

Epidemics in Networks

Part 2 — Compartmental Disease Models

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17–19 July 2017

Introduction to Compartmental Models

Dynamics

\mathcal{R}_0

Epidemic Probability

Epidemic size

References

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 interaction of u is with a randomly chosen other individual.

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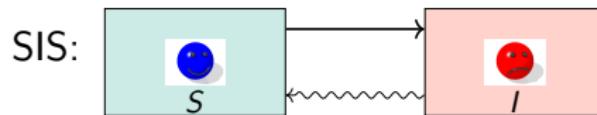
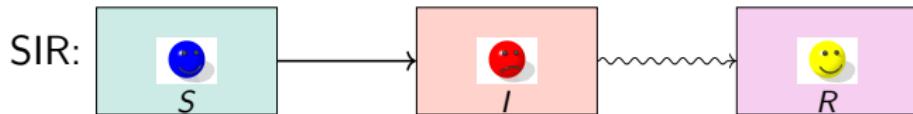
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Throughout:

$$S + I + R = N$$

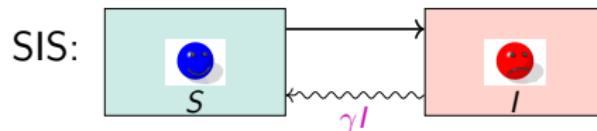
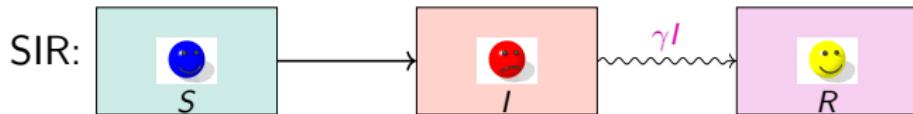
[That is, we look at absolute number rather than proportions of the population. Unfortunately this is standard across much of the field and it causes our equations and initial conditions to be littered with N s that do nothing to help us understand what is happening. I haven't used this convention in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

Continuous time: Kermack–McKendrick



Assumptions:

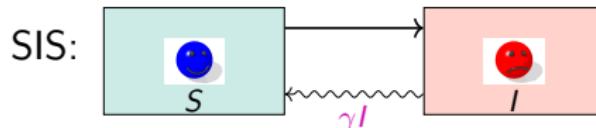
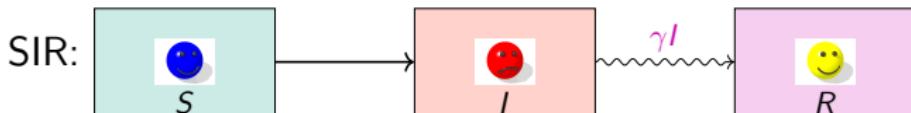
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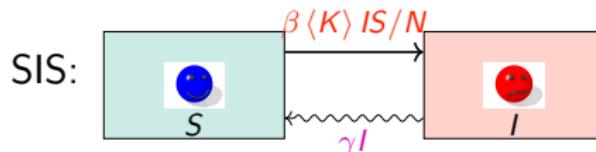
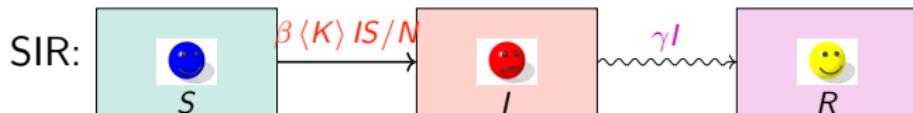
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- ▶ Individuals **recover** with rate γ .
- ▶ Infected individuals **transmit to others** at rate $\beta \langle K \rangle$ (usually we combine these into a single parameter).
 - ▶ β represents the transmission rate of the disease per partnership.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

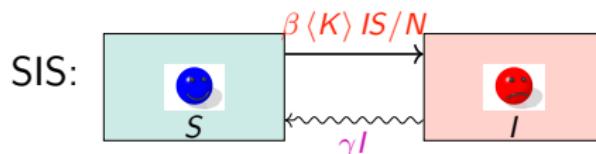
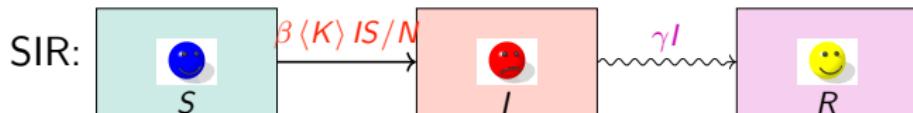
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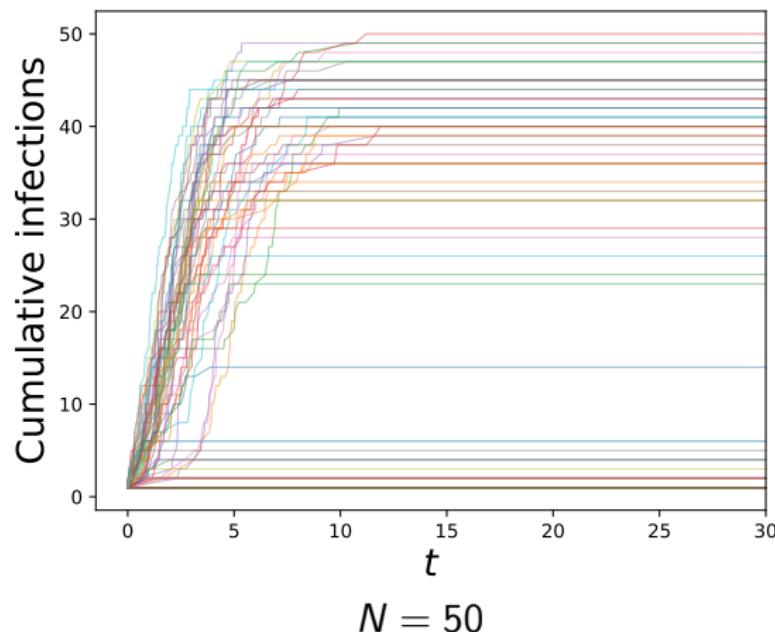
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- ▶ An implicit assumption is that each interaction is with a new randomly infected individual.

