

DS8104: Network Science

Class 22: Spreading Phenomena

a.k.a. Epidemics, Cascades, Walks

Alexander Gates



THE SCIENCE OF **SUPERSPREADING**

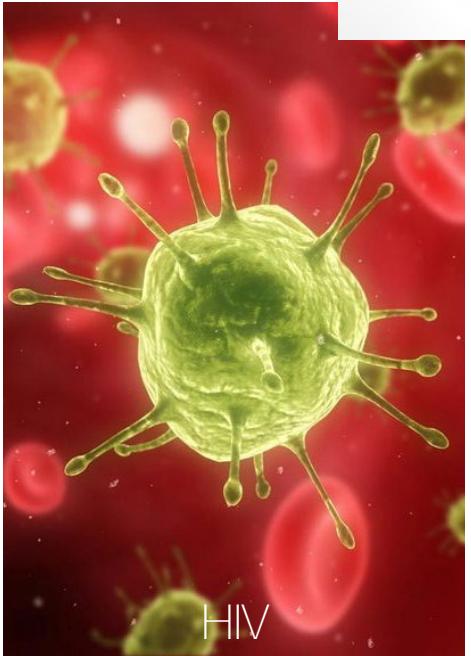
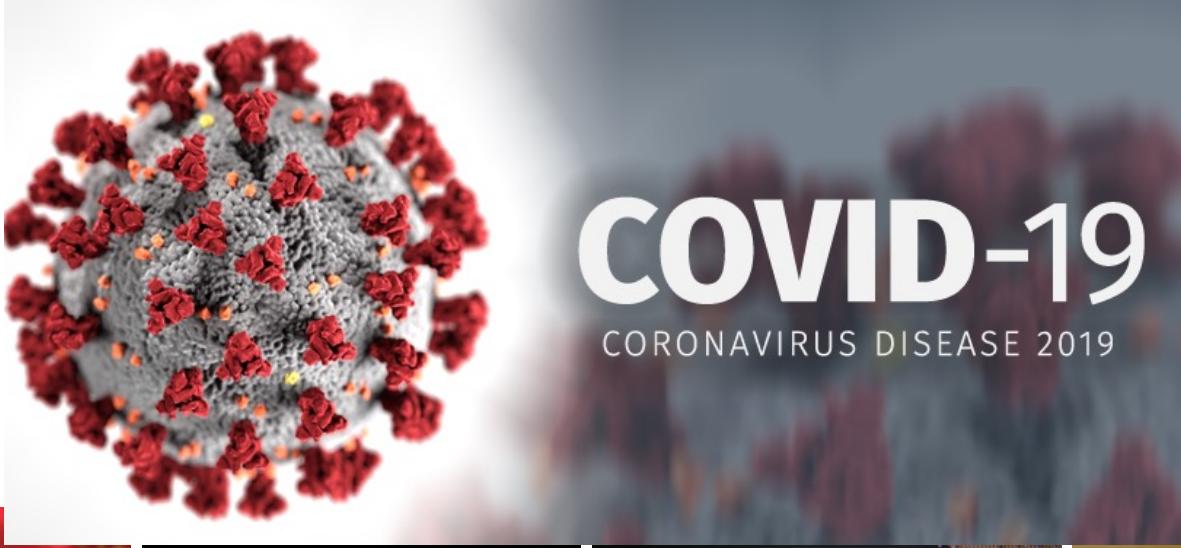
Why preventing hot spots of transmission is key to stopping the COVID-19 pandemic

