

Epidemics in Networks

Basic Properties

Joel C. Miller & Tom Hladish

20–22 July 2016

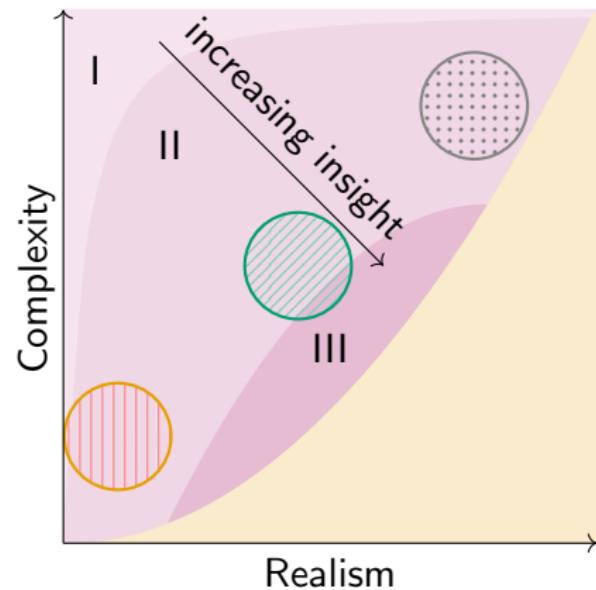
Introduction

Compartmental Models

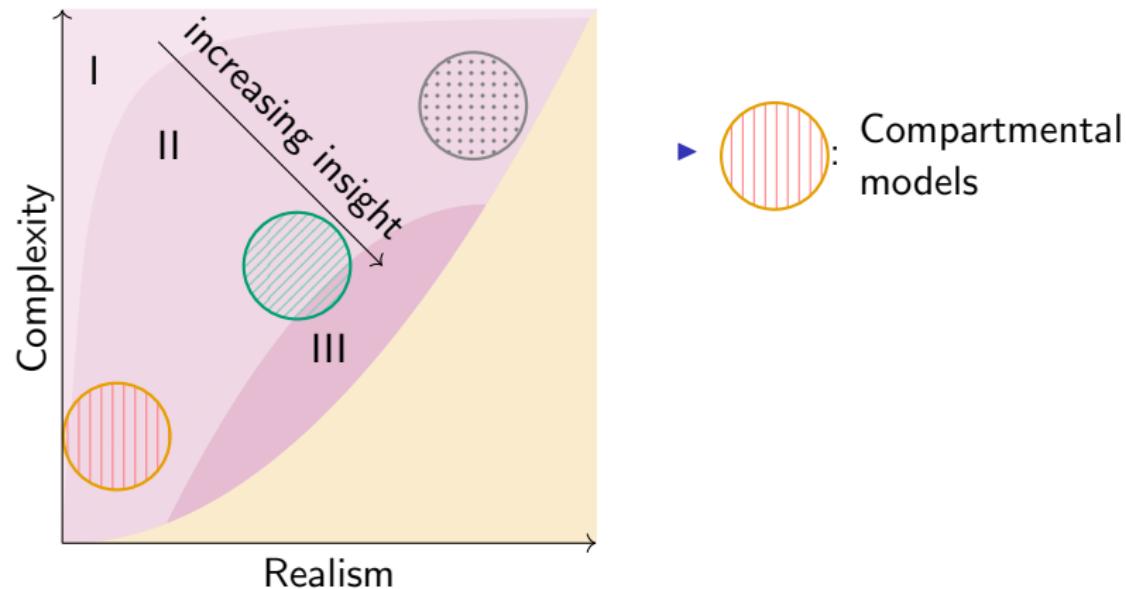
Network Disease Models

References

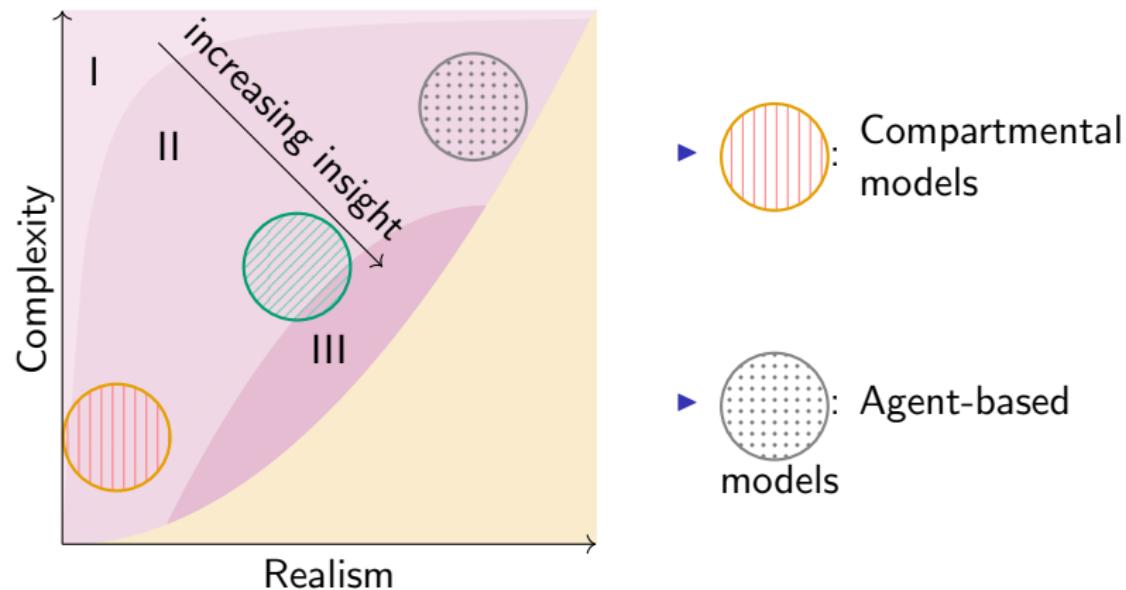
Modeling options



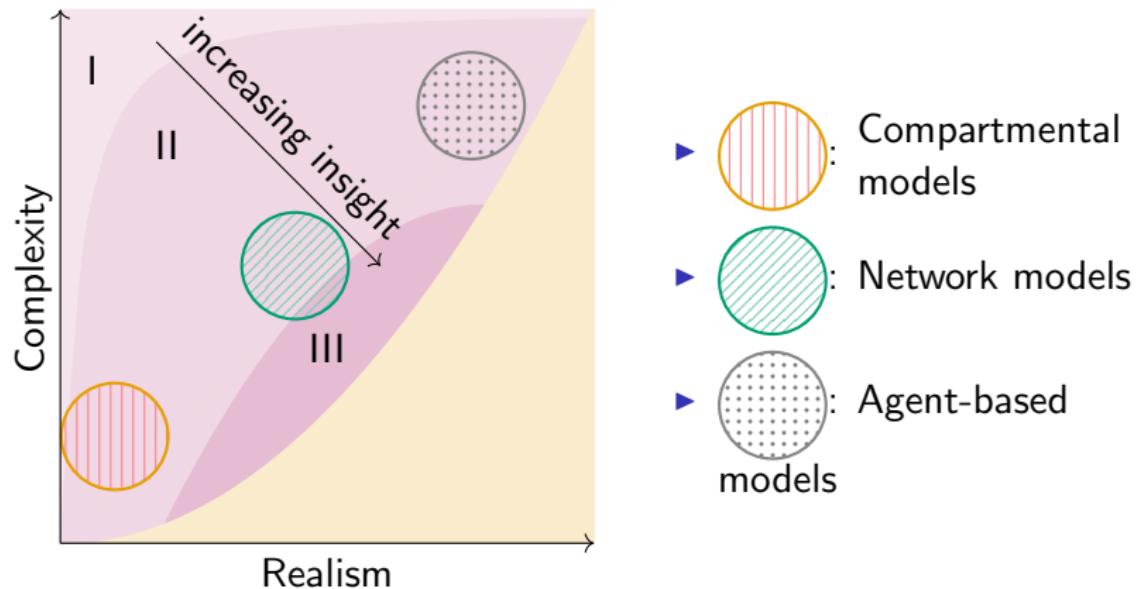
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Simple Compartmental Models

- ▶ Continuous time or Discrete time
- ▶ SIR or SIS

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- ▶ SIR or SIS

The major assumptions:

- ▶ Every individual is average.
- ▶ Every interaction of u is with a randomly chosen other individual.

