Epidemics in Networks
SIR: Final Size and Dynamics

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Introduction

We now consider the final size and the temporal dynamics of SIR epidemics in static configuration model networks.

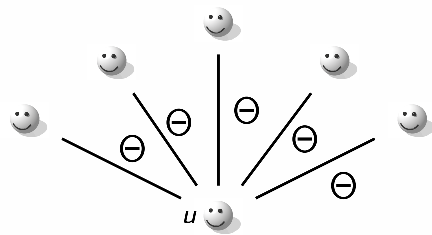
Applying percolation results

- I claimed that for unclustered networks, final size depends on distribution of susceptibility.
- For both Reed-Frost and continuous time epidemics, susceptibility is uniform.
- So they should have the same final size.
- Also, we have proven that for Reed–Frost epidemics $\mathcal{P} = \mathcal{A}$. We'll calculate $\mathcal{A}$ anyways, using a very similar method.
- To introduce something new, assume that at $t = 0$ some nodes are chosen to be infected so that $S(k, 0)$ is the probability a degree k individual is susceptible [1].

Setting up size calculations

- Assuming an epidemic occurs, the probability a random node u is infected equals the proportion of the population that is infected.
- The probability a random node u is infected is unaltered if we prevent u from transmitting to its partners.
- So consider a random test node u which is prevented from transmiting to its partners, we want to know the probability u is infected if an epidemic occurs.

Reed Frost final size in configuration model networks



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

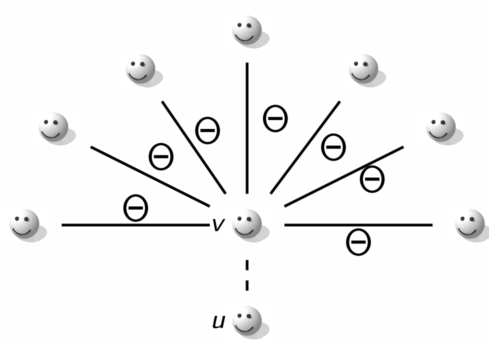
Probability a random ~~degree k~~ test individual is susceptible is

$$S = \sum_k P(k)S(k,0)\Theta^k = \hat{\psi}(\Theta)$$

where

$$\hat{\psi}(x) = \sum_k P(k)S(k,0)x^k$$

Finding Θ



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

$$\phi_S = \sum_k \frac{kP(k)}{\langle K \rangle} S(k,0)\Theta^{k-1} = \frac{\hat{\psi}'(\Theta)}{\langle K \rangle}$$

If p, then probability partner does not transmit to u is

$$\Theta = \phi_S + (1-p)(1-\phi_S) = 1 - p + p\frac{\hat{\psi}'(\Theta)}{\langle K \rangle}$$

Final Size

So

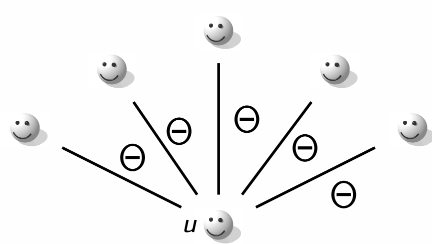
$$R = 1 - \hat{\psi}(\Theta)$$

where

$$\Theta = 1 - p + p\frac{\hat{\psi}'(\Theta)}{\langle K \rangle}$$

Contuous time case

To look at the coninuous time case, we use the same figure.



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

Here each Θ is uncorrelated with the other Θs.

- Transmission to all partners of an individual v are not independent because they depend on the duration of v's infection.
- However, transmissions from different partners to u are independent.
- So the identical calculation applies.

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SIR dynamic equations

- We now derive the equations for the time dependent case, assuming continuous time.
- The derivation is almost identical to the final size derivation, except that we calculate the probability transmission happened by time t rather than by the end.
- This is not the only approach [2, 3, 4, 5], but the predictions of the models are identical (subject to some small caveats) [6].

