Percolation approaches to SIR disease spread

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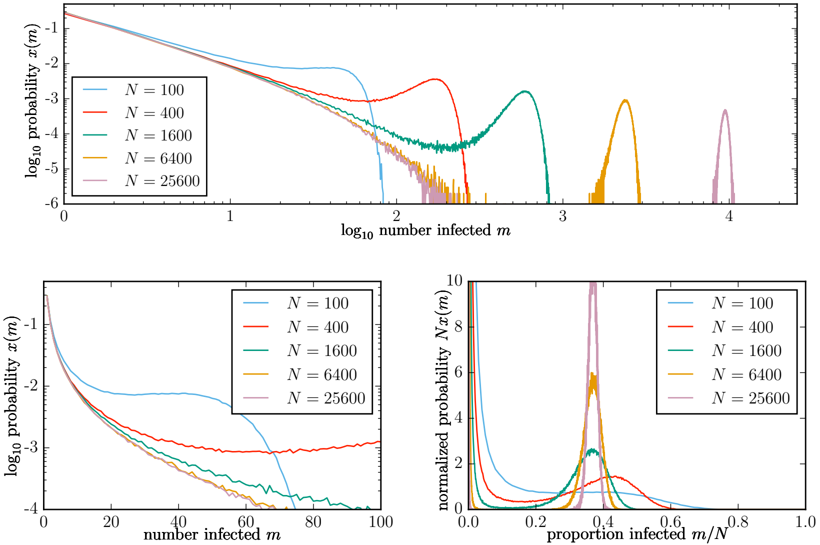
Percolation

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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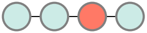
- An infected node transmits to a neighbor with probability p.

Modeling Disease Spread in a network



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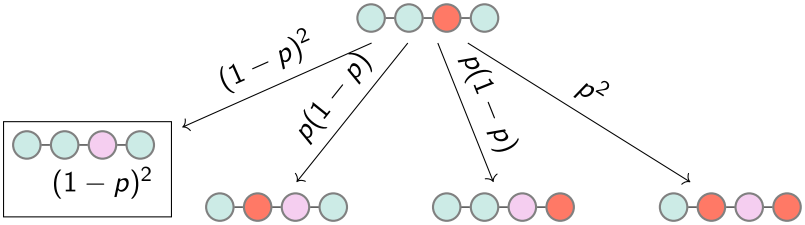

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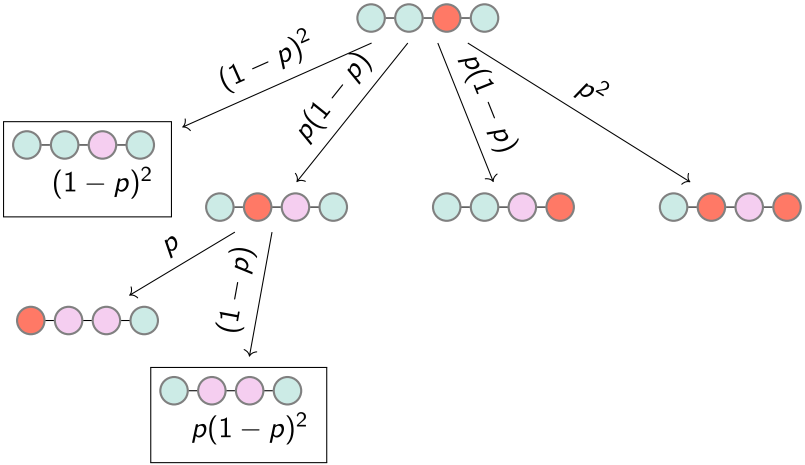

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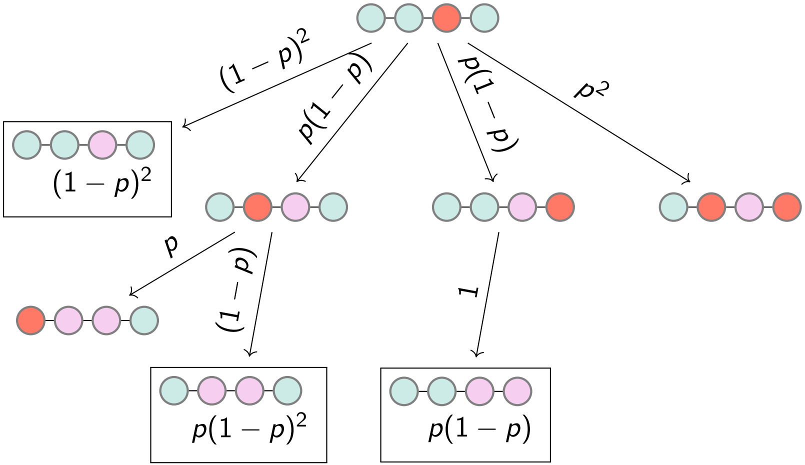

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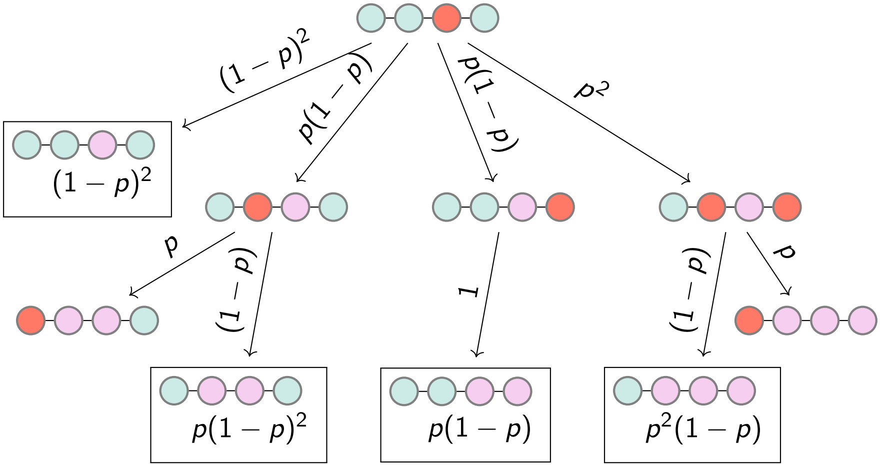

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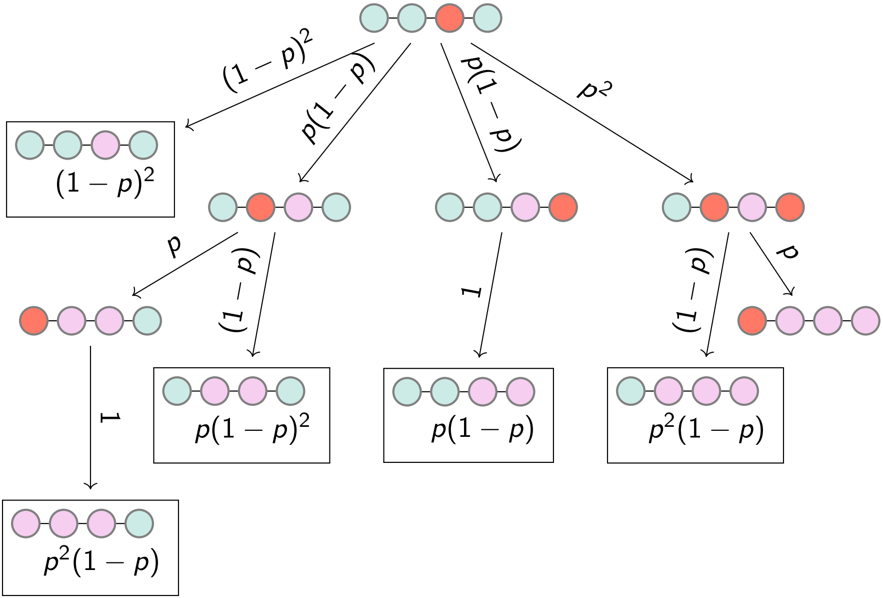

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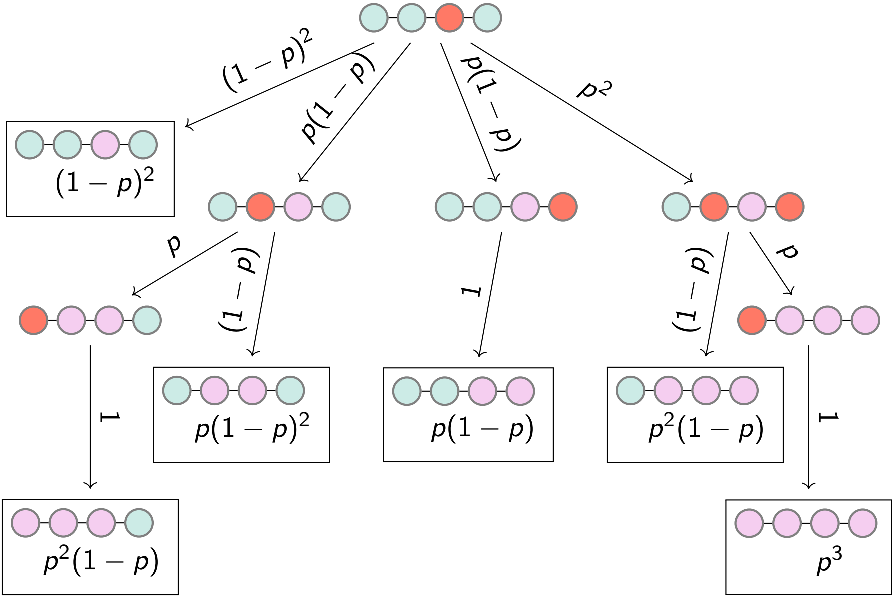
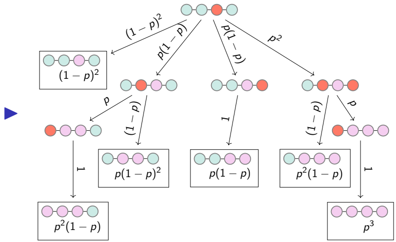


Alternative perspective



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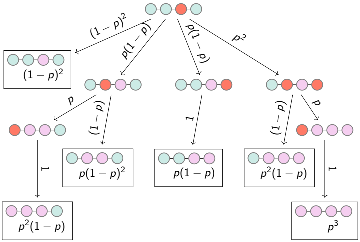
- 

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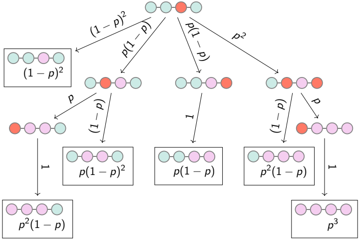
- 

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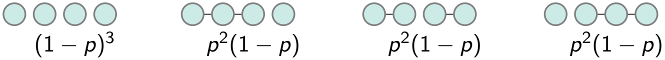

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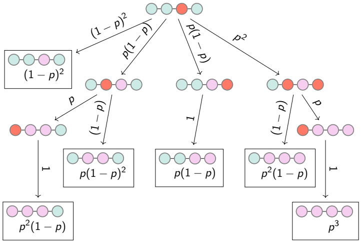
- 

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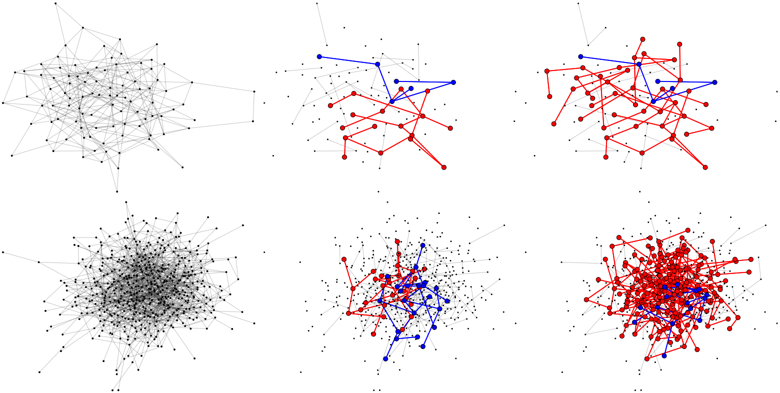
Percolation in different size networks

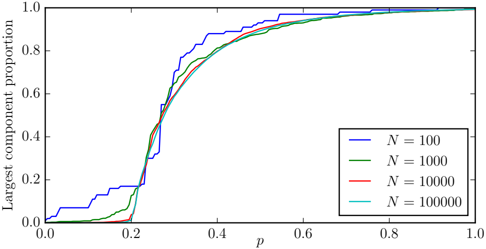
Comparison of largest (red) and second largest (blue) components in different size networks below and above percolation threshold.



- Below threshold largest and second largest are about the same size as each other
- Below threshold largest and second largest are about the same size in both networks

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

More detailed comparison of network size



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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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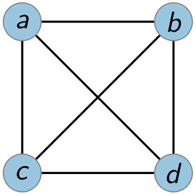
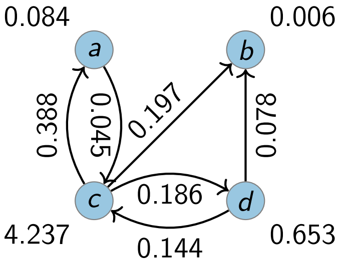
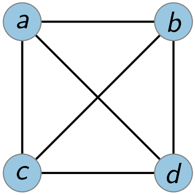
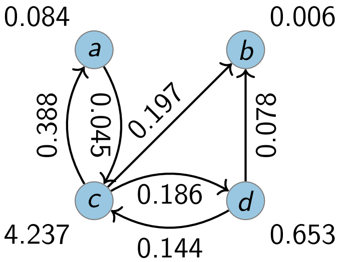
  - For each node Tom assigns the duration its infection will last if infected.
  - Once the duration is chosen, Tom decides which neighbors it will transmit to and how long it will take.
  - Then he reports those to me when I ask.
- Is it possible for me to know whether he is calculating in advance or not?


a
b
c
d

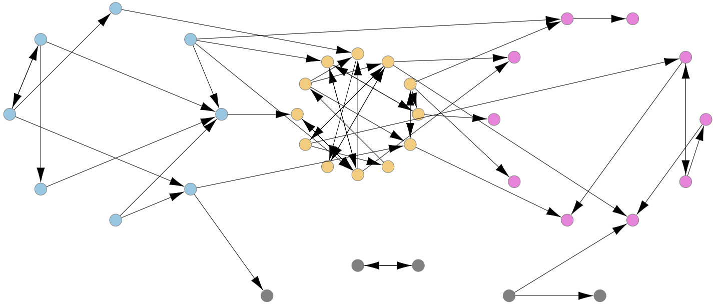

0.084
0.006
a
b
0.388
0.045
0.197
0.078
c
0.186
d
4.237
0.144
0.653





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, transmitting after given time if an edge is in the new network.

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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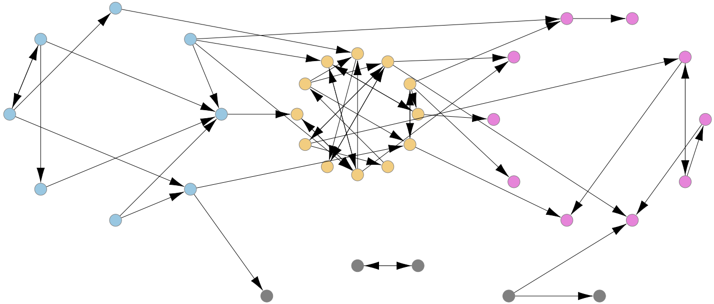

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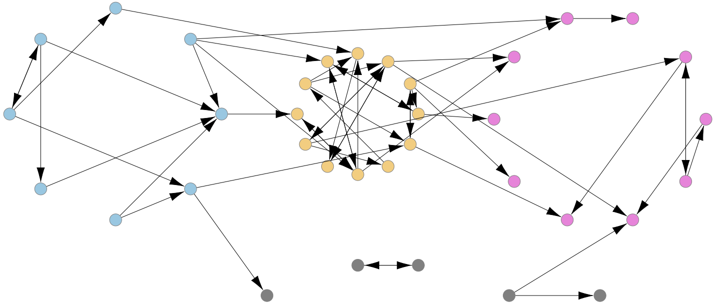

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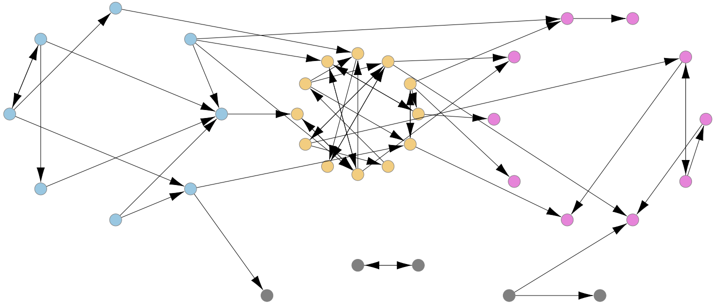

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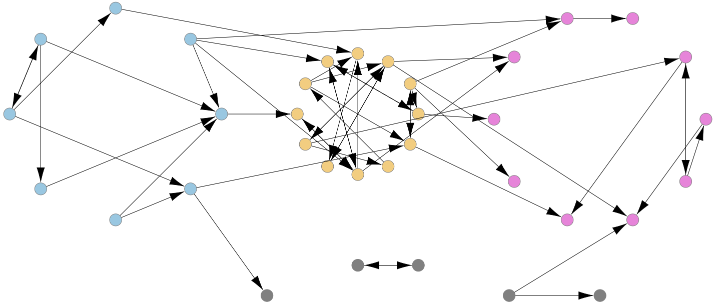

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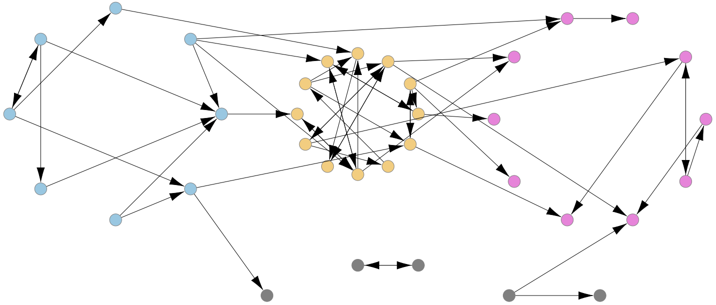

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- If the index case is in H_{IN} or H_{SCC} then all of H_{SCC} and H_{OUT} are eventually infected.
- So Epidemic Probability $\mathcal{P} = \mathbb{E}(|H_{IN} \cup H_{SCC}|)/N$ and Attack rate $\mathcal{A} = \mathbb{E}(|H_{SCC} \cup H_{OUT}|)/N$.

SIR epidemic size

- 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.
- What proportion end up susceptible or recovered?

Changing the question

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

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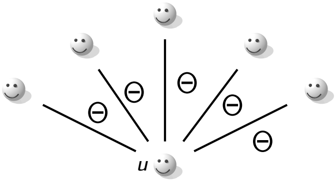
What is the probability a random node does not have a transmission path to it from one of the index nodes?



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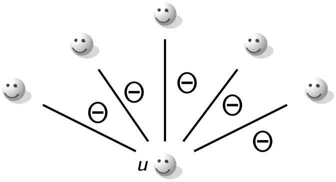

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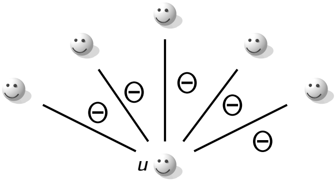
Probability a random degree k test individual is susceptible at the end is

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



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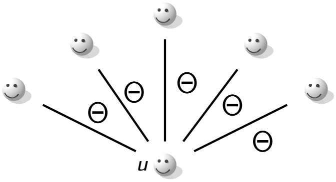

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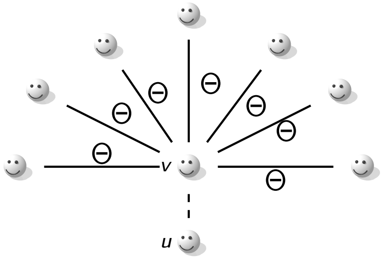
$$S = \sum_k P(k)(1-\rho)\Theta^k = \hat{\psi}(\Theta)$$

where

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

Finding Θ



Probability a random degree k partner never infected is

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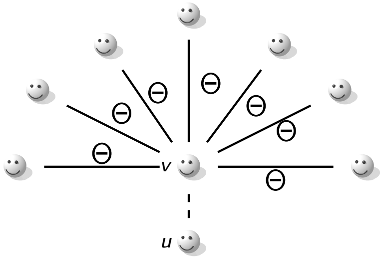

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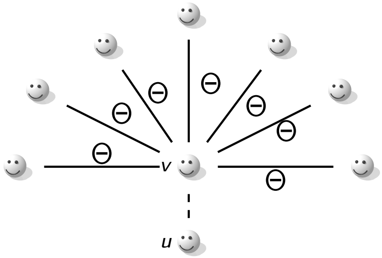

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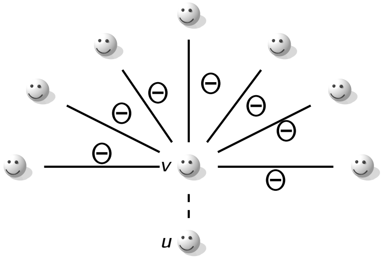

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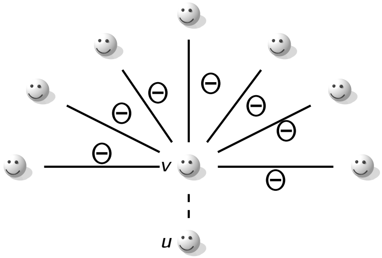

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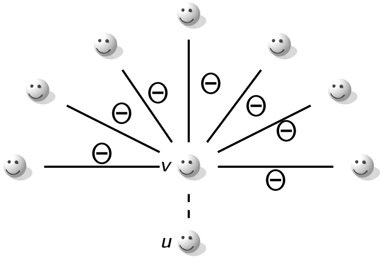

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Final Size

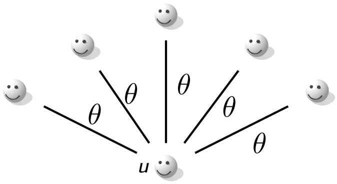
So

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

where

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

Finding $S(t)$



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

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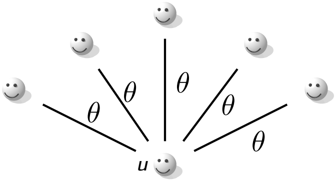

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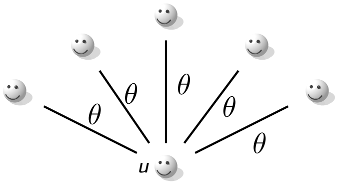

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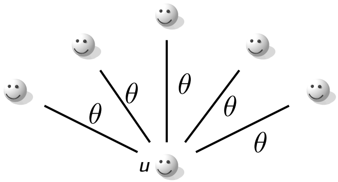

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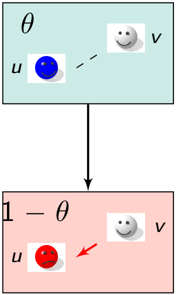

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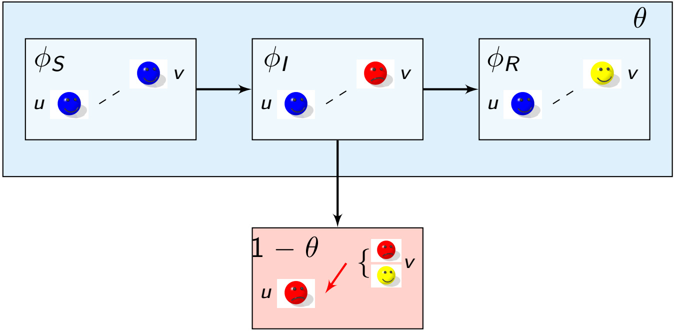
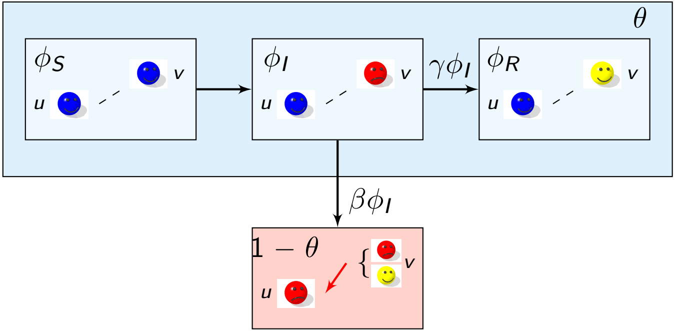


