Part 4 — Equation-based models of disease spread in networks

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18–20 July 2018

Challenges for an analytic model

- When we rigorously derive

  $$\begin{aligned}\dot{S} &= -\beta \frac{IS}{N}\\ \dot{I} &= \beta \frac{IS}{N} - \gamma I\end{aligned}$$

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  for the compartmental model, we use the fact that it does not matter which individuals are susceptible or infected.
- If there are S susceptible and I infected individuals, the combined infection rate is $\beta IS/N$. Similarly the combined recovery rate is γI.
- In a network, it matters exactly which nodes are susceptible or infected.

Triangle example

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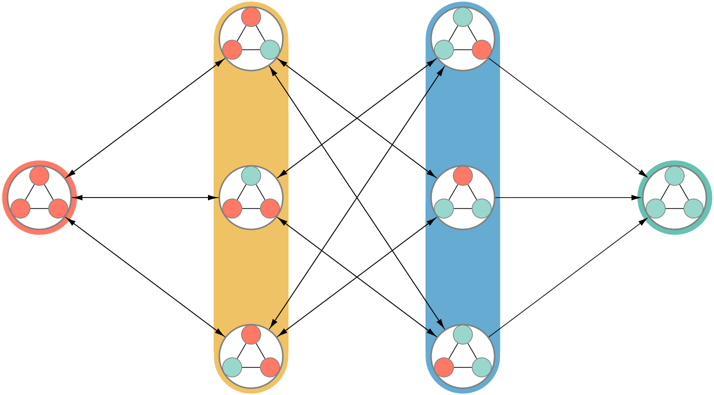

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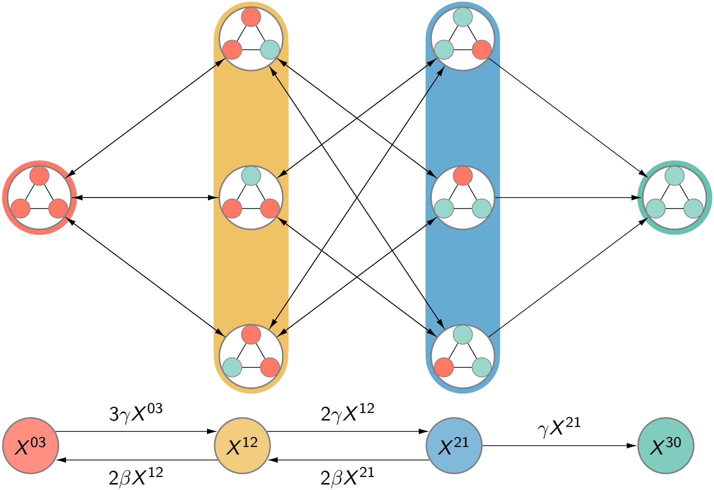

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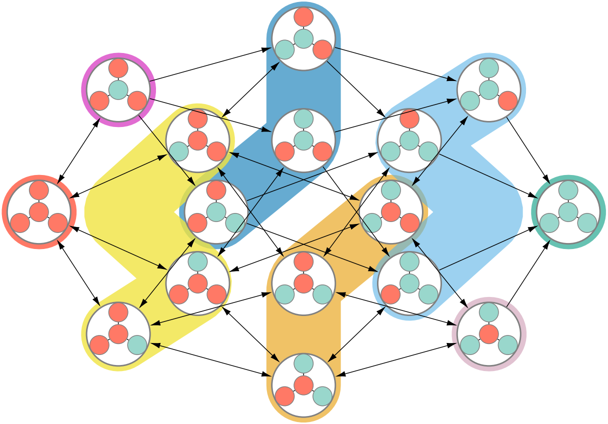

