1-14 Poster

ROBUSTNESS OF ALTERNATE CODING TABLES - A STATISTICAL ANALYSIS

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Since the identification of the Standard Coding Table, exceptions to this rule have been reported. There are nearly 20 alternate coding tables; in addition to different genetic code tables used by different organisms, even within the same organism the nuclear and mitochondrial genes may use two different coding tables. In an attempt to understand the advantages and disadvantages these coding tables may bring to an organism, we have decided to analyze various coding tables on genes subject to mutations, and have estimated their robustness. We have used this as indicative of the "evolutionary" success of that particular coding table. We show that two of the alternate coding tables, The Ciliate, Dasycladacean and Hexamita Nuclear Code (CDH) and The Flatworm Mitochondrial Code (FMC), are most robust, while others such as The Yeast Mitochondrial Code (YMC) are at a significant disadvantage, in terms of robustness.

Our study shows that, given the assumptions in our model, Standard Genetic Code is less robust when compared to other alternate coding tables. This brings about the question of why Standard Code has been so widely accepted, which needs to be addressed for a full understanding of genetic code evolution. We propose that the Standard Code is likely to have emerged as a "local minimum" and that the "coding landscape" is still being searched for a "global" minimum.