By Martin Eserink, Kai Kupferschmidt, and Nirja Desai

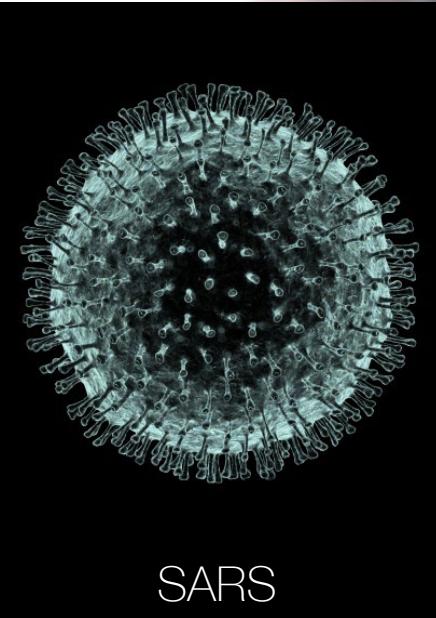
30 October 2020



<https://vis.sciencemag.org/covid-clusters/>



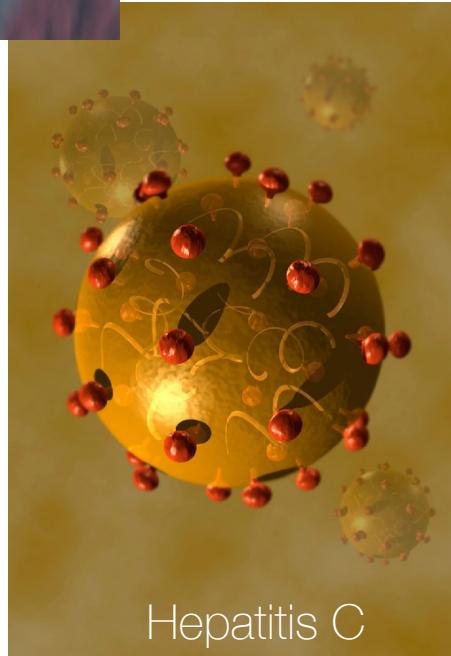
HIV



SARS

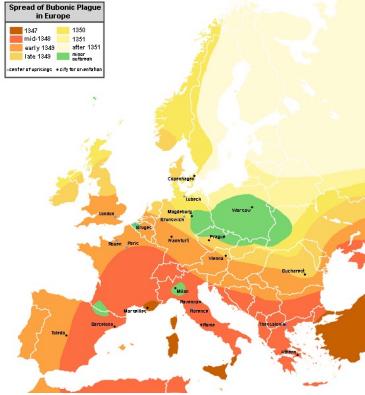


Influenza

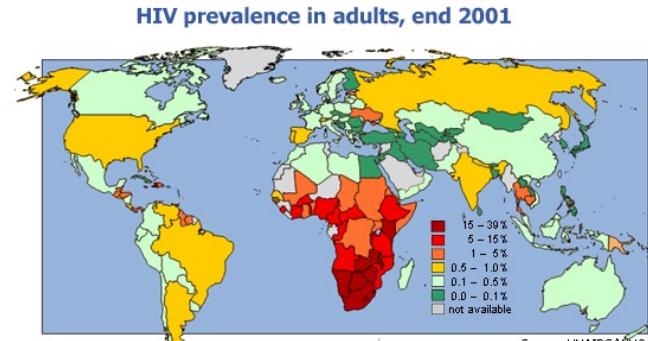


Hepatitis C

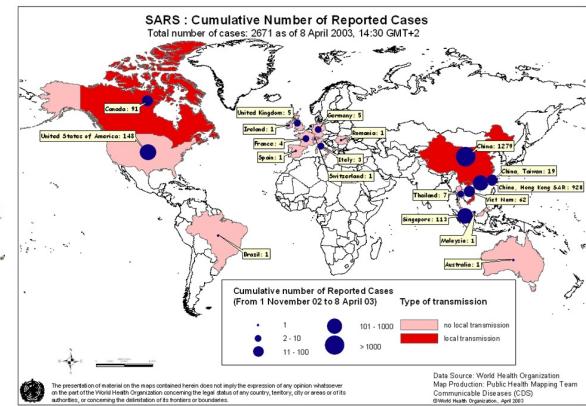
The Great Plague



HIV



SARS



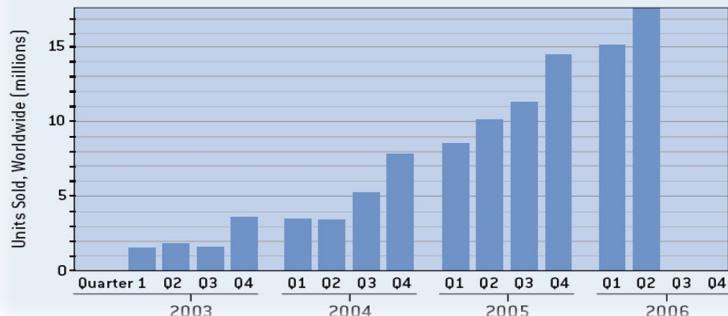
1918 Spanish flu

H1N1 flu



Computer viruses

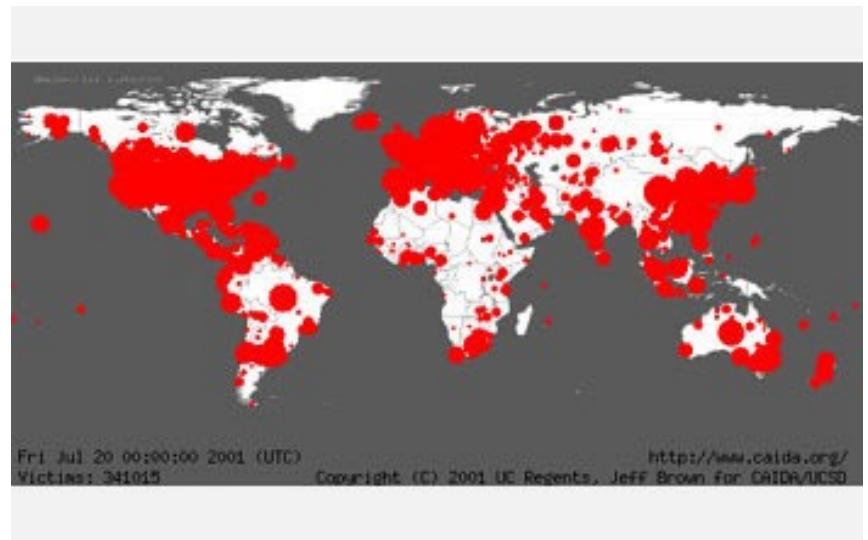
SMARTPHONES ON THE RISE



GROWTH IN MOBILE MALWARE

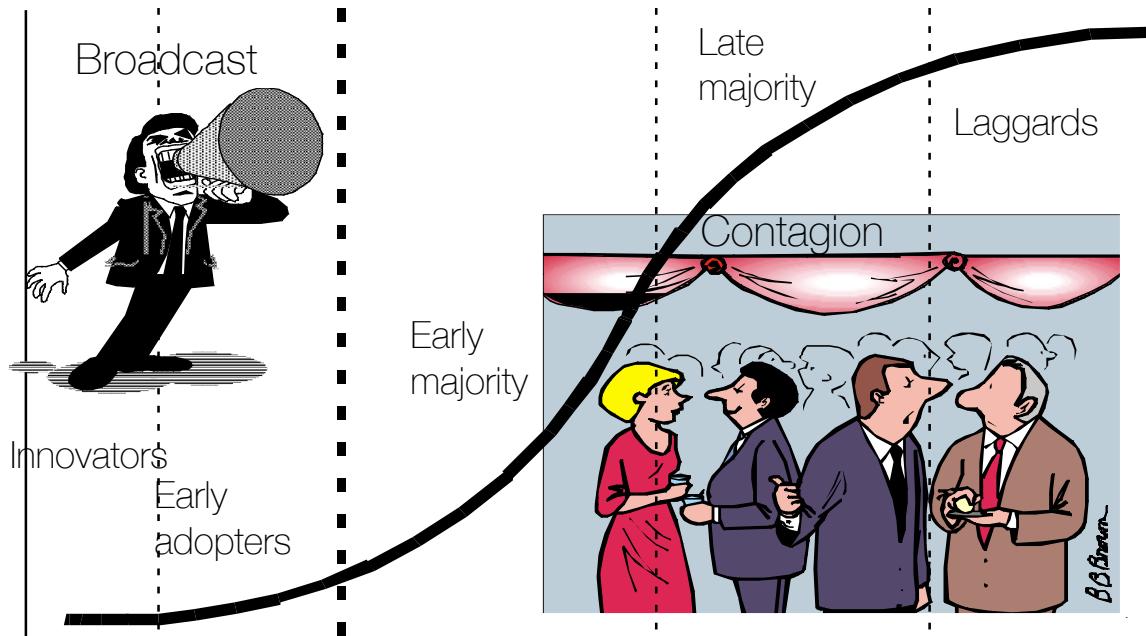


Code Red Worm paralyzed many countries' Internet



<http://www.caida.org/publications/visualizations/>

The spread of innovations = The Adoption Curve



Rogers, 1962

PHENOMENA	AGENT	NETWORK
Venereal Disease	Pathogens	Sexual Network
Rumor Spreading	Information, Memes	Communication Network
Diffusion of Innovations	Ideas, Knowledge	Communication Network
Computer Viruses	Malwares, Digital viruses	Internet
Mobile Phone Virus	Mobile Viruses	Social Network/Proximity Network
Bedbugs	Bedbugs	Hotel - Traveler Network
Malaria	Plasmodium	Mosquito - Human network

Epidemic Modeling (classical models)

