

Percolation approaches to disease spread

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SIR and percolation

SIS disease

Last details

References

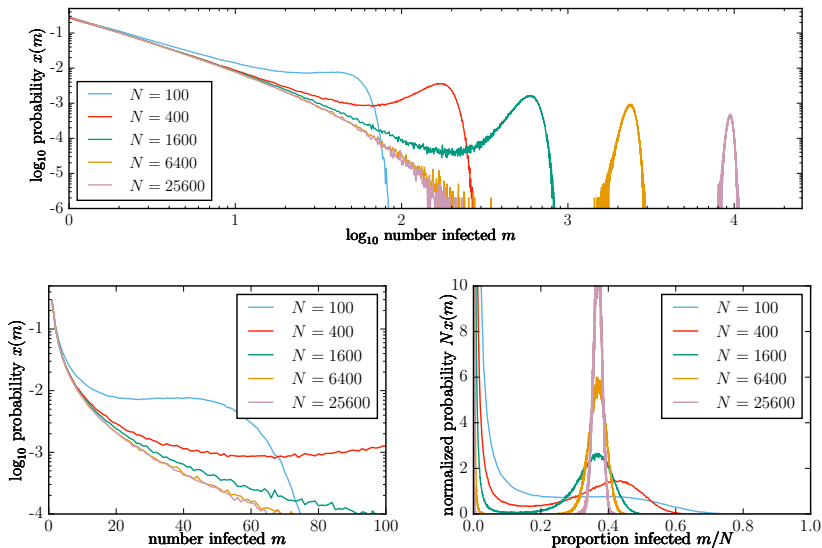
Percolation

We are going to explore a relationship between SIR disease and percolation.

This will lead to methods to

- ▶ predict epidemic probability from a single infection.
- ▶ predict final size of an epidemic.
- ▶ predict the dynamics of an epidemic.

Recall SIR behavior



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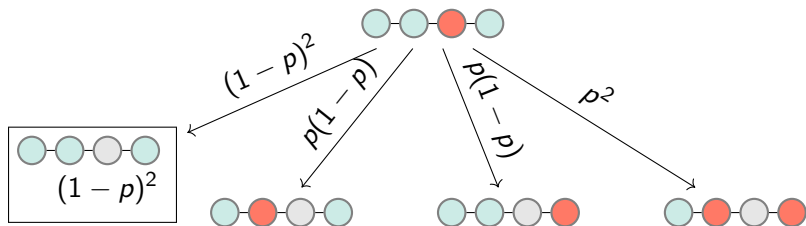
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- ▶ Warning — no longer assuming continuous time

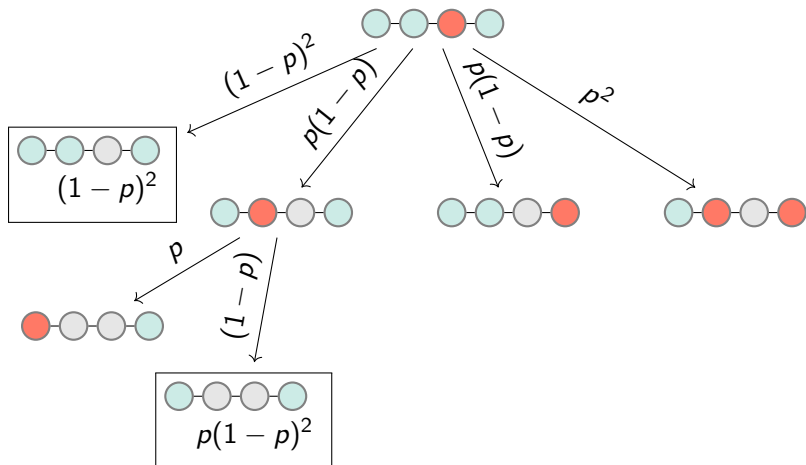
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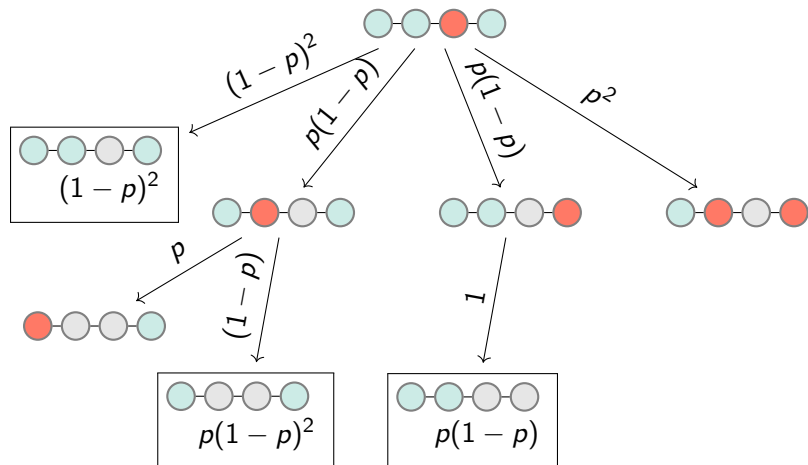
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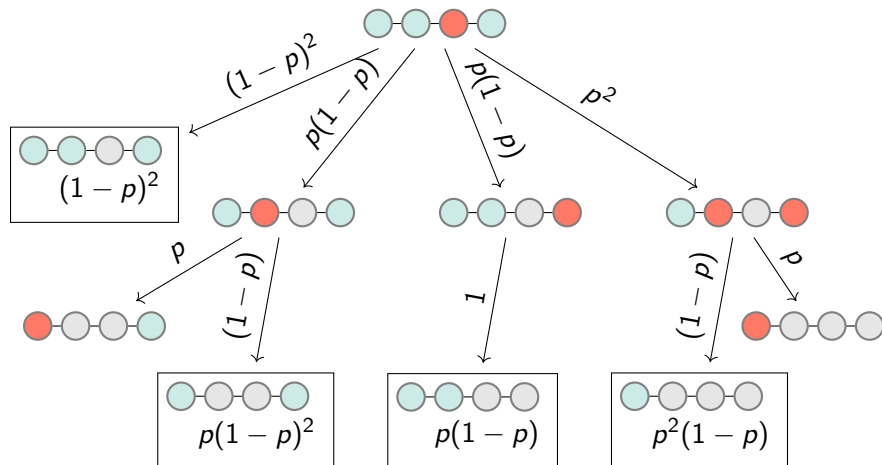
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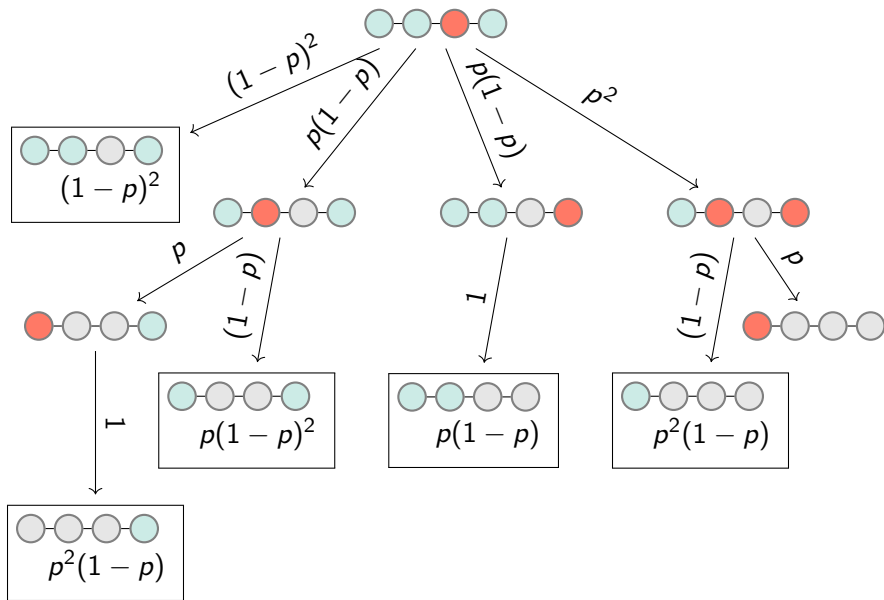
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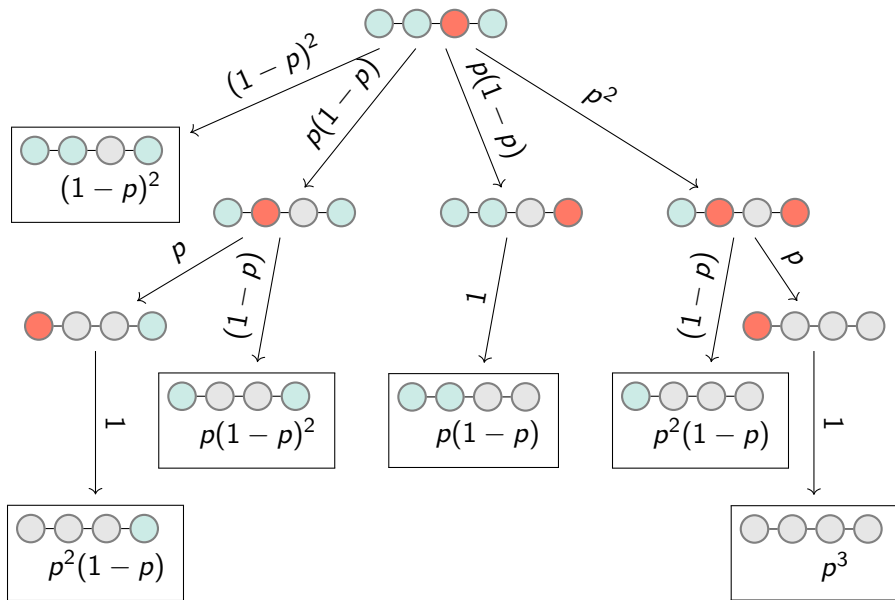
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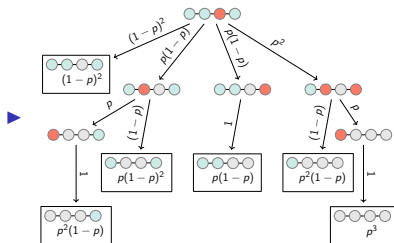
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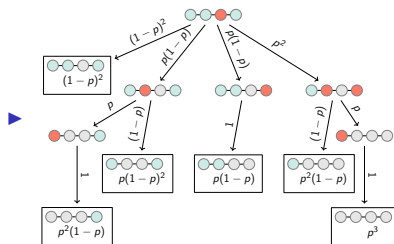