Stochastic simulation — SIR case

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

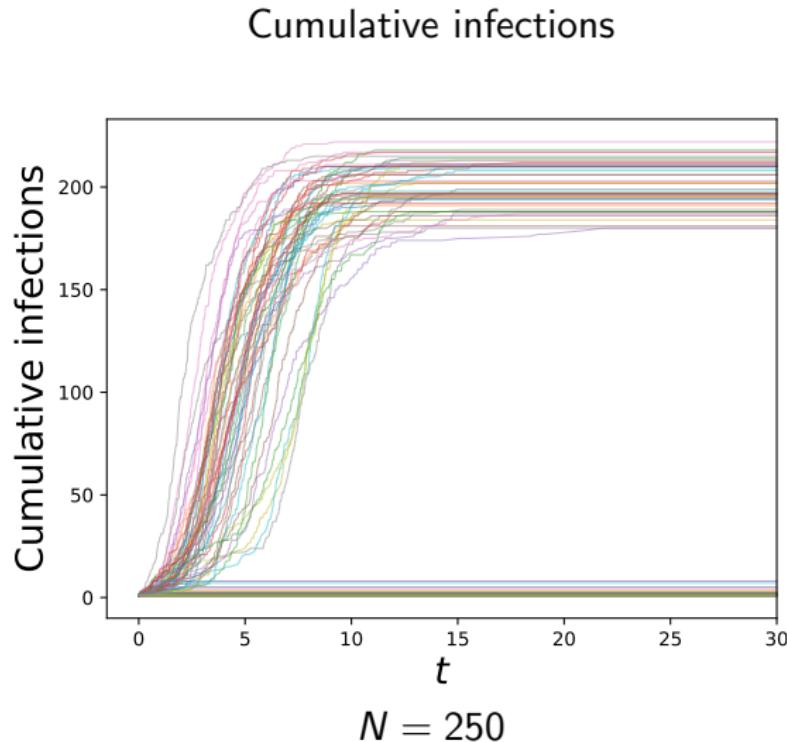
Cumulative infections



$$N = 50$$

Stochastic simulation — SIR case

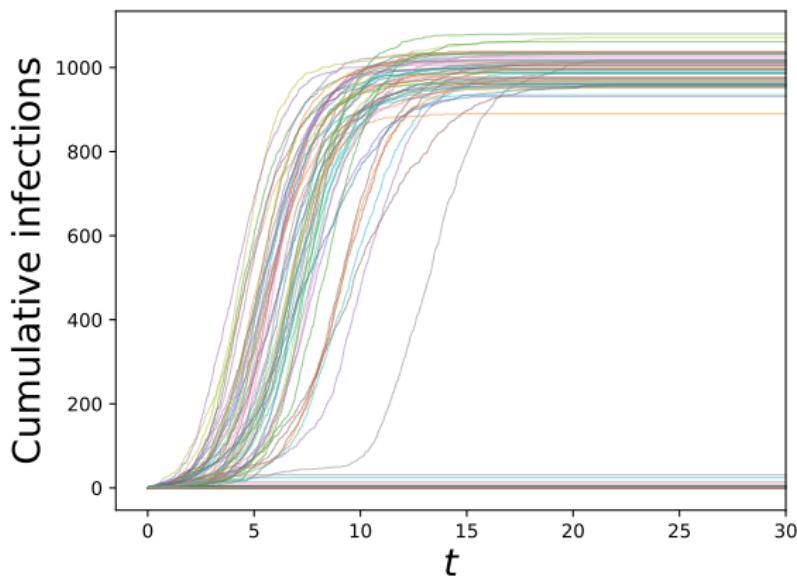
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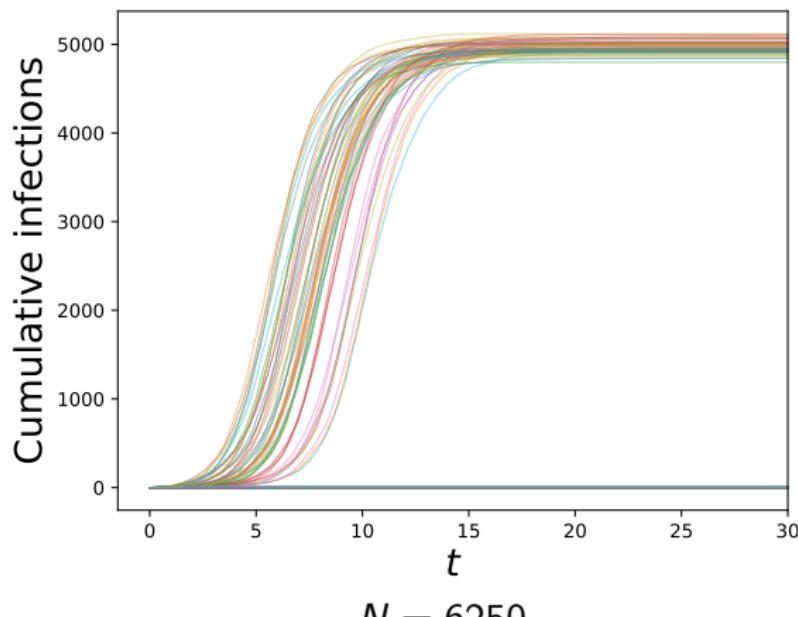


