CSE 8803 EPI: Data Science for Epidemiology, Fall 2022

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Lecture 6: Dynamics of modeling

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1 Overview of Dynamics of Models

In this lecture we broadly covered the Dynamics of Models: looking at how models behave long-term and what factors influence their long-term behavior. In particular, we are focusing on Thresholds and Stability Points with respect to single-virus models and competing contagion models.

Thresholds are boundary points where a model's long-term behavior goes from one phase too another phase (e.g. dying out vs epidemic). Stability Points are positions a model tends to return to or oscillate around over the long term regardless of perturbations. In addition to Threshold and Stable points there are also Unstable points. Perturbations to these points tend to lead to large changes in model behavior. In order to better understand this behavior this lecture introduces us to a couple of concepts to make it easier to analyze such system in the context of a more general framework. [2]

The first concept is the generalized S*I*V* model which can be seen as a more general model that encompasses SIR, SIS, and SIRS models. The second concept introduced is the idea of Effective Strength. The third concept introduced is the idea of modelling epidemics as networks being modified by an Non-Linear Dynamic System (NLDS)

1.1 A Fundamental Question

How do we determine a condition where a virus will go extinct quickly regardless of the initial infection conditions? We can determine this condition mathematically by finding a threshold at which a given virus will either go extinct or become invasive.

Establishing this threshold for a given virus is important for multiple reason. For example, when a virus is below a threshold, we might not have to 'worry' so much and take less precautionary steps, such as social distancing and lock-downs, to reduce its spread. Or when it is above the threshold, we can consider stronger measures like vaccination efforts. It can also help enhance forecasting of 'what-if' scenarios. Please look at slide 6 of this lecture for further information. [2]

An example of such threshold behavior can be seen in figure 1.

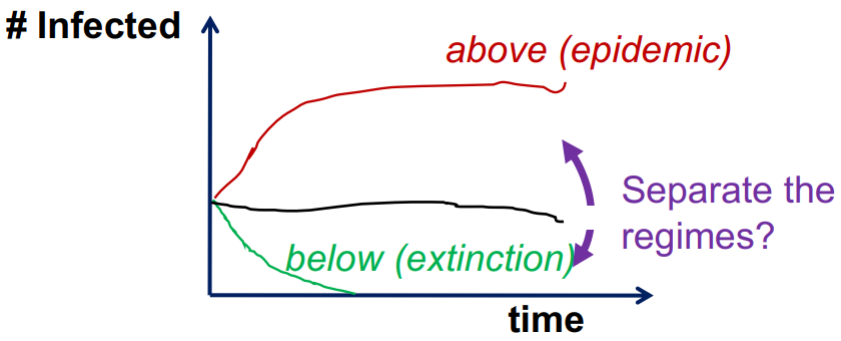

Figure 1: Black line indicated threshold tipping point where below the line a virus would go towards extinction and above the line would move towards and epidemic. Figure from [2]

In addition to threshold points, we can also look at stable, unstable, and neutral points. Stable points are characterized by the fact that small perturbations to the system will not lead to large changes in long term behavior. As seen in the phase plot in figure 2, you can see that all the trajectory arrows in the neighborhood of the stable point point towards the stable point. [2]

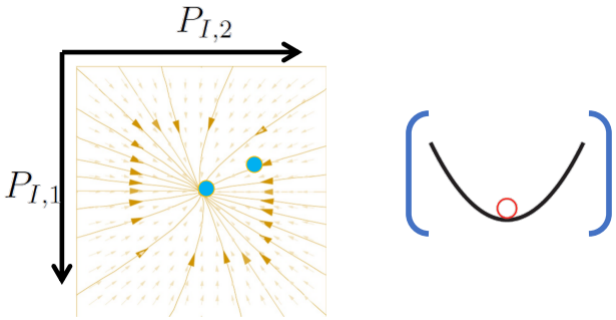

Figure 2: As seen in the phase plot above, stable points are kind of like a concave bowl. All the trajectory arrows in the neighborhood of the stable point point towards that point. Modified figure pulled from lecture [2]

Unstable points are characterized by the fact that large perturbations to the system will

lead to large changes in long term behavior. As illustrated in the phase plot in figure 3, you can see that all the trajectory arrows in the neighborhood of the unstable point point away from the point. This means that a small change from the stable point will result in a very different final state. [2]

