1. RNAs adopt complex 3d structures that are important for biological functions. Pairs of positions in RNA with complimentary nucleotides can form bonds. Bonds between locations \((i, j)\) and \((i', j')\) are interleaving if \(i < i' < j < j'\) and are noninterleaving otherwise; see the figure below.

Every set of noninterleaving bonds corresponds to a potential RNA structure. In a very naive formulation of RNA folding, one simply tries to find a maximum set of non-interleaving bonds. Design a dynamic programming algorithm for finding the largest set of noninterleaving bonds, given an RNA sequence as input.

(Note: There are more adequate folding models, which attempt to minimize energy - these are quite a bit more difficult!)
2. (a) Consider a model of virus infection where a virus infects a bacterium, and modifies a replication process by inserting:
- at every A, between 1 and 5 additional A’s
- at every C, a run of 1 to 10 additional C’s
- at every G, a run of of G’s of arbitrary length ≥ 1
- at every T, a run of of T’s of arbitrary length ≥ 1

The gaps or insertions are allowed for in this virally modified final DNA sequence. For example, the sequence AAATAAAGGGGCCCCCTTTTTTTTTCC is an infected version of ATAGCTC; however, AAAAAAAATAAAGGGGCCCCCTTTTTTTTTCC would not be, since it inserts too many A’s in the first slot and did not insert any extra G’s.

Given two sequences $v$ and $w$, give an efficient algorithm (including run time and space) that will determine if $v$ could be an invected version of $w$.

(b) Now consider a version where the virus will either delete a letter or will insert a run of arbitrary length, for each A,G,T,C it encounters in the original DNA. Give an efficient algorithm to decide if $v$ could be an infected version of $w$ under these circumstances.

3. Recall the dynamic programming solution to local alignment that we covered in class (or go re-read it in the textbook); this algorithm required O(mn) time and space. Adapt the divide and conquer framework from chapter 7 to get a linear space solution. (Your running time can still stay higher, though.)