

Modeling and Simulating Disease Outbreaks for Arbitrary Topological Systems

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1 Abstract

2 Introduction

While most papers are dedicated to modeling the progression of disease, our focus lies somewhere else entirely. We want to know whether or not diseases will successfully spread amongst the population, as well as understand the impact topology has on our results. In addition, we analyze specific models to determine key nodes, so that one can effectively combat possible epidemics. Lastly, since not all connections between two players in an agent-based-system are equal, we will show how results differ, when this additional parameter is taken into account.

To better understand the mechanics of analyzing disease outbreaks, the next chapter describes the theory behind our models. In later chapters, we will then apply these concepts and show our findings.

3 Theoretical Tools for Arbitrary Cascade Models

For any given epidemiological model, there are two key components that will describe our system; namely the virus propagation model and the topological constraints of the system. It will be shown that these two components can in fact be de-coupled and described by two constants. To fully describe arbitrary systems, some definitions must be introduced.

Definition:

The connectivity matrix is a symmetric $n \times n$ matrix, where n is the number of nodes in the system. If two nodes, i and j , are connected, the $(i, j)^{th}$ entry is equal to 1. Otherwise it is equal to 0. In addition, all diagonal entries are automatically set to 0.

Throughout this paper, the connectivity matrix will fully describe the interaction between two different people. In later chapters, we may allow values ranging from 0 to 1, to better describe the relationship of any two given nodes. To mathematically characterize any given virus propagation model (VPM), the following parameters are needed.

Parameters:

- (i) β is the attack or transmission probability via a link between two nodes
- (ii) γ is the immunization loss probability after a node has recovered
- (iii) δ is the healing probability once a node has been infected
- (iv) ϵ is the virus maturation probability after a node has been exposed. This therefore means that $1 - \epsilon$ defines the virus incubation probability
- (v) θ is the direct immunization probability whilst a node is susceptible to the virus

We now have the tools to prove the theorem, which not only allows us to decouple the topology from the VPM, but also determines whether or not viruses exceed the epidemic threshold.

3.1 G2-Threshold Theorem

For any given VPM that can be thought of as a $S^*I^2V^*$ model (there are two infectious states, but not conditions for the number of susceptible and vigilant states), which operates on an arbitrary topology, the virus will be eradicated if

$$s < 1 \quad (1)$$

where s is the effective strength and is defined as

$$s = \lambda_1 \cdot C_{VPM} \quad (2)$$

Here, λ_1 is the largest eigenvalue of the connectivity matrix and C_{VPM} is a constant that is derived from the VPM.

3.2 Proof Overview

We shall start by first giving a broad overview of why the G2-Threshold Theorem makes sense and in the following subsection we shall go into more detail.

Terminology:

In the general $S^*I^2V^*$ model, we have the following three classes:

- (i) Susceptible Class: Elements of this state can be infected by neighboring elements; i.e. the i^{th} node can be infected by the j^{th} node if $A_{i,j} = 1$. We can have $n \geq 0$ arbitrary susceptible states. In addition, nodes can only enter this class via endogenous transitions from the two other classes. This means that these transitions do not depend on neighboring elements. Transitions within this class are also endogenous.
- (ii) Infected Class: Elements in one of the two possible infected classes can

spread the infection to susceptible neighbors with a certain probability. For those wondering why we have two classes instead of one, I need only give the following example. If infectious state I has a transmissibility parameter $\beta_I > 0$ and infectious state E with $\beta_E = 0$, we can elegantly describe scenarios where the disease need not always be contagious. Elements can enter this class via exogenous transitions (neighbor-dependent) from susceptible states. Transitions within this class are endogenous.

(iii) Vigilant Class: Elements of these states can neither infect, nor be infected. This class can be used to describe dead, vaccinated, and/or recovered(Only in models, where recovered patients are no longer susceptible) nodes. Once again, there can be $m \geq 0$ possible states in this class. Elements can enter this class via endogenous transitions from all other states. Transitions within this class are also endogenous.

Assumptions:

We will be making two assumptions, which not only simplify calculations, but are rather intuitive.

