

# Epidemics in Networks

## Part 3 — Network-based Disease Models

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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

References

# Assumptions

We start with some simple assumptions:

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

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

Introduction

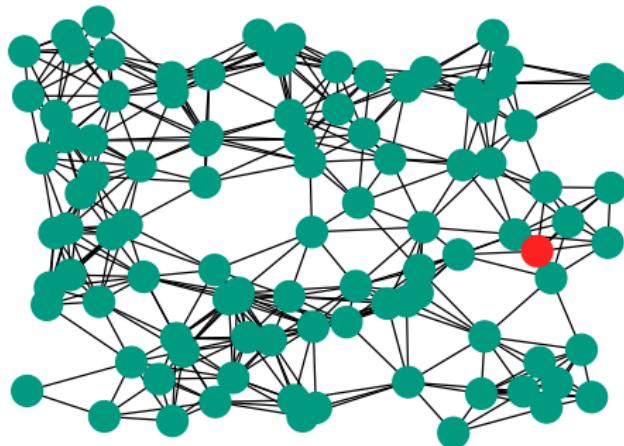
Sample stochastic simulations

Impact of network properties

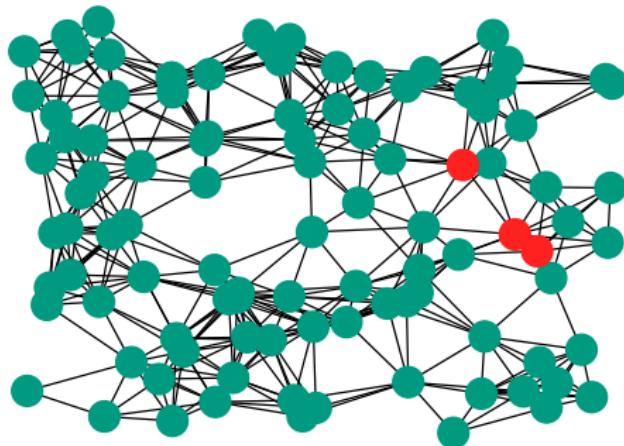
Deriving equations

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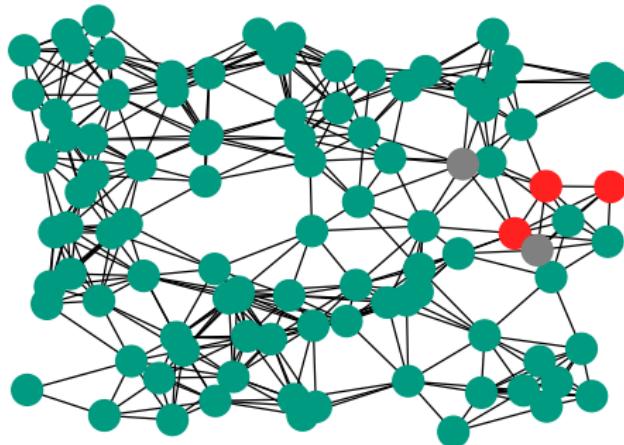
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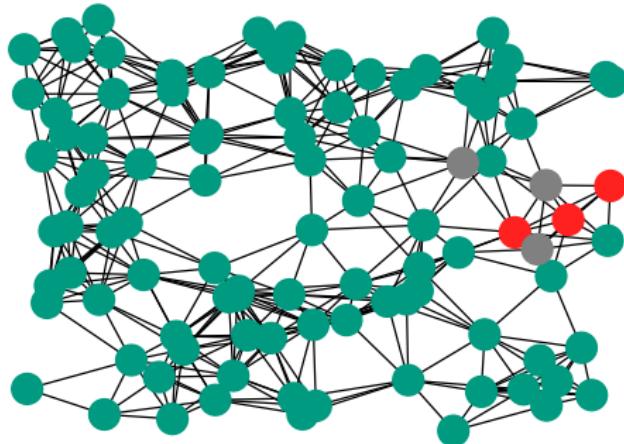
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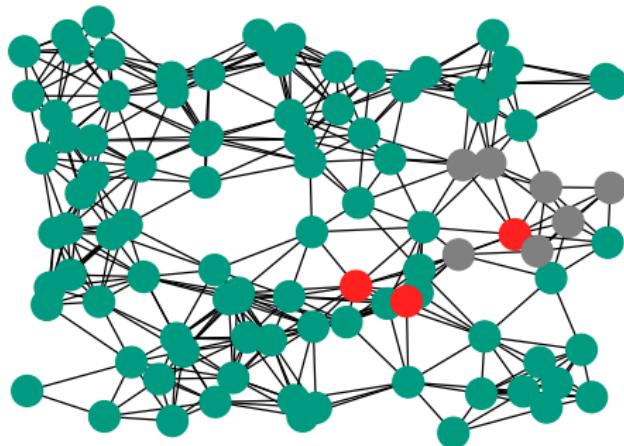
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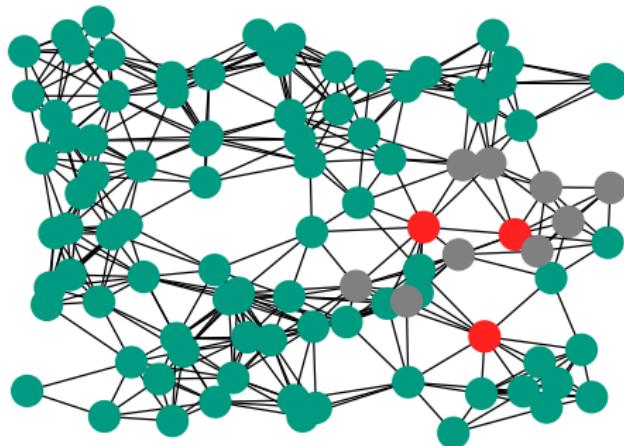
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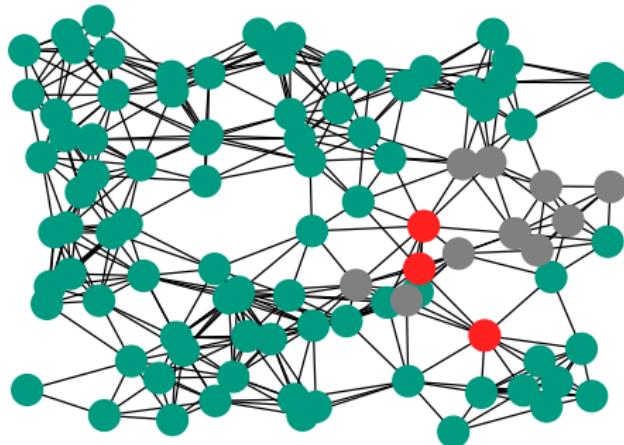
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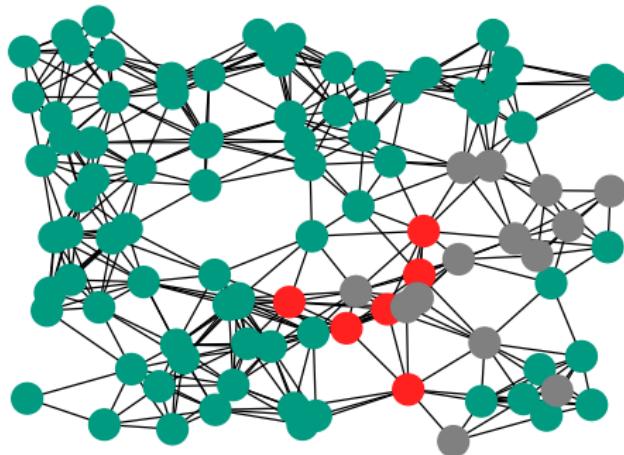
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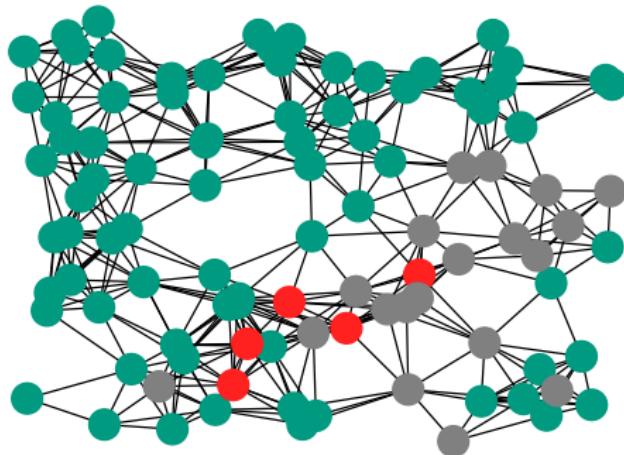
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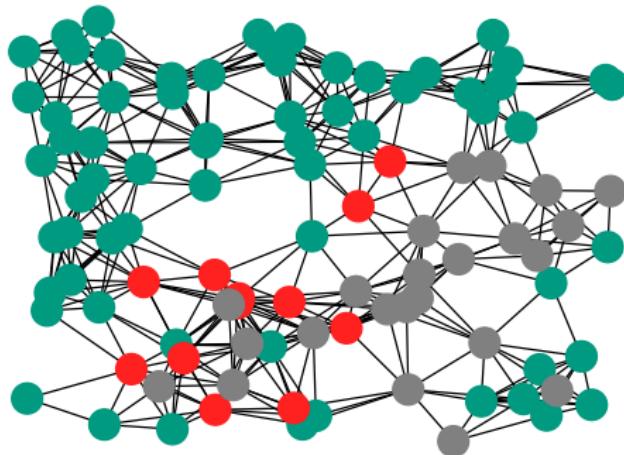
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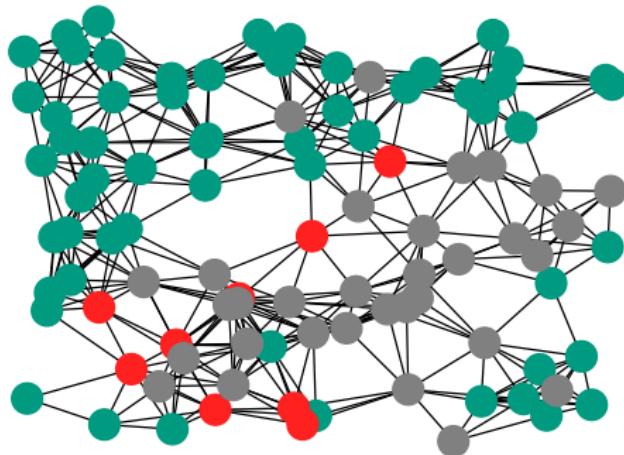
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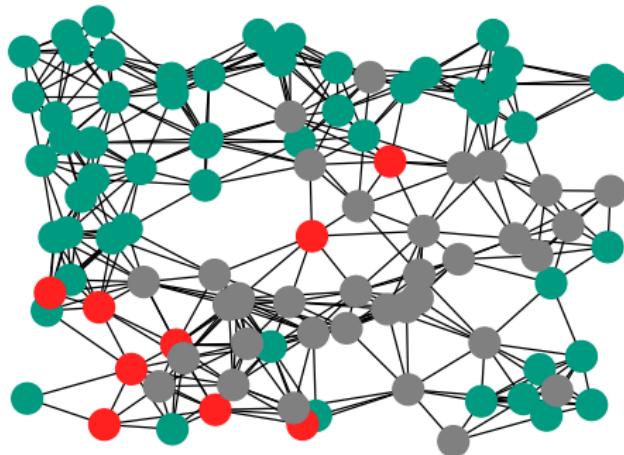