$$N = 1250$$

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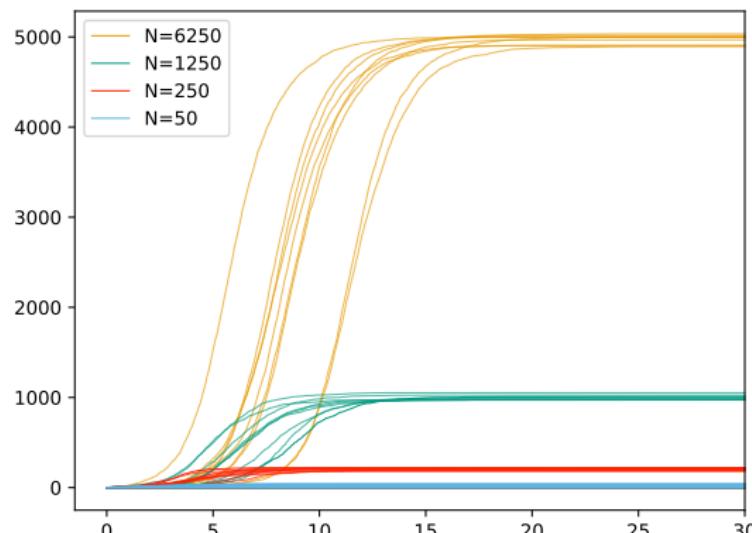
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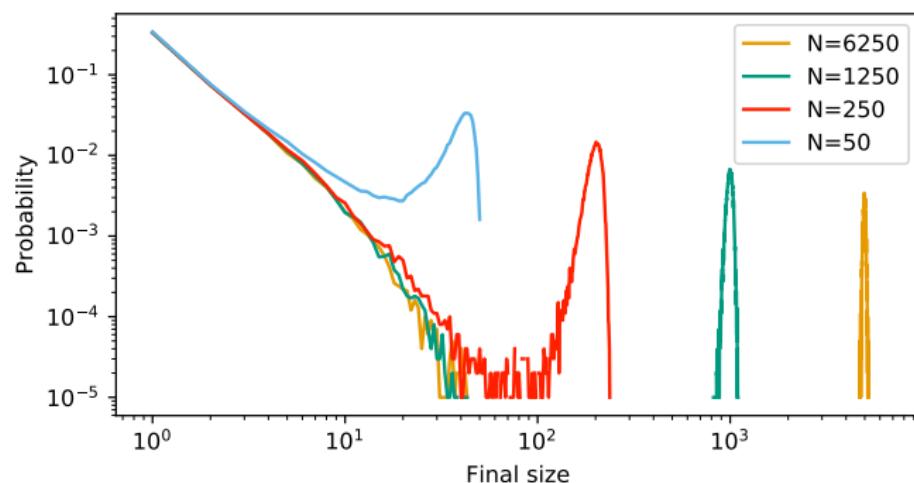
The distinction between small and large outbreaks becomes clear as N increases.

Stochastic simulation — SIR case

What does the final size distribution look like?

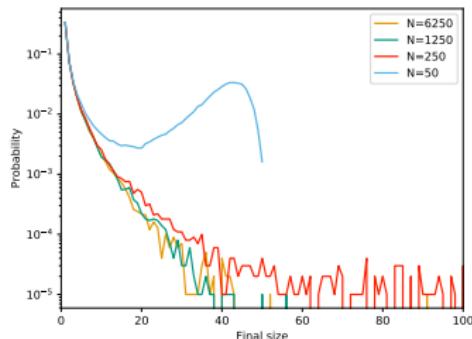
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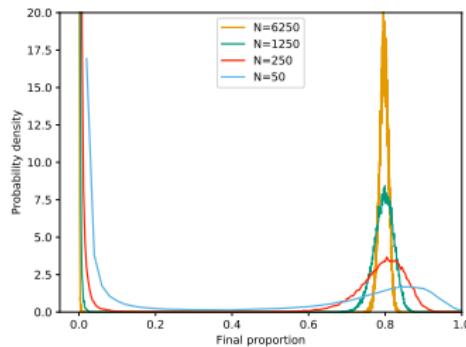
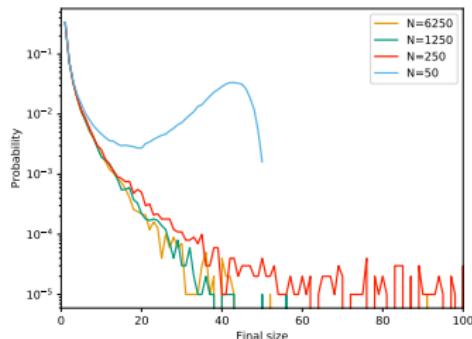


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Small outbreaks affect the same **number** of individuals.

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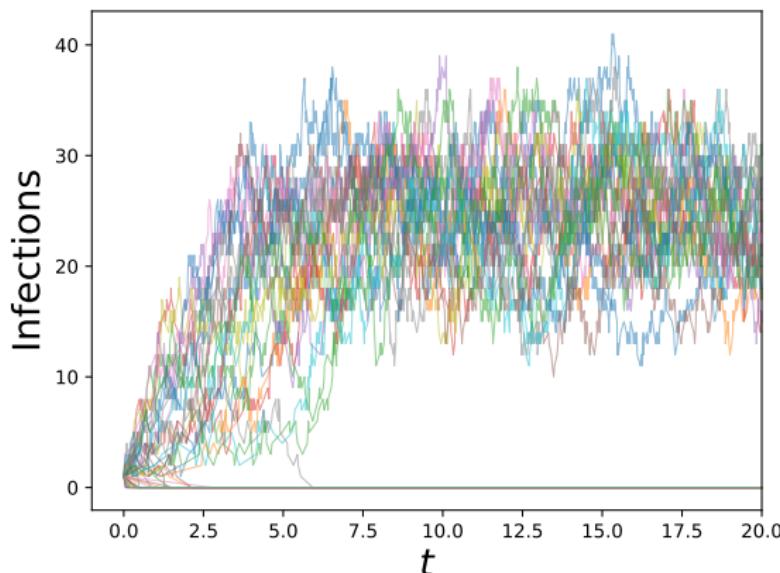
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Epidemics affect approximately the same proportion of the population