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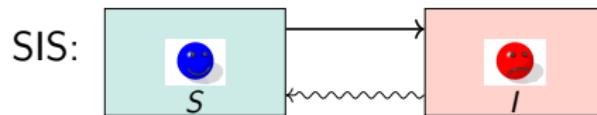
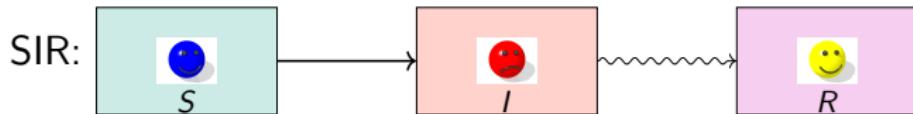
Throughout:

$$S + I + R = 1$$

That is, we look at proportions in each state, not absolute number:

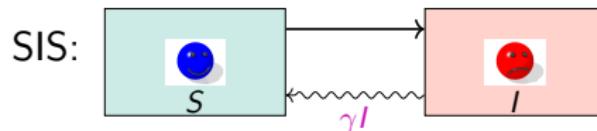
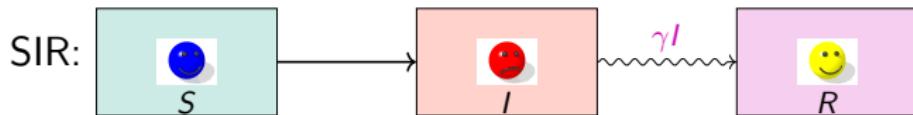
$$S + I + R \neq N.$$

Continuous time: Kermack–McKendrick



Assumptions:

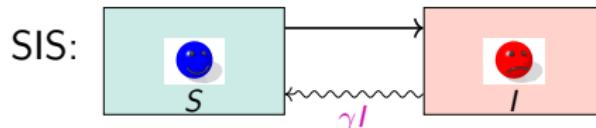
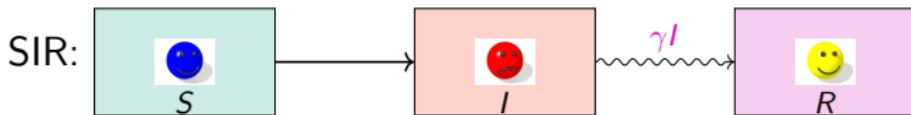
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Assumptions:

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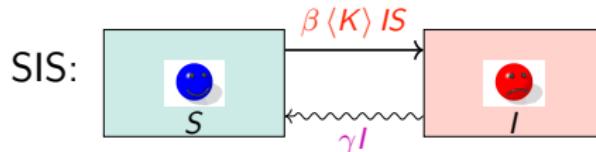
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- ▶ Infected individuals **transmit to others** at rate $\beta \langle K \rangle$ (usually we combine these into a single parameter).
 - ▶ β represents the transmission rate of the disease per partnership.
 - ▶ $\langle K \rangle$ represents the typical number of partners of an infected individual at any time.

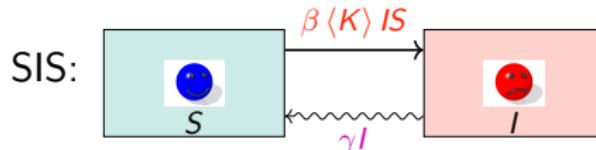
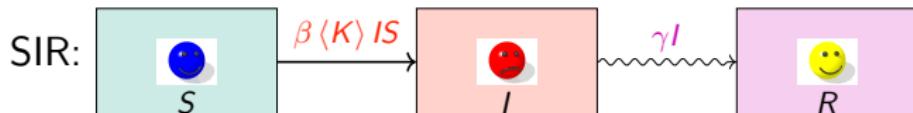
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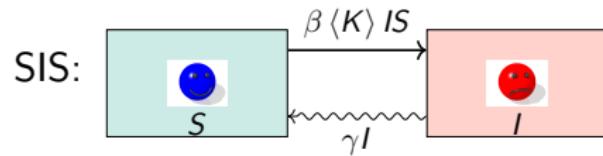
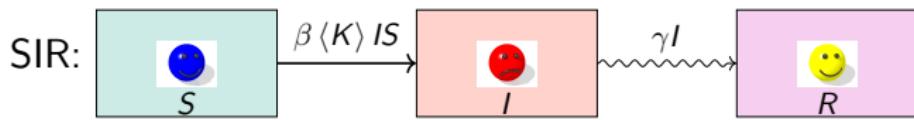
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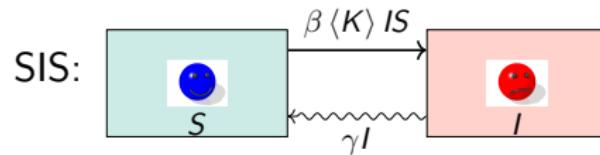
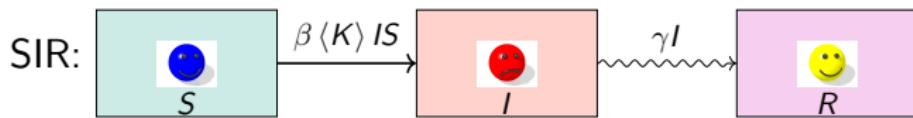
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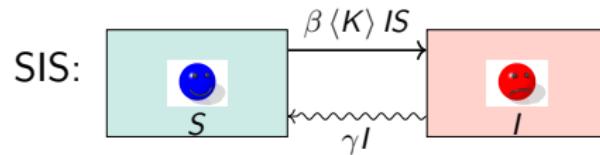
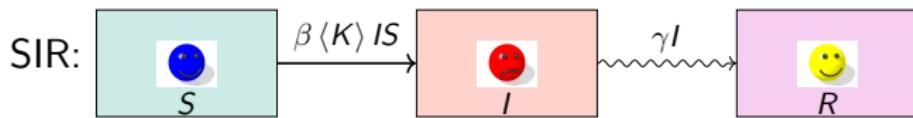
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- ▶ An implicit assumption is that each interaction is with a new randomly infected individual.





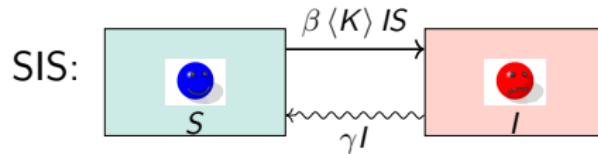
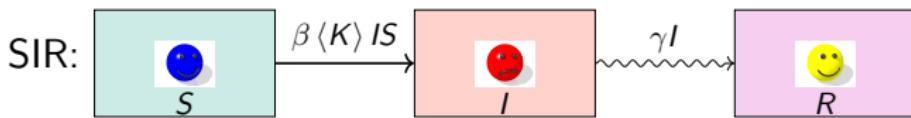
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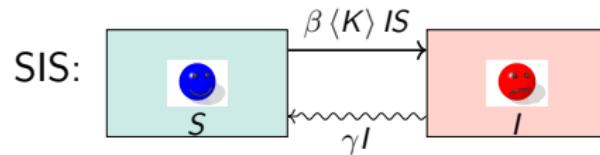
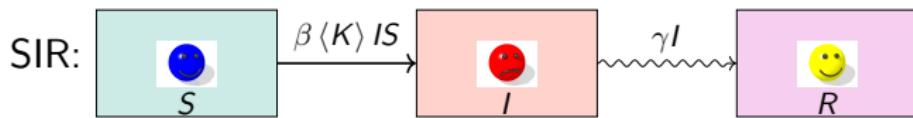
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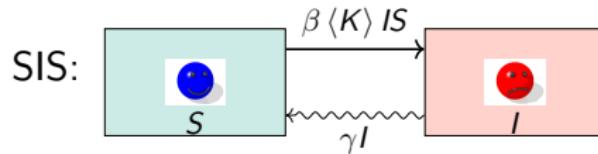
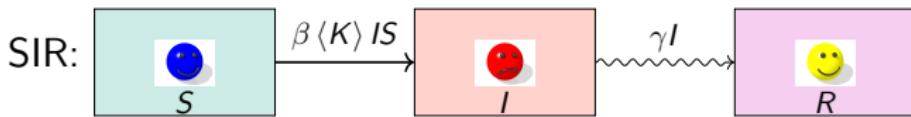
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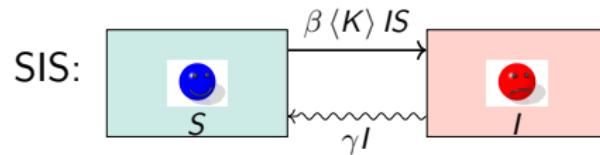
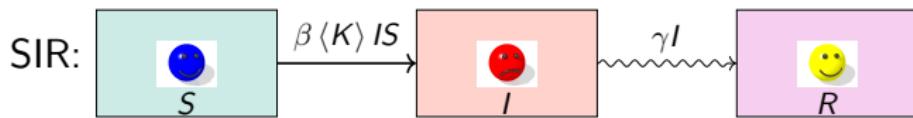


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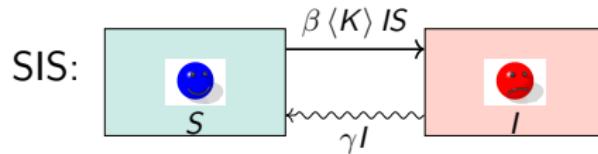
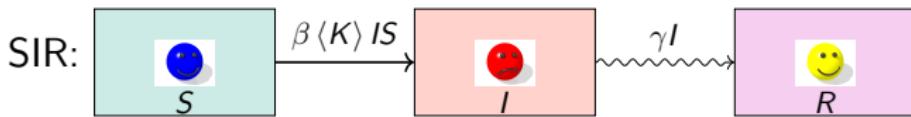


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So it's an important threshold parameter, but it doesn't address the probability of epidemics.

