

1 Spreading Processes on Networks

In the lectures so far, we have mainly focused on the structure of networks, building intuition about how networks can vary in their shape in different ways, and developing techniques to quantify or even predict that shape and variability. In reality, networks are usually not static objects, but are instead models of dynamical systems. One of the most general forms of *dynamics* on a network is a *spreading process*.

Spreading processes take place on networks all around us. Diseases spread through contact networks. Gossip, memes, and fashions spread through social networks. Computer viruses and malware can spread through digital communication networks. Avalanches of excitation spread through the neuronal networks. Research topics spread through academic conferences and hiring networks. Blackouts cascade through electrical grids.

Each of these is an example of a complicated dynamical process that we can model (represent) using a network. To capture the dynamics of a spreading process with a network, we annotate each node u with a *state* variable $x_u \in \Gamma$ that indicates whether or not u has contracted the disease, knows the gossip, has adopted the fashion, has been infected with the malware, has activated, or has shutdown, etc. The set of possible states Γ always contains at least two states, but can contain many more. Finally, to create the dynamics, we must define a set of rules that represent how a node's state updates, as a function of its neighbors' states, i.e., $x_u^{t+1} = f(\{x_{\nu(u)}^t\})$, where $\nu(u)$ is a function that returns the set of neighbors of u . Usually, we assume the network itself is fixed, although in advanced models, we may relax this assumption.¹

The central assumption of network spreading process models is that

edges are the mechanisms of transmission.

In order for a thing that is spreading to go from a node u to a node v , it has to travel along a sequence of edges $u \rightarrow \dots \rightarrow v$, with the shortest possible sequence being a single edge (u, v) . Because of this requirement, the structure of the network shapes the possible dynamics of the spreading, and hence structural variables like the degrees of the nodes, the length of the geodesic paths, the density of triangles, and the presence and form of communities will influence the particular way the spreading unfolds.

¹Hence, we might say “dynamics *on* a network,” because the dynamics flow across a fixed set of nodes and edges. In contrast, dynamics *of* a network would indicate that the edges themselves are changing. In the most sophisticated models of spreading processes, both can happen, in which the network’s structure responds to or *adapts* to the changes in node states. For example, self-quarantining behavior or various non-pharmaceutical interventions (NPIs) to suppress an epidemic by modifying the social network over which the pathogen spreads.

There are many different types of models of spreading processes on networks; each varies in how it defines the update function $f()$, but all share the central assumption. Here are a few broad classes.

- **Epidemic models**, which represent the way biological pathogens spread across social networks, as in the case of influenza, HIV, COVID, malaria, etc. Examples include the SI-X family models, which can be very elaborate.
- **Social adoption models**, which represent how social behaviors spread across social networks, as in the spread of ideas, or purchasing behavior, etc. Examples include the Independent Cascade (IC) model and Linear Threshold models.²
- **Biological computation models**, which represent how activation spreads across biological networks, as in neuronal networks, genetic regulatory networks, or signaling networks. Examples include neural cascade models, and boolean networks.

Across these models, there are two useful dichotomies to bear in mind.

1. *Continuous time vs. discrete time dynamics.* Just as in other dynamical systems, some models of spreading take place in continuous time, like standard epidemic models, while others take place in discrete time, like many simulations of network epidemic models.
2. *Simple vs. complex contagions.* A simple contagion is one in which a single exposure can cause transmission of the contagion across a network link. Measles is a good example of such a contagion, since a single exposure is all it takes for transmission to occur. A complex contagion, on the other hand, is one in which multiple exposure are required before the contagion is transmitted. Fashion trends or choices about technology purchases are often of this type, as an individual may be unlikely to change their clothing styles unless (or until) many peers have already made the change.

In this lecture, we will focus on network epidemiology models, building up basic ideas and concepts first and then adapting them to networks.

2 Network Epidemiology

Epidemiology is the study of diseases, in all ways and in all aspects. Network epidemiology generally focuses on infectious diseases, meaning diseases that can spread from one person to another. This usually excludes diseases like heart disease or cancer, and focuses instead on transmissible diseases like influenza, coronavirus, dengue, malaria, etc.

²For a thorough study of these models, see the book chapter by Kleinberg, “Cascading Behavior in Networks: Algorithmic and Economic Issues,” in *Algorithmic Game Theory* (2007).

The details of infectious diseases can be enormously complicated, and span all scales in biology, from molecular to populations, and even across species. Do we consider the molecular mechanisms of infection, e.g., how a virus gets into a cell? Do we consider what happens to individual cells, e.g., how a virus hijacks a cell’s machinery to reproduce, or how bacteria behave in the body? Do we account for how the immune system responds? These are all important questions, but most network-based epidemiological models focus on population dynamics, i.e., how many people are sick, how many could get sick, and how many have recovered.

The combination of population-level dynamics and a network representing people and their interactions is called *network epidemiology*, in which the shape of the network—who connects to whom— influences the spread of the disease. The central assumption of network spreading processes has an interesting implication here: because edges are the mechanisms of transmission, two nodes are linked if and only if the interact in a way that could allow the disease to spread.

This fact implies that there are many different epidemiological networks. If two disease are transmitted by different biology, e.g., gonorrhea (a sexually transmitted disease) vs. influenza (an airborne disease), then the corresponding “networks” will be different. Hence, in a room full of people sitting at desks, many links could exist in the influenza network but none in the gonorrhea network.

2.1 The simplest epidemic : the compartmental model

The simplest epidemiological model is the **compartmental model**, which lacks any population structure. It was first proposed and analyzed by Kermack and McKendrick in 1927.³ From a network perspective, we imagine the epidemic unfolding on a fully connected network, in which every person could be infected by, or could infect, any other person in the population. Hence, we say our modeled population is “well mixed.”

