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Introducing secondary structure profiling for small RNAs

The biomedical importance of small RNA molecules only continues to grow. Yet, even at this length scale, reliably predicting the native base pairings of an RNA sequence remains a significant open problem in computational molecular biology. We present a novel combinatorial method, RNA profiling, for identifying the most probable combinations of native base pairs across a Boltzmann ensemble of secondary structures. Proof-of-principle results show that profiling is straightforward, stable and surprisingly comprehensive for sequences on the order of 150 nt, which includes numerous classes of small RNA molecules.