Chapter 14

# 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

# Epidemic

**Biological:**
- Airborne diseases (flu, SARS, …)
- Venereal diseases (HIV, …)
- Other infectious diseases (HPV, …)
- Parasites (bedbugs, malaria, …)

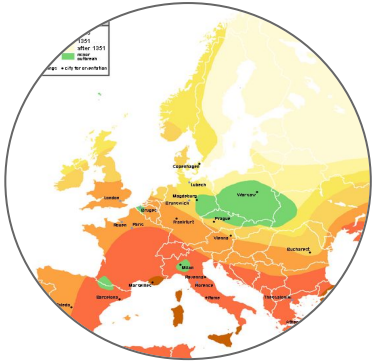
**Digital**:
- Computer viruses, worms
- Mobile phone viruses

**Conceptual/Intellectual**:
- Diffusion of innovations
- Rumors
- Memes
- Business practices

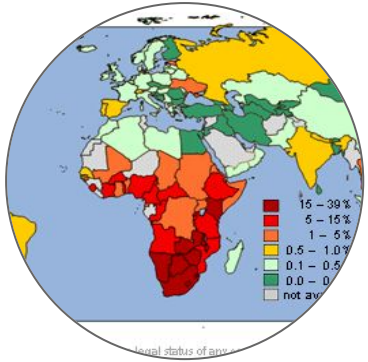
*Epi + demos*

*upon* *people*

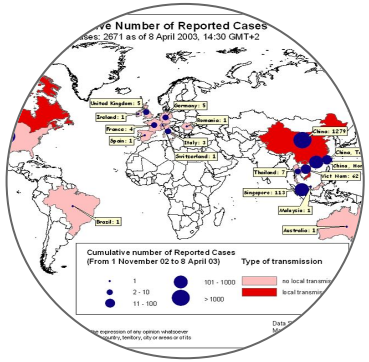
The Great Plague



HIV

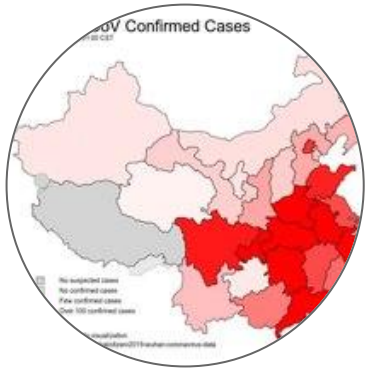



SARS



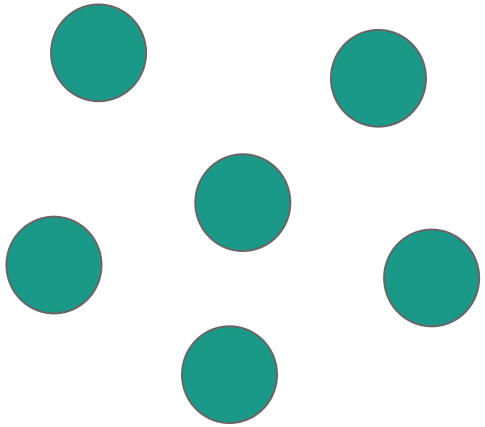

1918 Spanish flu

H1N1 flu

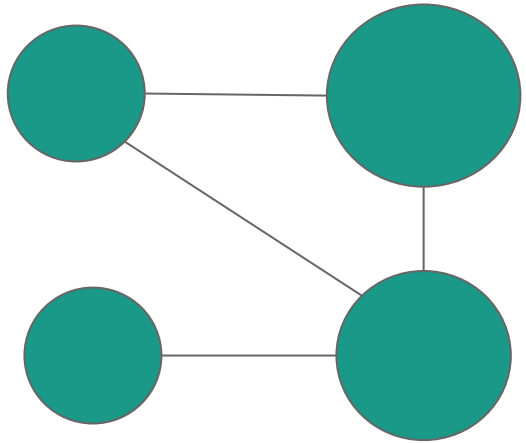



2019-nCoV

Biological: Notable Epidemic Outbreaks



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

# Compartmental Models

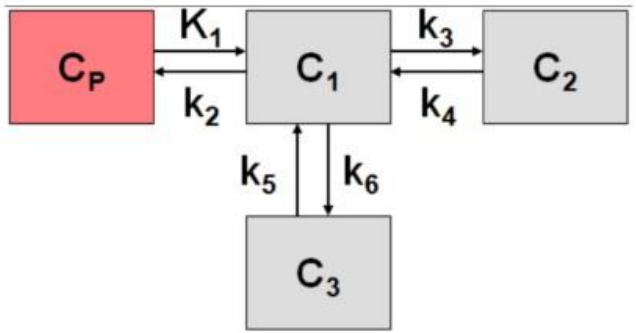
The framework is based on two hypotheses:

### Compartmentalization:

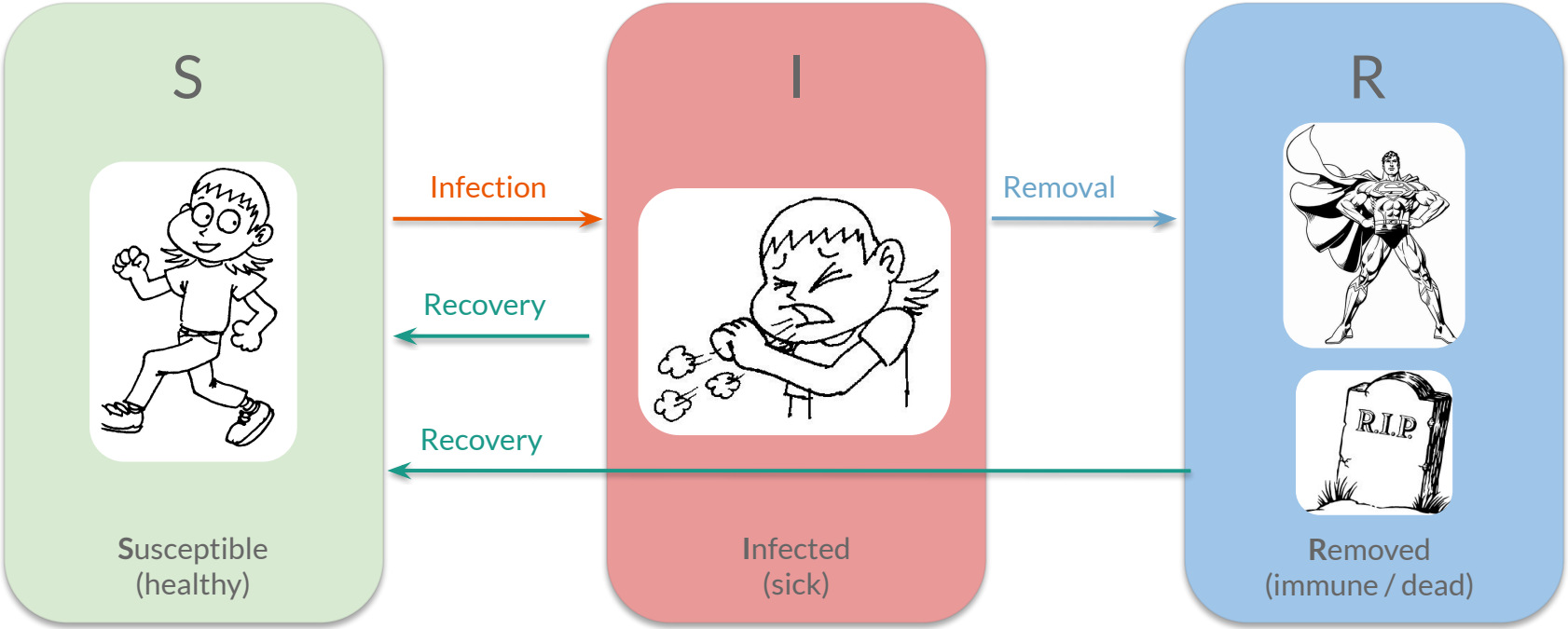
each individual is classified into distinct statuses. The simplest classification assumes that an individual can be in one of the states.

### Homogeneous Mixing:

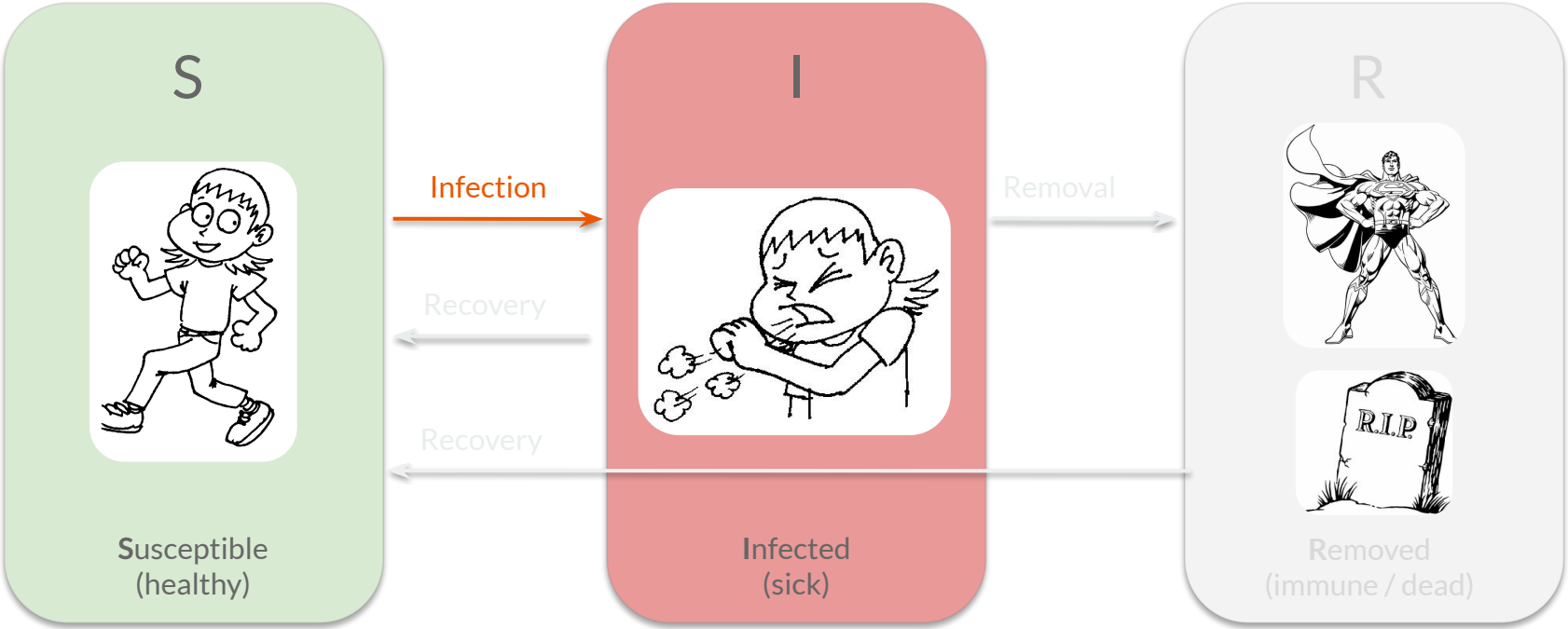
each individual has the same chance of coming into contact with an infected individual.



