

# Percolation approaches to disease spread

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SIR and percolation

SIS disease

Gratuitous advertisement

References

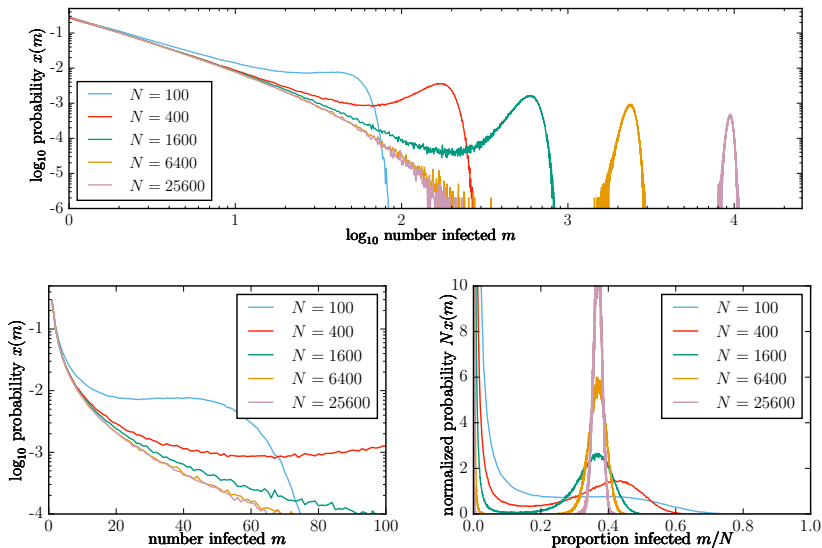
# Percolation

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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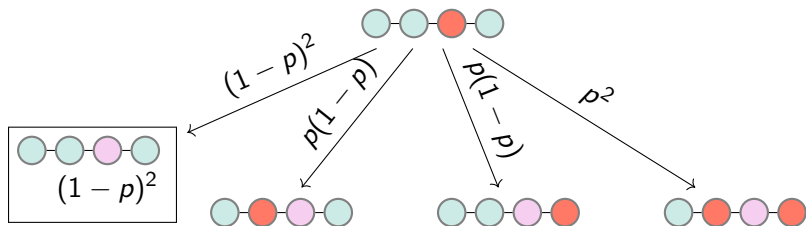
- ▶ An edge represents a potential transmission path (unweighted, bidirectional).
- ▶ An infected node remains infected for a single time step.
- ▶ An infected node transmits to a neighbor with probability  $p$ .

