

Digital health and computational epidemiology

Lesson 10

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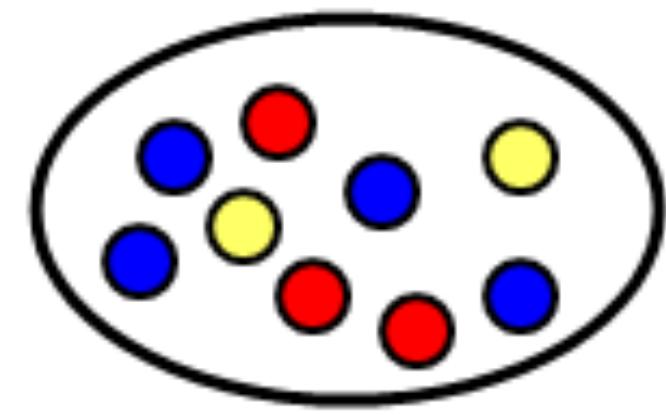
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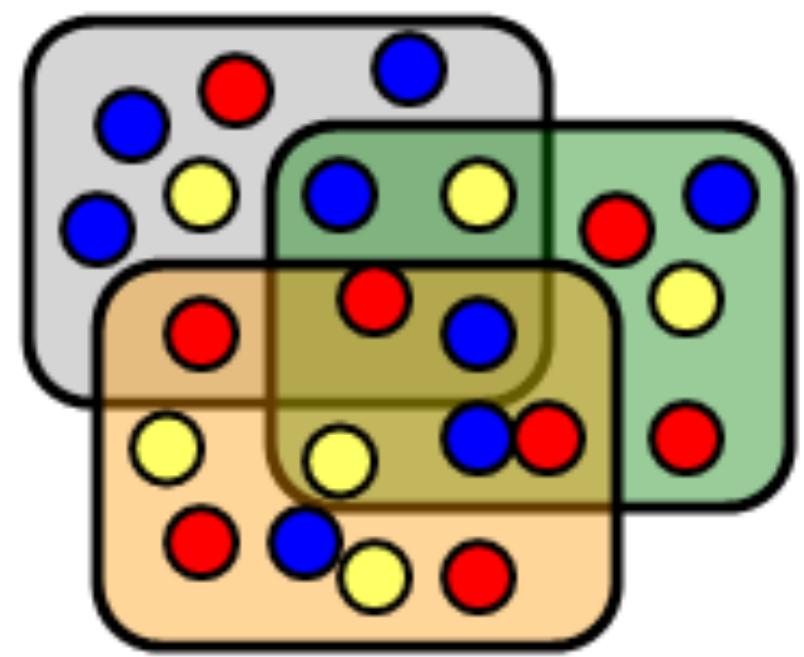
Center for
Computational Social Science
and Human Dynamics

