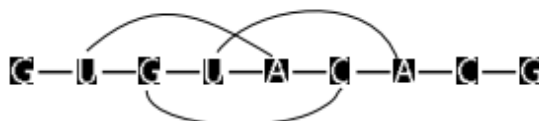


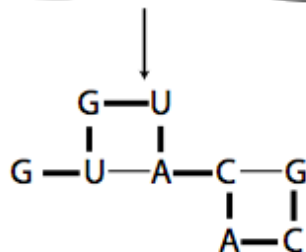
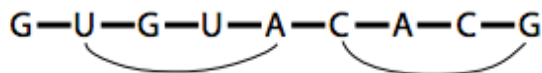
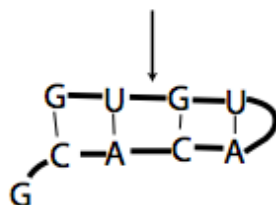
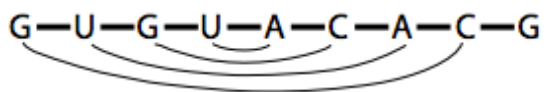
## BCB 5300

Homework 3:  
More fun with dynamic programming

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.



(a) Interleaving bonds



(b) Non-interleaving bonds

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  $\geq 1$
  - at every T, a run of of T's of arbitrary length  $\geq 1$

The gaps or insertions are allowed for in this virally modified final DNA sequence. For example, the sequence AAATTAAAGGGGCCCTTTTTTTTCC is an infected version of ATAGCTC; however, AAAAAAAAAATTAAAGGCCCTTTTTTTTCC 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 infected 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.)