Alternative perspective



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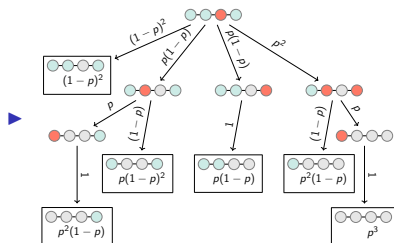
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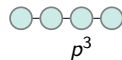
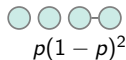
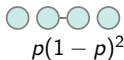
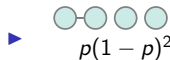
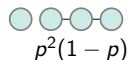
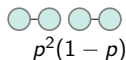
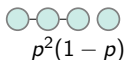
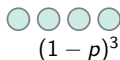
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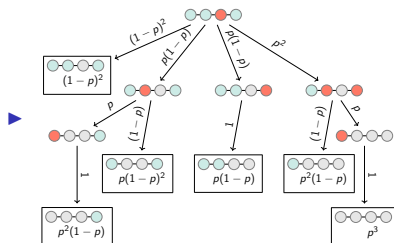


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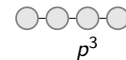
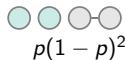
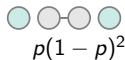
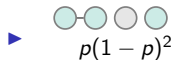
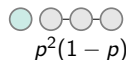
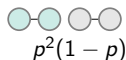
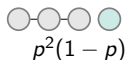
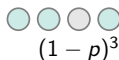


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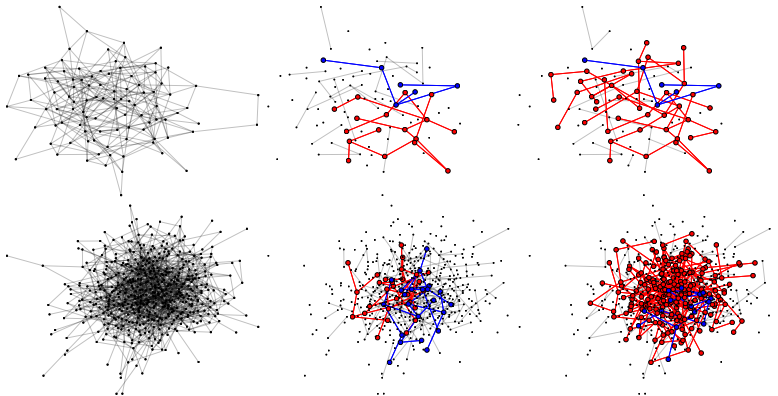
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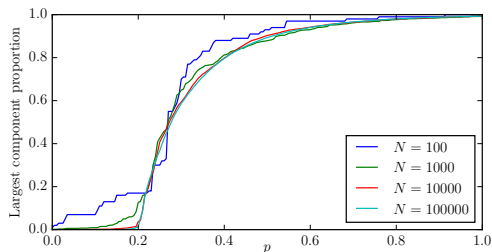
Percolation in different size networks

Comparison of largest (red) and second largest (blue) components in different size networks below and above percolation threshold.

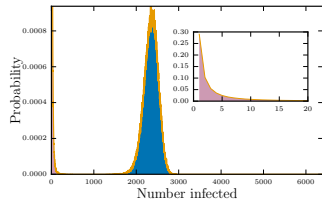
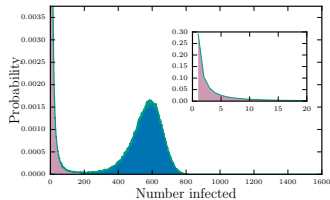
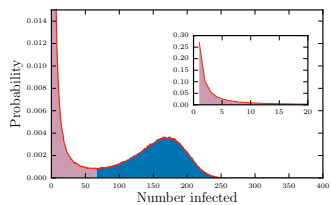
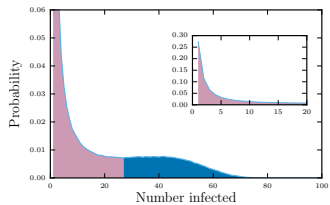


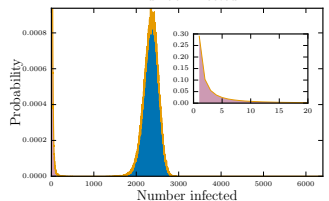
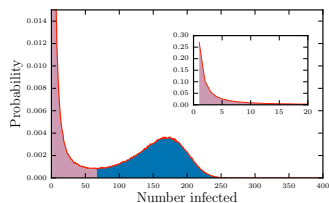
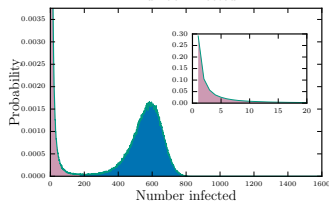
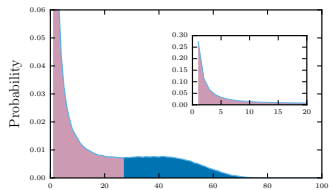
- ▶ Below threshold largest and second largest in a network are about the same size as each other and similar size in both networks
- ▶ Above threshold largest is proportional to network size.

