

Epidemics in Networks

Part 2 — Compartmental Disease Models

Joel C. Miller & Tom Hladish

18–20 July 2018

Introduction to Compartmental Models

Dynamics

\mathcal{R}_0

Epidemic Probability

Epidemic size

Review

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
- ▶ $I(t)$

Simple Compartmental Models

The most common models are compartmental models.

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

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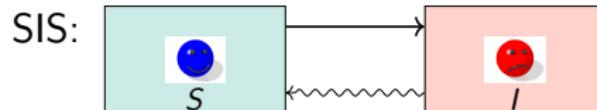
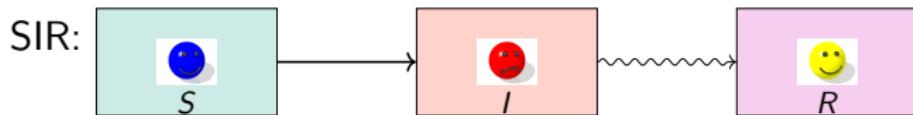
- ▶ Every individual is average.
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Throughout:

$$S + I + R = N$$

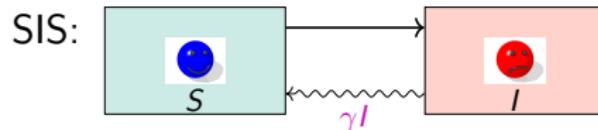
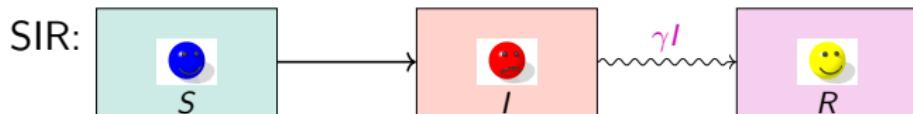
[That is, we look at absolute number rather than proportions of the population. Unfortunately this is standard across much of the field and it causes our equations and initial conditions to be littered with N s that do nothing to help us understand what is happening. I haven't used this convention in past years' notes, so there may be typos occasionally. I've given up fighting this.]

Continuous time: Kermack–McKendrick



Assumptions:

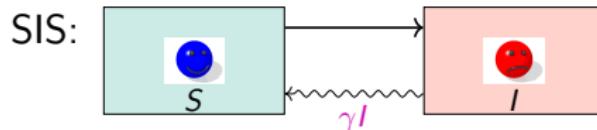
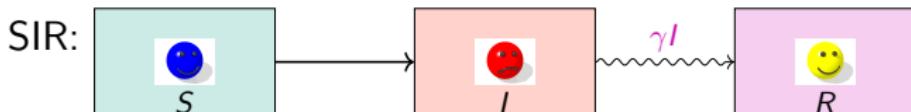
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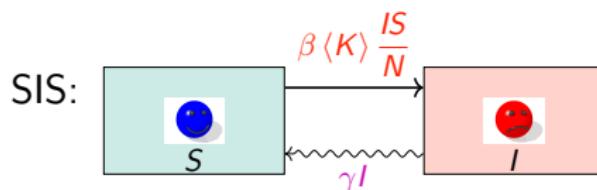
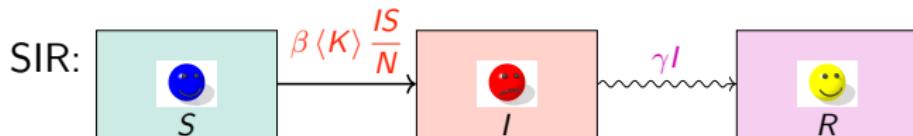
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Assumptions:

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

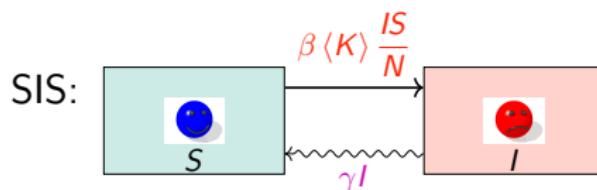
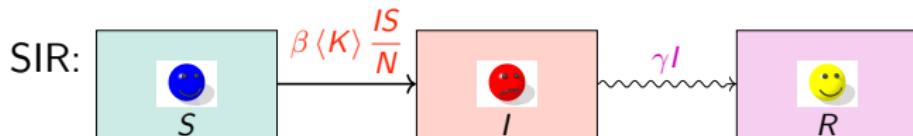
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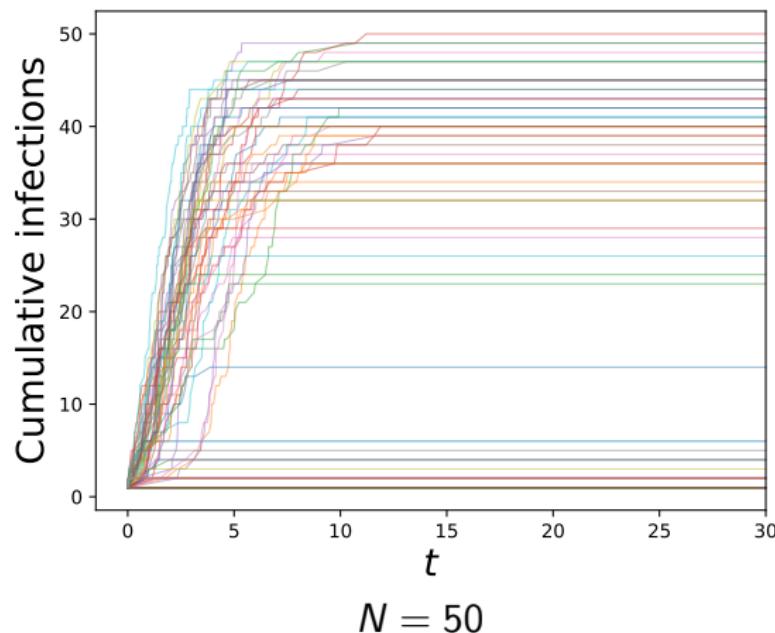
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- ▶ The proportion of transmissions that go to susceptible individuals is S/N .
- ▶ An implicit assumption is that each interaction is with a new

Stochastic simulation — SIR case

What behavior do we see with $\beta \langle K \rangle = 2$, $\gamma = 1$?