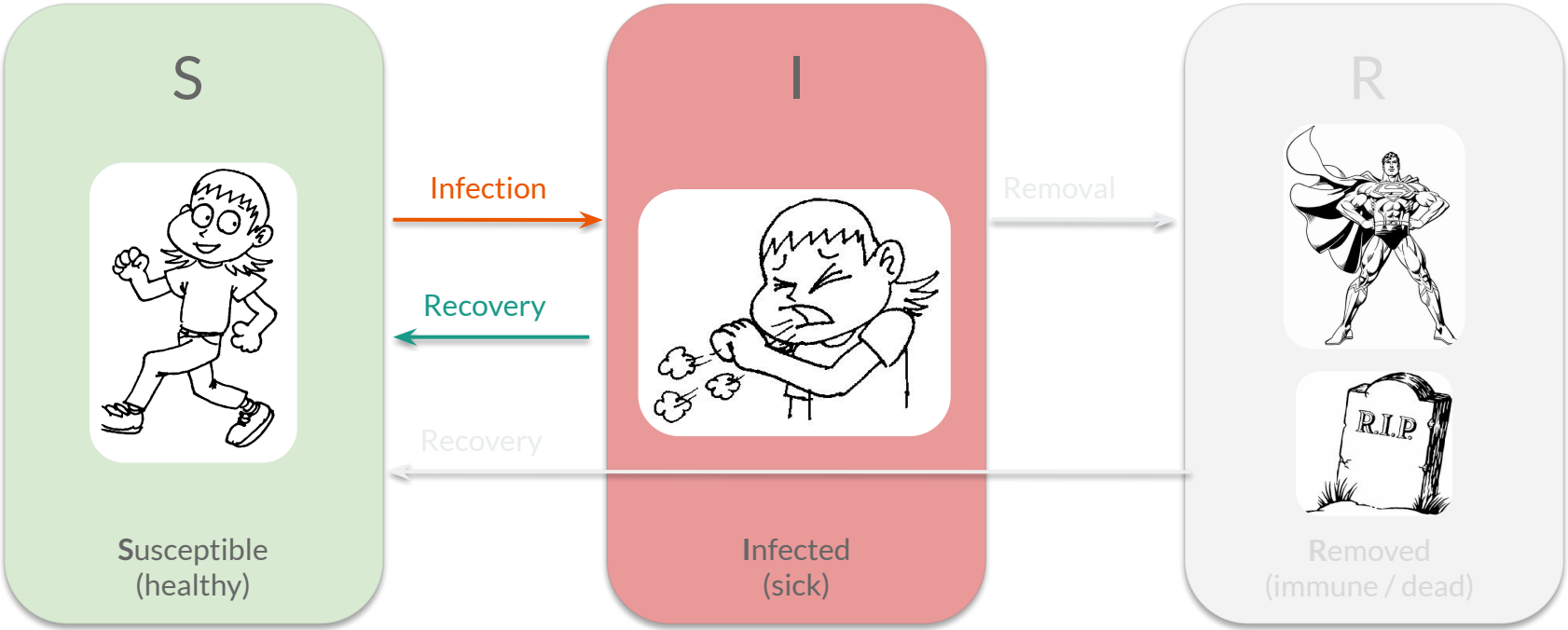

*W. O. Kermack and Ag McKendrick. A Contribution to the Mathematical Theory of Epidemics. 1927*