\mathcal{R}_0 calculation

Calculate \mathcal{R}_0 for:

$$\dot{S} = -\beta IS$$

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- ▶ So $\mathcal{R}_0 = \beta \langle K \rangle / \gamma$.

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We can get the final size from this, but let's see how far we can go.

New System

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$$S = S(0)e^{-\xi}$$

$$\dot{\xi} = -\beta \langle K \rangle (1 - S - R) = \beta \langle K \rangle \left(1 - S(0)e^{-\xi} - R(0) - \frac{1}{R_0} \xi \right)$$

$$R = R(0) + \frac{1}{R_0} \xi$$

$$I = 1 - S - R$$

We can write $\dot{\xi}$ entirely in terms of ξ and initial conditions.

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Taking $t \rightarrow \infty$, we have $\dot{\xi} \rightarrow 0$, so $R(\infty) = 1 - S(\infty)$.

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Assuming at time 0 a fraction ρ is initially infected, $R(0) = 0$ and $S(0) = 1 - \rho$.

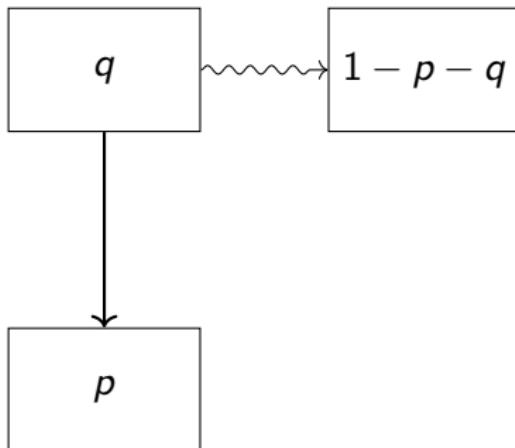
$$R(\infty) = 1 - (1 - \rho)e^{-\mathcal{R}_0 R(\infty)}$$

and the final size can be found by iteration.

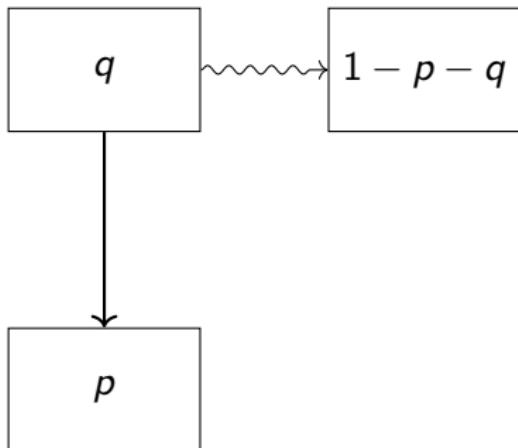
Epidemic probability \mathcal{P}

Consider an index infection u .

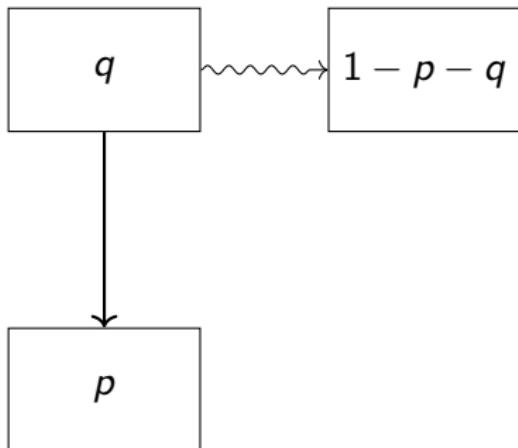
- ▶ The probability u sparks an epidemic is \mathcal{P} .
- ▶ But it's also the probability u infects at least one individual who would spark an epidemic.
- ▶ If u infects v , the probability v sparks an epidemic (if no-one else u infects does) is \mathcal{P} .



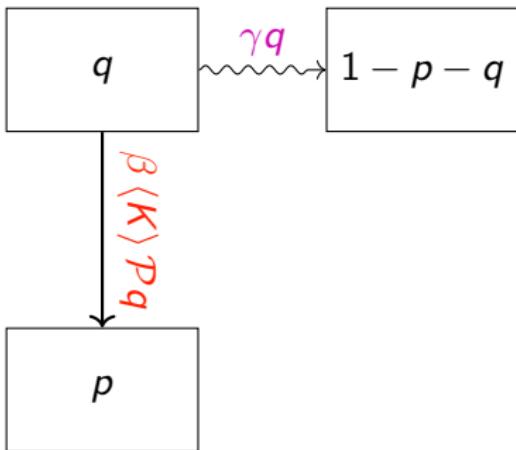
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- ▶ If u is infected, the rate of causing an infection that starts an epidemic is $\beta \langle K \rangle \mathcal{P}$.



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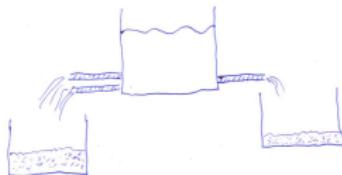
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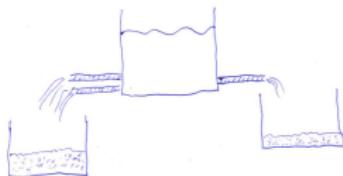
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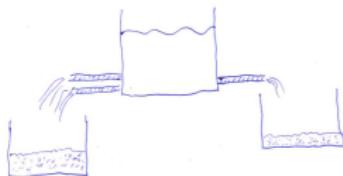


- ▶ If both pools start empty, and at all times one receives c times as much flow as the other, then it will always have c times as much water in it.

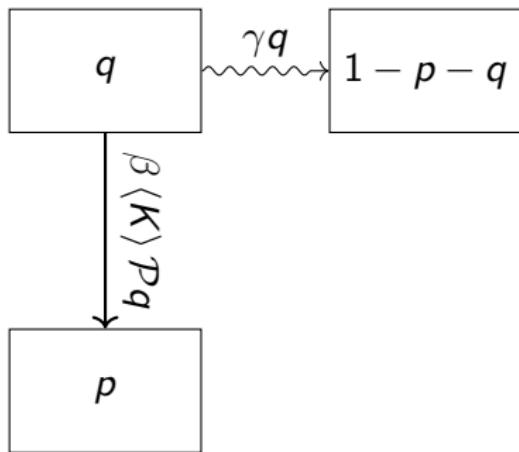
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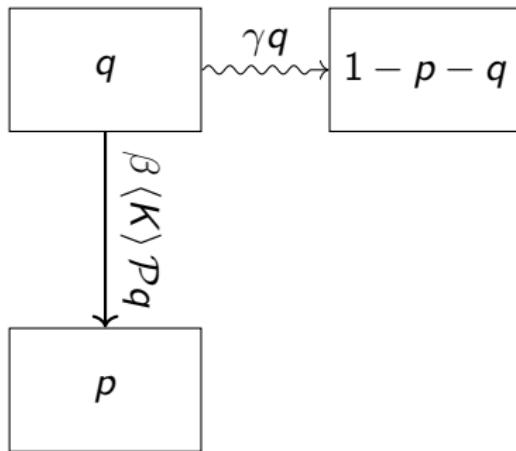
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- ▶ If both pools start empty, and at all times one receives c times as much flow as the other, then it will always have c times as much water in it.
- ▶ If the source is additionally finite, then when all the water has left the source, the first will have $c/(1 + c)$ of the initial water and the second will have $1/(1 + c)$ of the initial water.





$$\mathcal{P} = p(\infty) = \frac{\beta \langle K \rangle \mathcal{P}}{\beta \langle K \rangle \mathcal{P} + \gamma}$$

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We assume

- ▶ SIS disease on a fixed static network.
- ▶ Susceptible nodes  and infected nodes 

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- ▶ Disease transmits on an edge with rate β (many authors use τ)
- ▶ Infected individuals recover with rate γ

