

# Thresholds, localization and centrality in epidemic spreading on networks

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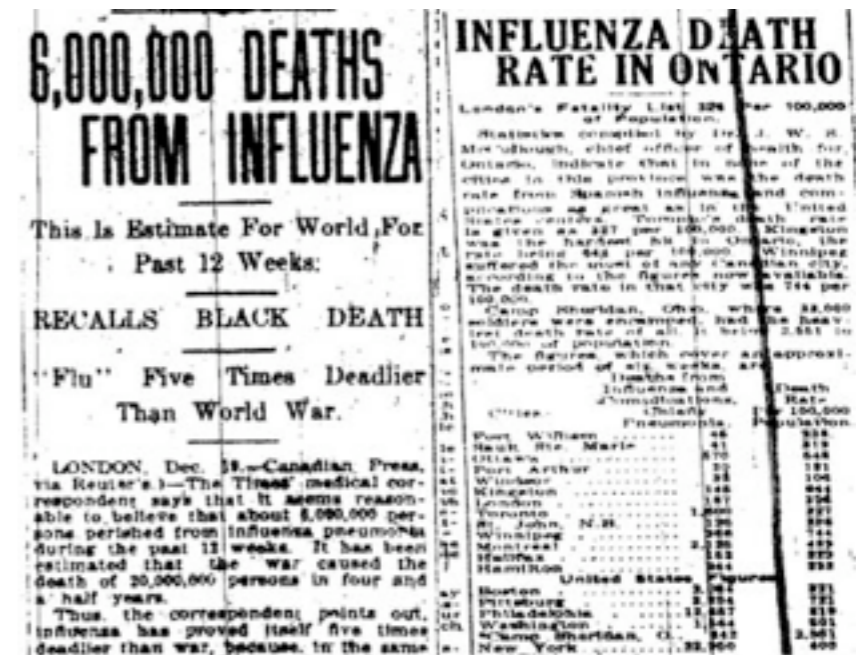
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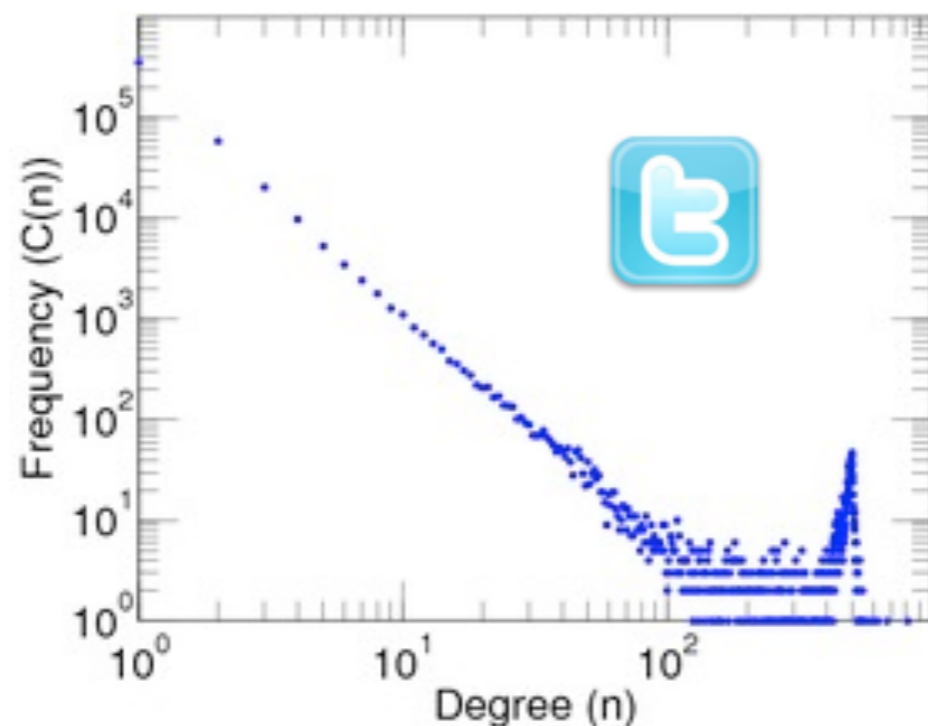
Disease epidemics have been a constant threat to mankind

- Black death epidemics killed one third of europeans between 1347 and 1353
- In 1918 spanish flu killed 40-50 million people, many more than world war I
- New epidemics constantly appear (HIV, SARS, Ebola...)



