The physics of epidemics spreading

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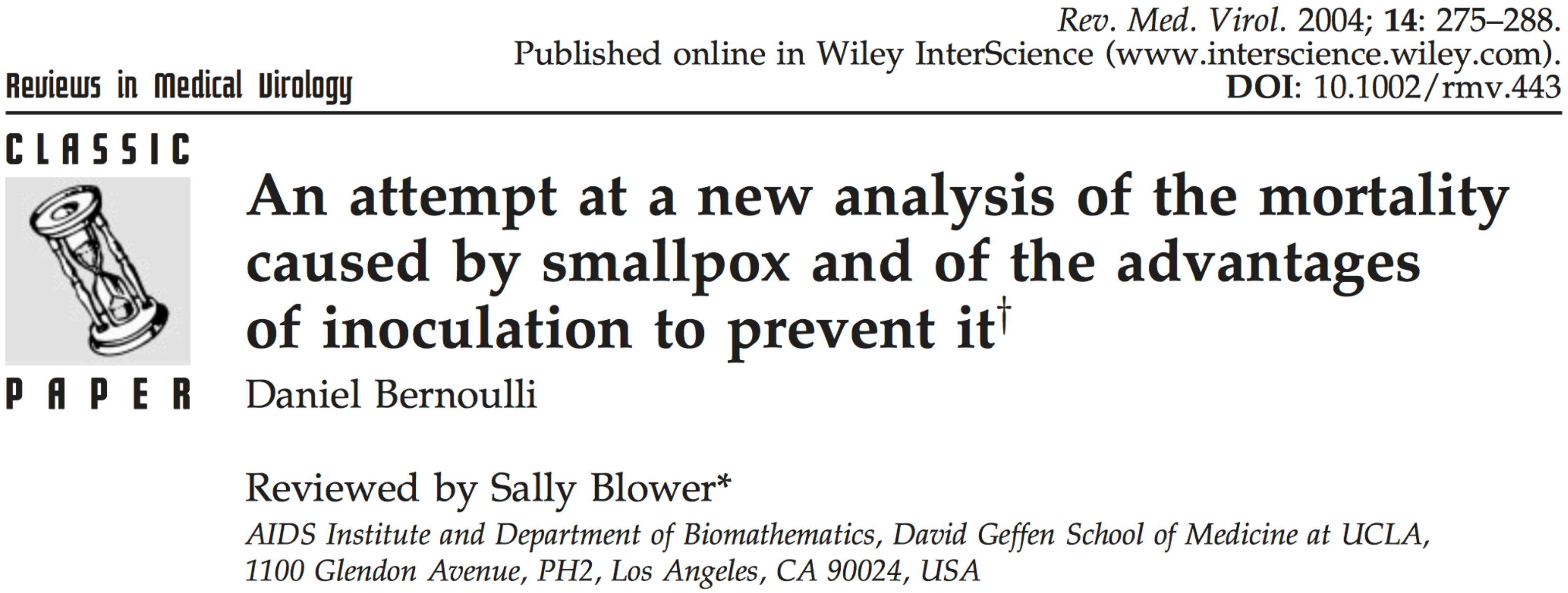
UNIVERSITAT ROVIRA i VIRGILI

Daniel Bernoulli 1700-1782

First mathematical epidemic model
Mem Math Phy Acad Roy Sci Paris 1766



Rev. Med. Virol. 2004; **14**: 275–288.
Published online in Wiley InterScience (www.interscience.wiley.com).
DOI: 10.1002/rmv.443

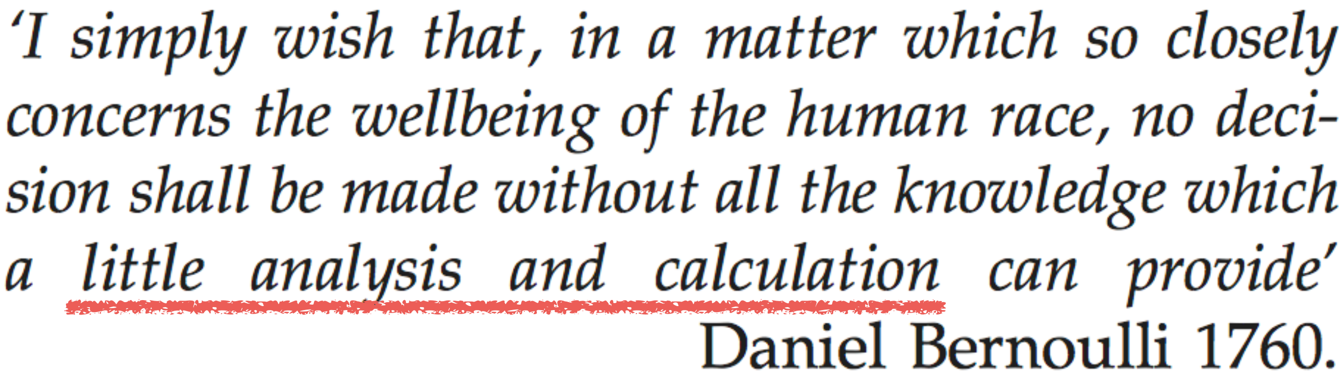
Reviews in Medical Virology

CLASSIC PAPER

An attempt at a new analysis of the mortality caused by smallpox and of the advantages of inoculation to prevent it[†]

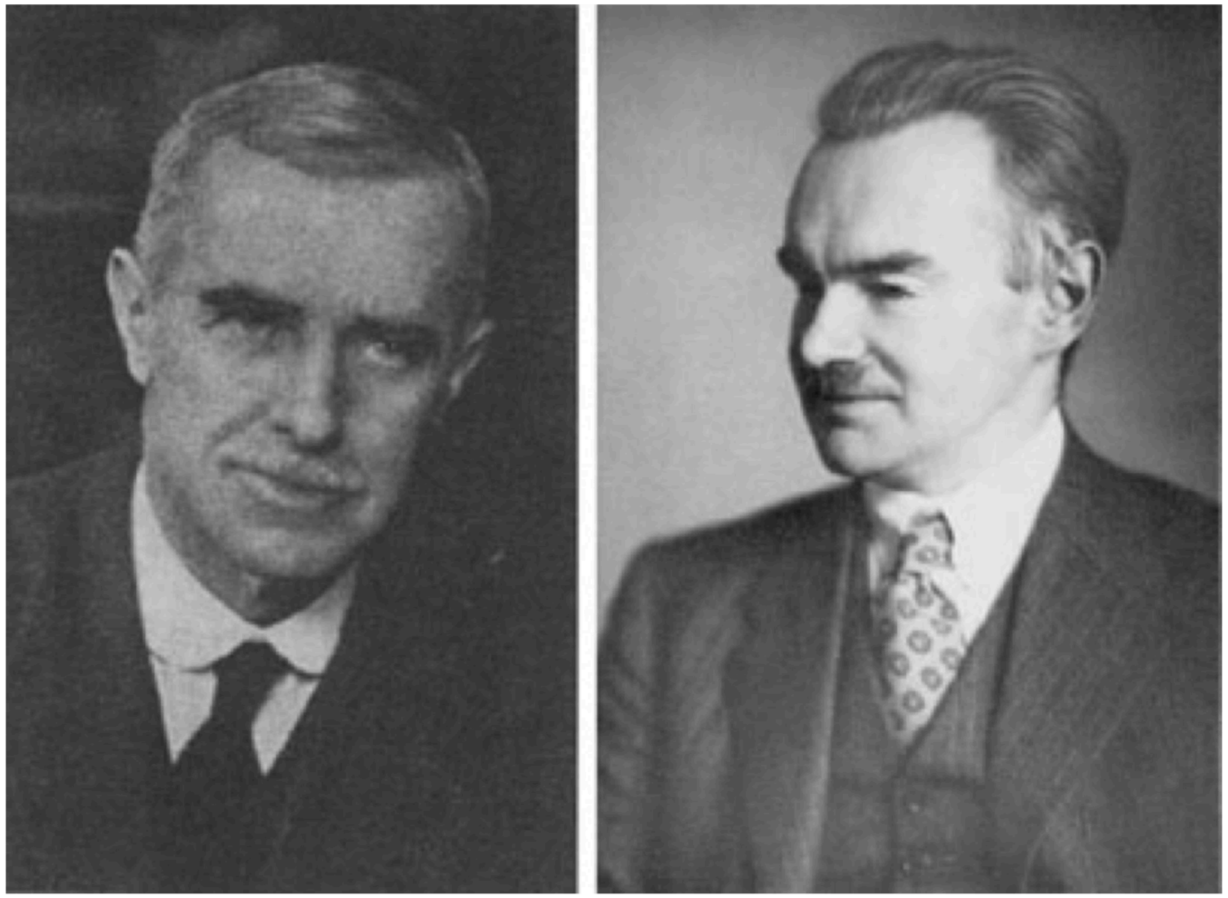
Daniel Bernoulli

Reviewed by Sally Blower*
AIDS Institute and Department of Biomathematics, David Geffen School of Medicine at UCLA, 1100 Glendon Avenue, PH2, Los Angeles, CA 90024, USA



'I simply wish that, in a matter which so closely concerns the wellbeing of the human race, no decision shall be made without all the knowledge which a little analysis and calculation can provide'
Daniel Bernoulli 1760.

150 years later … statistical physics started to shape the story of epidemic modelling



McKendrick and Kermack

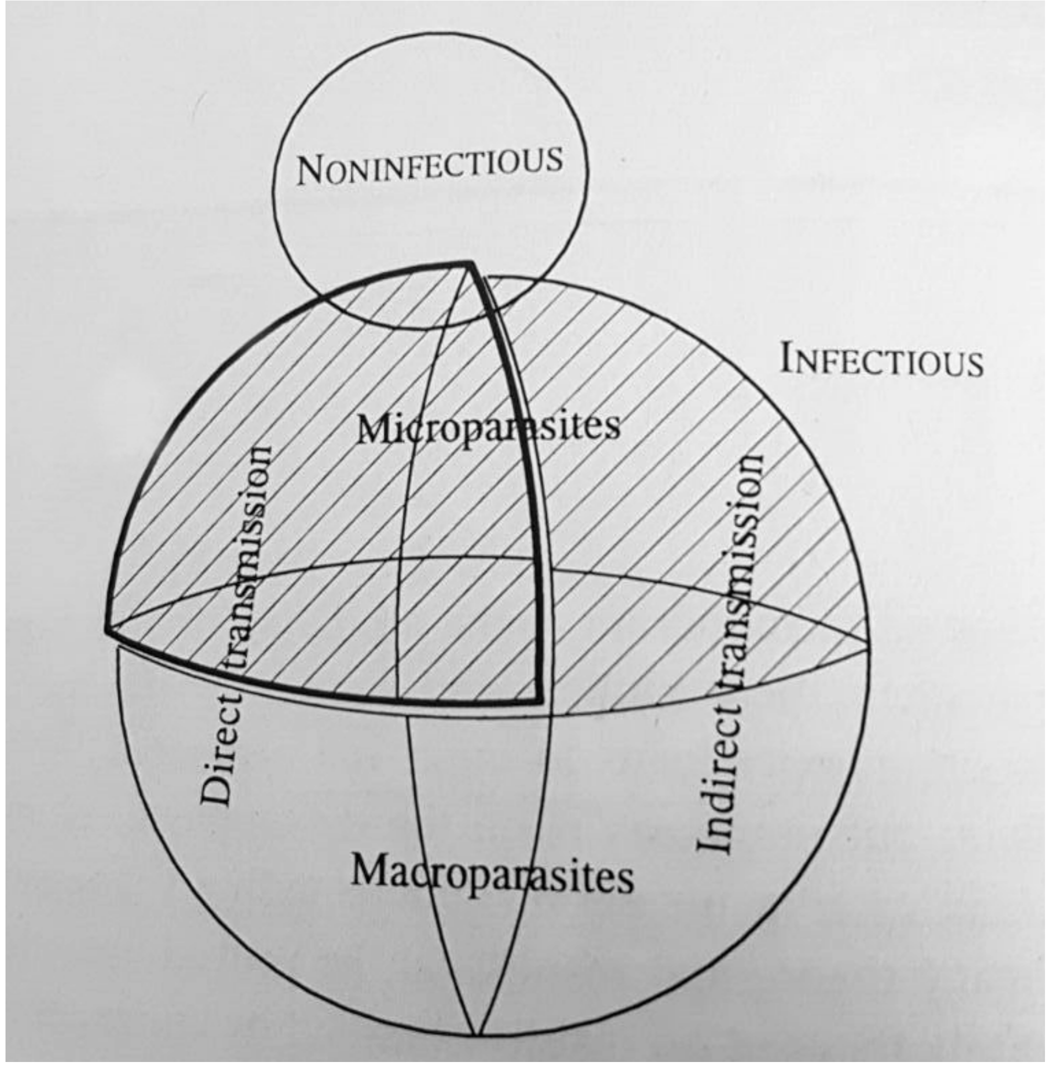
Essentially, they introduce the “Law of mass-action” in epidemic modelling

$$S + I \xrightarrow{\beta} I + I$$
$$I \xrightarrow{\mu} S$$

Scope: types of disease

- **Noninfectious diseases**: developed during an individual lifespan (e.g. arthritis)
  - Epidemiology: study of risk factors associated with the chance of developing the disease.

- **Infectious diseases**: can be passed between individuals (humans, animals, plants)
  - Epidemiology: the main risk factor is the presence of infectious cases in the local population.



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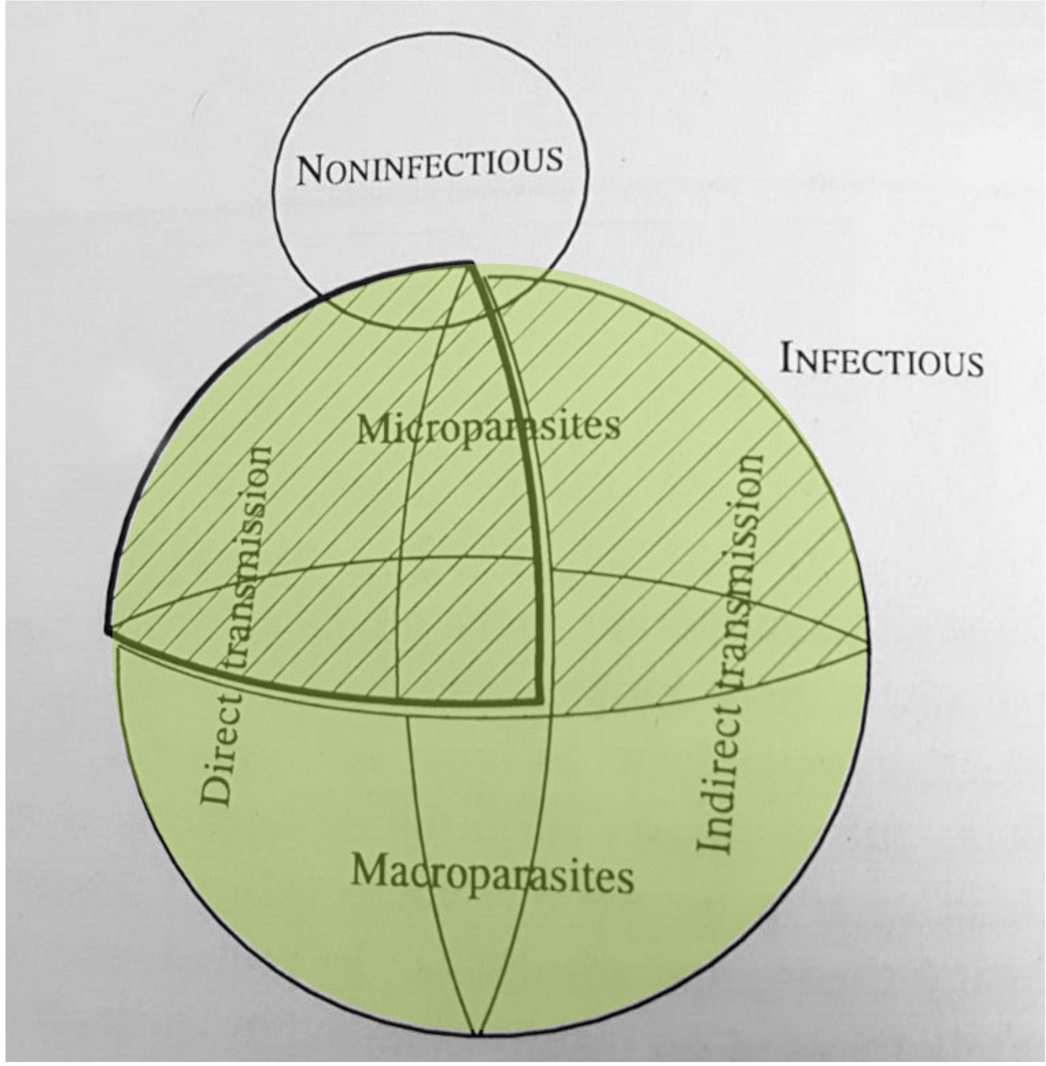
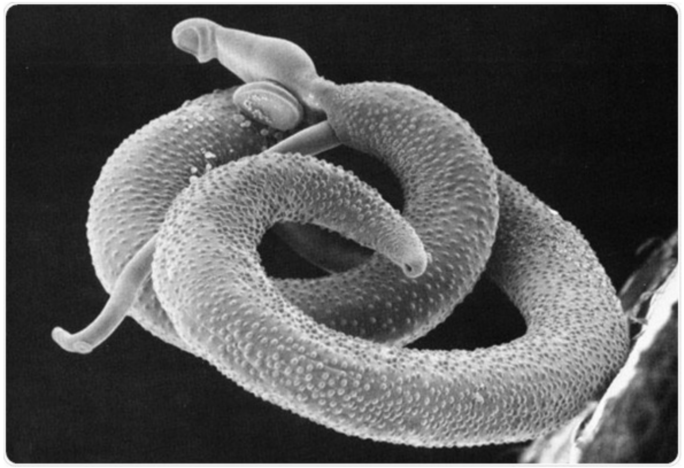
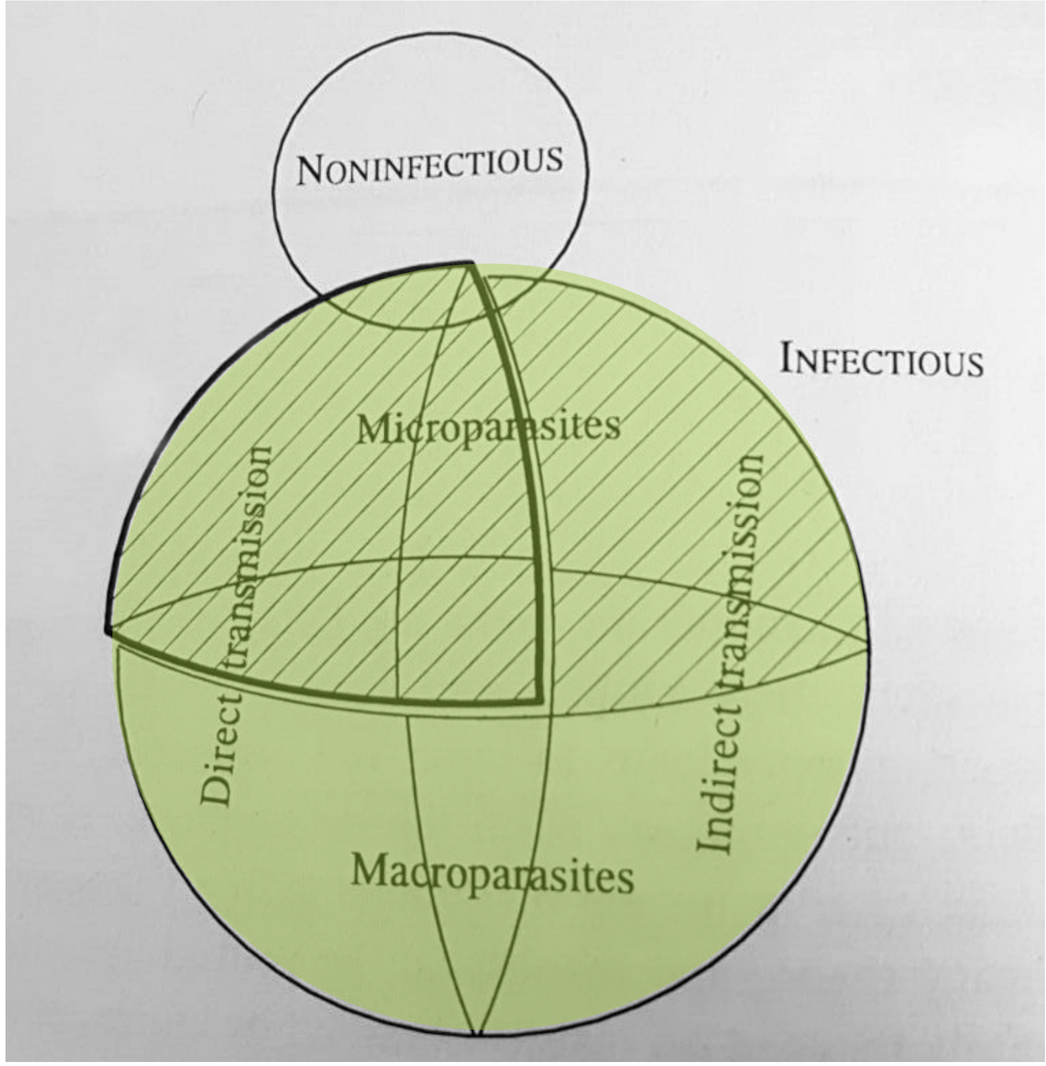


Scope: types of disease

- **Microparasites**: small, single-cell. Viruses, bacteria, protozoa.

- **Macroparasites**: bigger. Helminths and flukes.





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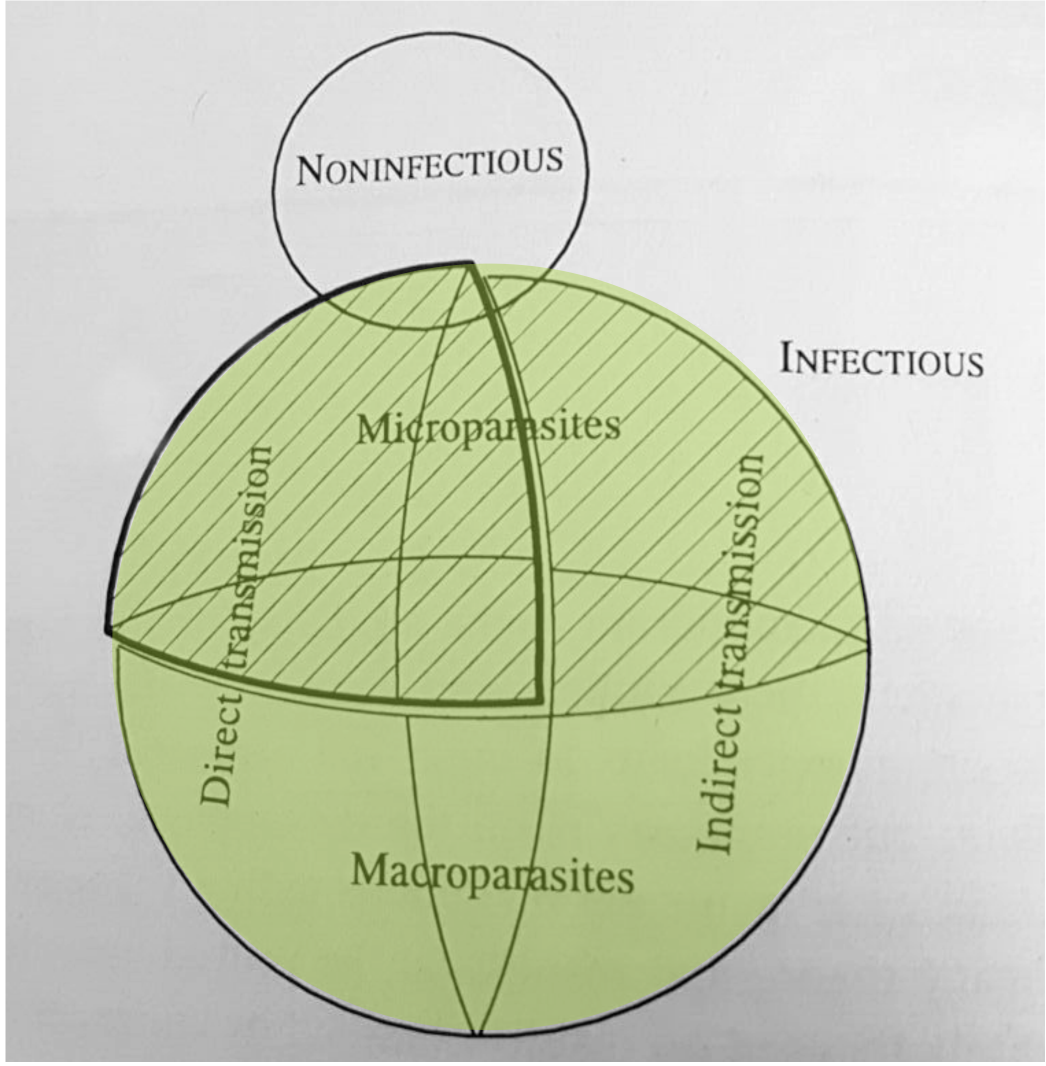
  - On the other hand, macroparasites have a complex life cycle within the host that needs to be modeled explicitly.



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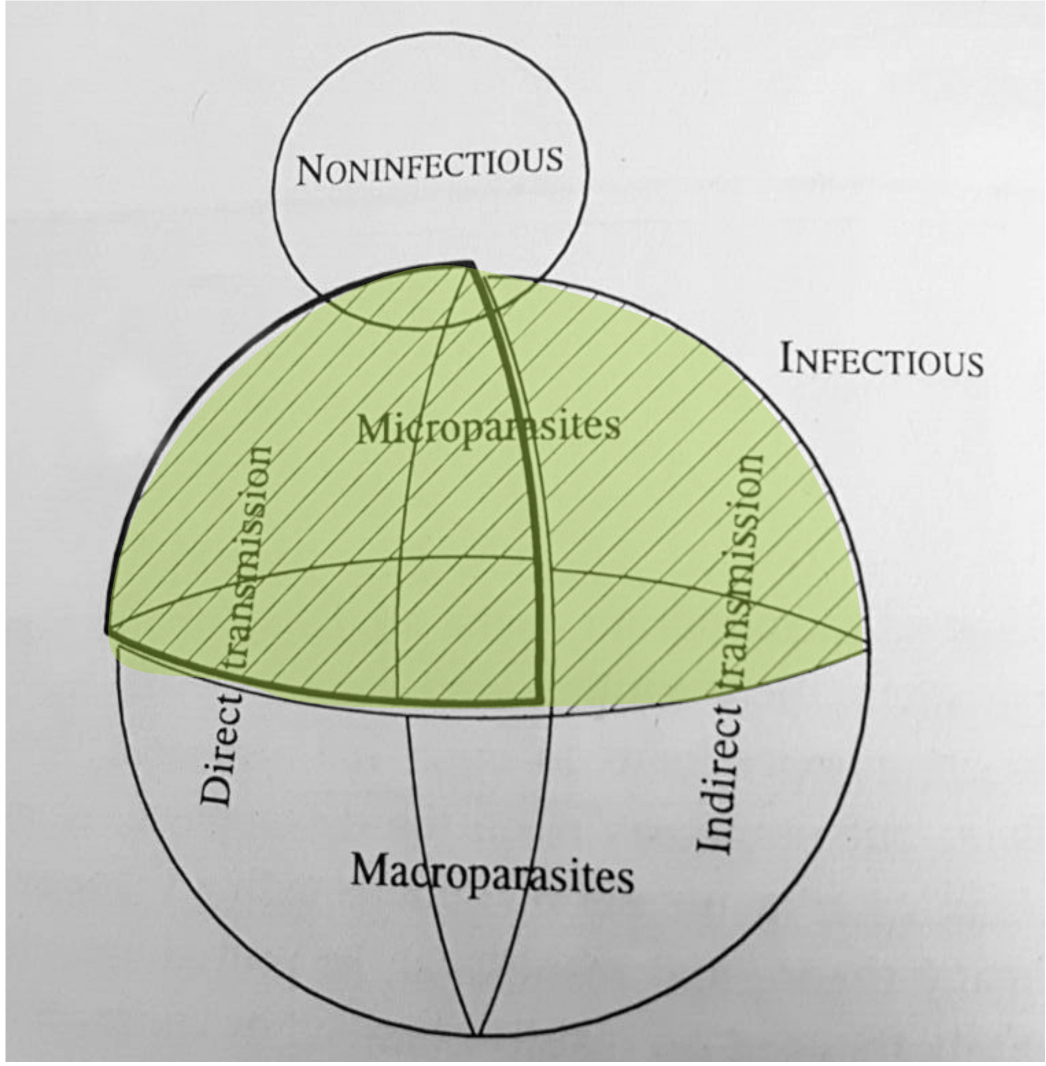
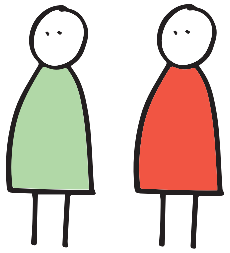
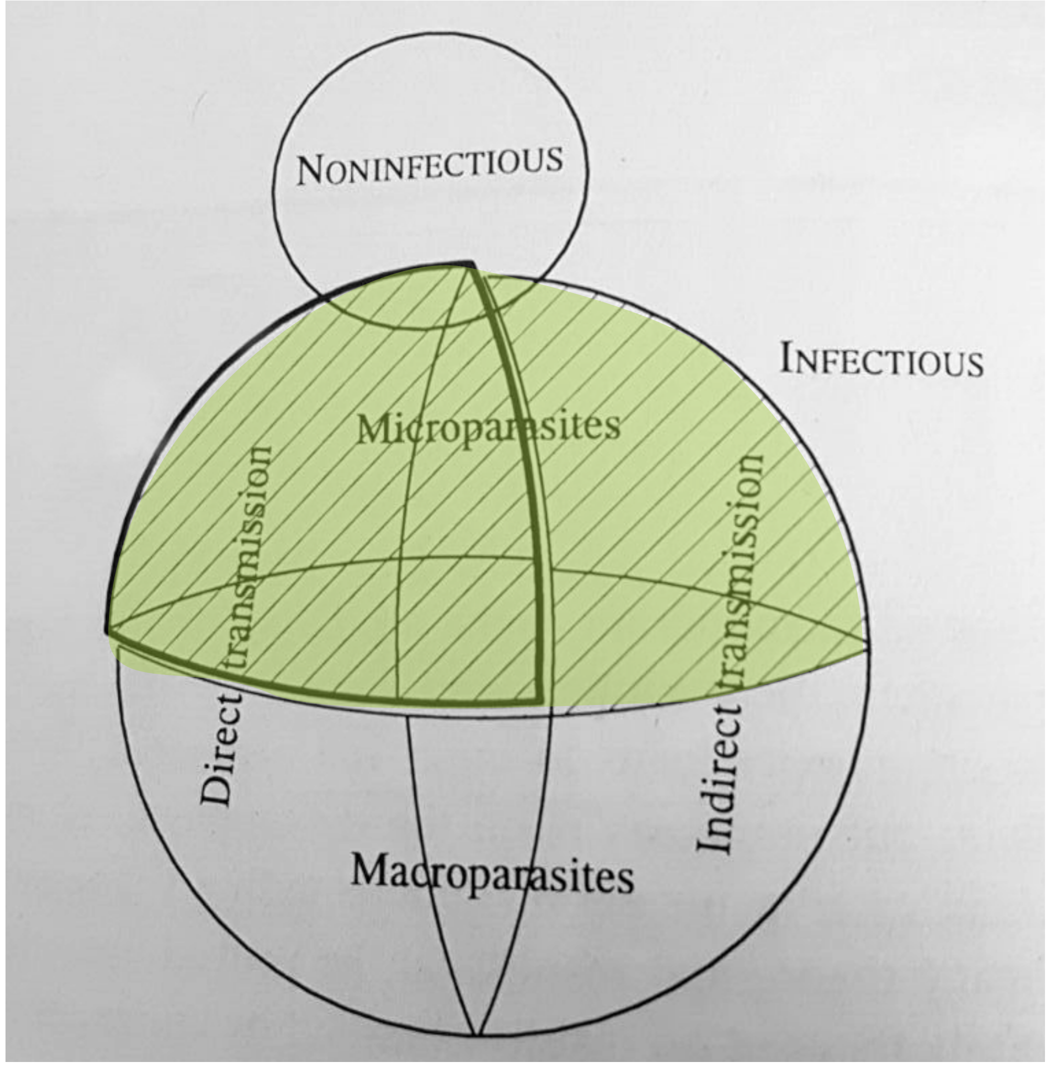


Scope: types of disease

- **Direct transmission**: there is direct physical contact between subjects exposed to the disease.



