Epidemics in Networks
Part 2 — Compartmental Disease Models

Joel C. Miller & Tom Hladish

17–19 July 2017

Recall our key questions

For SIR:

- $\mathcal{P}$, the probability of an epidemic.
- $\mathcal{A}$, the "attack rate": the fraction infected if an epidemic happens (better named the attack ratio).
- $\mathcal{R}_0$, the average number of infections caused by those infected early in the epidemic.
- $I(t)$, the time course of the epidemic.

For SIS:

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

Simple Compartmental Models

The most common models are compartmental models.

- Continuous time or Discrete time
- SIR or SIS

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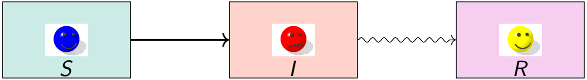
Throughout:

$$S + I + R = N$$

[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 Ns 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.]

Continuous time: Kermack–McKendrick

SIR:



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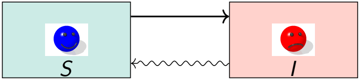

Assumptions:

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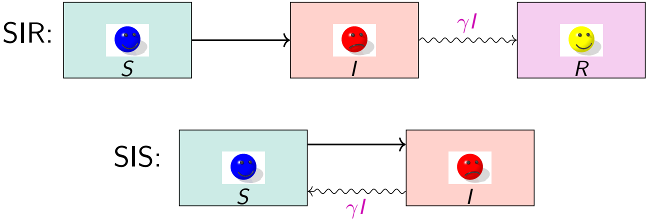

Assumptions:

- Individuals recover with rate γ.

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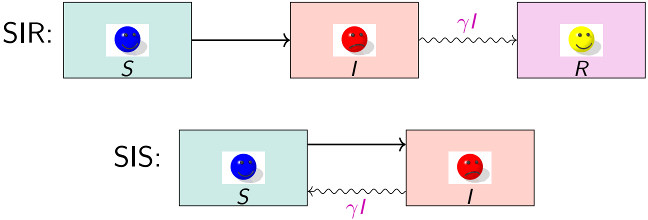

Assumptions:

- 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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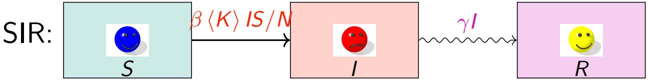

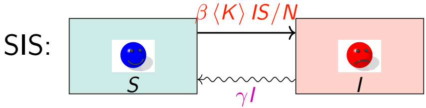

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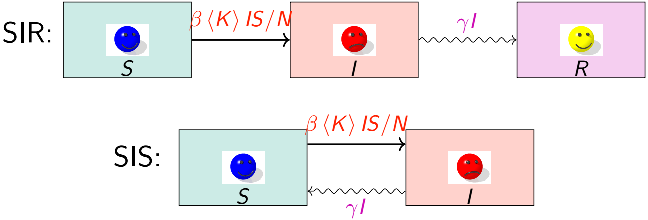

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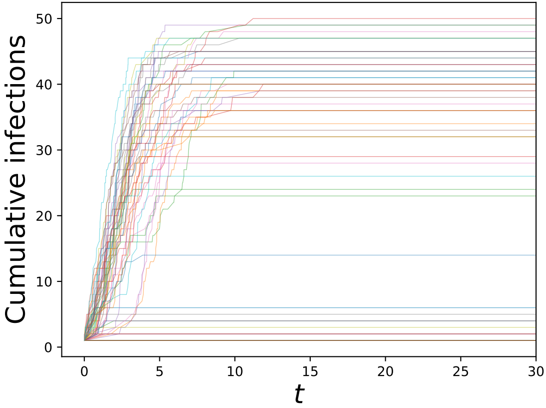
- The proportion of transmissions that go to susceptible individuals is S/N.
- An implicit assumption is that each interaction is with a new randomly infected individual.