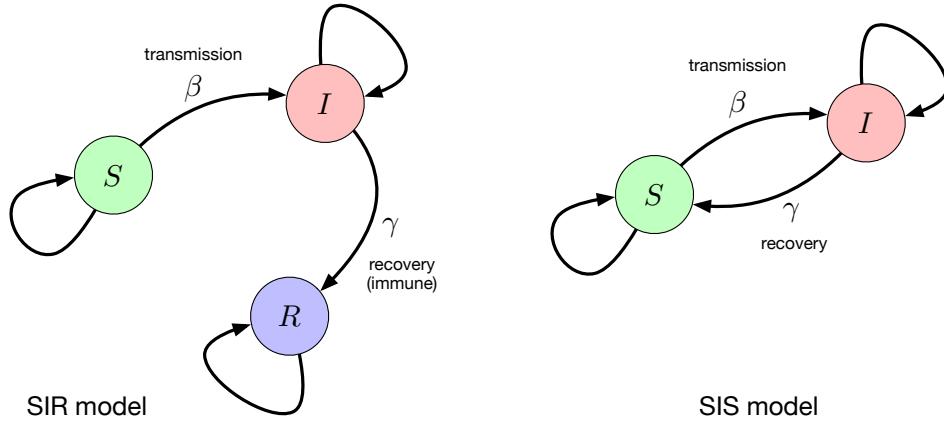
To answer questions at the population level, we need to model how individuals can change their “state” with respect to the spreading disease. In this simplest model, the network structure, such as it is, remains fixed, and each node has a *state variable* $x_i \in \{S, I, R\}$ or $x_i \in \{S, I\}$ that indicates which “compartment” a node is currently in. This model further assumes the population doesn’t change size on the timescale over which the dynamics occur, e.g., by births, or immigration.

The model’s dynamics then come from defining a set of “transition” rules that describe how a node’s state switches from one compartment to another. By tracking the counts of nodes in different compartments, we can track the evolution of an epidemic through the population. The basic compartmental model defines one compartment S for “susceptible” individuals, one compartment I for “infected” individuals, and, optionally, one compartment R for “recovered” individuals.

³See Kermack and McKendrick, “A contribution to mathematical theory of epidemics,” *Proc. Roy. Soc. Lond. A* **115**, 700721 (1927).

Transitions between these compartments then define events like a susceptible individual becoming infected $S \rightarrow I$, an infected individual recovering with immunity $I \rightarrow R$ or without immunity $I \rightarrow S$.

The most basic two epidemiology models are the Susceptible-Infected-Recovered or SIR model, with transitions $S \rightarrow I \rightarrow R$, and the Susceptible-Infected-Susceptible or SIS model, with transitions $S \rightarrow I \rightarrow S$. As state diagrams, we can draw these models like so:

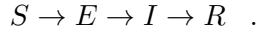


- **SIS** can model diseases like influenza or the common cold, where recovery does not imply immunity (because there are other strains circulating, or because natural immunity wanes quickly).
- **SIR** is more realistic for diseases like chickenpox and measles, where recovery usually implies lasting immunity (because there's only one strain in circulation over the course of a human lifetime, or because the disease is strongly immunogenic).

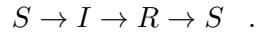
A set of states (“compartments”) and transitions among them fully specifies a compartmental model. In general, we have enormous flexibility in choosing the states and transitions, so long as each transition has a “rate” parameter for how quickly people flow from one state to another. The SIR and SIS models are the most basic compartmental models. If we wanted to model a disease in which infection proceeds in stages, we can break the usual I compartment into a sequence, e.g., perhaps an initial asymptomatic but contagious stage I_1 followed by a symptomatic stage I_2 , leading to this state diagram:

$$S \rightarrow I_1 \rightarrow I_2 \rightarrow R .$$

Or, if an individual can be infected and not yet contagious before later becoming contagious, we can insert an “exposed” state E , yielding the popular SEIR model:



Or, we might want a model in which recovery or immunity is only temporary, as with many respiratory diseases:



Or, we could have multiple types of susceptible states, each capturing a different kind of susceptibility. Or, we could model vaccinated immunity V as distinct from natural immunity R , and have different rates of transition from those states back to infected I , in order to capture different efficiencies of immunity.⁴ This kind of flexibility means that there are *many different* “SI-X” models of disease spread, e.g., a model for how influenza spreads should be different from a model of ebola because these diseases spread through different means, and have different disease progressions for the hosts.

2.2 Specifying a SIR or SIS model

Both SIR and SIS models have parameters β, γ . These represent, respectively, the rate or probability of becoming infected, given an exposure, and the rate or likelihood of recovery, given an infection. The higher the value of β , the more likely an exposure leads to an infection. For instance, a highly contagious disease like measles will have a very high value of β , while something like the common cold will have a much lower value. Similarly, the higher the value of γ , the faster an infected individual recovers to become non-infectious again. The ratio β/γ provides a simple quantitative measure of the relative flow into the I compartment, and in the compartmental model, it is equivalent to R_0 , which is defined as *the average number of secondary infections* per infected individual early in the epidemic. The higher R_0 , the faster an epidemic will tend to grow.

2.2.1 Epidemic dynamics in SIS

The dynamics of the basic SIS compartmental model provide a reference point for our intuition about epidemic dynamics on a network. We can mathematically model the number of individuals in each of the two S, I compartment as follows. This model runs in continuous time; later, when we describe network epidemiology simulations, the dynamics will run in discrete time (with synchronous updates). More on that below.

- Let N be the total population (number of nodes), which we assume to be constant.
- An infected person infects some susceptible person with probability $\bar{\beta}$ per unit time.
- An infected person recovers, becoming susceptible again, with probability γ per unit time.

⁴For a nicely elaborate SEIR model with vaccinations, see Figure S1 in Bubar et al., “Model-informed COVID-19 vaccine prioritization strategies by age and serostatus.” *Science* 371, 916-921 (2021).

- Let $S(t)$ and $I(t)$ denote the number of susceptible and number of infected individuals, and note that $N = S(t) + I(t)$.