## Networks are relevant

At the scale of individuals  
interaction patterns are not regular



## Heterogeneous networks are relevant

HIV “patient zero” infected 40 of the 284 first cases of AIDS in the USA

Networks are relevant

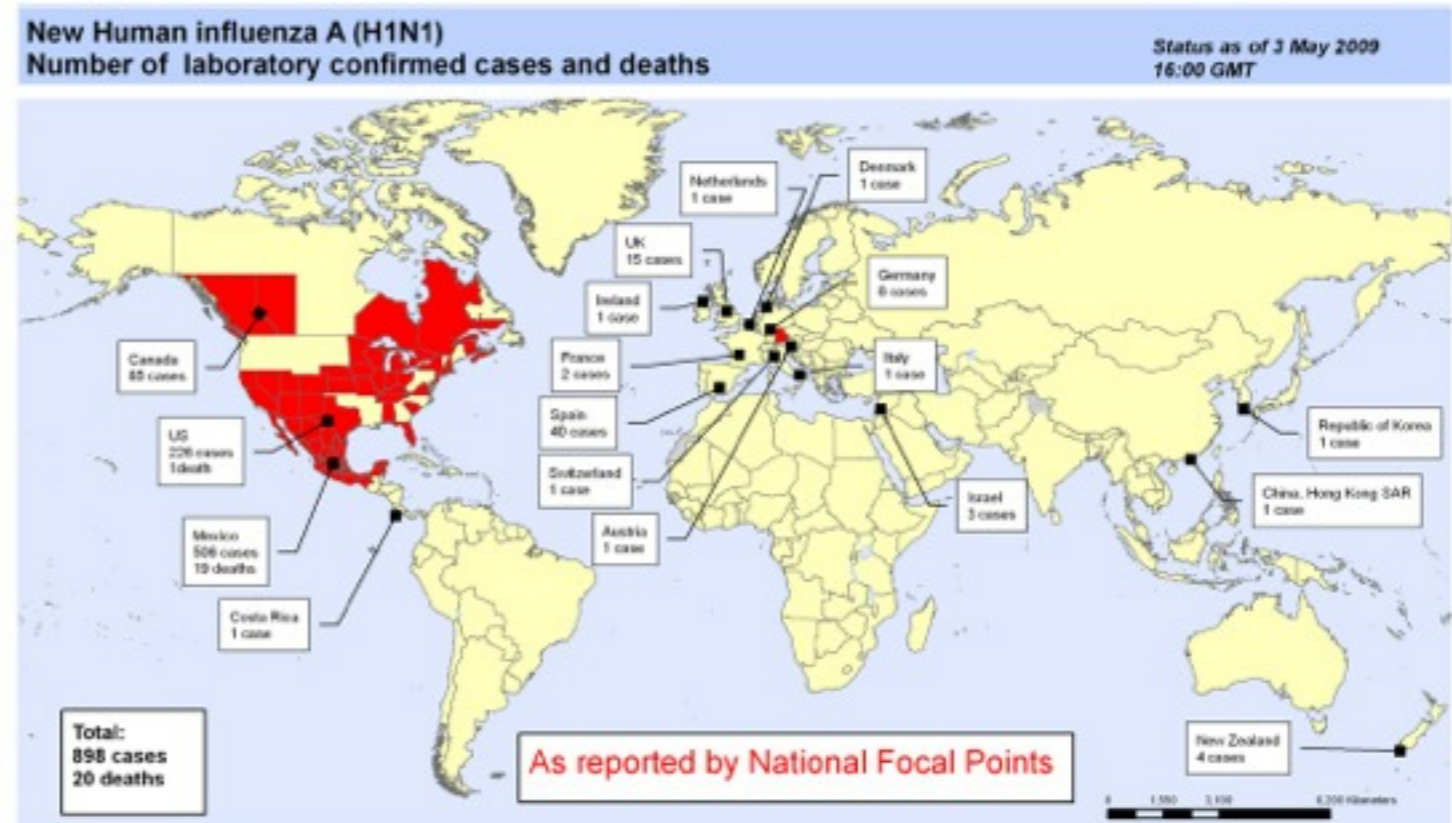


Black death

Fast and long-range travel is crucial

Large-scale heterogeneous transportation networks are relevant

H1N1 2009 pandemics



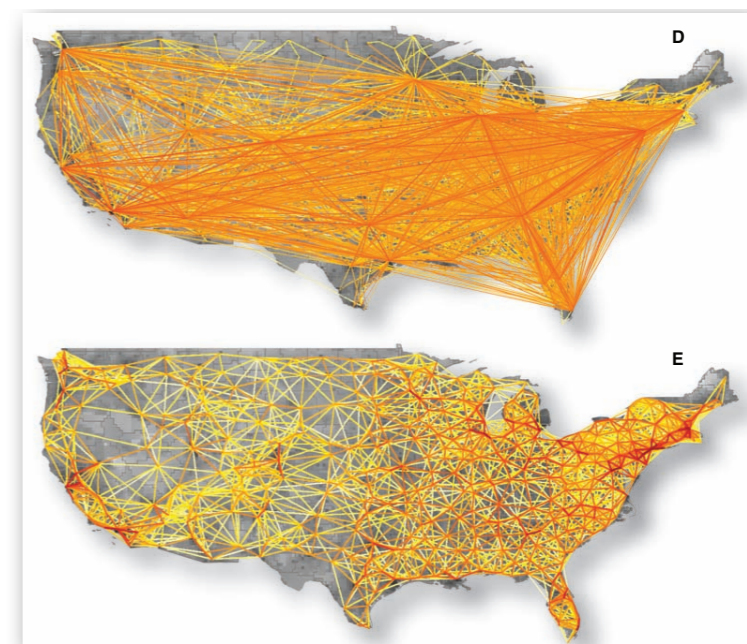
The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted lines on maps represent approximate border lines for which there may not yet be full agreement.

Map produced: 3 May 2009 18:17 CET

Data Source: World Health Organization  
Map Production: Public Health Information  
and Geographic Information Systems (GIS)  
World Health Organization



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# Modeling epidemics on networks

- Practical interest
  - Crucial problem throughout human history
- Theoretical interest
  - Nontrivial dynamics (percolation, branching processes, absorbing phase transitions)
    - What is the value of the epidemic threshold?
    - How does the prevalence varies?
    - Which immunization protocols control the epidemics?
    - Which spreaders are most influential?
    - How can the origin of an outbreak be reconstructed?

## SIR class

- Permanent immunity
- Individuals are infected at most once
- Outbreaks have finite duration

## SIS class

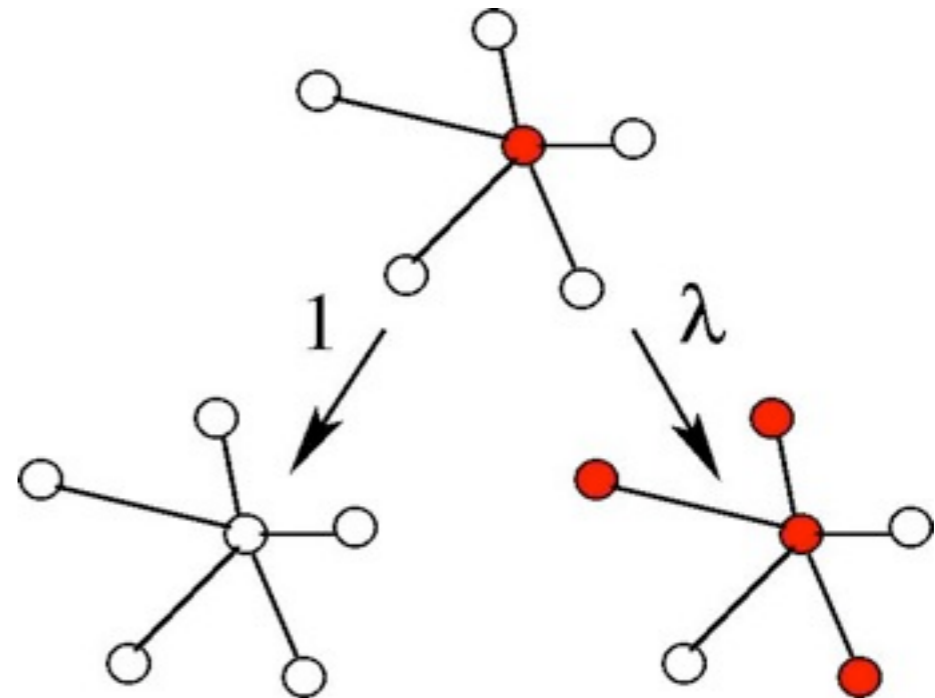
- Temporal/no immunity
- Individuals can be infected many times
- Outbreaks can persist forever

