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Analyzing RNA structure data with tree polynomials

Advancements in innovative technology such as high-throughput sequencing, cryogenic electron microscopy and artificial intelligence have enabled production of myriad data of RNA structures. Analyzing these data allows us to better understand the functions of RNAs and their roles in various biological processes. However, studying extensive RNA structure data poses challenges without proper representations. Polynomial invariants, such as the Tutte polynomial for graphs and the Jones polynomial for knots, are essential mathematical objects in algebraic combinatorics and algebraic topology. They encode structural information and are compatible with modern data analytic tools. In this talk, we introduce a computationally efficient, interpretable and complete polynomial invariant for trees. We apply this tree polynomial and its generalizations to the study of RNA secondary structures.