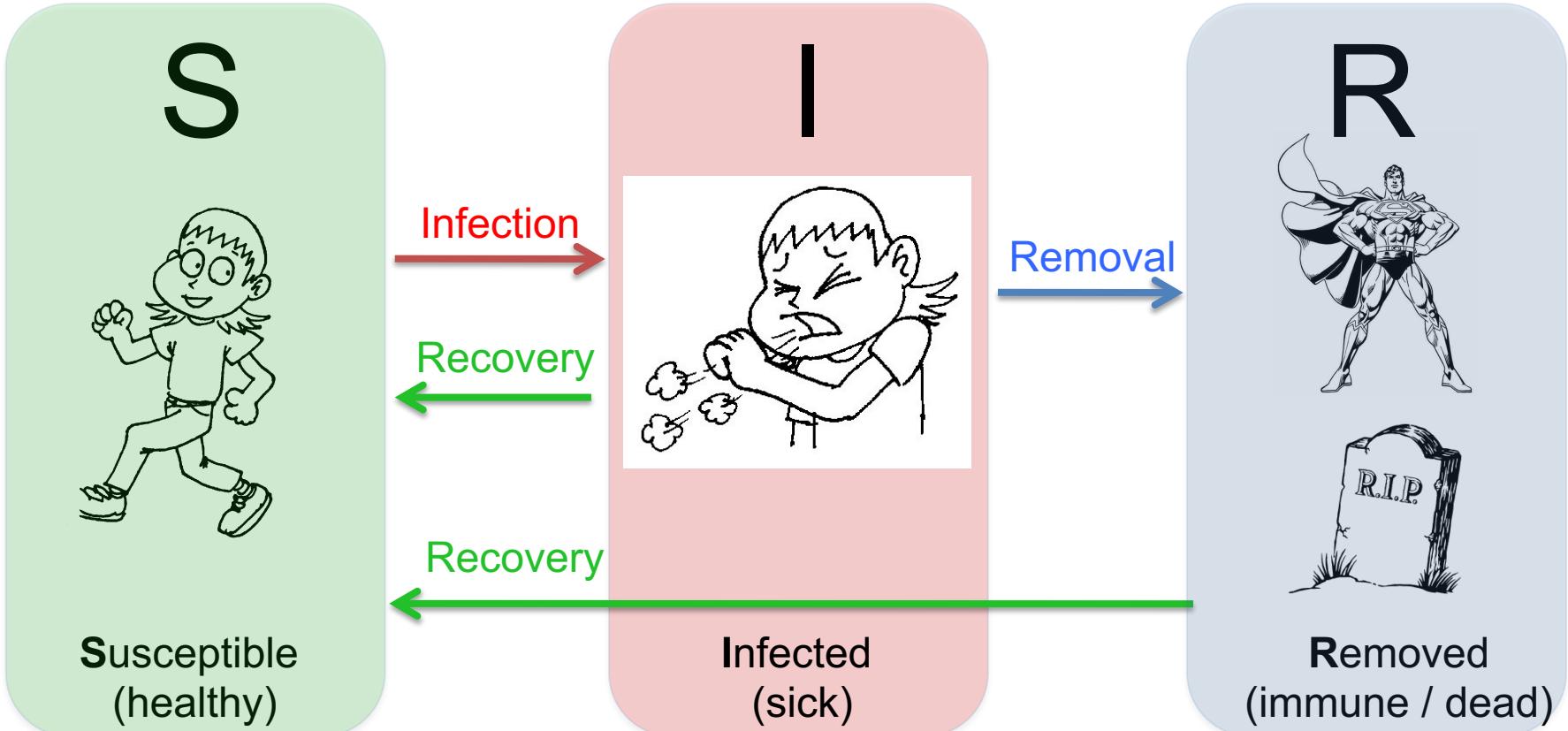
i. Compartmentalization

Epidemic models classify each individual into distinct states, based on the stage of the disease affecting them. The simplest classification assumes that an individual can be in one of three states (or compartments):

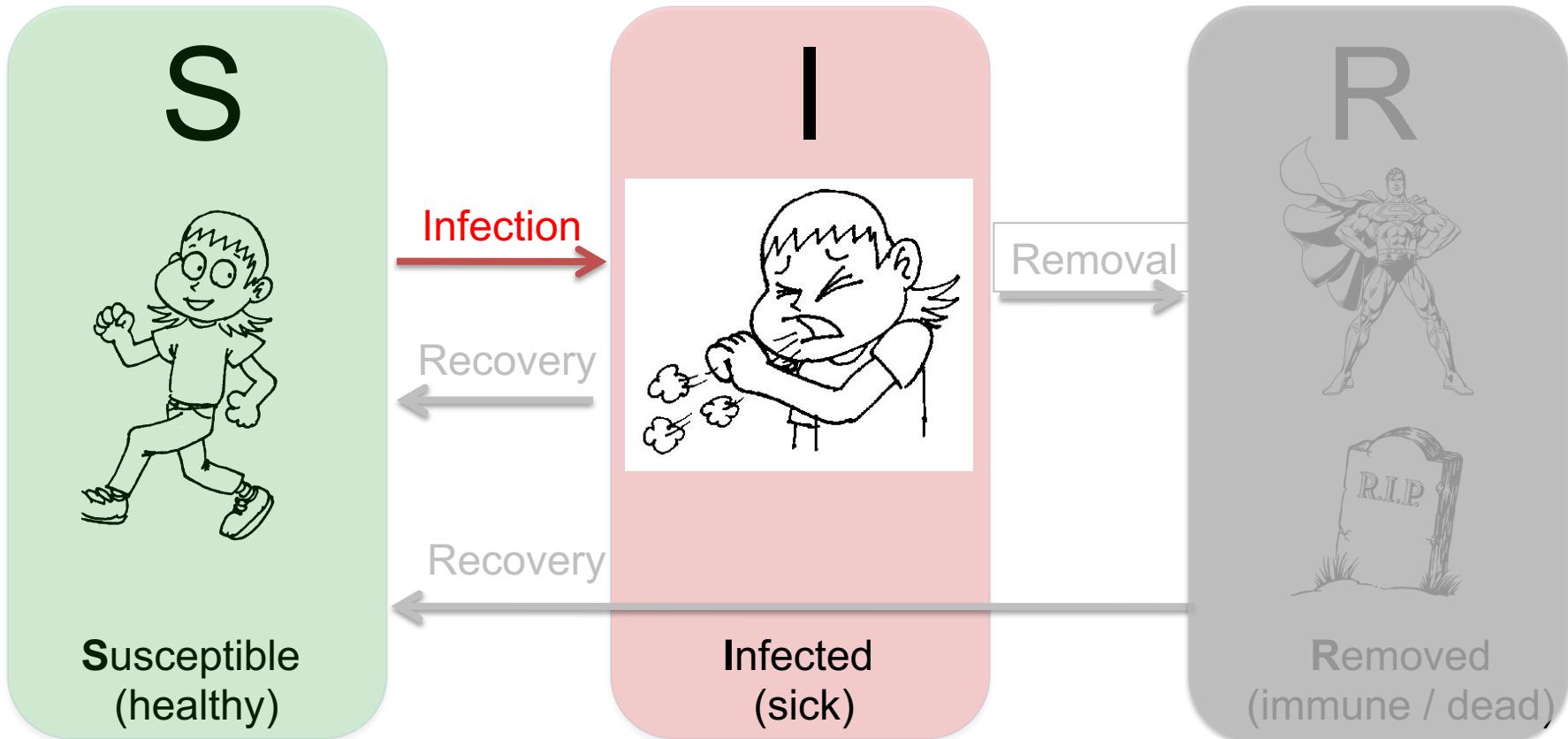
- *Susceptible (S)*: Healthy individuals who have not yet contacted the pathogen.
- *Infectious (I)*: Contagious individuals who have contacted the pathogen and hence can infect others.
- *Recovered (R)*: Individuals who have been infected before, but have recovered from the disease, hence are not infectious.

ii. Homogenous Mixing

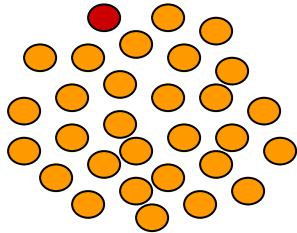
The homogenous mixing hypothesis (also called fully mixed or mass-action approximation) assumes that each individual has the same chance of coming into contact with an infected individual. This hypothesis eliminates the need to know the precise contact network on which the disease spreads, replacing it with the assumption that anyone can infect anyone else.