Spatial epidemic models

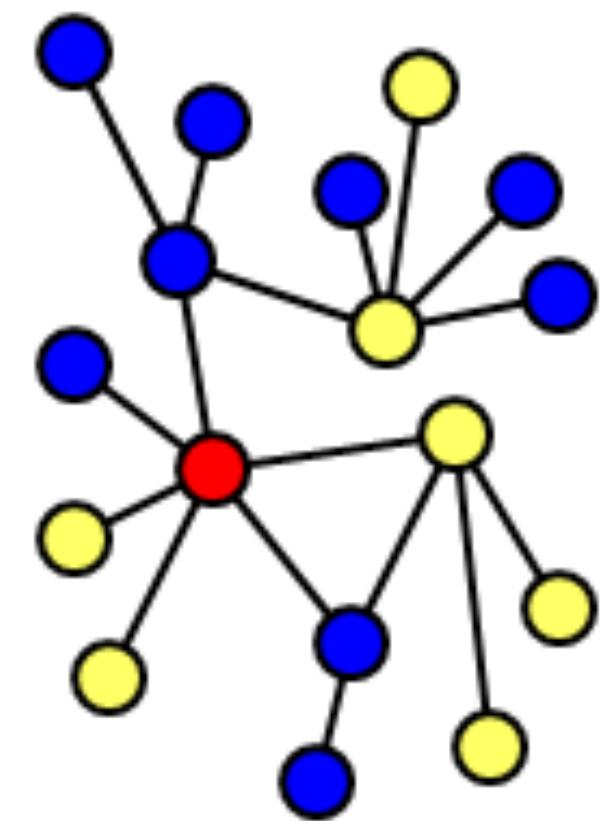
Models



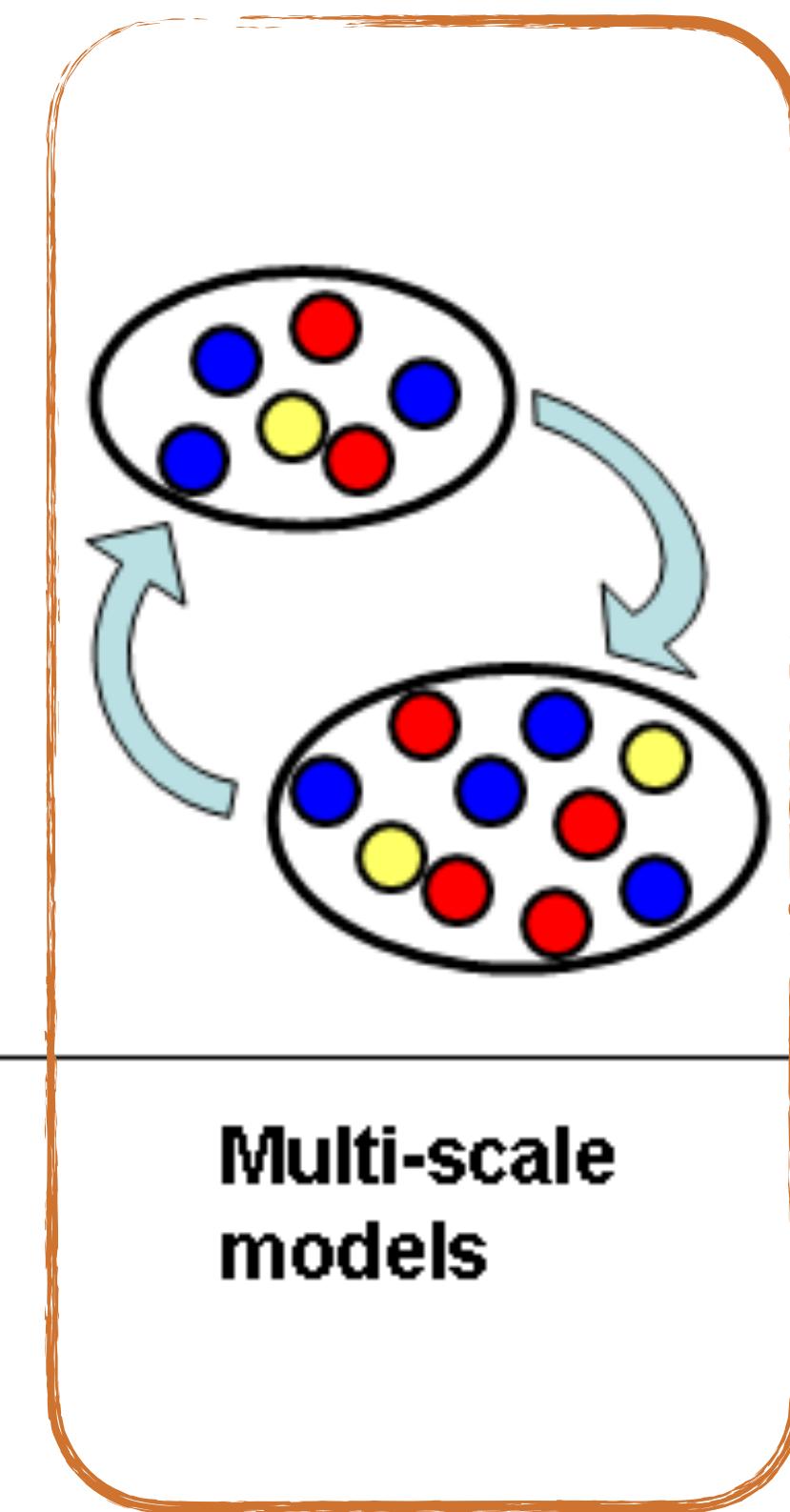
Homogeneous
mixing



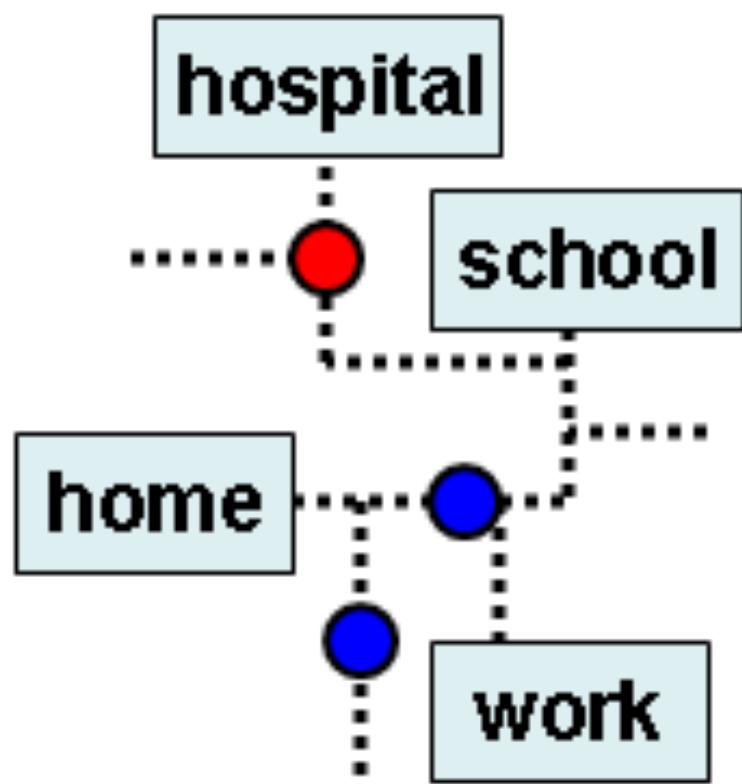
Social structure



Contact network
models

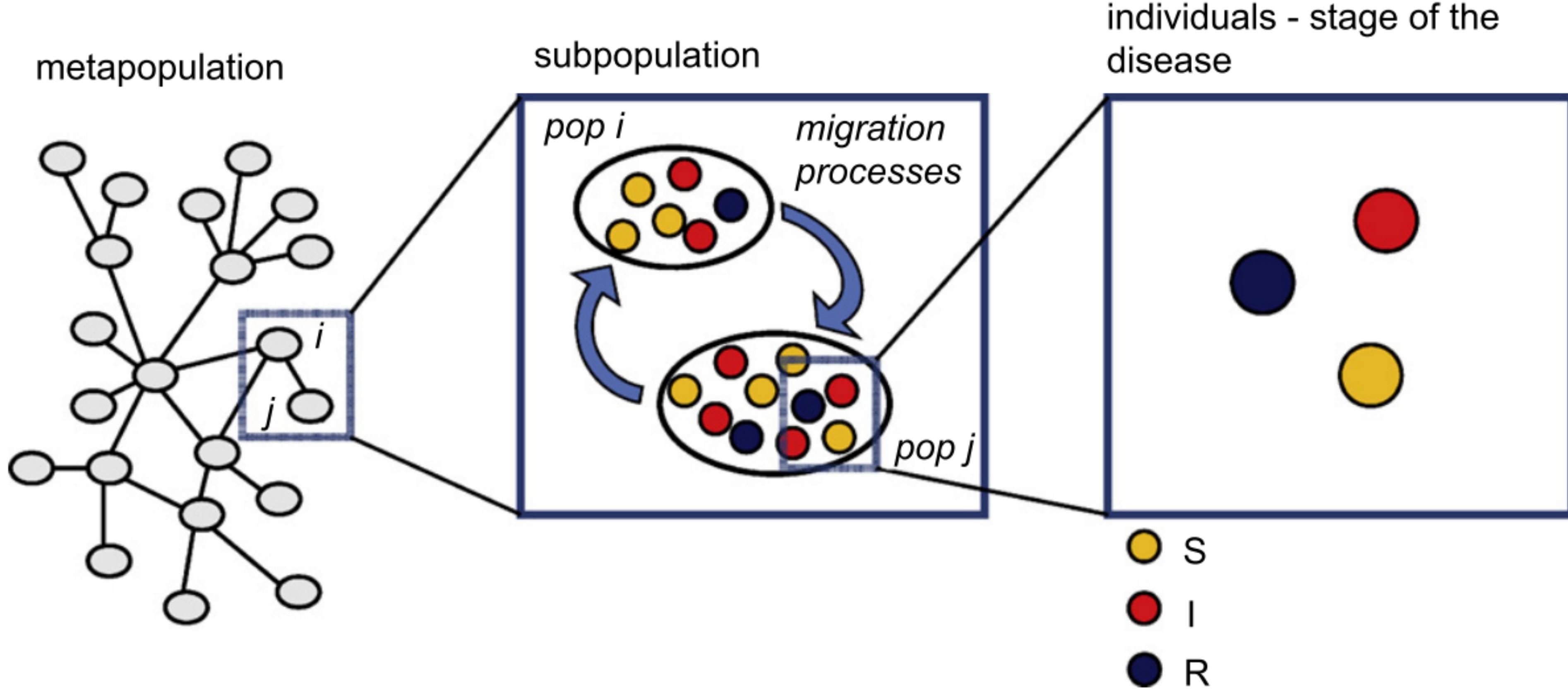


Multi-scale
models



Agent Based
models

Metapopulation models

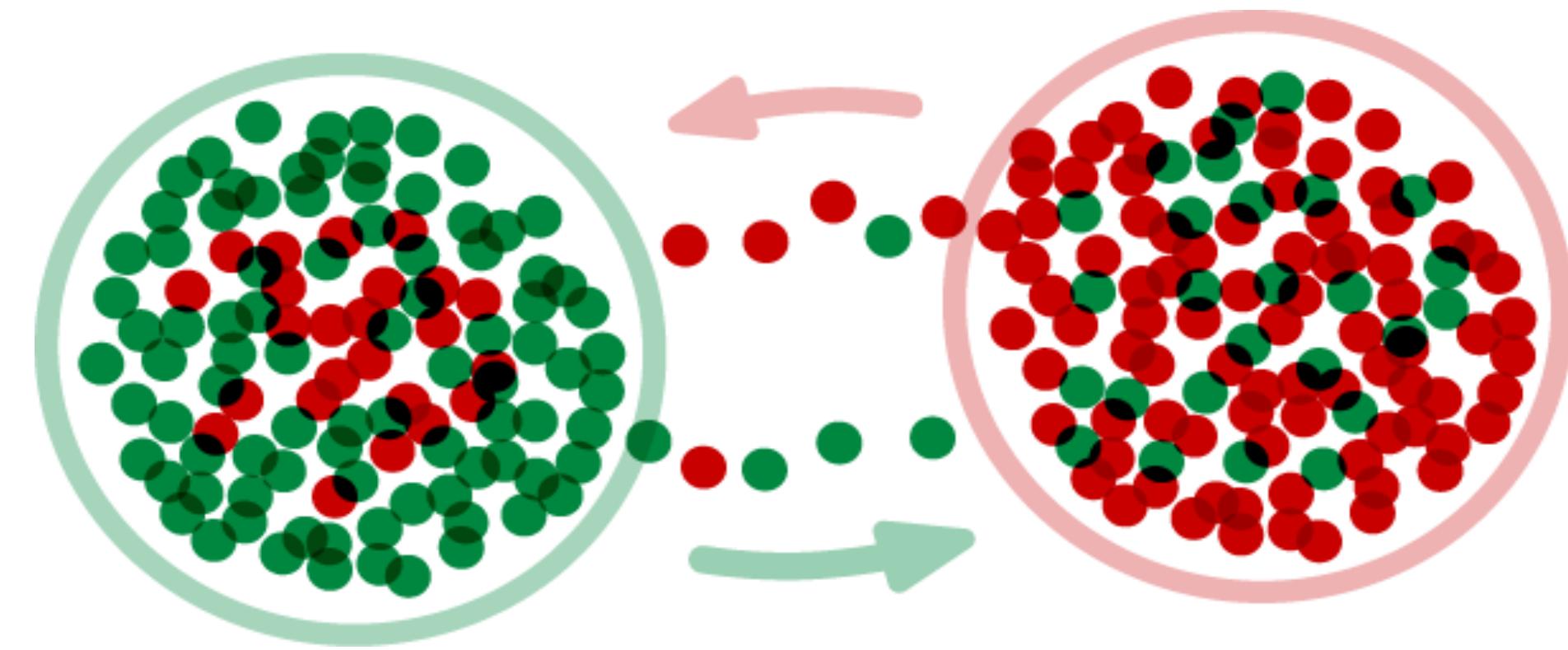


Reaction-diffusion

- 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

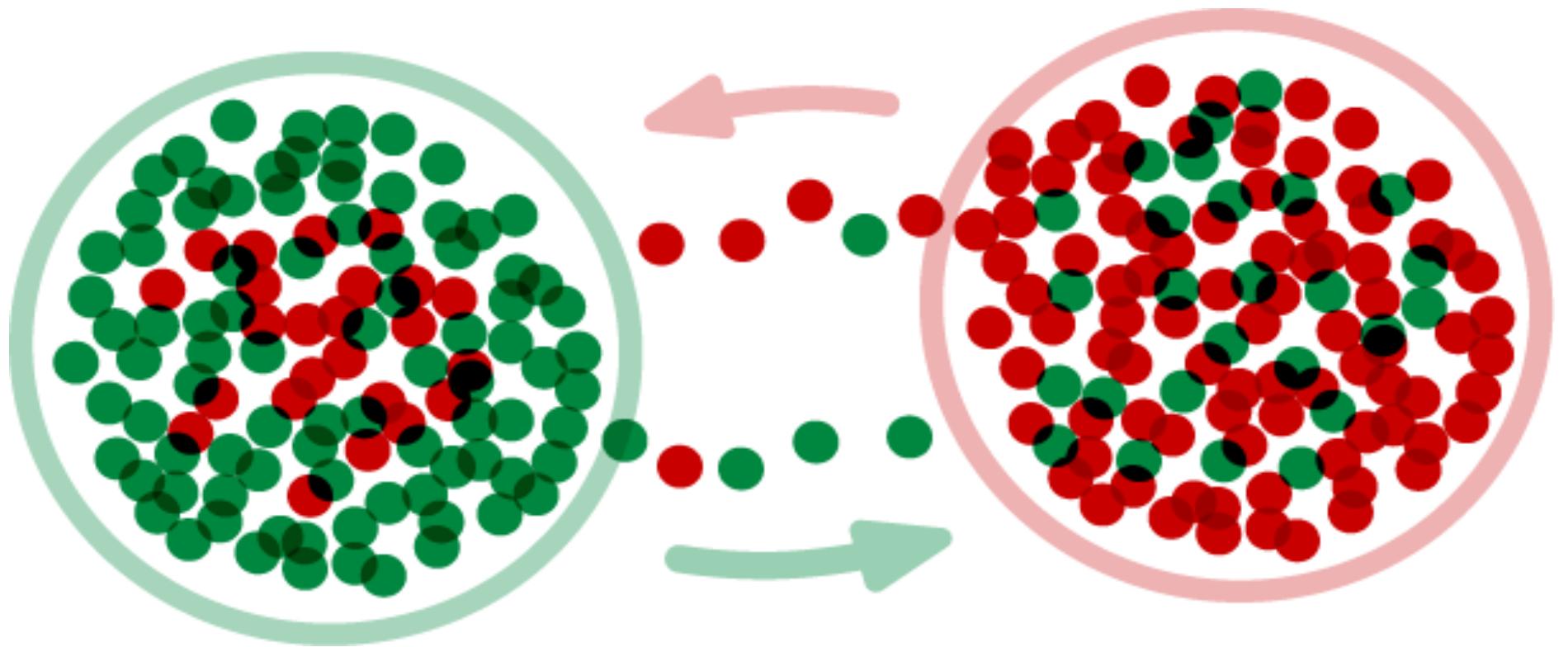
I. Diffusion process

Diffusion process



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

Diffusion process

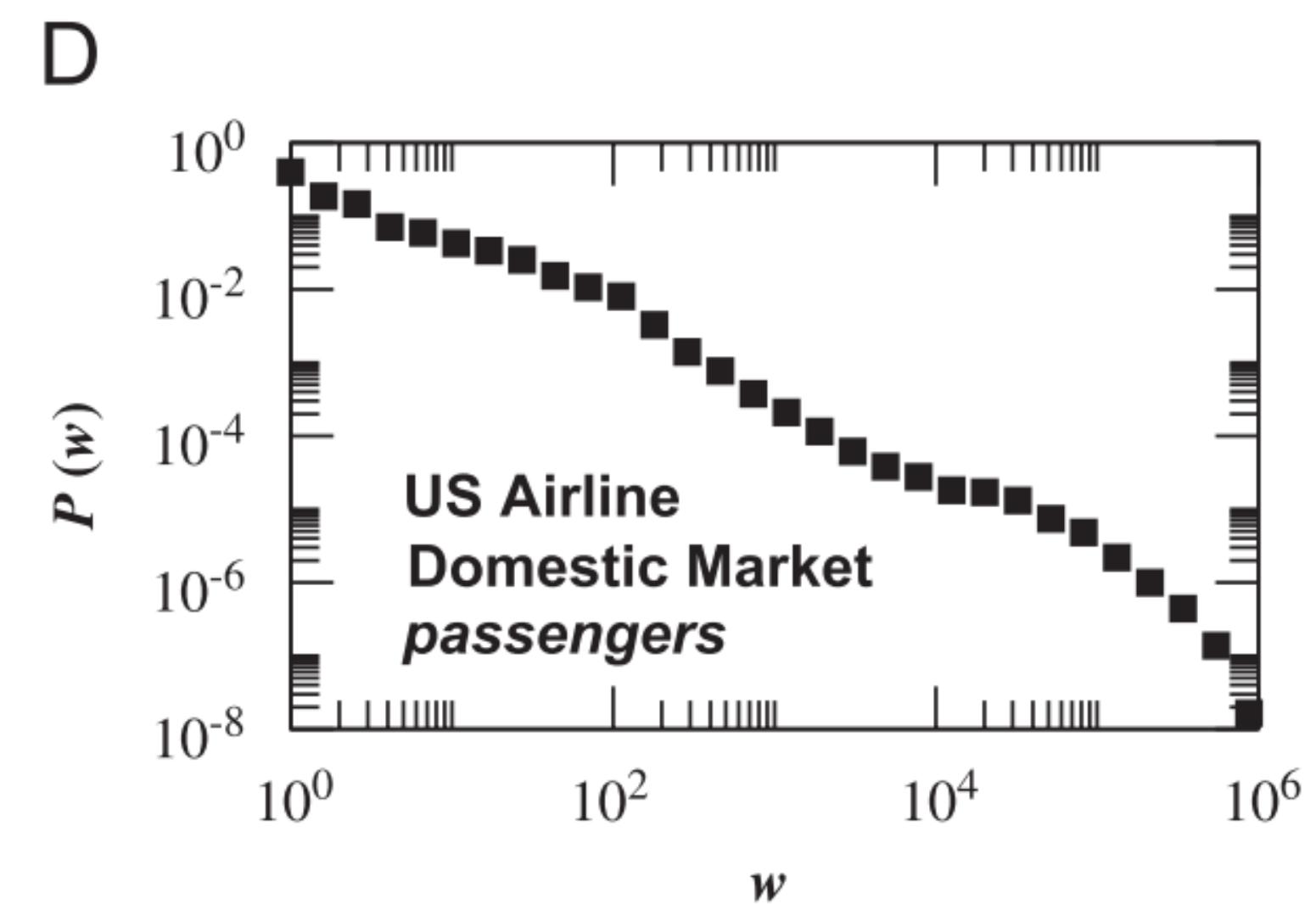
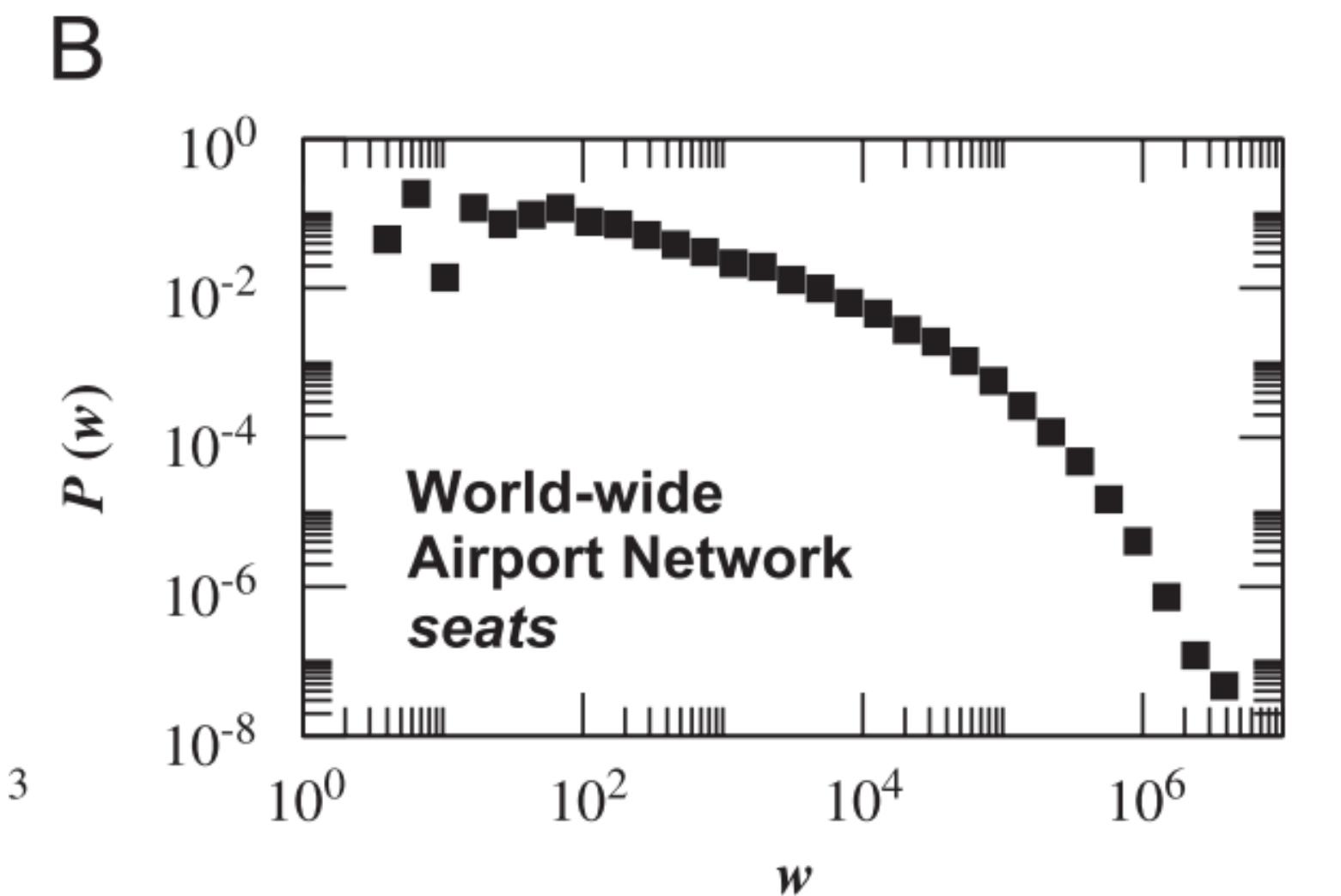