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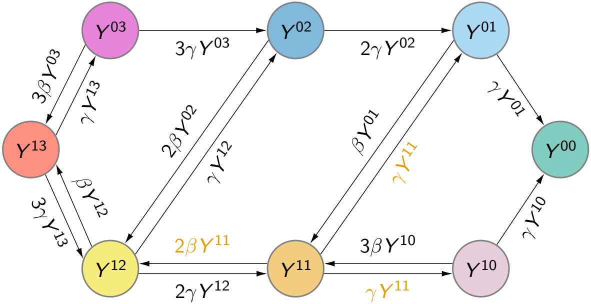
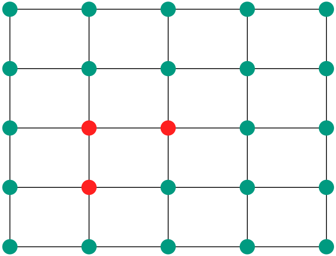


(numbered based on whether the central node is infected or not and how many peripheral nodes are infected)

Towards an analytic model*



- How many I nodes?

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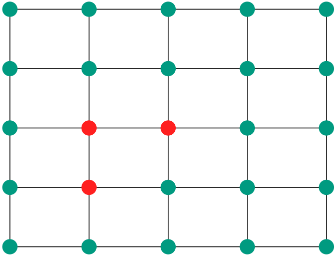

- How many I nodes? $[I] = 3$.

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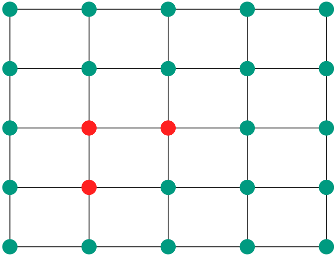

- How many I nodes? $[I] = 3$.
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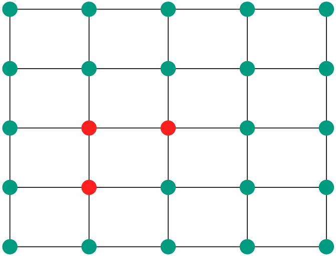

- How many I nodes? $[I] = 3$.
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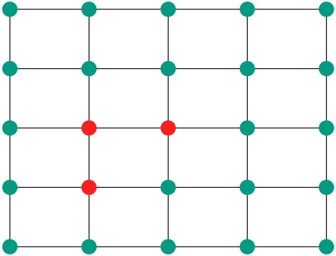

- How many I nodes? $[I] = 3$.
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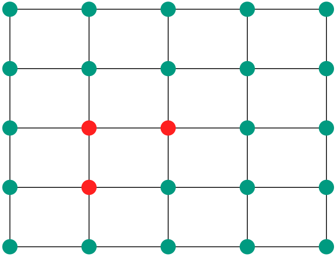

- How many I nodes? $[I] = 3$.
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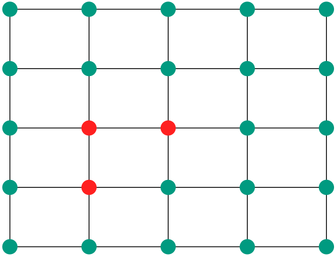

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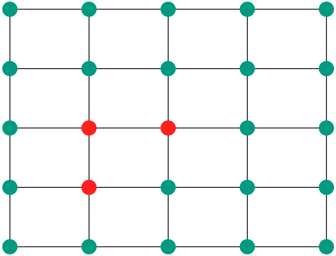

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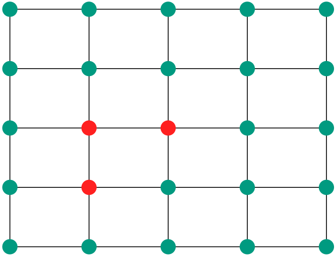

- How many I nodes? $[I] = 3$.
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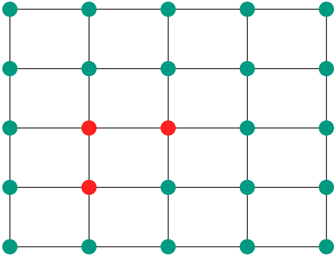

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- How many ISI triples? $[ISI] = 2$.