- **Indirect transmission**: the transmission of the disease among subjects is done by a third agent. Vectors. Eg. mosquitoes



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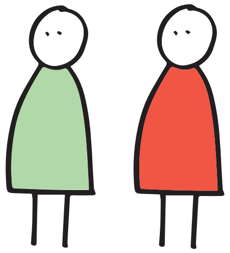

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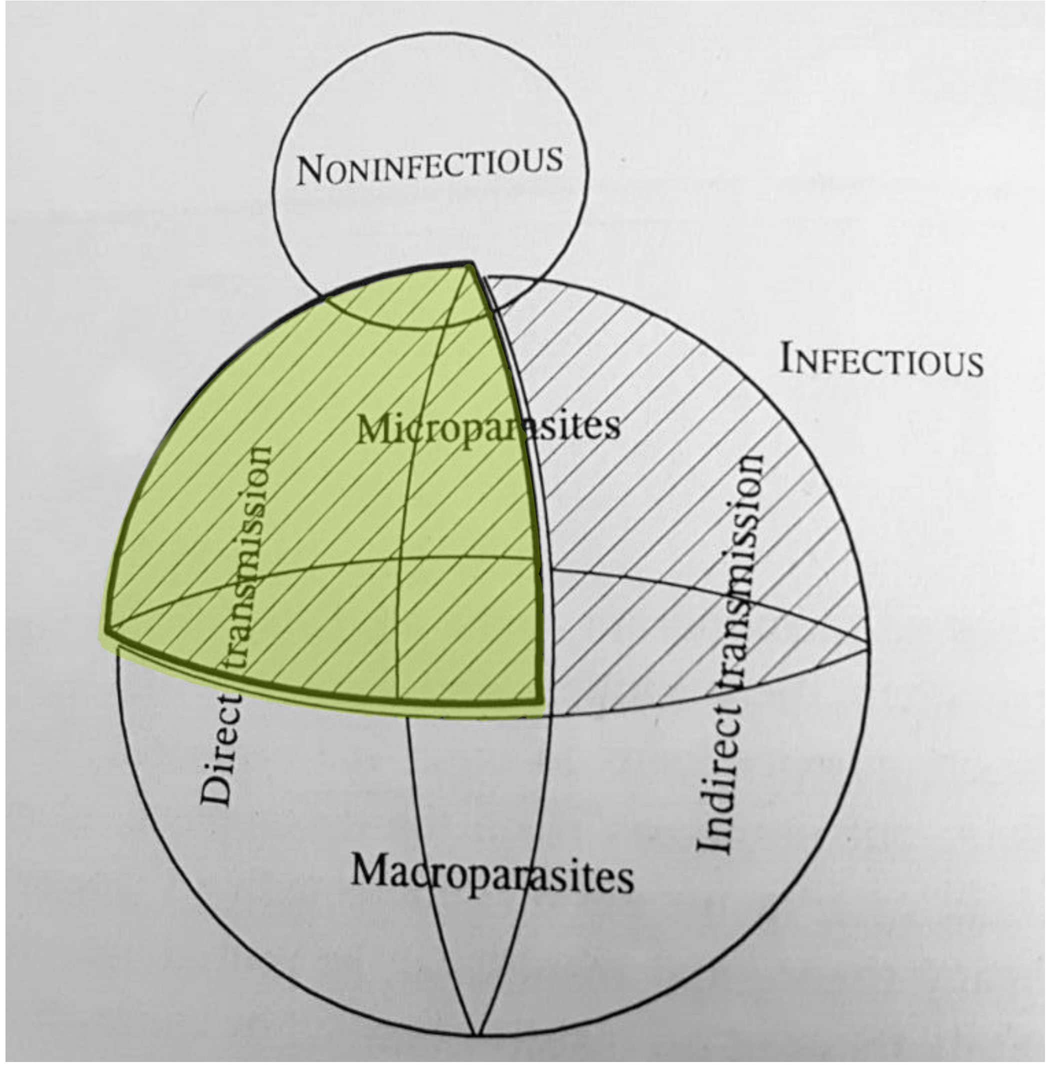

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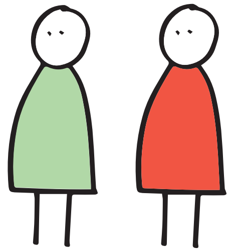
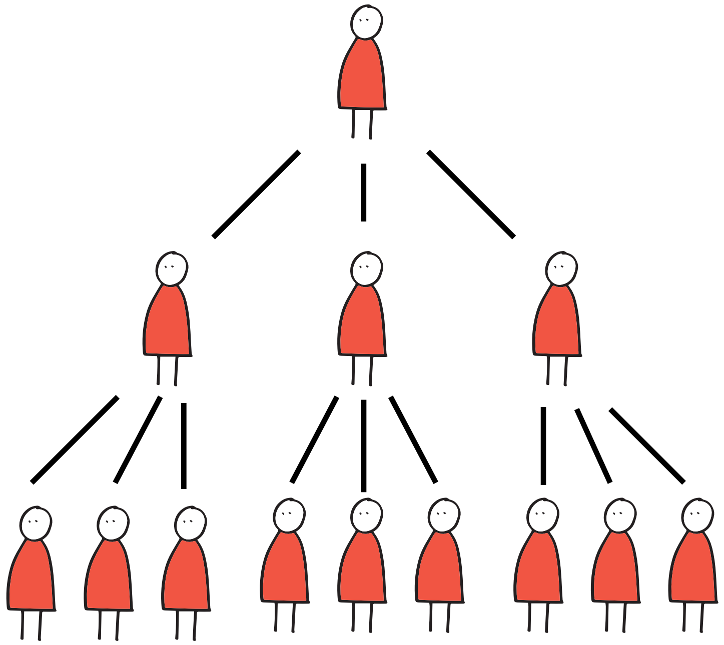


Basic reproduction number R: the expected number of cases directly generated by one case in a population where all individuals are susceptible to infection



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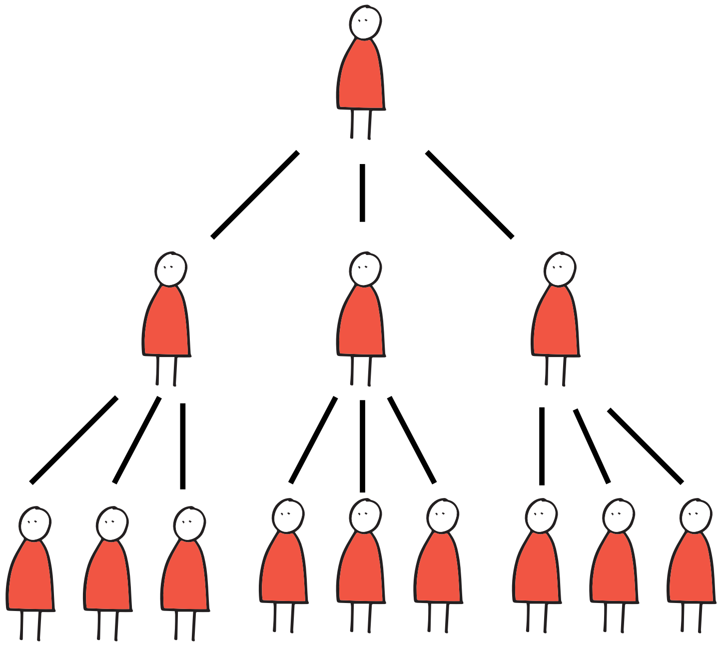

	R~1.4	R~2.0	R~3.0
DAY	INFLUENZA	EBOLA	COVID
1	2	3	4
2	5	8	14
3	12	20	46
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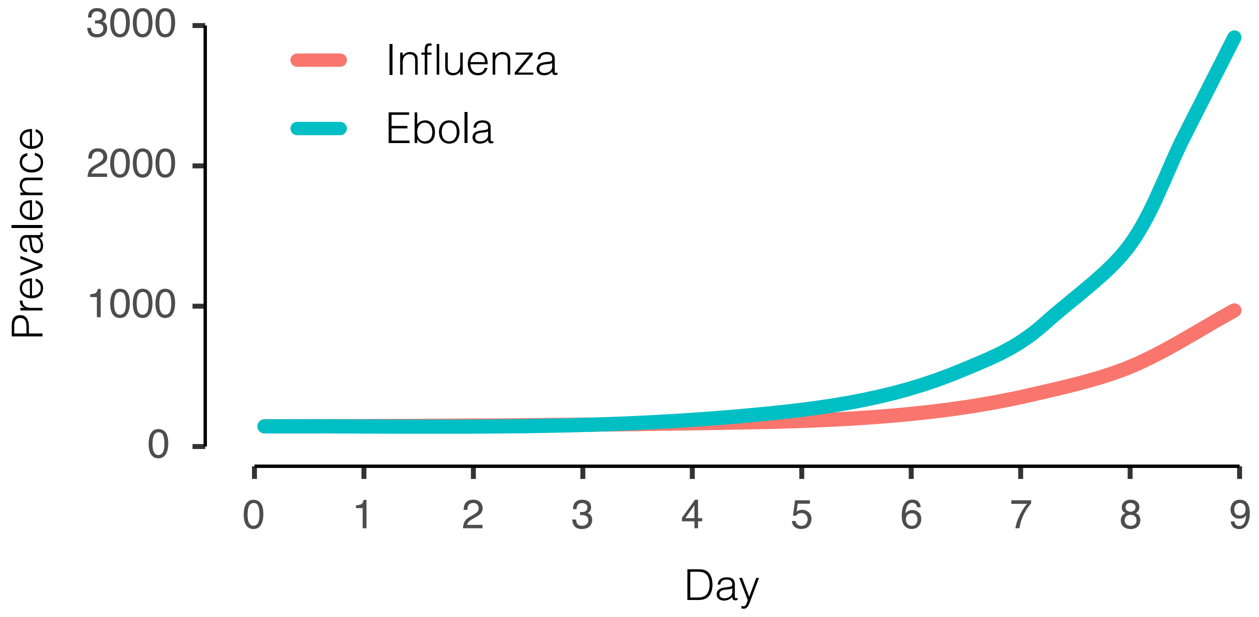

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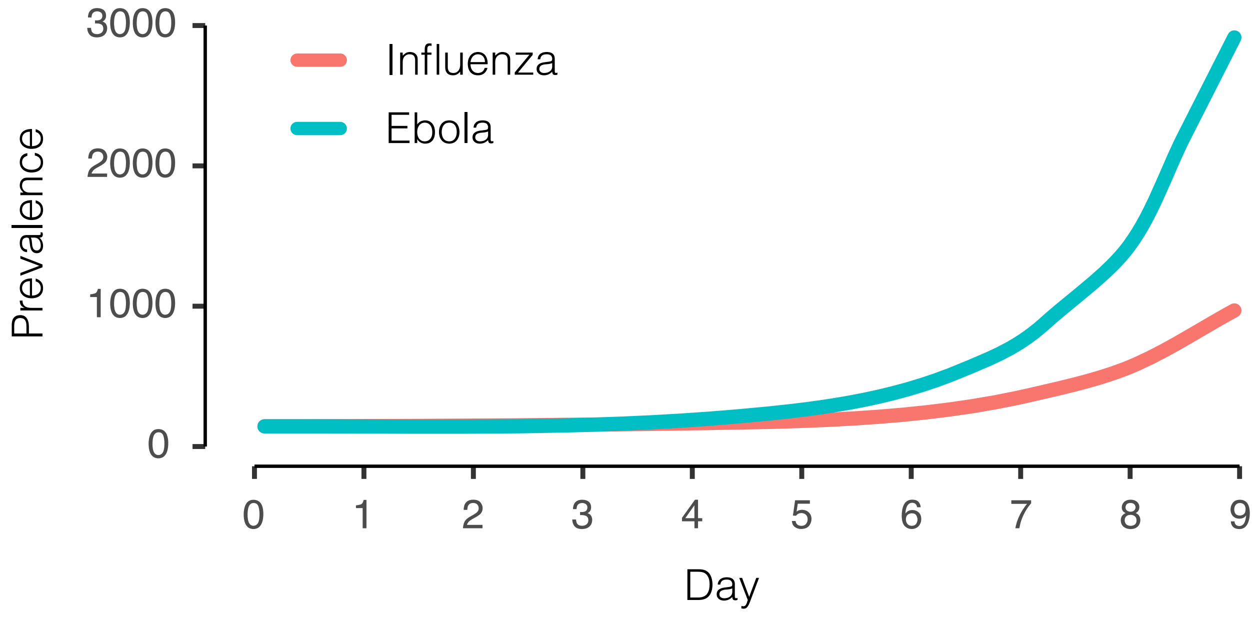

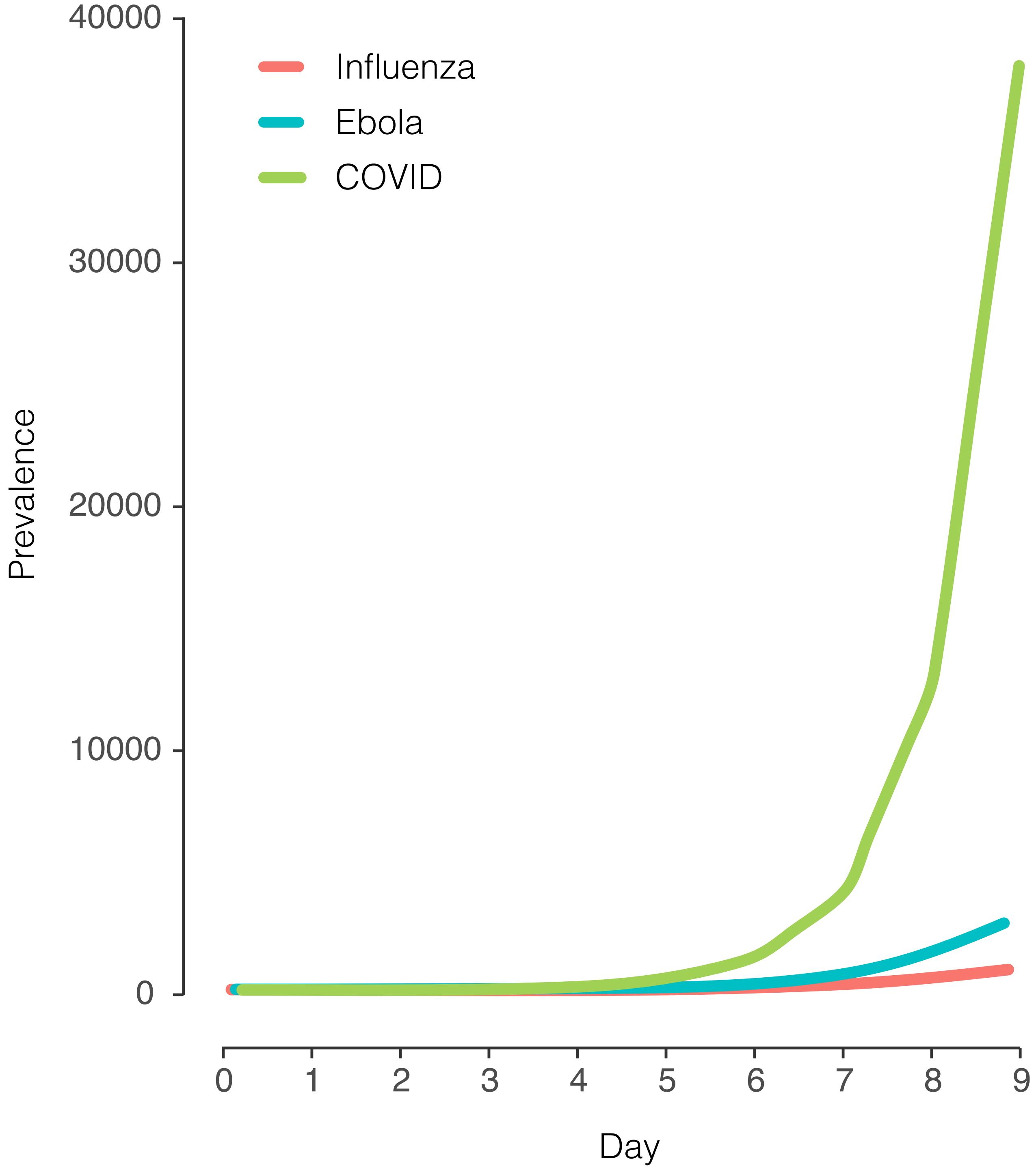

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To control de epidemics, **reduce R below 1**, we can only act on these parameters:

Reduce τ by early detection and isolation
Reduce β by drugs or physical protection
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Reduce ρ_S by vaccination, confinement or infection immunity

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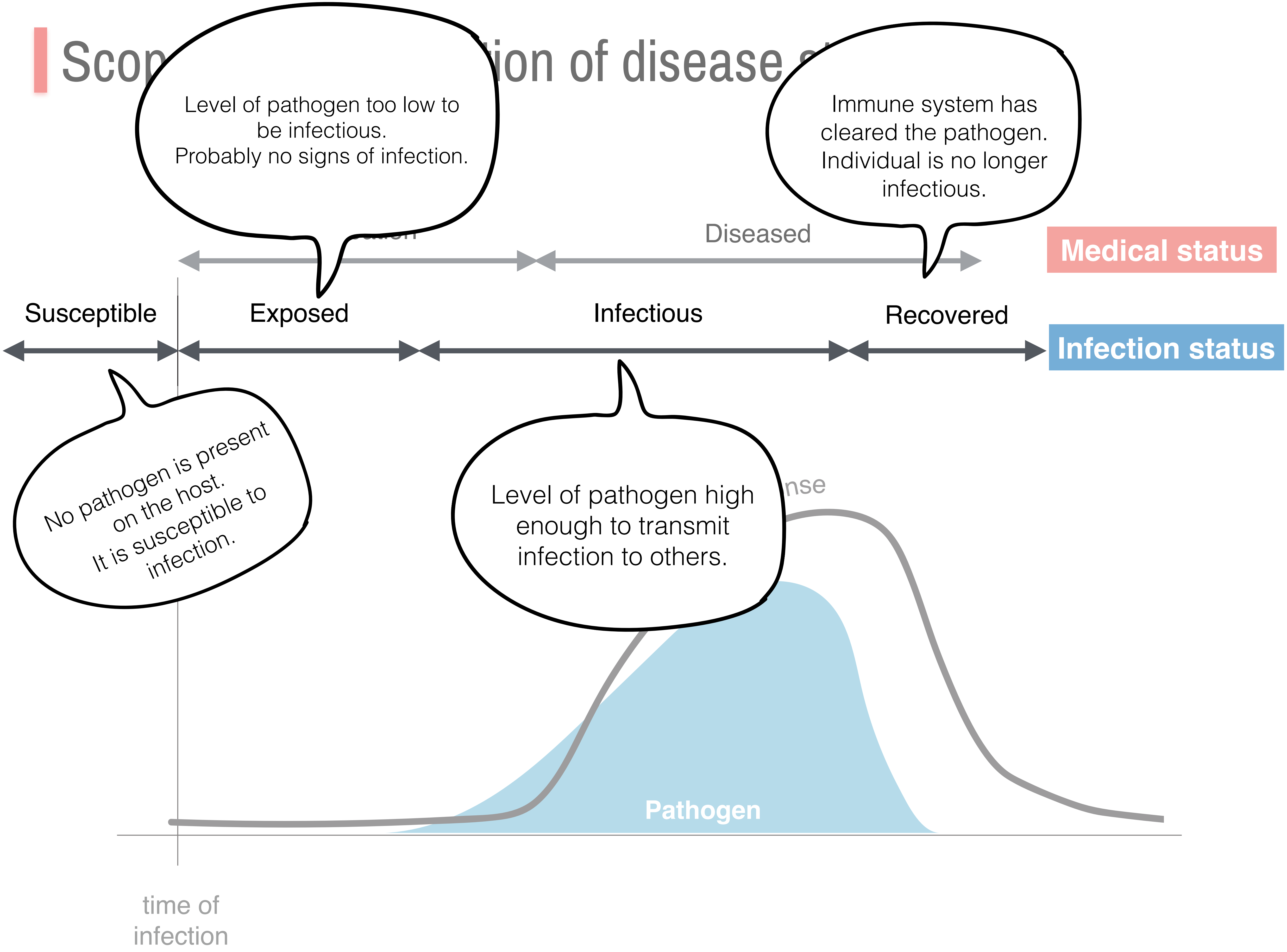
Scop ion of disease s



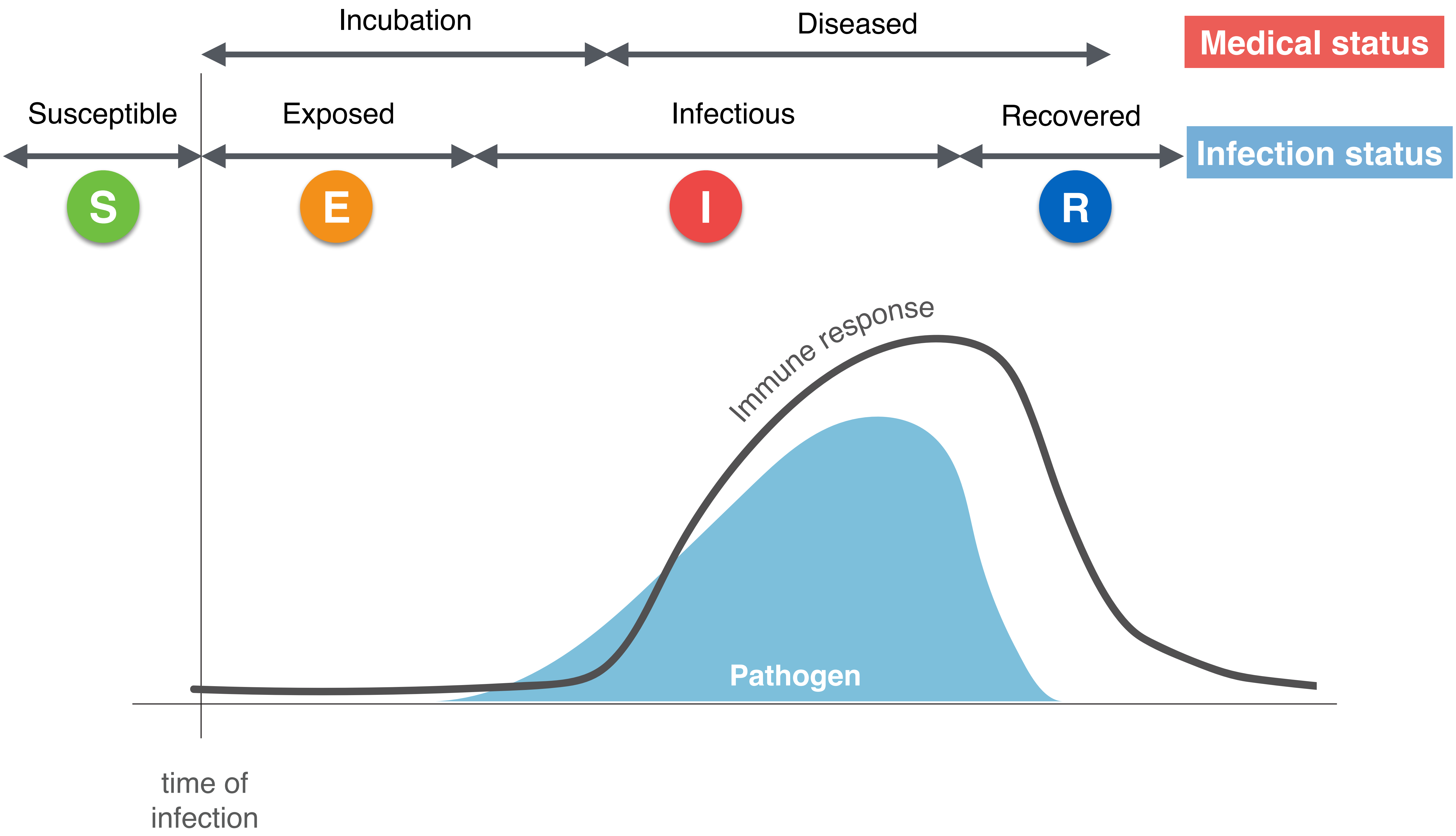
Level of pathogen too low to be infectious.
Probably no signs of infection.

Immune system has cleared the pathogen. Individual is no longer infectious.

No pathogen is present on the host.
It is susceptible to infection.

Level of pathogen high enough to transmit infection to others.

Scope: characterization of disease states



Incubation

Diseased

Medical status

Susceptible

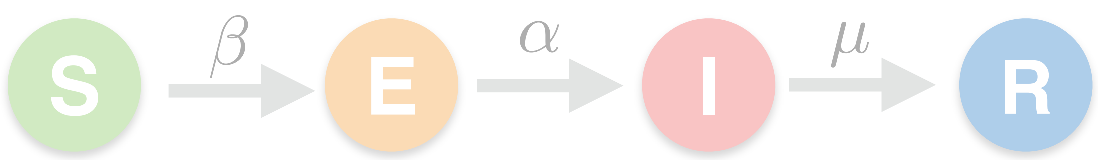
Exposed

Infectious

Recovered

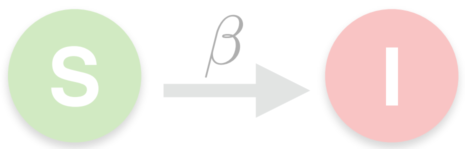
Infection status

Scope: compartmental models



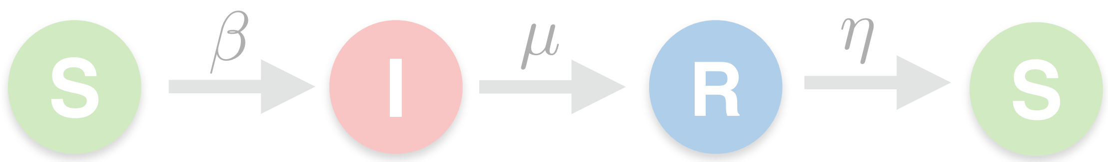
Chickenpox, measles, rubella

Often the exposed class is ignored, so that the mathematical model is simpler.



Some infections are better modeled by SI. In this case the host becomes infectious very fast and they remain infected until death. Plants.

Other diseases are better described by SIS. Here the host once recovered is soon again susceptible. Influenza, STDs.