More detailed comparison of network size



- ▶ Above the threshold, an epidemic occurs if the initial node is in the giant component.
- ▶ The entire component containing the index is infected.
- ▶ For a large network with given p , the giant component's size is remarkably consistent. So the probability of an epidemic equals the proportion infected.





N	\mathcal{P}	\mathcal{A}
100	0.237	0.423
400	0.340	0.387
1600	0.339	0.350
6400	0.365	0.366
25600	0.368	0.368

Now return back to transmitting with rate β and recovering with rate γ .

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- ▶ Transmission is at rate β , and recovery is at rate γ . The probability of transmitting before recovering is $\beta/(\beta + \gamma)$.
- ▶ Note: v transmitting to u and to w are correlated events (both depend on duration of v 's infection), but transmissions from different nodes to a single node are independent.

Directed percolation analogy

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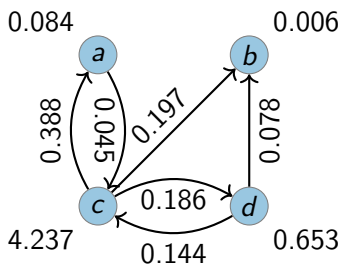
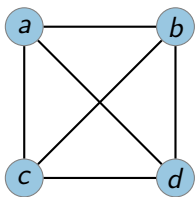
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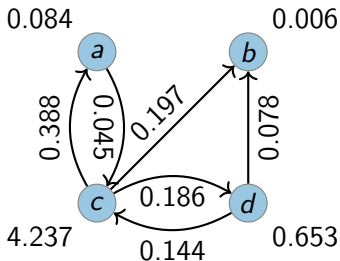
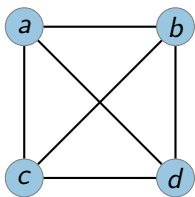
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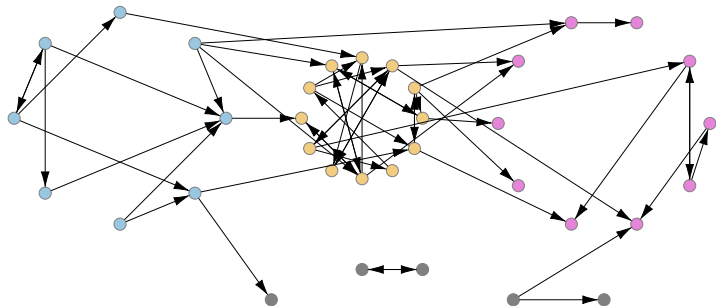
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 - ▶ Then he reports those to me when I ask.
- ▶ Is it possible for me to know whether he is calculating in advance or not?





Every number that Tom gives me is a random number that is generated independently of every other number. It doesn't matter when he generates it.

Typical structure



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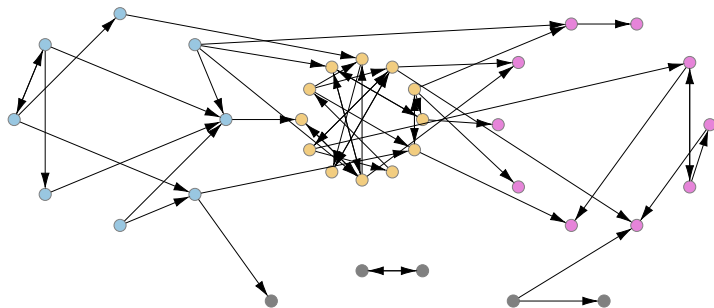
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 - ▶ Choose an initial infected individual.
 - ▶ Trace the disease spread following edges in H , transmitting after the given time.

Comments on directed percolation

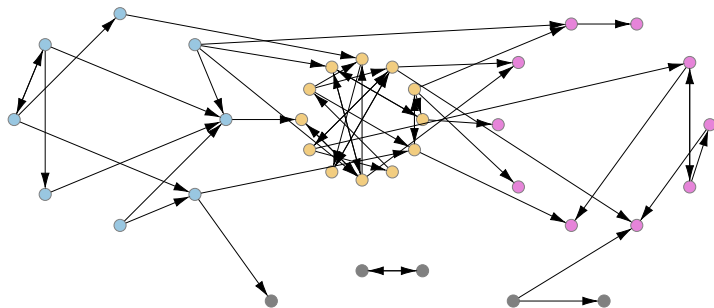
- ▶ Directed percolation can be used more generally when there are other sources of heterogeneity in infectiousness and/or susceptibility.
- ▶ The eventually infected nodes are exactly those nodes in the out-component of the index case.
- ▶ The probability a random node is infected follows from the size of its in-component.

Typical structure



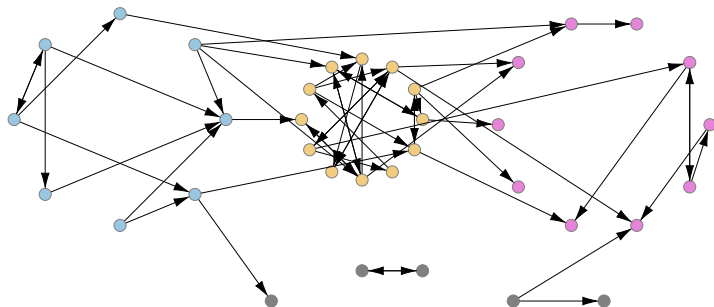
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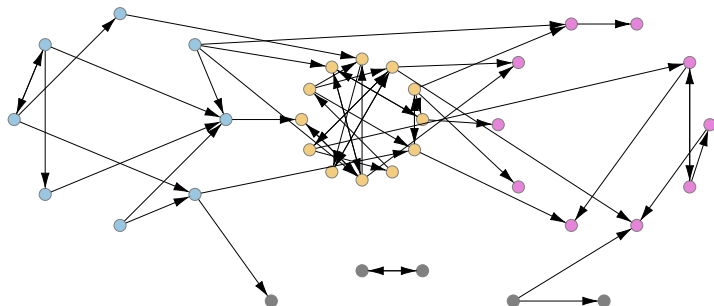
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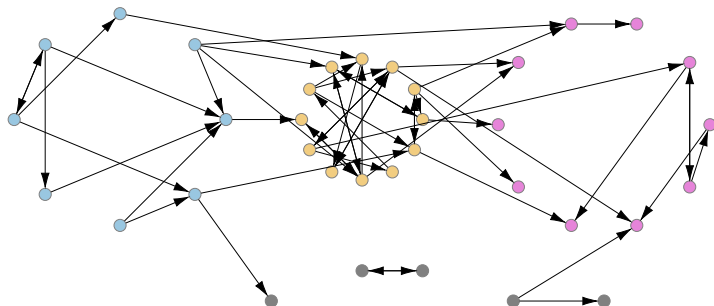
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- ▶ It has an in-component H_{IN} and an out-component H_{OUT} .
- ▶ If the index case is in H_{IN} or H_{SCC} then all of H_{SCC} and H_{OUT} are eventually infected.
- ▶ So Epidemic Probability $\mathcal{P} = \mathbb{E}(|H_{IN} \cup H_{SCC}|)/N$ and Attack rate $\mathcal{A} = \mathbb{E}(|H_{SCC} \cup H_{OUT}|)/N$.

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- ▶ The probability of an epidemic is the proportion of nodes from which there is a long chain of transmissions in H .
- ▶ The final size of an epidemic with a **very small** initial proportion infected is the proportion of nodes which are the target of a long chain of transmissions in H .

SIR epidemics in Configuration Model networks

- ▶ Consider a Configuration Model network in which we infect a (probably small) fraction of the population ρ .
- ▶ Allow the SIR disease to spread.
- ▶ We assume ρN is large enough that stochastic die-out does not play a major role.

