

Epidemics in Networks

Basic Properties

Joel C. Miller & Tom Hladish

13–15 July 2015

Introduction

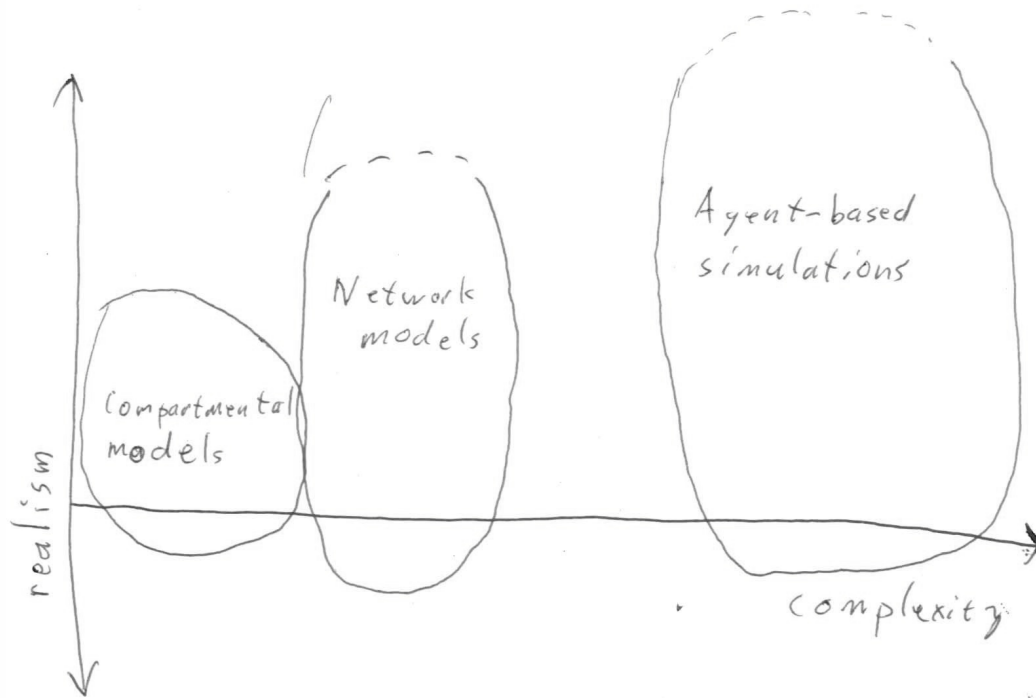
Mass Action Models

Key Epidemic Quantities

Introducing Networks

References

Modeling options



Our scope

- ▶ SIS
- ▶ SIR
- ▶ Networks of individuals
- ▶ Mostly static, unweighted networks

Simulation vs Analytic models

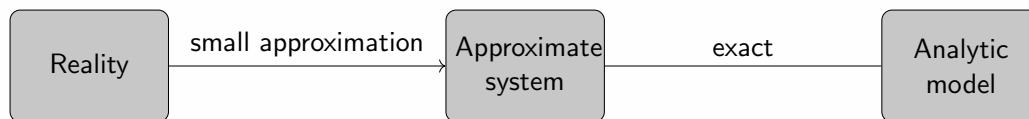
Usually simulation is more flexible, but an analytic model gives better results.

My (biased) opinion:

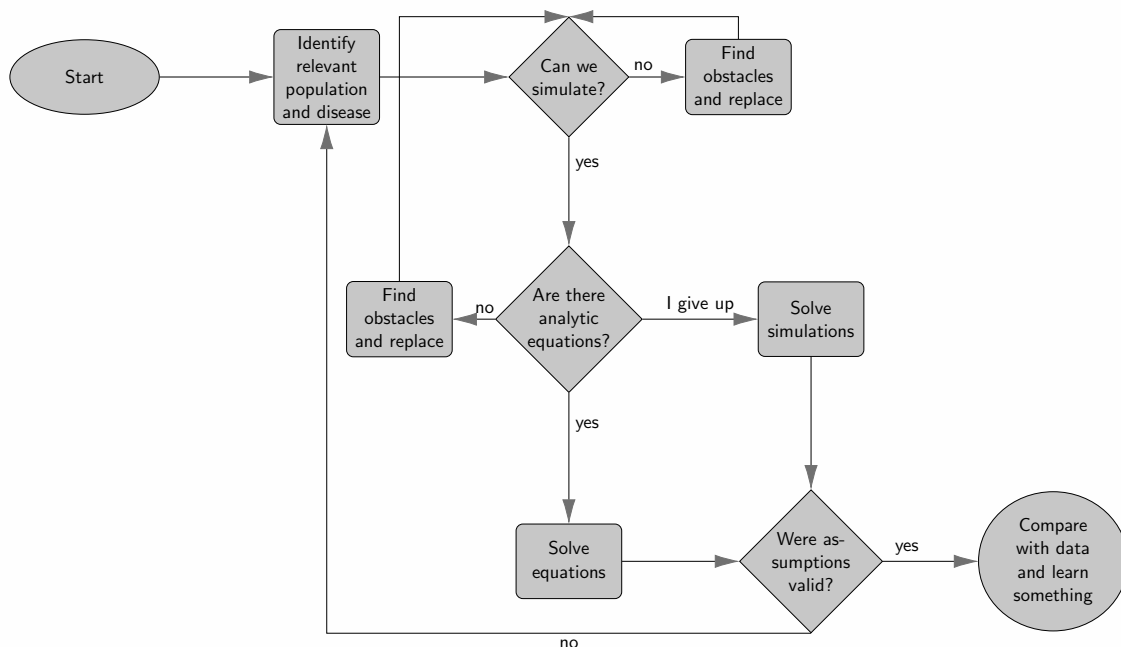
If you can't create a simulation that matches your analytic model, then either:

- ▶ You are a very good mathematician working on a very difficult problem, and you've put in a lot of effort to determine the limits of your model or
- ▶ You are doing something wrong.

We want



Basic approach to creating a mathematical model



Introduction

Mass Action Models

Key Epidemic Quantities

Introducing Networks

References

Simple Mass Action Models

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

The major assumptions:

- ▶ Every individual is average.
- ▶ Every interaction of u is with a randomly chosen other individual.

Throughout:

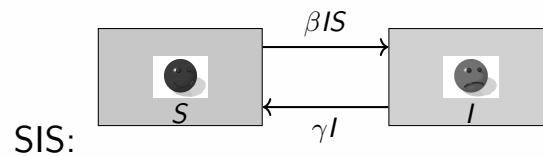
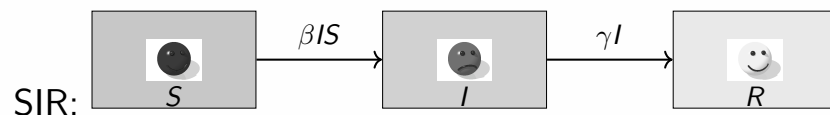
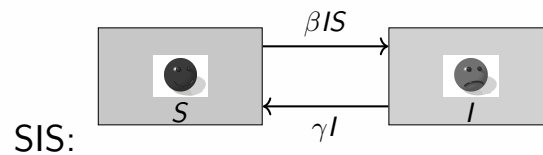
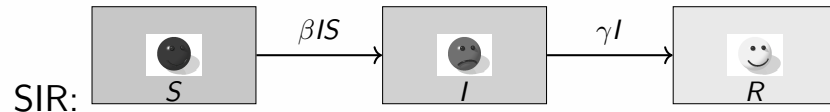
$$S + I + R = 1$$

That is, we look at proportions in each state, not absolute number.

Continuous time: Kermack–McKendrick

Assumptions:

- Individuals recover with rate γ .
- Infected individuals transmit at rate β .
- The proportion of transmissions that go to susceptible individuals is S .