Temporary immunity

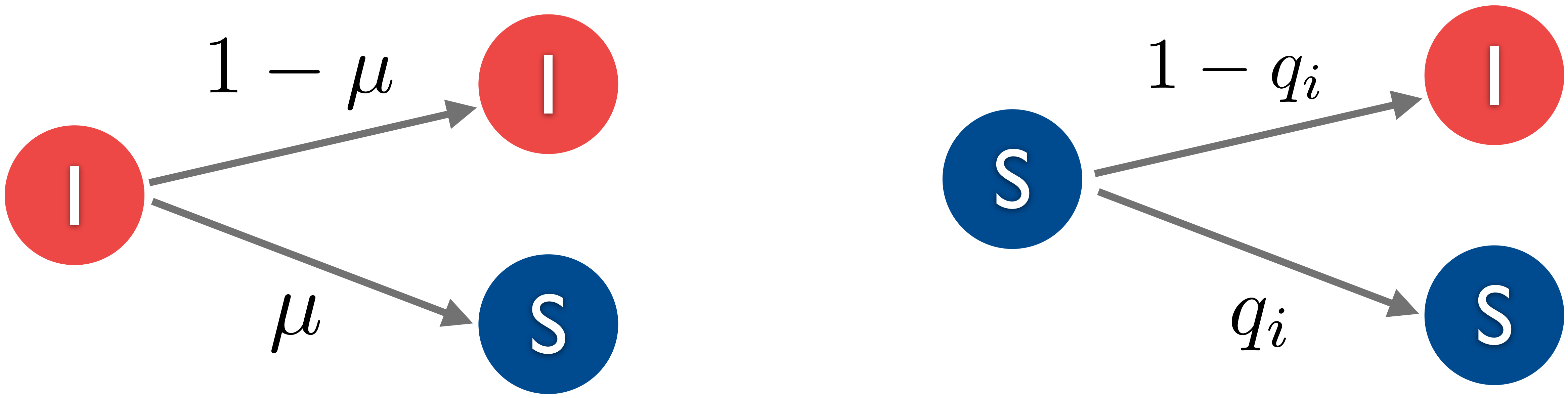
Microscopic Markov Chain Approach (MMCA)

Main ideas:

- Instead of discrete states of individuals, describe their individual probabilities of being in a certain state
- Deterministic maps for the evolution of these probabilities
- Accounting for the specific contact matrix between individuals, instead of an ensemble, allows for a more accurate description of spreading in real networks
- Easy to model from the Markov chain of possible states in discrete time steps
- Define the macrostate as the order parameter accounting for the average fraction of infected individuals

Discrete-time Markov chain approach to contact-based disease spreading in complex networks S. Gomez, AA, J. Borge-Holthoefer, S. Meloni and Y. Moreno**, Europhysics Letters, 89, 38009 (2010)**

SIS, reactive process, without reinfections



$$p_i^I(t+1) = p_i^I(t)(1-\mu) + p_i^S(t)[1-q_i(t)]$$

$$p_i^S(t+1) = p_i^I(t)\mu + p_i^S(t)q_i(t)$$

$$q_i(t) = \prod_{j=1}^{N}(1-\beta r_{ji}p_j(t))$$

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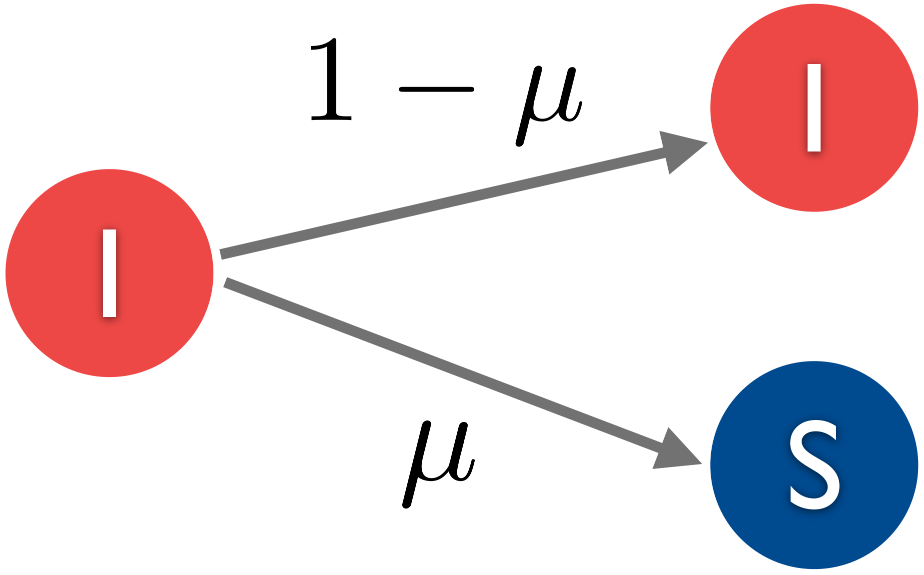

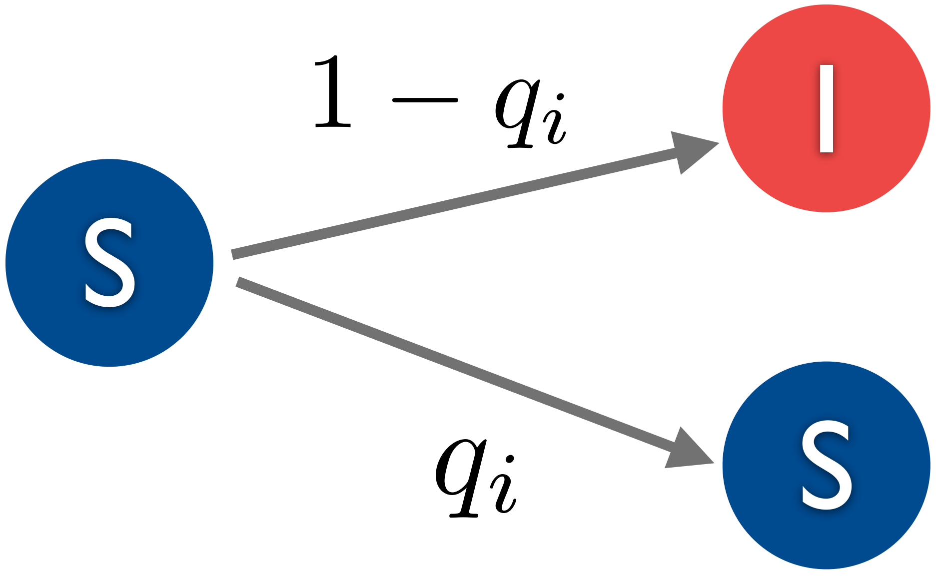

$$p_i(t+1) = (1-p_i(t))(1-q_i(t)) + (1-\mu)p_i(t)$$

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Dynamical system of N map equations with N time-dependent variables

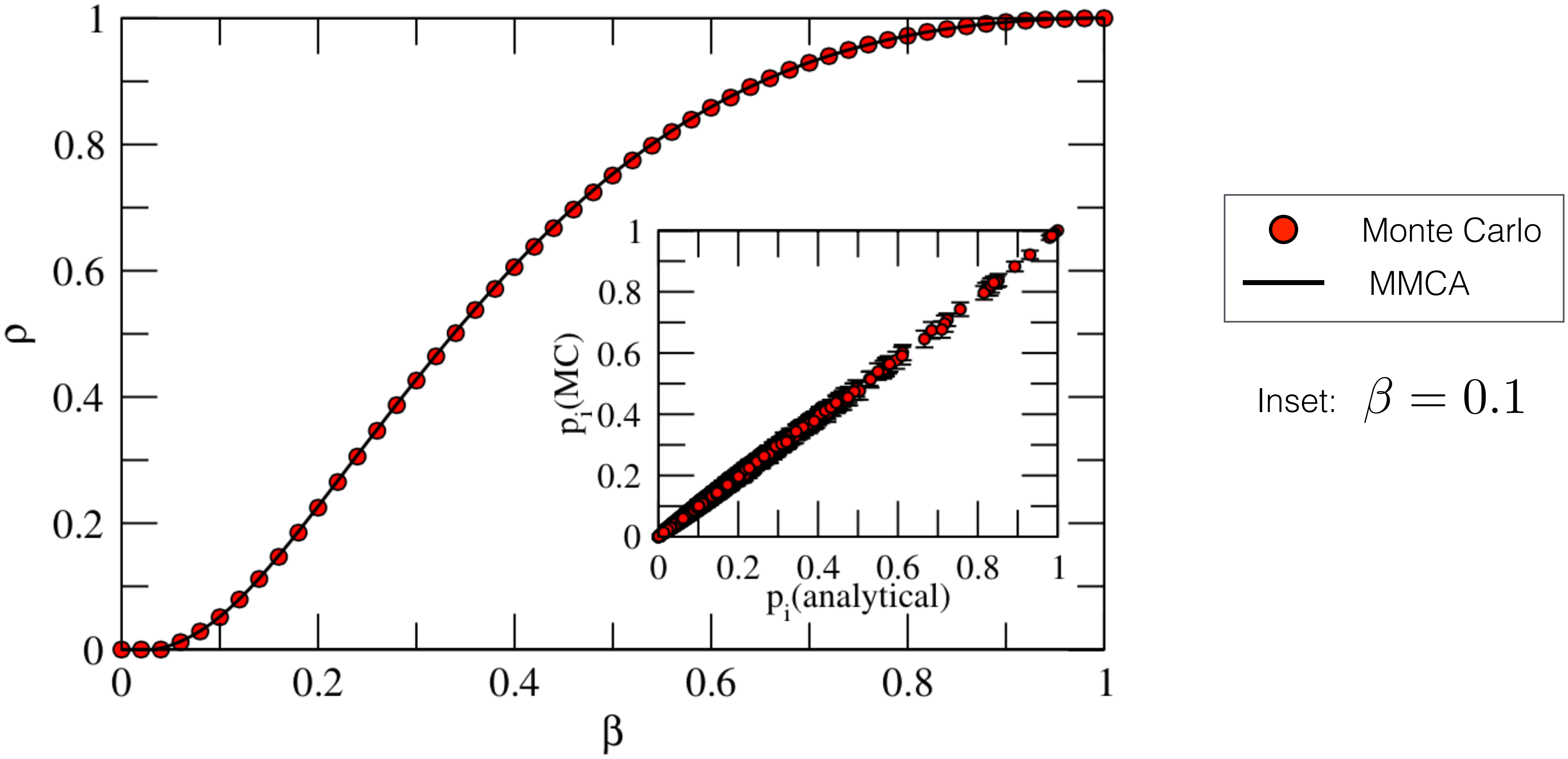
Parameters:

- initial conditions at time t=0
- r_{ji} : contact matrix
- β: infection rate
- μ : recovery rate

The system is a contraction mapping for every value of the parameters beyond β_c in the interval (0,1], and then the existence of fixed points is guaranteed by the Banach fixed point theorem. We can solve the system by iteration.

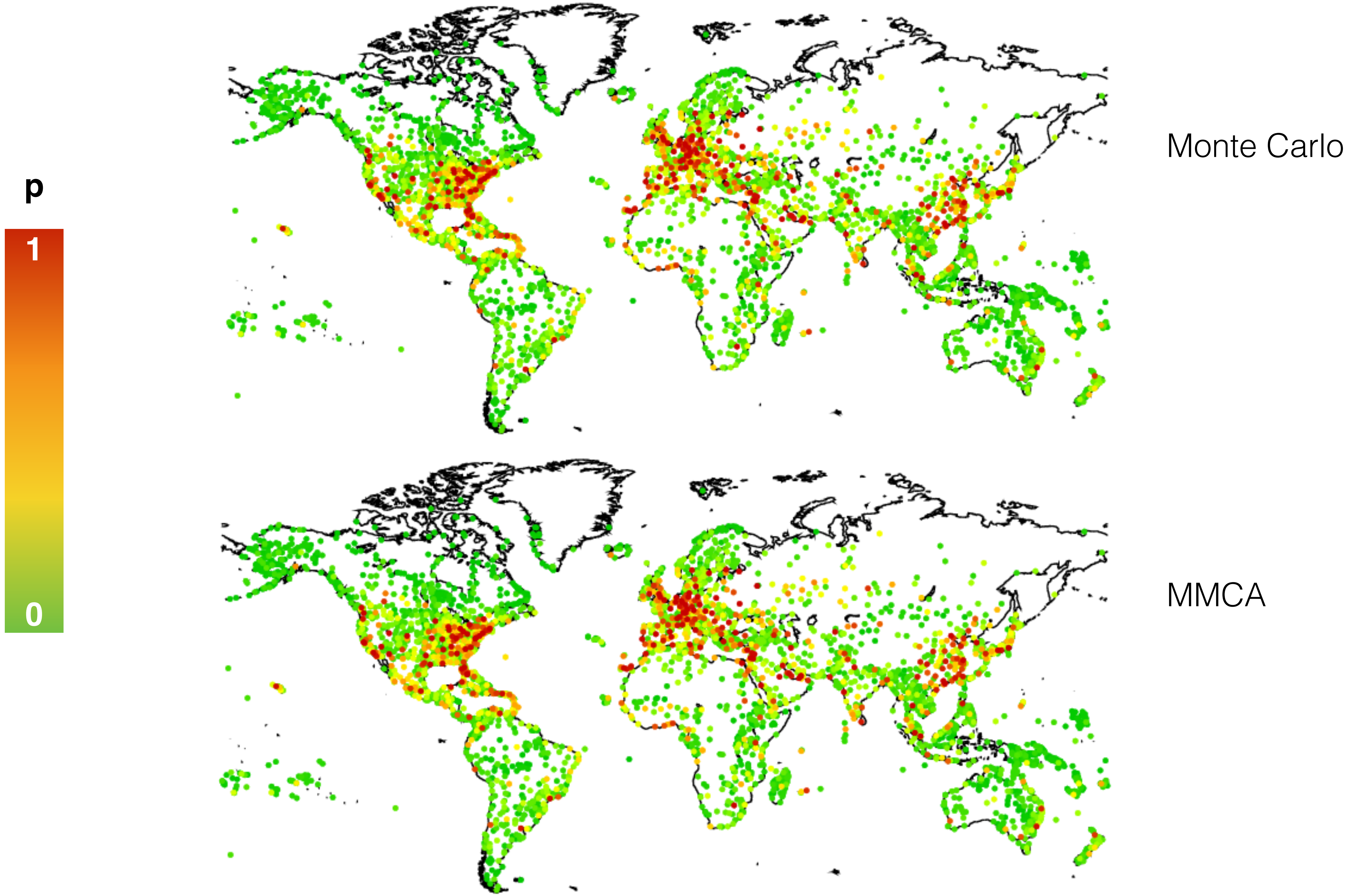
Microscopic Markov Chain Approach (MMCA)

- SIS model (reactive process)
- Recovery $\mu = 1.0$
- Scale-free network with $p(k) \sim k^{-\gamma}$ $N = 10^4, \gamma = 2.7$



Inset: $\beta = 0.1$

Results of the simulations and model for an infection starting in Oaxaca using the global air transportation network



Microscopic Markov Chain Approach (MMCA)

Calculation of the epidemic threshold

In the steady state

$$p_i = (1 - p_i)(1 - q_i) + (1 - \mu)p_i$$

Near the critical point:

$$0 \leq p_i \ll 1 \qquad q_i \approx 1 - \beta \sum_{j=1}^{N} r_{ji} p_j$$

A first order expansion in the probabilities yields:

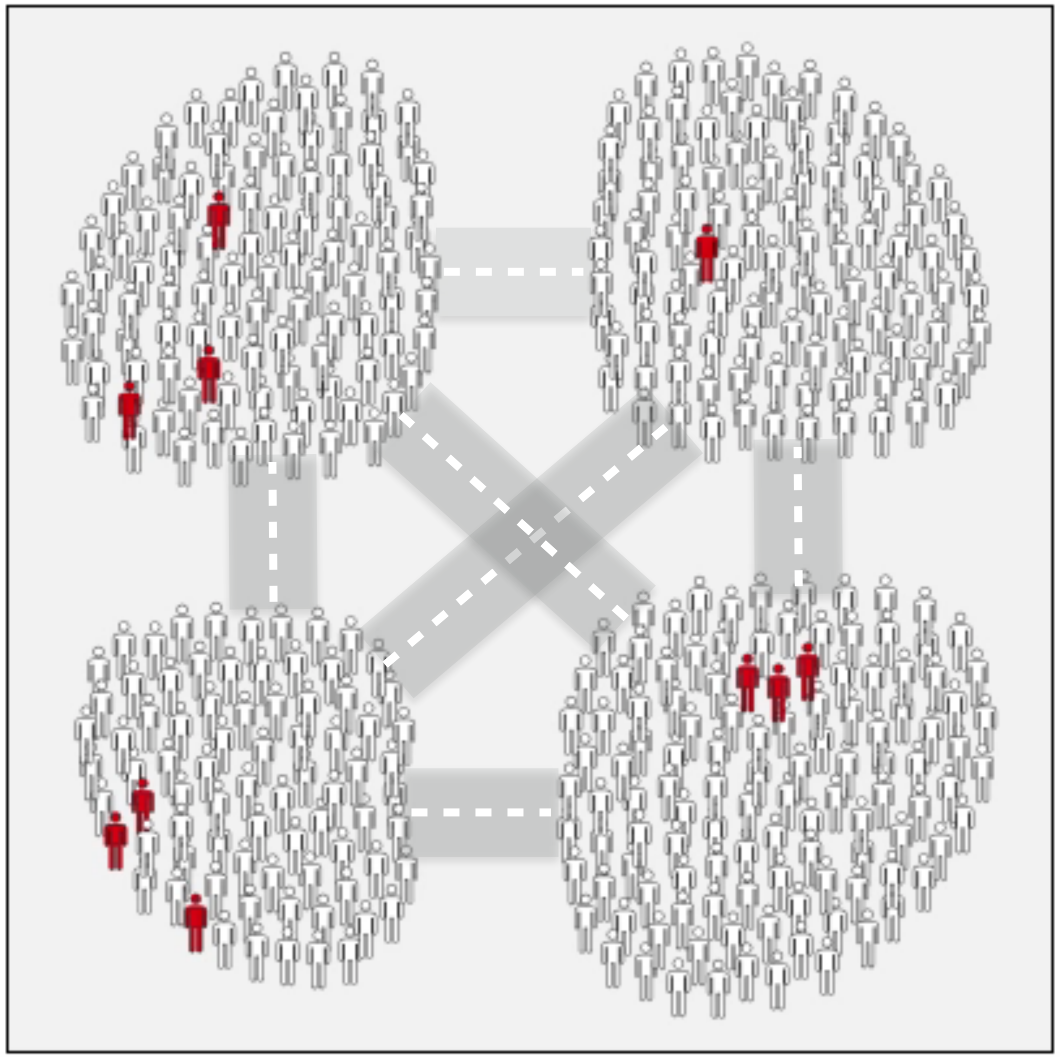
$$\sum_{j=1} \left(r_{ji} - \frac{\mu}{\beta} \delta_{ji} \right) p_j = 0 \longrightarrow \mathbf{R}\vec{p} = \frac{\mu}{\beta}\vec{p}$$

Solving the eigenvalue problem, the epidemic threshold is found as:

$$\beta_c = \frac{\mu}{\Lambda_{\max}(\mathbf{R})}$$

MMCA model for metapopulations

Metapopulations:
Networks of patches of individuals whose interactions are also driven by **mobility**



Adapted from Dirk Brockman's Complexity Explorables
http://www.complexity-explorables.org

MMCA model for metapopulations

We can adapt the MMCA model for SIS or SIR to **metapopulations** with **recurrent mobility**:

- Each patch is labeled as a node of the network, and the density of infected individuals is denoted by ρ_i

$$\rho_i(t+1) = \rho_i(t)(1-\mu) + (1-\rho_i)\Pi_i(t)$$

Probability that a healthy individual associated to node i is infected at time t

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Probability that a healthy individual associated to node i is infected at time t

- Compute $\Pi_i(t)$ as a function of the mobility *p*

$$\Pi_i(t) = (1-p)P_i(t) + p\sum_{j=1}^{N} R_{ij}P_j(t)$$

Probability that an individual being at node i (j) is infected at time t

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MMCA model for metapopulations

$$\rho_i(t+1) = \rho_i(t)(1-\mu)+$$

$$+(1-\rho_i(t))(1-p)\left[1-\prod_{j=1}^{N}(1-\beta\rho_j(t))^{n_{j\to i}}\right]+$$

$$+(1-\rho_i(t))p\sum_{j=1}^{N}R_{ji}\left[\prod_{j=1}^{N}(1-\beta\rho_j(t))^{n_{i\to j}}\right]$$

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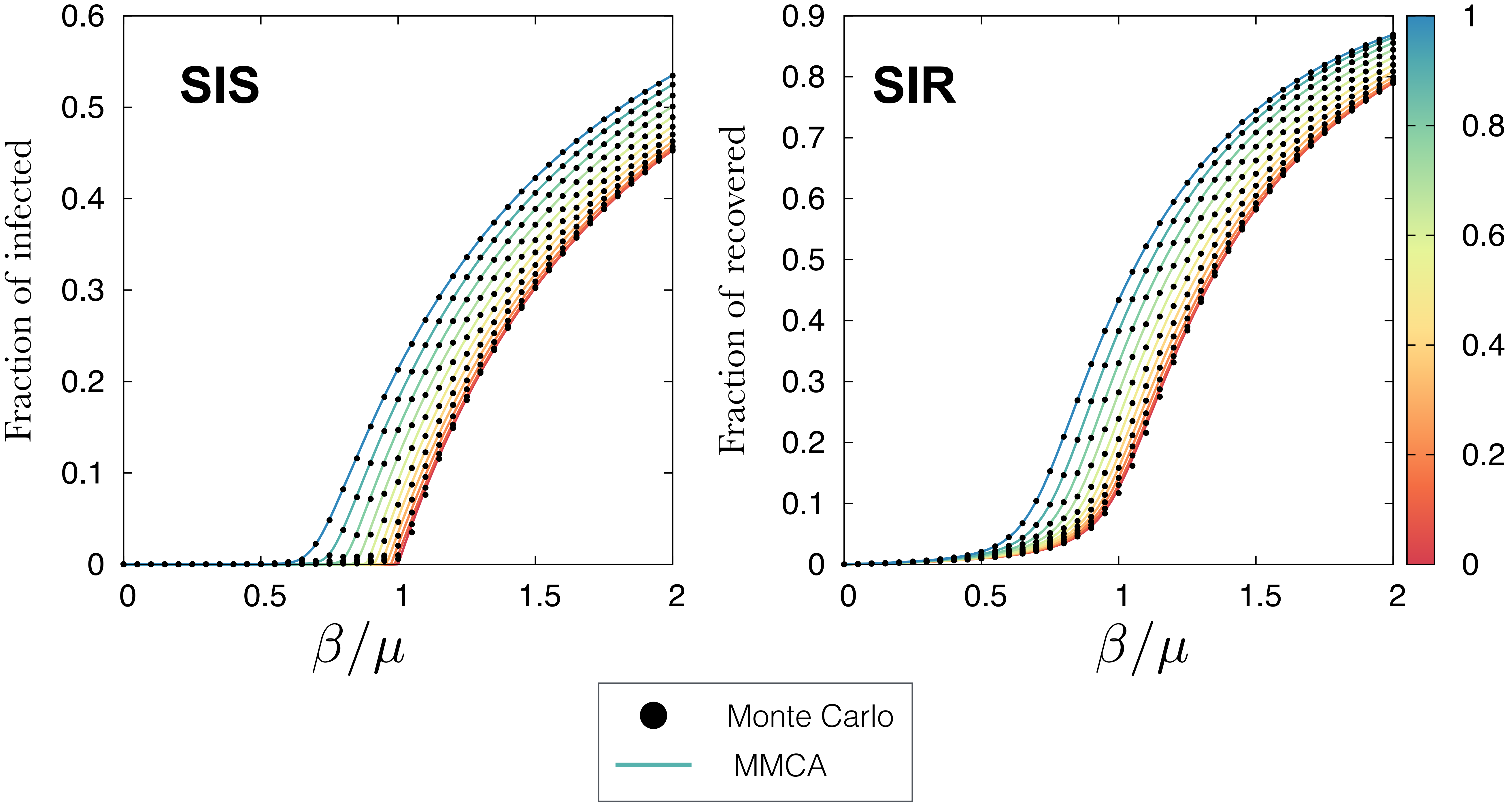
MMCA model for metapopulations

Results: comparison between Monte Carlo simulations and MMCA



MMCA model for metapopulations

Calculation of the epidemic threshold

$$\rho_i(t+1) = (1-\mu)\rho_i(t) + (1-\rho_i(t))\Pi_i(t)$$

$$\Big\downarrow \text{ Stationary state}$$

$$\mu\rho_i^* = (1-\rho_i^*)\Pi_i$$

$$\Pi_i = (1-p)\left(1 - \prod_{j=1}^{N}(1-\beta\rho_j^*)^{n_{j\to i}}\right) + p\sum_{j=1}^{N} R_{ij}\left(1 - \prod_{l=1}^{N}(1-\beta\rho_l^*)^{n_{l\to j}}\right)$$

$$\text{Linearize} \;\Big\downarrow\; \rho_i^* = \epsilon_i^* << 1 \;\; \forall\, i$$

$$\Pi_i \simeq (1-p)\sum_{j=1}^{N}\beta\epsilon_j^* n_{j\to i} + p\sum_{j=1}^{N}R_{ij}\sum_{l=1}^{N}\beta\epsilon_l^* n_{l\to j}$$

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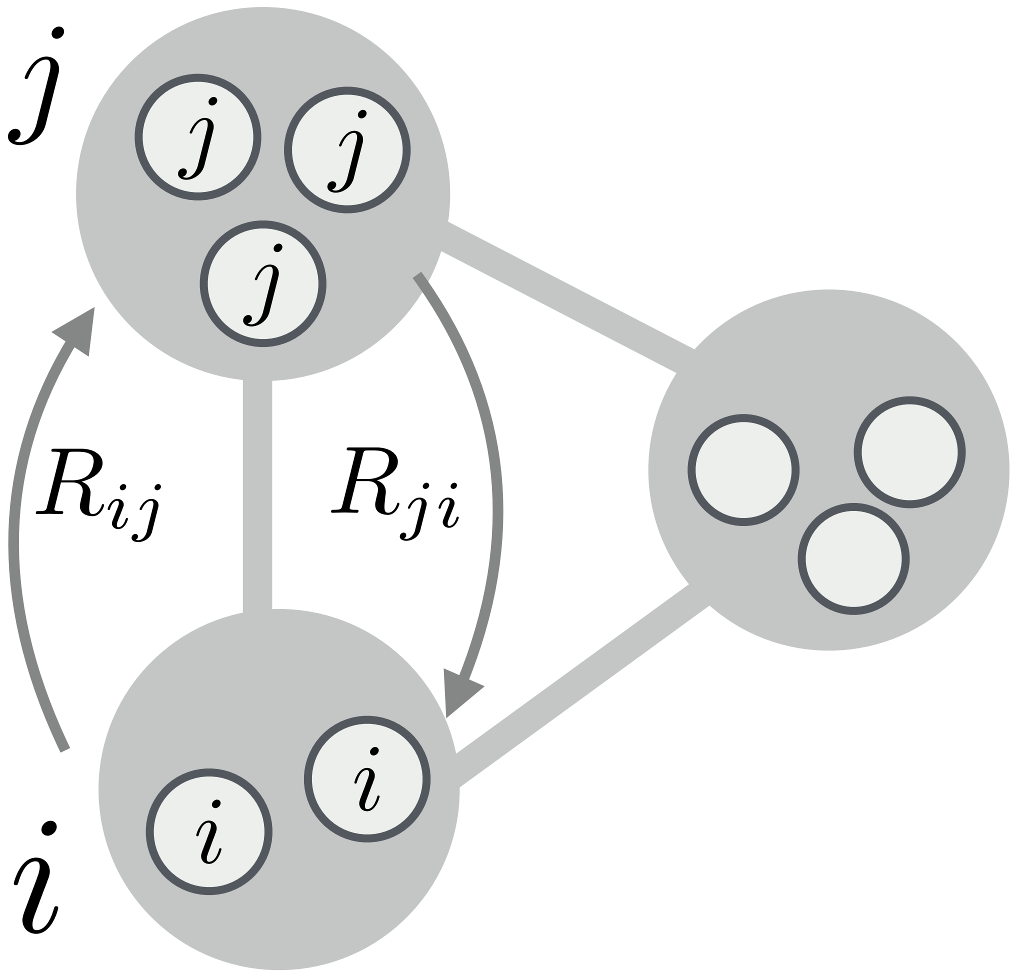
$$\Pi_i \simeq (1-p)\sum_{j=1}^{N}\beta\epsilon_j^*\left[(1-p)\delta_{ij}n_j + pR_{ji}n_j\right] + p\sum_{j=1}^{N}R_{ij}\sum_{l=1}^{N}\beta\epsilon_l^*\left[(1-p)\delta_{jl}n_l + pR_{lj}n_l\right]$$

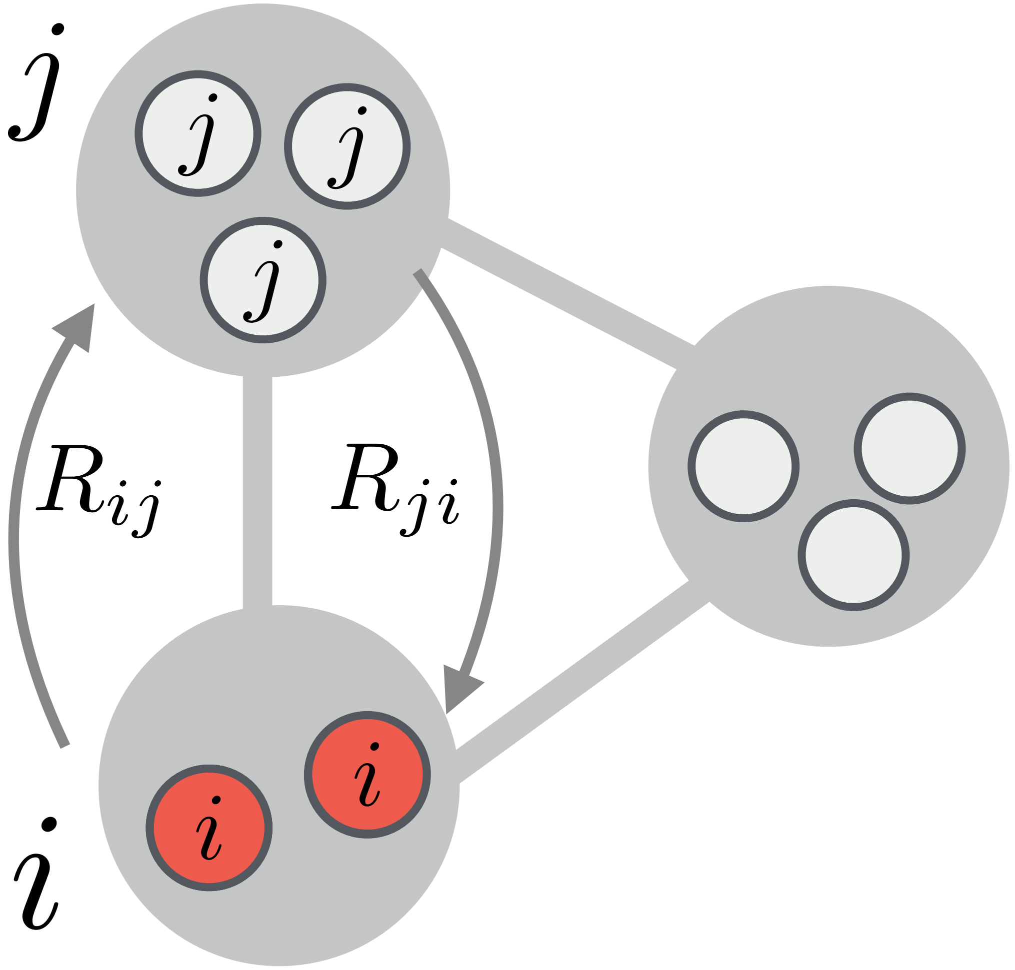
$$= \beta\textstyle\sum_{j=1}^{N}\underbrace{\left[(1-p)^2\delta_{ij}n_j + p(1-p)n_j(\mathbf{R}+\mathbf{R^T})_{ij} + p^2 n_j(\mathbf{R}\cdot\mathbf{R^T})_{ij}\right]}_{M_{ij}}\epsilon_j^*$$

