

# Digital epidemiology

## Lesson 10

**Michele Tizzoni**

Dipartimento di Sociologia e Ricerca Sociale  
Via Verdi 26, Trento  
Ufficio 6, 3 piano

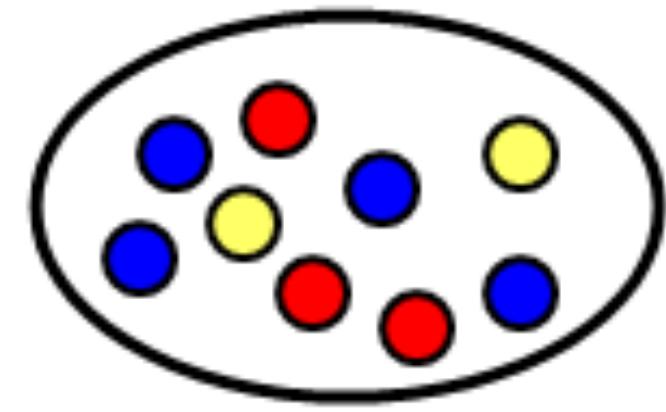


UNIVERSITÀ  
DI TRENTO

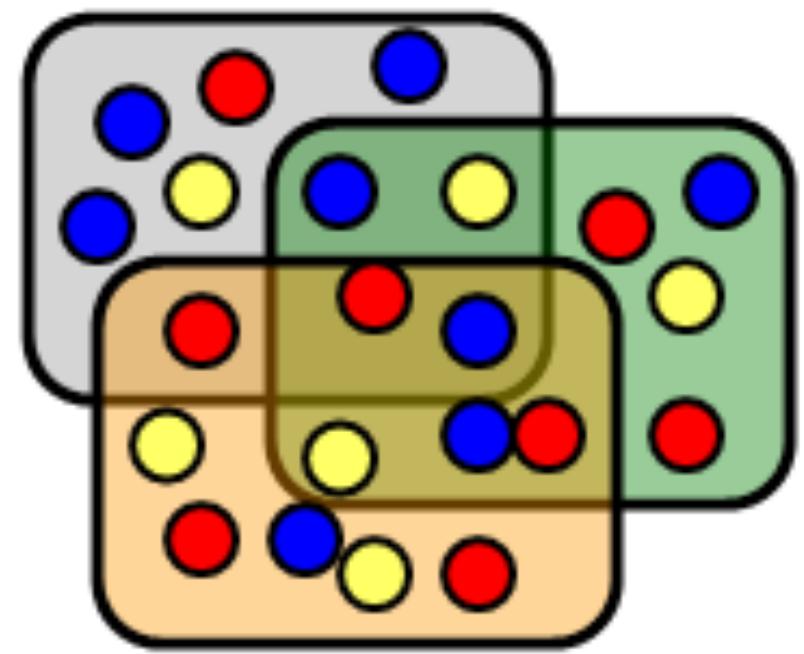


# Spatial epidemic models

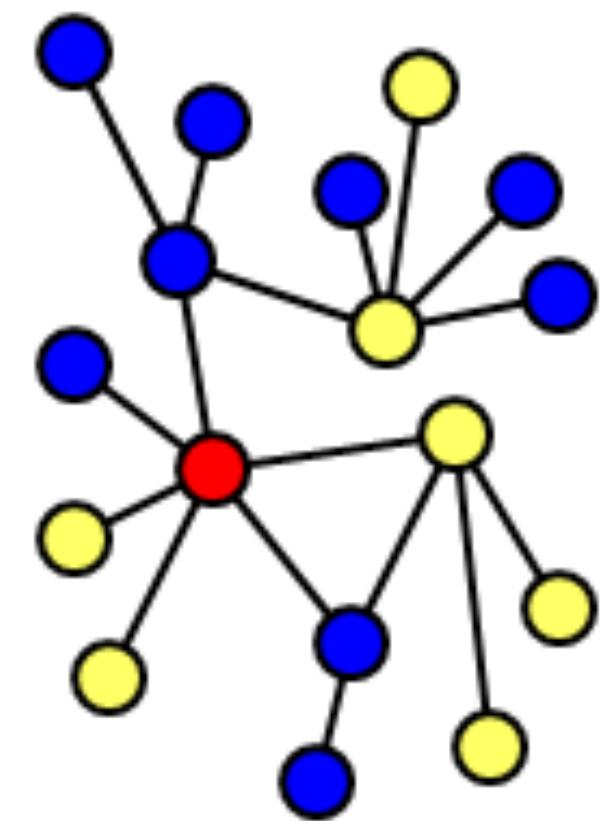
# Models



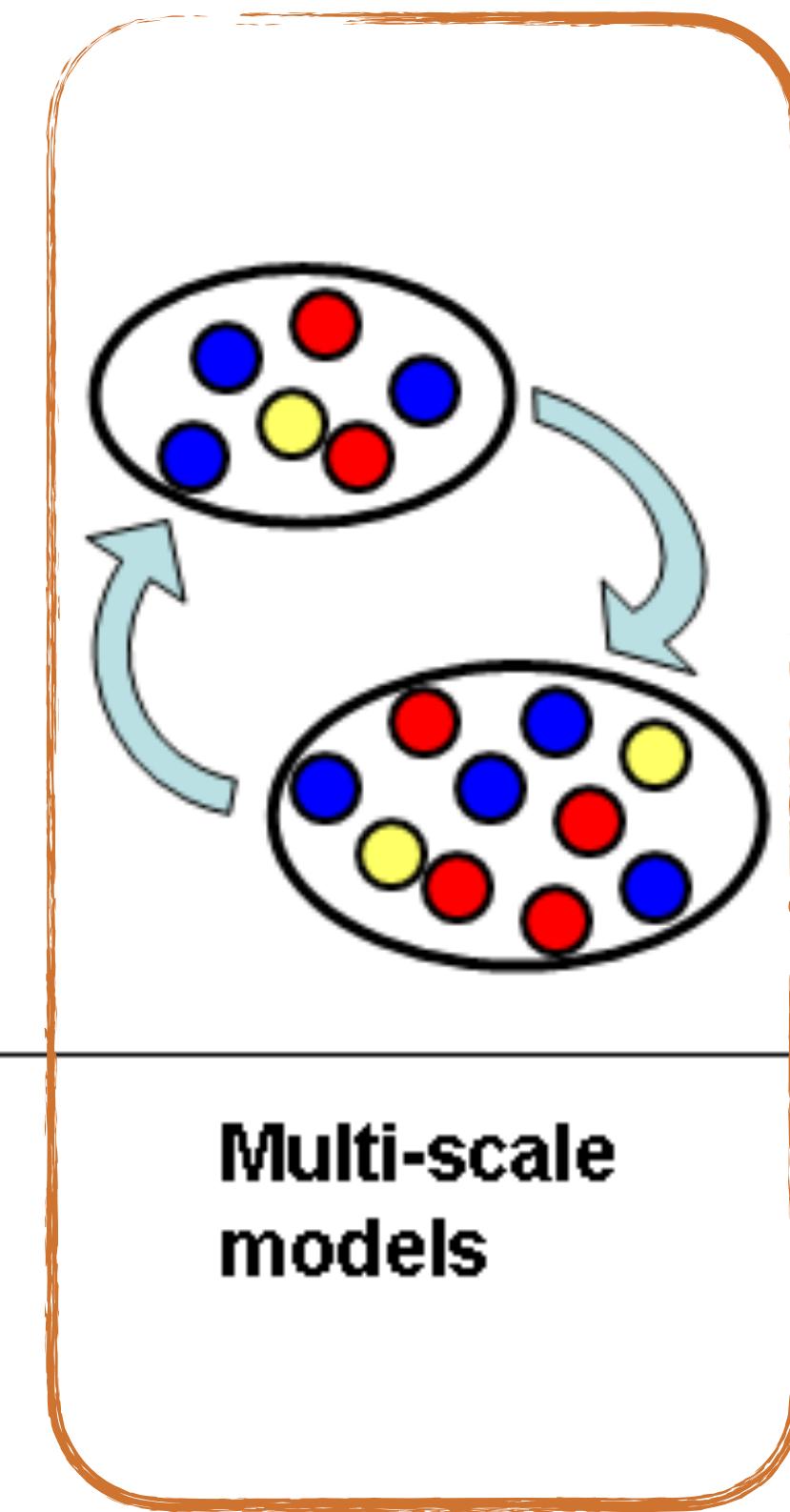
Homogeneous  
mixing



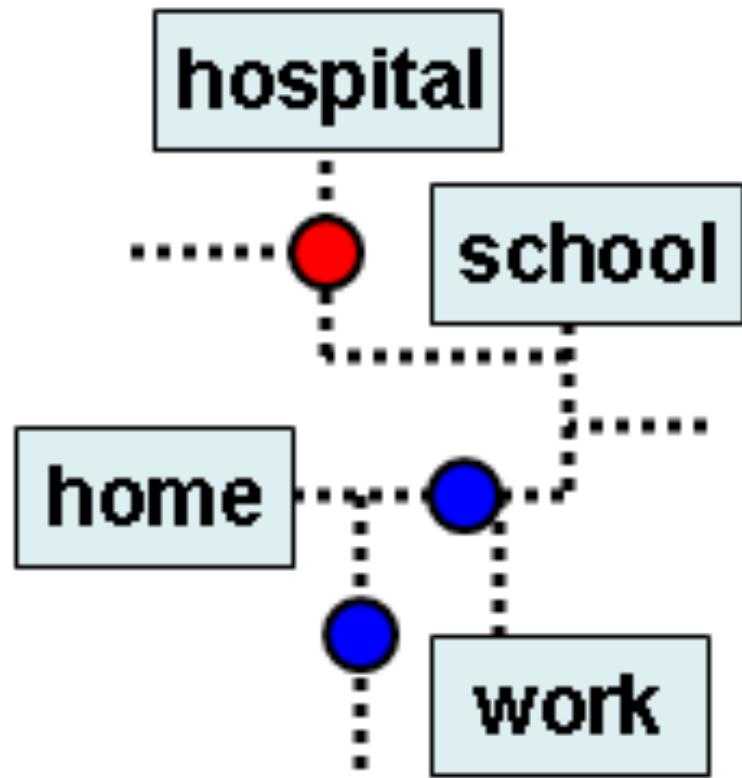
Social structure



Contact network  
models

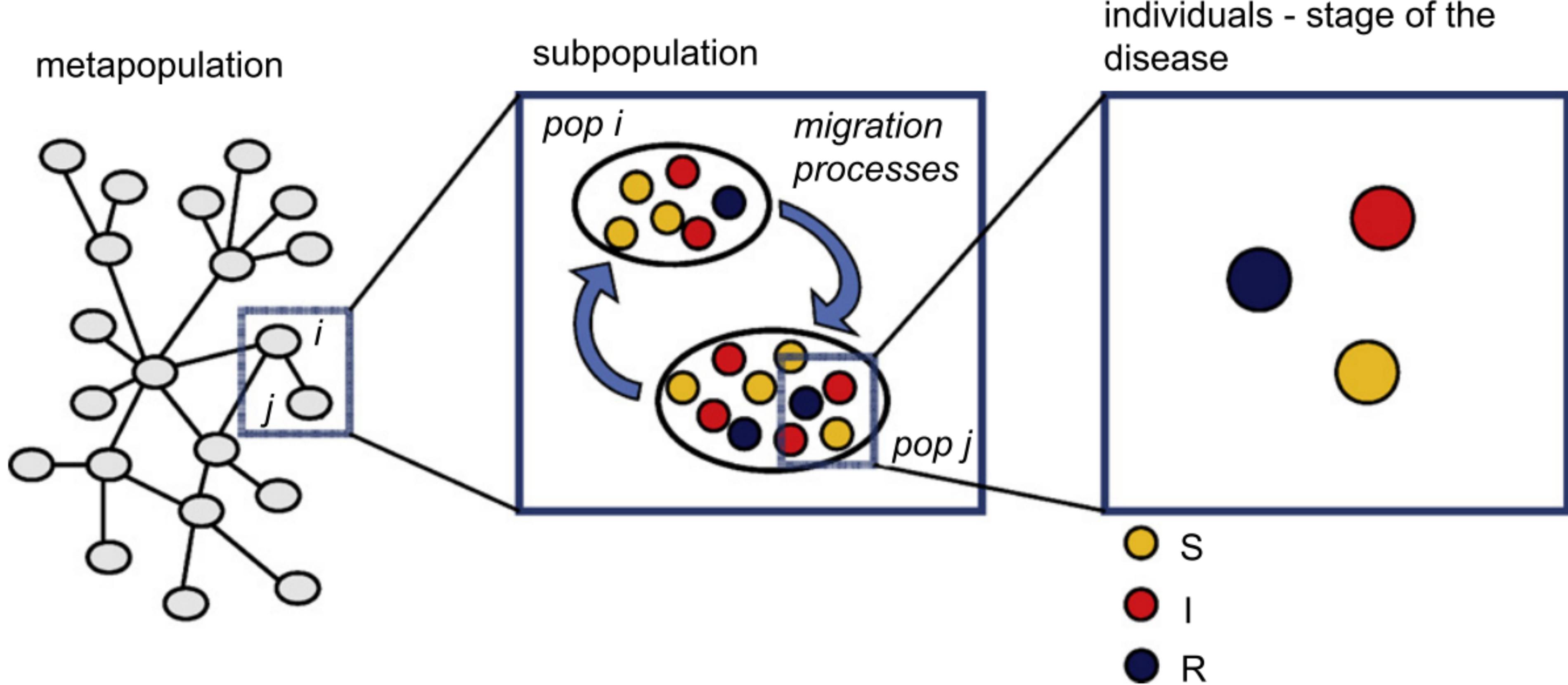


Multi-scale  
models



Agent Based  
models

# Metapopulation models

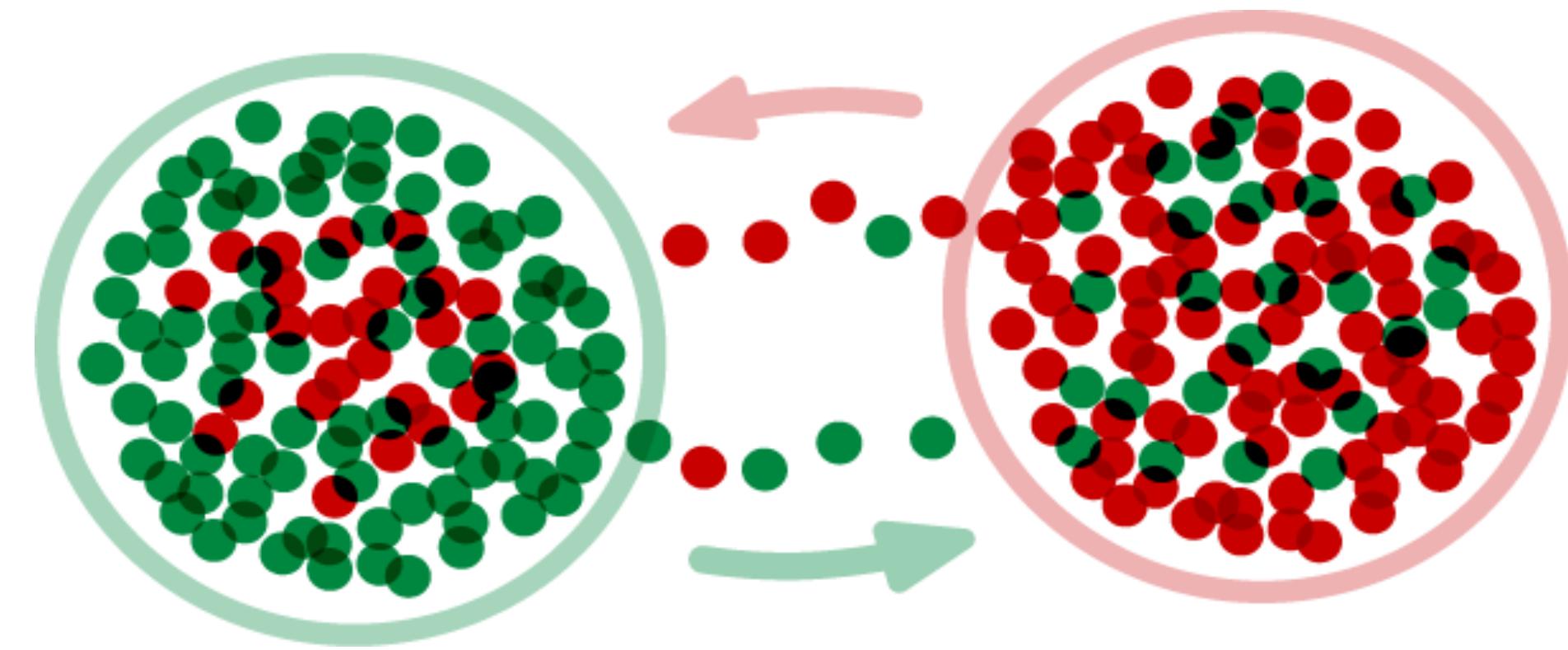


