

Epidemics in Networks

Part 3 — Network-based Disease Models

Joel C. Miller & Tom Hladish

17–19 July 2017

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
- ▶ $I(t)$

Introduction

Sample stochastic simulations

Impact of network properties

Deriving equations

Simple heterogeneous model

References

Assumptions

We start with some simple assumptions:

- ▶ SIS or SIR disease on a fixed static network.
- ▶ Susceptible nodes , infected nodes , and recovered nodes .

Assumptions

We start with some simple assumptions:

- ▶ SIS or SIR disease on a fixed static network.
- ▶ Susceptible nodes , infected nodes , and recovered nodes .
- ▶ Disease transmits along an edge with rate β (many authors use τ)
- ▶ Infected individuals recover with rate γ

Introduction

Sample stochastic simulations

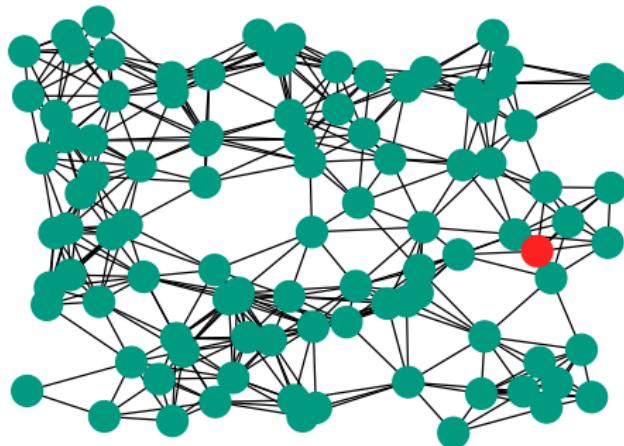
Impact of network properties

Deriving equations

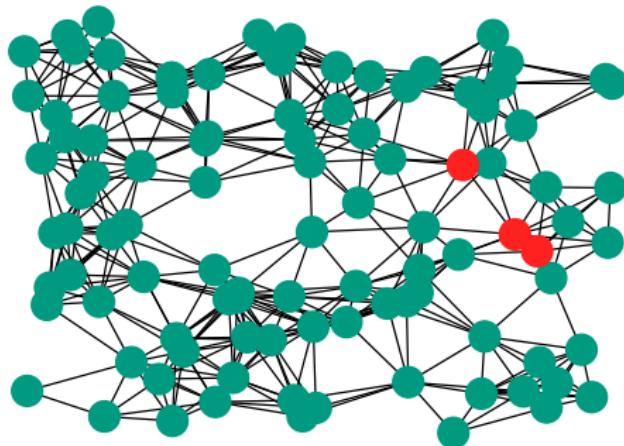
Simple heterogeneous model

References

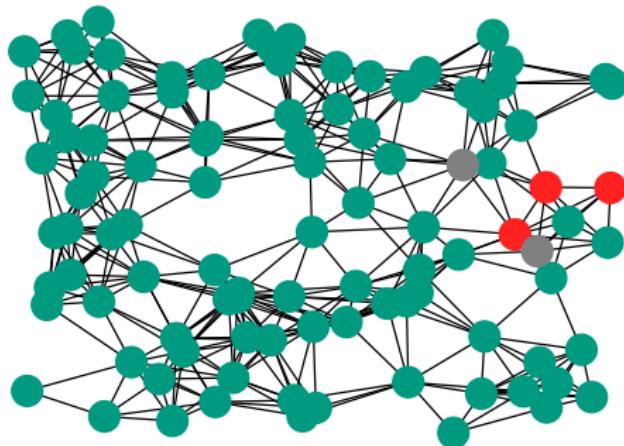
Sample SIR epidemic



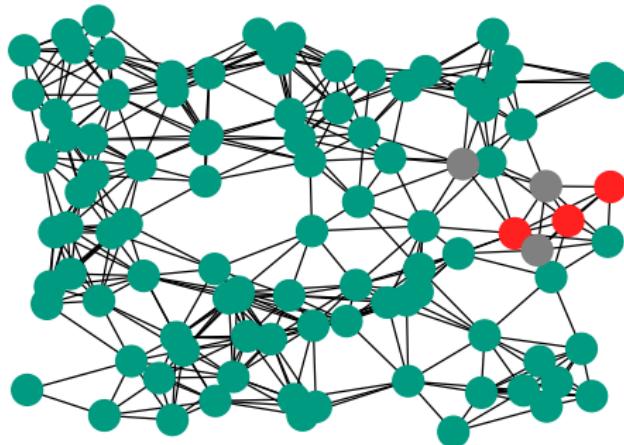
Sample SIR epidemic



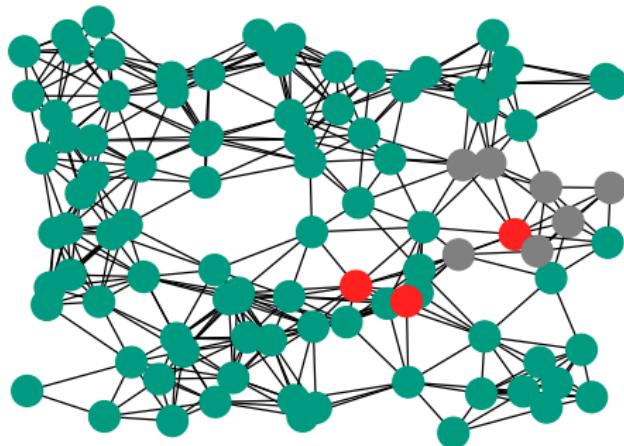
Sample SIR epidemic



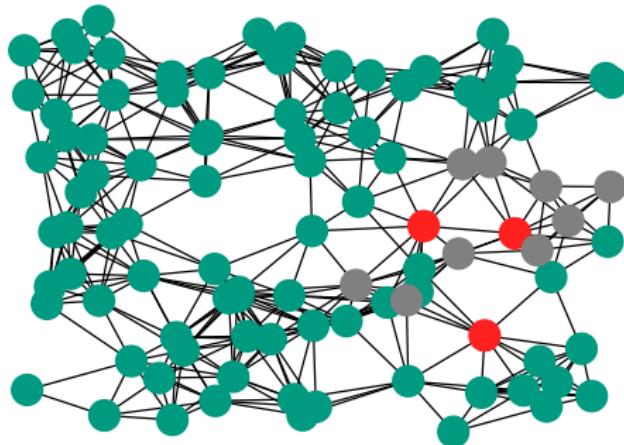
Sample SIR epidemic



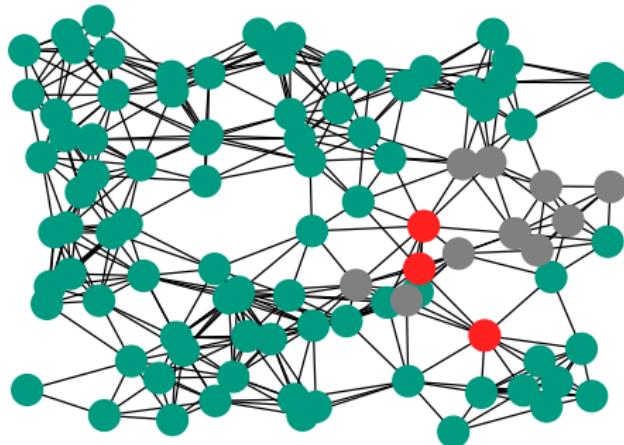
Sample SIR epidemic



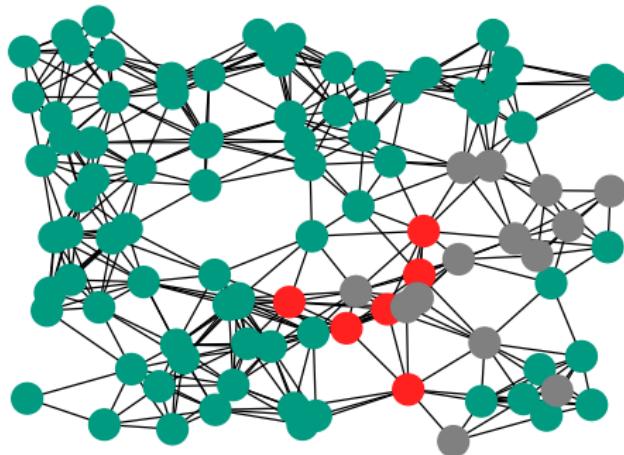
Sample SIR epidemic



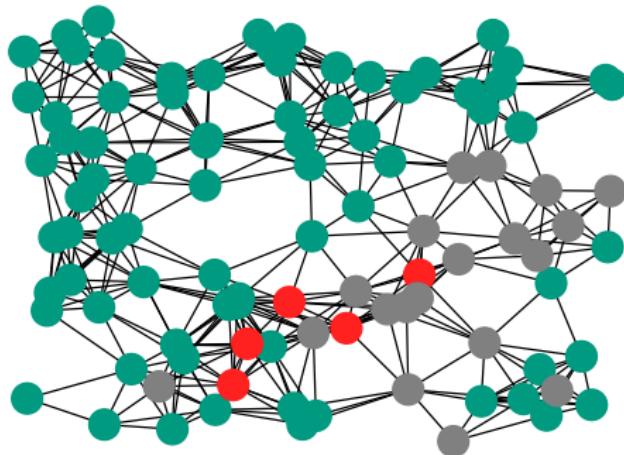
Sample SIR epidemic



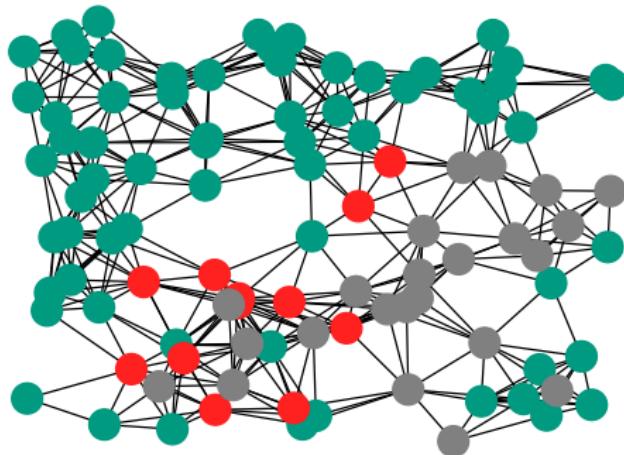
Sample SIR epidemic



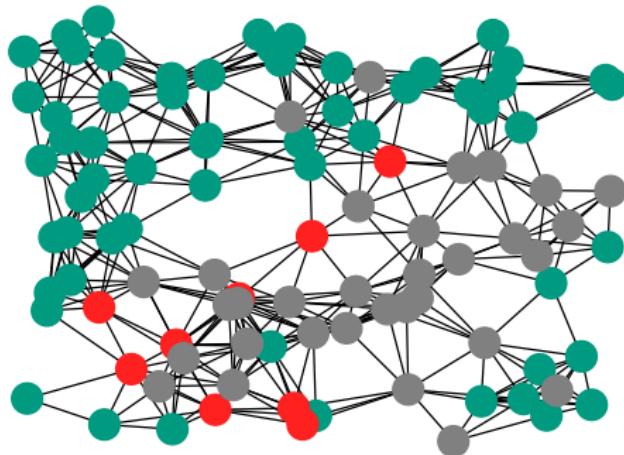
Sample SIR epidemic



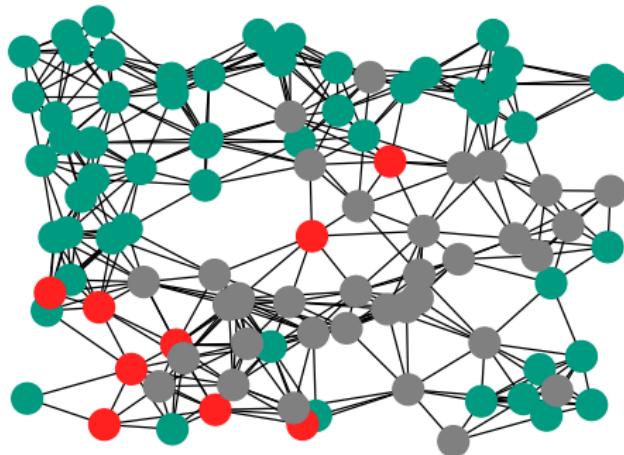
Sample SIR epidemic



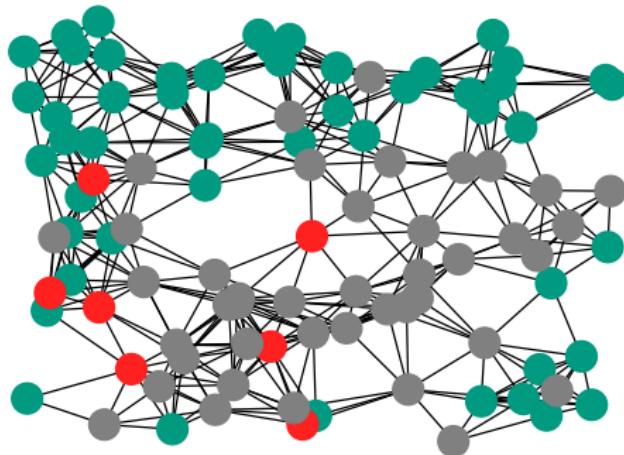
Sample SIR epidemic



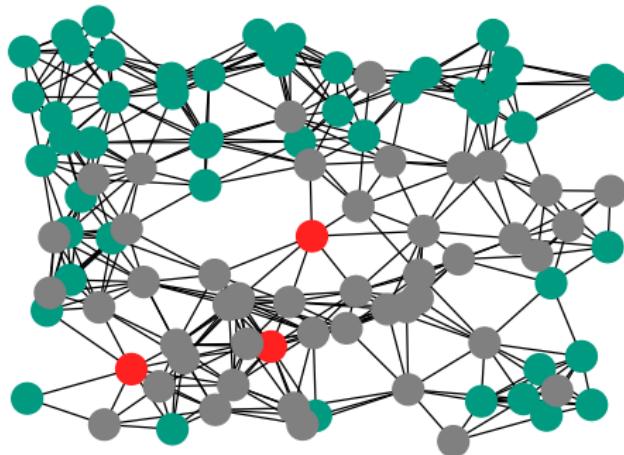
Sample SIR epidemic



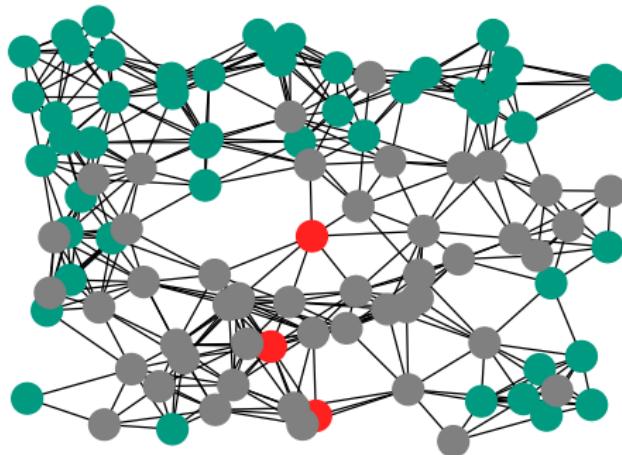