# Modeling Disease Spread in a network

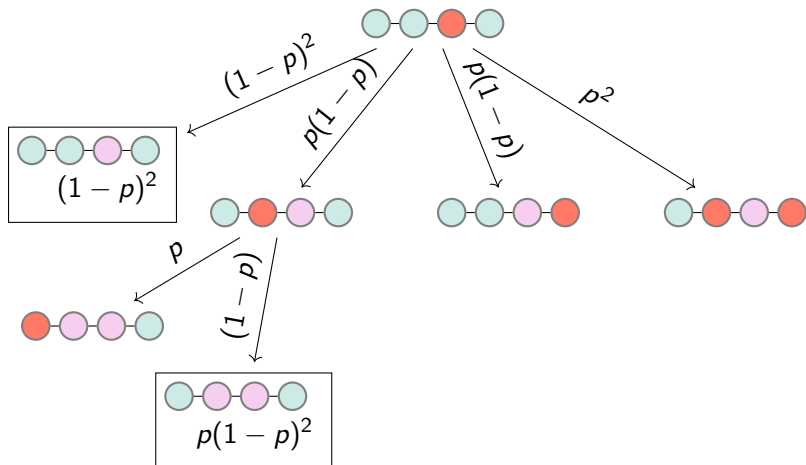




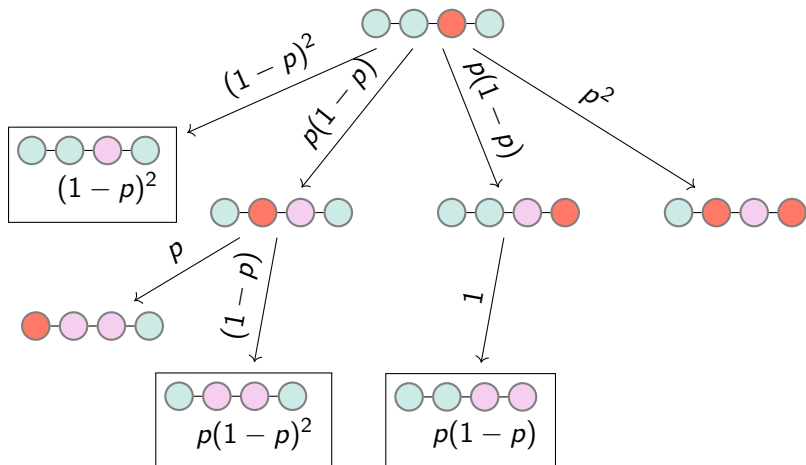
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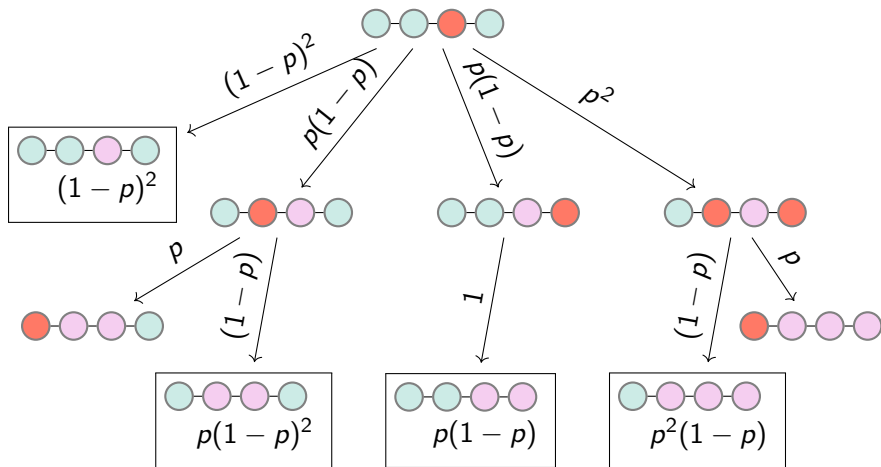
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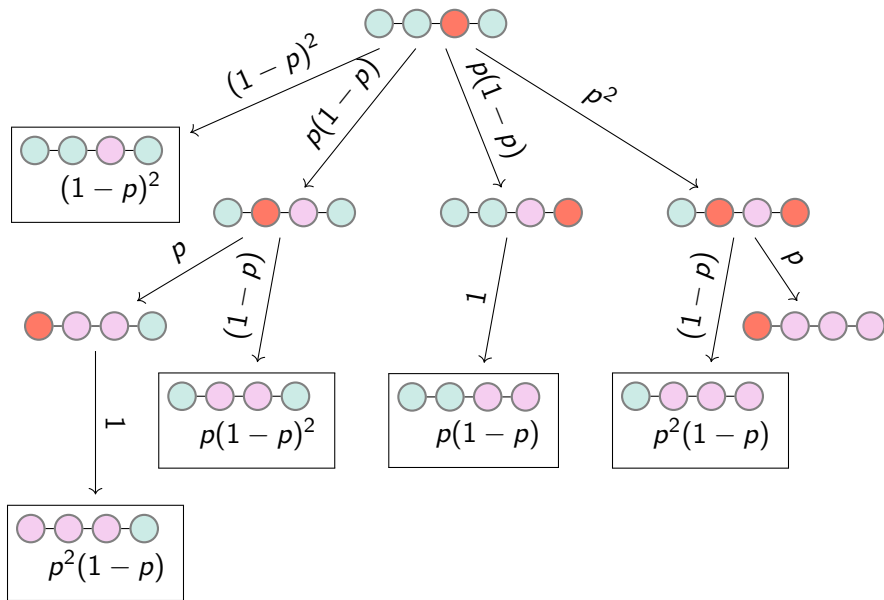
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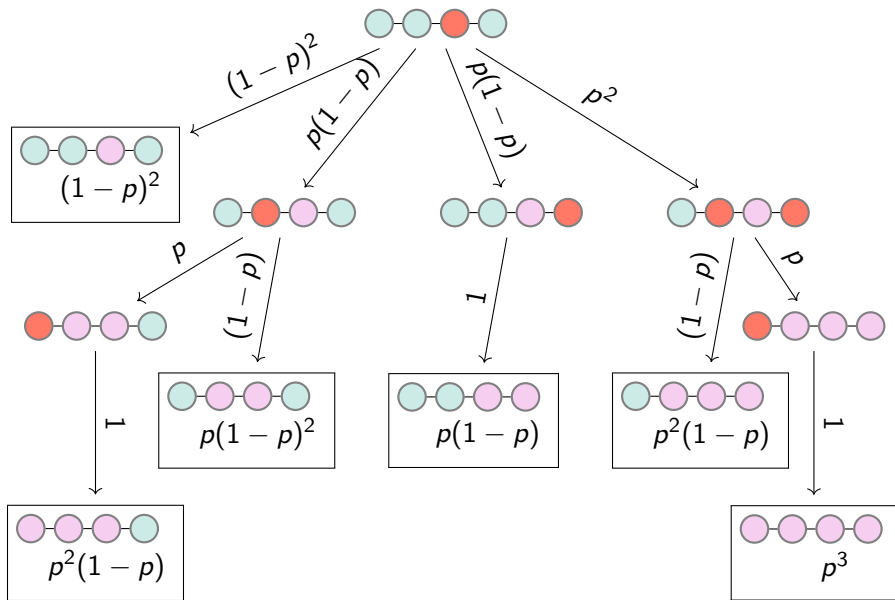
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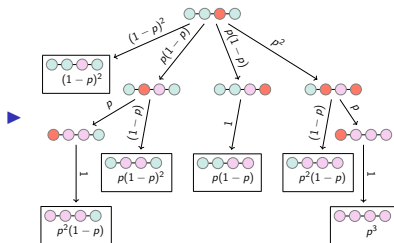
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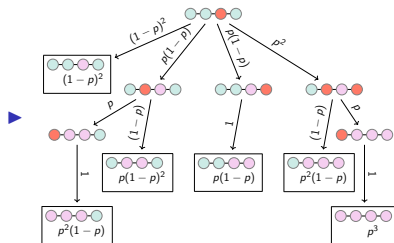


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At each step, if there is an edge to cross, it is crossed with probability  $p$ . No edge is ever crossed twice.

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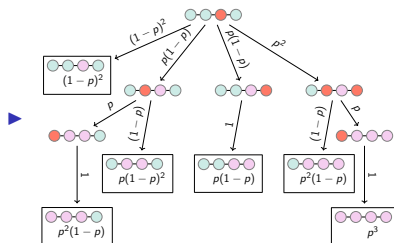


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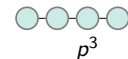
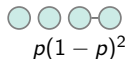
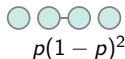
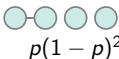
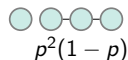
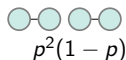
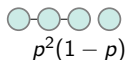
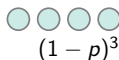


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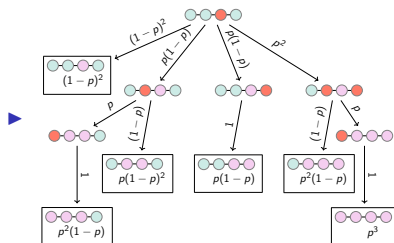


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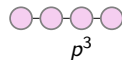
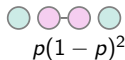
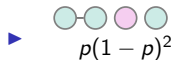
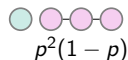
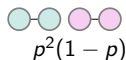
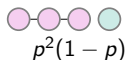


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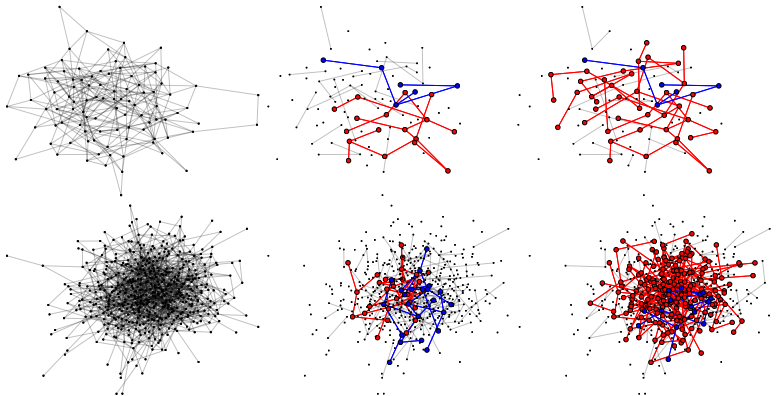
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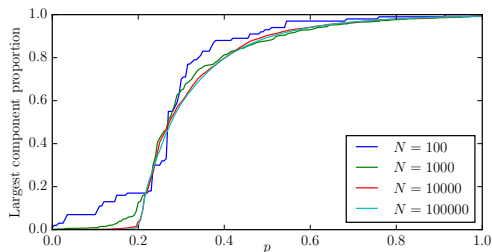
## Percolation in different size networks

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

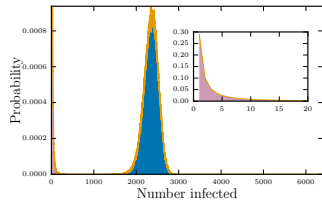
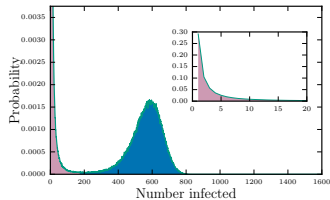
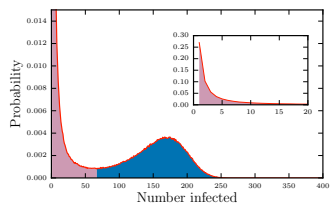
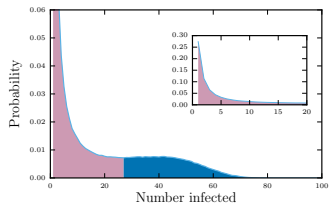


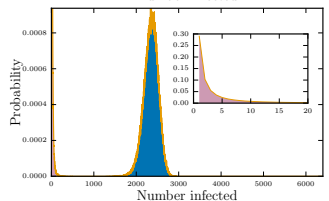
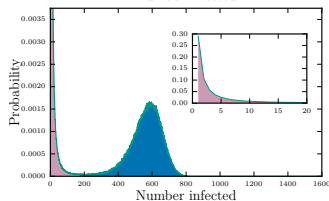
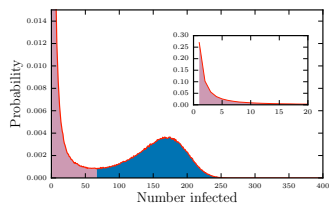
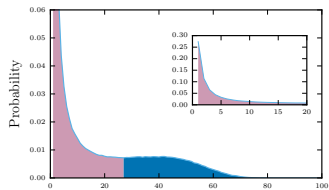
- ▶ Below threshold largest and second largest in a network are about the same size as each other and similar size in both networks
- ▶ Above threshold largest is proportional to network size.

# 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  $\beta$  and recovering with rate  $\gamma$ .

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- ▶ 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.

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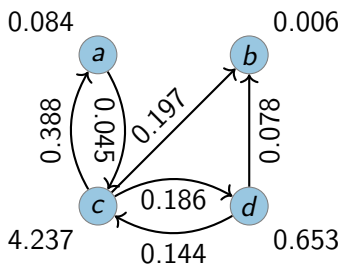
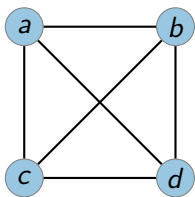
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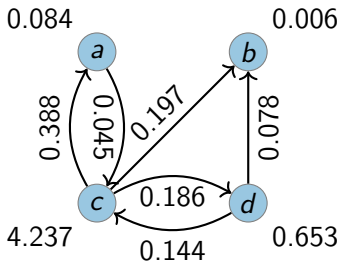
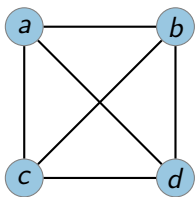
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- ▶ Is it possible for me to know whether he is calculating in advance or not?

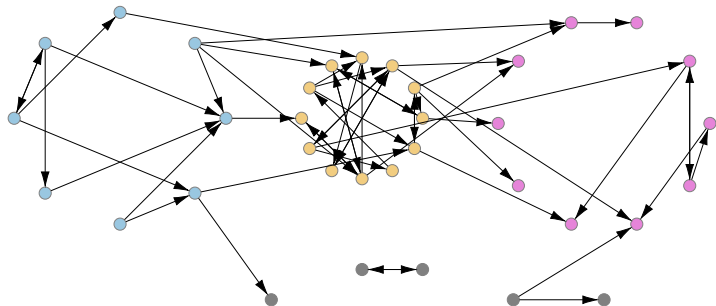






Every number that Tom gives me is a random number that is generated independently of every other number. It doesn't matter when he generates it.

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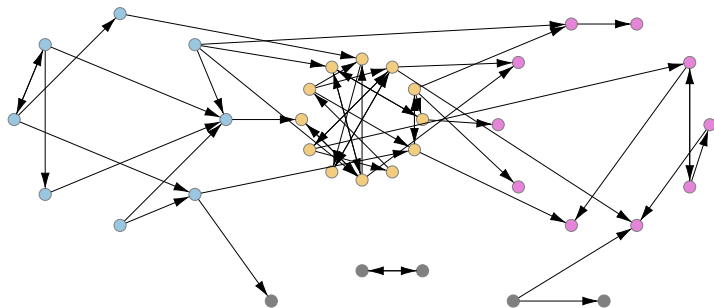
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    - ▶ If  $\tau < d$ , place directed edge into network with associated time.
  - ▶ Choose an initial infected individual.
  - ▶ Trace the disease spread following edges in  $H$ , transmitting after the given time.

# Comments on directed percolation

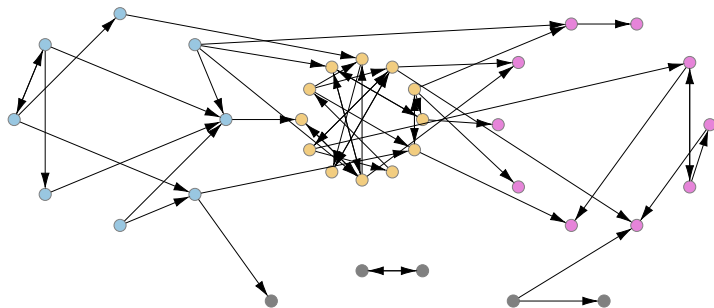
- ▶ Directed percolation can be used more generally when there are other sources of heterogeneity in infectiousness and/or susceptibility.
- ▶ The eventually infected nodes are exactly those nodes in the out-component of the index case.
- ▶ The probability a random node is infected follows from the size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

## Typical structure



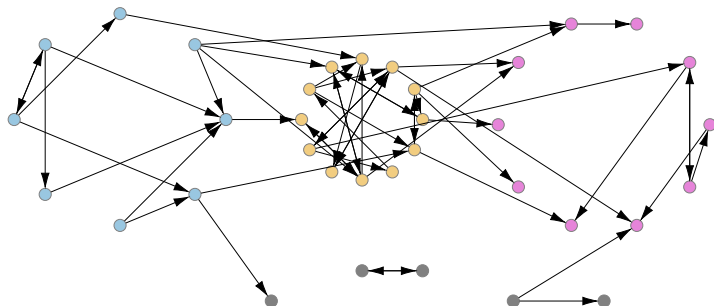
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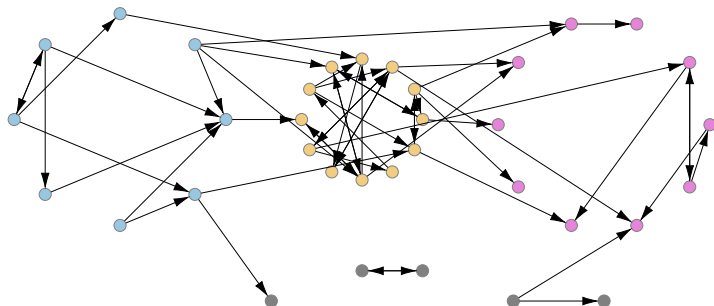
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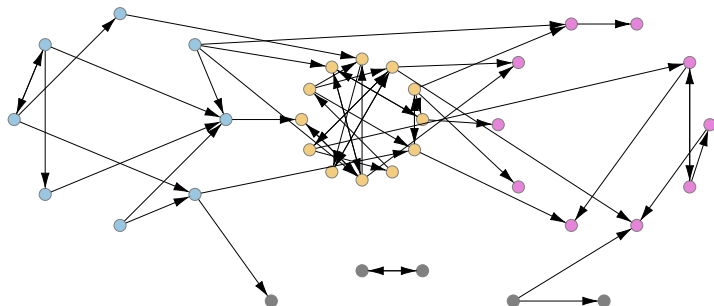
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- ▶ So Epidemic Probability  $\mathcal{P} = \mathbb{E}(|H_{IN} \cup H_{SCC}|)/N$  and Attack rate  $\mathcal{A} = \mathbb{E}(|H_{SCC} \cup H_{OUT}|)/N$ .

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- ▶ The 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  $H$ .

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- ▶ Allow the SIR disease to spread.
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  - ▶ What is the probability of an epidemic started from a single node?

# $\mathcal{R}_0$ calculation

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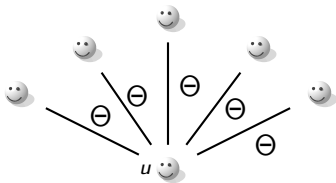
# Changing the final size question

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

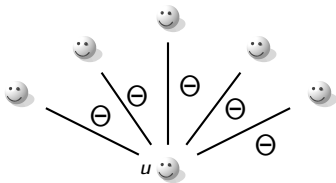
## Changing the final size question

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?



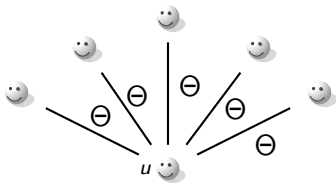
$$\Theta = P(v \text{ did not transmit to } u)$$



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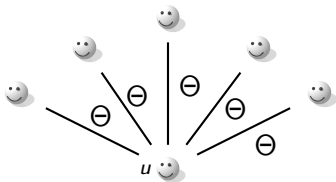
$$(1 - \rho)\Theta^k$$



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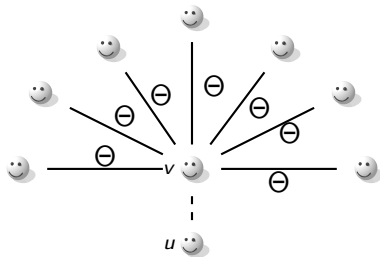
Probability a random ~~degree- $k$~~  test individual is susceptible at the end is

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

where

$$\hat{\psi}(x) = (1 - \rho) \sum_k P(k)x^k$$

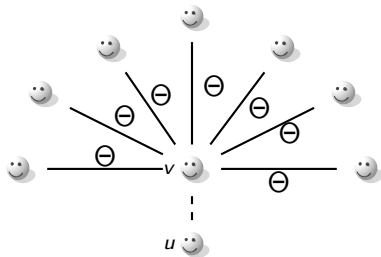
# Finding $\Theta$



Probability a random degree  $k$  partner never infected is

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

## Finding $\Theta$

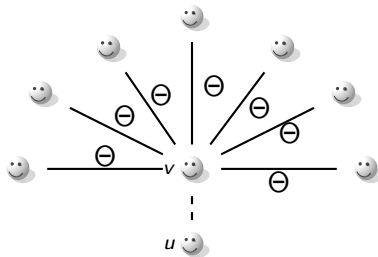


Probability a random ~~degree- $k$~~  partner never infected is

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



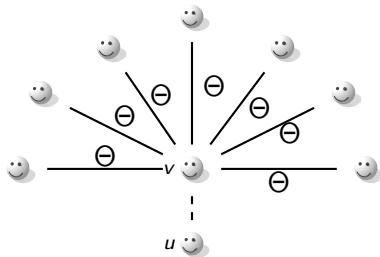
# Finding $\Theta$



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

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

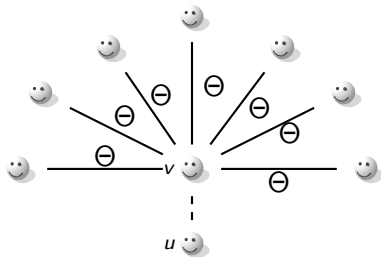
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Probability a random ~~degree- $k$~~  partner never infected is

