Structure and dynamics of complex networks

April 14, 2020

SPREADING ON NETWORKS

Why is spreading on networks important?

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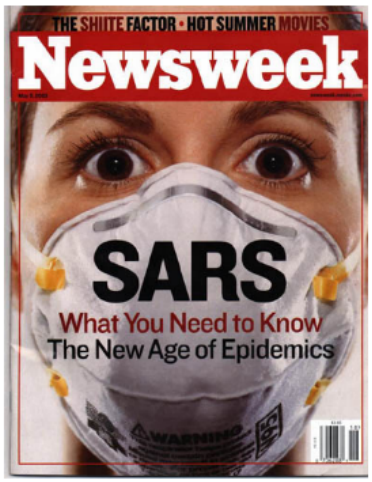
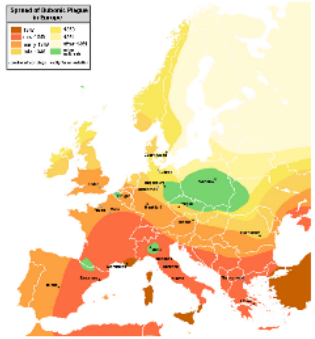
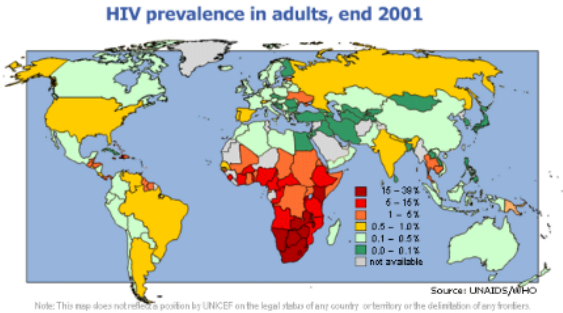


Famous epidemic outbreaks

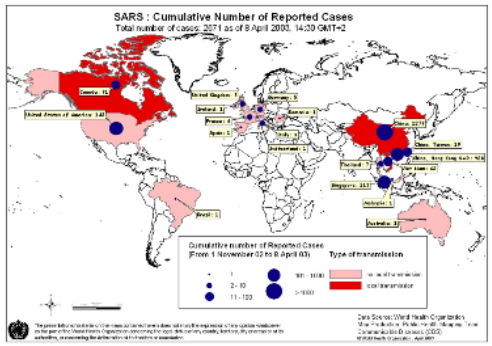
The Great Plague



HIV



SARS



1918 Spanish flu

H1N1 flu

COVID-19

A few dashboards monitoring the spread of the diseases:

- Center for Systems Science and Engineering (CSSE) at John Hopkins University (JHU):

  `https://gisanddata.maps.arcgis.com/apps/opsdashboard/index.html#/bda7594740fd40299423467b48e9ecf6`

- World Health Organisation (WHO):

  `https://who.sprinklr.com/`

- The New York Times (NYT):

  `https://www.nytimes.com/interactive/2020/world/coronavirus-maps.html`

- The Baselab:

  `https://coronavirus.thebaselab.com/`

- NextStrain:

  `https://nextstrain.org/ncov/global`

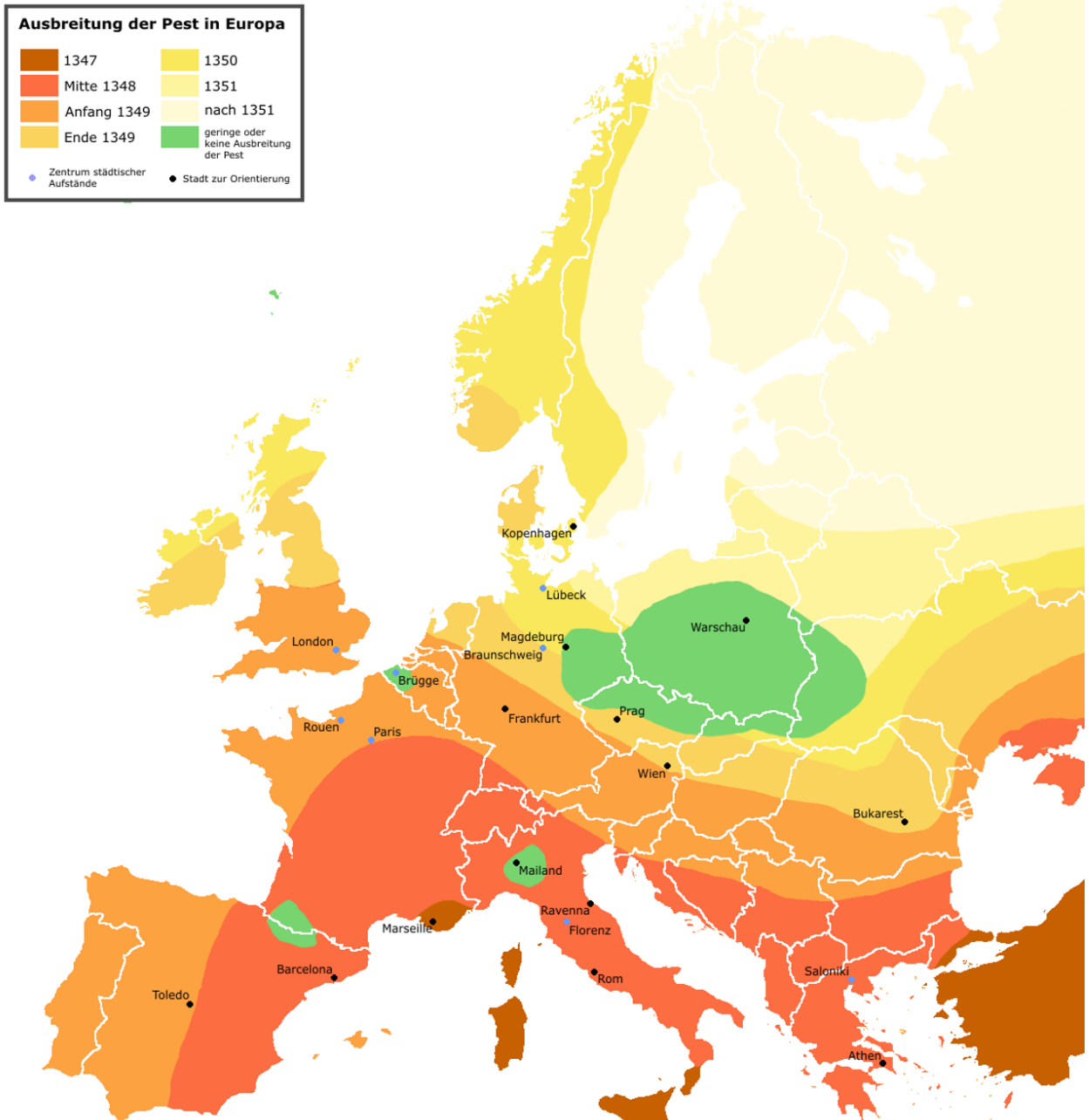
- Eötvös University:

  `http://csabaibio.elte.hu/tools/veo/covid19.html`

Famous epidemic outbreaks

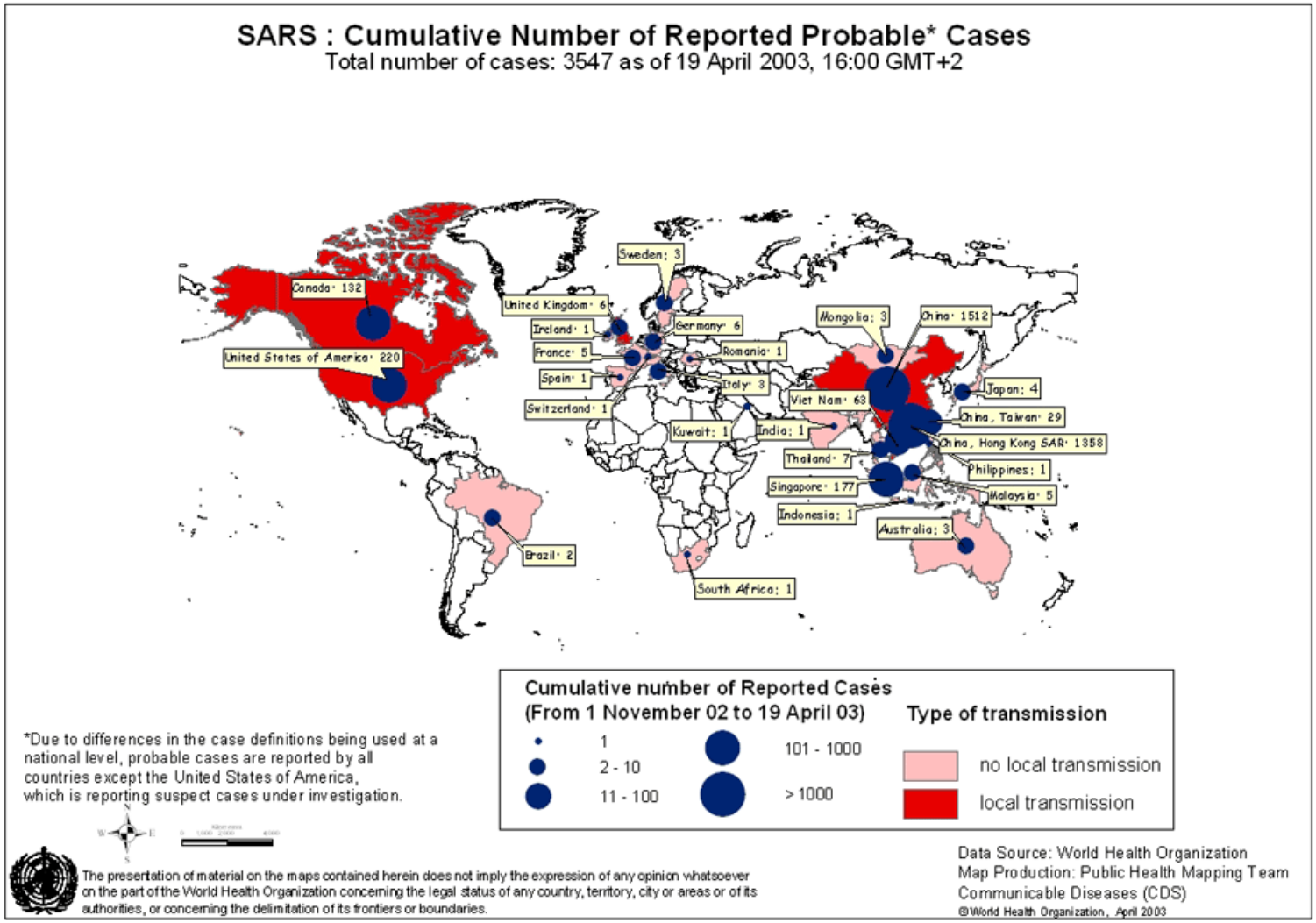
If we compare the **speed** of the spreading worldwide, global pandemics seemed to happen at a slower pace back in history...

Famous epidemic outbreaks
Speed?



Famous epidemic outbreaks

Speed?



Famous epidemic outbreaks
Speed?

- Why did the spreading speed up on the world wide scale?

Famous epidemic outbreaks
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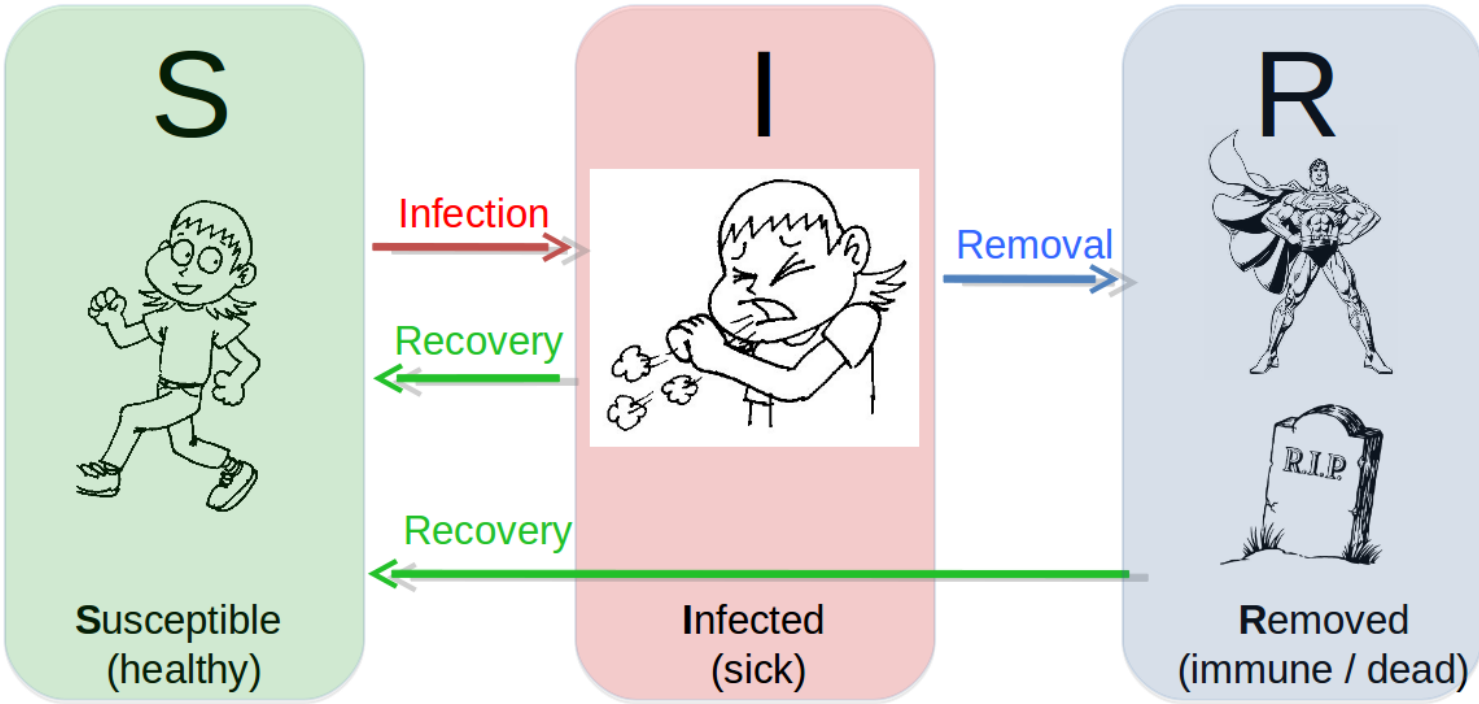
- Please watch a simulation comparing the historical and modern scenario on youtube:

  `http://www.youtube.com/watch?v=eJ5mKFNcfHg`

Famous epidemic outbreaks
Speed?

- Why did the spreading speed up on the world wide scale?
- Please watch a simulation comparing the historical and modern scenario on youtube:

  `http://www.youtube.com/watch?v=eJ5mKFNcfHg`
- The simple explanation is that the global human travel network has become very fast nowadays, basically you can travel anywhere in just a few days at most.



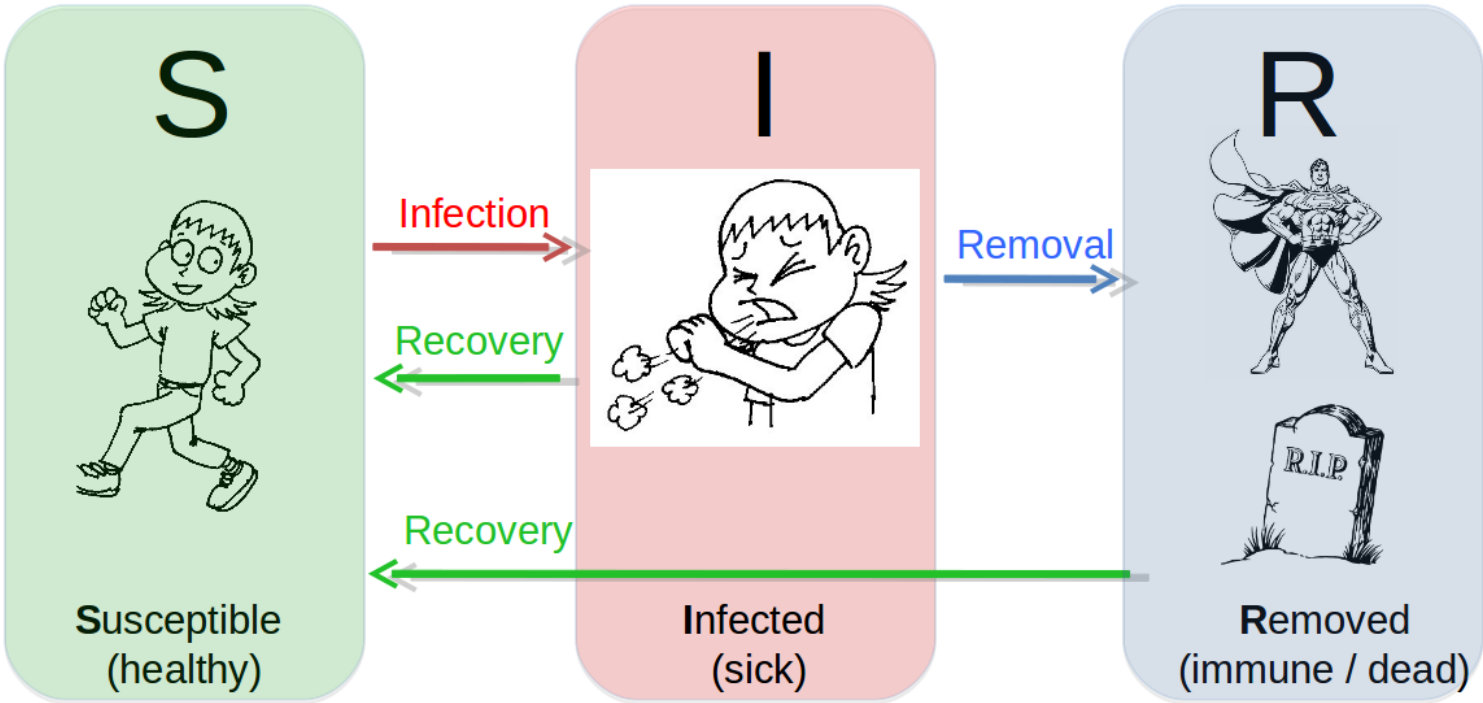
EPIDEMIC MODELS

Basic epidemic models

- In this section we review the basic epidemic models studied on networks.
- A common feature of these models is that they assume a few possible discrete states for the nodes describing whether the given node is healthy or infectious.
- The infection can spread over the links, and in the mean time, infected nodes may recover over time in most of the scenarios.