# Susceptible-Infected-Susceptible (SIS) model

- Two possible states:

○ susceptible (S)

● infected (I)

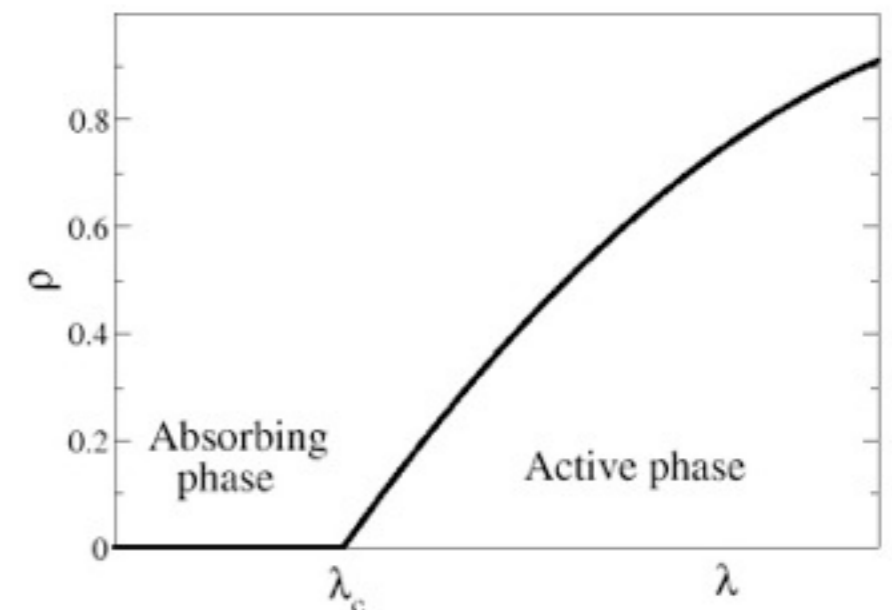


- Two possible events for infected nodes:

★ Recovery  $I \rightarrow S$  (rate  $\mu=1$ )

★ Infection to neighbors  $S+I \rightarrow I+I$  (rate  $\lambda$ )

- Order parameter  
 $\rho$  = fraction of infected nodes  
in the stationary state



# Heterogeneous Mean-Field theory (HMF) for SIS

*Pastor-Satorras and Vespignani (Phys. Rev. Lett., 2001)*

- Standard MF theory:  $\dot{\rho} = -\rho + \lambda k \rho (1 - \rho)$   $\lambda_c = \frac{1}{k}$
- What happens for heterogeneous networks ( $P(k) \sim k^{-\gamma}$ )?
- Assumption: degree determines the state of the node
- $\rho_k$  = fraction of infected nodes of degree  $k$

