Population and Virality Network Modeling

Mario Rodriguez-Montoya
ESE 217
Washington University in St. Louis
St. Louis, USA
mario.rodriguez-montoya@wustl.edu

Leela Srinivas
ESE 217
Washington University in St. Louis
St. Louis, USA
l.srinivas@wustl.edu

Hannah King
ESE 217
Washington University in St. Louis
St. Louis, USA
h.l.king@wustl.edu

***Abstract*—To explore equilibrium in population and virality network modeling, a generalization of the Lotka-Volterra differential equation and a linear model for virus propagation through a lattice network were applied. Through these ideas, the existence of stable and freely determinable points of equilibrium were explored, as well as interaction with the models to enact certain effects. These interactions included the implementation of an external factor into the Lotka-Volterra model and the "Small-World" topology idea into the lattice network and were done to allow for the examination of equilibriums given a shift in the inner workings of the model.**

I. Part I

A. Recreating the Modified Lotka-Volterra Model

The Lotka-Volterra predator prey model was further developed in the paper 'Asymptotic stability of a modified Lotka-Volterra model with small immigrations' by Tahara et. al. The original model includes a death rate and birth rate for each population, but it does not include immigration. As such, there is no stable equilibrium in either population; they oscillate with one population following the other. In the paper, the effect of immigration is implemented and simulated, and the result is stable equilibria for both populations under certain conditions of immigration, i.e. whether there's immigration or emigration, from which population the migration occurs, and how much is occurring.

A Runge-Kutta method was used to recreate the exploration of the Lotka-Volterra model and used the following general set of Lotka-Volterra equations with the addition of $C(x)$ and $D(y)$.

$$\frac{dx}{dt} = 0.1x - 0.1xy + C(x). \tag{1}$$

$$\frac{dy}{dt} = 0.3xy - 0.2y + D(y). \tag{2}$$

The migration terms C and D depend on how much migration there is. If there is no migration, they would be zero, whereas if there is emigration, they would be a negative constant. If there is small immigration, they would be a positive constant divided by whichever variable they are a function of.

B. Modifying the Model Further

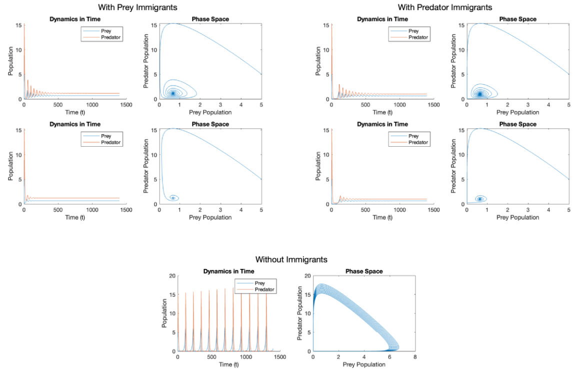

Fig. 1. Reproduction of phase space and long-term population dynamic graphs of the Lotka-Volterra system with parameter values: Initial Populations = 5, r = 0.1, α = 0.1, β = 0.3, m = 0.2, c = 0.01, d = 0.01.

To find a way to keep the populations at the same level, we needed a way to adjust them based on the difference between the two populations. This led to the modified equations shown below.

$$\frac{dx}{dt} = 0.1x - 0.1xy + C(x) + (c - x). \tag{3}$$

$$\frac{dy}{dt} = 0.3xy - 0.2y + D(y) + (d - x). \tag{4}$$

In this case, c and d would be constants. It should be noted that this might not be practical in the case of a real forestry service. This model implies that the service has a reserve of predator and prey that it can take from in case one population needs to increase and that they have some means to take out some individuals from whichever population needs to be decreased.

Using this method, it became possible to determine an equilibrium point using variable values of c and d, where they are treated as arbitrary constants, and would realistically be some adjustment rate dependent on the current population, where the result of (c-x) and (d-x) could be some result of wildlife control.

This is seen in 2, and again with different values of c and d in 3.

To implement these equations in practice, it would a wildlife preservation strategy which would adjust the population by some constant through each time step, meaning certain amounts of wildlife are added or taken from the environment depending on the difference of the constant and the total

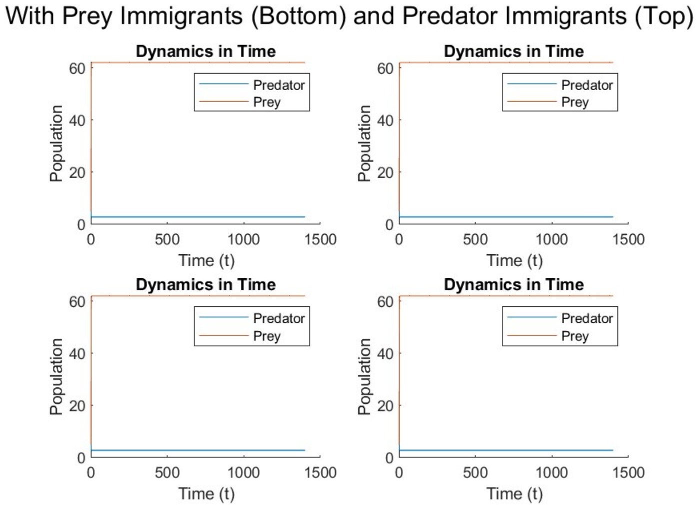

Fig. 2. Using the above sets of equations with c and d values of 20 and 22 respectively, the equilibrium points were determined to be about 2.8 for Prey and 62 for Predators. The leftmost equations are constant immigrations, with the rightmost being immigration that is dependent on the total population of either the predator or prey.