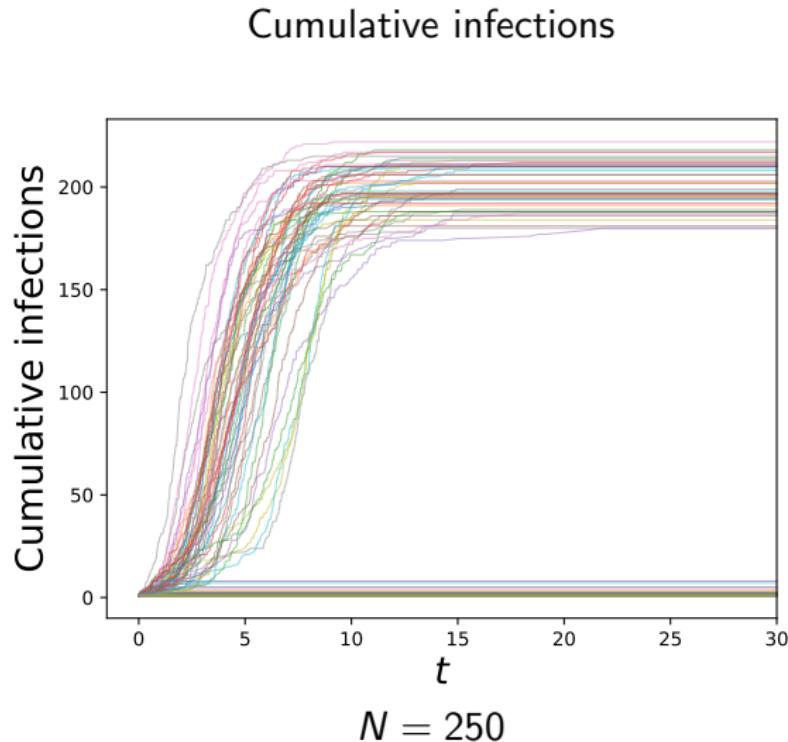
Cumulative infections



$$N = 50$$

Stochastic simulation — SIR case

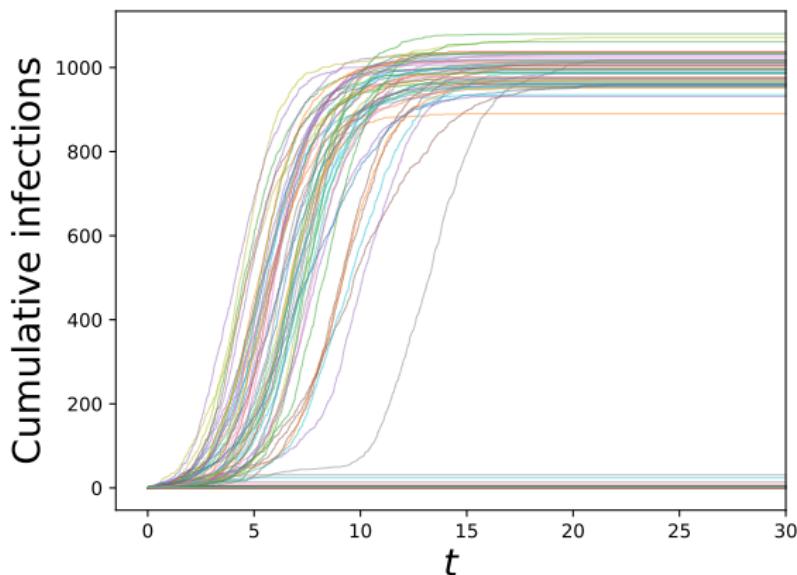
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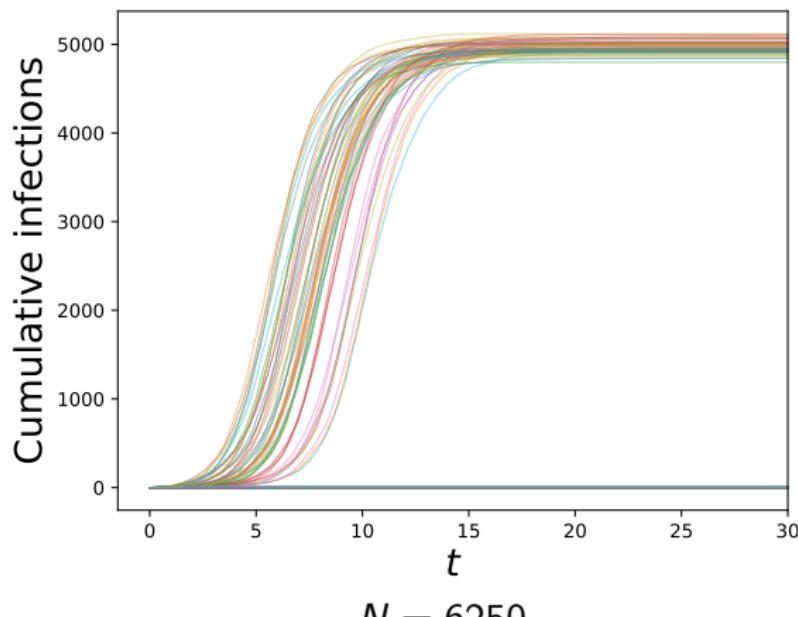


$$N = 1250$$

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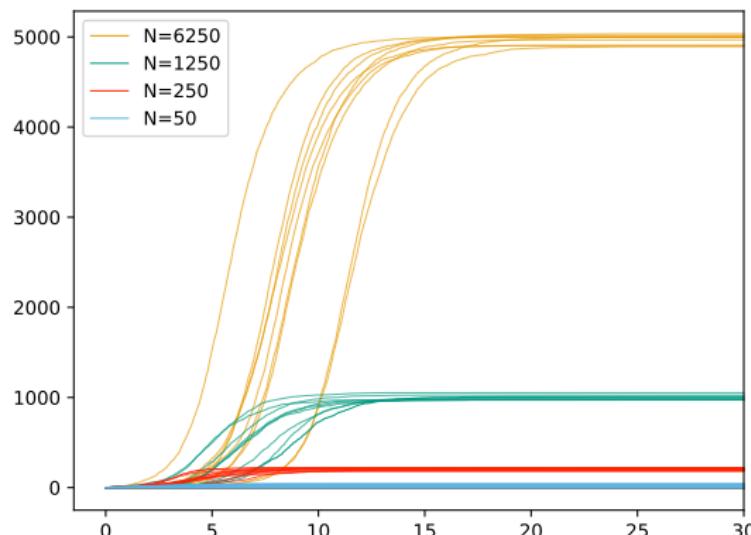
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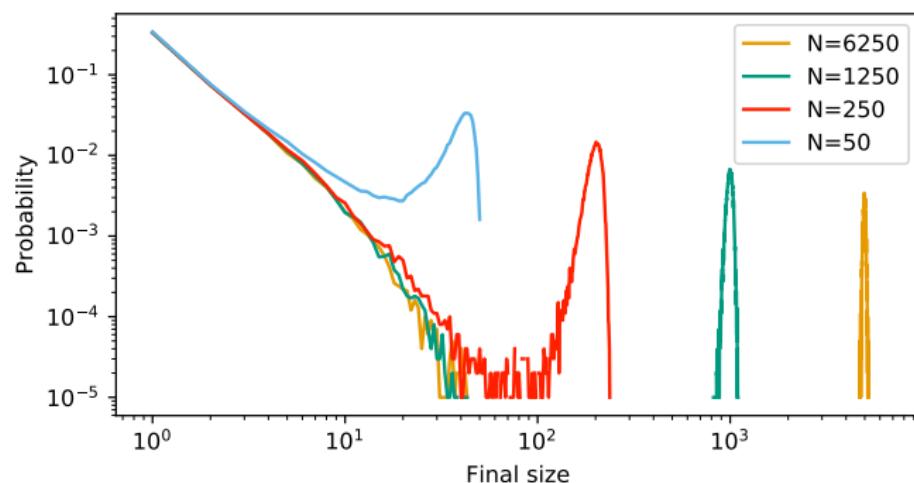
The distinction between small and large outbreaks becomes clear as N increases.