Calculating Dynamics

The network structure alters the infection process (but not the recoveries)

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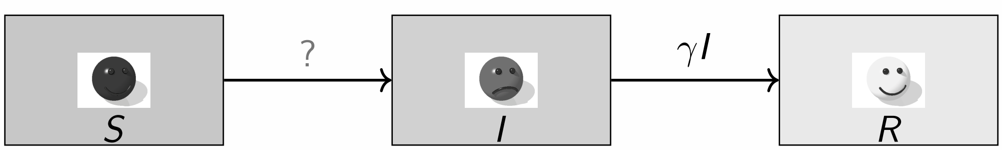


$$I = 1 - S - R\,, \qquad \dot{R} = \gamma I$$

We will switch to a partnership-based perspective to find $S(t)$.

Revisiting the test individual

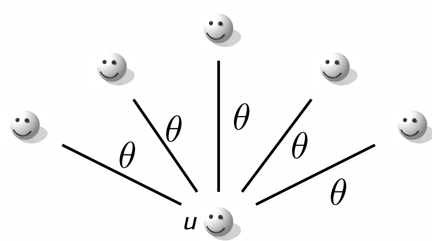
- Consider a randomly chosen test individual u in the population.
- Disallow infection from u to its partners (allows independence assumption for partners).
- The probability u is Susceptible, Infected, or Recovered at time t is affected by the status of its partners.
- The fraction of the population that is susceptible $S(t)$ equals the probability u is susceptible.

$$S(t) = P(u \text{ is susceptible})$$

- Let v be a random partner of u.
- Define

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

Finding $S(t)$



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

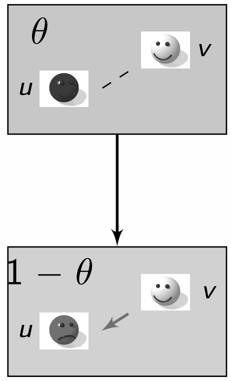
Probability a random ~~degree k~~ test individual still susceptible is

$$S(t) = \sum_k P(k)S(k,0)\theta(t)^k = \hat{\psi}(\theta(t))$$

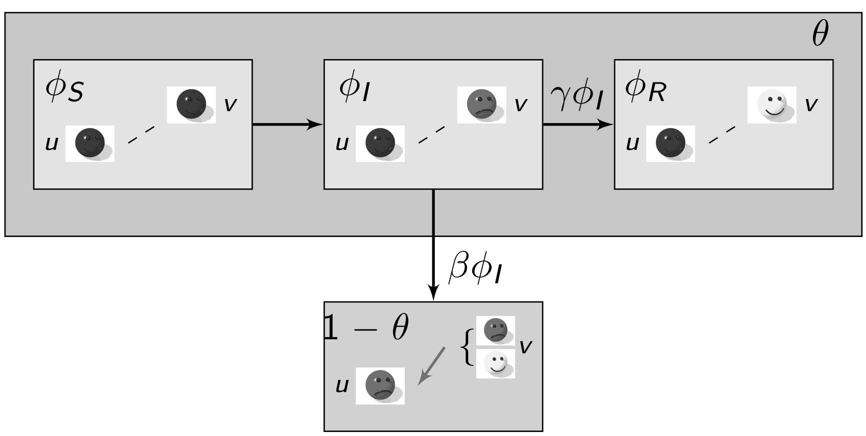
where

$$\hat{\psi}(x) = \sum_k S(k,0)P(k)x^k$$

How does θ evolve?