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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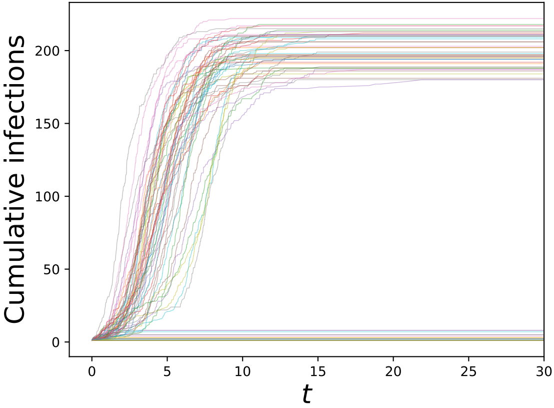

$N = 250$

Stochastic simulation — SIR case

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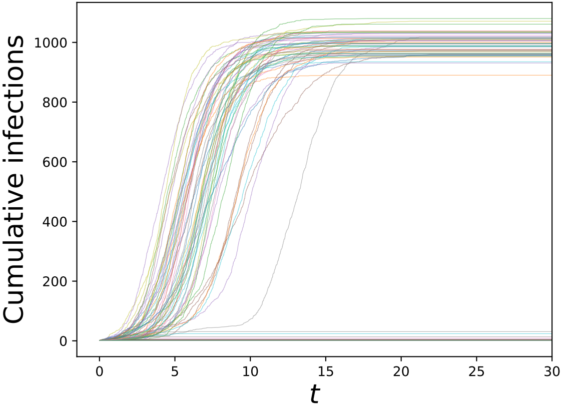
Cumulative infections



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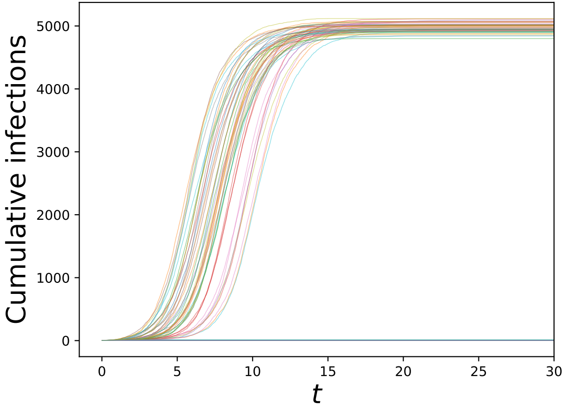

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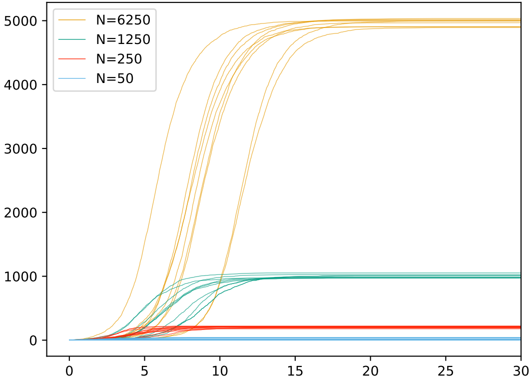

The distinction between small and large outbreaks becomes clear as N increases.

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What does the final size distribution look like?

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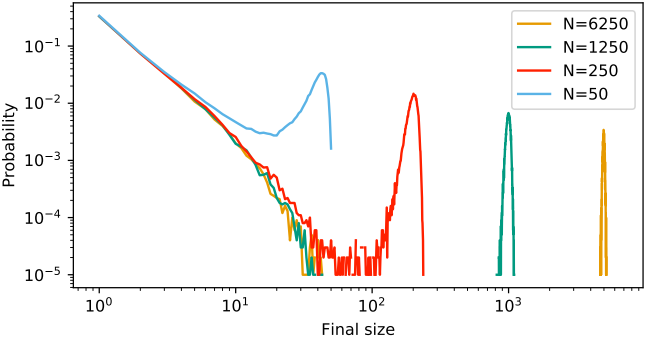

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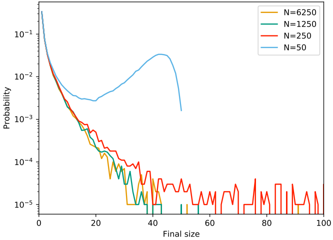

In large populations:

Small outbreaks affect the same number of individuals.