The SI model



The SI model



- Each individual has $\langle k \rangle$ contacts with randomly chosen others individuals per unit time.
- The likelihood that the disease will be transmitted from an infected to a healthy individual in a unit time: β

If there are I infected individuals and S susceptible individuals, the average rate of new infection is $\beta S I / N$

$$\beta \langle k \rangle \frac{S(t)I(t)}{N} dt.$$

$$\frac{dI(t)}{dt} = \beta \langle k \rangle \frac{S(t)I(t)}{N}.$$

The SI model

$$\frac{dI(t)}{dt} = \beta\langle k \rangle \frac{S(t)I(t)}{N}.$$

$$s = S/N, \quad i = I/N$$

$$\frac{di}{dt} = \beta si = \beta i(1 - i)$$

$\beta\langle k \rangle$ is called the *transmission rate* (or transmissibility).

$$\frac{di}{i} + \frac{di}{(1 - i)} = \beta\langle k \rangle dt. \quad \ln i - \ln(1 - i) + c = \beta\langle k \rangle t.$$

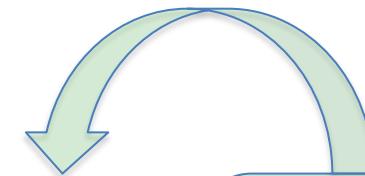
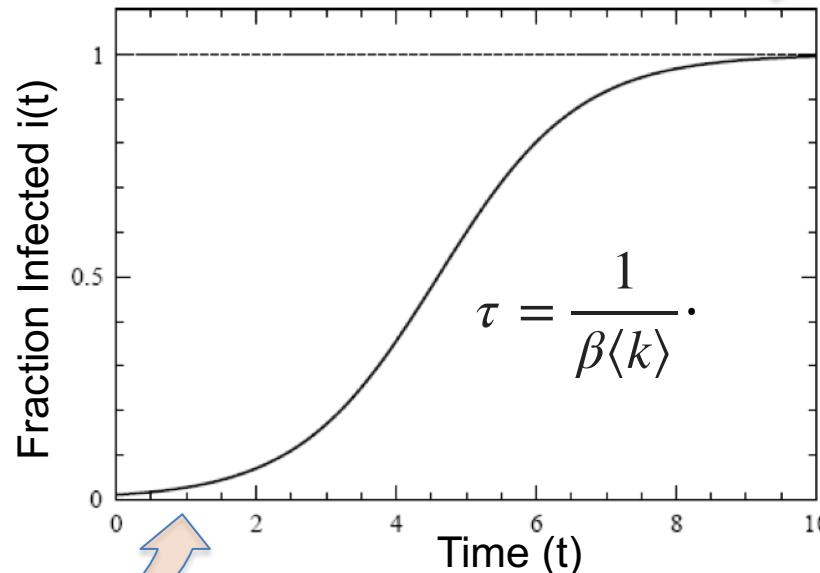
$$i(t) = \frac{i_0 \exp(\beta t)}{1 - i_0 + i_0 \exp(\beta t)}$$

The SI model

$$\frac{di}{dt} = \beta i(1 - i)$$

If $i(t)$ is small,
 $\frac{di}{dt} \approx \beta i$
 $i \approx i_0 \exp(\beta t)$
exponential outbreak

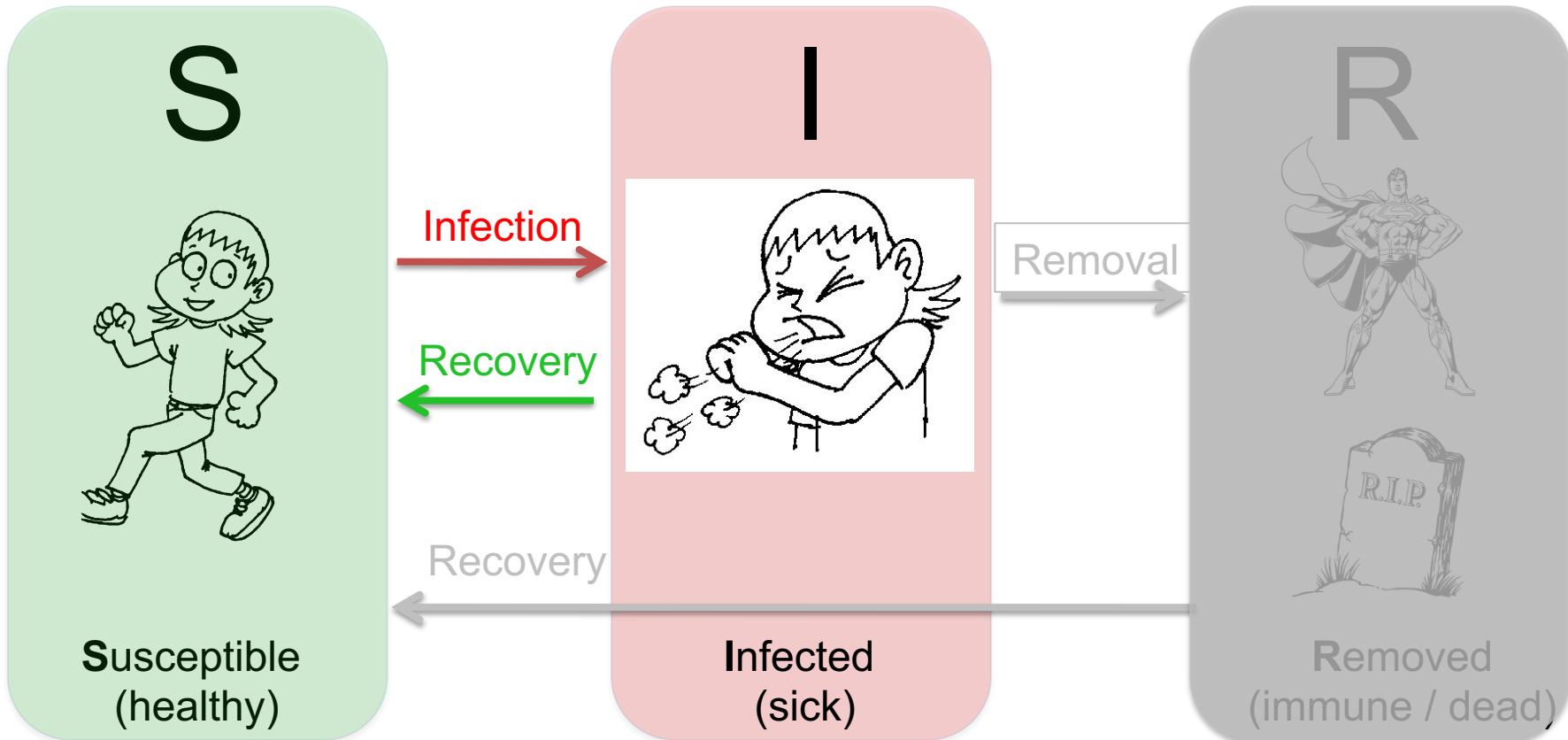
$$i(t) = \frac{i_0 \exp(\beta t)}{1 - i_0 + i_0 \exp(\beta t)}$$



