Getting Cryptic with Bioinformatics!

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This investigation researches if using amino acids instead of nitrogenous bases in bacterial data storage systems protects against the corruption of the stored data due to mutations. The hypothesis was the storage system that utilizes amino acids as the foundation instead of nucleotides (currently used system) will result in more accurate RNA and the least amount of errors due to mutation. Python was used to conduct a simulation of a randomized codex assigned to a message. The message was decoded through the nitrogenous based system and an amino acid codex. Analysis of the data shows that the amino acid system was more efficient in maintaining the message's integrity than the nitrogenous base system. The nitrogenous base system consistently showed the corruption of the message by allowing the mutation to directly impact the decoded message. In later trials, where mutation rates of 7 and 14 mutations per strand were applied, the nitrogenous base results yielded all of the trials being corrupted. The amino acid-based system tells a different story, for even as mutations increased, amino acid systems were consistently lower than the binary results (e. g. Binary System with 3 and 7 mutations=534 failures while Amino Acid System with 3 and 7 mutations=499, Binary System 5 mutations= 35 while Amino Acid System 5 mutations=26). The amino acid systems consistently yielded close to or zero corruptions, but the nitrogenous base system had many corruptions after decoding, therefore proving that this new system may lead to further data storage innovation.

Awards Won: