Part 5 — Percolation approaches to disease spread

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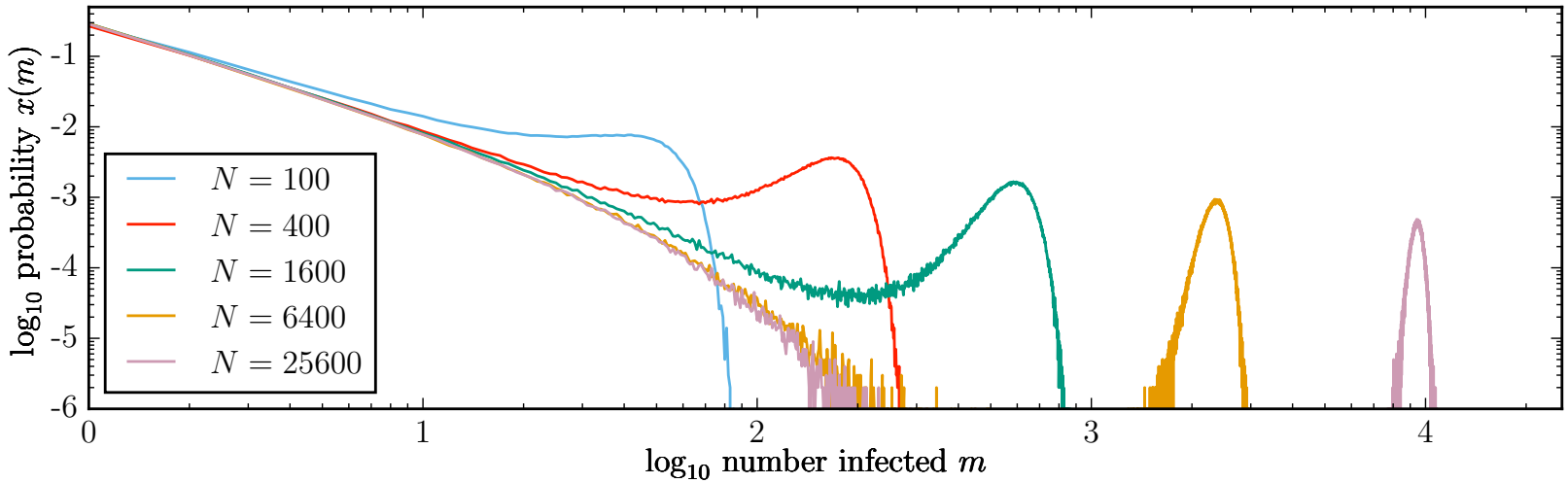
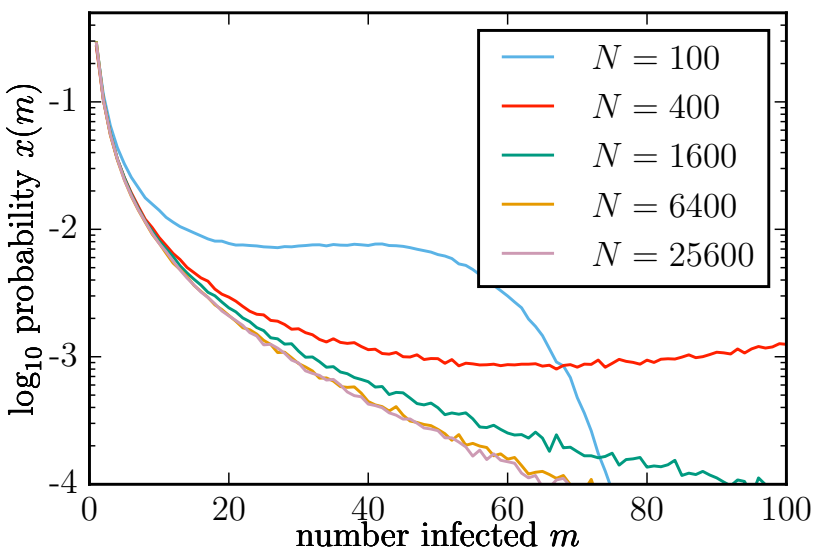
Percolation

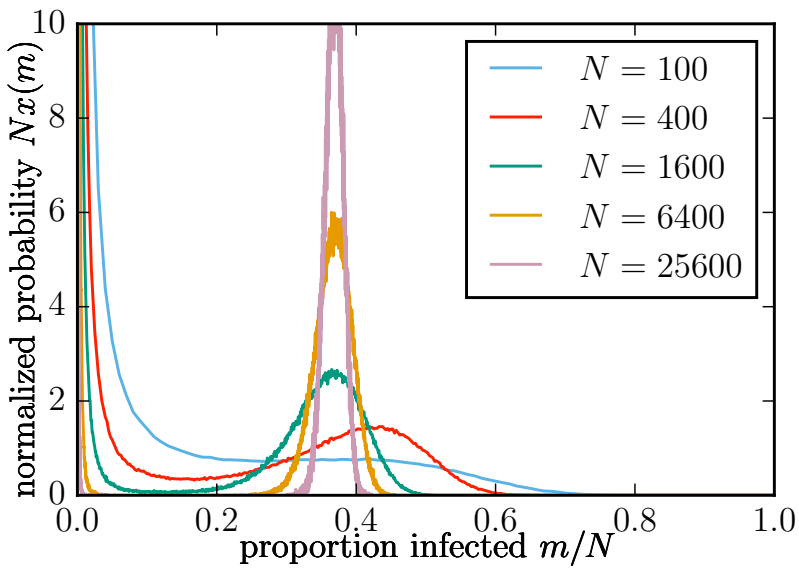
We are going to explore a relationship between SIR disease and percolation.
This will lead to methods to

- 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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- Warning — no longer assuming continuous time

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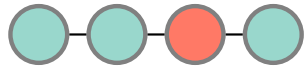

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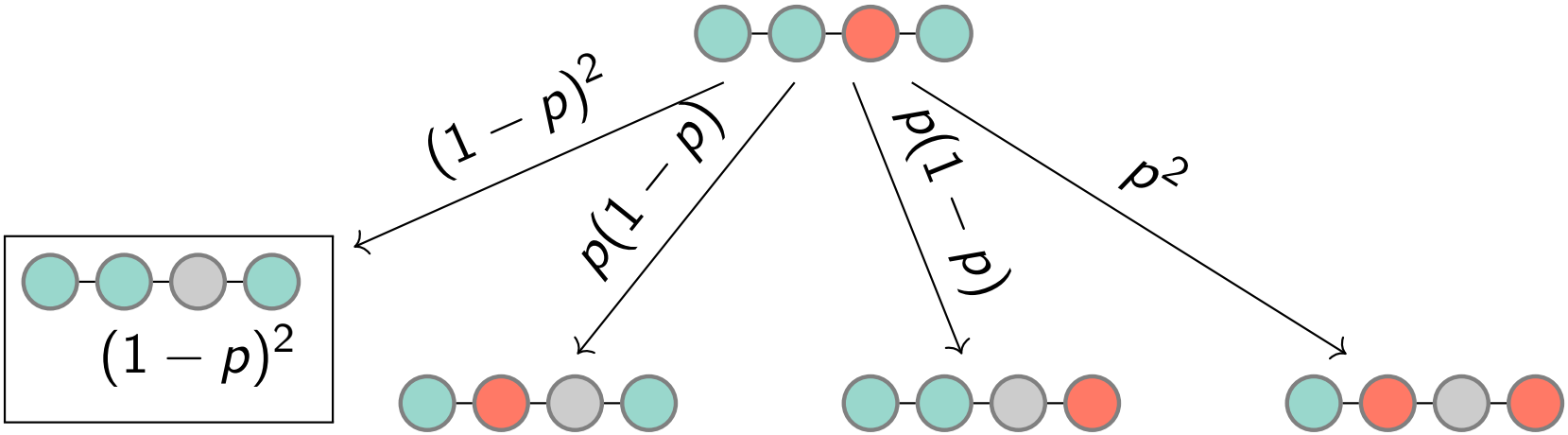

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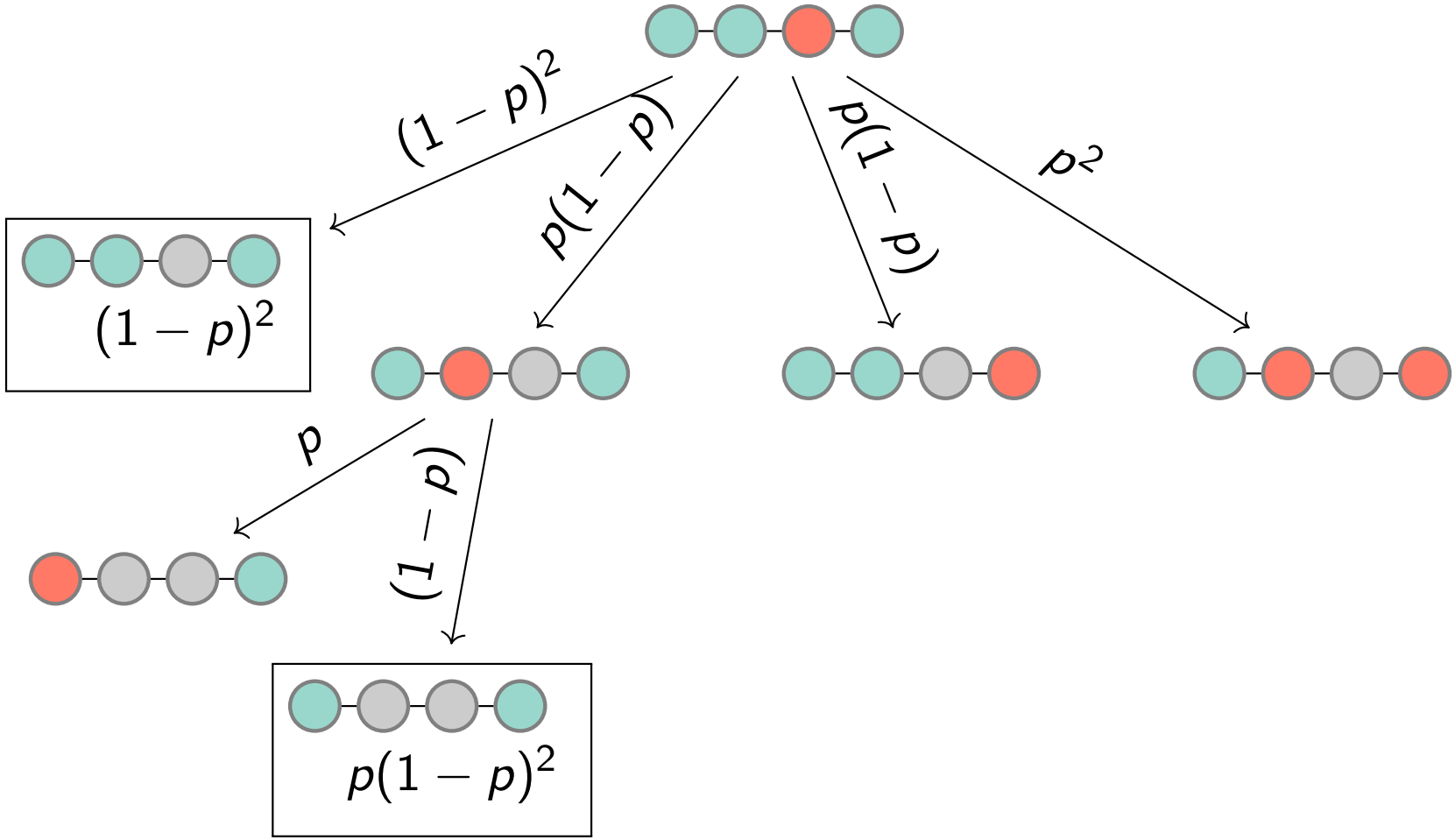

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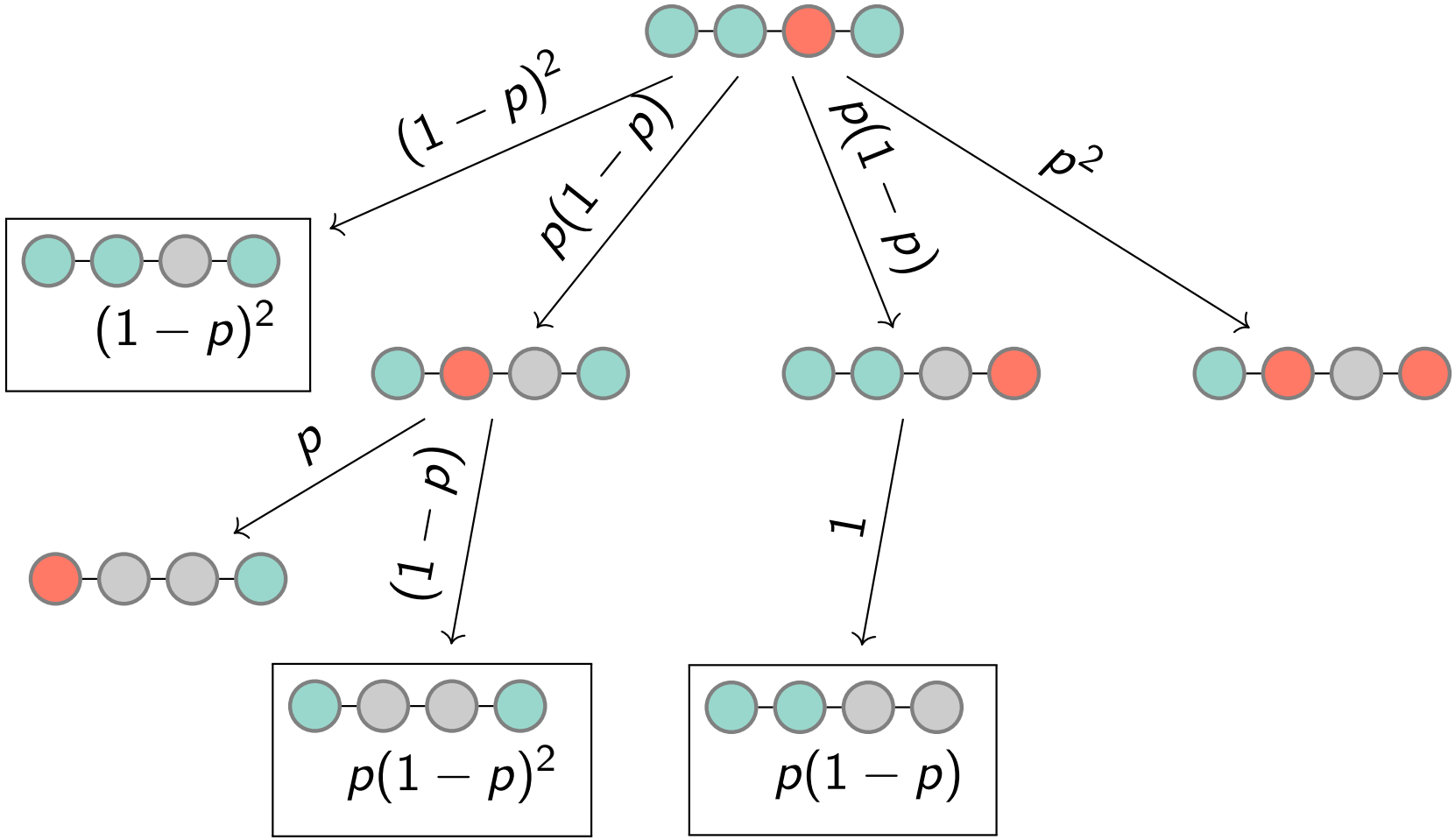

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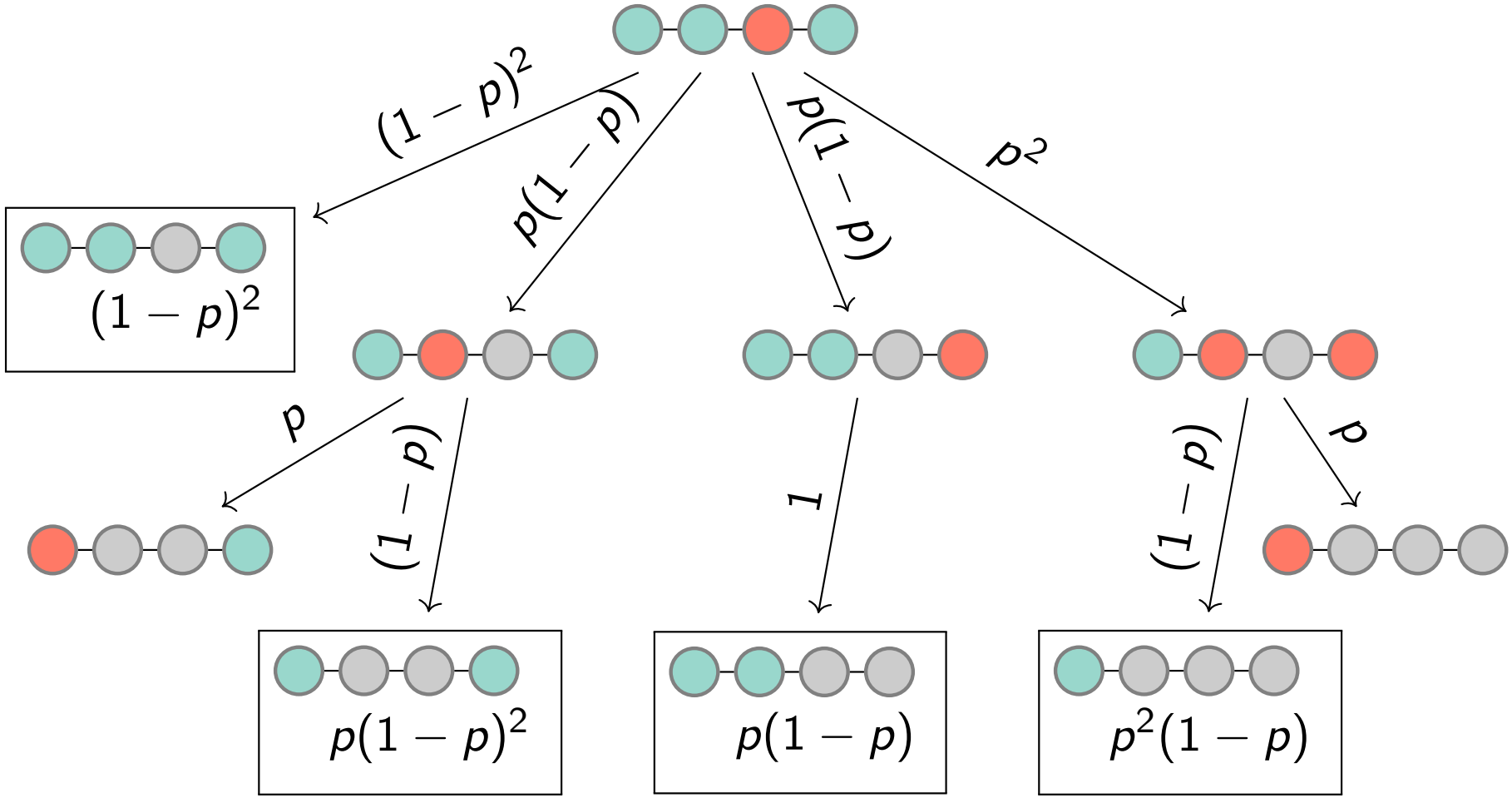

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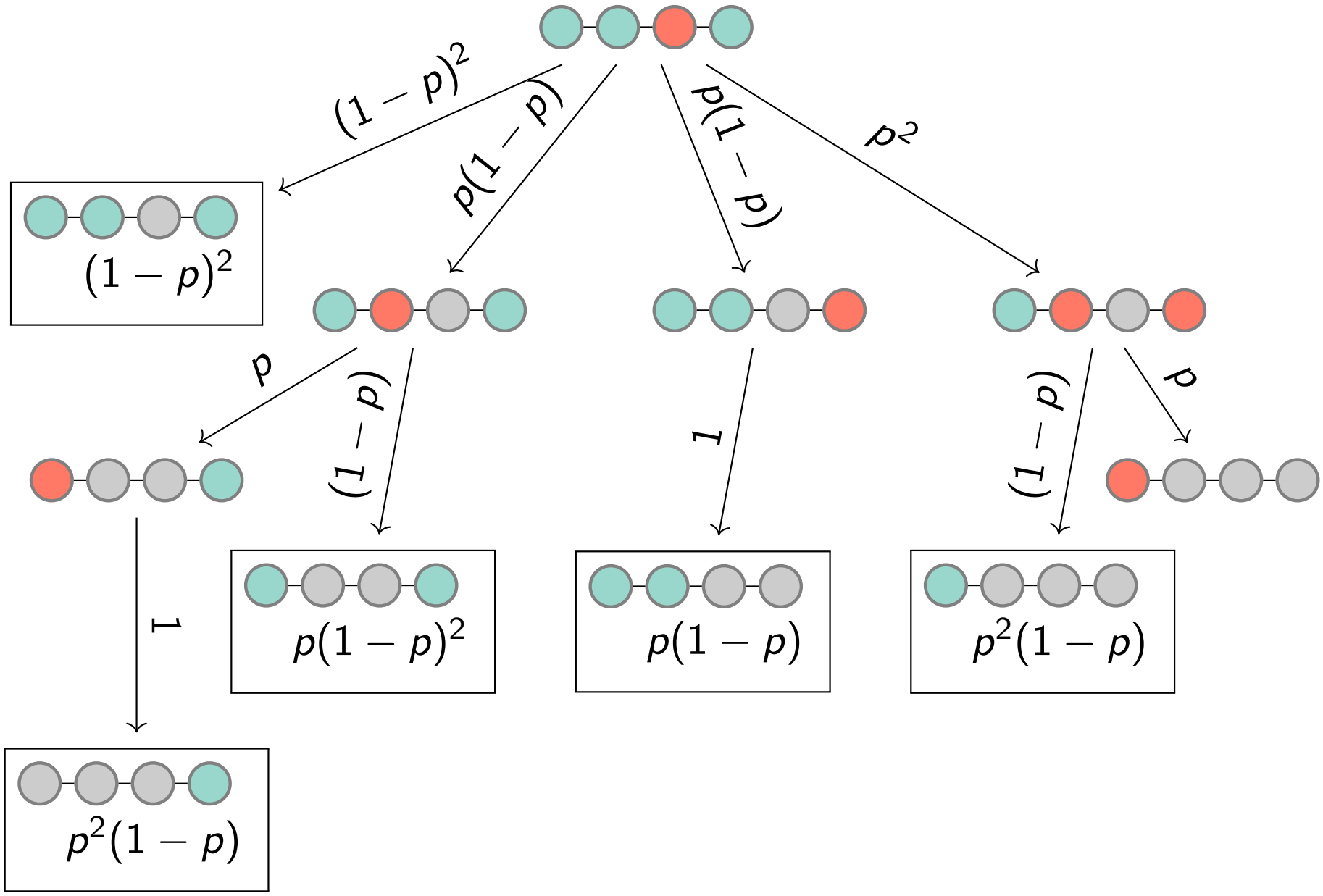

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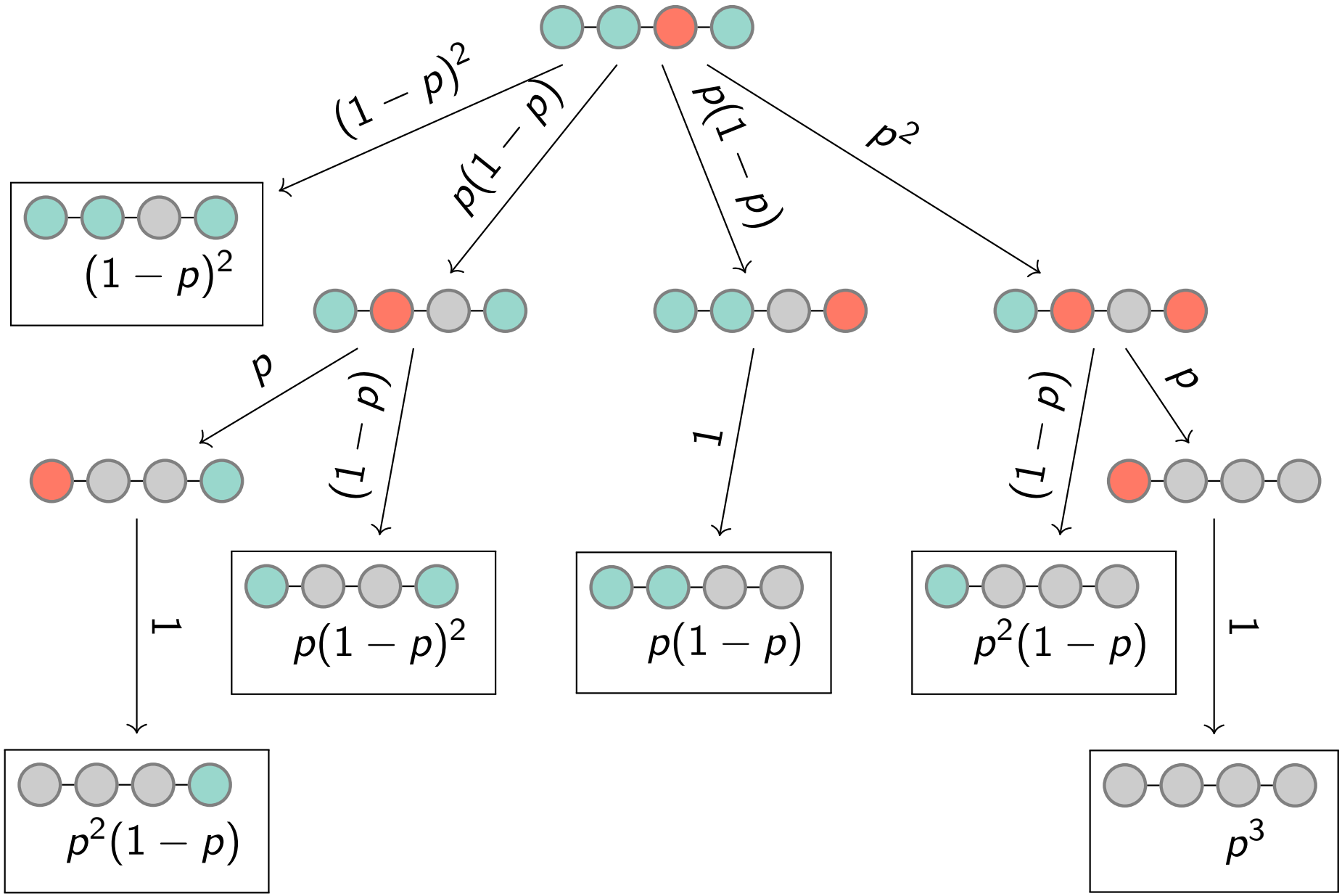
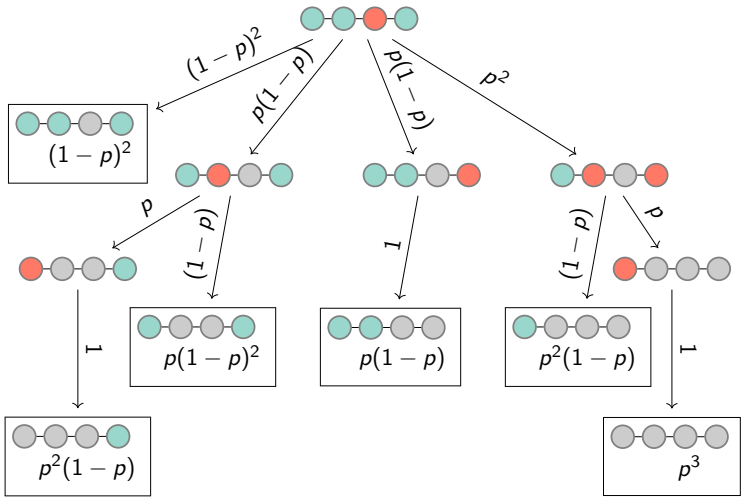


Alternative perspective



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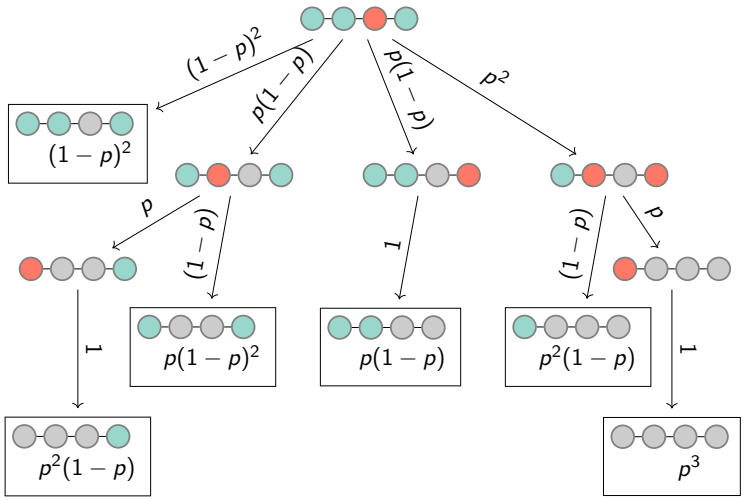
- 

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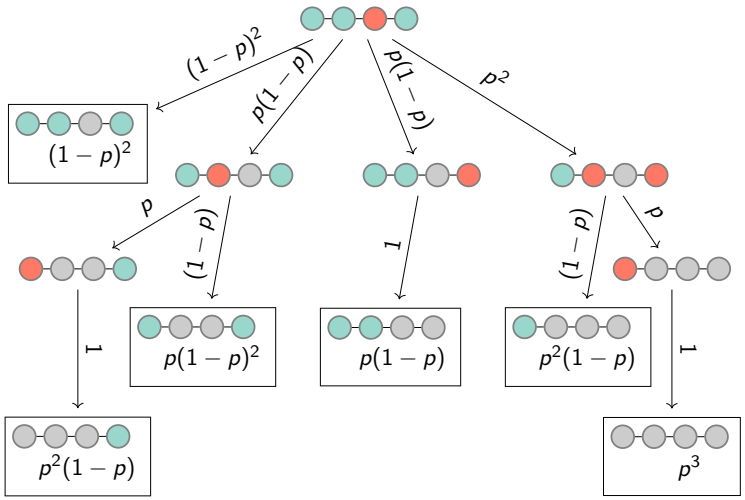
- 

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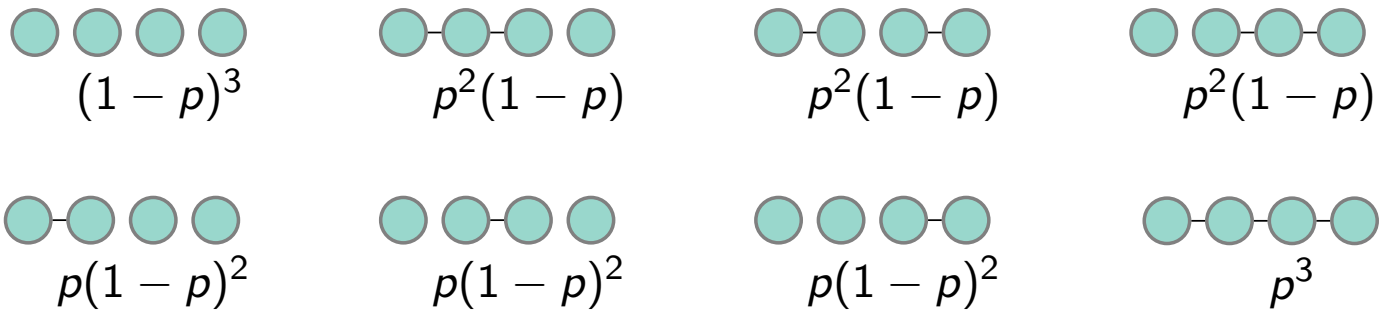
- 

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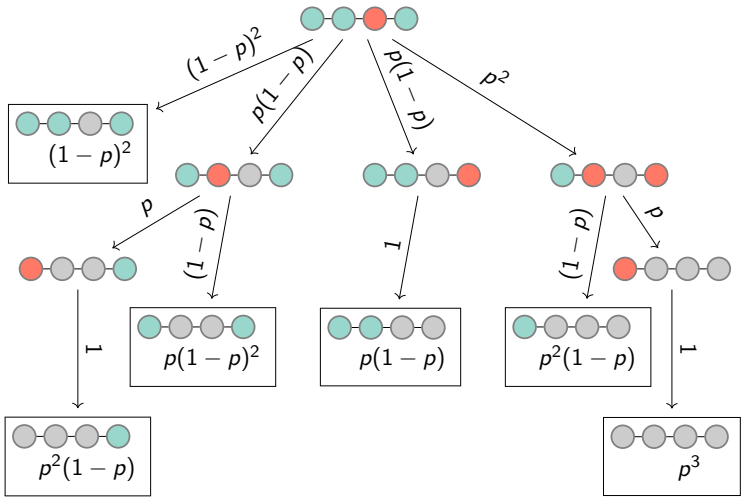
- 

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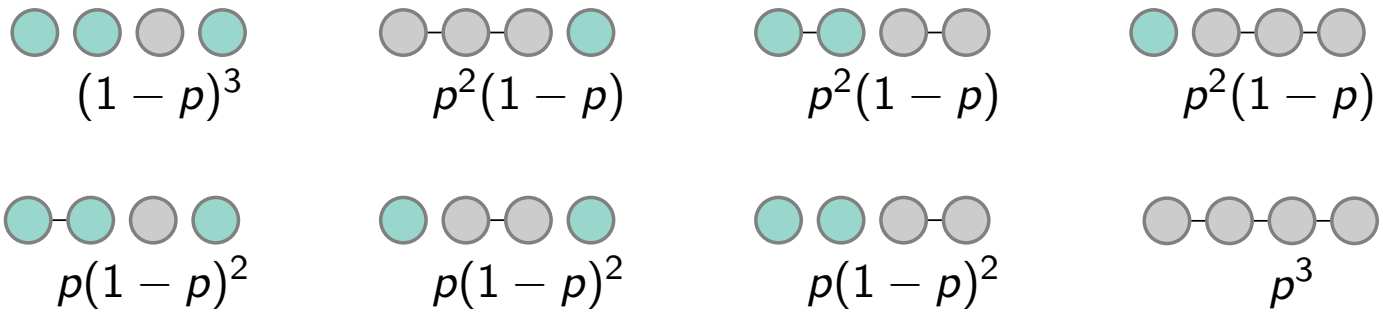
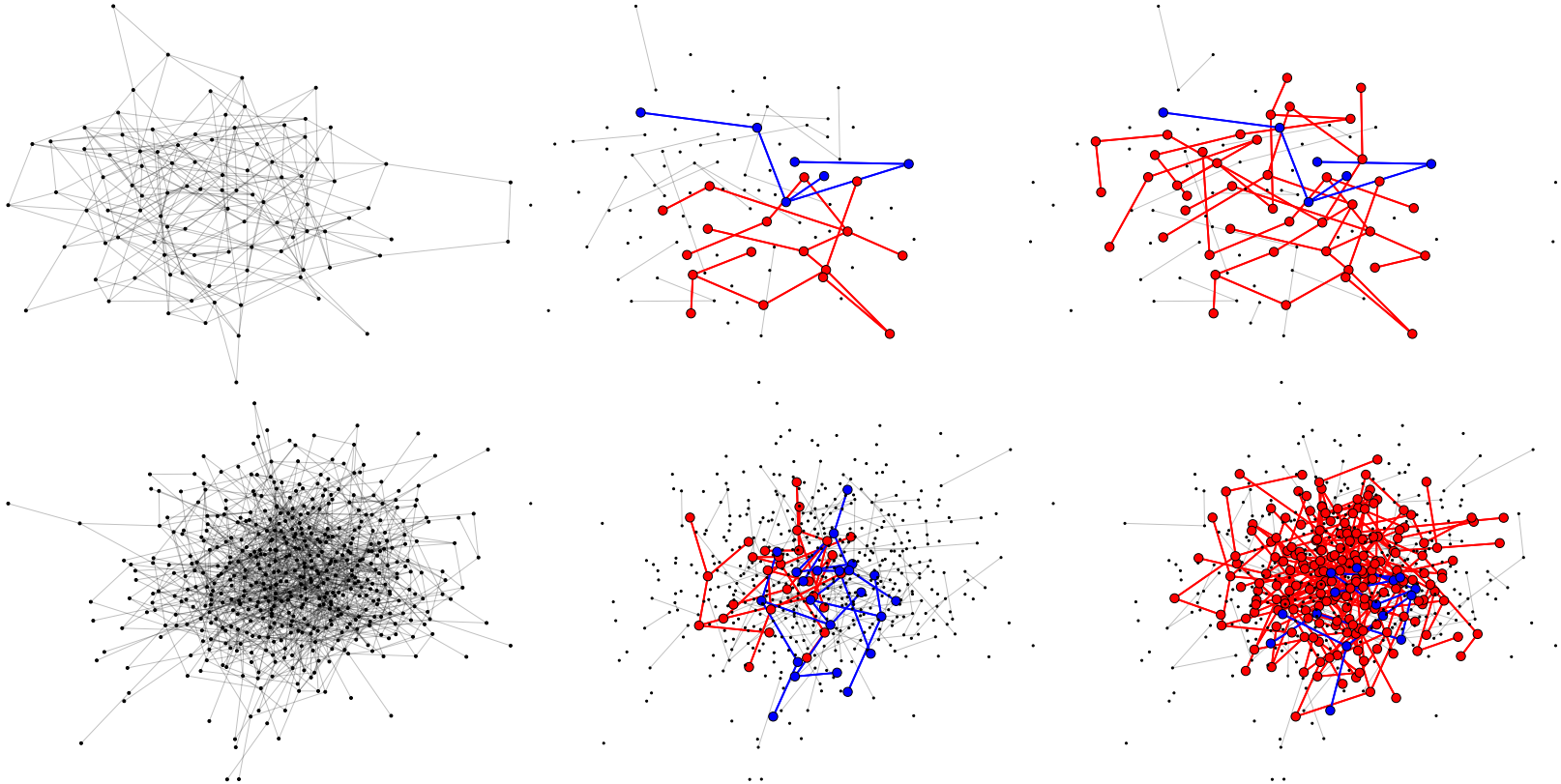
- 

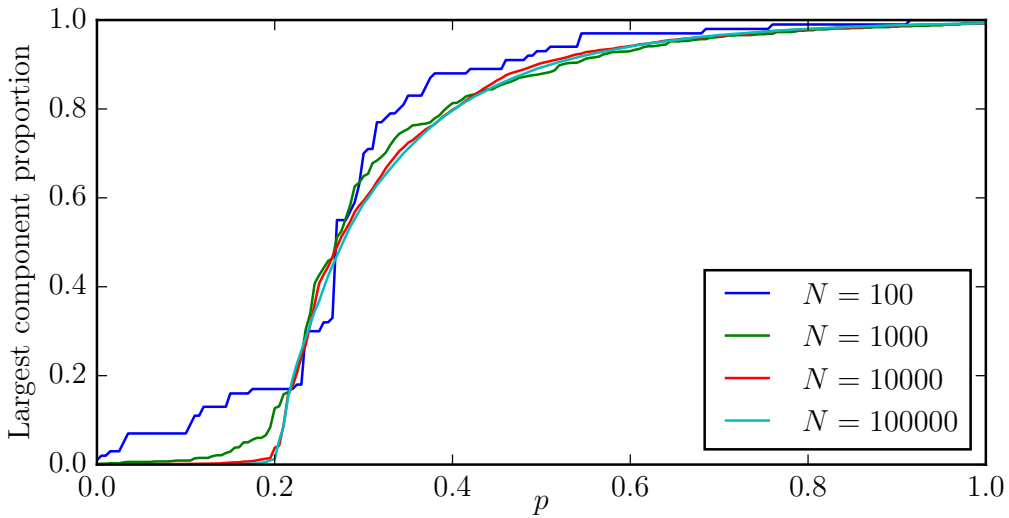
Percolation in different size networks

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

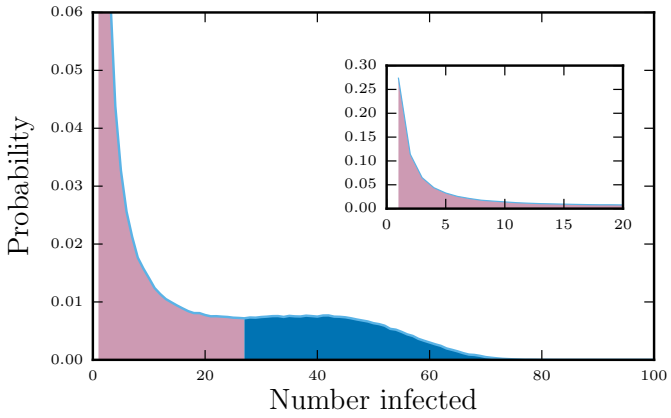


- Below threshold largest and second largest in a network are about the same size as each other and similar size in both networks
- Above threshold largest is proportional to network size.

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.


Probability
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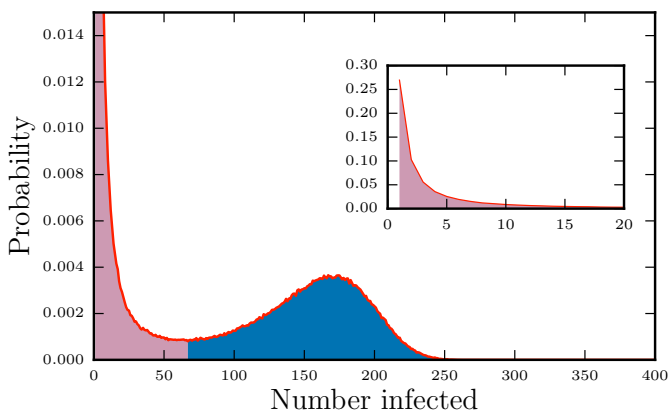
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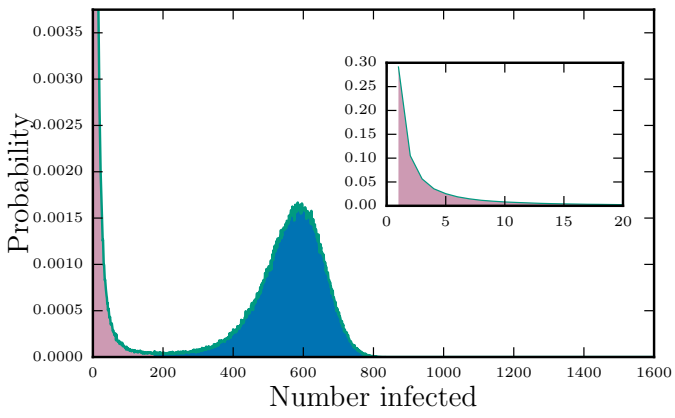
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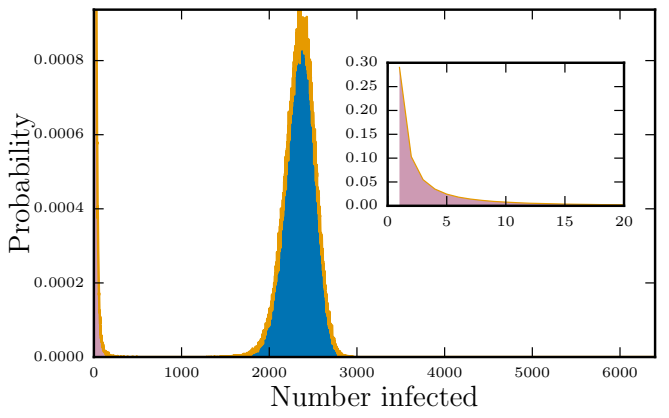
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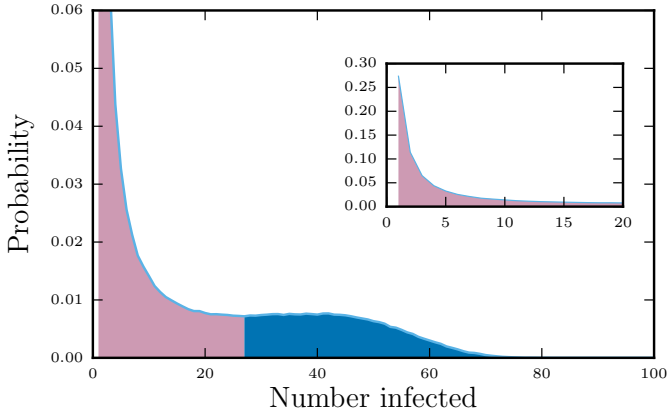

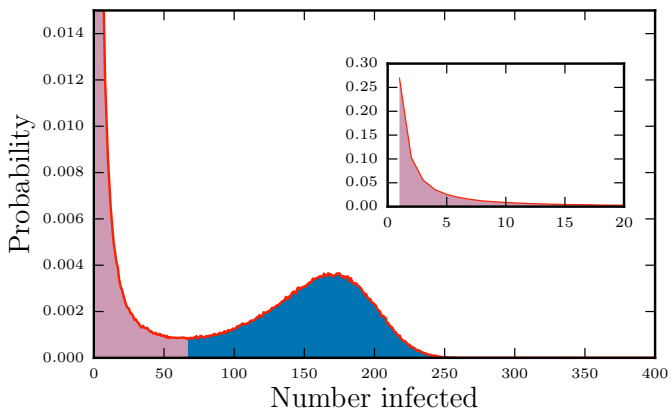

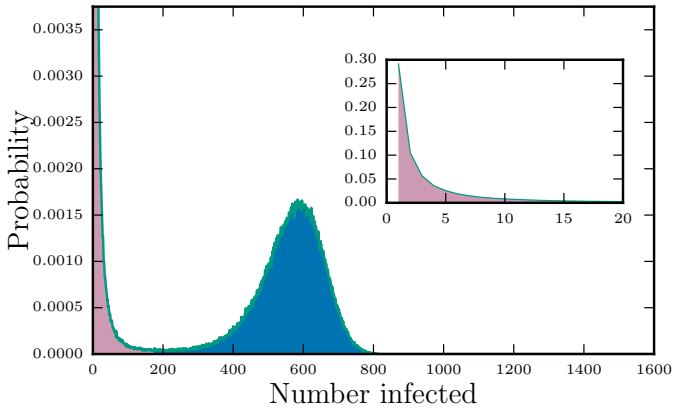

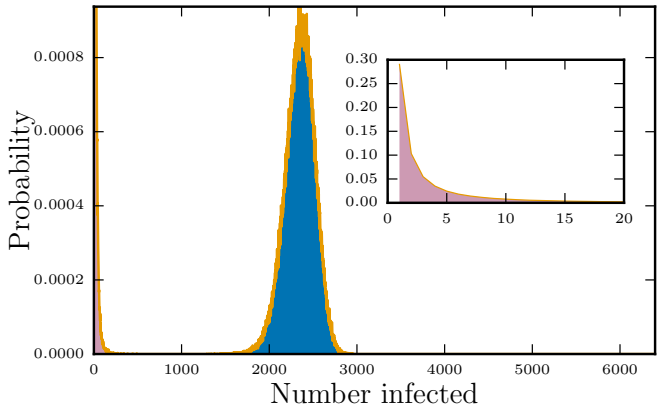

N	$\mathcal{P}$	$\mathcal{A}$
100	0.237	0.423
400	0.340	0.387
1600	0.339	0.350
6400	0.365	0.366
25600	0.368	0.368

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.

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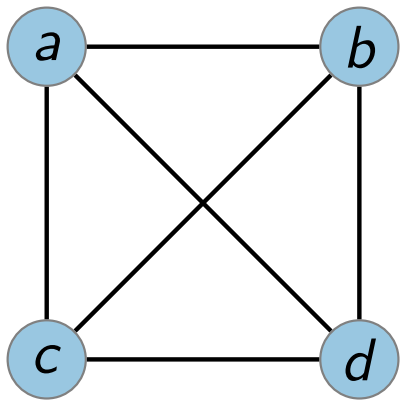
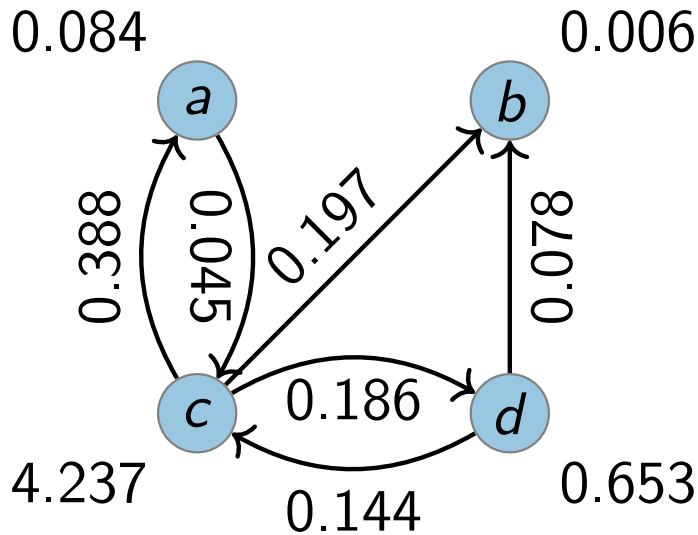
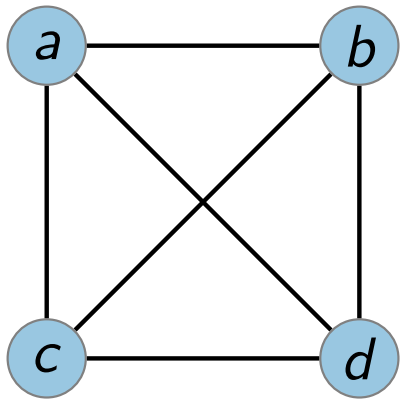
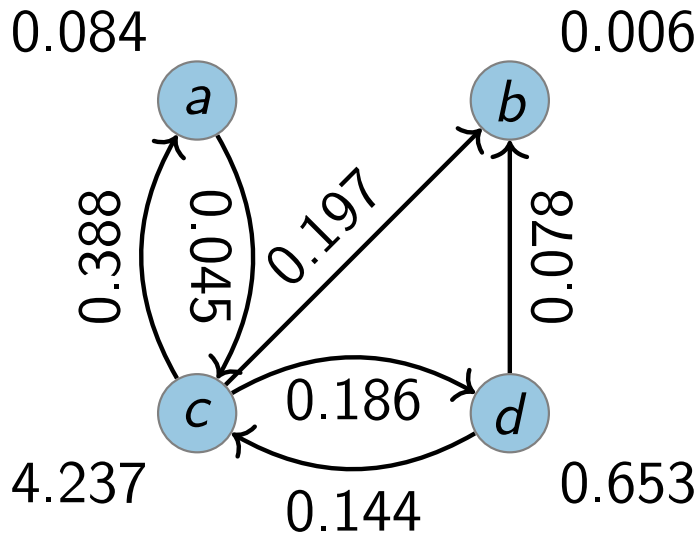
- Is it possible for me to know whether he is calculating in advance or not?


a
b
c
d

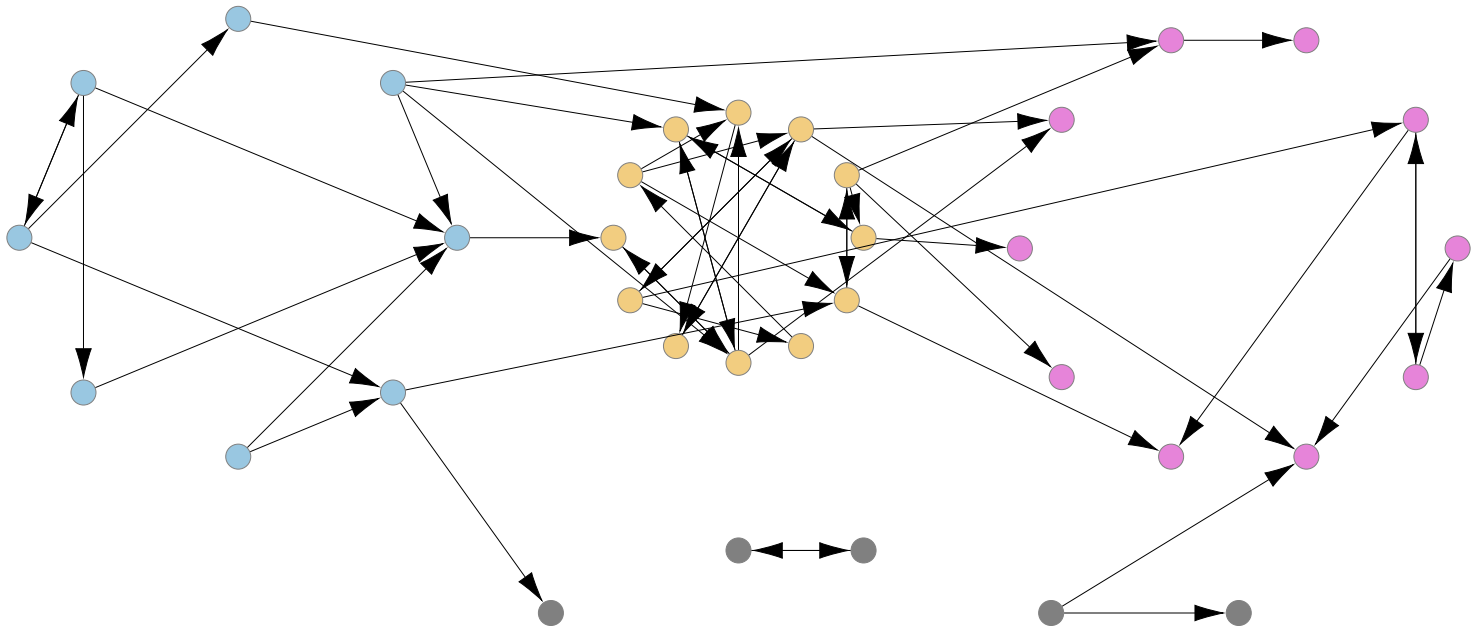

0.084
0.006
a
b
0.388
0.045
0.197
0.078
c
0.186
d
4.237
0.144
0.653





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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  - 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.

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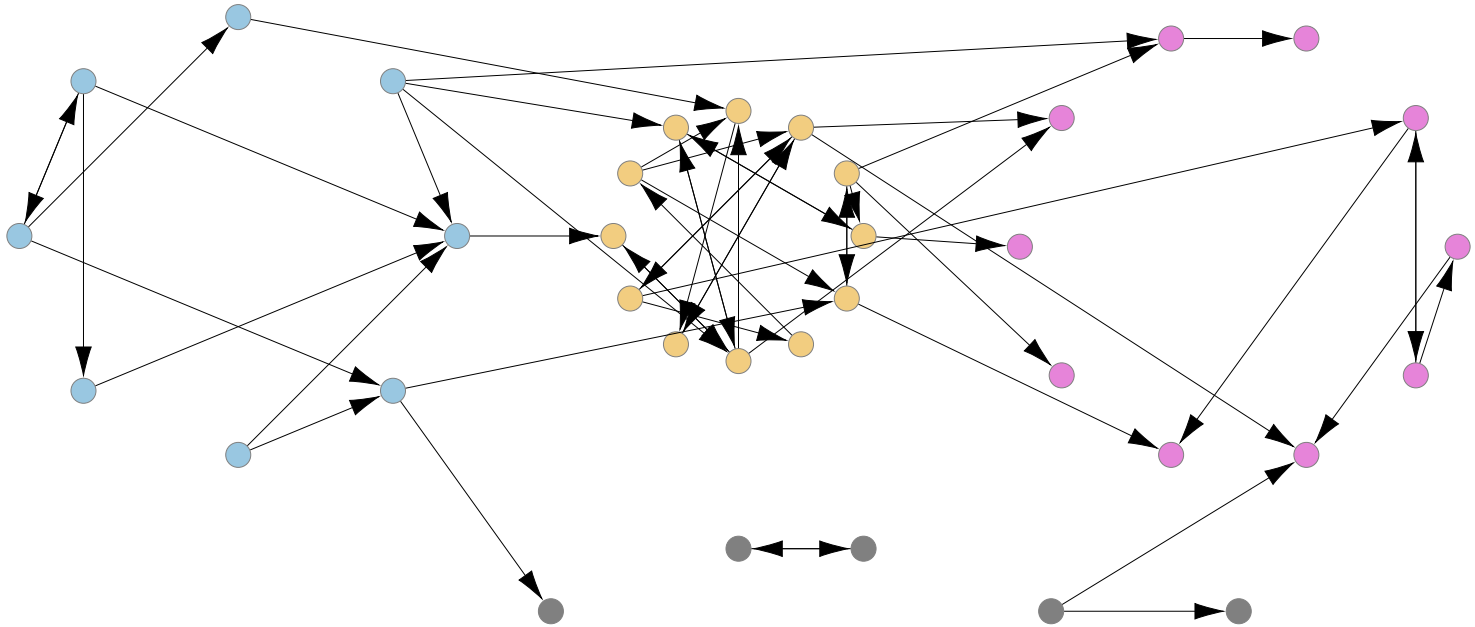

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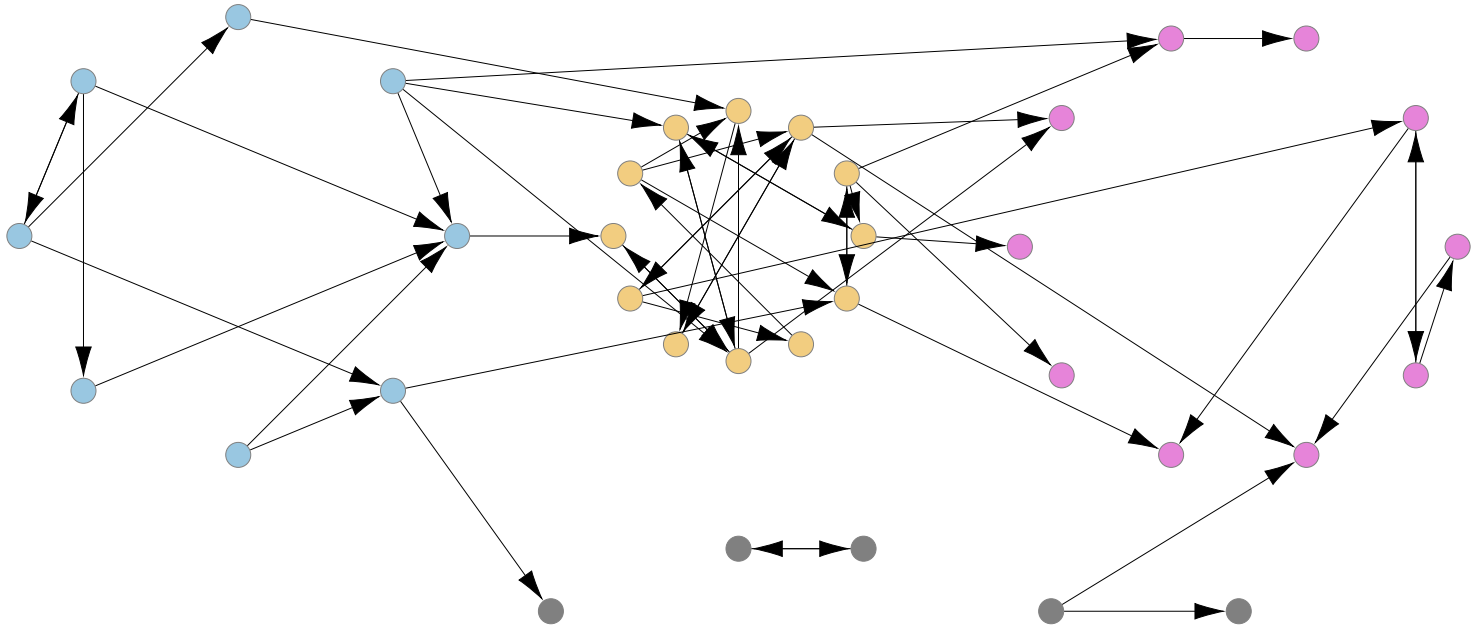

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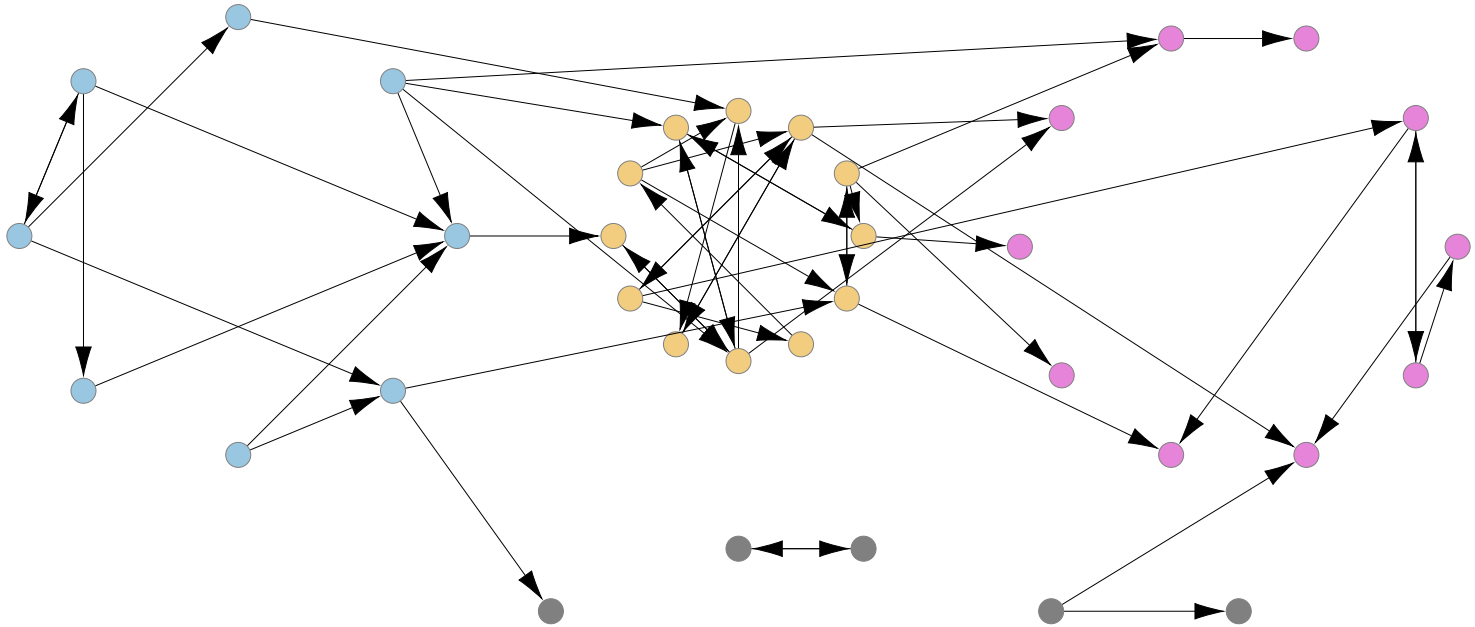

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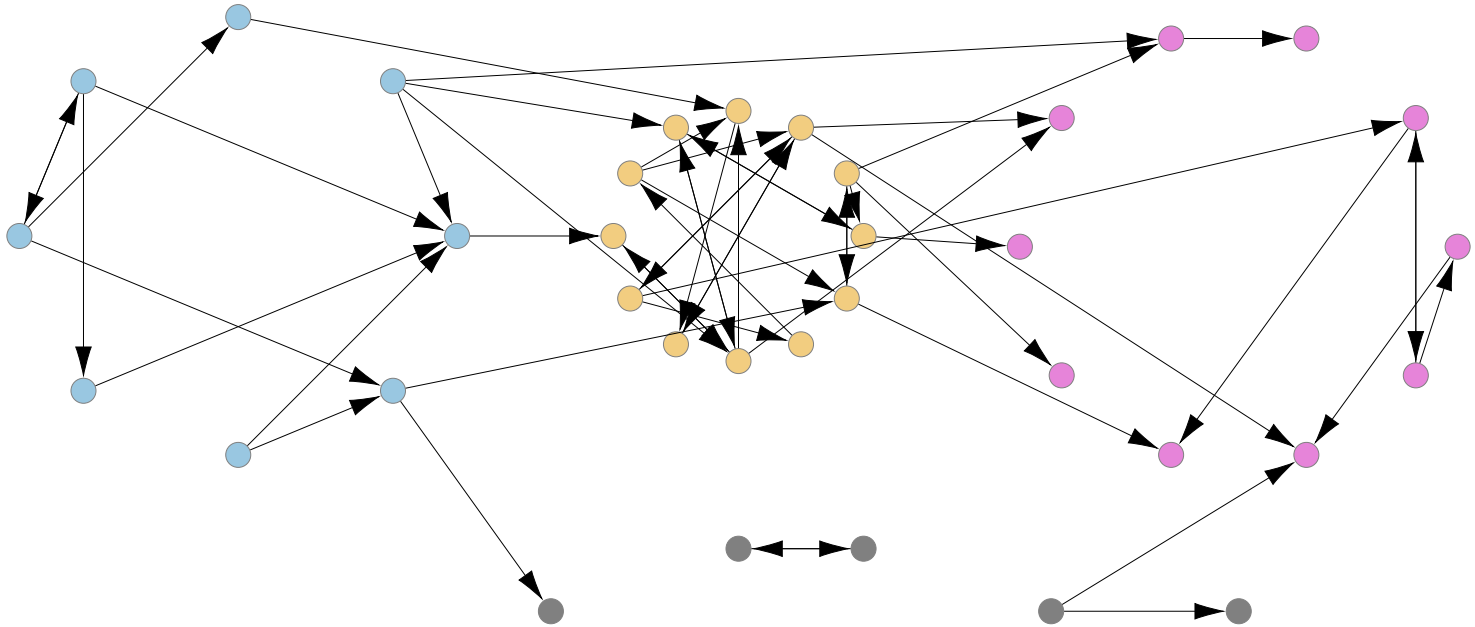

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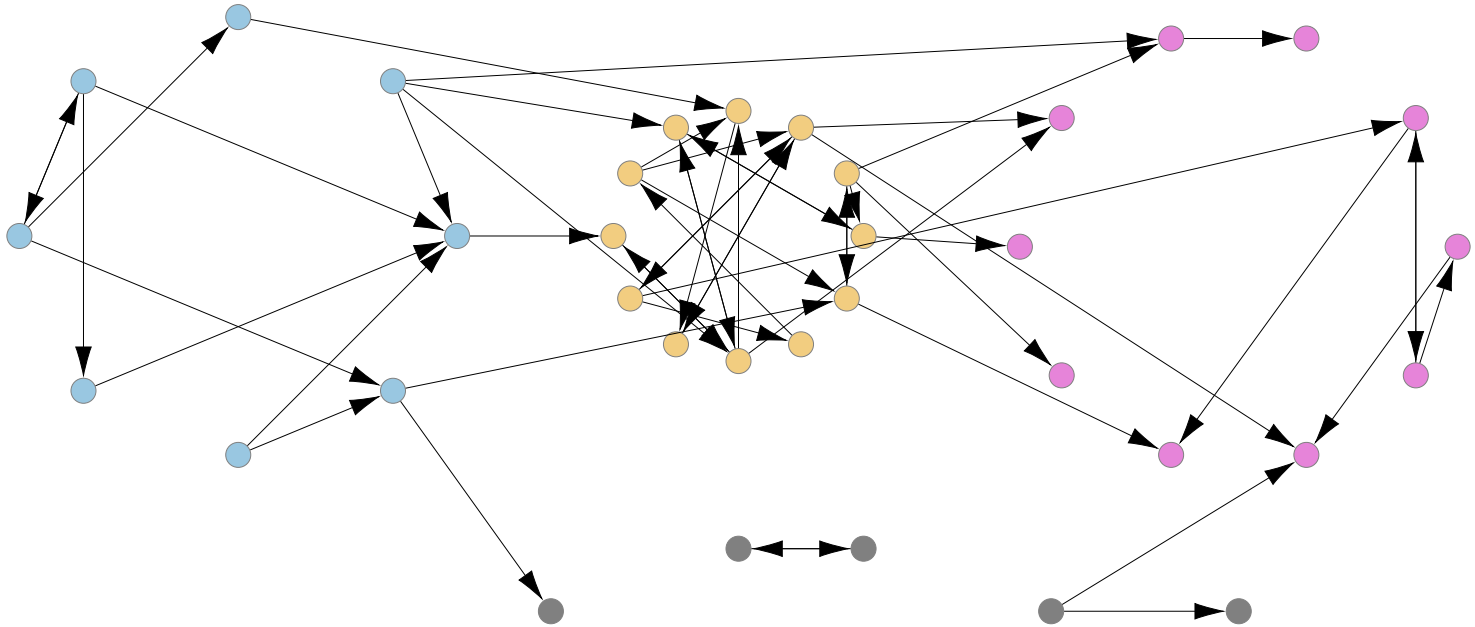

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- If the index case is in H_{IN} or H_{SCC} then all of H_{SCC} and H_{OUT} are eventually infected.
- So Epidemic Probability $\mathcal{P} = \mathbb{E}(|H_{IN} \cup H_{SCC}|)/N$ and Attack rate $\mathcal{A} = \mathbb{E}(|H_{SCC} \cup H_{OUT}|)/N$.

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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
- $\mathcal{R}_0$
- $I(t)$

$\mathcal{R}_0$ calculation

For SIR disease:

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Recall our key questions

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- $\mathcal{P}$, the probability of an epidemic.
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- $\mathcal{R}_0$, the average number of infections caused by those infected early in the epidemic.
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For SIS:

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Changing the final size question

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

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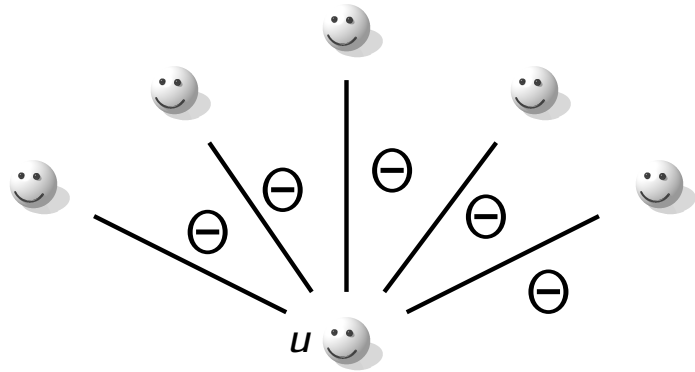
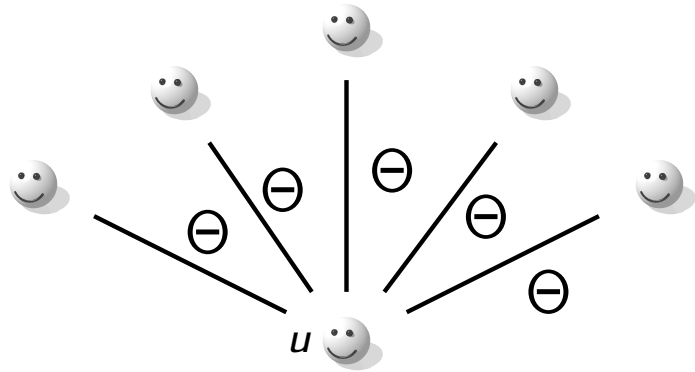
What is the probability a random node does not have a transmission path to it from one of the index nodes?



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



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

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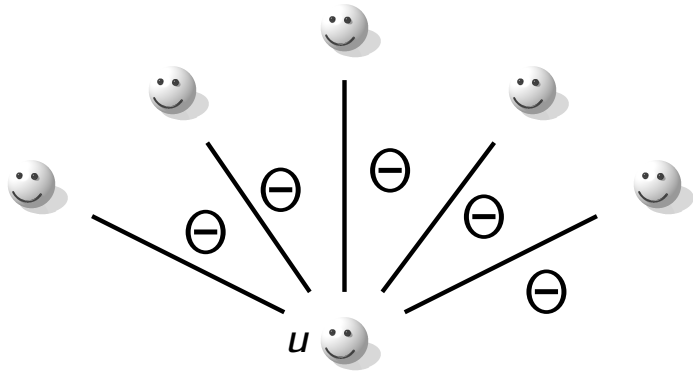

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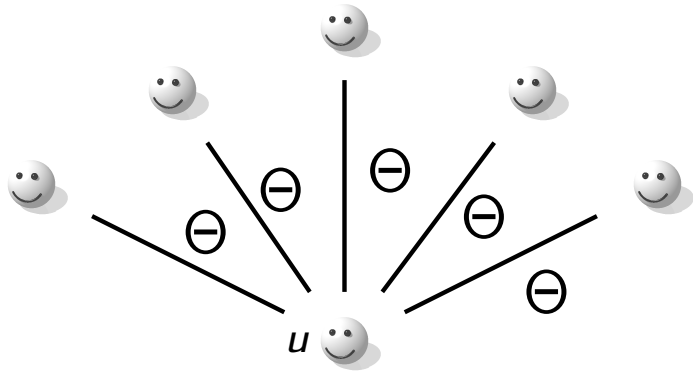

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where

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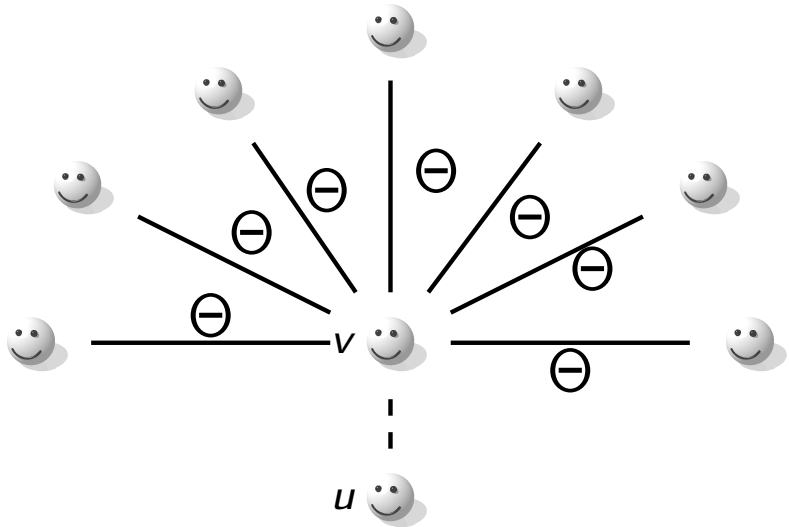
Finding Θ



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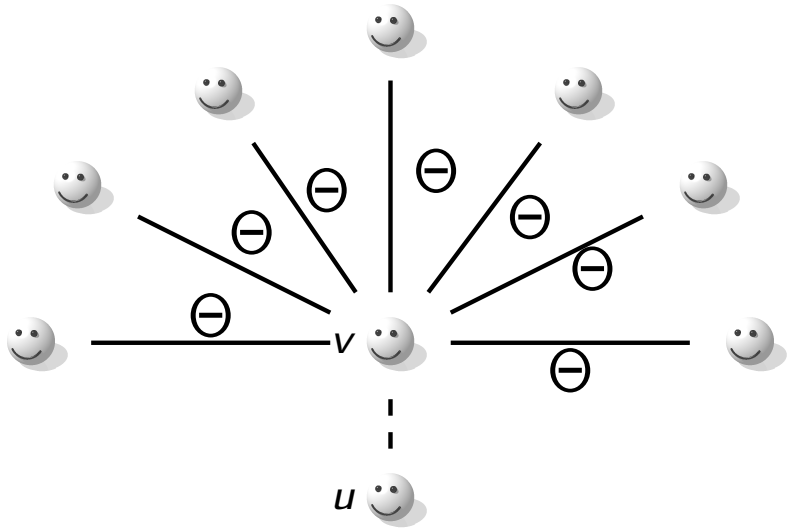

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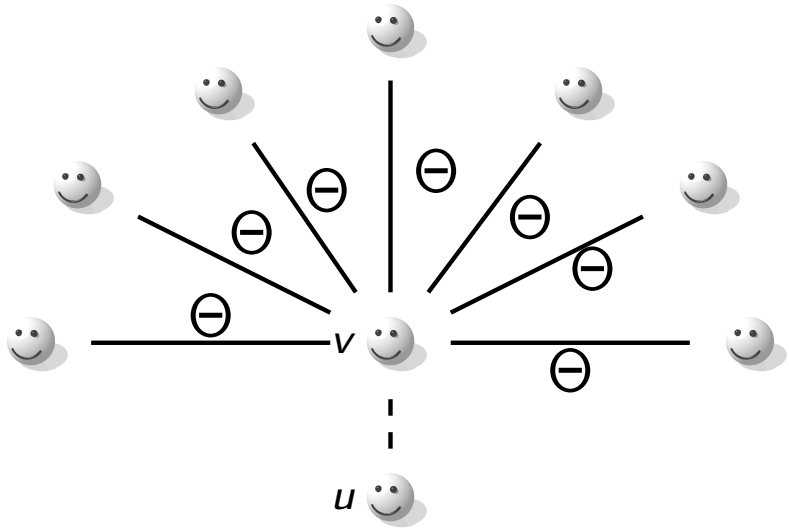