Now, consider how $S(t)$ changes over a small interval of time:

$$S(t + \Delta t) = S(t) - [S(t) \times \bar{\beta} \Delta t I(t)] + [I(t) \times \gamma \Delta t] . \quad (1)$$

Let's consider the structure of the equation:

- The first term is just the number of susceptibles we began with.
- The second term measures the flow of individuals out of the susceptible S compartment (and into the infected I compartment) due to new infections. This term is proportional to the product $S(t)I(t)$, because each susceptible is connected to every infected, and we assume that transmissions are independent (as in the configuration or Chung-Lu models).
- Finally, the third term measures the flow of individuals back into the susceptible S compartment (and out of the infected I compartment) due to recovery.⁵

We can convert this difference equation into a differential equation by dividing S , I , and $\bar{\beta}$ by the population size N and unit time Δt , yielding

$$s = S/N \quad i = I/N \quad \beta = \bar{\beta}N . \quad (2)$$

Changing from $\bar{\beta}$ to β lets us interpret β as the expected number of new infections resulting from an infected node in an uninfected population, per unit time.

Making these changes of variables yields a rate equation for the number of infected individuals

$$\frac{di}{dt} = \beta i(1 - i) - \gamma i . \quad (3)$$

Given this equation for the dynamics of the infected population, we use it to answer the most fundamental question: will a new epidemic spread? That is, if a small fraction of the population becomes infected by a new pathogen, will the infection spread or will it die out?

We can answer this question by setting i to be very small (few individuals infected, relative to N), and asking under what conditions will i grow. Under this assumption, we make the approximation $(1 - i) \approx 1$, which yields

$$\frac{di}{dt} \approx \beta i - \gamma i = i(\beta - \gamma) . \quad (4)$$

⁵In the SIR model, this term would instead appear in the update equation for $I(t + \Delta t)$, because it represents the flow from I to R , the “recovered” (or “removed”) compartment.

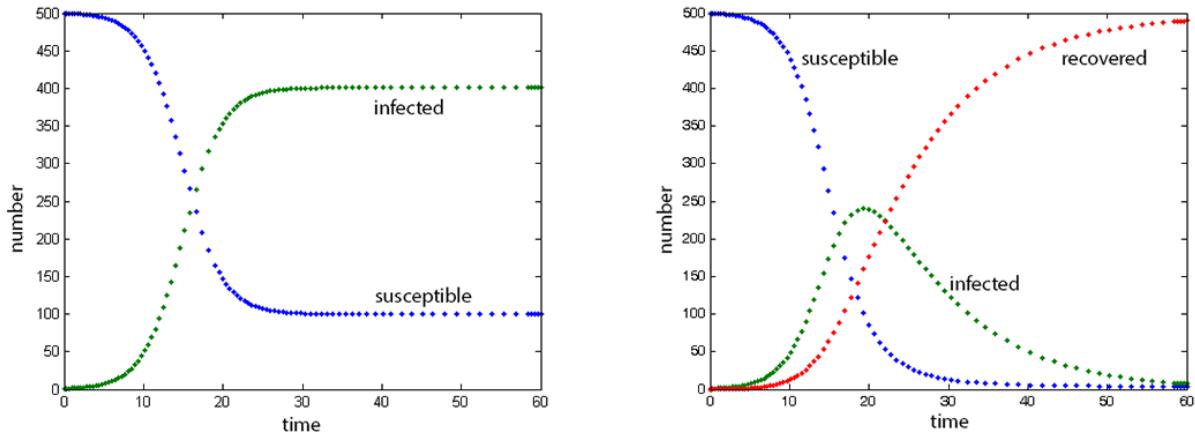
This is an ordinary differential equation, whose solution is a logistic function, given a fraction i_0 of initially infected individuals. That means the initial behavior of i is an exponential function that grows whenever $\beta > \gamma$, because the compartment I 's *rate* of in-flow exceeds its *rate* of out-flow. In contrast, when $\beta < \gamma$, the I compartment will tend to empty out more quickly than it fills up, and the epidemic dies out. The ratio β/γ is equivalent to R_0 , the so-called “basic reproduction number” of an epidemic, or the average number of secondary infections an infected individual produces. For this reason, the special point

$$\frac{\beta}{\gamma} = 1 \quad , \quad (5)$$

is called the *epidemic threshold*.⁶

2.2.2 SIS and SIR dynamics

The population's states S, I under the SIS model evolve like the figure above, on the left.⁷ Because individuals can go back and forth between the two compartments, the relative proportion of individuals in each will eventually stabilize. The value it converges on is given by setting Eq. (3) equal to 0, and solving, which yields a steady state of $i(\infty) = 1 - \beta/\gamma$.



Under the SIR model, the population's states S, I, R evolve like the figure above, on the right.⁸

⁶Recall the critical value of the average degree $c = 1$ in the Erdős-Rényi random graph model, where if the average degree $c > 1$, a giant connected component of size $\Theta(n)$ exists, while if the average degree $c < 1$, the largest connected component is $O(1)$ in size. The mathematics there and here are the same.

⁷Adapted from: <https://en.wikiversity.org/wiki/File:Sissys.png>

⁸Adapted from: <https://en.wikiversity.org/wiki/File:Sirsys-p9.png>

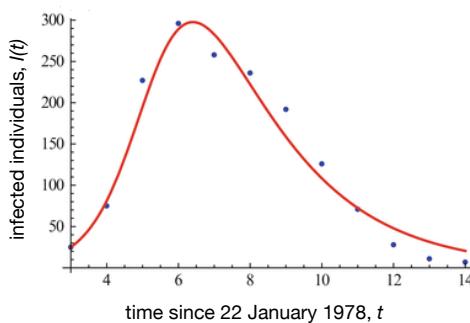
Based on the dynamics you see, what value do you think was chosen for the ratio β/γ ?

Initially, $I(t)$ grows exponentially in both cases. But, its behavior later differs—in the SIS case, the sizes of S and I eventually stabilize, at the point where the rate of infection $S \rightarrow I$ equals the rate of recovery $I \rightarrow S$. In the SIR case, the R compartment collects individuals over time so that eventually all individuals are either S (never infected) or R (all others recovered). As the fraction of individuals in S decreases, there are relatively fewer individuals to move to the I compartment, and this “emptying out” produces a characteristic peak in the $I(t)$ function. Because the early growth of $I(t)$ is exponential, the peak occurs sooner, and is reached more quickly, if $R_0 = \beta/\gamma$ is high, and the height of the peak is governed by the absolute value of γ , which determines how long an individual stays in the I state before transitioning to R . (Do you see why?)

