The Spread of Epidemic Disease on Networks

Libao Jin

University of Wyoming

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Epidemiological Models

Susceptible/Infective/Removed (SIR) Model

Motivation: Dynamic Vertex Coloring

- A simple graph G consisting of N vertices of three colors: red (R), green (G), and blue (B).
- The rate β of red vertices converting to green vertices is proportional to the product of the numbers of red and green vertices, and green vertices can be converted to the blue vertices at an average rate γ per unit time.
- In the limit of large N, this model is governed by the coupled nonlinear differential equations:

$$\frac{dr}{dt} = -\beta rg, \quad \frac{dg}{dt} = \beta rg - \gamma g, \quad \frac{db}{dt} = \gamma g,$$

where $r(t)$, $g(t)$, and $b(t)$ are the fractions of the vertices in each of three colors.

SIR Model

- A closed population of N individuals with no births or deaths is divided into three states: susceptible (S), infective (I), and removed/recovered (R).
- Infective individuals have contacts with randomly chosen individuals of all states at an average rate β per unit time, and recover and acquire immunity (or die) at an average rate γ per unit time.
- In the limit of large N, this model is governed by the coupled nonlinear differential equations:

$$\frac{ds}{dt} = -\beta is, \quad \frac{di}{dt} = \beta is - \gamma i, \quad \frac{dr}{dt} = \gamma i,$$

where $s(t)$, $i(t)$, and $r(t)$ are the fractions of the population in each of three states, and the last equation is redundant, due to $s + i + r = 1$.

Susceptible/Exposed/Infective/Removed (SEIR) Model

SEIR Model

- Many diseases have a latent phase during which the individual is infected but not yet infectious. This delay between the acquisition of infection and the infectious state can be incorporated within the SIR model by adding a latent/exposed population, E, and letting infected (but not yet infectious) individuals move from S to E and from E to I.
- SIR: $S \to I \to R$.
- SEIR: $S \to E \to I \to R$.

SEIR Model

- A closed population of N individuals with no births or deaths is divided into four states: susceptible (S), exposed (E), infective (I), and removed/recovered (R).
- Infective individuals have contacts with randomly chosen individuals of all states at an average rate β per unit time; exposed individuals become infective at an average rate σ per unit time, and recover and acquire immunity (or die) at an average rate γ per unit time.
- In the limit of large N, this model is governed by the coupled nonlinear differential equations:

$$\frac{ds}{dt} = -\beta is, \frac{de}{dt} = \beta is - \sigma e, \frac{di}{dt} = \sigma e - \gamma i, \frac{dr}{dt} = \gamma i,$$

where $s(t)$, $e(t)$, $i(t)$, and $r(t)$ are the fractions of the population in each of four states.

SEIRS Model

SEIRS Model

The SIR or SEIR model assumes people carry lifelong immunity to a disease upon recovery, but for many diseases the immunity after infection wanes over time. In this case, the SEIRS model is used to allow recovered individuals to return to a susceptible state.

SEIRS Model

- A closed population of N individuals with no births or deaths is divided into four states: susceptible (S), exposed (E), infective (I), and removed/recovered (R).
- Infective individuals have contacts with randomly chosen individuals of all states at an average rate β per unit time; exposed individuals become infective at an average rate σ per unit time, recover and acquire immunity (or die) at an average rate γ per unit time, and the recovered individuals return to the susceptible state due to loss of immunity at an average rate ξ per unit time.

SEIRS Model

- In the limit of large N, this model is governed by the coupled nonlinear differential equations:

$$\begin{aligned}
\frac{ds}{dt} &= -\beta i s + \xi r, \\
\frac{de}{dt} &= \beta i s - \sigma e, \\
\frac{di}{dt} &= \sigma e - \gamma i, \\
\frac{dr}{dt} &= \gamma i - \xi r,
\end{aligned}$$

where $s(t)$, $e(t)$, $i(t)$, and $r(t)$ are the fractions of the population in each of four states.