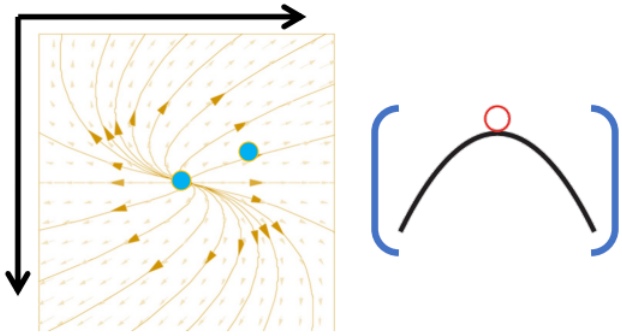

Figure 3: As seen in the phase plot above, unstable points are kind of like a convex hill. All the trajectory arrows in the neighborhood of the stable point point away from that point. Modified figure pulled from the lecture [2]

Finally neutral points are characterized as neither stable nor unstable. They can be thought of as a ball on a flat plane or a phase plot full of dots (zero magnitude trajectory arrows).

2 Model Generalization

All of the SIR, SIS, SIRS,... models that we have looked at so far can be seen as specialized forms of a more general S*I*V* model where they can be an arbitrary number of "susceptible" S states, one or more "infections" I states, and zero or more "vigilant" V states. An outline of this general state transition graph can be seen in figure 4. [2]

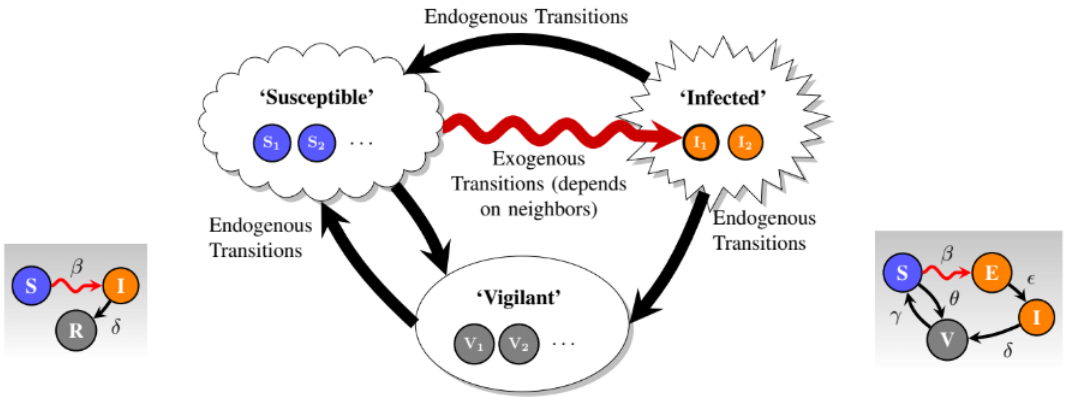

Figure 4: Diagram outlining the S*I*V* transition diagram. Figure pulled from [4]

As seen in figure 4, "Susceptible" states can transition to "Infected" states via "Exogenous" transitions that depend on the states of neighbors, and "Infected" states can

revert back to an "Susceptible" state via an "Endogenous" transition that can happen independently of neighboring states. "Infected" states can transition to "Vigilant" states via Endogenous transitions. Finally, "Vigilant" and "Susceptible" states can endogenously transition between each other.

To form the more specific models such as SIR and SIS, we just restrict the number of states and transition pathways accordingly. For example an SIR model can be viewed as an S*I*V* model with just one susceptible state, one infectious state, and one vigilant state (recovered); where the transition pathways between each state have been restricted to an exogenous infection pathway from the susceptible state and the infected state, and a recovery endogenous pathway between the infected state and the recovered state.

