

Digital Epidemiology

Mobility impact on epidemics spread

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Human mobility impact on epidemics

Metapopulation models with markovian mobility

- The metapopulation scheme
- Diffusion: Degree block approximation
- Diffusion analogy for mobility
 - solution for traffic dependent diffusion rate
 - solution population dependent diffusione rate
- Global epidemic threshold in metapopulation networks

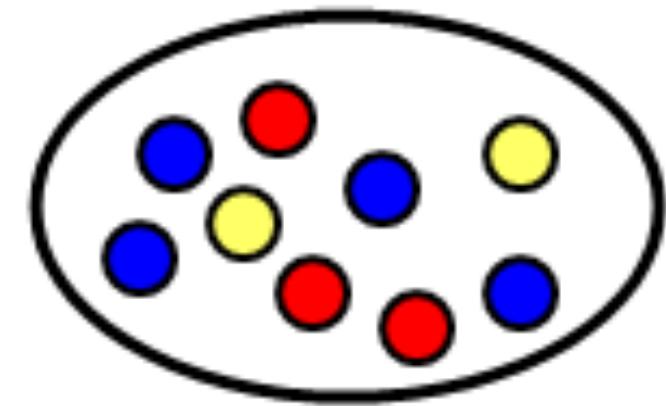
Metapopulation models with non-markovian mobility

- Force of infection with returning rate
- Markovian mobility bias on epidemic threshold

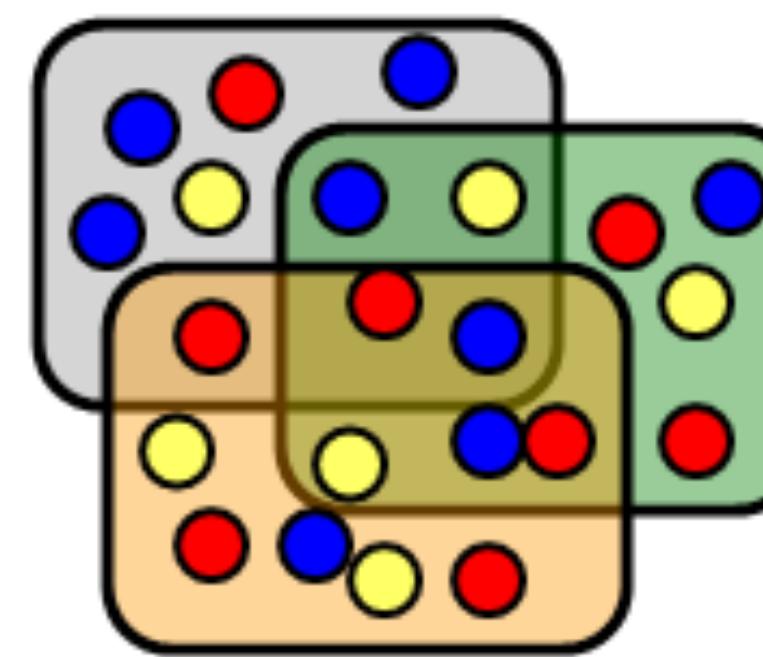


<https://www.onlymyhealth.com/>

The metapopulation scheme



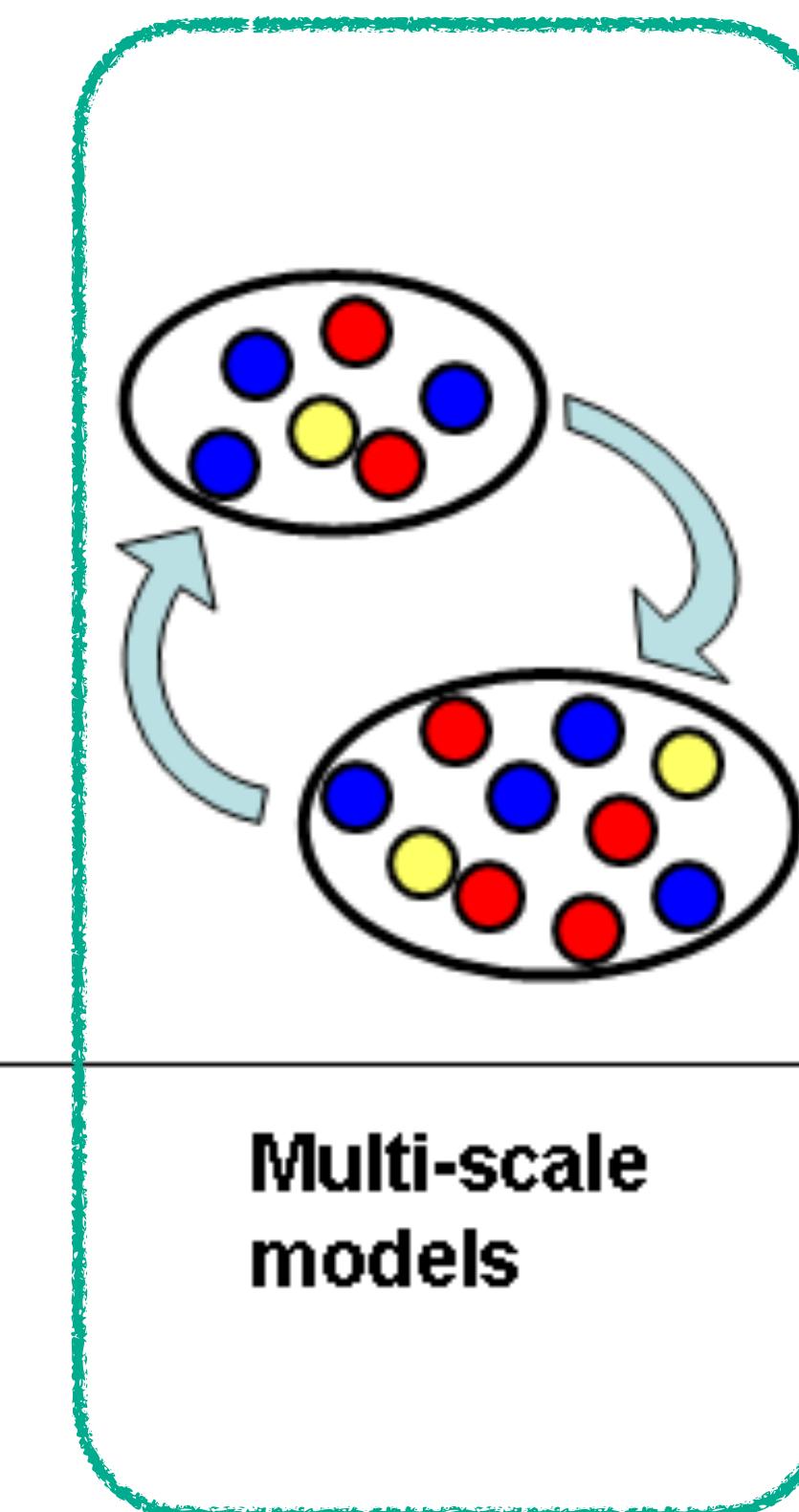
Homogeneous
mixing



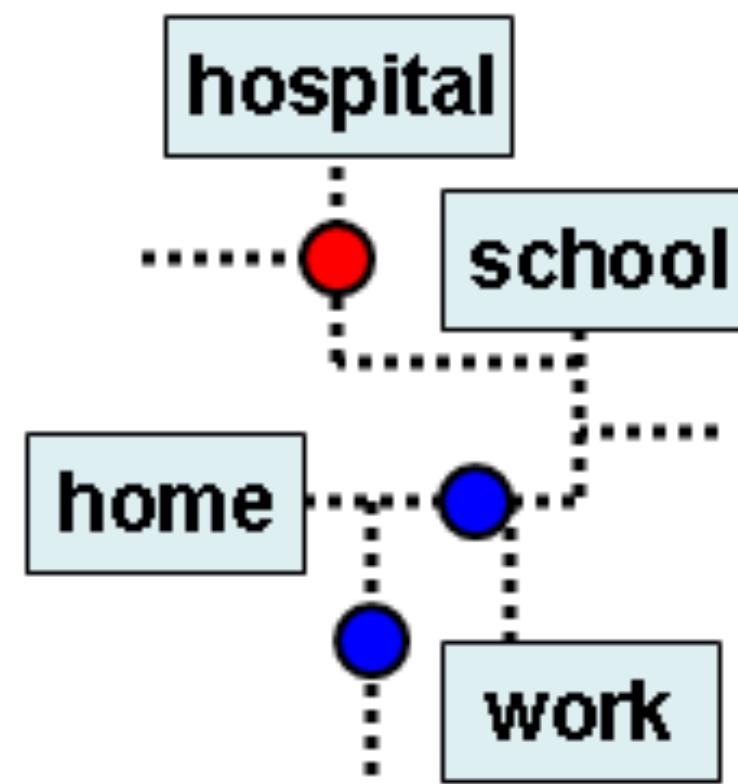
Social structure



Contact network
models

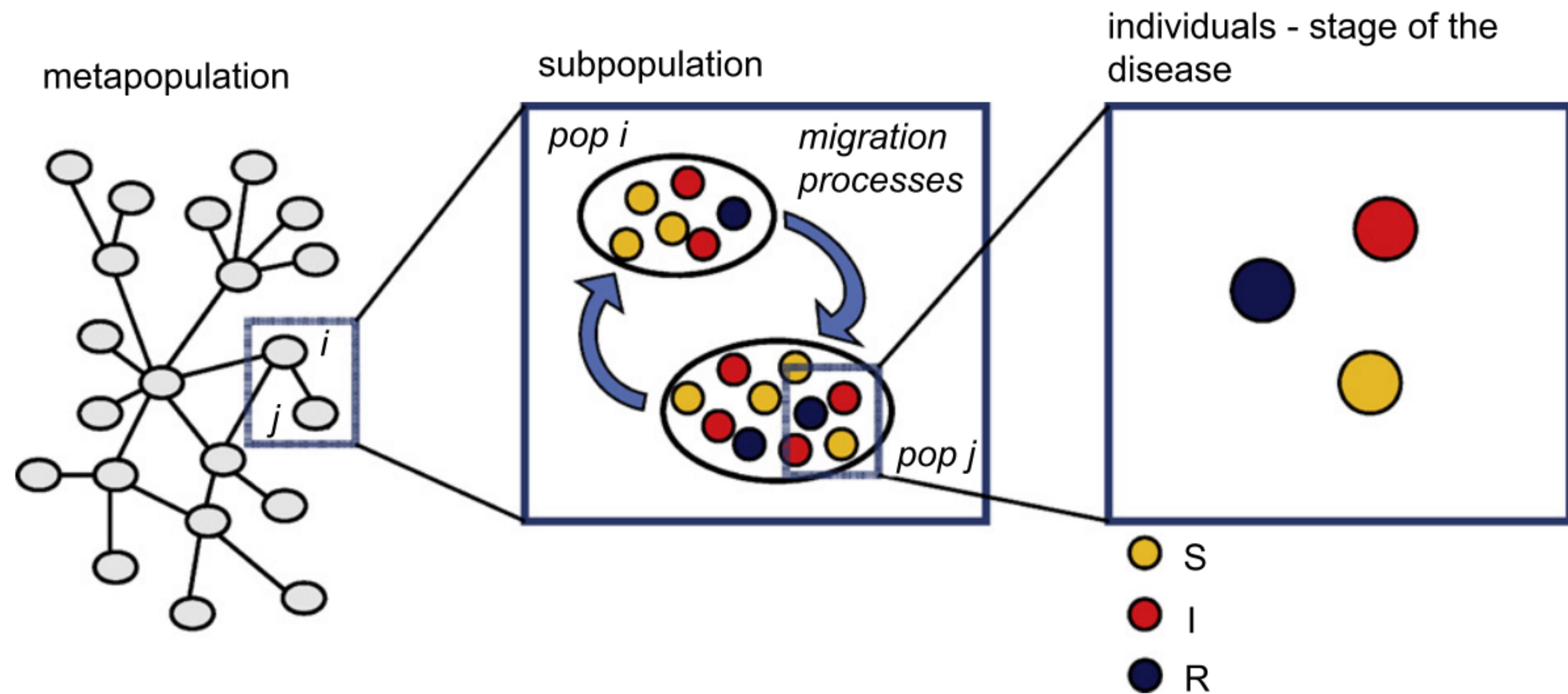


Multi-scale
models



Agent Based
models

The metapopulation scheme



Spatially structured subpopulations (city, regions, etc.).