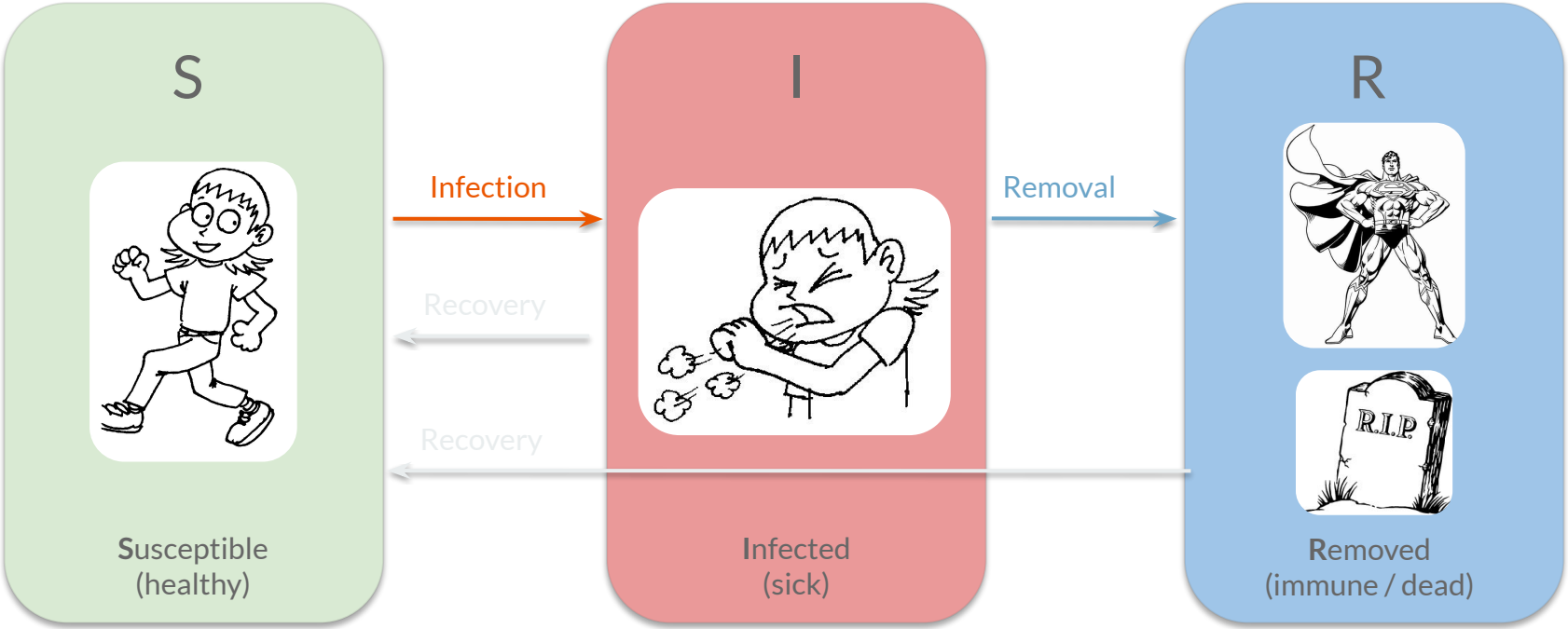

Classic Models Compartments




**SI**: The simplest model




**SIS**: Common Cold




**SIR**: Flu, SARS, Plague

# Mean Field formulation

(Homogeneous mixing)

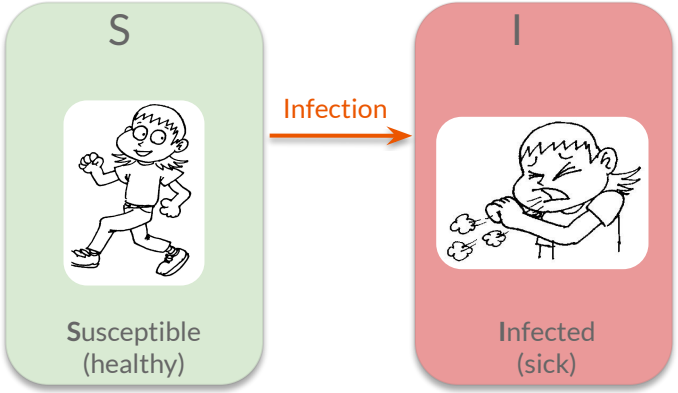
# SI model

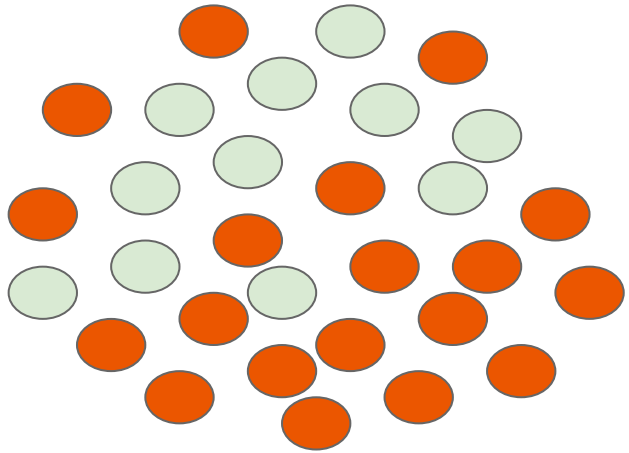
Each individual has β contacts with randomly chosen others individuals per unit time.

If there are *I* infected individual and *S* susceptible individuals, the average rate of new infection is βsi/N

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

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



SI model

# Dynamics

Logistic equation:
a basic model of population growth.

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

*http://en.wikipedia.org/wiki/Logistic_function*
*http://mathworld.wolfram.com/LogisticEquation.html*

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

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

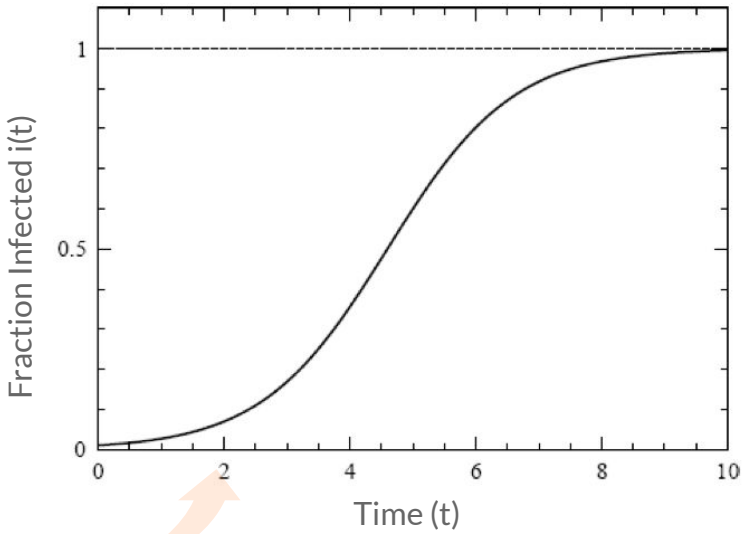
$$\ln\frac{i}{1-i} = c + \beta t$$

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

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

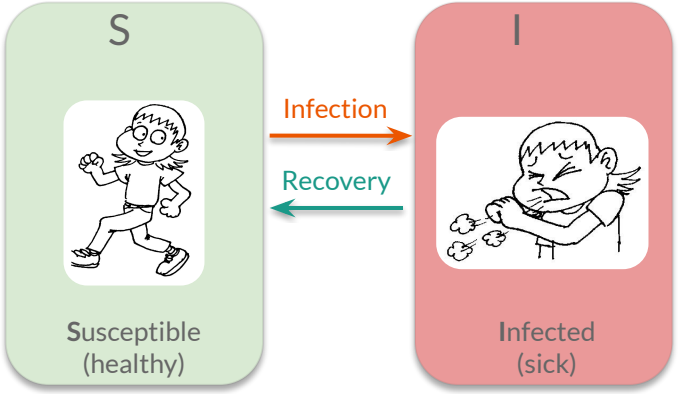
As i(t)~ 1.