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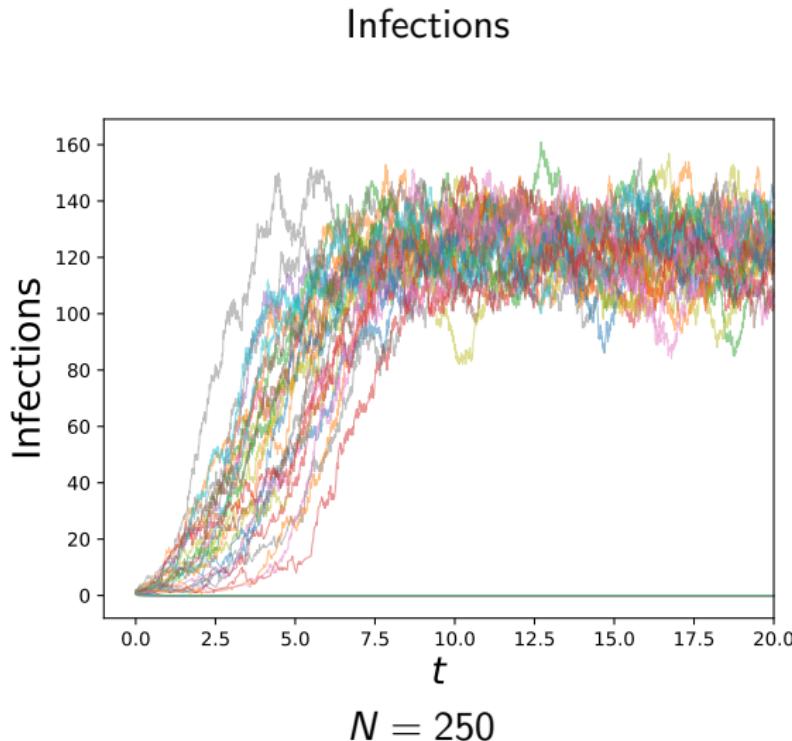
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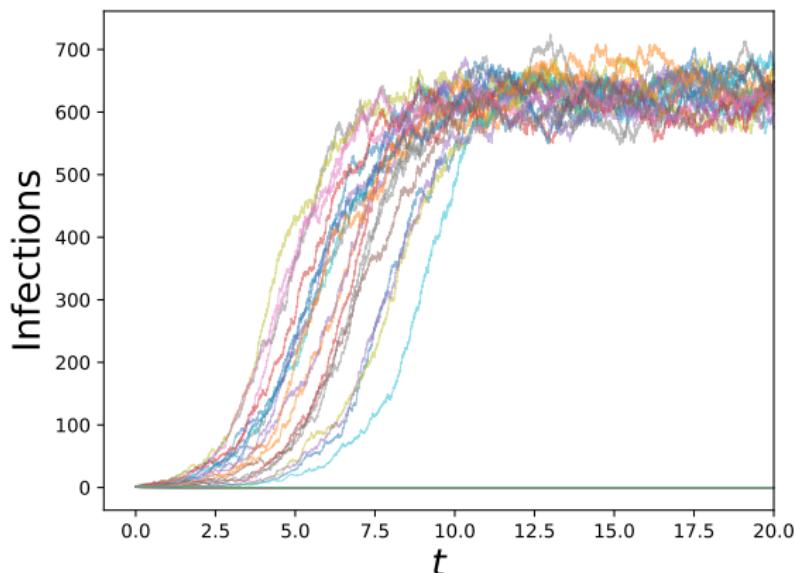
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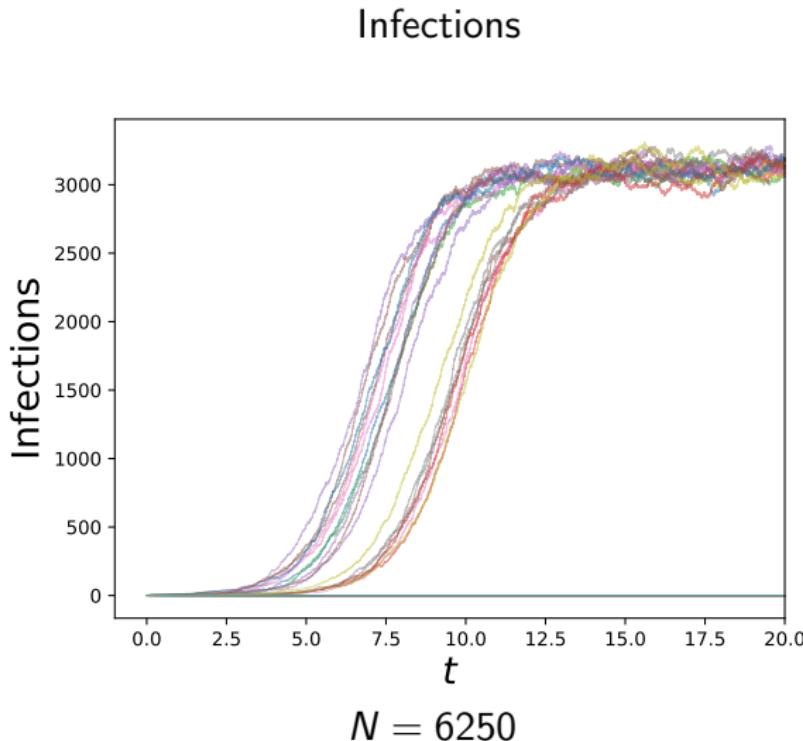
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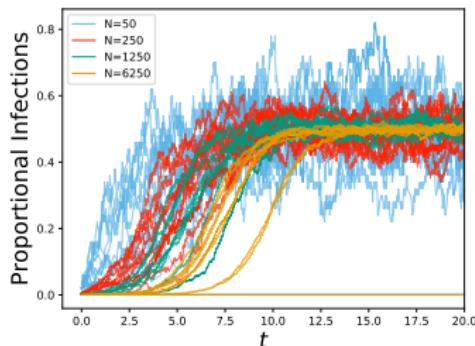
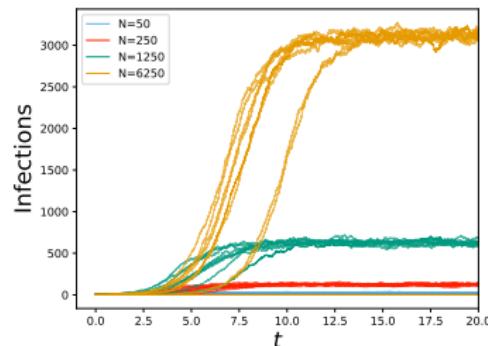
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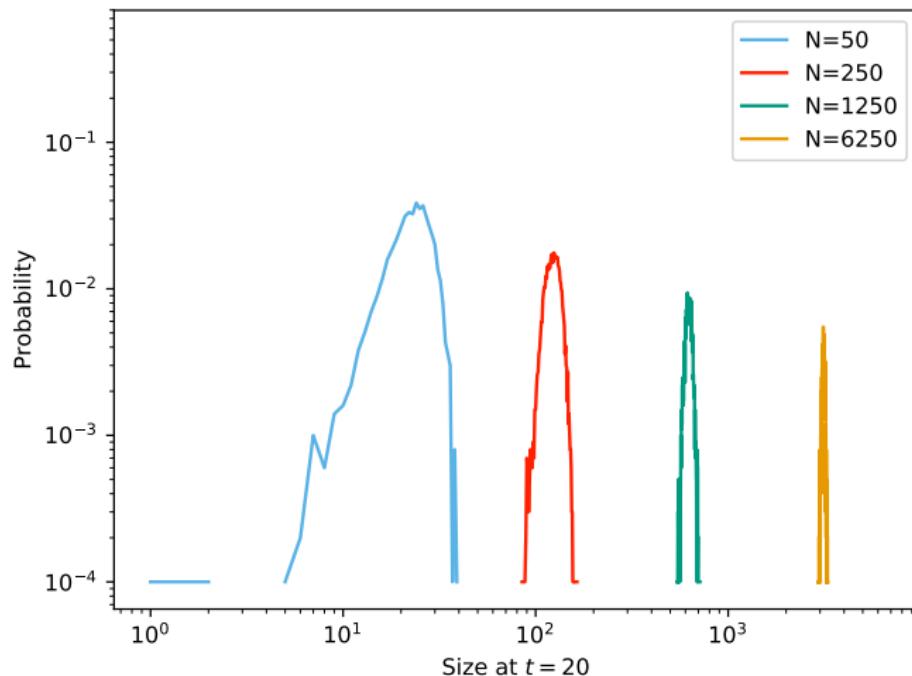
Typically extinction occurs either early or after exponentially long time. The **proportion** infected at equilibrium is approximately the same for different population sizes.