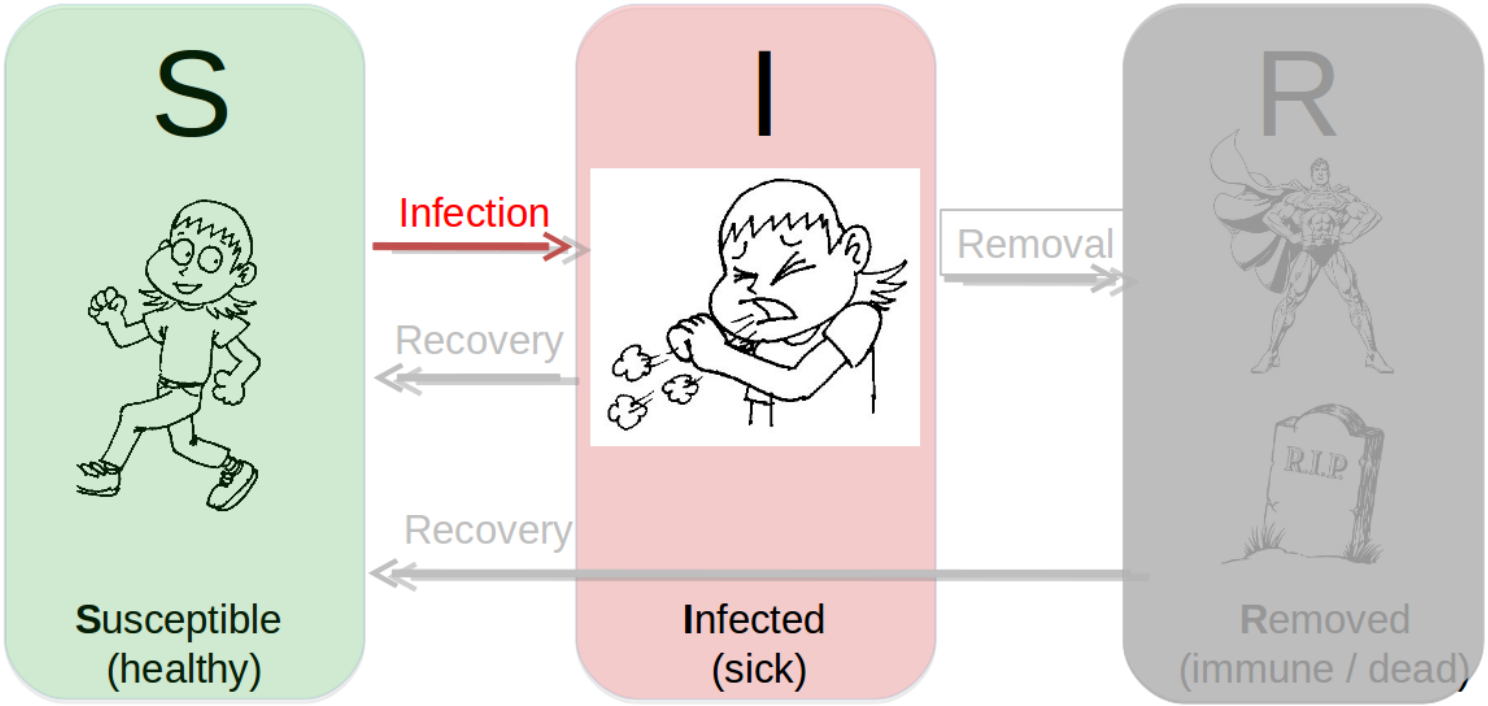
Basic epidemic models
Basic states

The basic states in epidemics:



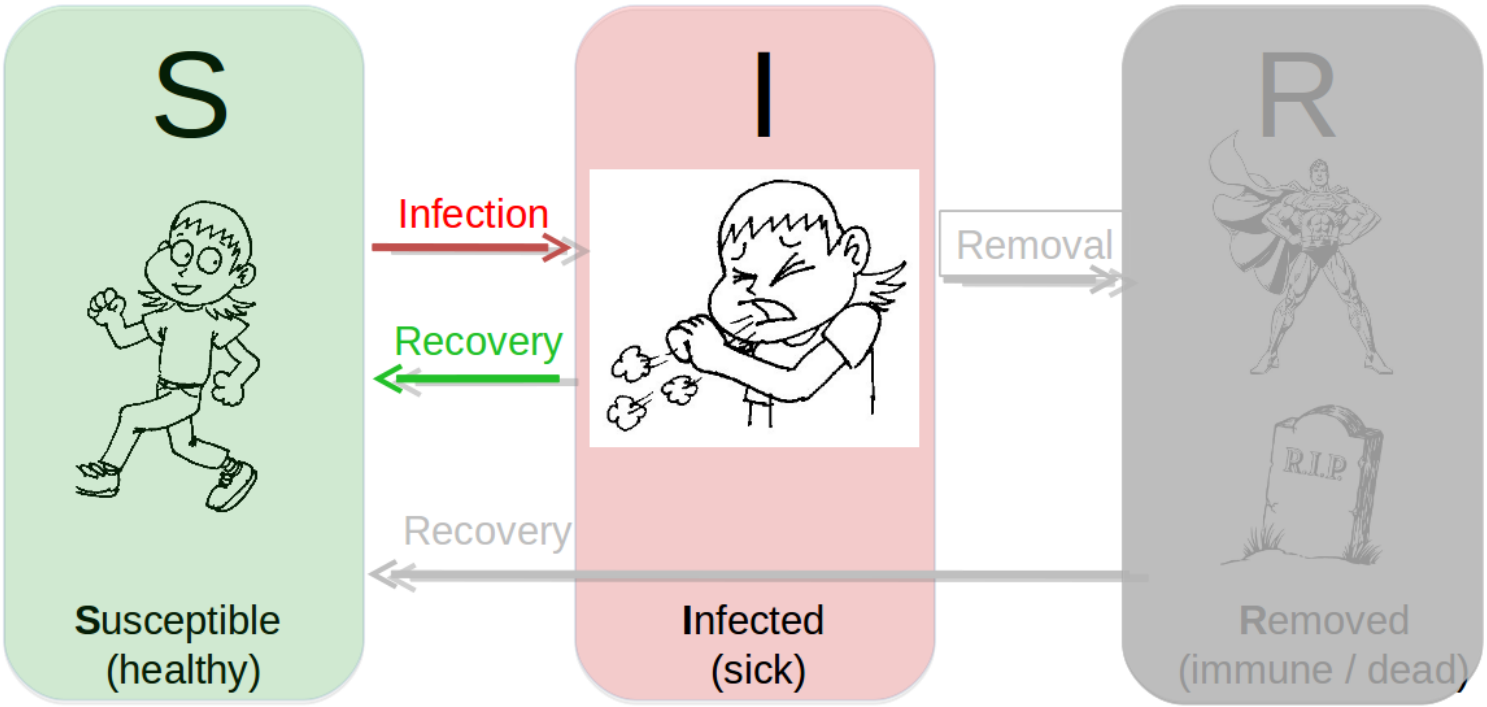
Basic epidemic models
SI

The SI model:



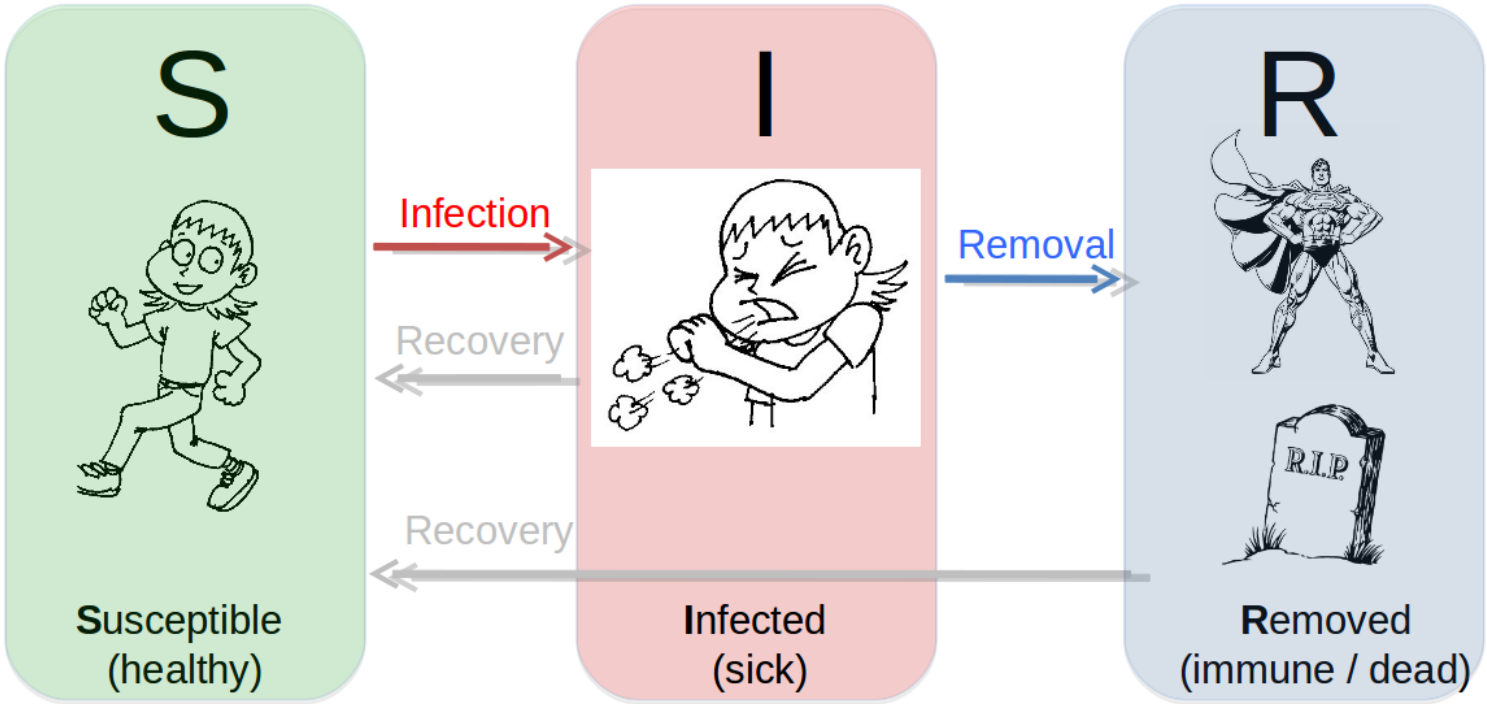
Basic epidemic models
SIS

The SIS model: (e.g., common cold)



Basic epidemic models
SIR

The SIR model: (e.g.,flu, SARS, plague)



SIS model on networks

- In the following we are going to study the SIS model on networks in an analytic framework.
- We begin with homogeneous networks such as the E-R graph, regular lattices, etc., where it is more easy to introduce the basic concepts such as the spreading rate and the epidemic threshold.
- Once we understand the behaviour in the homogeneous case, we can move onto to in-homogeneous systems such as scale-free networks.

SIS model on homogeneous networks

Model assumptions:

- **Homogeneous mixing** hypothesis:
  - The network is homogeneous, (e.g., E-R graph), every node has more or less $\langle k \rangle$ connections.
  - Every node has the same probability to be linked to an infected one.
- If a susceptible node is attached to an infected one, the probability of transaction per unit time is λ. (Spreading rate)
- For an infected node, the probability of the recovery per unit time is μ.
- At $t = 0$ we start with an infinitesimal $\rho(t = 0) = \rho_0 \ll 1$ fraction of infected nodes.

The diff. eq. for the time evolution of $\rho(t)$:

$$\frac{d\rho}{dt} = \underbrace{\lambda \underbrace{\langle k \rangle \rho}_{\text{linked to I}} \underbrace{(1 - \rho)}_{\text{S}}}_{\text{S}\to\text{I}} - \mu\rho$$

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SIS model on homogeneous networks

Solving the diff. eq. (the logistic equation):

$$\frac{d\rho}{dt} = \lambda \langle k \rangle \rho(1-\rho) - \mu\rho, \qquad \rho(t=0) = \rho_0,$$

$$\rightarrow \rho(t) = \left(1 - \frac{\mu}{\lambda \langle k \rangle}\right) \frac{c e^{(\lambda\langle k\rangle - \mu)t}}{1 + c e^{(\lambda\langle k\rangle - \mu)t}} \qquad c = \frac{\rho_0}{1 - \frac{\mu}{\lambda\langle k\rangle} - \rho_0}$$