Transmission on Networks

Transmission on Fully Mixed Networks vs. General Networks

Transmission on Fully Mixed Networks

Assumptions:

- The population is fully mixed, meaning that the individuals with whom a susceptible individual has contact are chosen at random from the whole population;
- All individuals have approximately the same number of contacts in the same time;
- All contacts transmit the disease with the same probability.

Transmission on General Networks

- Replace "fully mixed" aspect with a network of connections between individuals. Individuals have disease-causing contacts only alone the connections in the network.
- Connections vs. contacts:
  - Connections between pairs of individuals predispose those individuals to disease-causing contact, but do not guarantee it.
  - An individuals' connections are the set of people with whom the individual may have contact during the time he or she is infective — People that the individual lives with, works with, sits next to on the bus an so forth.
- Vary the number of connections each person has with others by choosing a particular degree distribution for the network.
- Allow the probability of disease-causing contact between pairs of individuals who have a connection to vary, so that some pairs have higher probability of disease transmission than others.

Transmissibility

Probability of Transmission

Consider a pair of individuals who are connected, one of whom i is infective and the other j susceptible. Suppose that the average rate of disease-causing contacts between them is r_{ij}, and that the infective individual remains infective for a time τ_i. Then the probability $1 - T_{ij}$ that the disease will *not* be transmitted from i to j is

$$\begin{aligned} 1 - T_{ij} &= \lim_{\delta t \to 0} (1 - r_{ij}\delta t)^{\tau_i/\delta t} \\ &= \lim_{-r_{ij}\delta t \to 0} \left\{ [1 + (-r_{ij}\delta t)]^{\frac{1}{-r_{ij}\delta t}} \right\}^{-r_{ij}\tau_i} \\ &= e^{-r_{ij}\tau_i}, \qquad \left[\lim_{x \to 0} (1+x)^{1/x} = e\right] \end{aligned}$$

Probability of Transmission

The probability of transmission is

- Continuous case:

$$1 - T_{ij} = e^{-r_{ij}\tau_i} \implies T_{ij} = 1 - e^{-r_{ij}\tau_i}.$$

- Discrete case: Set $\delta t = 1$, then

$$1 - T_{ij} = (1 - r_{ij}\delta t)^{\tau_i/\delta t} \implies T_{ij} = 1 - (1 - r_{ij})^{\tau_i},$$

where τ_i is measured in time-steps.

Priori Probability of Transmission

In general, r_{ij} and τ_i will vary between individuals, so that the probability of transmission also varies. Assume that initially these two quantities are i.i.d. random variables chosen from some appropriate distributions $P(r)$ and $P(\tau)$, note that $r_{ij} \neq r_{ji}$. Observe that T_{ij} is also an i.i.d. random variable, hence the *a priori* probability of transmission of the disease between two individuals is simply the average T of T_{ij} over the distributions $P(r)$ and $P(\tau)$.

Priori Probability of Transmission (Continuous Case)

For the continuous time case,

$$
\begin{aligned}
T &= \langle T_{ij} \rangle \\
&= \int_0^\infty \int_0^\infty T_{ij} P(r,\tau)\, dr\, d\tau \\
&= \int_0^\infty \int_0^\infty (1 - e^{-r\tau}) P(r) P(\tau)\, dr\, d\tau \\
&= \int_0^\infty \int_0^\infty P(r) P(\tau)\, dr\, d\tau - \int_0^\infty \int_0^\infty P(r) P(\tau) e^{-r\tau}\, dr d\tau, \\
&= 1 - \int_0^\infty \int_0^\infty P(r) P(\tau) e^{-r\tau}\, dr d\tau.
\end{aligned}
$$

Priori Probability of Transmission (Discrete Case)

For the discrete time case,

$$
\begin{aligned}
T &= \langle T_{ij} \rangle \\
&= \int_0^\infty \sum_{\tau=0}^{\infty} P(r,\tau)[1-(1-r)^\tau]\, dr \\
&= \int_0^\infty \sum_{\tau=0}^{\infty} P(r)P(\tau)\, dr - \int_0^\infty \sum_{\tau=0}^{\infty} P(r)P(\tau)(1-r)^\tau\, dr \\
&= 1 - \int_0^\infty \sum_{\tau=0}^{\infty} P(r)P(\tau)(1-r)^\tau\, dr.
\end{aligned}
$$