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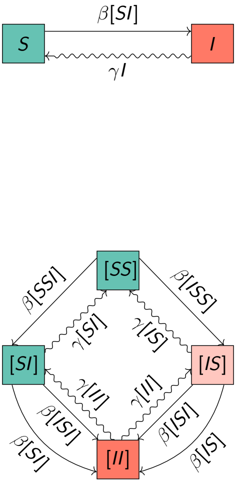
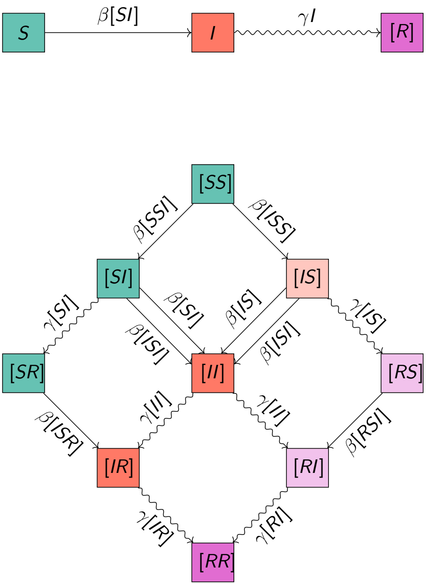
Towards an analytic model

$$\frac{\mathrm{d}}{\mathrm{d}t}[X] = \sum_{\substack{\text{possible}\\ \text{transitions}}} \text{rate(transition)} \times \Delta[X]\text{(transition)}$$

That is, the rate of change of $[X]$ is the sum over all possible transitions of the rate of the transition times the resulting change in $[X]$ if that transition occurs.



SIS



SIR

[Adapted from [1]]

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- What is $\frac{\mathrm{d}}{\mathrm{d}t}[SI]$?

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- What is $\frac{\mathrm{d}}{\mathrm{d}t}[I]$?
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    - An *I* is created whenever an SI edge transmits
    - $\frac{\mathrm{d}}{\mathrm{d}t}[I] = \beta[SI] - \gamma I$
- What is $\frac{\mathrm{d}}{\mathrm{d}t}[SI]$?
    - An *SI* edge is removed whenever the infected node transmits.
    - An *SI* edge is removed whenever the infected node recovers.
    - For each *SSI* triple that contains an *SI* edge that transmits, a new *SI* edge is created.
    - For each *ISI* triple, when the first node transmits it removes the second *SI* pair as well.
    - $\frac{\mathrm{d}}{\mathrm{d}t}[SI] = -(\beta+\gamma)[SI] + \beta([SSI] - [ISI])$

Finding SIR equations

So we have

$$\begin{aligned}
\frac{\mathrm{d}}{\mathrm{d}t}[S] &= -\beta[SI] \\
\frac{\mathrm{d}}{\mathrm{d}t}[I] &= \beta[SI] - \gamma[I] \\
\frac{\mathrm{d}}{\mathrm{d}t}[SI] &= -(\beta+\gamma)[SI] + \beta([SSI] - [ISI]) \\
\frac{\mathrm{d}}{\mathrm{d}t}[SSI] &= \cdots \\
\frac{\mathrm{d}}{\mathrm{d}t}[ISI] &= \cdots
\end{aligned}$$

Finding SIS equations

The equations for SIS are very similar. Let's look specifically at the $[SI]$ equation:

$$\frac{\mathrm{d}}{\mathrm{d}t}[SI] = \beta[SSI] - \beta[ISI] - \beta[SI] - \gamma[SI]$$

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- The second term represents the susceptible node in an SI pair being infected by another neighbor.
- The third term represents the susceptible node in an SI pair being infected by the infected node in the pair.

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- The second term represents the susceptible node in an SI pair being infected by another neighbor.
- The third term represents the susceptible node in an SI pair being infected by the infected node in the pair.
- The fourth term represents the infected node in an SI pair recovering.

Closures

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$$[SI] = [S][I]\left\langle K \right\rangle / N$$

where $\left\langle K \right\rangle$ is the average degree. So we replace the $\frac{\mathrm{d}}{\mathrm{d}t}[SI]$ equation with $[SI] = [S][I]\left\langle K \right\rangle / N$.