Stochastic simulation — SIR case

What does the final size distribution look like?

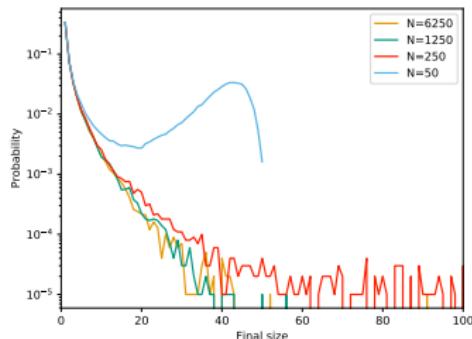
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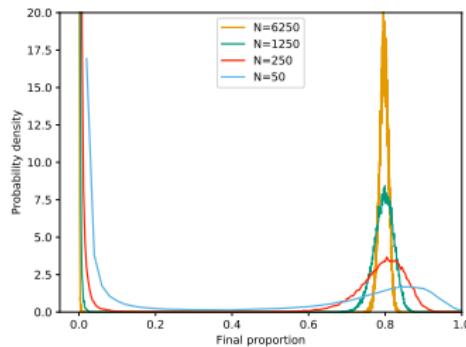
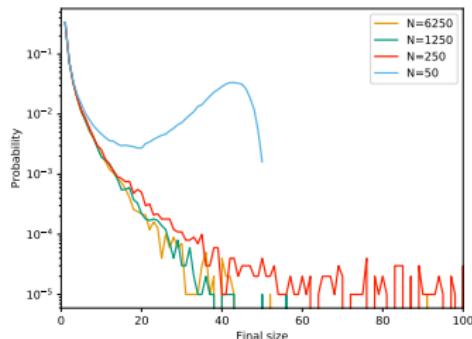


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Small outbreaks affect the same **number** of individuals.

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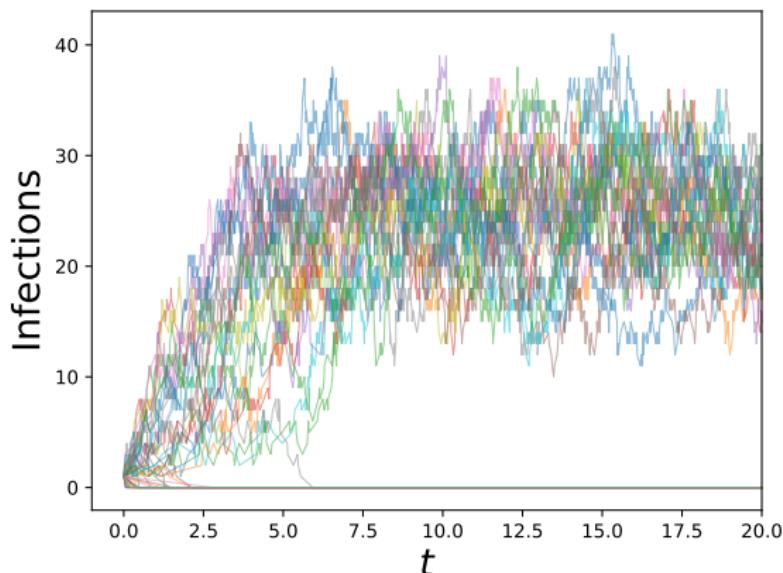
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Epidemics affect approximately the same proportion of the population

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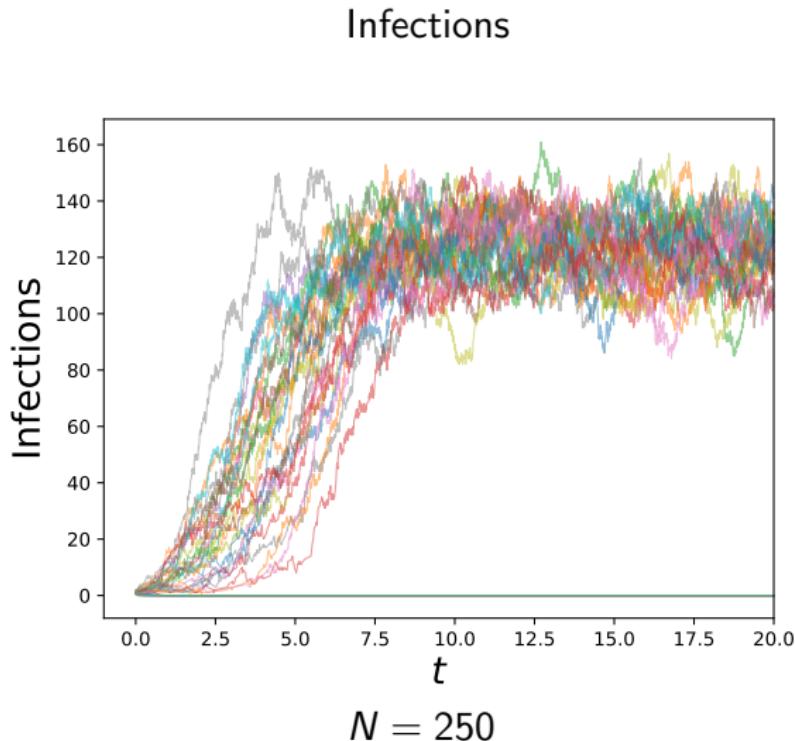
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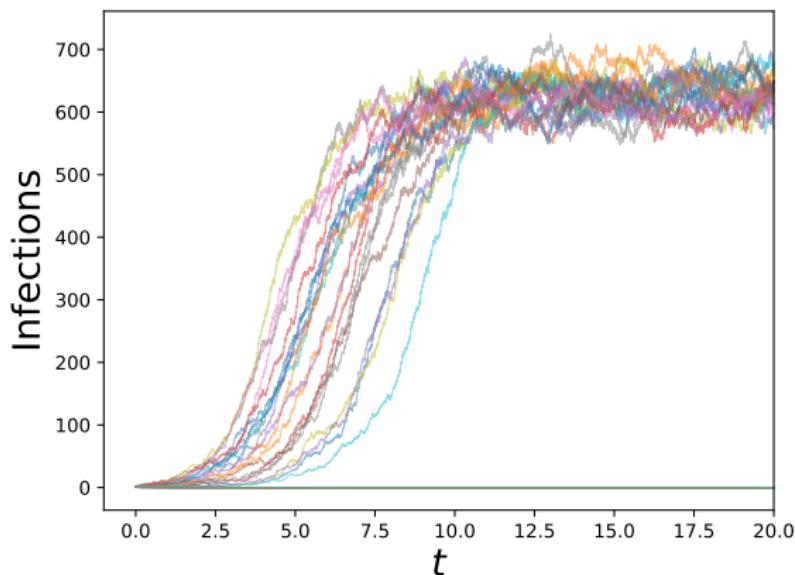
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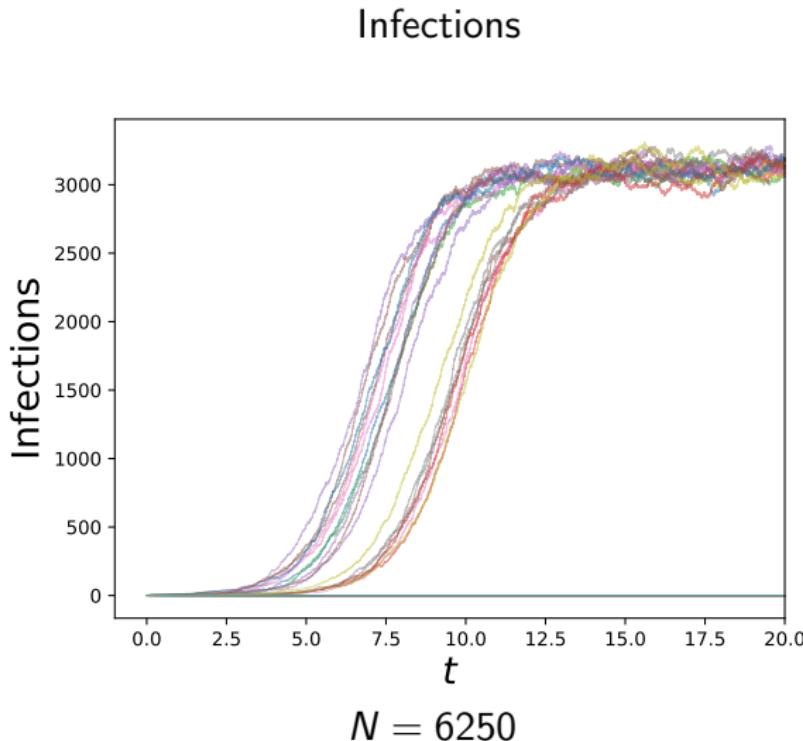
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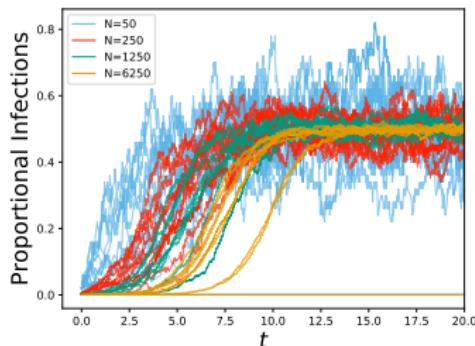
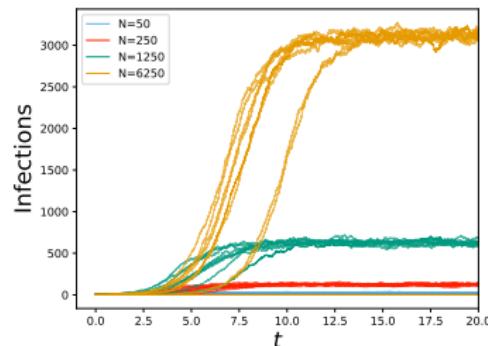
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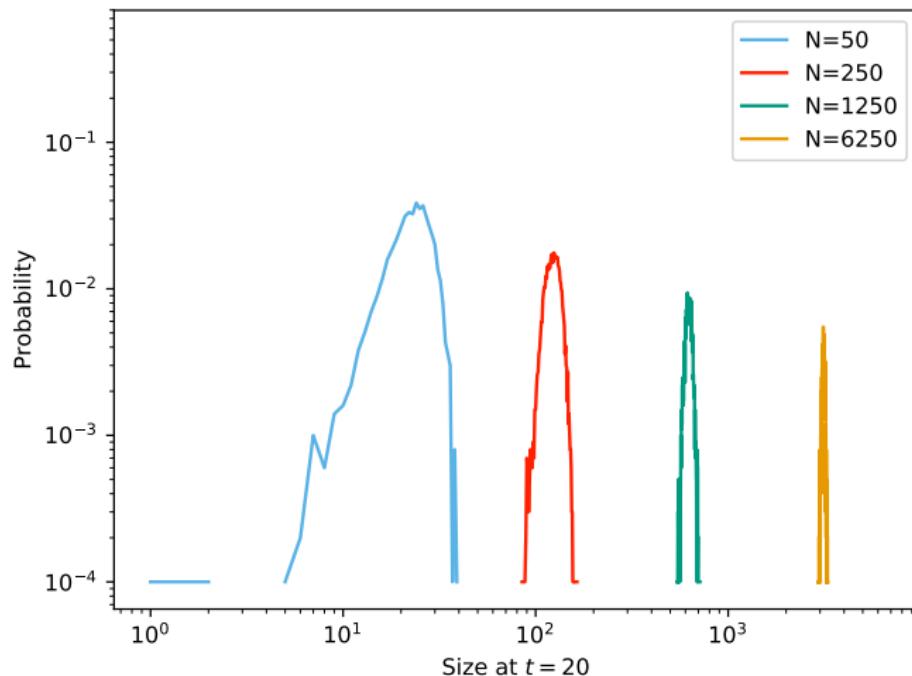
Typically extinction occurs either early or after exponentially long time. The **proportion** infected at equilibrium is approximately the same for different population sizes.

Stochastic simulation — SIS case

What does the “equilibrium” distribution look like?

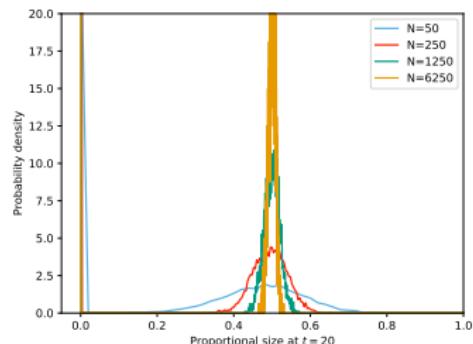
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What does the “equilibrium” distribution look like?



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The equilibrium proportion infected is about the same for different population sizes.

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\mathcal{R}_0

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Review

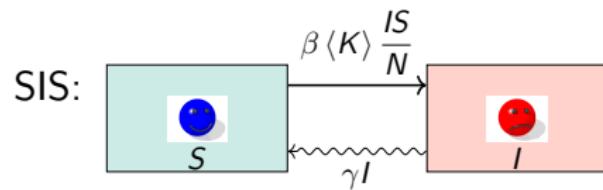
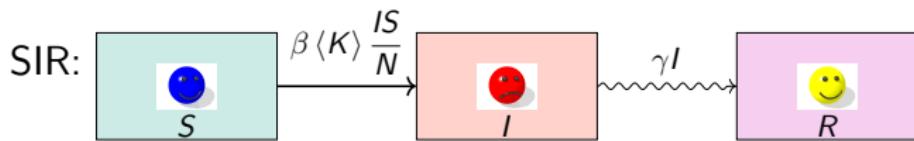
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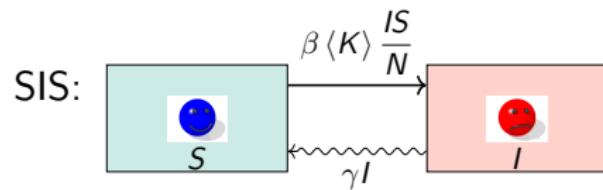
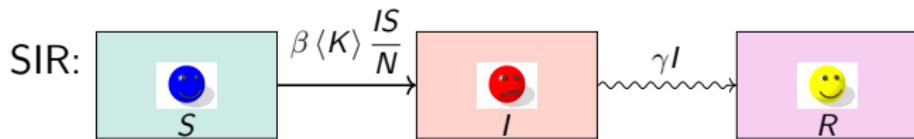
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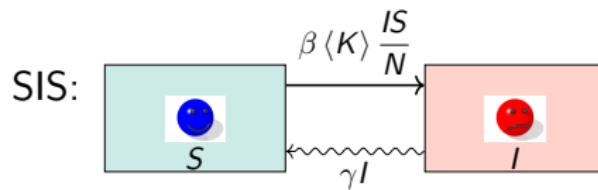
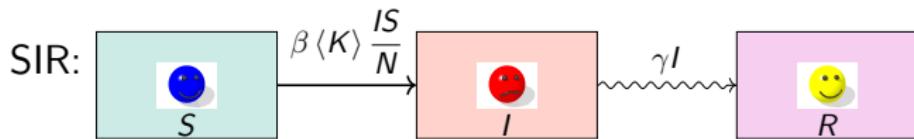
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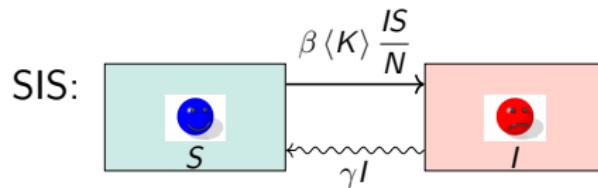
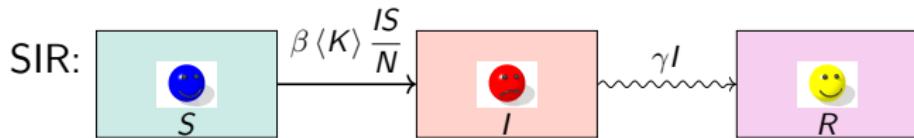
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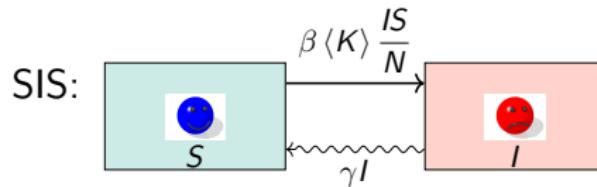
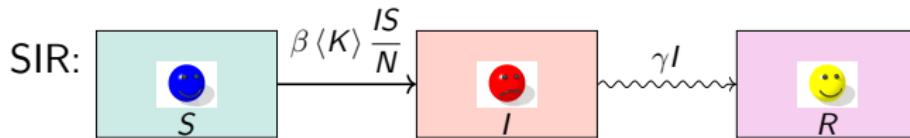
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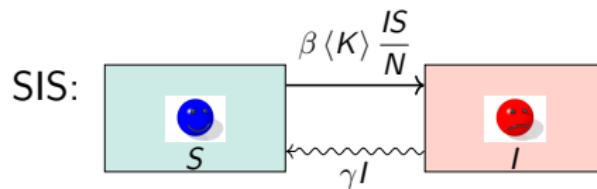
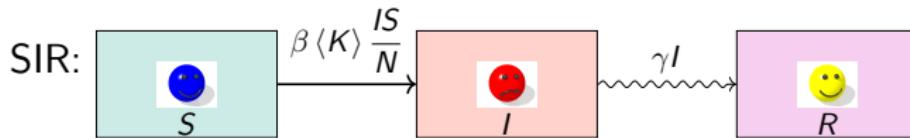
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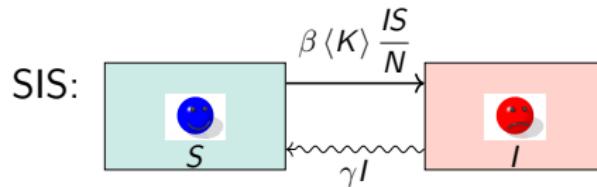
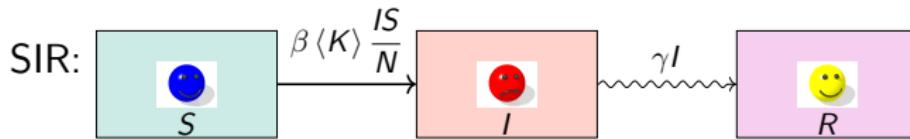


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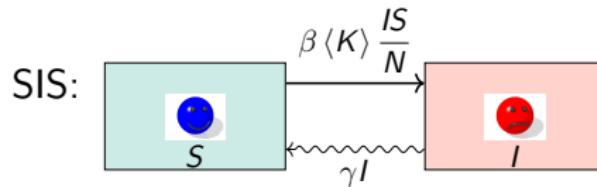
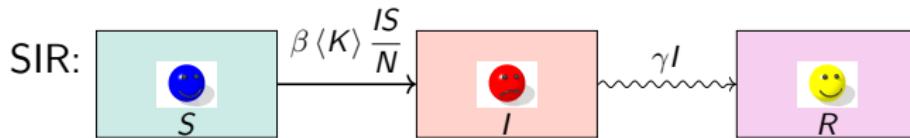


