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Christine E Heitsch* (heitsch@math.gatech.edu). *Branching polytopes for RNA sequences.*

The branching of an RNA secondary structure is an important molecular characteristic, yet often difficult to predict correctly by optimizing under the nearest-neighbor thermodynamic model (NNTM). Prior results for a combinatorial model of RNA folding analyzed the expected degree of branching, and demonstrated that changes in the NNTM parameters can significantly affect this distribution. This insight was fully developed using methods from geometric combinatorics to give a parametric analysis of the optimal configurations, addressing the dependence of prediction results on the objective function parameters. Furthermore, it is now possible to compute a branching polytope and associated normal fan subdivision of the dual space for any RNA sequence, yielding new insights into the accuracy and robustness of RNA secondary structure prediction. (Received January 19, 2016)