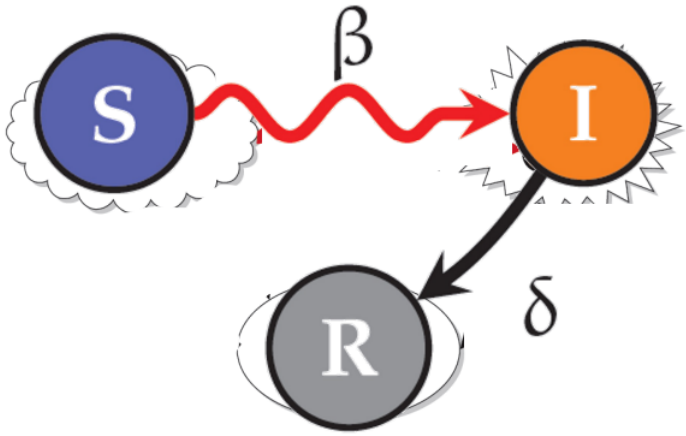

Figure 5: The state transition diagram for an SIR infection model. Figure pulled from [2]

3 Thresholds for arbitrary static networks

A long standing question in epidemiology has been determination the epidemic threshold, which has been defined in the literature as, 'the minimum level of virulence to prevent a viral contagion from dying out quickly' [2]. Given that the epidemic threshold can be challenging to determine depending on a contagion's virulence. In this lecture, we were introduced to a generalized framework for analyzing thresholds for static graphs based off of a factor called Effective Strength (s), which can be thought as similar, if not the same, as the reproductive number (R0) which we have learned of in previous lectures. Thus, if $s < 1$ it is below the threshold for mass spreading event, if $s > 1$ then it is above the threshold for an epidemic, and if $s = 1$ then it is at a tipping point [2].

The Effective Strength factor (s) consists of two components, λ (the largest eigenvalue of the network's adjacency matrix) and some constant C_{VPM} that is dependent on the virus propagation model being used.

$$s = \lambda * C_{VPM}$$

The constant C_{VPM} typically consists of constants describing the state transition probabilities between the various epidemic states. For example, if we consider the SIS model,

then:

$$s = \lambda * \frac{\beta}{\gamma}$$

where γ is the recovery probability, β is the viral transmission probability, and λ is the largest eigenvalue determined in from the network's adjacency matrix (A).

Other effective strength formulations can be found in the table in figure 6

Table III

Models	Effective Strength (s)	Threshold (tipping point)
SIS, SIR, SIRS, SEIR	$s = \lambda_1 \cdot \left(\frac{\beta}{\delta}\right)$	$s = 1$
SIV, SEIV	$s = \lambda_1 \cdot \left(\frac{\beta\gamma}{\delta(\gamma+\theta)}\right)$	
$SI_1I_2V_1V_2$ ($\sim$ H.I.V.)	$s = \lambda_1 \cdot \left(\frac{\beta_1 v_2 + \beta_2 \epsilon}{v_2(\epsilon+v_1)}\right)$	

Figure 6: Table containing the effective strengths for various Virus Propagation Models. Figure pulled from [4]

3.1 A deeper dive into λ

If we consider the fact that an adjacency matrix represents all connections between all nodes in a graph, then the largest λ value of an adjacency matrix represents the strength of connectivity [4] between all nodes in the graph. For example, figure 7 shows how λ is empirically correlated with higher levels of inter-node connectivity within the given graph.

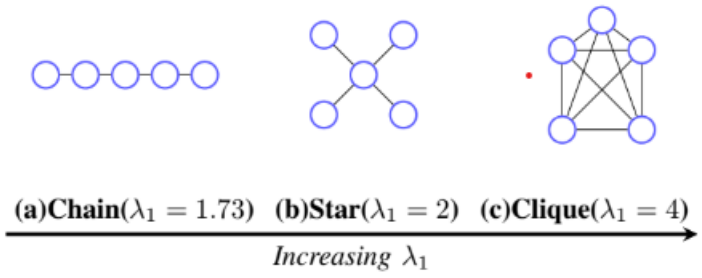

Figure 7: Diagram illustrating how higher λ values are correlated with higher inter-node connectivity in a graph. Figure pulled from [4]

When we examine the graphs from Figure 7a and b, each graph has an equal number of nodes and edges, and there respective λ values are relatively close in value. However, Figure 7c has the same number of nodes but has more edges and thus is more connected. From graphs a and b, we determine that what influences the strength of λ is not the number of edges but the way nodes are connected. In the Chain graph, for any susceptible node to be infected at a future time point, an infected node can only infect its neighbor node(s) as their connection is linear. From the Star graph, if the central node is infected then there is a higher probability that in will infect at least one node it is connected with. However

if the central node moves to the recovered state before infecting other nodes, the infection will die out and its connected nodes will not become infected. However, when we examine Figure 7c, we can see that the connection between every node increases the likelihood that all nodes will eventually become infected at some future time point. Finding the largest λ of each graphs adjacency matrix shows a strong correlations with the strength of connectivity within a graph. Overall, what λ tells us is that the chance of an epidemic increases when the inter-node connectivity is high, especially when λ is large. Using λ to make forecasting predictions of a virus with increase infectivity could have suggested better ways to take precautionary steps to reduce the transmission of the Omicron variant.