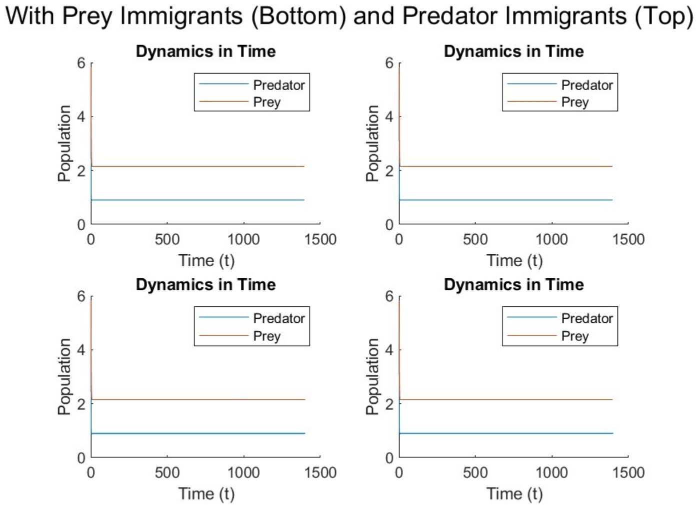

Fig. 3. Using the above sets of equations with c and d values of 1 and 2 respectively, the equilibrium points were determined to be about 2 for the Prey and 0.89 for the Predators. As is would be difficult for there to be 0.89 predators, the number is seen as scaled by some unknown order of magnitude when applied in terms of the real world.

population at any given timestep. This would mean, depending on the time step, precise records would have to be kept of the magnitude of the population while limiting interactions between the animals and any extraneous factors.

II. Part II

A. Simulation of Virus Propagation through a Lattice Network

The network trajectories of a lattice system consisting of only two nodes produce the general solutions for node one (x_1) and node two (x_2) as is seen in Eq. 5 and 6, respectively, where c_i is some constant, α_i is the self-influence term, and λ_i is the interaction strength term. When the square root portion of the root solutions is real, the trajectories will exhibit exponential

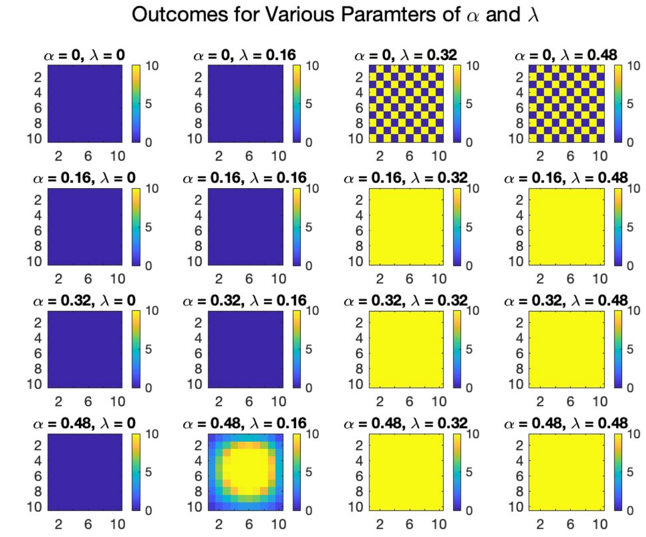

Fig. 4. Simulation of virality model for 90 time steps with α and λ values between 0 and 0.48.

$$x_1(t) = c_1 e^{r_1 t} + c_2 e^{r_2 t}. \tag{5}$$

$$x_2(t) = c_3 e^{r_1 t} + c_4 e^{r_2 t}. \tag{6}$$

$$r_1, r_2 = \frac{-(\alpha_1 + \alpha_2) \pm \sqrt{(\alpha_1 + \alpha_2)^2 - 4(\alpha_1 \alpha_2 - \lambda_1 \lambda_2)}}{2}. \tag{7}$$

behavior i.e. tending toward zero when the roots are negative and increasing indefinitely when the roots are positive. When the square root portion of the solutions is imaginary, which generally occurs when the λ values are much greater than the α values, the trajectories will exhibit sinusoidal behavior with some unstable equilibrium value around which the trajectories will oscillate.

This behavior is apparent even when the model is extended to a greater number of nodes as seen in Figure 2. We see the greater the values of the parameters, the wider the spread which makes intuitive sense given the nature of the general solutions of such a system. It is interesting to note that the presence of great values of α does not necessarily indicate greater spread when the values for λ are low. On the other hand, even without great values for α, a greater value of λ often takes over and increases spread. Considering our derived solutions, this makes sense as the roots will become increasingly positive and yield trajectories that increase exponentially.