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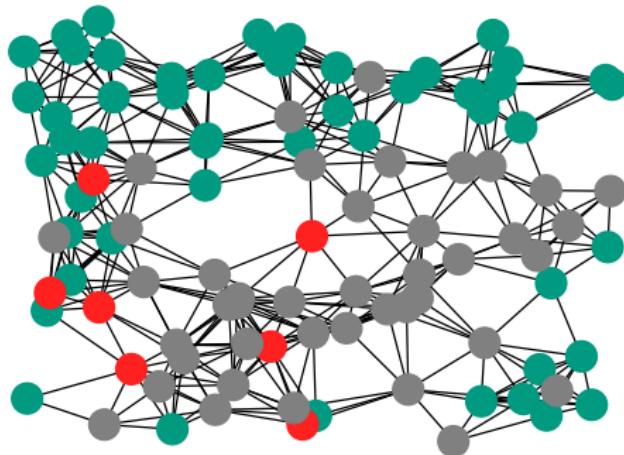
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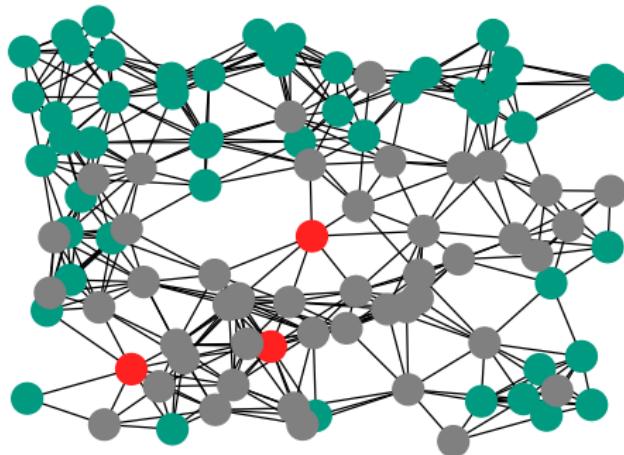
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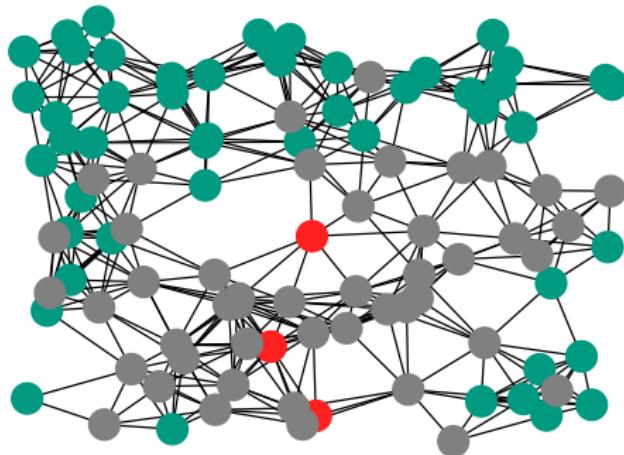
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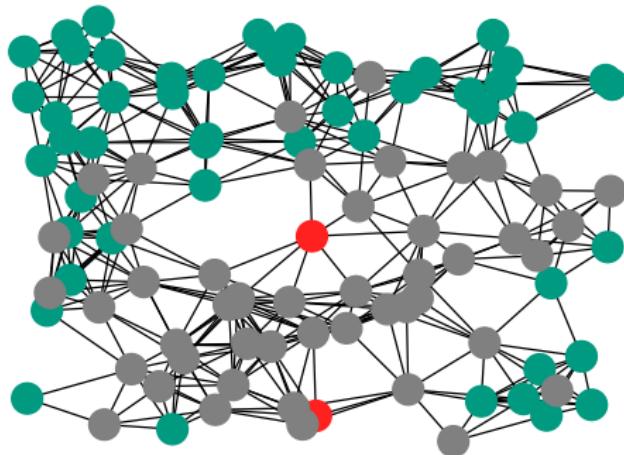
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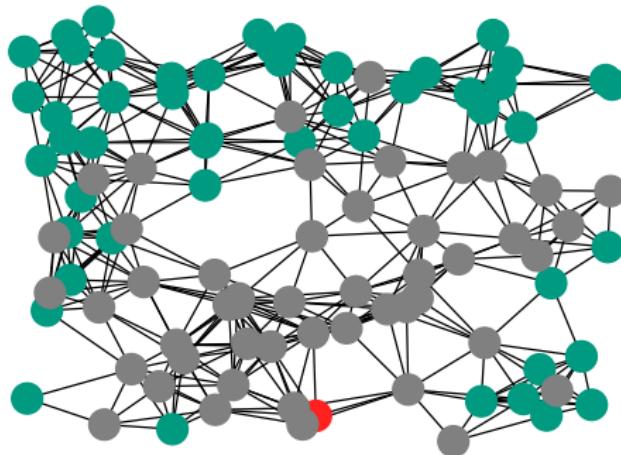
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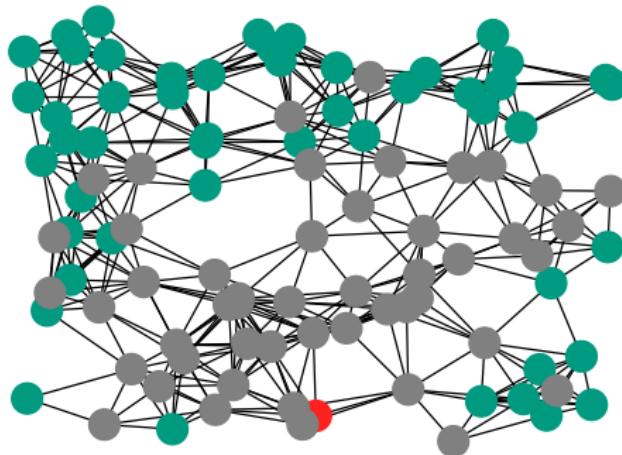
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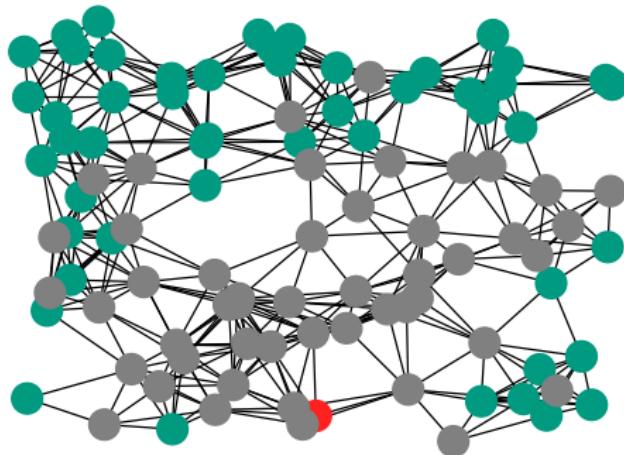
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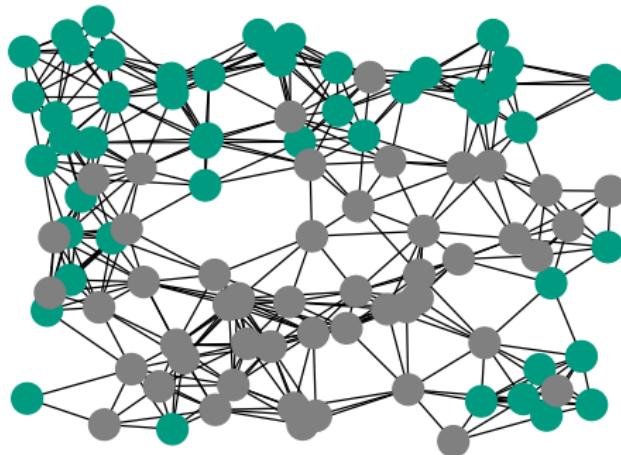
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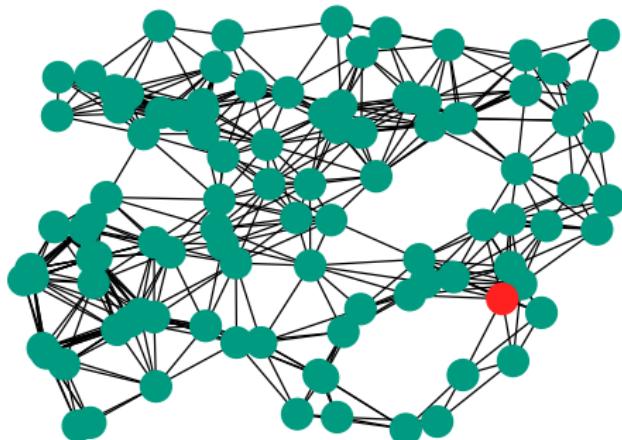
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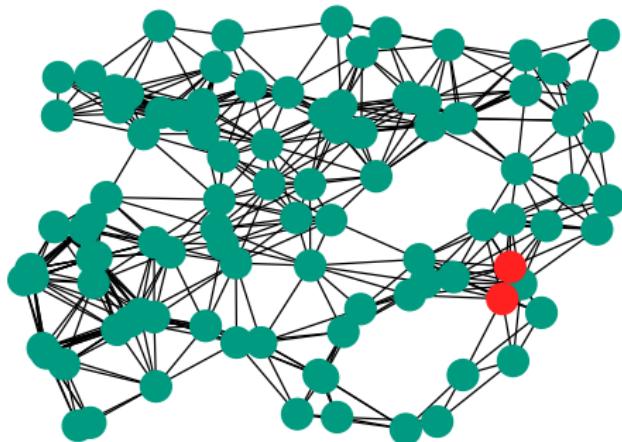
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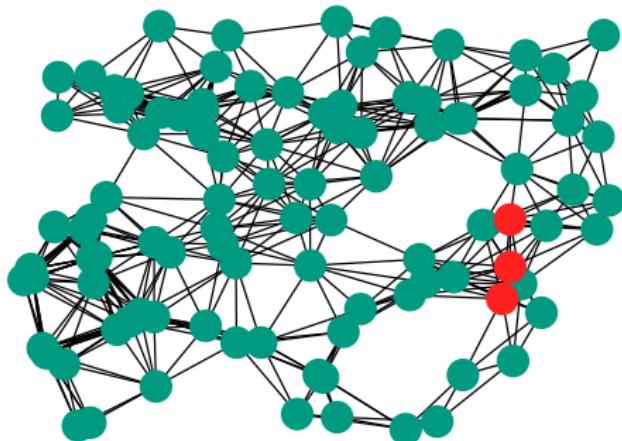
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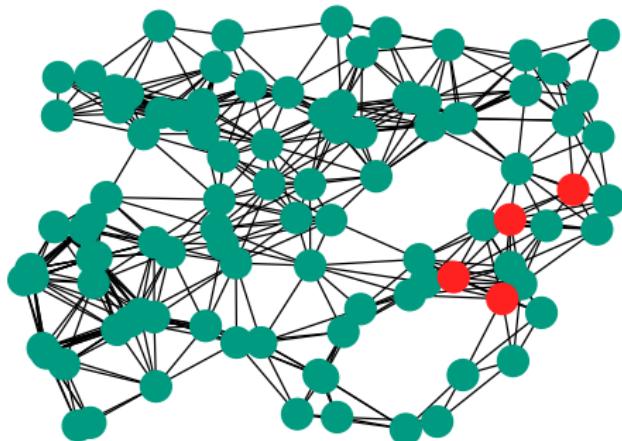
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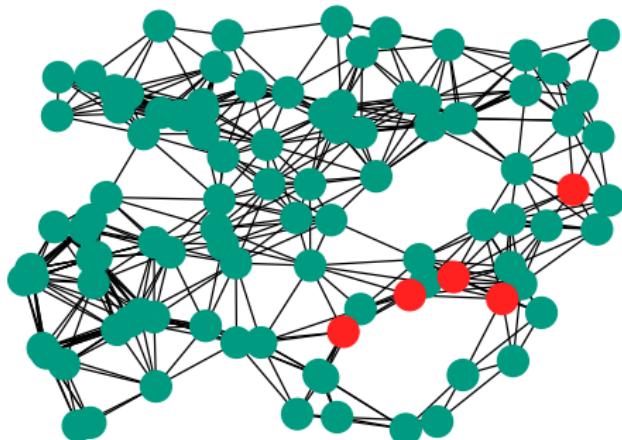
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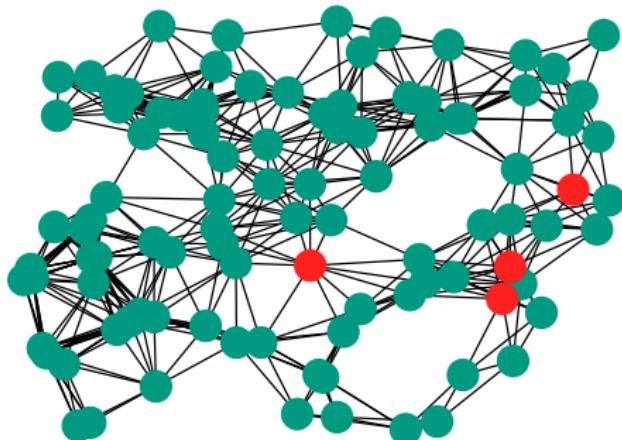
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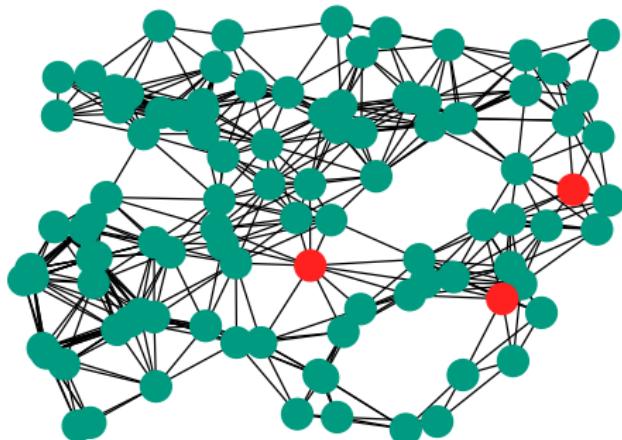
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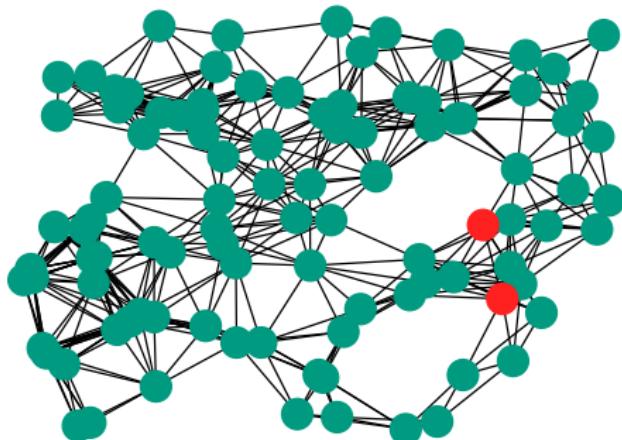
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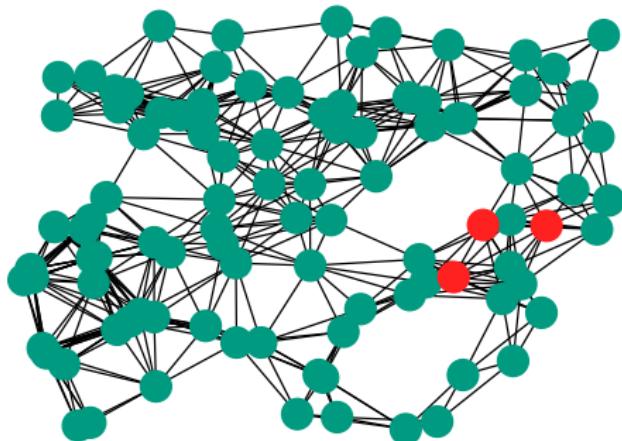
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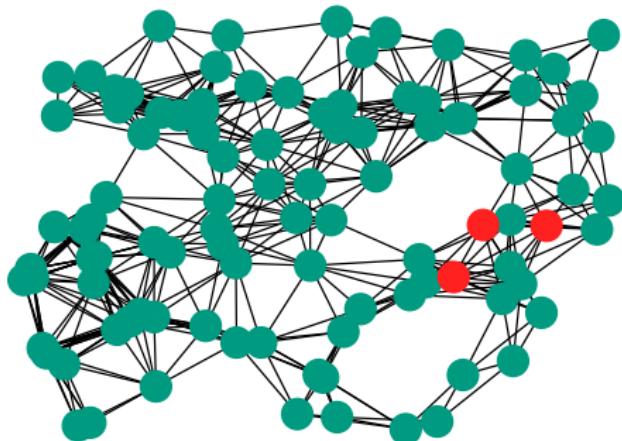
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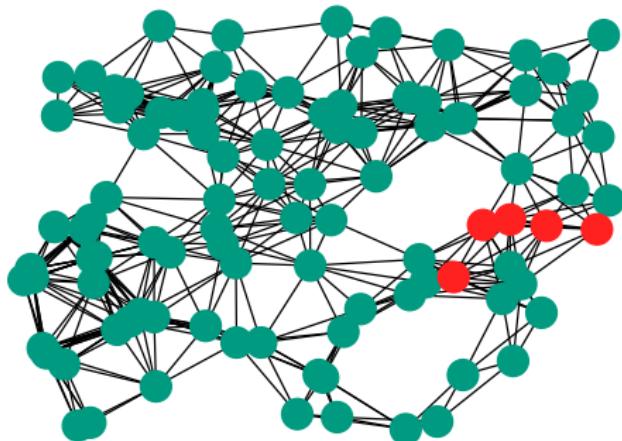
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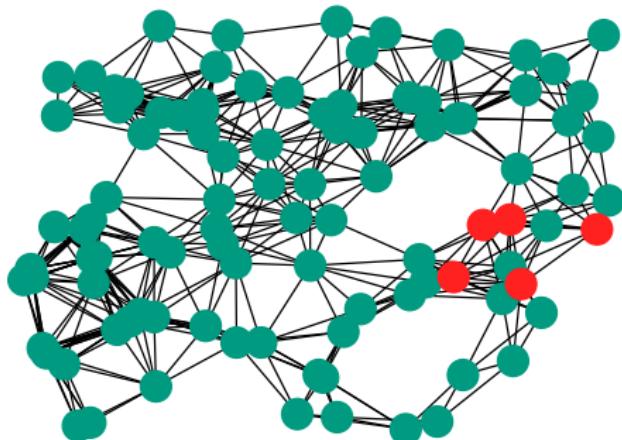
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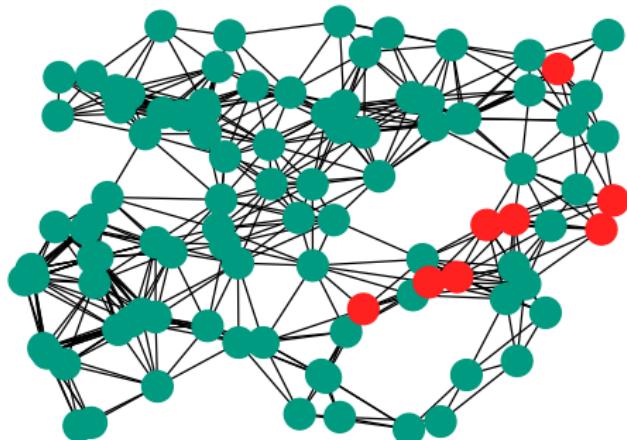
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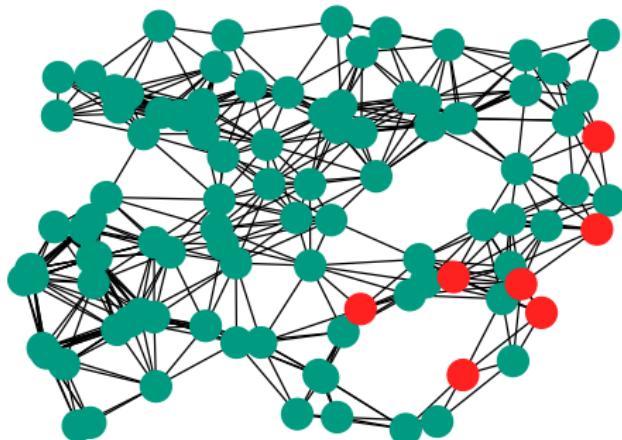
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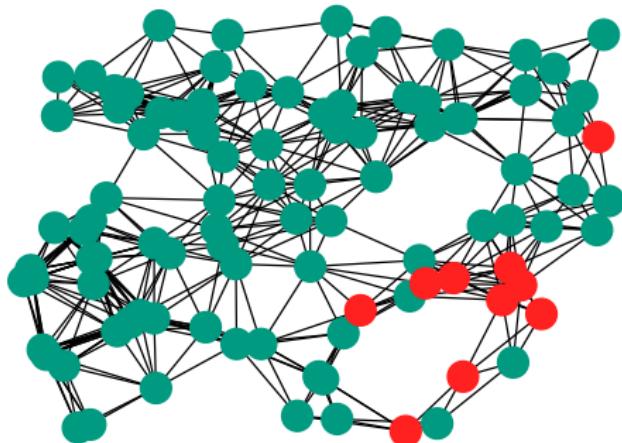
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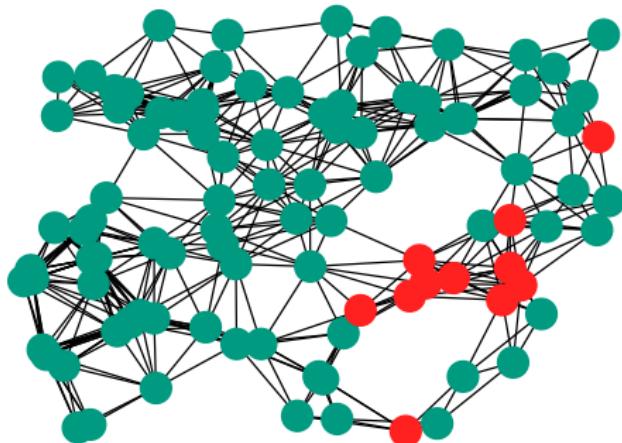
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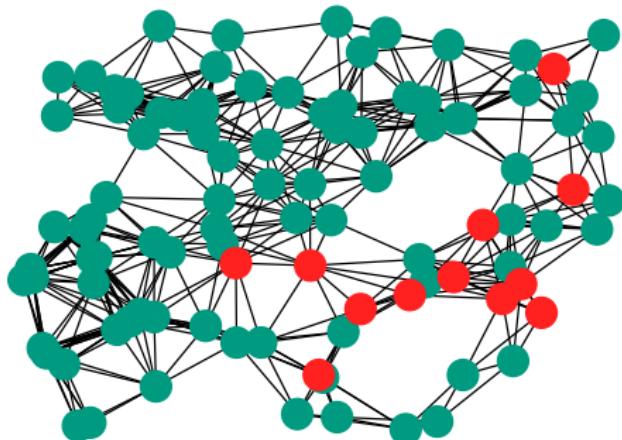
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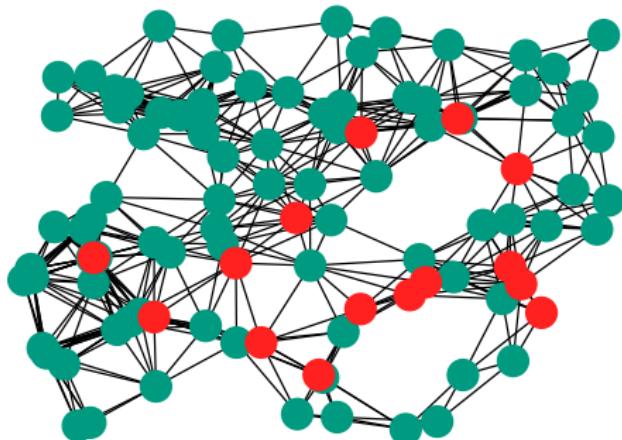
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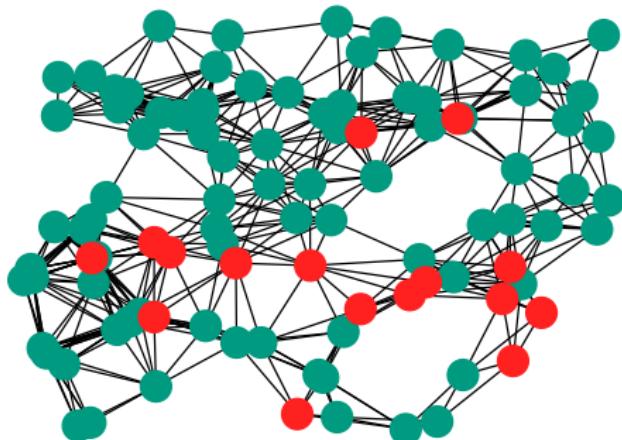
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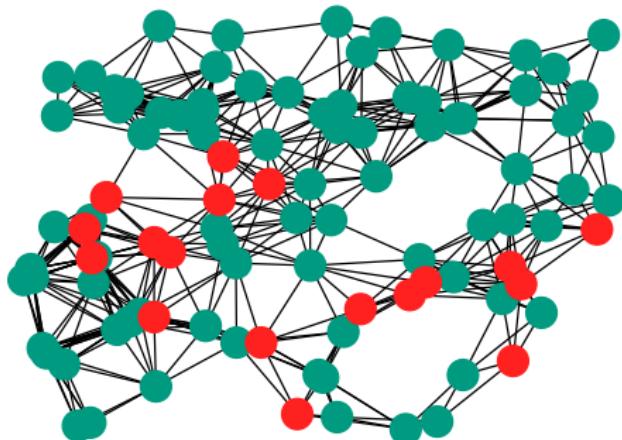
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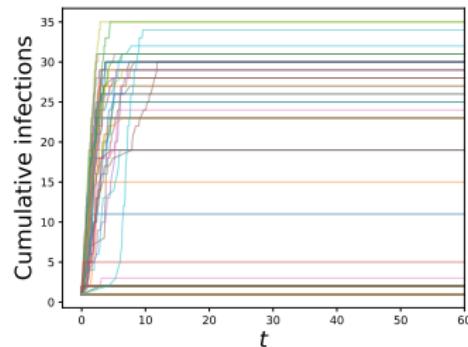
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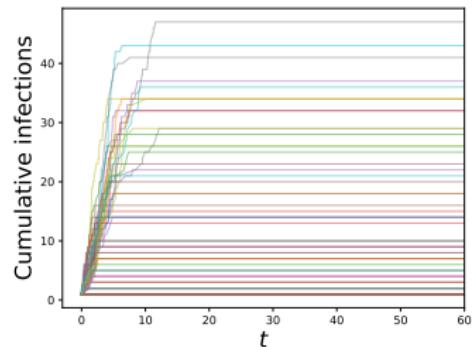
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SIR disease spread with  $\langle K \rangle = 5$ ,  $\beta = 0.4$ , and  $\gamma = 1$ .

