

## Chapter 13

# Diffusion: Epidemics

### Summary

- Probabilistic Epidemic Models
  - SI/SIS/SIR
- Mean Field Formulation
- Epidemics on Networks

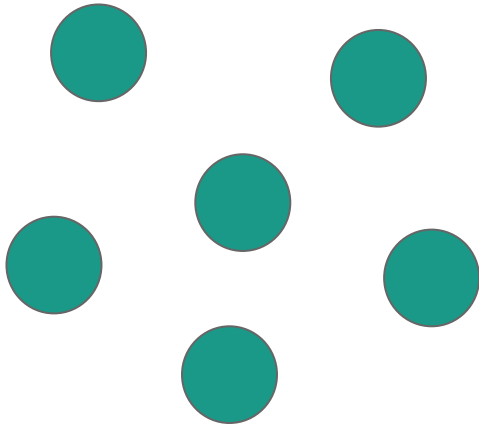
### Reading

- Chapter 21 of Kleinberg's book
- Chapter 10 of Barabasi's book

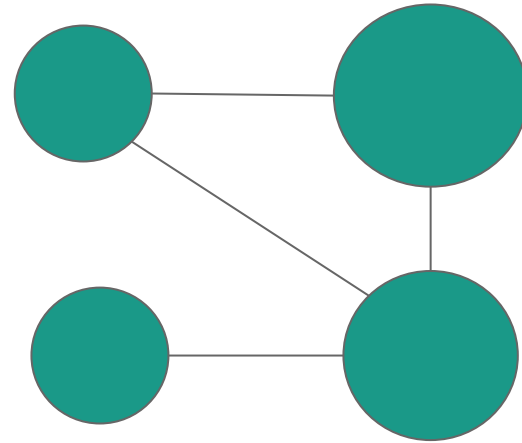








Separate, small population  
(hunter-gatherer society, wild animals)



Connected, highly populated areas  
(cities)

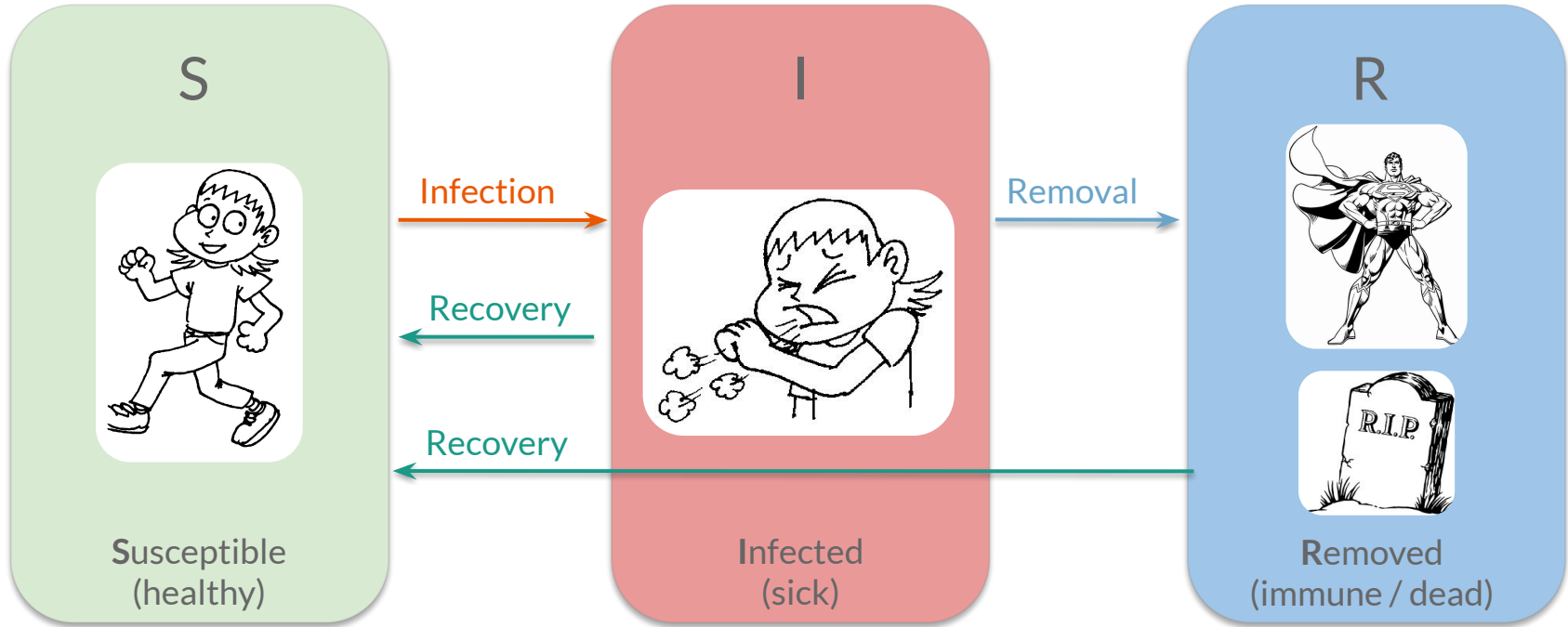
Human societies have “**crowd diseases**”, which are the consequences of large, interconnected populations (Measles, tuberculosis, smallpox, influenza, common cold, ...)