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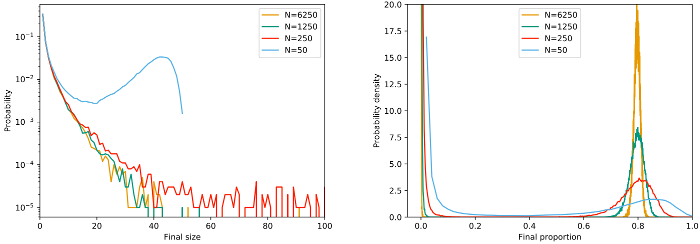

In large populations:

Small outbreaks affect the same number of individuals.

Epidemics affect approximately the same proportion of the population

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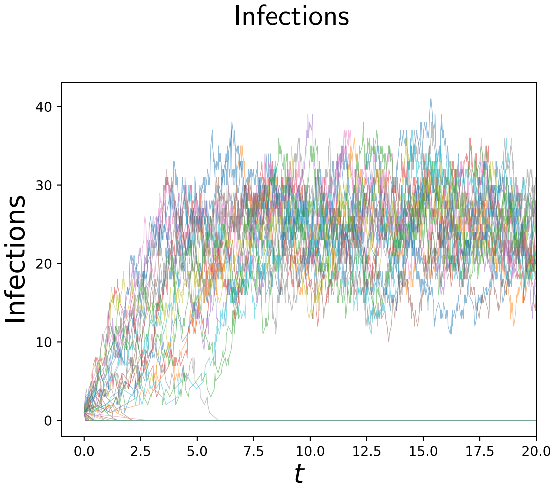

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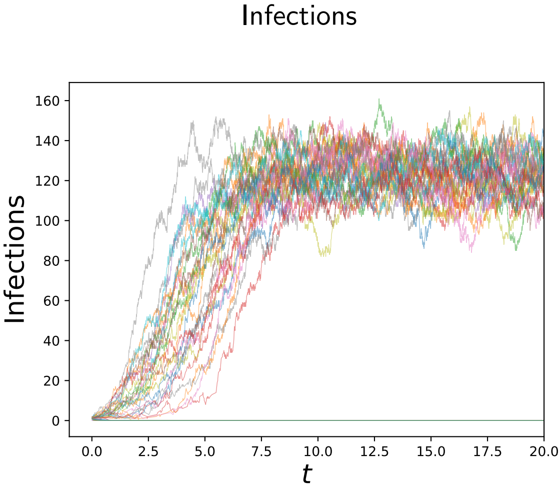

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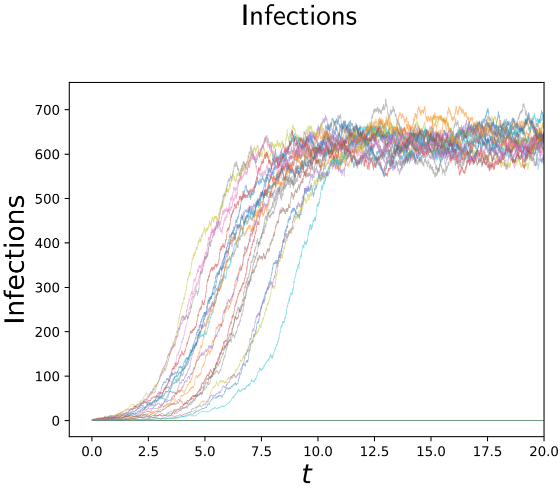

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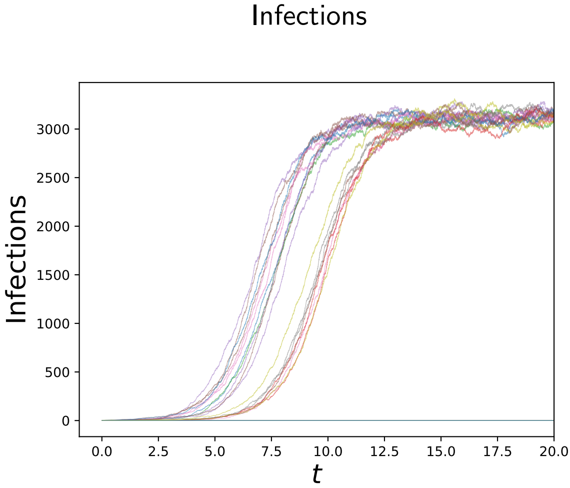