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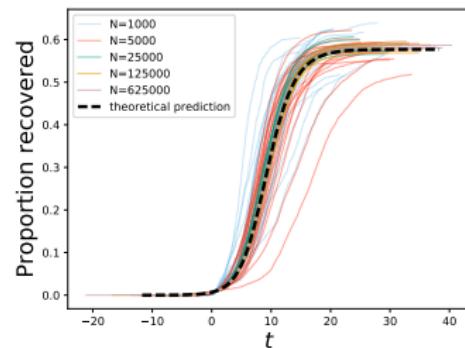
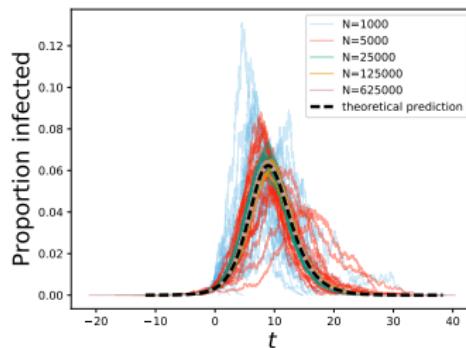
$$\dot{S} = -\beta \langle K \rangle IS/N + \gamma I$$

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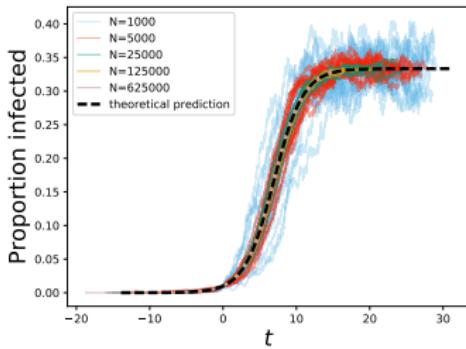
Comparison

We compare our differential equations predictions with simulations having transmission rate $\beta \langle K \rangle IS/N$ and recovery rate γI .

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

\mathcal{R}_0 calculation

The calculation of \mathcal{R}_0 is the same for SIR and SIS:

- ▶ Under our assumptions, every interaction an infected individual has is with a new randomly chosen individual.
- ▶ Early in the epidemic, the probability it is with a susceptible individual is $S/N \approx 1$.
- ▶ The typical infection duration is $1/\gamma$.
- ▶ The transmission rate during infection is $\beta \langle K \rangle$.
- ▶ So the number of new infections is $\mathcal{R}_0 = \beta \langle K \rangle / \gamma$.

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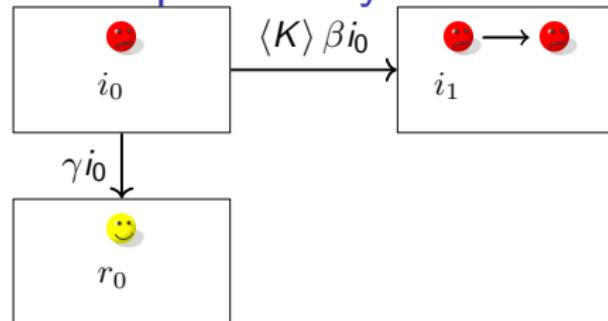


i_0

Consider an individual u who becomes infected at time $t = t_0$.

Define $i_m(t)$ and $r_m(t)$ to be the probability u has transmitted to m individuals and is infectious or recovered.

Epidemic probability

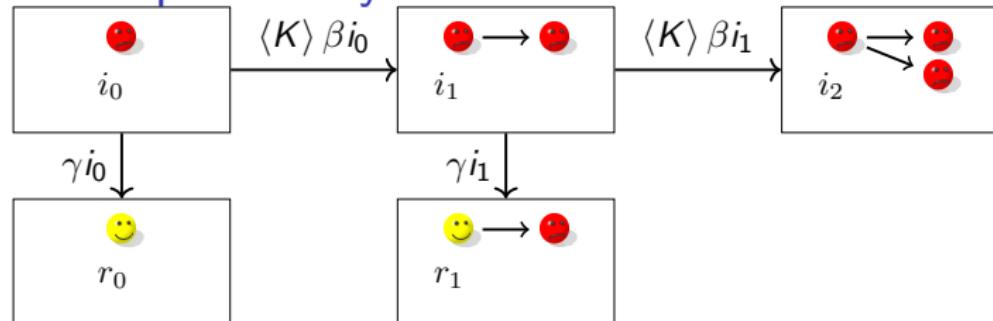


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- ▶ The probability of transmitting at least once before recovering is $\frac{\langle K \rangle \beta}{\langle K \rangle \beta + \gamma}$.

Epidemic probability

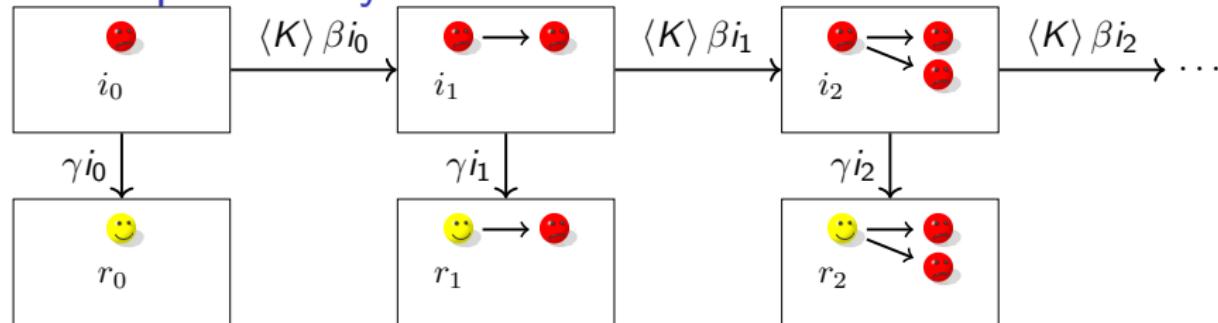


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- ▶ The probability the first m events are transmissions is $\left[\frac{\langle K \rangle \beta}{\langle K \rangle \beta + \gamma} \right]^m$.
- ▶ For exactly m transmissions before recovery it is

$$r_m(\infty) = \left(\frac{\langle K \rangle \beta}{\langle K \rangle \beta + \gamma} \right)^m \frac{\gamma}{\langle K \rangle \beta + \gamma}$$

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$$f(x) = \sum_m r_m(\infty) x^m = \frac{\gamma}{(\langle K \rangle \beta + \gamma) \left(1 - \frac{\langle K \rangle \beta x}{\langle K \rangle \beta + \gamma}\right)} = \frac{\gamma}{\langle K \rangle \beta (1 - x) + \gamma}$$

- ▶ The probability of extinction after the first individual is the probability it recovers without transmitting.