As $i(t) \rightarrow 1$.
 $\frac{di}{dt} \rightarrow 0$
saturation

SI model: the fraction infected increases until everyone is infected.

The SIS model: Common Cold



The SIS model

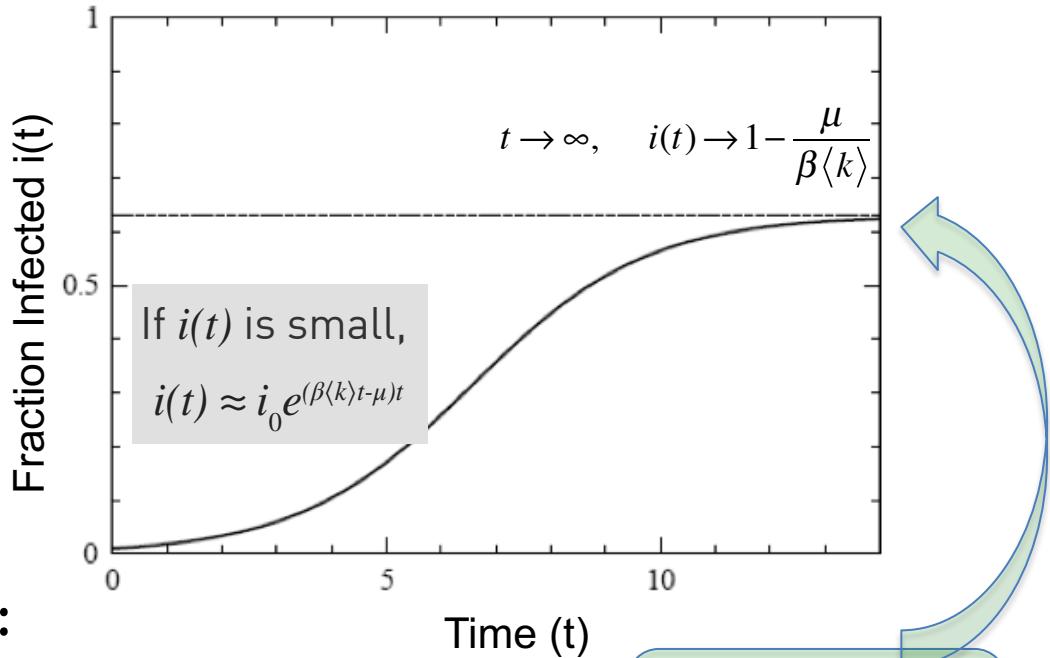
$$\frac{di}{dt} = \beta \langle k \rangle i(1 - i) - \mu i$$

I S I → S

$$i = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{Ce^{(\beta \langle k \rangle - \mu)t}}{1 + Ce^{(\beta \langle k \rangle - \mu)t}}.$$

Endemic state ($\mu < \beta \langle k \rangle$):

Disease-free state ($\mu > \beta \langle k \rangle$):



Stationary state:

$$\frac{di}{dt} = \beta i(1 - i) - \mu i = 0$$

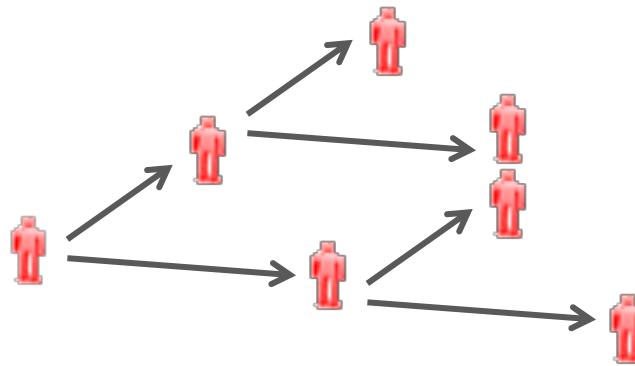
The SIS model: Reproductive Number

$$i = \left(1 - \frac{\mu}{\beta\langle k \rangle}\right) \frac{Ce^{(\beta\langle k \rangle - \mu)t}}{1 + Ce^{(\beta\langle k \rangle - \mu)t}}.$$

Characteristic Time: $\tau = \frac{1}{\mu(R_0 - 1)}$, $R_0 = \frac{\beta\langle k \rangle}{\mu}$.

Reproductive Number R_0 : average # of infectious individuals generated by one infected in a fully susceptible population.

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Choose
transmission
scenario

2

mild

$R_0=1.5$

medium

$R_0=1.9$

high

$R_0=2.3$

very high

$R_0=2.7$

Reproductive Number R_0 : average # of infectious individuals generated by one infected in a fully susceptible population.

Disease	Transmission	R_0
Measles	Airborne	12-18
Pertussis	Airborne droplet	12-17
Diphtheria	Saliva	6-7
Smallpox	Social contact	5-7
Polio	Fecal-oral route	5-7
Rubella	Airborne droplet	5-7
Mumps	Airborne droplet	4-7
HIV/AIDS	Sexual contact	2-5
SARS	Airborne droplet	2-5
Influenza (1918 strain)	Airborne droplet	2-3

COVID-19:
1.5 – 5+

depends on variant,
masking, isolation, etc.