Solving SIR on Networks with Arbitrary Degree Distribution

Degree Distribution & Distribution of Number of Occupied Edges

Percolation Problem

We would use the bond percolation and generating function methods to solve the percolation problem on random graphs with arbitrary degree distributions, to find the exact solutions for the typical size of outbreaks, presence of an epidemic, size of the epidemic (if there is one).

Generating Function of Degree Distribution

Assume that graphs are simply defined with certain degree distribution by giving the properly normalized probabilities p_k that randomly chosen vertex has degree k. We define a generating function for the *degree distribution*:

$$G_0(x) = \sum_{k=0}^{\infty} p_k x^k.$$

Properties of Generating Function

- Normality: $G_0(1) = \sum_k p_k = 1$.
- Reconstruction of the distribution by repeated differentiation:

$$p_k = \frac{1}{k!}\frac{d^k G_0}{dx^k}\bigg|_{x=0}.$$

- Moments: The mean degree z of a vertex is given by

$$z = \langle k \rangle = \sum_k k p_k = G_0'(1).$$

Higher moments of the distribution can be calculated from

$$\langle k^n \rangle = \sum_k k^n p_k = \left[\left(x\frac{d}{dx}\right)^n G_0(x)\right]\bigg|_{x=1}.$$

Degree Distribution of Vertices Reached by Following a Randomly Chosen Edge $\{q_k\}$

We also need a different generating function for the distribution of the degrees of vertices reached by following a randomly chosen edge. If we follow an edge to the vertex at one of its ends, then that vertex is more likely to be of high degree than is a randomly chosen vertex, since high-degree vertices have more edges attached to them than low-degree ones.

Proposition

Given a finite simple graph G consisting of n vertices whose degree distribution is $\{p_k\}_{k=0}^{n-1}$, the probability q_k that the vertex reached by following a randomly chosen edge has degree k is proportional to kp_k, i.e., $q_k \propto kp_k$.

Proof of Proposition: $q_k \propto kp_k$

Proof.

Observe that the number of vertices of degree k is np_k, then each vertex of degree k has knp_k edges attached to it. Each edge must connect two vertices, so each edge is counted twice when sum up knp_k over k, then the number of edges of G is

$$\frac{1}{2}\sum_{k=0}^{n-1} knp_k = \frac{n}{2}\sum_{k=0}^{n-1} kp_k.$$

Thus q_k can be obtained as follows,

$$q_k = \frac{knp_k}{2 \cdot \frac{n}{2}\sum_{k=0}^{n-1} kp_k} = \frac{kp_k}{\sum_{k=0}^{n-1} kp_k} = \alpha k p_k,$$

where $\alpha = 1/\sum_{k=0}^{n-1} kp_k$ is a constant. The proof is complete. □

Example

Given a simple graph as shown in Figure 1.

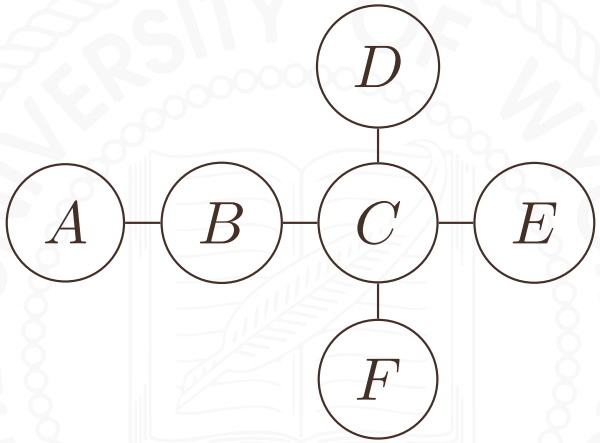

Figure 1:A simple graph of 6 vertices.