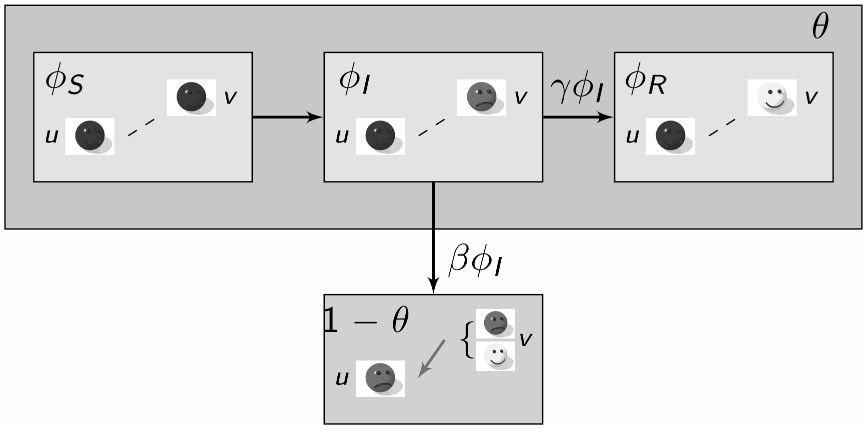


How does θ evolve?



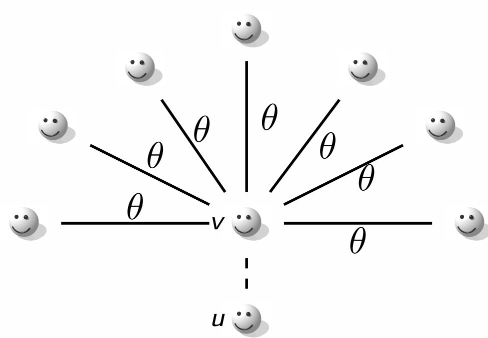
- $\theta = \phi_S + \phi_I + \phi_R$.
- $\dot{\theta} = -\beta\phi_I$.
- Our goal is to find ϕ_I in terms of θ.

Finding $\phi_R(t)$



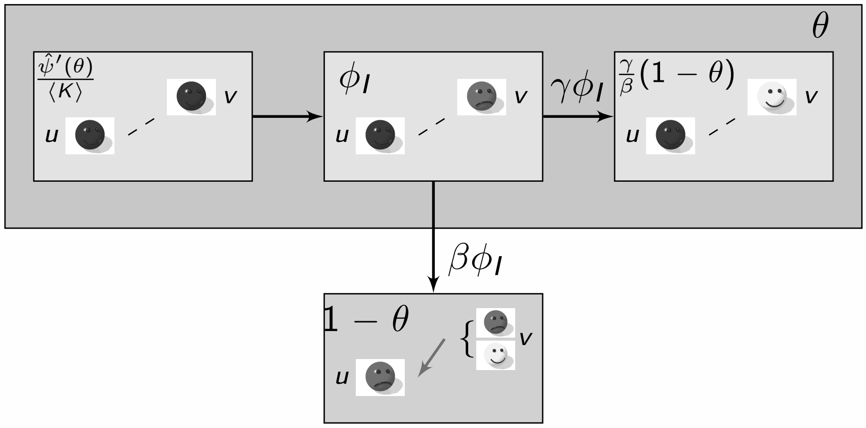
Because derivatives are proportional, $\phi_R = \frac{\gamma}{\beta}(1-\theta)$

Finding $\phi_S(t)$



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

$$\phi_S(t) = \sum_k \frac{kP(k)}{\langle K \rangle} S(k,0)\theta(t)^{k-1} = \frac{\hat{\psi}'(\theta)}{\langle K \rangle}$$