**Large population can provide the “fuel”**

# Probabilistic Epidemic Models



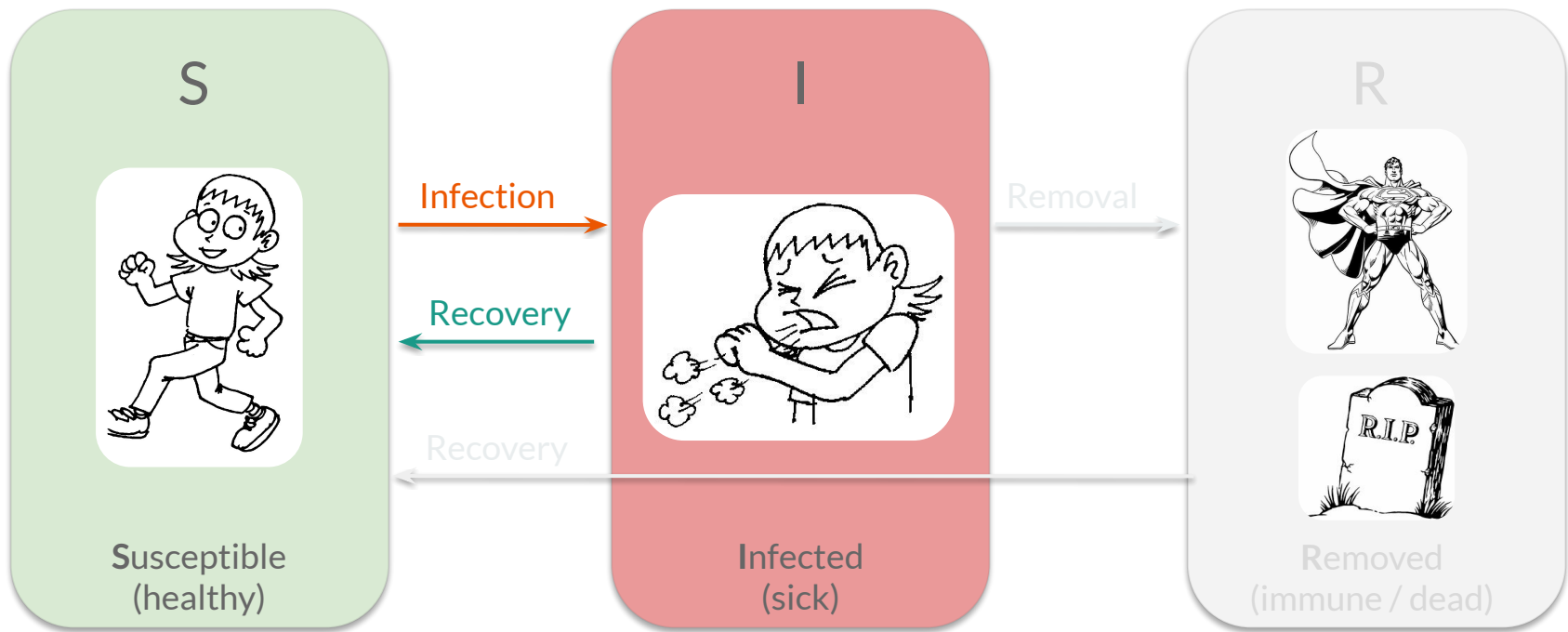




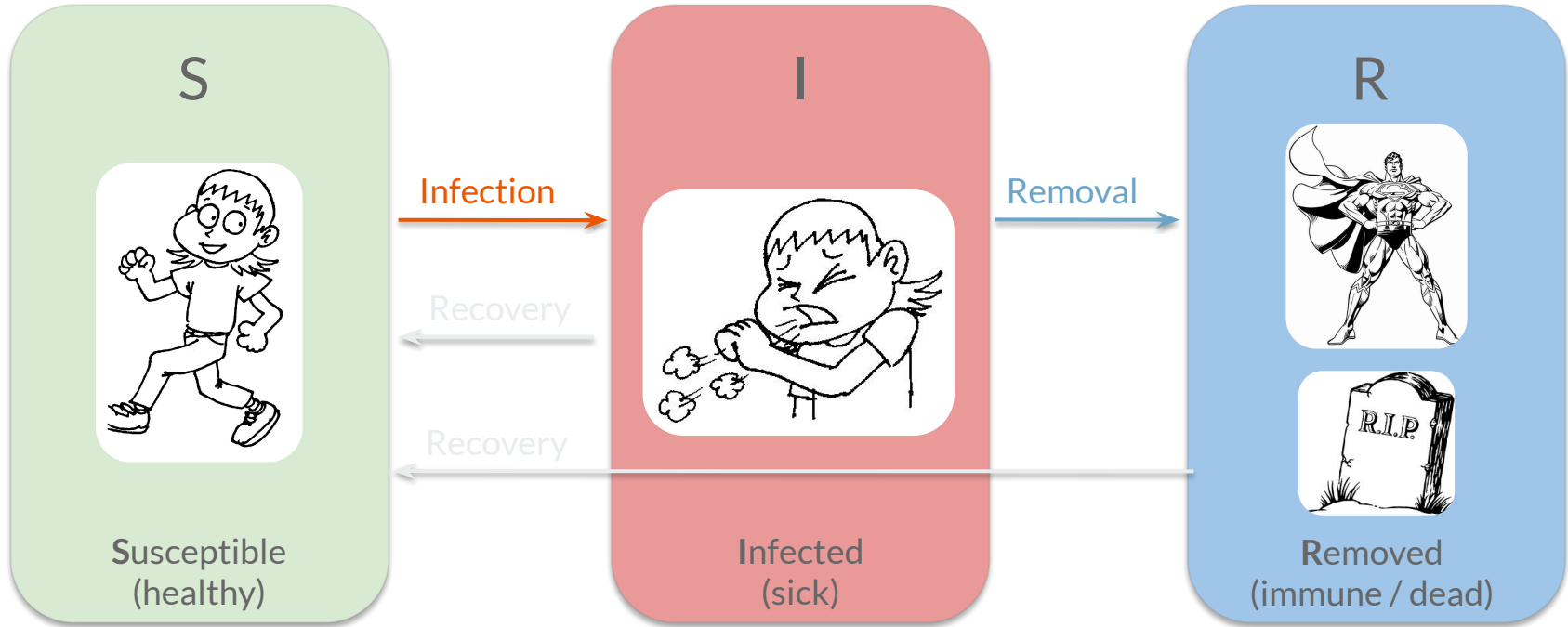
Classic Models Compartments







**SIS:** Common Cold



**SIR:** Flu, SARS, Plague

# Mean Field formulation

(Homogeneous mixing)



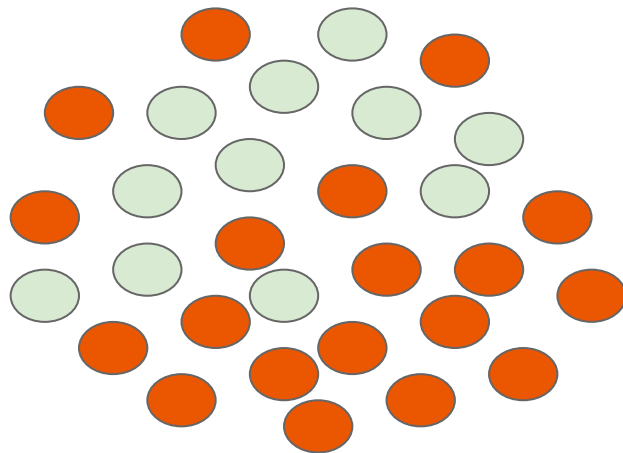
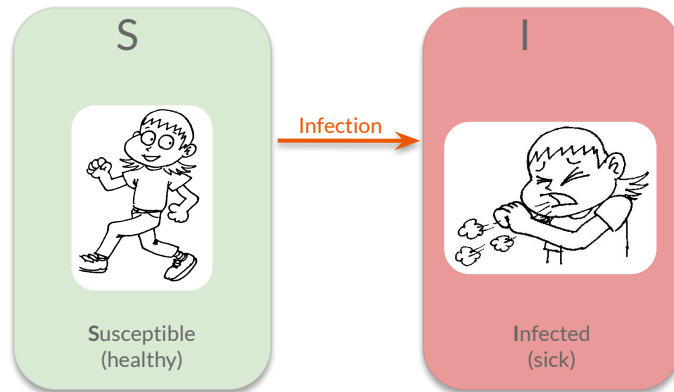
# SI model

Each individual has  $\beta$  contacts with randomly chosen others individuals per unit time.

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

with  $s = S/N$ ,  $i = I/N$

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



# SI model

## Dynamics

Logistic equation:  
a basic model of population growth.