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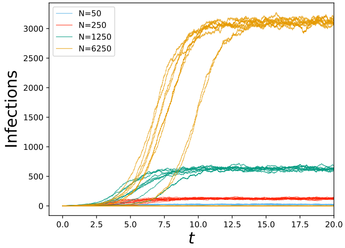
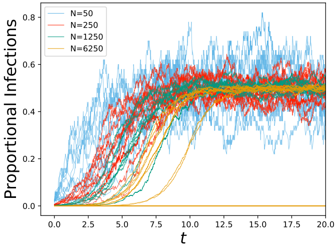
Infections





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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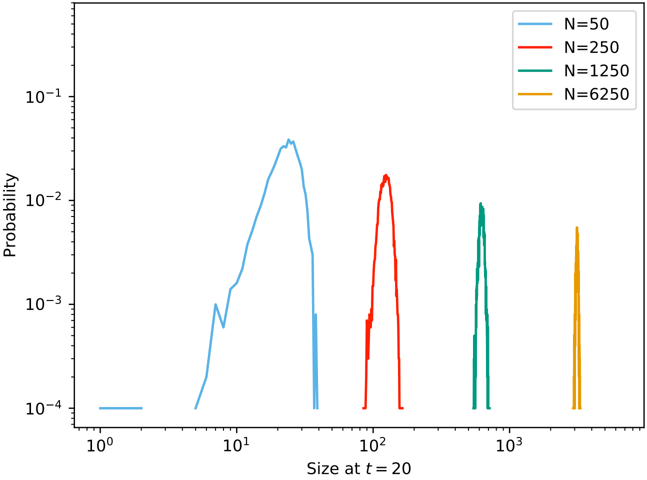

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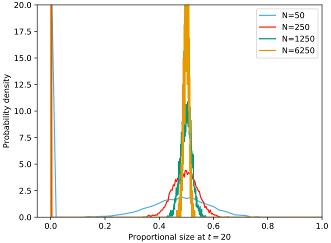

The equilibrium proportion infected is about the same for different population sizes.

Recall our key questions

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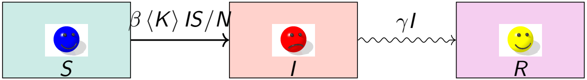
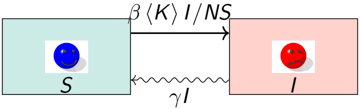


$\beta \langle K \rangle IS/N$
γI
S
I
R

SIS:



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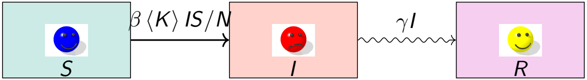

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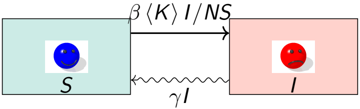

- SIR equations are:

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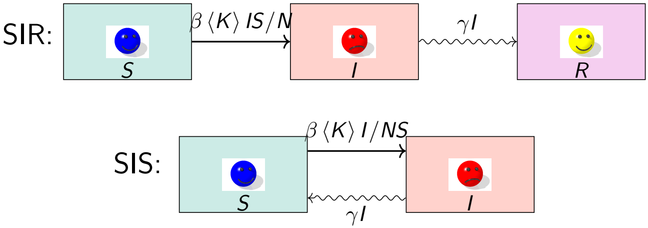

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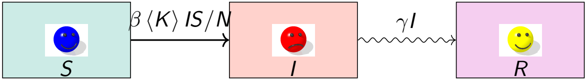
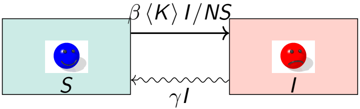