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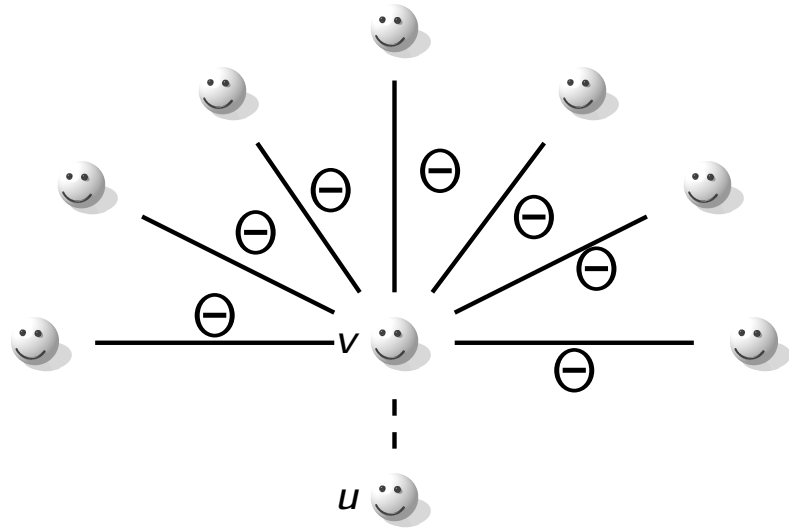

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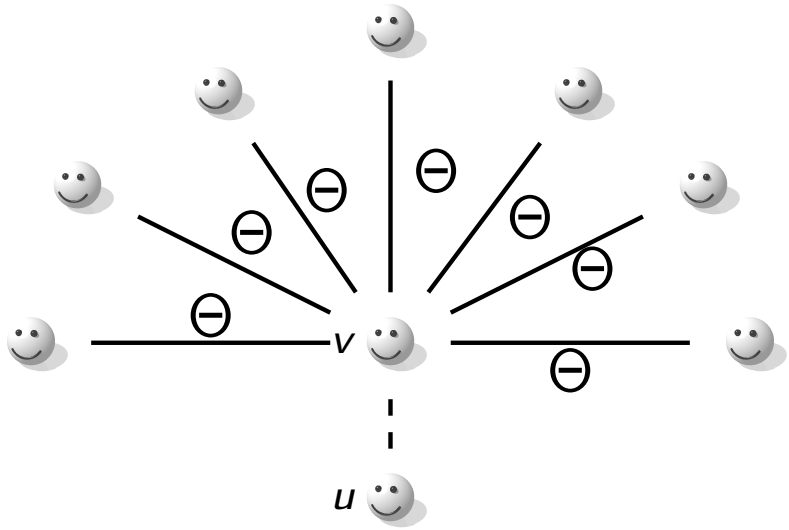

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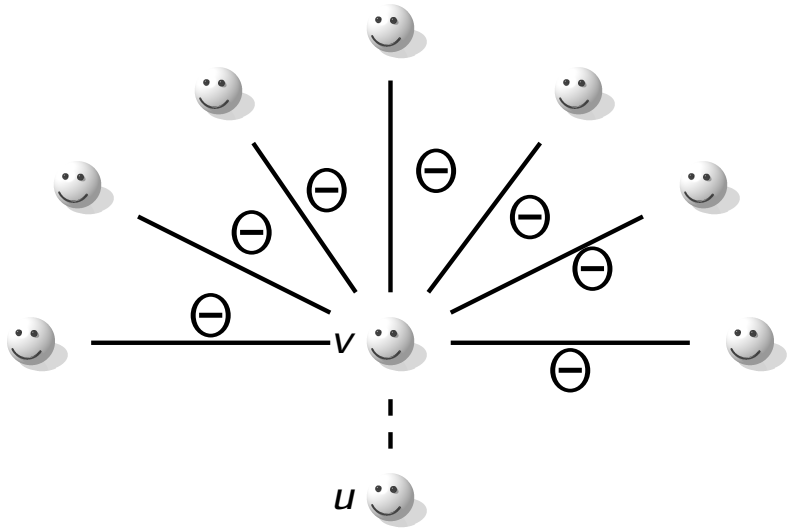

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Final Size

So

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

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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.

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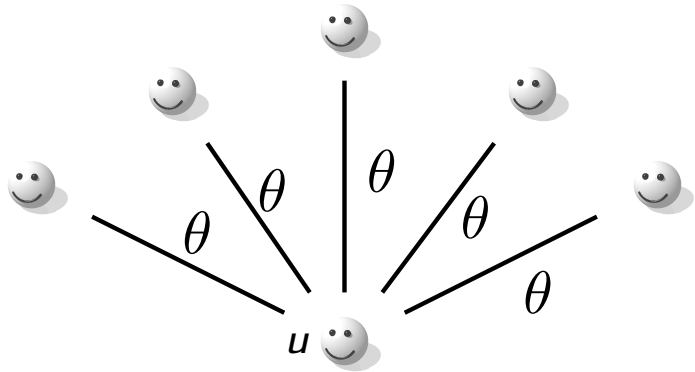
Finding $S(t)$ for SIR disease



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

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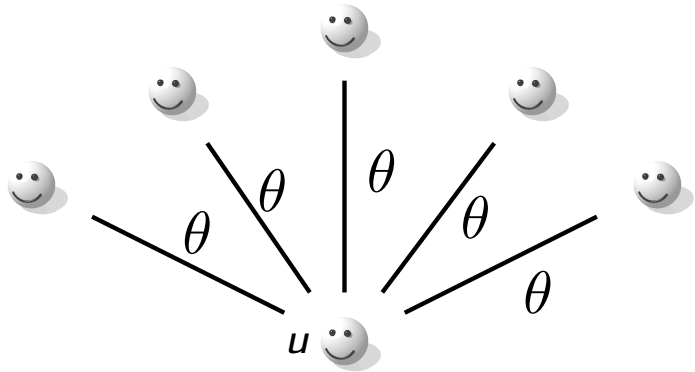

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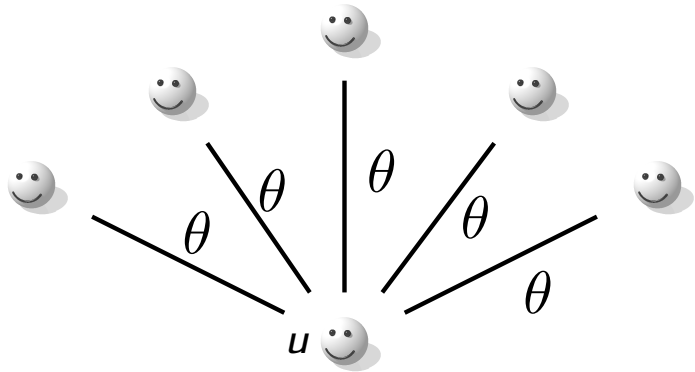

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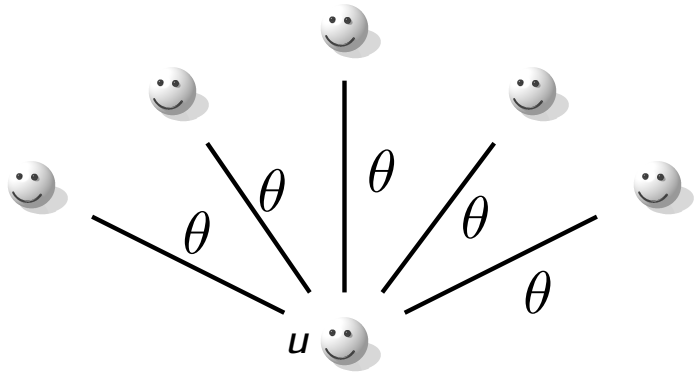

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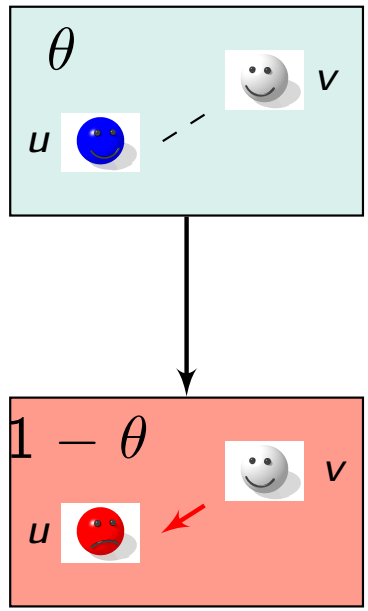
How does θ evolve?



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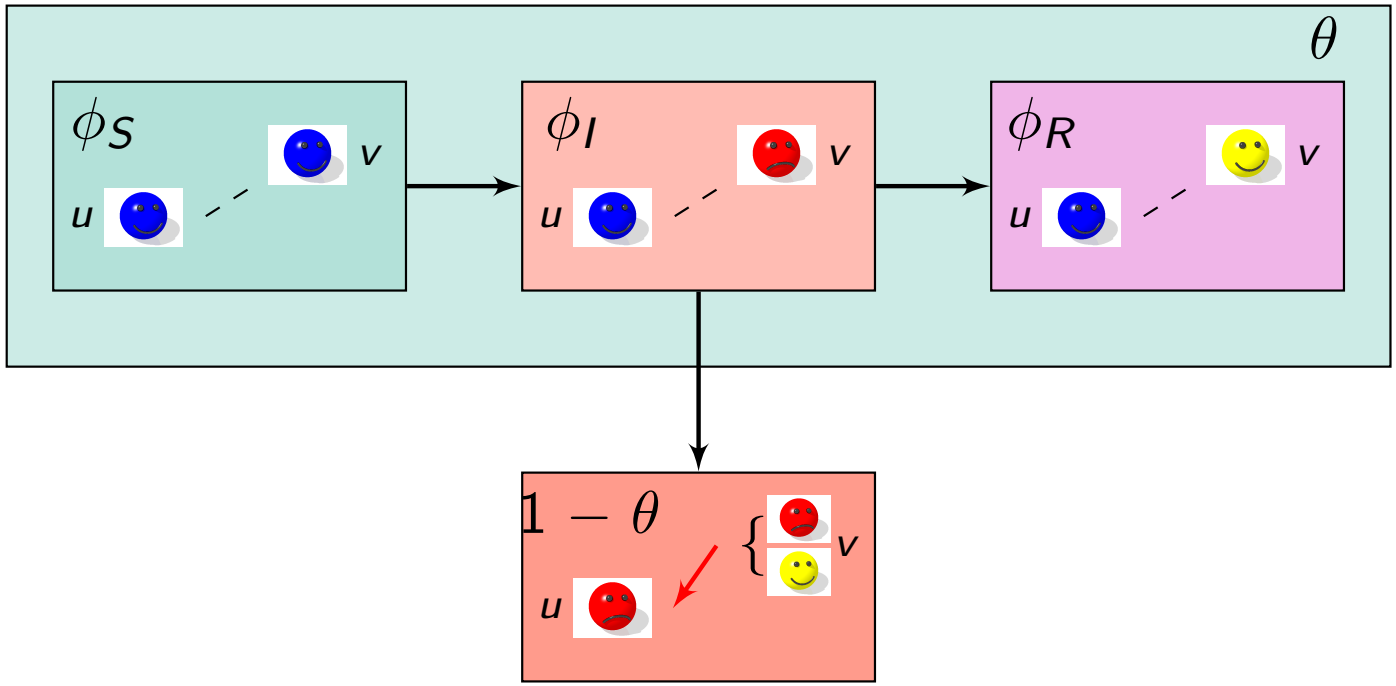

- $\theta = \phi_S + \phi_I + \phi_R$.

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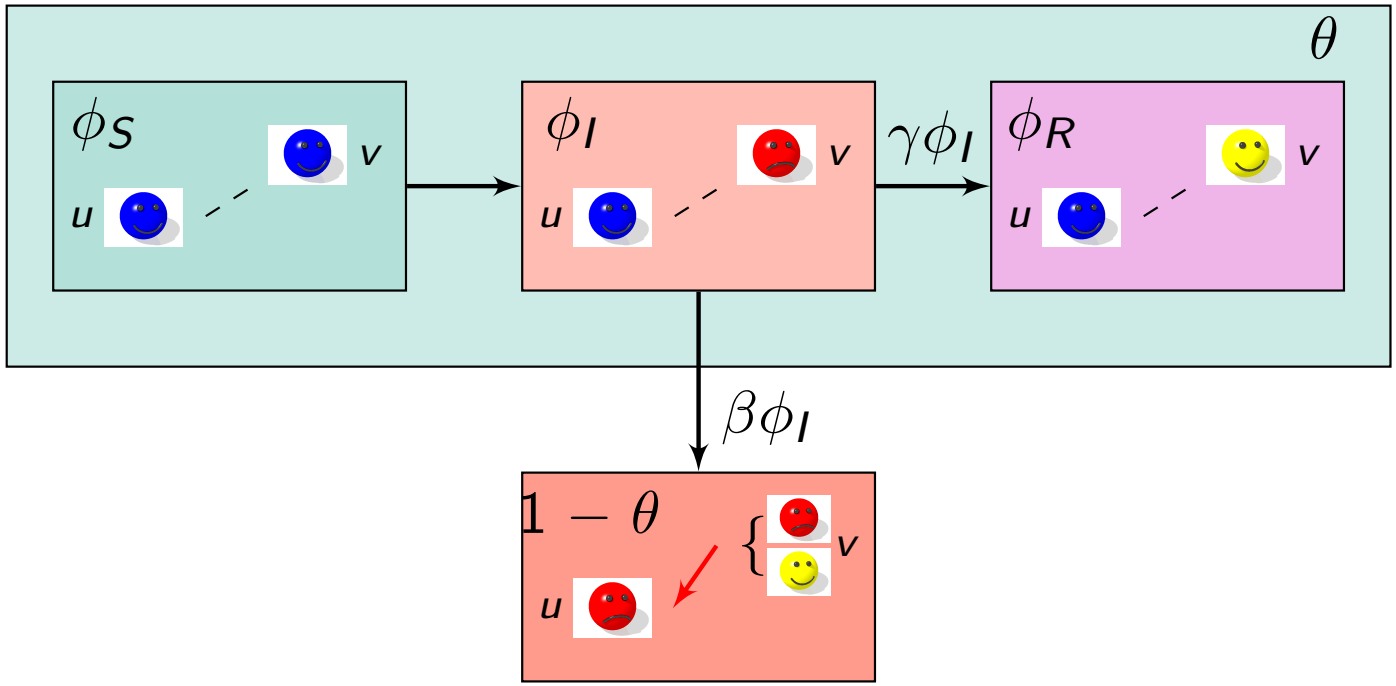

- $\theta = \phi_S + \phi_I + \phi_R$.
- $\dot{\theta} = -\beta\phi_I$.

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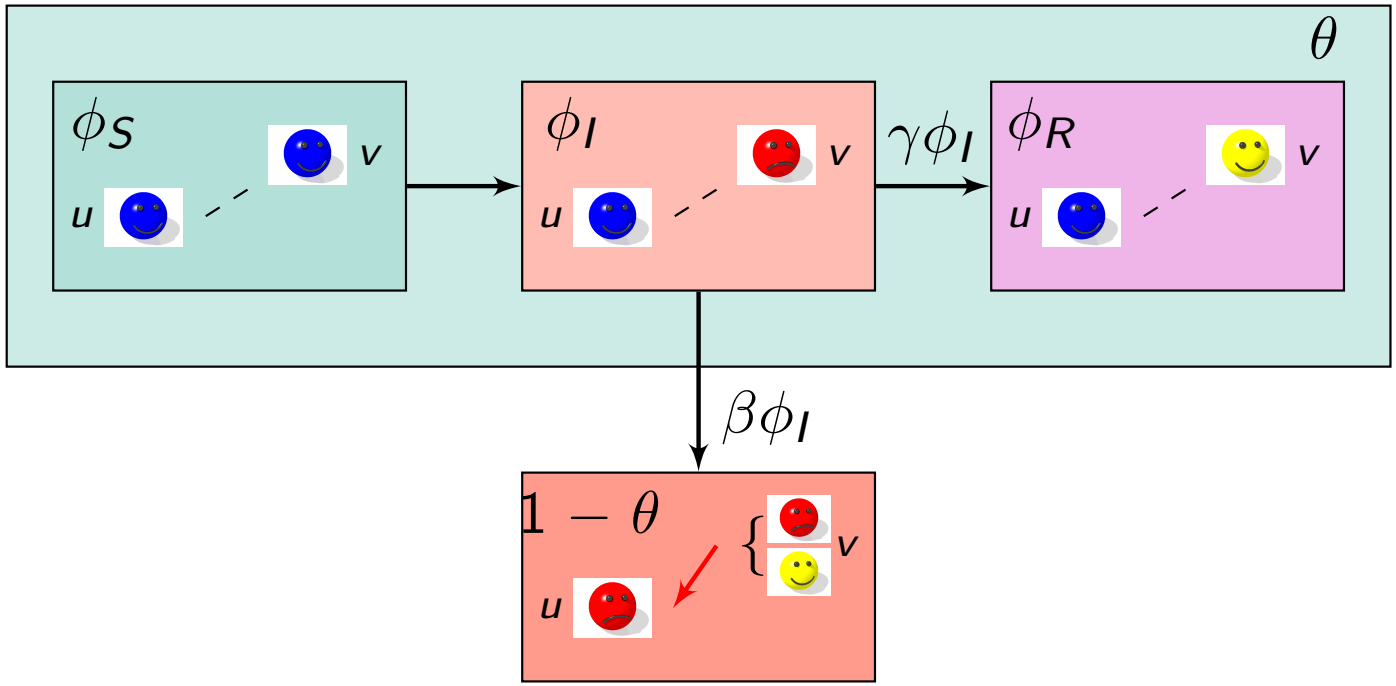
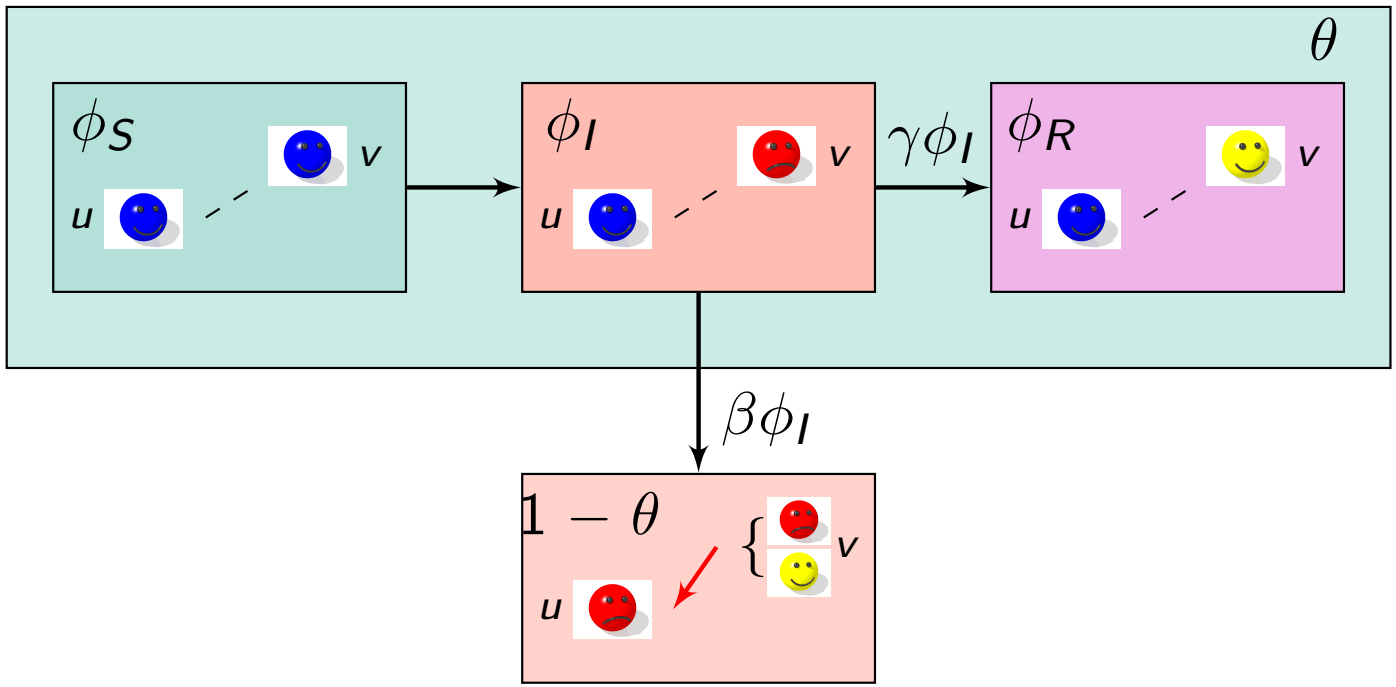


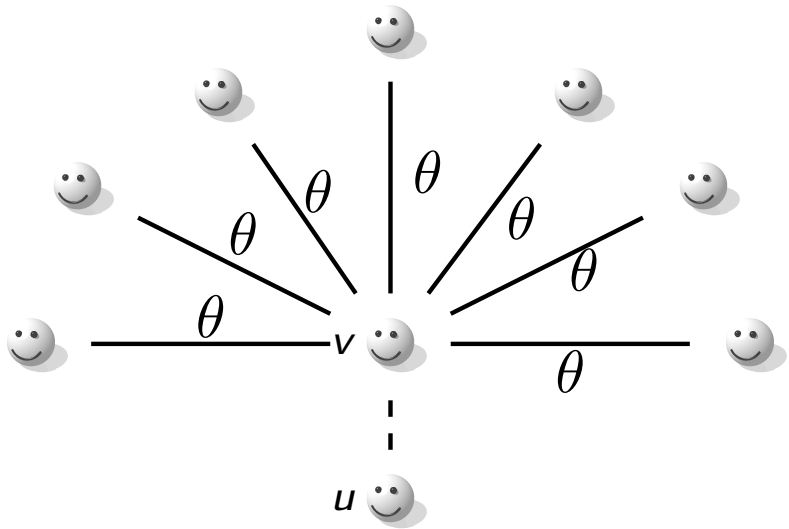
- $\theta = \phi_S + \phi_I + \phi_R$.
- $\dot{\theta} = -\beta\phi_I$.
- Our goal is to find ϕ_I in terms of θ.