$$\frac{di}{dt} = \beta \underbrace{i}_{I} (1 - \underbrace{i}_{S})$$

[http://en.wikipedia.org/wiki/Logistic\\_function](http://en.wikipedia.org/wiki/Logistic_function)  
<http://mathworld.wolfram.com/LogisticEquation.html>

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

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

$$\ln \frac{i}{1-i} = c + \beta t$$

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

SI model

## Behaviour

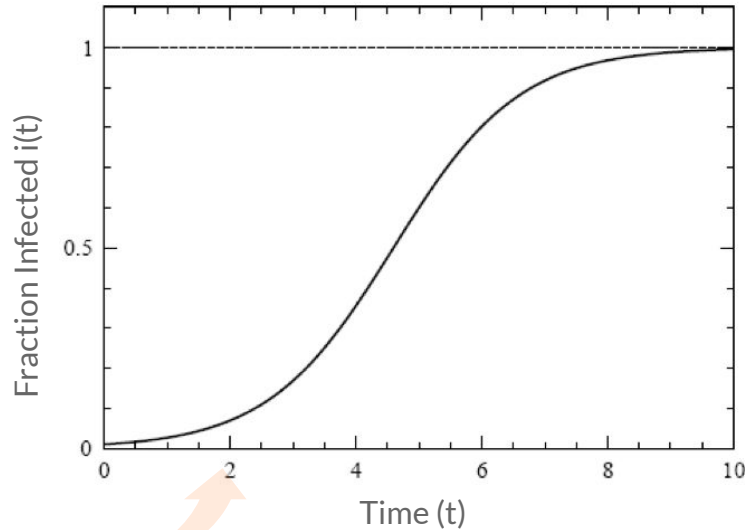
$$i(t) = \frac{i_0 \exp(\beta t)}{1 - i_0 + i_0 \exp(\beta t)}$$

If  $i(t)$  is small,

$$\frac{di}{dt} \approx \beta i$$

$$i \approx i_0 \exp(\beta t)$$

exponential  
outbreak



As  $i(t) \sim 1$ .