Network disease models

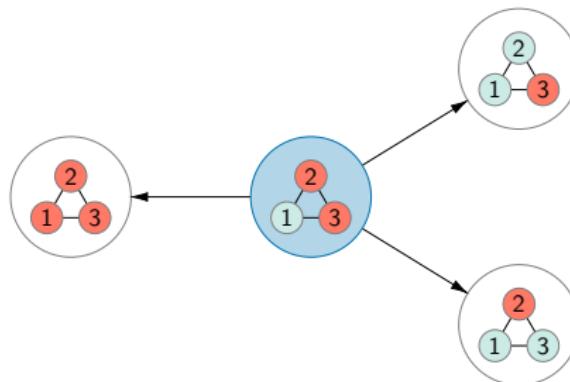
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- ▶ Susceptible nodes  and infected nodes 
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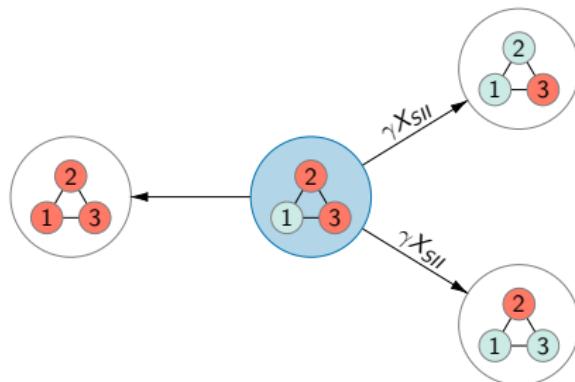
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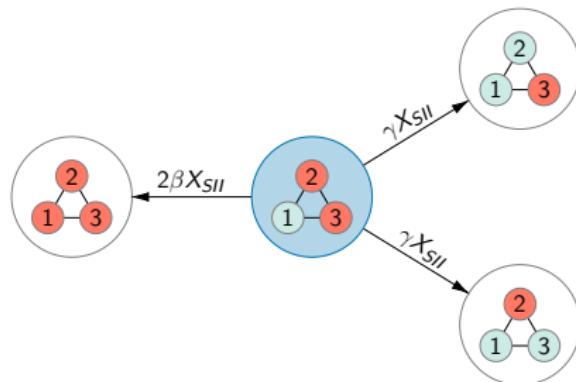
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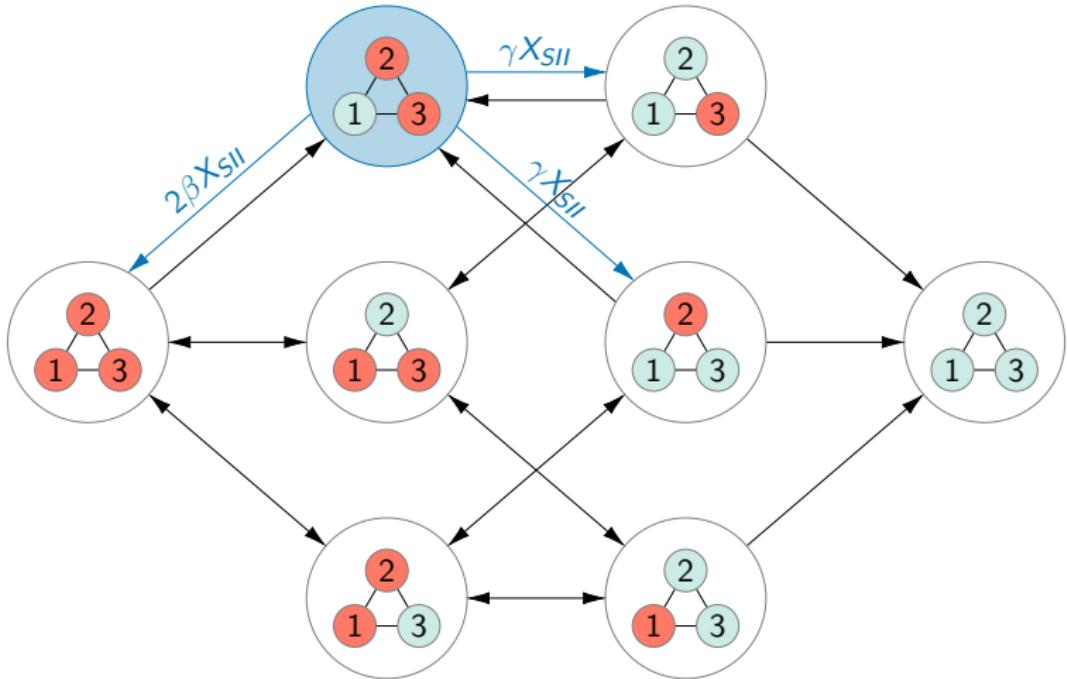


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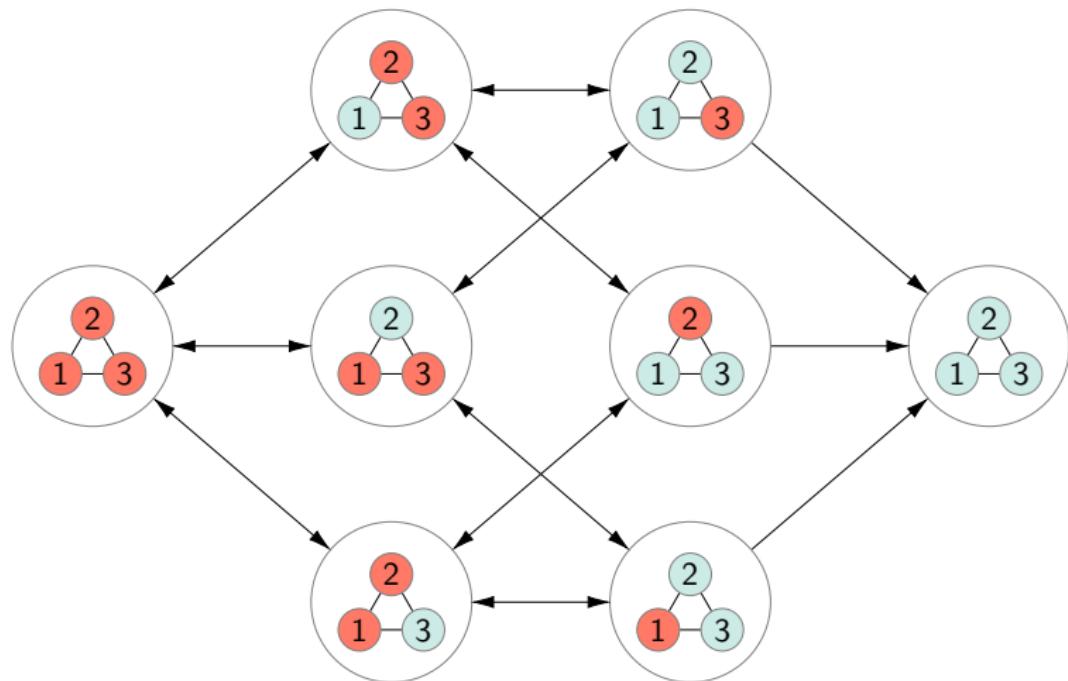


Master Equations

The Master Equations (aka Kolmogorov Equations)

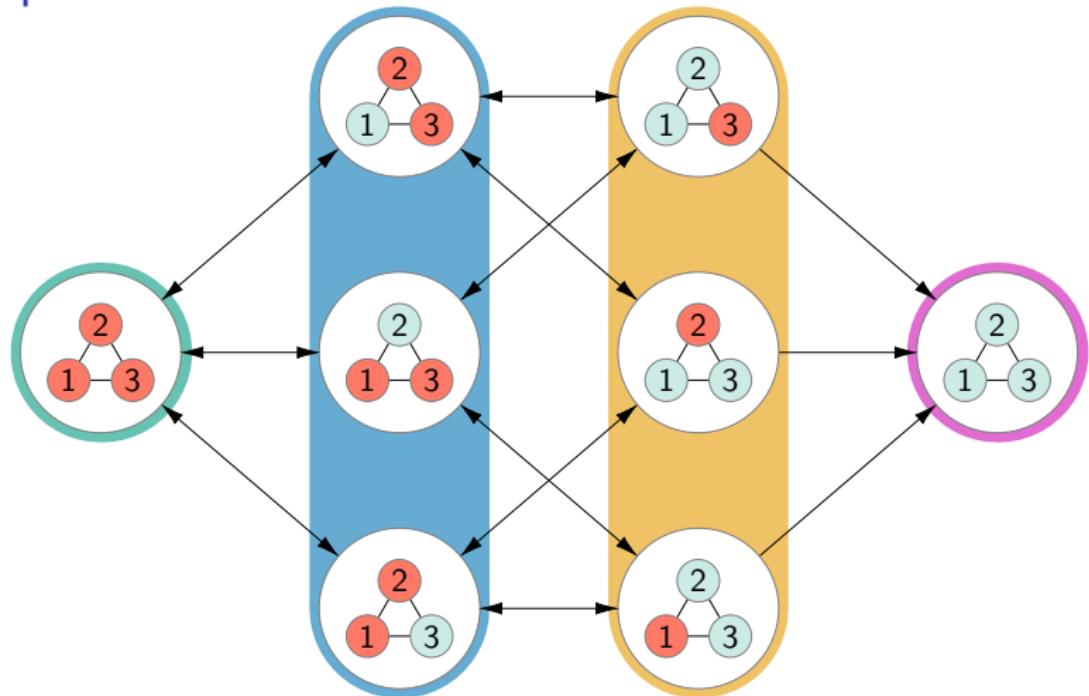
$$\begin{aligned}\dot{X}_{SSS} &= \gamma(X_{SSI} + X_{SIS} + X_{ISS}), \\ \dot{X}_{SSI} &= \gamma(X_{SII} + X_{ISI}) - (2\beta + \gamma)X_{SSI}, \\ \dot{X}_{SIS} &= \gamma(X_{SII} + X_{IIS}) - (2\beta + \gamma)X_{SIS}, \\ \dot{X}_{ISS} &= \gamma(X_{ISI} + X_{IIS}) - (2\beta + \gamma)X_{ISS}, \\ \dot{X}_{SII} &= \gamma X_{III} + \beta(X_{SSI} + X_{SIS}) - 2(\beta + \gamma)X_{SII}, \\ \dot{X}_{ISI} &= \gamma X_{III} + \beta(X_{SSI} + X_{ISS}) - 2(\beta + \gamma)X_{ISI}, \\ \dot{X}_{IIS} &= \gamma X_{III} + \beta(X_{SIS} + X_{ISS}) - 2(\beta + \gamma)X_{IIS}, \\ \dot{X}_{III} &= -3\gamma X_{III} + 2\beta(X_{SII} + X_{ISI} + X_{IIS}).\end{aligned}$$

Simplifications



There's a lot of symmetry here.