$$P(5) = 1,$$



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

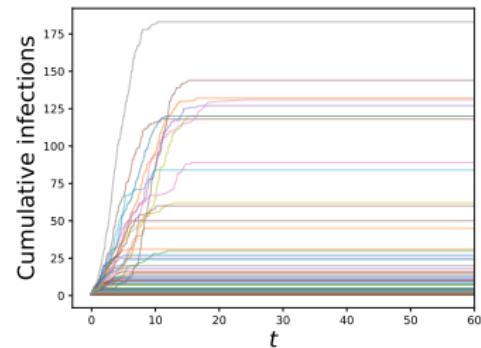
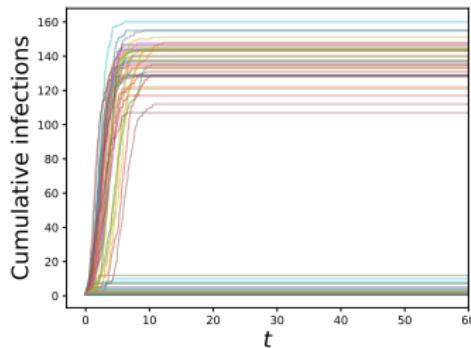


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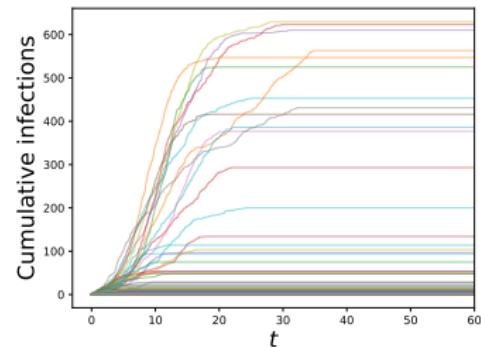
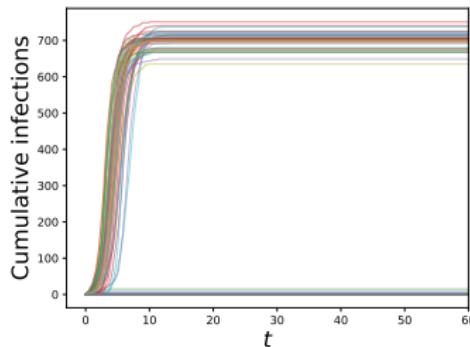


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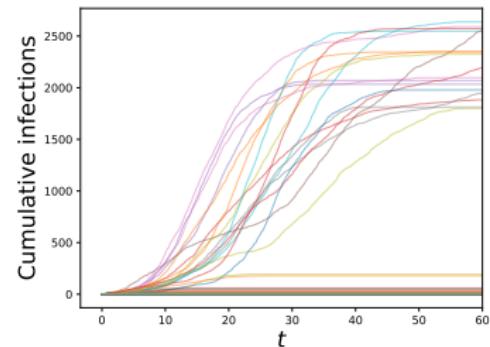
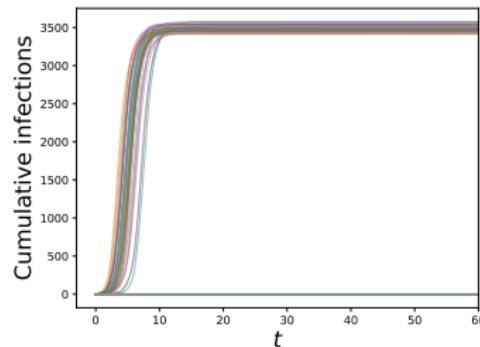


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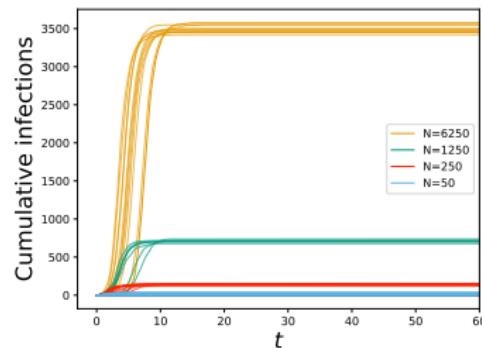
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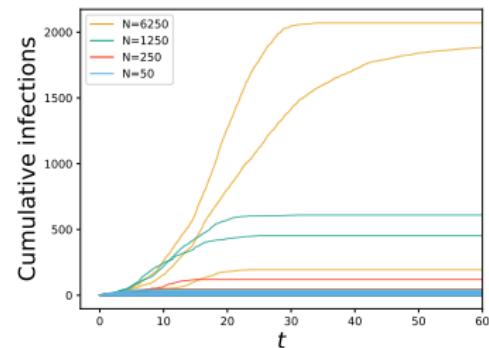
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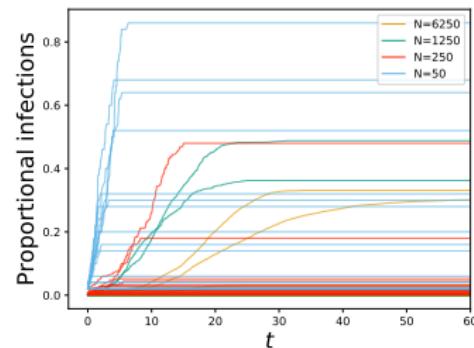
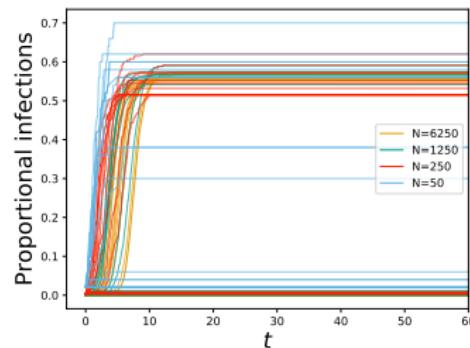


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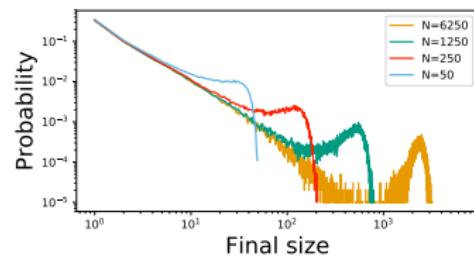
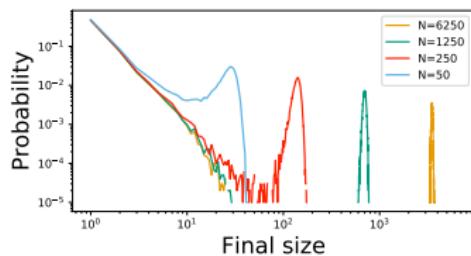


## Stochastic simulation — SIR case

What does the final size distribution look like?