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

saturation

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

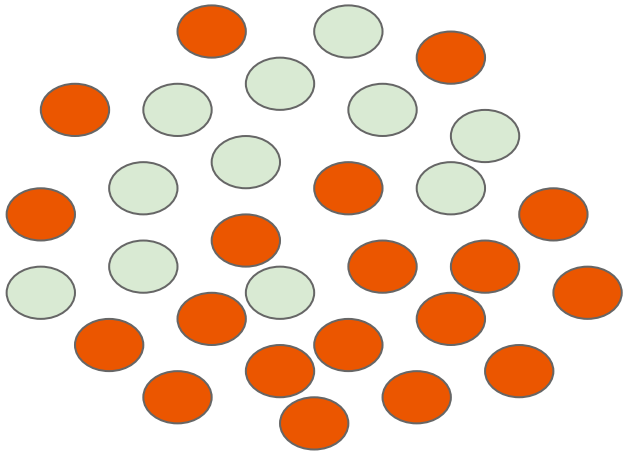
# SIS model




## Modeling Common Cold

Each individual has β contacts with randomly chosen others individuals per unit time.

Each infected individual has μ probability of revert its status to susceptible



SIS model

# Behaviour

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

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

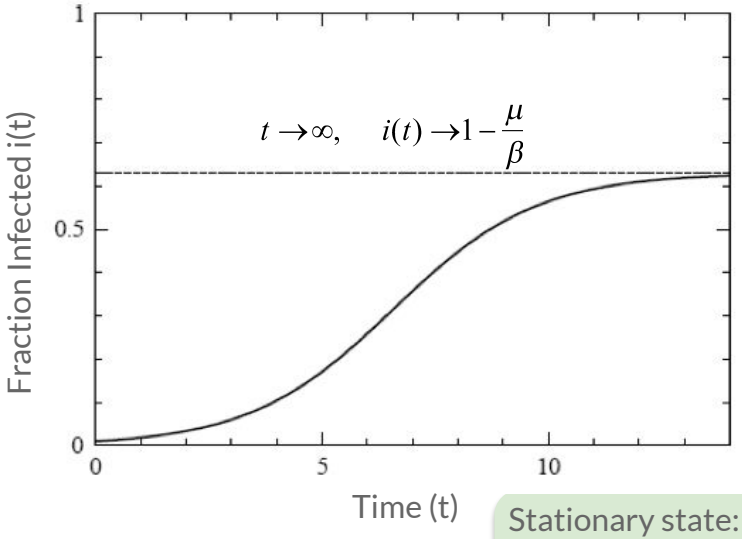
$$\ln(i) - \ln(1-\mu/\beta - i) = (\beta - \mu)t + c$$

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

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

SIS model

# Dynamics




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

**SIS model:**
the fraction of infected individual saturates below 1

Stationary state:

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

SIS model

# Basic Reproductive Number

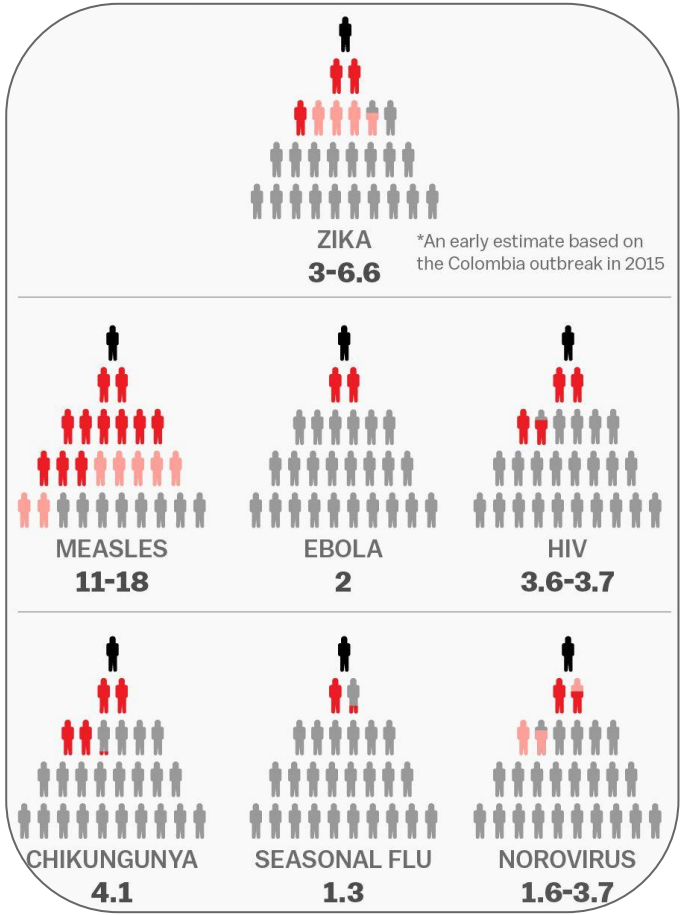
**ƛ** (also identified with $R_0$):
average # of infectious individuals generated by one infected in a fully susceptible population.