w_{ij} = number of individuals
traveling between i and j

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
- 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

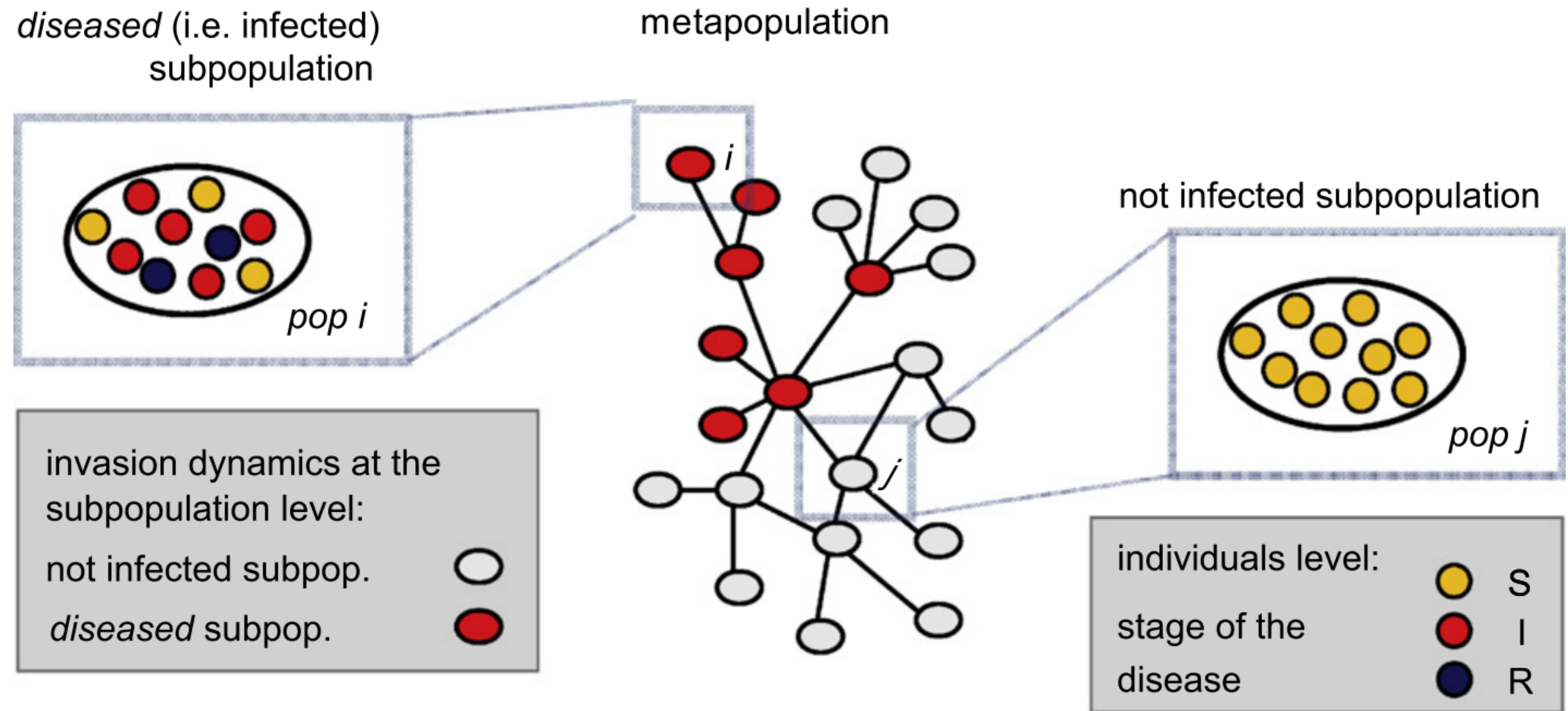
- We want to consider the population of each node as **independent variables**
- We want any initial conditions for the population size to satisfy the stationary state.
- This can be obtained by setting $p_k = T_k/N_k$

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

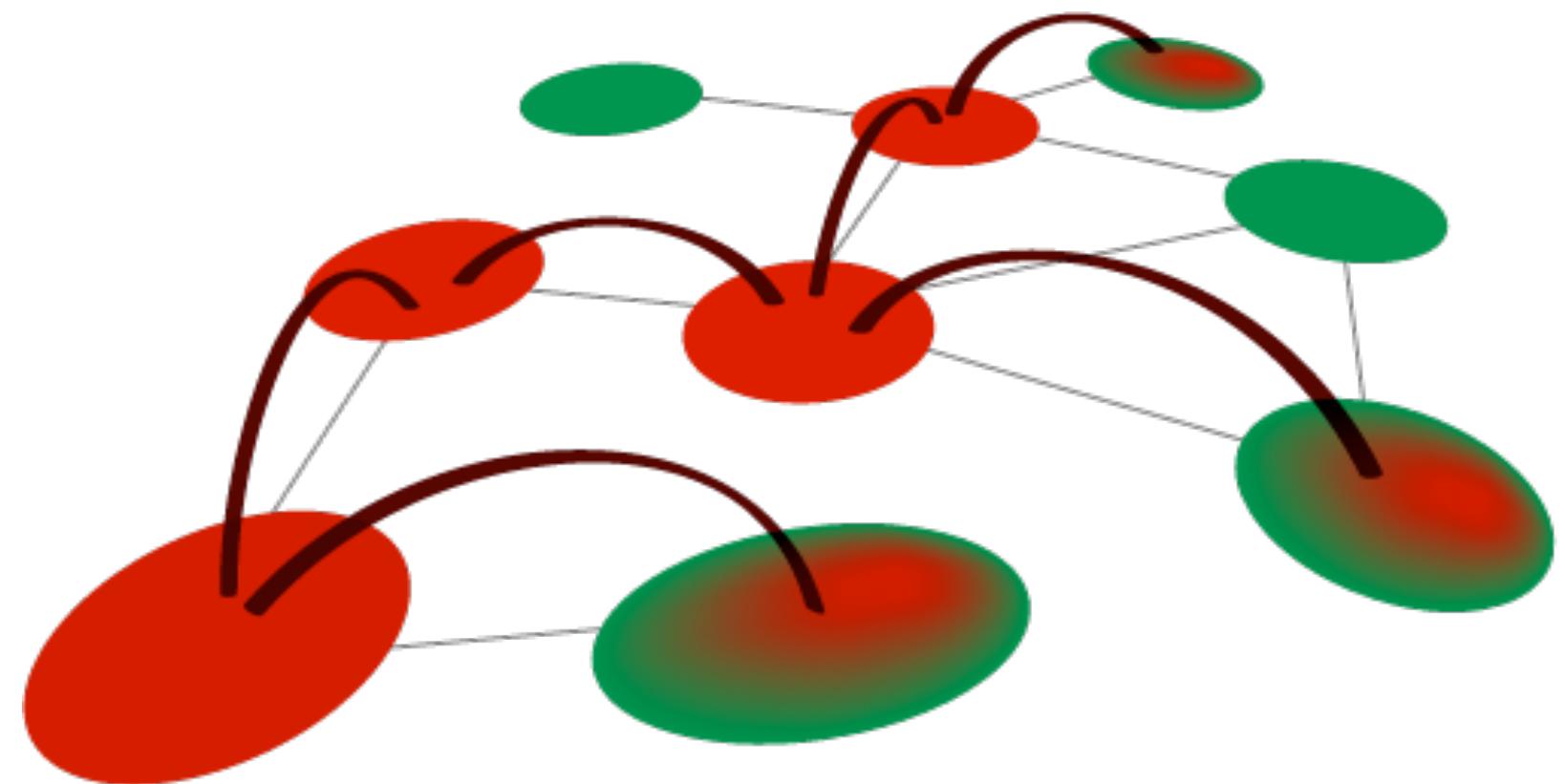
A population dependent diffusion process does not fix the subpopulation size, which can be given as a parameter of the model.

II. Reaction process

Reaction process

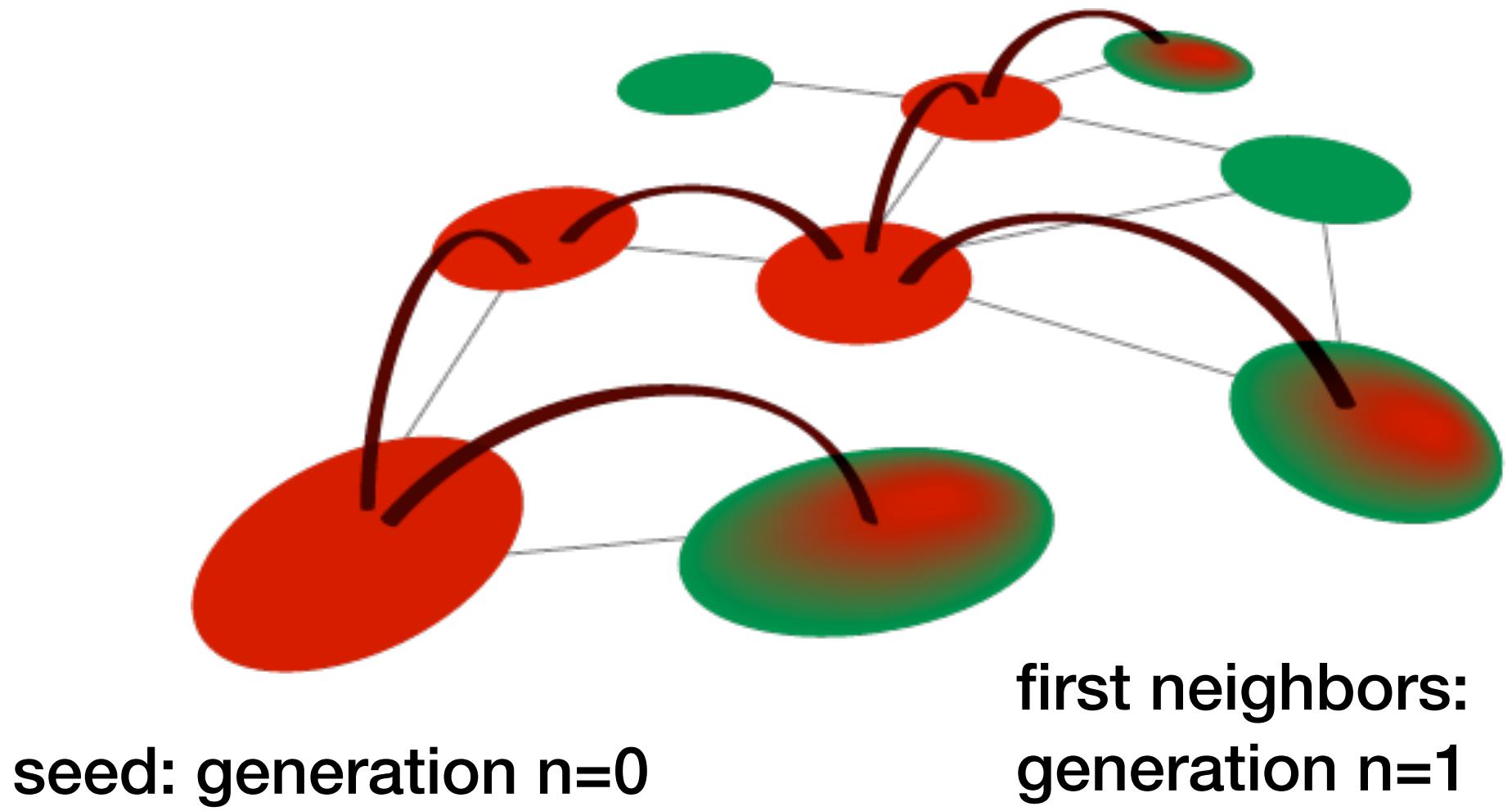


Invasion threshold



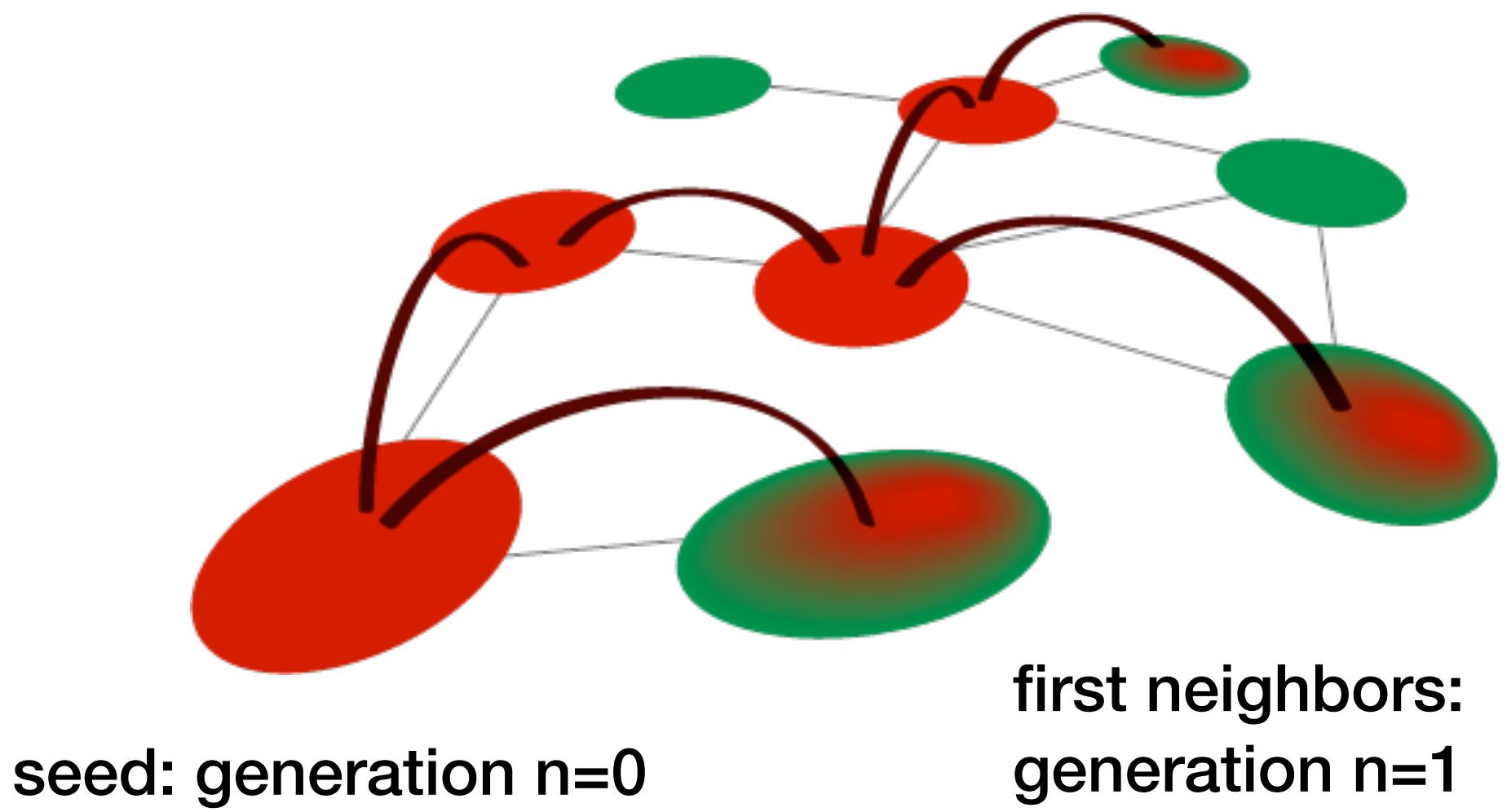
- In each node we consider a SIR model, with parameters β and μ
- The basic reproductive number is $R_0 = \frac{\beta}{\mu}$
- There is a **local epidemic threshold** $R_0 > 1$ that defines the condition for an outbreak to occur within a node
- We look for a **global invasion threshold** that defines 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 $R_0 \sim 1$, $(1 - R_0^{-\lambda_{kk'}}) \simeq \lambda_{kk'}(R_0 - 1)$
- 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

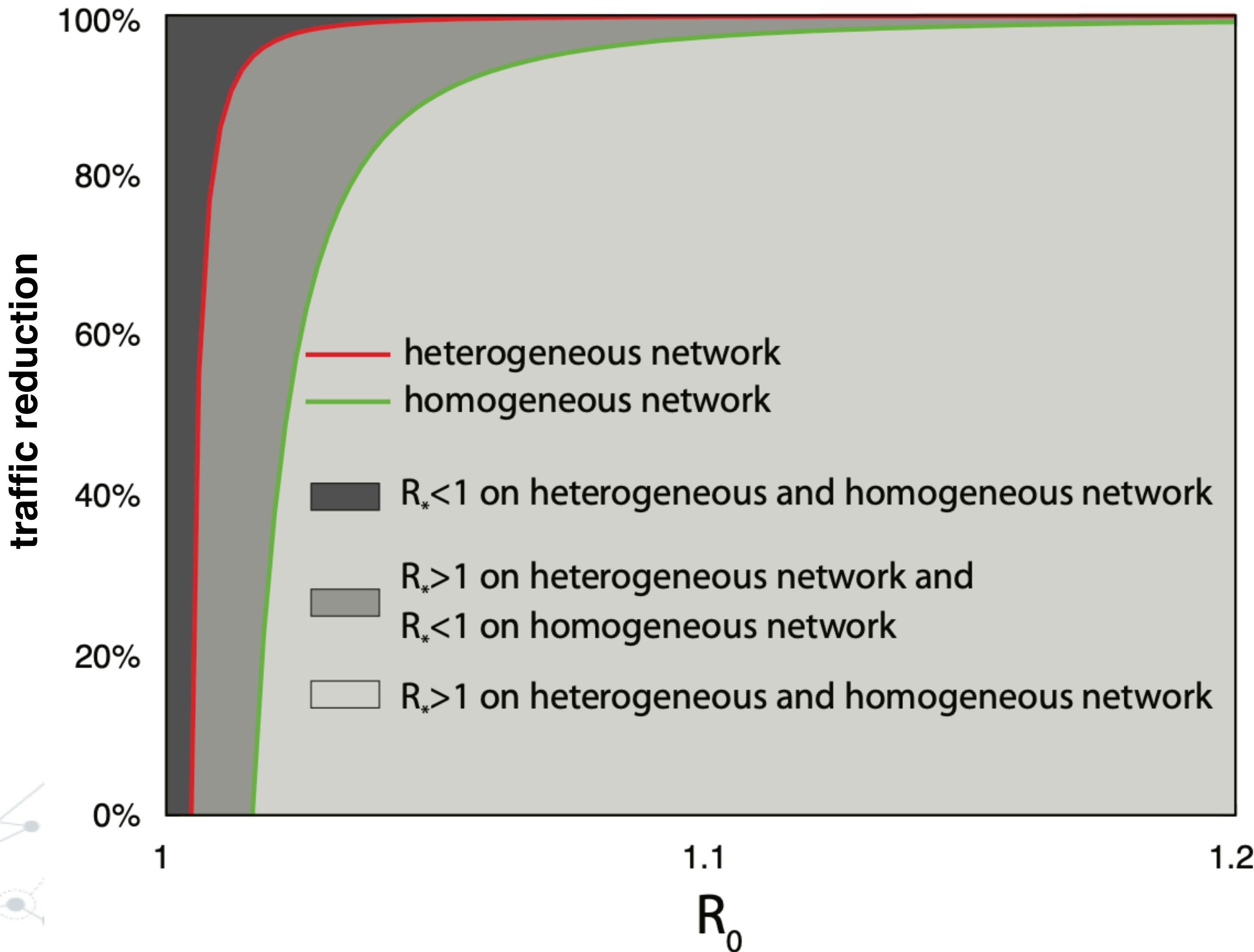
$$R_* = (R_0 - 1) \frac{\langle k^{2+2\theta} \rangle - \langle k^{1+2\theta} \rangle}{\langle k \rangle} \frac{w_0 \alpha}{\mu} > 1$$