We can obtain the following degree distribution of randomly chosen vertex:

$$p_0 = p_3 = p_5 = 0, p_1 = \frac{2}{3}, p_2 = \frac{1}{6}, p_4 = \frac{1}{6} \Longrightarrow \sum_{k=0}^{5} kp_k = \frac{5}{3}.$$

Example

Then by the proof of Proposition 1, we have the following the number of edges connecting vertices of degree k as follows,

$$k = 1 : knp_k = 1 \times 6 \times p_1 = 1 \times 6 \times \frac{2}{3} = 4;$$

$$k = 2 : knp_k = 2 \times 6 \times p_2 = 2 \times 6 \times \frac{1}{6} = 2;$$

$$k = 4 : knp_k = 4 \times 6 \times p_4 = 4 \times 6 \times \frac{1}{6} = 4.$$

It follows that the total number of edges is

$$\frac{1}{2} \sum_{k=0}^{5} knp_k = \frac{4+2+4}{2} = 5.$$

Example

Then the corresponding distribution of degrees of the vertices reached by following edges is

$$q_1 = \frac{4}{2 \cdot 5} = \frac{2}{5} \implies \frac{q_1}{1 \cdot p_1} = \frac{2/5}{2/3} = \frac{3}{5},$$
$$q_2 = \frac{2}{2 \cdot 5} = \frac{1}{5} \implies \frac{q_2}{2 \cdot p_2} = \frac{1/5}{2 \cdot 1/6} = \frac{3}{5},$$
$$q_4 = \frac{4}{2 \cdot 5} = \frac{2}{5} \implies \frac{q_4}{4 \cdot p_4} = \frac{2/5}{4 \cdot 1/6} = \frac{3}{5}.$$

Calculating α

Here is another way to find the above α. By Proposition 1, assume that $\{q_k\}$ is the distribution of degrees of the vertices reached by following edges, then

$$q_k = \alpha k p_k,$$

where $\alpha \in \mathbb{R}$ is a constant. By normality of q_k,

$$1 = \sum_k q_k = \sum_k \alpha k p_k = \alpha \sum_k k p_k \implies \alpha = \frac{1}{\sum_k k p_k}.$$

Generating Function of Degree Distribution $\{q_k\}$

It follows that the generating function for the degrees of the vertices reached by following edges is

$$\sum_k q_k x^k = \alpha \sum_k k p_k x^k = \frac{\sum_k k p_k x^k}{\sum_k k p_k} = x \frac{\sum_k k p_k x^{k-1}}{\sum_k k p_k} = x \frac{G_0'(x)}{G_0'(1)}.$$

In general, we will be concerned with the number of ways leaving such a vertex *excluding* the edge we arrived along, which is the degree minus 1. To allow for this, we simply divide the function above by one power of x, thus arriving at a new generating function

$$G_1(x) = \frac{G_0'(x)}{G_0'(1)} = \frac{1}{z} G_0'(x),$$

where z is the average degree.

Distribution of Number of Occupied Edges $\{r_m\}$

In order to solve the percolation problem, we will also need generating functions $G_0(x;T)$ and $G_1(x;T)$ for the distribution of the number of *occupied* edges attached to a vertex, as a function of the transmissibility T. The probability of a vertex having exactly m of the k edges emerging from it occupied is given by the binomial distribution

$$\binom{k}{m} T^m (1-T)^{k-m}.$$

Then the probability of a vertex having exactly m edges emerging from it occupied is

$$r_m = \sum_{k=m}^{\infty} p_k \binom{k}{m} T^m (1-T)^{k-m}.$$

Generating Function of $\{r_m\}$

Hence the probability distribution of the number m of occupied edges attached to a vertex is generated by

$$\begin{aligned} G_0(x;T) &= \sum_{m=0}^{\infty} r_m x^m \\ &= \sum_{m=0}^{\infty} \sum_{k=m}^{\infty} p_k \binom{k}{m} T^m (1-T)^{k-m} x^m \\ &= \sum_{k=0}^{\infty} p_k \sum_{m=0}^{k} \binom{k}{m} (xT)^m (1-T)^{k-m} \\ &= \sum_{k=0}^{\infty} p_k (1-T+xT)^k \\ &= G_0(1+(x-1)T). \end{aligned}$$

