

Visualizing the Effects of Single Point Mutations on RNA Codons Using Graph Theory

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The genetic code serves as the blueprint of life, guiding the synthesis of proteins from RNA sequences. Although extensively studied, new methodologies can provide fresh perspectives on its intricate nature. In this work, utilizing graph theory and aided by Centaur Intelligence, we dissected the genetic code to illuminate the potential impacts of single point mutations on RNA codons.

Introduction: Every RNA codon, a triplet of nucleotides, translates to an amino acid or a stop signal. A single point mutation in this codon can either have no effect or result in the coding of a different amino acid. Understanding these potential transitions provides insights into the robustness and vulnerabilities of the genetic code.

YouTube video:

<https://www.youtube.com/watch?v=WsGw5w6tiyE>

Methods:

1. **Graph Construction:** In our graph, vertices represent the 20 amino acids and the "Stop" signal. An edge connects two vertices if the amino acids they represent can be interchanged through a single point mutation in their corresponding codons. This graph is not just a visualization but an analytical tool, spotlighting the possible amino acid replacements due to minor genetic variations.
2. **Highlighting Mechanism:** Using the computational capabilities of Mathematica, and with the expertise provided by Centaur Intelligence, each amino acid (and the Stop signal) is successively emphasized. When highlighted, all directly reachable amino acids through a single point mutation are illuminated, thus displaying the mutation landscape for each amino acid.

Results: The resultant graph unravels the dense web of interconnections among amino acids based on single point mutations. As we animate through each amino acid, patterns emerge, revealing which amino acids can easily mutate into others and which remain more isolated.

Discussion: This visualization offers a unique vantage point on the genetic code. For instance, amino acids with numerous connections can transition to a variety of other amino acids with just a minor mutation. This might imply a greater evolutionary flexibility but also suggests vulnerabilities to mutations causing diseases.

In addition, by utilizing a graphical approach, the often abstract concept of single point mutations becomes tangible and comprehensible, even for those not deeply versed in genetics.

Conclusion:

In collaboration with Centaur Intelligence, we have married biology with mathematics to yield a fresh, intuitive perspective on the genetic code. This method not only aids in comprehension but also serves as a foundation for further explorations into the resilience and adaptability of life at the molecular level.