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

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

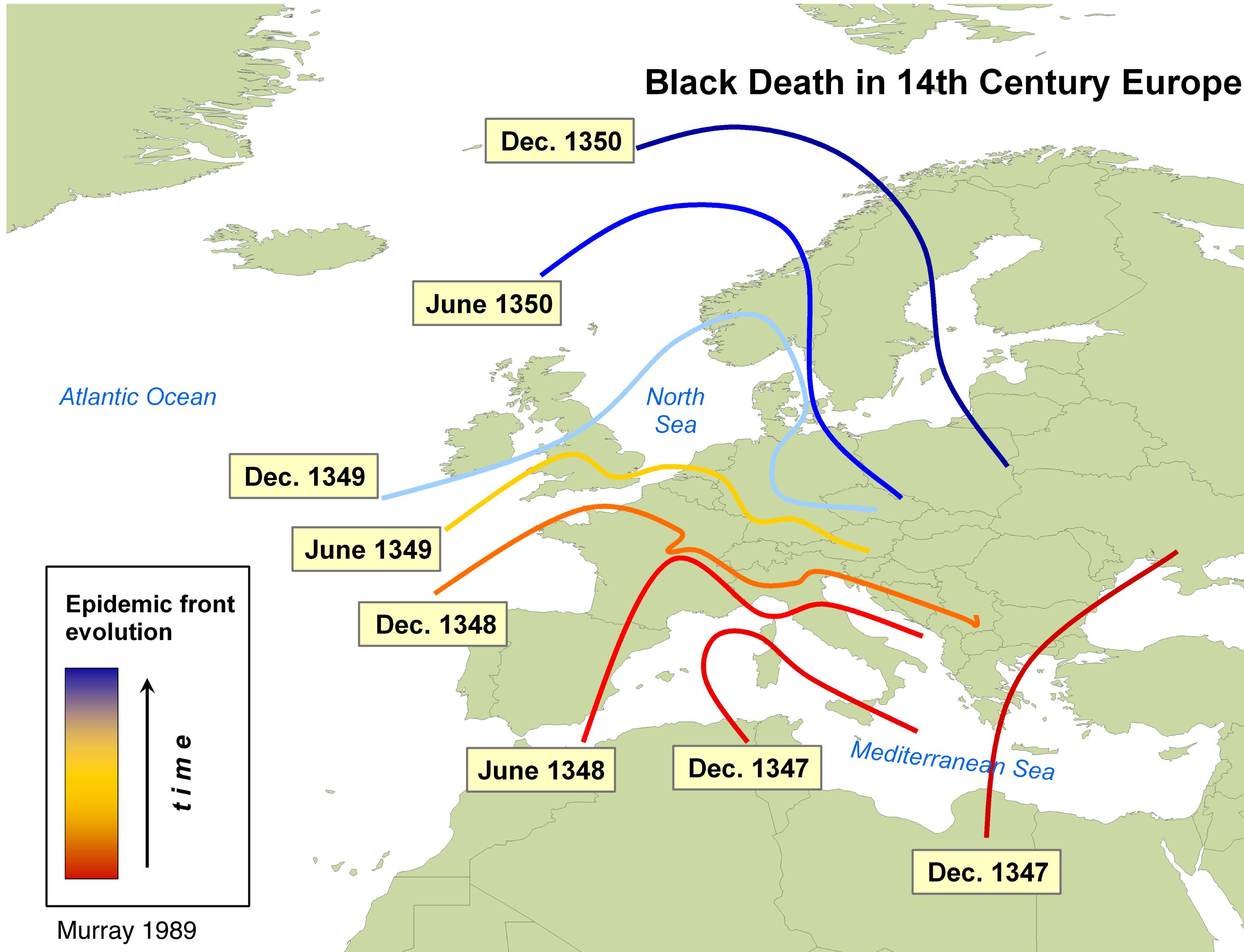
In an infinite scale-free network: $\frac{\langle k \rangle}{\langle k^{2+2\theta} \rangle - \langle k^{1+2\theta} \rangle} \rightarrow 0$

Travel restrictions



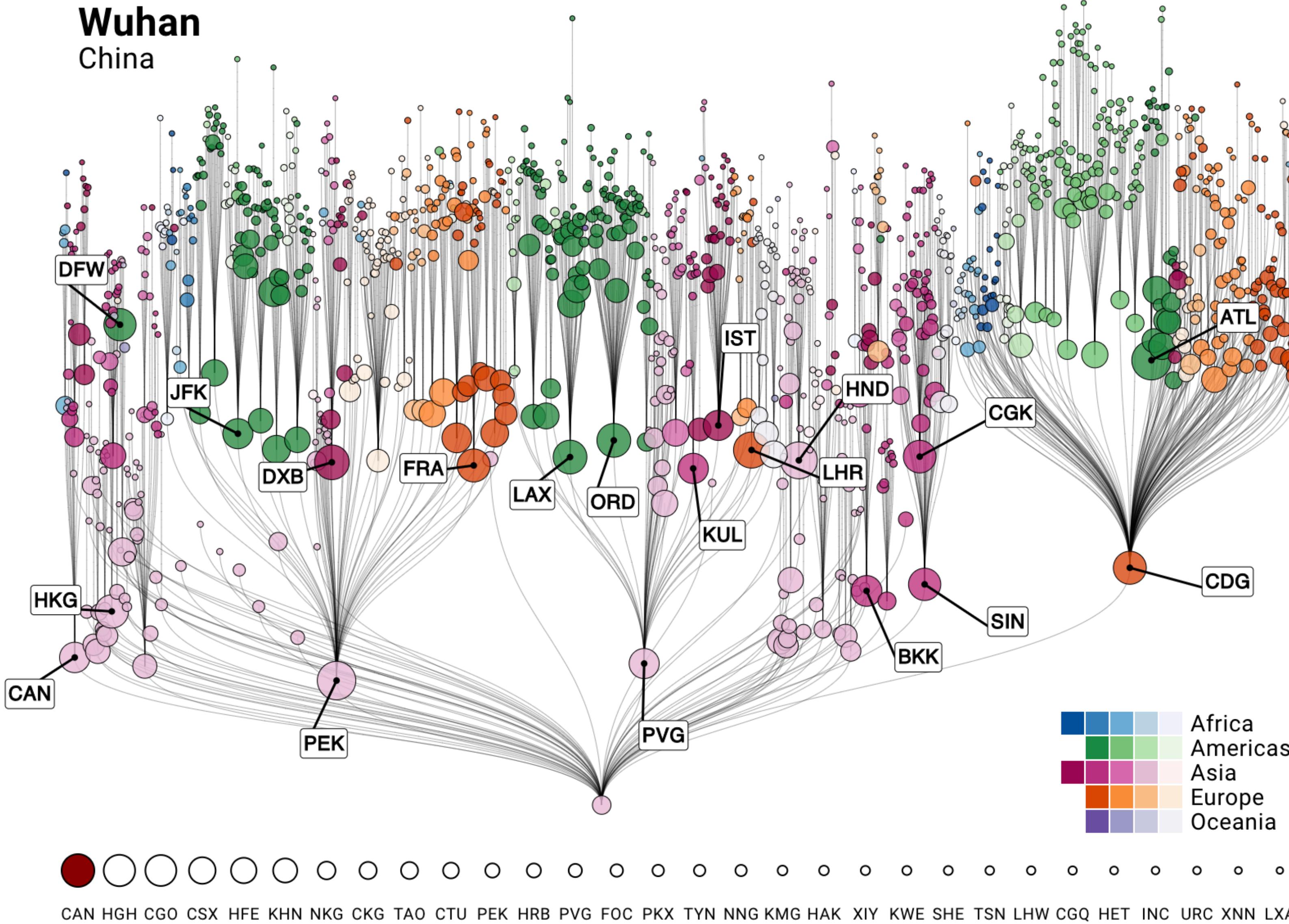
travel restrictions are generally ineffective unless traffic reduction is equal to 100%

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



SARS-CoV-2 in the XXI century
a network driven diffusion process

GLEAM: a data-driven metapopulation model



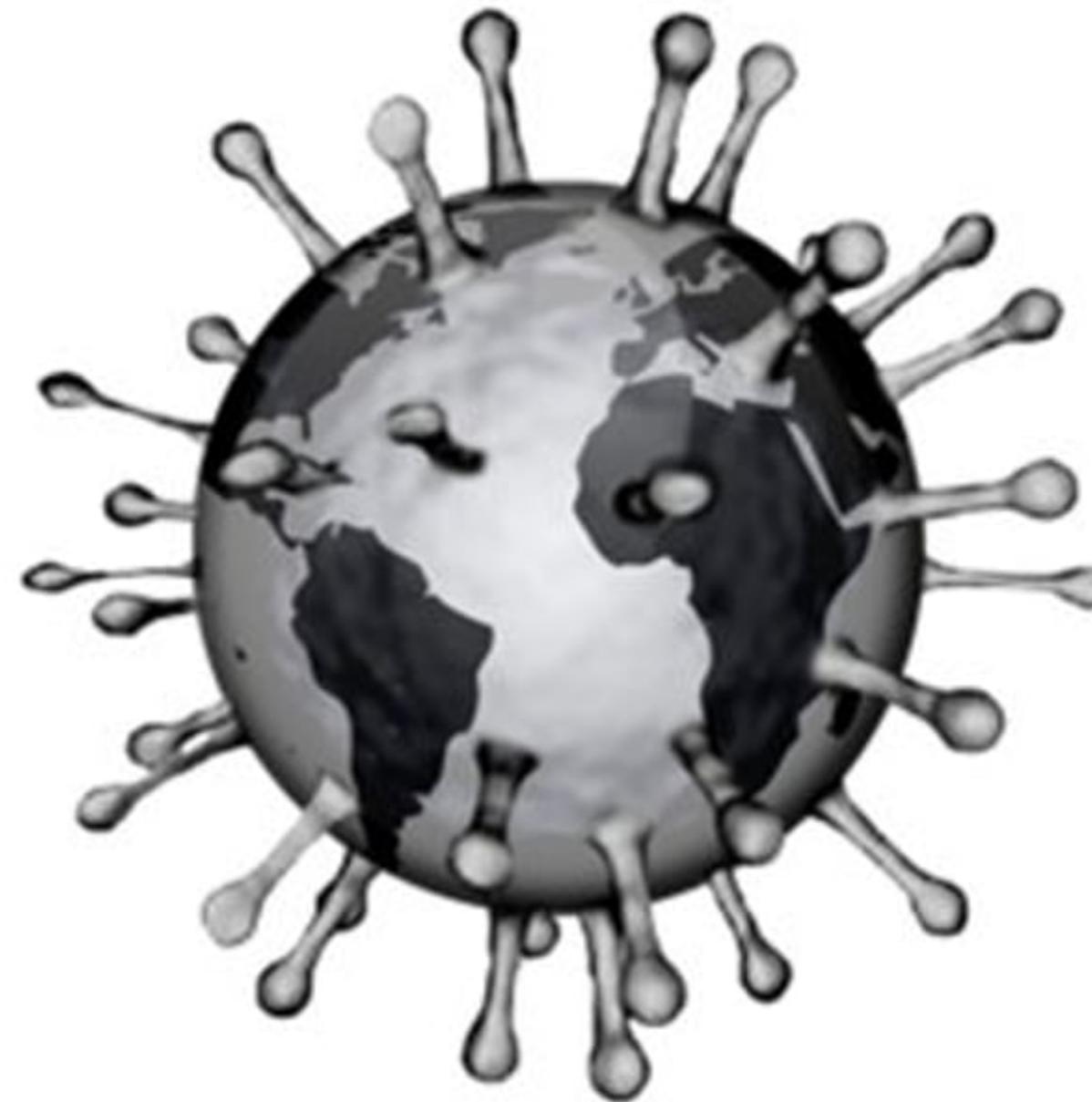
Using big data and computational
modeling to fight infectious diseases