Epidemic dynamic in each subpopulation is the same as in the single population scheme, but individuals travel

Reaction-diffusion analogy for mobility

We consider a network of V populations (nodes), where each node hosts N_i individuals, which can be in state S, I or R

The total population is preserved as: $N = \sum_i N_i$

each individual moves from i to j with a diffusion rate d_{ij} ~ node degree or population size or mobility matrix

Diffusion: individuals travel from one node to another

d_{ij} : rate at which an individual is moving from subpopulation i to subpopulation j

$d_{ij} = \frac{w_{ij}}{N_i}$ where w_{ij} is known real-world mobility between subpopulations

Reaction: in each subpopulation, individuals interact according to an epidemic compartmental model in homogenous mixing
(mass action principle)

Recap on the mass-action principle

Force of infection: the rate at which susceptible individuals become infectious

$$\lambda = \beta i = \beta \frac{I}{N} \text{ force of infection acting within the population at each subpopulation}$$

Mass-action: within each population, new infections are produced by the density of contacts of susceptible and infected individuals

$S + I \rightarrow 2I$ principle of mass-action: chemical reagents amount determines the product amount

Homogenous mixing: all individuals interact with the same rate, like particles in a box at given temperature T

$$\frac{dI}{dt} = \lambda S - \mu I = \beta S \frac{I}{N} - \mu I$$

Recap on the mass-action principle

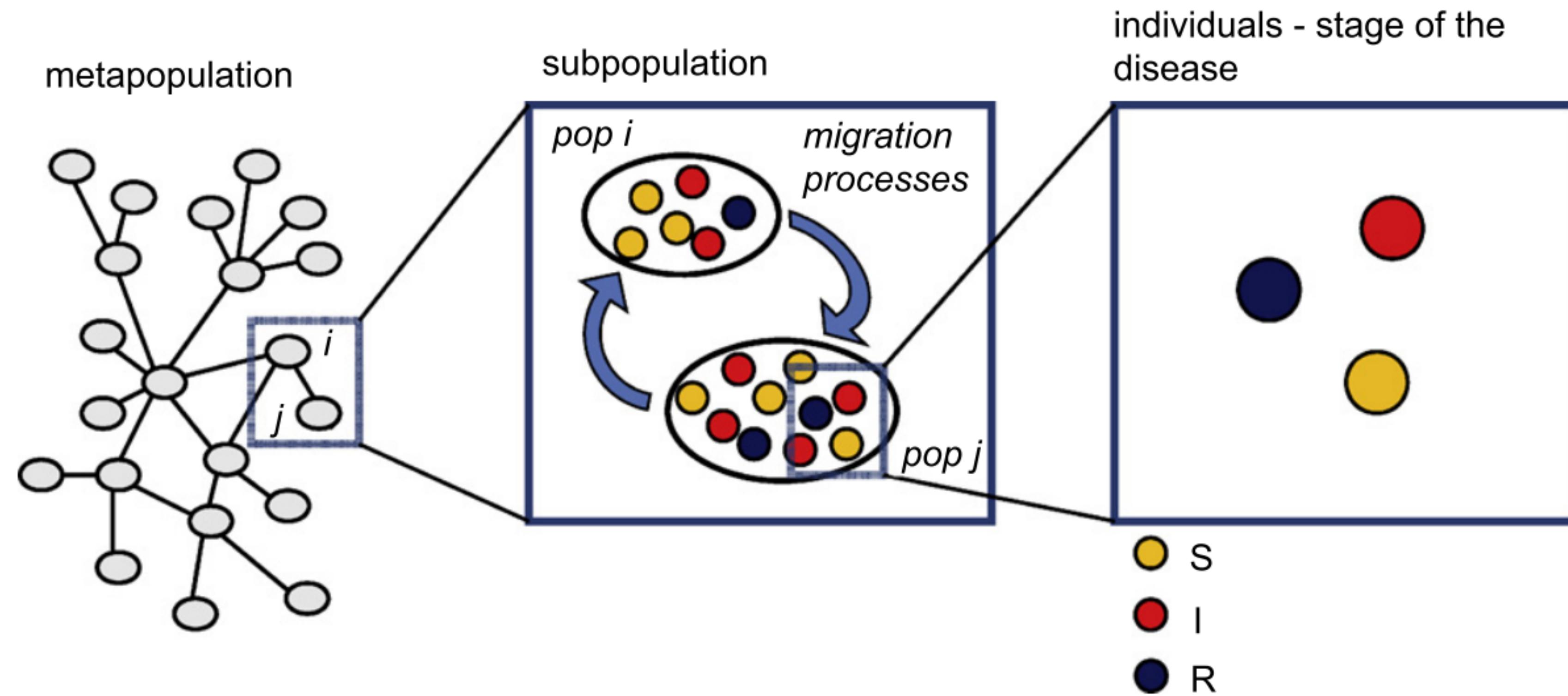
Asymptotic state: no more infections or infected to recover

$$\left\{ \begin{array}{l} \frac{dS_i}{dt} = -\beta \frac{S_i I_i}{N_i} \\ \frac{dI_i}{dt} = \beta \frac{S_i I_i}{N_i} - \mu I_i = 0 \\ \frac{dR_i}{dt} = \mu I_i \end{array} \right. \quad \left\{ \begin{array}{l} \frac{dS_i}{dt} = -\beta \frac{S_i I_i}{N_i} \\ I_i = \frac{1}{\mu} \frac{dR_i}{dt} \end{array} \right. \quad \left\{ \begin{array}{l} \frac{dS_i}{dt} = -\beta \frac{S_i}{N_i} \frac{1}{\mu} \frac{dR_i}{dt} = -R_0 \frac{S_i}{N_i} \frac{dR_i}{dt} \\ I_i = \frac{1}{\mu} \frac{dR_i}{dt} \end{array} \right.$$

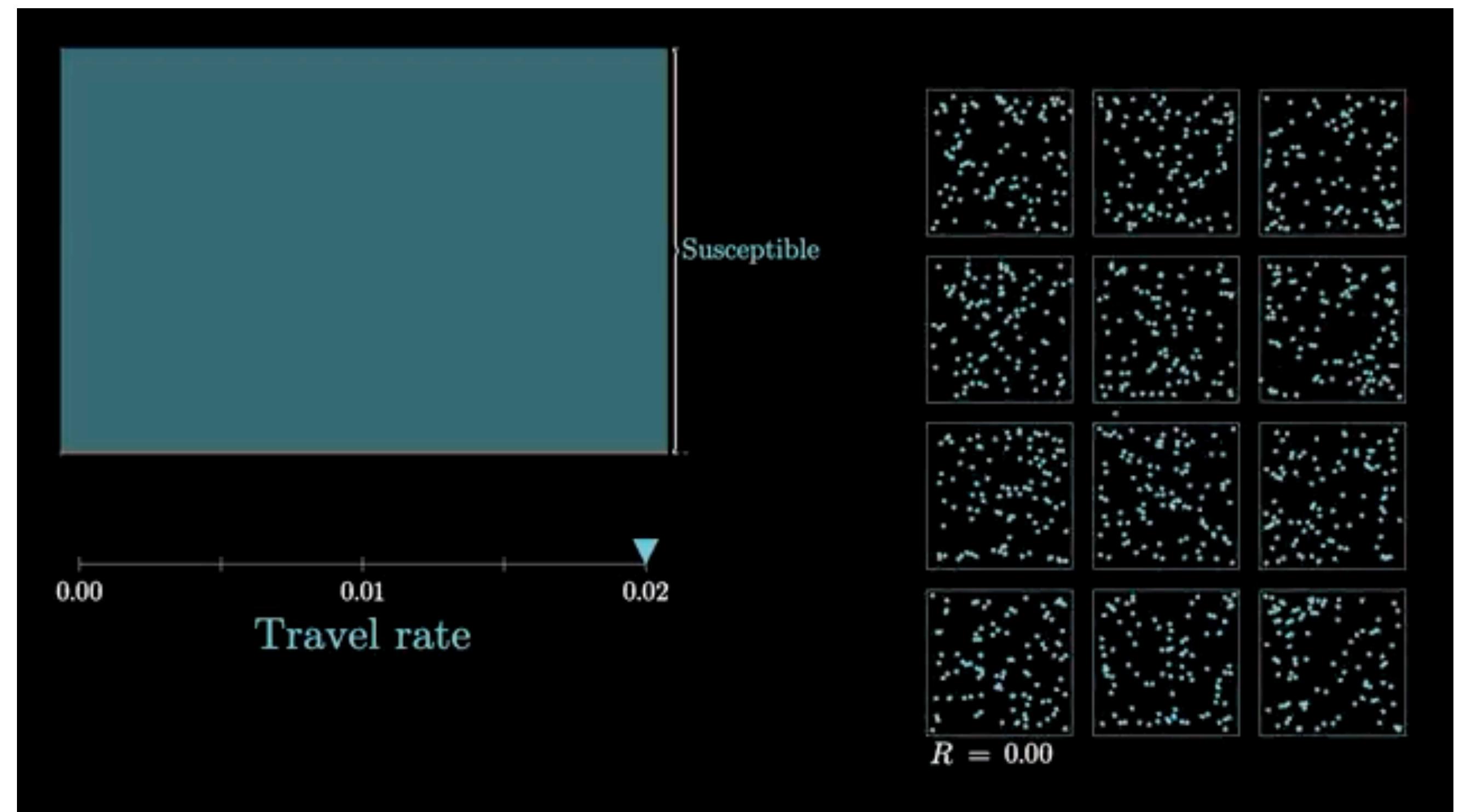
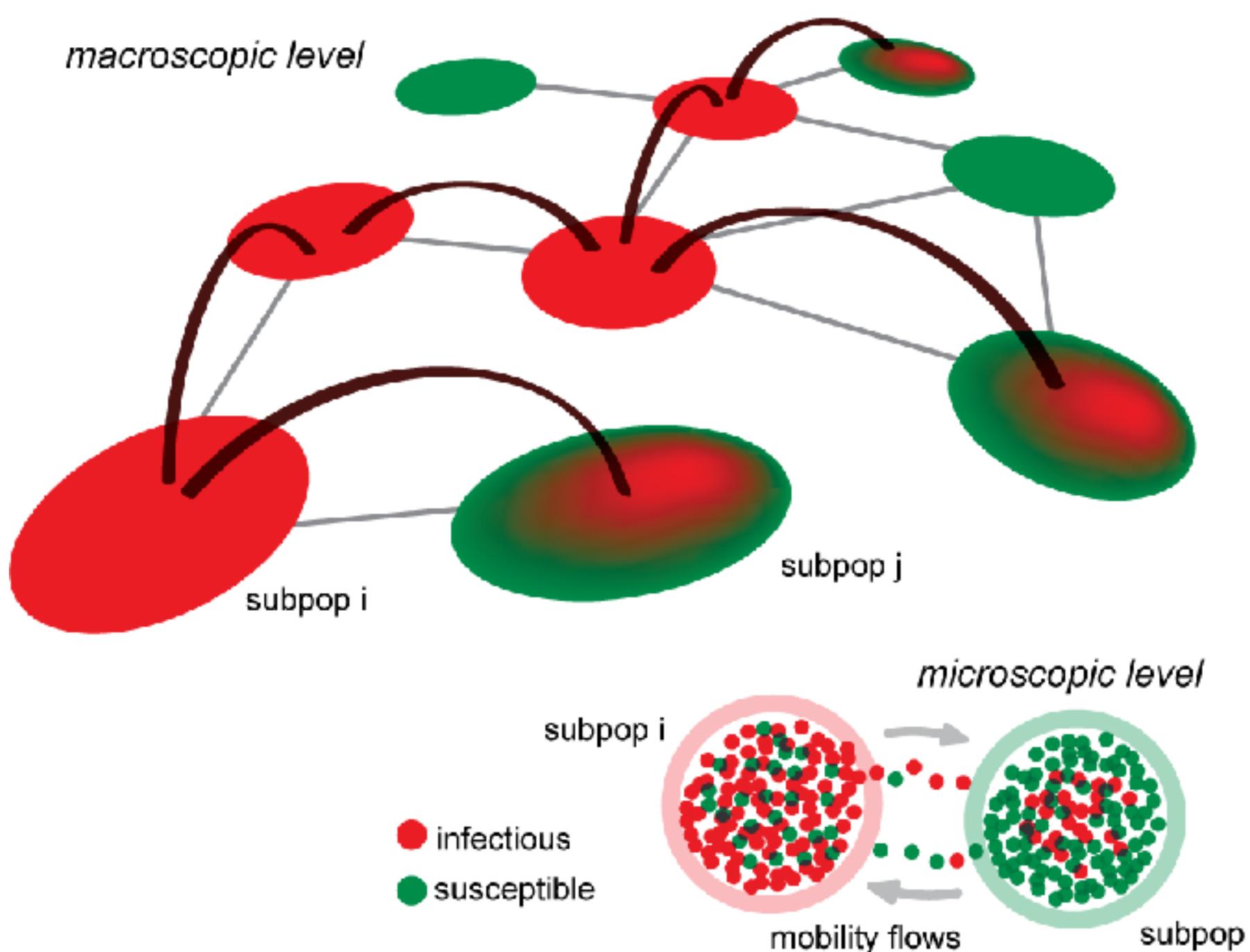
hence $\frac{dS_i}{dR_i} = -R_0 \frac{S_i}{N_i}$, so we can write the final n of susceptibles as $S(\infty) = S_{0i} e^{-R_0 \frac{R_i(\infty)}{N_i}}$