Choose
transmission
scenario

2

mild

$R_0=1.5$

medium

$R_0=1.9$

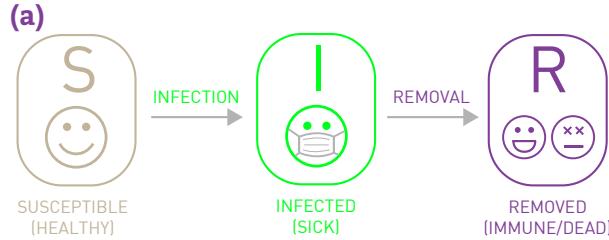
high

$R_0=2.3$

very high

$R_0=2.7$

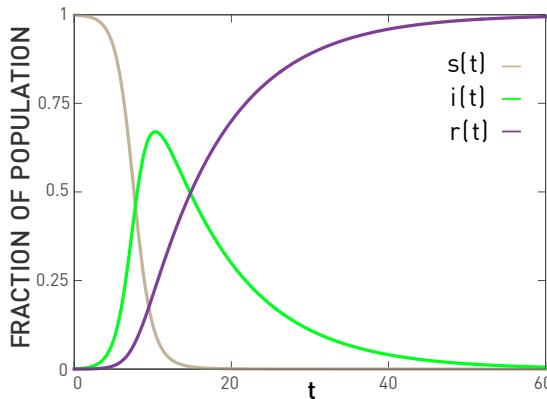
The SIR model

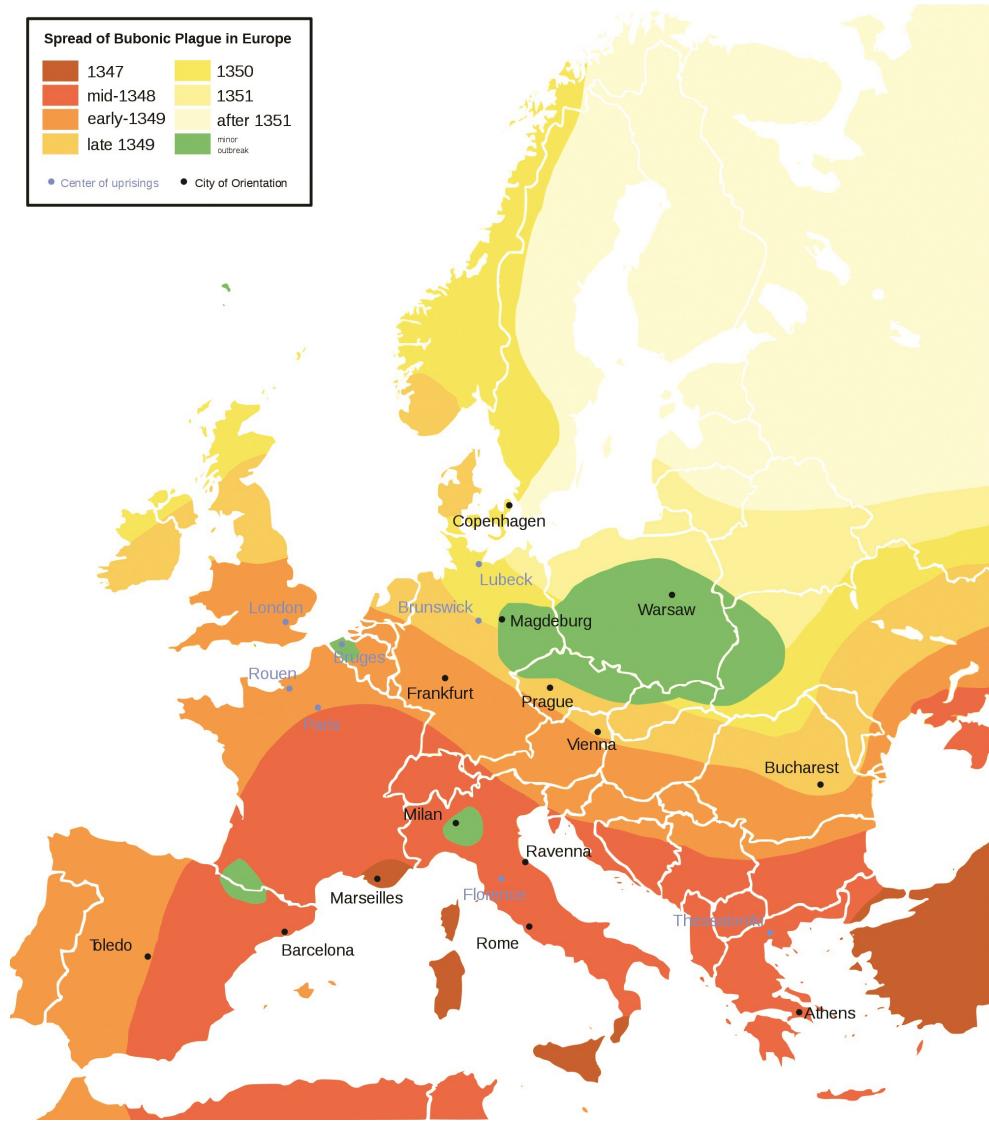
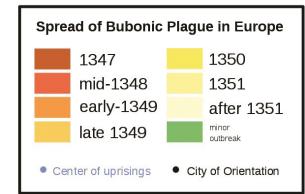


(b)

$$\begin{aligned}\frac{ds(t)}{dt} &= -\beta \langle k \rangle i(t) [I - r(t) - i(t)] \\ \frac{di(t)}{dt} &= -\mu i(t) + \beta \langle k \rangle i(t) [I - r(t) - i(t)] \\ \frac{dr(t)}{dt} &= \mu i(t).\end{aligned}$$

(c)