2.2.3 SIR in the wild

Meeting the conditions of the SIR model in the real-world is complicated: we need a closed population, it needs to be well-mixed socially, and recovery from the disease needs to imply strong immunity. If these conditions are met, then we can observe the entire course of the epidemic dynamics and compare them to an SIR model. If these conditions are not met, then the SIR model is only reasonable for the very beginning of the epidemic.

In the first two months of 1978, an influenza epidemic swept through an English boarding school containing 763 boys.⁹ Returning for the Spring term on January 10, one boy arrived and developed a fever. By January 22, three boys were unwell. This number reached 25 on day 3, 75 on day 4, etc., and in the end, only 19 boys escaped the flu. The original 1978 report on the epidemic says boys recovered in the infirmary, in isolation, but spent on average 2.1 days mixing with the fellows before that. From these numbers, the SIR model parameters can be estimated as $\hat{\beta} \approx 0.00234$ and $\hat{\gamma} = 1/2.1 \approx 0.476$, which parameterizes a beautifully best-fit $I(t)$ function for the case-count data.



⁹This example and figure reproduced from Martcheva, “Introduction to Epidemic Modeling.” In: *An Introduction to Mathematical Epidemiology*. Texts in Applied Mathematics, vol 61. Springer (2015)

2.2.4 Exponential growth in a real epidemic: covid-19

Without a closed system, the SI-X dynamics are mainly useful as a guide for the beginning of an epidemic, when the vast majority of the population is susceptible, and the epidemic is growing exponentially.

Exponential growth is very fast. A simple way to make this growth more intuitive is the “doubling time” of an epidemic: how many days τ (time steps) are required for the number of infected individuals to double, i.e., $I(t + \tau) = 2 I(t)$? Because $I(t) \sim (R_0)^t$ early in the epidemic, we can calculate the doubling time no matter what value of t we choose. (Do you see why?)

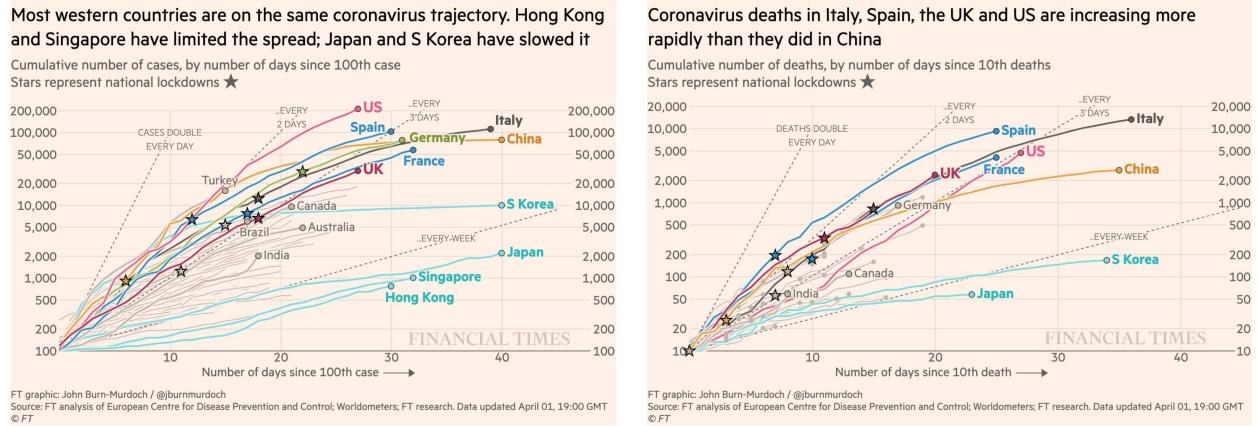


Figure 1: Official case and death counts, early in the covid-19 pandemic.

The doubling time τ of a real epidemic depends on many factors, including the scale and type of public health response, the temperature sensitivity of transmission, etc., all of which can impact the observed R_0 . In the first few months of the covid-19 pandemic of 2020, the empirical doubling time varied across countries, but was roughly 3–4 days in most developed nations, including Italy, Spain, and the United States. Here are Italy’s early case numbers, from the World Health Organization:¹⁰

24 Feb.	27 Feb.	1 Mar.	4 Mar.	8 Mar.	11 Mar.	15 Mar.
124	400	1128	2502	7375	10149	21157

Over these 27 days, the case count increased by a factor of 170, which gives a doubling time of $\tau = (t_2 - t_1)/\log_2[I(t_2)/I(t_1)] = 3.64$ days. Were this rate to continue unabated, Italy would reach 3,600,000 cases a month later, and then over 14,000,000 a week after that. In the space of

¹⁰Data from the World Health Organization’s covid-19 Situation Reports:

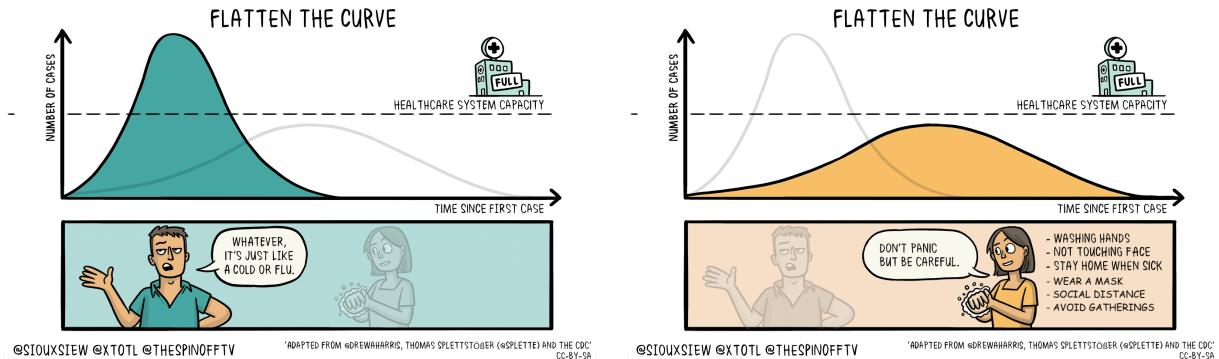
https://en.wikipedia.org/wiki/Template:201920_coronavirus_pandemic_data/WHO_situation_reports

just 9 weeks, the epidemic would have spread to 24% of Italy's population, killing 84,000 people (infected fatality rate of 0.6%). For reference, influenza kills about 17,000 Italians per year.