meaning that the final number of infected (attack ratio) will be $1 - s(\infty) = 1 - s_{0i} e^{-R_0 r_i(\infty)}$

Reaction-diffusion analogy for mobility



The metapopulation scheme



Degree block approximation

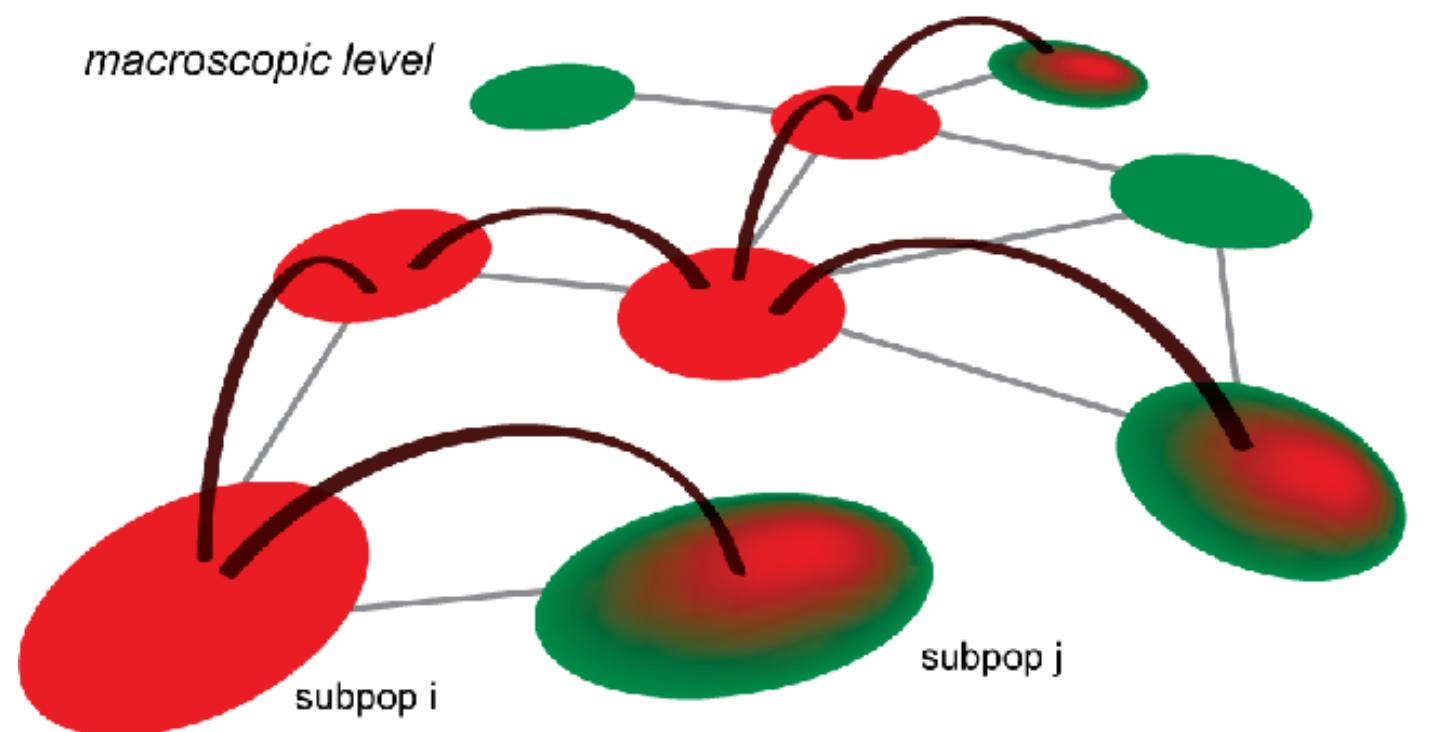
All nodes of degree k behave **statistically the same**.

For a degree-block k , the average population of nodes with degree k is: $N_k = \frac{1}{V_k} \sum_{i|k_i=k} N_i$

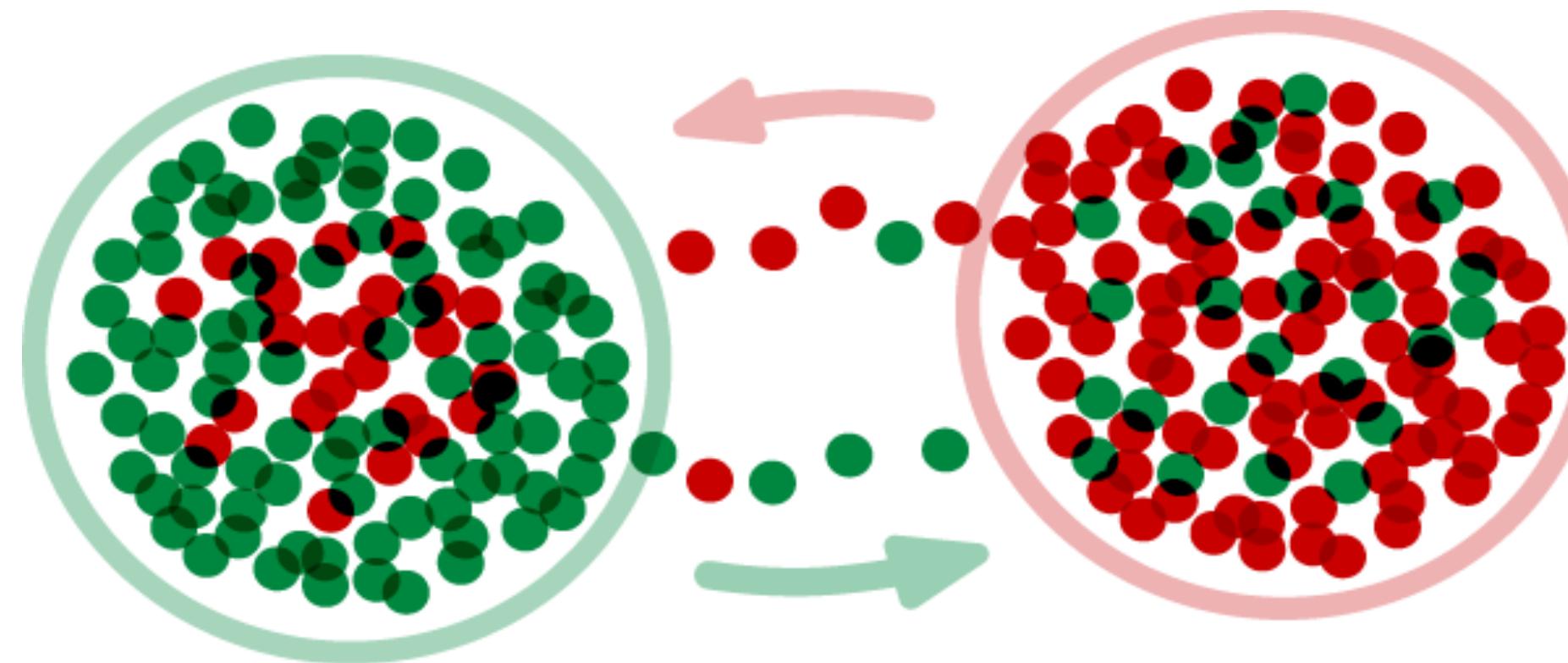
where i are populations with degree k and V_k are the n of nodes with that degree

The total population is preserved as: $N = \sum_k N_k$

$d_{kk'}$ is the **diffusion rate** between nodes of degree k and k'