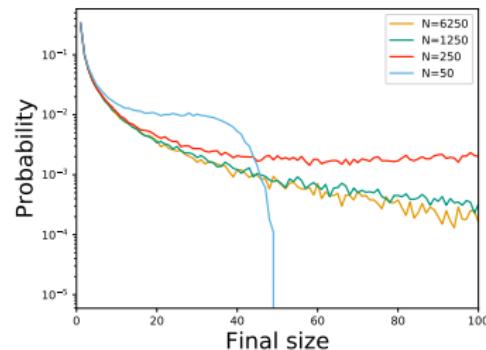
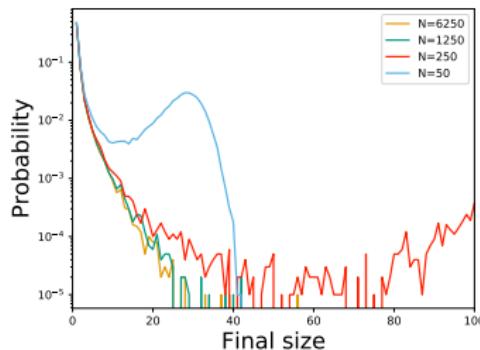
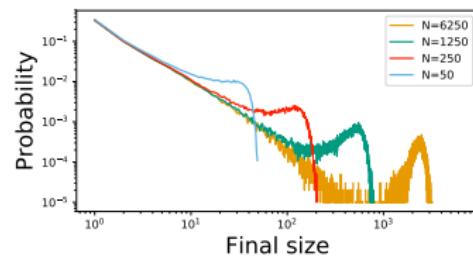
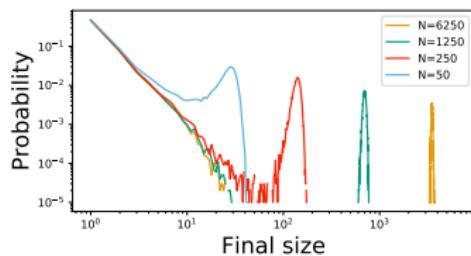
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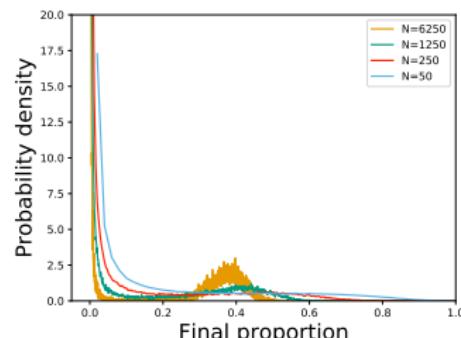
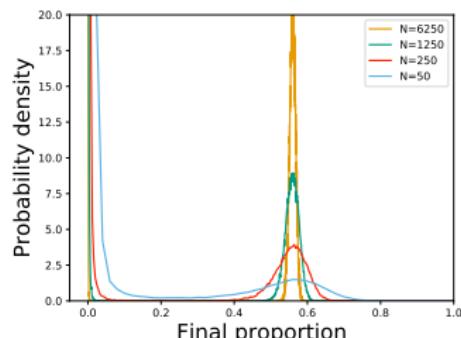
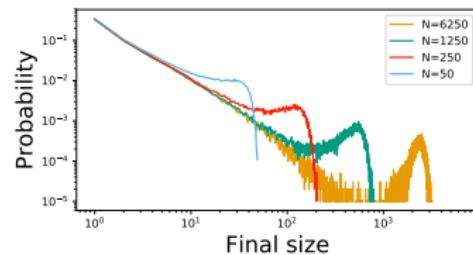
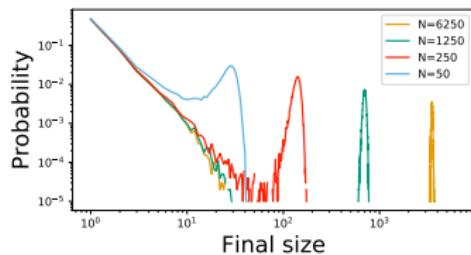
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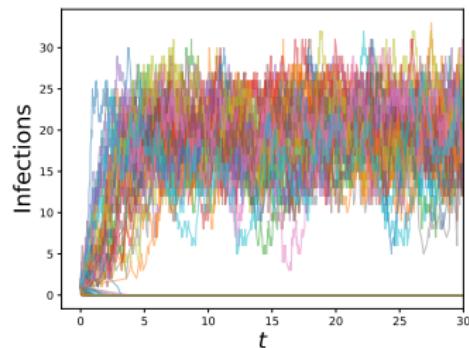
## SIR observations

- ▶ 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.

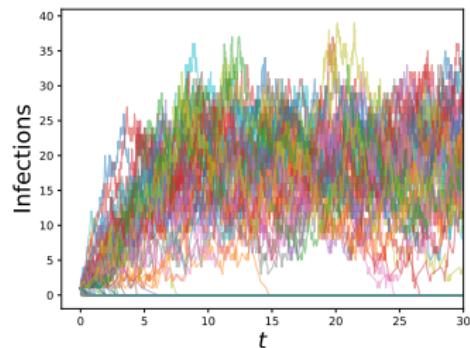
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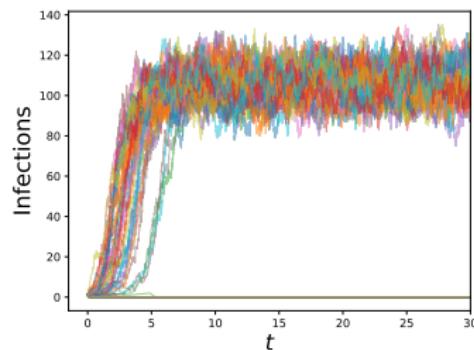


$$N = 50$$

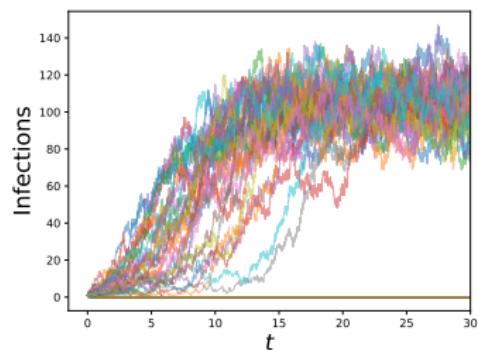
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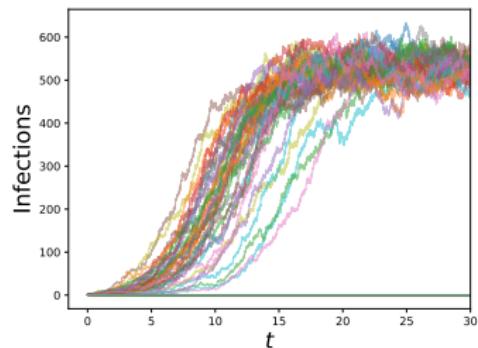
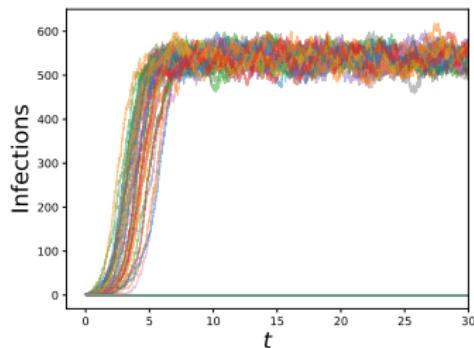
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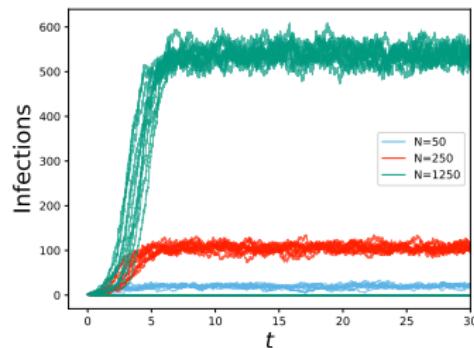


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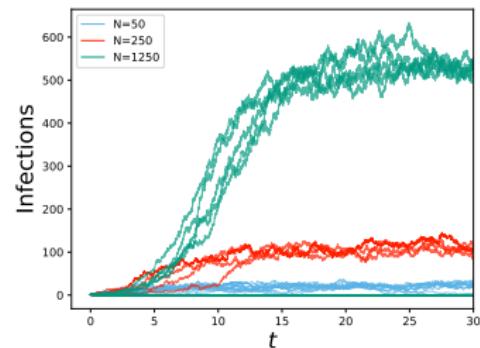
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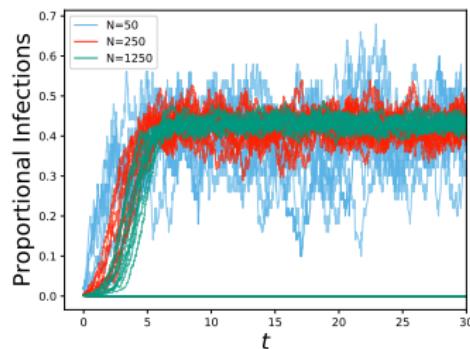
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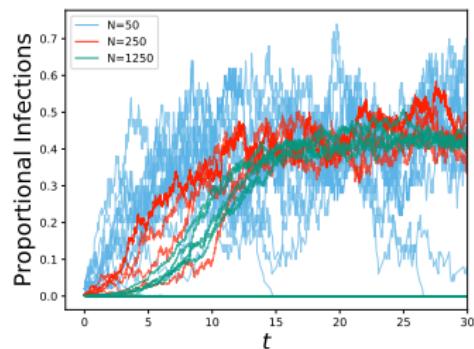
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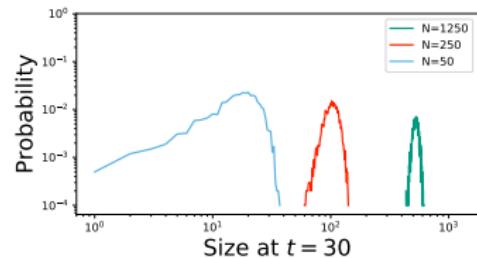
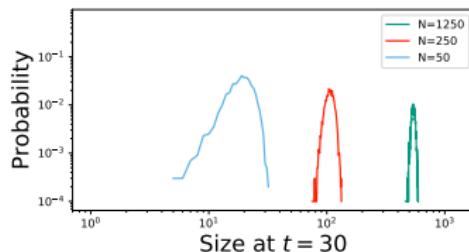
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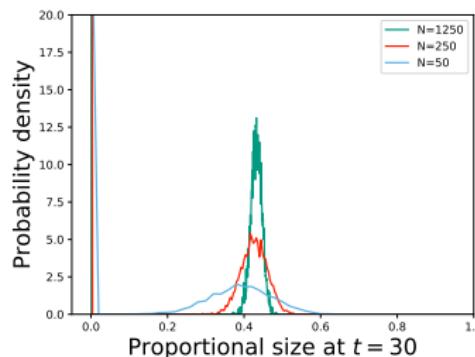
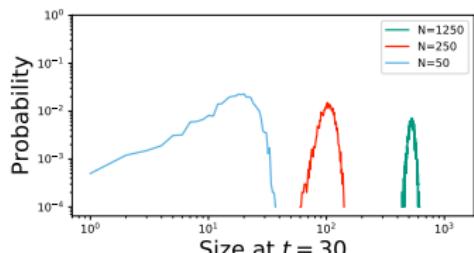
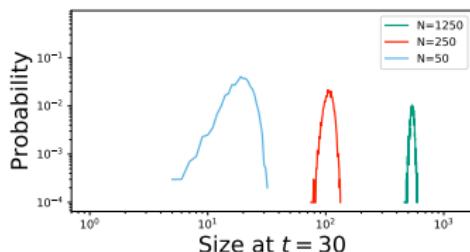