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

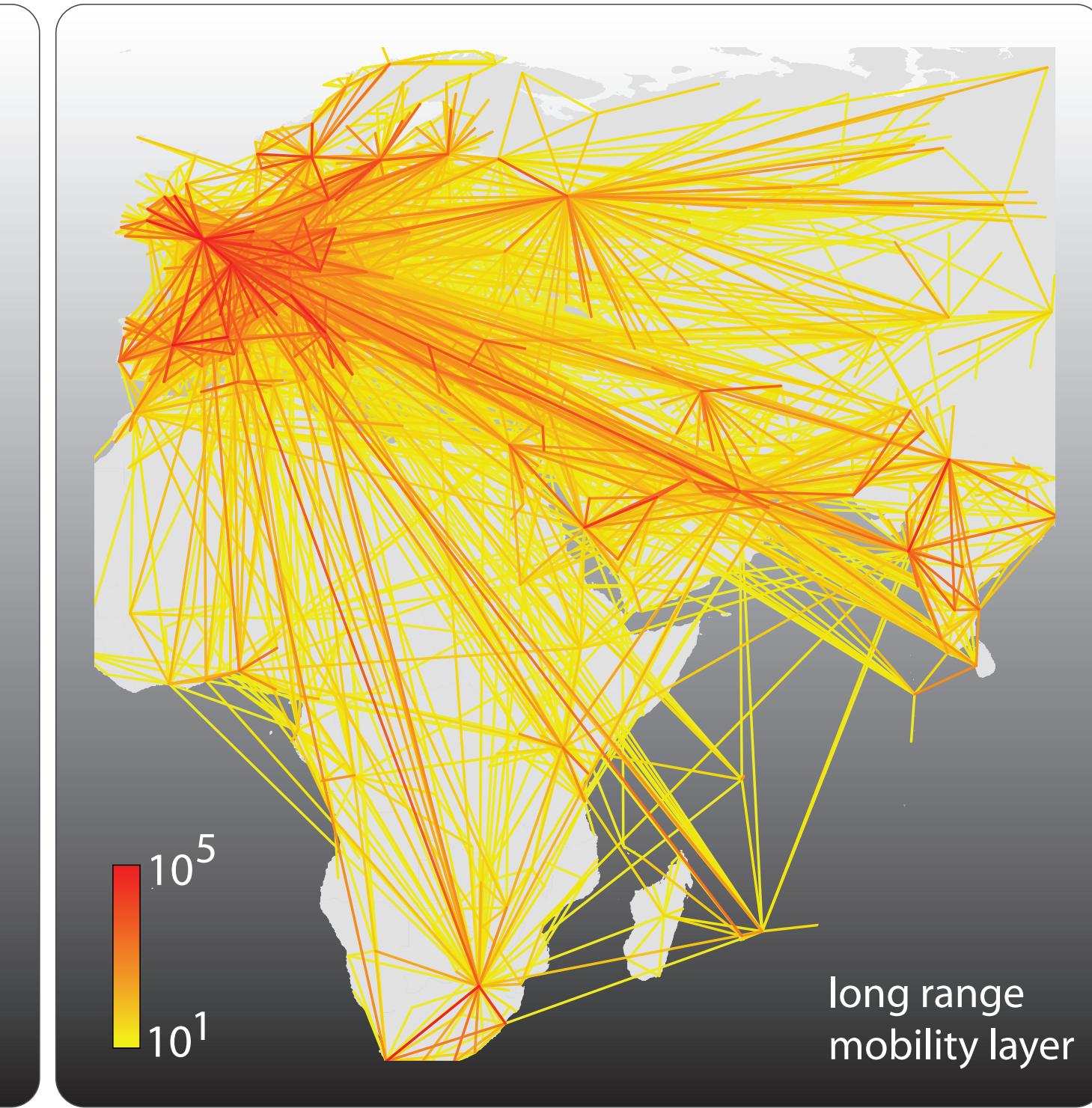
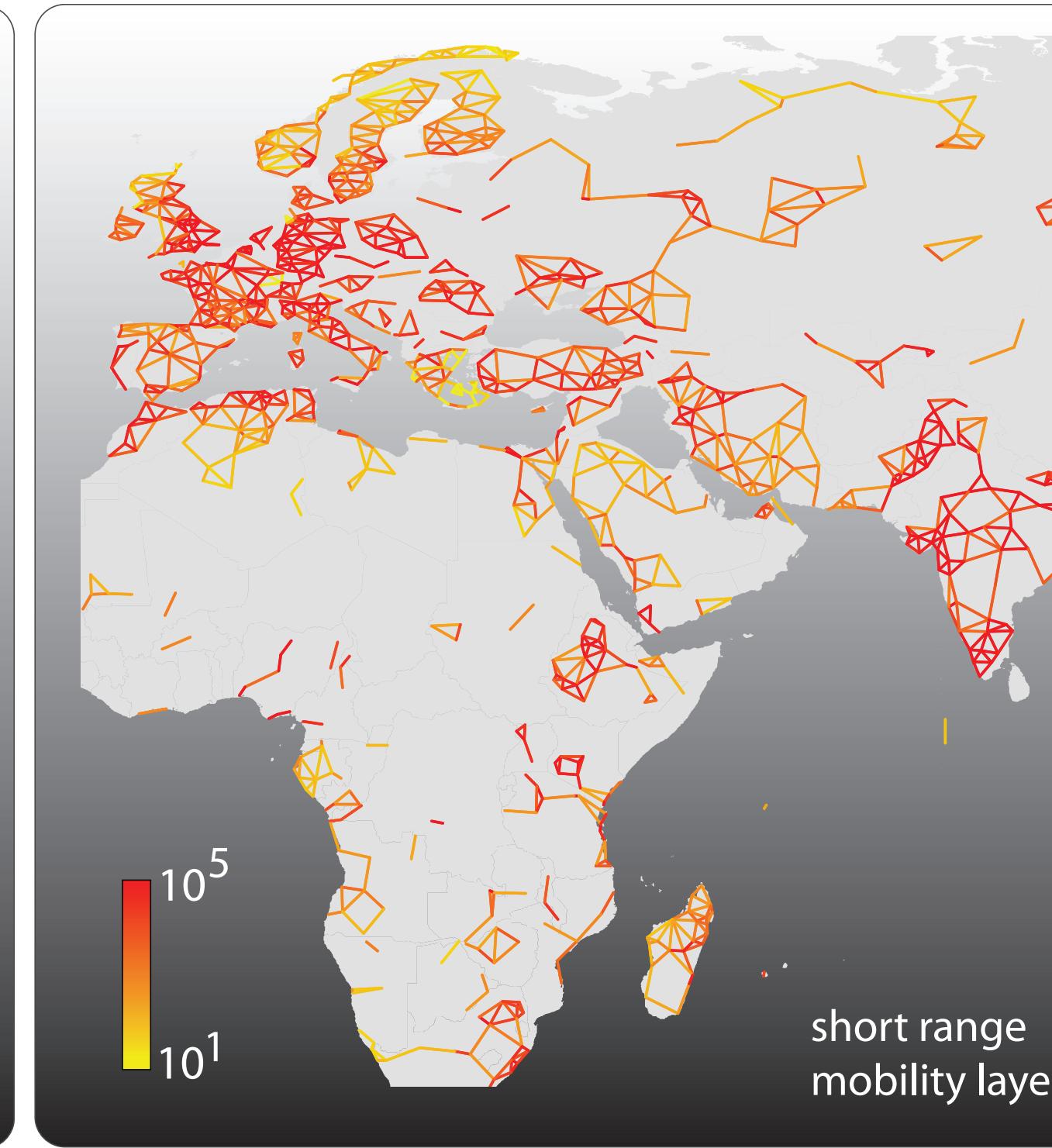
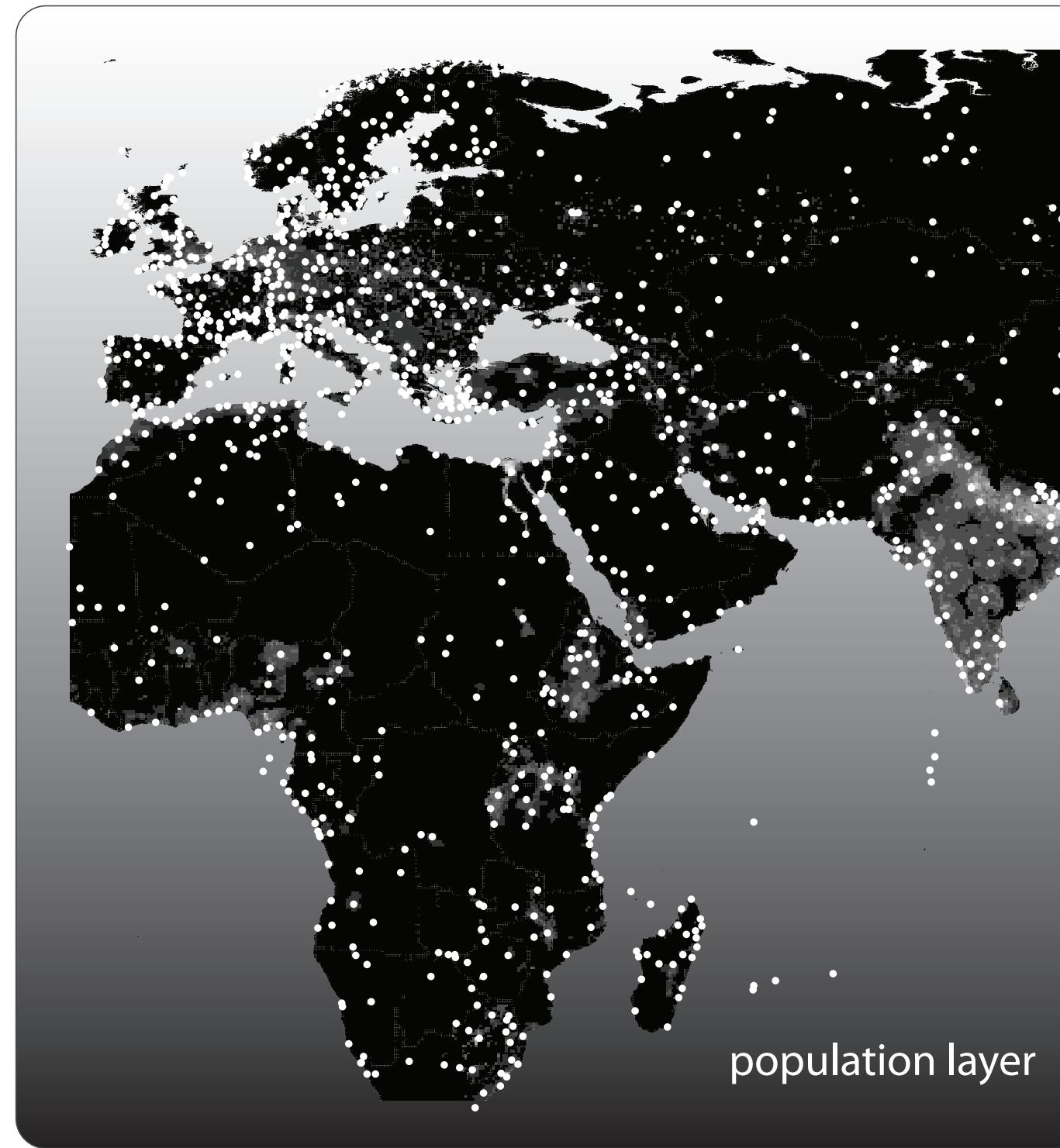