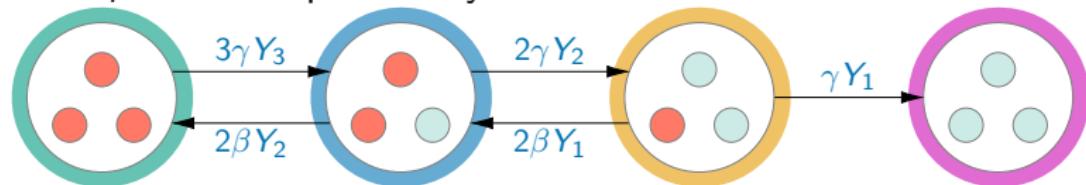
Simplifications



Set Y_i to be the probability i are infected.

Simplifications

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$$\dot{Y}_0 = \gamma Y_1$$

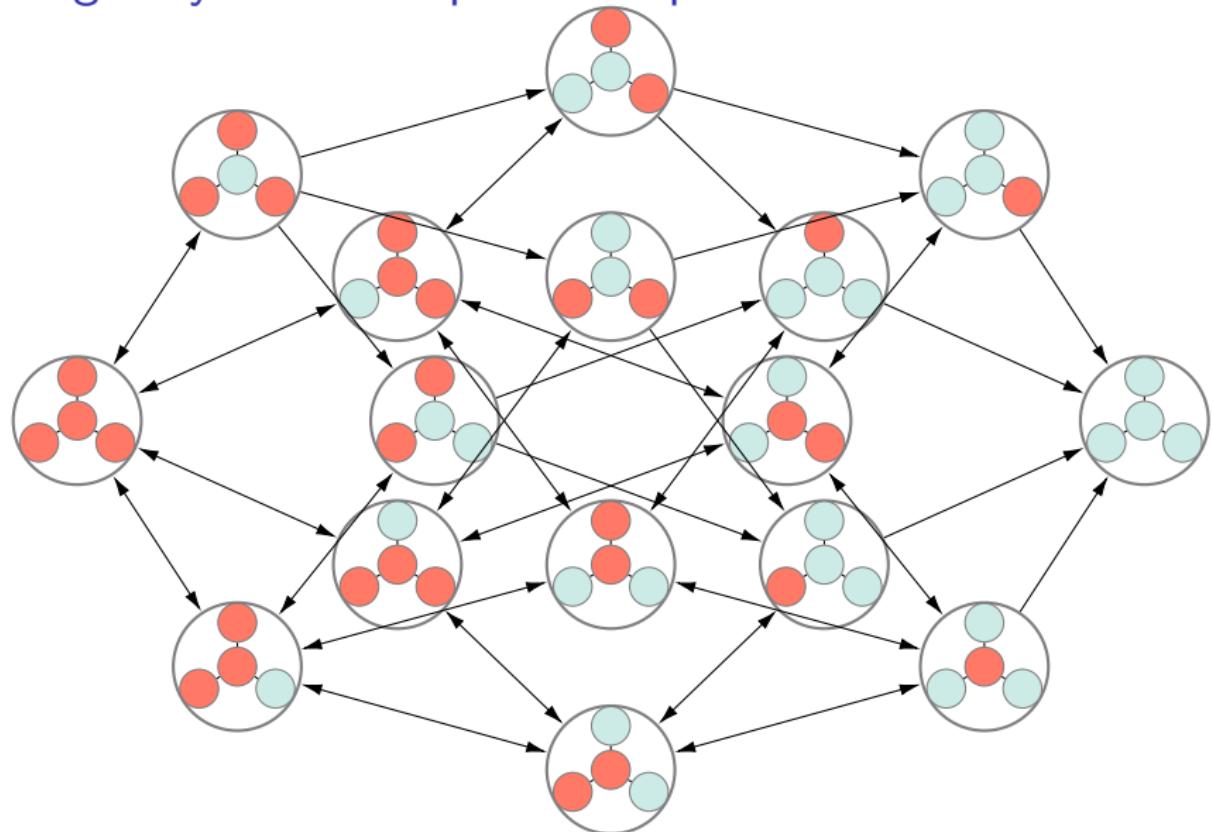
$$\dot{Y}_1 = 2\gamma Y_2 - (2\beta + \gamma) Y_1$$

$$\dot{Y}_2 = 3\gamma Y_3 + 2\beta Y_1 - (2\gamma Y_2 + 2\beta Y_2)$$

$$\dot{Y}_3 = 2\beta Y_2 - 3\gamma Y_3$$

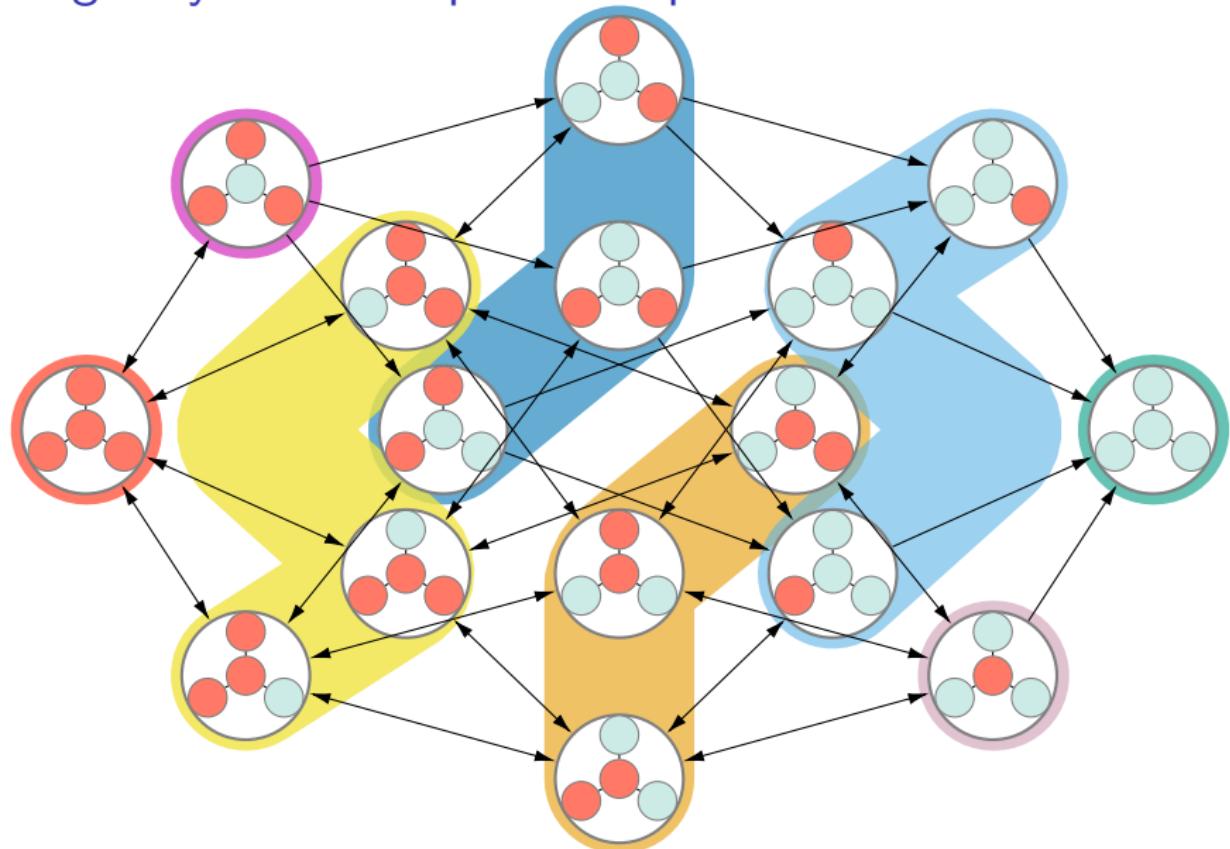
That's not so bad!

