Epidemics in Networks
SIR: $\mathcal{R}_0$ and Probability

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$\mathcal{R}_0$

Consequences of Percolation

Probability

References

$\mathcal{R}_0$

How would you calculate $\mathcal{R}_0$?

- It is actually more subtle than many realize.
- I have seen people with PhDs, who I respect, take a random node in the network, "infect" it, and check how many infections it would cause.
- They do this because people usually say "$\mathcal{R}_0$ is the number of infections caused by a single infected individual in a fully susceptible population."
- In fact to calculate $\mathcal{R}_0$, we must determine what a typical infected individual looks like early in the epidemic.

$\mathcal{R}_0$ SIR for Reed–Frost Configuration Model

- The probability a newly infected individual has degree k is $P_n(k)$.
- The expected number of infections it causes given k is $p(k-1)$ [it cannot reinfect the source of its infection].
- So

$$\mathcal{R}_0 = \sum_k P_n(k) p(k-1) = p \sum_k \frac{kP(k)(k-1)}{\langle K \rangle} = p \frac{\langle K^2 - K \rangle}{\langle K \rangle}$$

$\mathcal{R}_0$ for continuous time SIR on Configuration Model

- The only difference is that the probability of transmitting to each neighbor is $\beta/(\beta+\gamma)$ and the transmissions not independent.
- However, given k, the expected number of transmissions is still $k\beta/(\beta+\gamma)$
- So

$$\mathcal{R}_0 = \frac{\beta}{\beta+\gamma}\frac{\langle K^2 - K\rangle}{\langle K\rangle}$$

Comparison with simulation

Exercise

What happens if the degree distribution scales like:

$$P(k) \sim k^{-\alpha}$$

for what α are epidemics possible for any $\beta > 0$?

General SIR definition

For a general class of networks, we assume we can take arbitrarily large networks.

- We define I_r to be the number of infected individuals in "rank" or "generation" r.
- We take $\mathbb{E}(I_r)$ to be the expected value and define

$$\mathcal{R}_{0,r} = \frac{\mathbb{E}(I_{r+1})}{\mathbb{E}(I_r)}$$

- We need to let the epidemic run long enough that any residue of the initial infection is removed, but not so long that the disease starts to see that the network is finite.

$$\mathcal{R}_0 = \lim_{r\to\infty} \lim_{N\to\infty} \mathcal{R}_{0,r}$$

- In my experience $r = 2$ is close enough to infinity.

$\mathcal{R}_0$ for SIS

- The usual value given for $\mathcal{R}_0$ for an SIS epidemic is
$$\mathcal{R}_0 = \frac{\beta}{\gamma}\frac{\langle K^2\rangle}{\langle K\rangle}$$
Which is very close to what we find in the SIR model.
- This is only correct for an annealed network. If used for a Configuration Model network (as it usually is), there are errors
- High degree nodes can form a local island of infection that lasts a long time, occassionally causing a chain of infection that reaches another high degree node [1], resulting in physicists making errors.

- Assume partnerships change quickly, so that every transmission is to a new individual.
- The probability a newly infected node has degree k is $P_n(k)$.
- Each stub transmits on average β/γ times, each transmission is to a new individual.
- So
$$\mathcal{R}_0 = \sum_k P_n(k)k\beta/\gamma = \frac{\beta}{\gamma}\sum \frac{kP(k)}{\langle K\rangle}k = \frac{\beta}{\gamma}\frac{\langle K^2\rangle}{\langle K\rangle}$$
- This calculation also applies to SIR for the annealed model