MMCA model for metapopulations



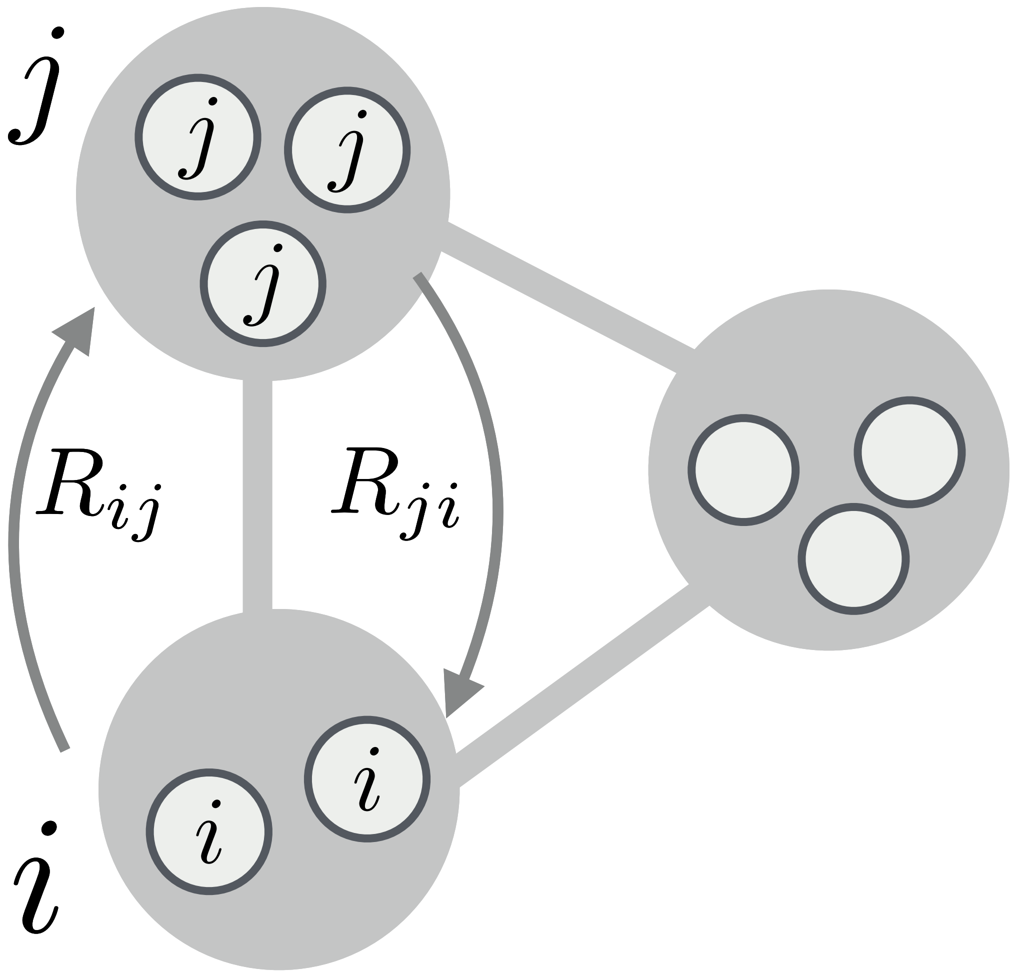
$$= \beta \sum_{j=1}^{N} \underbrace{\left[(1-p)^2 \delta_{ij} n_j + p(1-p) n_j (\mathbf{R} + \mathbf{R^T})_{ij} + p^2 n_j (\mathbf{R} \cdot \mathbf{R^T})_{ij}\right]}_{M_{ij}} \epsilon_j^*$$

MMCA model for metapopulations



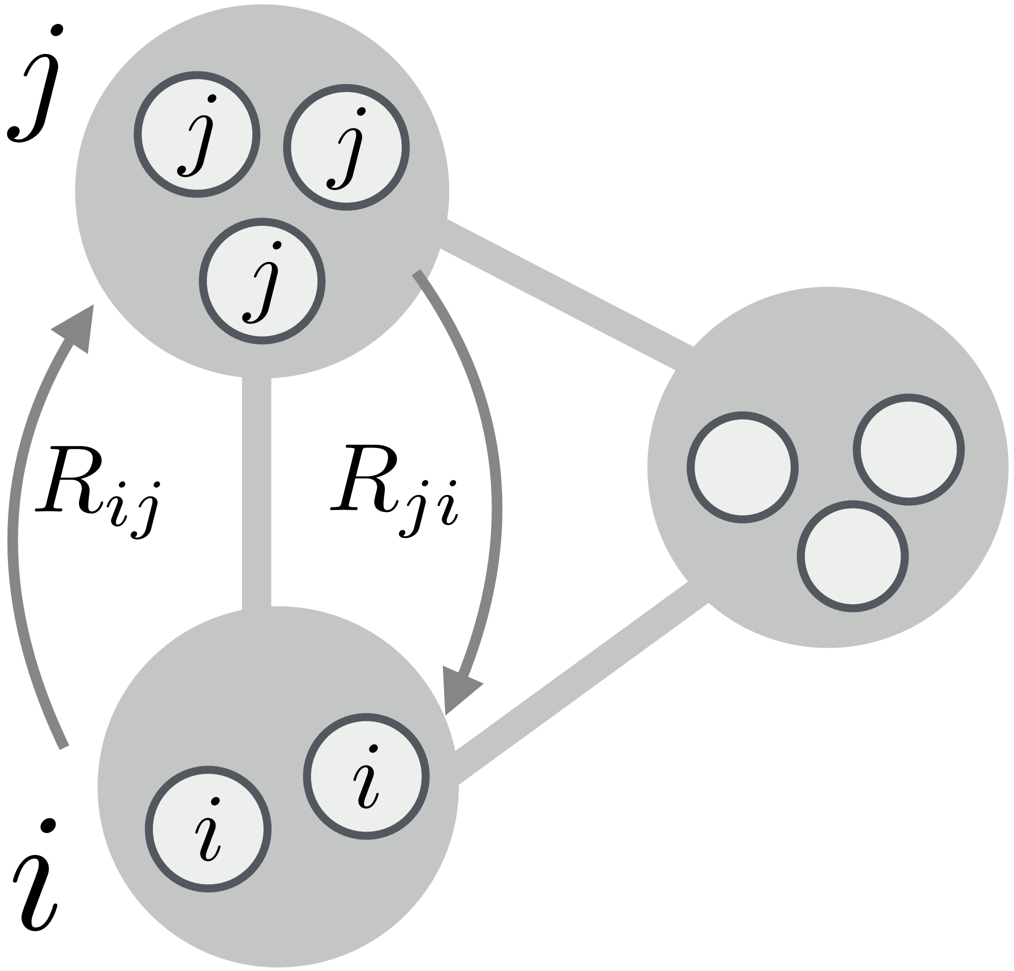
$$= \beta \sum_{j=1}^{N} \underbrace{\left[(1-p)^2 \delta_{ij} n_j + p(1-p) n_j (\mathbf{R} + \mathbf{R^T})_{ij} + p^2 n_j (\mathbf{R} \cdot \mathbf{R^T})_{ij} \right]}_{M_{ij}} \epsilon_j^*$$

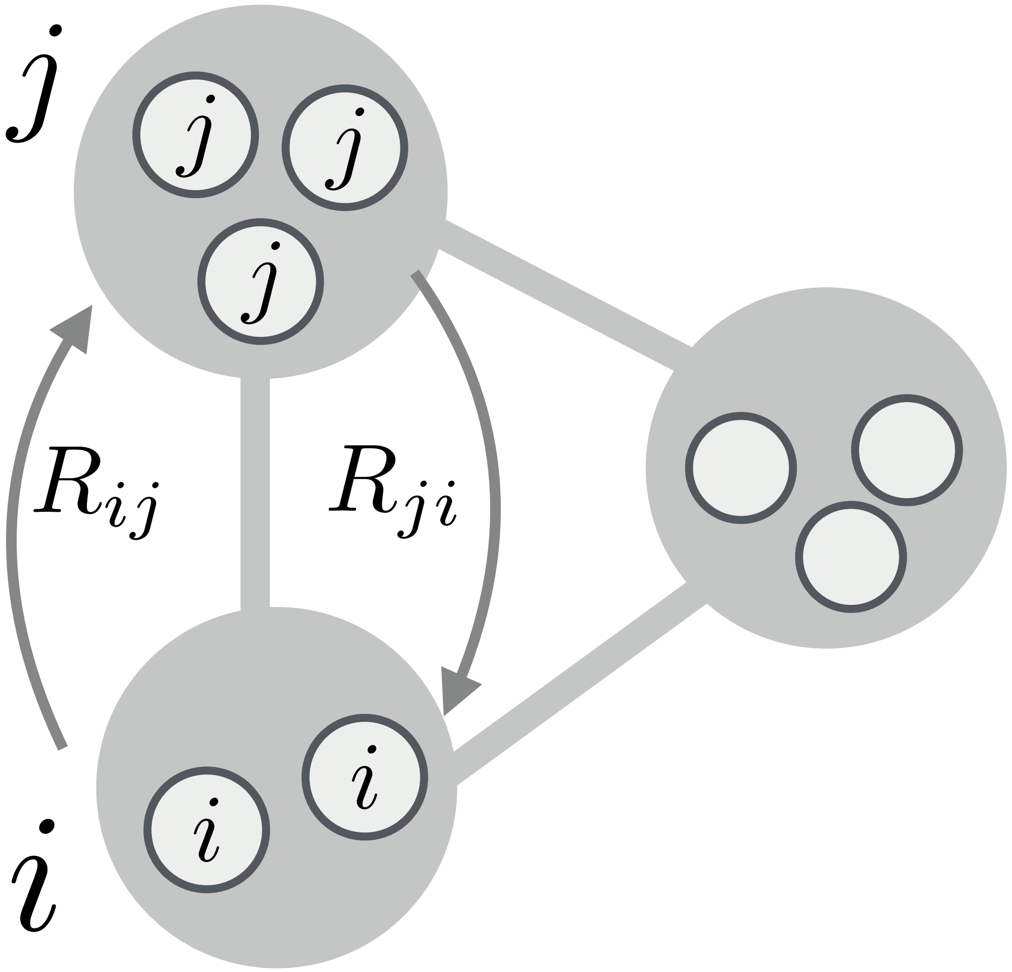
MMCA model for metapopulations



$$= \beta \sum_{j=1}^{N} \underbrace{\left[(1-p)^2 \delta_{ij} n_j + p(1-p) n_j (\mathbf{R} + \mathbf{R}^{\mathbf{T}})_{ij} + p^2 n_j (\mathbf{R} \cdot \mathbf{R}^{\mathbf{T}})_{ij}\right]}_{M_{ij}} \epsilon_j^*$$

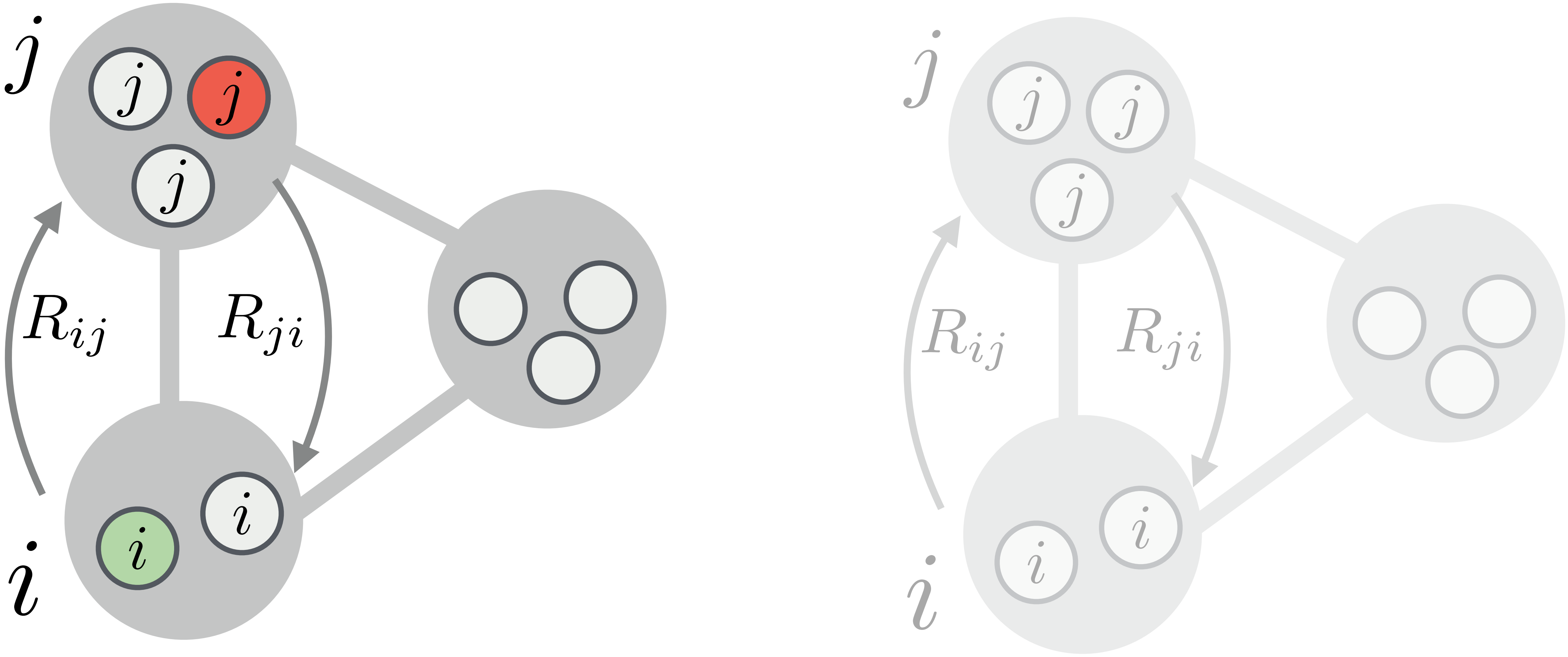
MMCA model for metapopulations





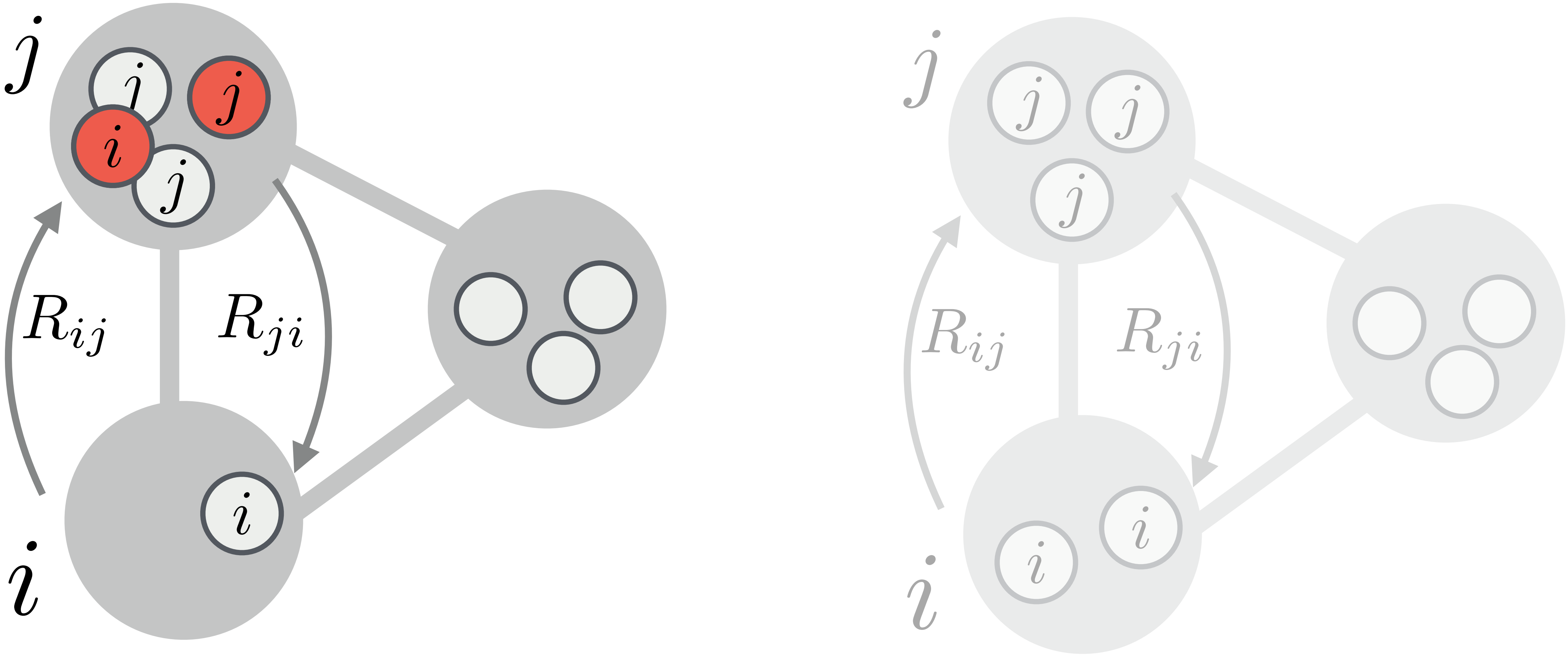
$$= \beta \sum_{j=1}^{N} \underbrace{\left[(1-p)^2 \delta_{ij} n_j + p(1-p) n_j (\mathbf{R} + \mathbf{R}^{\mathbf{T}})_{ij} + p^2 n_j (\mathbf{R} \cdot \mathbf{R}^{\mathbf{T}})_{ij}\right]}_{M_{ij}} \epsilon_j^*$$

MMCA model for metapopulations



$$= \beta \sum_{j=1}^{N} \underbrace{\left[(1-p)^2\delta_{ij}n_j + p(1-p)n_j(\mathbf{R}+\mathbf{R}^{\mathbf{T}})_{ij} + p^2 n_j(\mathbf{R}\cdot\mathbf{R}^{\mathbf{T}})_{ij}\right]}_{M_{ij}} \epsilon_j^*$$

MMCA model for metapopulations



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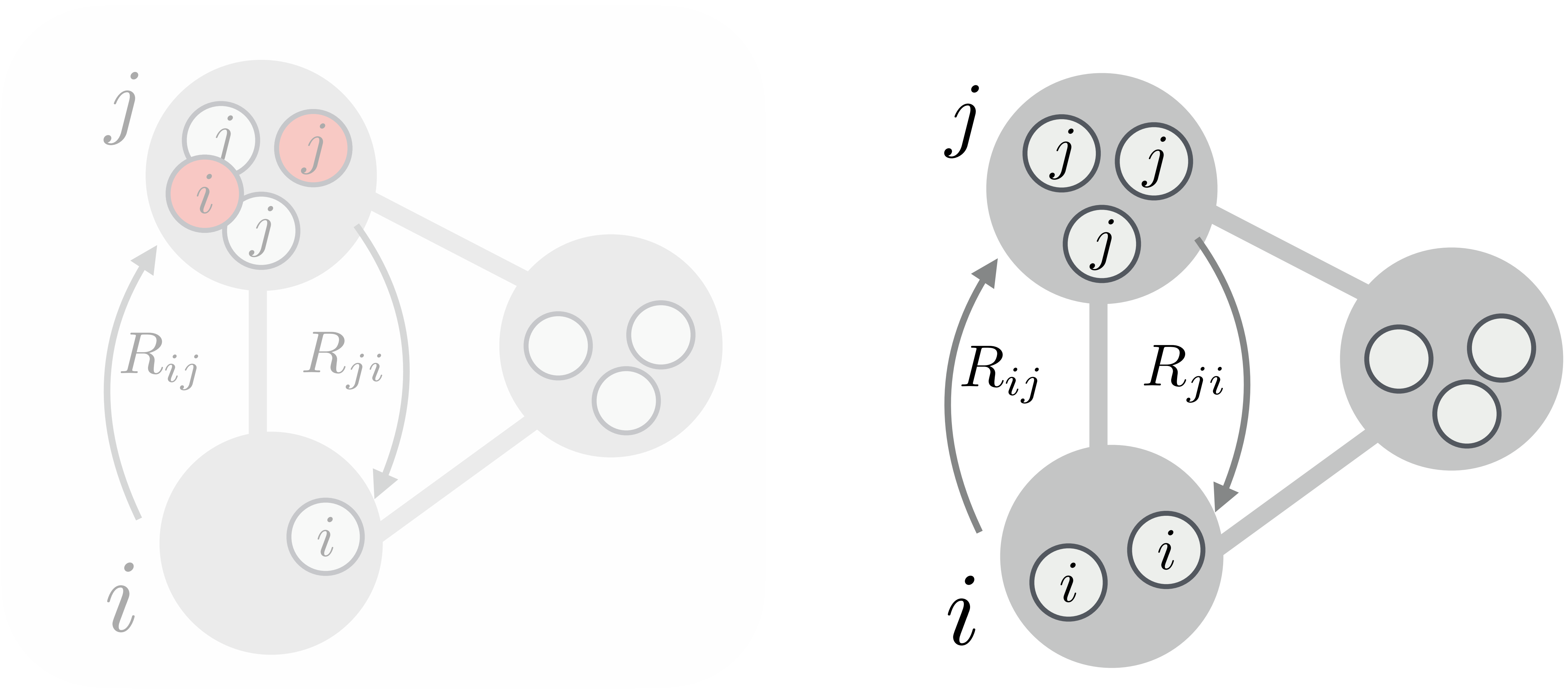
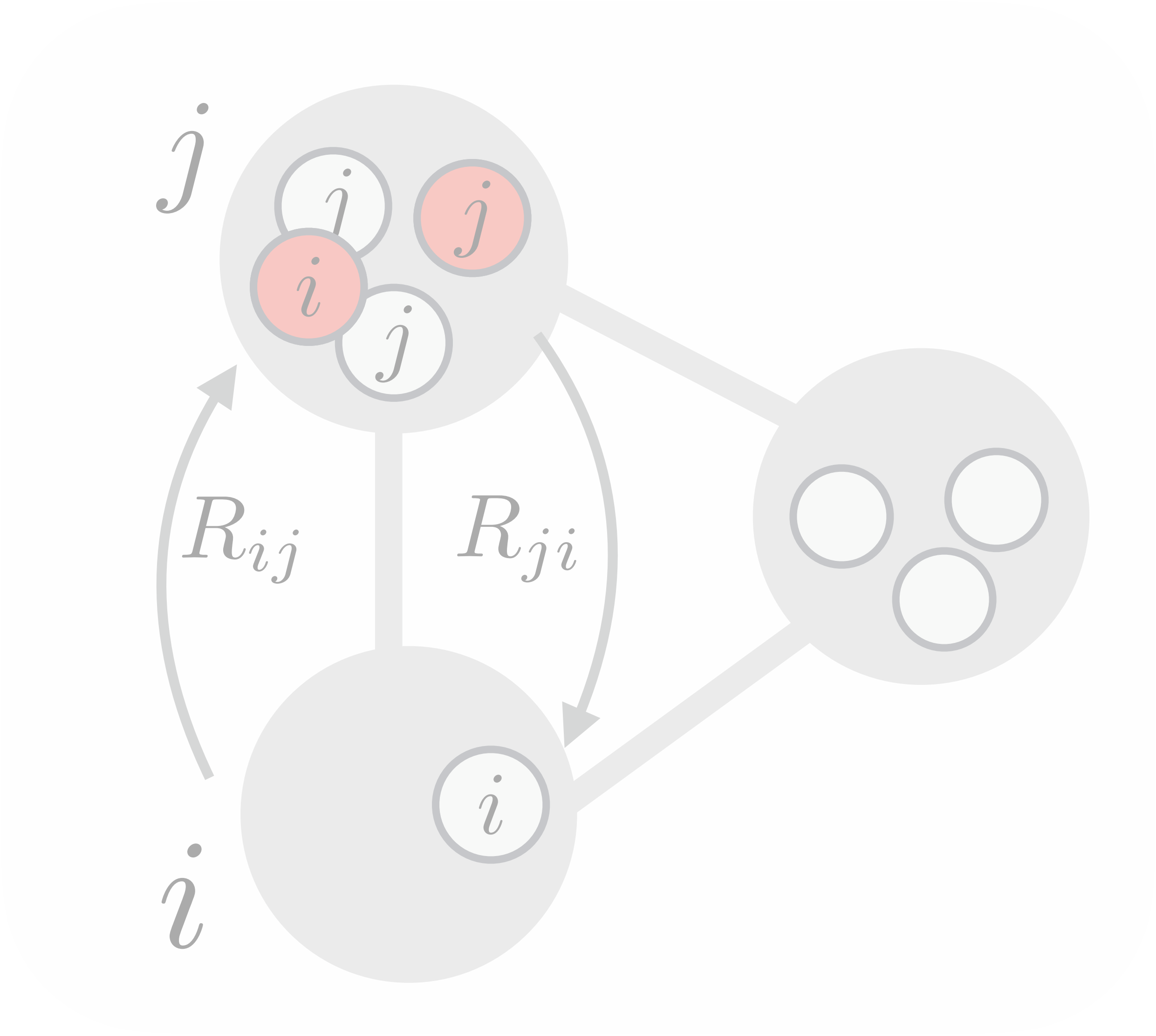
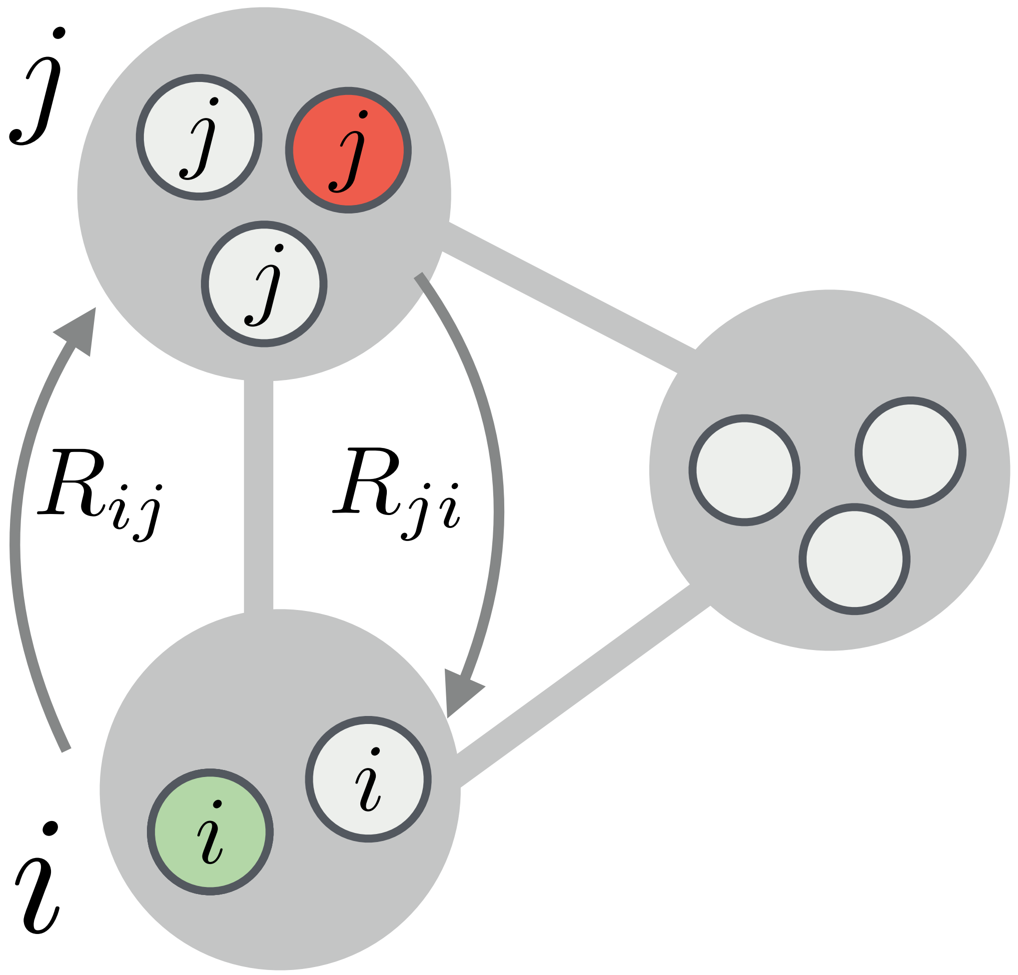
MMCA model for metapopulations



$$= \beta \sum_{j=1}^{N} \underbrace{\left[(1-p)^2\delta_{ij}n_j + p(1-p)n_j(\mathbf{R}+\mathbf{R}^{\mathbf{T}})_{ij} + p^2 n_j(\mathbf{R}\cdot\mathbf{R}^{\mathbf{T}})_{ij}\right]}_{M_{ij}} \epsilon_j^*$$