SIS:



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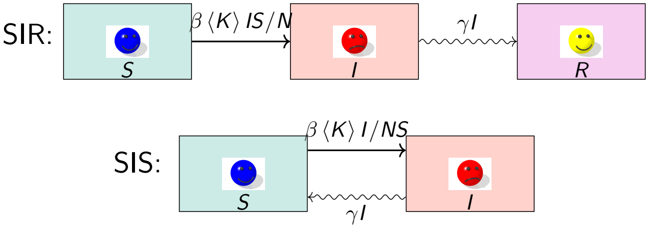

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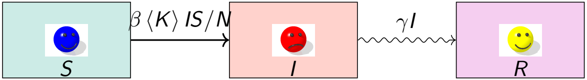

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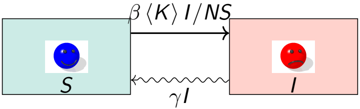

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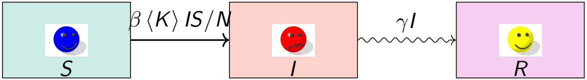

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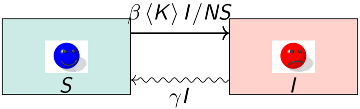

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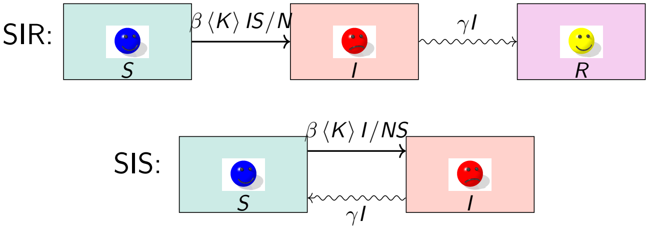

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Comparison

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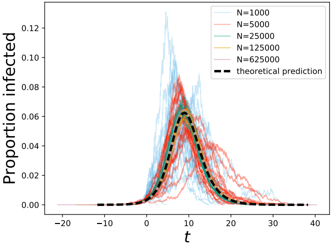

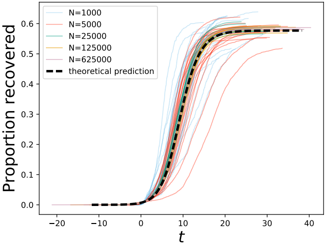

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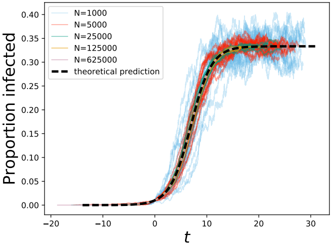

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$\mathcal{R}_0$

An important quantity in disease modeling is $\mathcal{R}_0$.

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- If $\mathcal{R}_0 < 1$ epidemics cannot occur.
- If $\mathcal{R}_0 > 1$ epidemics can occur, but are not guaranteed.

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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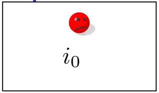
SIS epidemic probability on annealed networks



Consider an individual u with degree k 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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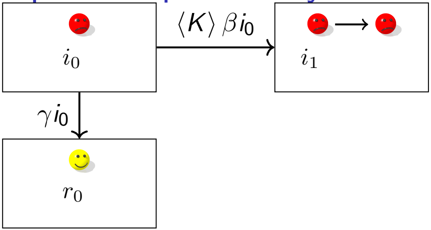

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- The probability of transmitting at least once before recovering is $\frac{\langle K \rangle \beta}{\langle K \rangle \beta + \gamma}$.

