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*From Nucleotide Sequences to Secondary Structures, and Back Again*  

The formation of base pairs within single-stranded RNA molecules, known as the "secondary structure," is an essential part of their overall structure and function. With the variety of biomedical roles performed by RNA molecules, understanding how structure and function are encoded in RNA sequences is a fundamental scientific challenge. We address this challenge by focusing on the design and analysis of RNA secondary structures based on a discrete mathematical model. Single-stranded RNA sequences are understood to self-bond with a complex interplay between energetically beneficial stacked base pairs, or "helices," and destabilizing single-stranded structures called "loops." We give results demonstrating the importance of local helical constraints in specifying a global structure and characterizing minima in loop energy configurations. These results suggest new insights into the folding of RNA molecules as well as motivating a combinatorial approach to designing RNA secondary structures.