

Britton Boras

Modeling the Kinetics of DNA Proofreading in Evolving Cell Lines

This paper will examine how proof reading in different types of cells works. Specifically it will use statistical mechanics to examine the probability of inserting an incorrect base based solely on the energy difference between a correct base pair and an incorrect. However, there are 3.2 billion basepairs in the human genome and if there was no proof reading mechanism then we would be riddled with mutations in every single generation. The number of basepairs the polymerase would get right is way too low to allow a cell pass down their genes to the next generation. Therefore, in order for the cell to function from generation to generation there must be significant proofing of the sequence as the polymerase moves down the DNA. We will identify the machinery used by the cell as well as amino acid redundancy and programmed cell death to attempt to model mathematically how the code for many proteins can proceed from one generation to the next while at the same time allowing the mutations that make evolution possible. We will also examine the probability that a protein will be able to function with a mutation and the survivability bonus/ deficit caused by these changes in the genetic code. There will be a lot of stat mech in this project and a good deal of probability.

(One question I would ask would be if you would suggest that I focus on one organism or should I try to tackle how many types of cells perform this needed operation.