Degree block approximation

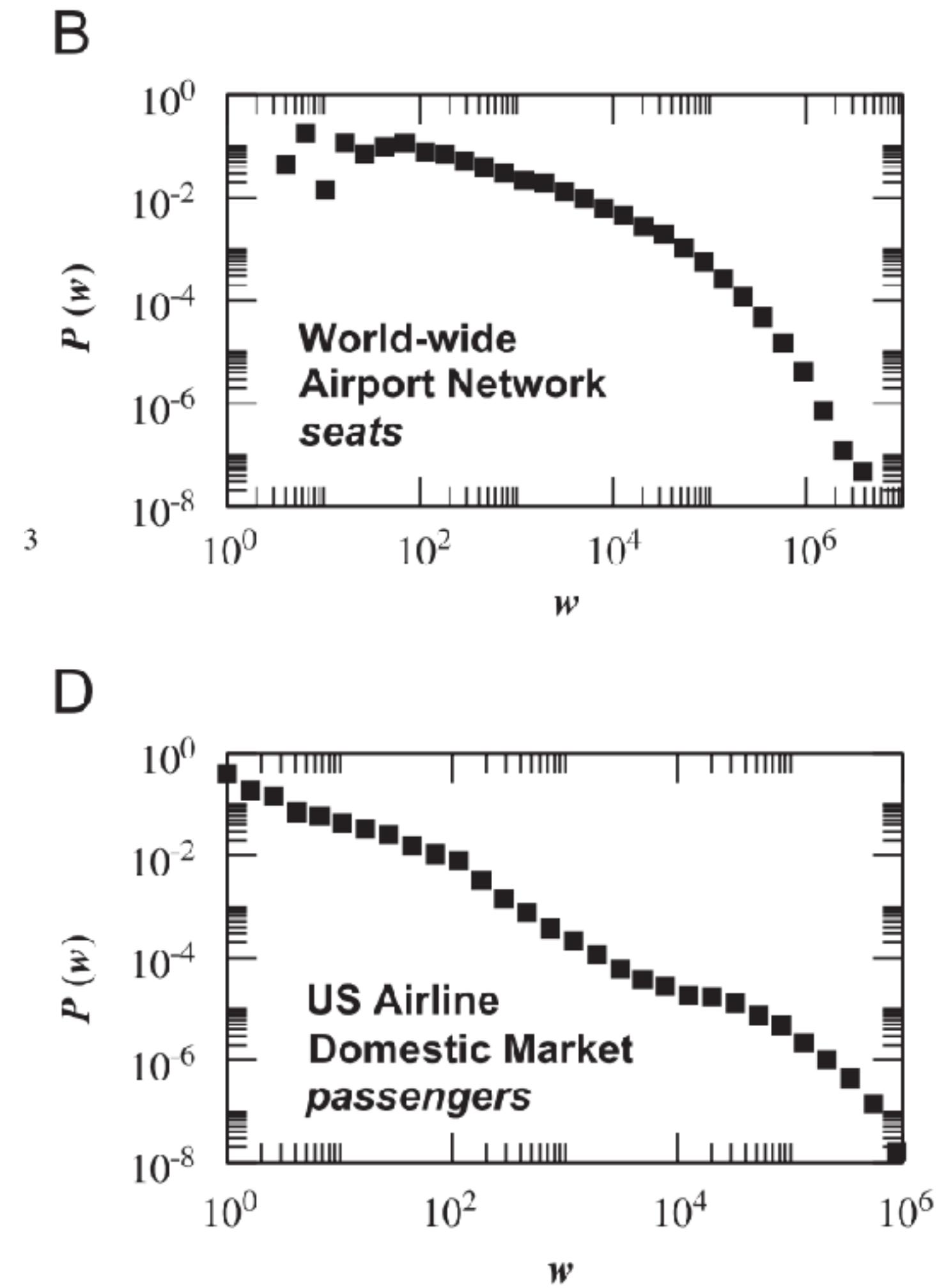


w_{ij} = number of individuals traveling
between i and j

in real world networks:

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

$$\theta \sim 0.5$$

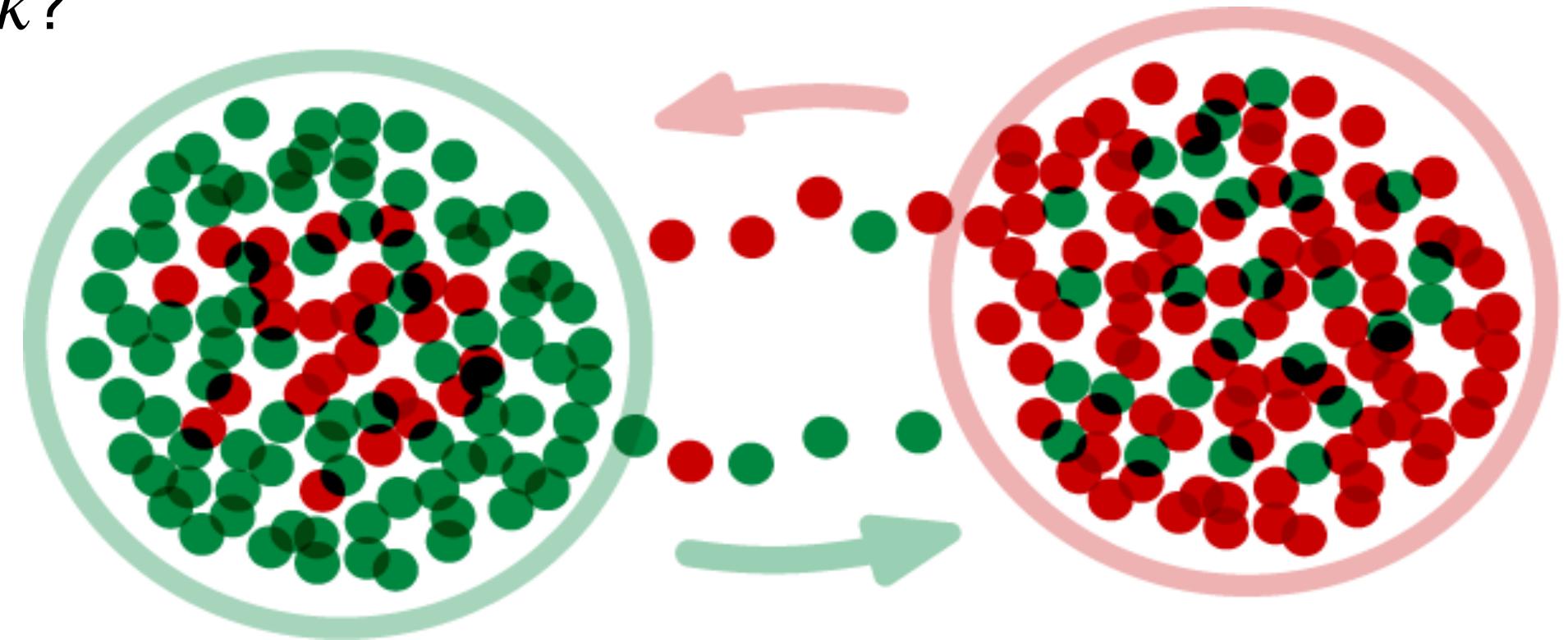


Degree block approximation

What is the total **average traffic** per unit time of populations with degree k ?

$$T_k = k \sum_{k'} P(k'|k) \langle w_{kk'} \rangle$$

$P(k'|k)$: conditional probability for an edge of k to be linked to k'



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

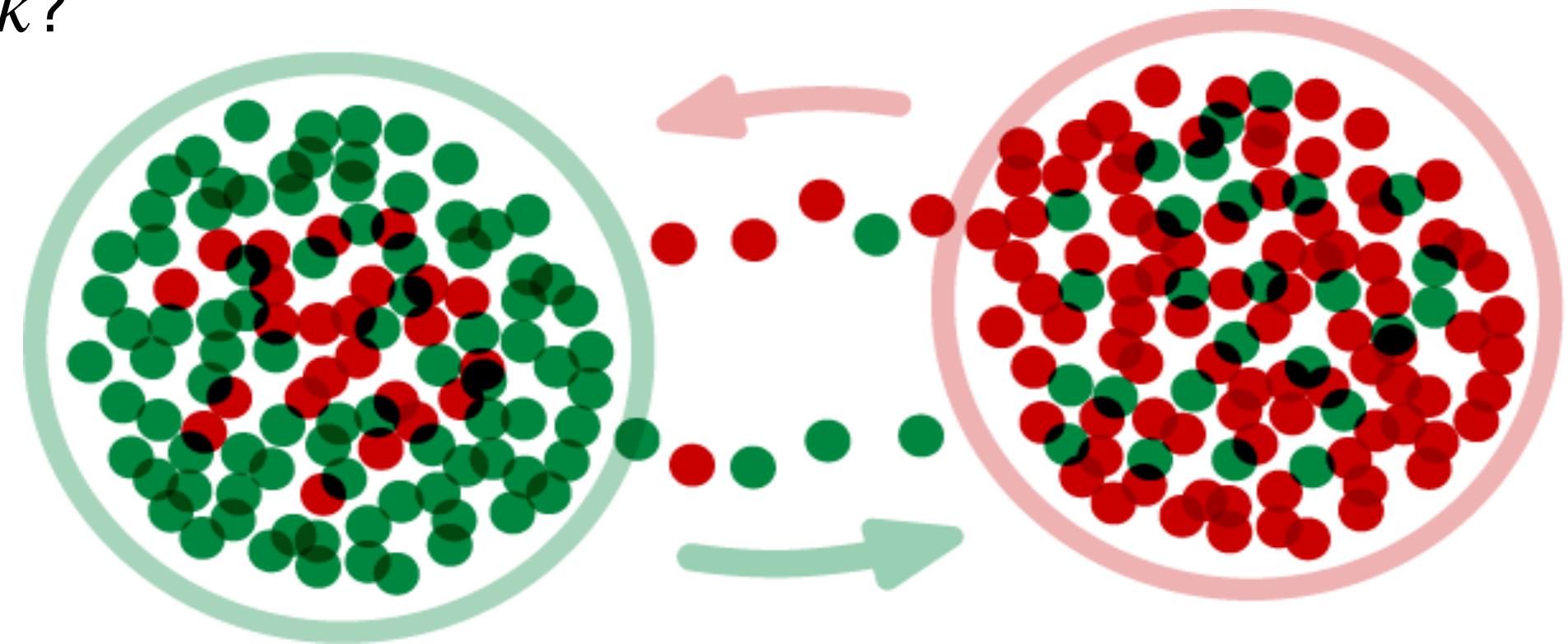
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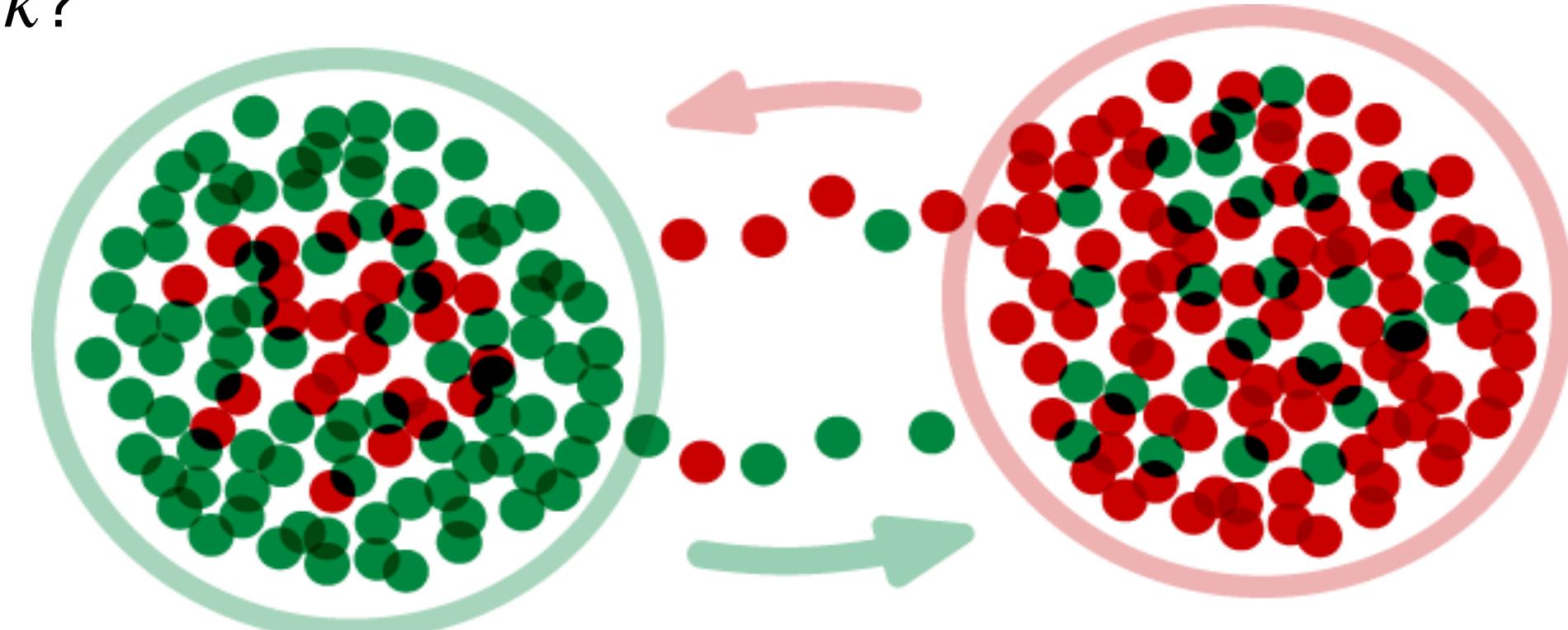
$P(k'|k)$: conditional probability for an edge of k to be linked to k'