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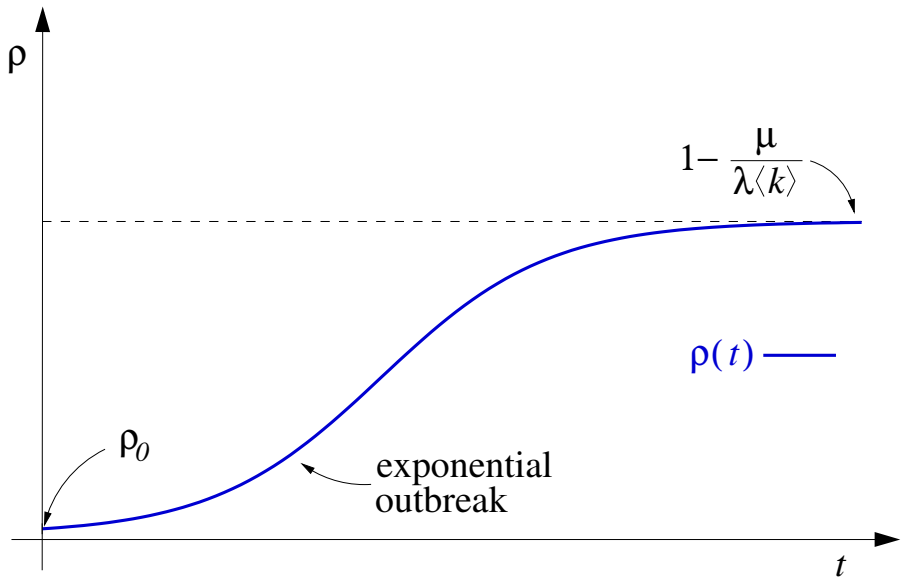
If $\lambda \langle k \rangle > \mu$:



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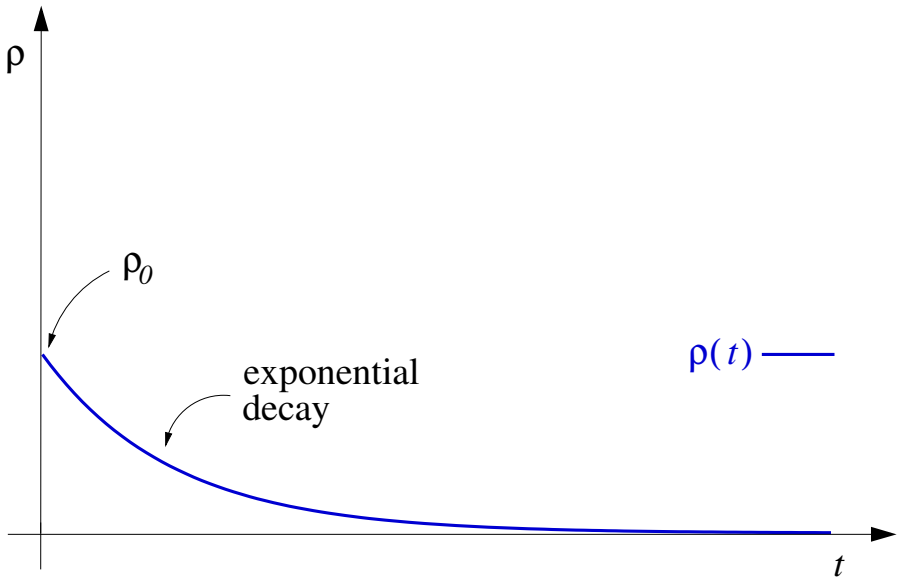

SIS model on homogeneous networks

EPIDEMIC THRESHOLD:

$$\lambda_c \langle k \rangle = \mu \quad \rightarrow \quad \lambda_c = \frac{\mu}{\langle k \rangle} \quad \leftrightarrow \quad \begin{cases} \lambda > \lambda_c : & \text{exp. outbreak} \\ \lambda < \lambda_c : & \text{exp. decay} \end{cases}$$

For simplicity, let us assume $\mu = 1$:

$$\lambda_c \langle k \rangle = 1 \quad \rightarrow \quad \lambda_c = \frac{1}{\langle k \rangle}$$

This becomes very intuitive in discrete time dynamics:

- an infected node recovers in one time step,
- it has $\langle k \rangle$ neighbors, thus, on average it can infect $\lambda \langle k \rangle$ other nodes during this time step,
  - if $\lambda \langle k \rangle < 1$ the infection dies out quickly,
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SIS model on inhomogeneous networks

- The network now is assumed to be inhomogeneous, (i.e., scale-free).

→ We need to treat the HUBS and ordinary nodes separately:

- We define ρ_k, as the fraction of infected nodes with degree k.

$$\rightarrow \rho = \frac{1}{N}\sum_k \rho_k N_k = \sum_k \rho_k p(k).$$

- The probability for a link pointing to an infected node: Γ.

  We assume Γ depends only on ρ, (not on e.g., the node degree at the other endpoint).

The diff.eq. for the time evolution of $\rho_k(t)$:

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- Let's assume we reach a stationary phase: $\frac{d\rho_k}{dt} = 0$

$$\rightarrow \mu\rho_k = \lambda k\Gamma\left[1-\rho_k\right] \quad \rightarrow \quad \rho_k = \frac{\lambda k\Gamma}{\mu+\lambda k\Gamma}$$

- Let's also calculate Γ. If $\mathcal{P}_k$ denotes the probability for a randomly chosen link pointing to a node with degree k, we have $\Gamma = \sum_k \rho_k \mathcal{P}_k$.
- How to express $\mathcal{P}_k$?

- However, since the infected nodes must have obtained the infection on another link, we use

$$\Gamma = \frac{1}{\langle k\rangle}\sum_k (k-1)p(k)\rho_k = \frac{1}{\langle k\rangle}\sum_k (k-1)p(k)\frac{\lambda k\Gamma}{\mu+\lambda k\Gamma}$$

$\rightarrow$ A self-consistent equation for Γ!

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- Let's assume we reach a stationary phase: $\frac{d\rho_k}{dt} = 0$

$$\rightarrow \mu\rho_k = \lambda k\Gamma\left[1-\rho_k\right] \quad \rightarrow \quad \rho_k = \frac{\lambda k\Gamma}{\mu+\lambda k\Gamma}$$

- Let's also calculate Γ. If $\mathcal{P}_k$ denotes the probability for a randomly chosen link pointing to a node with degree k, we have $\Gamma = \sum_k \rho_k \mathcal{P}_k$.
- How to express $\mathcal{P}_k$?

$$\rightarrow \mathcal{P}_k = \frac{kp(k)}{\langle k\rangle}.$$

- However, since the infected nodes must have obtained the infection on another link, we use

$$\Gamma = \frac{1}{\langle k\rangle}\sum_k (k-1)p(k)\rho_k = \frac{1}{\langle k\rangle}\sum_k (k-1)p(k)\frac{\lambda k\Gamma}{\mu+\lambda k\Gamma}$$

$\rightarrow$ A self-consistent equation for Γ!