- SIR equations are:

$$\dot{S} = -\beta IS$$

$$\dot{I} = \beta IS - \gamma I$$

$$\dot{R} = \gamma I$$

- SIS equations are

$$\dot{S} = -\beta IS + \gamma I$$

$$\dot{I} = \beta IS - \gamma I$$

Non-dimensionalizing

If we measure time in terms of $1/\gamma$, then in the new units the average infection duration is 1.

The new SIR equations are

$$\dot{S} = -\mathcal{R}_0 IS$$

$$\dot{I} = \mathcal{R}_0 IS - I$$

$$\dot{R} = I$$

The new SIS equations are

$$\dot{S} = -\mathcal{R}_0 IS + I$$

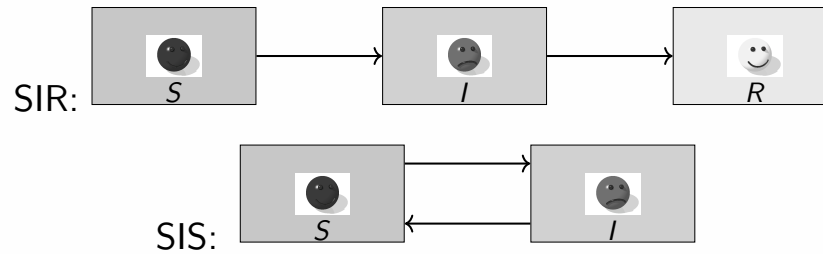
$$\dot{I} = \mathcal{R}_0 IS - I$$

Where

$$\mathcal{R}_0 = \frac{\beta}{\gamma}$$

Fit to simulation

Discrete time: Reed–Frost



- ▶ Each individual u is infectious for a single timestep.
- ▶ In that timestep u will transmit to each other individual in the population independently with probability \mathcal{R}_0/N .
- ▶ The probability a susceptible node v remains infected is thus $(1 - \mathcal{R}_0/N)^{I^N} \approx e^{-\mathcal{R}_0 I}$ for large N .

The equations are

$$S_{t+1} = e^{-\mathcal{R}_0 I_t} S_t \approx (1 - \mathcal{R}_0 I_t) S_t$$

$$I_{t+1} = S_t (1 - e^{-\mathcal{R}_0 I_t}) \approx \mathcal{R}_0 I_t S_t$$

$$R_{t+1} = R_t + I_t$$

Fit to simulation

Interpreting \mathcal{R}_0

In these simple models, \mathcal{R}_0 can be interpreted as

the expected number of infections a single infected individual will cause in an otherwise fully susceptible population.

More generally, we define \mathcal{R}_0 to be

the expected number of secondary cases produced by a typical infected individual early in an epidemic

We'll return to this subtle difference later.

Introduction

Mass Action Models

Key Epidemic Quantities

Introducing Networks

References

Lots of things to think about

For SIR, we are typically interested in

- ▶ \mathcal{P} , the probability of an epidemic.
- ▶ \mathcal{A} , the “attack rate”: the fraction infected (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, we are typically interested in

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

Introduction

Mass Action Models

Key Epidemic Quantities

Introducing Networks

References

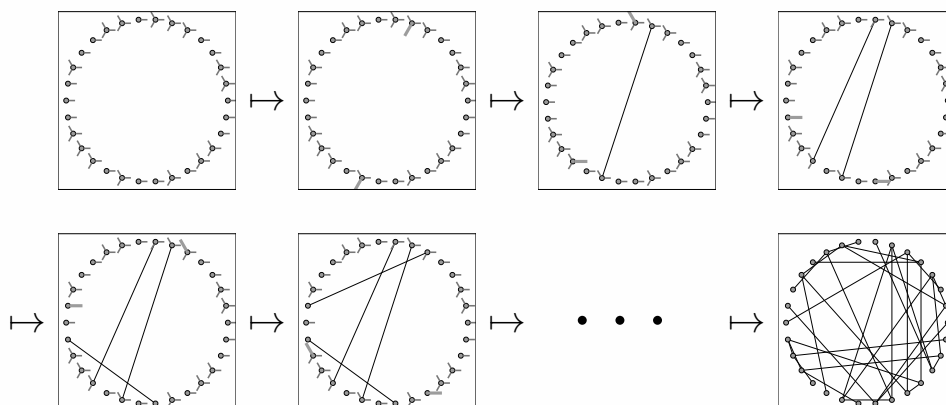
Network Assumptions

We begin with basic assumptions about contact structure.