In we have an **uncorrelated network**:

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

we can write:

$$T_k = k \sum_{k'} \frac{k' P(k')}{\langle k \rangle} w_0 (kk')^\theta = \frac{k^{1+\theta}}{\langle k \rangle} \sum_{k'} k'^{1+\theta} P(k') w_0$$



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

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

Degree block approximation

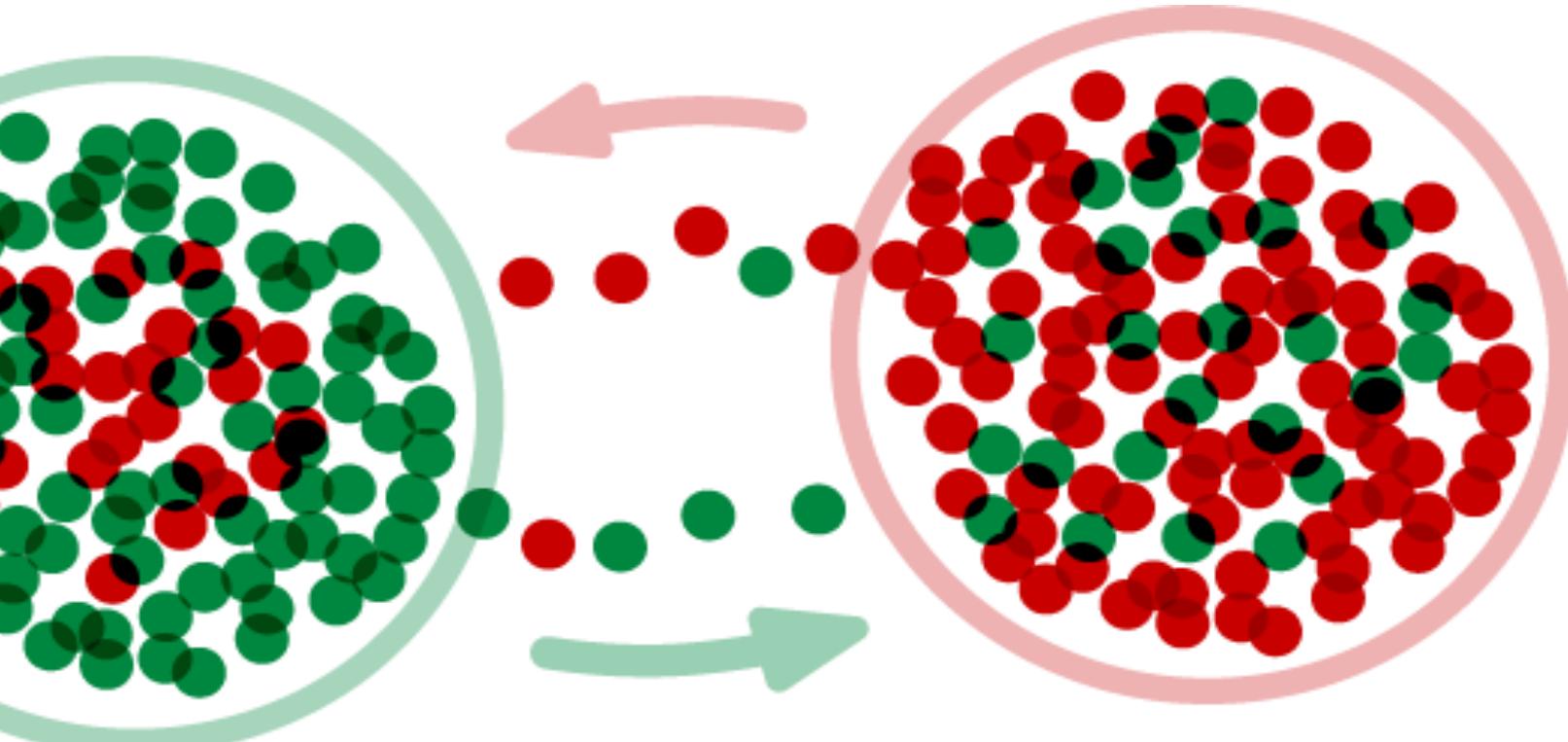
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$$T_k = k \sum_{k'} \frac{k' P(k')}{\langle k \rangle} w_0 (kk')^\theta = \frac{k^{1+\theta}}{\langle k \rangle} \sum_{k'} k'^{1+\theta} P(k') w_0 = \frac{\langle k^{1+\theta} \rangle}{\langle k \rangle} w_0 k^{\theta+1} = A k^{\theta+1}$$

Degree block approximation

Individuals travel from populations of degree k with rate: $p_k = k \sum_{k'} P(k' | k) d_{kk'}$

For a degree-block k , the average population of nodes with degree k is: $N_k = \frac{1}{V_k} \sum_{i|k_i=k} N_i$

The dynamics of individuals can be expressed as:

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

left term: fraction of population leaving nodes of degree k
right term: fraction of population from neighbors moving in

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 parameterization of the **diffusion rate**, $d_{kk'}$ leads to different analytical solutions.

Traffic dependent mobility

The probability of departing from a node does not depend on k , it is a constant $p_k = p$.

Define the diffusion rate $d_{kk'} = p \frac{w_0(kk')^\theta}{T_k}$ Travelers are distributed among links according to the observed flows.

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

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

$$N_k(t) = \frac{w_0}{A \langle k \rangle} \bar{N} k^{1+\theta} \quad \text{where} \quad \bar{N} = \sum_{k'} P(k') N_{k'}(t) \quad \text{repartition of populations dependent on degree}$$

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 $p_k = T_k/N_k$

Define the diffusion rate

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

Travelers are distributed among links according to the populations.

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

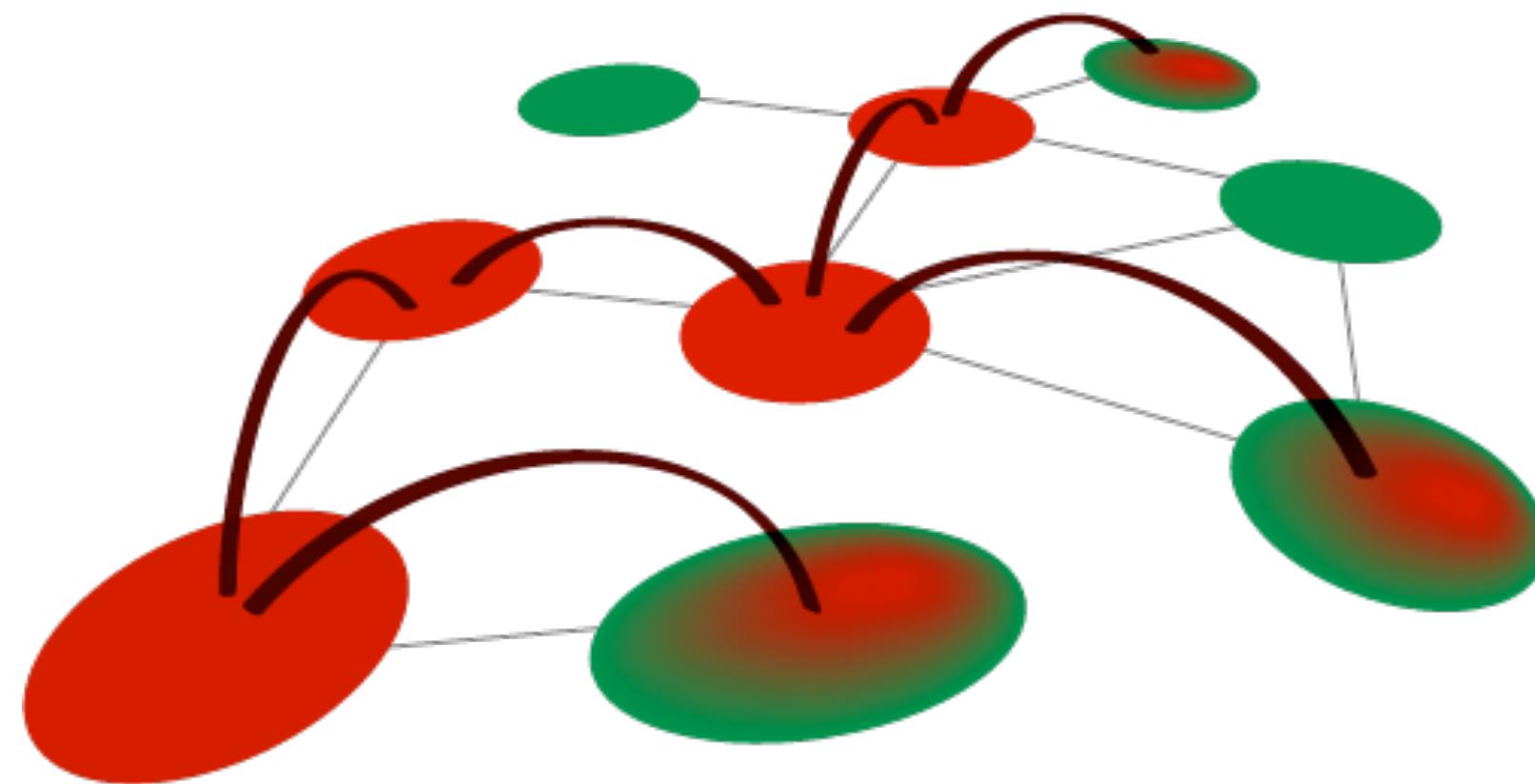
hence

$$\partial_t N_k(t) = -T_k + \frac{\langle k^{1+\theta} \rangle}{\langle k \rangle} w_0 k^{1+\theta} = 0$$

By normalisation
of sum of probs

A population dependent diffusion process does not alter the populations' sizes, which can be given as a parameter of the model.