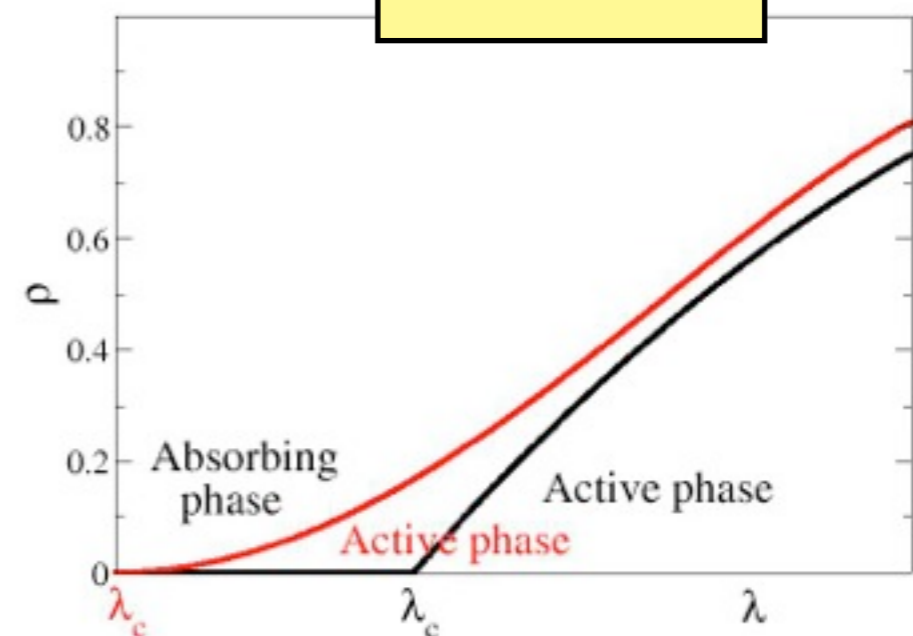
$$\dot{\rho}_k = -\rho_k + \lambda k [1 - \rho_k] \sum_{k'} P(k'|k) \rho_{k'}$$

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

- In the limit of large system size

$$\lambda_c \rightarrow \begin{cases} 0 & \gamma \leq 3 \\ \text{finite} & \gamma > 3 \end{cases}$$

**Zero threshold for scale-free networks**





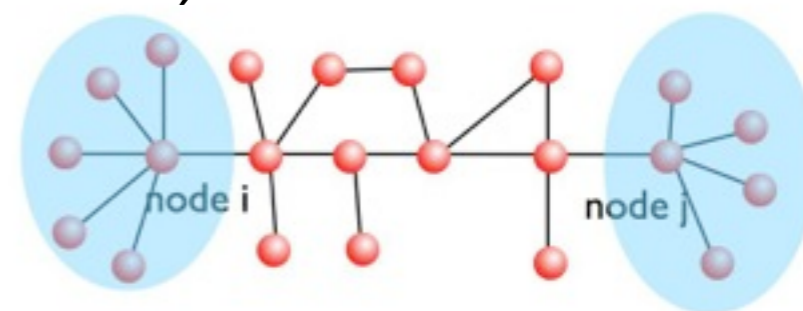
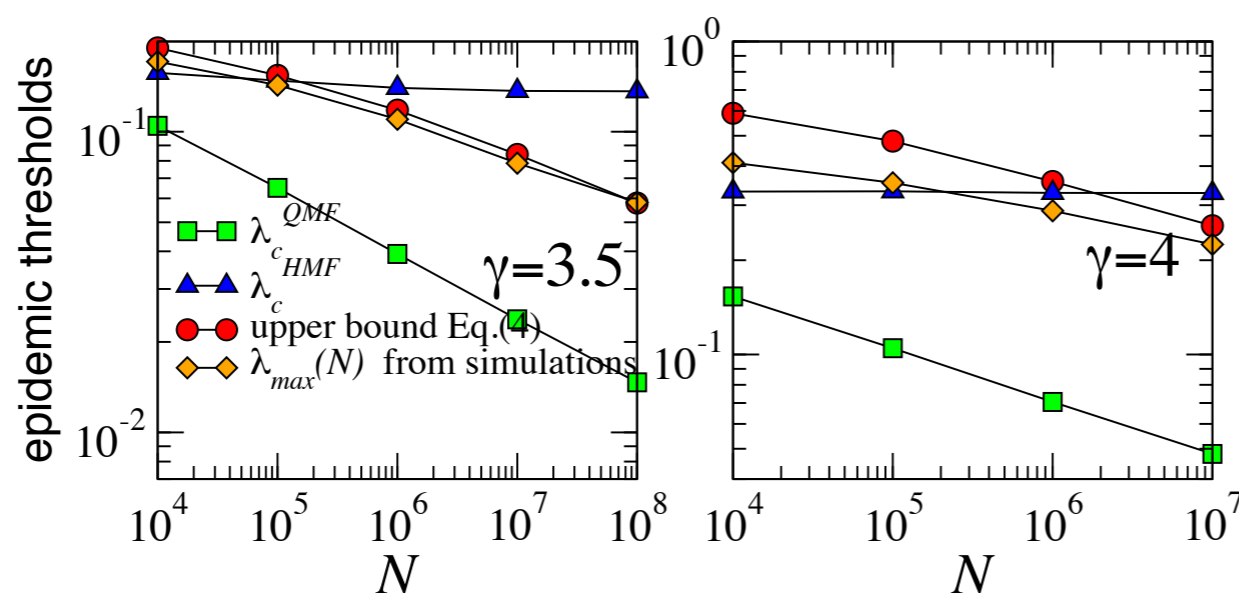
# Beyond Heterogeneous Mean Field