Understanding λ as a threshold has real-world implication. For example, removing nodes from a given graph with greater connectivity will decrease the size of λ. In a real-world example, we could vaccinate specific individuals (nodes) that have the highest connectivity to help reduce the the size of λ so that the number of future infections drops beneath the effective strength (s) threshold. Additionally, λ has implications for 'what-if' scenarios (briefly mentioned in 1.1 above) as it can be used to forecast future epidemics if a virus becomes more infections/virulent. A very good and relatable real-world example of this is the current COVID epidemic. In October of 2021, the Delta variant was still the dominant strain causing infections in the USA. By mid-January 2022, the Omicron strain swept through the US generating the greatest number of infections within a short period of time at an alarmingly fast rate.

4 Non-Linear Dynamic Systems (NLDS)

In general, we can model the spread of a contagion through a network via the use of Non-Linear Dynamic Systems (NLDS). To do this we store connectivity and node attribute information within a graph, and each node's probabilistic "state" with respect to the contagion over time in a series of time-stepped Probability Vectors $\vec{P}_t$. [2]

For example in, Figure 8, you can see that each probability vector has a size of $mN \times 1$ where N is the number of nodes in the graph and m is the number of states a node can be in with respect to the contagion. This allows us to keep track of how likely each node is in a particular contagion state at a particular time. [2]

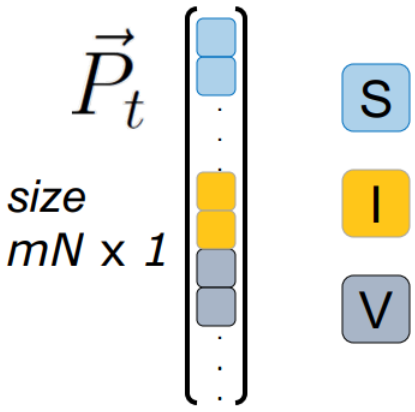

Figure 8: At each point in time in the simulation there is an $mN \times 1$ probability vector $\vec{P}_t$ representing how likely each of the N nodes are in any one of the m (in this case 3) contagion states. Figure adapted from [2]

We can then use a NLDS $G(\vec{P}_t)$ to model how those probabilities change over time as the contagion propagates through the system. This process is kind of like a stop motion animation where each $\vec{P}_t$ is an image and the transition between each image time-step is defined by the non linear function 'G'. [2]

For example if we wanted to simulate a SIR VPM as an aformementioned NLDS, the dimensions of each $\vec{P}_t$ vector would be $3N \times 1$ as an SIR model has 3 epidemiological states.

$$\vec{P}_{t+1} = G(\vec{P}_t)$$

where

$$G : \mathbb{R}^{mN} \to \mathbb{R}^{mN}$$

is defined as the following system of equations:

$$P_{S,i,t+1} = P_{S,i,t}\zeta_{i,t}(I)$$
$$P_{I,i,t+1} = P_{S,i,t}(1 - \zeta_{i,t}(I)) + (1 - \delta)P_{I,i,t}$$
$$P_{R,i,t+1} = P_{I,i,t} + P_{R,i,t}$$

Where $\zeta_{i,t}$ is the probability that the node i is not attacked by any of its infections neighbors. [2]

5 Analyzing Dynamics in Multiple Situations

5.1 Synchronization

Synchronization is a special case where the long term behavior of a graph enters a periodic state. This typically happens when a SIRS disease periodically cascades through a highly connected parts of the system leading to a wave in infections and then slowly burns through more sparsely connected parts of the system to form a trough before burning through the highly connected parts of the system once all the recovered nodes have become susceptible again. Examples of this in the real world include measles cases in the UK as seen in Figure 9 [2] [1]

