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Enumerating secondary structures and structural moieties for circular RNAs

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Abstract

A quantitative characterization of the relationship between molecular sequence and structure is essential to improve our understanding of how function emerges. This particular genotype-phenotype map has been often studied in the context of RNA sequences, with the folded configurations standing as a proxy for the phenotype. Here, we count the secondary structures of circular RNAs of length n and calculate the asymptotic distributions of different structural moieties, such as stems or hairpin loops, by means of symbolic combinatorics. Circular RNAs differ in essential ways from their linear counterparts. From the mathematical viewpoint, the enumeration of the corresponding secondary structures demands the use of combinatorial techniques additional to those used for linear RNAs. The asymptotic number of secondary structures for circular RNAs grows as $a^n n^{-5/2}$, with a depending on particular constraints applied to the secondary structure. As it occurs with linear RNA, the abundance of any structural moiety is normally distributed in the limit $n \rightarrow \infty$, with a mean and a variance that increase linearly with n .

Keywords: genotype-phenotype map, analytic combinatorics, viroids

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