Generating Function of $\{r_m\}$

For $G_0(x;T) = G_0(1+(x-1)T)$, we have the following:.

$$G_0(x;1) = G_0(x),$$
$$G_0(1;T) = G_0(1),$$
$$G_0(x;0) = G_0(1),$$
$$G_0'(1;T) = TG_0'(1).$$

Similarly, the probability distribution of occupied edges leaving a vertex arrived at by following a randomly chosen edge is generated by

$$G_1(x;T) = G_1(1+(x-1)T).$$

Outbreak Size Distribution

Generating Function of Outbreak Size

We want to find the distribution $P_s(T)$ of the sizes s of outbreaks of the disease on the network, which is also the distribution of sizes of clusters of vertices connected together by occupied edges in the corresponding percolation model. Let $H_0(x;T)$ be the generating function for the distribution:

$$H_0(x;T) = \sum_{s=0}^{\infty} P_s(T)x^s.$$

Generating Function of Outbreak Size

By analogy, we also define $H_1(x;T)$ to be the generating function for the cluster of connected vertices we reach by following a randomly chosen edge. H_1 can be broken down into an additive set of contributions as follows. The cluster reached by following an edge may be:

1. a single vertex with no occupied edges attached to it, other than the one alone which we passed in order to reach it;
2. a single vertex attached to any number $m \geq 1$ of occupied edges other than the one we reached it by, each leading to another cluster whose size distribution is also generated by H_1.

Generating Function of Outbreak Size

Note that the chance that any two finite clusters that are attached to the same vertex will have an edge connecting them together directly goes as N^{-1} with the size N of the graph, and hence zero in the limit of $N \to \infty$. In other words, there are no loops in our clusters; their structure is entirely *tree-like*. We can express $H_1(x;T)$ in a Dyson-equation-like self-consistent form thus:

$$H_1(x;T) = xG_1(H_1(x;T);T).$$

Then the size of the cluster reachable from a randomly chosen starting vertex is distributed according to

$$H_0(x;T) = xG_0(H_1(x;T);T).$$

Outbreak Sizes and the Epidemic Transition

We can find the mean outbreak size as follows,

$$\begin{aligned}
\langle s \rangle &= \frac{d}{dx} H_0(x;T)\Big|_{x=1} \\
&= \frac{d}{dx}[xG_0(H_1(x;T);T)]\Big|_{x=1} \\
&= G_0(H_1(x;T);T) + xG_0'(H_1(x;T);T)H_1'(x;T)\Big|_{x=1} \\
&= 1 + G_0'(1;T)H_1'(1;T).
\end{aligned}$$

Recall that $H_1(1;T) = 1$, $G_0(1;T) = G_0(1) = \sum_k p_k = 1$.

Outbreak Sizes and the Epidemic Transition

Taking derivative of $H_1(x;T) = xG_1(H_1(x;T);T)$ with respect to x yields,

$$\begin{aligned} H_1'(1;T) &= \frac{d}{dx} H_1(x;T)\Big|_{x=1} \\ &= \frac{d}{dx} xG_1(H_1(x;T);T)\Big|_{x=1} \\ &= G_1(H_1(x;T);T) + G_1'(H_1(x;T);T)H_1'(x;T)\Big|_{x=1} \\ &= 1 + G_1'(1;T)H_1'(1;T). \end{aligned}$$

That implies that

$$H_1'(1;T) = \frac{1}{1 - G_1'(1;T)}.$$

Outbreak Sizes and the Epidemic Transition

Since $G_i'(1;T) = TG_i'(T), i = 0, 1,$

$$\langle s \rangle = 1 + \frac{G_0'(1;T)}{1 - G_1'(1;T)} = 1 + \frac{TG_0'(1)}{1 - TG_1'(1)}.$$

The transition takes place when T is equal to the critical transmissibility T_c, given by

$$T_c = \frac{1}{G_1'(1)} = \frac{G_0'(1)}{G_0''(1)} = \frac{\sum_k kp_k}{\sum_k k(k-1)p_k} = \frac{\langle k \rangle}{\langle k^2 \rangle - \langle k \rangle}.$$

Recall that $G_1(x) = G_0'(x)/G_0'(1)$.