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$$[\dot{S}] = -\beta\langle K\rangle [S][I]/N + \gamma[I]$$
$$[\dot{I}] = \beta\langle K\rangle [S][I]/N - \gamma[I]$$

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- SIS:

$$\begin{aligned}[\dot{S}] &= -\beta\langle K\rangle[S][I]/N + \gamma[I]\\ [\dot{I}] &= \beta\langle K\rangle[S][I]/N - \gamma[I]\end{aligned}$$

- SIR:

$$\begin{aligned}[\dot{S}] &= -\beta\langle K\rangle[S][I]/N\\ [\dot{I}] &= \beta\langle K\rangle[S][I]/N - \gamma[I]\\ [\dot{R}] &= \gamma[I]\end{aligned}$$

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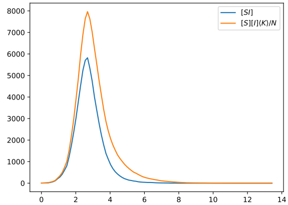
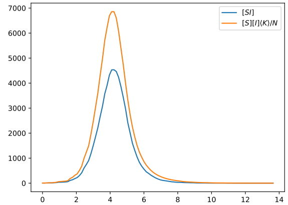
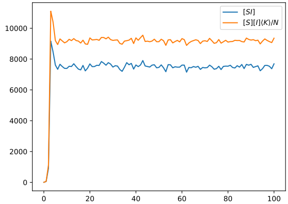
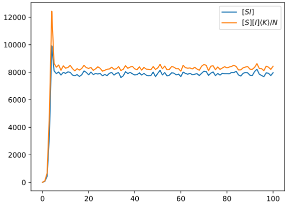
These are equivalent to the Kermack-McKendrick equations

Accuracy of $[SI] = \langle K \rangle [S][I]/N$

	Erdős–Rényi $\langle K \rangle = 5$	Config Model $P(5) = 1$
SIR		
SIS		

Appropriateness of $[SI] = \langle K \rangle [S][I]/N$

What assumptions are we making when we set $[SI] = \langle K \rangle [S][I]/N$?

- We're assuming that nodes are <u>not</u> preferentially infected by degree.
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When are these assumptions appropriate?

- Same degree, annealed network. Partnerships have zero duration.
- Large very similar degrees, transmission probability per edge very low, and low clustering.
- As a general rule — if the disease will never transmit across the same partnership twice, we can use models that ignore partnership duration.

A more accurate closure.

Our original equations are

$$\begin{aligned}
\frac{\mathrm{d}}{\mathrm{d}t}[S] &= -\beta[SI] \\
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\frac{\mathrm{d}}{\mathrm{d}t}[SI] &= -(\beta+\gamma)[SI] + \beta([SSI] - [ISI]) \\
\frac{\mathrm{d}}{\mathrm{d}t}[SSI] &= \cdots \\
\frac{\mathrm{d}}{\mathrm{d}t}[ISI] &= \cdots
\end{aligned}$$

Perhaps we can do a better job if we allow larger terms.

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- So we predict $[SSI] = [SS][SI](\langle K \rangle - 1)/\langle K \rangle [S]$.

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- Assuming $k_v = \langle K \rangle$, there are $\langle K \rangle - 1$ possible edges from v.
- The probability X is infected is $[SI]/\langle K \rangle [S]$.
- So we predict $[SSI] = [SS][SI](\langle K \rangle - 1)/\langle K \rangle [S]$.
- Unless knowing that u is susceptible would change the prediction for the probability X is infected. (not for SIR, but true for SIS since $[SS]$ edges may be concentrated around those who have not been infected recently.)