B. "Small-World" Topology Implementation

Upon implementing the topology, the network changes in the way it converges based on the specific amount of "randomness" applied to the edges of the network. This variable is defined as β, and as β increases, the network edge connections approach "random," or a system of edges independent of their original order.

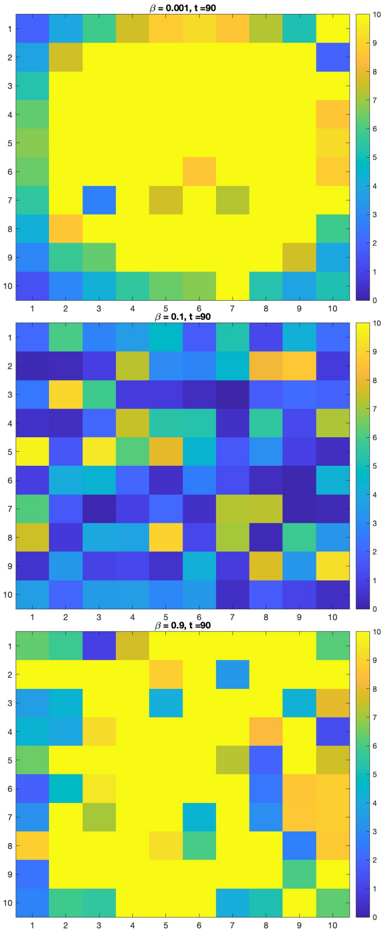

Fig. 5. State of network after 90 time steps with increasing β values

This is seen in the convergence of the system, as when β increases, the convergence of the virus becomes less like a steady circular spread from the epicenter of the outbreak and more like a sporadic spread. This falls in line with the definition of β being a measure of randomness, seen in Figure 3.

C. Control Strategy Design and Analysis

Under the assumption the state of each node x_i is known, a control vector was derived, in which after each time step, a scaling factor of τ was applied to each x_i. This limited the growth of each individual node while keeping the simulation within the bounds of a model applicable to real life, meaning the values for the "virality" within each node had a range of (0,10), where ten was designed to be the point of over-saturation in the model.

In a physical sense, the idea of knowing x_i, the "virality," to manipulate in the control vector at every step is like knowing the status of the outbreak at any point in time, which is not always the case. In real life, an engineer would have to estimate given prior data, which would take time to build up. Our control mechanism assumes a swift and immediate response, which assumes immediate awareness of the problem and immediate action, both of which are not particularly realistic.

To know the value of "virality" present in each node, a sort of documentation would need to be implemented, meaning each node would need to be investigated to find its value of "virality." Depending on the type of system being analyzed for its "virality", it would take varying degrees of effort to determine these values. To reduce the spread of a virus to a single number, incorporating all other factors into this number without making unreasonable assumptions would be near impossible, regardless of the specific virus or network used. Assuming this generalization was somehow possible, the recording of the factors necessary to make those calculations would likely be as difficult.

To reduce the amount of "virality" at each node by some proportion of the original amount of "virality" in a real-world situation, it would be necessary to implement a control strategy that applies to every individual. In terms of a real-world virality model, this could represent a strictly enforced mask mandate. This type of solution essentially proportionally decreases each individual's "virality" and is the closest real-world equivalent of an implementation of the control vector to our simulation.

D. Equilibrium Point of the System

The following proves the existence of an equilibrium point for two nodes at $x_i = 0$;

$$x_i(t) = c_1 e^{r_1 t} + c_2 e^{r_2 t}$$
$$-c_1 e^{r_1 t} = c_2 e^{r_2 t}$$
$$\frac{dx_i}{dt} = t(c_1 e^{r_1 t} + c_2 e^{r_2 t}) = 0$$
$$\frac{dx_i}{dt} = t(-c_2 e^{r_1 t} + c_2 e^{r_2 t}) = 0$$
$$\frac{dx_i}{dt} = x_i = 0 \tag{8}$$

This is true only when x equals 0 and is a point of stable equilibrium as long as the initial conditions of the nodes it is connected to are the same, because $\frac{dx_i}{dt}$ will always equal zero. The equation for x_i is seen in $Part II$ Section A, as the simplified two nodes model solution is the same for x_1 and x_2, and is independent of either variable. This trend then, should generalize between i nodes with j edges and each node's state should be entirely time dependent, according to the solution of the two nodes toy model. Then, if the initial conditions of the model are at $x_j(t) = 0$, where x_j is any of the nodes connected to any node x_i, then both x_i and all surrounding x_j will equal zero and remain at zero.

Using our control vector, any element x_i which is at zero with all of its connecting nodes x_j also at zero will remain at zero, and any values in which

$$x_i > x_i \tau \times (1 + dt) \tag{9}$$

is true, where $x_i \times dt$ equals the derivative over a time step, will also approach zero.