PROJECT DESCRIPTION: RNA EVOLUTIONARY ALGORITHMS

It has recently been shown that RNA molecules are able to replicate nucleic acids in the absence of protein [2]. This finding lends an important support to the RNA world hypothesis [1] which states that RNA is at the core of the origin of life as the first replicating molecules. Key functions such as self-replication, and any other catalytic activity performed by RNA are driven by the arrangement of the molecule’s backbone in space, also known as its secondary structure. Structure gives rise to function. With all this in mind, we ask what conditions are able to give rise to the structural complexity necessary for RNA to be functional. To do so, we build models of RNA evolution and simulate selection on populations of sequence, structure pairs. However, current RNA evolutionary algorithms are very simplistic and therefore are limited in that they quickly converge to local minima. As a result, populations are very uniform in structure, which is unlikely to represent the amount of structural diversity required for the emergence of complex function. In this project, you will extend existing RNA evolutionary algorithms to retain population diversity while still exploring the mutation landscape efficiently. This can be done introducing new parameters, adjusting selection criteria, mutation rate, nucleotide distribution, population size, molecule length, etc. The result should be an algorithm that is able to escape local minima and efficiently sample the space of possible structures by maintaining population diversity.

REFERENCES