CMSC 423 Homework #2:
Due: Sep. 28 at the start of class

You may discuss these problems with other students in this class, but you **must write up your solutions independently**, without using common notes or worksheets. You must indicate at the top of your homework who you worked with. Your write up should be clear, concise, and neat. You are trying to convince a skeptical reader that your algorithms or answers are correct. Messy or hard-to-read homeworks will not be graded.

1. Recall the RNA folding algorithm presented in class and in the lecture slides. Give pseudocode to find the actual optimal RNA structure (not just the optimal score) and briefly explain the idea behind your code.

2. A *monotonically increasing subsequence* of a sequence of $n$ integers $c_1, \ldots, c_n$ is a subset of the integers $c_{i_1}, \ldots, c_{i_k}$ such that $c_{i_1} < c_{i_2} < \ldots < c_{i_k}$ and $i_1 < i_2 < \ldots < i_k$. In other words, it is a subsequence of the input that is always increasing when considered in the order present in the input.

   Give an $O(n^2)$ dynamic programming algorithm to find the *longest* monotonically increasing subsequence of a given set $c_1, \ldots, c_n$ of integers. For example: $50, 75, 100$ is the longest increasing subsequence of input $80, 50, 75, 35, 100$.

3. Recall the algorithm for sequence alignment with affine gap penalties given in class, lecture slides, and section 6.9 of your book. This algorithm uses several parameters that define the scoring function: gap start, gap extend, and match(a,b). While the algorithm will work for any values of these parameters, some parameter settings produce more reasonable alignments than others.

   (a) For example, gap start + gap extend ought to be more than match(a,b) for any characters $a$ and $b$. Why is that?

   (b) Give two other conditions that the parameters “should” satisfy in order for the alignment to “make sense” and explain why it makes sense for those conditions to hold for most reasonable scoring functions.