# Reaction-diffusion

- We consider a network of  $V$  subpopulations where each node hosts  $N_i$  individuals, which can be in state S, I or R
- **Diffusion:** individuals migrate from one node to another with a rate  $d_{ij}$  depending on observed real-world weights:  $d_{ij} = \frac{w_{ij}}{N_i}$
- **Reaction:** in each subpopulation, individuals interact according to an epidemic compartmental model in homogenous mixing

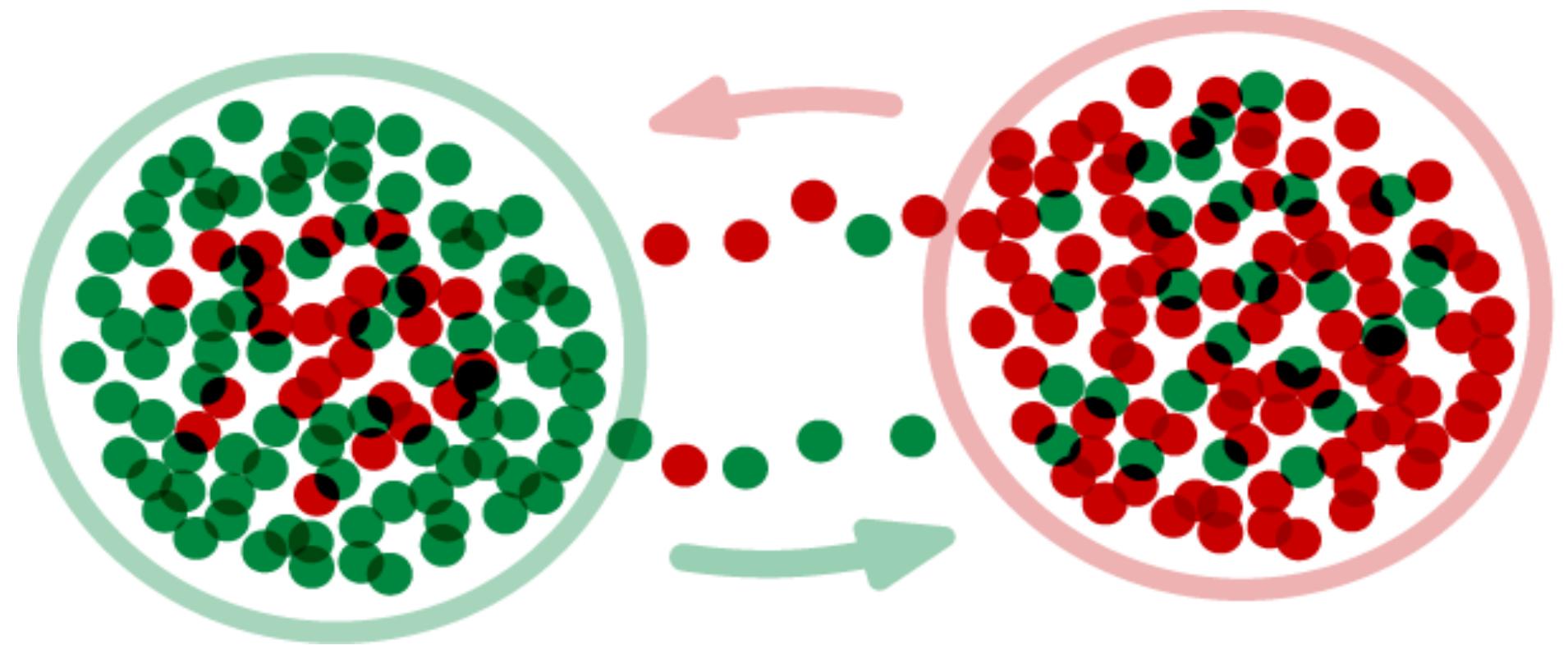
# I. Diffusion process

# Diffusion process



$w_{ij}$  = number of individuals  
traveling between i and j

# Diffusion process

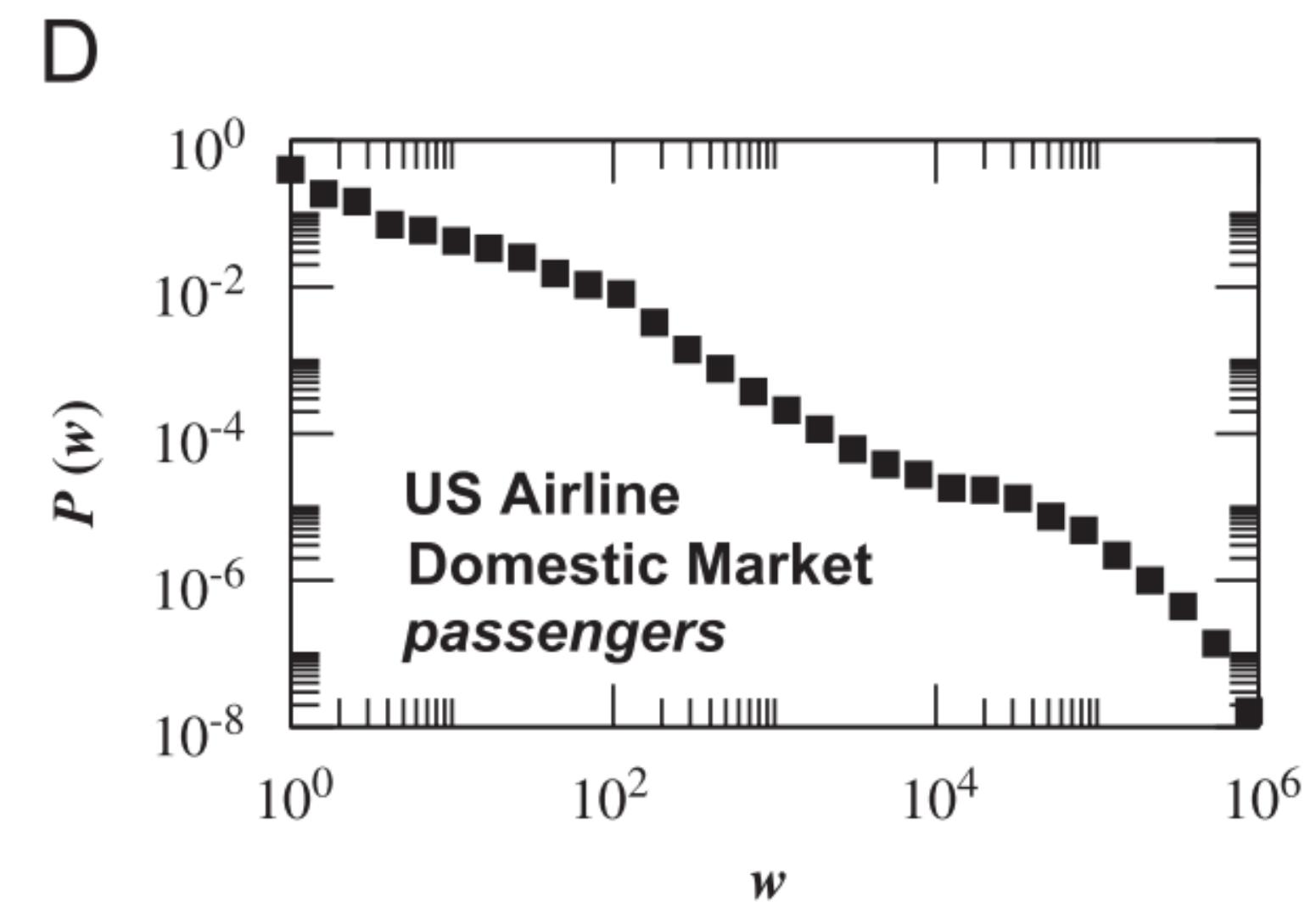
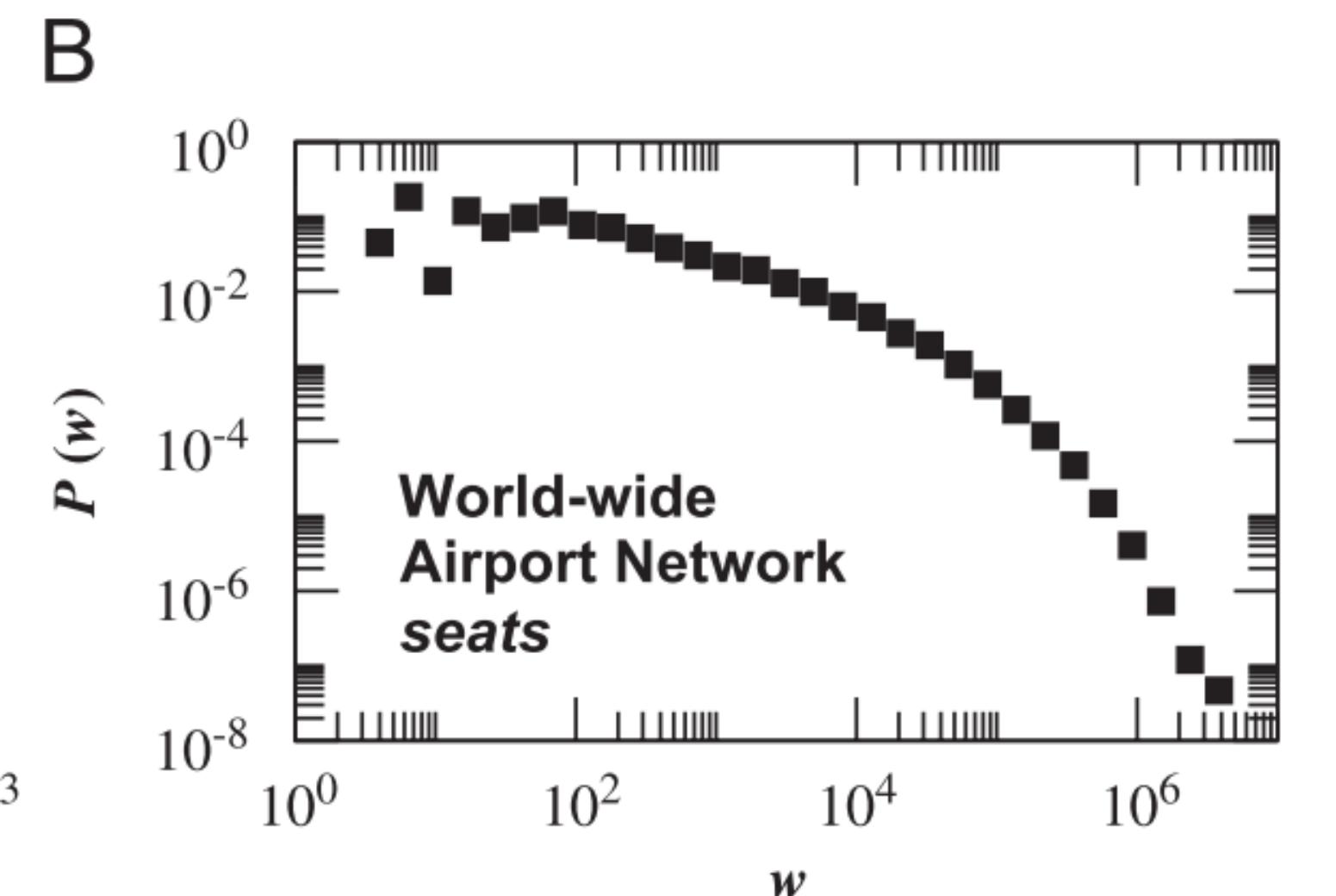