# Stochastic simulation — SIS on network case

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

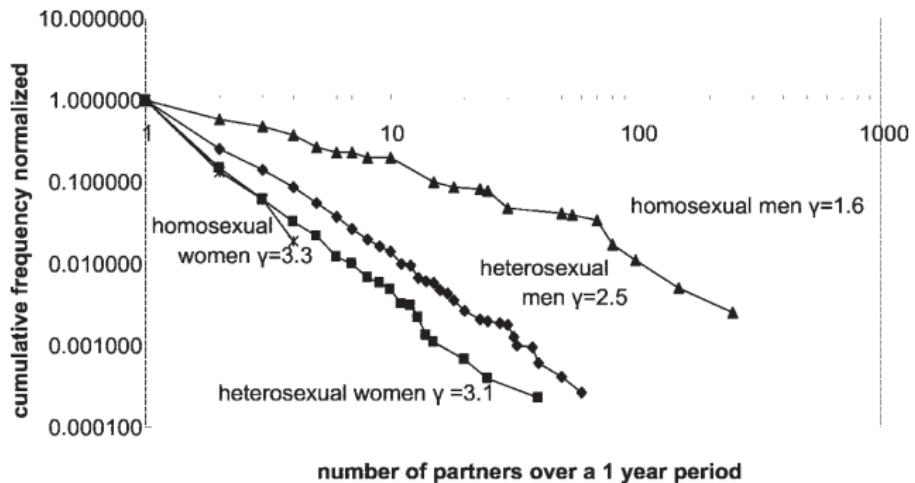
Impact of network properties

Deriving equations

References

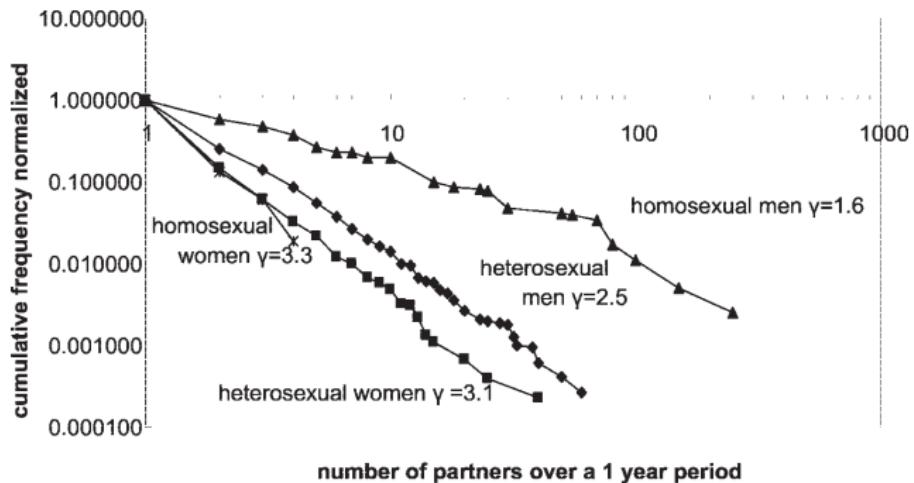
# Degree distribution

From [1]:



# Degree distribution

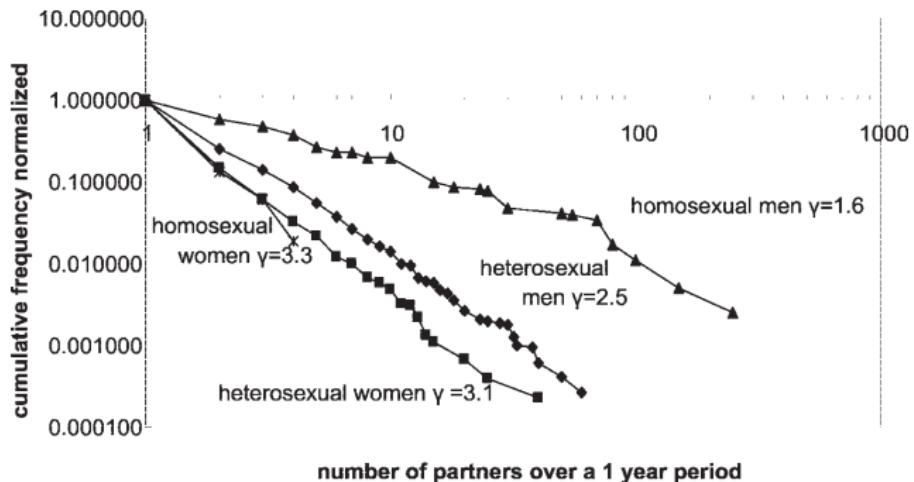
From [1]:



Impact on  $\mathcal{R}_0$ :

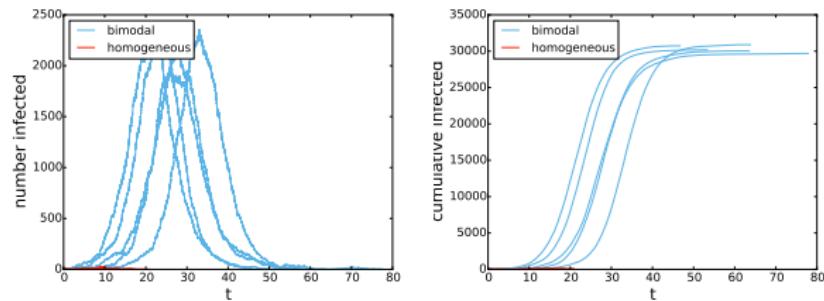
# Degree distribution

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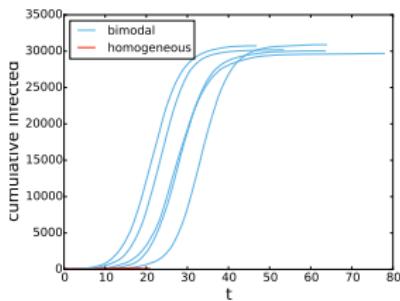
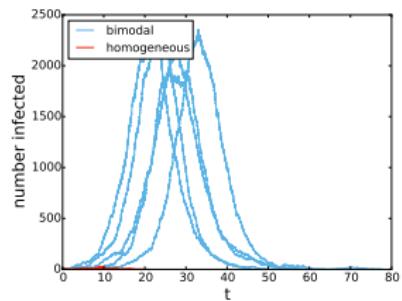
Impact on  $\mathcal{R}_0$ : Holding  $\langle K \rangle$  fixed, degree heterogeneity increases  $\mathcal{R}_0$  because of size-biased infection.

# Impact of degree distribution

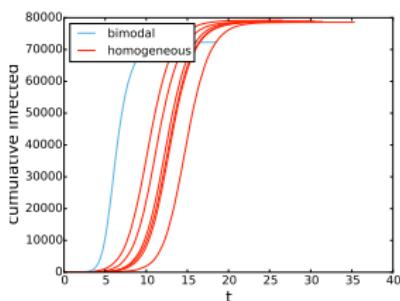
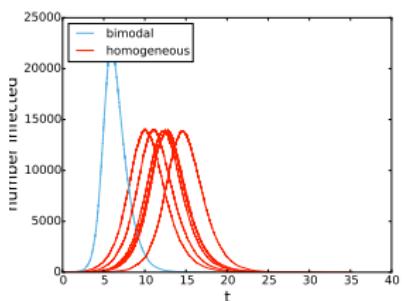


Small transmission rate

# Impact of degree distribution

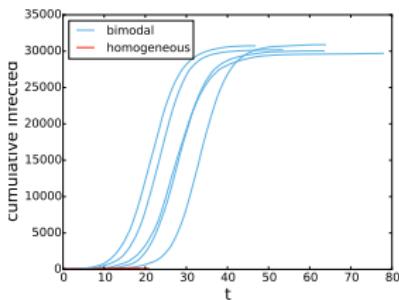
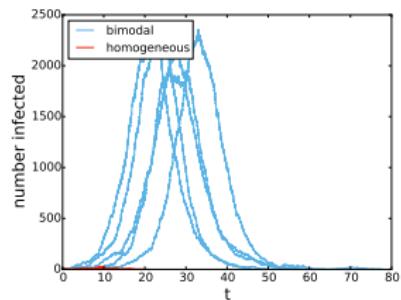


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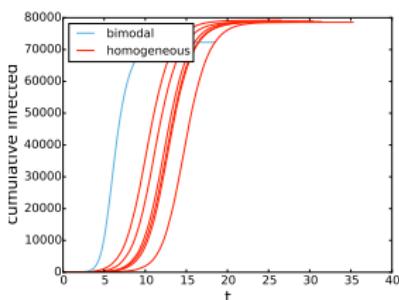
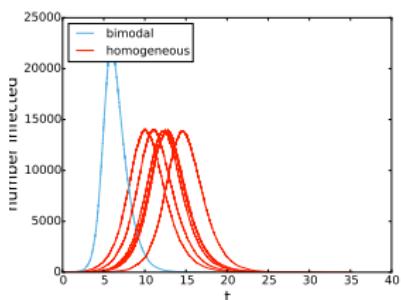


Large transmission rate

# 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

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

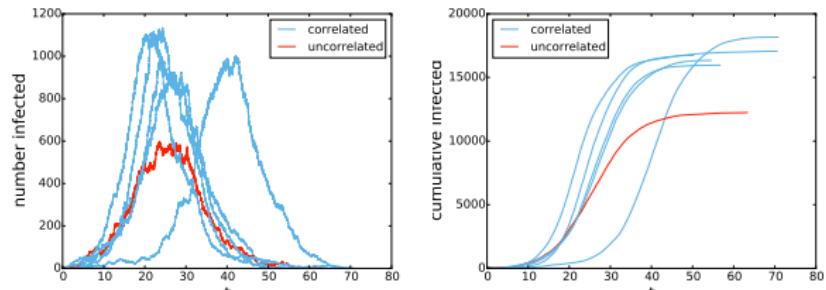
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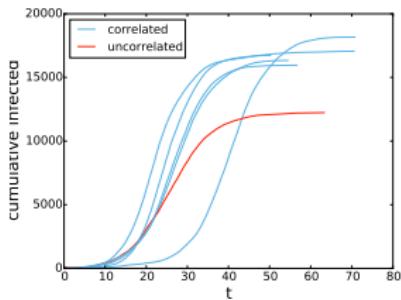
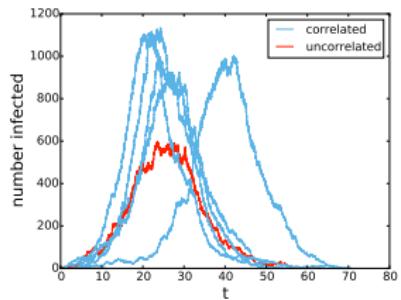
If high degree individuals preferentially contact high degree individuals, impact on  $\mathcal{R}_0$ : Increases it.