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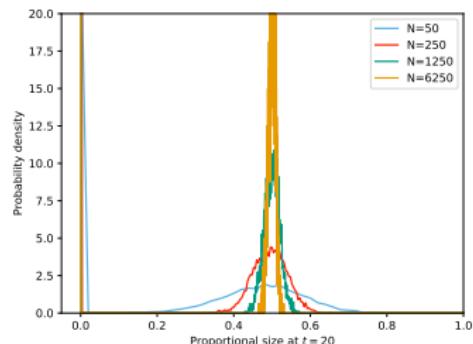
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What does the “equilibrium” distribution look like?



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\mathcal{R}_0

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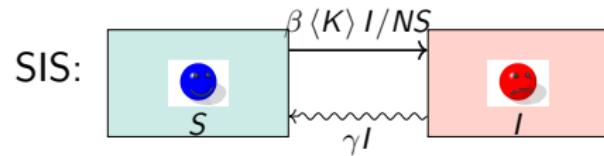
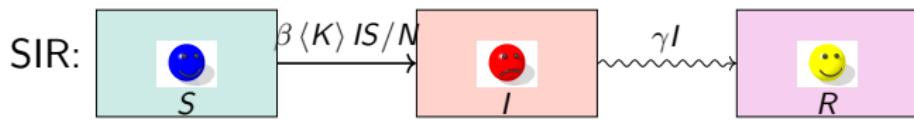
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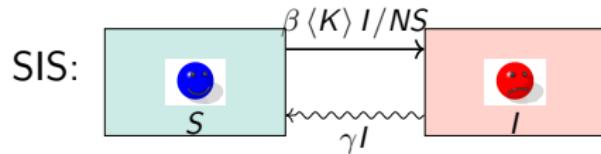
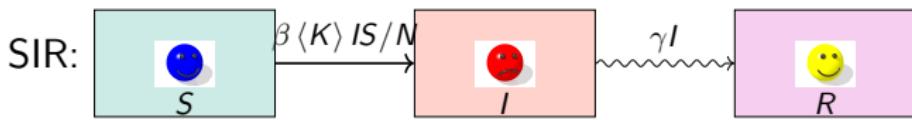
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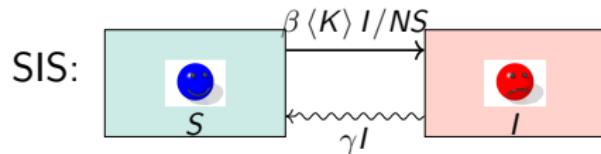
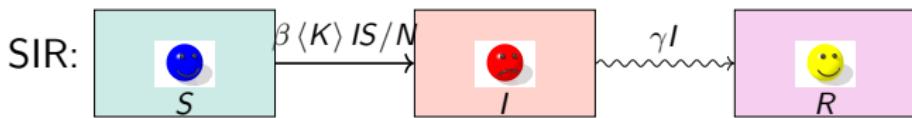
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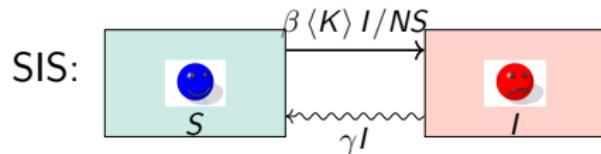
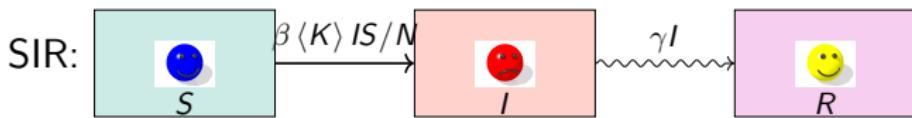
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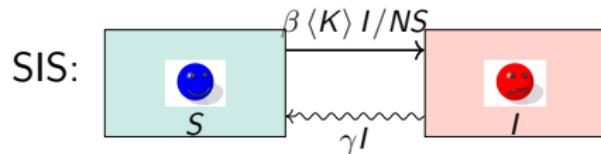
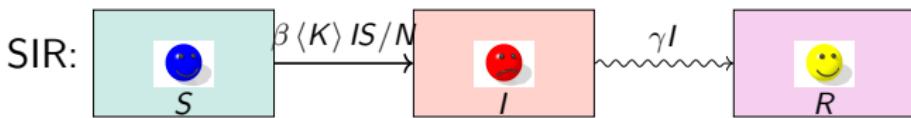
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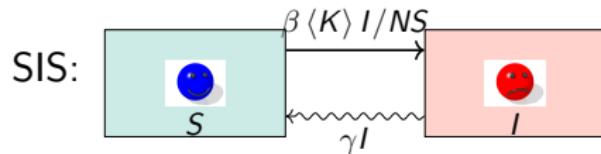
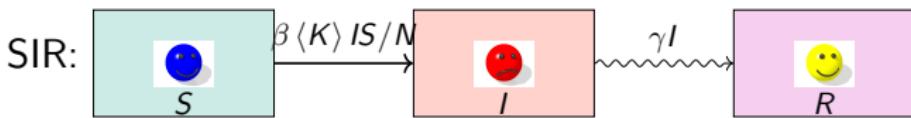
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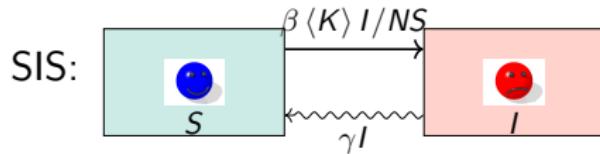
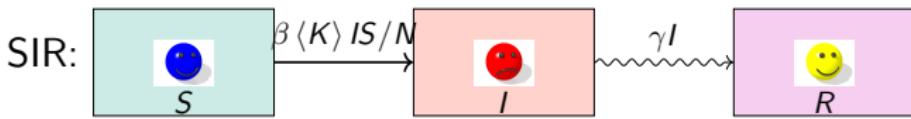