Sample SIR epidemic



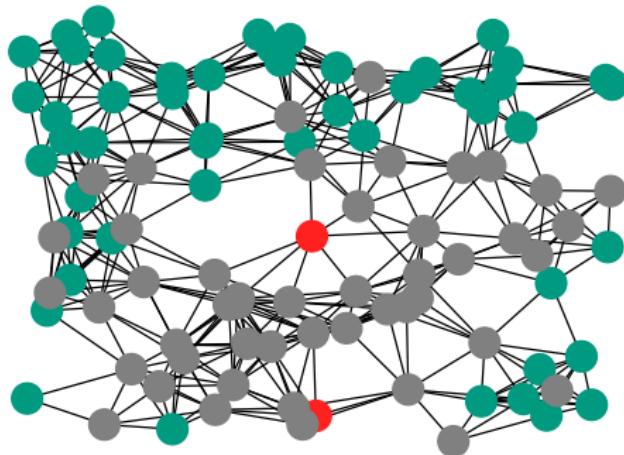
Sample SIR epidemic



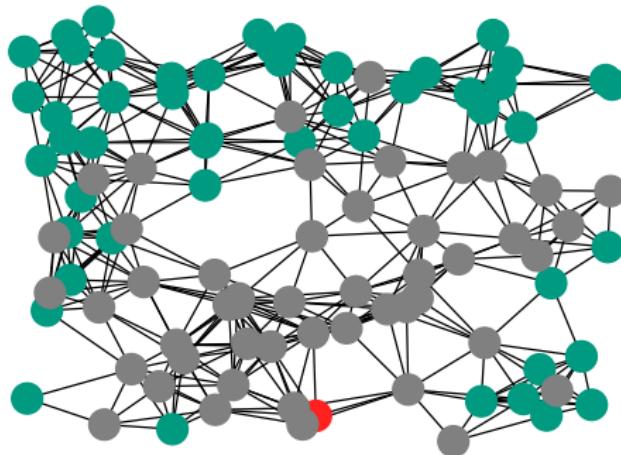
Sample SIR epidemic



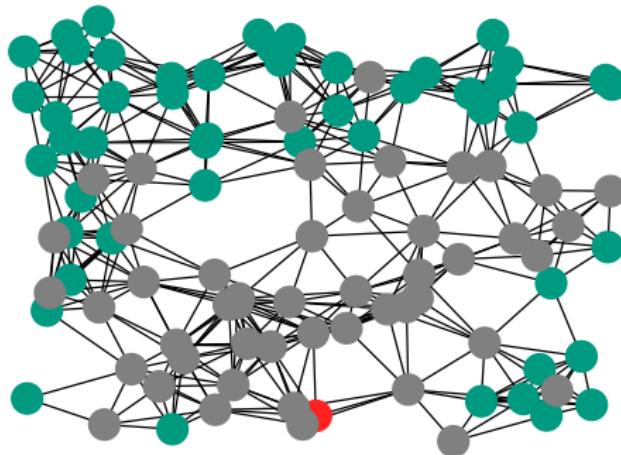
Sample SIR epidemic



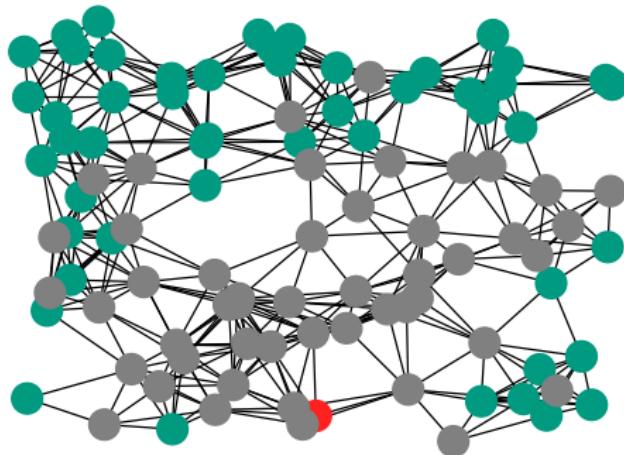
Sample SIR epidemic



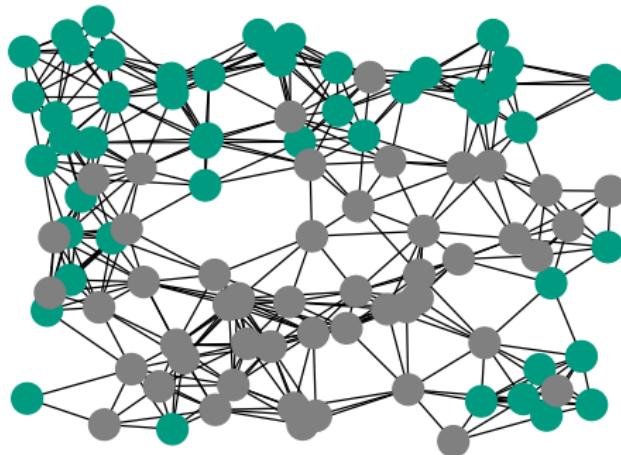
Sample SIR epidemic



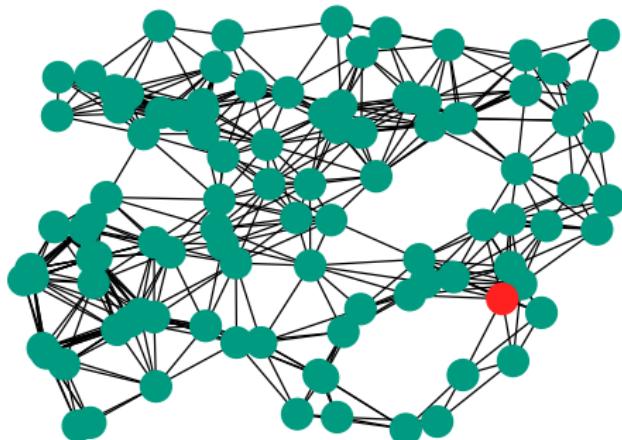
Sample SIR epidemic



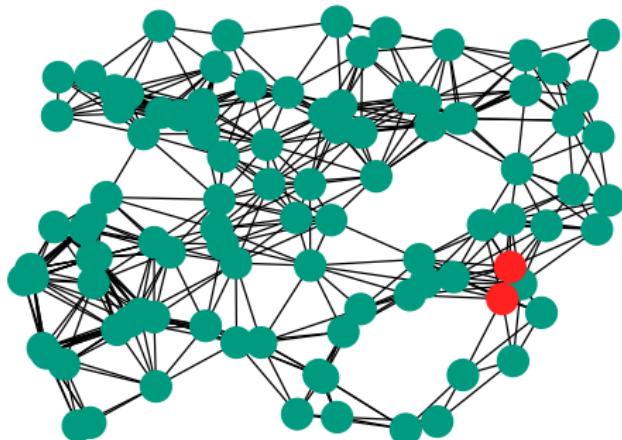
Sample SIR epidemic



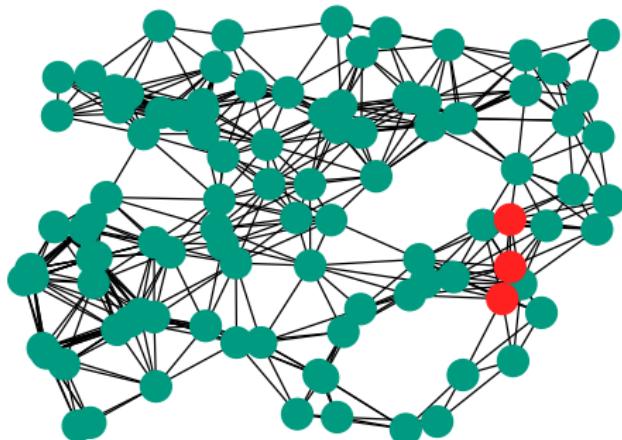
Sample SIS epidemic



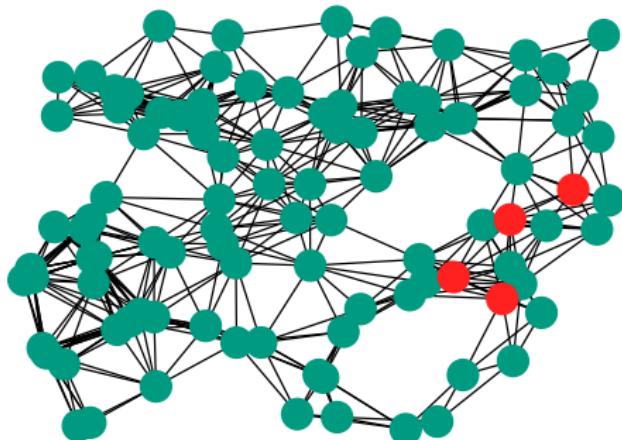
Sample SIS epidemic



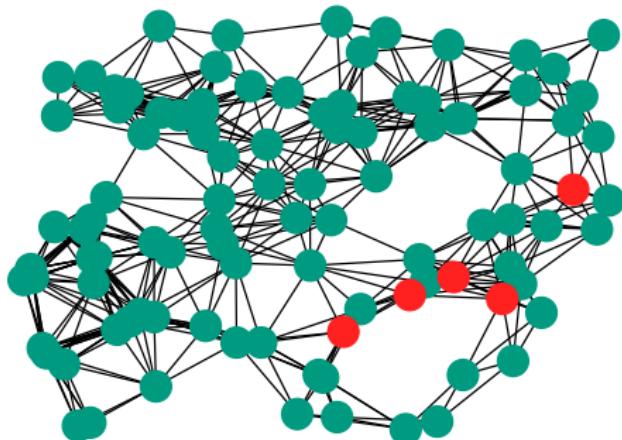
Sample SIS epidemic



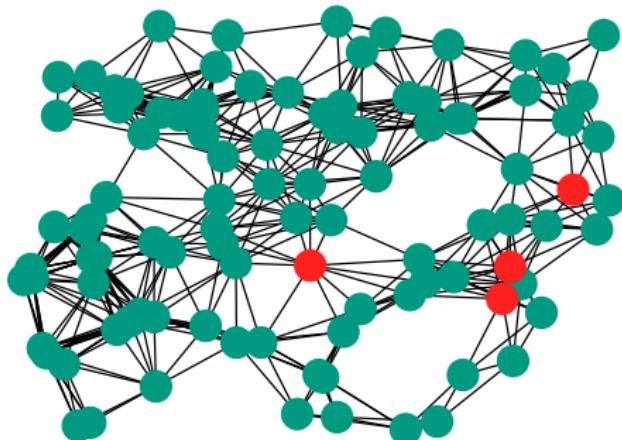
Sample SIS epidemic



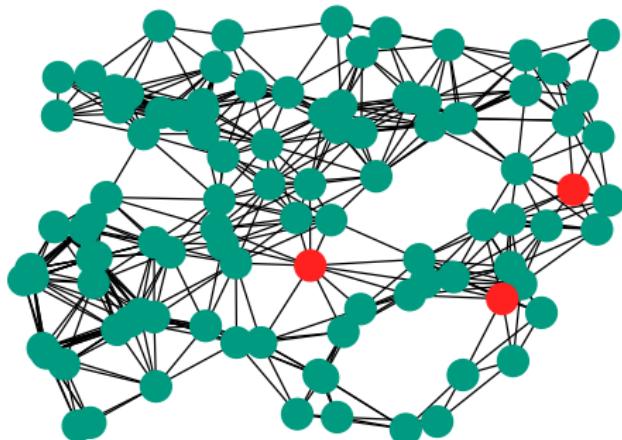
Sample SIS epidemic



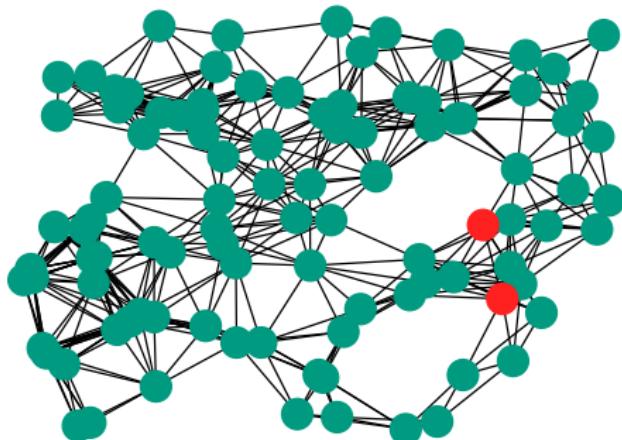
Sample SIS epidemic



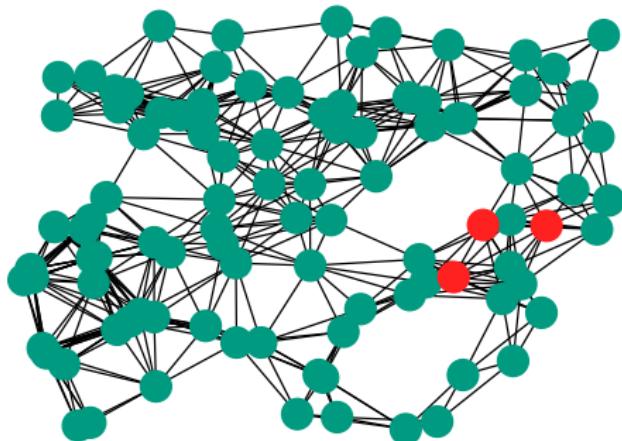
Sample SIS epidemic



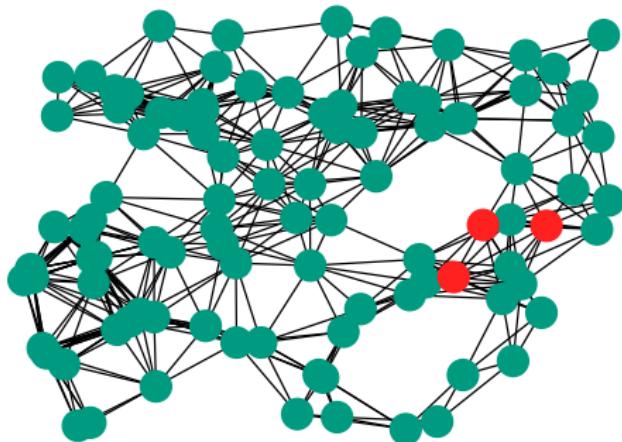
Sample SIS epidemic



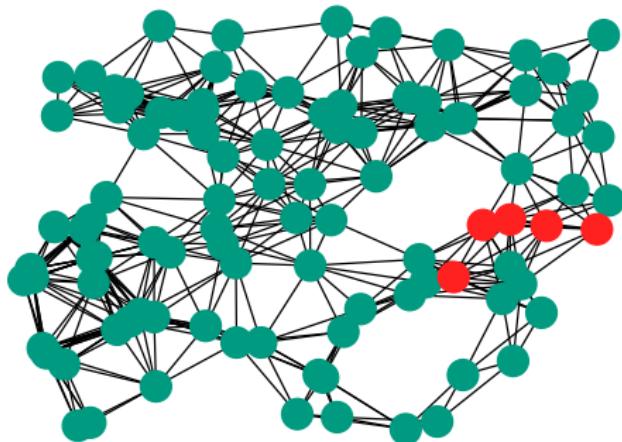
Sample SIS epidemic



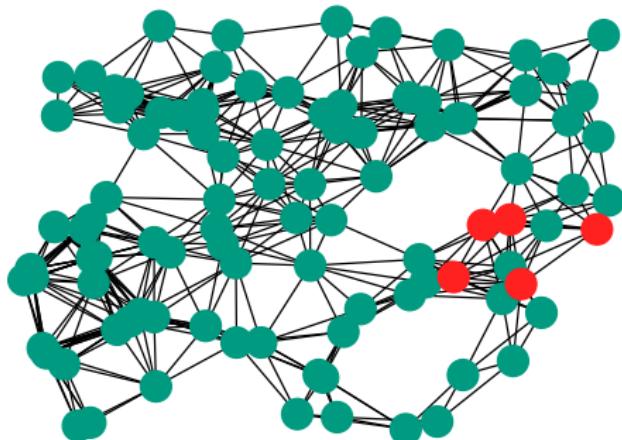
Sample SIS epidemic



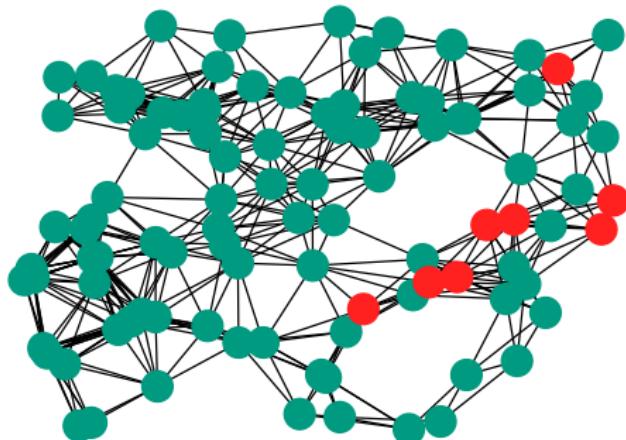
Sample SIS epidemic



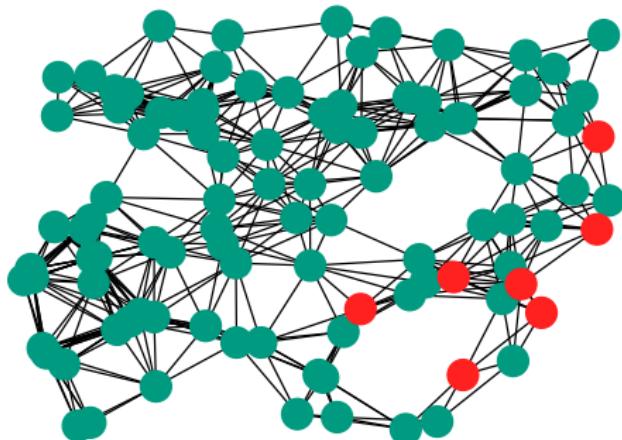
Sample SIS epidemic



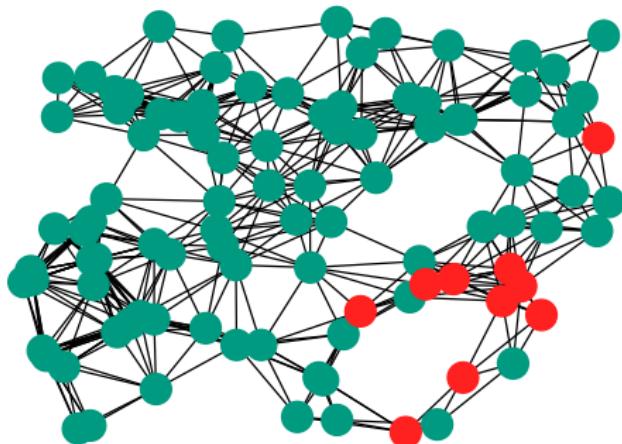
Sample SIS epidemic



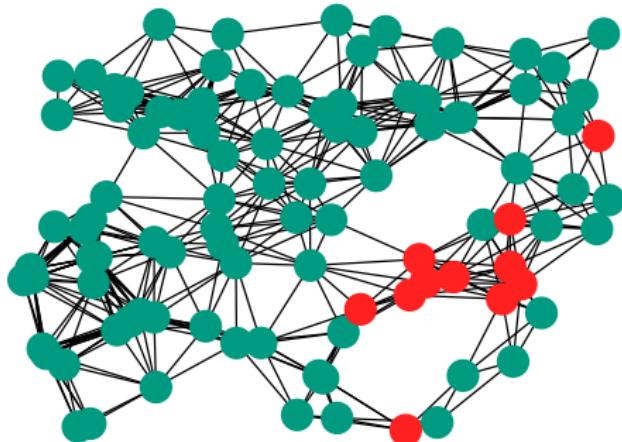
Sample SIS epidemic



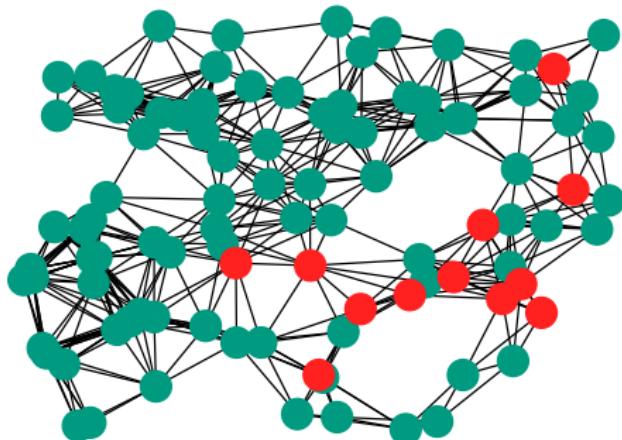
Sample SIS epidemic



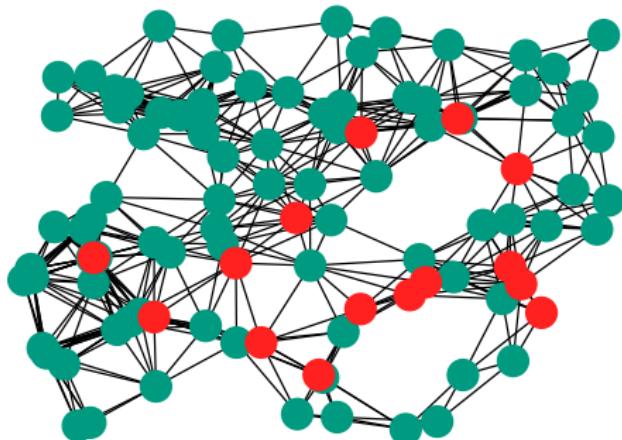
Sample SIS epidemic



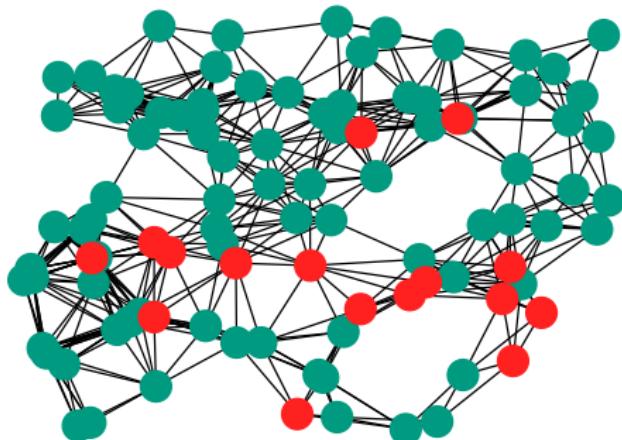
Sample SIS epidemic



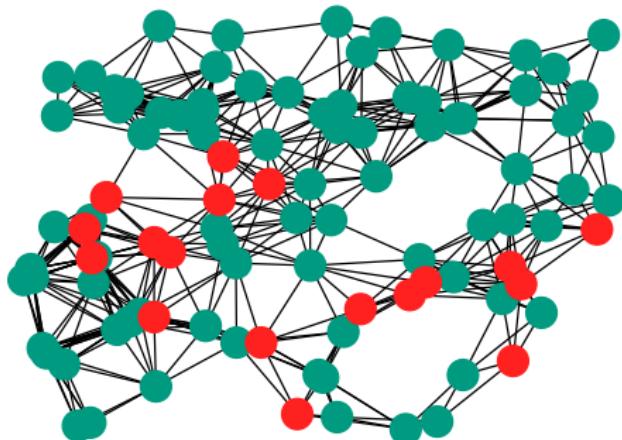
Sample SIS epidemic



Sample SIS epidemic



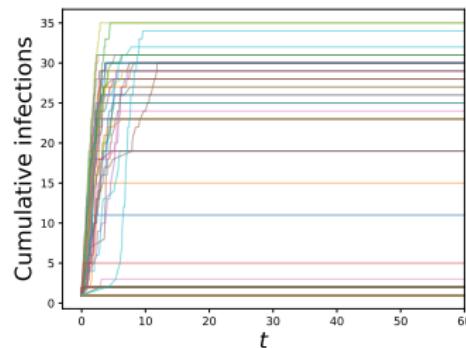
Sample SIS epidemic



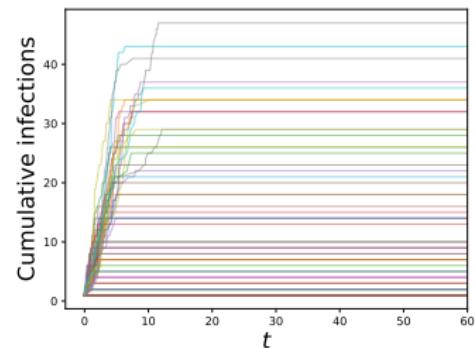
Stochastic simulation — SIR on network case