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

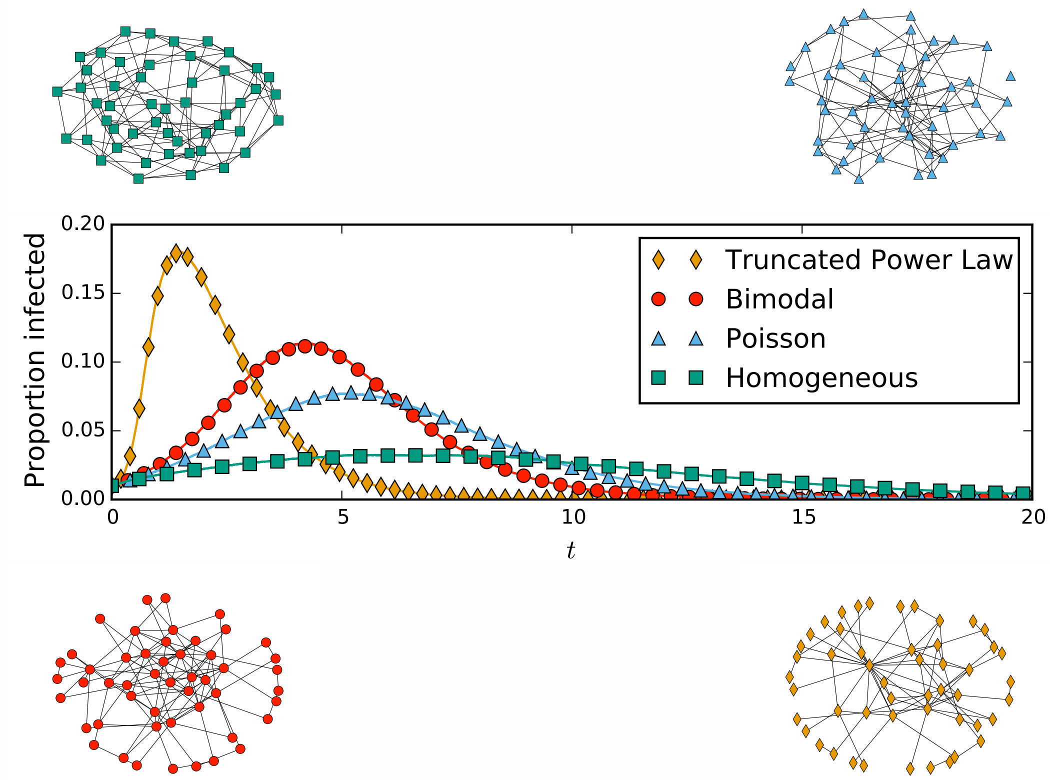
$$\dot{\theta} = -\beta\phi_I = -\beta\theta + \beta\frac{\hat{\psi}'(\theta)}{\langle K \rangle} + \gamma(1-\theta)$$

Final System

We finally have

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

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



Exercise

Derive the Reed–Frost version of this model [7]
Set the probability of transmitting in a time step to be β.

A major caveat

- All of this assumes that the strength of partnerships is not degree-dependent. This is a dangerous assumption.
- I suspect most results from the high-impact papers on powerlaw degree distributions will disappear if we make more realistic assumptions.

Generalizing

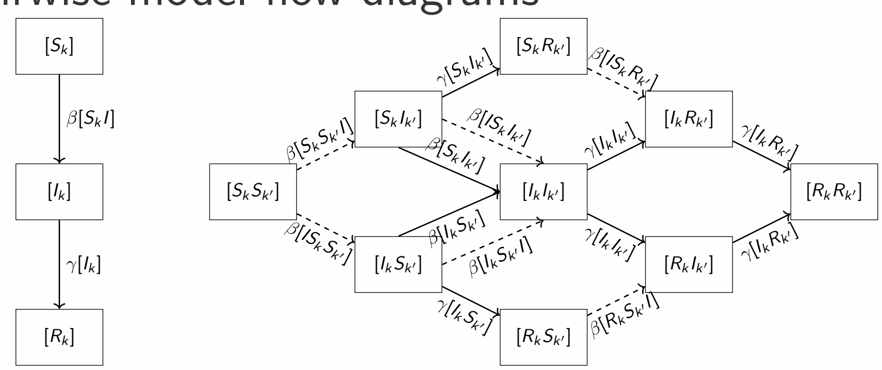
Many generalizations are possible:

- Dynamic networks, other classes of random networks [8].
- SEIR, demographic groups, different partnership types, asymmetric transmission, . . . [9].
- Competing diseases [10].
- Spread of ideas or behaviors [11].
- Including birth and death (ongoing)
- Degree-dependent transmission probabilities [12] (and ongoing work).