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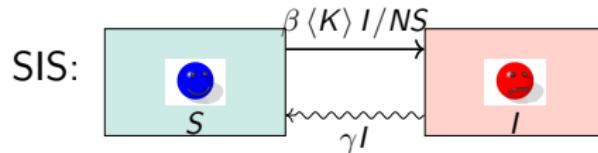
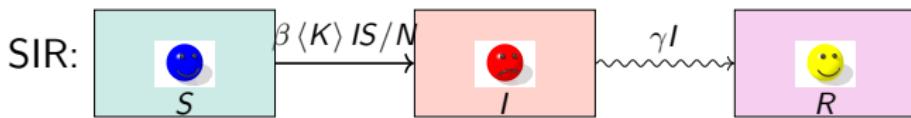


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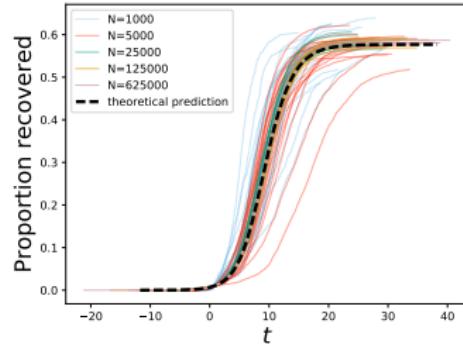
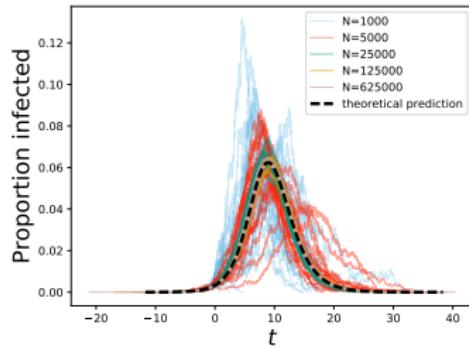
- ▶ SIS equations are

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

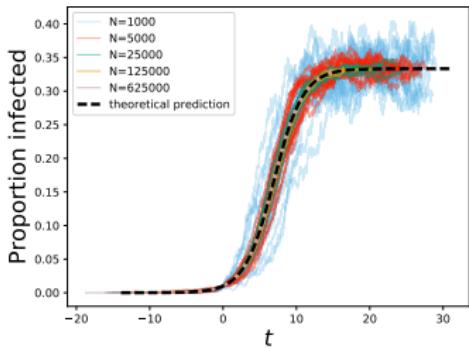
$$\dot{I} = \beta \langle K \rangle IS/N - \gamma I$$

Comparison

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SIS:



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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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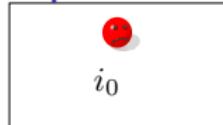
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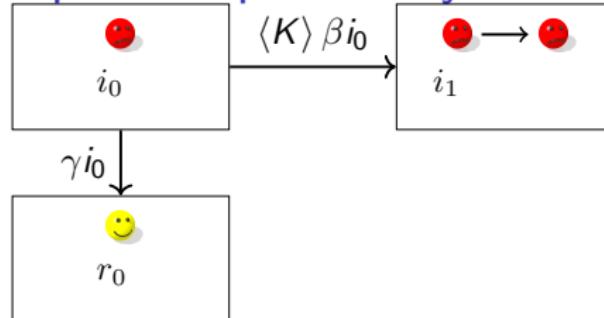
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SIS epidemic probability on annealed networks



