

# Epidemics in Networks

## Part 2 — Compartmental Disease Models

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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
- ▶  $\mathcal{R}_0$
- ▶  $I(t)$

# Simple Compartmental Models

The most common models are compartmental models.

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- ▶ SIR or SIS

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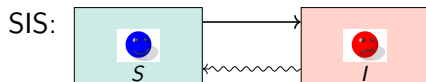
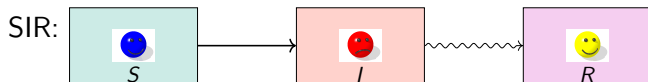
- ▶ Every individual is average.
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Throughout:

$$S + I + R = N$$

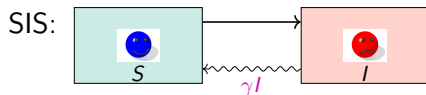
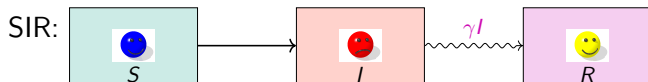
[That is, we look at absolute number rather than proportions of the population. Unfortunately this is standard across much of the field and it causes our equations and initial conditions to be littered with  $N$ s that do nothing to help us understand what is happening. I haven't used this convention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

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Assumptions:

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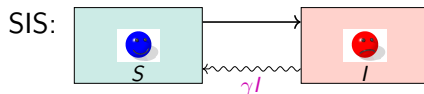
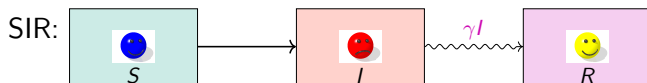


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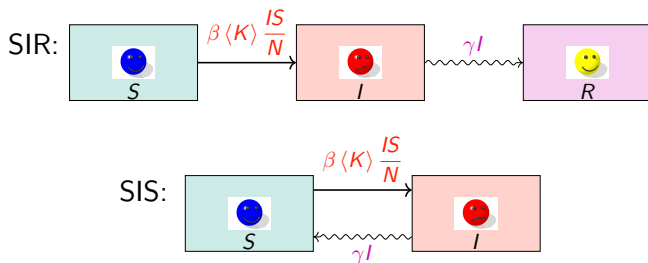
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- ▶ Individuals **recover** with rate  $\gamma$ .
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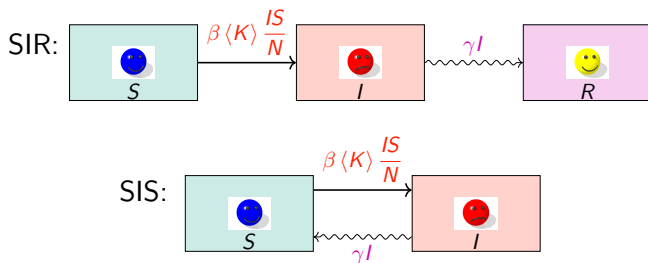
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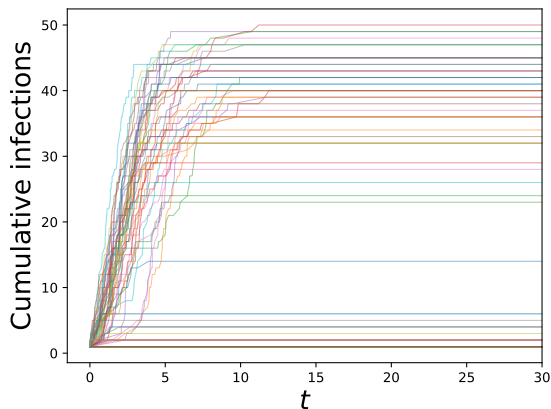
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- ▶ The proportion of transmissions that go to susceptible individuals is  $S/N$ .
- ▶ Implicitly assume each interaction is with a new randomly chosen individual.

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

Cumulative infections

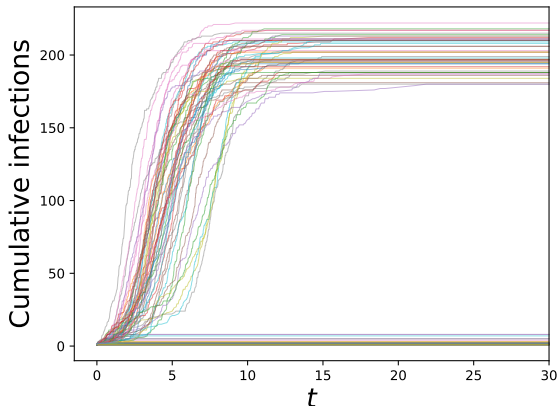


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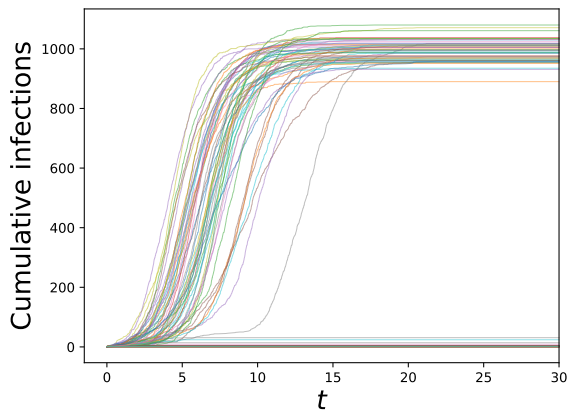


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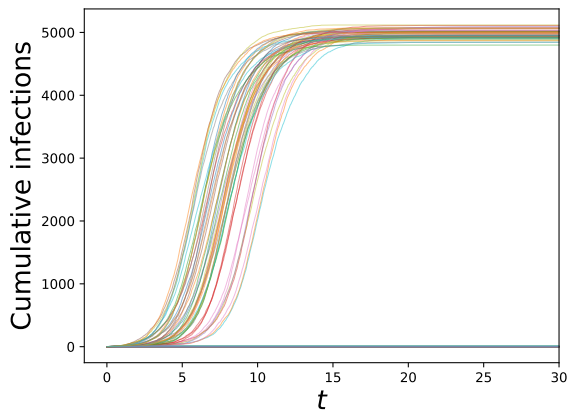


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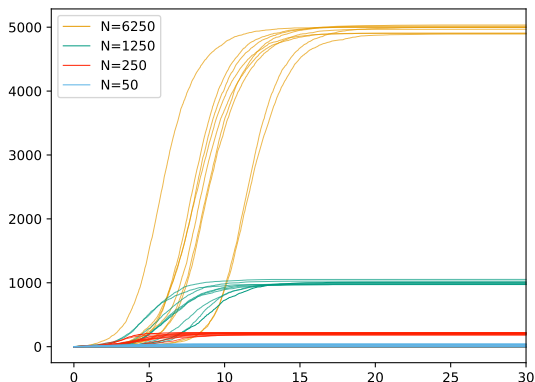


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The distinction between small and large outbreaks becomes clear as  $N$  increases.

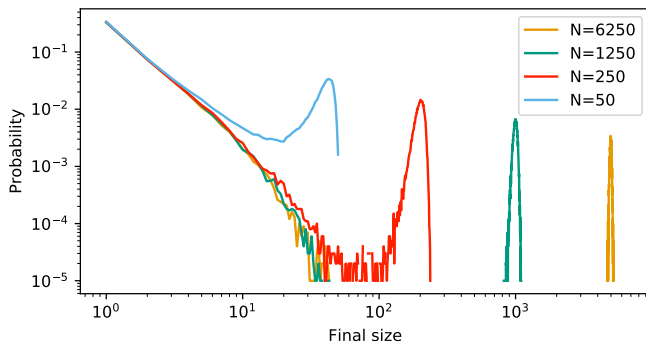


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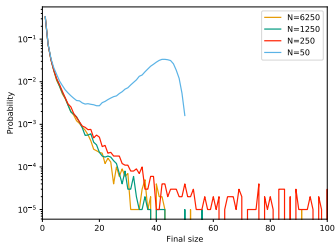
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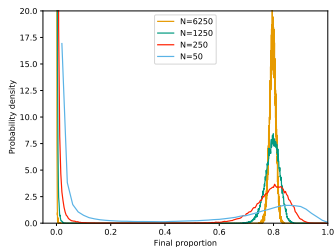
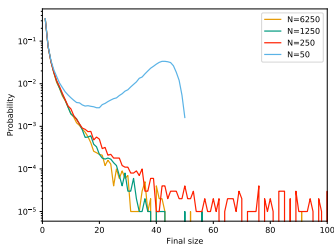


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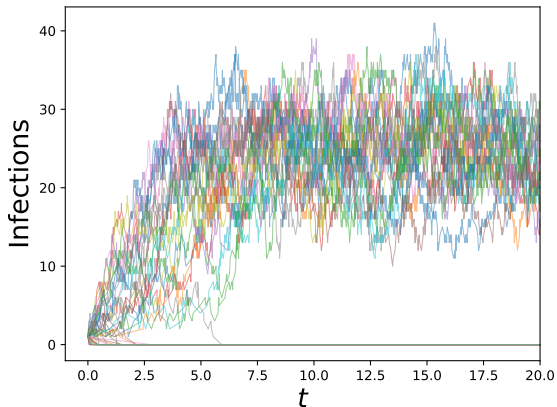
**Small outbreaks** affect the same **number** of individuals.

**Epidemics** affect approximately the same **proportion** of the population

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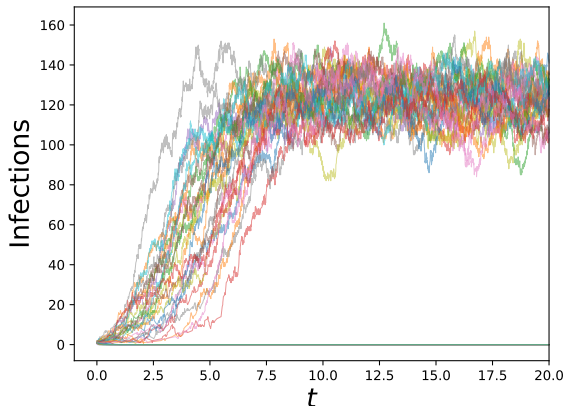


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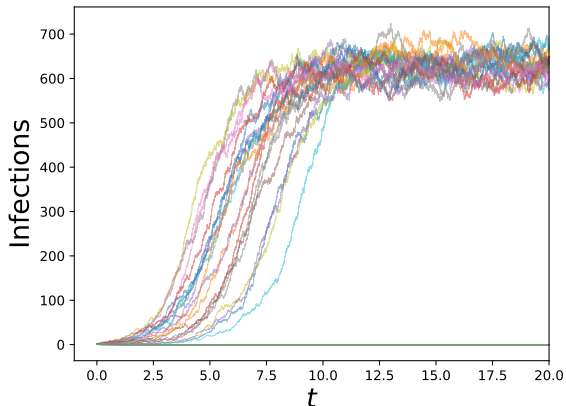


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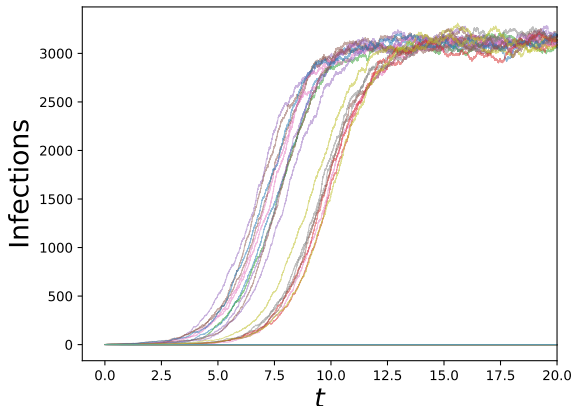


