**-20**	**-24**	**-28**	**-32**	**-36**
G	**-4**									
M	**-8**									
C	**-12**									
M	**-16**									
E	**-20**									
D	**-24**									
L	**-28**									

	C	S	T	P	A	G	N	D	E	Q	H	R	K	M	I	L	V	F	Y	W
C	9	-1	-1	-3	0	-3	-3	-3	-4	-3	-3	-3	-3	-1	-1	-1	-1	-2	-2	-2
S	-1	4	1	-1	1	0	1	0	0	0	-1	-1	0	-1	-2	-2	-2	-2	-2	-3
T	-1	1	4	1	-1	1	0	1	0	0	0	-1	0	-1	-2	-2	-2	-2	-2	-3
P	-3	-1	1	7	-1	-2	-1	-1	-1	-1	-2	-2	-1	-2	-3	-3	-2	-4	-3	-4
A	0	1	-1	-1	4	0	-1	-2	-1	-1	-2	-1	-1	-1	-1	-1	-2	-2	-2	-3
G	-3	0	1	-2	0	6	-2	-1	-2	-2	-2	-2	-2	-3	-4	-4	0	-3	-3	-2
N	-3	1	0	-2	-2	0	6	1	0	0	-1	0	0	-2	-3	-3	-3	-3	-2	-4
D	-3	0	1	-1	-2	-1	1	6	2	0	-1	-2	-1	-3	-3	-4	-3	-3	-3	-4
E	-4	0	0	-1	-1	-2	0	2	5	2	0	0	1	-2	-3	-3	-3	-3	-2	-3
Q	-3	0	0	-1	-1	-2	0	0	2	5	0	1	1	0	-3	-2	-2	-3	-1	-2
H	-3	-1	0	-2	-2	-2	1	1	0	0	8	0	-1	-2	-3	-3	-2	-1	2	-2
R	-3	-1	-1	-2	-1	-2	0	-2	0	1	0	5	2	-1	-3	-2	-3	-3	-2	-3
K	-3	0	0	-1	-1	-2	0	-1	1	1	-1	2	5	-1	-3	-2	-3	-3	-2	-3
M	-1	-1	-1	-2	-1	-3	-2	-3	-2	0	-2	-1	-1	5	1	2	-2	0	-1	-1
I	-1	-2	-2	-3	-1	-4	-3	-3	-3	-3	-3	-3	-3	1	4	2	1	0	-1	-3
L	-1	-2	-2	-3	-1	-4	-3	-4	-3	-2	-3	-2	-2	2	2	4	3	0	-1	-2
V	-1	-2	-2	-2	0	-3	-3	-3	-2	-2	-3	-3	-2	1	3	1	4	-1	-1	-3
F	-2	-2	-2	-4	-2	-3	-3	-3	-3	-3	-1	-3	-3	0	0	0	-1	6	3	1
Y	-2	-2	-2	-3	-2	-3	-2	-3	-2	-1	2	-2	-2	-1	-1	-1	-1	3	7	2
W	-2	-3	-3	-4	-3	-2	-4	-4	-3	-2	-2	-3	-3	-1	-3	-2	-3	1	2	11