$w_{ij}$  = number of individuals  
traveling between i and j

in real world networks:

$$\langle w_{kk'} \rangle \sim w_0(kk')^\theta$$

$$\theta \sim 0.5$$



# Diffusion process

We can define  $T_k = k \sum_{k'} P(k'|k) w_0(kk')^\theta$

as the **total average traffic** in unit time.

in real world networks:

$$\langle w_{kk'} \rangle \sim w_0(kk')^\theta$$

$$\theta \sim 0.5$$

Under the assumption of **uncorrelated network**:

$$P(k'|k) = \frac{k' P(k')}{\langle k \rangle}$$

$$T_k = \frac{\langle k^{1+\theta} \rangle}{\langle k \rangle} w_0 k^{\theta+1} = A k^{\theta+1}$$

# Degree based mean field

- We consider all nodes of degree  $k$  as **statistically equivalent**
- For a degree-block  $k$ , the population of the nodes:

$$N_k = \frac{1}{V_k} \sum_{i|k_i=k} N_i$$

# Degree based mean field

- ▶ Individuals leave subpopulations of degree  $k$  with rate:

$$p_k = k \sum_{k'} P(k' | k) d_{kk'}$$

- ▶  $d_{kk'}$  is the **diffusion rate** between nodes of degree  $k$  and  $k'$
- ▶ The dynamics of individuals in nodes of degree  $k$  can be expressed as:

$$\partial_t N_k(t) = - p_k N_k + k \sum_{k'} P(k' | k) d_{kk'} N_k(t)$$

# Degree based mean field

$$\partial_t N_k(t) = - p_k N_k + k \sum_{k'} P(k' | k) d_{kk'} N_{k'}(t)$$

- Assuming an uncorrelated network, it becomes:

$$\partial_t N_k(t) = - p_k N_k + \frac{k}{\langle k \rangle} \sum_{k'} k' P(k') d_{kk'} N_{k'}(t)$$

- The **choice of the diffusion rate**,  $d_{kk'}$  will lead to different results.

# I. Traffic dependent mobility

$$d_{kk'} = p \frac{w_0(kk')^\theta}{T_k}$$

- The probability of leaving a node is a constant  $p$ , independent of  $k$ .
- Travellers are distributed among links according to the observed weights (in real networks).

$$\partial_t N_k(t) = -pN_k + pk^{1+\theta} \frac{w_0}{A\langle k \rangle} \sum_{k'} P(k') N_{k'}(t)$$

- The stationary solution  $\partial_t N_k(t) = 0$  does not depend on  $p$  and it becomes

$$N_k(t) = \frac{w_0}{A\langle k \rangle} \bar{N} k^{1+\theta}$$

where  $\bar{N} = \sum_{k'} P(k') N_{k'}(t)$

# I. Traffic dependent mobility

$$d_{kk'} = p \frac{w_0(kk')^\theta}{T_k}$$



$$N_k(t) = \frac{k^{1+\theta}}{\langle k^{1+\theta} \rangle} \bar{N}$$

- the population of each node scales with the node degree in the stationary limit
- The above behavior is simply the effect of the diffusion process that brings a large number of individuals in well connected nodes
- In the case  $\theta = 0$  we obtain the result of a **homogeneous diffusion rate**  $d_{kk'} = \frac{p}{k}$

$$N_k(t) = \frac{k}{\langle k \rangle} \bar{N}$$

# II. Population dependent mobility

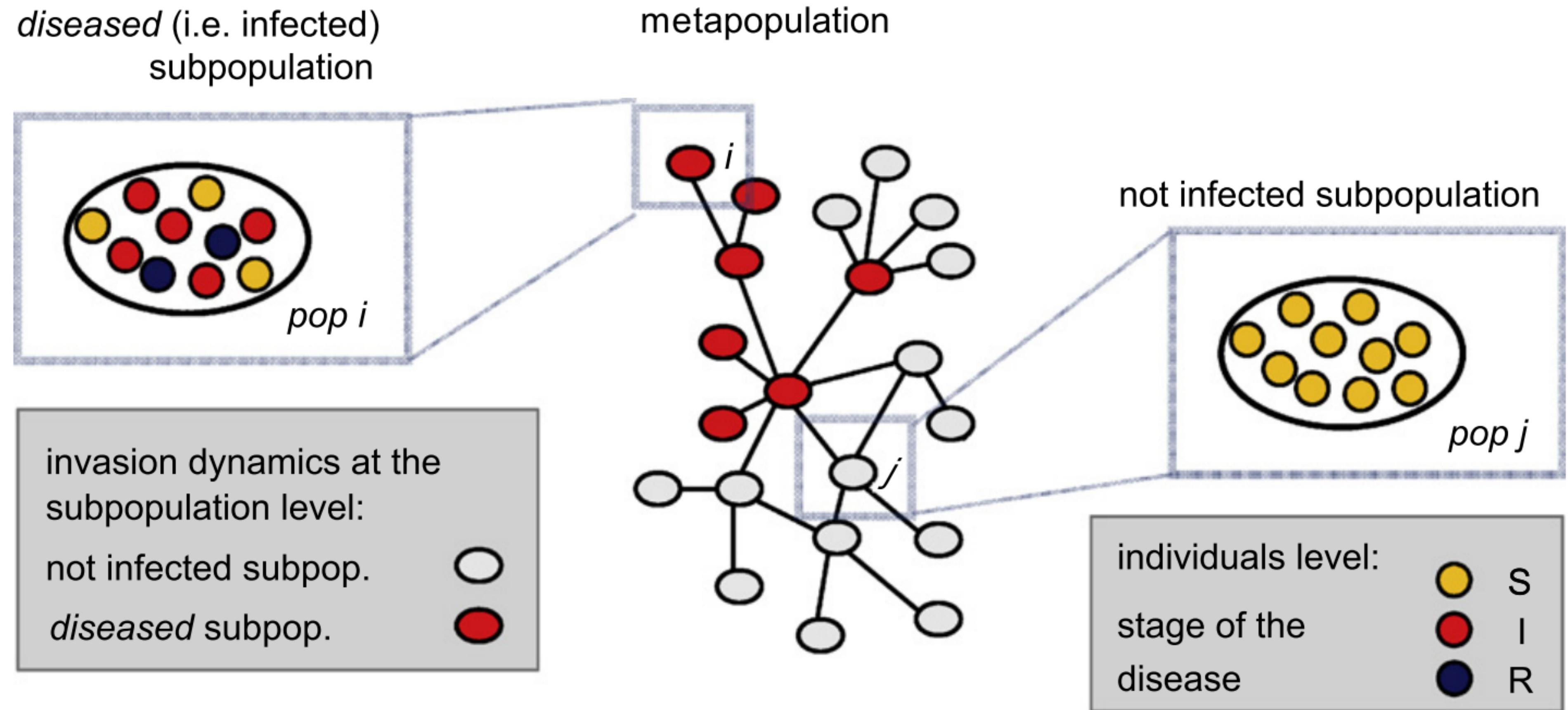
- We want to consider the population of each node as **independent variables**
- We want any initial conditions for the population size to satisfy the stationary state.
- This can be obtained by setting  $p_k = T_k/N_k$

$$d_{kk'} = \frac{w_0(kk')^\theta}{N_k} \quad \rightarrow \quad \partial_t N_k(t) = -T_k + \frac{\langle k^{1+\theta} \rangle}{\langle k \rangle} w_0 k^{1+\theta} = 0$$

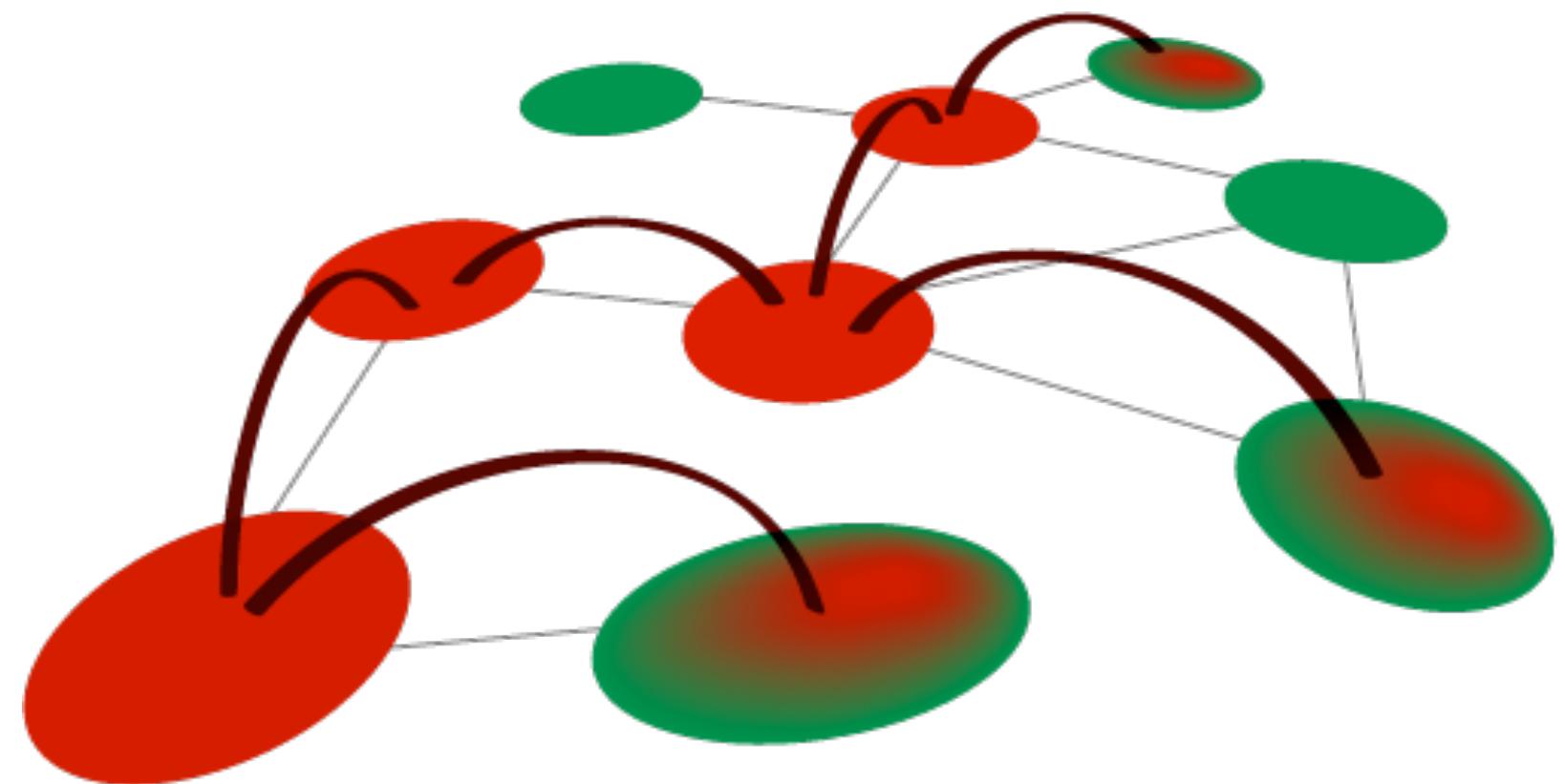
A population dependent diffusion process does not fix the subpopulation size, which can be given as a parameter of the model.