A marginally more complex example



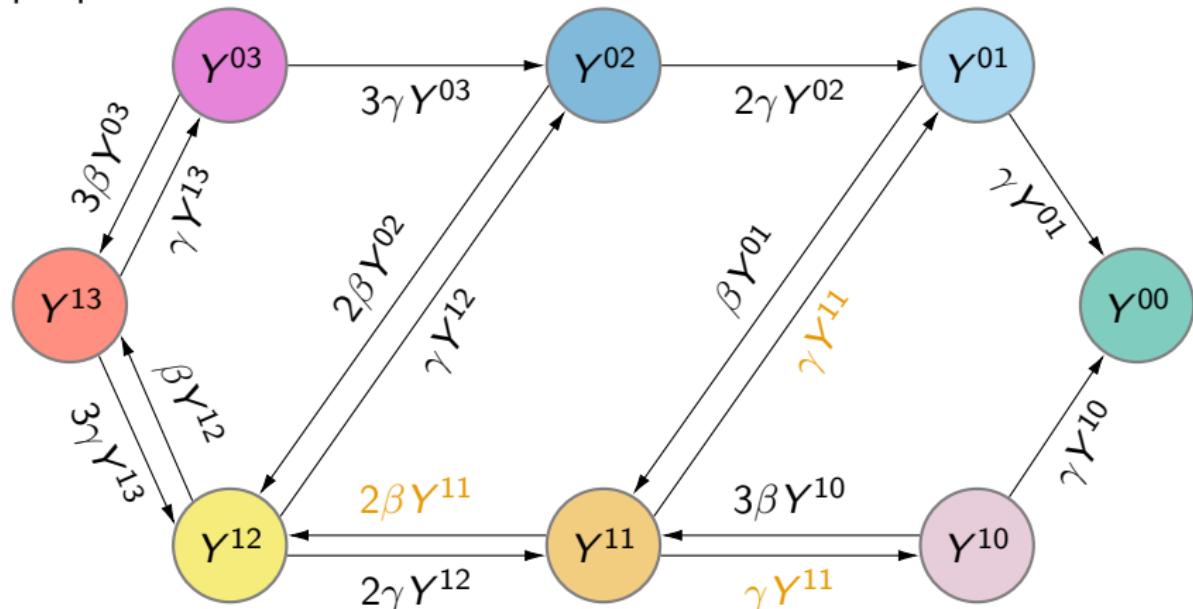
Can we take advantage of the symmetry?

A marginally more complex example



A marginally more complex example

Define Y^{ij} with $i = 1$ if central node infected and j the number of peripheral infections.



A marginally more complex example

$$\dot{Y}^{00} = \gamma(Y^{10} + Y^{01})$$

$$\dot{Y}^{01} = 2\gamma Y^{02} + \gamma Y^{11} - (\gamma + \beta) Y^{01}$$

$$\dot{Y}^{10} = \gamma Y^{11} - (\gamma + 3\beta) Y^{10}$$

$$\dot{Y}^{02} = 3\gamma Y^{03} + \gamma Y^{12} - (2\gamma + 2\beta) Y^{02}$$

$$\dot{Y}^{11} = 3\beta Y^{10} + \beta Y^{01} + 2\gamma Y^{12} - (2\gamma + 2\beta) Y^{11}$$

$$\dot{Y}^{03} = \gamma Y^{13} - (3\gamma + 3\beta) Y^{03}$$

$$\dot{Y}^{12} = 3\gamma Y^{13} + 2\beta(Y^{02} + Y^{11}) - (3\gamma + \beta) Y^{12}$$

$$\dot{Y}^{13} = 3\beta Y^{03} + \beta Y^{12} - 4\gamma Y^{13}$$

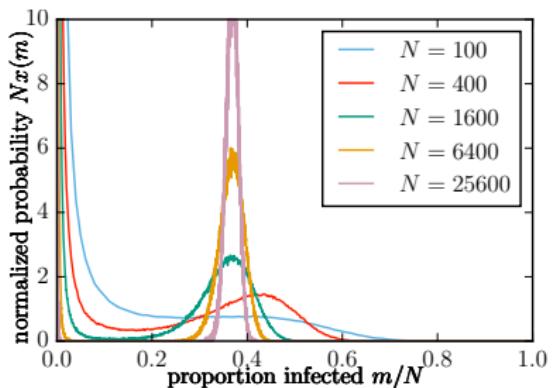
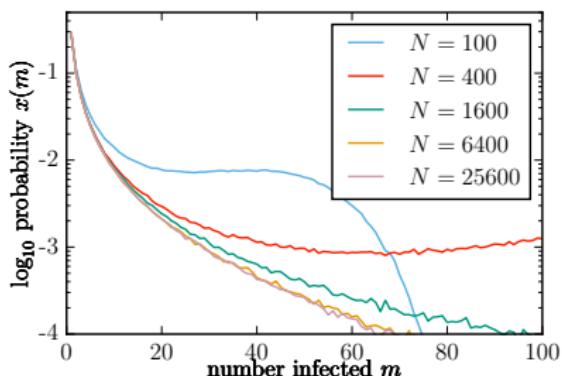
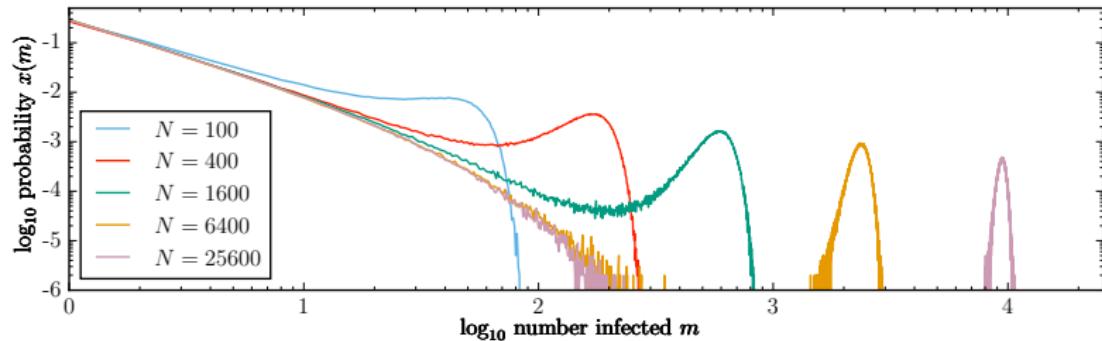
That got a lot worse. Without symmetry or larger networks would be really bad.

Larger networks

- ▶ It will be hopeless to find equations for all possible states: 2^N for SIS and 3^N for SIR.
- ▶ Even taking advantage of symmetries, it is impractical.
- ▶ Instead we can try to approximate “population-scale” quantities such as proportion infected.
- ▶ Perhaps surprisingly, eventually we will see that SIR is easier to work with. Although there are more states, there are fewer transitions possible.
- ▶ Working with SIS will require more dubious assumptions.

SIR in detail

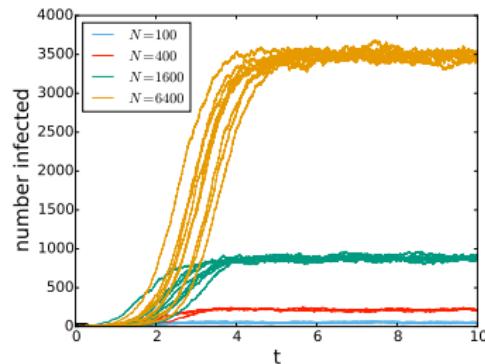
Set $x(m)$ to be the probability exactly m nodes infected:



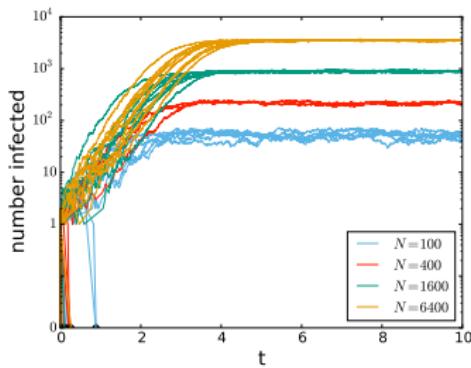
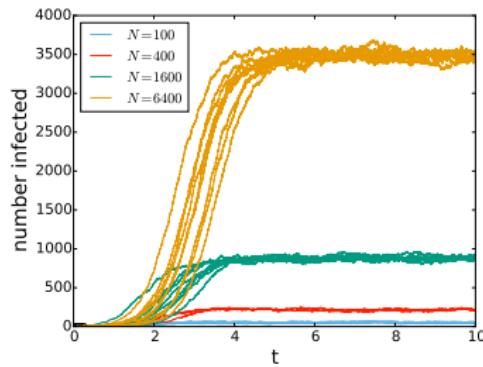
SIR observations

- ▶ In large networks outbreaks are either small (non-epidemic) or large (epidemic).
- ▶ Small outbreaks don't care about network size (once network is larger than some threshold).
- ▶ Epidemic sizes are proportional to network size.