Finding $\phi_R(t)$



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

Finding $\phi_S(t)$



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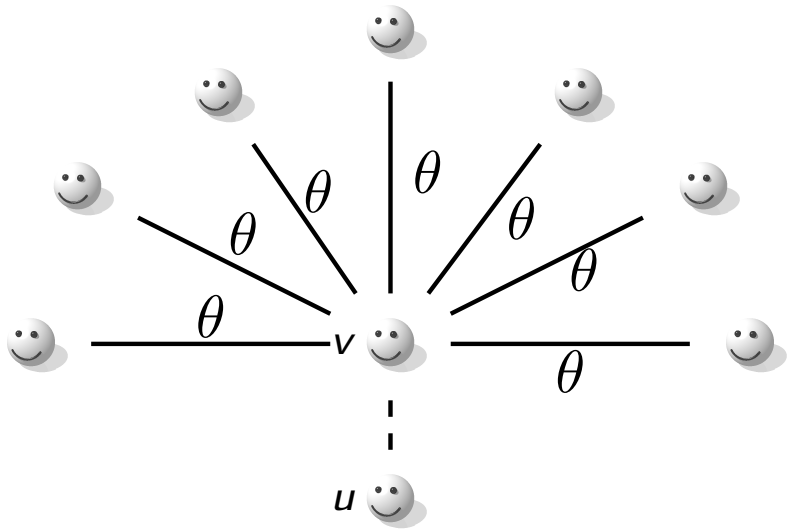

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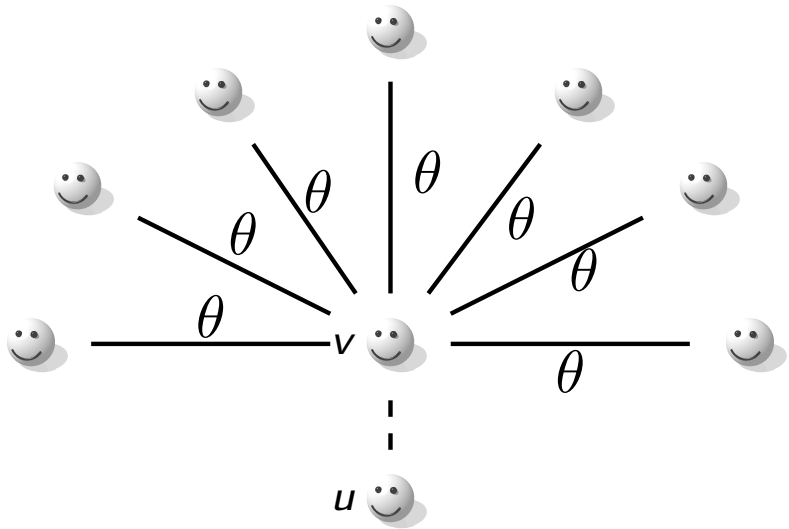

Probability a random ~~degree k~~ partner still susceptible is

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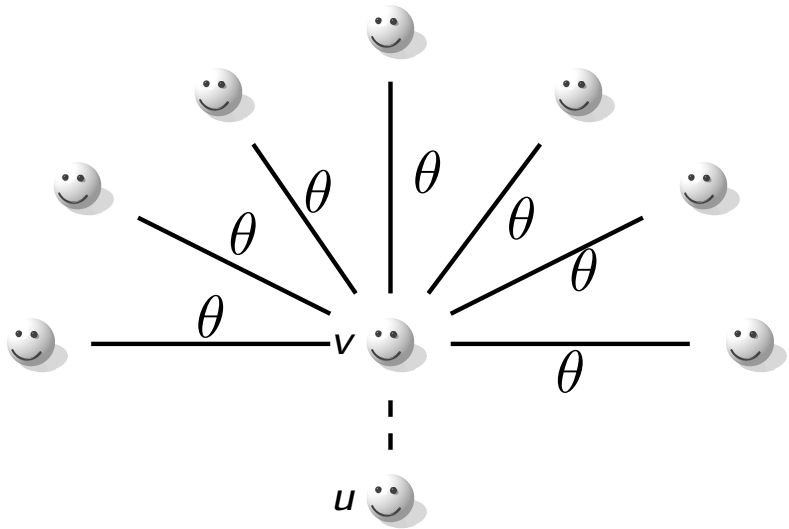

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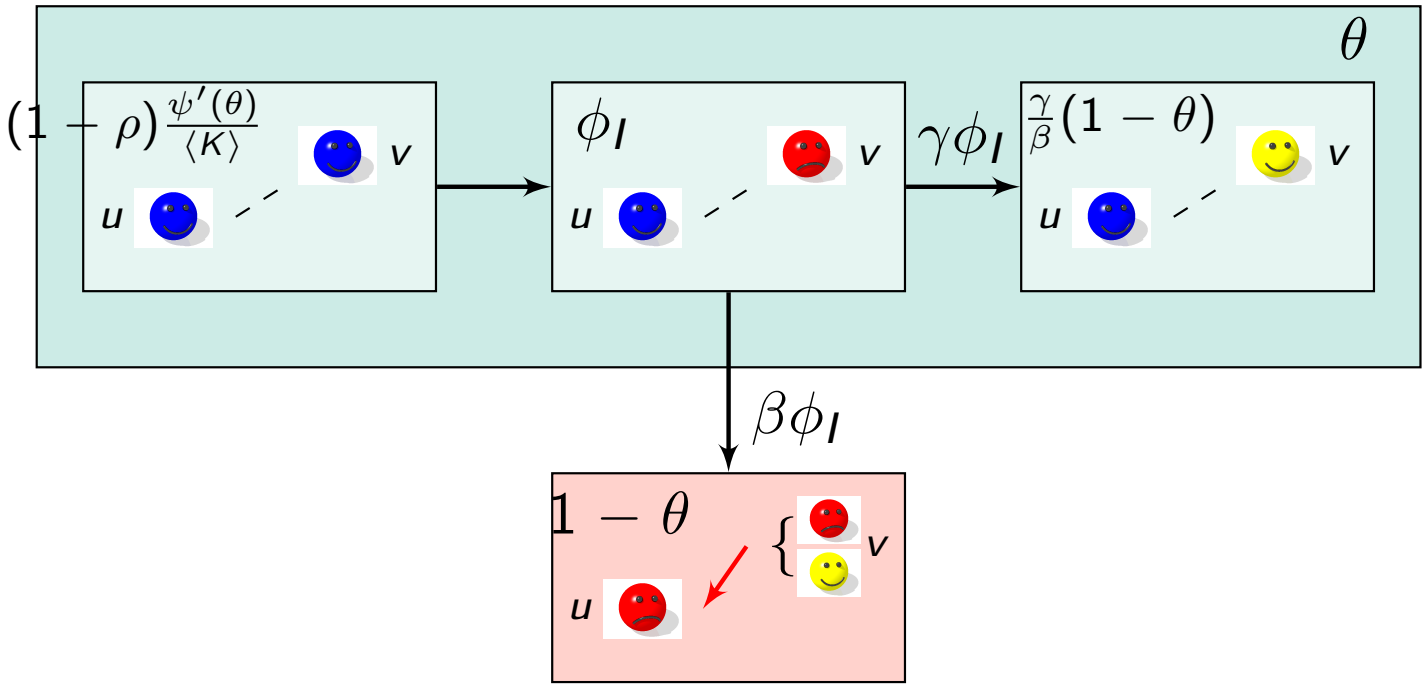
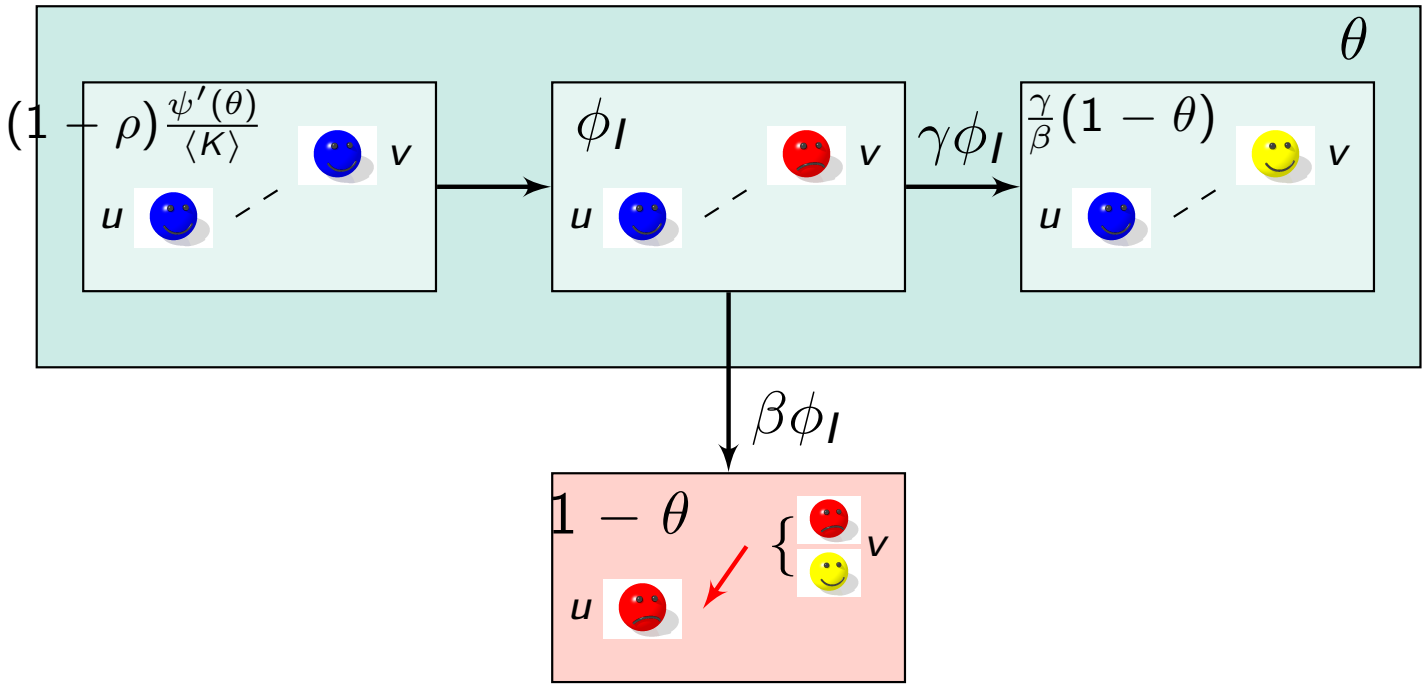


We have

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

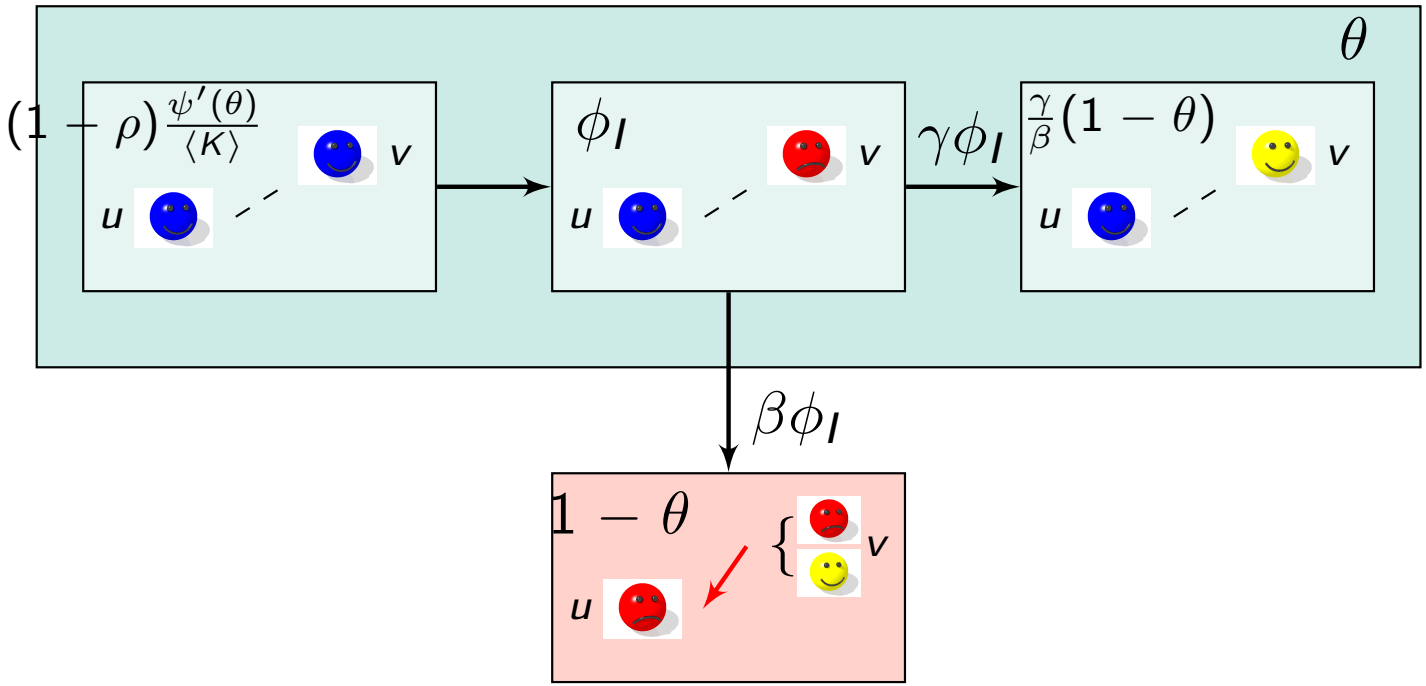
$$\dot{\theta} = -\beta\phi_I$$



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

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

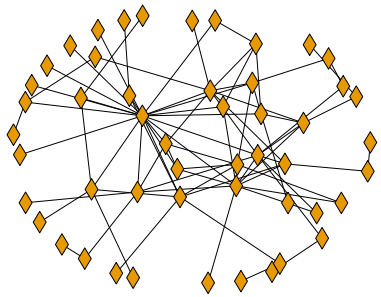
$$\dot{R} = \gamma I \qquad S = (1-\rho)N\psi(\theta) \qquad I = N - S - R$$

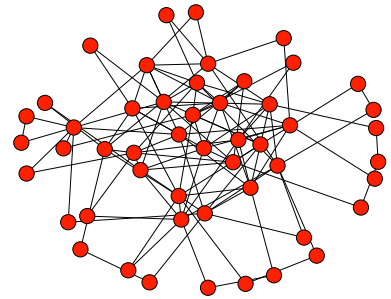
Compare with

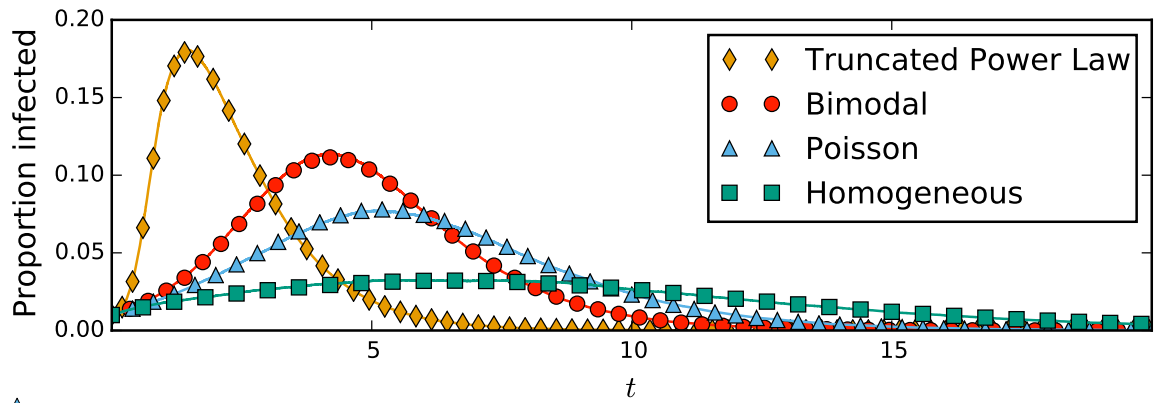
$$\dot{\theta} = -\beta\theta + \beta\theta^2\frac{(1-\rho)\psi'(\theta)}{\langle K\rangle} - \theta\gamma\ln\theta$$

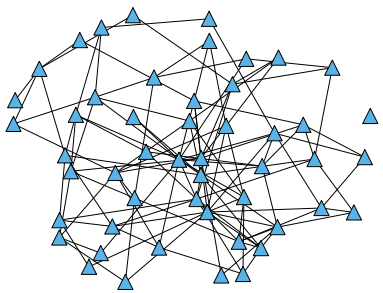
$$\dot{R} = \gamma I, \qquad S = (1-\rho)N\psi(\theta), \qquad I = N - S - R$$

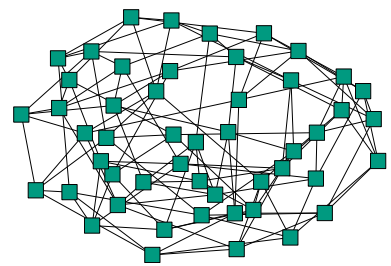
More details in [1, 2, 3]






Proportion infected
0.20
0.15
0.10
0.05
0.00
5
10
15
t
Truncated Power Law
Bimodal
Poisson
Homogeneous





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.

