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(spoznan@clemsn.edu). *The Structure of the Branching Polytopes for RNA Structures.*

Like proteins, RNA assumes complex three-dimensional structures to perform specific roles and understanding this structure helps our understanding of the ways the noncoding RNAs perform their regulatory functions. That is why the problem of finding methods 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 so called branching polytope. We discovered that there is a lot of structural similarity in the normal fans of these branching polytopes as the nucleotide sequences change. In this talk I will present our findings. (Received July 26, 2017)