(i) The infection can only be spread from node i to node j if $A_{i,j} = 1$. In essence, this means that the infection can only be spread via neighbors.

(ii) When an element from a susceptible state becomes infected, it must always transition into the "first" susceptible state I_1 . This is trivially fulfilled for models with one infectious state. Models with two susceptible states could then describe infections that first need an incubation period. In this case I_1 would be the state "E" that was mentioned before.

Proof Sketch:

We start by defining a vector \mathbf{P}_t that will describe the system at time t . In a model where m is the total number of states and n is the total number of nodes, this vector will have $m \times n$ entries, i.e. $\mathbf{P}_t \in \mathbb{R}^{m \times n}$. More specifically, we can write \mathbf{P}_t in the following way:

$$\mathbf{P}_t = (P_{s_1,1,t}, P_{s_1,2,t}, \dots, P_{s_1,n,t}, P_{s_2,1,t}, \dots, P_{s_m,n,t})^T, \quad (3)$$

where $P_{s_i,j,t}$ is given by the probability that node j is an element of state s_i at time t . For any given VPM, \mathbf{P}_{t+1} can be determined by \mathbf{P}_t , i.e.

$$\mathbf{P}_{t+1} = g(\mathbf{P}_t), \quad (4)$$

where g is a (potentially non-linear) function. For a fixed point, we have that

$$\mathbf{P}_{t+1} = \mathbf{P}_t. \quad (5)$$

At these points, one can calculate the stability, i.e. will we return to this fixed point under small perturbations or not, by analyzing the spectrum of the Jacobi matrix at these locations. We will in essence calculate the stability of systems, where no nodes are infected. As we will see, the constraints for the spectrum of the Jacobian will allow us to decouple the topology from the VPM and deliver the desired result.

3.3 Proof

To make the proof more readable, we shall introduce additional notation

3.3.1 Notation

- (i) m denotes the total number of states in the VPM.
- (ii) q denotes the total number of states in both the Susceptible, as well as the Vigilant class. This means that $m = q + 2$.
- (iii) w denotes the total number of states in the Susceptible Class.
- (iv) S_1, \dots, S_w denote the states in the Susceptible class.
- (v) E, I denote the two states in the Infected class.
- (vi) α_{KU} denotes the probability of a transition from state K to state U . We assume that α_{KU} is not only constant, but also given to us beforehand.
- (vii) β_1 denotes the transmission probability to for state E .
- (viii) β_2 denotes the transmission probability to for state I .
- (ix) $\zeta_{i,t}(E, I)$ denotes the probability of node i not being infected by E or I at time t .
- (x) \mathbf{x} denotes the fixed point vector of our system that has no infected node.
- (xi) $p_{S_y}^*$ denotes the probability of being an element of the S_y state at vector \mathbf{x} . We assume that this value is independent of the node.
- (xii) \mathcal{J} denotes the Jacobian matrix of the non-linear differential equation at \mathbf{x} .

3.3.2 Deriving the System Equations

We will now describe the function g in terms of our parameters. The first step will be to derive the probability that an arbitrary node i will not be infected by its neighbors during one time-step. In other words, we want to calculate $\zeta_{i,t}(E, I)$. We know that the virus will not be transmitted if one of the following holds:

- (i) The neighbor is not in any of the two infected states E or I .
- (ii) A neighbor is in state E , but the virus is not transmitted with a probability of $1 - \beta_1$
- (iii) A neighbor is in state I , but the virus is not transmitted with a probability of $1 - \beta_2$

To only consider first-order effects, we shall be assuming that our time steps are infinitesimal, i.e. $\Delta t \rightarrow 0$. In addition, we postulate that all neighbors are independent of one another. By doing so, we can write $\zeta_{i,t}(E, I)$ as follows:

$$\zeta_{i,t}(E, I) = \prod_{j \in N\mathcal{E}(i)} (P_{E,j,t}(1 - \beta_1) + P_{I,j,t}(1 - \beta_2) + (1 - (P_{E,j,t} + P_{I,j,t})), \quad (6)$$

where $N\mathcal{E}(i)$ is just the set of all neighboring nodes. This just says that for each neighbor, we must consider him to be in (i) state E with probability $P_{E,j,t}$ and not spread the disease with probability $(1 - \beta_1)$, (ii) state I with probability