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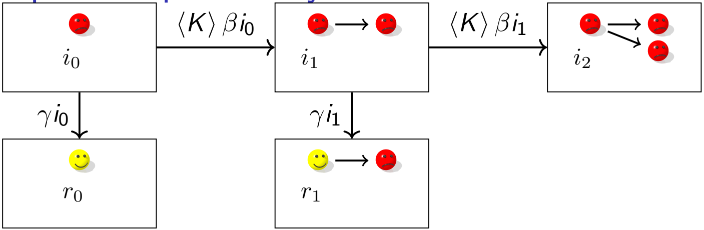

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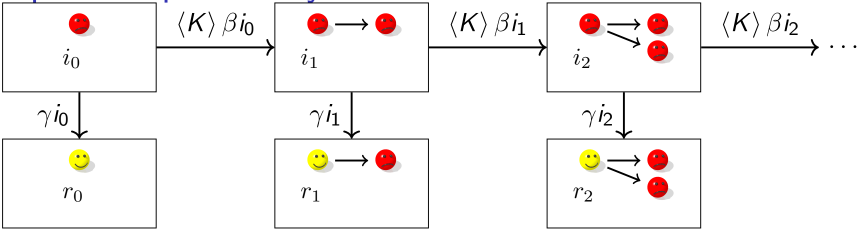

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- The probability the first m events are transmisions is $\left[\frac{\langle K \rangle \beta}{\langle K \rangle \beta + \gamma}\right]^m$.
- For exactly m transmissions before recovery it is

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

[The superscript with parentheses denotes function iteration]

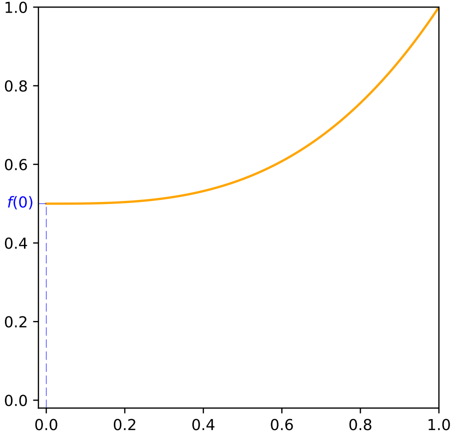
- The probability of reaching no further than generation g is the probability that none of the first generation individuals causes a transmission chain of length longer than $g-1$.

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

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

Cobweb diagrams

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



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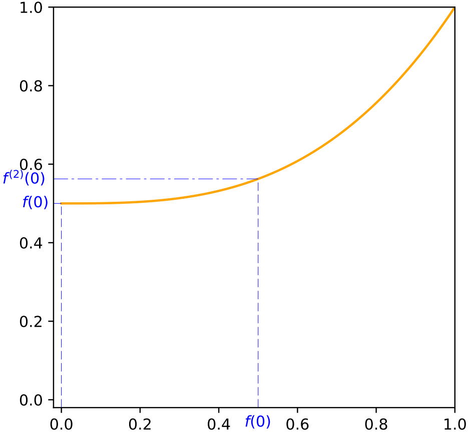

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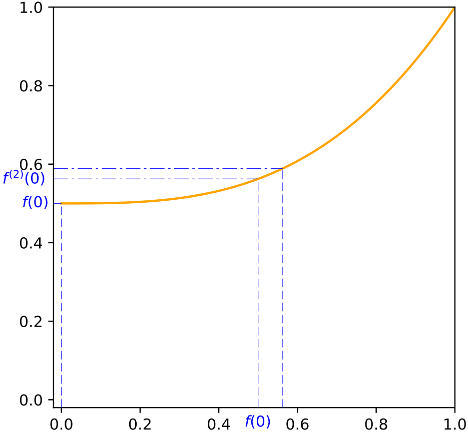

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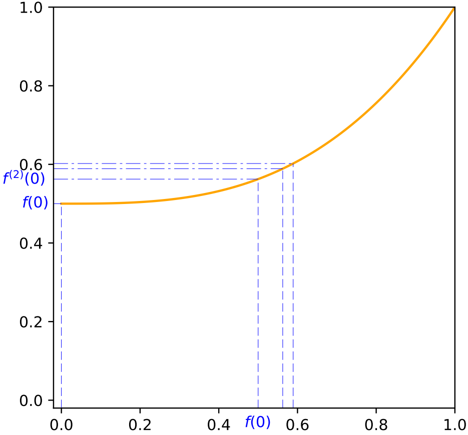