Outbreak Sizes and the Epidemic Transition

For $T > T_c$, we have an epidemic, or "giant component" in the language of percolation. Above the epidemic threshold, the equation $H_1(x;T) = xG_1(H_1(x;T);T)$ is no longer valid because the giant component is extensive and therefore can contain loops which destroys the assumption on which the equation was based.

The equation is valid however if we redefine H_0 to be the generating function only for outbreaks other than epidemic outbreaks, i.e., isolated clusters of vertices that are not connected to the giant component. Thus, above the epidemic transition, we have

$$H_0(1;T) = \sum_s P_s = 1 - S(T),$$

where $S(T)$ is the fraction of the population affected by the epidemic.

Outbreak Sizes and the Epidemic Transition

We find that the size of the epidemic is

$$S(T) = 1 - G_0(H_1(1, T); T) = 1 - G_0(u; T),$$

where $u = H_1(1; T)$ is the solution of the self-consistency relation

$$u = G_1(u; T).$$

Example of Disease Spreading

Define a Network of a Certain Degree Distribution

First, define a network of connections between individuals, which means choosing a degree distribution. Here we will consider graphs with the degree distribution

$$p_k = \begin{cases} 0 & \text{for } k = 0, \\ Ck^{-\alpha}e^{-k/\kappa} & \text{for } k \geq 1, \end{cases}$$

where $C = [\mathrm{Li}_\alpha(e^{-1/\kappa})]^{-1}$, α, and κ are constants, and

$$p_k = \frac{k^{-\alpha}e^{-k/\kappa}}{\mathrm{Li}_\alpha(e^{-1/\kappa})} \text{ for } k \geq 1,$$

where $\mathrm{Li}_n(x) = \sum_{k=1}^{\infty} \frac{x^k}{k^n}$ is the nth polylogarithm of x.

Generating Function of Degree Distribution $\{p_k\}$

Choose both $P(r)$ and $P(\tau)$ to be uniform distributions, $0 \leq r < r_{\max}$ and $1 \leq \tau \leq \tau_{\max}$. Then

$$\begin{aligned} G_0(x) &= \sum_{k=1}^{\infty} p_k x^k \\ &= \sum_{k=1}^{\infty} \frac{k^{-\alpha} e^{-k/\kappa} x^k}{\mathrm{Li}_\alpha(e^{-1/\kappa})} \\ &= \frac{1}{\mathrm{Li}_\alpha(e^{-1/\kappa})} \sum_{k=1}^{\infty} \frac{(xe^{-1/\kappa})^k}{k^\alpha} \\ &= \frac{\mathrm{Li}_\alpha(xe^{-1/\kappa})}{\mathrm{Li}_\alpha(e^{-1/\kappa})}. \end{aligned}$$

Generating Function of Degree Distribution $\{q_k\}$

In short,

$$G_0(x) = \frac{\mathrm{Li}_\alpha(xe^{-1/\kappa})}{\mathrm{Li}_\alpha(e^{-1/\kappa})}.$$

Then we have

$$\begin{aligned} G_0'(x) &= \frac{1}{\mathrm{Li}_\alpha(e^{-1/\kappa})} \frac{d}{dx} \sum_{k=1}^{\infty} \frac{(xe^{-1/\kappa})^k}{k^\alpha} \\ &= \frac{1}{x\,\mathrm{Li}_\alpha(e^{-1/\kappa})} \sum_{k=1}^{\infty} \frac{(xe^{-1/\kappa})^k}{k^{\alpha-1}} \\ &= \frac{\mathrm{Li}_{\alpha-1}(xe^{-1/\kappa})}{x\,\mathrm{Li}_\alpha(e^{-1/\kappa})}. \end{aligned}$$

