
Large Deviation Properties of RNA Neutral Set Size

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Abstract

The functionality of noncoding RNA molecules is mainly determined by their structure. Sequences with the same structure form the *neutral set*. The neutral set may be partitioned into several components, called neutral networks, traversable by structure-preserving point mutations. The neutral network size is biologically relevant: large neutral networks appear to be favourable in terms of mutational robustness and evolvability. We investigate the neutral set and neutral network size using computer simulations.

We apply a dynamic programming approach [1] to obtain the secondary structures of RNA sequences. The neutral set size can be estimated using a *Nested Set Monte Carlo* Simulation [2]. We implemented a combination of the algorithm with the *Ballistic Search* approach to estimate the neutral network size. The distribution of neutral set and network sizes is determined for randomly generated RNA and compared to biological RNA molecules. To improve the accuracy in the tails of the distribution, large-deviation simulations are used [3]. Furthermore, the correlation of the neutral set size to other observables like the number of base-pairs is investigated. [1] M. Zuker and P. Stiegler, Nucl. Acids Res. **9**(1), 133-148 (1981)

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