Mathematical Modeling Project

Tyler Lukasiewicz, Liana Severo, Caitlin Buttery

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Abstract

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1   Introduction

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2   Research and Methods

2.1   Immunal response to a single viral strain

$$
\begin{aligned}
\dot{v} &= v(r - ax) = f_1(v, x), \\
\dot{x} &= -bx + cv = f_2(v, x)
\end{aligned}
\tag{1}
$$

Where v is the viral strain and x is the specific immune response to the strain. r is the rate at which the virus reproduces. a is the rate at which the immune cells destroy the virus. b is the rate at which the immune cells die off. c is rate at which the immune cells reproduce. This is dependent on the number of viruses present, v.

2.1.1   Getting our eigenvalues

First we take the Jacobian

$$
J = \begin{pmatrix} r - ax & -av \\ c & -b \end{pmatrix}
\tag{2}
$$

Then we find the characteristic equations by evaluating the Jacobian at the two fixed points of our system $(0,0)$ and (α, β), where $\alpha = \frac{br}{ac}$ and let $\beta = \frac{r}{a}$

$$
\begin{aligned}
J|_{(0,0)} - \lambda I &= \lambda^2 + \lambda(b - r) - br = 0 \\
\implies \lambda_{1,2} &= r, -b \\
J|_{(\alpha,\beta)} - \lambda I &= \lambda^2 + \lambda\gamma + \delta \\
\implies \lambda_{1,2} &= \frac{-\gamma \pm \sqrt{\gamma^2 - 4\delta}}{2}
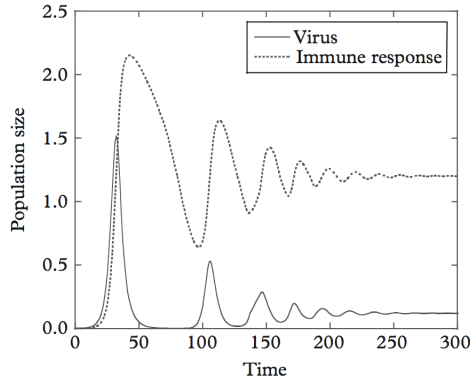\end{aligned}
\tag{3}
$$

where

$$
\gamma = b - r + a\beta, \text{ and } \delta = ac\alpha + ab\beta - rb
$$

2.1.2 modeling our system with one viral strain

We will now model our system of equations with conditions $r = 2.4, a = 2, b = 0.1,$ and $c = 1..$ We will also assume that we are starting with no viruses and no immune response.

The fixed point $(0, 0)$ coresponds to the eigenvalues $\lambda_1 = 2.4, \lambda_2 = -.1$, which implies that $(0, 0)$ is a saddle point. The fixed point $(\alpha, \beta) = (.12, 1.2)$ results in eigenvalues $\lambda_1 = -.05 + 4.873i, \lambda_2 = -.05 - 4873i$, which implies that the point $(.12, 1.2)$ is a spiral sink. So in this system both the viral strain and immune response will begin oscillating dramatically and then as time approaches infinity, they will settle to stable values. This is illustrated in figure 1

Figure 1: *Population size of the viral load and the immune response for a single virus strain with $r = 2.4$, $a = 2$, $b = 0.1$, $c = 1$.*

2.2 Modeling Our System with Multiple Viral Strains

Suppose there are N strains of the virus. The ith strain of the virus v_i and the immunal reaction x_i to it can be modeled by the system of equations

$$
\begin{aligned}
\dot{v}_i &= v_i(r - ax_i), \\
\dot{x}_i &= -bx_i + cv_i
\end{aligned}
\tag{4}
$$

This adds a degree of randomness to our behavior as new viruses can appear at any point in time. Each new virus strain should result in a new immune response. Eventually a global immune response will take care of all N viral strains regardless of mutation. This global response can be modeled by the system of equations

$$
\begin{aligned}
\dot{v}_i &= v_i(r - ax_i - qz) \\
\dot{x}_i &= -bx_i + cv_i \\
\dot{z} &= kv - bz
\end{aligned}
\tag{5}
$$

Where z is the cross reactive response that decays at rate b. $v = \sum_{i=1}^{N} v_i$ is the total viral load. q is the rate at which the virus evades the global response, k is the rate at which the global response grows in comparison to the number of preheat viral strains.

2.2.1 Getting Eigenvalues

2.3 HIV Section

2.4 Ebola Section

3 Conclusion

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Figure 2: ***Example of a cross-reactive immune response. The total population sizes of the viral load and the immune response are shown for r = 2.4, a = 2, b=0.1,c=1,q=2.4,k=1 with a random probability for the rise of new virus strains.***
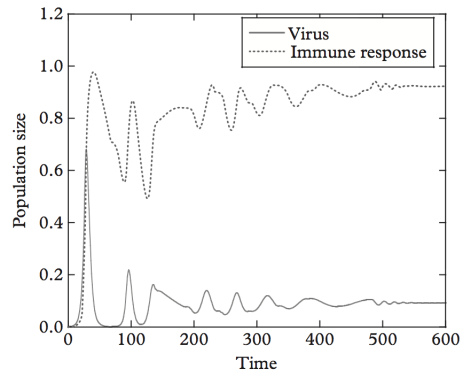
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References

[1] Michel Goossens, Frank Mittelbach, and Alexander Samarin. *The LATEX Companion*. Addison-Wesley, Reading, Massachusetts, 1993.