## II. Reaction process

# Reaction process

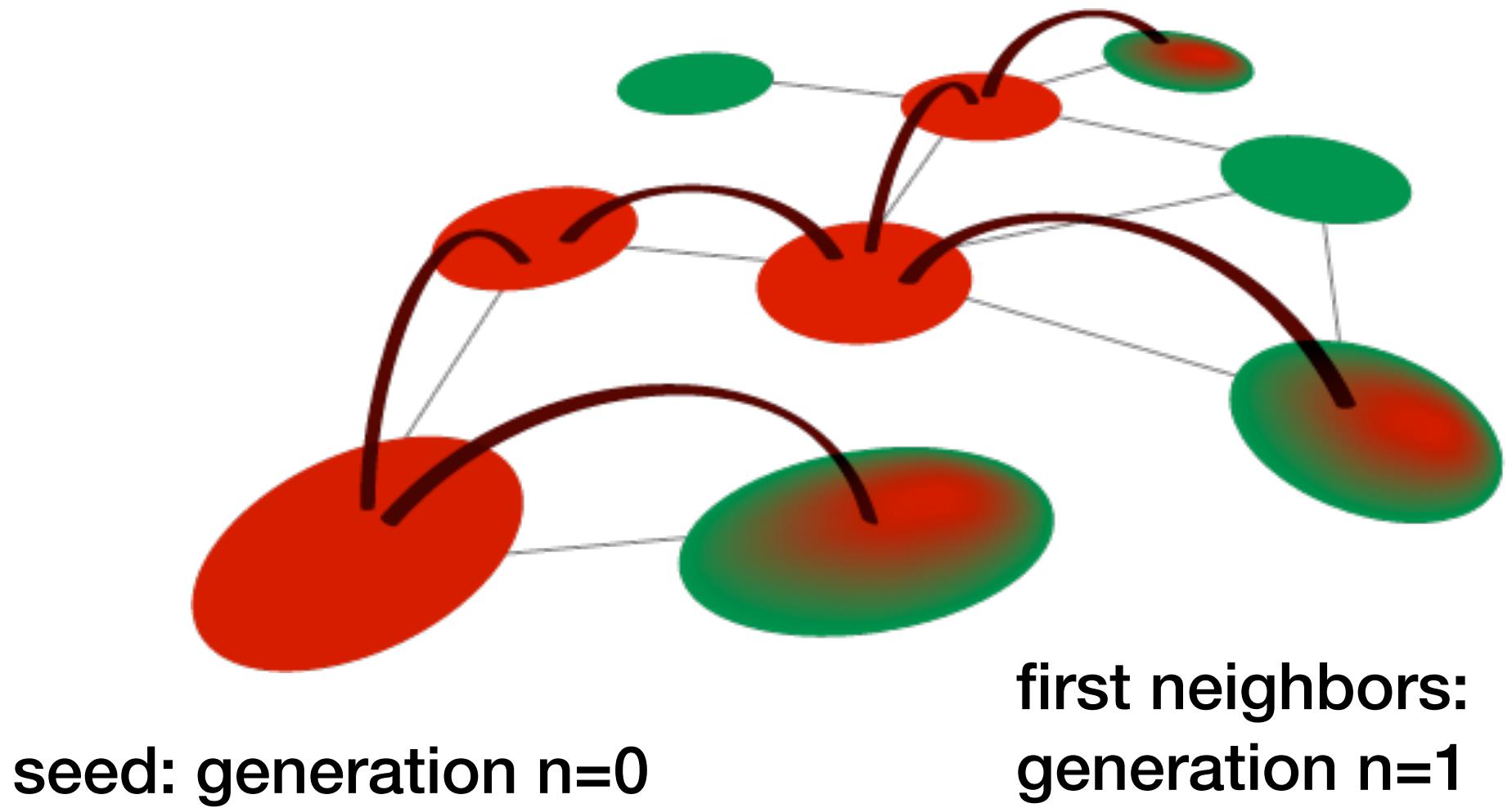


# Invasion threshold



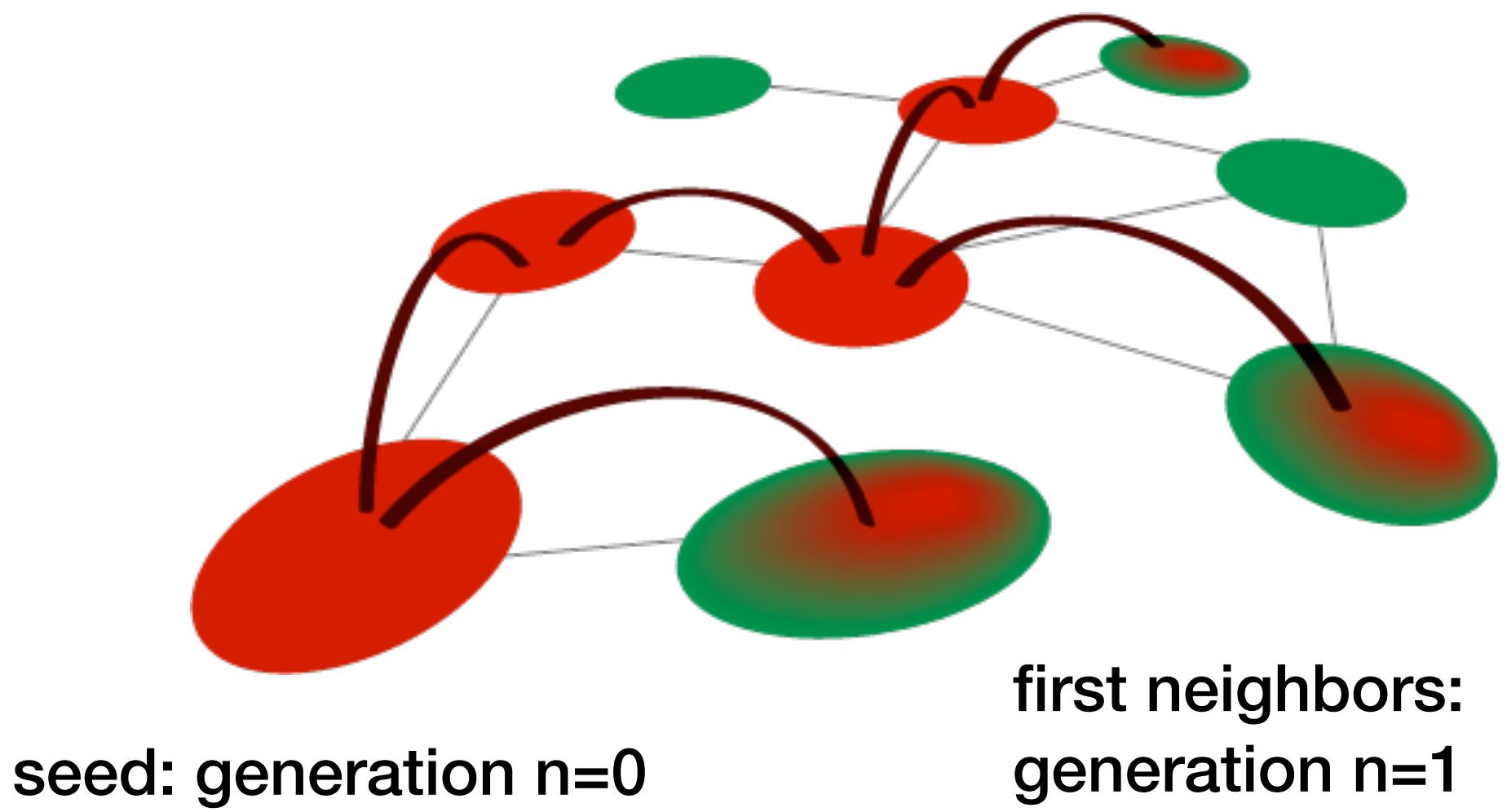
- In each node we consider a SIR model, with parameters  $\beta$  and  $\mu$
- The basic reproductive number is  $R_0 = \frac{\beta}{\mu}$
- There is a **local epidemic threshold**  $R_0 > 1$  that defines the condition for an outbreak to occur within a node
- We look for a **global invasion threshold** that defines the condition for an outbreak to reach a finite portion of the whole system

# Branching process



We denote as  $D_k^0, D_k^1, \dots$  the number of subpopulations of degree  $k$ , that are infected (with at least 1 infected individual) at generation  $n=0, 1, \dots$

# Branching process



We denote as  $D_k^0, D_k^1, \dots$  the number of subpopulations of degree  $k$ , that are infected (with at least 1 infected individual) at generation  $n=0, 1, \dots$

$$D_k^n = \sum_{k'} D_{k'}^{n-1} P(k | k') (k' - 1) \left( 1 - \frac{D^{n-1}}{V} \right) \left[ 1 - \frac{1}{R_0^{\lambda_{kk'}}} \right]$$

Connections k'-k      possible paths  
of infections      density of  
susceptible nodes      outbreak  
probability in a  
node

# Branching process

$$p_{outbreak} = \left[ 1 - \frac{1}{R_0^{\lambda_{kk'}}} \right]$$

Where  $\lambda_{kk'}$  is the number of infected individuals (seeds) traveling between subpopulations of degree  $k'$  to  $k$

$$\lambda_{kk'} = d_{kk'} \frac{\alpha N_{k'}}{\mu}$$

Epidemic size in the subpopulation  $N_{k'}$

$$d_{kk'} = \frac{w_0 (kk')^\theta}{N_{k'}}$$

**population dependent**  
mobility rates

# Branching process

$$D_k^n = \sum_{k'} D_{k'}^{n-1} P(k | k') (k' - 1) \left( 1 - \frac{D^{n-1}}{V} \right) \left[ 1 - \frac{1}{R_0^{\lambda_{kk'}}} \right]$$

- Early stage approximation:  $1 - D^{n-1}/V \sim 1$
- For  $R_0 \sim 1$ ,  $(1 - R_0^{-\lambda_{kk'}}) \simeq \lambda_{kk'}(R_0 - 1)$  (Taylor expansion)
- Uncorrelated networks:  $P(k | k') = \frac{kP(k)}{\langle k' \rangle}$

# Branching process

$$D_k^n = (R_0 - 1) \frac{k^{1+\theta} P(k)}{\langle k \rangle} \frac{w_0 \alpha}{\mu} \sum_{k'} D_{k'}^{n-1} k'^\theta (k' - 1)$$

Let's define the auxiliary function:  $\Theta^n = \sum_k D_k^n k^\theta (k - 1)$

$$\Theta^n = (R_0 - 1) \frac{\langle k^{2+2\theta} \rangle - \langle k^{1+2\theta} \rangle}{\langle k \rangle} \frac{w_0 \alpha}{\mu} \Theta^{n-1}$$



Global epidemic threshold > 1

# Global epidemic threshold

$$R_* = (R_0 - 1) \frac{\langle k^{2+2\theta} \rangle - \langle k^{1+2\theta} \rangle}{\langle k \rangle} \frac{w_0 \alpha}{\mu} > 1$$

This **threshold** defines the condition for an outbreak to reach a finite portion of the whole system.

It answers the question: **when does a local epidemic become a global pandemic?**

# Global epidemic threshold

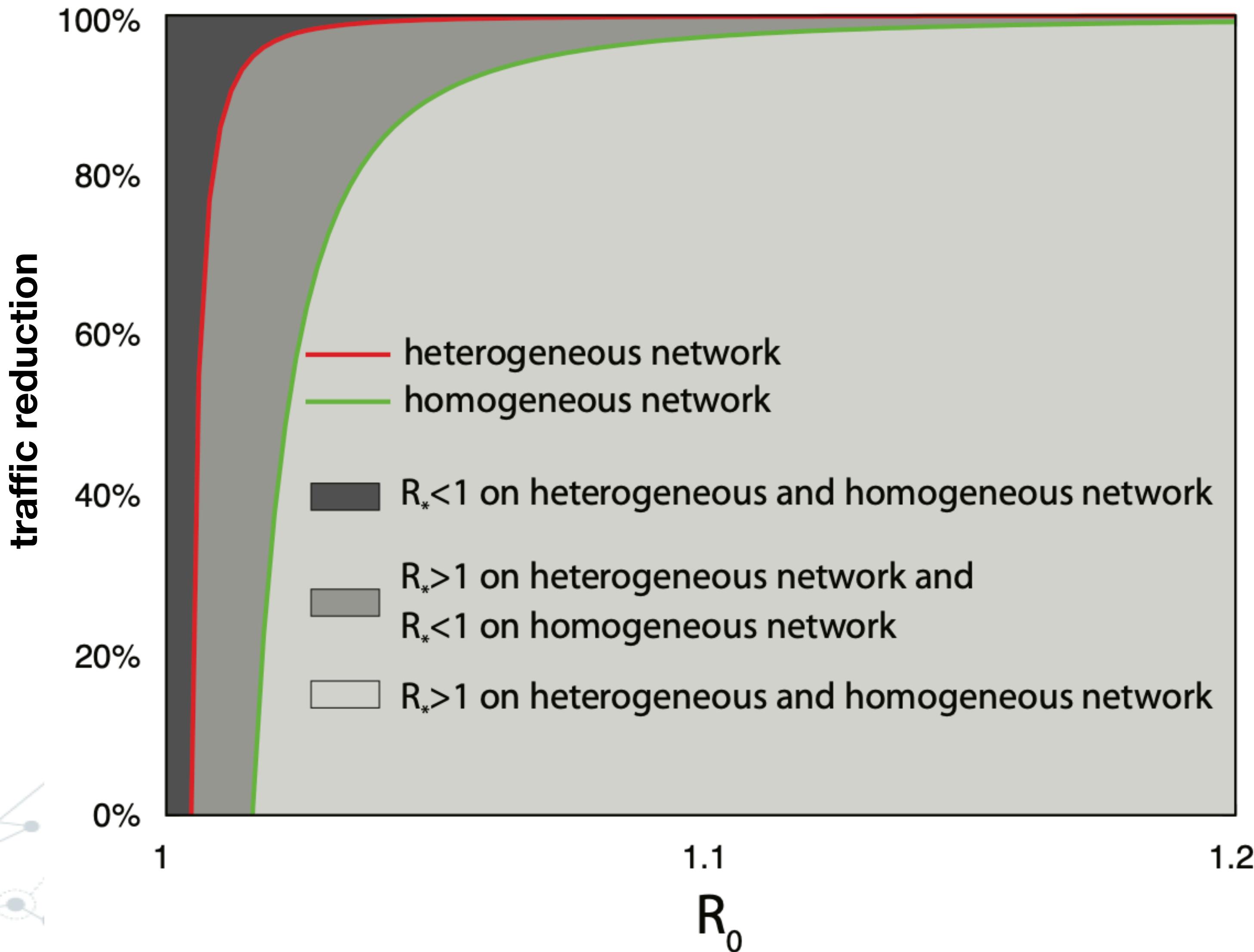
$$R_* = (R_0 - 1) \frac{\langle k^{2+2\theta} \rangle - \langle k^{1+2\theta} \rangle}{\langle k \rangle} \frac{w_0 \alpha}{\mu} > 1$$