Of course, exponential growth cannot go on forever. The doubling time's utility as a measure of an epidemic's speed R_0 or its peak size $\max_t I(t)$ depends on how long the exponential growth holds. Population is an obvious long-term limiting factor: once a large fraction of the population becomes infected, the supply of susceptible individuals $S(t)$ is no longer large compared to the number of infected individuals $I(t)$, and the epidemic will begin to decelerate.

2.2.5 Flattening the curve

To limit the speed or peak size of an epidemic in the compartment model, we can change either β , the rate at which individuals become infected, or γ , the rate at which they recover. How much we can change either depends on the details of the pathogen and our public health system. For instance, in viral infections, like influenza and covid-19, where treatments are rudimentary, there are fewer things we can do directly to increase the recovery rate γ . In such a case, we instead focus our public health efforts on β , transmissibility. In contrast, in bacterial infections like *E. coli*, we can increase γ substantially, if a suitable antibiotic is available.



For a seasonal pandemic like influenza, a modern health care system tends to have enough capacity to provide adequate care to all individuals with serious cases: because it's seasonal and widespread, the peak number of cases is fairly predictable and treatment resources widely available.

However, if the health care system is overwhelmed by cases, i.e., $I(t)$ grows so rapidly that there are more serious cases than available hospital beds or intensive care units, this "collapse" of the health care system would itself cause γ to decrease (for all diseases), leading to many more deaths.¹¹

¹¹In such a case, doctors will likely be forced to ration life-saving resources using "wartime" triage protocols. Such a situation occurred in both Italy and Arizona during the covid-19 pandemic:
<https://www.theatlantic.com/ideas/archive/2020/03/who-gets-hospital-bed/607807/>.

In such an “explosive” pandemic situation, e.g., the covid-19 pandemic of 2020, a good public health strategy aims to “flatten the curve” (see cartoon above, from March 2020, which predates the understanding that wearing a facial covering also lowers β). By lowering β , we aim to *slow* the exponential growth of $I(t)$ so that it peaks lower (ideally, low enough that it is below the health care system’s capacity) and later, so as to buy time for the development of novel treatments (vaccines, etc.) and the construction of adequate resources (more ICUs, etc.). At worst, these actions won’t change the total number of infections over the epidemic, but by prolonging its duration, the health care system is better able to keep up with the peak case load, keeping γ high for all cases (including other medical needs, e.g., broken bones, cancer, etc.), and more time is created to find effective medical treatments or management strategies.

A key strategy to flatten the curve is “social distancing,” a kind of network intervention, in which we modify the contact network the disease exploits so that fewer secondary cases are produced by every new infection. Social distancing explicitly targets the exposure network G in order to lower R_0 and decelerate the exponential growth. We’ll discuss this idea in more detail later.

2.3 Epidemics on a network

There are two primary differences between a compartment model and a network model of an epidemic. First, real-world networks are typically sparse, while the compartment model is unrealistically dense. And second, the network is an explicit representation of which pairs of individuals actually interact, and hence could infect each other. As a result, the shape of the network constrains the dynamics of the epidemic.

We begin by answering the two fundamental questions for using a network $G = (V, E)$ in this setting: *What are nodes? And, what are edges?*

Typically, nodes are individuals (humans or animals), and edges are potential exposures, given the biology of transmission. Two nodes i, j are only connected if i can expose j to an illness. If not, then there cannot be an edge between i, j . We call this set of edges the *exposure network* G . For example, where are several different ways we could define an exposure interaction:

- close proximity (influenza, common cold)
- physical contact with a fomite (inanimate object harboring live pathogen, e.g., pink eye)
- physical contact with fluids (STDs)
- contact with an animal vector (mosquitos and malaria).

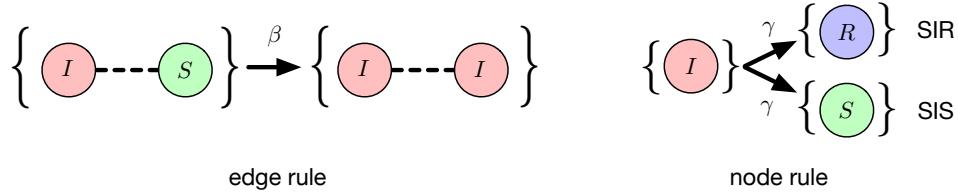
But not all potential exposures result in actual *transmissions*. A second network we can define is the network of actual transmissions $G_T = (V, E_T)$, whose edges E_T are a subset of the potential exposures $E_T \subseteq E$. In the transmission network, every edge represents a *directed* transmission, in which

j became infected by its interaction with i . If infection events are unique for an individual (as in SIR), then edges are directed and G_T is always a tree, whose root is the “patient 0” of the epidemic.

2.3.1 Dynamics on the network

Because not every susceptible individual connects to every infected individual, the structure of the potential exposure network G shapes both which and when nodes get infected.

In the simplest network epidemiology model, time progresses synchronously in discrete steps. To manage the transitions of nodes from one state $x_i(t)$ to another $x_i(t+1)$, we define a set of update rules for the network, one for the edges, and one for the nodes:



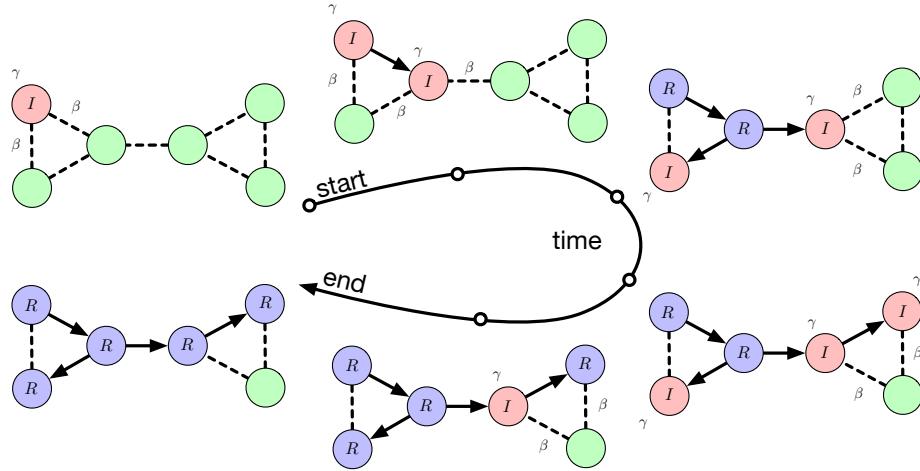
The conceptual meanings of β and γ here are the same as in the compartment model, but mathematically, their meaning have changed slightly. Here, when we find a motif of the form on the left, we transform it into the motif on the right with probability β for an edge update (transmission) and γ for a node update (recovery). Hence, β in a network model is the independent probability that an exposure leads to infection, and γ is the independent probability that an infected node recovers.

The conceptual meaning of R_0 is also the same as in the compartment model: it denotes the expected number of secondary infections early in the epidemic. But, in a network model, $R_0 \approx \beta/\gamma \times \langle k \rangle$, i.e., the number of secondary infections is governed by both the relative transmission probability *and* the network structure. That means an epidemic can spread faster by increasing either its transmissibility *or* the density of connections. Thus, R_0 is not an intrinsic property of a disease, and instead it depends both on how easily humans transmit the disease to one another (β/γ , which can be modified by hygiene, demographics, etc.) and on how many opportunities an infected human has to spread it ($\langle k \rangle$, on average, which can be modified by social structure, lifestyle, etc.), both of which can change over time or context.

2.3.2 An example on a network

Given a network where some node is the initial infection (the “patient 0”), we can apply the rules to simulate the spread of the infection across the network. The simulation halts when there are no

infected nodes. In the example below, edges in the potential exposure network G are dashed, while edges in the transmission network G_T are solid.



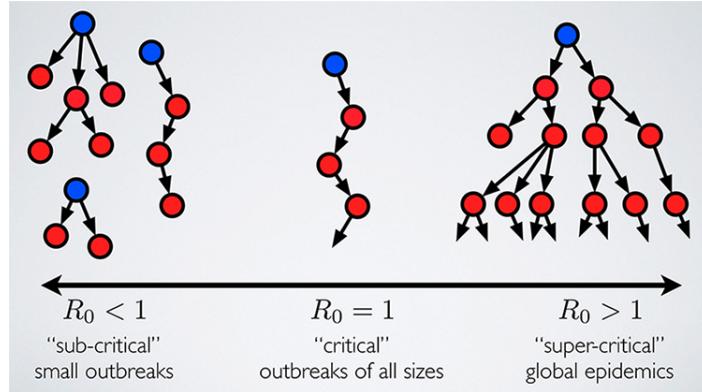
At the end of this epidemic, there is only one node (bottom right) that escaped infection entirely. The bottom-left node could have been infected by either of its neighbors, but only one of those edges is included in the final transmission network.

2.3.3 The role of R_0

The basic reproduction number R_0 plays a critical role in giving us a sense of what kind of an epidemic an infection will produce. Remember that in the network, $R_0 \approx \beta/\gamma \times \langle k \rangle$, meaning that we can increase it by either increasing the transmission probability or increasing the network's connectivity.

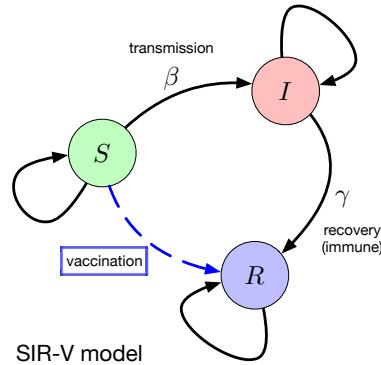
When it is below the epidemic threshold, the transmission graphs (trees) tend to be small. Above the threshold, and the expected number of additional infections is greater than 1, which implies an exponential growth process (consider $R_0 = 2$; what kind of a tree does this create?) that will eventually consume every node reachable from the initial infection. At the critical value of $R_0 = 1$, we get outbreaks of all different sizes.

In fact, we've seen (mathematically) exactly this behavior before! It was in the *phase transition* in the size of the giant component for the Erdos-Renyi random graph model $G(n, p)$. Look back at the figure that visualized ER graphs for different choices of mean degree $c = \{0.5, 1, 2, 4\}$. There, the mean degree c plays exactly the same role as R_0 here.



2.4 Stopping an epidemic on a network

Vaccination is a remarkably achievement of public health: for most people, it provides a means to transition from a susceptible state S to a “recovered” (immune) state R , without having to go through the experience of being infected I .



This state-change is useful for individuals, but also useful for the population, because placing an individual into the R state effectively deletes their edges from the potential exposure graph G . And, deleting many edges from G necessarily reduces the mean out-degree R_0 in the transmission graph G_T , and, ideally, moves it below the critical threshold of $R_0 = 1$. That is, vaccinations break up the network into small, disconnected components, any one of which could host a small epidemic, but such an outbreak cannot spread to the other components. Vaccination thus protects the rest of the network, and this is called *herd immunity*.

The higher the value of R_0 for a disease, the greater a fraction of the population needs to be vaccinated in order to push the transmission graph below the critical threshold. Under the compartment

model, we can derive an equation that relates the fraction of the population needed to be vaccinated in order to push $R_0 < 1$: vaccination rate = $1 - 1/R_0$. Hence, as R_0 increases, a greater fraction of the population needs to be vaccinated in order to create herd immunity.

But, recall that R_0 depends on the structure of network. If the mean degree is high enough, or, in fact, if the variance of the degree distribution is large enough, large components in the exposure graph can persist, even under very high vaccination rates, and the existence of these components means an epidemic can still spread.