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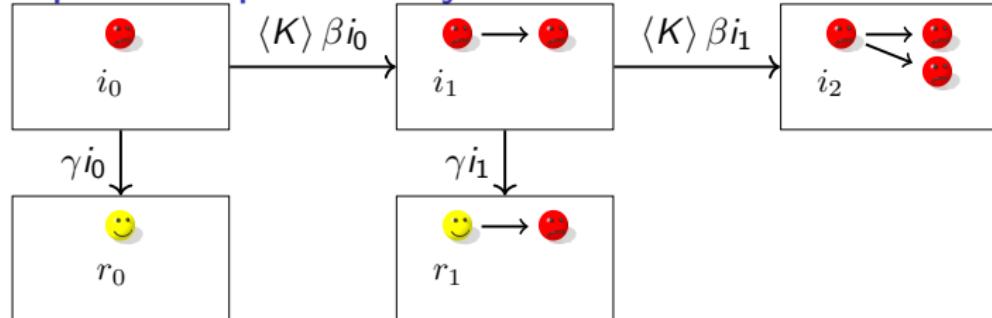
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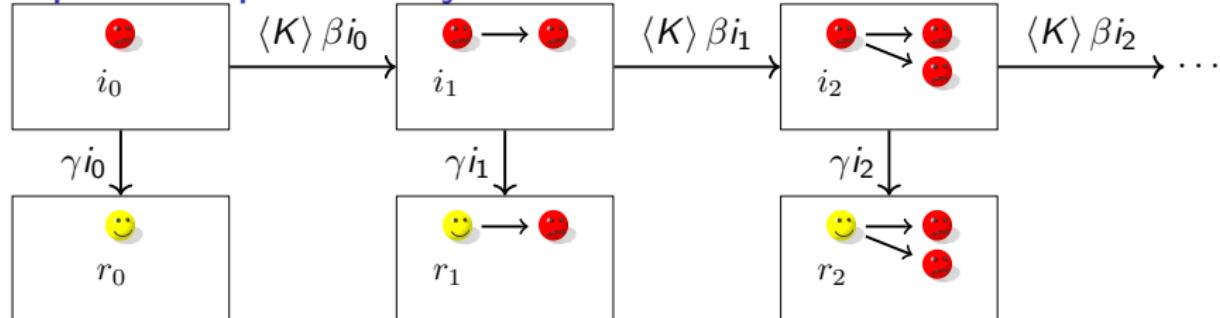
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- ▶ For exactly m transmissions before recovery it is

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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]

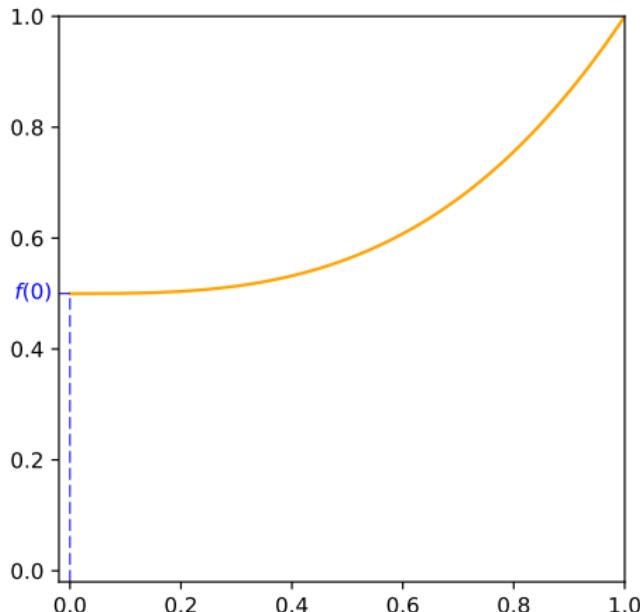
- ▶ The probability of reaching no further than generation g is the probability that none of the first generation individuals causes a transmission chain of length longer than $g - 1$.