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# Finding $\Theta$



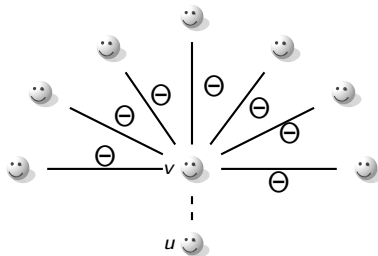
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Given  $\beta$  and  $\gamma$ , partner does not transmit to  $u$  with probability

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

# Finding $\Theta$



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

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Given  $\beta$  and  $\gamma$ , partner does not transmit to  $u$  with probability

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

# Final Size

So

$$R = 1 - \hat{\psi}(\Theta)$$

where

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

# Final Size

So

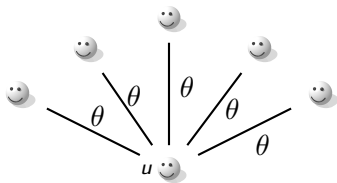
$$R = 1 - \hat{\psi}(\Theta)$$

where

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

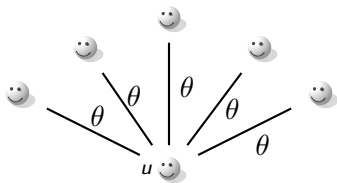
A more rigorous definition would be that  $\Theta$  is the probability that the given edge isn't the final edge of a directed path from an index node to  $u$  in the percolated network  $H$ .

# Finding $S(t)$



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

# Finding $S(t)$



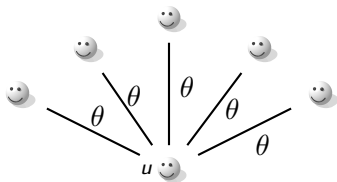
$$\theta(t) = P(v \text{ not yet transmitted to } u)$$

Probability a random degree  $k$  test individual still susceptible is

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



# Finding $S(t)$

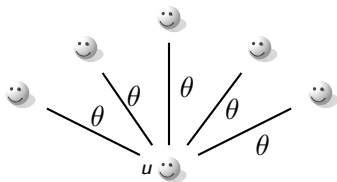


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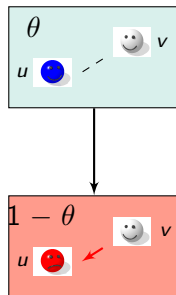
Probability a random ~~degree- $k$~~  test individual still susceptible is

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

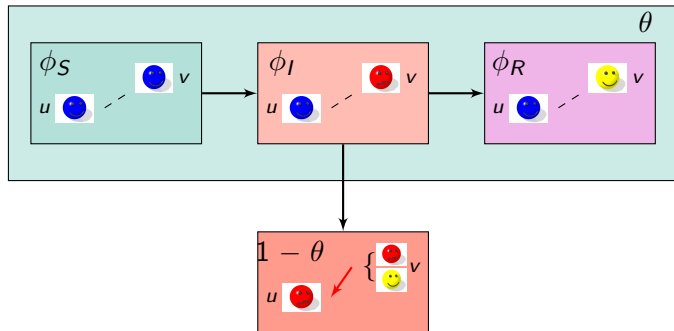
where

$$\hat{\psi}(x) = (1 - \rho) \sum_k P(k)x^k$$

# How does $\theta$ evolve?

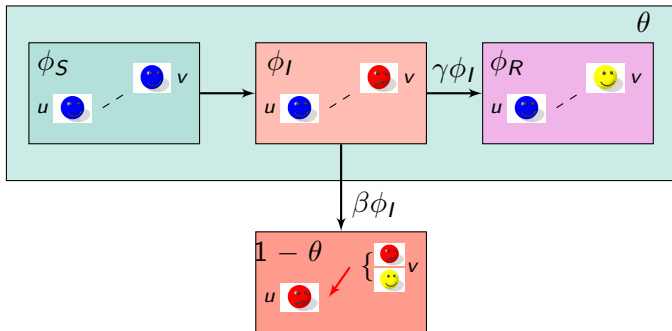


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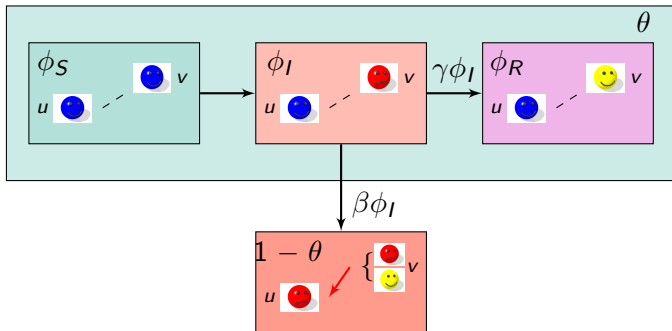
►  $\theta = \phi_S + \phi_I + \phi_R.$

# How does $\theta$ evolve?



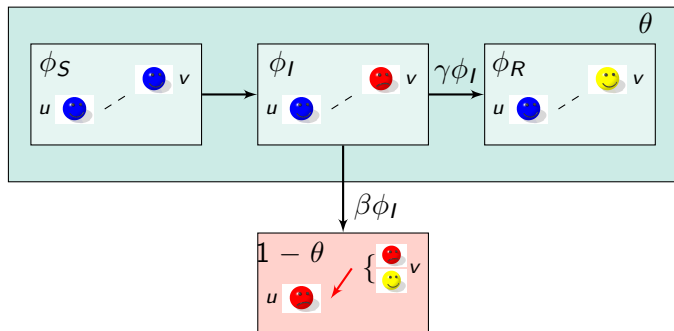
- ▶  $\theta = \phi_S + \phi_I + \phi_R$ .
- ▶  $\dot{\theta} = -\beta\phi_I$ .