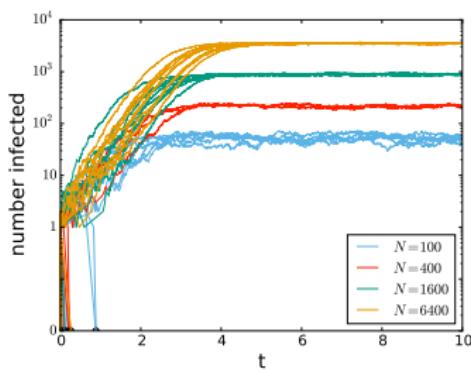
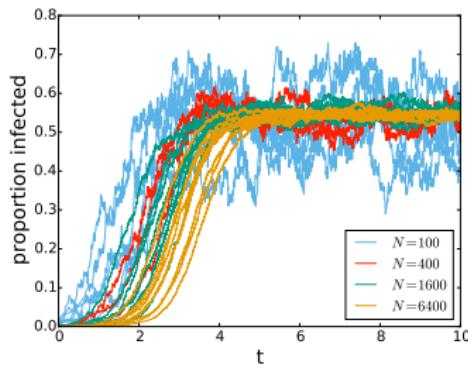
SIS in detail



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SIS in detail

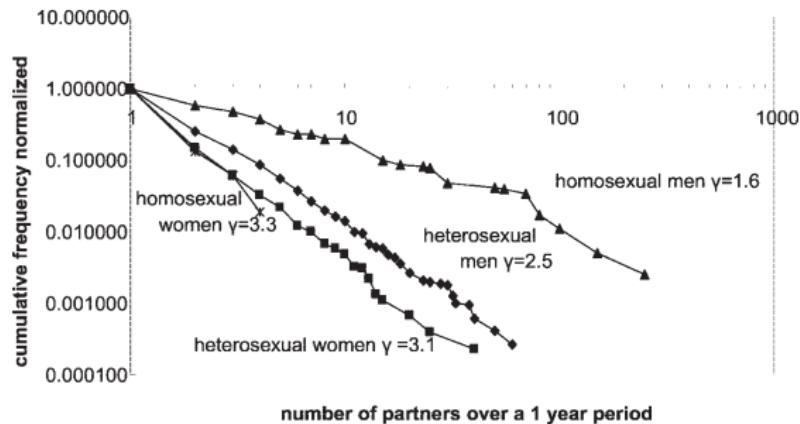


SIS observations

- ▶ In large networks outbreaks either go extinct quickly (non-epidemic) or reach an endemic equilibrium (epidemic).
- ▶ Small outbreak sizes don't care about network size.
- ▶ Endemic equilibrium sizes are proportional to network size.
- ▶ Variance decreases for large networks.

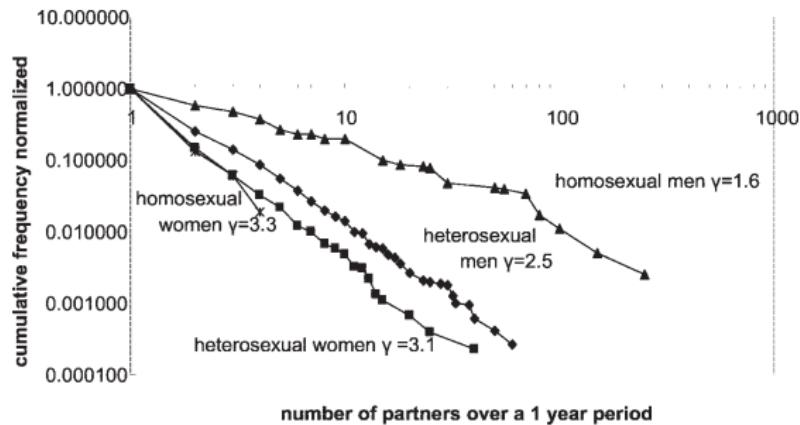
Degree distribution

From [1]:



Degree distribution

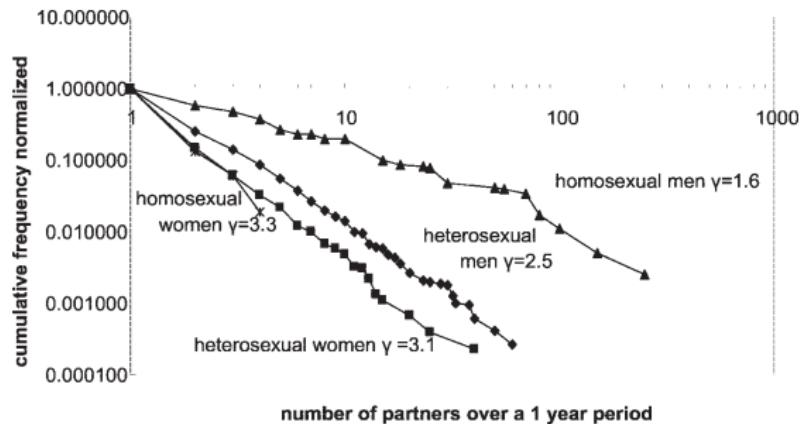
From [1]:



Impact on \mathcal{R}_0 :

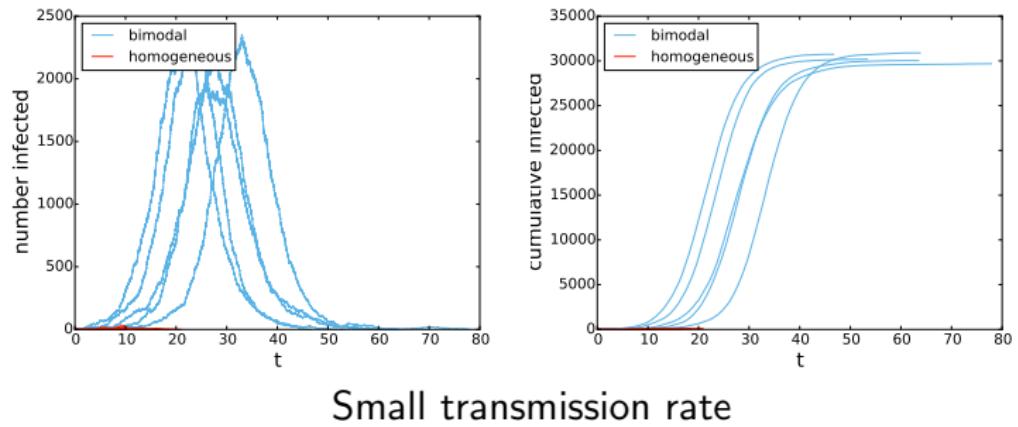
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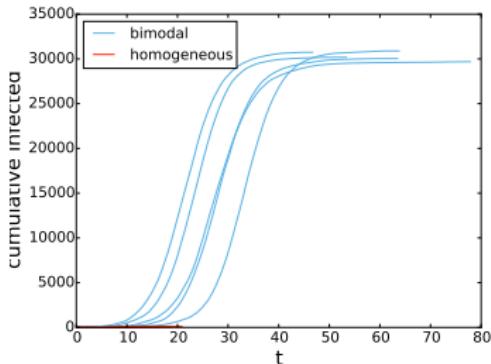
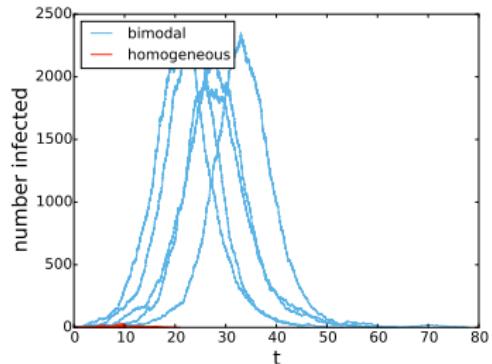


Impact on \mathcal{R}_0 : Increases it

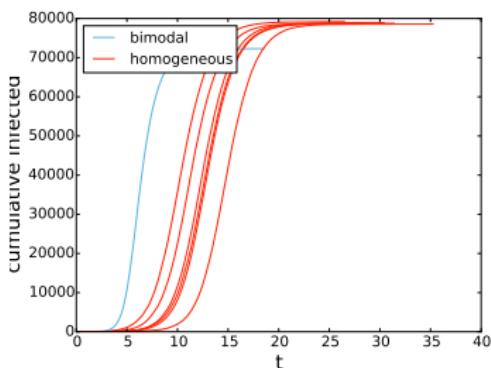
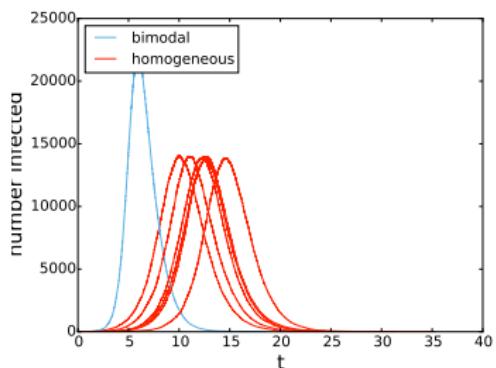
Degree distribution



Degree distribution



Small transmission rate



Large transmission rate

Degree correlations

Do opposites really attract?