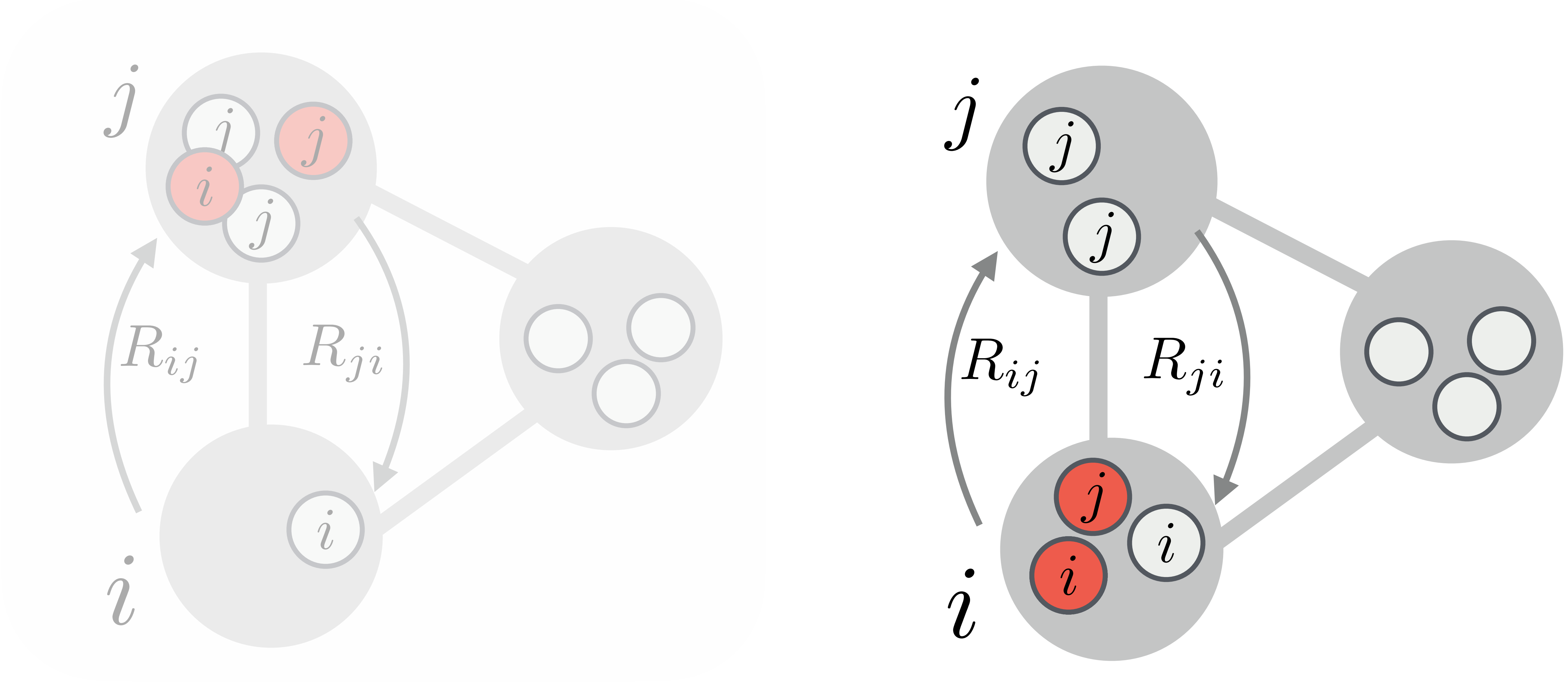
MMCA model for metapopulations





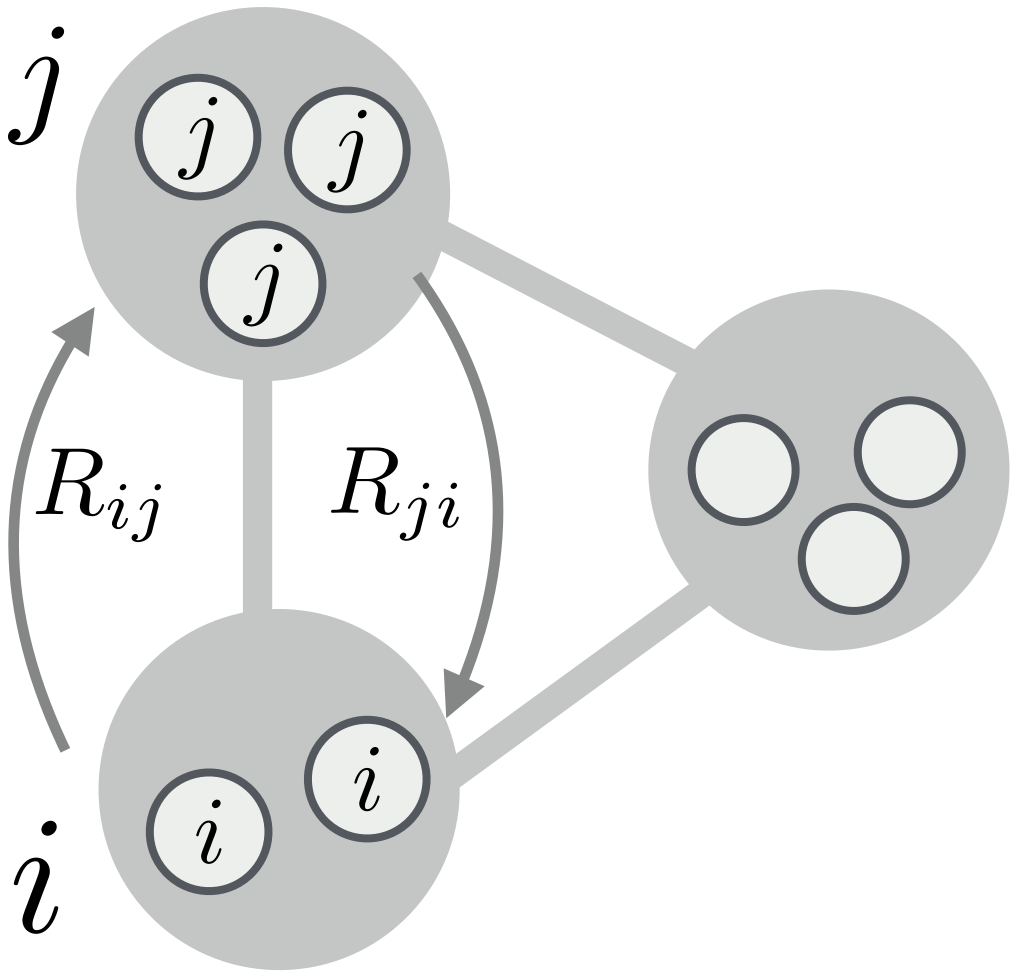
$$= \beta \sum_{j=1}^{N} \underbrace{\left[(1-p)^2\delta_{ij}n_j + p(1-p)n_j(\mathbf{R}+\mathbf{R^T})_{ij} + p^2 n_j(\mathbf{R}\cdot\mathbf{R^T})_{ij}\right]}_{M_{ij}} \epsilon_j^*$$

MMCA model for metapopulations



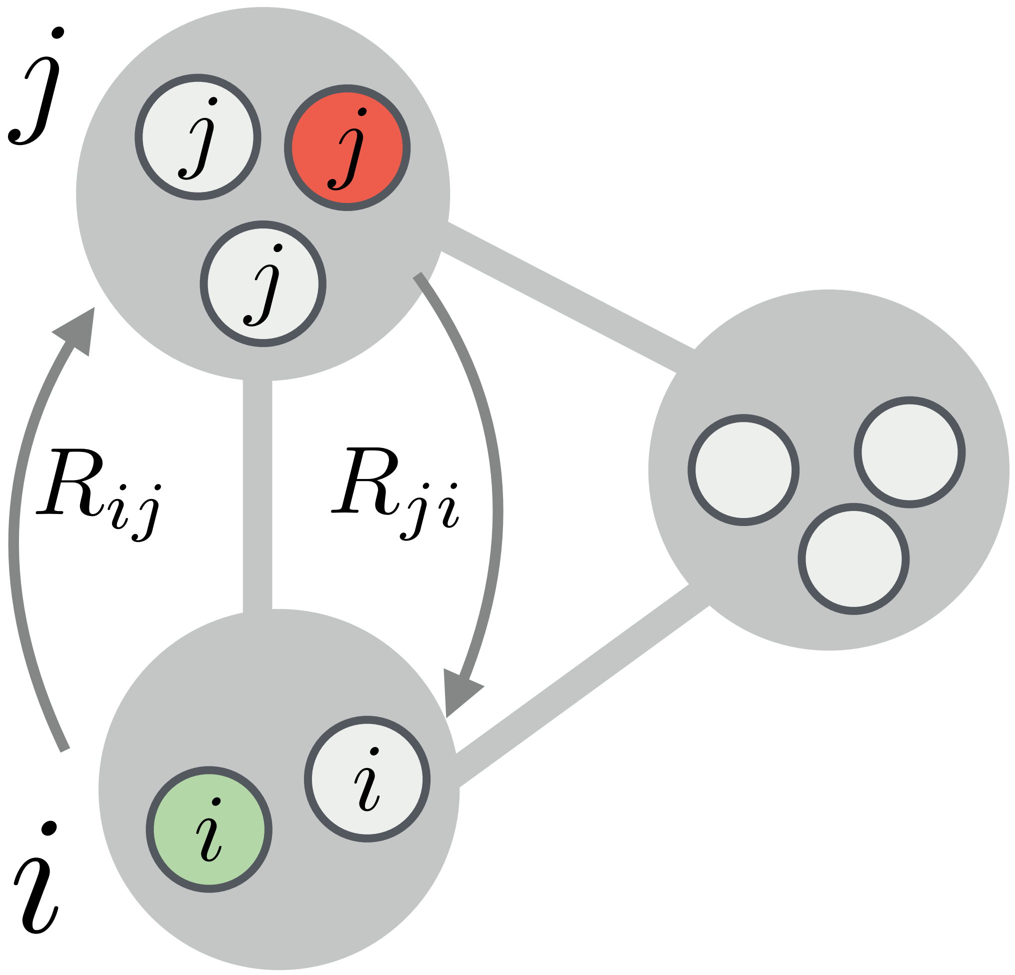
$$= \beta \sum_{j=1}^{N} \underbrace{\left[(1-p)^2\delta_{ij}n_j + p(1-p)n_j(\mathbf{R}+\mathbf{R}^{\mathbf{T}})_{ij} + p^2 n_j(\mathbf{R}\cdot\mathbf{R}^{\mathbf{T}})_{ij}\right]}_{M_{ij}} \epsilon_j^*$$

MMCA model for metapopulations



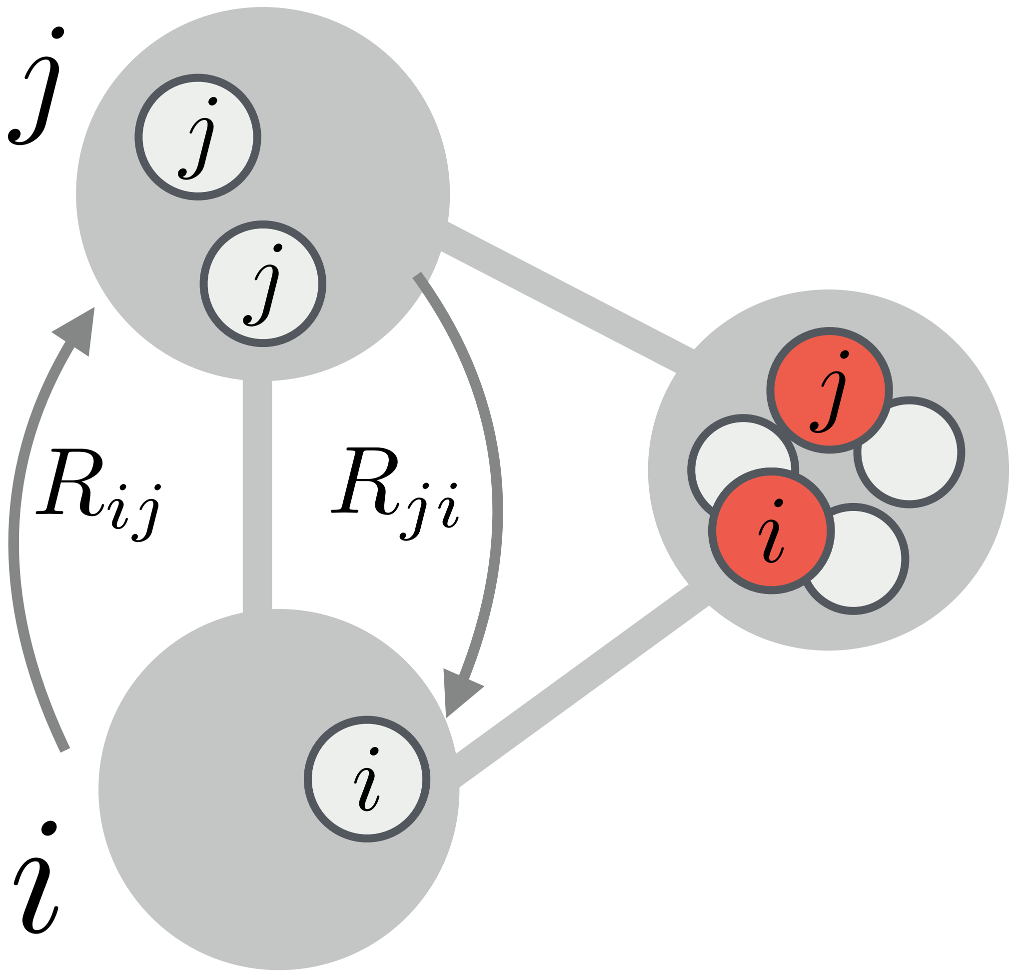
$$= \beta \sum_{j=1}^{N} \underbrace{\left[(1-p)^2 \delta_{ij} n_j + p(1-p) n_j (\mathbf{R} + \mathbf{R^T})_{ij} + p^2 n_j (\mathbf{R} \cdot \mathbf{R^T})_{ij}\right]}_{M_{ij}} \epsilon_j^*$$

MMCA model for metapopulations



$$= \beta \sum_{j=1}^{N} \underbrace{\left[(1-p)^2\delta_{ij}n_j + p(1-p)n_j(\mathbf{R}+\mathbf{R^T})_{ij} + p^2 n_j(\mathbf{R}\cdot\mathbf{R^T})_{ij}\right]}_{M_{ij}} \epsilon_j^*$$

MMCA model for metapopulations



$$= \beta \sum_{j=1}^{N} \underbrace{\left[(1-p)^2 \delta_{ij} n_j + p(1-p) n_j (\mathbf{R} + \mathbf{R}^\mathbf{T})_{ij} + p^2 n_j (\mathbf{R} \cdot \mathbf{R}^\mathbf{T})_{ij}\right]}_{M_{ij}} \epsilon_j^*$$

MMCA model for metapopulations

Calculation of the epidemic threshold

$$\Pi_i = (1-p)\left(1-\prod_{j=1}^{N}(1-\beta\rho_j^*)^{n_{j\to i}}\right) + p\sum_{j=1}^{N}R_{ij}\left(1-\prod_{l=1}^{N}(1-\beta\rho_l^*)^{n_{l\to j}}\right)$$

Linearize $\Big\downarrow$ $\rho_i^* = \epsilon_i^* << 1 \;\; \forall\, i$

$$\Pi_i \simeq (1-p)\sum_{j=1}^{N}\beta\epsilon_j^* n_{j\to i} + p\sum_{j=1}^{N}R_{ij}\sum_{l=1}^{N}\beta\epsilon_l^* n_{l\to j}$$

$$\Pi_i \simeq (1-p)\sum_{j=1}^{N}\beta\epsilon_j^*\left[(1-p)\delta_{ij}n_j + pR_{ji}n_j\right] + p\sum_{j=1}^{N}R_{ij}\sum_{l=1}^{N}\beta\epsilon_l^*\left[(1-p)\delta_{jl}n_l + pR_{lj}n_l\right]$$

$$= \beta\sum_{j=1}^{N}\underbrace{\left[(1-p)^2\delta_{ij}n_j + p(1-p)n_j(\mathbf{R}+\mathbf{R^T})_{ij} + p^2 n_j(\mathbf{R}\cdot\mathbf{R^T})_{ij}\right]}_{M_{ij}}\epsilon_j^*$$

MMCA model for metapopulations

Calculation of the epidemic threshold

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Recap:

$$\rho_i(t+1) = (1-\mu)\rho_i(t) + (1-\rho_i(t))\Pi_i(t)$$

$$\mu\epsilon_i^* = (1-\epsilon_i^*)\Pi_i$$

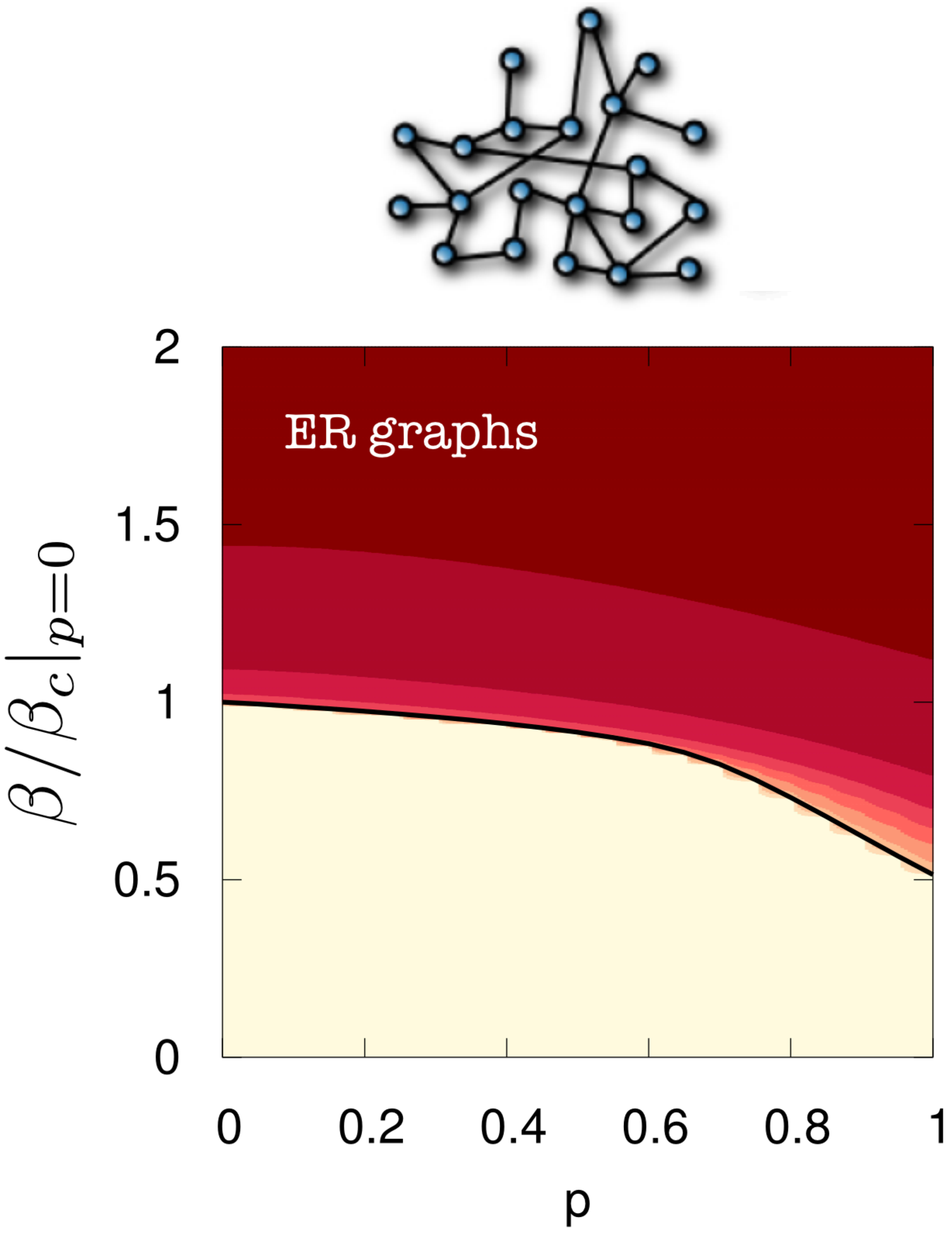
$$\mu\epsilon_i^* = \beta(1-\cancel{\epsilon_i^*})(\mathbf{M}\vec{\epsilon^*})_i$$

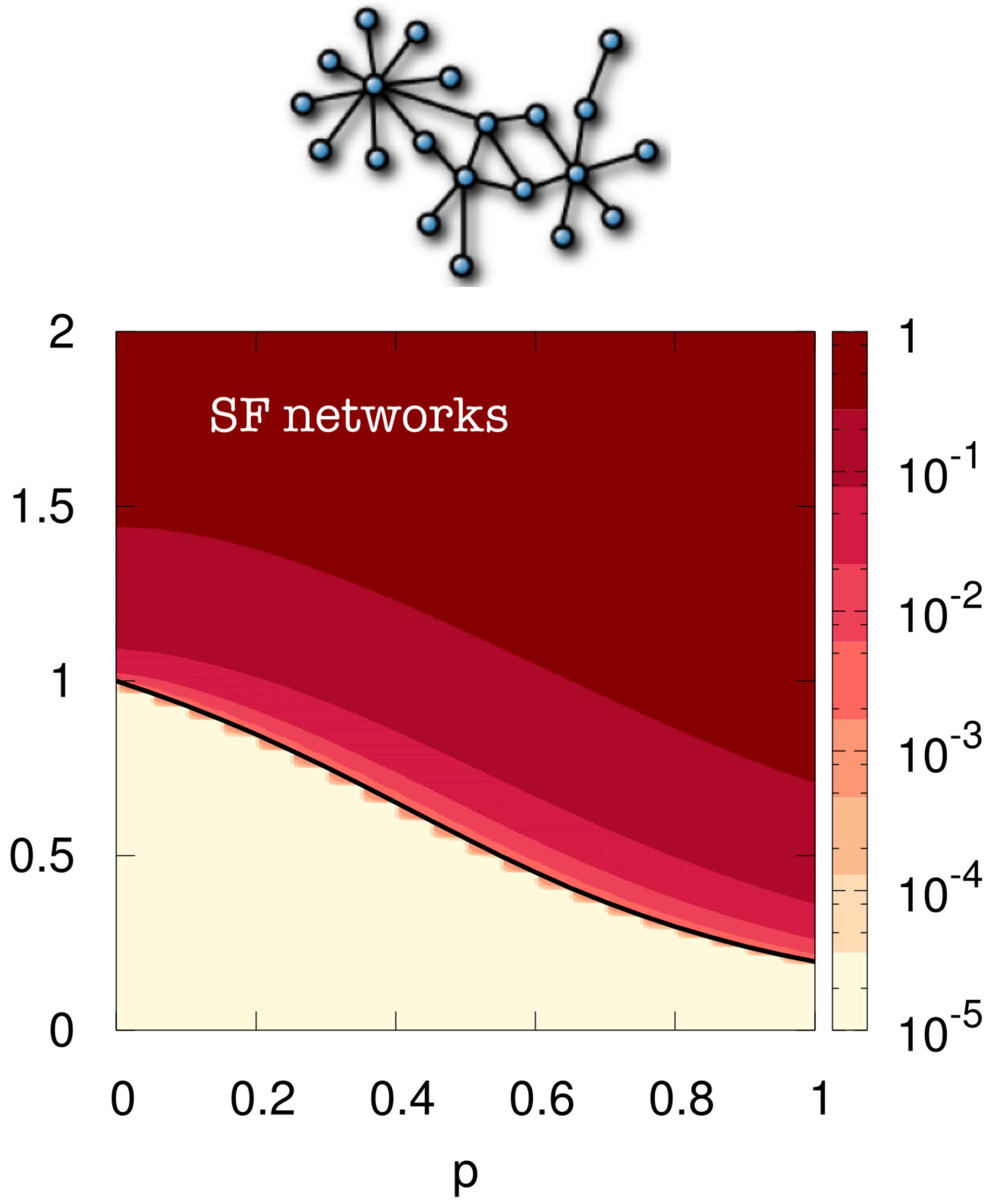
$$\frac{\mu}{\beta}\epsilon_i^* = (\mathbf{M}\vec{\epsilon^*})_i$$