$\mathcal{R}_0$

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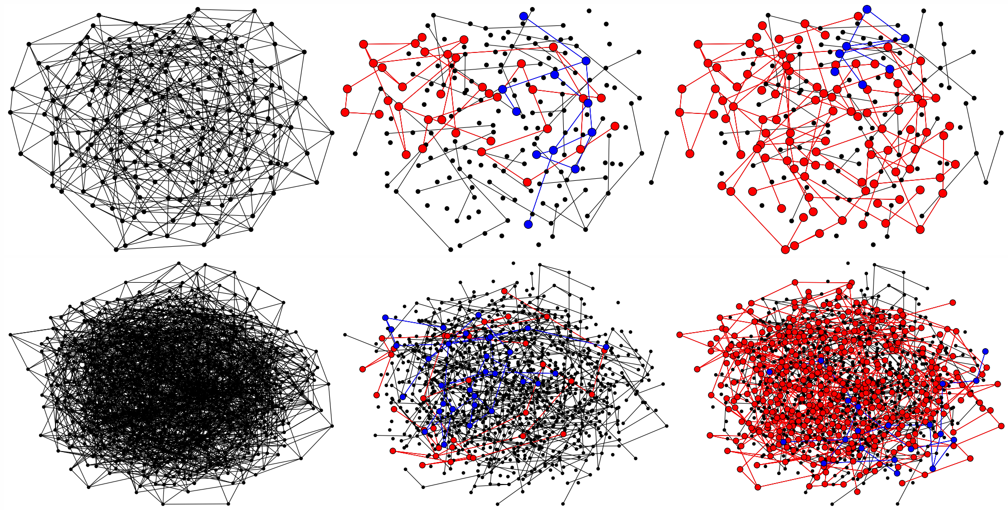
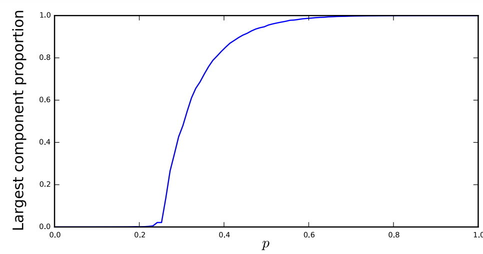
Reed–Frost

We can understand the Reed–Frost model as an application of percolation.
So to understand the epidemic spread, let's look at percolation.
Consider configuration model networks with $P(5) = 1$: all nodes have degree 5.





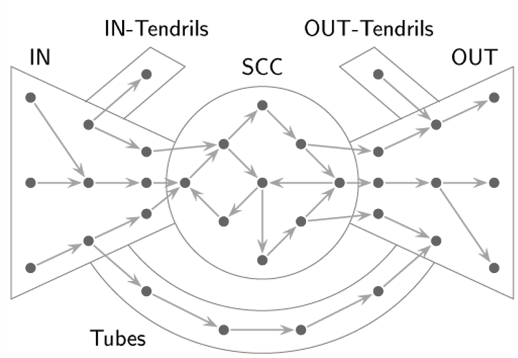
Observations

- Below a threshold, the largest component is small compared to the network.
- Its size is fairly independent of network size (I think it's perhaps logarithmic)
- Above a threshold, the largest component is proportional to network size. It is called the Giant Component.
- The size of the giant component is remarkably uniform across different realizations.
- All other components are small compared to the networks.

Consequences

- The eventually infected nodes are exactly the nodes in the same component as the index case.
- An epidemic happens iff the index case is in the giant component: $\mathcal{P}$ equals the expected proportion in the giant component
- If an epidemic happens, the entire giant component is infected: the $\mathcal{A}$ equals the expected proportion in the giant component.
- Thus for Reed–Frost epidemics, $\mathcal{P} = \mathcal{A}$.

Directed case



The Network of Global Corporate Control, PLoS One, 2011

- Above a threshold there is a Giant Strongly Connected Component G_{SCC}
- It has an in-component G_{IN} and an out-component G_{OUT}.
- If the index case is in G_{IN} or G_{SCC} then all of G_{SCC} and G_{OUT} are eventually infected.
- So $\mathcal{P} = \mathbb{E}(|G_{IN} \cup G_{SCC}|)/N$ and $\mathcal{A} = \mathbb{E}(|G_{SCC} \cup G_{OUT}|)/N$.
- There is a symmetry between $\mathcal{P}$ and $\mathcal{A}$: for each disease, there exists a symmetric disease which has $\mathcal{P}$ and $\mathcal{A}$ interchanged.

Example/exercise

Consider a configuration model network of 1000 nodes, all nodes having degree 6.

- Estimate $\mathcal{P}$ and $\mathcal{A}$ by simulating an epidemic with each edge transmitting independently with probability $p = 0.5$.
- Repeat, but this time half of the population is immune and the other half are guaranteed to become infected if a partner becomes infected.
- Repeat, but this time half of the population do not transmit and the other half are guaranteed to transmit to all of their partners if they become infected.

Now take a $10 \times 10 \times 10$ periodic cubic lattice [in `networkx` this is `grid_graph([10,10,10],periodic=True)`]. Repeat the steps above.
What cases minimize or maximize $\mathcal{P}$ and $\mathcal{A}$?