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- ▶ The probability of reaching no further than the first generation of offspring is the probability that none of the first generation individuals causes a transmission.

$$\sum_m r_m(\infty) [f^{(0)}]^m = f(f(0)) = f^{(2)}(0)$$

[The superscript with parentheses denotes function iteration]

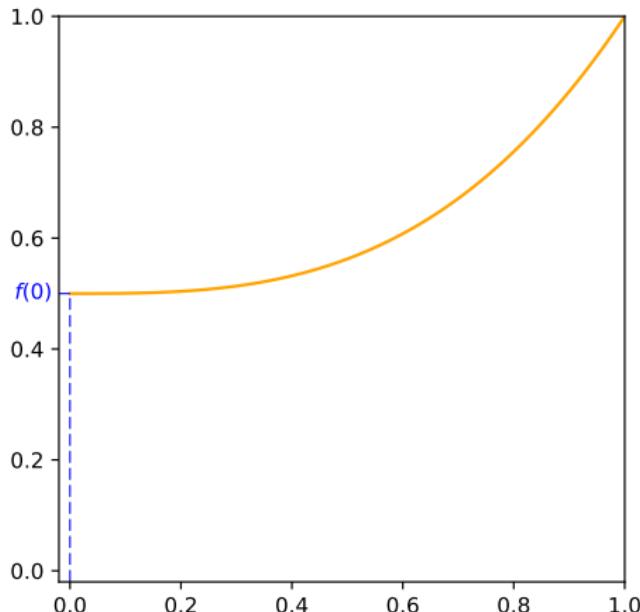
- ▶ The probability of reaching no further than generation g is the probability that none of the first generation individuals causes a transmission chain of length longer than $g - 1$.

$$\sum_m r_m(\infty) [f^{(g-1)}(0)]^m = f^{(g)}(0)$$

- ▶ The probability the outbreak goes extinct in a finite number of generations (in an infinite population) is $\lim_{g \rightarrow \infty} f^{(g)}(0)$.

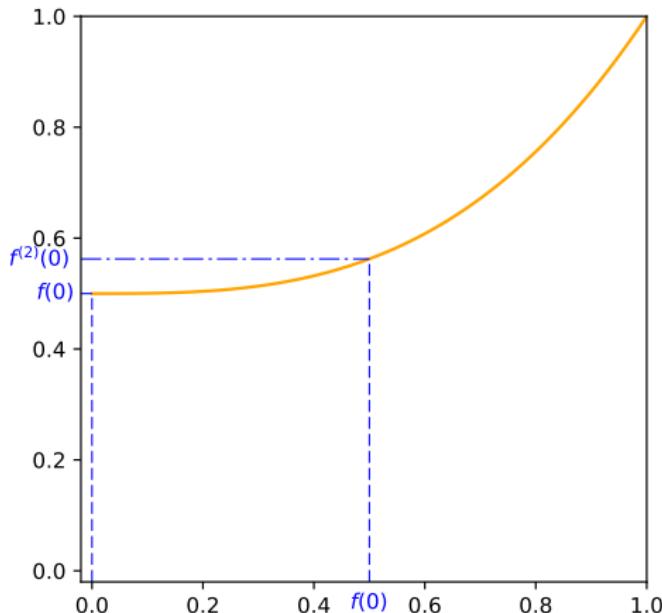
Cobweb diagrams

Consider $f(x) = \frac{1+x^3}{2}$. We can keep iterating f on 0.



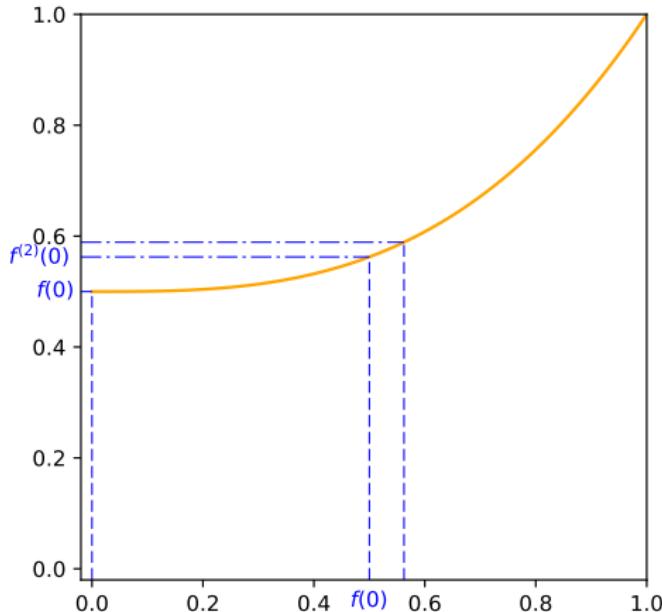
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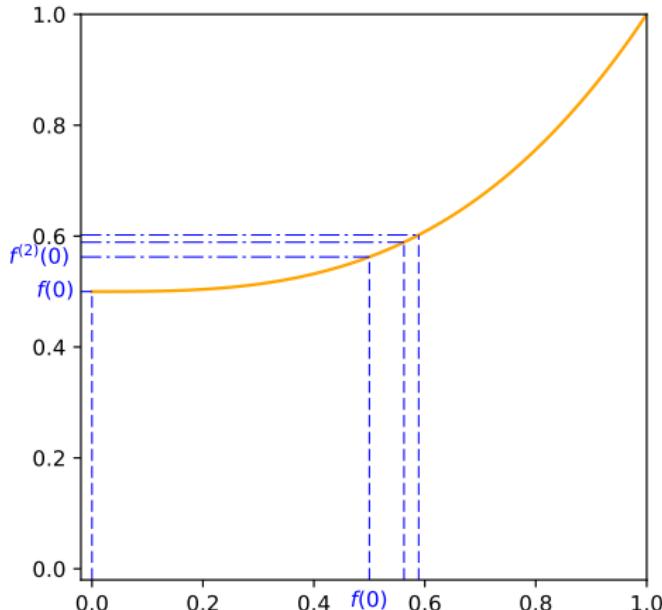
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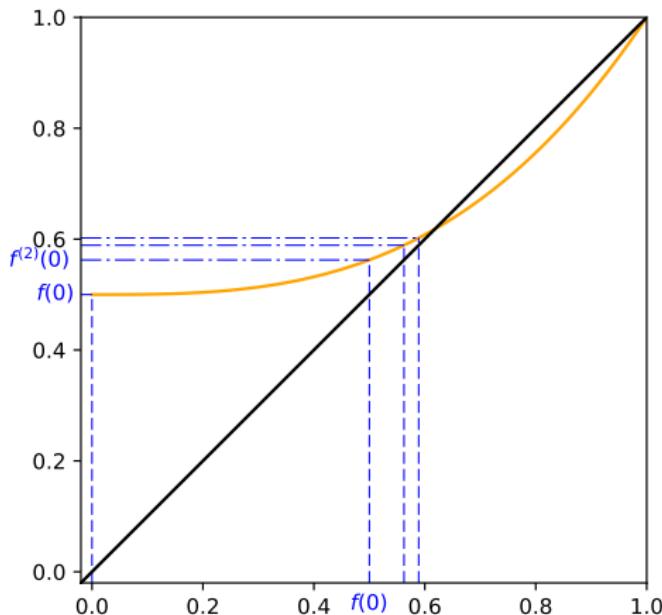
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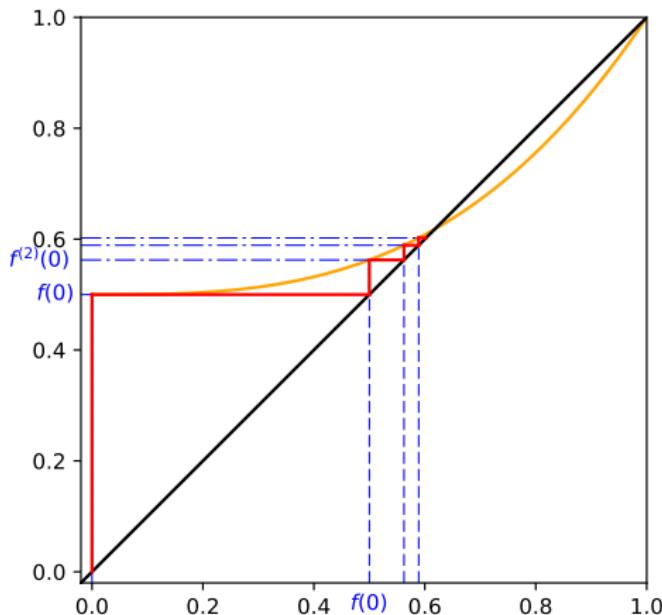
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Introduction to Compartmental Models