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

**ƛ > 1:** Outbreack

**ƛ < 1:** Die Out

Epidemic Threshold
if $\mu \approx$ □ then $i \longrightarrow 0$

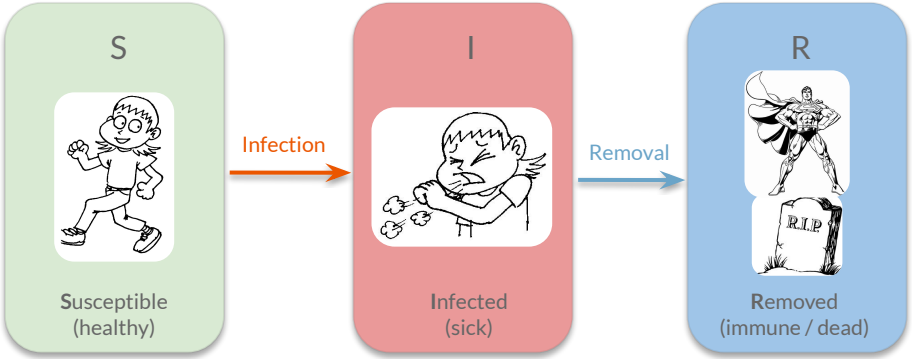


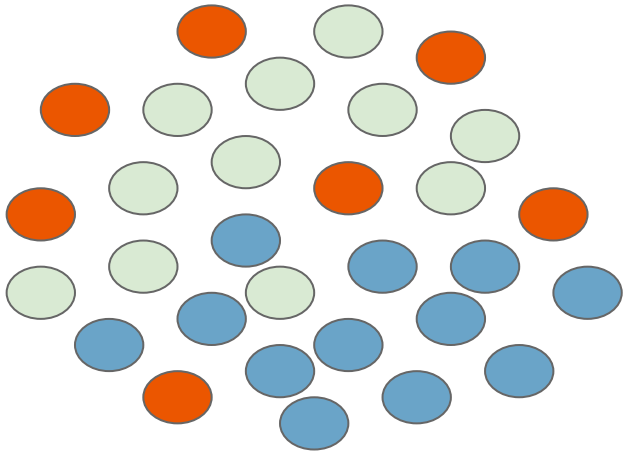
# SIR model

## Modeling Flu-like disease

Each individual has β contacts with randomly chosen others individuals per unit time.

Each infected individual has μ probability of becoming immune after being infected



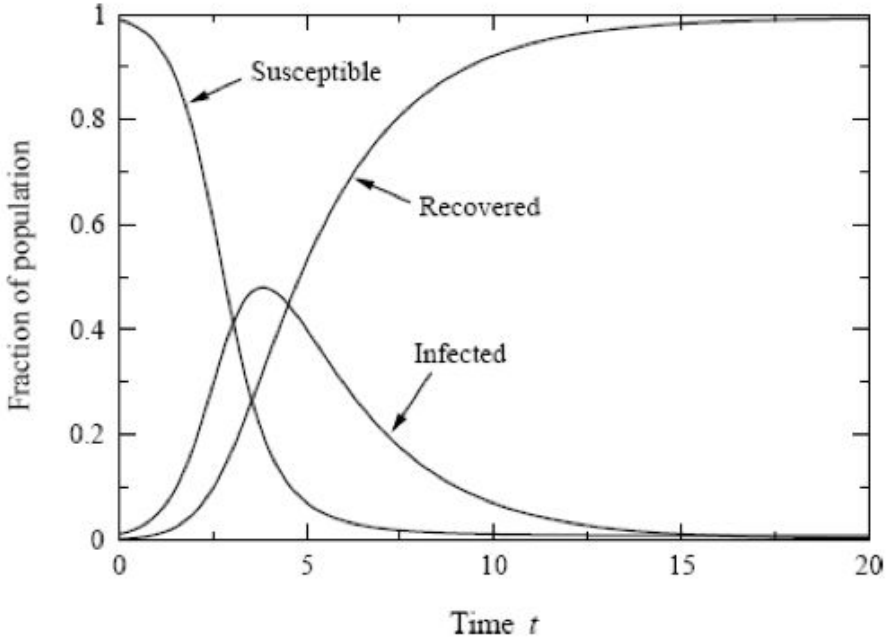



SIS model

# Behaviour

$$\frac{\mathrm{d}s(t)}{\mathrm{d}t} = \beta\langle k\rangle i(t)\,[1 - r(t) - i(t)]$$
$$\frac{\mathrm{d}i(t)}{\mathrm{d}t} = -\mu i(t) + \beta\langle k\rangle i(t)\,[1 - r(t) - i(t)]$$
$$\frac{\mathrm{d}r(t)}{\mathrm{d}t} = \mu i(t).$$

**SIR model:**
the fraction infected peaks and the fraction recovered saturates.



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

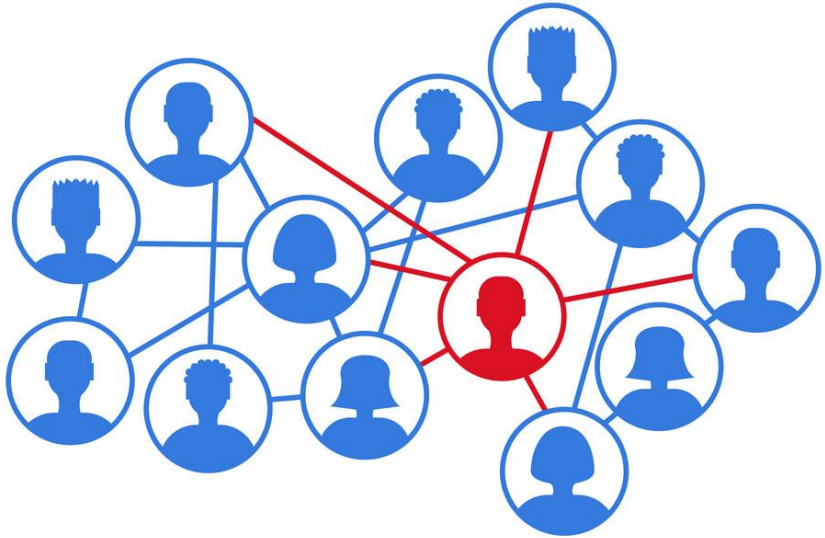
**Recap**: Basic Features of Epidemic Models