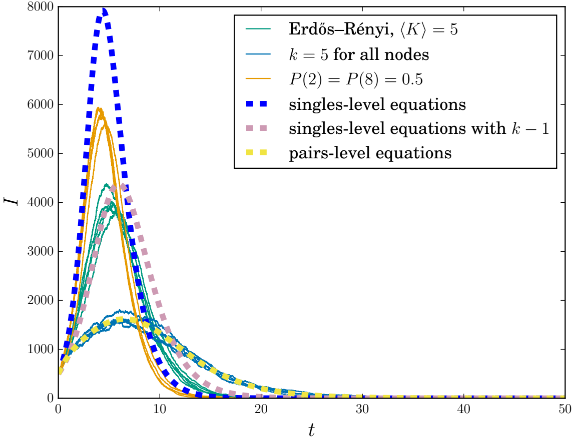
New equations

Our new equations are

$$\begin{aligned}
\frac{\mathrm{d}}{\mathrm{d}t}[S] &= -\beta[SI] \\
\frac{\mathrm{d}}{\mathrm{d}t}[I] &= \beta[SI] - \gamma[I] \\
\frac{\mathrm{d}}{\mathrm{d}t}[SI] &= -(\beta+\gamma)[SI] + \beta\frac{\langle K\rangle - 1}{\langle K\rangle}\left(\frac{([SS][SI] - [SI][SI])}{[S]}\right) \\
\frac{\mathrm{d}}{\mathrm{d}t}[SS] &= -2\beta\frac{\langle K\rangle - 1}{\langle K\rangle}\frac{[SI][SS]}{[S]}
\end{aligned}$$

(we need to add an $[SS]$ equation)

Theory versus stochastic simulation



Deriving equations

Simple heterogeneous model

References

A model for heterogeneous networks

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A model for heterogeneous networks

- We can develop a model that accounts for degree correlation.
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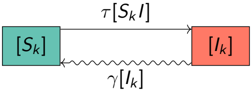
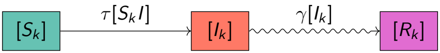
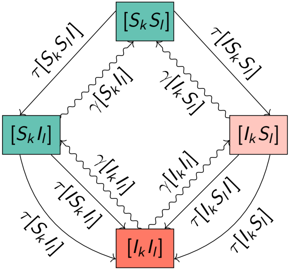
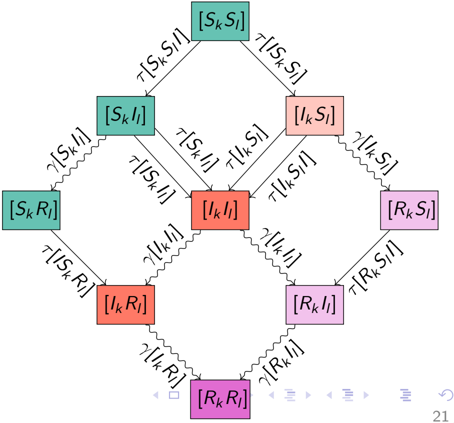
  To give the number of pairs involving a degree k node with status A and a degree l node with status B.
- We derive similar unclosed equations, and then use a closure.

Flow diagrams









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For SIS we get

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\begin{aligned}
\dot{[S_k]} &= \gamma[I_k] - \tau[S_k I], \\
\dot{[I_k]} &= \tau[S_k I] - \gamma[I_k], \\
\dot{[S_k I_l]} &= \gamma([I_k I_l] - [S_k I_l]) + \tau([S_k S_l I] - [I S_k I_l] - [S_k I_l]), \\
\dot{[S_k S_l]} &= \gamma([S_k I_l] + [I_k S_l]) - \tau([S_k S_l I] + [I S_k S_l]), \\
\dot{[I_k I_l]} &= \tau([S_k I_l] + [I_k S_l]) - 2\gamma[I_k I_l] + \tau([I S_k I_l] + [I_k S_l I])
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These models can account for degree assortativity or dissasortativity, but LOTS OF EQUATIONS.
We can do closures in terms of pairs, but do not show that here (see [1]).

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Simplest closure (annealed networks)

We can derive a model that accounts for degree distribution, but not partnership duration [2, 3, 4]:

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Recall our key questions

For SIR:

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

For SIS:

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

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$$\mathcal{R}_0 = \sum_k \frac{kP(k)}{\langle K \rangle} k \frac{\beta}{\gamma} = \frac{\beta}{\gamma} \frac{\langle K^2 \rangle}{\langle K \rangle}$$
- This is the same whether the model is SIS or SIR.

Errors

- It was rigorously proven by [5] that if $P(k) \sim k^{-\alpha}$ then for a Configuration Model network there is no epidemic threshold for SIS disease, even if $\left\langle K^2 \right\rangle$ is finite.