Degree correlations

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Individuals likely form partnerships with similar individuals.

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If high degree individuals preferentially contact high degree individuals, impact on \mathcal{R}_0 :

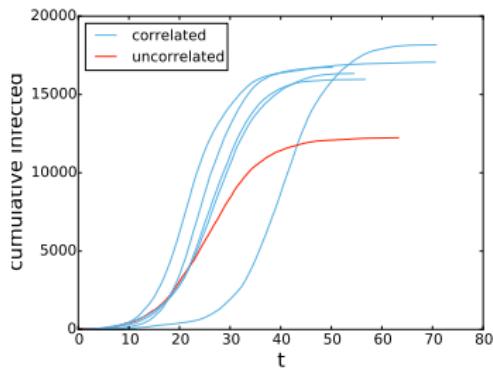
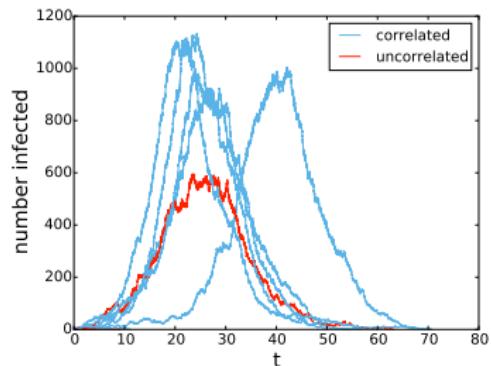
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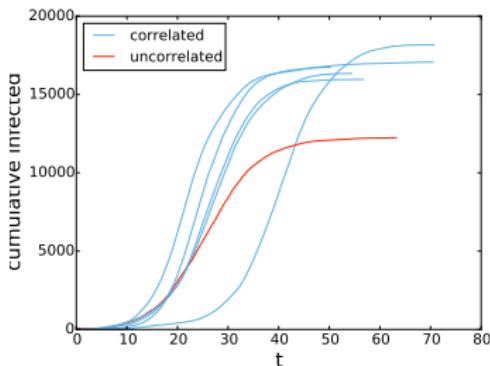
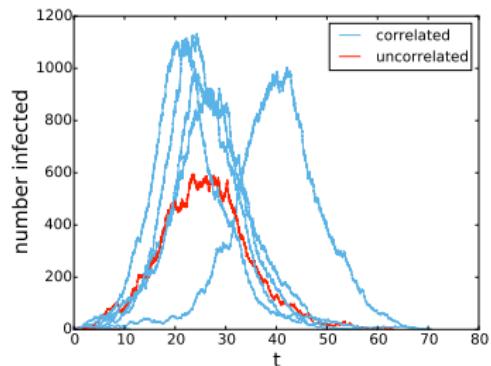
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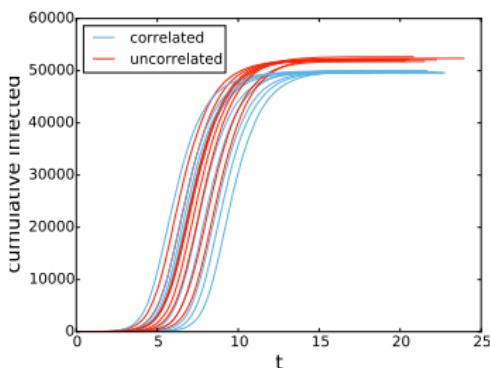
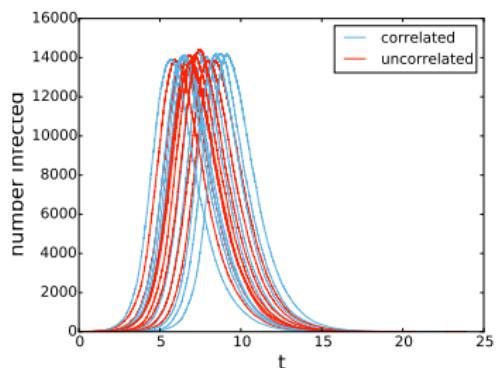


Small transmission rate

Degree correlations



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Large transmission rate

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If partnerships have long duration, people are likely to have some transmissions blocked, and are likely to reinfect their infector (in SIS) rather than someone else.

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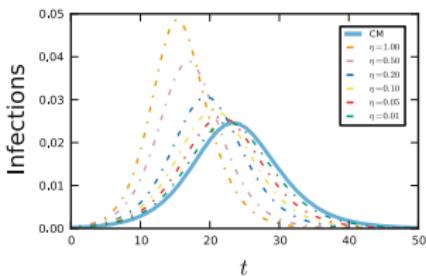
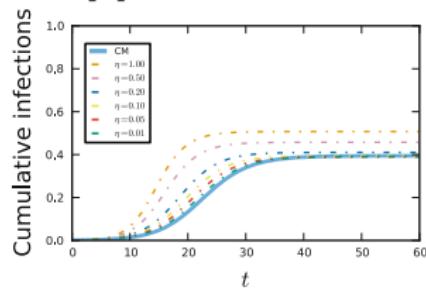
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Impact on \mathcal{R}_0 : For SIR, decreases it. For SIS, it is complex.

Partnership duration

From [2]



(η is inverse partnership duration, “CM” is static Configuration Model)

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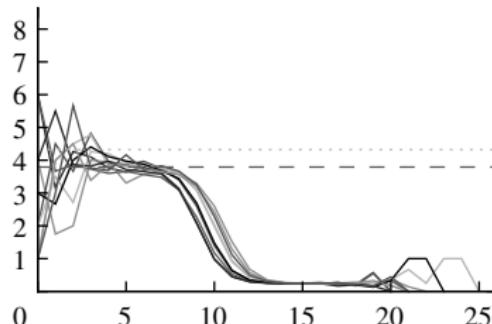
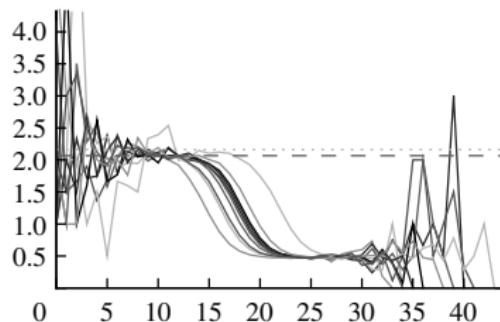
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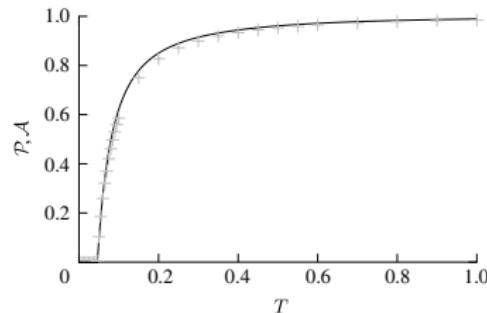
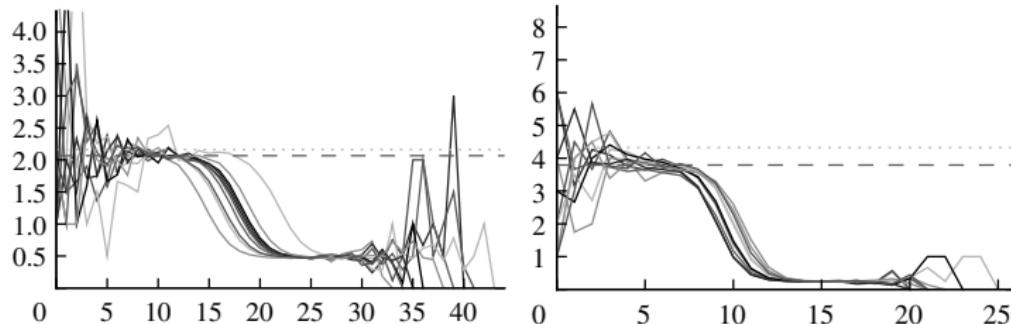
Clustering

From [3]



Clustering

From [3]



(horizontal axis is transmission probability)

Introduction

Compartmental Models

Network Disease Models

References

References |

- [1] Anne Schneeberger, Catherine H Mercer, Simon AJ Gregson, Neil M Ferguson, Constance A Nyamukapa, Roy M Anderson, Anne M Johnson, and Geoff P Garnett.
Scale-free networks and sexually transmitted diseases: a description of observed patterns of sexual contacts in britain and zimbabwe.
Sexually transmitted diseases, 31(6):380–387, 2004.
- [2] Joel C. Miller and Erik M. Volz.
Model hierarchies in edge-based compartmental modeling for infectious disease spread.
Journal of Mathematical Biology, 67(4):869–899, 2013.
- [3] Joel C. Miller.
Spread of infectious disease through clustered populations.
Journal of the Royal Society Interface, 6(41):1121, 2009.