# 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

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

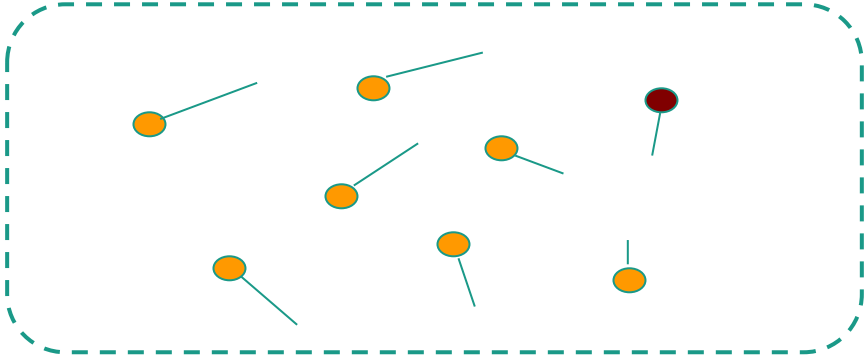
**Example SIS:**

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

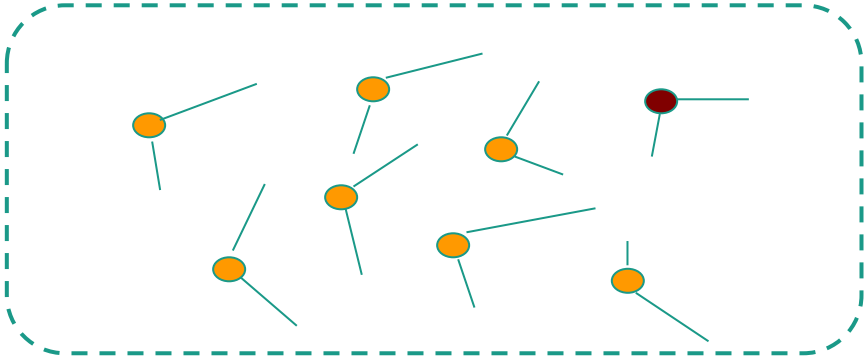
$$\frac{di_k(t)}{dt} = \beta(1 - i_k(t))k\Theta_k(t) - \mu i_k(t)$$

Proportional to k

Density of infected neighbors of nodes with degree *k*



Class of nodes with degree *k=1*



Class of nodes with degree k=2

# 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:**

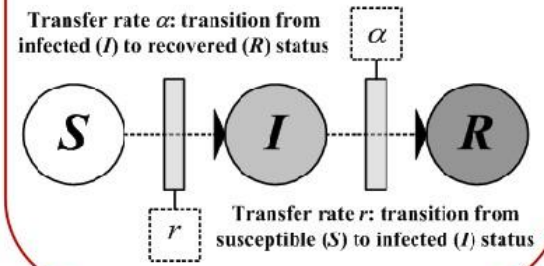
- Current node status S:
  Applicable rules: S→I
  If at least one of my neighbors is infected, with probability β change my status to infected.

- Current node status I:
  Applicable rules: I→R
  With probability $\mu$ turn my status to removed.

**Example**
**SIR model**

Three node statuses:
(**S**)uscepAble,
(**I**)nfected,
(**R**)ecovered

Two transition rules:
**S→I;**
**I→R**



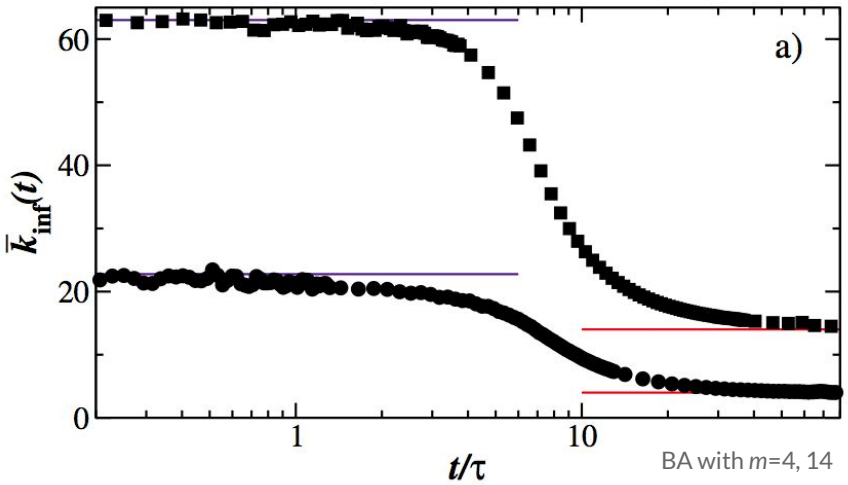
SI Model

# Early time behaviour

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

The timescale it takes for an epidemics to grow. The smaller is τ, the faster it grows.

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




BA with $m$=4, 14

Numerical Test:

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

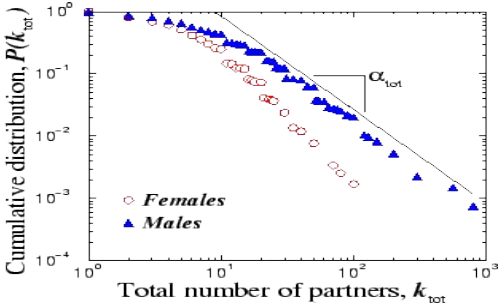
$$\bar{k}_{\text{inf}}(t) = \frac{\sum_k k\left(I_k(t) - I_k(t-1)\right)}{I(t) - I(t-1)}$$

SIS Model

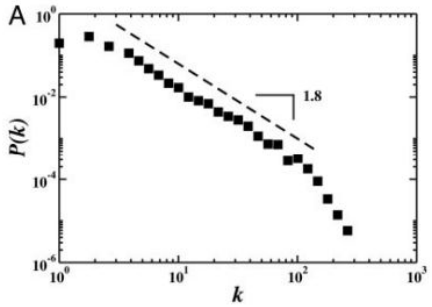
# No Epidemic Threshold

Many networks will have small or vanishing epidemic threshold.

