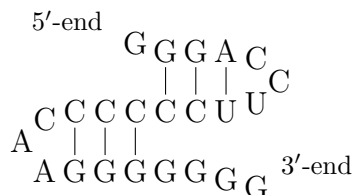
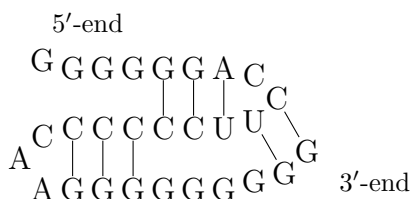


Read: Algebraic and Discrete Mathematical Methods for Modern Biology, Chapter 13: *RNA Secondary Structures: Combinatorial Models and Folding Algorithms*, by Q. He, M. Macauley, and R. Davies. Pages 321–345.

1. Consider the following fold of the RNA sequence GGGACCUCCCCCAAGGGGGG:



- (i) Draw the corresponding arc diagram.
 - (ii) Write out this secondary structure in point-bracket notation.
 - (iii) Draw the corresponding Motzkin path.
2. Consider the following fold of the same RNA sequence from the previous problem:



- (i) Draw the corresponding arc diagram. What is the smallest k for which this is k -noncrossing .
 - (ii) What if the first G bonds with the C “directly below” it (vertex 17). Does this change the k from the previous part?
 - (iii) Draw a picture of a folded RNA strand (like the one above) that is 4-noncrossing but not 3-noncrossing.
3. Consider the RNA sequence $\mathbf{b} = \text{GCUGCAUCUU}$. Find all possible ways that it can fold into a secondary structure S , without leaving any “allowed” unpaired bases. Draw the arc diagram and a “realistic sketch” of the folded RNA strand. Compute the energy score $E(\mathbf{b}, S)$ of each.

4. Use dynamic programming to fill out the remaining table to find the optimal fold of the RNA sequence $\mathbf{b} = \text{GCUGCAUCUU}$. Then, do the trace-back step to recover a structure that achieves this maximum energy score.

	G	C	U	G	C	A	U	C	U	U
G	0	0	0	0						
C		0	0	0	0					
U			0	0	0	0				
G				0	0	0	0			
C					0	0	0	0		
A						0	0	0	0	
U							0	0	0	0
C								0	0	0
U									0	0
U										0