$$\beta_c = \frac{\mu}{\Lambda_{\max}(\mathbf{M})}$$

MMCA model for metapopulations

Global Incidence for different mobility rates





MMCA on real metapopulations

Santiago de Cali

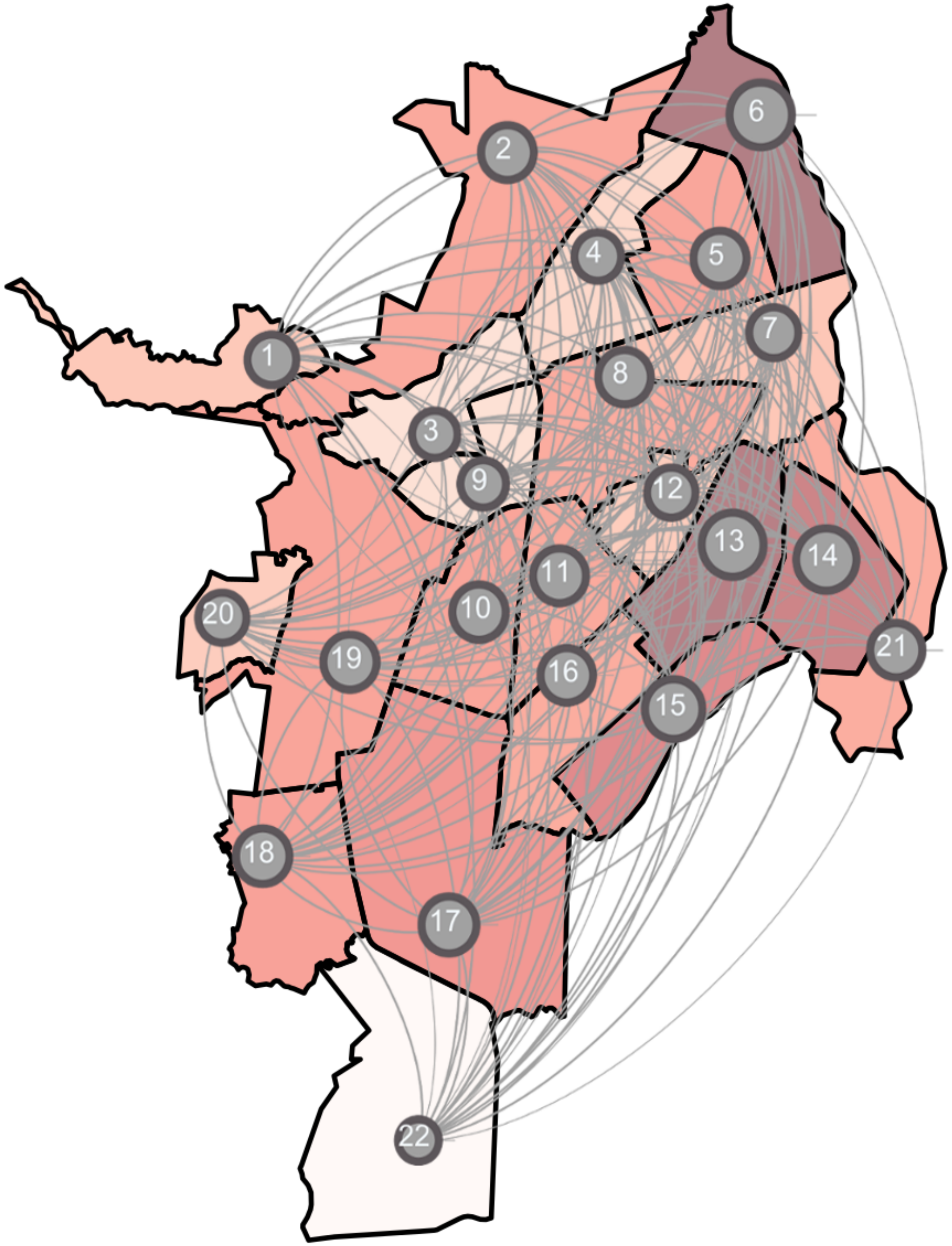
MMCA on real metapopulations

Santiago de Cali: our data

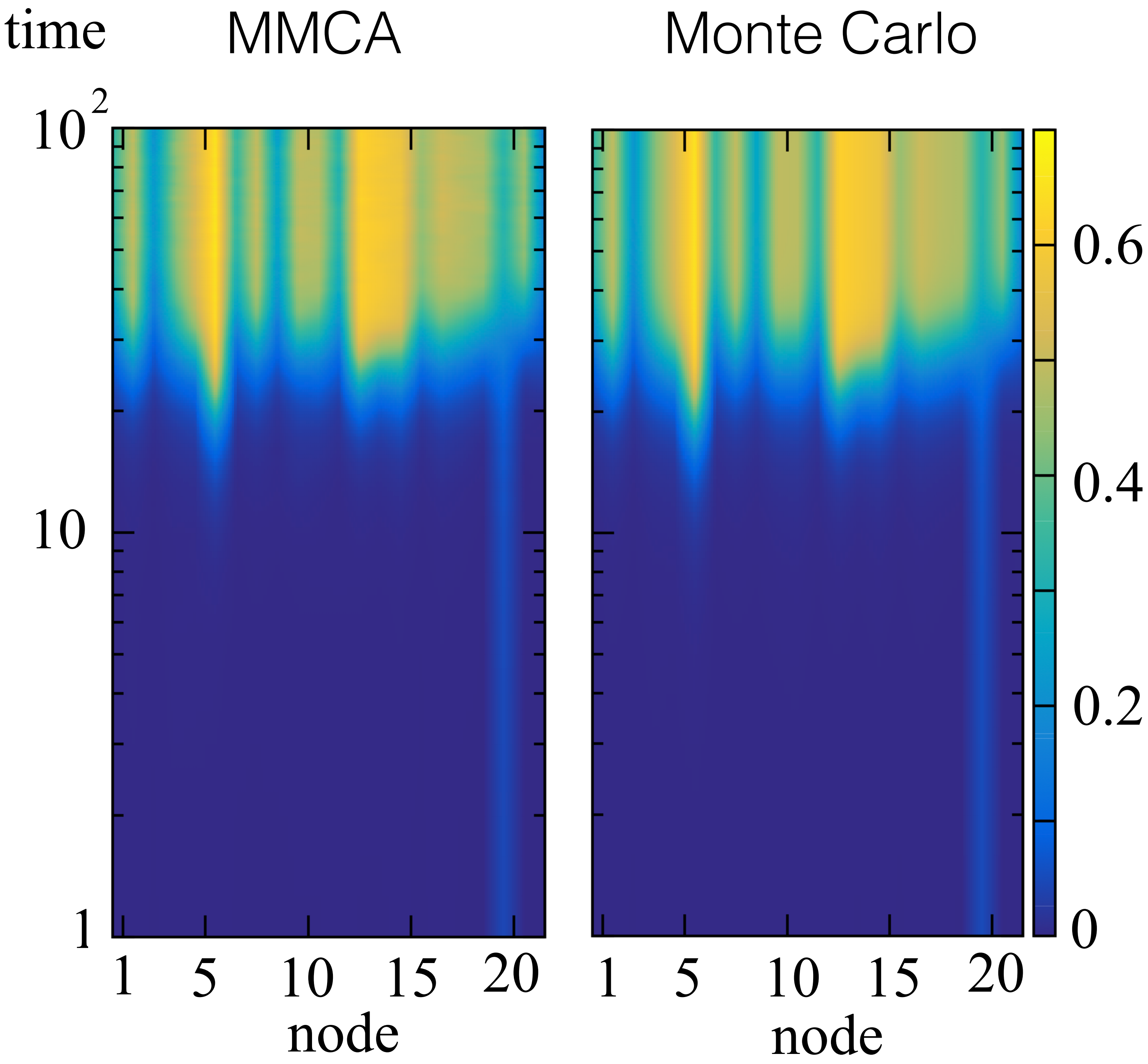
$$N = 2.2 \cdot 10^6$$

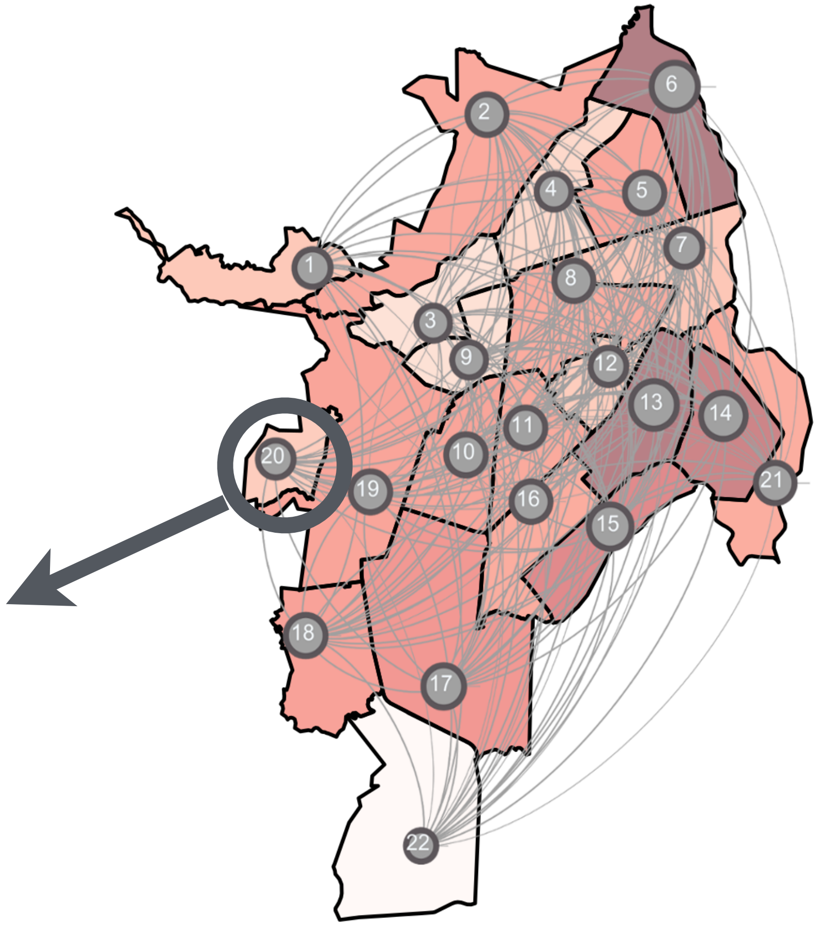
22 districts

$\sim 10^5$ trajectories

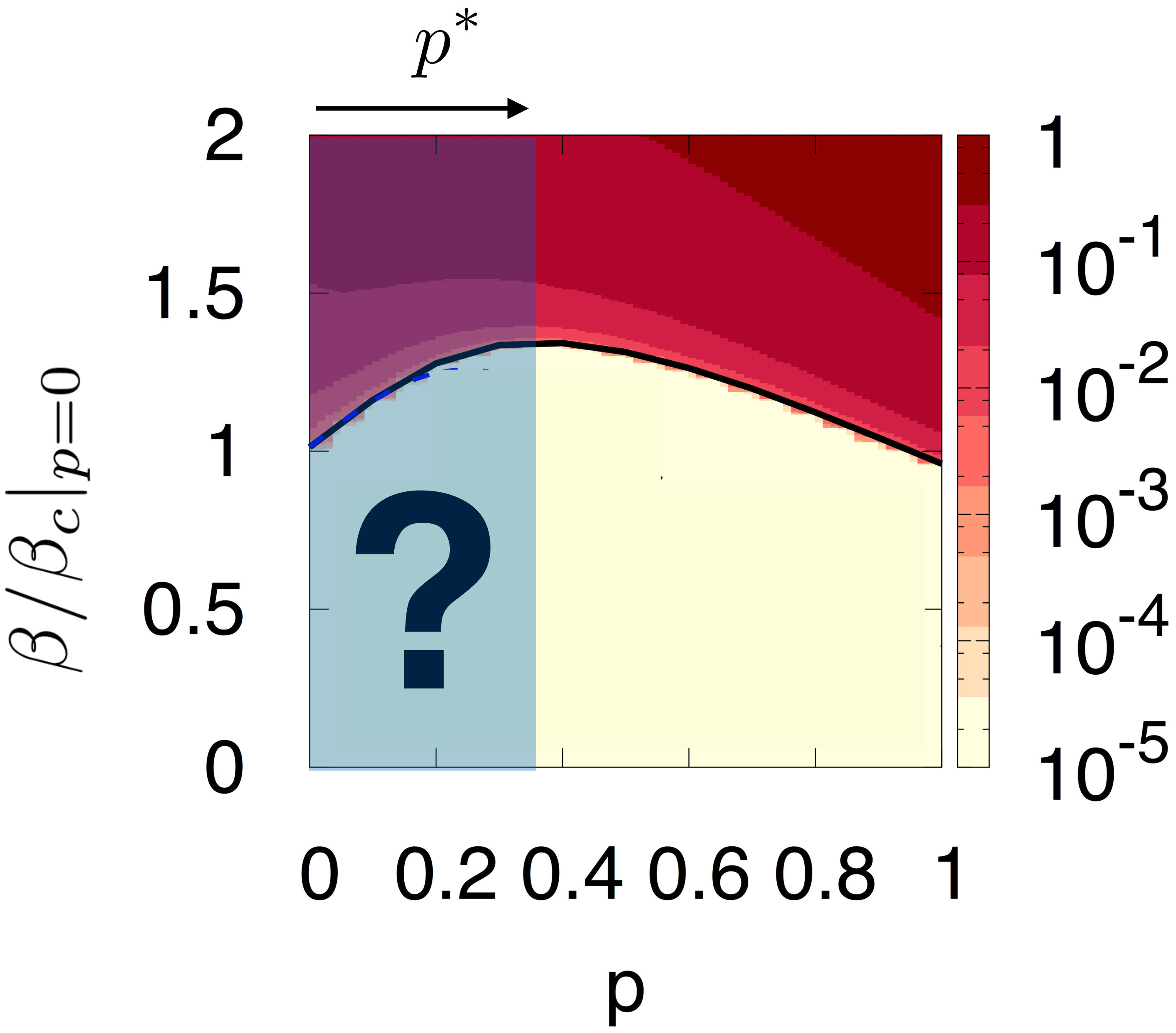


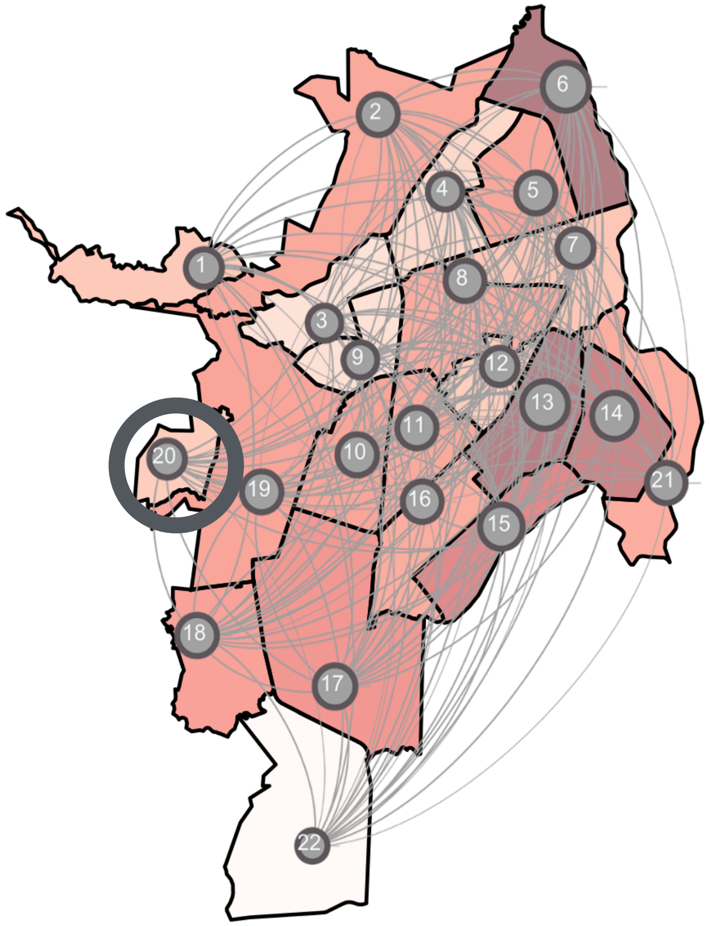
MMCA on real metapopulations

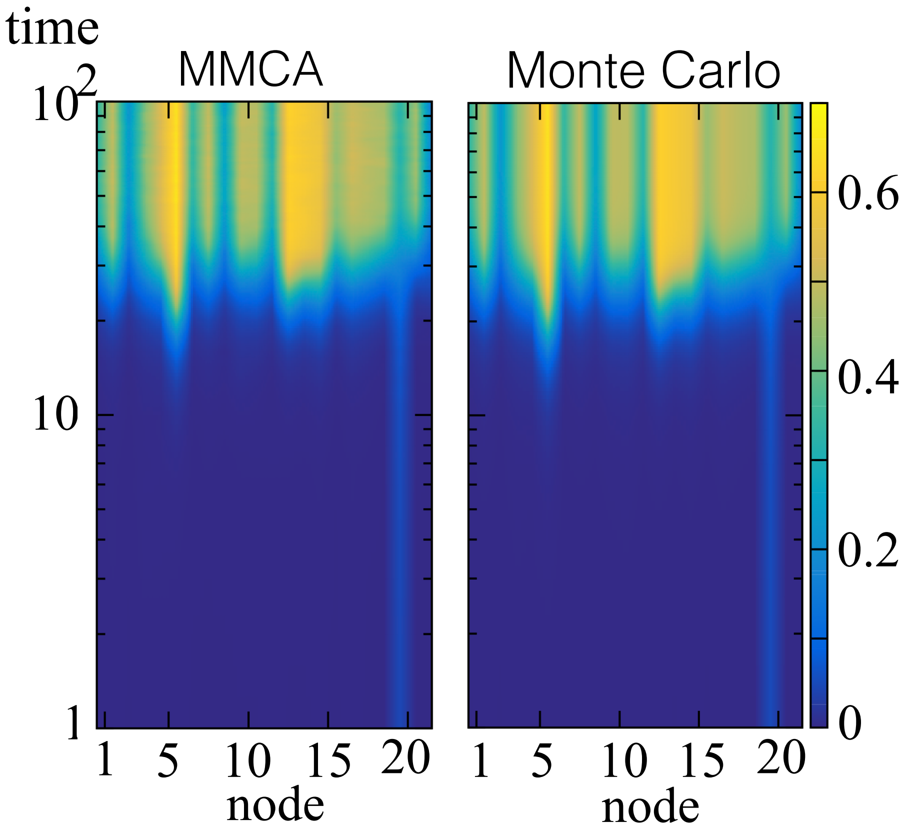




MMCA on real metapopulations







Epidemic detriment, the threshold increases!

MMCA on real metapopulations

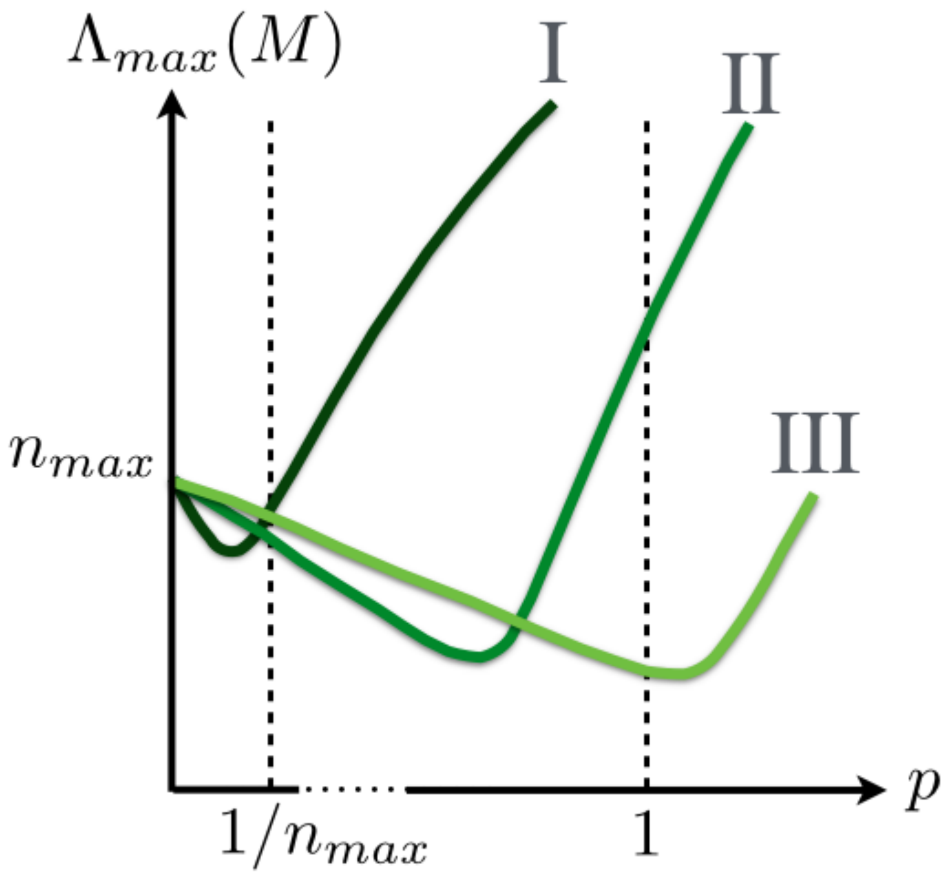
$$\beta_c = \frac{\mu}{\Lambda_{\max}(\mathbf{M})}$$

Asymptotic analysis for $p \to 0$

$$M_{ij} = (1-p)^2 \delta_{ij} n_j + p(1-p) n_j \left(\mathbf{R} + \mathbf{R}^{\mathbf{T}}\right)_{ij} + p^2 n_j \left(\mathbf{R} \cdot \mathbf{R}^{\mathbf{T}}\right)_{ij}$$

$$M_{ij}(p=0) = \delta_{ij} n_j \longrightarrow \Lambda_{\max}[M(p=0)] = n_{\max}$$

$$M_{ij}(p \ll 1) \longrightarrow \Lambda_{\max}[M(p \ll 1)] = n_{\max} + Ap + Bp^2$$



There are three different regimes

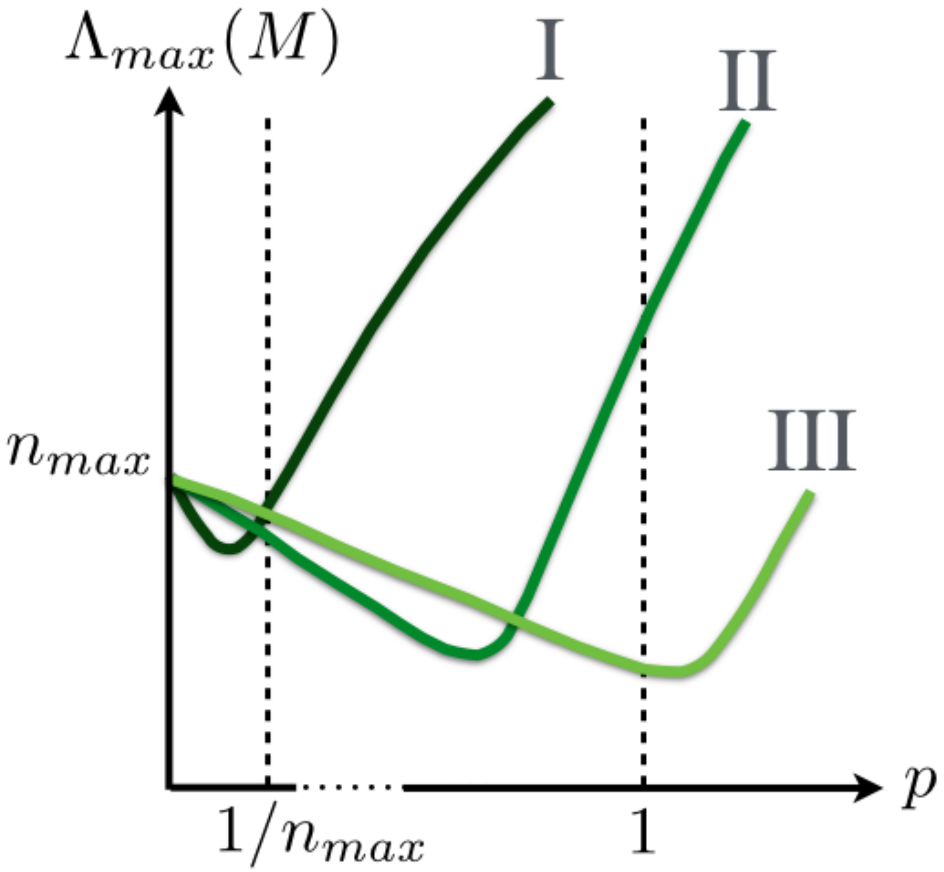
Epidemic Threshold

$$\beta_c = \frac{\mu}{\Lambda_{\max}(\mathbf{M})}$$

$$M_{ij} = (1-p)^2\delta_{ij}n_j + p(1-p)n_j\left(\mathbf{R}+\mathbf{R^T}\right)_{ij} + p^2 n_j\left(\mathbf{R}\cdot\mathbf{R^T}\right)_{ij}$$

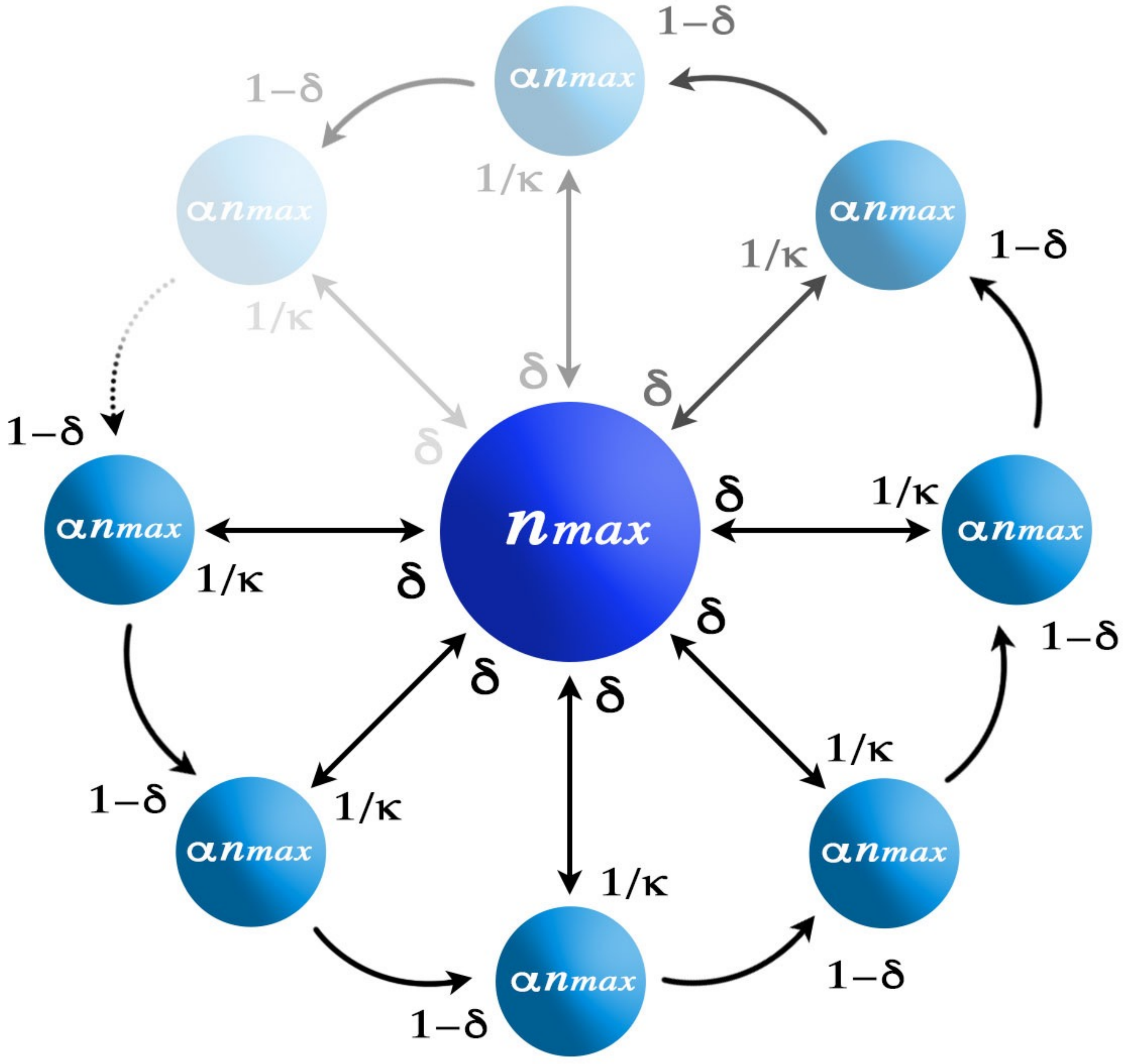
$$M_{ij}(p=0) = \delta_{ij}n_j \longrightarrow \Lambda_{max}[M(p=0)] = n_{max}$$

$$\Lambda_{max}[M(p \ll 1)] = n_{max} + 2pn_{max}(R_{max,max}-1)$$



$$+p^2 n_{max}\sum_{j\neq i}\frac{n_j(R_{max,j}+R_{j,max})^2}{n_{max}-n_j}$$

Three different regimes



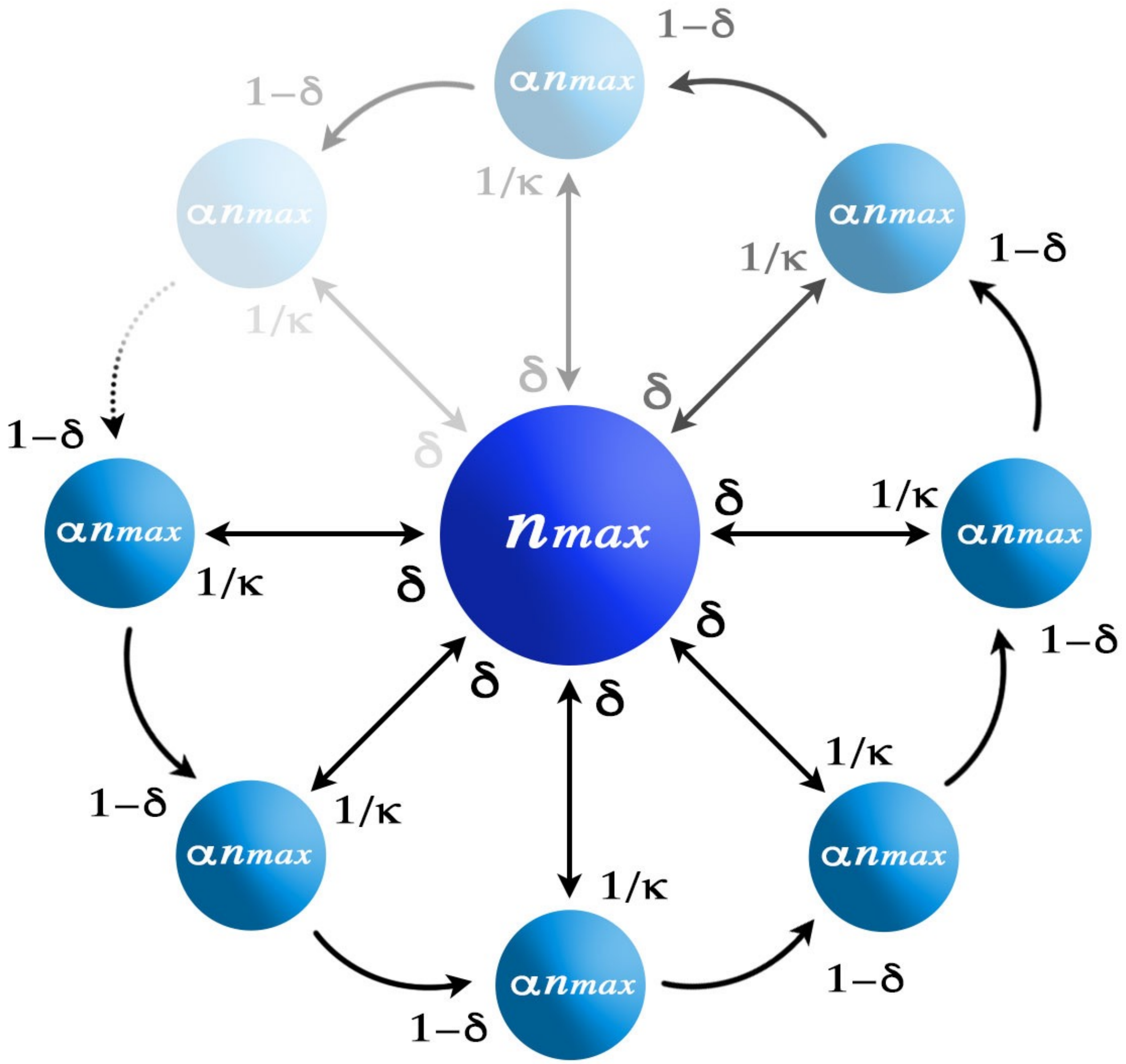
Starcity

n_{max} : Population of hub

k : Number of leaves

α : Scaling factor of leaves population

δ : Fraction of trips from leaf to hub



Starcity

n_{max} : Population of hub

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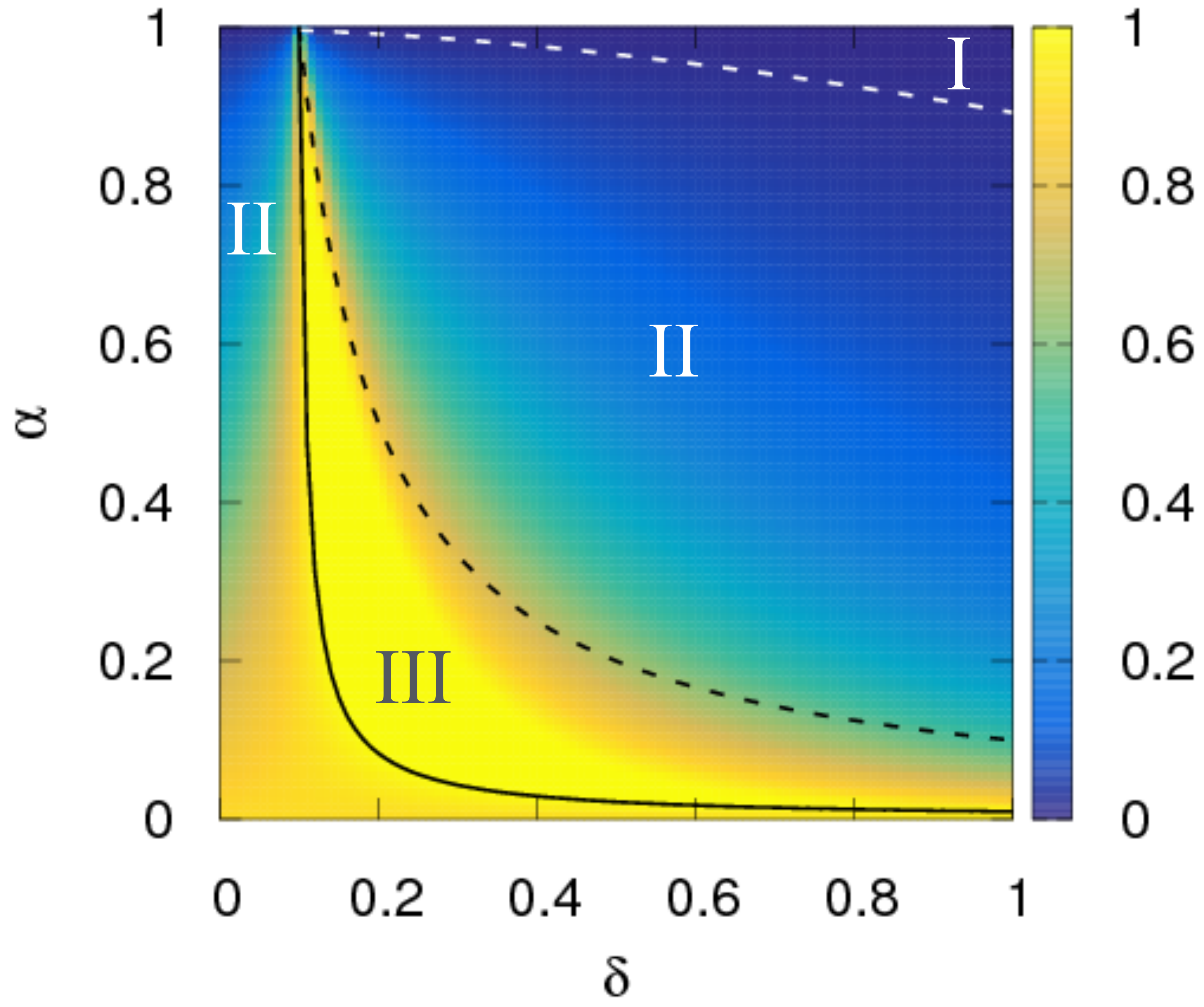
2x2 matrix $\mathbf{M}$

$$\mathbf{M} = \begin{pmatrix} n_{\max}\left[(1-p)^2 + \frac{p^2}{k}\right] & n_{\max}\alpha\left[p\,(1-p)\,(1+k\delta) + p^2\,(1-\delta)\right] \\ n_{\max}\left[p\,(1-p)\left(\frac{1}{k}+\delta\right) + p^2\frac{1}{k}\,(1-\delta)\right] & n_{\max}\alpha\left[(1-p\delta)^2 + kp^2\delta^2\right] \end{pmatrix}$$