- Inclusion of detailed structure of the network:  
Quenched Mean Field

$$\lambda_c = \frac{1}{\Lambda_N}$$

$\Lambda_N$  = Largest eigenvalue of adjacency matrix

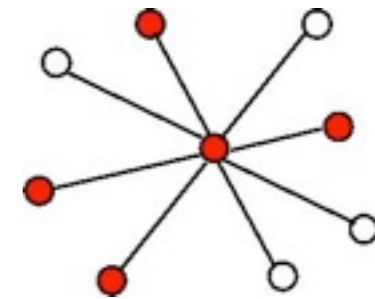
- Eigenvector localization for  $\gamma > 5/2$ : global activity slightly decays over time (Griffiths phase)?
- Inclusion of dynamical correlations between distant neighbors (reinfection among distant hubs)



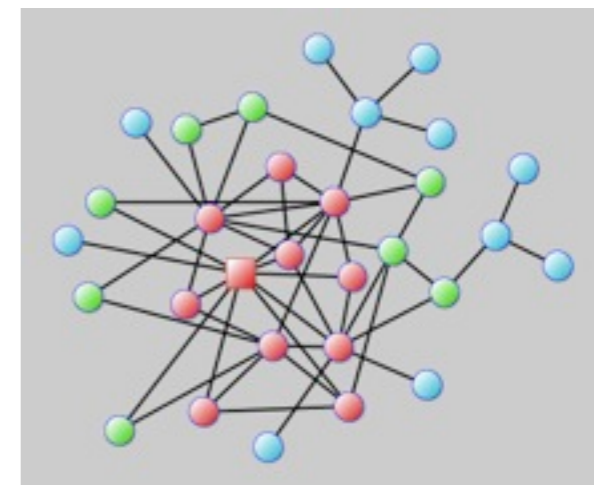
The epidemic threshold goes to zero for any  $\gamma$

# Distinct triggering mechanisms

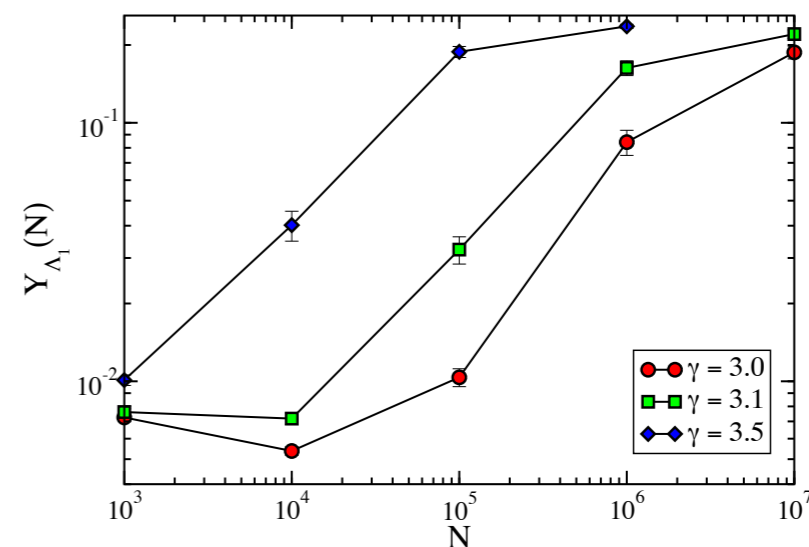
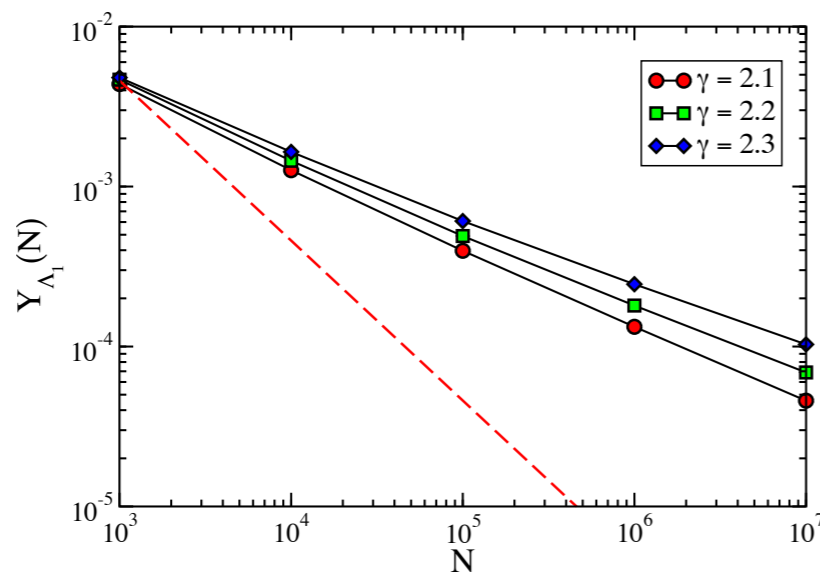
- $\gamma > 5/2$ : single hub triggers the epidemics