SIR disease spread with $\langle K \rangle = 5$, $\beta = 0.4$, and $\gamma = 1$.

$$P(5) = 1,$$



$$P(1) = P(9) = 0.5$$

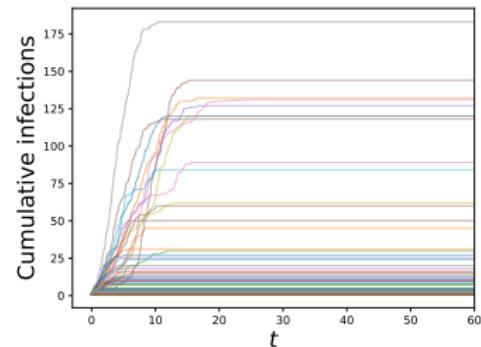
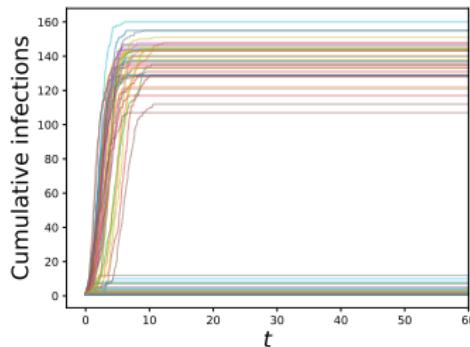


Stochastic simulation — SIR on network case

SIR disease spread with $\langle K \rangle = 5$, $\beta = 0.4$, and $\gamma = 1$.

$$P(5) = 1,$$

$$P(1) = P(9) = 0.5$$

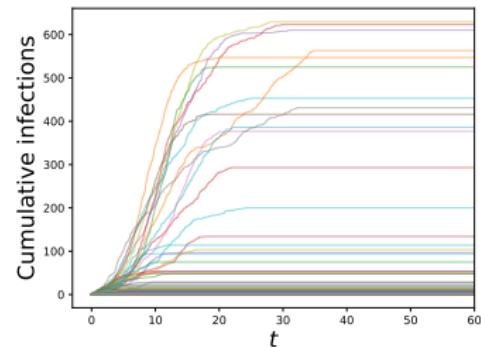
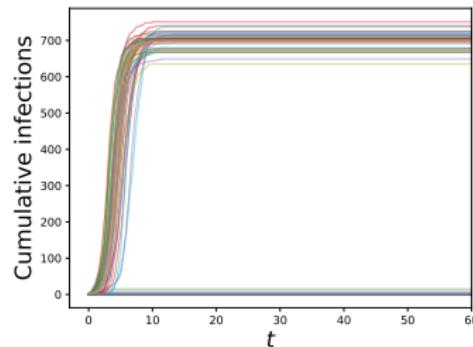


Stochastic simulation — SIR on network case

SIR disease spread with $\langle K \rangle = 5$, $\beta = 0.4$, and $\gamma = 1$.

$$P(5) = 1,$$

$$P(1) = P(9) = 0.5$$

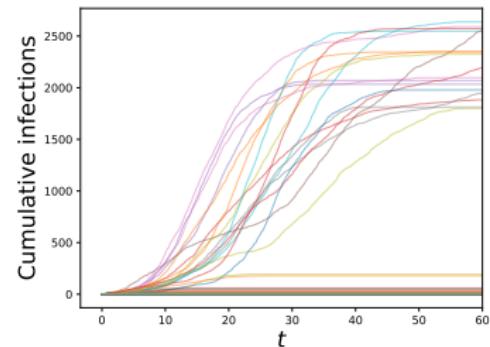
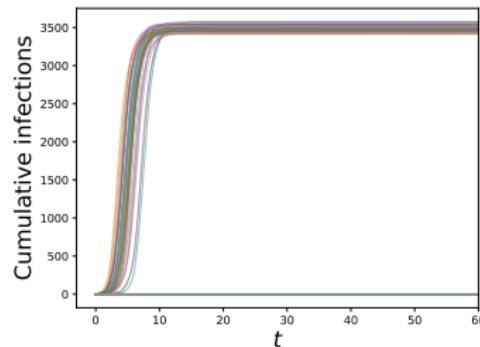


Stochastic simulation — SIR on network case

SIR disease spread with $\langle K \rangle = 5$, $\beta = 0.4$, and $\gamma = 1$.

$$P(5) = 1,$$

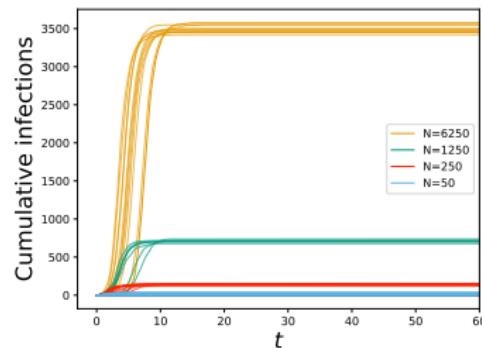
$$P(1) = P(9) = 0.5$$



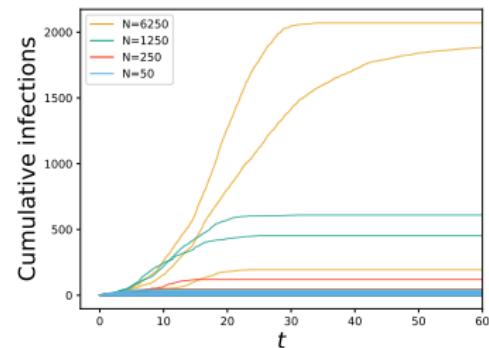
Stochastic simulation — SIR on network case

SIR disease spread with $\langle K \rangle = 5$, $\beta = 0.4$, and $\gamma = 1$.

$$P(5) = 1,$$



$$P(1) = P(9) = 0.5$$

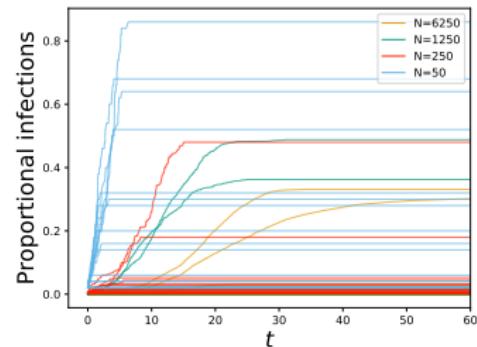
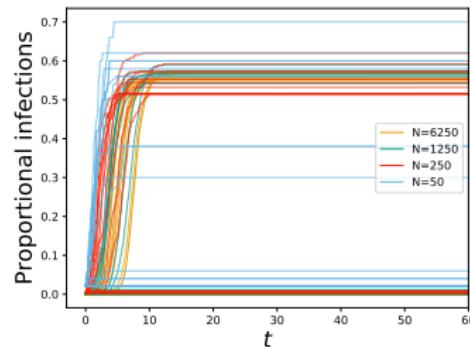


Stochastic simulation — SIR on network case

SIR disease spread with $\langle K \rangle = 5$, $\beta = 0.4$, and $\gamma = 1$.

$$P(5) = 1,$$

$$P(1) = P(9) = 0.5$$

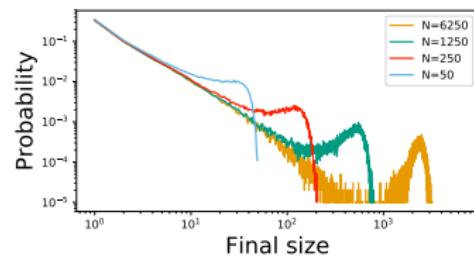
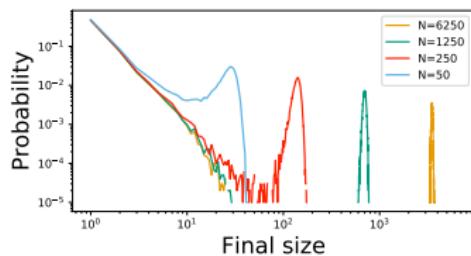


Stochastic simulation — SIR case

What does the final size distribution look like?

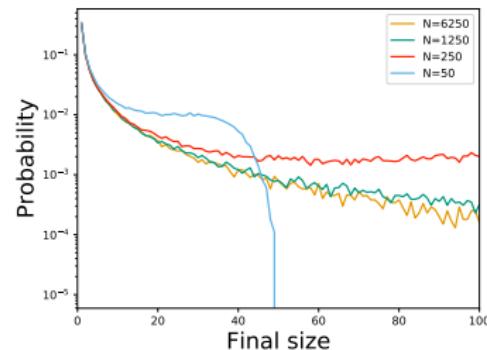
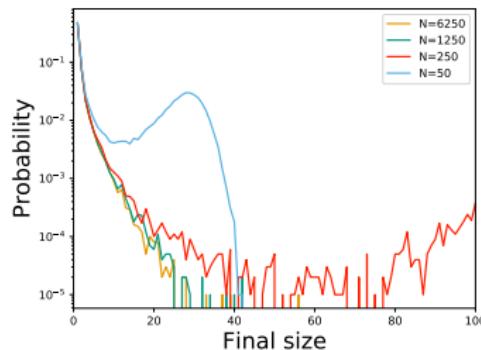
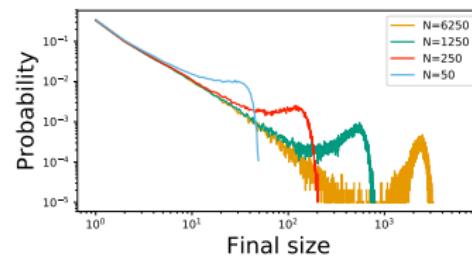
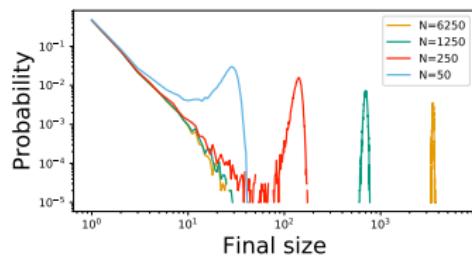
Stochastic simulation — SIR case

What does the final size distribution look like?