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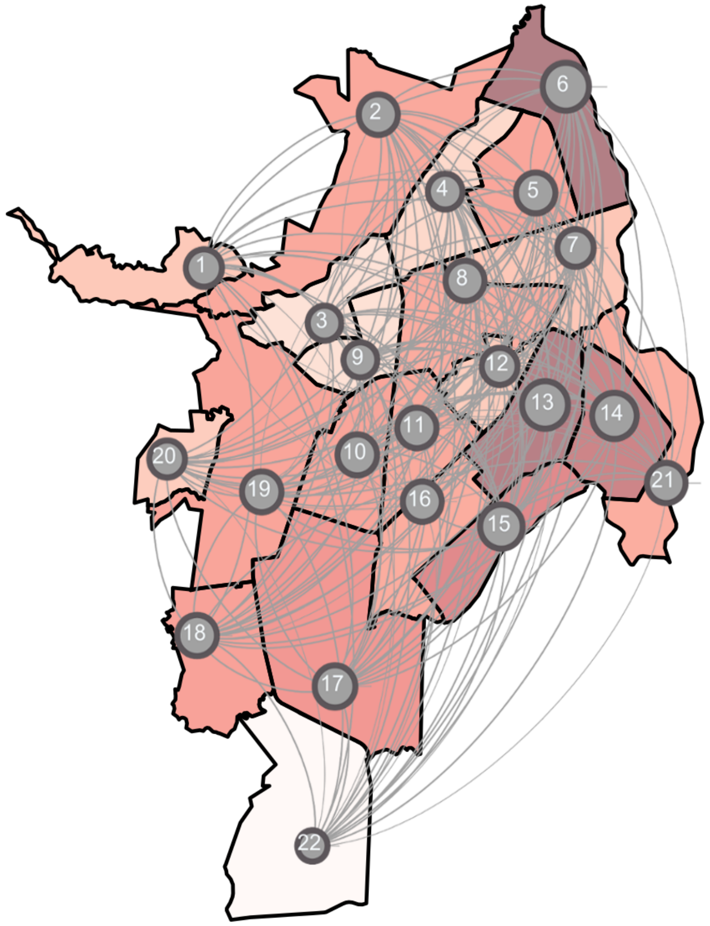
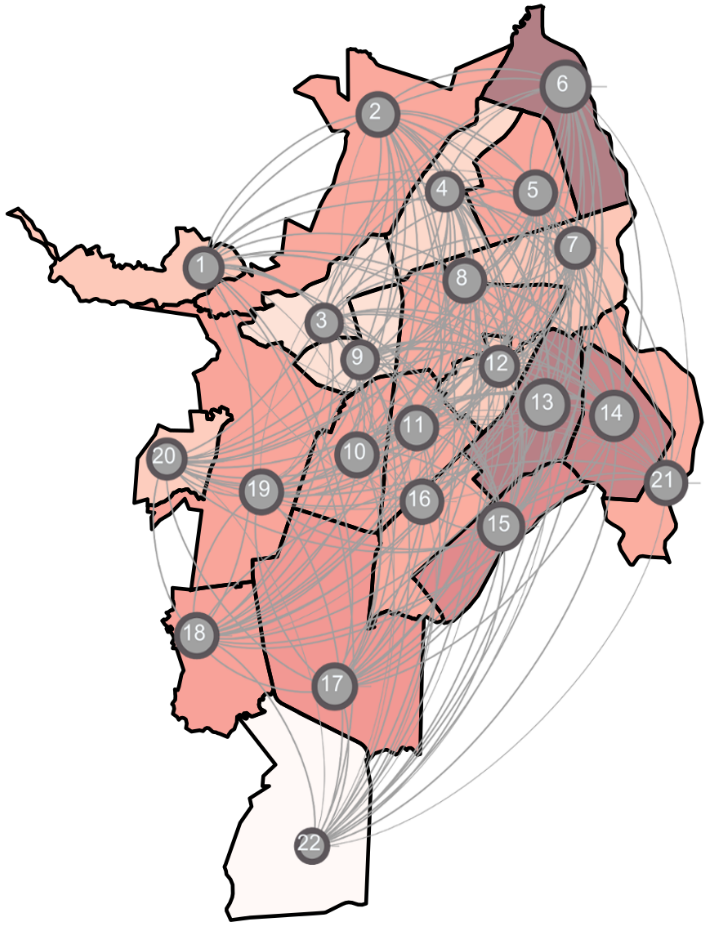
MMCA on real metapopulations

Santiago de Cali

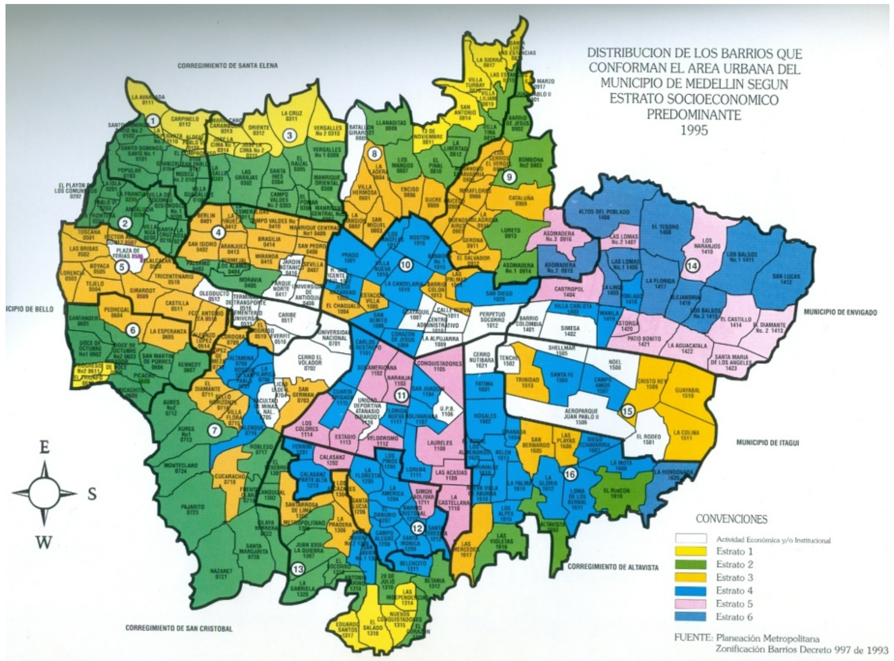


MMCA on real metapopulations

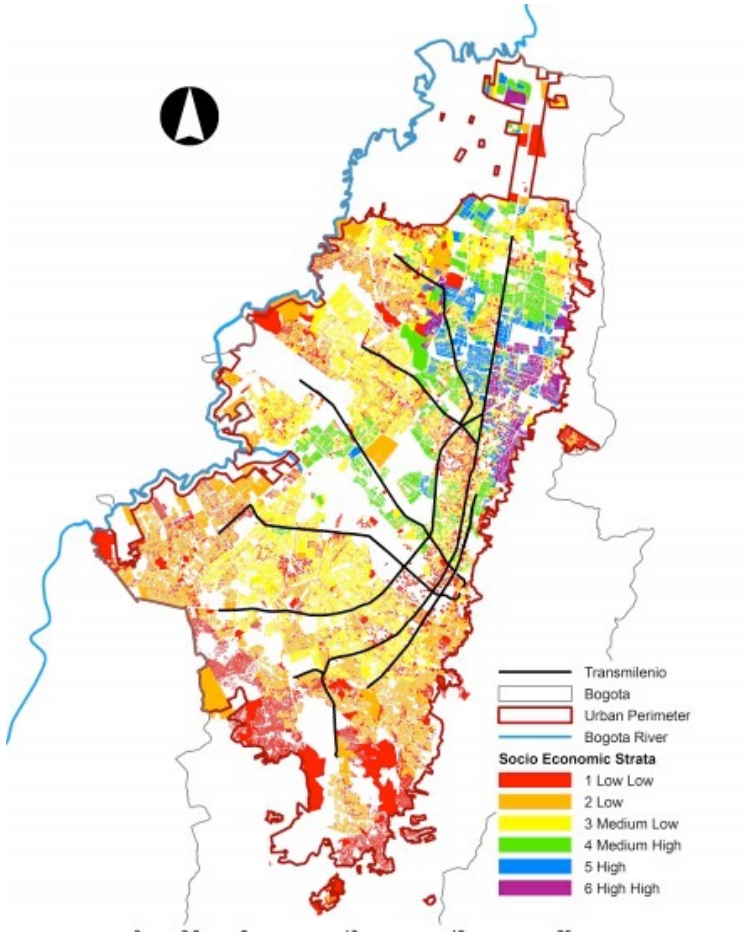
Santiago de Cali



Medellín

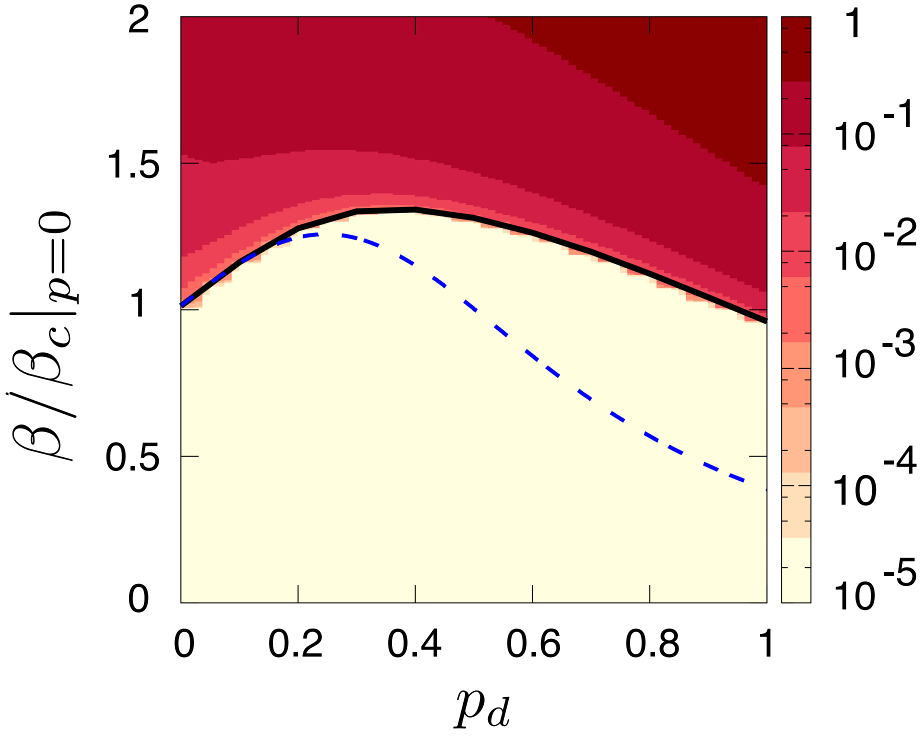


Bogotá



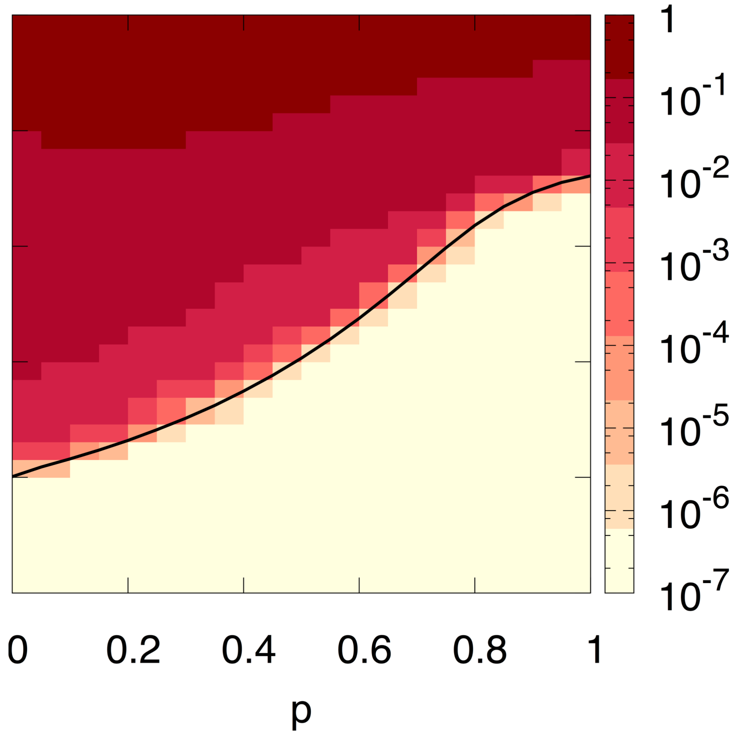
MMCA on real metapopulations

Santiago de Cali



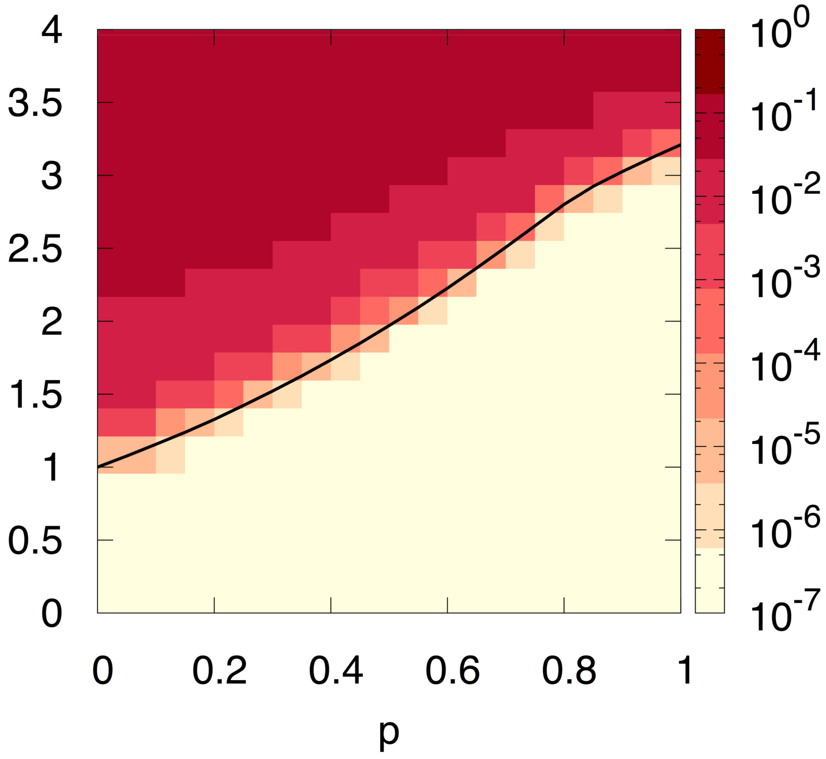
Type II

Medellín



Type III

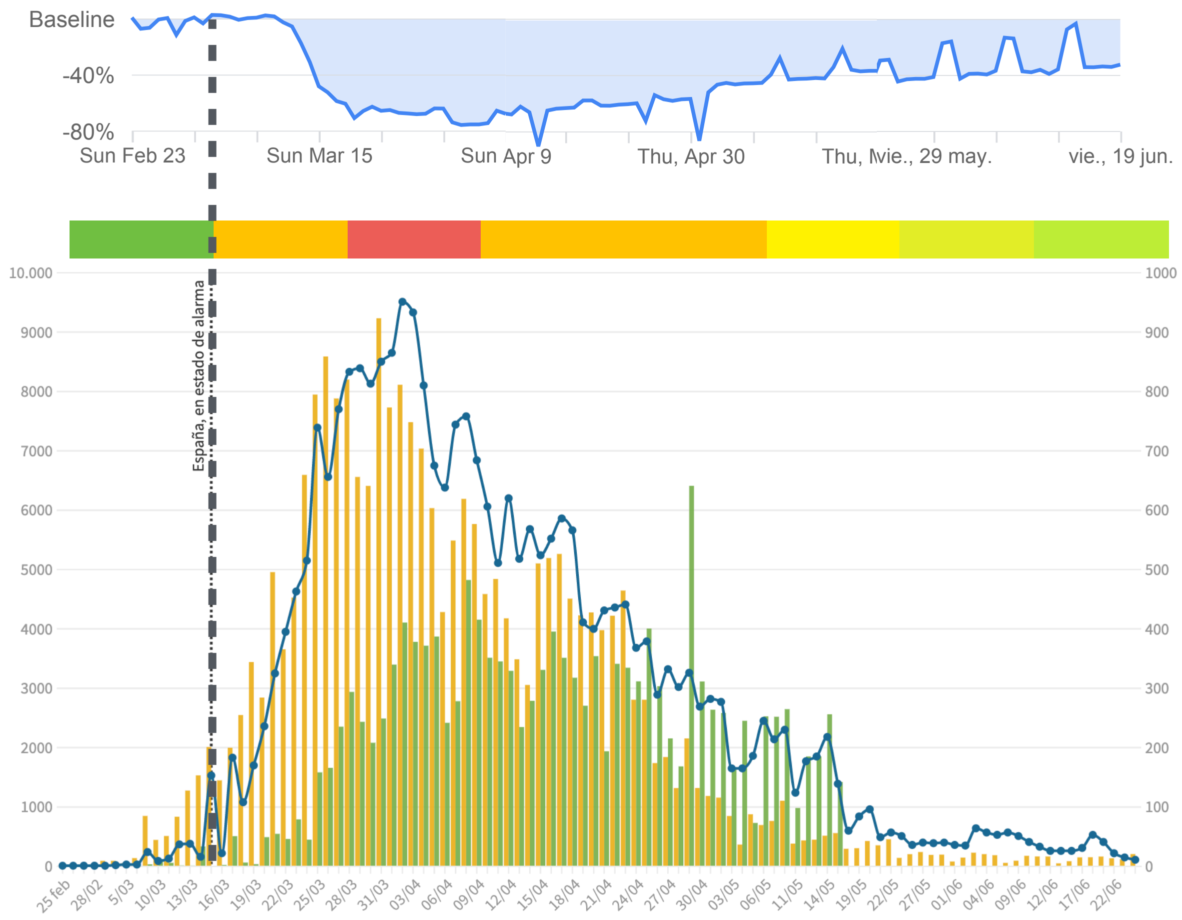
Bogotá

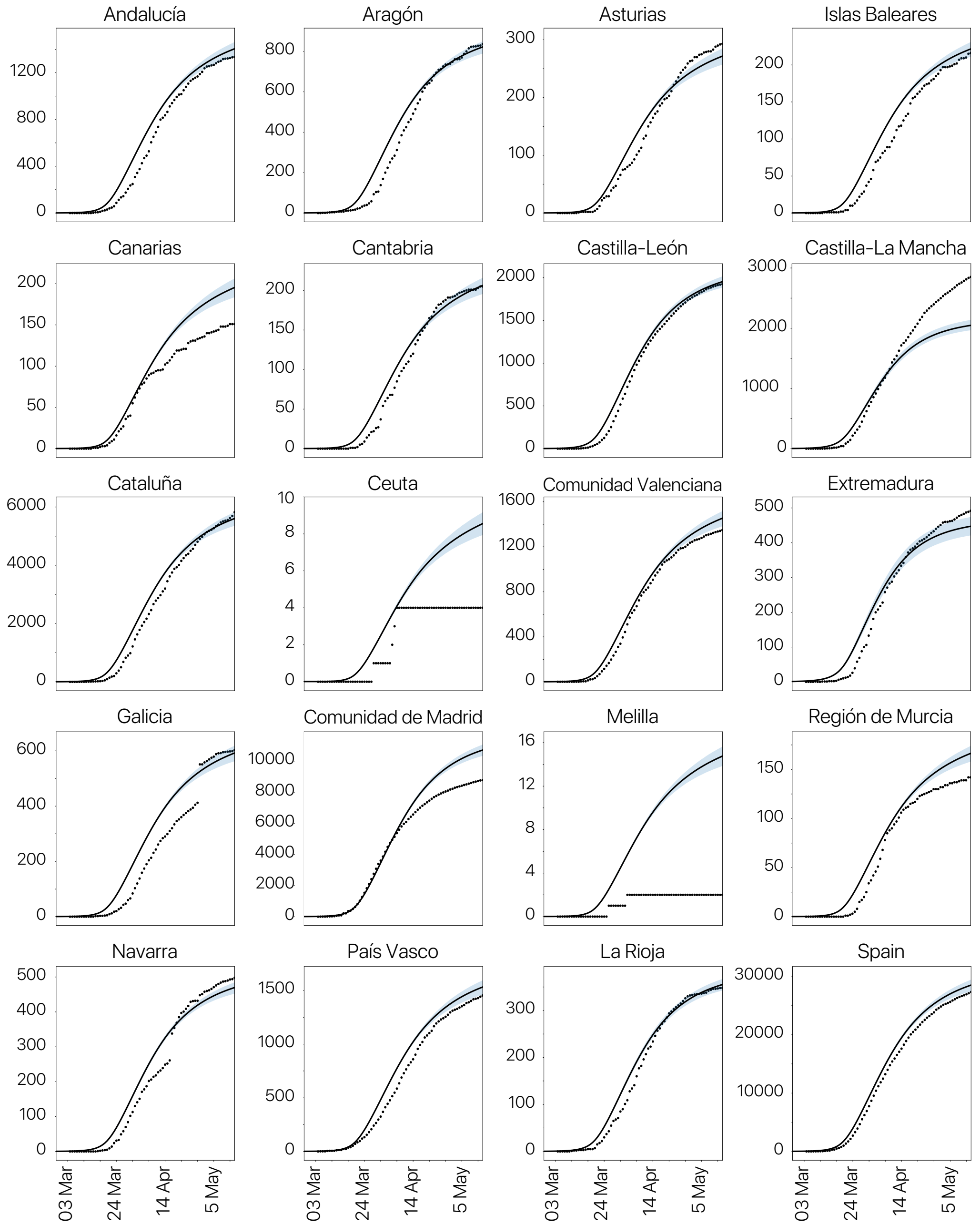


Type III

Modelling COVID

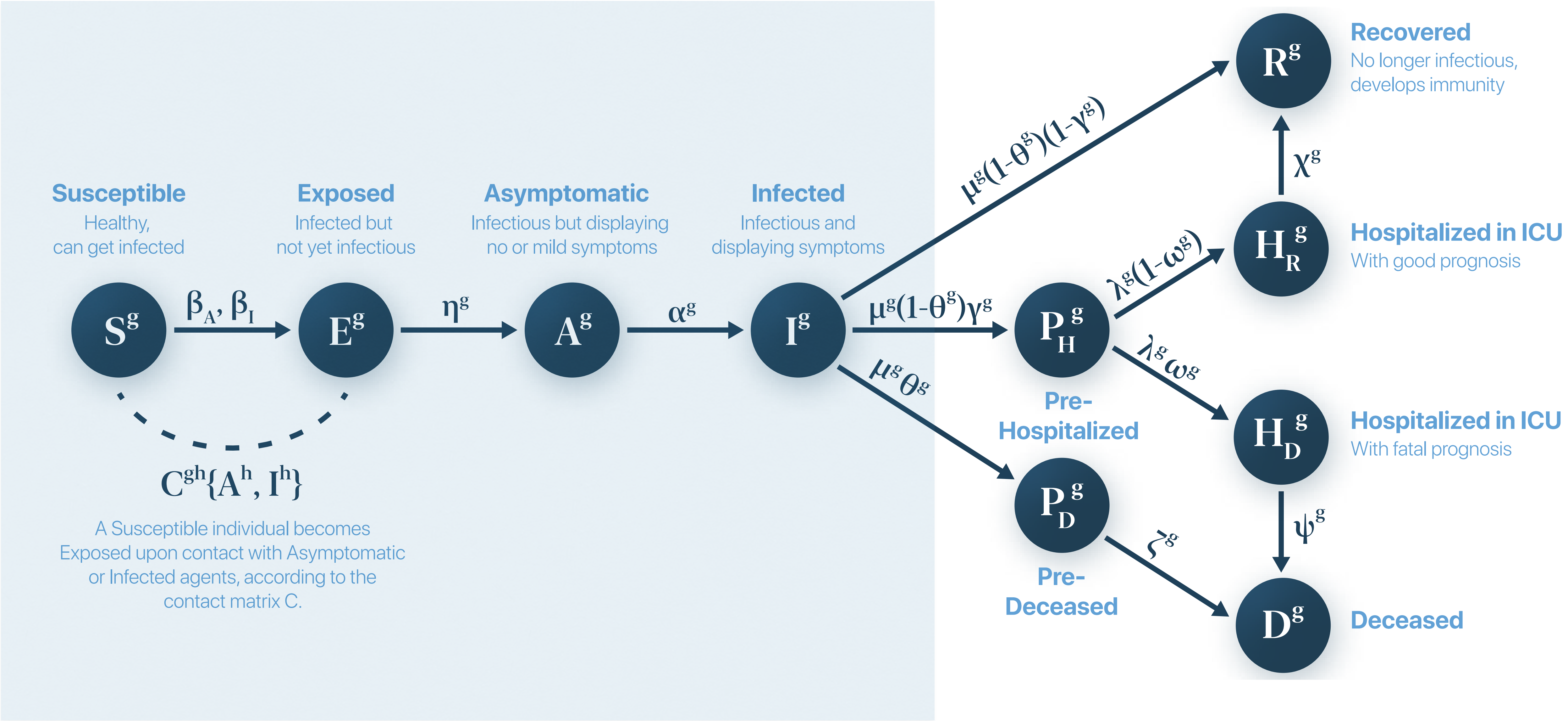
We used the formalism to model the spatio-temporal evolution of COVID19 in Spain





Modelling COVID

Compartmental model



Susceptible
Healthy,
can get infected

Exposed
Infected but
not yet infectious

Asymptomatic
Infectious but displaying
no or mild symptoms

Infected
Infectious and
displaying symptoms

A Susceptible individual becomes
Exposed upon contact with Asymptomatic
or Infected agents, according to the
contact matrix C.

Pre-Hospitalized

Pre-Deceased

Recovered
No longer infectious,
develops immunity

Hospitalized in ICU
With good prognosis

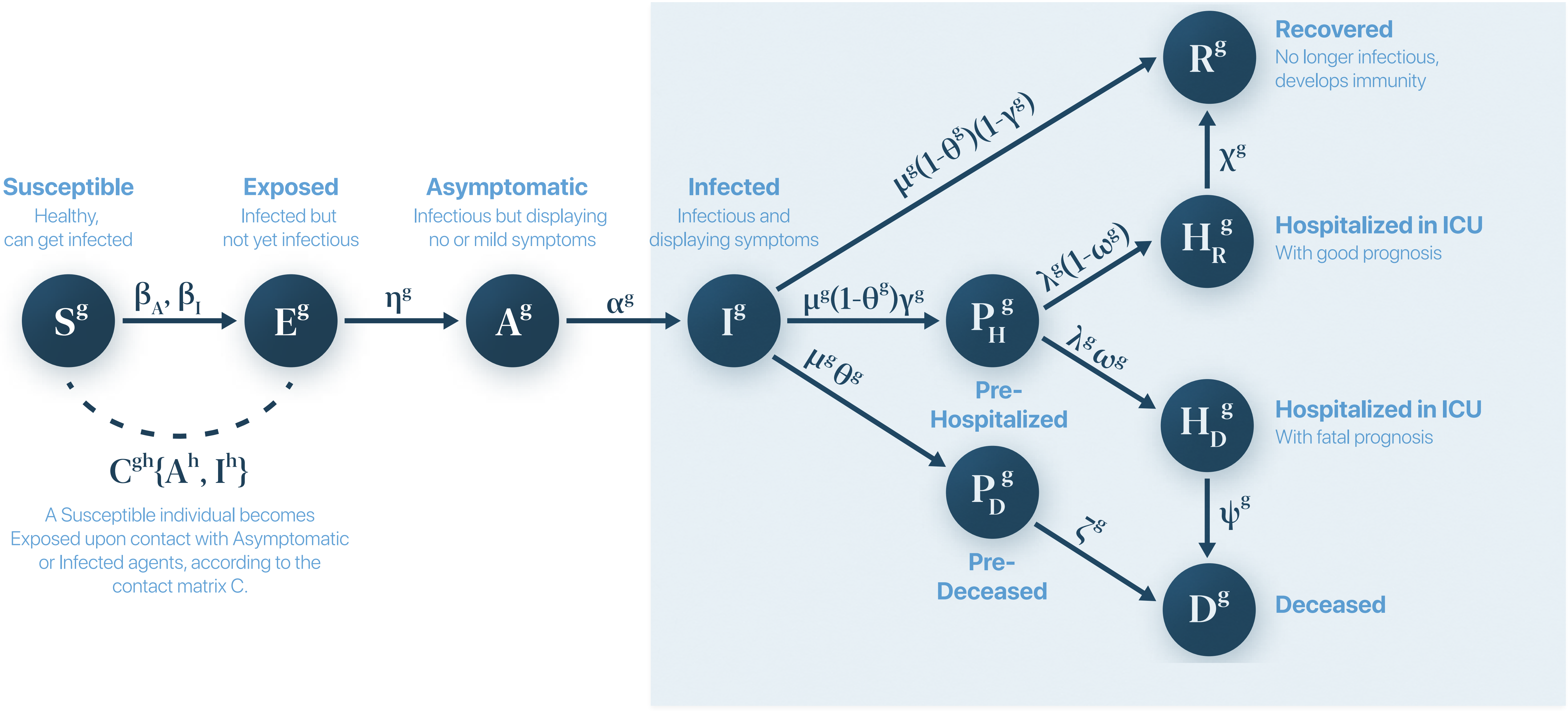
Hospitalized in ICU
With fatal prognosis

Deceased

Epidemiological dynamics

Modelling COVID

Compartmental model



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Infected but
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Asymptomatic
Infectious but displaying
no or mild symptoms

Infected
Infectious and
displaying symptoms

Pre-Hospitalized

Pre-Deceased

Recovered
No longer infectious,
develops immunity

Hospitalized in ICU
With good prognosis

Hospitalized in ICU
With fatal prognosis

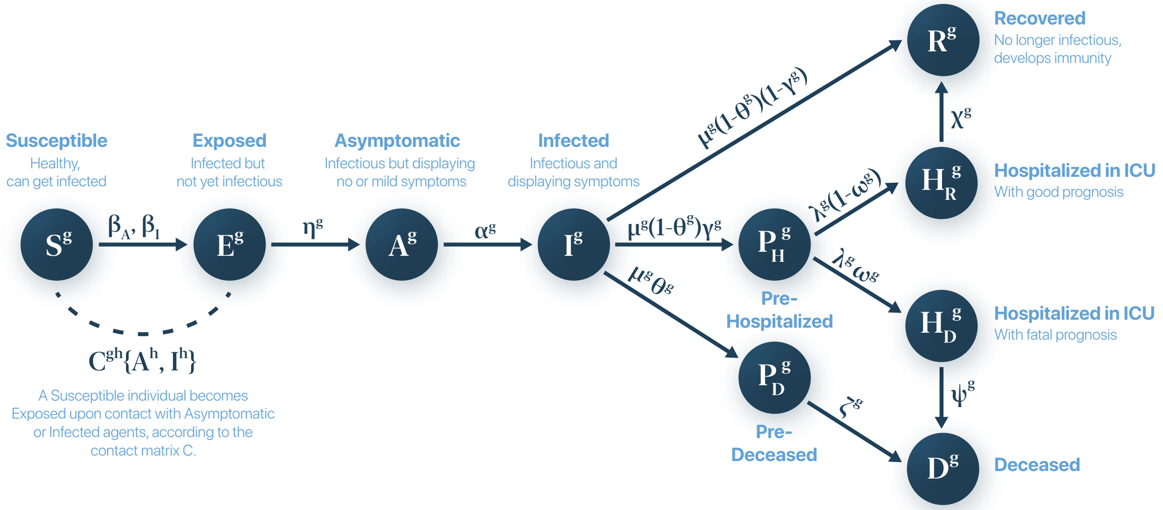
Deceased

A Susceptible individual becomes Exposed upon contact with Asymptomatic or Infected agents, according to the contact matrix C.