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$$\Gamma = \frac{1}{\langle k \rangle} \sum_k (k-1) p(k) \frac{\lambda k \Gamma}{\mu + \lambda k \Gamma}$$

- How to solve it?

→ Graphically, since we are interested only in the qualitative behavior.

- $\Gamma = 0$ is always a solution, however this is trivial, no infection.
- The condition for a non-trivial solution:

$$\frac{d}{d\Gamma} \left[\frac{1}{\langle k \rangle} \sum_k (k-1) p(k) \frac{\lambda k \Gamma}{\mu + \lambda k \Gamma} \right] \Bigg|_{\Gamma=0} \geq 1$$

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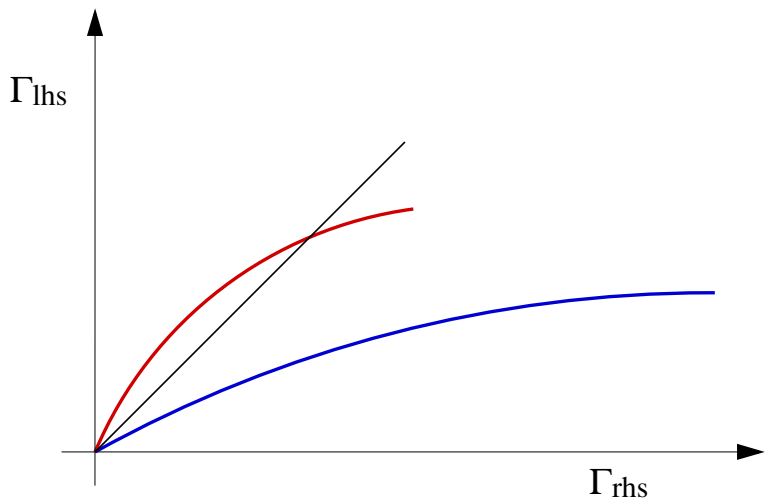

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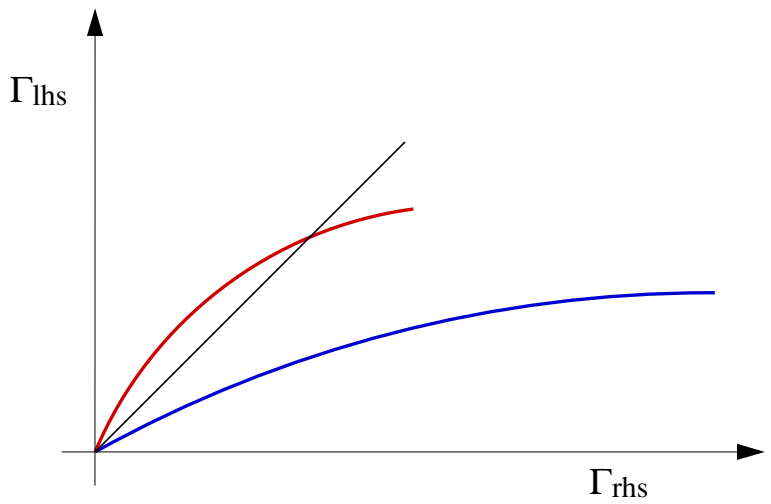

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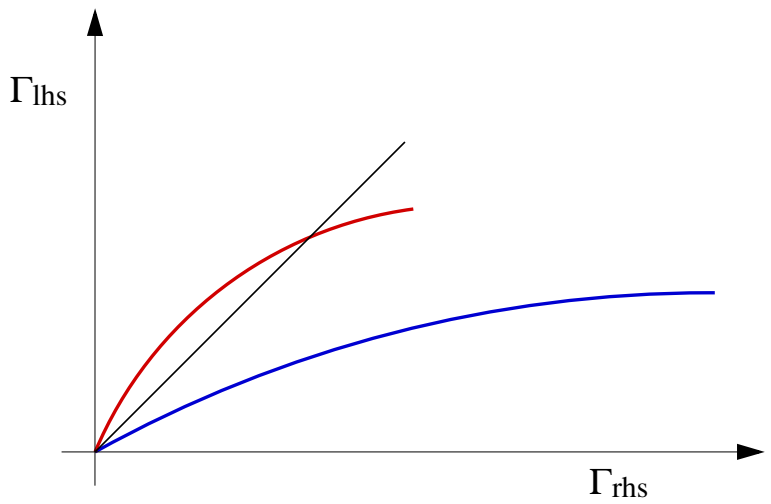

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$$\frac{\lambda}{\mu} \geq \frac{\langle k\rangle}{\langle k^2\rangle - \langle k\rangle}$$

Assuming $\mu = 1$ we have $\lambda \geq \frac{\langle k\rangle}{\langle k^2\rangle - \langle k\rangle}$.

- For networks with $\langle k^2\rangle \to \infty$ we have $\lambda_c = 0$!
- → **Scale-free networks with $\gamma < 3$ have zero epidemic threshold!**

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Consequences of $\lambda_c = 0$

- No matter how weak is the infection, it will prevail,
- No matter how weak is the infection, a finite fraction of the nodes will eventually become infected.

SIR model on networks

- Let us now move onto the SIR model.
- In some sense this seems to be more complicated compared to the SIS, since we have 3 possible states (also called as compartments) instead of 2.
- On the other hand, it is more simple in the sense that here everybody must ends up in the R state, unless the disease has died out early.