In a SIR model:  $\alpha \simeq \frac{2(R_0 - 1)}{R_0^2}$

$$w_0 > \frac{\langle k \rangle}{\langle k^{2+2\theta} \rangle - \langle k^{1+2\theta} \rangle} \frac{\mu R_0^2}{2(R_0 - 1)^2}$$

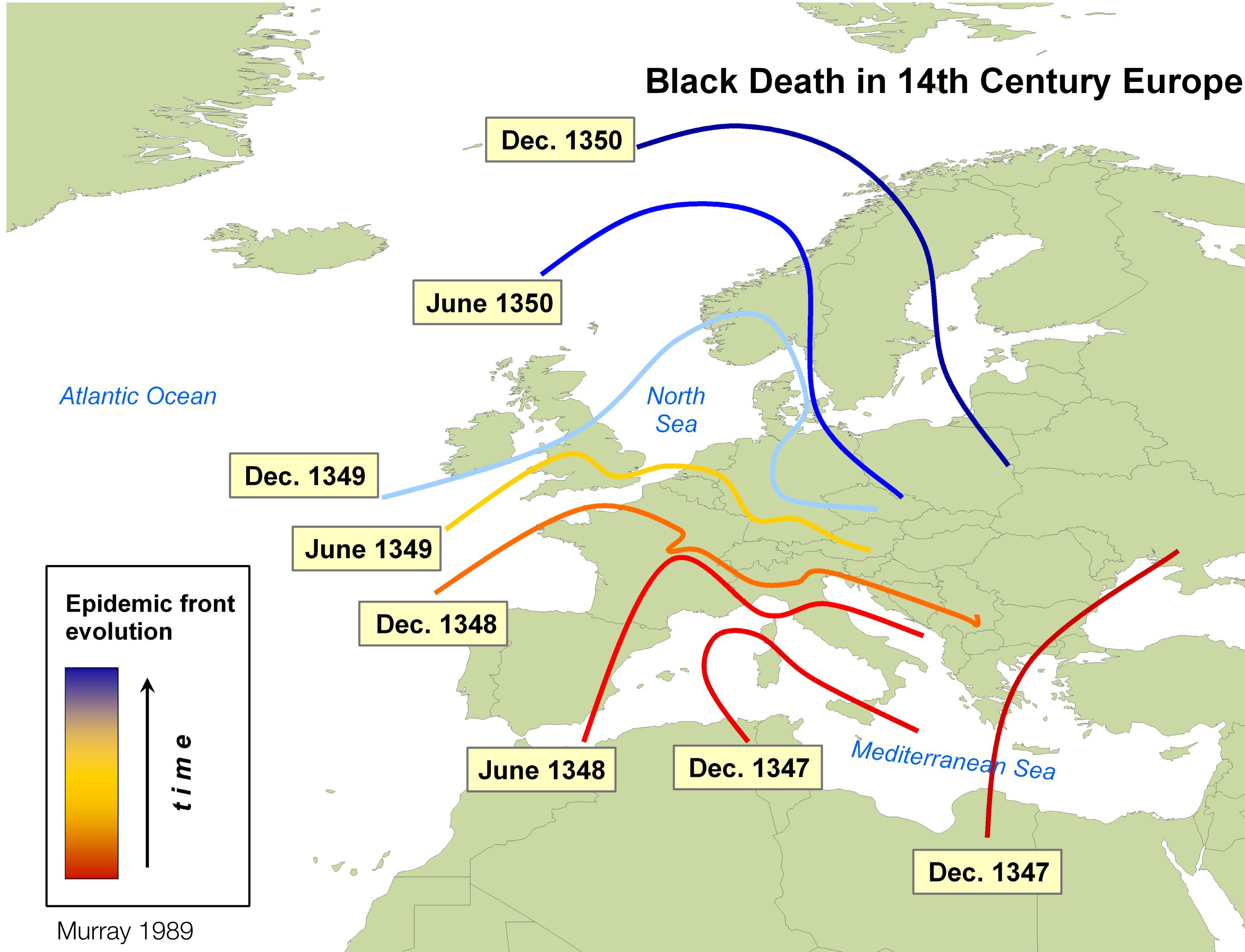
In an infinite scale-free network:  $\frac{\langle k \rangle}{\langle k^{2+2\theta} \rangle - \langle k^{1+2\theta} \rangle} \rightarrow 0$

# Travel restrictions



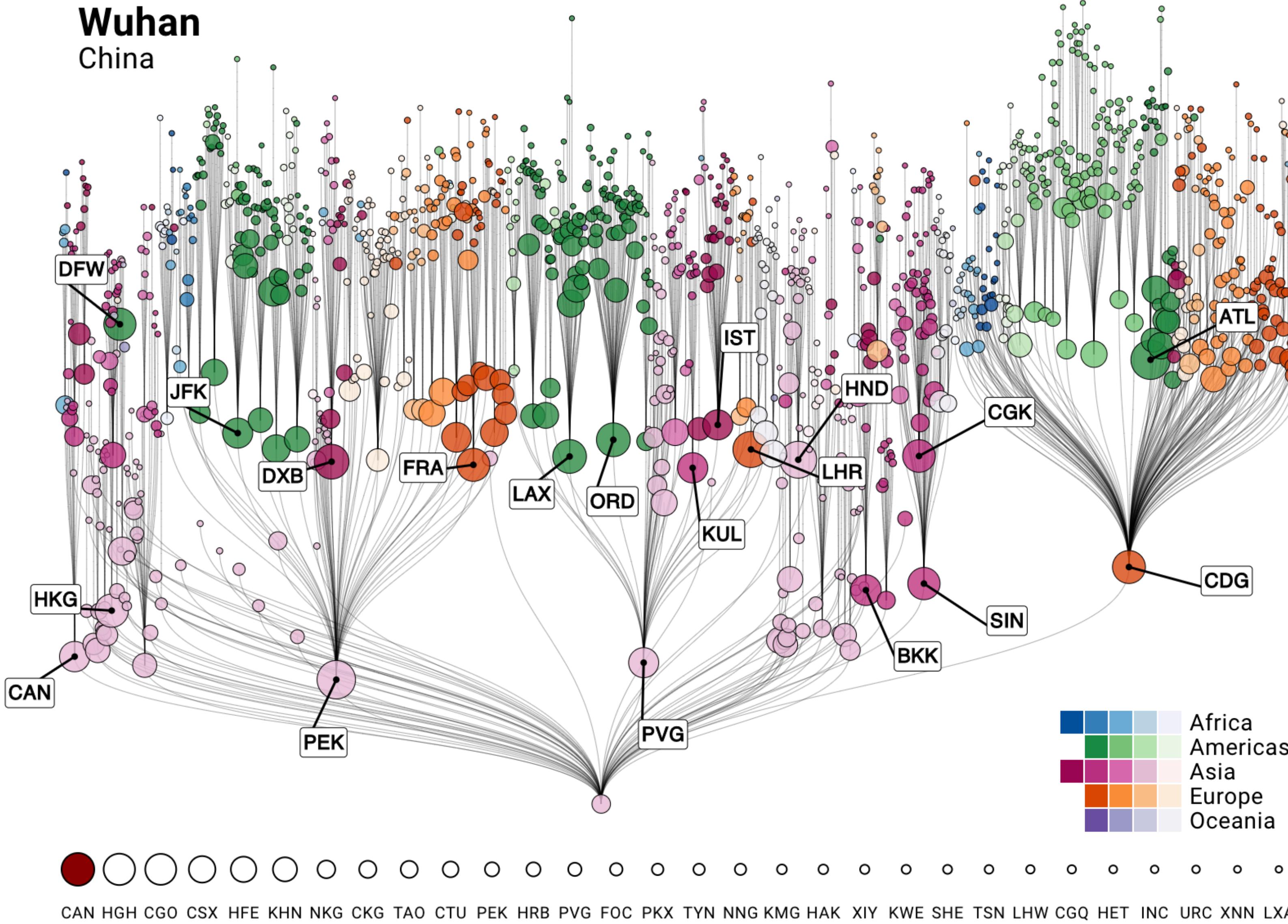
travel restrictions are generally ineffective unless traffic reduction is equal to 100%

# Human mobility drives the spread of infectious diseases



The black death in the  
XIV century  
a continuous diffusion  
wave process

# Human mobility drives the spread of infectious diseases



# GLEAM: a data-driven metapopulation model



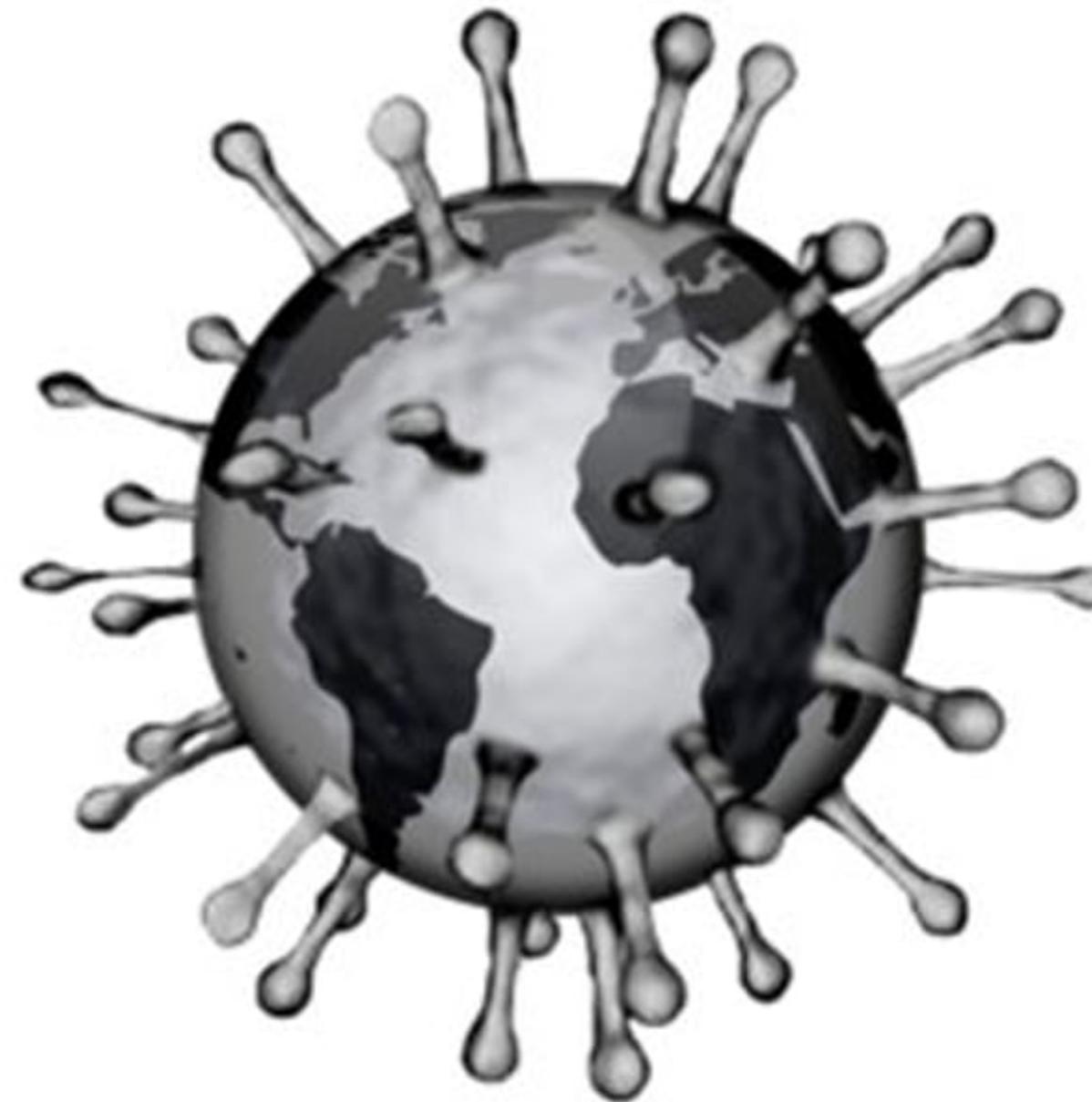
Using big data and computational  
modeling to fight infectious diseases