Recall our key questions

For SIR:

- ▶ \mathcal{P} , the probability of an epidemic.
- ▶ \mathcal{A} , the “attack rate”: the fraction infected if an epidemic happens (better named the attack ratio).
- ▶ \mathcal{R}_0 , the average number of infections caused by those infected early in the epidemic.
- ▶ $I(t)$, the time course of the epidemic.

For SIS:

- ▶ \mathcal{P}
- ▶ $I(\infty)$, the equilibrium level of infection
- ▶ \mathcal{R}_0
- ▶ $I(t)$

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$$\begin{aligned}\mathcal{R}_0 &= \mathbb{E}(\text{number infections caused} | \text{infected early}) \\ &= \sum_k P(k | \text{infected early}) \mathbb{E}(\text{number infections} | k) \\ &= \sum_k P_n(k) (k-1) \frac{\beta}{\beta+\gamma} \\ &= \frac{\beta}{\beta+\gamma} \sum_k \frac{kP(k)(k-1)}{\langle K \rangle}\end{aligned}$$

\mathcal{R}_0 calculation

For SIR disease:

- ▶ The probability a newly infected individual has degree k is $P_n(k)$.
- ▶ The expected number of infections it causes given k is $(k-1)\frac{\beta}{\beta+\gamma}$ [it cannot reinfect the source of its infection].
- ▶ So

$$\begin{aligned}\mathcal{R}_0 &= \mathbb{E}(\text{number infections caused} | \text{infected early}) \\ &= \sum_k P(k | \text{infected early}) \mathbb{E}(\text{number infections} | k) \\ &= \sum_k P_n(k) (k-1) \frac{\beta}{\beta+\gamma} \\ &= \frac{\beta}{\beta+\gamma} \sum_k \frac{kP(k)(k-1)}{\langle K \rangle} \\ &= \frac{\beta}{\beta+\gamma} \frac{\langle K^2 - K \rangle}{\langle K \rangle}\end{aligned}$$

Recall our key questions

For SIR:

- ▶ \mathcal{P} , the probability of an epidemic.
- ▶ \mathcal{A} , the “attack rate”: the fraction infected if an epidemic happens (better named the attack ratio).
- ▶ \mathcal{R}_0 , the average number of infections caused by those infected early in the epidemic.
- ▶ $I(t)$, the time course of the epidemic.

For SIS:

- ▶ \mathcal{P}
- ▶ $I(\infty)$, the equilibrium level of infection
- ▶ \mathcal{R}_0
- ▶ $I(t)$

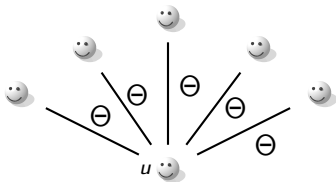
Changing the final size question

Instead of asking what proportion end up susceptible or recovered ask:

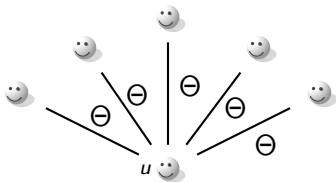
Changing the final size question

Instead of asking what proportion end up susceptible or recovered ask:

What is the probability a random node does not have a transmission path to it from one of the index nodes?



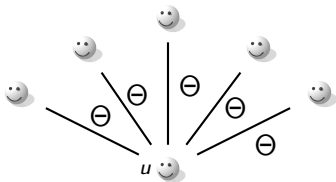
$$\Theta = P(v \text{ did not transmit to } u)$$



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Probability a random degree k test individual is susceptible at the end is

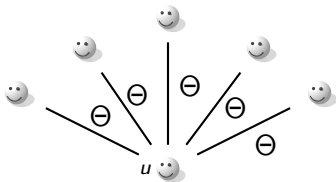
$$(1 - \rho)\Theta^k$$



$$\Theta = P(v \text{ did not transmit to } u)$$

Probability a random ~~degree- k~~ test individual is susceptible at the end is

$$\frac{S}{N} = \sum_k P(k)(1 - \rho)\Theta^k$$



$$\Theta = P(v \text{ did not transmit to } u)$$

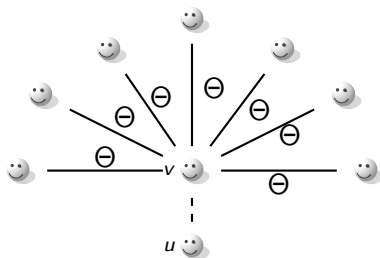
Probability a random ~~degree- k~~ test individual is susceptible at the end is

$$\frac{S}{N} = \sum_k P(k)(1 - \rho)\Theta^k = (1 - \rho)\psi(\Theta)$$

where

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

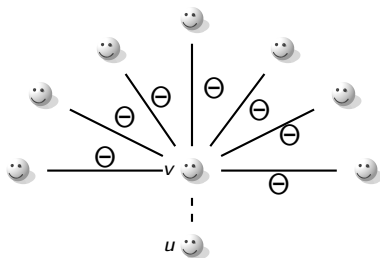
Finding Θ



Probability a random degree k partner never infected is

$$(1 - \rho)\Theta^{k-1}$$

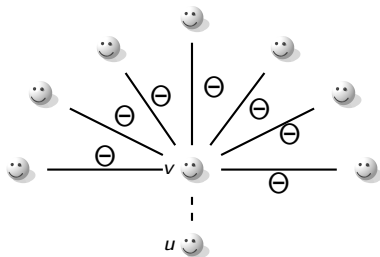
Finding Θ



Probability a random ~~degree- k~~ partner never infected is

$$\phi_S = \sum_k P_n(k)(1 - \rho)\Theta^{k-1}$$

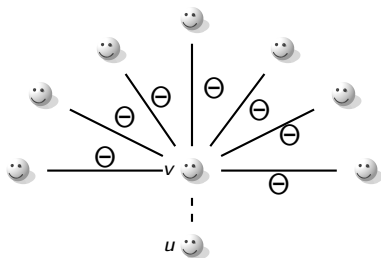
Finding Θ



Probability a random ~~degree- k~~ partner never infected is

$$\phi_S = \sum_k \frac{kP(k)}{\langle K \rangle} (1 - \rho) \Theta^{k-1}$$

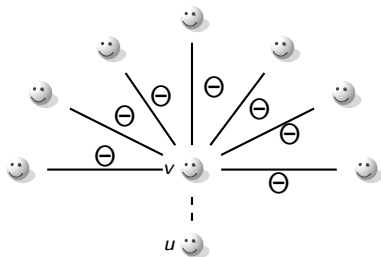
Finding Θ



Probability a random ~~degree- k~~ partner never infected is

$$\phi_S = \sum_k \frac{kP(k)}{\langle K \rangle} (1 - \rho) \Theta^{k-1} = (1 - \rho) \frac{\psi'(\Theta)}{\langle K \rangle}$$

Finding Θ



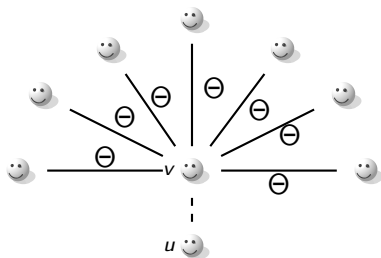
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Given β and γ , partner does not transmit to u with probability

$$\Theta = \phi_S + \left(1 - \frac{\beta}{\beta + \gamma}\right) (1 - \phi_S)$$

Finding Θ



Probability a random ~~degree- k~~ partner never infected is

$$\phi_S = \sum_k \frac{kP(k)}{\langle K \rangle} (1 - \rho) \Theta^{k-1} = (1 - \rho) \frac{\psi'(\Theta)}{\langle K \rangle}$$

Given β and γ , partner does not transmit to u with probability

$$\Theta = \phi_S + \left(1 - \frac{\beta}{\beta + \gamma}\right) (1 - \phi_S) = 1 - \frac{\beta}{\beta + \gamma} + \frac{\beta}{\beta + \gamma} \frac{(1 - \rho) \psi'(\Theta)}{\langle K \rangle}$$

Final Size

So

$$\mathcal{A} = 1 - (1 - \rho)\psi(\Theta)$$

where

$$\Theta = \frac{\gamma}{\beta + \gamma} + \frac{\beta}{\beta + \gamma}(1 - \rho)\frac{\psi'(\Theta)}{\langle K \rangle}$$

Final Size

So

$$\mathcal{A} = 1 - (1 - \rho)\psi(\Theta)$$

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$$\Theta = \frac{\gamma}{\beta + \gamma} + \frac{\beta}{\beta + \gamma}(1 - \rho)\frac{\psi'(\Theta)}{\langle K \rangle}$$

A more rigorous definition would be that Θ is the probability that the given edge isn't the final edge of a directed path from an index node to u in the percolated network H .