$P_{I,j,t}$ and not spread the disease with probability $(1 - \beta_2)$, and (iii) none of the Infectious states with probability $(1 - (P_{E,j,t} - (P_{I,i,t}))$, where he cannot spread the disease at all. As all neighbors are independent, we must multiply the probabilities. We can rewrite equation (6) and attain

$$\zeta_{i,t}(E, I) = \prod_{J \in \{1, \dots, n\}} (1 - \mathbf{A}_{i,j}(\beta_1 P_{E,j,t} + \beta_2 P_{I,j,t})). \quad (7)$$

Here, we just count over all the indices and if i and j are neighbors $A_{i,j} = 1$ and we get the same terms as above. If, on the other hand i and j are not neighbors, $A_{i,j} = 0$ and we are in essence multiplying everything by 1, which changes absolutely nothing.

We also demand that for any node i at any given time t , it must be in exactly one of the states. This just means that

$$\forall i, t : \sum_K P_{K,i,t} = 1. \quad (8)$$

Having finally found a formula for $\zeta_{i,t}(E, I)$, we are now ready determine g . If a node is in a particular state S_y , which is located in the Susceptible class at time $t + 1$, it must be for one of the following reasons:

- (i) The node was already an element of the state S_y and stayed there.
- (ii) The node was in a different state U and transitioned into that state during our time step. This transition must of course be internal (See Terminology).

We can now use this information to attain the following result:

$$\forall y = 1, 2, \dots, w : P_{S_y,i,t+1} = \sum_{K \neq S_y} \alpha_{KS_y} P_{K,i,t} + P_{S_y,i,t} \left(\zeta_{i,t}(E, I) - \sum_{K \neq E, S_y, I} \alpha_{S_y,K} \right) \quad (9)$$

The term $\alpha_{KE} P_{K,i,t}$ denotes all the transitions from other susceptible state to S_y , whereas the second term gives us the probability that the element in S_y stays in S_y . Through analogous reasoning we attain similar results for elements in state E at time $t + 1$

$$P_{E,i,t+1} = \sum_{K \neq S_1, \dots, S_w} \alpha_{KE} P_{K,i,t} + \sum_{y=1}^w P_{S_y,i,t} (1 - \zeta_{i,t}(E, I)), \quad (10)$$

as well as for all other states $U \neq \{S_1, \dots, S_w, E\}$ at time $t + 1$

$$P_{U,i,t+1} = \sum_K \alpha_{KU} P_{K,i,t}. \quad (11)$$

Equations (9) to (11) now define g , which is what we wanted.

We will now need a theorem, which will not be proven.

Asymptotic Stability Theorem:

A system that is determined by $\mathbf{P}_{t+1} = g(\mathbf{P}_t)$ is asymptotically stable at some fixed point $\mathbf{P} = \mathbf{x}$, if the absolute value of all eigenvalues of the Jacobian $\mathcal{J} = \nabla g(\mathbf{x})$ are less than one. The entries of the Jacobian matrix are given by

$$\mathcal{J}_{i,j} = [\nabla g(\mathbf{x})]_{i,j} = \frac{\partial g_i}{\partial x_j}|_{\mathbf{x}} \quad (12)$$

3.3.3 A More Thorough Analysis of Fixed Points

We are only interested in fixed points, where none of the nodes are infected. If that is the case, the only possible transitions will be from endogenous transitions within and between the Susceptible and Vigilant class. This means that now the topology plays no role whatsoever in determining our preferred fixed point, which allows us to use the Markov Chain model. Using this method, we will attain a unique steady state probability for each node(same for each one). The steady state vector π^* , whose entries will contain the probability that any node is found in an arbitrary state (In either the Susceptible or Vigilant class). It therefore is a vector with q entries, where q is the number of states in the Susceptible and Vigilant class. We then know from Markov chain analysis that