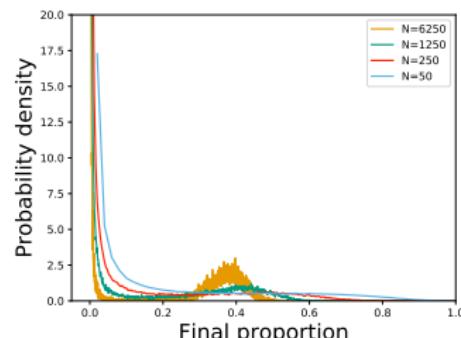
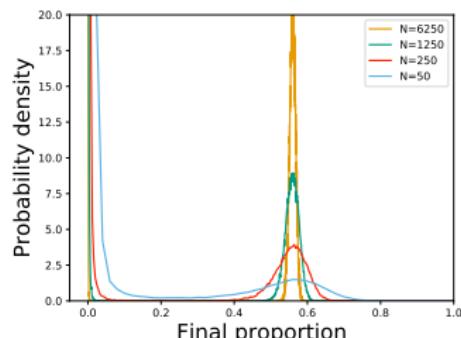
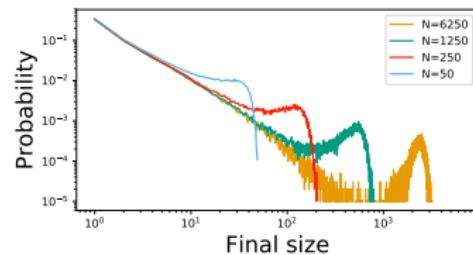
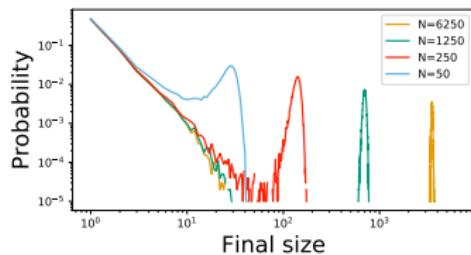
Stochastic simulation — SIR case

What does the final size distribution look like?



Stochastic simulation — SIR case

What does the final size distribution look like?



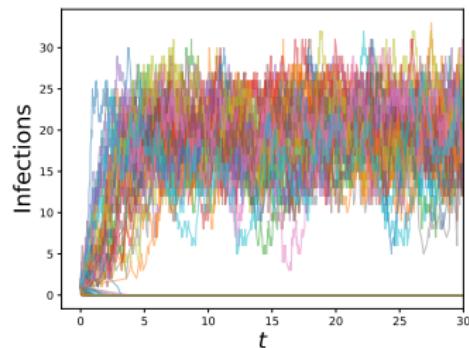
SIR observations

- ▶ 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.
- ▶ The degree distribution affects the final size and the early growth.

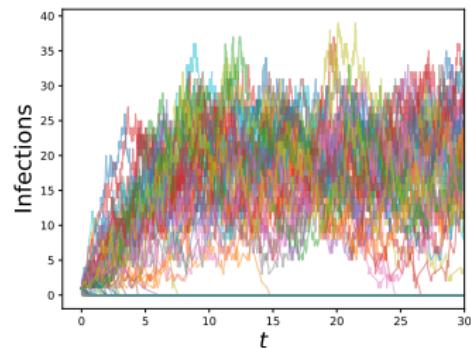
Stochastic simulation — SIS on network case

SIS disease spread with $\langle K \rangle = 5$, $\beta = 0.4$, and $\gamma = 1$.

$$P(5) = 1,$$



$$P(1) = P(9) = 0.5$$

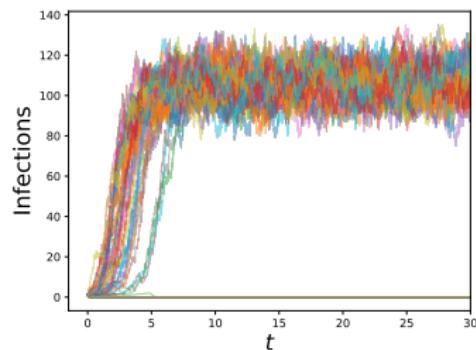


$$N = 50$$

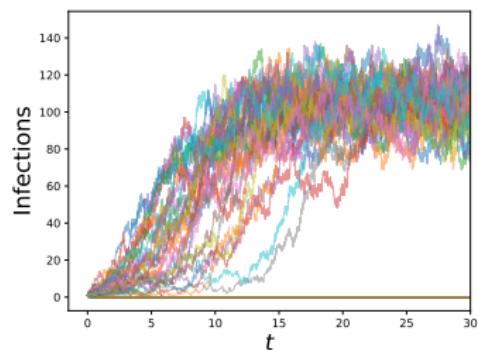
Stochastic simulation — SIS on network case

SIS disease spread with $\langle K \rangle = 5$, $\beta = 0.4$, and $\gamma = 1$.

$$P(5) = 1,$$



$$P(1) = P(9) = 0.5$$



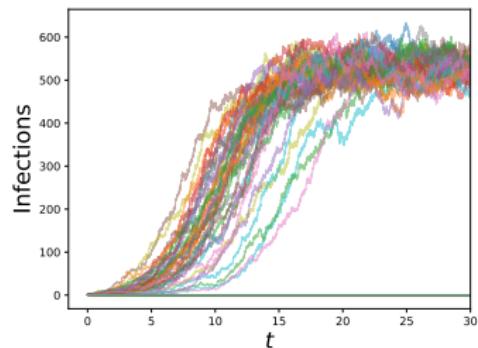
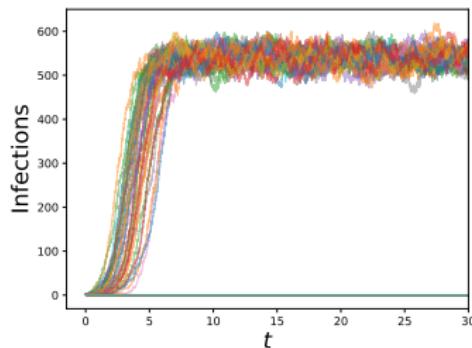
$$N = 250$$

Stochastic simulation — SIS on network case

SIS disease spread with $\langle K \rangle = 5$, $\beta = 0.4$, and $\gamma = 1$.

$$P(5) = 1,$$

$$P(1) = P(9) = 0.5$$

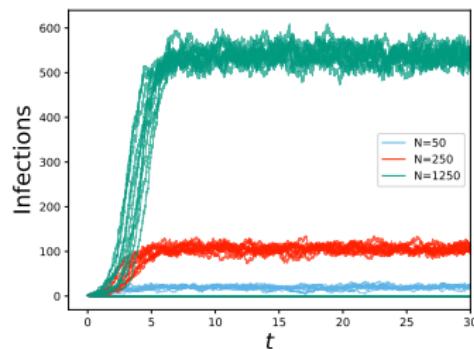


$$N = 1250$$

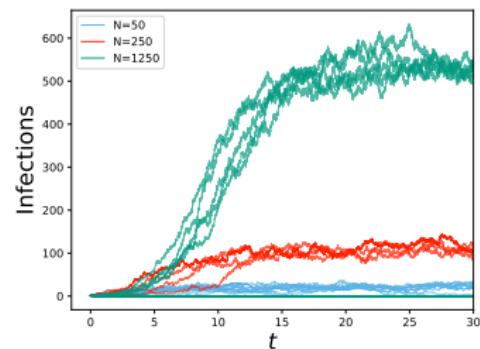
Stochastic simulation — SIS on network case

SIS disease spread with $\langle K \rangle = 5$, $\beta = 0.4$, and $\gamma = 1$.

$$P(5) = 1,$$



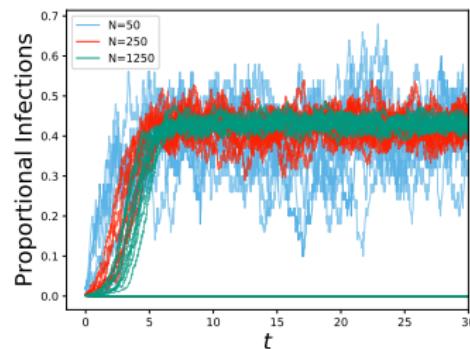
$$P(1) = P(9) = 0.5$$



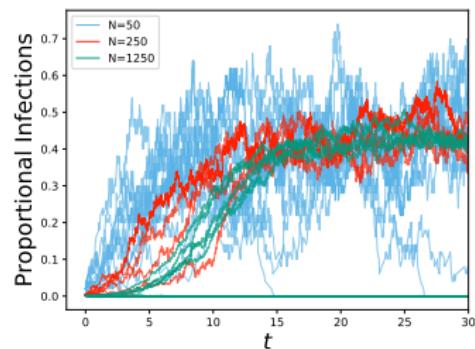
Stochastic simulation — SIS on network case

SIS disease spread with $\langle K \rangle = 5$, $\beta = 0.4$, and $\gamma = 1$.

$$P(5) = 1,$$



$$P(1) = P(9) = 0.5$$



Stochastic simulation — SIS on network case

What does the “equilibrium” distribution look like?

$$P(5) = 1,$$

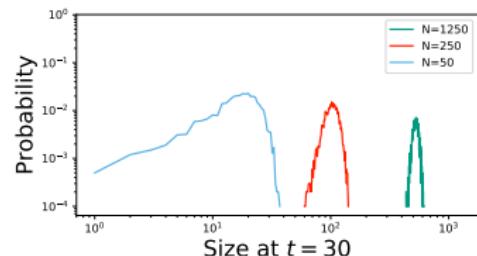
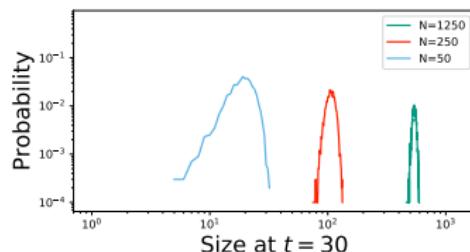
$$P(1) = P(9) = 0.5$$

Stochastic simulation — SIS on network case

What does the “equilibrium” distribution look like?

$$P(5) = 1,$$

$$P(1) = P(9) = 0.5$$

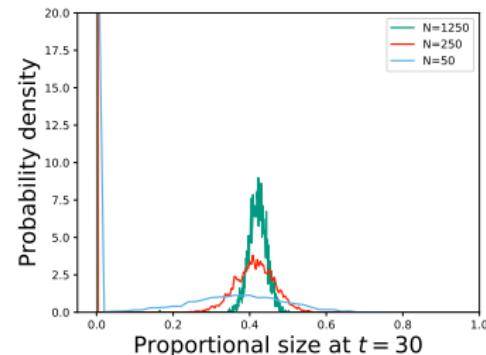
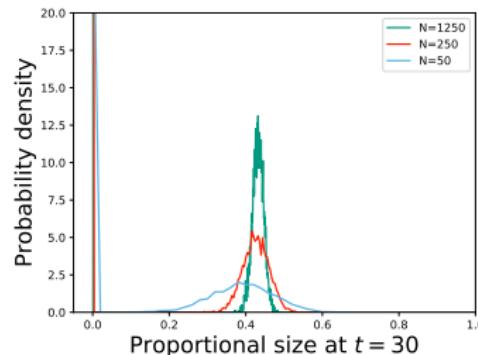
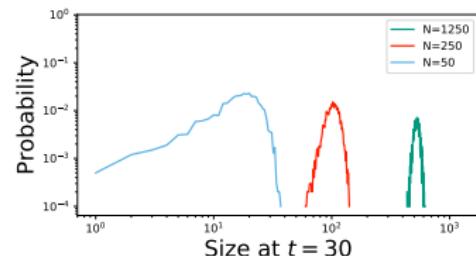
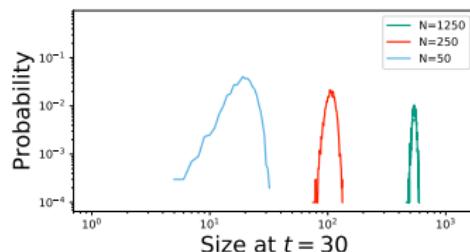


Stochastic simulation — SIS on network case

What does the “equilibrium” distribution look like?

$$P(5) = 1,$$

$$P(1) = P(9) = 0.5$$



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.
- ▶ Coefficient of variation decreases for large networks. [typical deviation from mean is small compared to mean.]

Introduction

Sample stochastic simulations

Impact of network properties

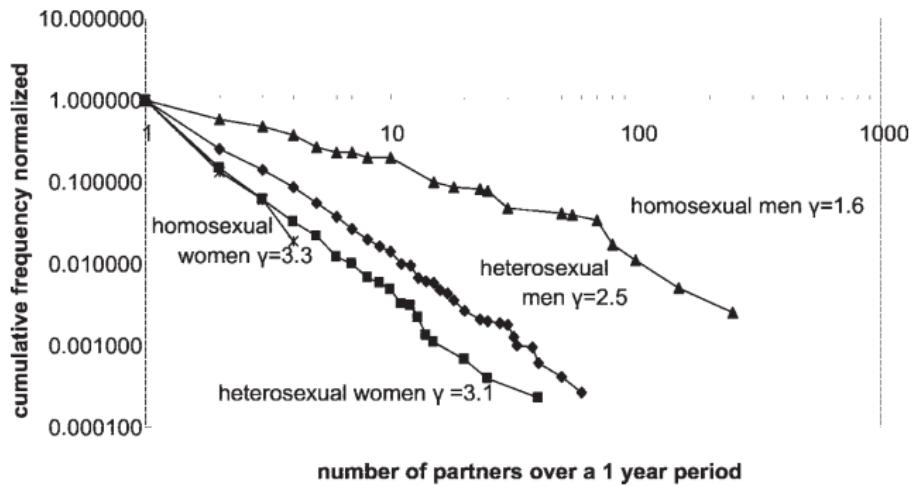
Deriving equations

Simple heterogeneous model

References

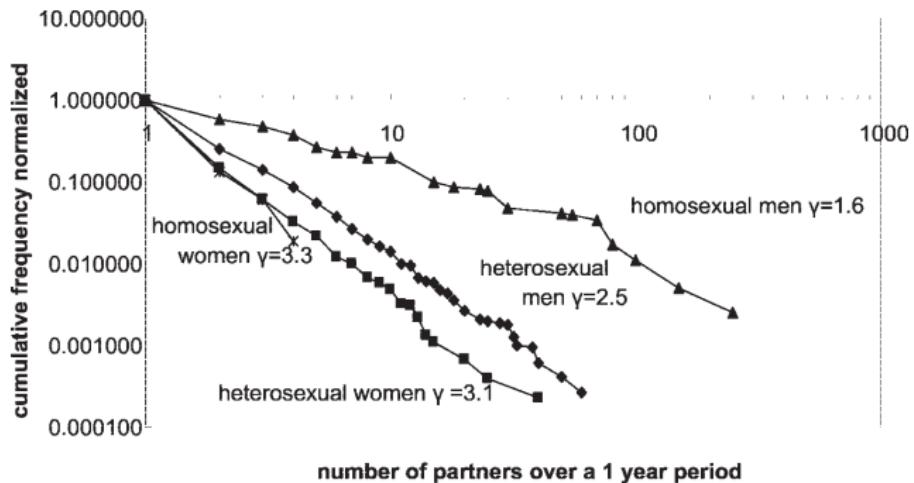
Degree distribution

From [1]:



Degree distribution

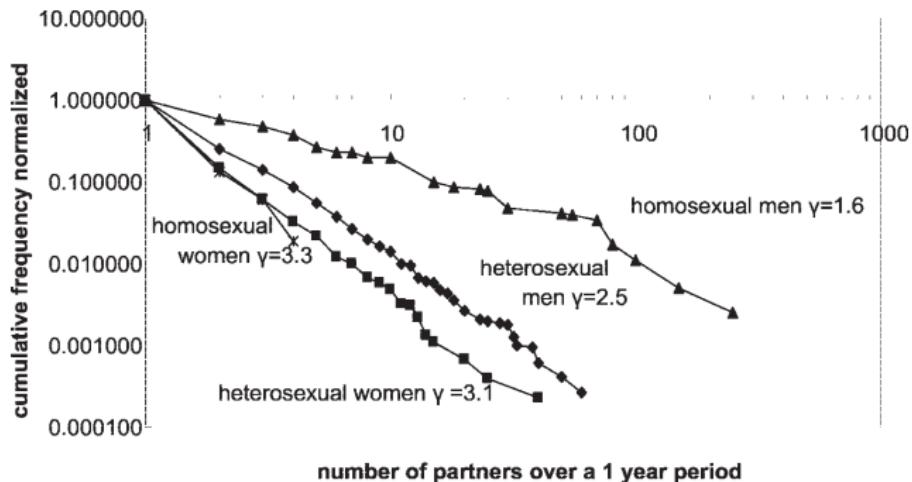
From [1]:



Impact on \mathcal{R}_0 :

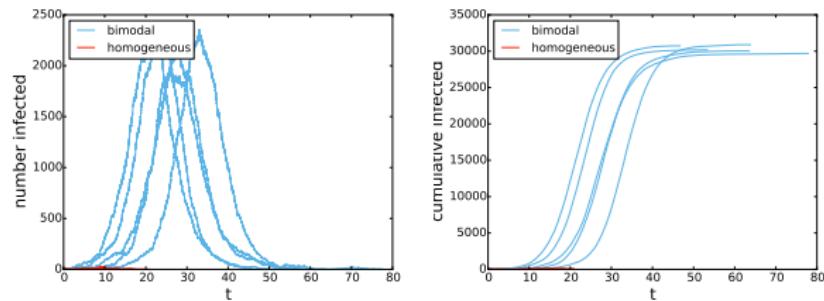
Degree distribution

From [1]:



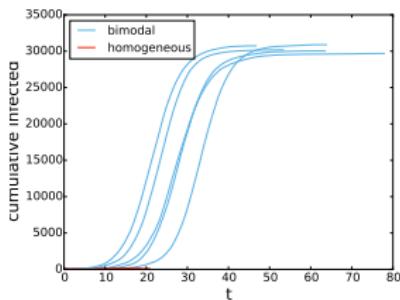
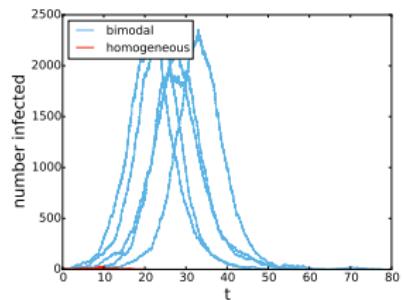
Impact on \mathcal{R}_0 : Holding $\langle K \rangle$ fixed, degree heterogeneity increases \mathcal{R}_0 because of size-biased infection.