Global invasion threshold



In each node we consider a SIR model, with parameters β and μ

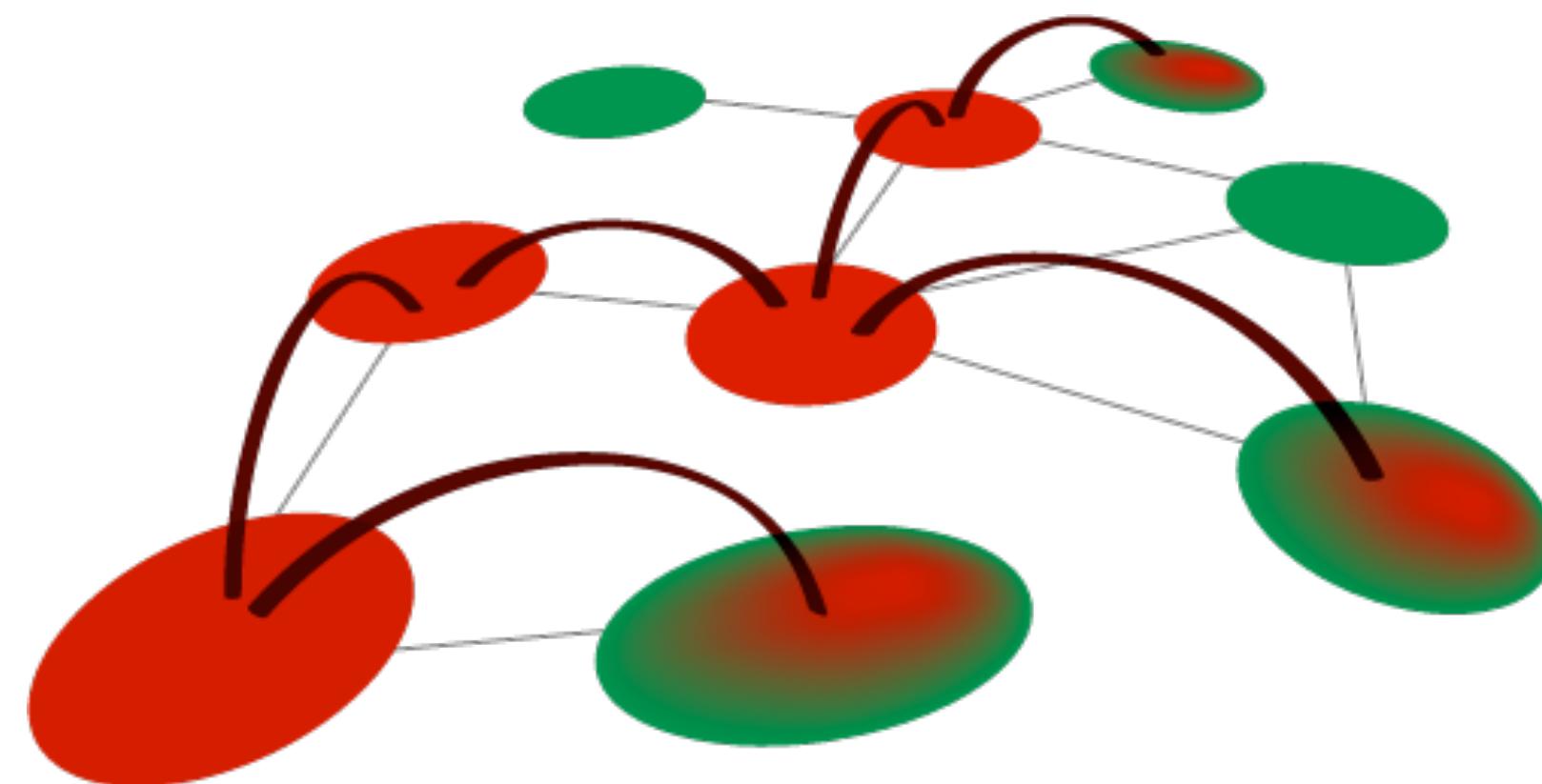
$$\text{The basic reproductive number is then } R_0 = \frac{\beta}{\mu}$$

There is a **local epidemic threshold** $R_0 > 1$ that defines the condition for an outbreak to occur within a node (population)

We look for a **global invasion threshold** that defines the condition for an outbreak to reach a finite portion of the whole system

We solve this for the case of population dependent mobility rates

Global invasion threshold



Branching process: each individual in generation produces some random number of individuals in generation

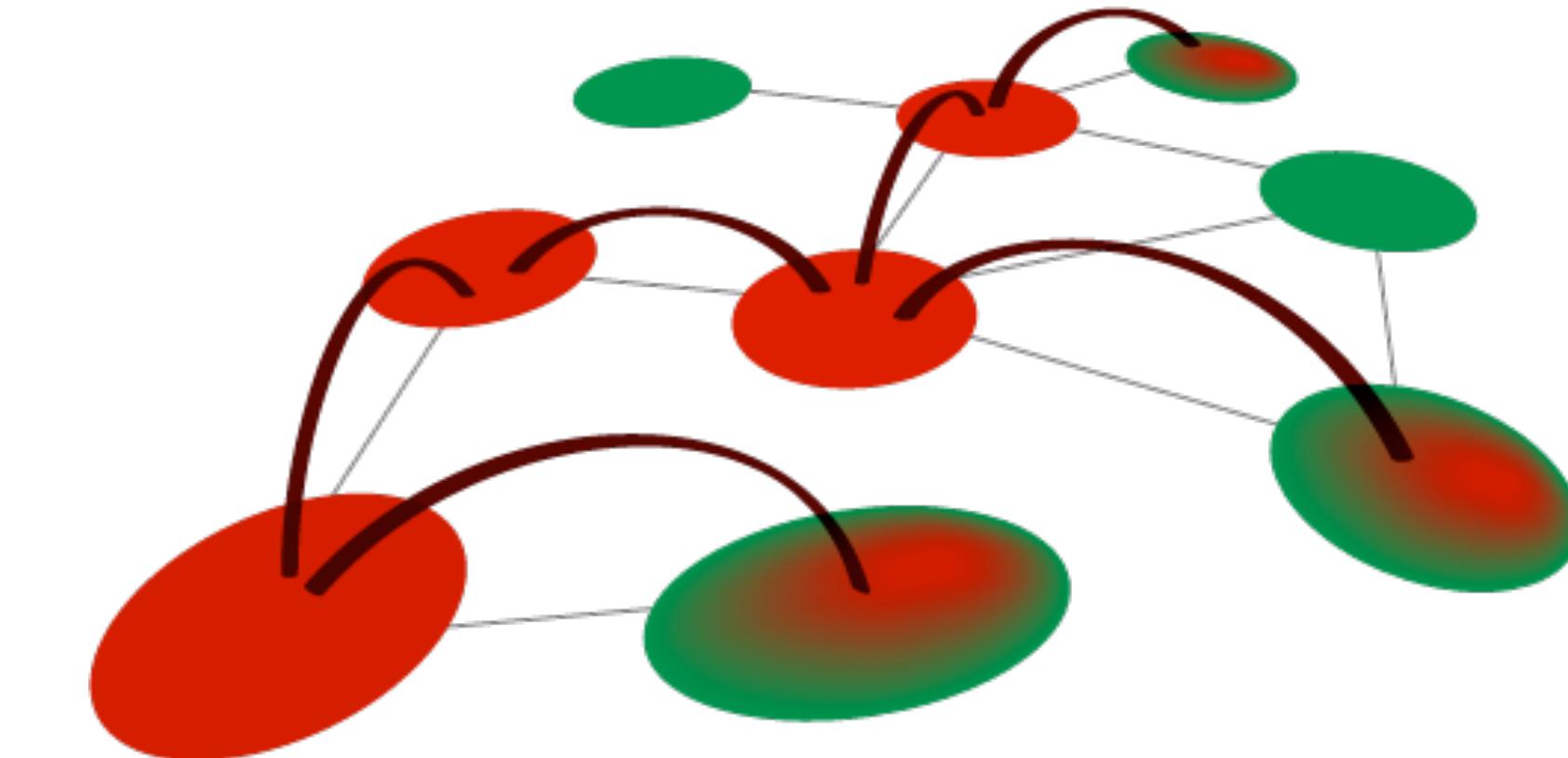
We denote as D_k^0, D_k^1, \dots the number of subpopulations of degree k , that are infected (with at least 1 infected individual) at generation $n=0, 1, \dots$

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

Annotations below the equation:

- A bracket under the term $D_{k'}^{n-1}$ has a red arrow pointing down to the text "Connections k'-k".
- A bracket under the term $P(k | k')(k' - 1)$ has a red arrow pointing down to the text "possible paths of infections".
- A bracket under the term $\left[1 - \frac{1}{R_0^{\lambda_{kk'}}} \right]$ has a red arrow pointing down to the text "density of susceptible".
- A red arrow points from the term $\left[1 - \frac{1}{R_0^{\lambda_{kk'}}} \right]$ to the text "outbreak probability in a node".

Global invasion threshold



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

↓
 Connections
 $k'-k$
 ↓
 possible paths
 of infections
 ↓
 density of
 susceptible

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

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

$$\begin{cases} \lambda_{kk'} = d_{kk'} \frac{\alpha N_k}{\mu} \\ d_{kk'} = \frac{w_0(kk')^\theta}{N_k} \end{cases}$$

Epidemic size in the subpopulation $N_{k'}$
 population dependent mobility rates

$$\lambda_{kk'} = \frac{w_0(kk')^\theta}{N_k} \frac{\alpha N_k}{\mu} = w_0(kk')^\theta \frac{\alpha}{\mu}$$

outbreak probability in
 a node

Global invasion threshold

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

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

For $R_0 \sim 1$ we can expand $(1 - R_0^{-\lambda_{kk'}}) \simeq \lambda_{kk'}(R_0 - 1)$ hence $D_k^n = \sum_{k'} D_{k'}^{n-1} P(k|k')(k' - 1) \lambda_{kk'}(R_0 - 1)$

Now i can make explicit $\lambda_{kk'} = w_0(kk')^\theta \frac{\alpha}{\mu}$, moreover for uncorrelated networks we have $P(k|k') = \frac{kP(k)}{\langle k \rangle}$