$$\pi^{*T} \text{Trans}_{MC_{SV}} = \pi^*, \quad (13)$$

where we set the constraint that

$$\sum_{i=1}^q \pi^* = 1. \quad (14)$$

Here, $\text{Trans}_{MC_{SV}}$ denotes the stochastic matrix of the Markov chain MC_{SV} . To create a probability vector for an arbitrary node i with n entries for all states, including the Infected states, we just add two 0 entries to π^* . We shall call this new vector p^* . To finally attain the fixed point that describes all nodes, we define \mathbf{x} to be

$$\mathbf{x} = [p^*, p^*, \dots, p^*]^T, \quad (15)$$

where p^* is included n times. We define $p_{S_y}^*$ to be the steady state probability of an arbitrary node i being an element in state S_y . In addition, let

$$p_S^* = \sum_{y=1}^w p_{S_y}^*. \quad (16)$$

This can be interpreted as the probability of any given node i being in the Susceptible class.

3.3.4 Deriving the Jacobian

Here, we rely on equations (9) to (11) to express g and then take all of the partial derivatives. As all of our n nodes can be elements of m possible states, we expect our Jacobian matrix to be of the form $(m \times n) \times (m \times n)$. By plugging in the values, we get the following results:

$$\text{Plug in Matrix} \quad (17)$$

Here, the state K denotes all states not equal to E or I , whereas $U \neq \{S_1, \dots, S_w, E, I\}$. We shall now recall one of our previous assumptions, namely that there can be

no endogenous transitions into the Infected class. Mathematically speaking this means

$$\forall K \neq E, I : \alpha_{KE} = \alpha_{KI} = 0 \quad (18)$$

This, of course simplifies our Jacobian, which is reduced to

$$Plug in Matrix \quad (19)$$

Now that we have attained our matrix, we must calculate all of its eigenvalues.

3.3.5 Calculating the Eigenvalues of our Jacobian

As we can see in (19), the Jacobian is of the form

$$\mathcal{J} = \begin{pmatrix} \mathbf{B}_1 & \mathbf{B}_2 \\ \mathbf{0} & \mathbf{B}_1 \end{pmatrix} \quad (20)$$

where \mathbf{B}_1 is a $((m-2) \cdot n) \times ((m-2) \cdot n)$ matrix, \mathbf{B}_2 is a $((m-2) \cdot n) \times (2 \cdot n)$ matrix, and \mathbf{B}_3 is a $(2 \cdot n) \times (2 \cdot n)$ matrix. Any eigenvector \mathbf{v} with eigenvalue $\lambda_{\mathcal{J}}$ can now be thought of a composition of two smaller vectors, \mathbf{v}_1 and \mathbf{v}_2 , such that

$$\mathbf{v} = (\mathbf{v}_1, \mathbf{v}_2)^T. \quad (21)$$

Since \mathbf{v} is an eigenvector, we know that

$$\begin{pmatrix} \mathbf{B}_1 & \mathbf{B}_2 \\ \mathbf{0} & \mathbf{B}_1 \end{pmatrix} \begin{pmatrix} \mathbf{v}_1 \\ \mathbf{v}_2 \end{pmatrix} = \lambda_{\mathcal{J}} \begin{pmatrix} \mathbf{v}_1 \\ \mathbf{v}_2 \end{pmatrix}. \quad (22)$$

This, in turn, can be written as

$$\mathbf{B}_1 \mathbf{v}_1 + \mathbf{B}_2 \mathbf{v}_2 = \lambda_{\mathcal{J}} \mathbf{v}_1 \quad (23)$$

$$\mathbf{B}_3 \mathbf{v}_2 = \lambda_{\mathcal{J}} \mathbf{v}_2, \quad (24)$$

which tells us that one of the following must be true:

- (i) $\mathbf{v}_2 = 0$
 - (ii) \mathbf{v}_2 can be thought of as an eigenvector of \mathbf{B}_3 with eigenvalue $\lambda_{\mathcal{J}}$
- We shall now examine both cases.