Recall our key questions

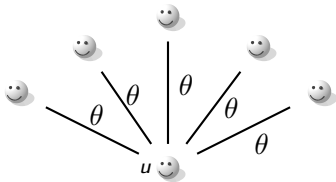
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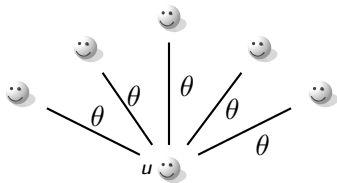
- ▶ \mathcal{P}
- ▶ $I(\infty)$, the equilibrium level of infection
- ▶ \mathcal{R}_0
- ▶ $I(t)$

Finding $S(t)$ for SIR disease



$$\theta(t) = P(v \text{ not yet transmitted to } u)$$

Finding $S(t)$ for SIR disease

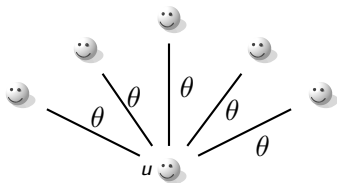


$$\theta(t) = P(v \text{ not yet transmitted to } u)$$

Probability a random degree k test individual still susceptible is

$$(1 - \rho)\theta(t)^k$$

Finding $S(t)$ for SIR disease

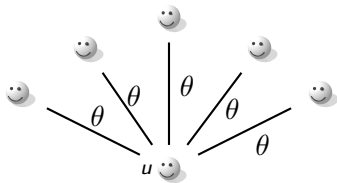


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$$\frac{S(t)}{N} = \sum_k P(k)(1 - \rho)\theta(t)^k$$

Finding $S(t)$ for SIR disease



$$\theta(t) = P(v \text{ not yet transmitted to } u)$$

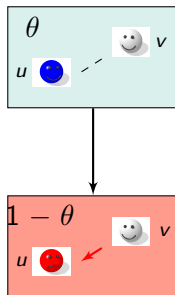
Probability a random ~~degree- k~~ test individual still susceptible is

$$\frac{S(t)}{N} = \sum_k P(k)(1 - \rho)\theta(t)^k = (1 - \rho)\psi(\theta(t))$$

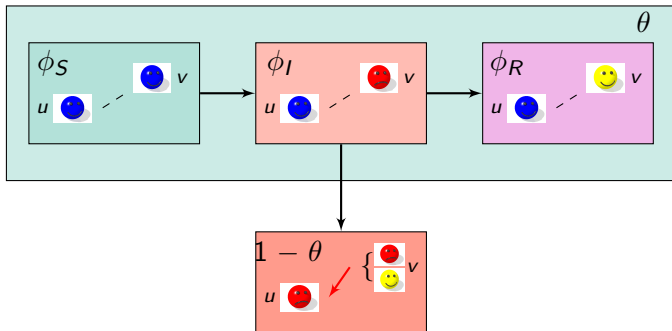
where

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

How does θ evolve?

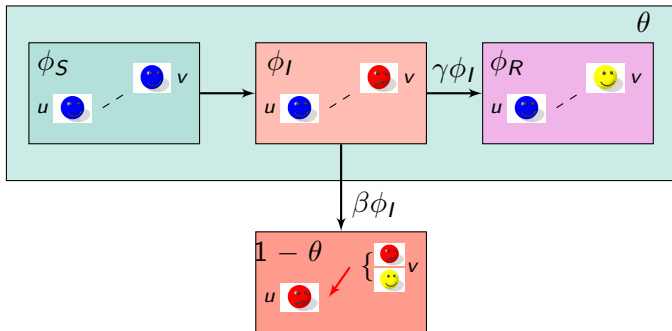


How does θ evolve?



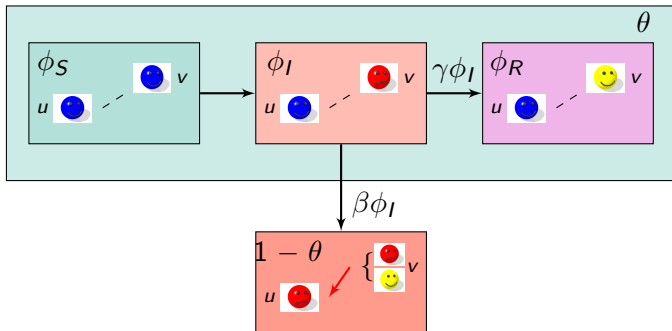
► $\theta = \phi_S + \phi_I + \phi_R.$

How does θ evolve?



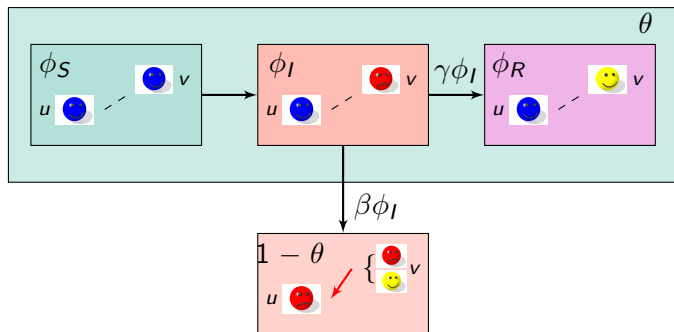
- ▶ $\theta = \phi_S + \phi_I + \phi_R$.
- ▶ $\dot{\theta} = -\beta\phi_I$.

How does θ evolve?



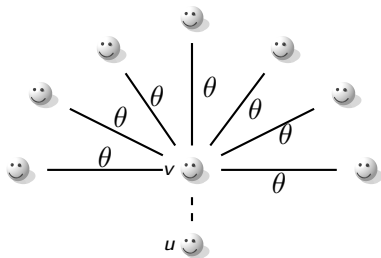
- ▶ $\theta = \phi_S + \phi_I + \phi_R$.
- ▶ $\dot{\theta} = -\beta\phi_I$.
- ▶ Our goal is to find ϕ_I in terms of θ .

