

Due Date: March 20, 2007 (in class)

**CENG 465
Spring 2006-2007**

Written Assignment #1

Problem 1 (50 Points): Given the following dynamic programming score table constructed using the Smith-Waterman algorithm, find the match score, mismatch penalty, and gap penalty parameters. Show your reasoning. Also, show the best local alignment of the two sequences. What is the score of the local alignment?

Additional information: 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): What is the maximum length of the DNA sequence that is expected to occur at least once in its entirety in another DNA sequence of length 600? In other words given two DNA sequences, A and B , where $length(A)=600$, what should be the maximum length of B , so that it is expected to observe a perfect local alignment (all matches, no mismatch or gap) between A and B ? Show the steps of your calculation.