Impact of degree distribution

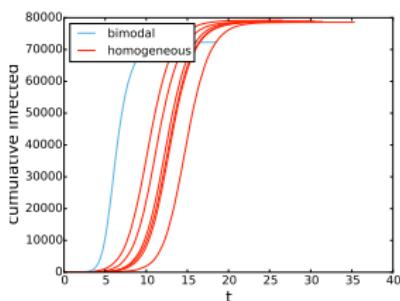
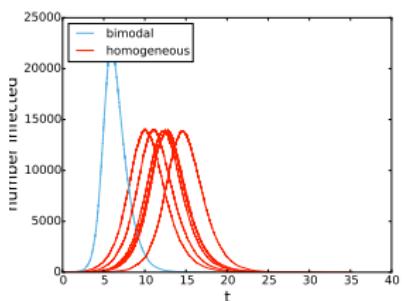


Small transmission rate

Impact of degree distribution

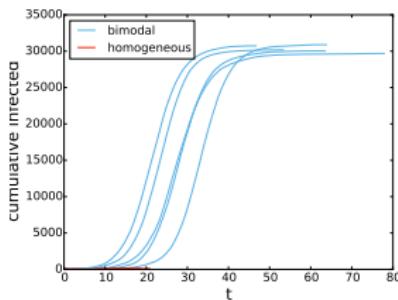
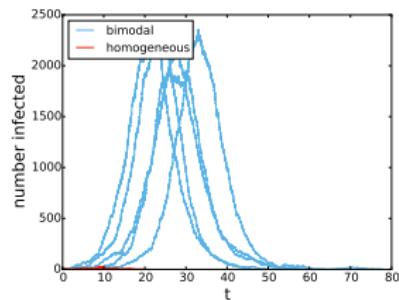


Small transmission rate

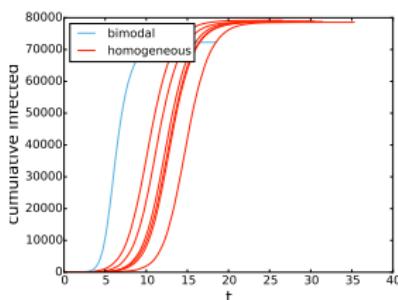
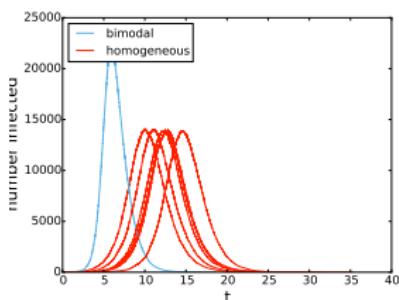


Large transmission rate

Impact of degree distribution



Small transmission rate



Large transmission rate

Depending on transmission rates, heterogeneous degree can increase or reduce the size of epidemics.

Degree correlations

Do opposites really attract?

Degree correlations

Do opposites really attract?

Individuals likely form partnerships with similar individuals.

Degree correlations

Do opposites really attract?

Individuals likely form partnerships with similar individuals.

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

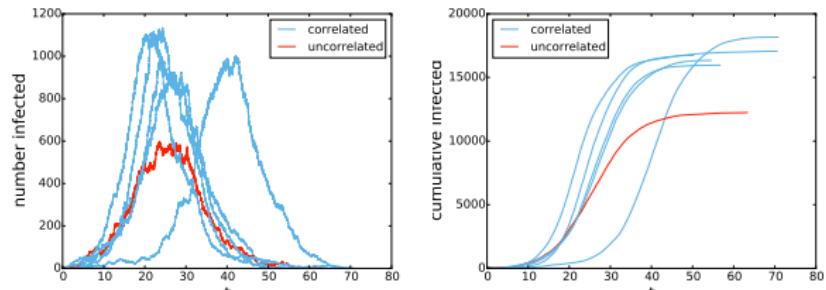
Degree correlations

Do opposites really attract?

Individuals likely form partnerships with similar individuals.

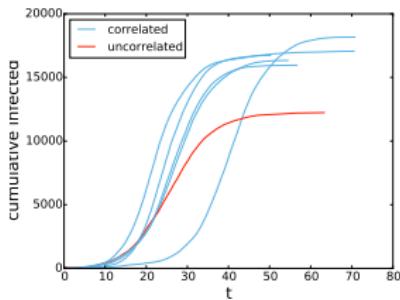
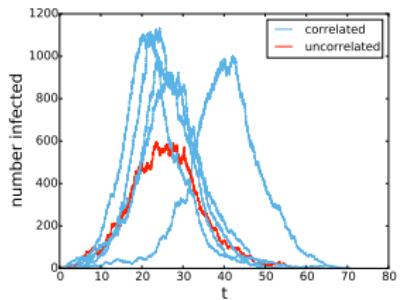
If high degree individuals preferentially contact high degree individuals, impact on \mathcal{R}_0 : Increases it.

Degree correlations

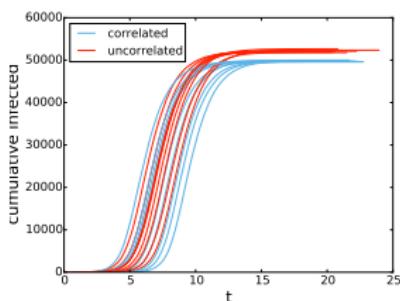
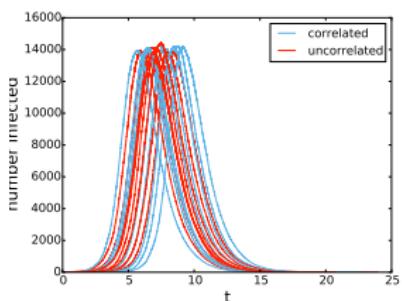


Small transmission rate

Degree correlations

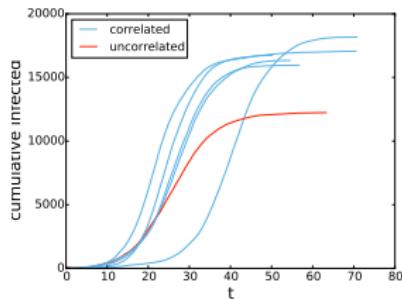
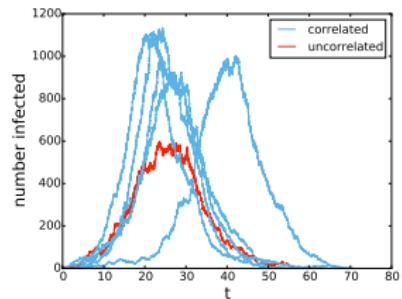


Small transmission rate

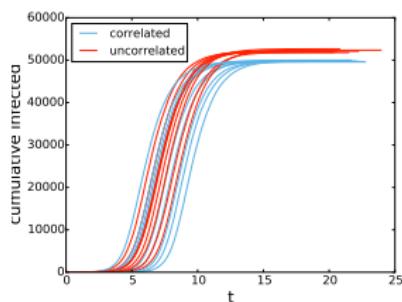
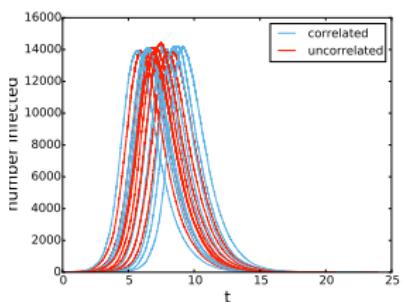


Large transmission rate

Degree correlations



Small transmission rate



Large transmission rate

Degree correlations can increase or decrease epidemic sizes, depending on transmission rate.

Partnership duration

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.

Partnership duration

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.

Impact on \mathcal{R}_0 :

Partnership duration

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.

Impact on \mathcal{R}_0 :

For SIR, long partnership duration decreases \mathcal{R}_0 because repeated transmissions are wasted.

Partnership duration

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.

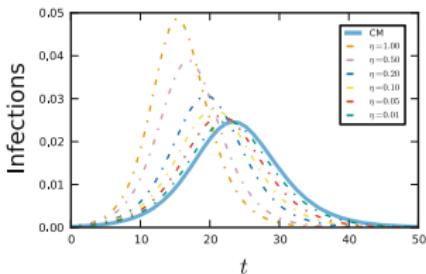
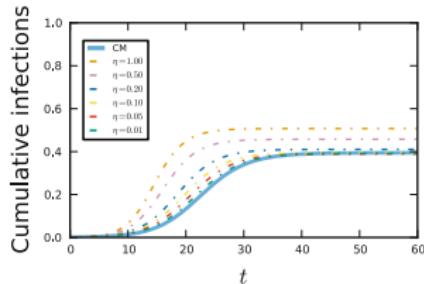
Impact on \mathcal{R}_0 :

For SIR, long partnership duration decreases \mathcal{R}_0 because repeated transmissions are wasted.

For SIS, it is complex — repeated transmissions are wasted, but long-lasting partnerships help ensure that high degree nodes are quickly reinfected [2].

Partnership duration

Sample SIR epidemics from [3]



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

Clustering

If partnerships are clustered, even early on individuals who become infected are likely to have partners who are infected by others.

Clustering

If partnerships are clustered, even early on individuals who become infected are likely to have partners who are infected by others.

Impact on \mathcal{R}_0 :

Clustering

If partnerships are clustered, even early on individuals who become infected are likely to have partners who are infected by others.

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

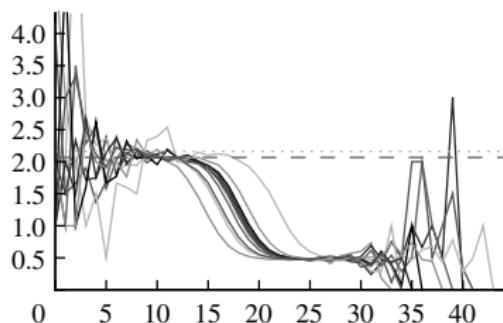
Clustering

Ratio of successive generation sizes from [4]

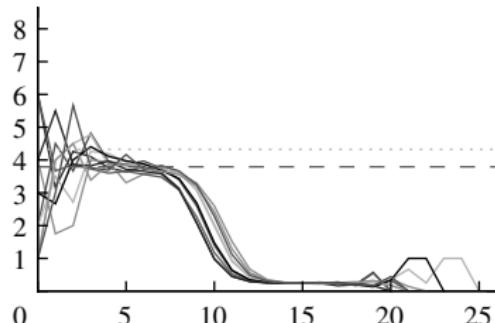
Clustering

Ratio of successive generation sizes from [4]

lower transmission rate

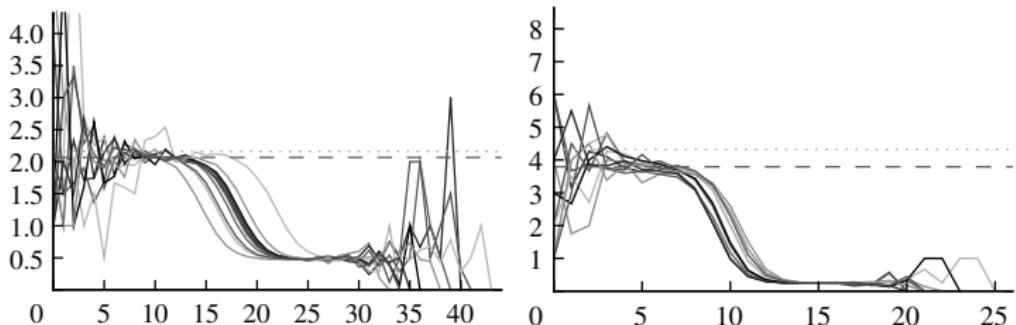


higher transmission rate



Clustering

Ratio of successive generation sizes from [4]
 lower transmission rate higher transmission rate



Dotted line is prediction ignoring clustering. Dashed line is correction accounting for triangles and squares.

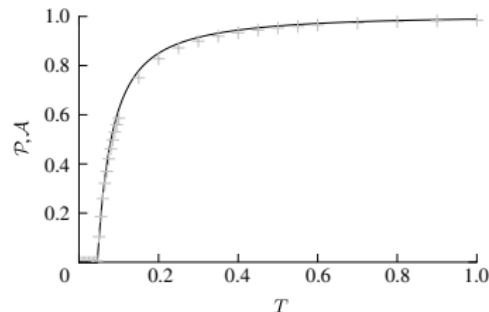
Clustering

But the size is not so affected:

Clustering

But the size is not so affected:

Comparison of unclustered prediction (line) with stochastic simulation (symbols)



(horizontal axis is transmission probability, vertical is fraction infected.)

Introduction

Sample stochastic simulations

Impact of network properties

Deriving equations

Simple heterogeneous model

References

Challenges for an analytic model

- ▶ When we rigorously derive

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

$$I = \beta \frac{IS}{N} - \gamma I$$

for the compartmental model, we use the fact that it does not matter which individuals are susceptible or infected.

Challenges for an analytic model

- ▶ When we rigorously derive

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

$$i = \beta \frac{IS}{N} - \gamma I$$

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 .

Challenges for an analytic model

- ▶ When we rigorously derive

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

$$i = \beta \frac{IS}{N} - \gamma I$$

for the compartmental model, we use the fact that it does not matter which individuals are susceptible or infected.

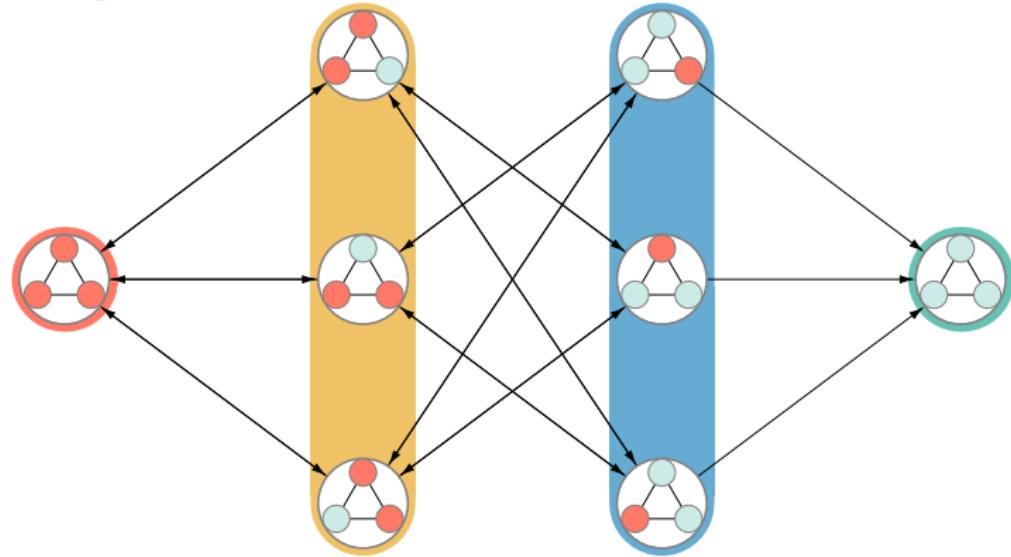
- ▶ If there are s susceptible and i infected individuals, the combined infection rate is $\beta is/N$. Similarly the combined recovery rate is γi .
- ▶ In a network, it matters exactly which nodes are susceptible or infected.

Triangle example

All that we need to predict the rate of change of S and I in a triangle is the current value of S and I .