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

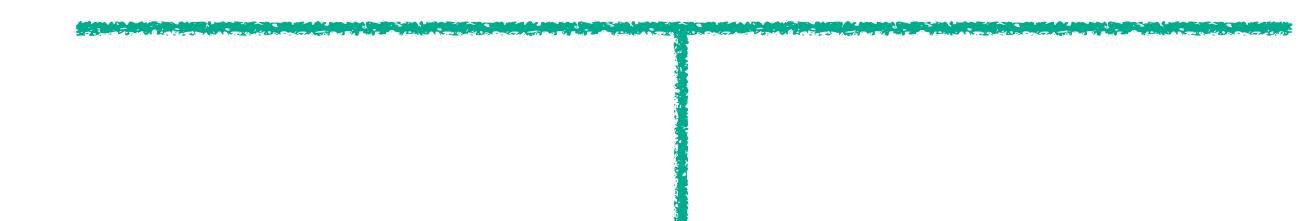
Global invasion threshold

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

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

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

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



Global epidemic threshold > 1

Global invasion threshold

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

Increases with
Network heterogeneity

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

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

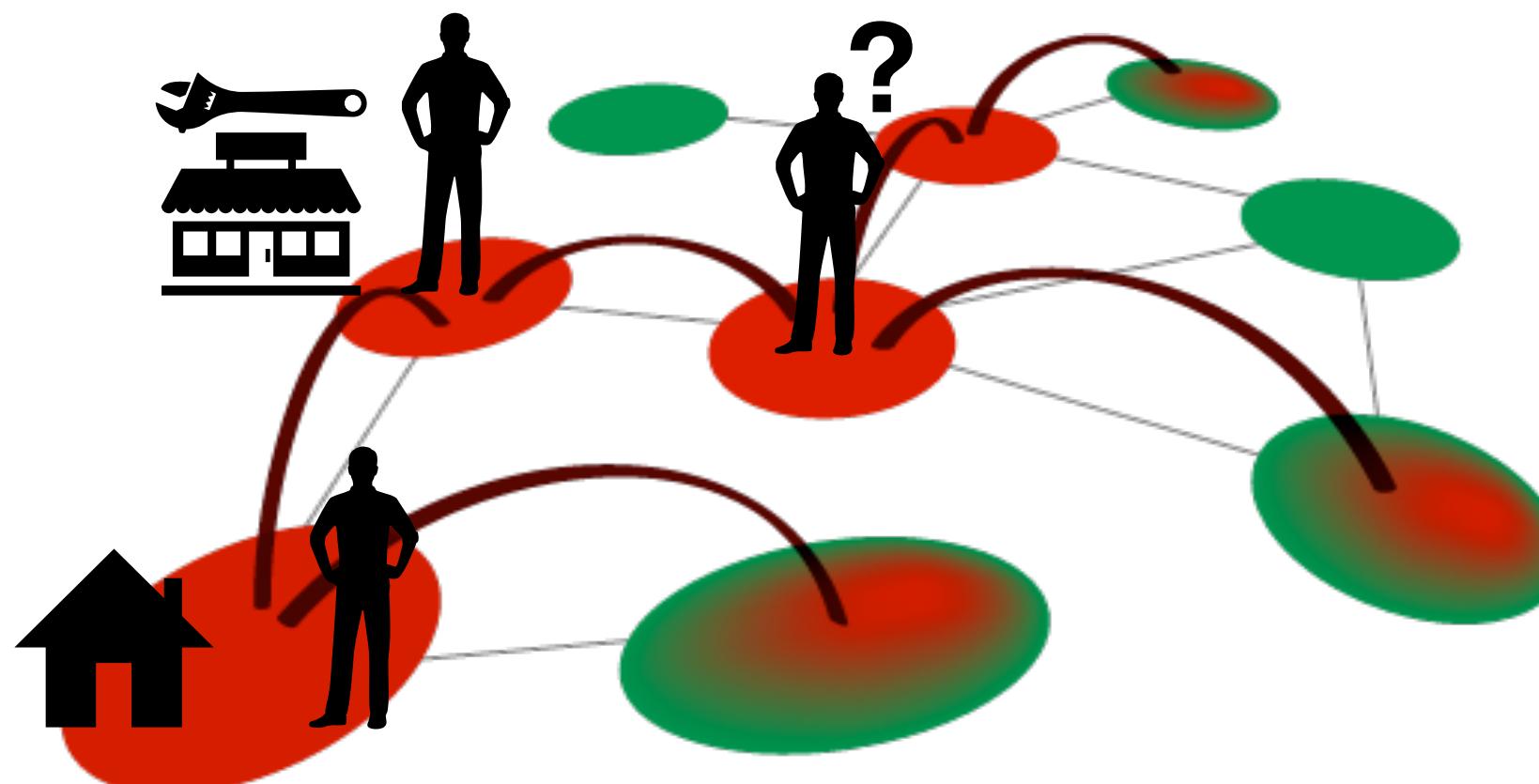
Mobility threshold is lowered
by increasing heterogeneity

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

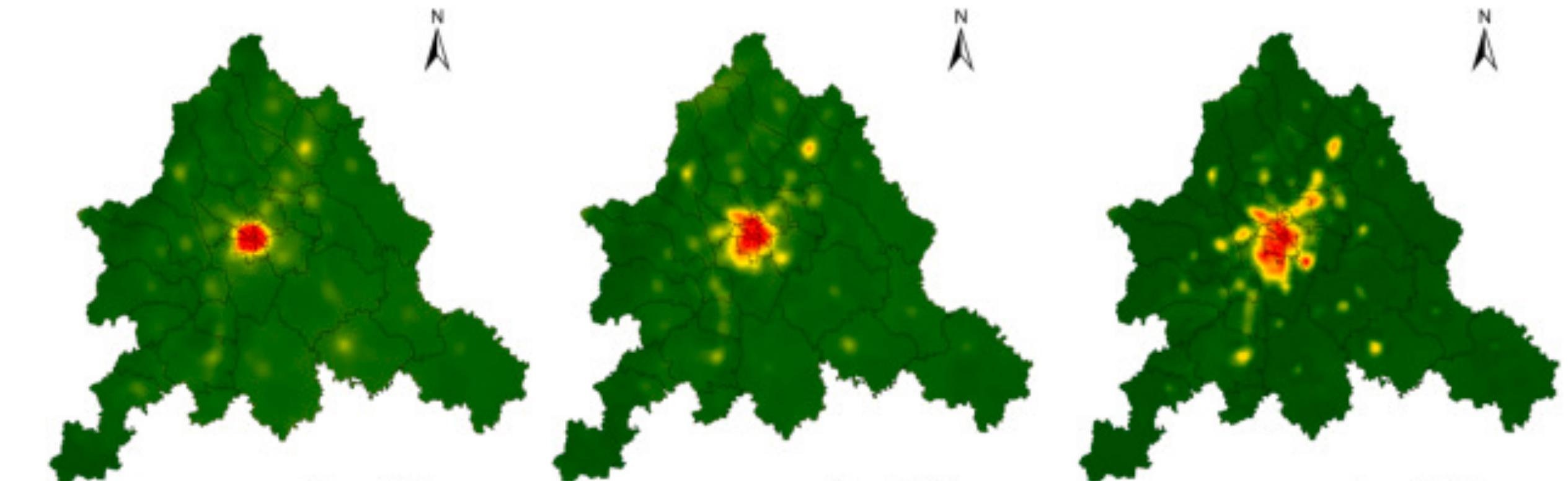
Metapopulation models with markovian mobility

Markovian mobility: individuals move among populations without memory, the probability of moving from i to j depends only on the average flows between i and j

Indistinguishability: individuals are not distinguishable, i.e. not labelled, they do not belong to a patch.
A susceptible in i moving in j might come from anywhere



non-markovianity of mobility impacts invasion threshold



Rvachev-Longini model

Rvachev-Longini model (1985):

first model of global spread using diffusion rates in compartmental models

$x_i(t)$: number of susceptibles in i at time t

$u_i(\tau, t)$: n of exposed in i at time t who were infected at $t-\tau$

$y_i(\tau, t)$: n of infected in i at time who were infected at $t-\tau$

$z_i(t)$: n of recovered in i at time t

$\gamma(\tau)$: incubation period distribution

τ_1 : max of incubation period

$\delta(\tau)$: infectious period distribution

τ_2 : max of infectious period

n : n of populations $p_i(t)$: population of i, preserved

$n[1 + (\tau_1 + 1) + (\tau_2 + 1)]$ ODEs

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τ_2 : max of infectious period

n : n of populations $p_i(t)$: population of i, preserved

$n[1 + (\tau_1 + 1) + (\tau_2 + 1)]$ ODEs

$$x_i(t) + \sum_{\tau=0}^{\tau_1} u_i(\tau, t) + \sum_{\tau=0}^{\tau_2} y_i(\tau, t) + z_i(t) = p_i, \forall t$$

$$x_i(t+1) = \Omega[x_i(t)] - u_i(0, t), \quad (9)$$

$$u_i(\tau+1, t+1) = [1 - \gamma(\tau)] \Omega[u_i(\tau, t)], \quad \tau = 0, 1, \dots, \tau_1 - 1, \quad (10)$$

$$y_i(\tau+1, t+1) = \begin{cases} \gamma(\tau) \Omega[u_i(\tau, t)] + [1 - \delta(\tau)] y_i(\tau, t), & \tau = 0, 1, \dots, \tau_1, \\ [1 - \delta(\tau)] y_i(\tau, t), & \tau = \tau_1 + 1, \tau_1 + 2, \dots, \tau_2 - 1, \end{cases} \quad (11)$$

$$w_i(t+1) = \sum_{\tau=0}^{\tau_1} \gamma(\tau) \Omega[u_i(\tau, t)], \quad (12)$$

Output

$w_i(t)$: new infected on time t

Rvachev-Longini model

Rvachev-Longini model (1985):

first model of global spread using diffusion rates in compartmental models

σ_{ij} : $n \times n$ matrix of trips from i to j (symmetric!)

$p_i(t)$: population of i , preserved

$$x_i(t+1) = \Omega[x_i(t)] - u_i(0, t), \quad (9)$$

$$u_i(\tau+1, t+1) = [1 - \gamma(\tau)] \Omega[u_i(\tau, t)], \quad \tau = 0, 1, \dots, \tau_1 - 1, \quad (10)$$

$$y_i(\tau+1, t+1) = \begin{cases} \gamma(\tau) \Omega[u_i(\tau, t)] + [1 - \delta(\tau)] y_i(\tau, t), & \tau = 0, 1, \dots, \tau_1, \\ [1 - \delta(\tau)] y_i(\tau, t), & \tau = \tau_1 + 1, \tau_1 + 2, \dots, \tau_2 - 1, \end{cases} \quad (11)$$

Transport operator

$$\Omega[A_i(t)] = A_i(t) + \sum_{j=1}^n \left[A_j \frac{\sigma_{ji}}{p_j} - A_i \frac{\sigma_{ij}}{p_i} \right]$$

travel rates

$$w_i(t+1) = \sum_{\tau=0}^{\tau_1} \gamma(\tau) \Omega[u_i(\tau, t)], \quad (12)$$

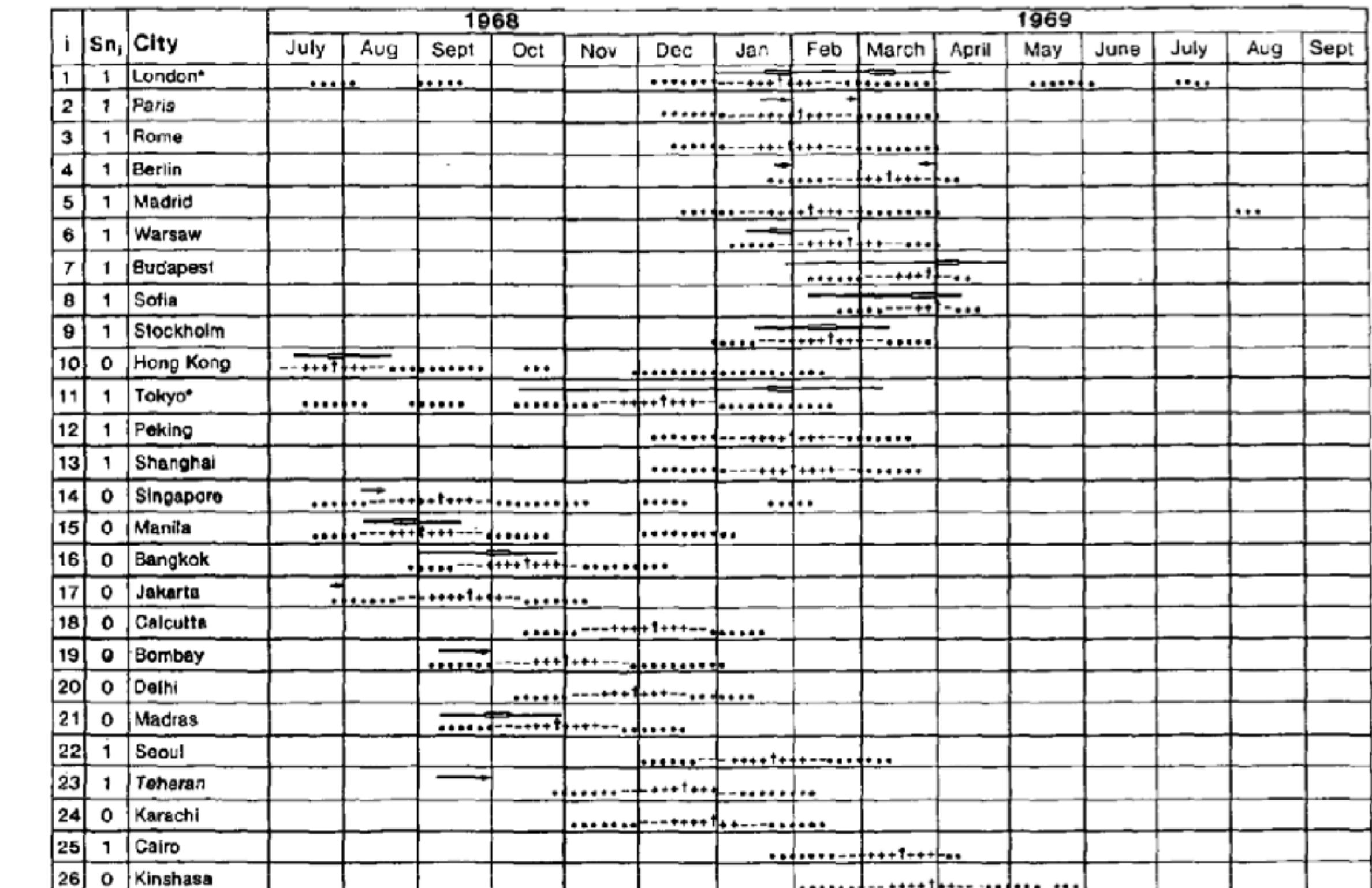
Rvachev-Longini model

Rvachev-Longini model (1985):

first model to introduce diffusion rates in compartmental models

Very complex model, high n of ODEs

Fitted very well the intensity of influenza pandemic of 1968-69 from Hong Kong in 52 cities of the world



* Empirical data are joint with the surrounding region.