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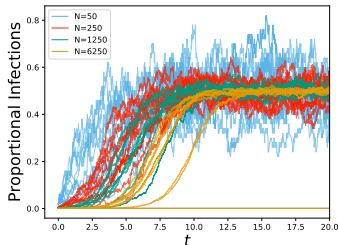
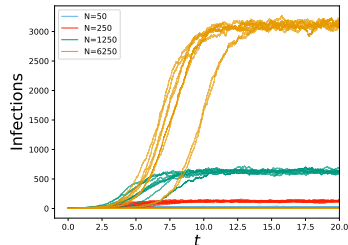
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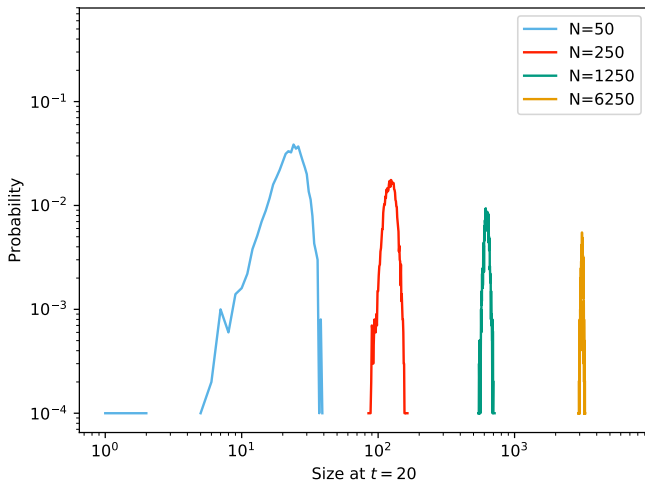
Typically extinction occurs either early or after exponentially long time. The **proportion** infected at equilibrium is approximately the same for different population sizes.

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What does the “equilibrium” distribution look like?

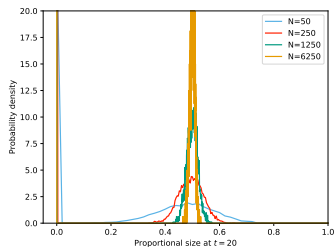
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The equilibrium proportion infected is about the same for different population sizes.

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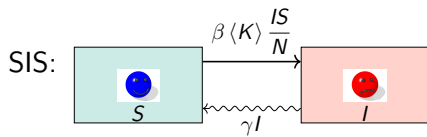
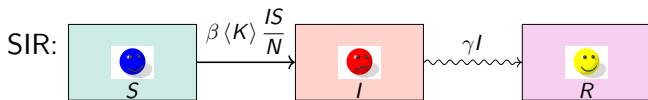
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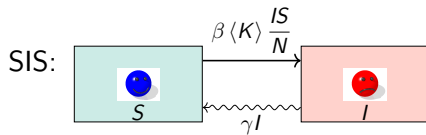
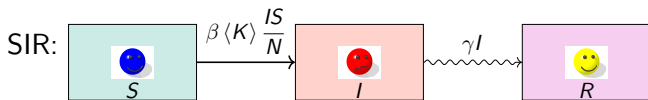
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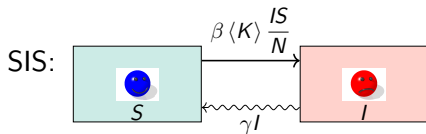
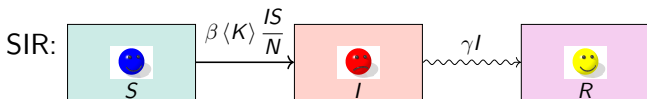