Vittoria
Colizza



- 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

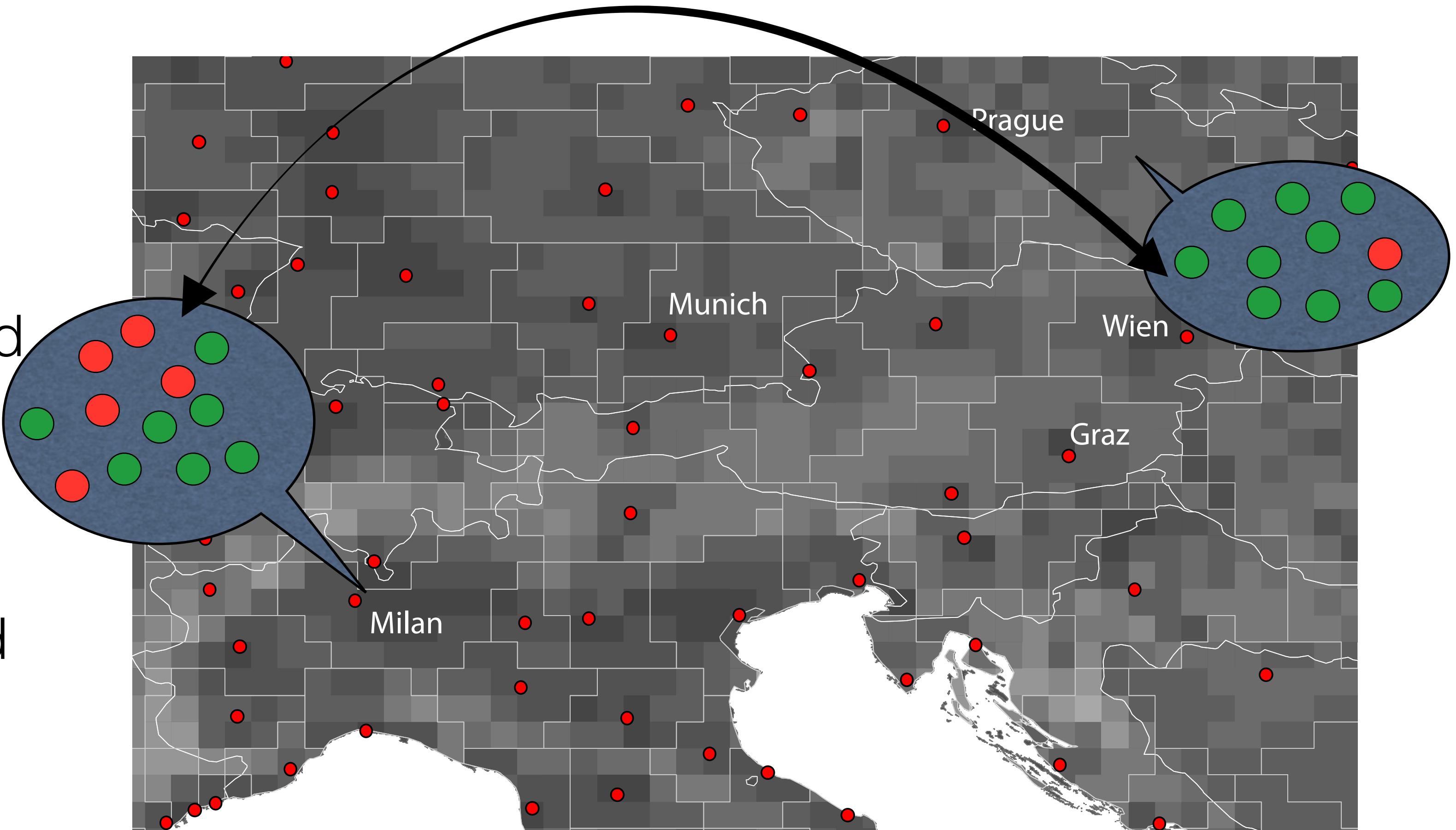
Short range
mobility
(commuting)

Air travel

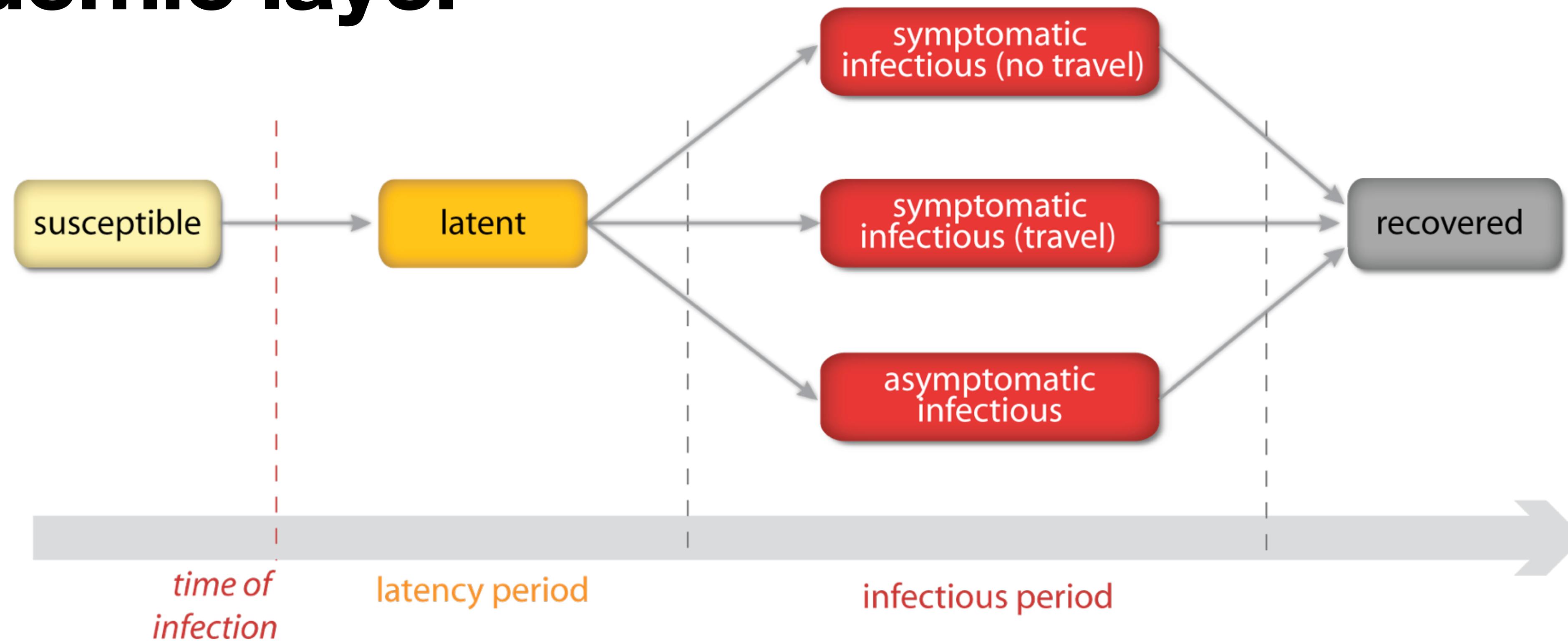
Balcan et al. PNAS 2009

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



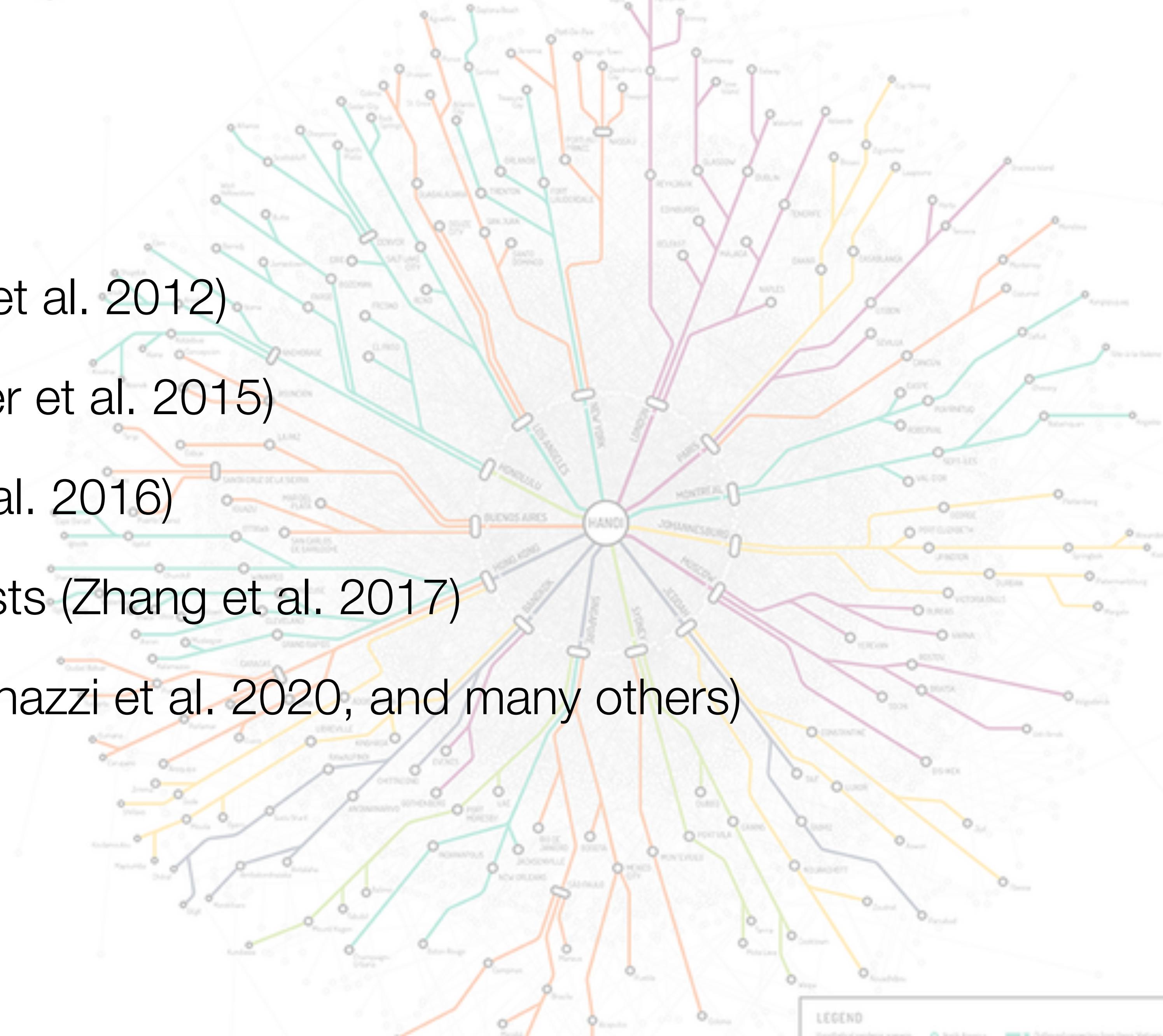
Parameters are estimated from clinical data.

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 Chinazzi¹, Jessica T. Davis¹, Marco Ajelli², Corrado Gioannini³,  Maria Litvinova³, Stefano Merler², Ana Pastore y Piontti¹, Kunpeng Mu¹, Luca Rossi³,  Kaiyuan Sun⁴,  Cécile Viboud⁴, Xinyue Xiong¹,  Hongjie Yu⁵,  M. Elizabeth Halloran^{6,7},  Ira M. Longini Jr.^{8,*},  Alessandro Vespignani^{1,3,*}

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⁶Fred Hutchinson Cancer Research Center, Seattle, WA, USA.