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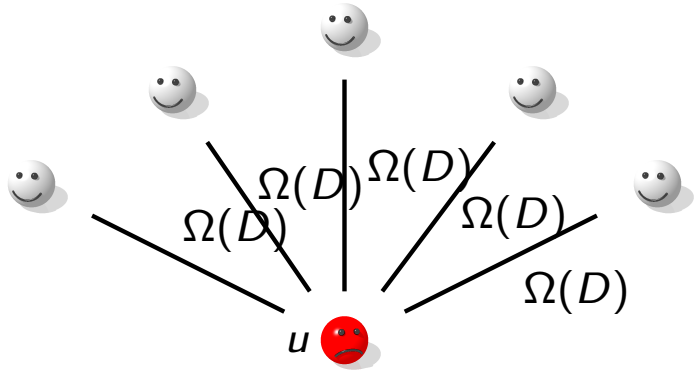
- $\psi(x) = \sum_k P(k)x^k$ is the probability generating function for the degree distribution.

Calculating epidemic probability



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

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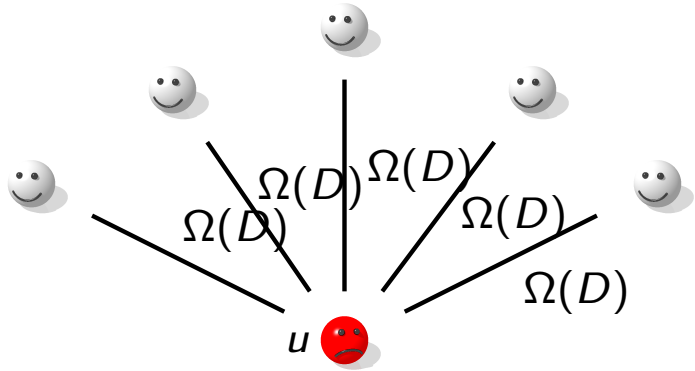

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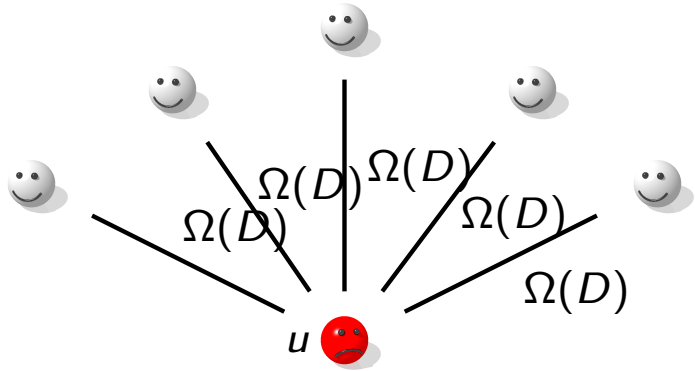

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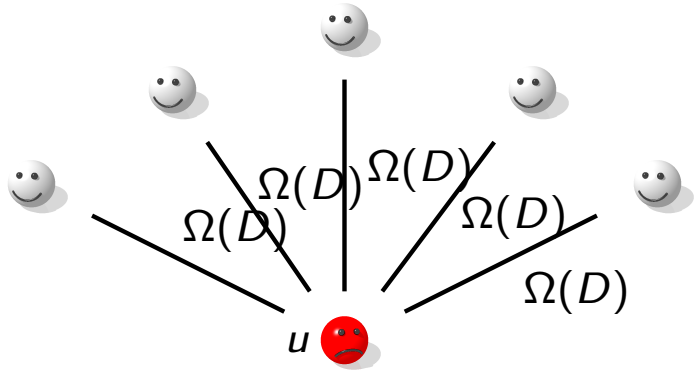
$$\sum_k P(k)\Omega(D)^k$$

Calculating epidemic probability



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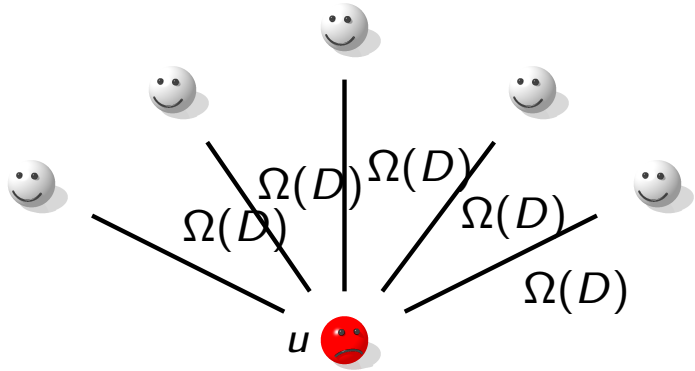

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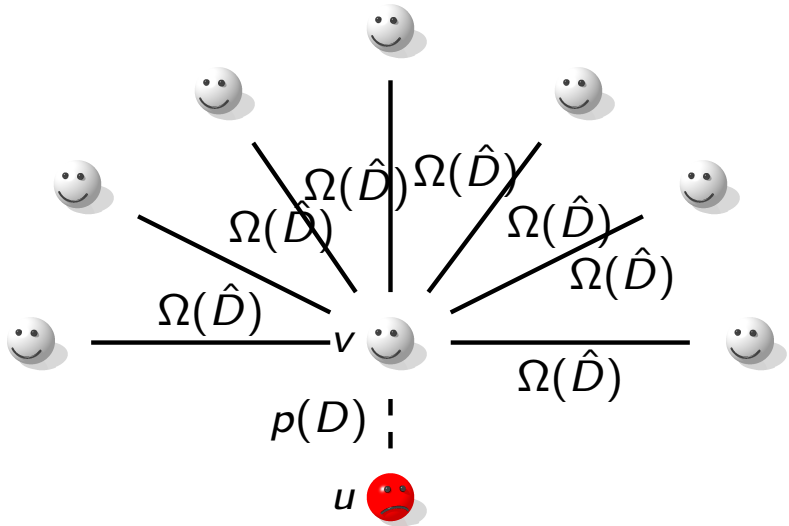
where

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

Finding Ω



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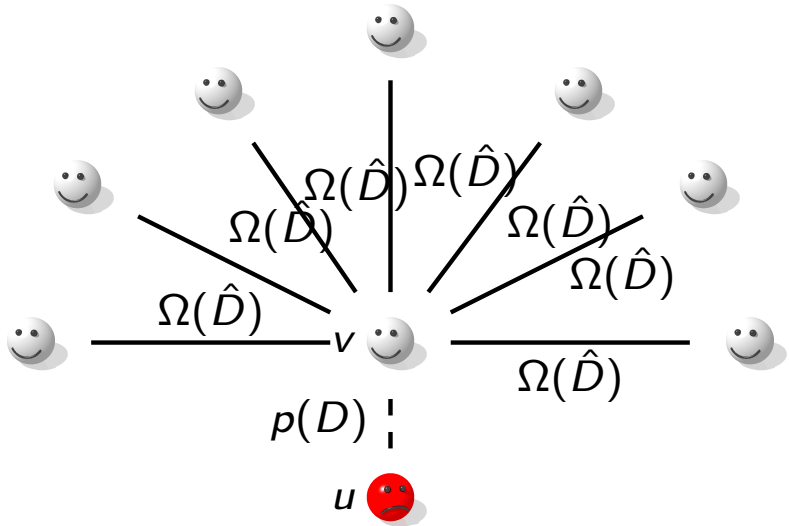

Probability a random partner of the index case having degree $\hat{k}$ whose infection duration is $\hat{D}$ does not start an epidemic is

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

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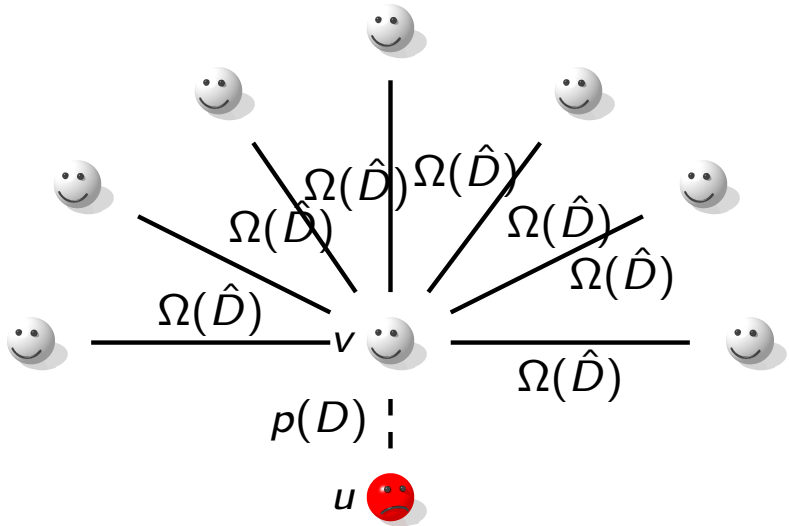

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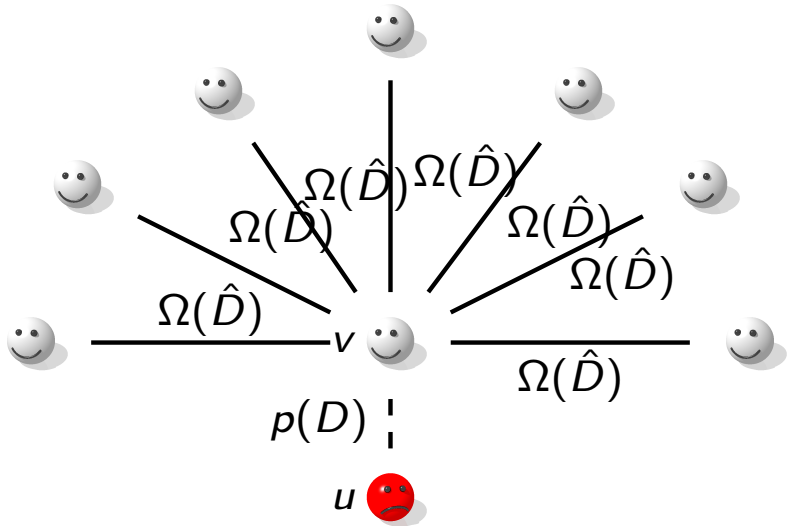

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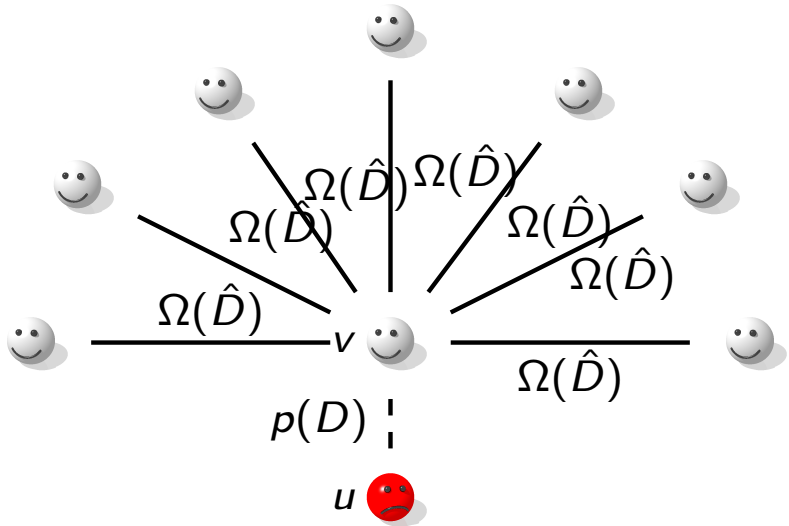

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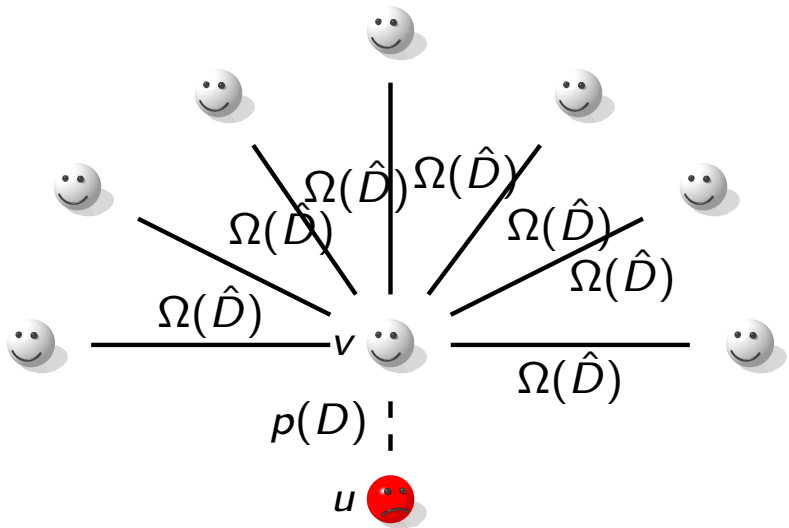

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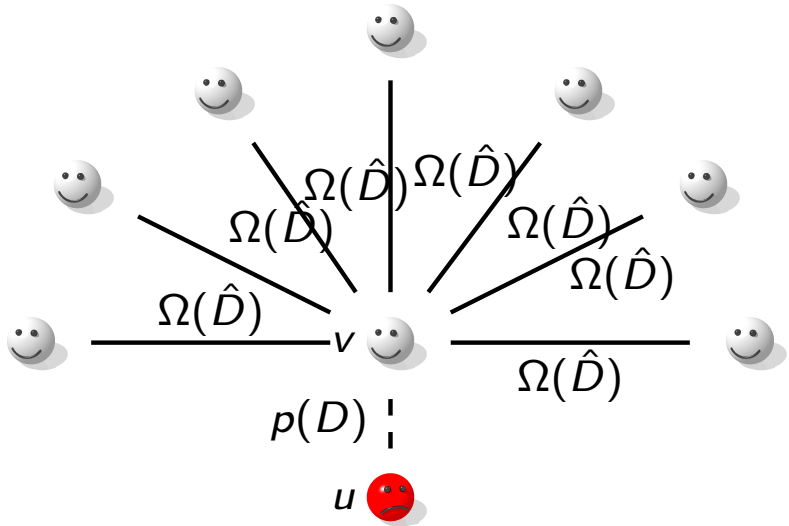

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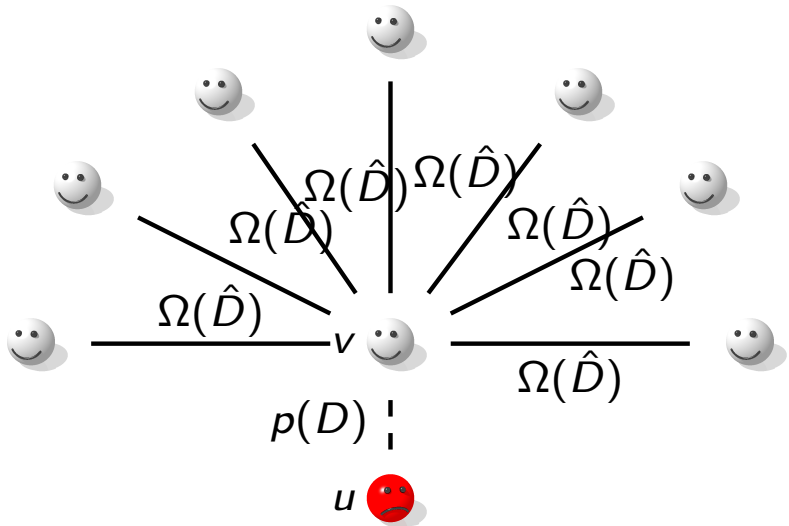

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Calculating epidemic probability

We arrive at

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

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

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 nth iteration will give the probability that the disease spreads at least n generations.

SIR and percolation

SIS disease

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

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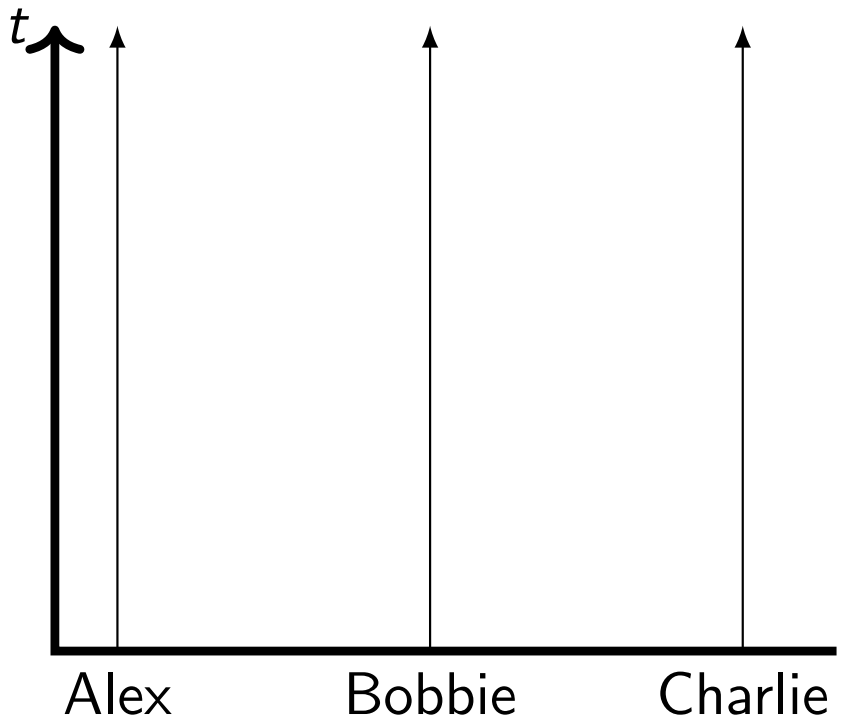
Percolation-like results and SIS