- $\gamma < 5/2$ : mesoscopic subgraph of densely connected nodes triggers the epidemics



- Distinct triggering mechanisms correspond to distinct eigenvector localizations in networks

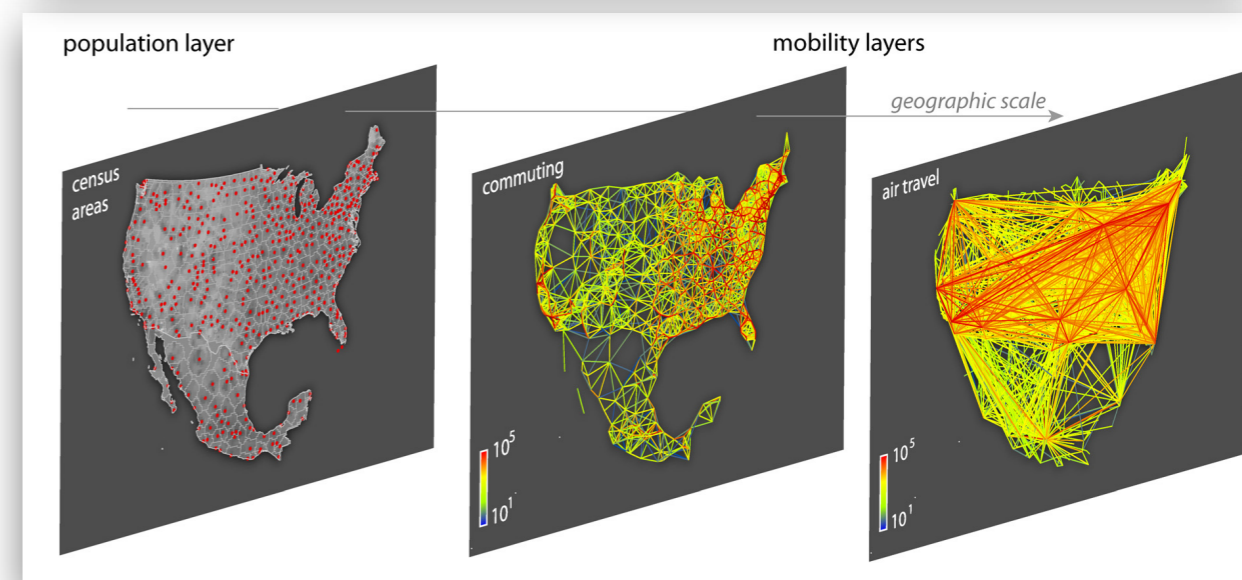
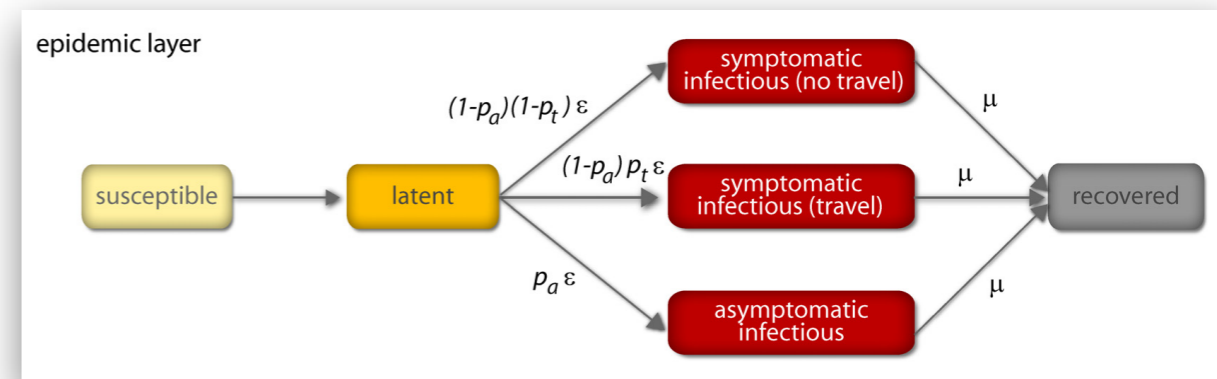