Dynamics

\mathcal{R}_0

Epidemic Probability

Epidemic size

Review

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 equilibrium size

- The SIS equations are

$$\dot{S} = -\beta \langle K \rangle \frac{IS}{N} + \gamma I$$

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

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- ▶ If $\gamma > \beta \langle K \rangle$ the disease must die out.
- ▶ If $\gamma < \beta \langle K \rangle$ at equilibrium the disease has died out or reaches an equilibrium having a fraction $\gamma / \beta \langle K \rangle$ susceptible and the rest infected.

Alternate equations for SIR

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Alternate equations for SIR

Before deriving the final size relation, we derive an alternate system of equations. The system has some important properties:

- ▶ There is a single governing ODE.
- ▶ It will make the final size relation trivial.
- ▶ It has a useful alternate interpretation that gives insight into equations for disease on networks.

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$$\frac{d}{dt} Se^\xi = \dot{S}e^\xi + S\dot{\xi}e^\xi = 0$$

where $\xi(0) = 0$

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- ▶ Finally

$$I = N - R - S = N - \frac{N\xi}{\mathcal{R}_0} - R(0) - S(0)e^{-\xi}$$

SIR final size

- Our full equations are thus

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- ▶ Assuming $R(0) \approx 0$ and rearranging gives

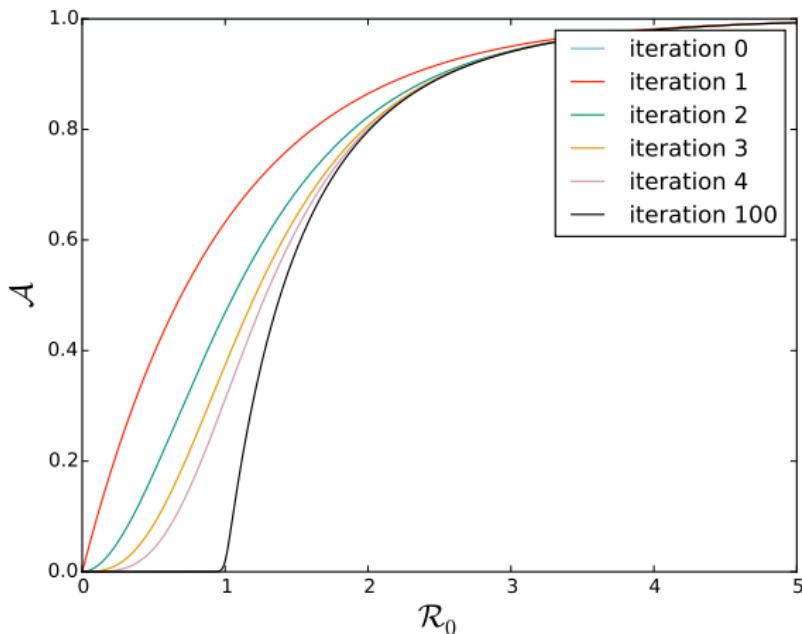
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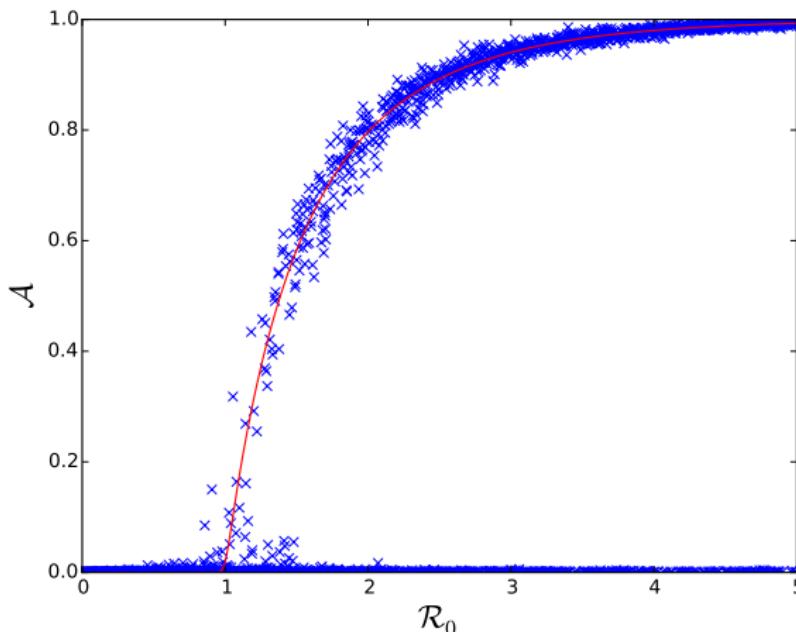
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We can solve this iteratively, starting from a guess $\mathcal{A} = 1$.

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The results are in good agreement with simulation (subject to the simulation satisfying the assumptions made in the equation derivation).

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We will give a direct derivation of these new equations, and later use this approach to derive SIR equations for diseases in networks.

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- ▶ So

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- ▶ Thus $\hat{\xi}$ satisfies the same relations as ξ , and we can conclude that $\hat{\xi} = \xi$.

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\mathcal{R}_0

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Review

Review

- ▶ We can write down fairly simple equations for mass-action mixing of SIS and SIR disease.
- ▶ The sizes of epidemics are proportional to the population size.
- ▶ The sizes of small outbreaks are independent of (large enough) population size.
- ▶ We can calculate epidemic probability and final size through iteration.
- ▶ The mass-action SIR model can be reduced to a single ODE.