$$\frac{di}{dt} \rightarrow 0$$

saturation

**SI model:**

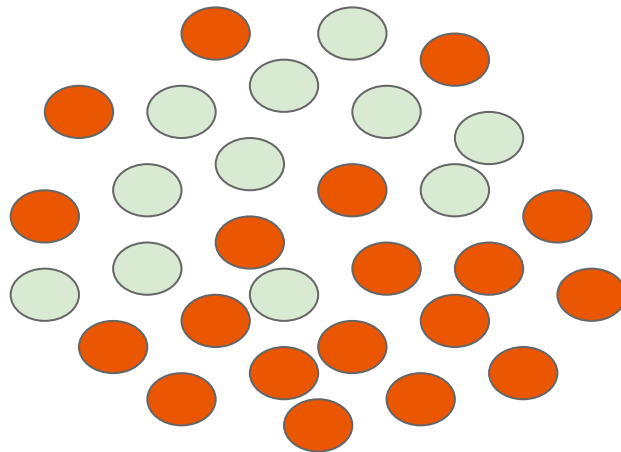
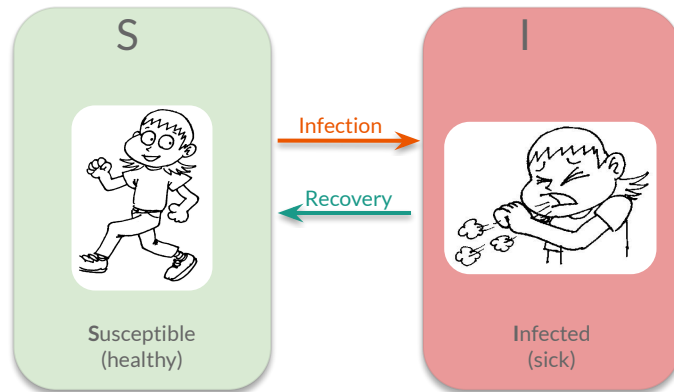
the fraction infected increases  
until everyone is infected.

# SIS model

## Modeling Common Cold

Each individual has  $\beta$  contacts with randomly chosen others individuals per unit time.

Each infected individual has  $\mu$  probability of revert its status to susceptible



SIS model

## Behaviour

$$\frac{di}{dt} = \underbrace{\beta i(1-i)}_{\text{I} \rightarrow \text{S}} - \underbrace{\mu i}_{\text{I} \rightarrow \text{S}} = i(\beta - \mu - \beta i)$$

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

$$\ln(i) - \ln(1 - \mu/\beta - i) = (\beta - \mu)t + c$$

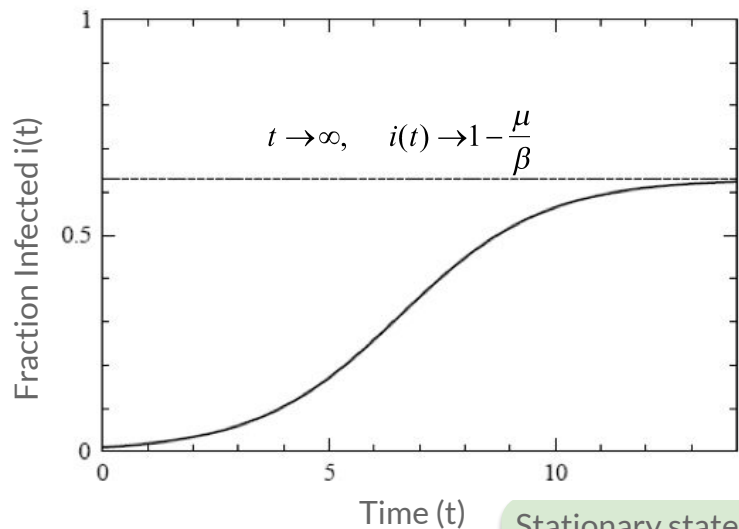
$$\frac{i}{1 - \mu/\beta - i} = Ce^{(\beta - \mu)t}$$

$$\therefore i(t) = \left(1 - \frac{\mu}{\beta}\right) \frac{Ce^{(\beta - \mu)t}}{1 + Ce^{(\beta - \mu)t}}$$



## SIS model

# Dynamics



Stationary state:

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

$$\therefore i(t) = \left(1 - \frac{\mu}{\beta}\right) \frac{C e^{(\beta - \mu)t}}{1 + C e^{(\beta - \mu)t}}$$

**SIS model:**

the fraction of infected individual saturates below 1

SIS model

# Basic Reproductive Number

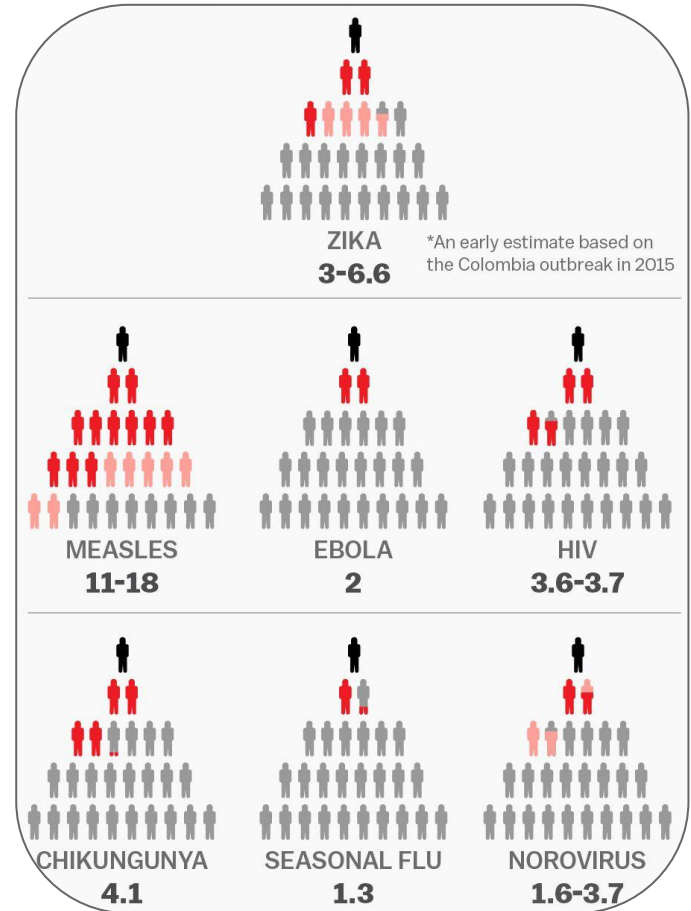
$\lambda$  (also identified with  $R_0$ ):  
average # of infectious individuals  
generated by one infected in a fully  
susceptible population.