# How does $\theta$ evolve?



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

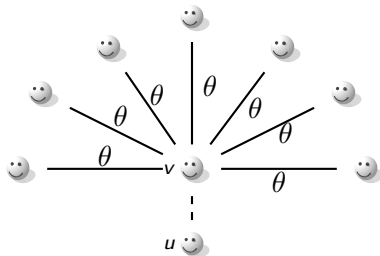
# Finding $\phi_R(t)$



Because derivatives are proportional (swimming pool analogy),

$$\phi_R = \frac{\gamma}{\beta}(1 - \theta)$$

## Finding $\phi_S(t)$

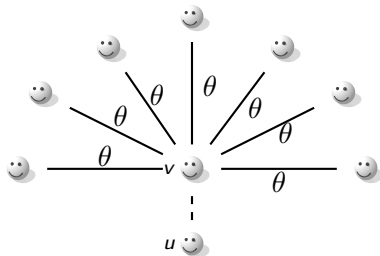


Probability a random degree  $k$  partner still susceptible is

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



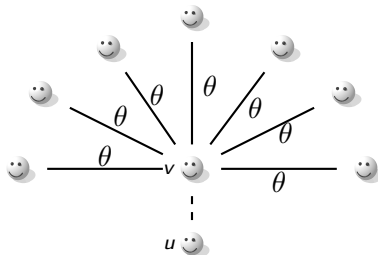
## Finding $\phi_S(t)$



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

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

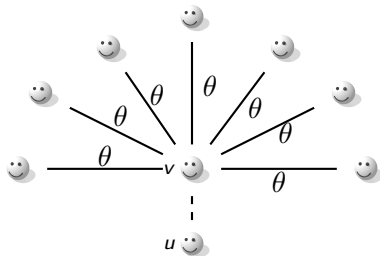
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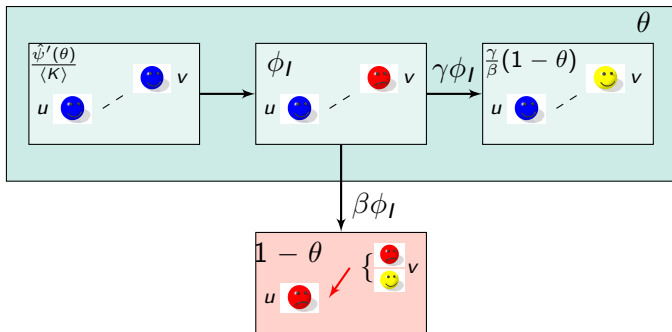
$$\phi_S(t) = \sum_k \frac{kP(k)}{\langle K \rangle} (1 - \rho) \theta(t)^{k-1}$$

## Finding $\phi_S(t)$



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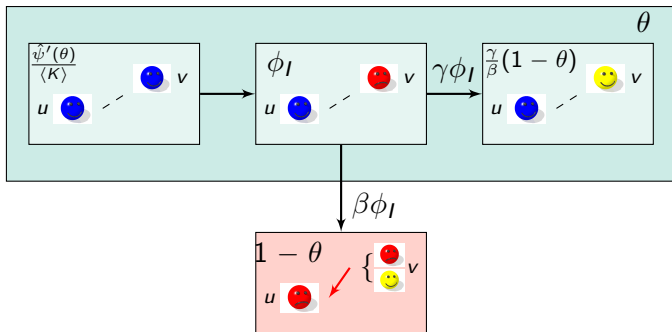
$$\phi_S(t) = \sum_k \frac{kP(k)}{\langle K \rangle} (1 - \rho) \theta(t)^{k-1} = \frac{\hat{\psi}'(\theta)}{\langle K \rangle}$$



We have

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

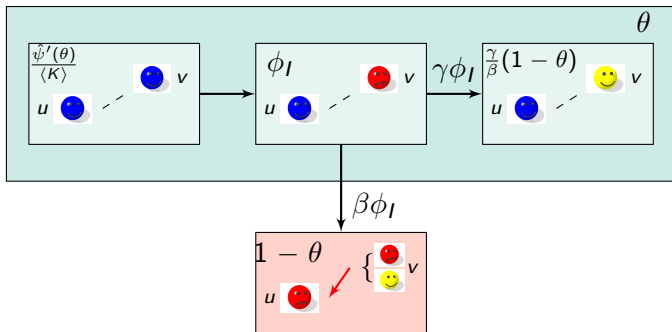
$$\dot{\theta} = -\beta\phi_I$$



We have

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

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



We have

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

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

# Final System

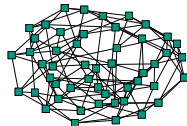
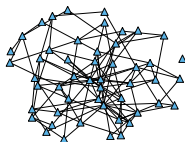
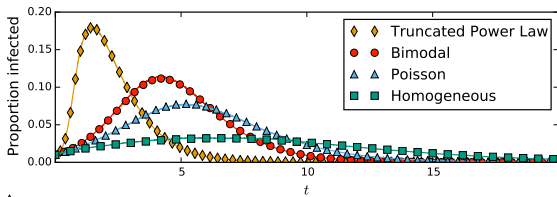
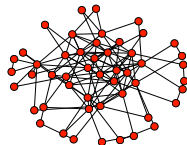
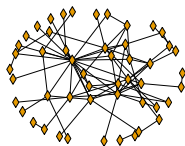
We finally have

$$\begin{aligned}\dot{\theta} &= -\beta\theta + \beta \frac{\hat{\psi}'(\theta)}{\langle K \rangle} + \gamma(1 - \theta) \\ \dot{R} &= \gamma I \quad S = \hat{\psi}(\theta) \quad I = 1 - S - R\end{aligned}$$