Generating Function of Degree Distribution $\{q_k\}$

It follows that

$$G_0'(1) = \frac{\mathrm{Li}_{\alpha-1}(e^{-1/\kappa})}{\mathrm{Li}_{\alpha}(e^{-1/\kappa})}.$$

That implies

$$G_1(x) = \frac{G_0'(x)}{G_0'(1)} = \frac{\mathrm{Li}_{\alpha-1}(xe^{-1/\kappa})}{x\,\mathrm{Li}_{\alpha}(e^{-1/\kappa})} \frac{\mathrm{Li}_{\alpha}(e^{-1/\kappa})}{\mathrm{Li}_{\alpha-1}(e^{-1/\kappa})} = \frac{\mathrm{Li}_{\alpha-1}(xe^{-1/\kappa})}{x\,\mathrm{Li}_{\alpha-1}(e^{-1/\kappa})}.$$

Critical Transmissibility T_c

Moreover, taking derivative of $G_1(x)$ with respect to x yields

$$\begin{aligned} G_1'(x) &= \frac{1}{\mathrm{Li}_{\alpha-1}(e^{-1/\kappa})} \frac{d}{dx} \frac{\mathrm{Li}_{\alpha-1}(xe^{-1/\kappa})}{x} \\ &= \frac{1}{\mathrm{Li}_{\alpha-1}(e^{-1/\kappa})} \frac{x\,\mathrm{Li}'_{\alpha-1}(xe^{-1/\kappa}) - \mathrm{Li}_{\alpha-1}(xe^{-1/\kappa})}{x^2} \\ &= \frac{\mathrm{Li}_{\alpha-2}(xe^{-1/\kappa}) - \mathrm{Li}_{\alpha-1}(xe^{-1/\kappa})}{x^2\,\mathrm{Li}_{\alpha-1}(e^{-1/\kappa})}. \end{aligned}$$

Critical Transmissibility T_c

Thus the epidemic transition occurs at

$$\begin{aligned} T_c &= \frac{1}{G_1'(1)} \\ &= \frac{x^2 \operatorname{Li}_{\alpha-1}(e^{-1/\kappa})}{\operatorname{Li}_{\alpha-2}(xe^{-1/\kappa}) - \operatorname{Li}_{\alpha-1}(xe^{-1/\kappa})}\Big|_{x=1} \\ &= \frac{\operatorname{Li}_{\alpha-1}(e^{-1/\kappa})}{\operatorname{Li}_{\alpha-2}(e^{-1/\kappa}) - \operatorname{Li}_{\alpha-1}(e^{-1/\kappa})}. \end{aligned}$$

Mean Outbreak Size

Below this value of T there are only small (non-epidemic) outbreaks, which have mean outbreak size

$$\begin{aligned}\langle s\rangle &= 1+\frac{TG_0'(1)}{1-TG_1'(1)}\\ &= 1+\frac{T\frac{\mathrm{Li}_{\alpha-1}(e^{-1/\kappa})}{\mathrm{Li}_{\alpha}(e^{-1/\kappa})}}{1-T\frac{\mathrm{Li}_{\alpha-2}(e^{-1/\kappa})-\mathrm{Li}_{\alpha-1}(e^{-1/\kappa})}{\mathrm{Li}_{\alpha-1}(e^{-1/\kappa})}}\\ &= 1+\frac{T[\mathrm{Li}_{\alpha-1}(e^{-1/\kappa})]^2}{\mathrm{Li}_{\alpha}(e^{-1/\kappa})[(T+1)\,\mathrm{Li}_{\alpha-1}(e^{-1/\kappa})-T\,\mathrm{Li}_{\alpha-2}(e^{-1/\kappa})]}.\end{aligned}$$