$$\lambda \equiv \frac{\beta}{\mu}$$

$\lambda > 1$ : Outbreak

$\lambda < 1$ : Die Out

Epidemic Threshold  
if  $\mu \approx 0$  then  $i \rightarrow 0$

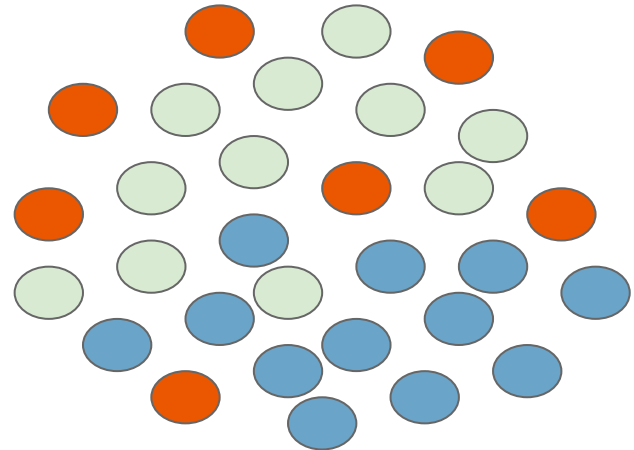
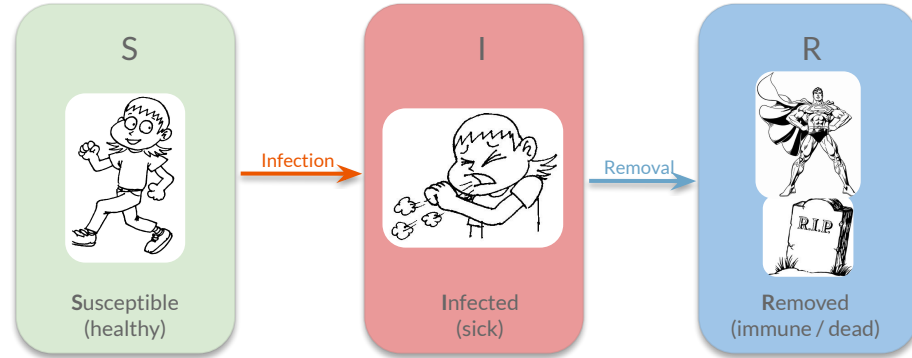


# SIR model

## Modeling Flu-like disease

Each individual has  $\beta$  contacts with randomly chosen others individuals per unit time.

Each infected individual has  $\mu$  probability of becoming immune after being infected



SIS model

## Behaviour

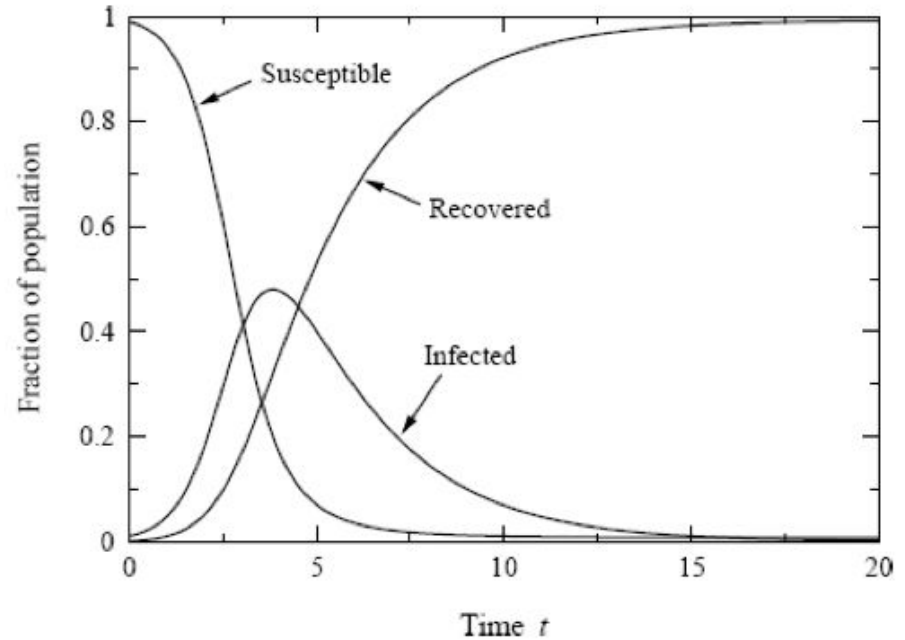
$$\frac{ds(t)}{dt} = \beta \langle k \rangle i(t) [1 - r(t) - i(t)]$$

$$\frac{di(t)}{dt} = -\mu i(t) + \beta \langle k \rangle i(t) [1 - r(t) - i(t)]$$

$$\frac{dr(t)}{dt} = \mu i(t).$$

**SIR model:**

the fraction infected peaks and the fraction recovered saturates.