Finding $\phi_R(t)$



Because derivatives are proportional, $\phi_R = \frac{\gamma}{\beta}(1 - \theta)$

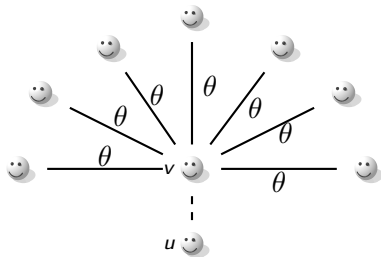
Finding $\phi_S(t)$



Probability a random degree k partner still susceptible is

$$(1 - \rho)\theta(t)^{k-1}$$

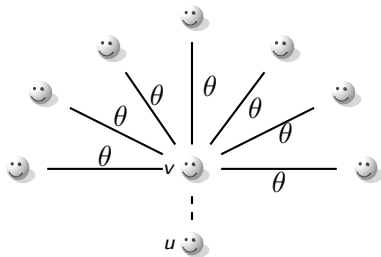
Finding $\phi_S(t)$



Probability a random ~~degree- k~~ partner still susceptible is

$$\phi_S(t) = \sum_k P_n(k) (1 - \rho) \theta(t)^{k-1}$$

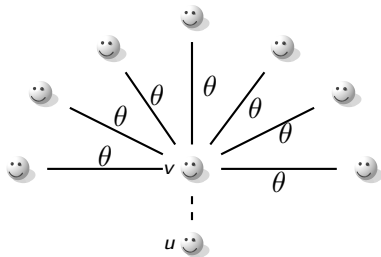
Finding $\phi_S(t)$



Probability a random ~~degree- k~~ partner still susceptible is

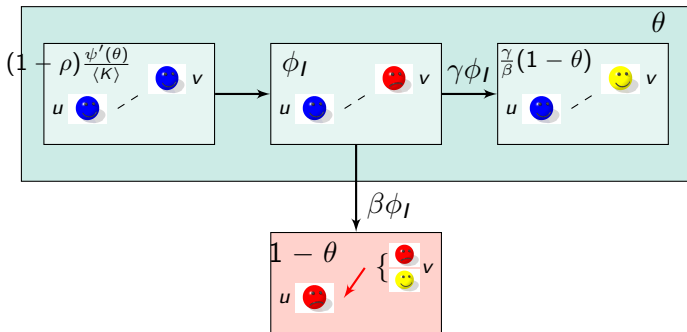
$$\phi_S(t) = \sum_k \frac{kP(k)}{\langle K \rangle} (1 - \rho) \theta(t)^{k-1}$$

Finding $\phi_S(t)$



Probability a random ~~degree- k~~ partner still susceptible is

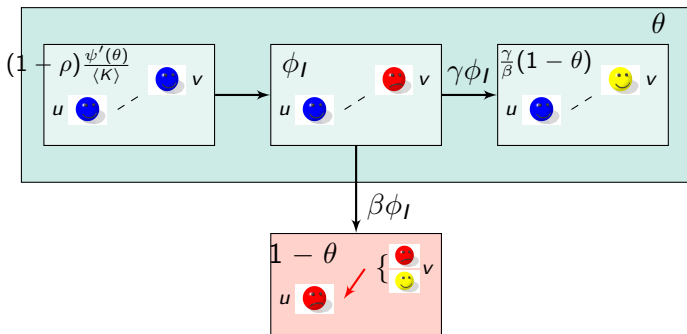
$$\phi_S(t) = \sum_k \frac{kP(k)}{\langle K \rangle} (1 - \rho) \theta(t)^{k-1} = (1 - \rho) \frac{\psi'(\theta)}{\langle K \rangle}$$



We have

$$\phi_I = \theta - \phi_S - \phi_R$$

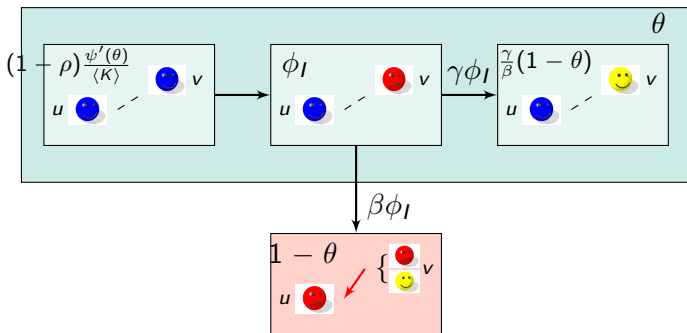
$$\dot{\theta} = -\beta \phi_I$$



We have

$$\phi_I = \theta - \phi_S - \phi_R = \theta - \frac{(1 - \rho)\psi'(\theta)}{\langle K \rangle} - \frac{\gamma}{\beta}(1 - \theta)$$

$$\dot{\theta} = -\beta\phi_I$$



We have

$$\phi_I = \theta - \phi_S - \phi_R = \theta - \frac{(1 - \rho)\psi'(\theta)}{\langle K \rangle} - \frac{\gamma}{\beta}(1 - \theta)$$

$$\dot{\theta} = -\beta\phi_I = -\beta\theta + \beta \frac{(1 - \rho)\psi'(\theta)}{\langle K \rangle} + \gamma(1 - \theta)$$

Final System

We finally have

$$\dot{\theta} = -\beta\theta + \beta \frac{(1-\rho)\psi'(\theta)}{\langle K \rangle} + \gamma(1-\theta)$$

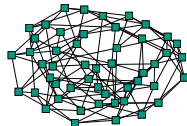
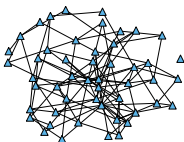
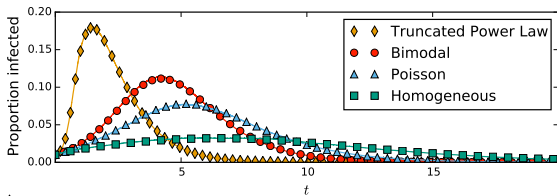
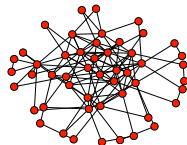
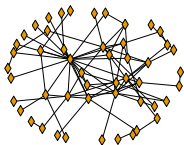
$$\dot{R} = \gamma I \quad S = (1-\rho)N\psi(\theta) \quad I = N - S - R$$

Compare with

$$\dot{\theta} = -\beta\theta + \beta\theta^2 \frac{(1-\rho)\psi'(\theta)}{\langle K \rangle} - \theta\gamma \ln \theta$$

$$\dot{R} = \gamma I, \quad S = (1-\rho)N\psi(\theta), \quad I = N - S - R$$

More details in [1, 2, 3]



A good exercise

Repeat this derivation for a model in which infections last for one time step and transmission occurs with probability p .

Epidemic probability

- ▶ To calculate epidemic probability, we consider a single introduced node, randomly chosen in the population.

Epidemic probability

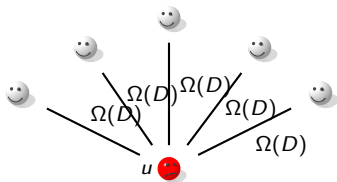


- ▶ To calculate epidemic probability, we consider a single introduced node, randomly chosen in the population.
- ▶ $\rho = 0$.

Epidemic probability

- ▶ To calculate epidemic probability, we consider a single introduced node, randomly chosen in the population.
- ▶ $\rho = 0$.
- ▶ $\psi(x) = \sum_k P(k)x^k$ is the probability generating function for the degree distribution.

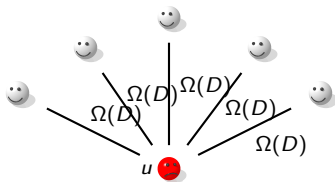
Calculating epidemic probability



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



Calculating epidemic probability

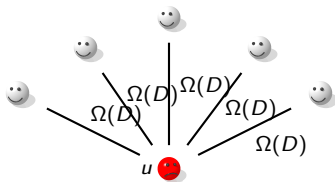


$$\Omega(D) = P(u \text{ does not transmit to a neighbor} | D) + P(u \text{ transmits, but neighbor doesn't lead to an epidemic})$$

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

$$\Omega(D)^k$$

Calculating epidemic probability

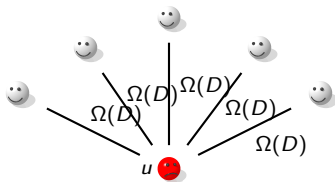


$$\Omega(D) = P(u \text{ does not transmit to a neighbor} | D) + P(u \text{ transmits, but neighbor doesn't lead to an epidemic})$$

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

$$\sum_k P(k) \Omega(D)^k$$

Calculating epidemic probability

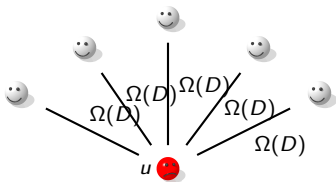


$$\Omega(D) = P(u \text{ does not transmit to a neighbor} | D) + P(u \text{ transmits, but neighbor doesn't lead to an epidemic})$$