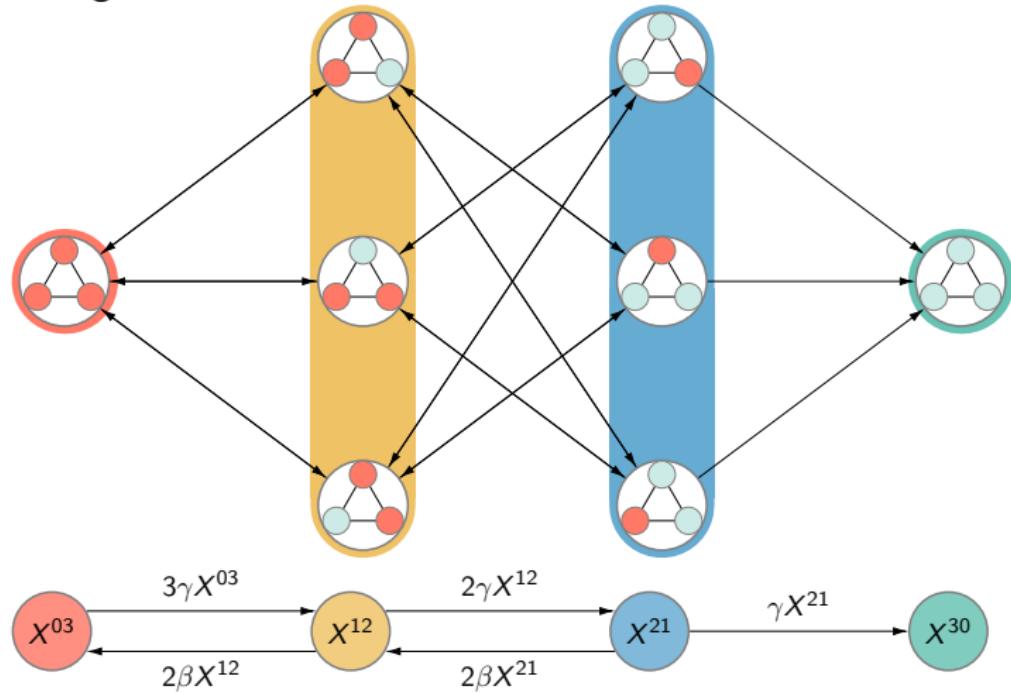
Triangle example

All that we need to predict the rate of change of S and I in a triangle is the current value of S and I .



Triangle example

All that we need to predict the rate of change of S and I in a triangle is the current value of S and I .

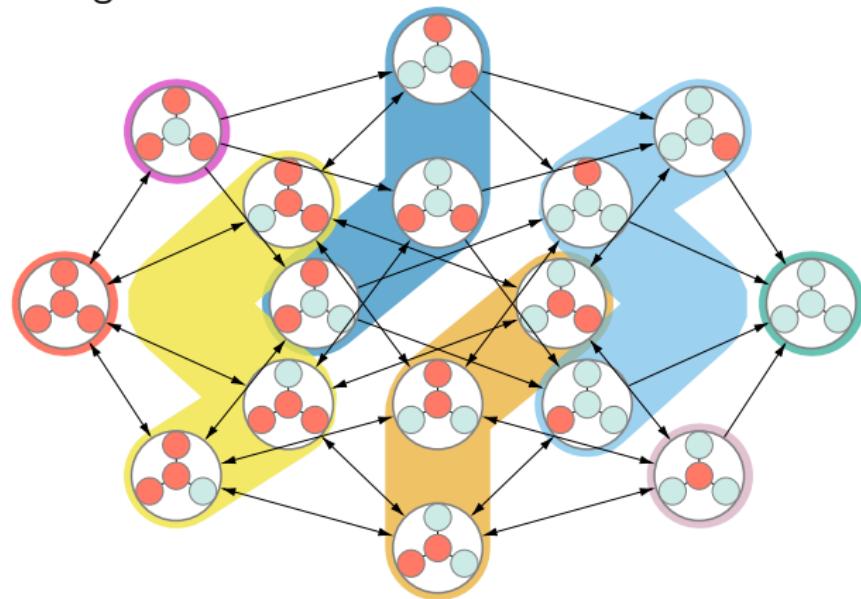


Star example

For a star however, having just the current values of S and I is not enough.

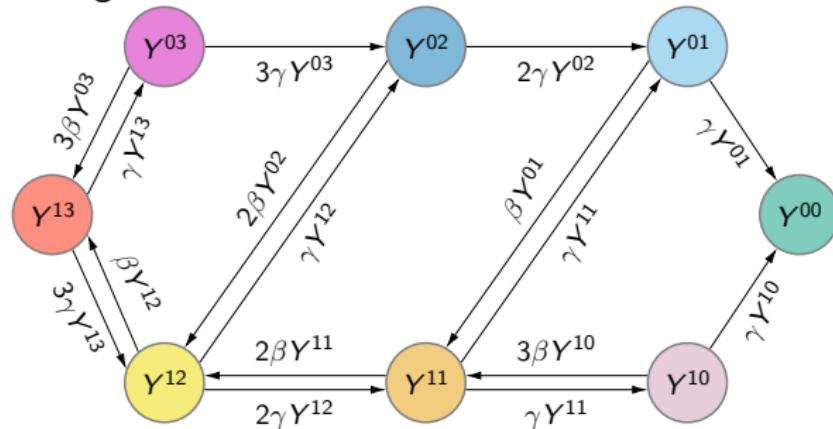
Star example

For a star however, having just the current values of S and I is not enough.

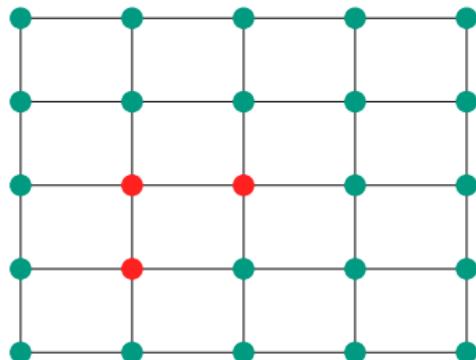


Star example

For a star however, having just the current values of S and I is not enough.



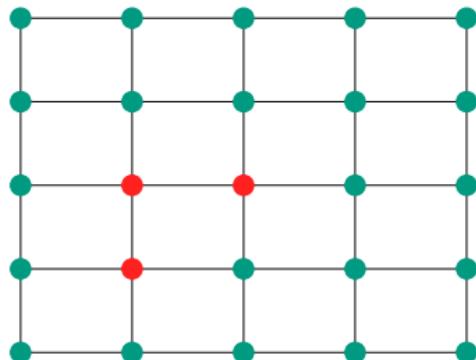
Towards an analytic model*



- ▶ How many I nodes?

*By “analytic” I mean we can write down deterministic equations rather than simply describe the transitions of a stochastic process.

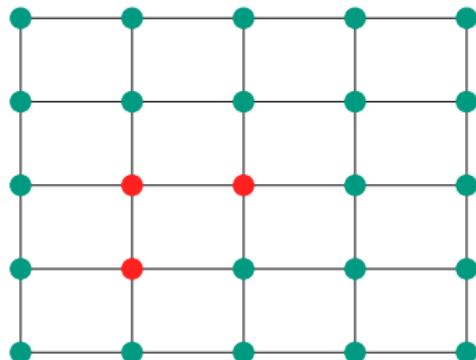
Towards an analytic model*



- ▶ How many I nodes? $[I] = 3$.

*By “analytic” I mean we can write down deterministic equations rather than simply describe the transitions of a stochastic process.

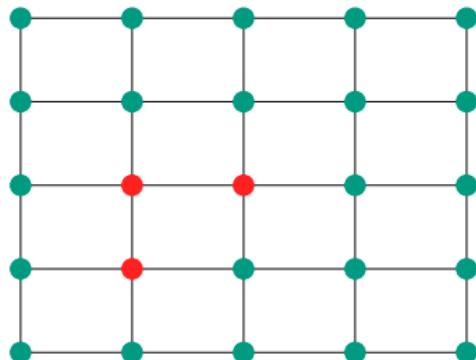
Towards an analytic model*



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

*By “analytic” I mean we can write down deterministic equations rather than simply describe the transitions of a stochastic process.

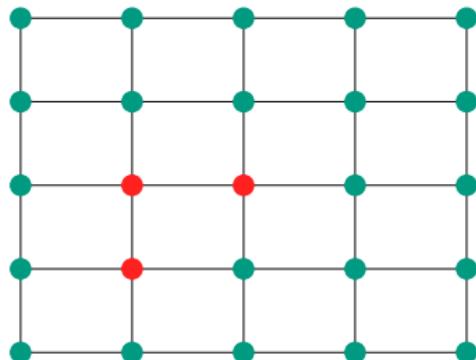
Towards an analytic model*



- ▶ How many I nodes? $[I] = 3$.
- ▶ How many S nodes? $[S] = 22$.

*By “analytic” I mean we can write down deterministic equations rather than simply describe the transitions of a stochastic process.

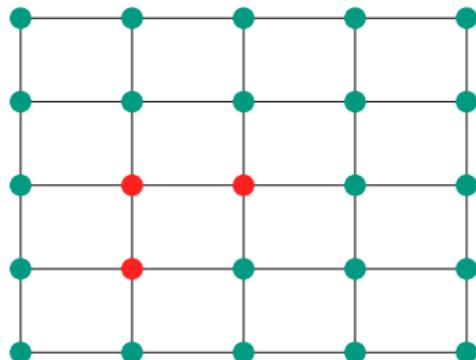
Towards an analytic model*



- ▶ How many I nodes? $[I] = 3$.
- ▶ How many S nodes? $[S] = 22$.
- ▶ How many SI edges?

*By “analytic” I mean we can write down deterministic equations rather than simply describe the transitions of a stochastic process.

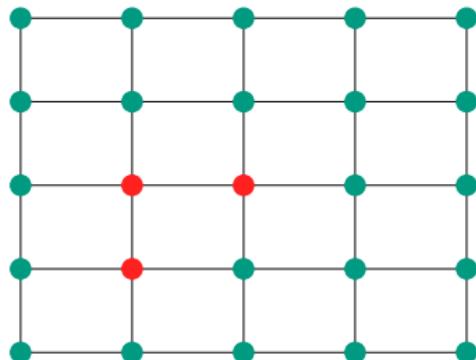
Towards an analytic model*



- ▶ How many I nodes? $[I] = 3$.
- ▶ How many S nodes? $[S] = 22$.
- ▶ How many SI edges? $[SI] = 8$.

*By “analytic” I mean we can write down deterministic equations rather than simply describe the transitions of a stochastic process.

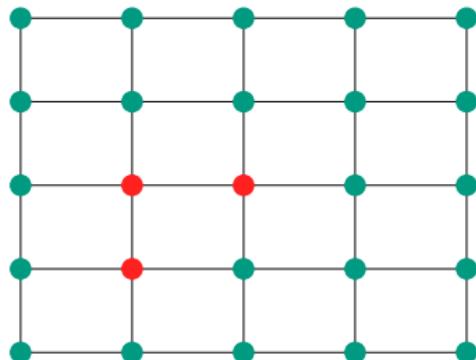
Towards an analytic model*



- ▶ How many I nodes? $[I] = 3$.
- ▶ How many S nodes? $[S] = 22$.
- ▶ How many SI edges? $[SI] = 8$.
- ▶ How many SSI triples?

*By “analytic” I mean we can write down deterministic equations rather than simply describe the transitions of a stochastic process.

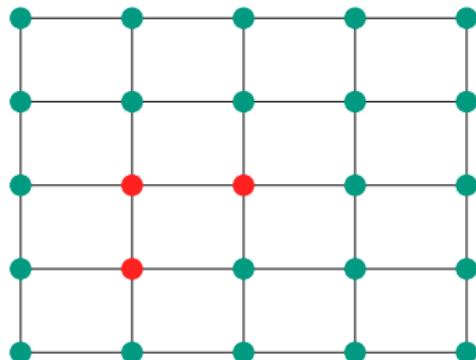
Towards an analytic model*



- ▶ How many I nodes? $[I] = 3$.
- ▶ How many S nodes? $[S] = 22$.
- ▶ How many SI edges? $[SI] = 8$.
- ▶ How many SSI triples? $[SSI] = 19$.

*By “analytic” I mean we can write down deterministic equations rather than simply describe the transitions of a stochastic process.

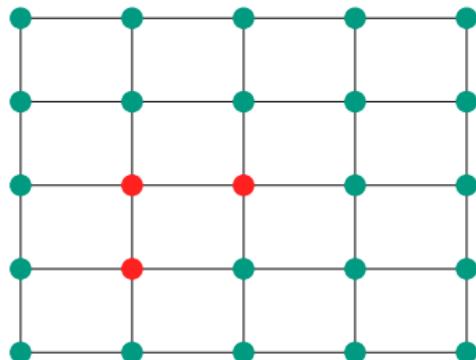
Towards an analytic model*



- ▶ How many I nodes? $[I] = 3$.
- ▶ How many S nodes? $[S] = 22$.
- ▶ How many SI edges? $[SI] = 8$.
- ▶ How many SSI triples? $[SSI] = 19$.
- ▶ How many ISI triples?

*By “analytic” I mean we can write down deterministic equations rather than simply describe the transitions of a stochastic process.

Towards an analytic model*



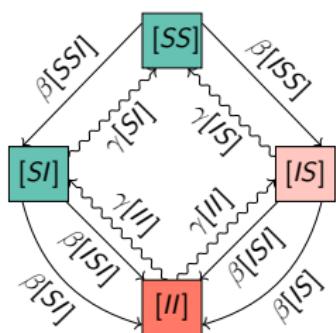
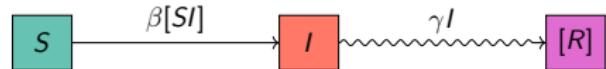
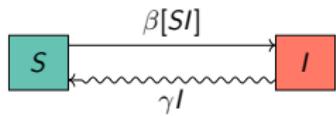
- ▶ How many I nodes? $[I] = 3$.
- ▶ How many S nodes? $[S] = 22$.
- ▶ How many SI edges? $[SI] = 8$.
- ▶ How many SSI triples? $[SSI] = 19$.
- ▶ How many ISI triples? $[ISI] = 2$.

*By “analytic” I mean we can write down deterministic equations rather than simply describe the transitions of a stochastic process.

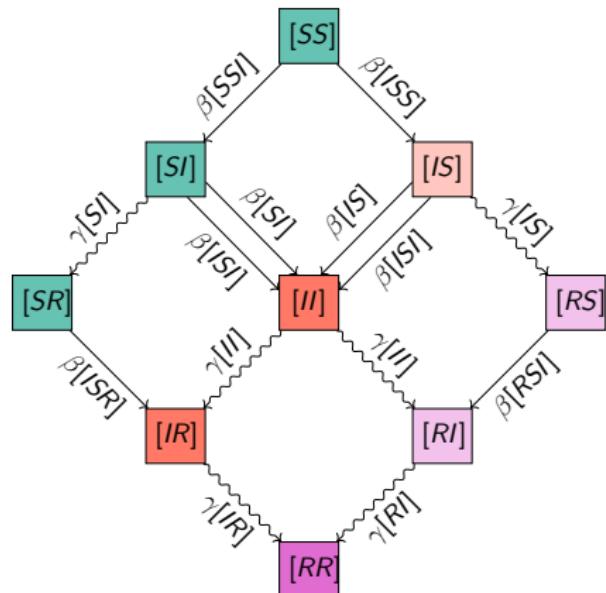
Towards an analytic model

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

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



[Adapted from [5]]

Finding SIR equations

- ▶ What is $\frac{d}{dt}[S]$?

Finding SIR equations

- ▶ What is $\frac{d}{dt}[S]$?
 - ▶ 1 is removed whenever an SI edge transmits. So
 - ▶ $\frac{d}{dt}[S] = -\beta[SI]$

Finding SIR equations

- ▶ What is $\frac{d}{dt}[S]$?
 - ▶ 1 is removed whenever an SI edge transmits. So
 - ▶ $\frac{d}{dt}[S] = -\beta[SI]$
- ▶ What is $\frac{d}{dt}[I]$?

Finding SIR equations

- ▶ What is $\frac{d}{dt}[S]$?
 - ▶ 1 is removed whenever an SI edge transmits. So
 - ▶ $\frac{d}{dt}[S] = -\beta[SI]$
- ▶ What is $\frac{d}{dt}[I]$?
 - ▶ An I is removed whenever a recovery occurs.
 - ▶ An I is created whenever an SI edge transmits
 - ▶ $\frac{d}{dt}[I] = \beta[SI] - \gamma I$

Finding SIR equations

- ▶ What is $\frac{d}{dt}[S]$?
 - ▶ 1 is removed whenever an SI edge transmits. So
 - ▶ $\frac{d}{dt}[S] = -\beta[SI]$
- ▶ What is $\frac{d}{dt}[I]$?
 - ▶ An I is removed whenever a recovery occurs.
 - ▶ An I is created whenever an SI edge transmits
 - ▶ $\frac{d}{dt}[I] = \beta[SI] - \gamma I$
- ▶ What is $\frac{d}{dt}[SI]$?