- ▶ The number of partners an individual has is its “degree” k .
- ▶ k varies from individual to individual.
- ▶ $P(k)$ is the proportion of the population with degree k .
- ▶ We seek the simplest model that satisfies these assumptions.
- ▶ Partners are randomly chosen.
- ▶ The network connections do not change (static network).
This assumption is appropriate if the timescale of the epidemic is less than the typical partnership duration.

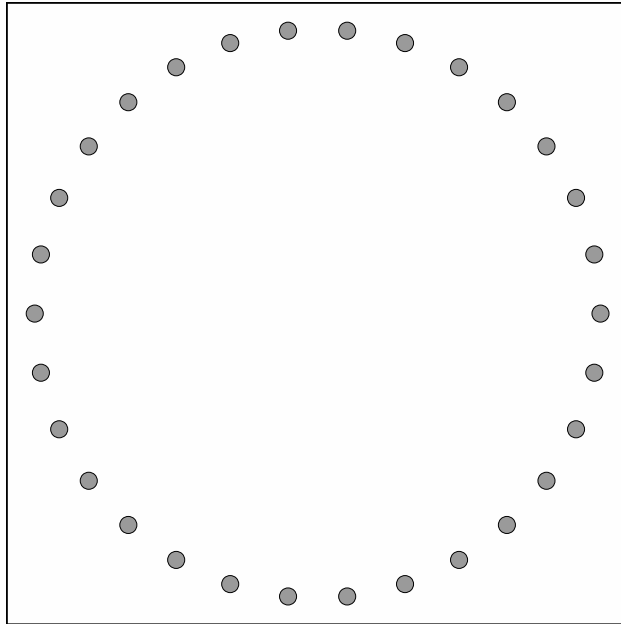
Configuration Model Networks

- ▶ Each individual has a “degree” k , its number of partners distributed randomly with probability $P(k)$.
- ▶ Pairs of stubs are chosen and joined into edges.
- ▶ This yields a null model: a random “Configuration Model Network” chosen to satisfy the degree distribution and nothing else.



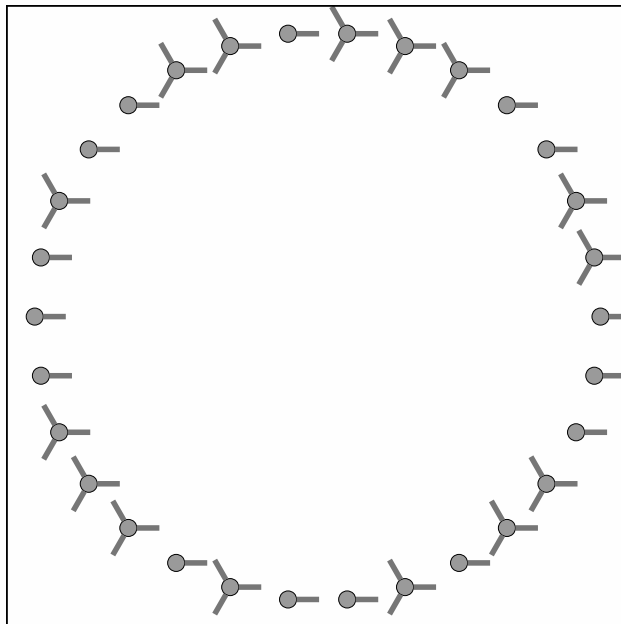
Size Bias

Do your friends have more friends than you do (on average)?