	SI	SIS
<b>1</b> <b>Early Behaviour</b> Exponential growth of infected individuals	$i(t) = \left(1 - \frac{\mu}{\beta}\right) \frac{Ce^{(\beta-\mu)t}}{1 + Ce^{(\beta-\mu)t}}$	$i(t) = \frac{i_0 \exp(\beta t)}{1 - i_0 + i_0 \exp(\beta t)}$
<b>2</b> <b>Late Behaviour</b> Saturation at $t \rightarrow \infty$	$i(t) \rightarrow 1$	$i(t) \rightarrow 1 - \frac{\mu}{\beta}$
<b>3</b> <b>Epidemic Threshold</b> Disease not always spread	No Threshold	$\lambda_c = 1$

Recap: Basic Features of Epidemic Models

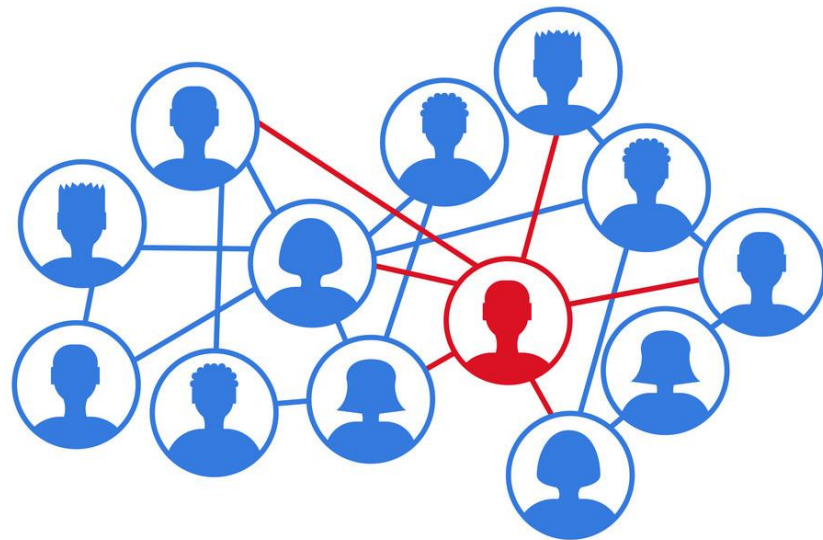
# Epidemics on Networks



# Topology matters

The described approaches assumed *homogenous mixing*, which means that each individual can infect *any* other individual.

In reality, epidemics spread along *links in a network*: we need to explicitly account for the role of the network in the epidemic process.



# Modeling choices

## Degree based representation:

split nodes by degree

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

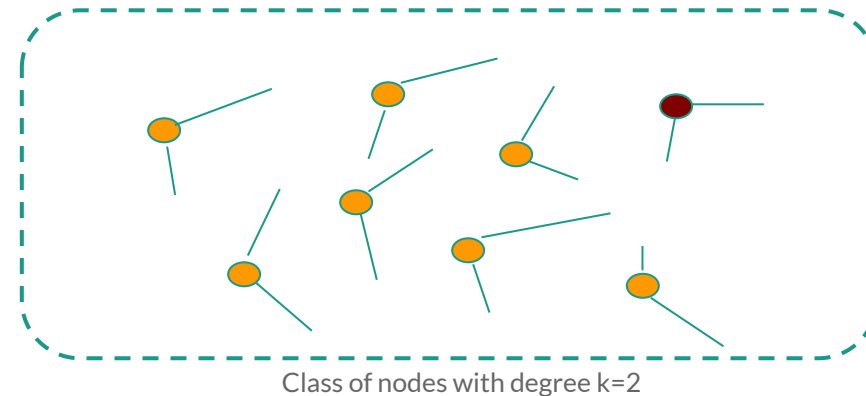
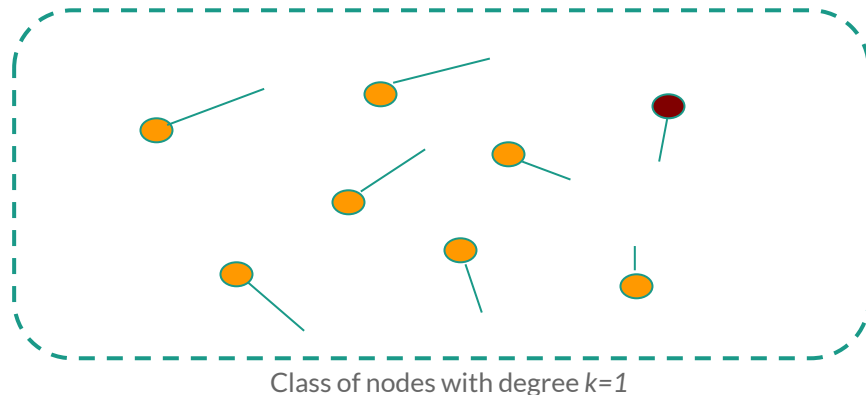
## Example SIS:

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

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

Proportional to  $k$

Density of infected  
neighbors of nodes with  
degree  $k$





# Modeling choices

## Agent based representation:

Each node is an agent having a current status (S/I/R...) and subject to probabilistic transition rules

## Example SIR:

- Current node status S:  
Applicable rules:  $S \rightarrow I$   
If at least one of my neighbors is infected, with probability  $\beta$  change my status to infected.
- Current node status I:  
Applicable rules:  $I \rightarrow R$   
With probability  $\mu$  turn my status to removed.

