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The Structure of the Branching Polytopes for RNA Structures

Finding a method that can quickly and reliably identify the structure of a given RNA has been an important problem in computational biology. However, the methods developed still vary widely in the prediction accuracy. An important component of this problem is predicting the secondary structure, which identifies both the canonically base-paired regions (helices) and non-paired regions (loops). In this work we focus on understanding the effects of the parameters used for scoring the multibranch loops in the nearest-neighbor thermodynamic model. For this purpose, for each RNA we built and analyzed a branching polytope. Here I will present our findings.