# Degree correlations

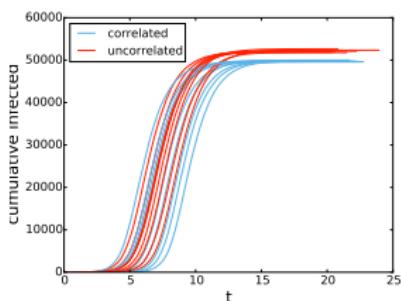
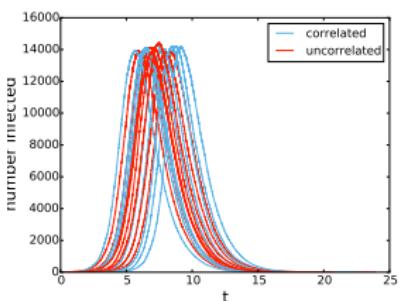


Small transmission rate

# Degree correlations

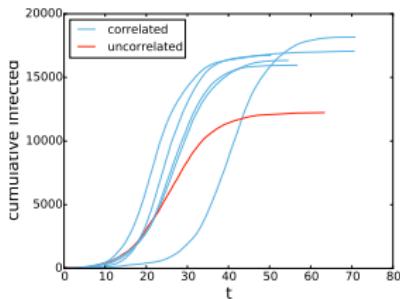
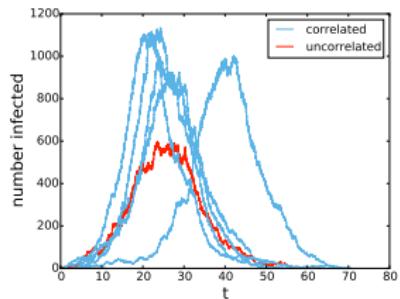


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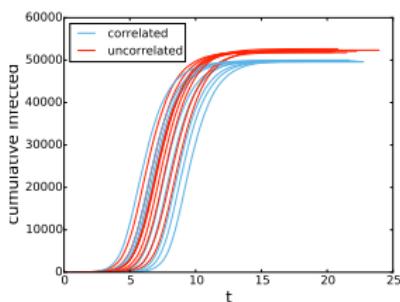
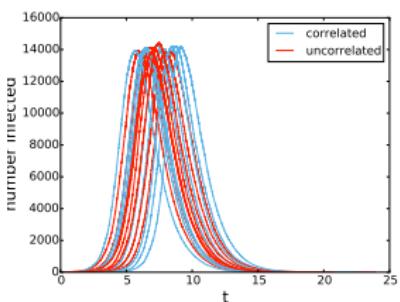


Large transmission rate

# 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.

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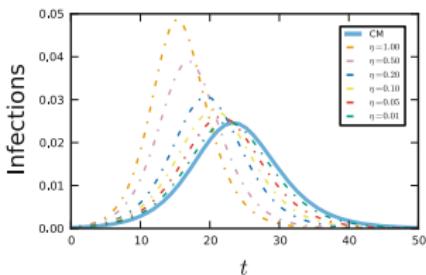
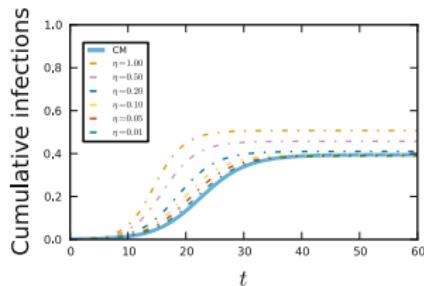
Impact on  $\mathcal{R}_0$ :

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]



( $\eta$  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.

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# Clustering

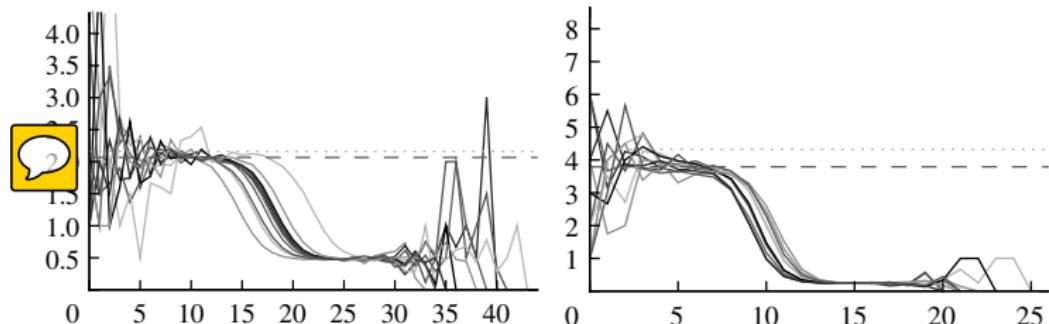
Ratio of successive generation sizes from [4]

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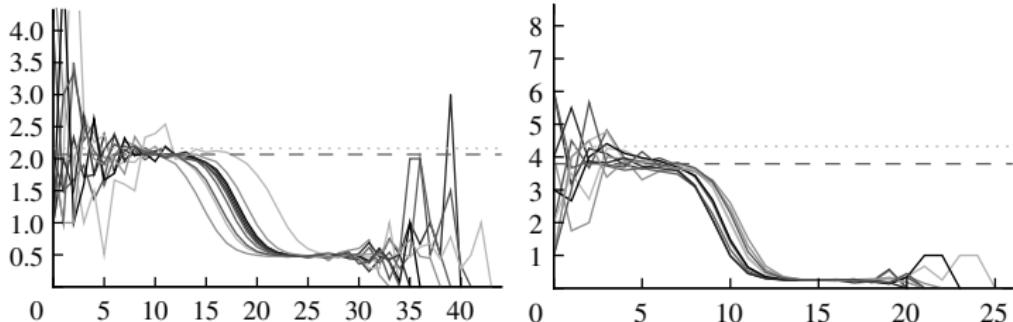
Ratio of successive generation sizes from [4]

lower transmission rate

higher transmission rate



# Clustering



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

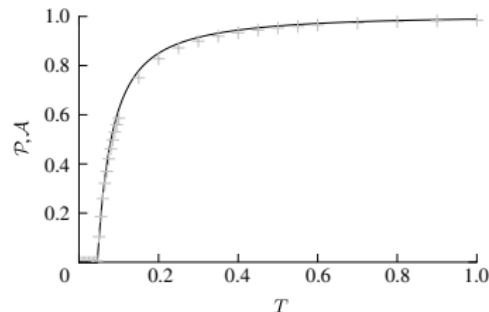
# Clustering

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

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## 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.

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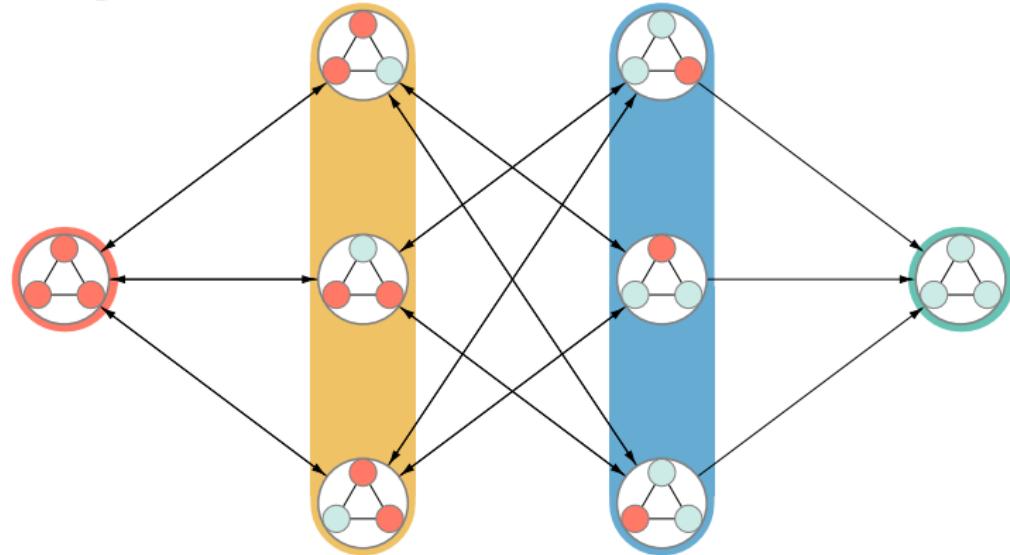
- ▶ If there are  $s$  susceptible and  $i$  infected individuals, the combined infection rate is  $\beta is/N$ . Similarly the combined recovery rate is  $\gamma i$ .
- ▶ In a network, it matters exactly which nodes are susceptible or infected.

## 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  $I$ .

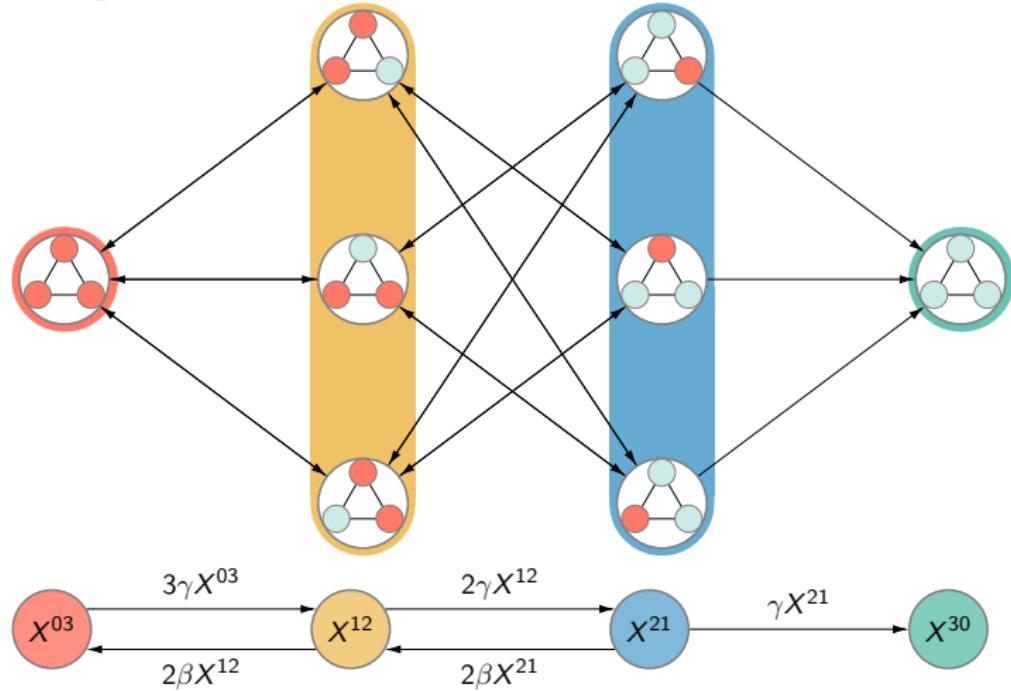
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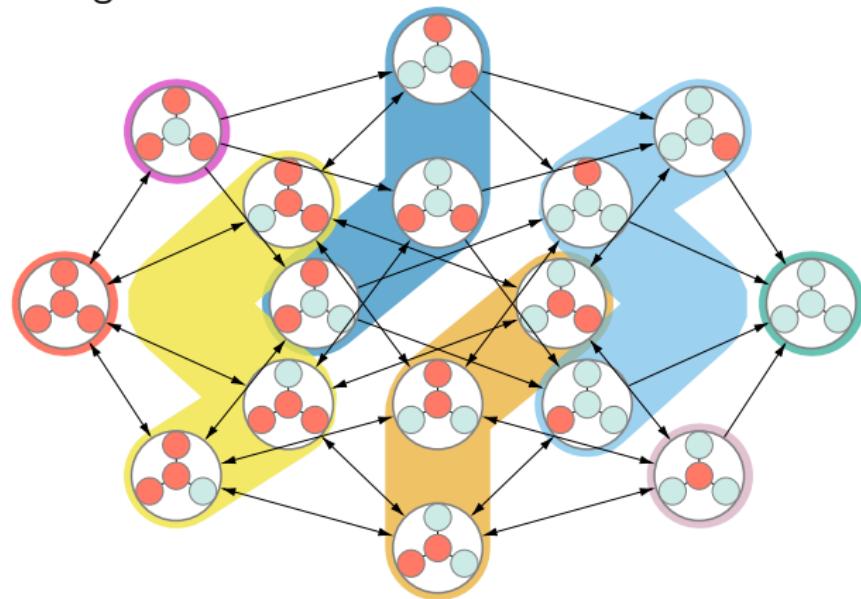