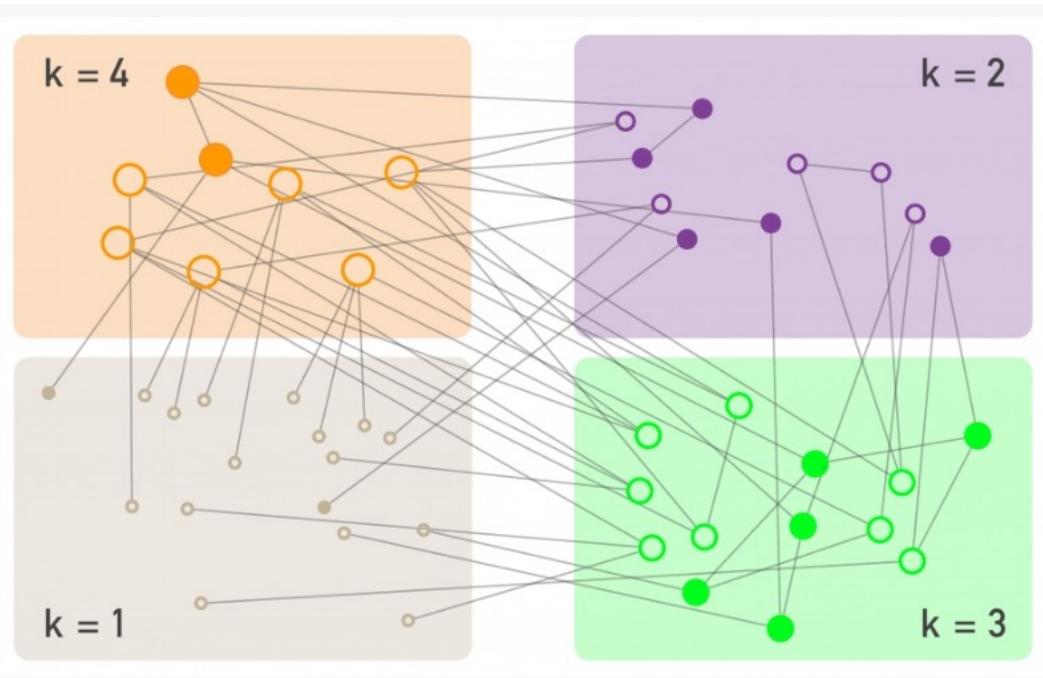


4 years from France to Sweden

Limited by the speed of human travel

The SIS network model: degree mean-field

Split nodes by their degrees

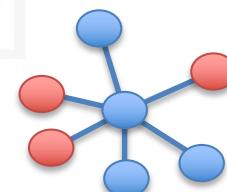


$$i_k = \frac{I_k}{N_k}, \quad i = \sum_k P(k)i_k$$

$$\frac{di_k(t)}{dt} = \beta(1 - i_k(t))k\Theta_k(t) - \mu i_k(t)$$

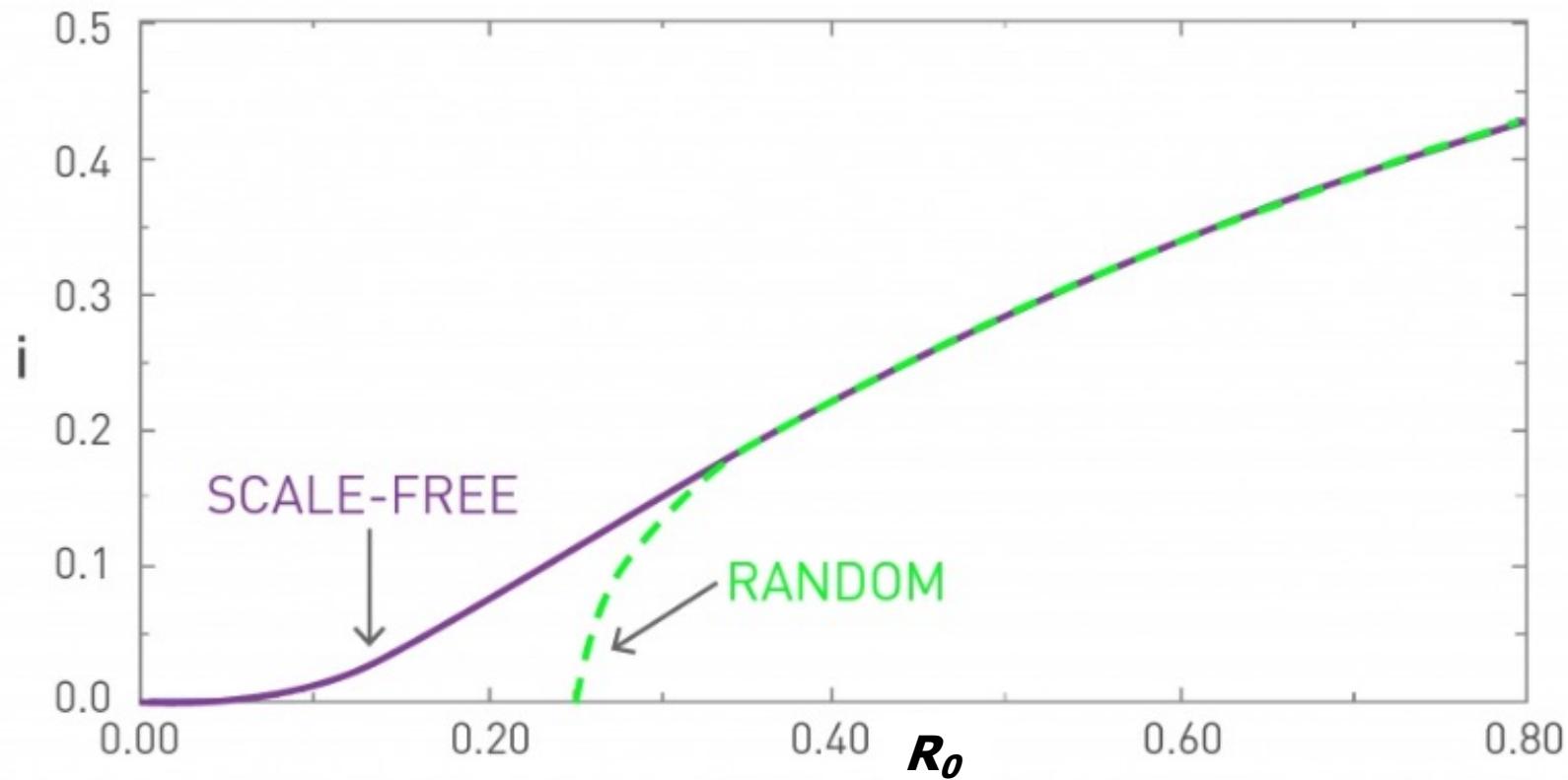
Proportional to k

Density of infected neighbors of nodes with degree k

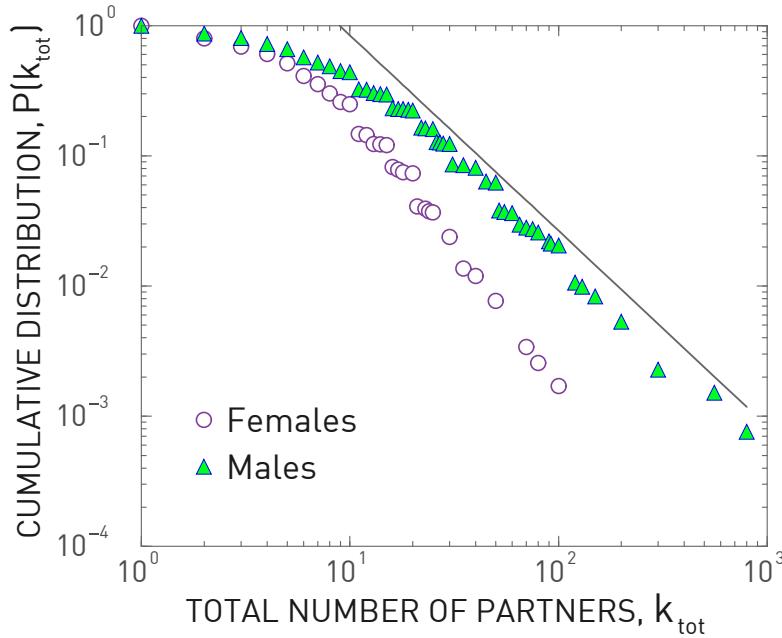


I am susceptible with k neighbors, and $\Theta_k(t)$ of my neighbors are infected.