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

$$1 - \mathcal{P} = \int_0^{\infty} \gamma e^{-\gamma D} \sum_k P(k) \Omega(D)^k dD$$

Calculating epidemic probability



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

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

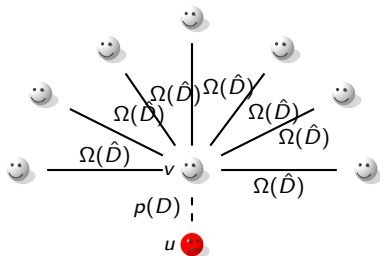
$$1 - \mathcal{P} = \int_0^{\infty} \gamma e^{-\gamma D} \sum_k P(k) \Omega(D)^k dD = \int_0^{\infty} \gamma e^{-\gamma D} \psi(\Omega(D)) dD$$

where

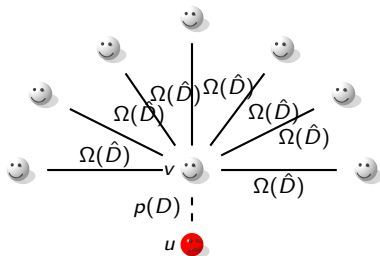
$$\psi(x) = \sum_k P(k) x^k$$



Finding Ω



Finding Ω

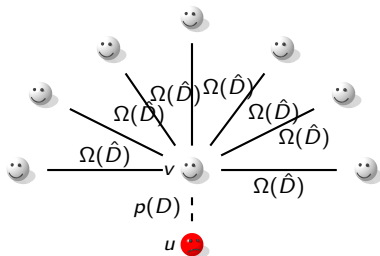


Probability a random partner of the index case having degree \hat{k} whose infection duration is \hat{D} does not start an epidemic is

$$[1 - p(D)] + \text{[speech bubble icon]} p(D)\Omega(\hat{D})^{\hat{k}-1}$$

$p(D) = 1 - e^{-\beta D}$ is the probability of transmitting given infection duration of D

Finding Ω

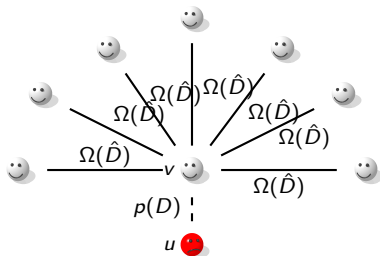


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Finding Ω

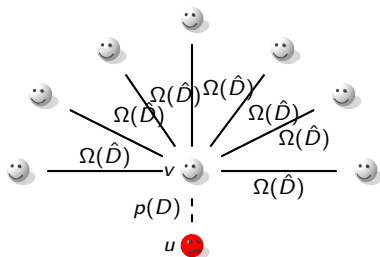


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$$\Omega(D) = [1 - p(D)] + \int_0^\infty \gamma e^{-\gamma \hat{D}} \sum_{\hat{k}} P_n(\hat{k}) p(D) \Omega(\hat{D})^{\hat{k}-1} d\hat{D}$$

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Finding Ω

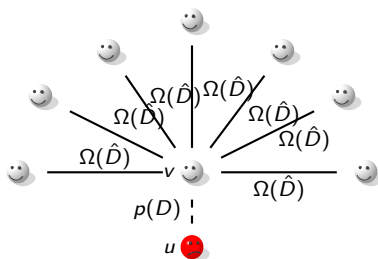


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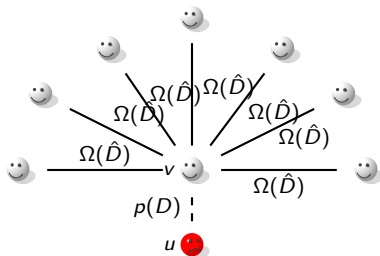


Probability a random partner of the index case ~~having degree \hat{k}~~
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$$\Omega(D) = [1 - p(D)] + p(D) \int_0^\infty \gamma e^{-\gamma \hat{D}} \sum_{\hat{k}} \frac{\hat{k} P(\hat{k})}{\langle K \rangle} \Omega(\hat{D})^{\hat{k}-1} d\hat{D}$$

$p(D) = 1 - e^{-\beta D}$ is the probability of transmitting given infection duration of D

Finding Ω

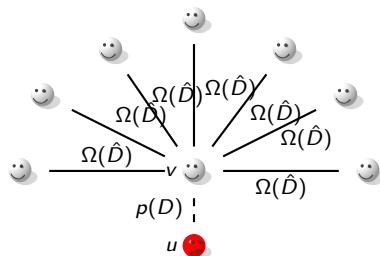


Probability a random partner of the index case ~~having degree \hat{k}~~
~~whose infection duration is \hat{D}~~ does not start an epidemic is

$$\Omega(D) = [1 - p(D)] + p(D) \int_0^\infty \gamma e^{-\gamma \hat{D}} \frac{\sum_{\hat{k}} \hat{k} P(\hat{k}) \Omega(\hat{D})^{\hat{k}-1}}{\langle K \rangle} d\hat{D}$$

$p(D) = 1 - e^{-\beta D}$ is the probability of transmitting given infection duration of D

Finding Ω



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

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

$p(D) = 1 - e^{-\beta D}$ is the probability of transmitting given infection duration of D

Calculating epidemic probability

We arrive at

$$1 - \mathcal{P} = \int_0^\infty \gamma e^{-\gamma D} \psi(\Omega(D)) \, dD$$

$$\Omega(D) = e^{-\beta D} + \left(1 - e^{-\beta D}\right) \int_0^\infty \gamma e^{-\gamma \hat{D}} \frac{\psi'(\Omega(\hat{D}))}{\langle K \rangle} \, d\hat{D}$$

In general we can only solve this numerically, but it is straightforward. We start with a guess that $\Omega(D) = 1$, plug it in and iterate.

In fact the n th iteration will give the probability that the disease spreads at least n generations.

SIR and percolation

SIS disease

Last details

References

SIS disease

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- ▶ This has policy implications: how much will it reduce MRSA transmission if we clear the disease from a hospital or a prison?
- ▶ So for SIS disease simulation is likely to play a major role.

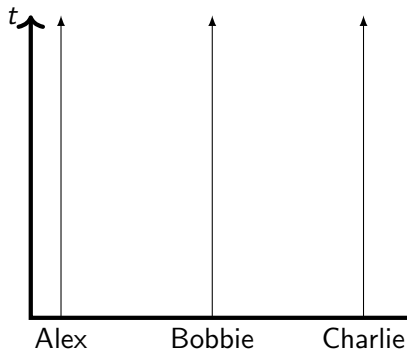
Percolation-like results and SIS

- ▶ It is possible to use percolation-like results to for rigorous conclusions about SIS disease.

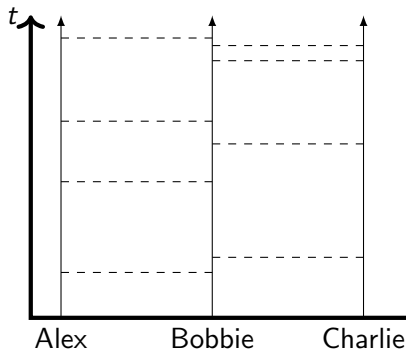
Percolation-like results and SIS

- ▶ It is possible to use percolation-like results to for rigorous conclusions about SIS disease.
- ▶ As a general rule, these rigorous results do not generalize if we do not assume constant infection and transmission rates.