3.3.6 Case (i)

Scenario (i) simplifies equation (23) considerably, as the second term is dropped and we left with

$$\mathbf{B}_1 \mathbf{v}_1 = \lambda_{\mathcal{J}} \mathbf{v}_1, \quad (25)$$

which then again implies one of the following:

- (i) $\mathbf{v}_1 = 0$

(ii) \mathbf{v}_1 is an eigenvector

Since $\mathbf{v}_2 = 0$ by assumption, $\mathbf{v}_1 = 0$ would yield a zero vector as the solution to (22), which is not a very interesting outcome (as $\mathbf{v} = 0$ would not be considered an eigenvector). We can therefore consider \mathbf{v}_1 to be an eigenvector of \mathbf{B}_1 .

Definition: For two arbitrary matrices A and B , where A and B are of the form $m \times n$ and $r \times s$, respectively, the Kronecker product $A \otimes B$ is defined as

$$A \otimes B = \begin{pmatrix} a_{11} \cdot B & \dots & a_{1n} \cdot B \\ \dots & \dots & \dots \\ a_{m1} \cdot B & \dots & a_{mn} \cdot B \end{pmatrix}. \quad (26)$$

This is clearly a $(m \cdot r) \times (n \cdot s)$ matrix.

We shall now note that with the help of the Kronecker product, \mathbf{B}_1 can be written as

$$\mathbf{B}_1 = \mathbf{T} \otimes \mathbb{1}, \quad (27)$$

where \mathbf{T} is given by

$$\mathbf{T} = \begin{pmatrix} \left(1 - \sum_{K \neq S_y, E}\right) & \alpha_{KS_y} & \dots \\ \dots & \dots & \dots \\ \alpha_{S_y U} & \alpha_{KU} & \dots \\ \dots & \dots & \dots \end{pmatrix}. \quad (28)$$

It can be shown that if $A = B \otimes C$, $A_{diag} = B_{diag} \otimes C_{diag}$. This means that if we diagonalize A , we have diagonalized B and C as well. Now, since in our case C is the identity, \mathbf{T} will have the same eigenvalues as \mathbf{B}_1 . We shall now analyze case (ii).

3.3.7 Case (ii)

Here, we know that \mathbf{v}_2 is an eigenvector of \mathbf{B}_3 . From (19) it follows that

$$\mathbf{B}_3 = \begin{pmatrix} \alpha_{EE} \mathbb{1} + p_S^* \beta_1 \mathbf{A} & \alpha_{IE} \mathbb{1} + p_S^* \beta_2 \mathbf{A} \\ \alpha_{EI} \mathbb{1} & \alpha_{II} \mathbb{1} \end{pmatrix}. \quad (29)$$

For pragmatic reasons, we shall split \mathbf{v}_2 into components, \mathbf{u}_1 and \mathbf{u}_2 , such that both are vectors of length n . Since \mathbf{v}_2 is an eigenvector with eigenvalue λ_J , we know that the two components satisfy:

$$(\alpha_{EE} \mathbb{1} + p_S^* \beta_1 \mathbf{A}) \mathbf{u}_1 + (\alpha_{IE} \mathbb{1} + p_S^* \beta_2 \mathbf{A}) \mathbf{u}_2 = \lambda_J \mathbf{u}_1 \quad (30)$$

$$\alpha_{EI} \mathbf{u}_1 + \alpha_{II} \mathbf{u}_2 = \lambda_J \mathbf{u}_2 \quad (31)$$

Equation (31) tells us that

$$\mathbf{u}_1 = \left(\frac{\lambda_J - \alpha_{II}}{\alpha_{EI}} \right) \mathbf{u}_2, \quad (32)$$

which can be plugged into (30) to get:

$$\left((\alpha_{EE} \mathbb{1} + p_S^* \beta_1 \mathbf{A}) \left(\frac{\lambda_J - \alpha_{II}}{\alpha_{EI}} \right) + (\alpha_{IE} \mathbb{1} + p_S^* \beta_2 \mathbf{A}) \right) \mathbf{u}_2 = \lambda_J \left(\frac{\lambda_J - \alpha_{II}}{\alpha_{EI}} \right) \mathbf{u}_2 \quad (33)$$

4 Conclusion