Stability Analysis of a Model for In Vitro Inhibition of Cancer Cell Mutation

Christopher G. Yakopcic

University of Dayton, stander@udayton.edu

Follow this and additional works at: http://ecommons.udayton.edu/stander_posters

Recommended Citation
http://ecommons.udayton.edu/stander_posters/183
**Abstract**

Human homeostasis is the body's ability to physiologically regulate its inner environment to ensure its stability in response to changes in the outside environment. An inability to maintain homeostasis may lead to death or disease, which is caused by a condition known as homeostatic imbalance. Normal cells follow the homeostasis when they proliferate and cancer cells do not.

This work describes a model consisting of three reaction-diffusion equations representing in vitro interaction between two drugs. One inhibits proliferation of cancerous cells, and the other destroys these cells. A stability analysis of the model is performed with and without diffusion applied to the model (similarly to in [1]). MATLAB is used to perform the stability analysis of the model.

**The Model**

A common method for modeling infectious diseases is known as the SIR Model. This model divides the host population into several categories. The host population is comprised of humans and the model divides them into three categories Susceptible (S), Infectious (I), and Recovered (R) [2]-[5]. The cancer mutation model analyzed in this work is an adaptation of the SIR model, and is used to characterize cancer growth. The three categories in this model are the concentration of cancerous cells (a), the concentration of the drug that inhibits the proliferation of a (b), and the concentration of the chemical that destroys cancerous cells (c).

**SIR Model**

\[
\frac{dS}{dt} = -\beta SI \\
\frac{dI}{dt} = \beta SI - \mu I \\
\frac{dR}{dt} = \mu I
\]

**Cancer Cell Mutation Model**

\[
\begin{aligned}
\frac{da}{dt} &= \frac{1}{1+kd} \left[ a^2 - ra^2 - r_1ca \right] \\
\frac{db}{dt} &= r_2a - r_2da - r_3da \\
\frac{dc}{dt} &= r_4a - r_4ca - r_5ca
\end{aligned}
\]

**Results**

| Without Diffusion | 0.172064710740 | 0.0001256877081 | 0.0000001516208 | 0.0000214749783 |
| With Diffusion | 0.172067449556 | 0.001257303164 | 0.000001518678 | 0.000214822271 |
| Bifurcation of k (Root for each function) | Without Diffusion | -0.0000008266602 | 0.000635387421 | 0.0000710399628 | 0.000634972328 |
| With Diffusion (n=1) | -0.0000008266602 | 0.000635357721 | 0.0000710422516 | 0.000634662628 |
| With Diffusion (n=2) | -0.0000008266602 | 0.000634876251 | 0.0000710498810 | 0.000634281158 |

**Bifurcation Plots Without Diffusion**

**Bifurcation Plots With Diffusion (n=1)**

The plots above were used to determine the stable region when sweeping the parameter k. It can be seen in both cases that the system is stable when k is approximately equal to 6(10)^n.

**References**