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Is it significant: A search for motifs and their possible significance

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Synthetic biology is an emerging field of study based on the chemistry of biological macromolecules. The function of these molecules is determined by their structure and the structures are determined by the sequence. One common type of molecule to study is ribozymes. Ribozymes are RNA molecules that fold into secondary and tertiary structures in order to function as enzymes. Previous work in our lab identified a population of 60 ribozymes that are able to utilize ATP or GTP. I found the sequences of the molecules in this population, and then it became apparent that the population could be split into 9 categories based on sequence similarities. Within each family, there was a single molecule that best represented that family. This representative molecule was identical within 3 mutations of all other molecules in the family. I used the m-fold web server to determine possible secondary structures of each of the representative molecules. One seemingly significant structural (and sequential) motif was present in 5 out of 6 of the families that utilize ATP and in none of the 3 families that utilize GTP. For the second part of my project I am determining rate constants and relative reactivity of kinetic reactions using the representative molecules of each family. This work will assist me in determining what types of structures and sequences yield the fastest and most reactive ribozymes.