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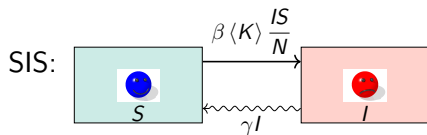
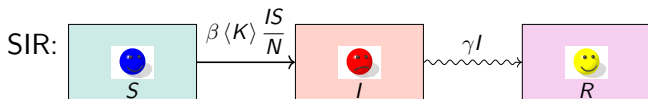
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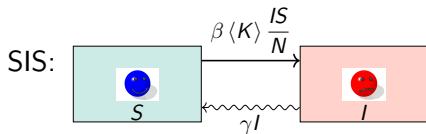
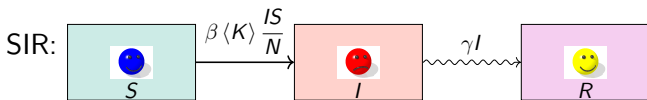
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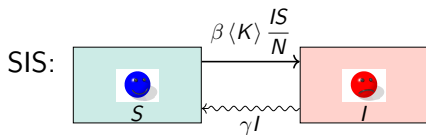
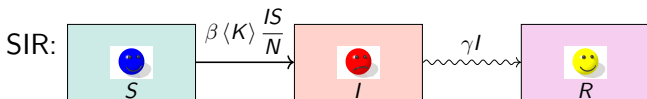
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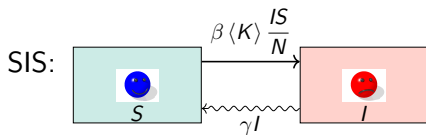
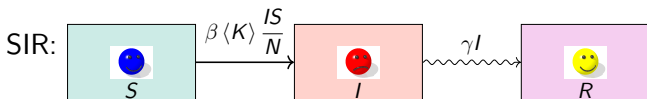


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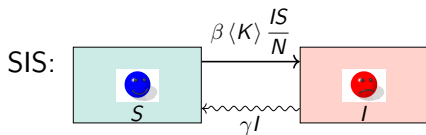
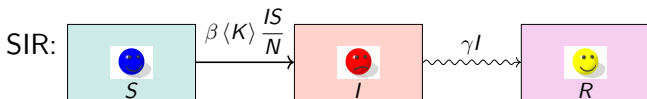


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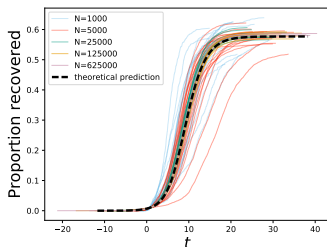
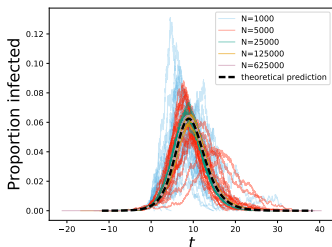
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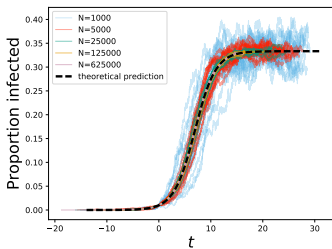
## Comparison

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

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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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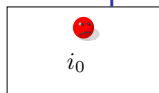
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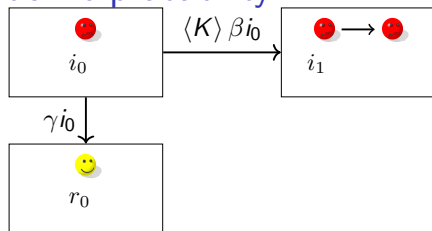


## Epidemic probability



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.