Other formulations

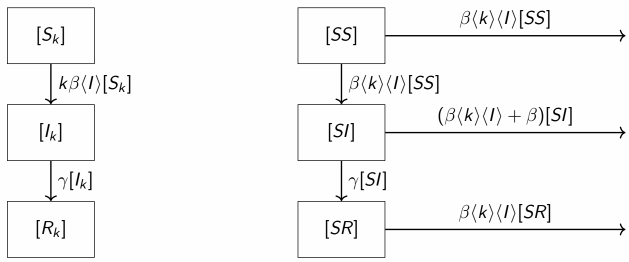
- Other variable choices exist, which lead to different equations.
- Subject to mild conditions the equations are all equivalent [6].
- The number of equations and compartments can vary substantially

Pairwise model flow diagrams



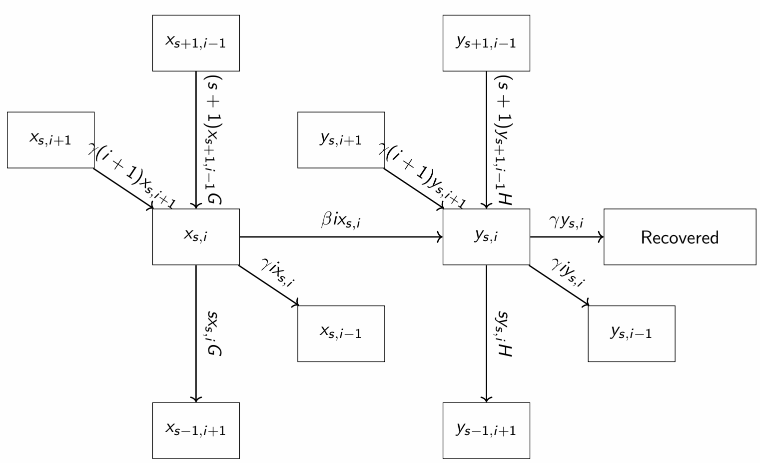
- The flow diagram underlying the basic pairwise model [2].
- We track individuals of each status and degree as well as partnerships between individuals of various statuses and degrees.
- Dashed lines denote transitions that rely on infection coming from a source outside the edge of interest.
- The triples $[A_{k'} S_k I]$ and $[I S_k A_{k'}]$ can be expressed in terms of the doubles and singles: $[A_{k'} S_k][S_k I]/[S_k]$

Reduced pairwise flow diagram



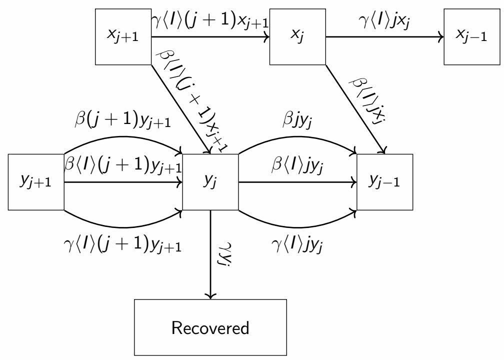
- The flow diagram for the reduced system of [4].
- The $[SS]$, $[SI]$, and $[SR]$ compartments correspond to the sum of the $[S_k S_{k'}]$, $[S_k I_{k'}]$ and $[S_k R_{k'}]$ compartments of the basic pairwise model.
- $\langle I\rangle = [SI]/([SS]+[SI]+[SR])$

Effective degree model flow diagram



- The flow diagram underlying the effective degree model of [3].
- We include just the fluxes involving the $x_{s,i}$ or $y_{s,i}$ compartments. Fluxes between other compartments exist but are not included.

Compact effective degree model flow diagram



- The flow diagram that underlies the model of [5].
- Only the fluxes into and out of y_j and x_j are included. Fluxes between other compartments exist, but are not included.
- An active edge is eliminated if the partner recovers or if it transmits infection in either direction. The quantity $\langle I\rangle$ represents the probability an active edge joins an individual with an infected partner.

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References

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