Rigorous bounds on $\mathcal{P}$, $\mathcal{A}$

Assume that a node's infectiousness and susceptibility are unrelated to one another.
Holding the average transmission probability p fixed:

- $\mathcal{P}$ and $\mathcal{A}$ are both maximized (and equal) if the transmission probability is p for every edge.
- If the network has very few short cycles:
  - $\mathcal{P}$ depends only on distribution of infectiousness, and is minimized when p transmit to all partners and $1 - p$ to none.
  - $\mathcal{A}$ depends only on distribution of susceptibility, and is minimized when p are infected if any partner infected and $1 - p$ never infected.
- If short cycles are allowed: Increasing heterogeneity can only reduce $\mathcal{P}$ and $\mathcal{A}$.

$\mathcal{R}_0$

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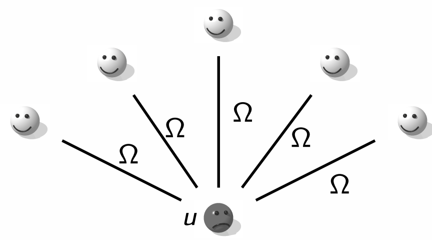
Probability Calculation Outline

We can exactly calculate the probability of an epidemic in Configuration Model networks.

- Calculate the probability that index case leads to "self-limiting" outbreak.
- Do this by calculating probability that all infections caused by index case lead to self-limiting outbreak.
- Will result in a consistency equation.
- We define $\psi(x) = \sum_k P(k)x^k$.

Calculating epidemic probability



$\Omega = P(u \text{ does not transmit to a neighbor}) + P(u \text{ transmits, but neighbor doesn't lead to an epidemic})$

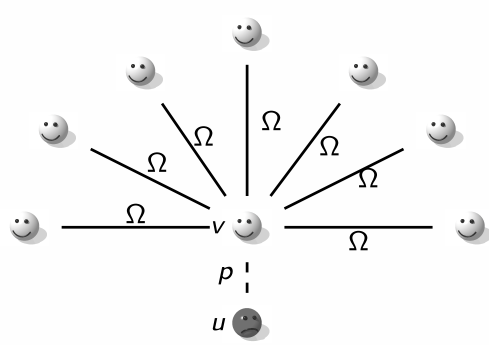
Probability a random ~~degree k~~ index case does not start an epidemic is

$$1 - \mathcal{P} = \sum_k P(k)\Omega^k = \psi(\Omega)$$

where

$$\psi(x) = \sum_k P(k)x^k$$

Finding Ω



Probability a random partner of the index case ~~having degree $\hat{k}$~~ does not start an epidemic is

$$\Omega = [1 - p] + p\frac{\psi'(\Omega)}{\langle K \rangle}$$

Calculating epidemic probability

We arrive at

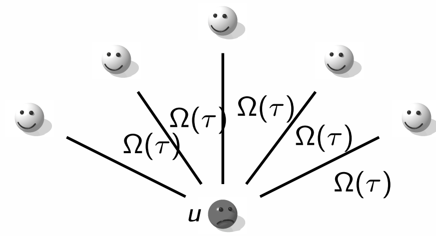
$$1 - \mathcal{P} = \psi(\Omega)$$
$$\Omega = 1 - p + p\frac{\psi'(\Omega)}{\langle K \rangle}$$

In general we can only solve this numerically, but it is straightforward: We guess $\Omega_0 = 0$ and iterate.

Continuous time case

Now consider the case with transmission at rate β and recovery at rate γ.

Calculating epidemic probability



$\Omega(\tau) = P(u \text{ does not transmit to a neighbor}|\tau) + P(u \text{ transmits, but neighbor doesn't lead to an epidemic})$

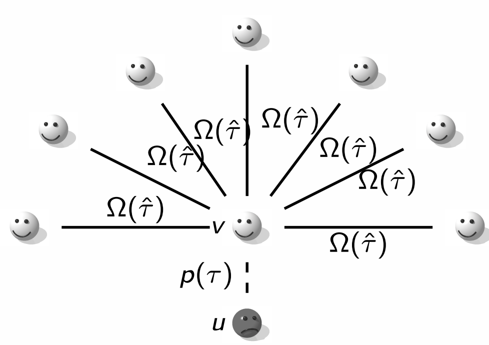
Probability a random ~~degree k~~ index case ~~whose infection duration is τ~~ does not start an epidemic is

$$1-\mathcal{P} = \int_0^\infty \gamma e^{-\gamma\tau} \sum_k P(k)\Omega(\tau)^k \,\mathrm{d}\tau = \int_0^\infty \gamma e^{-\gamma\tau} \psi(\Omega(\tau)) \,\mathrm{d}\tau$$

where

$$\psi(x) = \sum_k P(k) x^k$$

Finding Ω



Probability a random partner of the index case ~~having degree $\hat{k}$ whose infection duration is $\hat{\tau}$~~ does not start an epidemic is

$$\Omega(\tau) = [1 - p(\tau)] + p(\tau) \int_0^\infty \gamma e^{-\gamma\hat{\tau}} \frac{\psi'(\Omega(\hat{\tau}))}{\langle K \rangle} \,\mathrm{d}\hat{\tau}$$

