Simulating Mutations in the p53 Gene

Adventures in Supercomputing Challenge

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Executive Summary

Cancer has become a very important issue over the decade and many scientists are scrambling to find out what causes cancer and how they can stop it from forming. We have an insight to a gene that helps with cell regulation and replication. When the p53 gene itself mutates and deforms it can lead to unregulated cell replication. Our goal is to show how the p53's gene mutates and we will map our results graphically. With this information we can determine how often the p53 gene fails to do its task.

Introduction

About the p53 Gene

The p53 gene is commonly known as the "tumor suppressor gene." The gene is located on the 17th chromosome and it serves the purpose of binding DNA. When DNA is being bound the p53 gene stimulates another gene to produce the p21 protein. In turn the protein interacts with a "cell division-stimulating" protein known as "cdk2." When the two proteins combine the cell is incapable of passing to the next stage of cell division. If the p53 gene has mutated it cannot contribute to the regulation of cell division, therefore leading the cell to replicate uncontrollably.

Background Information

Some of the information we came across that pointed to three enzymes that fix and repair codon sequences within the p53 gene, however as of this writing we had neglected to record the site that the

names and numbers were on. Due to this we will simply use arbitrary numbers to represent these enzymes.

These enzymes regularly fix problems (Usually caused by frame shifts, deletions, and other phenomena) in the p53 gene, but in some cases they can actually cause more harm by deforming the gene by a error caused by the enzyme itself or by passing over a deformity.

Based off of material we have made, we will use the following letters and numbers to represent the probability that an enzyme will either fail to correct a deformity or whether or not it will cause a deformity.

Enzyme	Probability of Failure
A	1 in 100,000
B	1 in 1,000,000
C	1 in 1,000,000,000

Our Goal

We want to map out the gene, codon by codon, in StarLogo and by doing so we will manipulate three “turtles” to carry out the enzyme’s functions as they scan for errors in a normal copy of the p53 gene and in a deformed copy. We will perform the simulation at different lengths of time, print the screen and then compare the differences with the originals.

Mathematical Model

It has been difficult for us to explain how it our math model works, but we will show our understanding of how it would be as a conditional statement.

- Start at first codon
    - Run probability for Enzyme A.
        - If enzyme A succeeds in finding a deformation it will fix the deformation, however if it fails it will pass over the current deformity.
        - If there is no deformity, run probability again to determine if it will fail and cause a deformity. If it does record the deformity.
    - Run probability for Enzyme B.
        - If enzyme B succeeds in finding a deformation it will fix the deformation, however if it fails it will pass over the current deformity.
        - If there is no deformity, run probability again to determine if it will fail and cause a deformity. If it does record the deformity.
    - Run probability for Enzyme C.
        - If enzyme C succeeds in finding a deformation it will fix the deformation, however if it fails it will pass over the current deformity.
        - If there is no deformity, run probability again to determine if it will fail and cause a deformity. If it does record the deformity.
- Move to next codon and repeat process.

Results

When the program executes; Starlogo will run the probability for each of the enzyme's ability to fix or mutate a codon. When it is finished running those probabilities within the codon it is currently on, it will graphically mark if it has fixed the codon, deformed the codon, or simply just passed over the codon. Even though the probability that these enzymes will fail is relatively low, we expect to our simulation to show fragmentation from the original code base within the p53 gene after long periods of time.

After we run our program, we will print the results and compare them with the original sequence from a normal gene.

StarLogo Source Code

Source code is posted on our site at:

- " http://www.studiom500.com/challenge/ "

Resources

"The p53 tumor suppressor protein." Genes and Proteins. National Center for Biotechnology Information. <http://www.ncbi.nlm.nih.gov/books/bv.fcgi?call=bv.View..ShowSection&rid=gnd.section.107>.