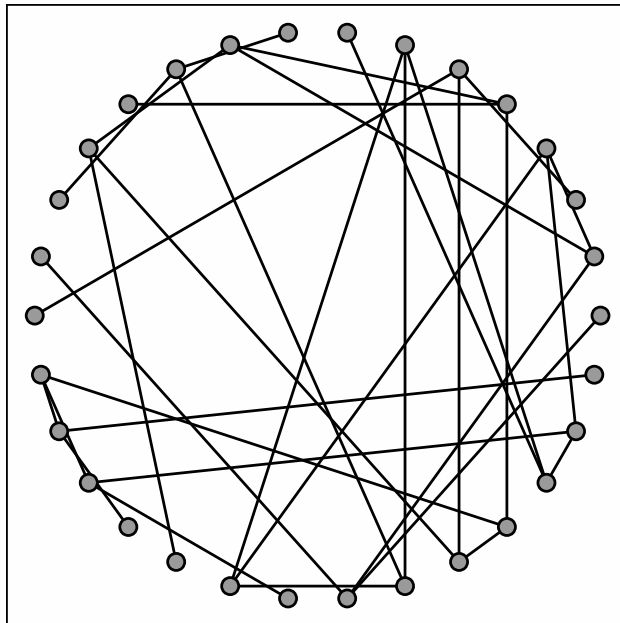
Size Bias

Do your friends have more friends than you do (on average)?



Size Bias

Do your friends have more friends than you do (on average)?



In fact $P_n(k) = kP(k) / \langle K \rangle$ where $\langle K \rangle$ is the average degree.

21 / 26

Size Bias

- ▶ A random individual has degree k with probability $P(k)$
- ▶ What about a random partner? What is the probability $P_n(k)$ a partner has degree k ?
- ▶ Because of how partners are selected, a random partner is likely to have higher degree than a random individual [2, 3].
- ▶ In fact $P_n(k) = kP(k) / \langle K \rangle$ where $\langle K \rangle$ is the average degree.
- ▶ Note that the degrees of a random individual and a random neighbor of a random individual have different distributions, but a random neighbor and a random neighbor's random neighbor are both from $P_n(k)$.

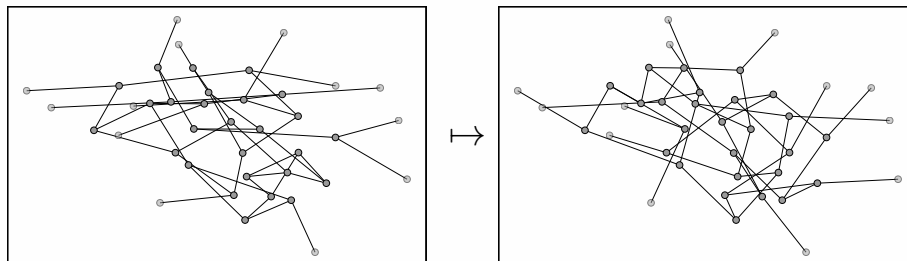
Size Bias

I cannot stress enough that if $P(k)$ is the probability a random individual has k partners, then

$$P_n(k) = kP(k)/\langle K \rangle$$

is the probability a random partner has k partners.

“Annealed” version



- ▶ The annealed network version assumes that at every moment the network looks like a Configuration model network.
- ▶ However, at every moment, an individual changes all of its partners.
- ▶ In practice this is appropriate if partnerships are so short or disease transmission so rare that an individual is unlikely to ever transmit to the same individual twice or transmit back to its infector.

Introduction

Mass Action Models

Key Epidemic Quantities

Introducing Networks

References

References I

- [1] Junling J. Ma and David J. D. Earn.
Generality of the final size formula for an epidemic of a newly invading infectious disease.
Bulletin of Mathematical Biology, 68(3):679–702, 2006.
- [2] Scott L. Feld.
Why your friends have more friends than you do.
American Journal of Sociology, 96(6):1464–1477, 1991.
- [3] N.A. Christakis and J.H. Fowler.
Social network sensors for early detection of contagious outbreaks.
PLoS ONE, 5(9):e12948, 2010.