- Forecasting simulation frameworks are nontrivial systems, implementing:

- Realistic models of disease propagation, based on real epidemiological data

- Different layers of social, population and mobility data

- Computational power



 **GLEaMviz.org**

### Introduction

GLEaM is a Global Epidemic and Mobility modeler that integrates sociodemographic and population mobility data in a spatially structured stochastic disease approach to simulate the spread of epidemics at the worldwide scale. [Read more about GLEaM.](#)

The GLEaMviz project covers the research conducted with GLEaM as well as the tools derived from it. This website reports on the progress of this project, its main results, [publications](#) of academic papers and editorial material, presentations at international conferences and workshops, and other outreach activities.

Please subscribe to our [RSS](#) or [Atom](#) feed or follow [gleamviz](#) on Twitter to stay up-to-date.

**New publication describing the data integration, modeling schemes and algorithmic implementations of GLEaM**  
September 20th, 2010

**TEXAS TAGG Texas Pandemic Flu Simulator**

Map showing the state of Texas with a grid overlay, indicating simulation results. The interface includes a sidebar with controls for simulation parameters and a main map area.

Current data set: 100 Run 8

Advertisement:

- Number of realizations: 100
- Reproduction number:  $R_0 = 1.5$
- Latency period: 1 day
- Infectious period: 4 days
- Mortality rate: 0.1
- Travel distribution strategy: Default

© 2010, Lauren Heffernan

## Epidemic-like phenomena are ubiquitous

- Computer viruses
- Information diffusion
- Rumor spreading
- Adoption of innovations
- Fashion
- Behavioral contagion
- .....

- SIS epidemic threshold always vanishes in the large size limit
- Mean-field approaches capture only part of the picture
- Depending on heterogeneity (value of  $\gamma$ )
  - Different mechanisms trigger the epidemic transition
  - Different types of eigenvector centrality localization may occur
- Networks with  $\gamma < 5/2$  are much different from those with  $\gamma > 5/2$

*C. Castellano and R. Pastor-Satorras, Phys. Rev. Lett., 105, 218701 (2010)*

*C. Castellano and R. Pastor-Satorras, Scientific Reports 2, 371 (2012)*

*S. Ferreira, C. Castellano and R. Pastor-Satorras Phys. Rev. E 86, 041125 (2012)*

*M. Boguñá, C. Castellano and R. Pastor-Satorras Phys. Rev. Lett. 111, 068701 (2013)*

*A. Mata, M. Boguñá, C. Castellano and R. Pastor-Satorras, Phys. Rev. E 91, 052117 (2015)*

*R. Pastor-Satorras and C. Castellano, arxiv: 1505.06024 (2015)*

*Review on epidemics in networks:*

*R. Pastor-Satorras, C. Castellano, P. Van Mieghem and A. Vespignani, Rev. Mod. Phys., 87, 925 (2015)*