Data Structures and Algorithms
Homework 2

1. What is the Manhattan Tourist Problem, and how does it apply to the comparison of biological sequences?

2. Hamming vs Edit Distance Methods:

a. Compute the Hamming distance for these two sequences: AATCGACTTAGCA and AGTCGACATACCA

b. Compute the Edit distance for these two sequences: the sequences AATCGACTTAGCA and AGTCGATACCA

c. Which of the two method (Hamming vs Edit) is more appropriate for biological sequence data, and why?

3. Consider the sequences S1 = TACGGGTAT and S2 = GGACGTACG. Assume that the match score is 1, mismatch score is -1, and gap penalty is d = -2. You must show the scoring matrix for full credit!

a. Find an optimal global alignment

b. Final an optimal local alignment

4. Given the following alignments of three sequences, what is the sum-of-pairs score? Assume that the scoring system: match score = 1, mismatch score = -2, gap score = -4. Show all of your work for full credit!

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ACCTCTGTC
AC-TGTAAC
ACCTGT-AC
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