SIR model on networks

Homogeneous networks:

$$
\begin{aligned}
1 &= S + \rho + R \\
\frac{dS}{dt} &= -\lambda \langle k \rangle \rho S \\
\frac{d\rho}{dt} &= \lambda \langle k \rangle \rho S - \mu \rho \\
\frac{dR}{dt} &= \mu \rho
\end{aligned}
$$

Inhomogeneous networks:

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\begin{aligned}
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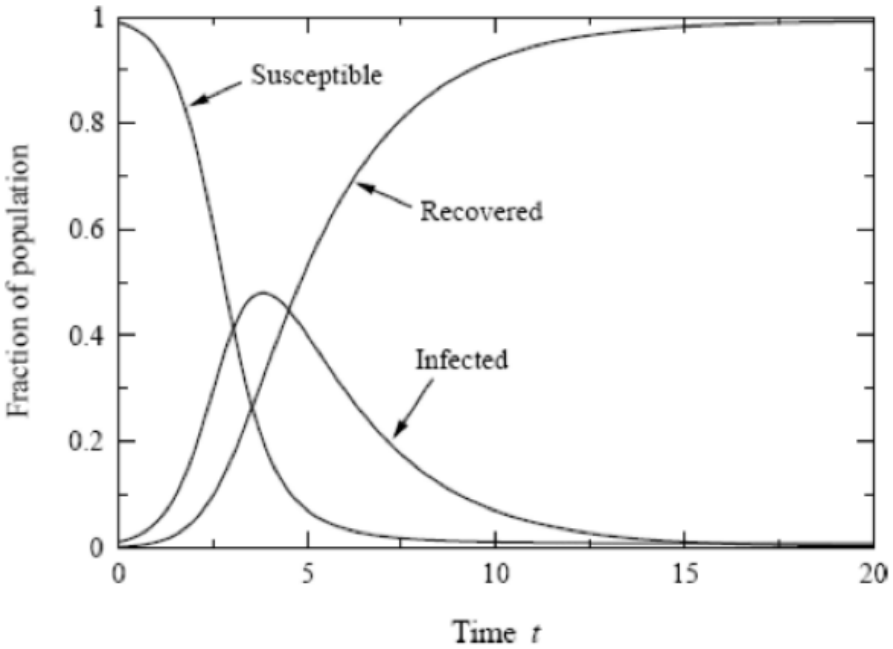

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SIR model on networks
Epidemic threshold

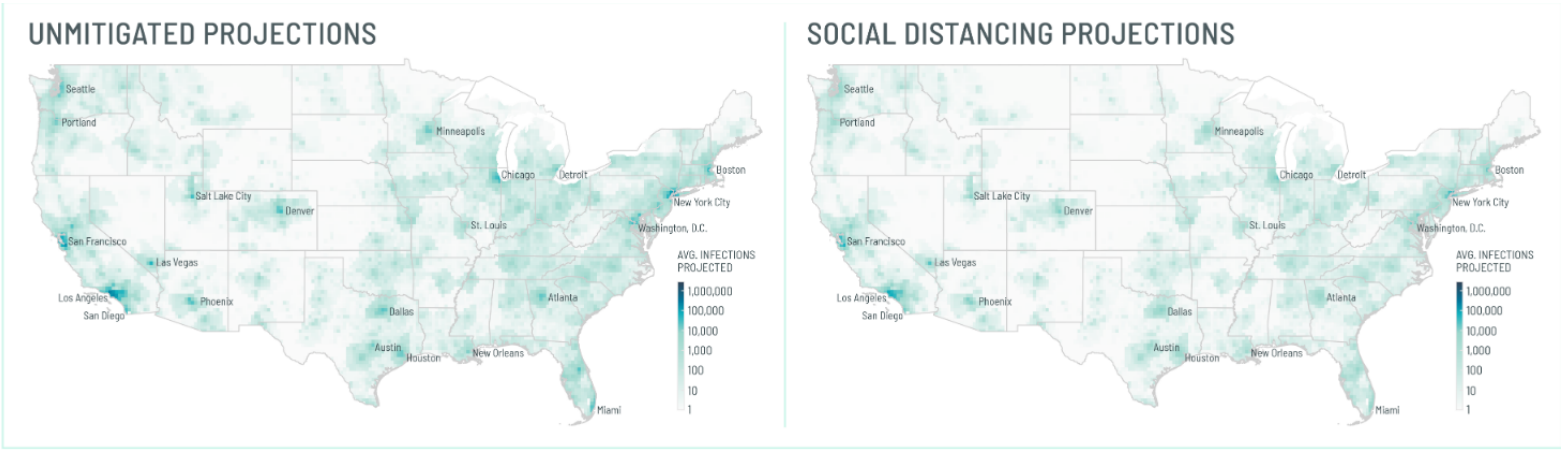
Early stages: qualitatively the same behavior as SIS:

Homogeneous networks:

$$\lambda_c = \frac{1}{\langle k \rangle}$$

Inhomogeneous networks:

$$\lambda_c = \frac{\langle k \rangle}{\langle k^2 \rangle - \langle k \rangle}$$



PREDICTING EPIDEMICS

Predicting epidemics

- How to predict epidemic spreading in a realistic scenario?

Predicting epidemics

- How to predict epidemic spreading in a realistic scenario?
- It is quite a difficult problem; the current state of the art method is provided by Prof. Allesandro Vespignani's group:
  - GLobal Epidemic And Mobility simulator (GLEAM): `http://www.gleamviz.org/simulator/`
  - COVID-19 related page (in general): `https://www.mobs-lab.org/2019ncov.html`
  - Modelling COVID-19 in the USA: `https://covid19.gleamproject.org/`
  - Group's home page: `https://www.mobs-lab.org/`

Predicting epidemics

The basic idea of the GLEAM approach:

- A model with 3 layers, where the bottom layer is corresponding to the population layer, divided into "cells" or regions on the World map, with a number of inhabitants associated to each unit.
- In the middle we have the mobility layer, having two important ingredients:
  - the global airline network,
  - and a local commuting network between neighbouring regions.
- The top layer is corresponding to the disease model we want to study, where we can define compartments such as S, I, R, Endemic, Hospitalised, etc., together with transition probabilities and infection rules.
- For more details please visit the model description part of the GLEAM site:
  `http://www.gleamviz.org/model/`

Summary

Short summary for spreading on networks

- Traditionally we model spreading phenomena by assuming a few states (compartments) describing different stages of the disease such as S, I and R.
- Homogeneous networks have a non-zero epidemic threshold, which means that the spreading rate λ has to be larger than a non-zero constant in order to induce an outbreak, otherwise the infection dies out exponentially.
- However, in the mean time for scale-free networks the epidemic threshold is zero, thus, in principle for any infinitesimally small λ the infection can still prevail. This property is connected to the divergence of the second moment of the degree distribution.

Further reading on network robustness (not compulsory):

Network science book by A.-L. Barabási, chapter 10:
`http://networksciencebook.com/chapter/10`