Here are some examples of real R_0 values for real diseases, along with the corresponding estimates of the required vaccination rate to produce herd immunity:

disease	R_0	transmission	vax.	data from
measles	12 – 18	airborne	90–95%	1912–1928 in US + 1944–1979 in UK
chickenpox	7 – 12		85–90%	
polio	5 – 7	fecal-oral route	82–87%	
small pox	1.5 – 20+	airborne droplet	70–80%	
H1N1 flu	1 – 3	airborne droplet		
ebola	1.5 – 2.5	bodily fluids		
zika	2			
covid-19 (wildtype)	≈ 2.4	aerosols	60–85%	
covid-19 (alpha)	4 – 5	aerosols	75–80%	
covid-19 (delta)	5 – 8	aerosols	80–88%	

The estimates of R_0 values are empirical, as the example of measles illustrates. That means that the value of R_0 for a particular disease depends on the current structure of human social organization and human behavior. The better the public health system, and the more isolated individuals are from each other, the lower the R_0 will be, even for the same disease. But, as we have seen with covid-19, R_0 can also change as a result of evolution, which can tend to select for greater transmissibility, and hence higher R_0 even in the face of changes in social behavior.

2.4.1 Network strategies for targeted vaccination

Suppose we had only a limited supply of vaccines, but we still wanted to stop an epidemic. The limited number means we cannot rely on the classic vaccination strategy of “vaccinate everyone who isn’t immuno-compromised.” Instead, we can try to exploit the network structure itself, by vaccinating nodes that would either *slow down* the epidemic (making it take longer paths through the network) or *break up* the network into smaller components.

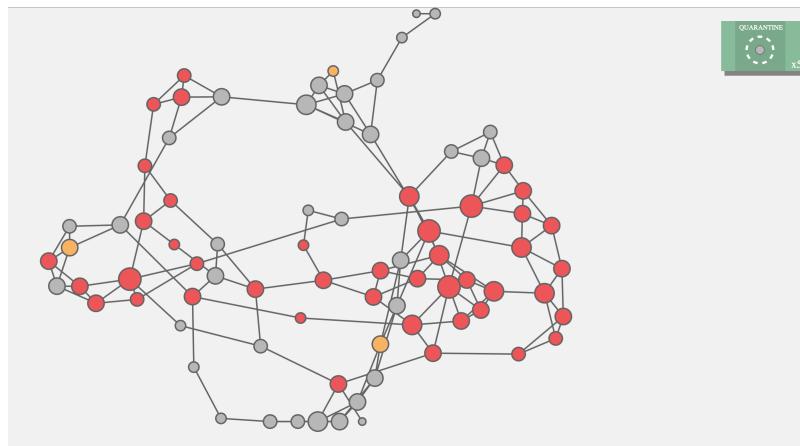
Here are some possible strategies:

- vaccinate by node attributes, e.g., the young and old (who are less likely to survive a bad infection)
- vaccinate randomly
- vaccinate higher-degree nodes first, e.g., teachers, doctors, service industry workers, etc.
- vaccinate “bridges” that link different social communities

2.4.2 Try your hand

Prof. Marcel Salathé’s group at EPFL in Switzerland has created a web game that challenges you to precisely the above problem: can you stop an outbreak through targeted interventions?

Try it out here: VAX! <https://vax.herokuapp.com>. The screenshot shows an example of an ongoing outbreak on a small social network.



2.5 Modeling Epidemics on Networks

There are several useful Python packages for modeling epidemics on networks:

- **Epidemics on Networks** (EoN) is a package for simulating SIS and SIR models on networks. EoN works on top of `networkx`, and allows event-based simulations on simple or weighted networks, synchronous updating, and visualization of the epidemic results, e.g., epidemic trajectories like $I(t)$.

Highlights and tutorial: <https://epidemicsonnetworks.readthedocs.io/en/latest/>

- **SEIR+ Model** is a package for simulating SEIR models on networks, where the E state represents individuals who are “exposed.” SEIR+ also works on top of `networkx`, and includes

additional states and transitions in order to model an epidemic like SARS-CoV-2, where testing and latent infections play a substantial role in the epidemic's trajectory.

Highlights and tutorial: <https://github.com/ryansmcgee/seirsplus>

Supplemental readings

1. van den Driessche, "Reproduction numbers of infectious disease models." *Infection Disease Modeling* **2**, 288–303 (2017)
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6002118/>
2. Delamater et al., "Complexity of the Basic Reproduction Number R_0 ." *Emerging Infectious Diseases* **25**(1), 1–4 (2019)
<https://www.ncbi.nlm.nih.gov/pubmed/30560777>
3. Bansal, Grenfell, and Meyers, "When individual behaviour matters: homogeneous and network models in epidemiology." *J. Royal Society Interface* **4**, 879–891 (2007)
<https://royalsocietypublishing.org/doi/full/10.1098/rsif.2007.1100>

3 SIS on a network, using math

How does a network of connections change the dynamics that we observe? One place to start is the epidemic threshold. For an all-to-all network, we found, above, that an epidemic would occur whenever $\bar{\beta}N/\gamma > 1$. Now, we consider the same process as above on an adjacency matrix, A , in which $A_{uv} = 1$ if and only if nodes u and v interact. We will still define $\bar{\beta}\Delta t$ as the probability that an infected node will pass the infection to an uninfected neighbor in a time Δt , and let $\gamma\Delta t$ be the probability that an infected node will spontaneously recover in time Δt .

To begin, let $i_u(t)$ be the probability that node u is infected at time t . Then

$$\begin{aligned} i_u(t + \Delta t) &= \Pr(\text{node } u \text{ is infected at time } t \text{ and does not heal.}) \\ &\quad + \Pr(\text{node } u \text{ is susceptible at time } t \text{ and gets infected by a neighbor}). \\ &= i_u(t)[1 - \gamma\Delta t] + [1 - i_u(t)] \sum_{v=1}^N A_{uv} i_v(t) \bar{\beta} \Delta t \end{aligned}$$

and this can be rearranged, as in the all-to-all case, to find that

$$\frac{di_u}{dt} = -\gamma i_u + (1 - i_u) \bar{\beta} \sum_{v=1}^N A_{uv} i_v . \quad (6)$$

How does the epidemic threshold change when we consider the dynamics of Eq. (6)? We will linearize as before, neglecting the products of $i_u i_v$, which will be very small when the typical i is small. This results in the equation:

$$\frac{di_u}{dt} = -\gamma i_u + \bar{\beta} \sum_{v=1}^N A_{uv} i_v \quad (7)$$

which in vector form is

$$\frac{di}{dt} = (-\gamma I + \bar{\beta} A) i \quad (8)$$

and which is solved by

$$i(t) = x e^{(\bar{\beta}\lambda - \gamma)t} . \quad (9)$$

One can check (you should!) that this is a solution provided that x is an eigenvector of A and λ is its corresponding eigenvalue. Which eigenvalue-eigenvector pair should we consider? As in previous lectures, this turns out to be the principal (largest) eigenvalue. For a network A which is irreducible (i.e., connected) this largest eigenvalue is unique and positive, and is referred to as the Perron-Frobenius eigenvalue.