- 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



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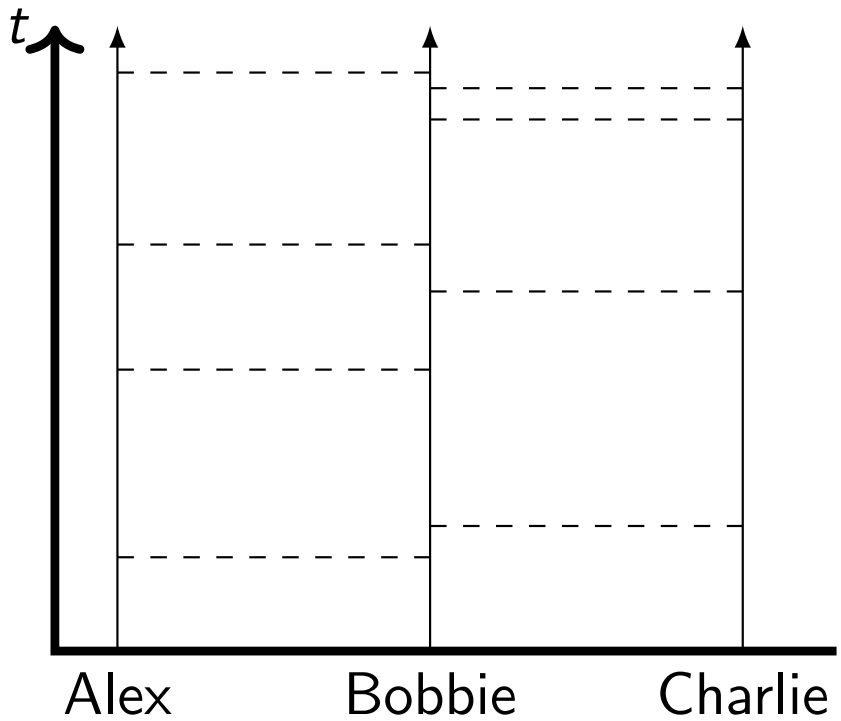
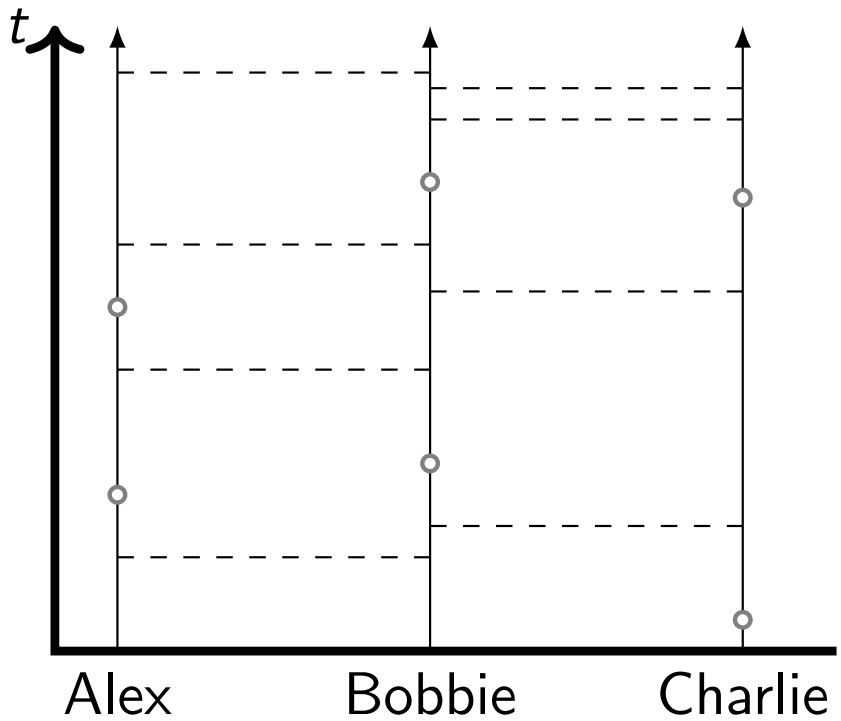


- Find transmission events as Poisson process

A percolation-like approach



- Find transmission events as Poisson process
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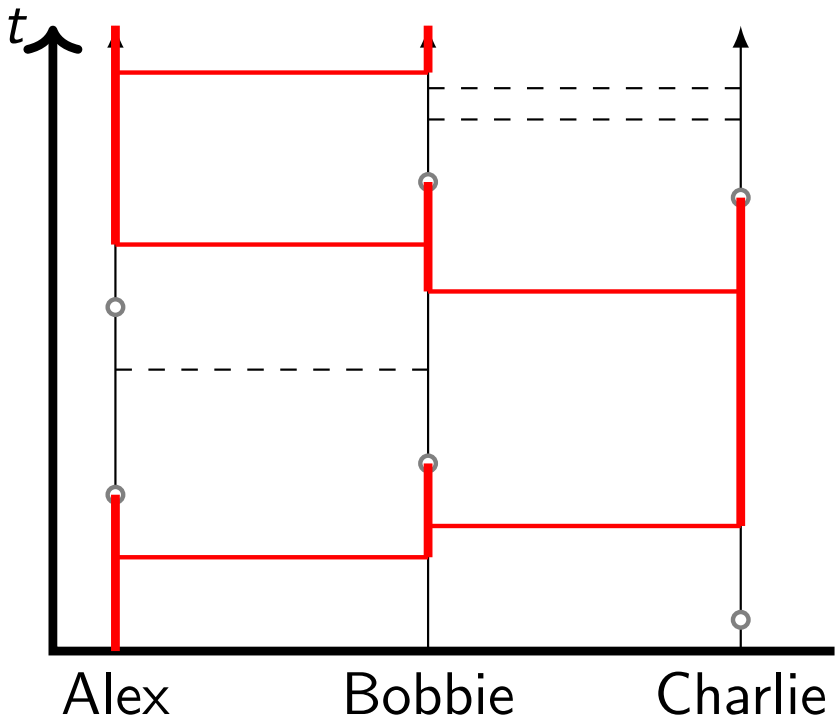
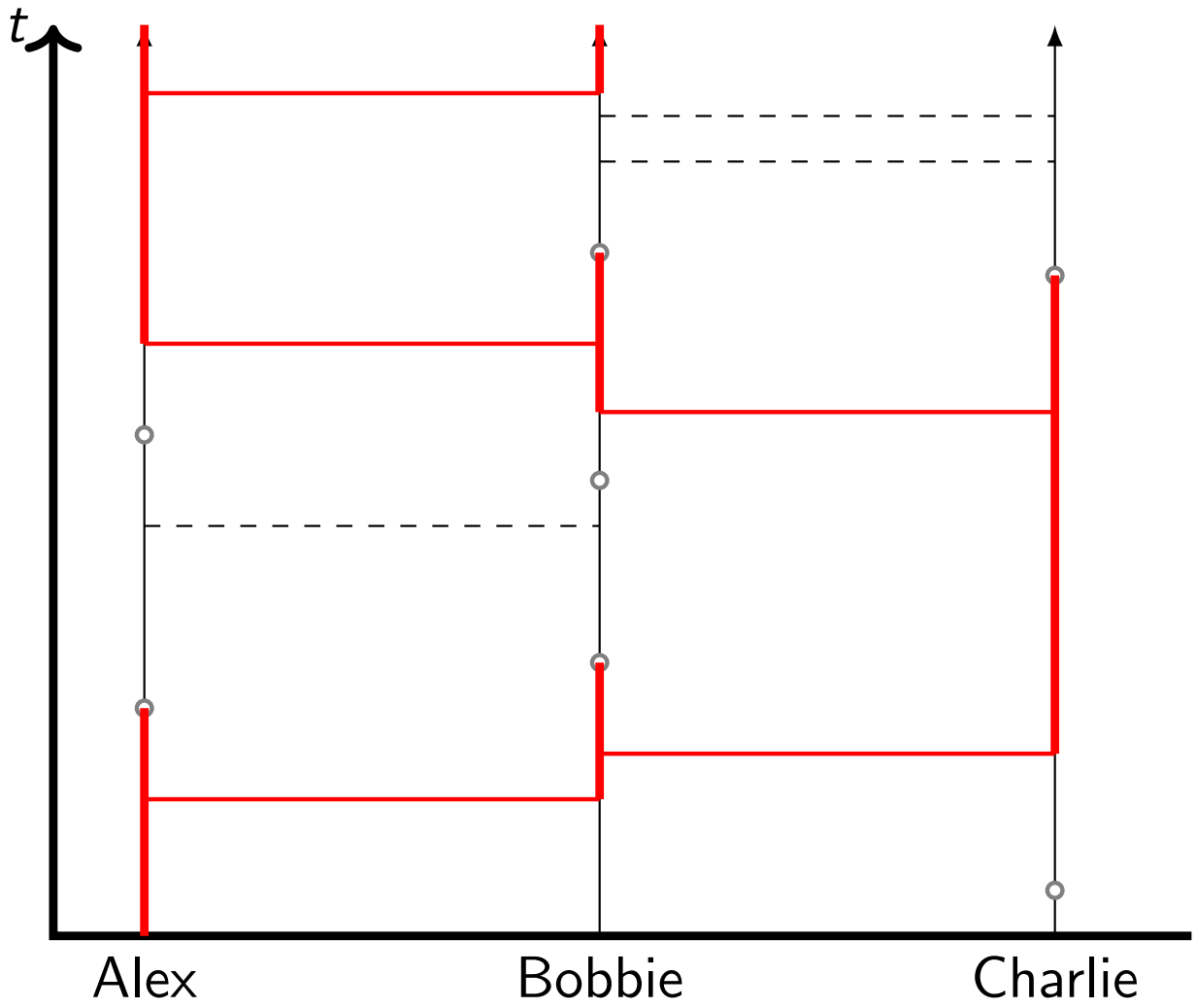
A percolation-like approach



- 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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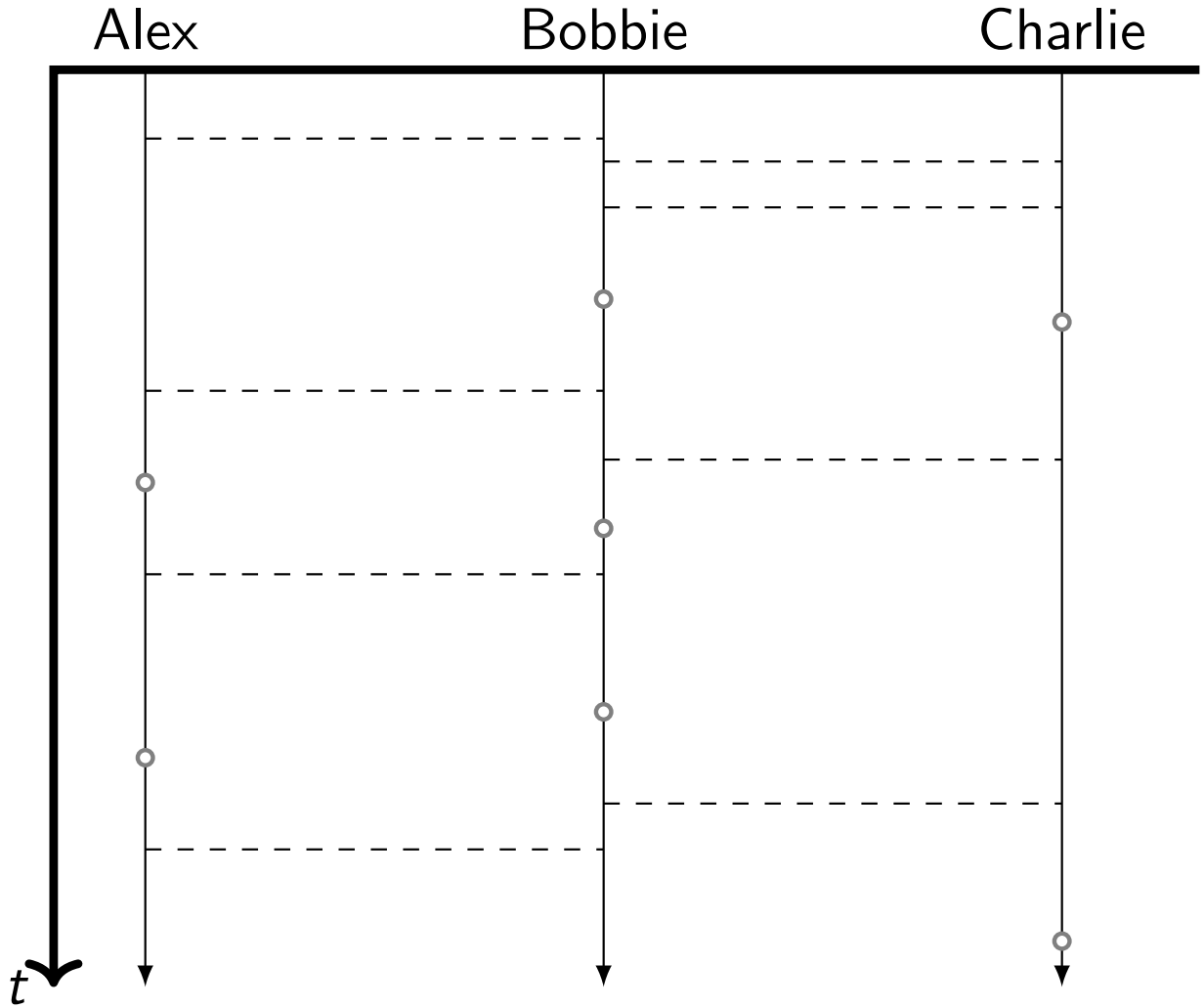

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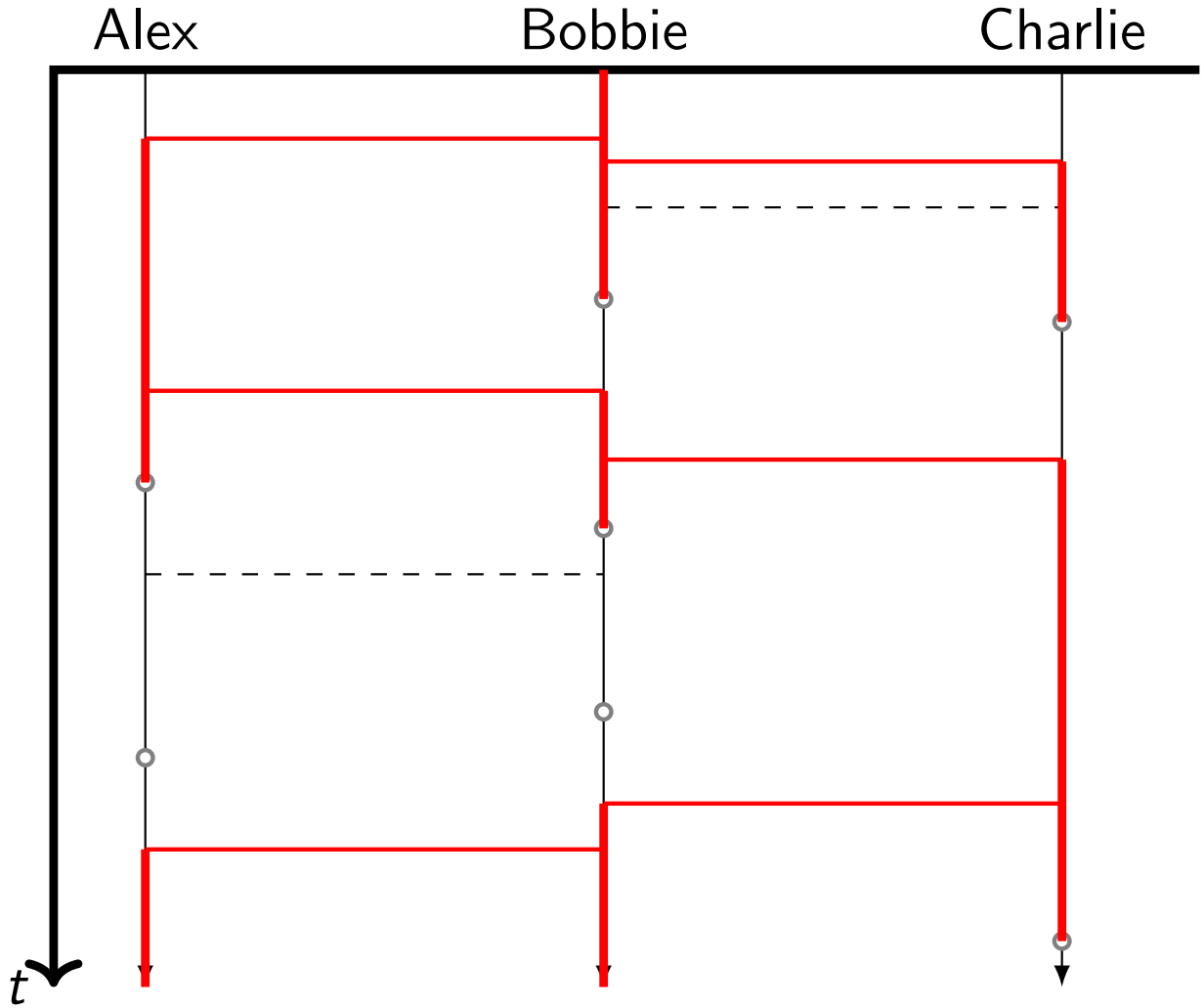

Some conclusions

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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.
- 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 $P(1) = P(5) = 0.5$.

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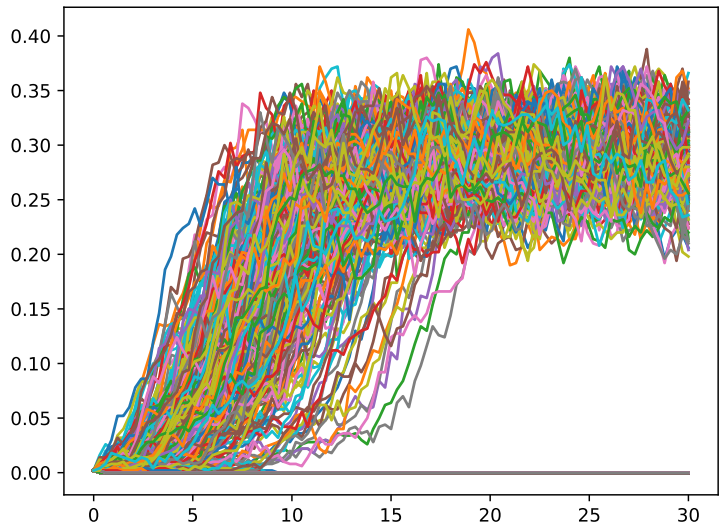

$\beta = 0.5, \quad \gamma = 1$

273 did not die out

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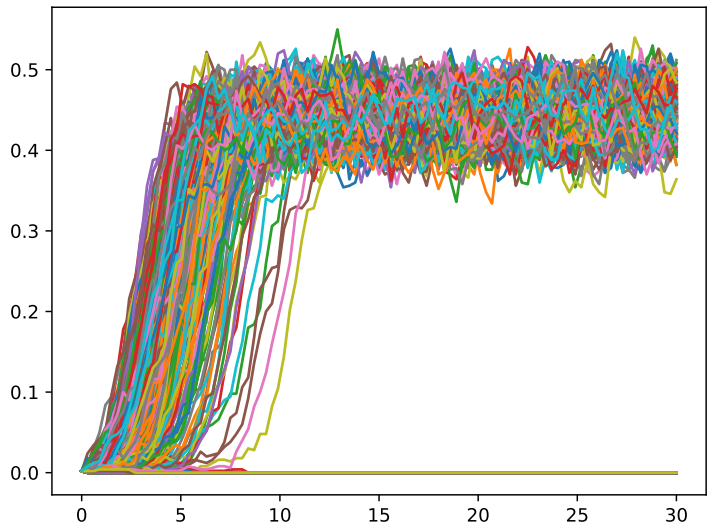

$\beta = 0.75, \ \gamma = 1$

448 did not die out

SIS size vs Probability

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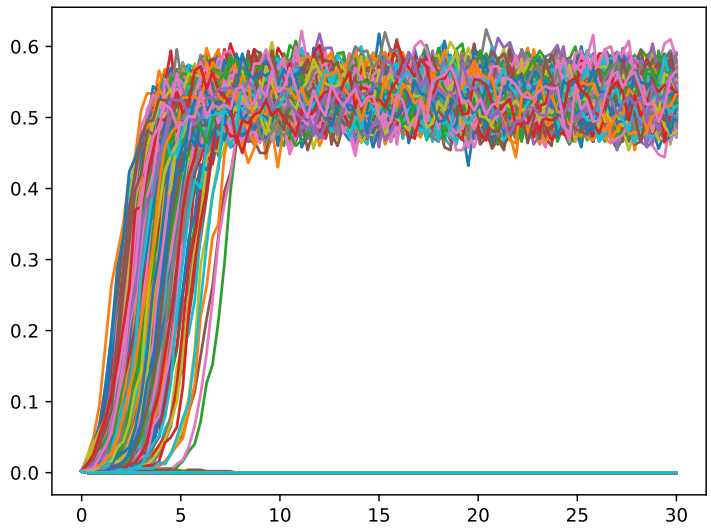

$\beta = 1, \ \gamma = 1$

537 did not die out

SIR and percolation

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References

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