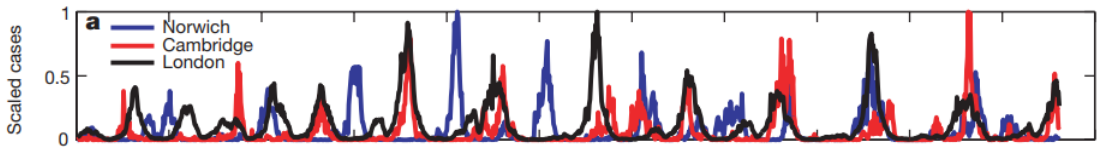

Figure 9: Case counts for measles across multiple cities in the UK. Figure originally from [1]

5.2 Multiple Competing Viruses

In general, when multiple viruses compete the strongest virus usually dominates. Where strength is measured by communicability and positioning. E.g. a highly transmissible on an isolated island is not going to dominate a less transmissible virus that starts out in a highly connected place like New York City. In addition, viruses that are too weak to propagate in the environment typically die out while mediocre propagators tend to go endemic. [2]

5.2.1 Strong vs Weak

For example in the Strong vs Weak case in Figure 10 we can easily see from the Time-Plot that the Infection count of the stronger virus 1 will usually dominate the weaker virus 2 over time. [2]

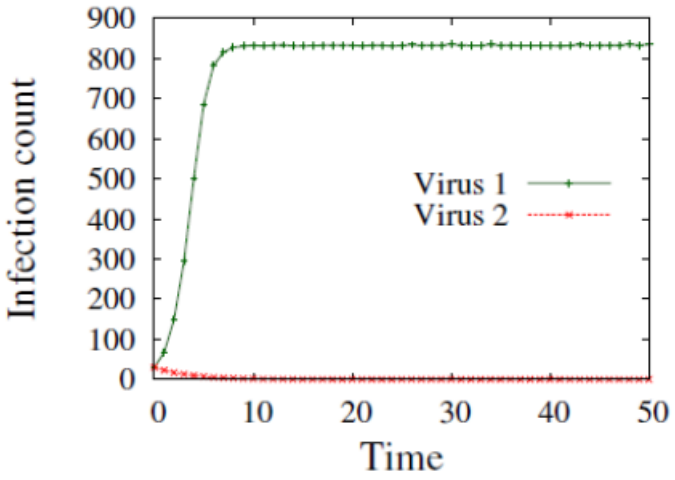

Figure 10: Over time the stronger Virus 1 dominates the weaker Virus 2 in terms of case counts. Figure pulled from [3]

Then in the corresponding phase-plot in figure 11 we can see that there are two fixed points fp_1 and fp_2. Since virus 2 is weak, there is no stability fixed point for virus 2 as at any population it's case count will drop to zero. There is a semi unstable fix point threshold at fp_1, where if there is any minor positive perturbation in the case count for virus 1 the graph will inexorably go to fp_2 where the stronger virus 1 has dominated the case count. However as long as the case count for virus 1 remains zero, any amount of the weaker virus two cases will go to zero over time. [2]

In addition the phase plot has a line representing the path followed by the time-plot in figure 10

5.2.2 Weak vs Weak

In the case of two weak virus, the case counts for both will drop to zero over time no matter the initial starting point. An example of this can be seen in figure 12

The fact that this drop to (0, 0) will happen for any initial case count for the weak viruses 1 and 2 is highlighted in figure 13 where all the trajectory arrows point to the stable fixed point fp_1 at (0, 0).

5.2.3 Strong vs Strong

Finally in the Strong vs Strong case, the stronger of the two viruses typically wins long term as seen in figure 14.

However there are certain unstable fixed points where the less strong virus will win out (e.g. if the less strong virus is the only one introduced to the environment). Otherwise as

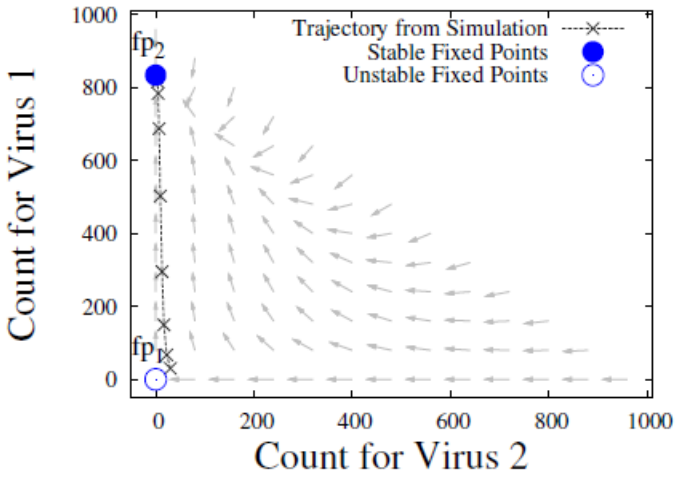

Figure 11: As seen in the phase plot above, under most conditions the simulation ends up at the stable fp_2 where the stronger virus 1 dominates and the weaker virus 1 has died out. The unstable fixed point (0, 0) at fp_1 is an exception to this. Figure pulled from [3]