A percolation-like approach

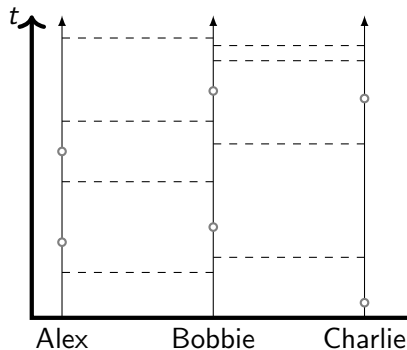


A percolation-like approach



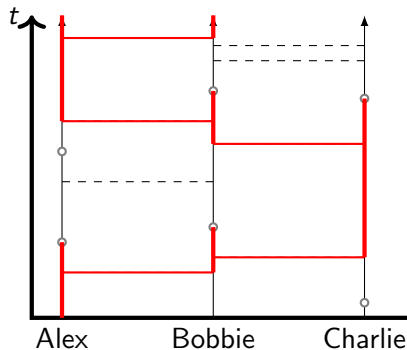
- Find transmission events as Poisson process

A percolation-like approach



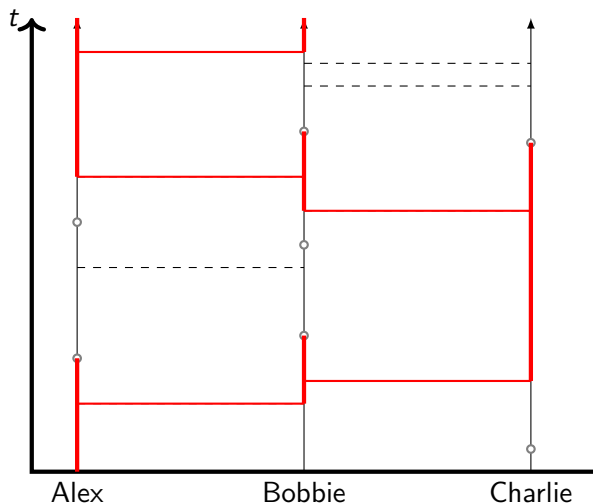
- ▶ Find transmission events as Poisson process
- ▶ Find recovery events as Poisson process

A percolation-like approach

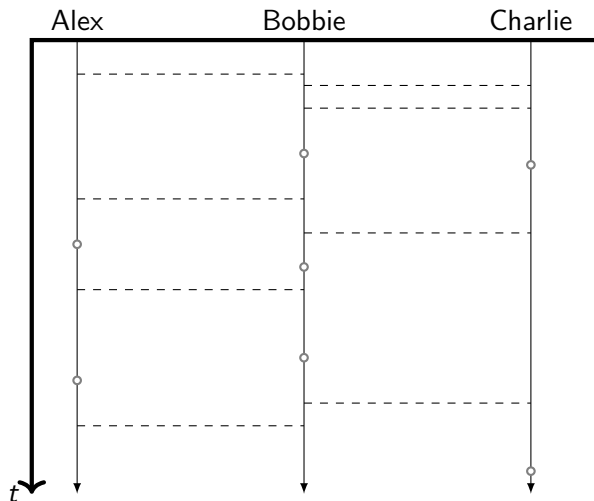


- ▶ Find transmission events as Poisson process
- ▶ Find recovery events as Poisson process
- ▶ Trace out from initial infection

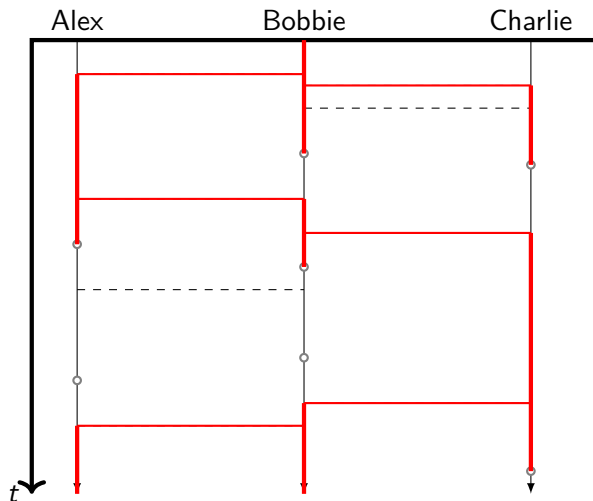
Now invert the picture



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Some conclusions

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- ▶ So the expected number of nodes infected at time t starting from infection of u at time 0 is equal to the probability u is infected at time t if we infect a random individual at time 0.

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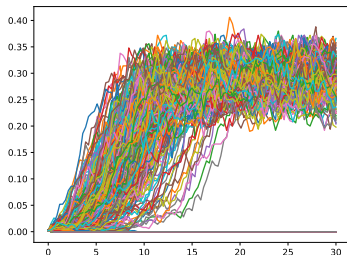
- ▶ An infection of u at time 0 leads to an infection of v at time t iff there is a path that doesn't go through a recovery event.
- ▶ That reversed path also works. So any node infected at time t would cause infection of the initial node at time 0 in the reversed process.
- ▶ So the expected number of nodes infected at time t starting from infection of u at time 0 is equal to the probability u is infected at time t if we infect a random individual at time 0.
- ▶ The equilibrium size of an SIS epidemic with Poissonian transmission and recovery equals the probability that an epidemic occurs.

SIS size vs Probability

1000 simulations starting with a single randomly chosen node in a Configuration model network with $P(1) = P(5) = 0.5$.

SIS size vs Probability

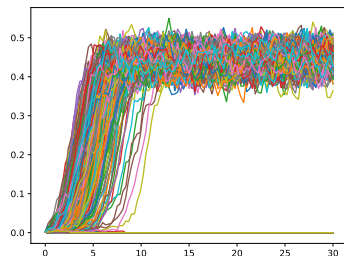
1000 simulations starting with a single randomly chosen node in a Configuration model network with $P(1) = P(5) = 0.5$.



$\beta = 0.5, \gamma = 1$
273 did not die out

SIS size vs Probability

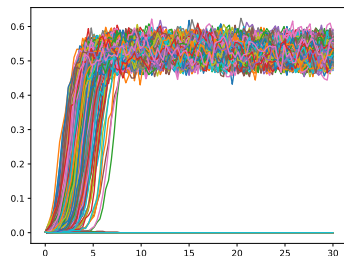
1000 simulations starting with a single randomly chosen node in a Configuration model network with $P(1) = P(5) = 0.5$.



$\beta = 0.75, \gamma = 1$
448 did not die out

SIS size vs Probability

1000 simulations starting with a single randomly chosen node in a Configuration model network with $P(1) = P(5) = 0.5$.



$\beta = 1, \gamma = 1$
537 did not die out

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A final SIS model

$$\frac{d}{dt}[S_k] = \gamma[I_k] - \tau[S_k I],$$

$$\frac{d}{dt}[I_k] = \tau[S_k I] - \gamma[I_k],$$

$$\frac{d}{dt}[S_k I_l] = \gamma([I_k I_l] - [S_k I_l]) + \tau([S_k S_l I] - [I S_k I] - [S_k I_l]),$$

$$\frac{d}{dt}[S_k S_l] = \gamma([S_k I_l] + [I_k S_l]) - \tau([S_k S_l I] + [I S_k S_l]),$$

$$\frac{d}{dt}[I_k I_l] = \tau([S_k I_l] + [I_k S_l]) - 2\gamma[I_k I_l] + \tau([I S_k I_l] + [I_k S_l I]),$$

with

$$[A_l S_k I]_s = \frac{k-1}{k} \frac{[A_l S_k]_s [S_k I]_s}{[S_k]_s}, \quad [I S_k A_l]_s = \frac{k-1}{k} \frac{[I S_k]_s [S_k A_l]_s}{[S_k]_s}.$$

Sample code

I plan to put sample code for the simulations I did up on Tom's webpage.

See also <http://epidemicsonnetworks.readthedocs.io/en/latest/>

SIR and percolation

SIS disease

Last details

References

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