### Example SIR model

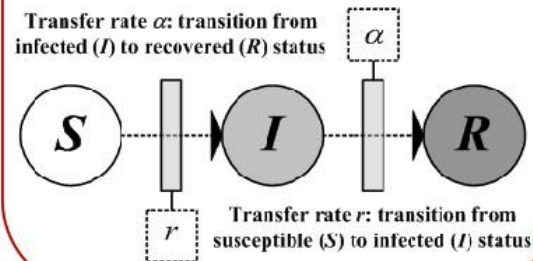
Three node statuses:

(S)uscepAble,  
(I)nfectd,  
(R)ecovered

Two transition rules:

$S \rightarrow I$ ;

$I \rightarrow R$



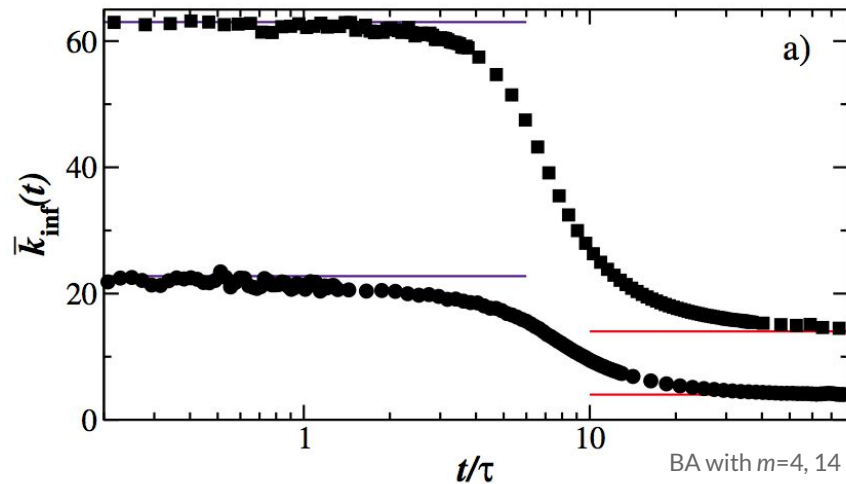
## SI Model

# Early time behaviour

$$\tau = \frac{\langle k \rangle}{\beta(\langle k^2 \rangle - \langle k \rangle)}$$

The **timescale** it takes for an epidemics to grow. The smaller is  $\tau$ , the faster it grows.

ER model	BA model
$\langle k^2 \rangle = \langle k \rangle (\langle k \rangle + 1)$  The more connected the network is, the faster does the epidemic spread.	$\langle k^2 \rangle \propto \infty$ for $N \propto \infty \Rightarrow \tau \propto 0$  The characteristic <b>time vanishes</b> : the epidemic becomes instantaneous.  <b>Reason:</b> the hubs get infected first, which then rapidly reach most nodes.



Numerical Test:

The average degree of newly infected nodes at time  $t$ :

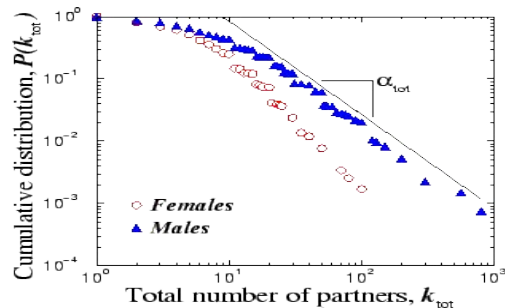
$$\bar{k}_{inf}(t) = \frac{\sum_k k(I_k(t) - I_k(t-1))}{I(t) - I(t-1)}$$

## SIS Model

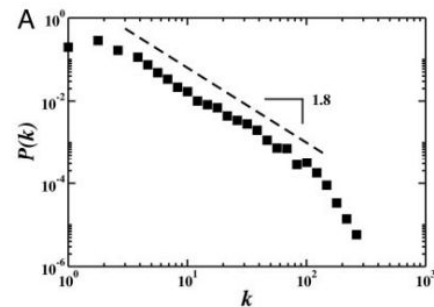
# No Epidemic Threshold

Many networks will have small or vanishing epidemic threshold.

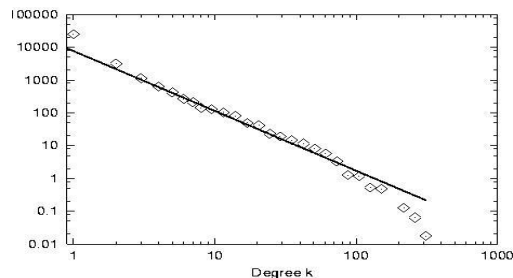
Diffusion will not die out.