What is the eigenvector x ? It turns out that if λ is the Perron-Frobenius eigenvalue, then x is the corresponding eigenvector which makes its entries the *eigenvector centralities of the nodes*. Therefore, nodes with higher eigenvector centrality will tend to have a higher probability of being infected than nodes with a lower eigenvector centrality. Can you build an intuitive understanding of this?

We've now solved the equation above, but have not computed an epidemic threshold. Based on the solution, the exponential term will grow whenever $\bar{\beta}\lambda - \gamma > 0$, meaning that the epidemic threshold here is

$$\frac{\bar{\beta}}{\gamma} = \frac{1}{\lambda}.$$

Recall that in the all-to-all case, we decided to change from $\bar{\beta}$ to β . We rescaled by N so that β was interpretable as the expected number of new infections resulting from an infected node in an uninfected population, per unit time. Previously, this meant that $\beta = \bar{\beta}N$, but here, to maintain the same interpretation, we set $\beta = \langle k \rangle \bar{\beta}$ since typically, each node connects to $\langle k \rangle$ other nodes. Therefore, our epidemic threshold becomes

$$\frac{\beta}{\gamma} = \frac{\langle k \rangle}{\lambda}. \quad (10)$$

What should we make of this equation? It looks just like our previous equation for the well-mixed case, except for that the right hand side now reads as a ratio of the mean degree to the principal eigenvalue instead of one. What does that mean?

3.1 A few notes on the largest eigenvalue

It turns out that the Perron-Frobenius eigenvalue comes up a lot. As a consequence, people have been very interested to know how it can be approximated from the values. For a network without degree correlations, it turns out that

$$\lambda \approx \frac{\langle k^2 \rangle}{\langle k \rangle}.$$

The value on the right hand side also appeared in our analyses of the configuration model's properties, and even appears in the mathematical analysis of the friendship paradox. Recall that $\langle k^2 \rangle \geq \langle k \rangle^2$ with equality only if the network is degree-regular. This means that $\lambda \geq \langle k \rangle$. Plugging the approximation above into Eq (10), we find that the epidemic threshold can be approximated as

$$\frac{\beta}{\gamma} \frac{\langle k^2 \rangle}{\langle k \rangle^2} = 1. \quad (11)$$

In networks where some nodes have exceptionally large degree, the approximation above is no longer good. Specifically,

$$\lambda \approx \sqrt{k_{\max}} \quad \text{if } \sqrt{k_{\max}} > \frac{\langle k^2 \rangle}{\langle k \rangle} \log^2 N.$$

These results are due to Chung and Lu, the very same as the Chung-Lu model of random graphs with specified expected degrees. They assume that there are no degree correlations. However, when there are degree correlations, correction terms are needed. For more details, see *Approximating the largest eigenvalue of network adjacency matrices* by Restrepo, Ott, and Hunt.

3.2 Vaccination and herd immunity, using math

Suppose that you vaccinate a fraction q of the nodes, chosen uniformly at random. How large does q need to be in order to prevent the disease from spreading? If we assume that the vaccine is perfectly protective, then the probability that an infected node passes the infection to an uninfected node is $\beta(1 - q)$, since the disease transmits only if the recipient is not vaccinated. Therefore, to understand the role of vaccination, we need only replace β in Eq. (12) with $\beta(1 - q)$,

$$\frac{\beta(1 - q)}{\gamma} \frac{\langle k^2 \rangle}{\langle k \rangle^2} = 1 . \quad (12)$$

A little algebra shows us that

$$\frac{\beta(1 - q)}{\gamma} \frac{\langle k^2 \rangle}{\langle k \rangle^2} \leq 1 \iff q \geq 1 - \frac{\gamma \langle k \rangle^2}{\beta \langle k^2 \rangle} . \quad (13)$$

When a fraction q of nodes are vaccinated satisfying Eq (13), it pushes the SIS dynamics into the subcritical regime in which epidemics do not spread to infect a large fraction of the network. Put differently, we need only vaccinate qN nodes to protect the population of N nodes from epidemics. This is herd immunity again. Simply due to the intrinsic dynamics of a disease, a vaccine for some can provide protection for all.

Note also that the fraction q can be nearly 1 whenever: (i) recovery is slow (γ is small), (ii) the disease is highly transmissible (β is large), or (iii) the network has an especially broad degree distribution $\langle k^2 \rangle \gg \langle k \rangle^2$. In fact, for some networks, $\langle k^2 \rangle$ diverges, meaning that no amount of vaccination can overcome the structural tendency toward epidemics!

To illustrate this latter point, suppose that you have degrees with a power-law degree distribution, $\Pr(k) = ck^{-\alpha}$ where c is the normalization constant. Suppose for convenience that $k \in [k_{\min}, \infty)$. Then, approximating the discrete power law with its continuous version,

$$\begin{aligned} \langle k^2 \rangle &= \int_{k_{\min}}^{\infty} k^2 \Pr(k) dk = \int_{k_{\min}}^{\infty} k^2 ck^{-\alpha} dk \\ &= c \int_{k_{\min}}^{\infty} k^{2-\alpha} dk \end{aligned} \quad (14)$$

This integral will diverge when $\alpha \leq 3$, which means that for sufficiently broad power-law degree distributions, the epidemic threshold is always satisfied, regardless of vaccination, β , or γ .