Compare with

$$\begin{aligned}\dot{\theta} &= -\beta\theta + \beta\theta^2 \frac{\hat{\psi}'(\theta)}{\langle K \rangle} - \theta\gamma \ln \theta \\ \dot{R} &= \gamma I, \quad S = \hat{\psi}(\theta), \quad I = 1 - S - R\end{aligned}$$

More details in [1, 2]





## 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.

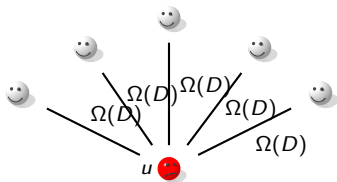
# Epidemic probability

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# Epidemic probability

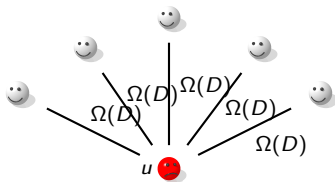
- ▶ To calculate epidemic probability, we consider a single introduced node, randomly chosen in the population.
- ▶  $\rho = 0$ .
- ▶  $\psi(x) = \sum_k P(k)x^k$  is the probability generating function for the degree distribution.

# 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

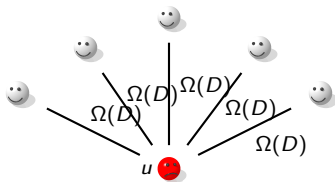


$$\Omega(D) = P(u \text{ does not transmit to a neighbor} | D) + P(u \text{ transmits, but neighbor doesn't lead to an epidemic})$$

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

$$\Omega(D)^k$$

# Calculating epidemic probability

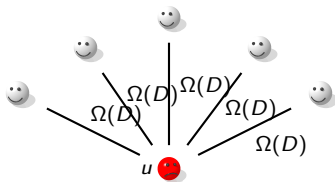


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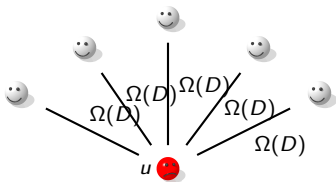
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Probability a random ~~degree  $k$~~  index case ~~whose infection duration is  $D$~~  does not start an epidemic is

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



# Calculating epidemic probability



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

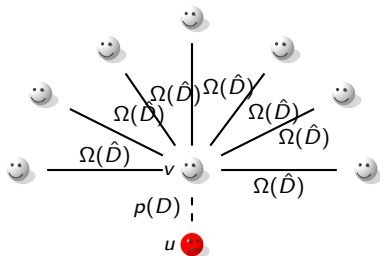
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$$1 - \mathcal{P} = \int_0^\infty \gamma e^{-\gamma D} \sum_k P(k) \Omega(D)^k dD = \int_0^\infty \gamma e^{-\gamma D} \psi(\Omega(D)) dD$$

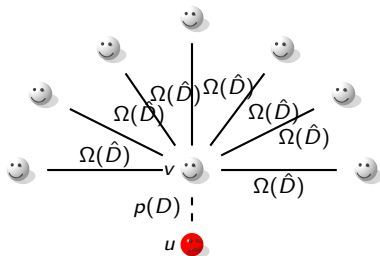
where

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

# Finding $\Omega$



# Finding $\Omega$

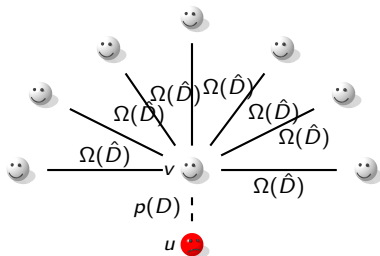


Probability a random partner of the index case having degree  $\hat{k}$  whose infection duration is  $\hat{D}$  does not start an epidemic is

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

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

# Finding $\Omega$

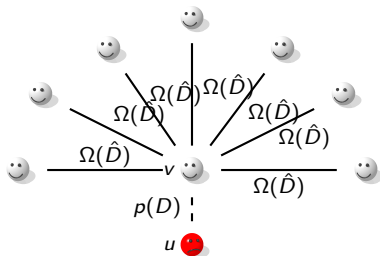


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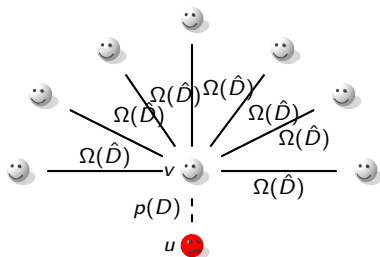


Probability a random partner of the index case ~~having degree  $\hat{k}$~~   
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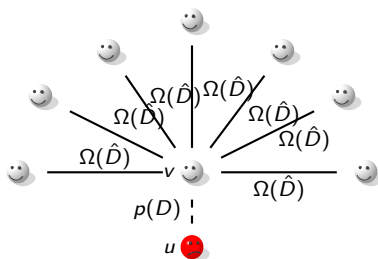


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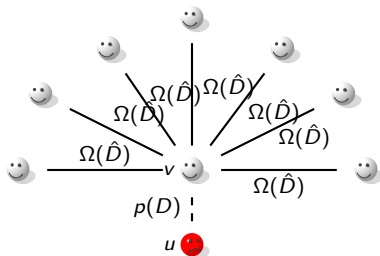


Probability a random partner of the index case ~~having degree  $\hat{k}$~~   
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$$\Omega(D) = [1 - p(D)] + p(D) \int_0^\infty \gamma e^{-\gamma \hat{D}} \sum_{\hat{k}} \frac{\hat{k} P(\hat{k})}{\langle K \rangle} \Omega(\hat{D})^{\hat{k}-1} d\hat{D}$$

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

# Finding $\Omega$



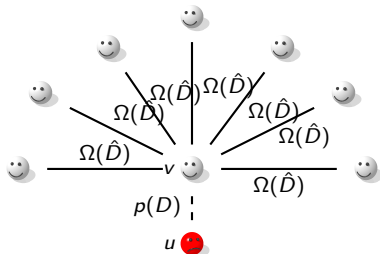
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# Calculating epidemic probability

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.