Finding SIR equations

- ▶ What is $\frac{d}{dt}[S]?$
 - ▶ 1 is removed whenever an SI edge transmits. So
 - ▶ $\frac{d}{dt}[S] = -\beta[SI]$
- ▶ What is $\frac{d}{dt}[I]?$
 - ▶ An I is removed whenever a recovery occurs.
 - ▶ An I is created whenever an SI edge transmits
 - ▶ $\frac{d}{dt}[I] = \beta[SI] - \gamma I$
- ▶ What is $\frac{d}{dt}[SI]?$
 - ▶ 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.
$$\frac{d}{dt}[SI] = -(\beta + \gamma)[SI] + \beta([SSI] - [ISI])$$

Finding SIR equations

So we have

$$\frac{d}{dt}[S] = -\beta[SI]$$

$$\frac{d}{dt}[I] = \beta[SI] - \gamma[I]$$

$$\frac{d}{dt}[SI] = -(\beta + \gamma)[SI] + \beta([SSI] - [ISI])$$

$$\frac{d}{dt}[SSI] = \dots$$

$$\frac{d}{dt}[ISI] = \dots$$

Finding SIS equations

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

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

Finding SIS equations

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

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

- ▶ The **first** term represents a node in an SS pair getting infected by another neighbor.

Finding SIS equations

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

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

- ▶ The first term represents a node in an SS pair getting infected by another neighbor.
- ▶ The **second** term represents the susceptible node in an SI pair being infected by another neighbor.

Finding SIS equations

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

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

- ▶ The first term represents a node in an SS pair getting infected by another neighbor.
- ▶ 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.

Finding SIS equations

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

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

- ▶ The first term represents a node in an SS pair getting infected by another neighbor.
- ▶ 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

Our equations require larger and larger terms.

Closures

Our equations require larger and larger terms. Let's try short circuiting that chain with a “closure approximation”:

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

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

Closures

Our equations require larger and larger terms. Let's try short circuiting that chain with a “closure approximation”:

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

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

- ▶ SIS:

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

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

Closures

Our equations require larger and larger terms. Let's try short circuiting that chain with a “closure approximation”:

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

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

- ▶ SIS:

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

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

- ▶ SIR:

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

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

$$\dot{[R]} = \gamma[I]$$

Closures

Our equations require larger and larger terms. Let's try short circuiting that chain with a “closure approximation”:

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

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

- ▶ SIS:

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

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

- ▶ SIR:

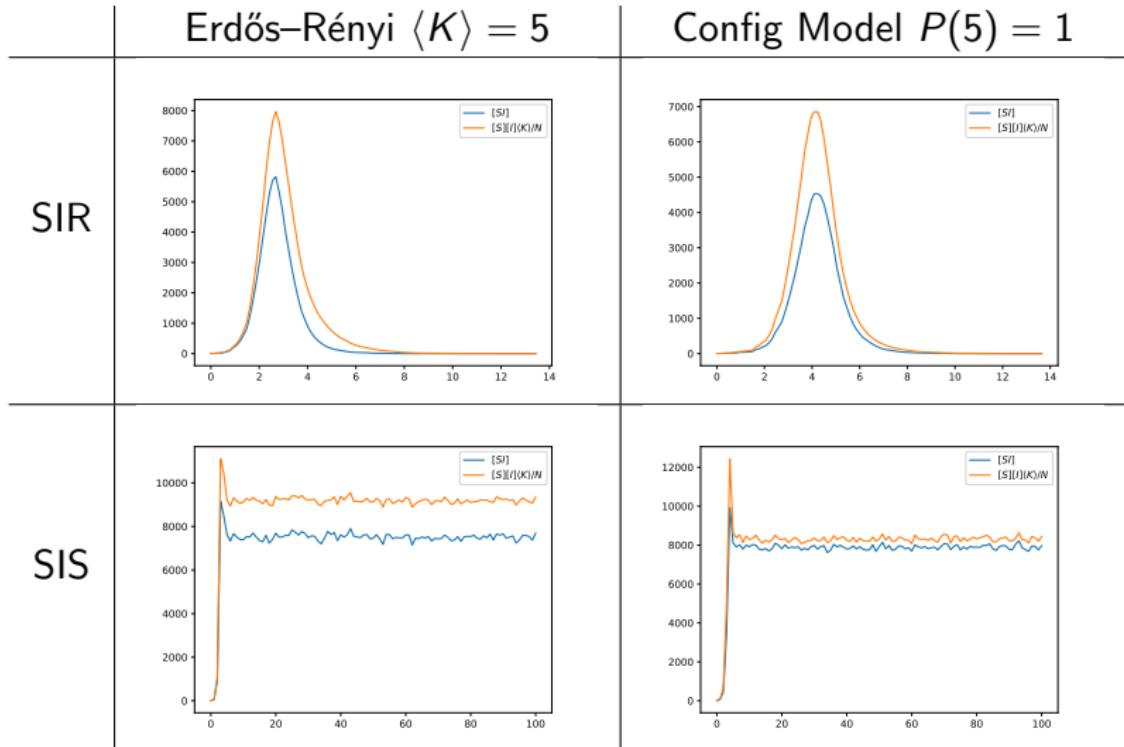
$$\dot{[S]} = -\beta \langle K \rangle [S][I]/N$$

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

$$\dot{[R]} = \gamma[I]$$

These are equivalent to the Kermack-McKendrick equations

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



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 not preferentially infected by degree.
- ▶ We're assuming that neighbors of infected nodes are no more likely to be infected than any other node.
- ▶ We implicitly assume partners change rapidly.

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 not preferentially infected by degree.
- ▶ We're assuming that neighbors of infected nodes are no more likely to be infected than any other node.
- ▶ We implicitly assume partners change rapidly.

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.

More accurate model

- ▶ We can develop a model that accounts for degree correlation.

More accurate model

- ▶ We can develop a model that accounts for degree correlation.
- ▶ Our model has terms like

$$[A_k B_l]$$

To give the number of pairs involving a degree k node with status A and a degree l node with status B .

More accurate model

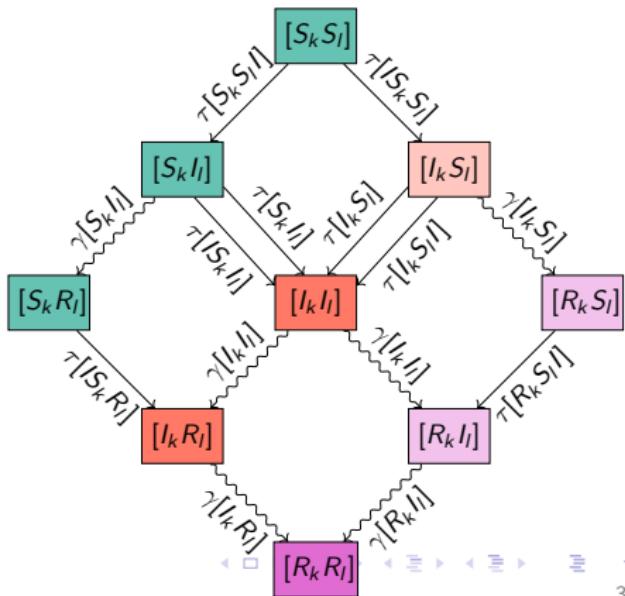
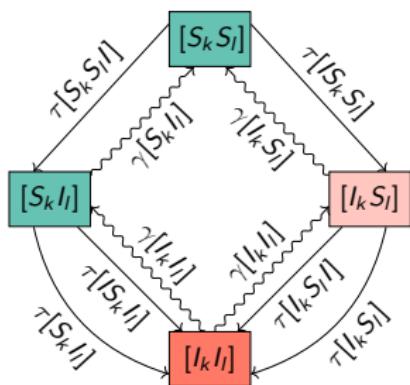
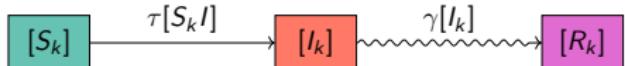
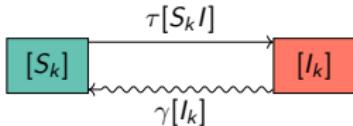
- ▶ We can develop a model that accounts for degree correlation.
- ▶ Our model has terms like

$$[A_k B_l]$$

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



Introduction

Sample stochastic simulations

Impact of network properties

Deriving equations

Simple heterogeneous model

References

A better closure

Using the notation $[S_k I] = \sum_l [S_k I_l]$,

These models can account for degree assortativity or dissassortativity, but **LOTS OF EQUATIONS**.

A better closure

Using the notation $[S_k I] = \sum_I [S_k I_I]$,



For SIS we get

$$\dot{[S_k]} = \gamma[I_k] - \tau[S_k I],$$

$$\dot{[I_k]} = \tau[S_k I] - \gamma[I_k],$$

$$\dot{[S_k I_I]} = \gamma([I_k I_I] - [S_k I_I]) + \tau([S_k S_I I] - [I S_k I_I] - [S_k I_I]),$$

$$\dot{[S_k S_I]} = \gamma([S_k I_I] + [I_k S_I]) - \tau([S_k S_I I] + [I S_k S_I]),$$

$$\dot{[I_k I_I]} = \tau([S_k I_I] + [I_k S_I]) - 2\gamma[I_k I_I] + \tau([I S_k I_I] + [I_k S_I I])$$

These models can account for degree assortativity or dissassortativity, but **LOTS OF EQUATIONS**.

A better closure

Using the notation $[S_k I] = \sum_l [S_k I_l]$,

For SIR we get

$$[\dot{S}_k] = -\tau[S_k I],$$

$$[\dot{I}_k] = \tau[S_k I] - \gamma[I_k],$$

$$[\dot{R}_k] = \gamma[I_k],$$

$$[\dot{S}_k I_l] = -\gamma[S_k I_l] + \tau([S_k S_l I] - [I S_k I_l] - [S_k I_l]),$$

$$[\dot{S}_k S_l] = -\tau([S_k S_l I] + [I S_k S_l])$$

These models can account for degree assortativity or dissassortativity, but **LOTS OF EQUATIONS**.

A heterogeneous population model

We derive a model that accounts for degree distribution, but not partnership duration [6, 7, 8]:

A heterogeneous population model

We derive a model that accounts for degree distribution, but not partnership duration [6, 7, 8]:

- ▶ This corresponds to the “annealed networks” mentioned earlier.

A heterogeneous population model

We derive a model that accounts for degree distribution, but not partnership duration [6, 7, 8]:

- ▶ This corresponds to the “annealed networks” mentioned earlier.
- ▶ We assume that

$$[S_k I] = k[S_k] \pi_I$$

A heterogeneous population model

We derive a model that accounts for degree distribution, but not partnership duration [6, 7, 8]:

- ▶ This corresponds to the “annealed networks” mentioned earlier.
- ▶ We assume that

$$[S_k I] = k[S_k] \pi_I$$

- ▶ where π_I is the probability a random stub in the population belongs to an infected node.

$$\pi_I = \sum_{\ell} \ell I_{\ell} / N \langle K \rangle$$

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
- ▶ $I(t)$

New equations

Our equations become

New equations

Our equations become

- ▶ SIS:

$$\begin{aligned}\frac{d}{dt}[S_k] &= \gamma[I_k] - \tau[S_k]k\pi_I \\ \frac{d}{dt}[I_k] &= \tau[S_k]k\pi_I - \gamma[I_k] \\ \pi_I &= \sum k[I_k]/N \langle K \rangle\end{aligned}$$

New equations

Our equations become

- ▶ SIS:

$$\begin{aligned}\frac{d}{dt}[S_k] &= \gamma[I_k] - \tau[S_k]k\pi_I \\ \frac{d}{dt}[I_k] &= \tau[S_k]k\pi_I - \gamma[I_k] \\ \pi_I &= \sum k[I_k]/N \langle K \rangle\end{aligned}$$

- ▶ SIR:

$$\begin{aligned}\frac{d}{dt}[S_k] &= -\tau[S_k]k\pi_I \\ \frac{d}{dt}[I_k] &= \tau[S_k]k\pi_I - \gamma[I_k] \\ \frac{d}{dt}[R_k] &= \gamma[I_k] \\ \pi_I &= \sum k[I_k]/N \langle K \rangle\end{aligned}$$

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

Early on,

\mathcal{R}_0

Early on,

- ▶ The degree of an infected person is chosen using
 $P_n(k) = kP(k)/\langle K \rangle$.

Early on,

- ▶ The degree of an infected person is chosen using $P_n(k) = kP(k)/\langle K \rangle$.
- ▶ The expected number of transmissions of a degree k individual before recovering is $k\beta/\gamma$.
[This uses the fact that partners are constantly replaced].

\mathcal{R}_0

Early on,

- ▶ The degree of an infected person is chosen using $P_n(k) = kP(k)/\langle K \rangle$.
- ▶ The expected number of transmissions of a degree k individual before recovering is $k\beta/\gamma$.
[This uses the fact that partners are constantly replaced].
- ▶ So

$$\mathcal{R}_0 = \sum_k \frac{kP(k)}{\langle K \rangle} k \frac{\beta}{\gamma} = \frac{\beta}{\gamma} \frac{\langle K^2 \rangle}{\langle K \rangle}$$

Early on,

- ▶ The degree of an infected person is chosen using $P_n(k) = kP(k)/\langle K \rangle$.
- ▶ The expected number of transmissions of a degree k individual before recovering is $k\beta/\gamma$.
[This uses the fact that partners are constantly replaced].
- ▶ So

$$\mathcal{R}_0 = \sum_k \frac{kP(k)}{\langle K \rangle} k \frac{\beta}{\gamma} = \frac{\beta}{\gamma} \frac{\langle K^2 \rangle}{\langle K \rangle}$$

- ▶ This is the same whether the model is SIS or SIR.

Errors

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

Errors

- ▶ It was rigorously proven by [2] that if $P(k) \sim k^{-\alpha}$ then for a Configuration Model network there is no epidemic threshold for SIS disease, even if $\langle K^2 \rangle$ is finite.
- ▶ That is, no matter how small β is, an epidemic is possible.

Errors

- ▶ It was rigorously proven by [2] that if $P(k) \sim k^{-\alpha}$ then for a Configuration Model network there is no epidemic threshold for SIS disease, even if $\langle K^2 \rangle$ is finite.
- ▶ That is, no matter how small β is, an epidemic is possible.
- ▶ This contradicts the prediction. How does this happen?

Errors

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

Errors

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

Errors

- ▶ It was rigorously proven by [2] that if $P(k) \sim k^{-\alpha}$ then for a Configuration Model network there is no epidemic threshold for SIS disease, even if $\langle K^2 \rangle$ is finite.
- ▶ 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. Eventually the disease spreads to other high degree nodes. So it can persist even if the naive estimate has $\mathcal{R}_0 < 1$.

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:

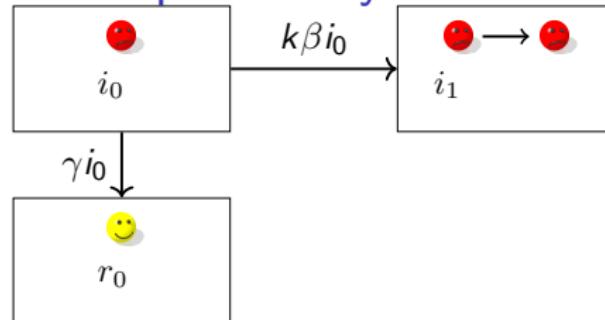
- ▶ \mathcal{P}
- ▶ $I(\infty)$, the equilibrium level of infection
- ▶ \mathcal{R}_0
- ▶ $I(t)$

Epidemic probability on annealed networks



Consider an individual u with degree k who becomes infected at time $t = t_0$. Define $i_{m|k}(t)$ and $r_{m|k}(t)$ to be the probability u has transmitted to m individuals and is infectious or recovered.

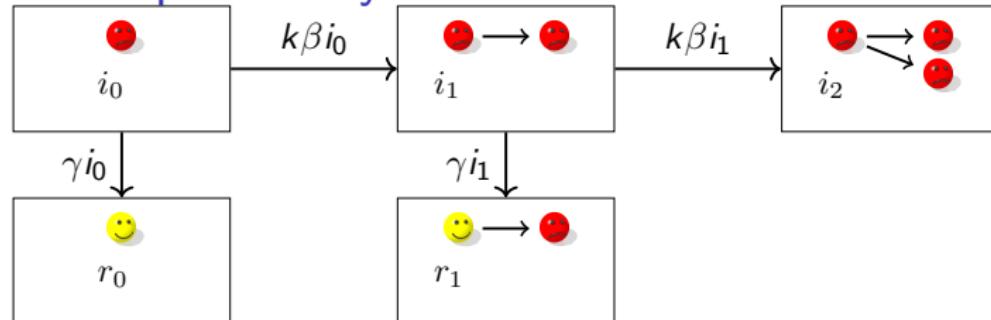
Epidemic probability on annealed networks



Consider an individual u with degree k who becomes infected at time $t = t_0$. Define $i_{m|k}(t)$ and $r_{m|k}(t)$ to be the probability u has transmitted to m individuals and is infectious or recovered.