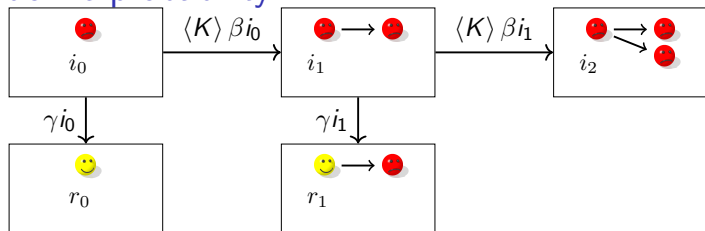
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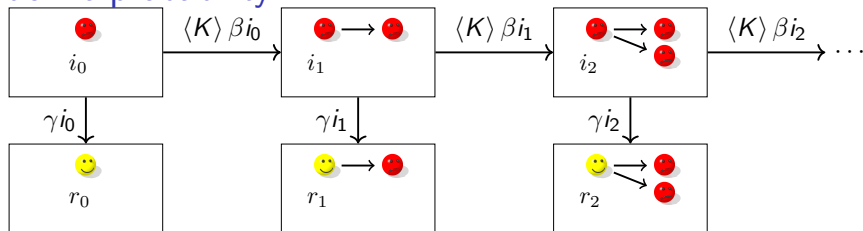
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- ▶ The probability the first  $m$  events are transmissions is  $\left[ \frac{\langle K \rangle \beta}{\langle K \rangle \beta + \gamma} \right]^m$ .
- ▶ For **exactly**  $m$  transmissions before recovery it is

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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]

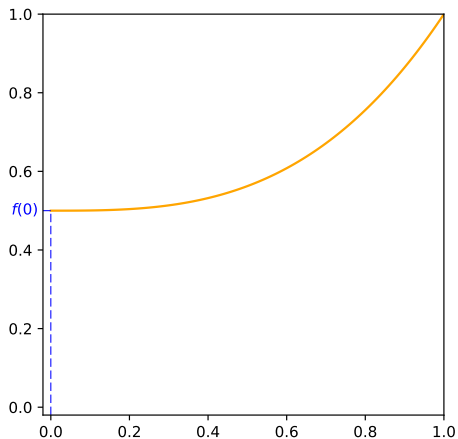
- ▶ The probability of reaching no further than generation  $g$  is the probability that none of the first generation individuals causes a transmission chain of length longer than  $g - 1$ .

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

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

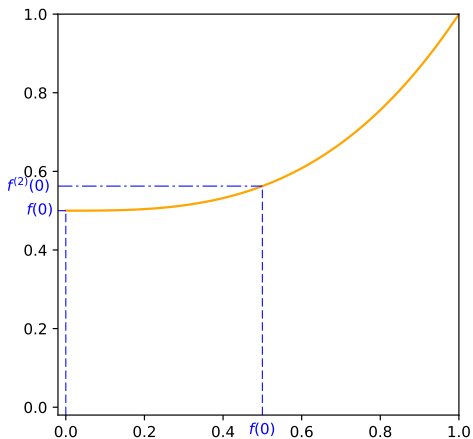
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Consider  $f(x) = \frac{1+x^3}{2}$ . We can keep iterating  $f$  on 0.