## COVID-19 Research

US COVID-19  
Modeling Dashboard

US COVID-19  
Mobility Dashboard

Italy COVID-19  
Modeling Dashboard



# The Global Epidemic and Mobility Model



Alessandro  
Vespignani

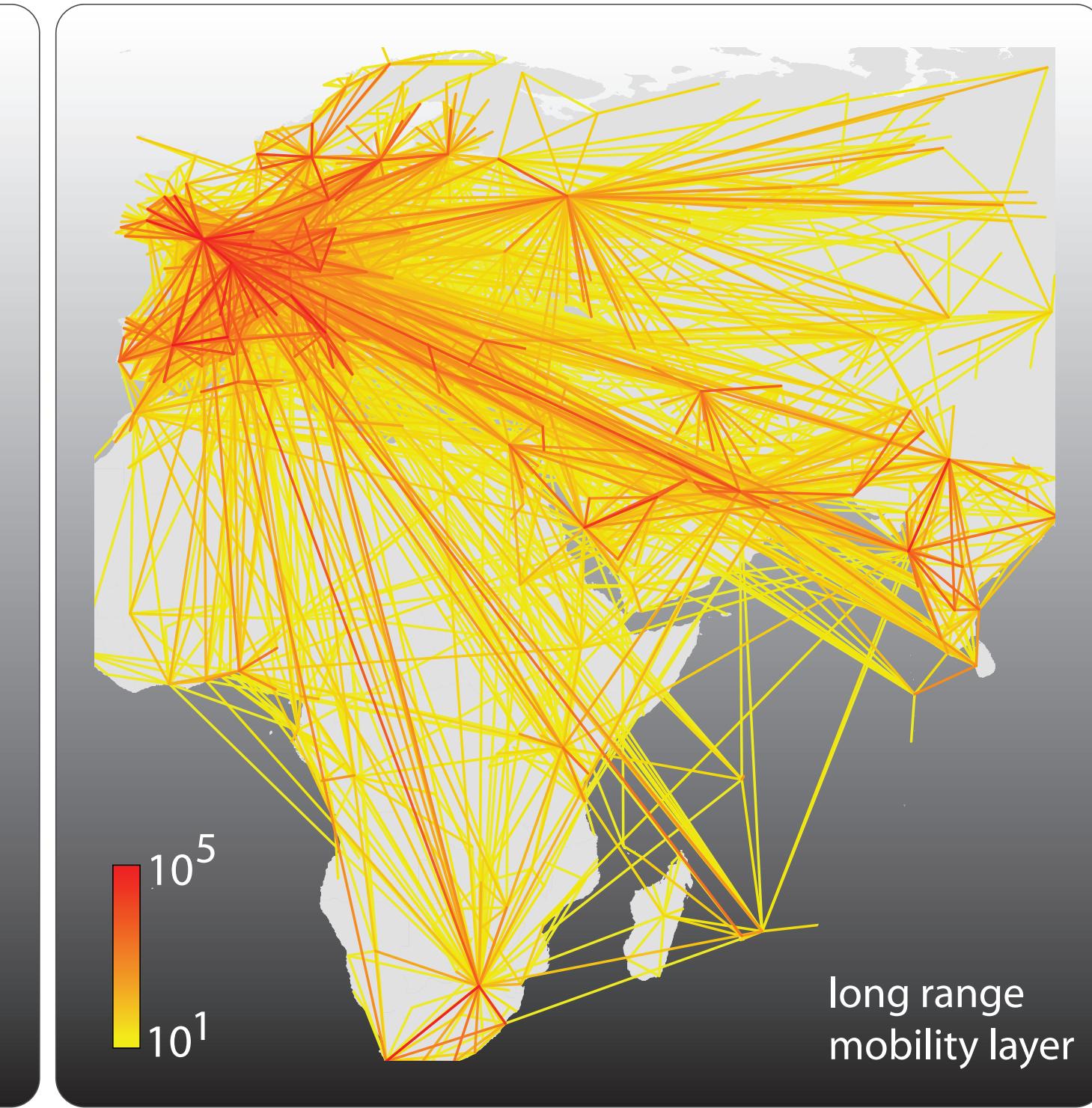
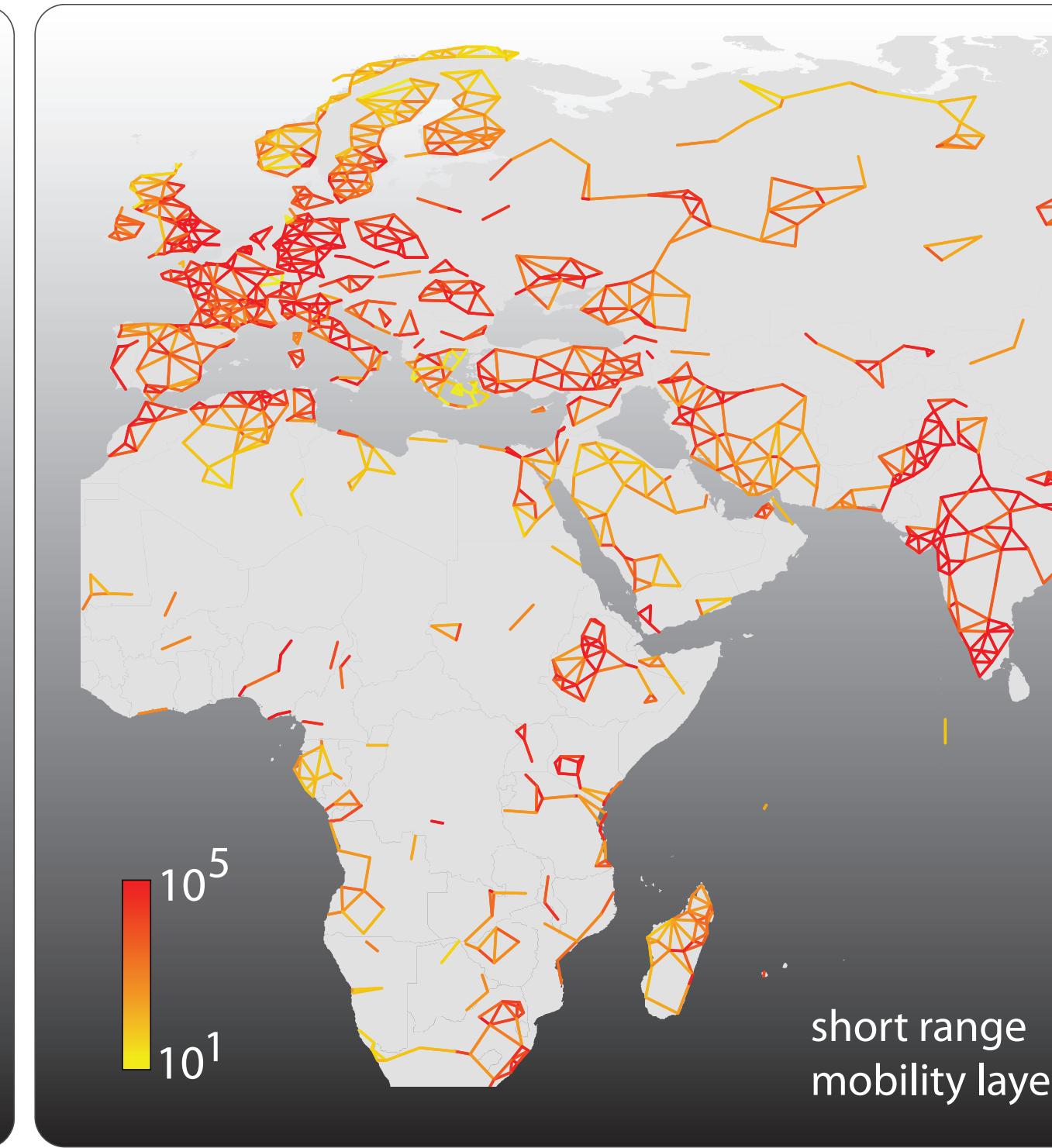
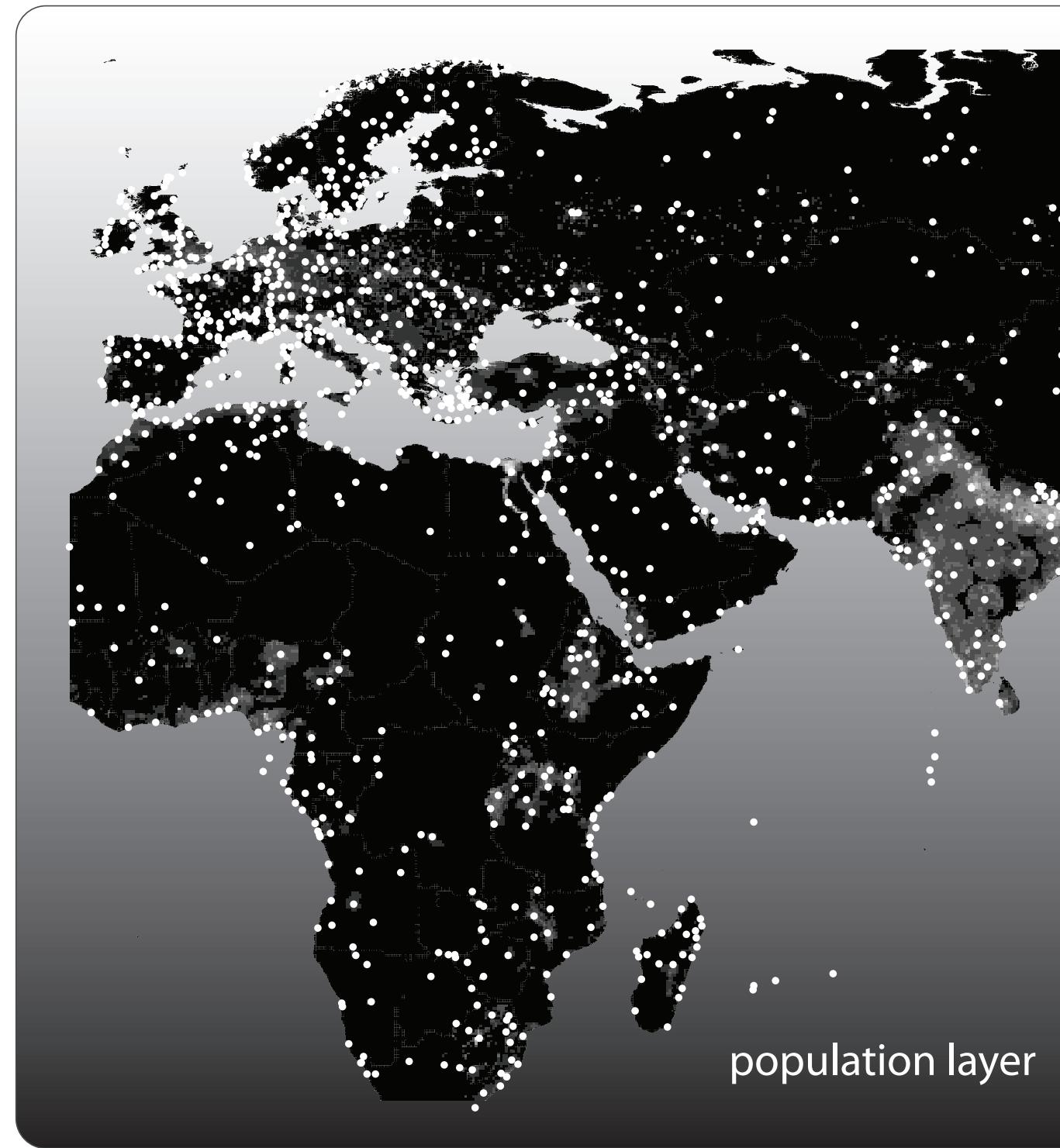


Vittoria  
Colizza



- D. Balcan
- B. Gonçalves
- M. Gomes
- H. Hu
- A. Pastore y Piontti
- N. Perra
- D. Mocanu
- L. Rossi
- Q. Zhang
- P. Bajardi
- C. Gioannini
- D. Paolotti
- C. Poletto
- M. Quaggiotto
- J. J. Ramasco
- W. Van Den Broeck
- M. Roncaglione
- S. Merler
- M. Ajelli
- N. Samay
- P. Milano
- M. Selim
- D. Perrotta
- F. Ciulla
- Kaiyuan Sun
- D. Mistry
- L. Fumanelli
- I. M. Longini
- E. Halloran
- M. Litvinova