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- That is, no matter how small β is, an epidemic is possible.
- This contradicts the prediction. How does this happen?
- High degree nodes get infected and infect their neighbors. Then they recover.
- So susceptible high degree nodes tend to have more infected neighbors.
- We expect to see islands of infection surrounding high degree nodes that persist long enough to spread the disease spreads to other high degree nodes. This holds even if the naive estimate has $\mathcal{R}_0 < 1$.

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- So $I_k = \beta k P(k) \pi_I / (\gamma + \beta k \pi_I)$

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- But $\pi_I = \sum kI_k / \langle K \rangle$. Substituting for I_k yields

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- Not pleasant to solve for π_I, but doable. There is a positive solution iff $\mathcal{R}_0 = \beta \left\langle K^2 \right\rangle / \gamma \langle K \rangle > 1$.

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- Set $\theta = e^{-\xi}$, so $S_k = S_k(0)\theta^k$ where $S_k(0) = (1-\rho)P(k)N$. Then

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

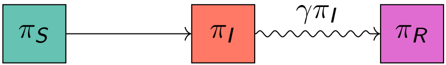
  is a probability generating function. We define $\psi(x) = \sum_k P(k)x^k$.

Consolidating and continuing

Our model is now

$$\begin{aligned}\dot{\theta} &= -\beta\pi_I\theta \\ S_k &= (1-\rho)NP(k)\theta^k \\ I_k &= NP(k) - S_k - R_k \\ \dot{R}_k &= \gamma I_k \\ \pi_I &= \sum_k kI_k \Bigg/ N\langle K\rangle \,.\end{aligned}$$

- We set $\pi_X = \sum_k kX_k/N\langle K\rangle$ to be the proportion of stubs belonging to status X nodes. We have



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- Further $\pi_S = (1-\rho)\sum_k NkP(k)\theta^k / N\langle K\rangle = (1-\rho)\theta\psi(\theta)/\langle K\rangle$.

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- Further $\pi_S = (1-\rho)\sum_k NkP(k)\theta^k/N\langle K\rangle = (1-\rho)\theta\psi(\theta)/\langle K\rangle$.
- So $\pi_I = 1 - \pi_S - \pi_R$. Substituting in terms of θ we have

$$\begin{aligned}
\dot{\theta} &= -\beta\theta\left(1-(1-\rho)\frac{\theta\psi'(\theta)}{\langle K\rangle}+\frac{\gamma\ln\theta}{\beta}\right)\\
S &= N(1-\rho)\psi(\theta)\\
I &= N-S-R\\
\dot{R} &= \gamma I
\end{aligned}$$

Final size

At $t \to \infty$, we have $\dot{\theta} \to 0$. We assume $\rho \to 0$. So

$$0 = 1 - \frac{\theta \psi'(\theta)}{\langle K \rangle} + \frac{\gamma \ln \theta}{\beta}$$

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Solving for $\theta(\infty)$:

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Then

$$S(\infty) = S(0)\psi(\theta(\infty)), \qquad R(\infty) = N - S(0)\psi(\theta(\infty))$$

Deriving equations

Simple heterogeneous model

References

References I

[1] Istvan Z Kiss, Joel C Miller, and Péter L Simon.
Mathematics of epidemics on networks: from exact to approximate models.
IAM. Springer, 2017.

[2] Romualdo Pastor-Satorras and Alessandro Vespignani.
Epidemic spreading in scale-free networks.
Physical Review Letters, 86(14):3200–3203, Apr 2001.

[3] Robert M. May and R. M. Anderson.
The transmission dynamics of human immunodeficiency virus (HIV).
Philosophical Transactions of the Royal Society London B, 321(1207):565–607, 1988.

[4] Annett Nold.
Heterogeneity in disease-transmission modeling.
Mathematical Biosciences, 52(3):227–240, 1980.

[5] S. Chatterjee and R. Durrett.
Contact processes on random graphs with power law degree distributions have critical value 0.
The Annals of Probability, 37(6):2332–2356, 2009.