Human Sexual network



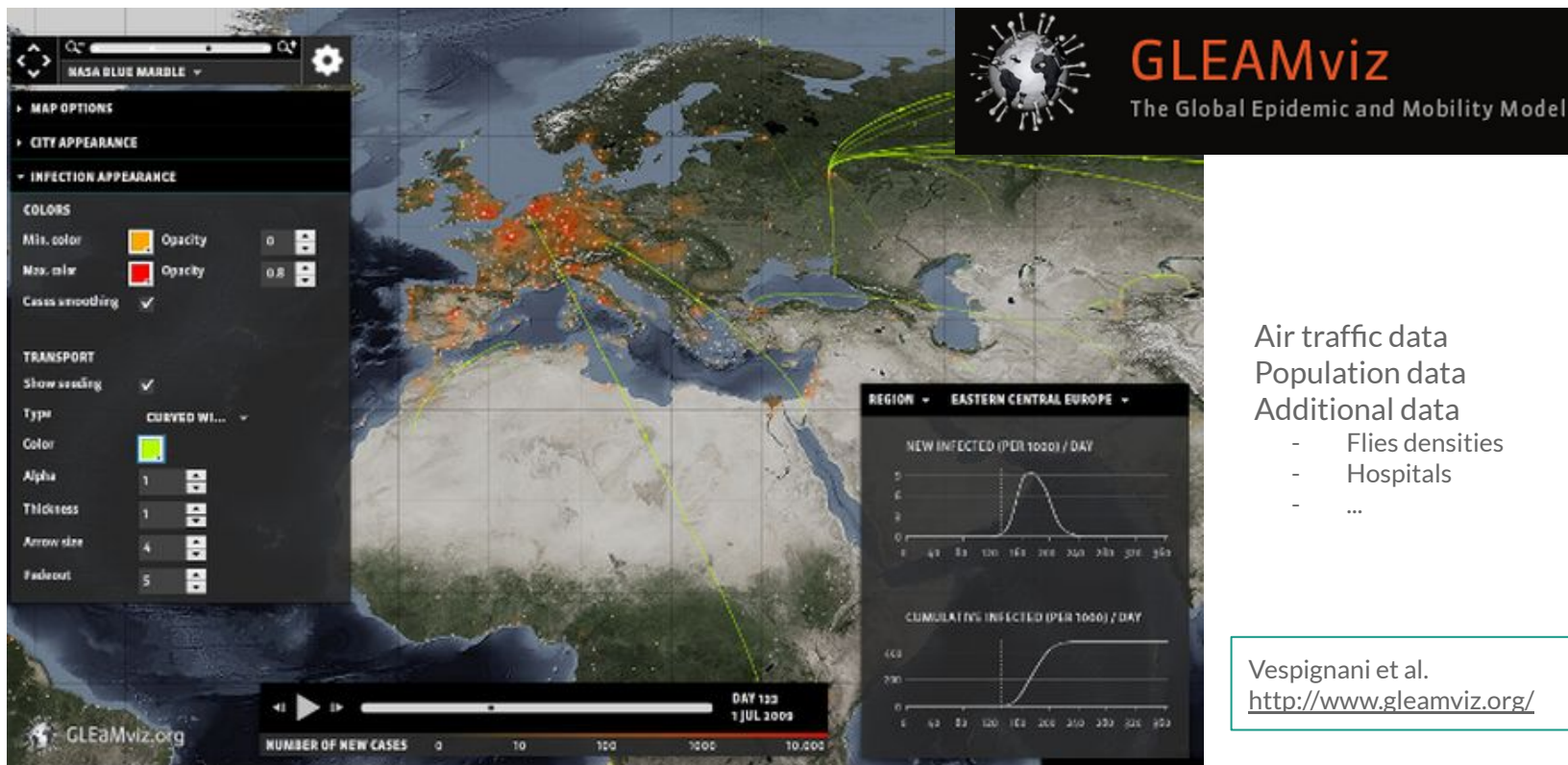
Air Transportation network



Email network

# Summarizing



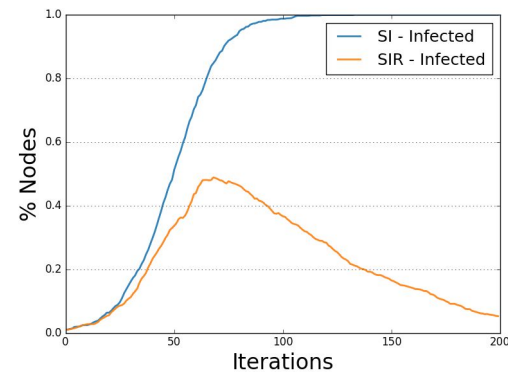
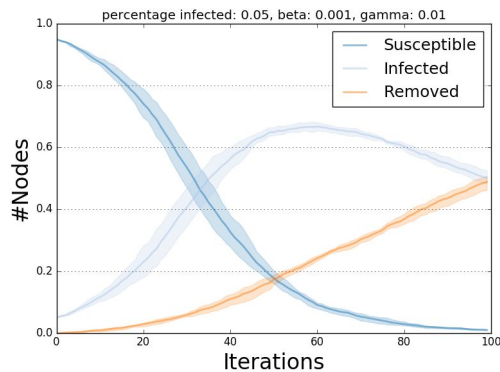


Air traffic data  
Population data  
Additional data

- Flies densities
- Hospitals
- ...

Vespignani et al.  
<http://www.gleamviz.org/>

GleamViz: leveraging mobility networks



#### Diffusion Models

# 12+5

Epidemics & Opinion Dynamics

pip install ndlib

#### User Base

# ~20.000

Installations  
(2019-Q1 only)

#### Research impact

# 20

Publications citing NDlib  
since 2018  
(First release 12/2017)



<https://ndlib.rtfd.io>

Rossetti, Giulio, et al. "NDlib: a python library to model and analyze diffusion processes over complex networks." *International Journal of Data Science and Analytics* (2018)



<https://bit.ly/2UcfDle>

## Chapter 13

# Conclusion

### Take Away Messages

1. Viruses spread over a population
2. Populations can be modeled with social networks topologies
3. Stochastic epidemic models can be leveraged to simulate and reason upon real world viruses diffusion

### Suggested Readings

- Chapter 21 of Kleinberg's book
- Chapter 10 of Barabasi's book

### What's Next

Chapter 14:  
**Diffusion: Opinion Dynamics**