# Data-driven



Worldwide  
population  
distribution

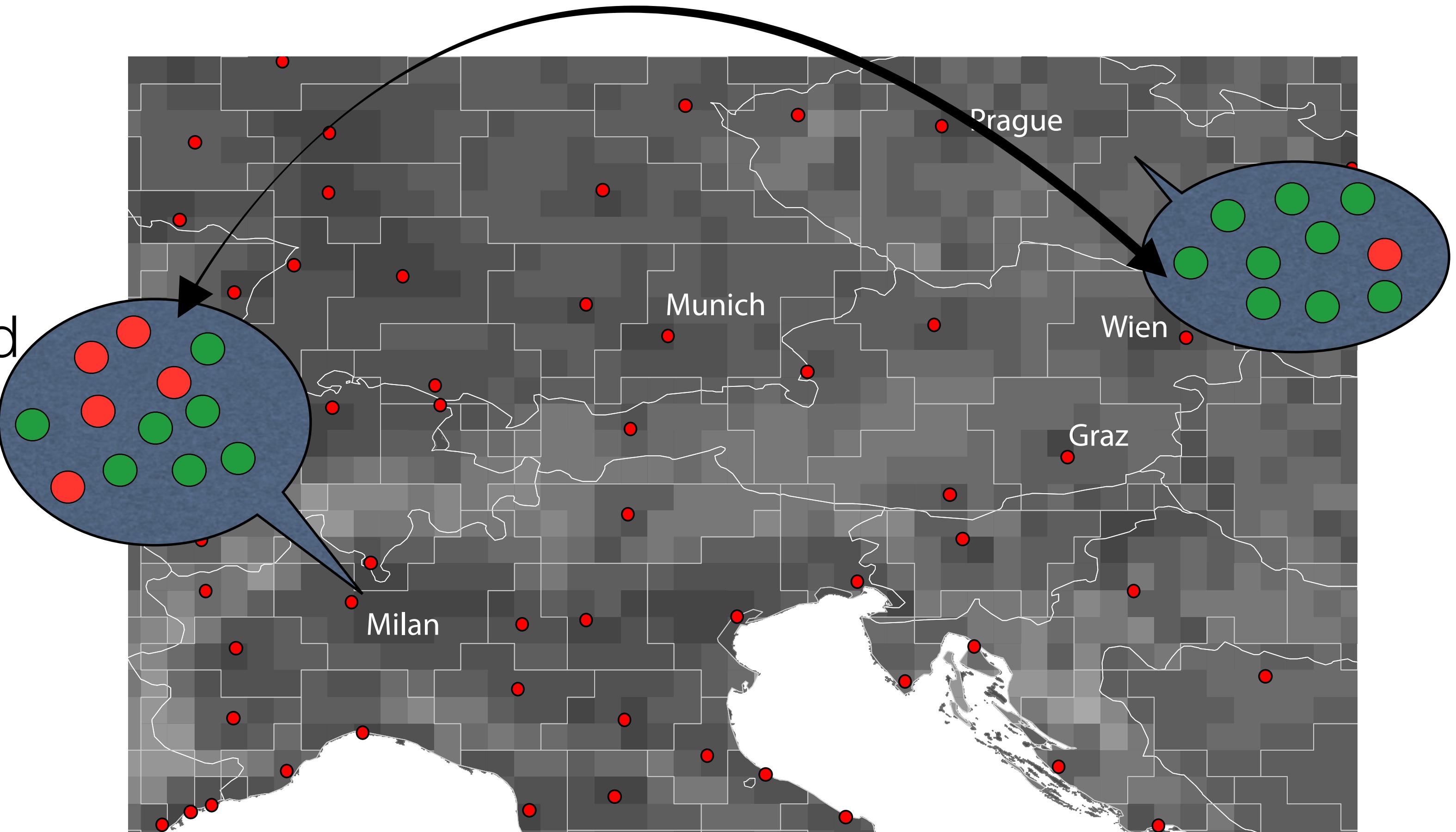
Short range  
mobility  
(commuting)

Air travel

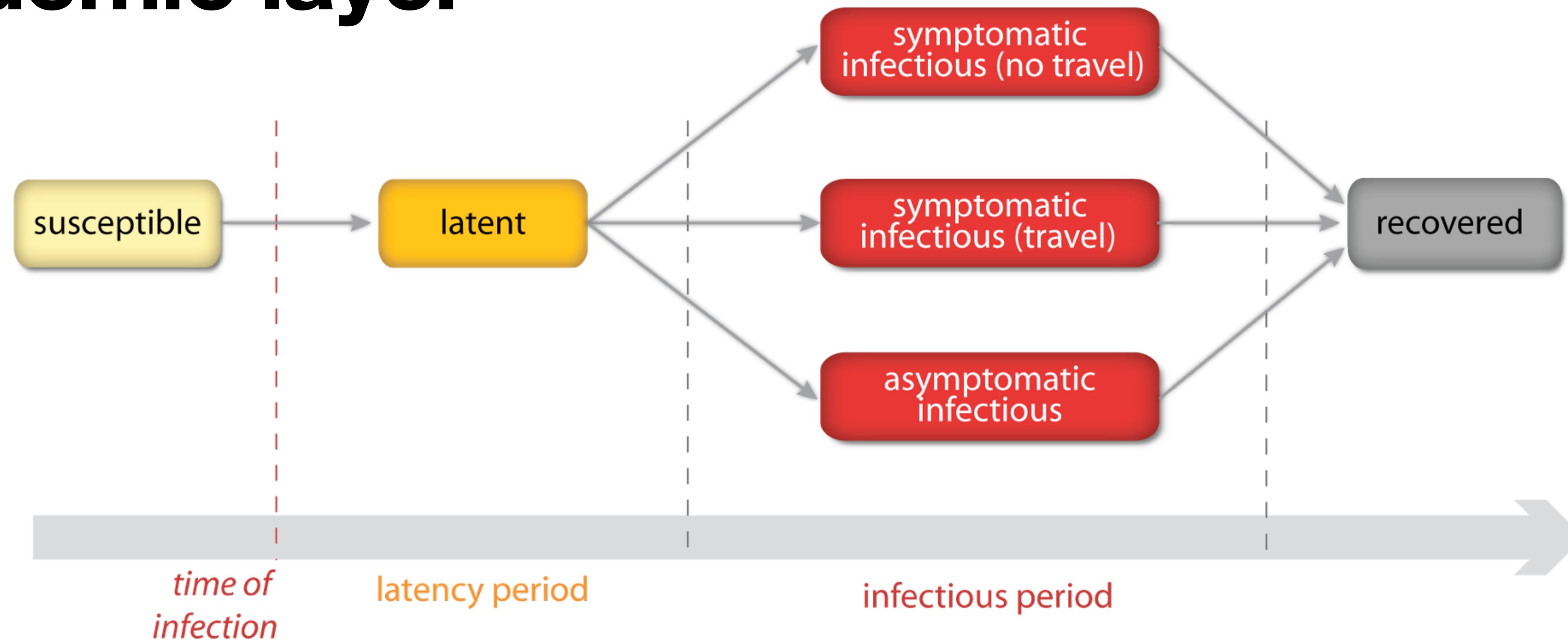
Balcan et al. PNAS 2009

# Metapopulation

- the world is divided into sub-populations centered around major hubs
- sub-populations are connected by the flux of individuals traveling daily among them
- inside each subpopulation the disease dynamics is described by a compartmental model in homogeneous mixing



# Epidemic layer



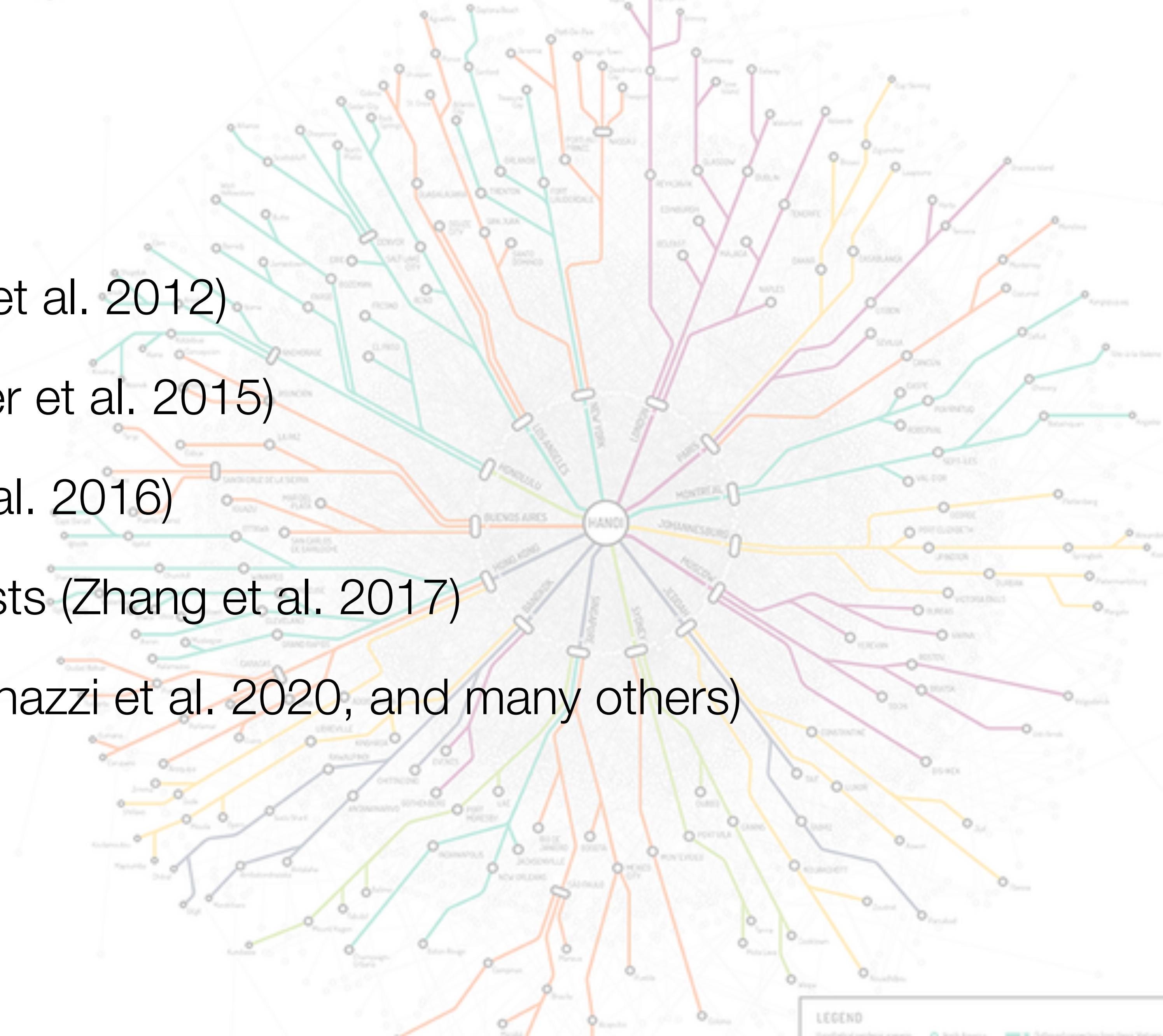
Parameters are estimated from clinical data.

For COVID-19 (Chinazzi et al. Science 2020):

- latency period: 3-6 days
- infectious period: 2-8 days

# GLEAM at work

- 2009 H1N1 pandemic (Tizzoni et al. 2012)
- 2014 WA Ebola outbreak (Merler et al. 2015)
- 2016 ZIKV epidemic (Zhang et al. 2016)
- 2014-2019 Seasonal flu forecasts (Zhang et al. 2017)
- 2020 COVID-19 pandemic (Chinazzi et al. 2020, and many others)



# COVID-19 and travel restrictions

RESEARCH ARTICLE

## The effect of travel restrictions on the spread of the 2019 novel coronavirus (COVID-19) outbreak

 Matteo Chinazzi<sup>1</sup>, Jessica T. Davis<sup>1</sup>, Marco Ajelli<sup>2</sup>, Corrado Gioannini<sup>3</sup>,  Maria Litvinova<sup>3</sup>, Stefano Merler<sup>2</sup>, Ana Pastore y Piontti<sup>1</sup>, Kunpeng Mu<sup>1</sup>, Luca Rossi<sup>3</sup>,  Kaiyuan Sun<sup>4</sup>,  Cécile Viboud<sup>4</sup>, Xinyue Xiong<sup>1</sup>,  Hongjie Yu<sup>5</sup>,  M. Elizabeth Halloran<sup>6,7</sup>,  Ira M. Longini Jr.<sup>8,\*</sup>,  Alessandro Vespignani<sup>1,3,\*</sup>

<sup>1</sup>Laboratory for the Modeling of Biological and Socio-technical Systems, Northeastern University, Boston, MA, USA.

<sup>2</sup>Bruno Kessler Foundation, Trento, Italy.

<sup>3</sup>ISI Foundation, Turin, Italy.

<sup>4</sup>Fogarty International Center, NIH, Bethesda, MD, USA.

<sup>5</sup>School of Public Health, Fudan University, Key Laboratory of Public Health Safety, Ministry of Education, Shanghai, China.

<sup>6</sup>Fred Hutchinson Cancer Research Center, Seattle, WA, USA.

<sup>7</sup>Department of Biostatistics, University of Washington, Seattle, WA, USA.

<sup>8</sup>Department of Biostatistics, College of Public Health and Health Professions, University of Florida, Gainesville, FL, USA.

\*Corresponding author. Email: [a.vespignani@northeastern.edu](mailto:a.vespignani@northeastern.edu) (A.V.); [ilongini@ufl.edu](mailto:ilongini@ufl.edu) (I.M.L.)