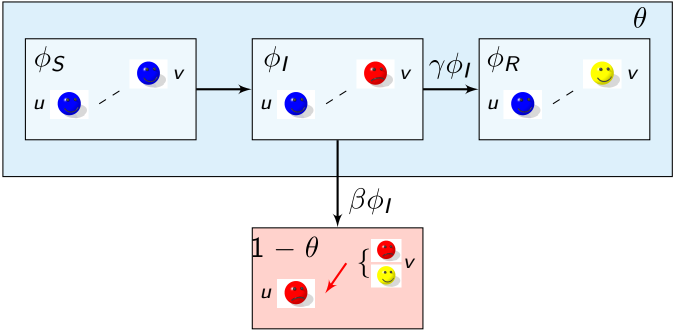
- $\theta = \phi_S + \phi_I + \phi_R$.

How does θ evolve?



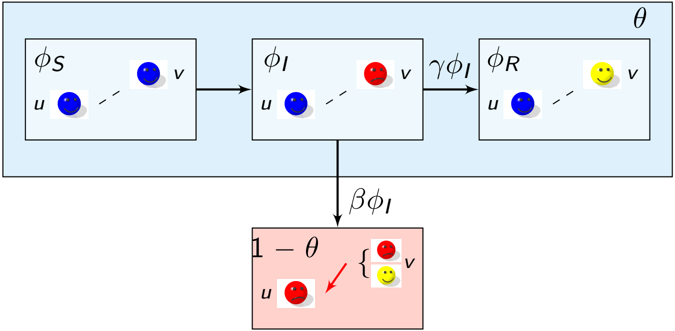
- $\theta = \phi_S + \phi_I + \phi_R$.
- $\dot{\theta} = -\beta\phi_I$.

How does θ evolve?



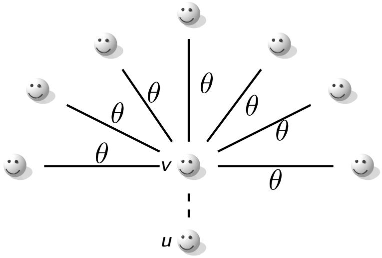
- $\theta = \phi_S + \phi_I + \phi_R$.
- $\dot{\theta} = -\beta\phi_I$.
- Our goal is to find ϕ_I in terms of θ.

Finding $\phi_R(t)$



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

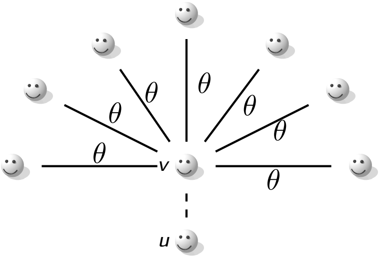
Finding $\phi_S(t)$



Probability a random degree k partner still susceptible is

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

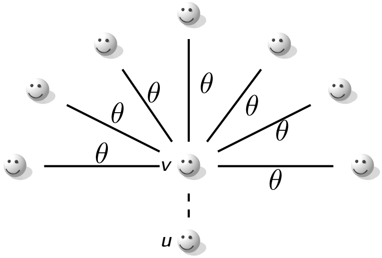
Finding $\phi_S(t)$



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

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

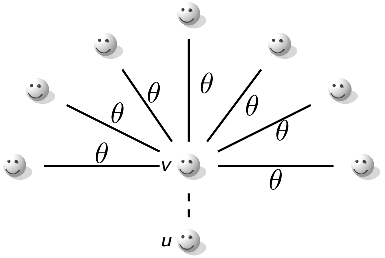
Finding $\phi_S(t)$



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

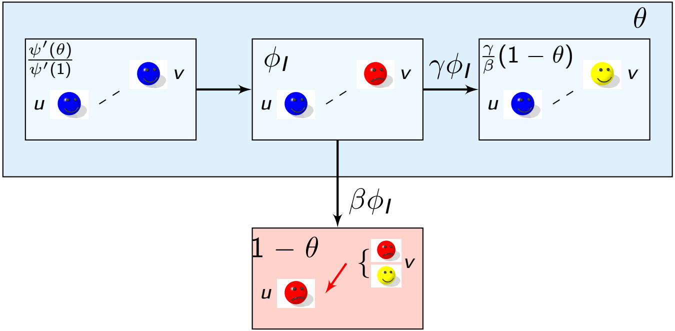
$$\phi_S(t) = \sum_k \frac{kP(k)}{\langle K \rangle}(1-\rho)\theta(t)^{k-1}$$