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

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

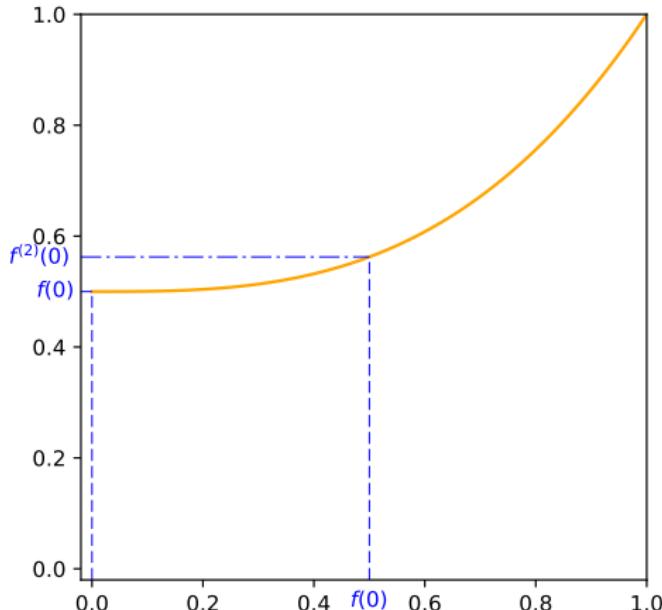
Cobweb diagrams

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



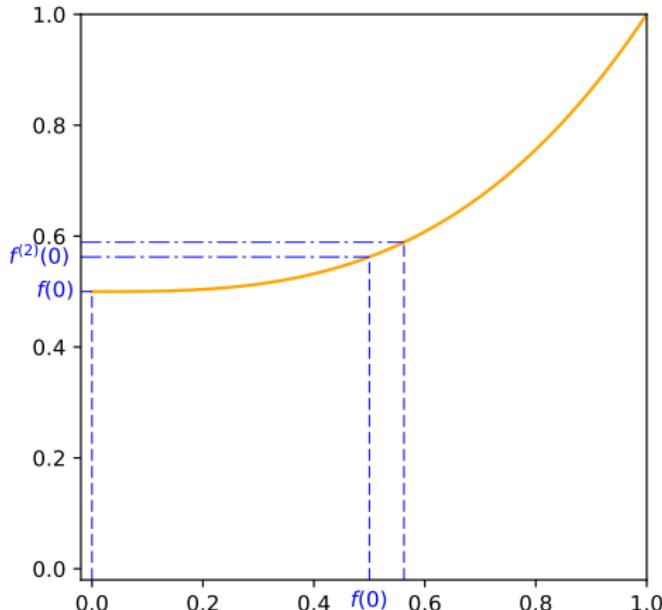
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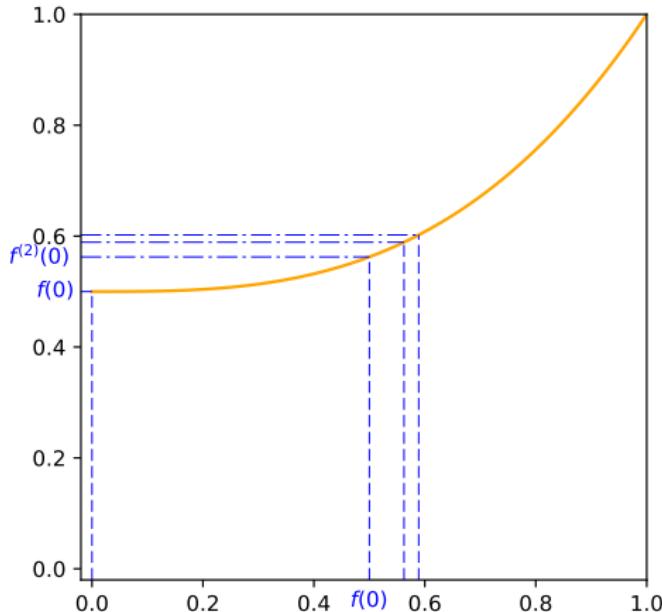
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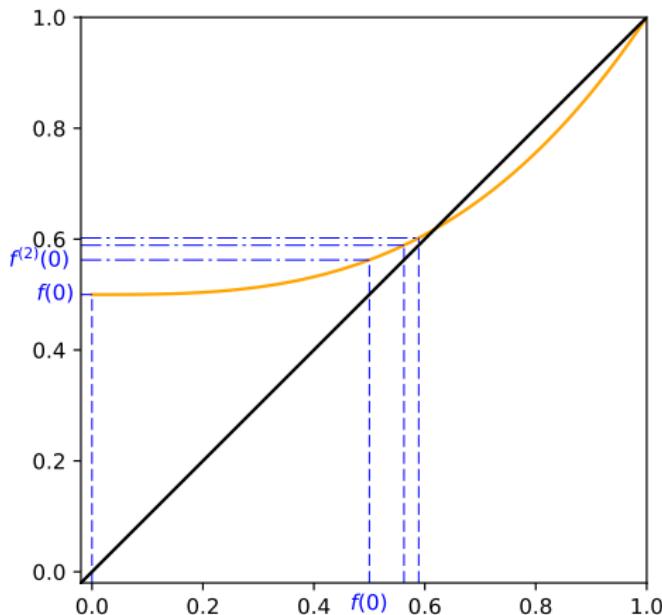
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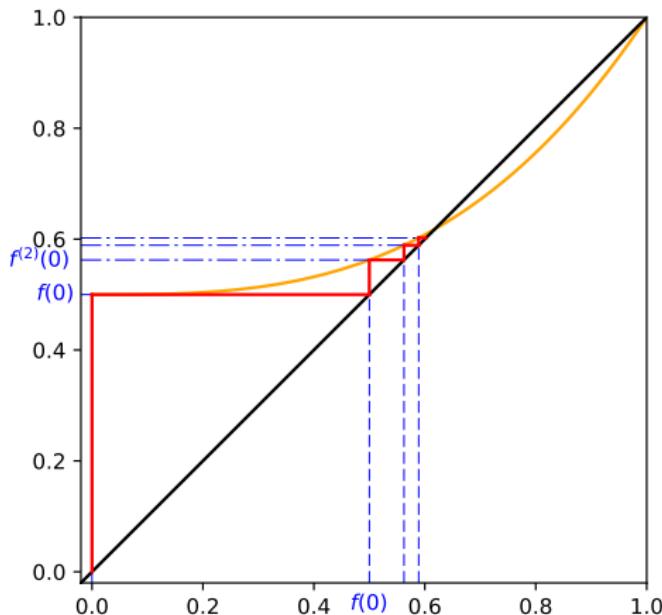
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Recall our key questions

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

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

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

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

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- Our full equations are thus

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

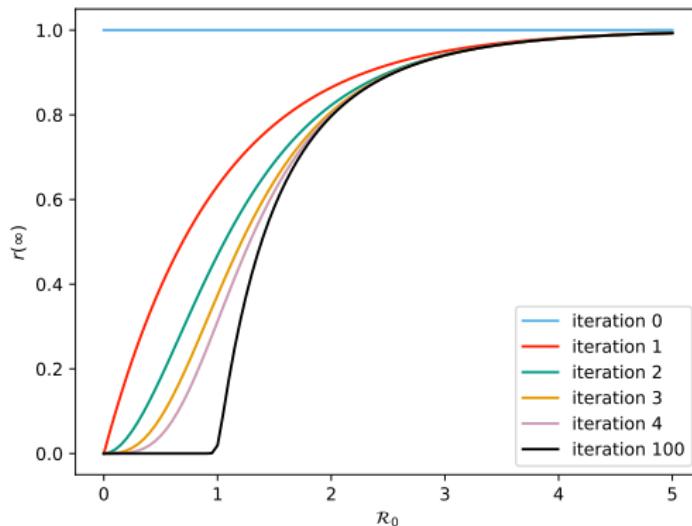
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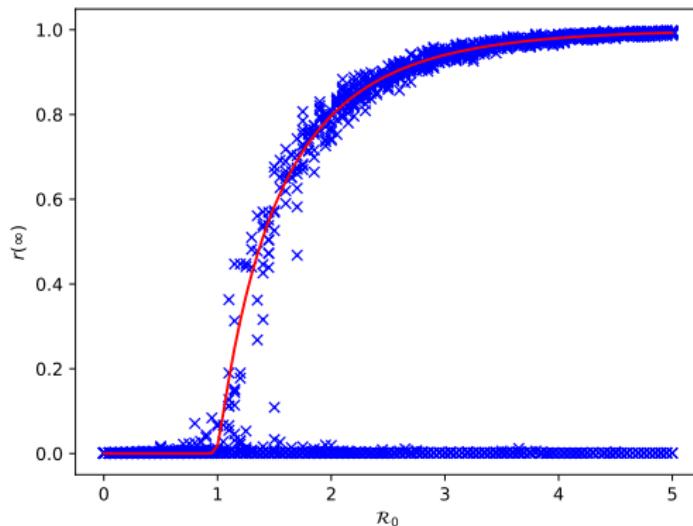
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We can solve this iteratively, starting from a guess $r = 1$.

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The results are in good agreement with simulation.

Direct derivation of alternate equations

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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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References

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