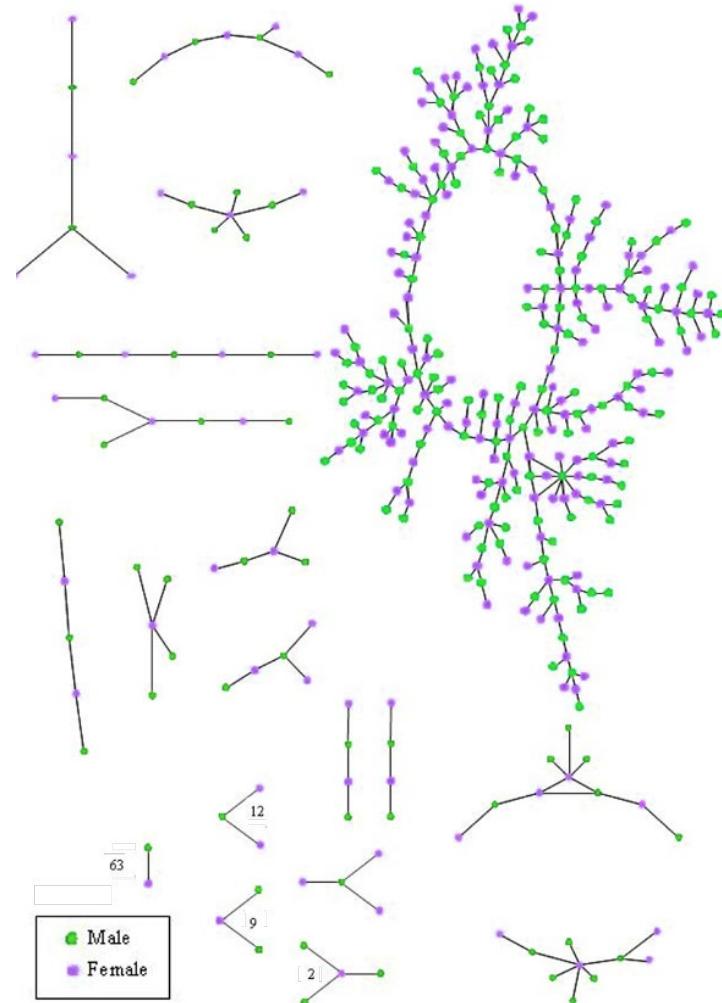
ER vs Scale-Free Networks



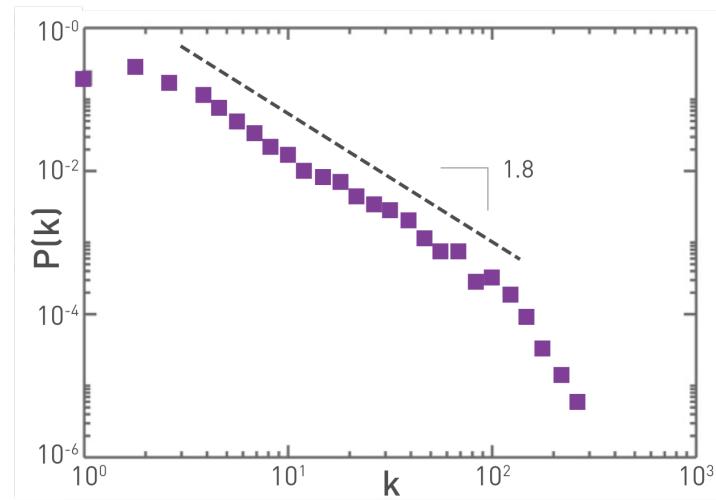
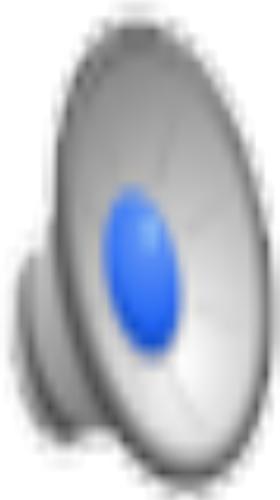
Contact Networks



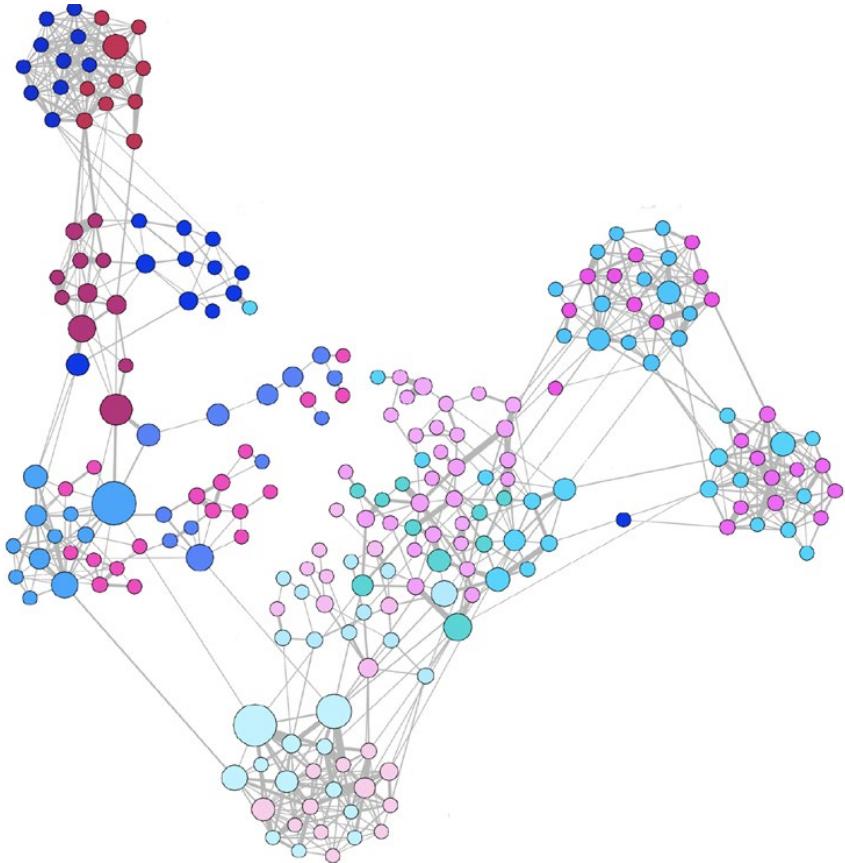
Through interviews and questionnaires, researchers collected information from 4,781 randomly chosen Swedes of ages 18 to 74. The participants were not asked to reveal the identity of their sexual partners, but only to estimate the number of sexual partners they had during their lifetime.



Transportation Networks



Face-to-Face Contact



A face-to-face contact network mapped out using RFA tags, capturing interactions between 232 students and 10 teachers across 10 classes in a school [31]. The structure of the obtained map depends on the context in which it is collected: the school network shown here reveals the presence of clear communities. In contrast, a study capturing the interactions between individuals that visited a museum reveal an almost linear network [29]. Finally, a network of attendees of a small conference is rather dense, as most participants interact with most others [29]. After [31].