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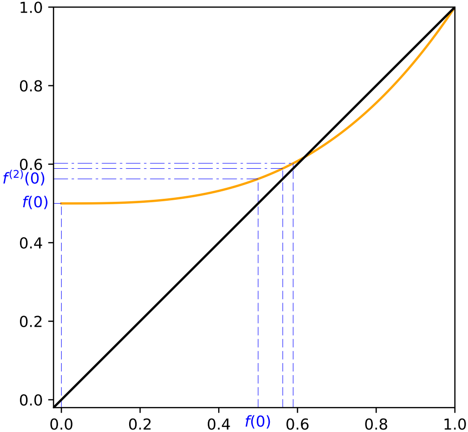

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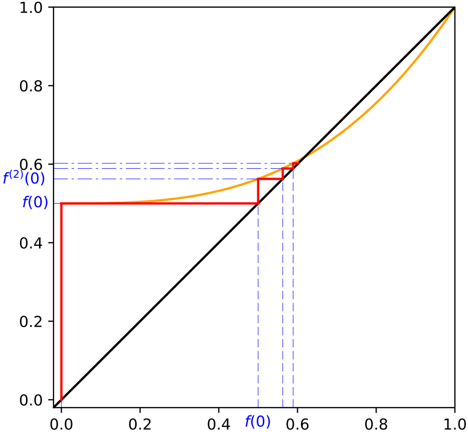

Recall our key questions

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

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

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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.

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

$$\dot{\xi} = \beta \langle K \rangle \frac{I}{N} = \beta \langle K \rangle \left(1 - \frac{\xi}{\mathcal{R}_0} - \frac{R(0)}{N} - \frac{S(0)e^{-\xi}}{N}\right)$$

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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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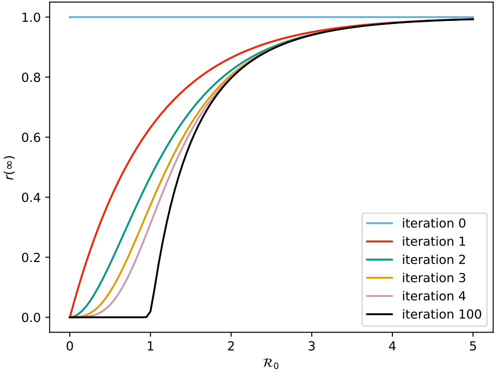

We can solve this iteratively, starting from a guess $r = 1$.

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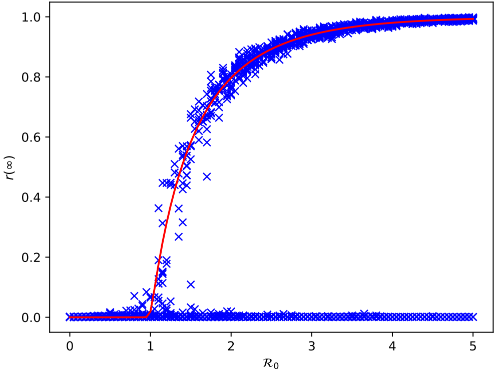

The results are in good agreement with simulation.

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
$$\frac{\mathrm{d}}{\mathrm{d}t}\hat{\xi} = \frac{\beta \langle K \rangle}{N} I$$
- Thus $\hat{\xi}$ satisfies the same relations as ξ, and we can conclude that $\hat{\xi} = \xi$.

References I

[1] Anne Schneeberger, Catherine H Mercer, Simon AJ Gregson, Neil M Ferguson, Constance A Nyamukapa, Roy M Anderson, Anne M Johnson, and Geoff P Garnett.
Scale-free networks and sexually transmitted diseases: a description of observed patterns of sexual contacts in britain and zimbabwe.
Sexually transmitted diseases, 31(6):380–387, 2004.

[2] Joel C. Miller and Erik M. Volz.
Model hierarchies in edge-based compartmental modeling for infectious disease spread.
Journal of Mathematical Biology, 67(4):869–899, 2013.

[3] Joel C. Miller.
Spread of infectious disease through clustered populations.
Journal of the Royal Society Interface, 6(41):1121, 2009.