# Discussion

- ▶ The number of equations is dramatically reduced by this model, and does not depend on the degrees in the network.
- ▶ The model does not appear applicable to SIS disease.
- ▶ Degree correlations can be introduced, but then the number of equations becomes proportional to the number of degrees.
- ▶ For an SIR disease in a Configuration Model network, these equations give the  $N \rightarrow \infty$  limit.
- ▶ For the earlier “effective degree” and the “pairwise” model I mentioned that we can reduce the number of equations to order  $M$  by making particular assumptions. By doing a lot of algebraic gymnastics, we can show that the model here is equivalent to these.

SIR and percolation

SIS disease

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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

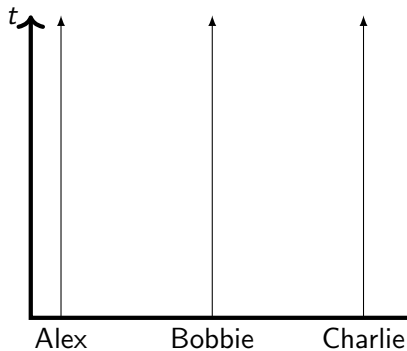
# Mathematically rigorous SIS

- ▶ It is possible to do some mathematically rigorous work with SIS.

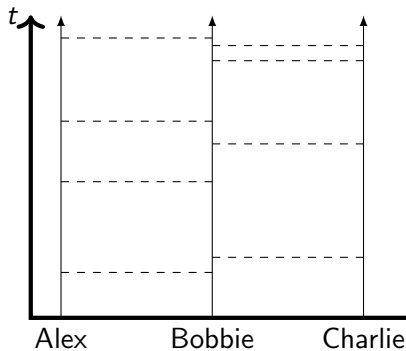
# Mathematically rigorous SIS

- ▶ It is possible to do some mathematically rigorous work with SIS.
- ▶ As a general rule, the rigorous results do not generalize if we do not assume constant infection and transmission rates.

## A percolation-like approach

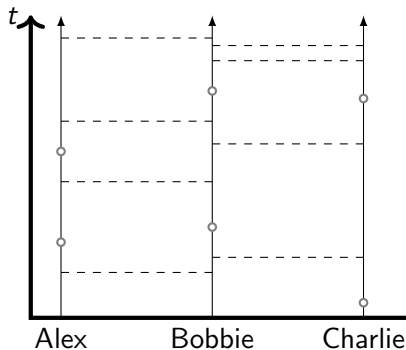


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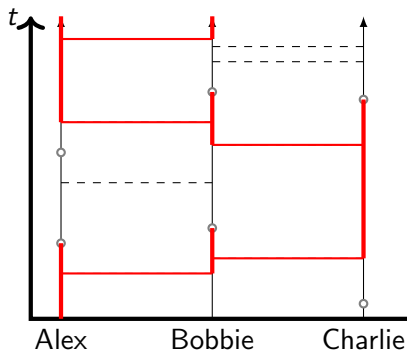
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## A percolation-like approach



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

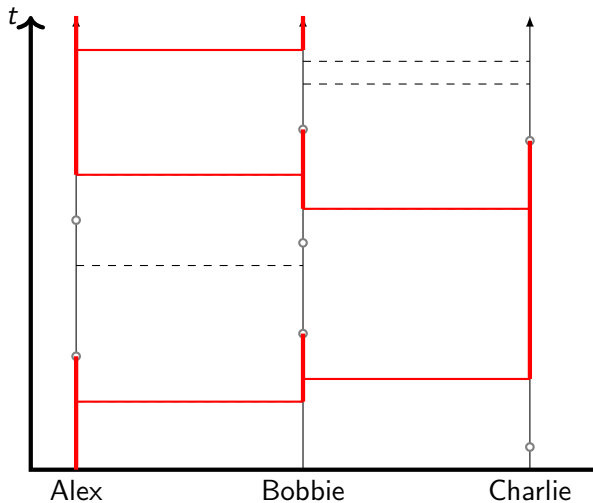
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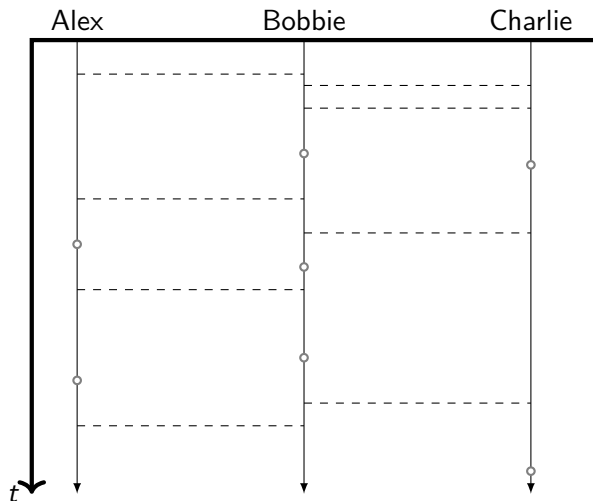
- ▶ Find transmission events as Poisson process
- ▶ Find recovery events as Poisson process
- ▶ Trace out from initial infection



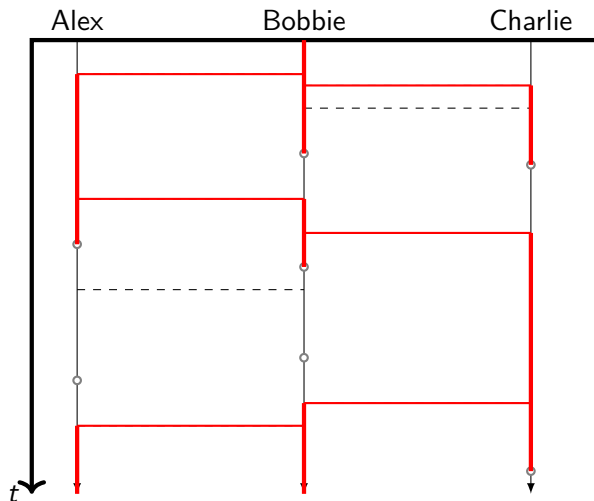
Now invert the picture



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## Some conclusions

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- ▶ The equilibrium size of an SIS epidemic equals the probability that an epidemic occurs.

SIR and percolation

SIS disease

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# Mathematics of network epidemics: from exact to approximate models

– Monograph –

To appear

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