- ▶ The probability of transmitting at least once before recovering is $\frac{k\beta}{k\beta + \gamma}$.

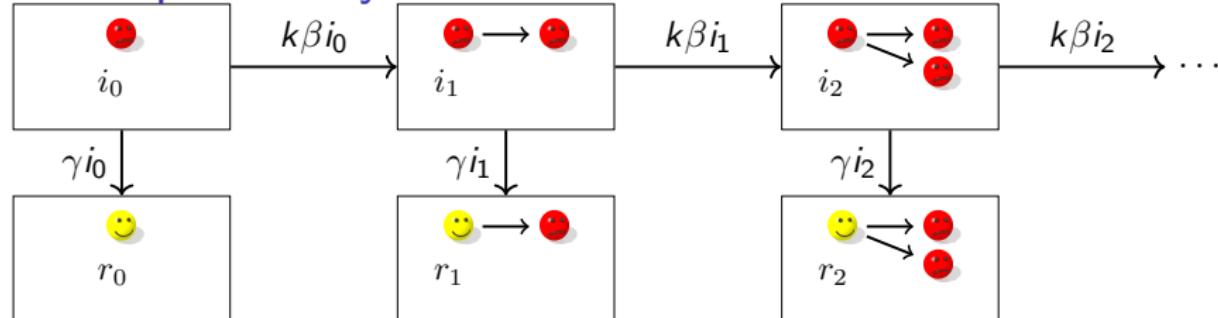
Epidemic probability on annealed networks



Consider an individual u with degree k who becomes infected at time $t = t_0$. Define $i_{m|k}(t)$ and $r_{m|k}(t)$ to be the probability u has transmitted to m individuals and is infectious or recovered.

- ▶ The probability of transmitting at least once before recovering is $\frac{k\beta}{k\beta+\gamma}$.
- ▶ The probability the first m events are transmissions is $\left[\frac{k\beta}{k\beta+\gamma}\right]^m$.

Epidemic probability on annealed networks



Consider an individual u with degree k who becomes infected at time $t = t_0$. Define $i_{m|k}(t)$ and $r_{m|k}(t)$ to be the probability u has transmitted to m individuals and is infectious or recovered.

- ▶ The probability of transmitting at least once before recovering is $\frac{k\beta}{k\beta + \gamma}$.
- ▶ The probability the first m events are transmissions is $\left[\frac{k\beta}{k\beta + \gamma} \right]^m$.
- ▶ For exactly m transmissions before recovery it is

$$r_{m|k}(\infty) = \left(\frac{k\beta}{k\beta + \gamma} \right)^m \frac{\gamma}{k\beta + \gamma}$$

\mathcal{P} calculation

- ▶ The probability a randomly chosen initial infection does not cause any further infections is

$$\sum_k P(k) r_{0|k}$$

\mathcal{P} calculation

- ▶ The probability a randomly chosen initial infection does not cause any further infections is

$$\sum_k P(k) r_{0|k}$$

- ▶ The probability any secondary case does not cause any further infections is

$$\sum_k P_n(k) r_{0|k} = \frac{\sum_k k P(k) r_{0|k}}{\langle K \rangle}$$

\mathcal{P} calculation

- ▶ The probability a randomly chosen initial infection does not cause any further infections is

$$\sum_k P(k) r_{0|k}$$

- ▶ The probability any secondary case does not cause any further infections is

$$\sum_k P_n(k) r_{0|k} = \frac{\sum_k k P(k) r_{0|k}}{\langle K \rangle}$$

- ▶ With a bit of effort we find that the probability of the index node causing m cases is

$$\sum_k P(k) r_{m|k}(\infty)$$

\mathcal{P} calculation

- ▶ The probability a randomly chosen initial infection does not cause any further infections is

$$\sum_k P(k) r_{0|k}$$

- ▶ The probability any secondary case does not cause any further infections is

$$\sum_k P_n(k) r_{0|k} = \frac{\sum_k k P(k) r_{0|k}}{\langle K \rangle}$$

- ▶ With a bit of effort we find that the probability of the index node causing m cases is

$$\sum_k P(k) r_{m|k}(\infty)$$

- ▶ And for a secondary case $\sum_k P_n(k) r_{m|k}$.

\mathcal{P} calculation

- ▶ The probability a randomly chosen initial infection does not cause any further infections is

$$\sum_k P(k) r_{0|k}$$

- ▶ The probability any secondary case does not cause any further infections is

$$\sum_k P_n(k) r_{0|k} = \frac{\sum_k k P(k) r_{0|k}}{\langle K \rangle}$$

- ▶ With a bit of effort we find that the probability of the index node causing m cases is

$$\sum_k P(k) r_{m|k}(\infty)$$

- ▶ And for a secondary case $\sum_k P_n(k) r_{m|k}$.
- ▶ Define $f(x) = \sum_m \sum_k P(k) r_{m|k} x^m$ and $g(x) = \sum_m \sum_k P_n(k) r_{m|k} x^m$.

\mathcal{P} calculation

- ▶ Let q_d be the probability a secondary case **does not** start a transmission chain of length greater than d .

\mathcal{P} calculation

- ▶ Let q_d be the probability a secondary case **does not** start a transmission chain of length greater than d .
- ▶ Then q_{d+1} is given by summing up the probability of causing m cases, but they do not start a chain longer than d .

$$\sum_m \left(\sum_k P_n(k) r_{m|k} \right) q_d^m = g(q_d)$$

\mathcal{P} calculation

- ▶ Let q_d be the probability a secondary case **does not** start a transmission chain of length greater than d .
- ▶ Then q_{d+1} is given by summing up the probability of causing m cases, but they do not start a chain longer than d .

$$\sum_m \left(\sum_k P_n(k) r_{m|k} \right) q_d^m = g(q_d)$$

- ▶ and $q_0 = \sum_k P_n(k) r_{0|k} = g(0)$.

\mathcal{P} calculation

- ▶ Let q_d be the probability a secondary case **does not** start a transmission chain of length greater than d .
- ▶ Then q_{d+1} is given by summing up the probability of causing m cases, but they do not start a chain longer than d .

$$\sum_m \left(\sum_k P_n(k) r_{m|k} \right) q_d^m = g(q_d)$$

- ▶ and $q_0 = \sum_k P_n(k) r_{0|k} = g(0)$.
- ▶ after a little more effort we have that the probability of no epidemic is

$$f(q_\infty)$$

where $q_\infty = \lim_{d \rightarrow \infty} g^{(d)}(0)$.

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
- ▶ $I(t)$

SIS endemic equilibrium prediction

Let's find the **predicted** endemic equilibrium:

- ▶ We set $I_k = 0$ for all k and solve for I_k in terms of π_I .

SIS endemic equilibrium prediction

Let's find the **predicted** endemic equilibrium:

- ▶ We set $I_k = 0$ for all k and solve for I_k in terms of π_I .
- ▶ Since we have π_I in terms of I_k , we get an equation to solve for π_I .

SIS endemic equilibrium prediction

Let's find the **predicted** endemic equilibrium:

- ▶ We set $I_k = 0$ for all k and solve for I_k in terms of π_I .
- ▶ Since we have π_I in terms of I_k , we get an equation to solve for π_I .
- ▶ This gives the equilibrium infection level.

SIS endemic equilibrium calculation

- ▶ Set $I_k = 0$:

$$\beta k S_k \pi_I - \gamma I_k = 0$$

SIS endemic equilibrium calculation

- ▶ Set $I_k = 0$:

$$\beta k S_k \pi_I - \gamma I_k = 0$$

- ▶ Since $S_k = P(k) - I_k$ we have

$$\beta k P(k) \pi_I - \beta k \pi_I I_k - \gamma I_k = 0$$

SIS endemic equilibrium calculation

- ▶ Set $I_k = 0$:

$$\beta k S_k \pi_I - \gamma I_k = 0$$

- ▶ Since $S_k = P(k) - I_k$ we have

$$\beta k P(k) \pi_I - \beta k \pi_I I_k - \gamma I_k = 0$$

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

SIS endemic equilibrium calculation

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

$$\pi_I = \frac{\beta\pi_I}{\langle K \rangle} \sum_k \frac{P(k)k^2}{(\gamma + \beta k\pi_I)}$$

SIS endemic equilibrium calculation

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

$$\pi_I = \frac{\beta\pi_I}{\langle K \rangle} \sum_k \frac{P(k)k^2}{(\gamma + \beta k\pi_I)}$$

- ▶ So if $\pi_I \neq 0$ then

$$1 = \frac{\beta}{\langle K \rangle} \sum_k \frac{P(k)k^2}{\gamma + \beta k\pi_I}.$$

SIS endemic equilibrium calculation

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

$$\pi_I = \frac{\beta\pi_I}{\langle K \rangle} \sum_k \frac{P(k)k^2}{(\gamma + \beta k\pi_I)}$$

- ▶ So if $\pi_I \neq 0$ then

$$1 = \frac{\beta}{\langle K \rangle} \sum_k \frac{P(k)k^2}{\gamma + \beta k\pi_I}.$$

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

SIR final size

To calculate the SIR final size, we assume that for the initial condition a proportion ρ of the nodes are randomly selected to be infected.

SIR final size

To calculate the SIR final size, we assume that for the initial condition a proportion ρ of the nodes are randomly selected to be infected.

- ▶ Using an integrating factor, we have

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

SIR final size

To calculate the SIR final size, we assume that for the initial condition a proportion ρ of the nodes are randomly selected to be infected.

- ▶ Using an integrating factor, we have

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

- ▶ 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

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

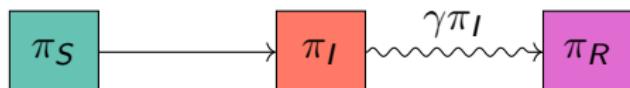
$$S_k = (1 - \rho) NP(k) \theta^k$$

$$I_k = NP(k) - S_k - R_k$$

$$\dot{R}_k = \gamma I_k$$

$$\pi_I = \sum_k k I_k \Big/ N \langle K \rangle .$$

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



Finishing up

- ▶ Note that $\dot{\pi}_R = \gamma\pi_I$ and $\dot{\theta} = -\beta\pi_I\theta$.

Finishing up

- ▶ Note that $\dot{\pi}_R = \gamma\pi_I$ and $\dot{\theta} = -\beta\pi_I\theta$.
- ▶ So $\dot{\pi}_R/\gamma = -\dot{\theta}/\beta\theta$. Thus

$$\frac{\pi_R}{\gamma} = -\frac{\ln \theta}{\beta}$$

Finishing up

- ▶ Note that $\dot{\pi}_R = \gamma\pi_I$ and $\dot{\theta} = -\beta\pi_I\theta$.
- ▶ So $\dot{\pi}_R/\gamma = -\dot{\theta}/\beta\theta$. Thus

$$\frac{\pi_R}{\gamma} = -\frac{\ln \theta}{\beta}$$

- ▶ Further

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

Finishing up

- ▶ Note that $\dot{\pi}_R = \gamma\pi_I$ and $\dot{\theta} = -\beta\pi_I\theta$.
- ▶ So $\dot{\pi}_R/\gamma = -\dot{\theta}/\beta\theta$. Thus

$$\frac{\pi_R}{\gamma} = -\frac{\ln \theta}{\beta}$$

- ▶ 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

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

$$S = N(1 - \rho)\psi(\theta)$$

$$I = N - S - R$$

$$\dot{R} = \gamma I$$

Final size

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

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

Final size

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

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

Solving for $\theta(\infty)$:

$$\theta(\infty) = \exp \left[-\frac{\beta}{\gamma} \left(1 - \frac{\theta(\infty)\psi'(\theta(\infty))}{\langle K \rangle} \right) \right]$$

Final size

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

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

Solving for $\theta(\infty)$:

$$\theta(\infty) = \exp \left[-\frac{\beta}{\gamma} \left(1 - \frac{\theta(\infty)\psi'(\theta(\infty))}{\langle K \rangle} \right) \right]$$

Then

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

Scale-free networks

- ▶ Many measurements of sexual partnership networks suggests the degree distribution scales like

$$P(k) \sim k^{-\alpha}$$

where α is in a range such that $\langle K \rangle$ is finite, but $\langle K^2 \rangle$ is infinite.

Scale-free networks

- ▶ Many measurements of sexual partnership networks suggests the degree distribution scales like

$$P(k) \sim k^{-\alpha}$$

where α is in a range such that $\langle K \rangle$ is finite, but $\langle K^2 \rangle$ is infinite.

- ▶ Such networks are called “scale-free”.

Scale-free networks

- ▶ Many measurements of sexual partnership networks suggests the degree distribution scales like

$$P(k) \sim k^{-\alpha}$$

where α is in a range such that $\langle K \rangle$ is finite, but $\langle K^2 \rangle$ is infinite.

- ▶ Such networks are called “scale-free”.
- ▶ For such a network, $\mathcal{R}_0 = \frac{\beta}{\gamma} \frac{\langle K^2 \rangle}{\langle K \rangle} = \infty$ if $\beta > 0$

Scale-free networks

- ▶ Many measurements of sexual partnership networks suggests the degree distribution scales like

$$P(k) \sim k^{-\alpha}$$

where α is in a range such that $\langle K \rangle$ is finite, but $\langle K^2 \rangle$ is infinite.

- ▶ Such networks are called “scale-free”.
- ▶ For such a network, $\mathcal{R}_0 = \frac{\beta}{\gamma} \frac{\langle K^2 \rangle}{\langle K \rangle} = \infty$ if $\beta > 0$ — No epidemic threshold! (if we believe that transmission rates are degree-independent)

Scale-free networks

- ▶ Many measurements of sexual partnership networks suggests the degree distribution scales like

$$P(k) \sim k^{-\alpha}$$

where α is in a range such that $\langle K \rangle$ is finite, but $\langle K^2 \rangle$ is infinite.

- ▶ Such networks are called “scale-free”.
- ▶ For such a network, $\mathcal{R}_0 = \frac{\beta}{\gamma} \frac{\langle K^2 \rangle}{\langle K \rangle} = \infty$ if $\beta > 0$ — No epidemic threshold! (if we believe that transmission rates are degree-independent)
- ▶ But if $\langle K^2 \rangle$ is finite, this predicts there is a β_c below which epidemics are impossible.

Direct derivation

We can directly derive the equations

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

$$S = N\psi(\theta)$$

$$I = N - S - R$$

$$\dot{R} = \gamma I$$

Direct derivation

We can directly derive the equations

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

$$S = N\psi(\theta)$$

$$I = N - S - R$$

$$\dot{R} = \gamma I$$

- ▶ Each individual has k stubs.

Direct derivation

We can directly derive the equations

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

$$S = N\psi(\theta)$$

$$I = N - S - R$$

$$\dot{R} = \gamma I$$

- ▶ Each individual has k stubs.
- ▶ Let $\theta(t)$ be the probability that transmission hasn't happened along a given stub.

Direct derivation

We can directly derive the equations

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

$$S = N\psi(\theta)$$

$$I = N - S - R$$

$$\dot{R} = \gamma I$$

- ▶ Each individual has k stubs.
- ▶ Let $\theta(t)$ be the probability that transmission hasn't happened along a given stub.
- ▶ Then $S(t) = (1 - \rho)N \sum_k P(k)\theta^k$, $I(t) = 1 - S(t) - R(t)$, and $\dot{R} = \gamma I$.

Direct derivation

- ▶ Then

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

where π_I is the proportion of stubs that belong to infected nodes.

Direct derivation

- ▶ Then

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

where π_I is the proportion of stubs that belong to infected nodes.

- ▶ The θ represents the probability the stub has not transmitted yet, π_I is the probability it connects to an infected node, and β is the transmission rate.

Direct derivation

- ▶ Then

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

where π_I is the proportion of stubs that belong to infected nodes.

- ▶ The θ represents the probability the stub has not transmitted yet, π_I is the probability it connects to an infected node, and β is the transmission rate.
- ▶ We calculate π_I as before and arrive at the equations.

Introduction

Sample stochastic simulations

Impact of network properties

Deriving equations

Simple heterogeneous model

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] 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.
- [3] 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.
- [4] Joel C. Miller.
Spread of infectious disease through clustered populations.
Journal of the Royal Society Interface, 6(41):1121, 2009.
- [5] Istvan Z Kiss, Joel C Miller, and Péter L Simon.
Mathematics of epidemics on networks: from exact to approximate models.
IAM. Springer, 2017.
- [6] Romualdo Pastor-Satorras and Alessandro Vespignani.
Epidemic spreading in scale-free networks.
Physical Review Letters, 86(14):3200–3203, Apr 2001.
- [7] 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.
- [8] Annett Nold.
Heterogeneity in disease-transmission modeling.
Mathematical Biosciences, 52(3):227–240, 1980.