FIG. 1. A schematic plot of the forecasted $b(t)$ and actual $a(t)$ course of the 1968-1969 influenza pandemic. Each of the following symbols represents the daily forecasted morbidity incidence per 10^5 over four calendar days: ● for $b_i(t) < 10$, - for $10 \leq b_i(t) \leq 100$, + for $100 > b_i(t)$, and † when the peak in morbidity occurred during the four days indicated. When a symbol falls directly on a border between months, this indicates two days in each month.

Simpler deterministic approach

$$\begin{cases} \frac{dS_i}{dt} = -\beta \frac{S_i I_i}{N_i} + \langle \Omega_i(S) \rangle \\ \frac{dI_i}{dt} = \beta \frac{S_i I_i}{N_i} - \mu I_i + \langle \Omega_i(S) \rangle \\ \frac{dR_i}{dt} = \mu I_i + \langle \Omega_i(S) \rangle \end{cases}$$

Encodes the average behavior
Transport operator is averaged

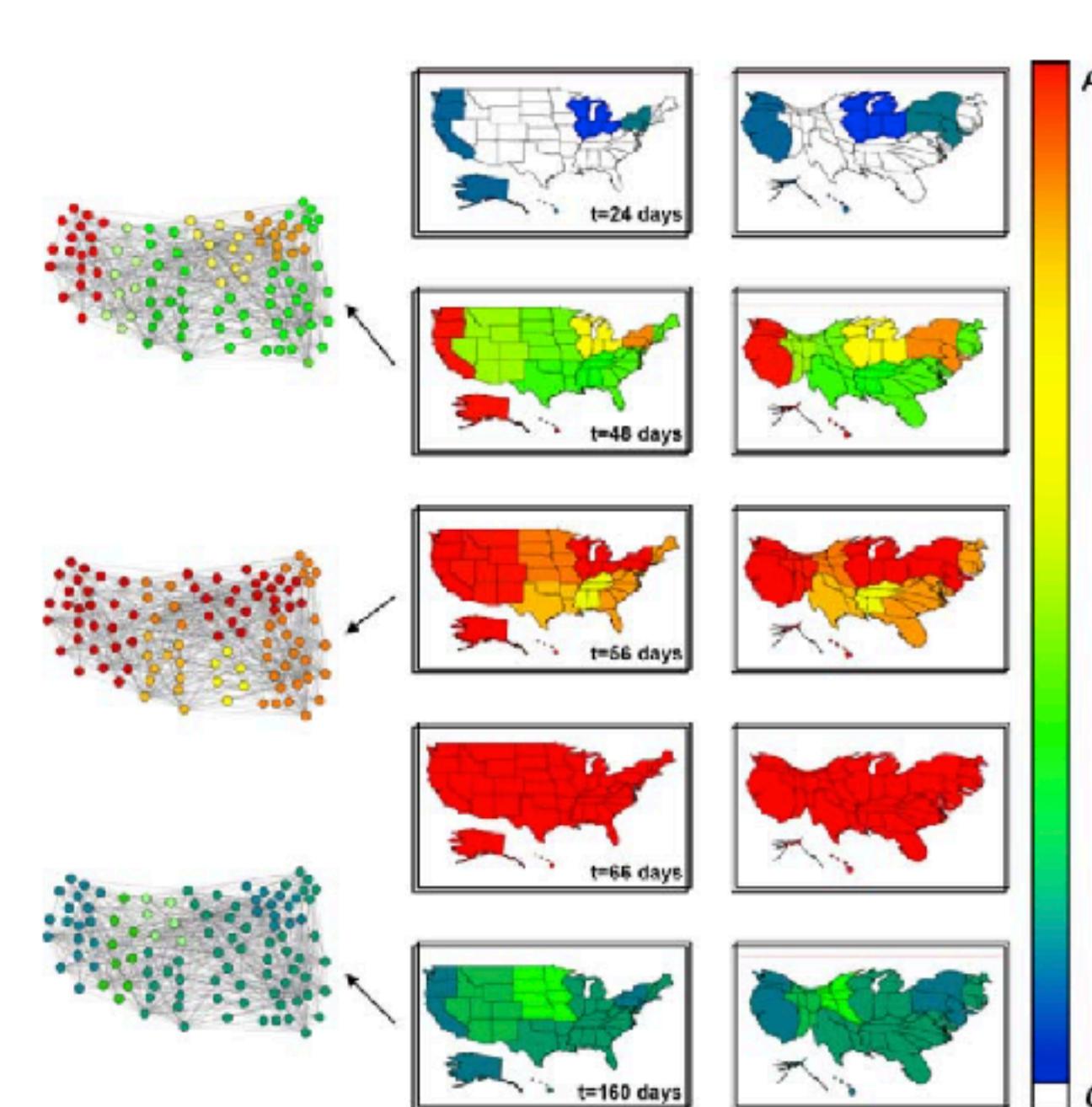


Fig. 4 Geographical representation of the evolution in the US of the SIR epidemic specified in the text with Hong Kong as initial seed. States are grouped according to the nine influenza surveillance regions. The color code corresponds to the prevalence in each region, from 0 to the maximum value reached (ρ_{max}). The first set of maps provides the original US maps, while the second shows the corresponding cartograms obtained by rescaling each region according to its population (Gastner and Newman, 2004). Three representations of the airport network restricted to the United States are also shown, corresponding to three different snapshots of the epidemic diffusion. For the sake of visualization, only the 100 airports with largest traffic in the US are shown, however the data have been obtained by using the full data set including 3100 airports. The color code is the same adopted for the maps.

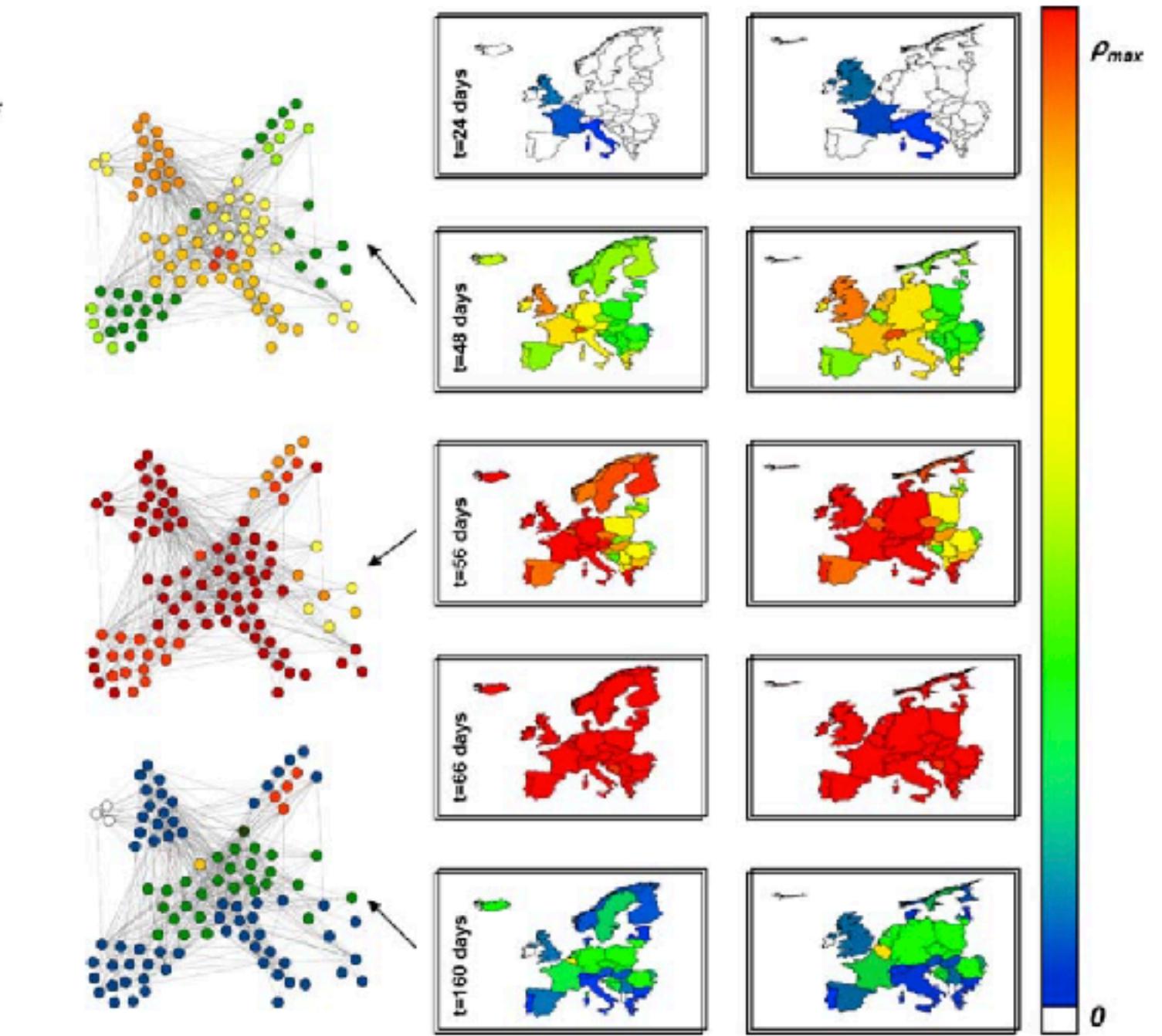


Fig. 5 Geographical representation of the evolution in Europe of the SIR epidemics starting in Hong Kong. The color code corresponds to the prevalence in each European country, from 0 to the maximum value reached (ρ_{max}). The first set of maps provides the original maps of Europe, while the second shows the corresponding cartograms obtained by rescaling each country according to its population (Gastner and Newman, 2004). Three representations of the airport network restricted to Europe are also shown, corresponding to three different snapshots of the epidemic diffusion. For the sake of visualization, only the 100 airports with largest traffic in Europe are shown, however the data have been obtained by using the full data set including 3100 airports. The color code is the same adopted for the maps.

Simpler deterministic approach

$$\begin{cases} \frac{dS_i}{dt} = -\beta \frac{S_i I_i}{N_i} + \langle \Omega_i(S) \rangle \\ \frac{dI_i}{dt} = \beta \frac{S_i I_i}{N_i} - \mu I_i + \langle \Omega_i(S) \rangle \\ \frac{dR_i}{dt} = \mu I_i + \langle \Omega_i(S) \rangle \end{cases}$$

Hands on session

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Notebook:
[**metapopulation_deterministic.ipynb**](#)