$p(\tau)$ is the probability of transmitting given infection duration of τ

Calculating epidemic probability

We arrive at

$$1 - \mathcal{P} = \int_0^\infty \gamma e^{-\gamma\tau} \psi(\Omega(\tau))\, \mathrm{d}\tau$$

$$\Omega(\tau) = 1 - p(\tau) + p(\tau) \int_0^\infty \gamma e^{-\gamma\hat{\tau}} \frac{\psi'(\Omega(\hat{\tau}))}{\langle K \rangle}\, \mathrm{d}\hat{\tau}$$

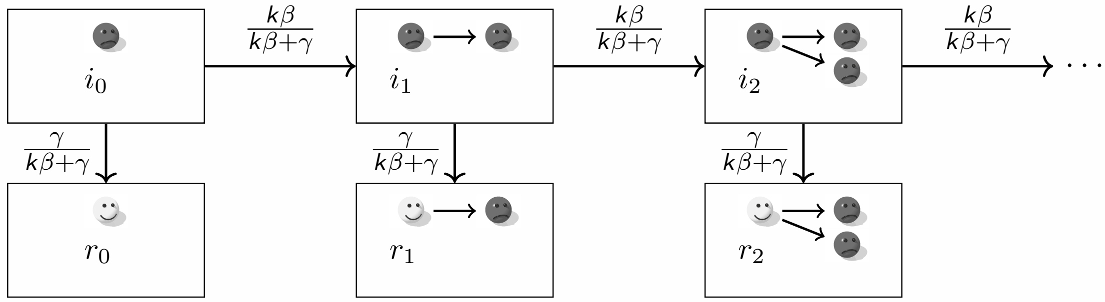
In general we can only solve this numerically, but it is straightforward.

SIS

I don't think anyone has a good calculation of epidemic probability for static networks.

- If we take static networks and assume that nodes cannot transmit back to their infector, then the derivation we did above works.
- Alternately, we can make progress with annealed networks.

SIS epidemic probability on annealed networks



Consider an individual u with degree k who becomes infected at time $t = 0$.

- The probability of transmitting at least once before recovering is $k\beta/(k\beta + \gamma)$.
- The probability of transmitting at least m times is $[k\beta/(k\beta + \gamma)]^m$.
- For exactly m times it is

$$\left(\frac{k\beta}{k\beta + \gamma}\right)^m \frac{\gamma}{k\beta + \gamma}$$

SIS probability

The probability of an infected partner not starting an epidemic is

$$\begin{aligned}
\hat{\Omega} &= \sum_{\hat{k}} \left(P_n(\hat{k}) \sum_m \left[\frac{\hat{k}\beta}{\hat{k}\beta + \gamma}\right]^m \frac{\gamma}{\hat{k}\beta + \gamma} \hat{\Omega}^m \right) \\
&= \sum_{\hat{k}} \left(P_n(\hat{k}) \frac{\gamma}{\hat{k}\beta + \gamma} \sum_m \left[\frac{\hat{k}\beta}{\hat{k}\beta + \gamma}\right]^m \hat{\Omega}^m \right) \\
&= \sum_{\hat{k}} \left(P_n(\hat{k}) \frac{\gamma}{\hat{k}\beta + \gamma} \frac{\hat{k}\beta + \gamma}{\hat{k}\beta + \gamma - \hat{k}\beta\hat{\Omega}} \right) \\
&= \sum_{\hat{k}} P_n(\hat{k}) \frac{\gamma}{\hat{k}\beta(1 - \hat{\Omega}) + \gamma}
\end{aligned}$$

SIS probability

So we find

$$1 - \mathcal{P} = \sum_k P(k) \frac{\gamma}{\hat{k}\beta(1 - \hat{\Omega}) + \gamma}$$
$$\hat{\Omega} = \sum_k P_n(k) \frac{\gamma}{\hat{k}\beta(1 - \hat{\Omega}) + \gamma}$$

References I

[1] S. Chatterjee and R. Durrett.
Contact processes on random graphs with power law degree distributions have critical value 0.
The Annals of Probability, 37(6):2332–2356, 2009.