## Star example

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

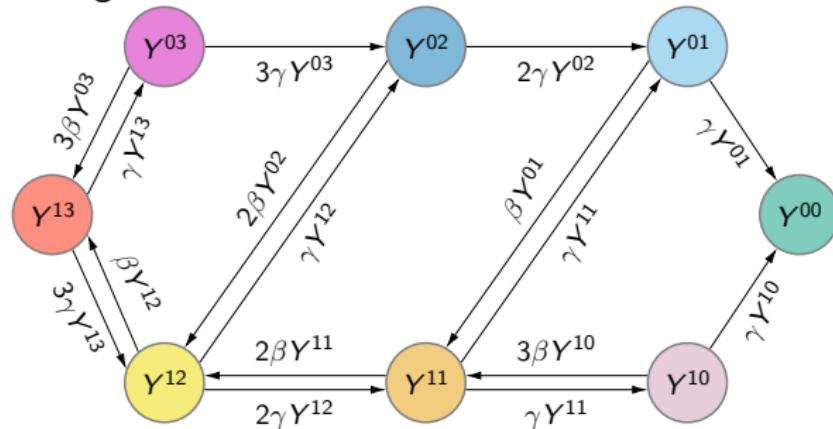
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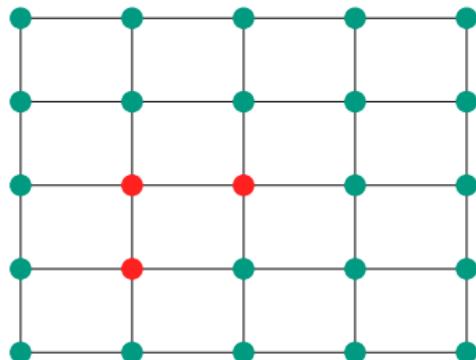


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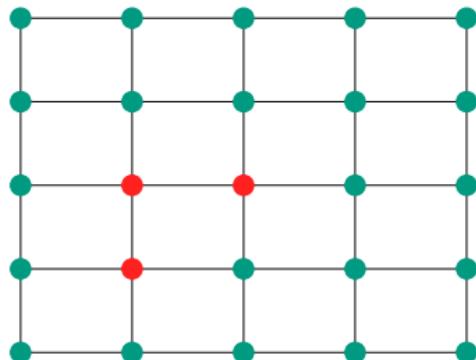
## Towards an analytic model\*



- ▶ How many  $I$  nodes?

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

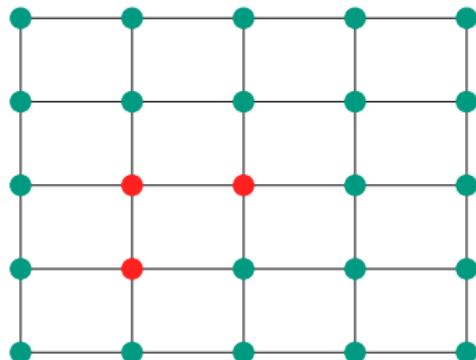
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- ▶ How many  $I$  nodes?  $[I] = 3$ .

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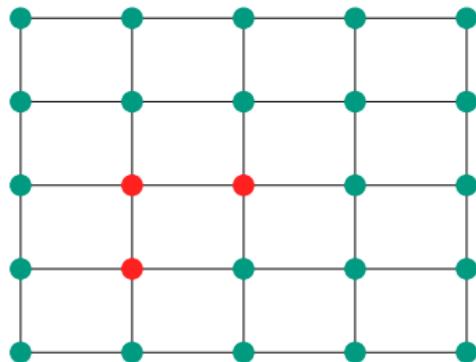
## Towards an analytic model\*



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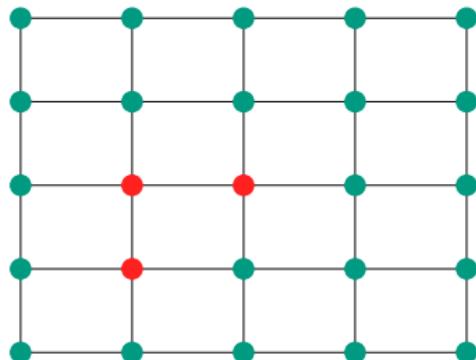
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- ▶ How many  $I$  nodes?  $[I] = 3$ .
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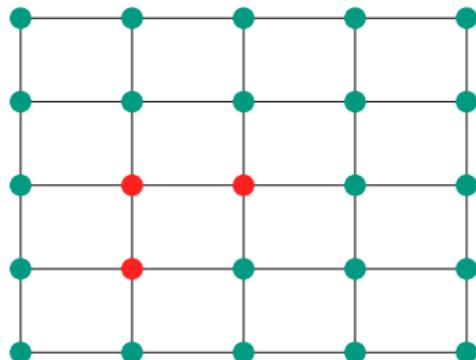
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- ▶ How many  $I$  nodes?  $[I] = 3$ .
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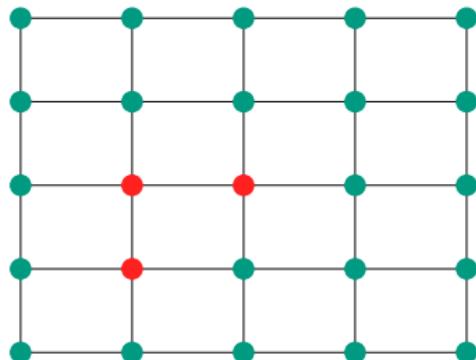
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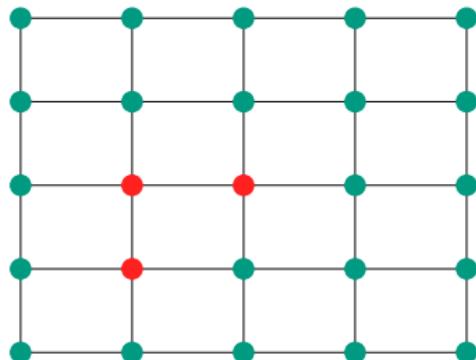
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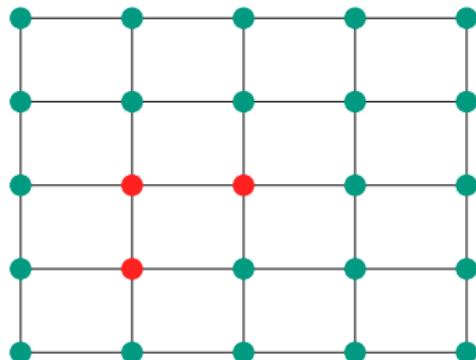
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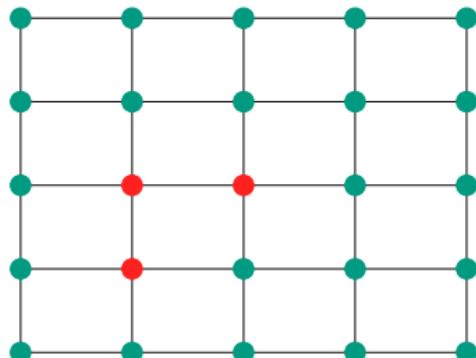
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- ▶ How many  $ISI$  triples?

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- ▶ How many  $SSI$  triples?  $[SSI] = 19$ .
- ▶ How many  $ISI$  triples?  $[ISI] = 2$ .



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

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.

# Finding SIR equations

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

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

$$[\dot{S}I] = \beta[SSI] - \beta[ISI] - \beta[SI] - \gamma[SI]$$

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

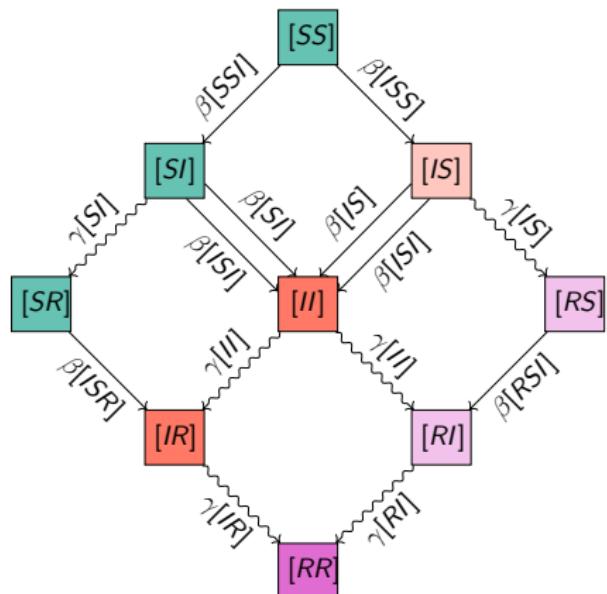
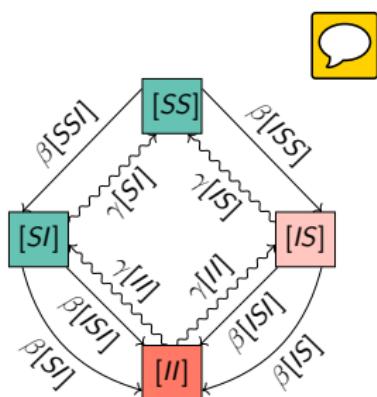
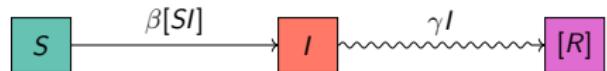
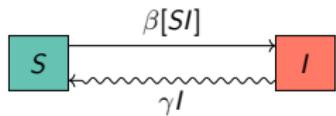
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- ▶ The second term represents the susceptible node in an SI pair being infected by another neighbor.
- ▶ The third term represents the susceptible node in an SI pair being infected by the infected node in the pair.
- ▶ The **fourth** term represents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



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These are equivalent to the Kermack-McKendrick equations

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

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.

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When are these assumptions appropriate?

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

Introduction

Sample stochastic simulations

Impact of network properties

Deriving equations

References

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