– Hide authors and affiliations

# COVID-19 and travel restrictions

RESEARCH ARTICLE

## The effect of travel restrictions on the spread of the 2019 novel coronavirus (COVID-19) outbreak

Matteo Chinazzi<sup>1</sup>, Jessy Piontti<sup>1</sup>, Kunpeng Mu<sup>1</sup>, Michael Halloran<sup>6,7</sup>, Ira M. Longini<sup>2</sup>

<sup>1</sup>Laboratory for the Modeling of Infectious Diseases, Fred Hutchinson Cancer Research Center, Seattle, WA, USA.

<sup>2</sup>Bruno Kessler Foundation, Trento, Italy.

<sup>3</sup>ISI Foundation, Turin, Italy.

<sup>4</sup>Fogarty International Center, NIH, Bethesda, MD, USA.

<sup>5</sup>School of Public Health, Fudan University, Key Laboratory of Public Health Safety, Ministry of Education, Shanghai, China.

<sup>6</sup>Fred Hutchinson Cancer Research Center, Seattle, WA, USA.

<sup>7</sup>Department of Biostatistics, University of Washington, Seattle, WA, USA.

<sup>8</sup>Department of Biostatistics, College of Public Health and Health Professions, University of Florida, Gainesville, FL, USA.

✉ Corresponding author. Email: a.vespignani@northeastern.edu (A.V.); ilongini@ufl.edu (I.M.L.)

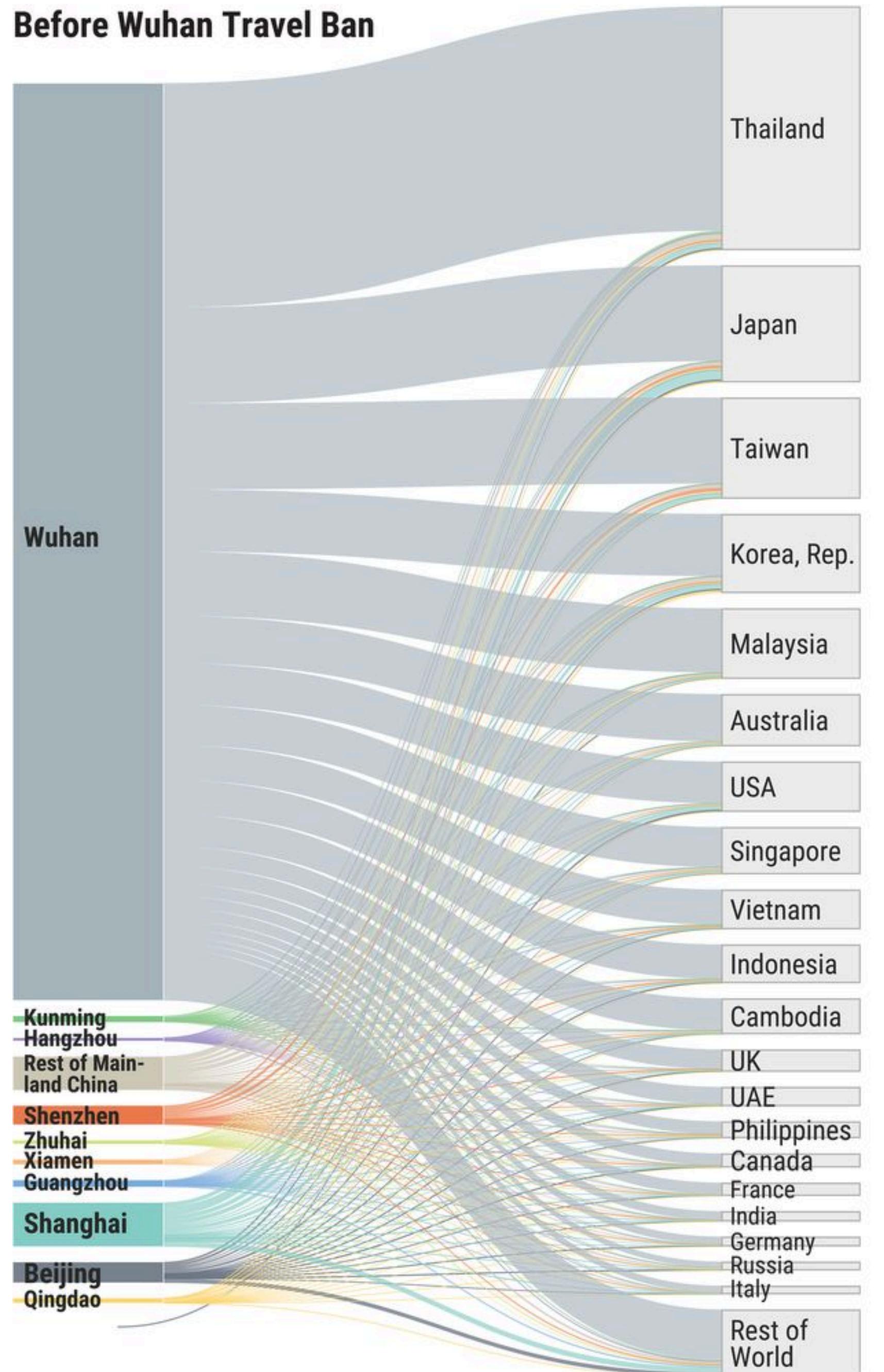
- Hide authors and affiliations

Science 24 Apr 2020:  
Vol. 368, Issue 6489, pp. 395-400  
DOI: 10.1126/science.aba9757

The travel quarantine of Wuhan delayed the overall epidemic progression by only 3 to 5 days in mainland China but had a more marked effect on the international scale, where case importations were reduced by nearly 80% until mid-February.

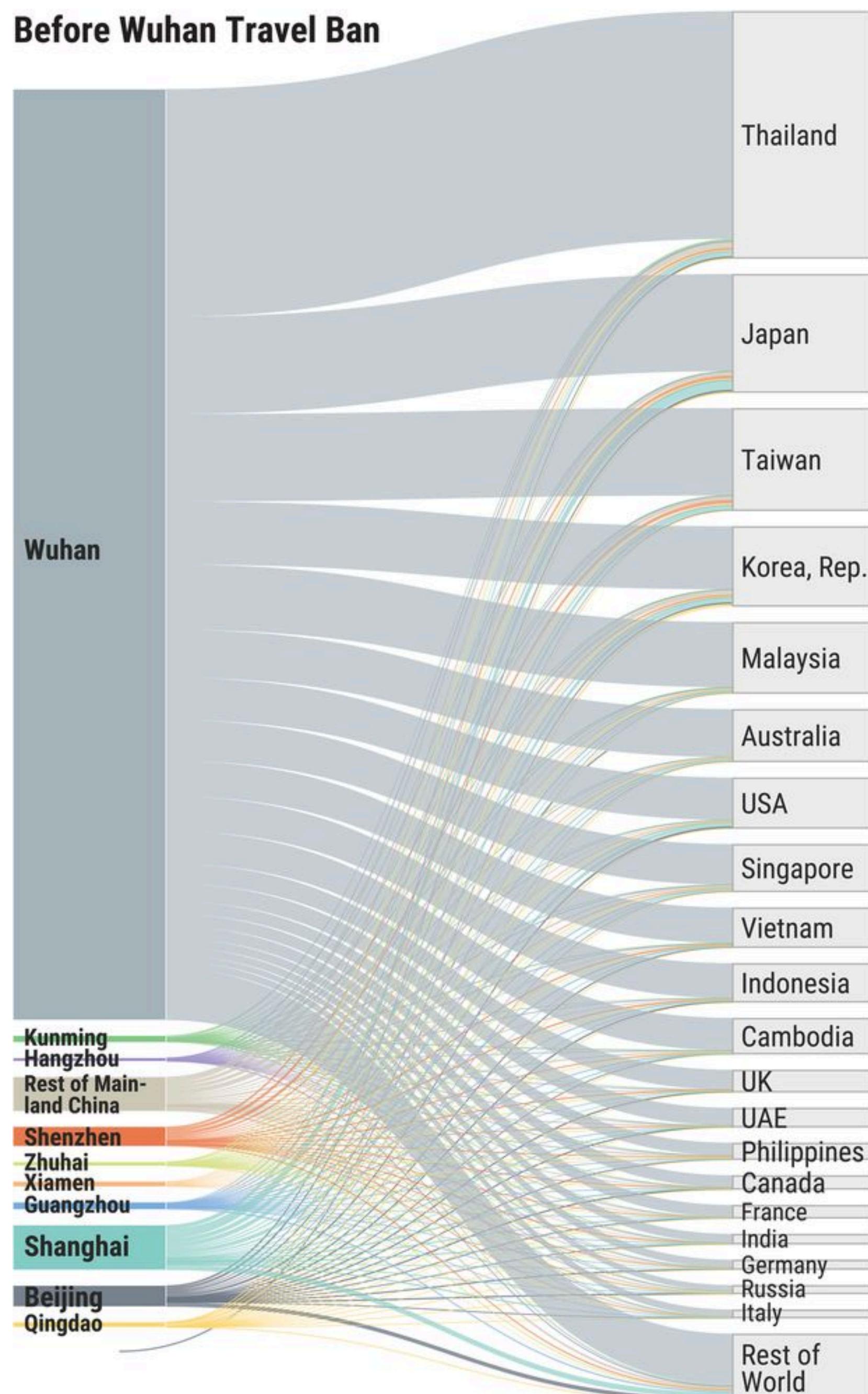
# Case Importations

## Before Wuhan Travel Ban

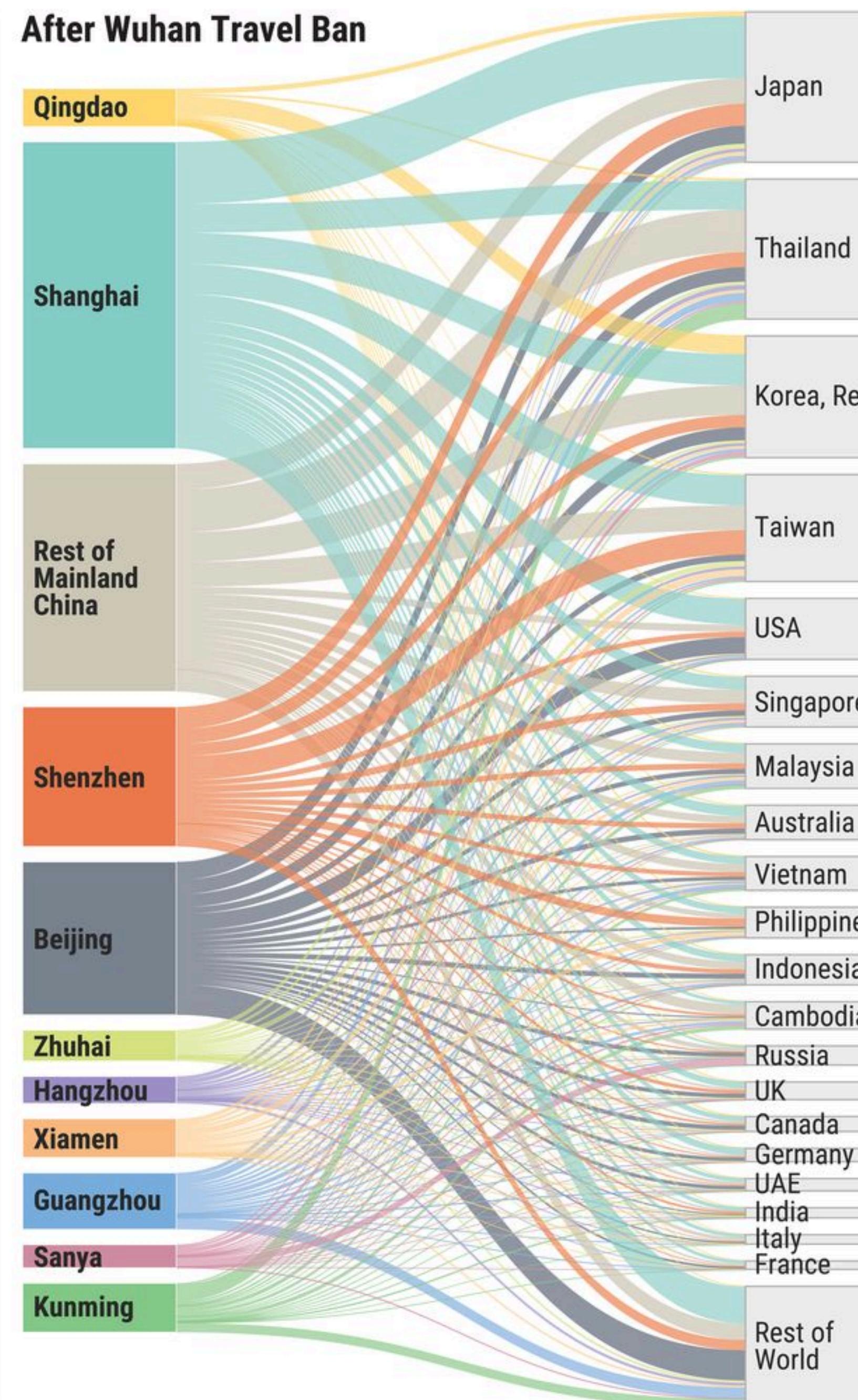


## Case Importations

### Before Wuhan Travel Ban



### After Wuhan Travel Ban



After the travel ban in Wuhan (January 23, 2020) the risk of importation has been redistributed from other major Chinese hubs

Next... modelling human mobility