Fraction S of Population Affected by the Epidemics

Above it, we are in the region in which epidemics can occur, and the affect a fraction S of the population in the limit of large graph size by solving the following numerically,

$$S(T) = 1 - G_0(u; T),$$

$$u = G_1(u; T).$$

Validity of the Model: Exact Solution vs. Simulation

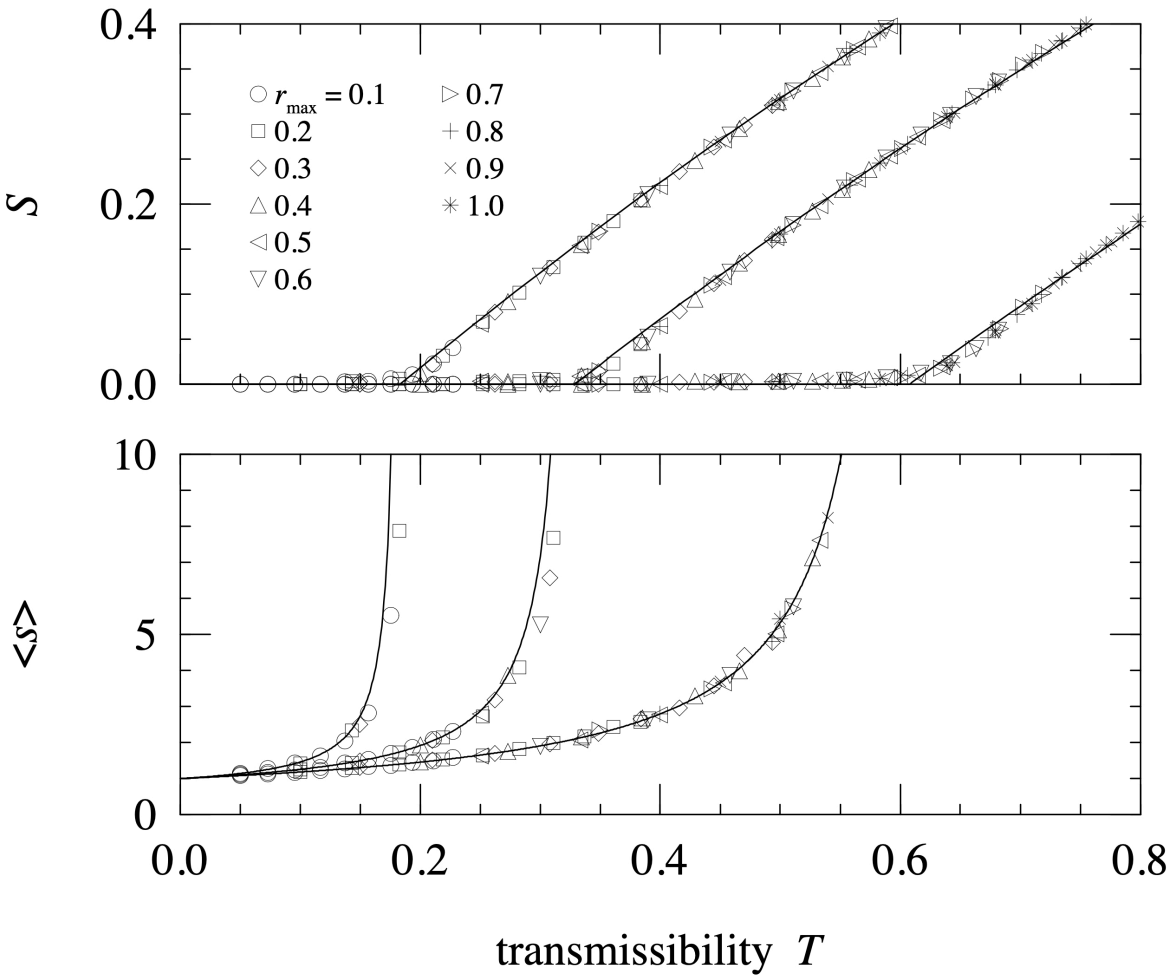

Figure 2:Exact Solution (solid line) vs. Simulation (points)

Questions?

Thank you!