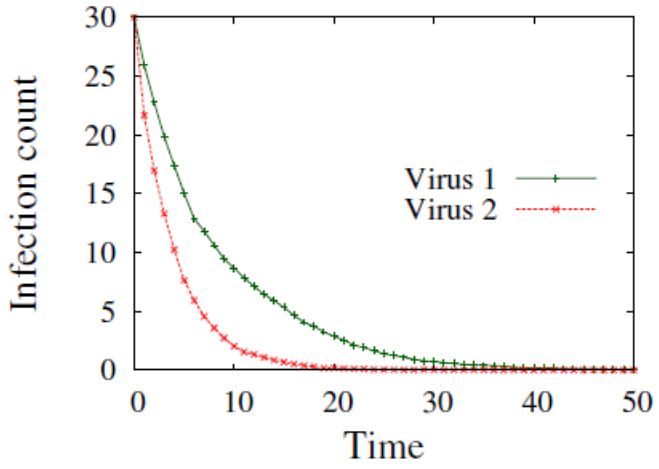

Figure 12: As seen in the time plot above, both weak viruses eventually die out. Figure pulled from [3]

evidenced by the trajectory arrows in 15, we tend to end up in the stable fixed point (fp_2) where the stronger virus dominates. [2]

5.2.4 Cooperation and mutual immunity

In addition to competing, viruses can also coexist in the same host at the same time. When this happens we often see examples of cooperation, partial mutual immunity, and full mutual immunity. For example in figure 16, we are using a modified flu-like SIIIS model to model browser adoption where a user can install either Chrome, Firefox, both browsers, or neither browsers. As seen in figure figure 16 users have some probability β_1 and β_2 of adopting

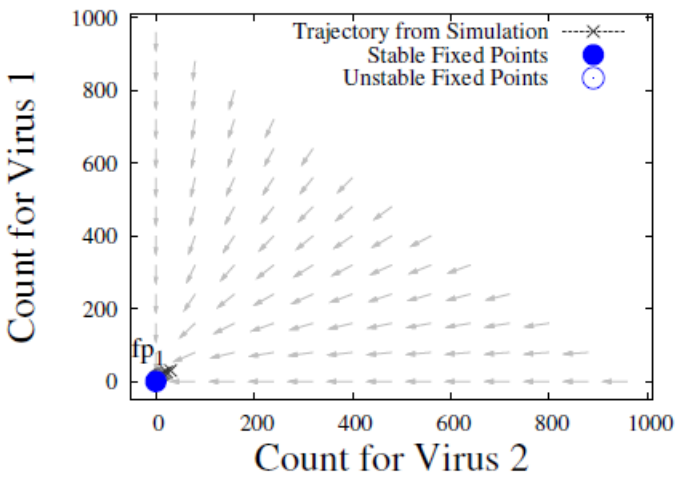

Figure 13: As seen in the phase plot above, the trajectory arrows for both weak viruses all end up in the fixed point fp_1 at (0, 0) Figure pulled from [3]

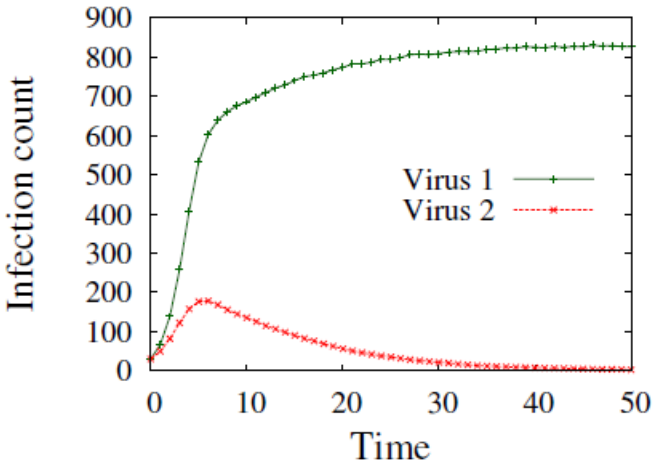

Figure 14: As seen in the time plot above, when two strong viruses compete the stronger one or the one in the better position will eventually win out. Diagram pulled from [3]