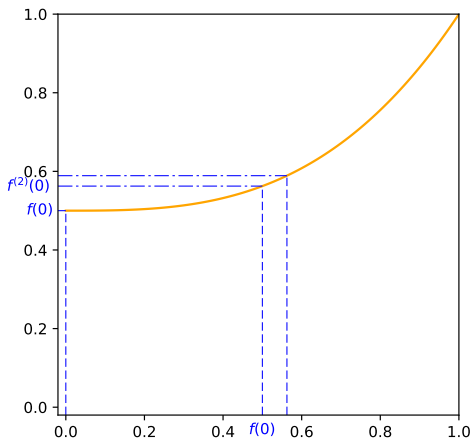
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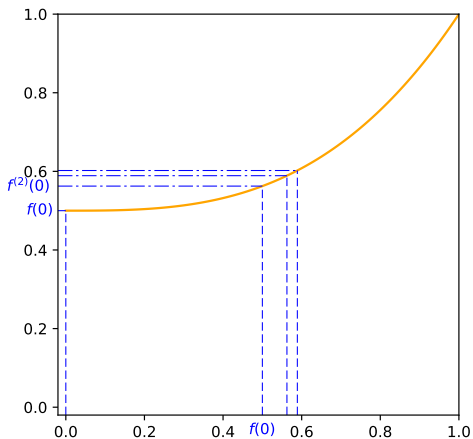
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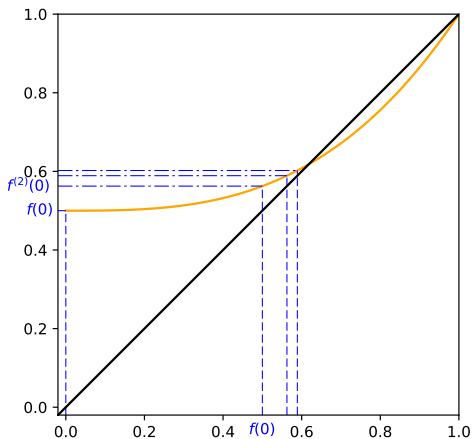
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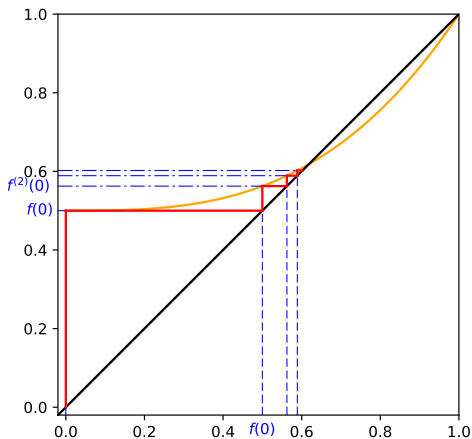
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# Introduction to Compartmental Models

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

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

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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.



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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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- ▶ We have

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

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

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

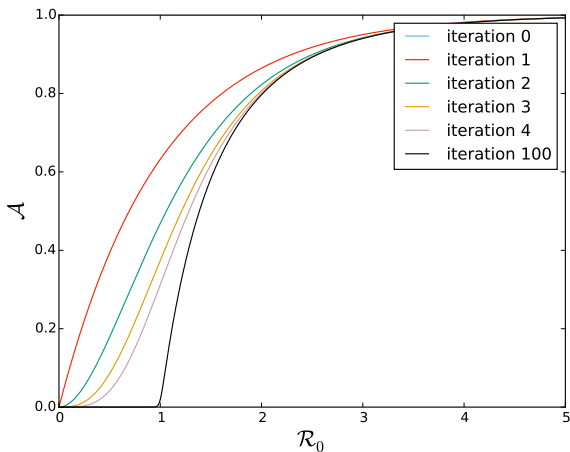


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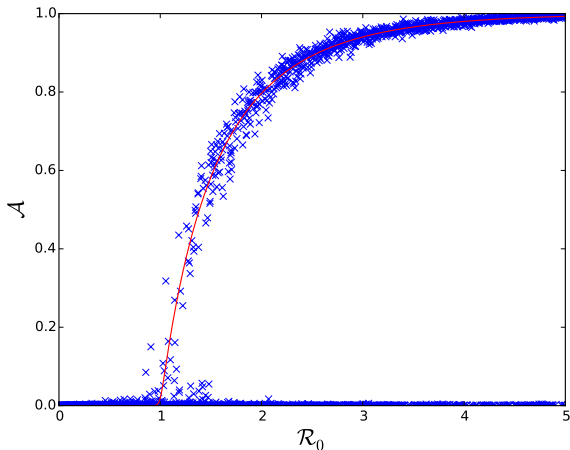
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We can solve this iteratively, starting from a guess  $\mathcal{A} = 1$ .

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

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

# Introduction to Compartmental Models

Dynamics

$\mathcal{R}_0$

Epidemic Probability

Epidemic size

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.