⁷Department of Biostatistics, University of Washington, Seattle, WA, USA.

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COVID-19 and travel restrictions

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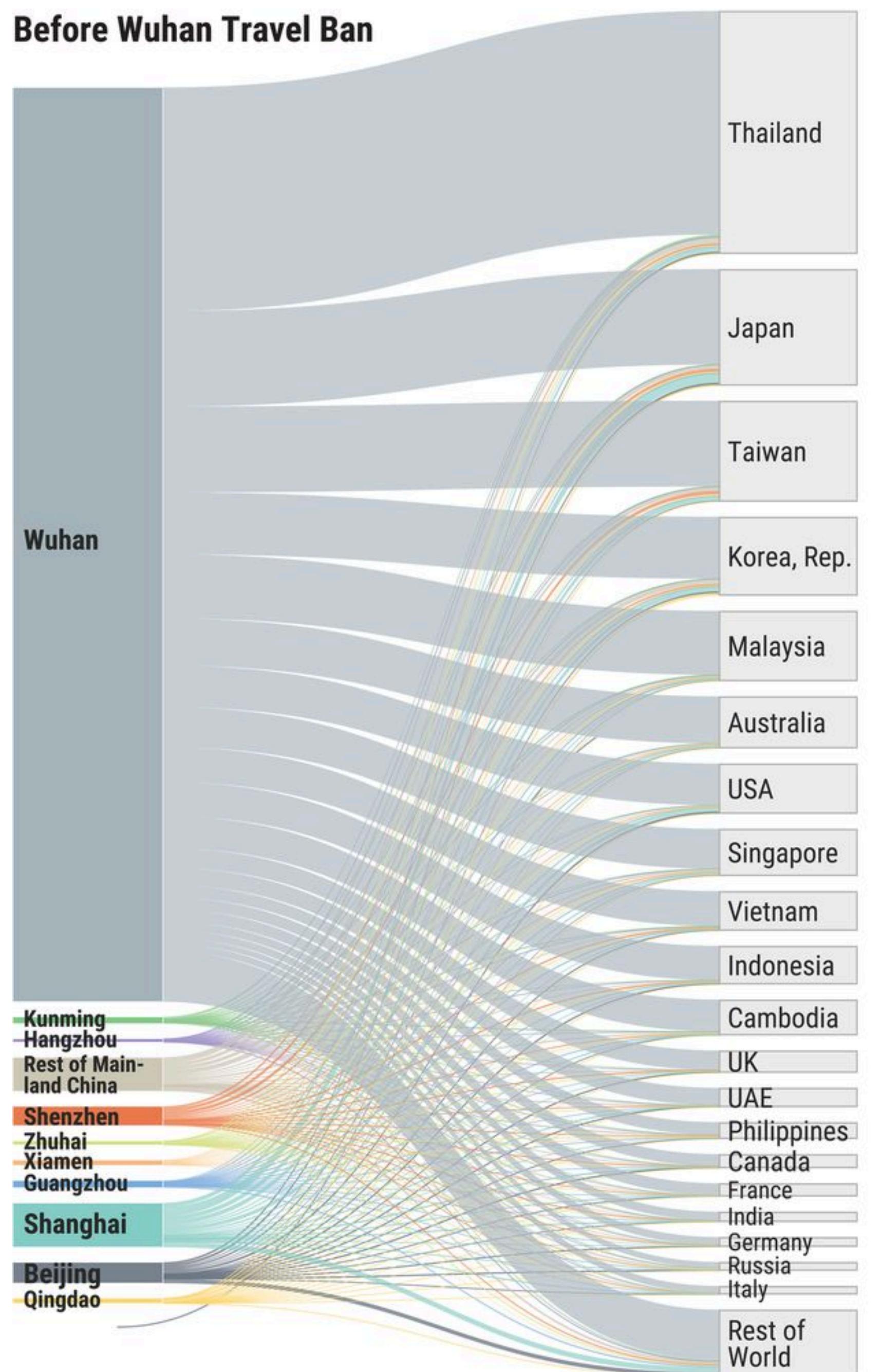
- Hide authors and affiliations

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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.

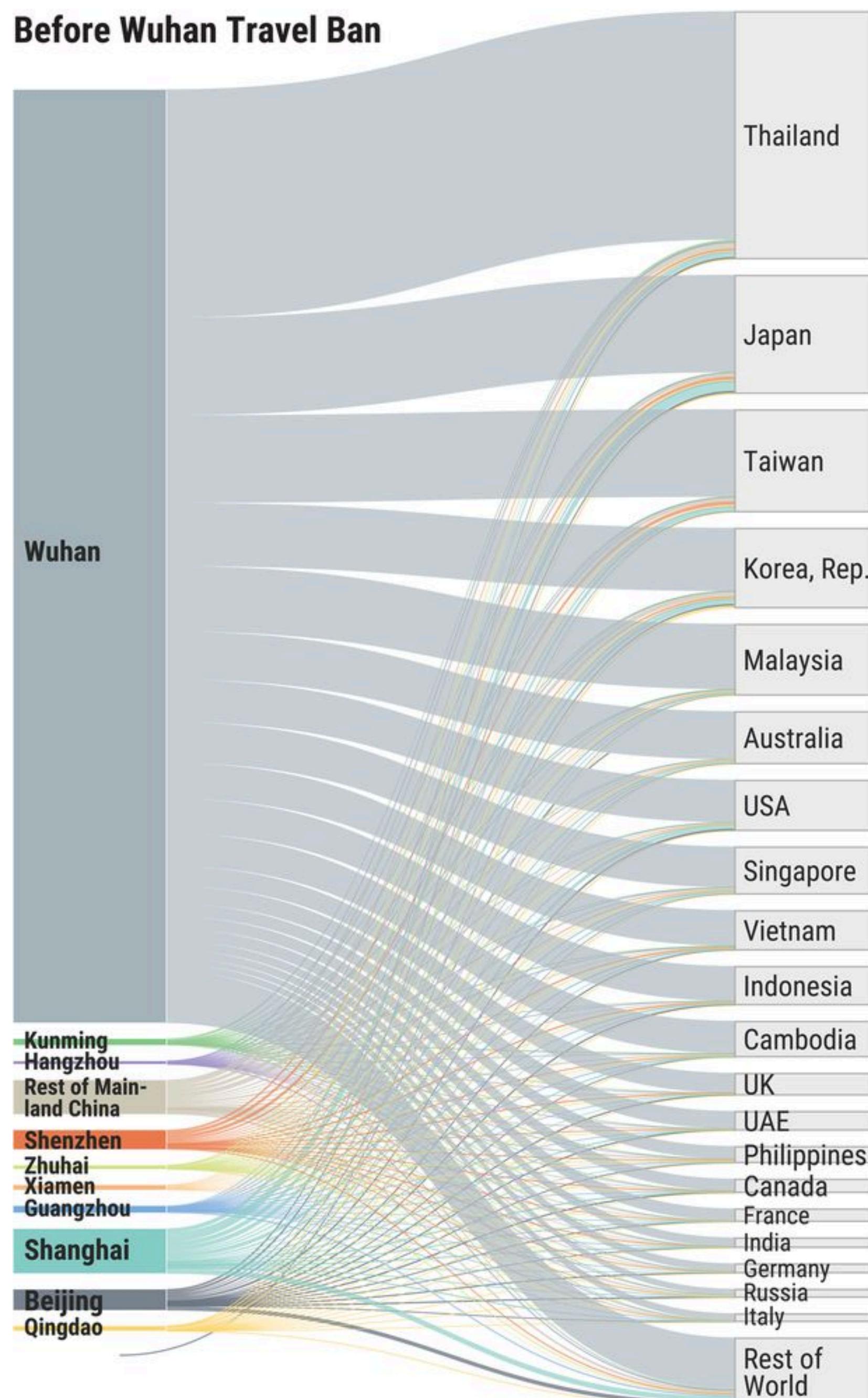
Case Importations

Before Wuhan Travel Ban

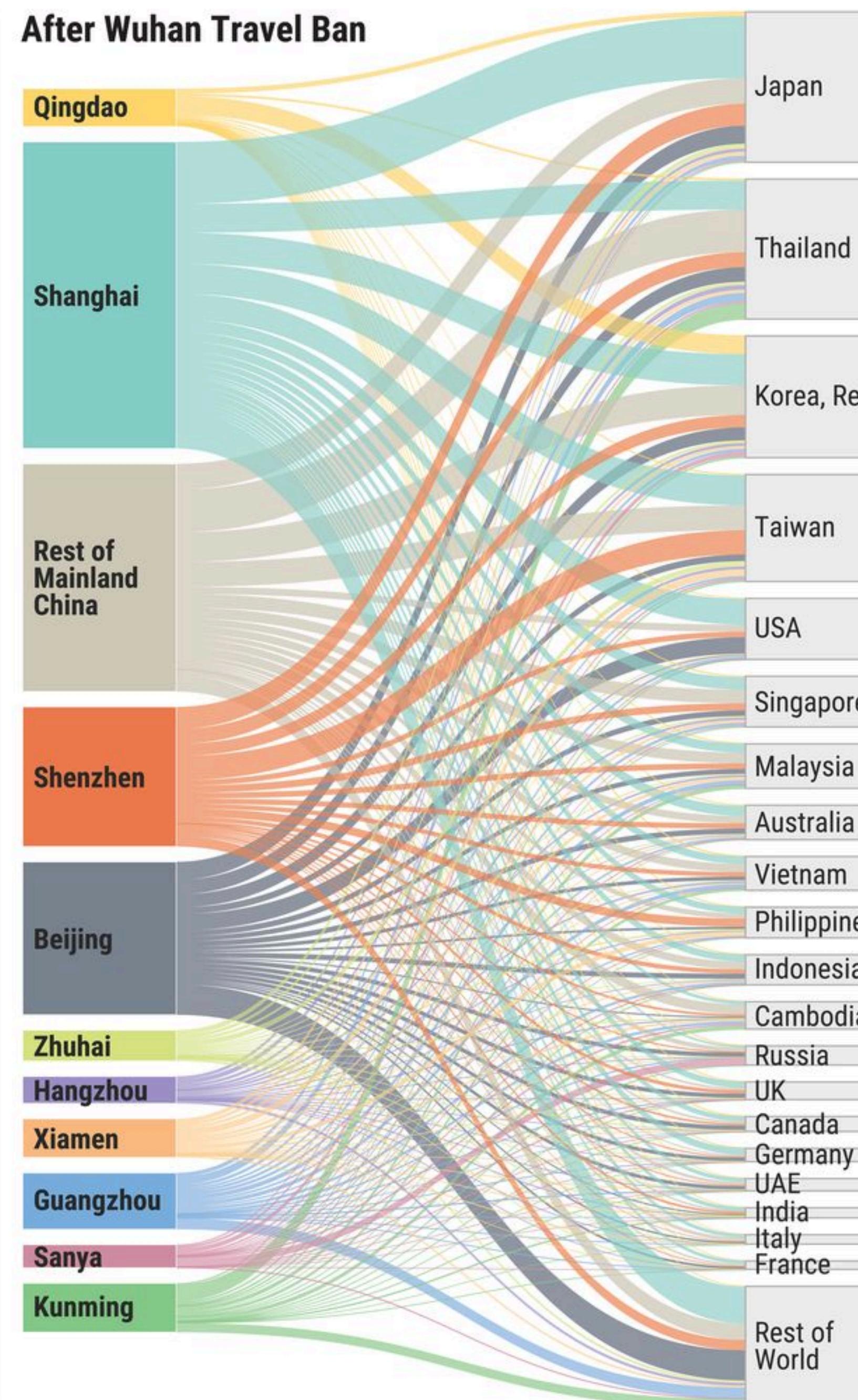


Case Importations

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

Epi-pop



Next... modelling human mobility