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The Combinatorics of RNA in the Polymere Zeta Model

Recently it has been observed that the computational prediction of RNA secondary structure can be speed-up by a linear factor on average. To this end, one has to assume the so-called polymere zeta property, i.e. two building blocks of an RNA molecule at distance m are paired (in folding) with probability b/m^c, for some constants $b, c > 0$. In this talk, we examine the averaged shape of an RNA folding in a polymere zeta model using generating functions and techniques form complex analysis. We find that some important structural motifs show a rather different behavior than observed in real world molecules.