Chrome or Firefox respectively. Once they have adopted either one of the browsers they have an $\epsilon\beta_2$ and $\epsilon\beta_1$ chance of adopting the other browser as well. [2]

This ϵ value is called the "Interaction Factor" and is used to model how the browser "contagions" affect each other's adoption rate once they have been established. If the adoption of one browser fully excludes the adoption of the other, then ϵ is zero and this is case of "Full Mutual Immunity". However, if the adoption of one browser simply reduces the probability of adoption of the other, then ϵ is less than 1 (but greater than zero) and this is case of "Partial Mutual Immunity". Lastly if the adoption of one browser increases the probability of adopting the other, then ϵ is greater than one and this is case of "Cooperation". [2]

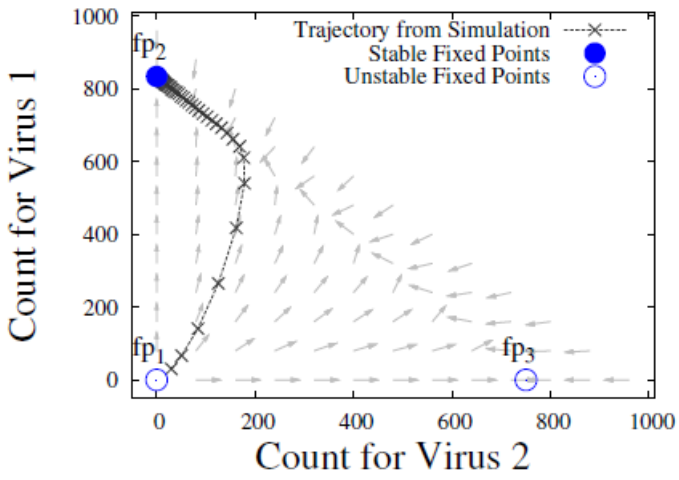

Figure 15: As seen in the phase plot above, the trajectory arrows indicate that most initial conditions end up at the stable fixed point fp_2 at (0, 800) where the stronger virus 1 dominates. Exceptions to this include the unstable fixed point fp_1 at (0, 0) and the semi-stable fixed point fp_3 at (0, 800). In the case of fp_3, it is the stable sink as long as the case count for virus 1 is held at zero and the case count for virus 2 is some non-zero positive number. Figure pulled from [3]

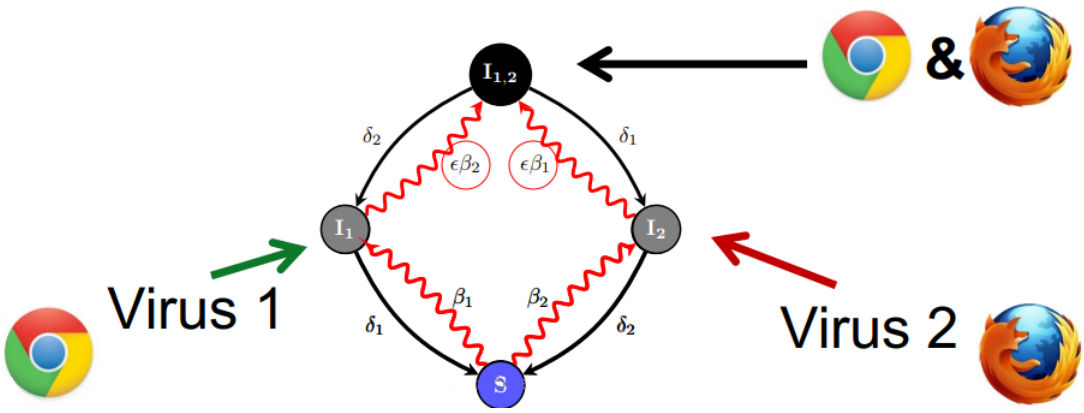

Figure 16: A modified SIIIS model for Web Browser adoption used to illustrate cooperation and mutual immunity. Diagram pulled from [2]

6 References

References

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