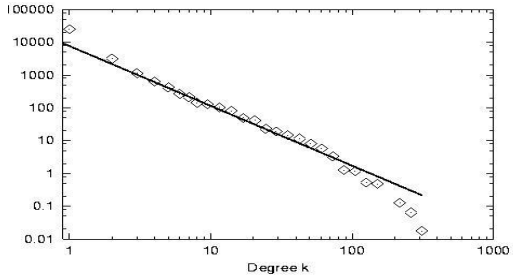
Diffusion will not die out.




Human Sexual network

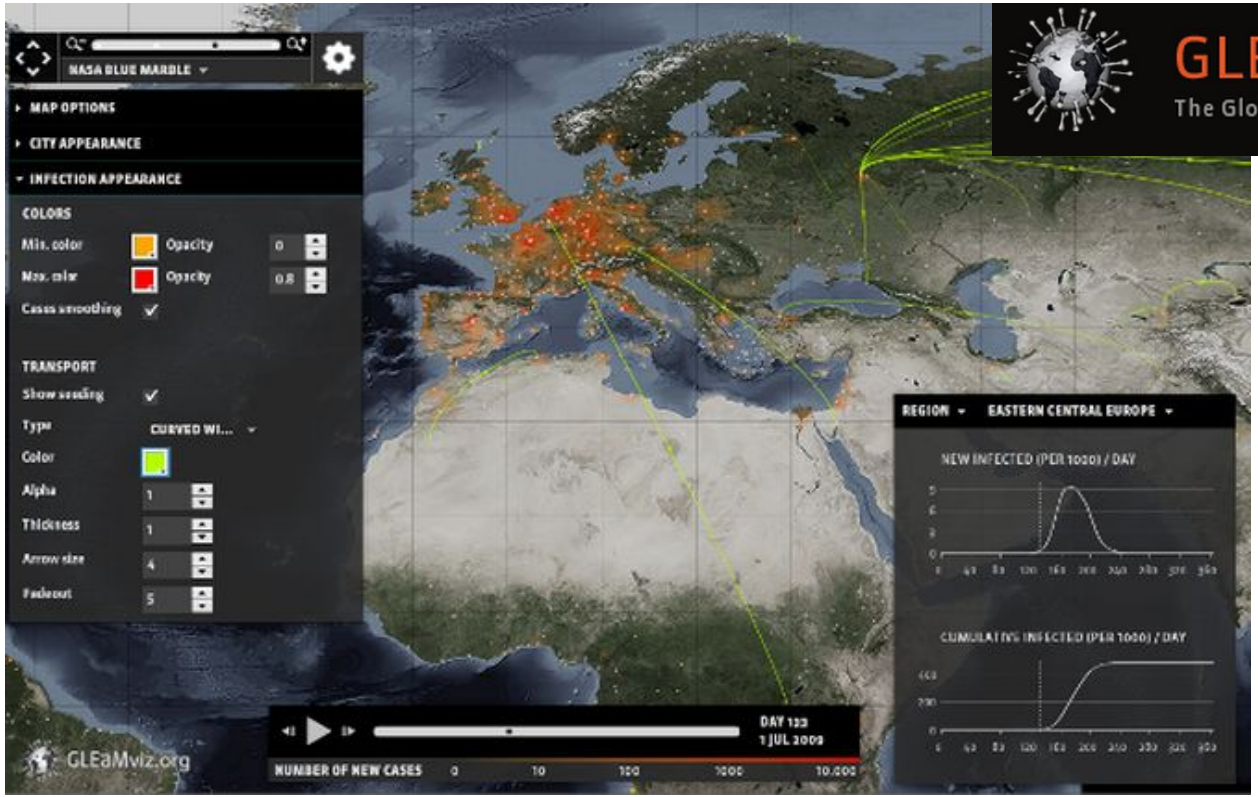



Air Transportation network




Email network

# Summarizing

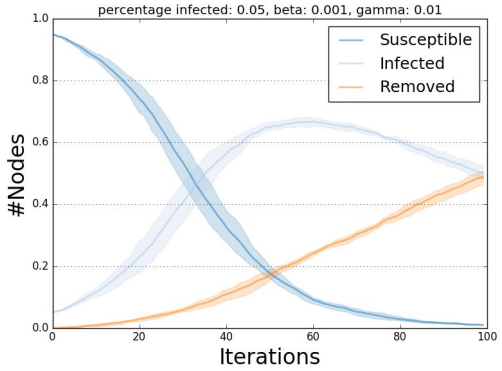



Air traffic data
Population data
Additional data

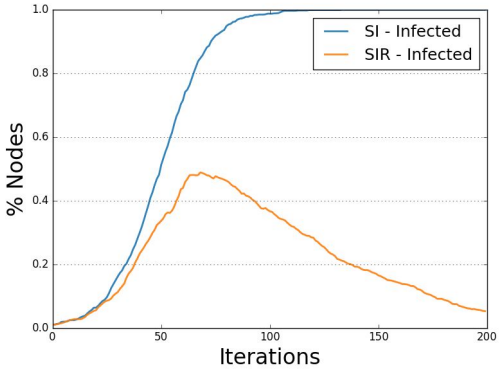
- Flies densities
- Hospitals
- ...

*Vespignani et al.*
*http://www.gleamviz.org/*

GleamViz: leveraging mobility networks




NDlib
Network Diffusion Library




Diffusion Models

12+5

Epidemics & Opinion Dynamics

pip install ndlib

User Base

~60k

Installations (2021-Q1 only)

Research impact

33

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/2UcfDIe

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 15:
**Diffusion: Opinion Dynamics**