Finding $\phi_S(t)$



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

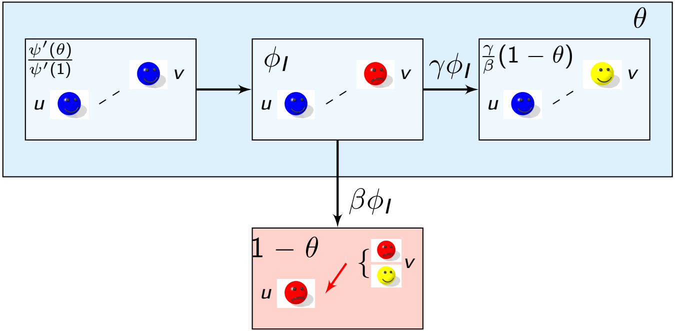
$$\phi_S(t) = \sum_k \frac{kP(k)}{\langle K \rangle}(1-\rho)\theta(t)^{k-1} = \frac{\hat{\psi}'(\theta)}{\langle K \rangle}$$



We have

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

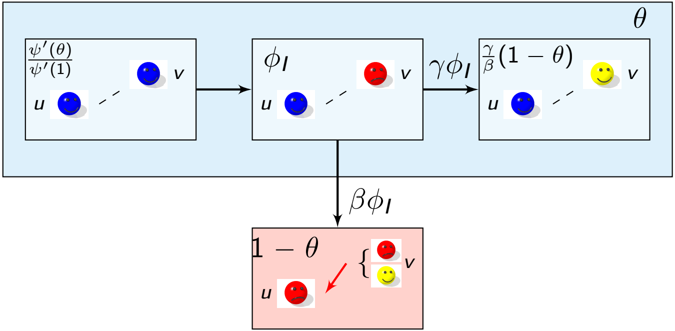
$$\dot{\theta} = -\beta\phi_I$$



We have

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

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



We have

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

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

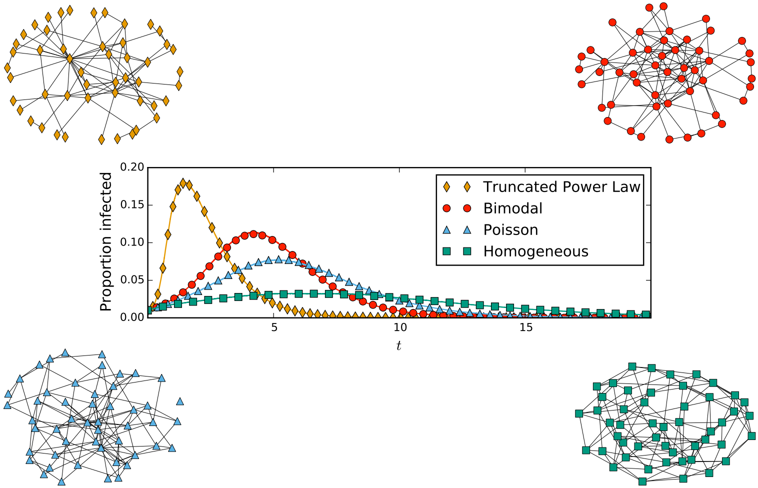
Final System

We finally have

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

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

More details in [1, 2]


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

A good exercise

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

References

References I

[1] Joel C. Miller, Anja C. Slim, and Erik M. Volz.
Edge-based compartmental modelling for infectious disease spread.
Journal of the Royal Society Interface, 9(70):890–906, 2012.

[2] Joel C. Miller.
Epidemics on networks with large initial conditions or changing structure.
PLoS ONE, 9(7):e101421, 2014.