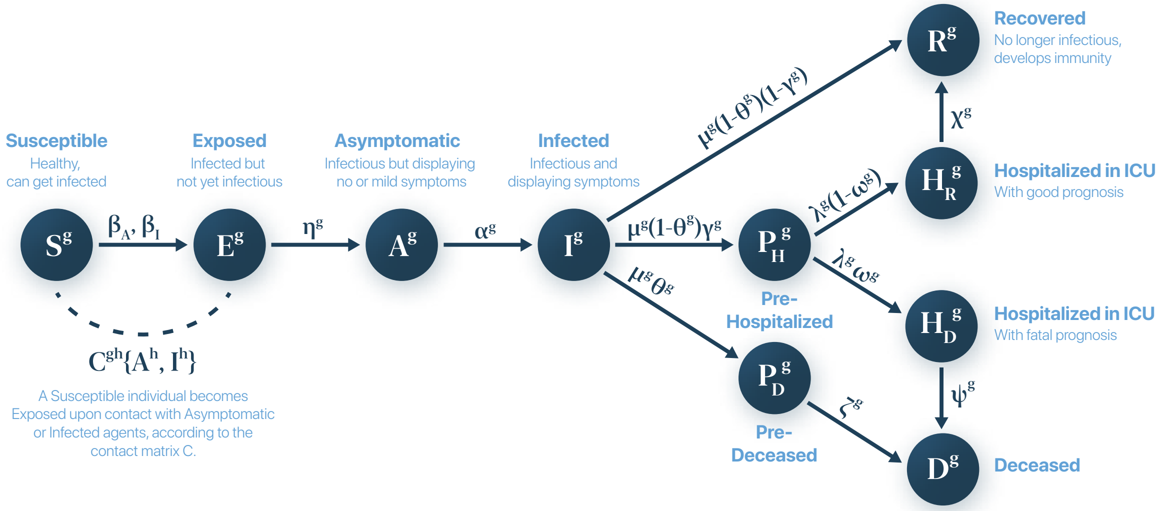
Clinical dynamics

Modelling COVID

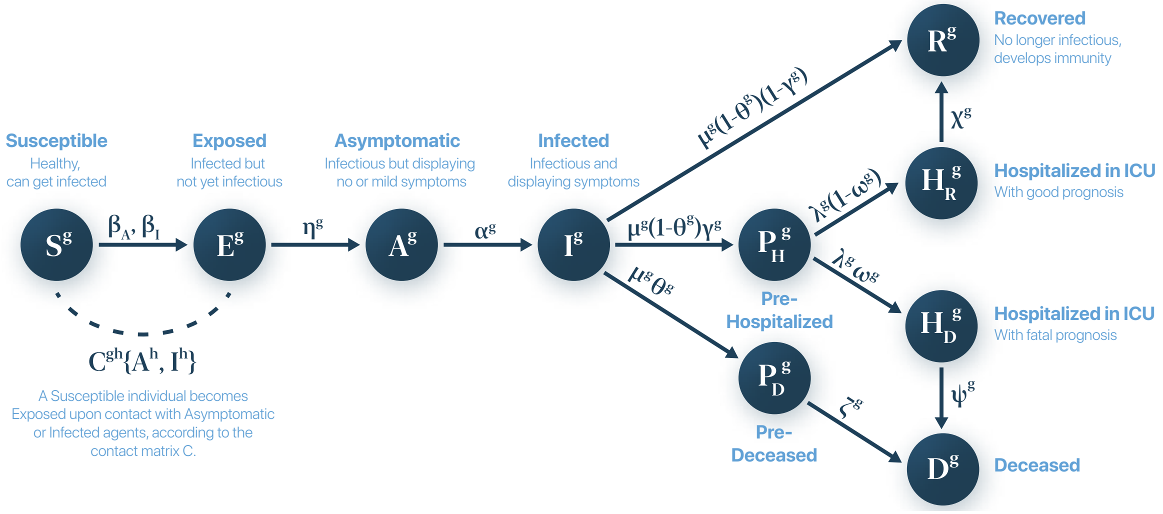
Age structured



A Susceptible individual becomes Exposed upon contact with Asymptomatic or Infected agents, according to the contact matrix C.



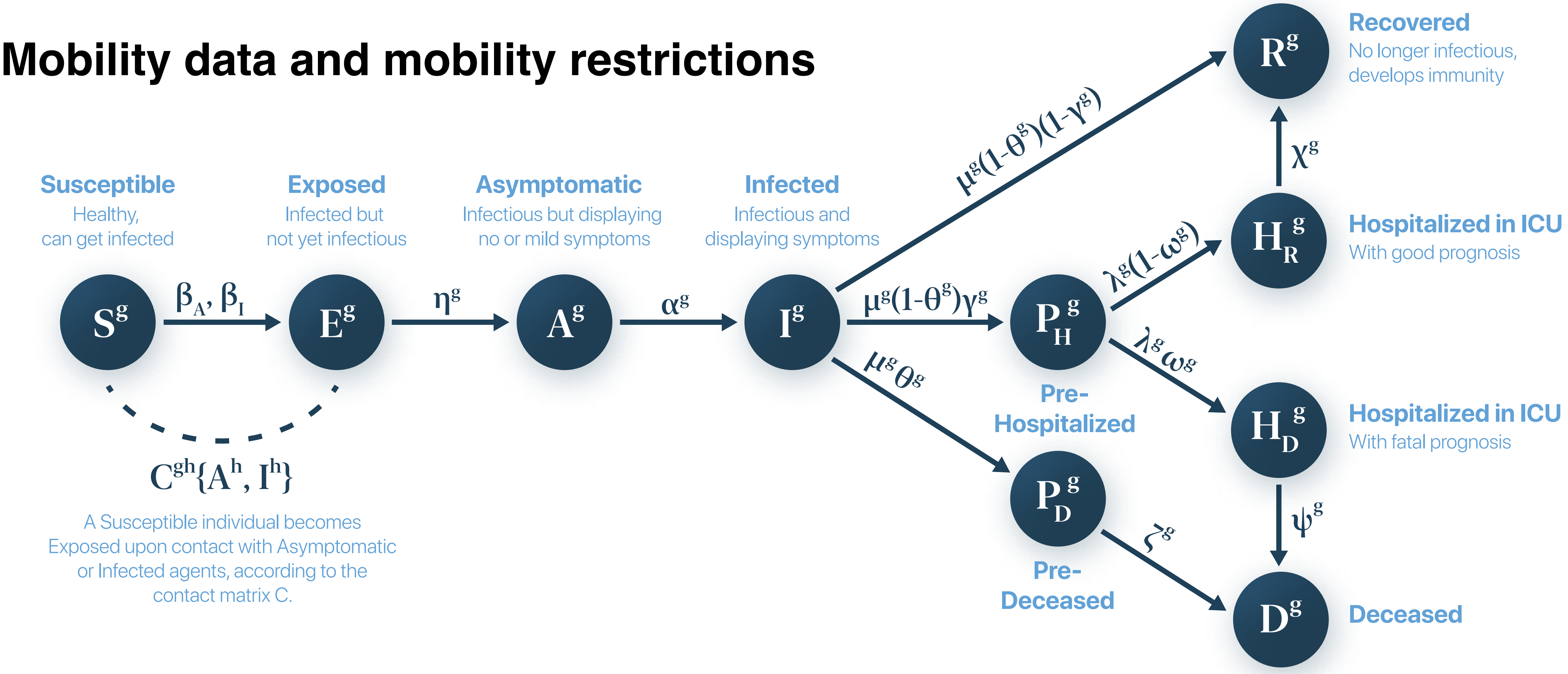
A Susceptible individual becomes Exposed upon contact with Asymptomatic or Infected agents, according to the contact matrix C.



A Susceptible individual becomes Exposed upon contact with Asymptomatic or Infected agents, according to the contact matrix C.

Modelling COVID

Mobility data and mobility restrictions



Susceptible
Healthy,
can get infected

Exposed
Infected but
not yet infectious

Asymptomatic
Infectious but displaying
no or mild symptoms

Infected
Infectious and
displaying symptoms

Recovered
No longer infectious,
develops immunity

Hospitalized in ICU
With good prognosis

Hospitalized in ICU
With fatal prognosis

Pre-Hospitalized

Pre-Deceased

Deceased

$C^{gh}\{A^h, I^h\}$

A Susceptible individual becomes
Exposed upon contact with Asymptomatic
or Infected agents, according to the
contact matrix C.

Mobility and confinement:

- Mobility data was gathered from INE on normal week and weekend statistics
- A fraction κ_0 of the population is confined in their households
- Confined population keep in contact with other confined households with probability ϕ
- Non-confined individuals reduce their contacts due to social distancing by a fraction δ

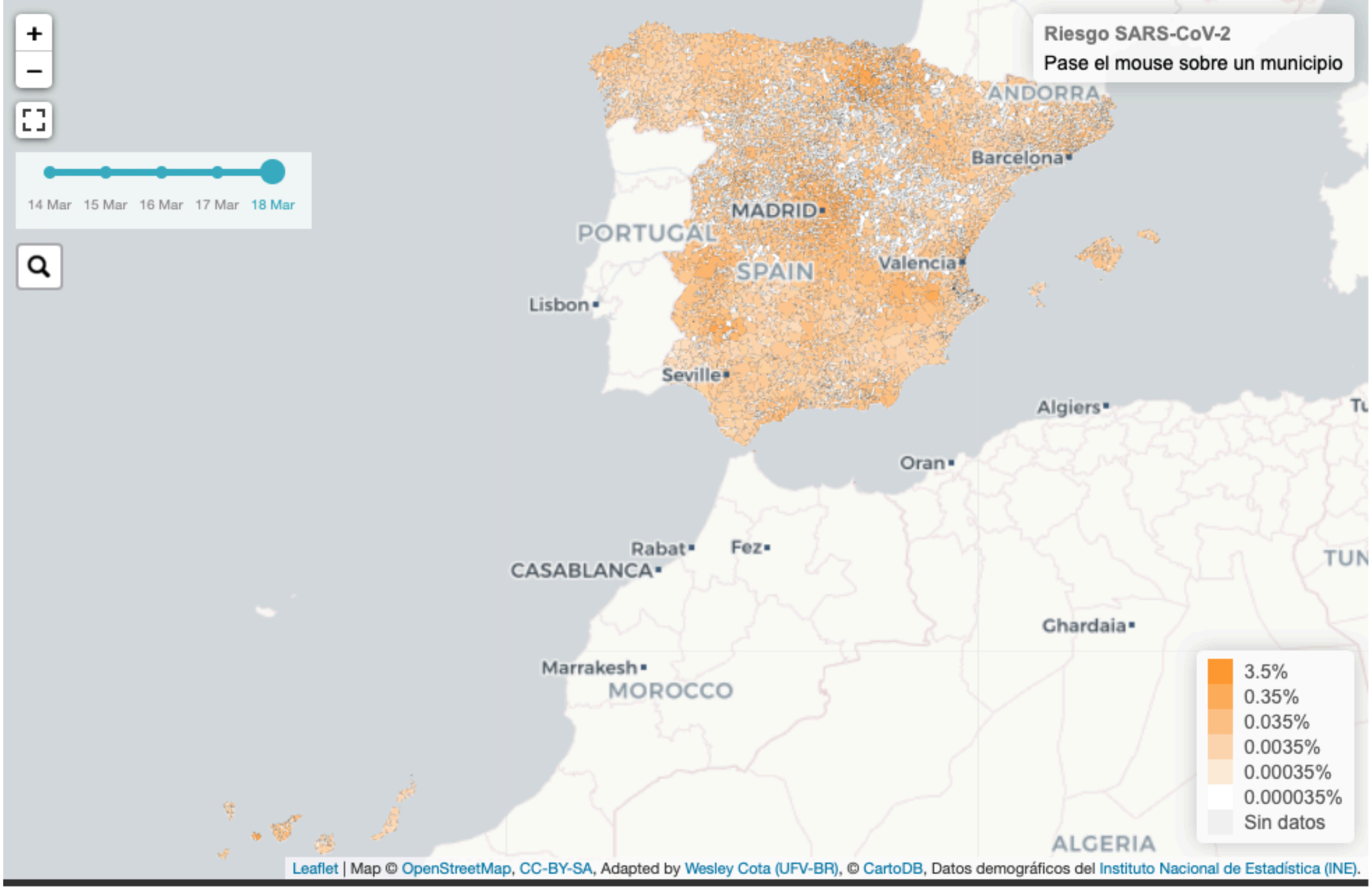
Modelling COVID

$$
\begin{aligned}
\rho_i^{S,g}(t+1) &= \rho_i^{S,g}(t)\,(1-\Pi_i^g(t))\,,\\
\rho_i^{E,g}(t+1) &= \rho_i^{S,g}(t)\,\Pi_i^g(t) + (1-\eta^g)\,\rho_i^{E,g}(t)\,,\\
\rho_i^{A,g}(t+1) &= \eta^g\,\rho_i^{E,g}(t) + (1-\alpha^g)\,\rho_i^{A,g}(t)\,,\\
\rho_i^{I,g}(t+1) &= \alpha^g\,\rho_i^{A,g}(t) + (1-\mu^g)\,\rho_i^{I,g}(t)\,,\\
\rho_i^{P_D,g}(t+1) &= \mu^g\,\theta^g\,\rho_i^{I,g}(t) + (1-\zeta^g)\,\rho_i^{P_D,g}(t)\,,\\
\rho_i^{P_H,g}(t+1) &= \mu^g\,(1-\theta^g)\,\gamma^g\,\rho_i^{I,g}(t) + (1-\lambda^g)\,\rho_i^{P_H,g}(t)\,,\\
\rho_i^{R,g}(t+1) &= \mu^g\,(1-\theta^g)\,(1-\gamma^g)\,\rho_i^{I,g}(t) + \chi^g\,\rho_i^{H_R,g}(t) + \rho_i^{R,g}(t)\,,\\
\rho_i^{H_D,g}(t+1) &= \lambda^g\,\omega^g\,\rho_i^{P_H,g}(t) + (1-\psi^g)\,\rho_i^{H_D,g}(t)\,,\\
\rho_i^{H_R,g}(t+1) &= \lambda^g\,(1-\omega^g)\,\rho_i^{P_H,g}(t) + (1-\chi^g)\,\rho_i^{H_R,g}(t)\,,\\
\rho_i^{D,g}(t+1) &= \zeta^g\,\rho_i^{P_D,g}(t) + \psi^g\,\rho_i^{H_D,g}(t) + \rho_i^{D,g}(t)\,.
\end{aligned}
$$

$$
\Pi_i^g(t) = (1-p^g)\,P_i^g(t) + p^g \sum_{j=1}^{N_P} R_{ij}^g\,P_j^g(t)\,,
$$

$$
P_i^g(t) = 1 - \prod_{h=1}^{N_G}\prod_{j=1}^{N_P} (1-\beta_A)^{z^g\,\langle k^g\rangle\, f\left(\frac{\tilde{n}_i}{s_i}\right) C^{gh}\, \frac{n_{j\to i}^{A,h}(t)}{\tilde{n}_i^h}}\;(1-\beta_I)^{z^g\,\langle k^g\rangle\, f\left(\frac{\tilde{n}_i}{s_i}\right) C^{gh}\, \frac{n_{j\to i}^{I,h}(t)}{\tilde{n}_i^h}}
$$

Results modelling COVID in Spain



Riesgo SARS-CoV-2

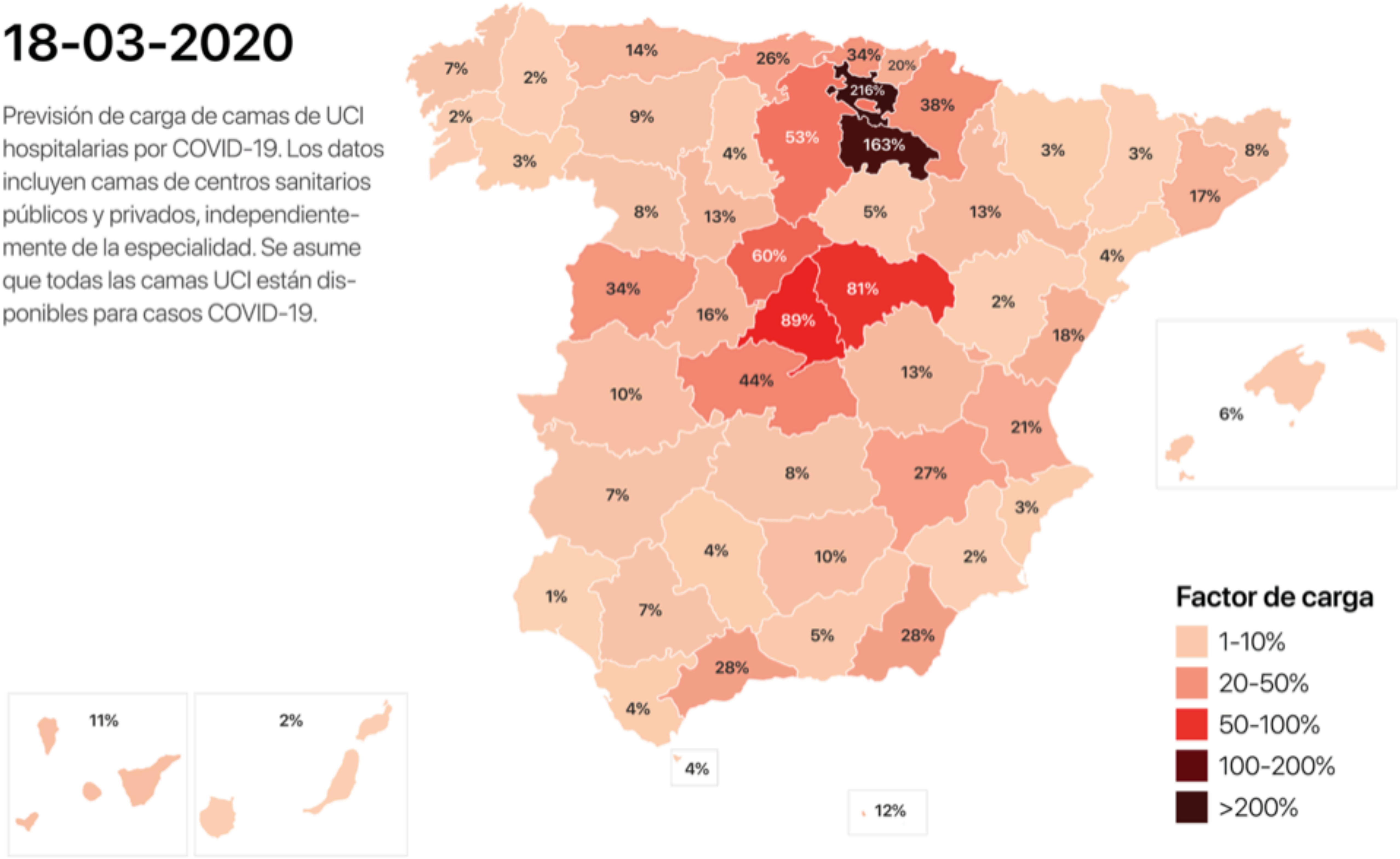
Pase el mouse sobre un municipio

Leaflet | Map © OpenStreetMap, CC-BY-SA, Adapted by Wesley Cota (UFV-BR), © CartoDB, Datos demográficos del Instituto Nacional de Estadística (INE).

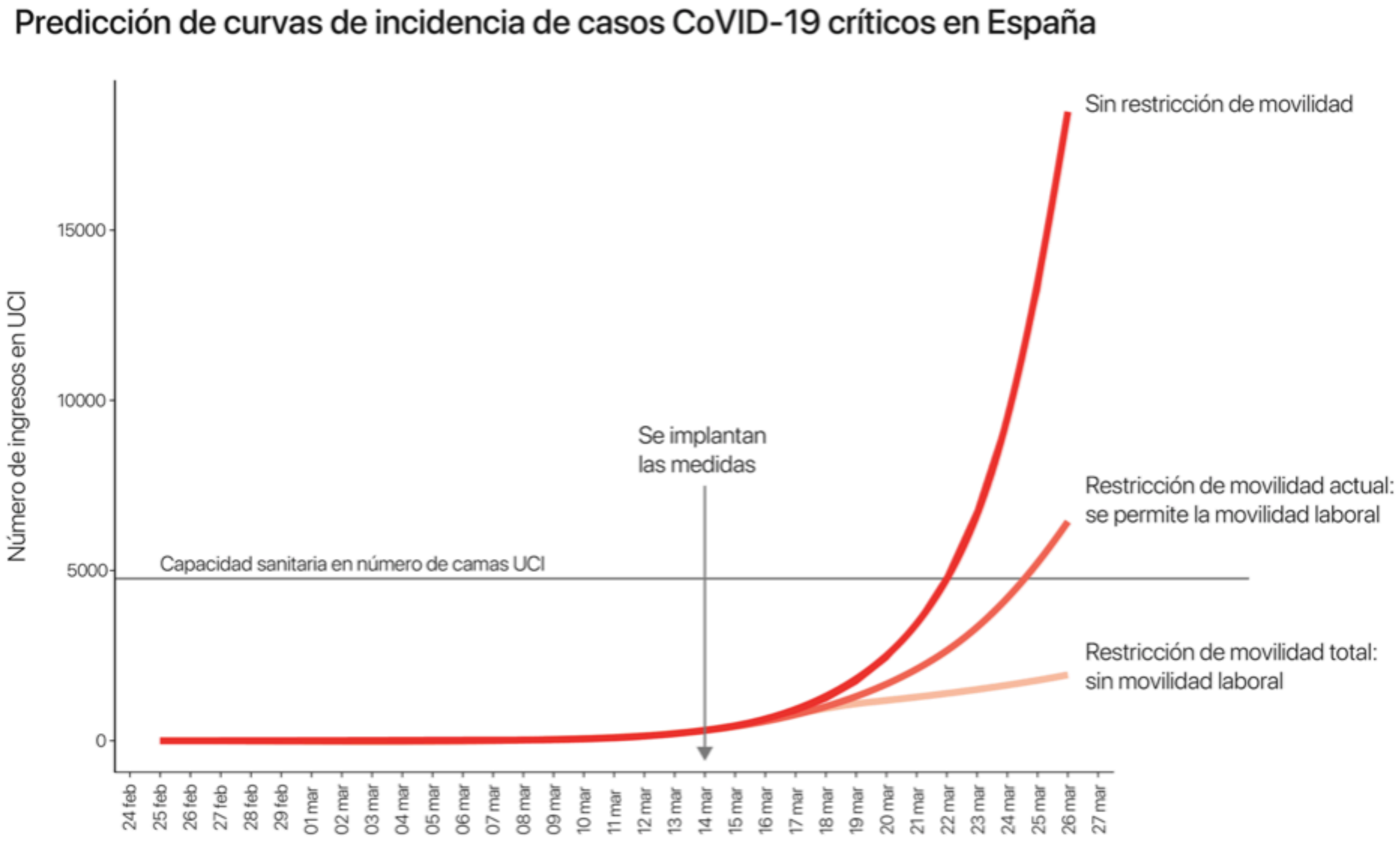
Results modelling COVID in Spain

18-03-2020

Previsión de carga de camas de UCI hospitalarias por COVID-19. Los datos incluyen camas de centros sanitarios públicos y privados, independientemente de la especialidad. Se asume que todas las camas UCI están disponibles para casos COVID-19.



Results modelling COVID in Spain



Modelling COVID

Basic reproduction number R: Assuming an infection probability per contact β, the expected number of individuals infected by an infected individual on a time period τ is

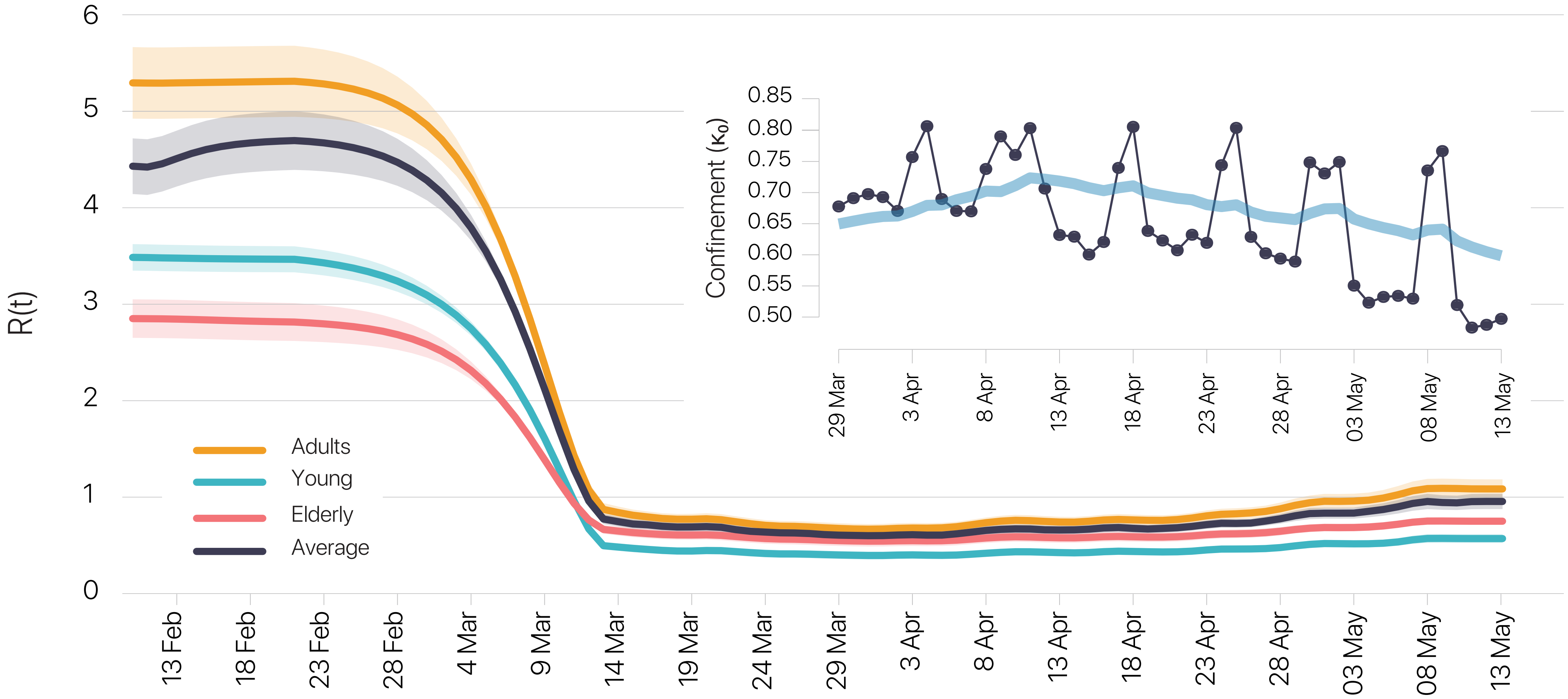
$$R = \tau\, \beta\, \langle k \rangle\, \rho_S$$

Basic reproduction number R for COVID using our model by patch and age

$$\mathscr{R}_i^g(t) = \sum_{s=t}^{\infty} \overset{\tau\, \beta}{\left[\zeta^{A,g}(s-t)\beta_A + \zeta^{I,g}(s-t)\,\beta_I\right]} \sum_{j=1}^{N} \sum_{h=1}^{G} \overset{\langle k \rangle\, \rho_S}{k_{ij}^{gh}(s)\, \tilde{\rho}_j^{S,h}(s)}$$

Modelling COVID

$$\mathscr{R}(t) = \frac{\sum_{i=1}^{N} \sum_{g=1}^{G} \left[\rho_i^{S,g}(t-1) - \rho_i^{S,g}(t)\right] n_i^g \, \mathscr{R}_i^g(t)}{\sum_{i=1}^{N} \sum_{g=1}^{G} \left[\rho_i^{S,g}(t-1) - \rho_i^{S,g}(t)\right] n_i^g}$$



Modelling COVID

$$\mathcal{R}(t) = \frac{\sum_{i=1}^{N}\sum_{g=1}^{G}\left[\rho_i^{S,g}(t-1)-\rho_i^{S,g}(t)\right] n_i^g\,\mathcal{R}_i^g(t)}{\sum_{i=1}^{N}\sum_{g=1}^{G}\left[\rho_i^{S,g}(t-1)-\rho_i^{S,g}(t)\right] n_i^g}$$

Grasping the physics:

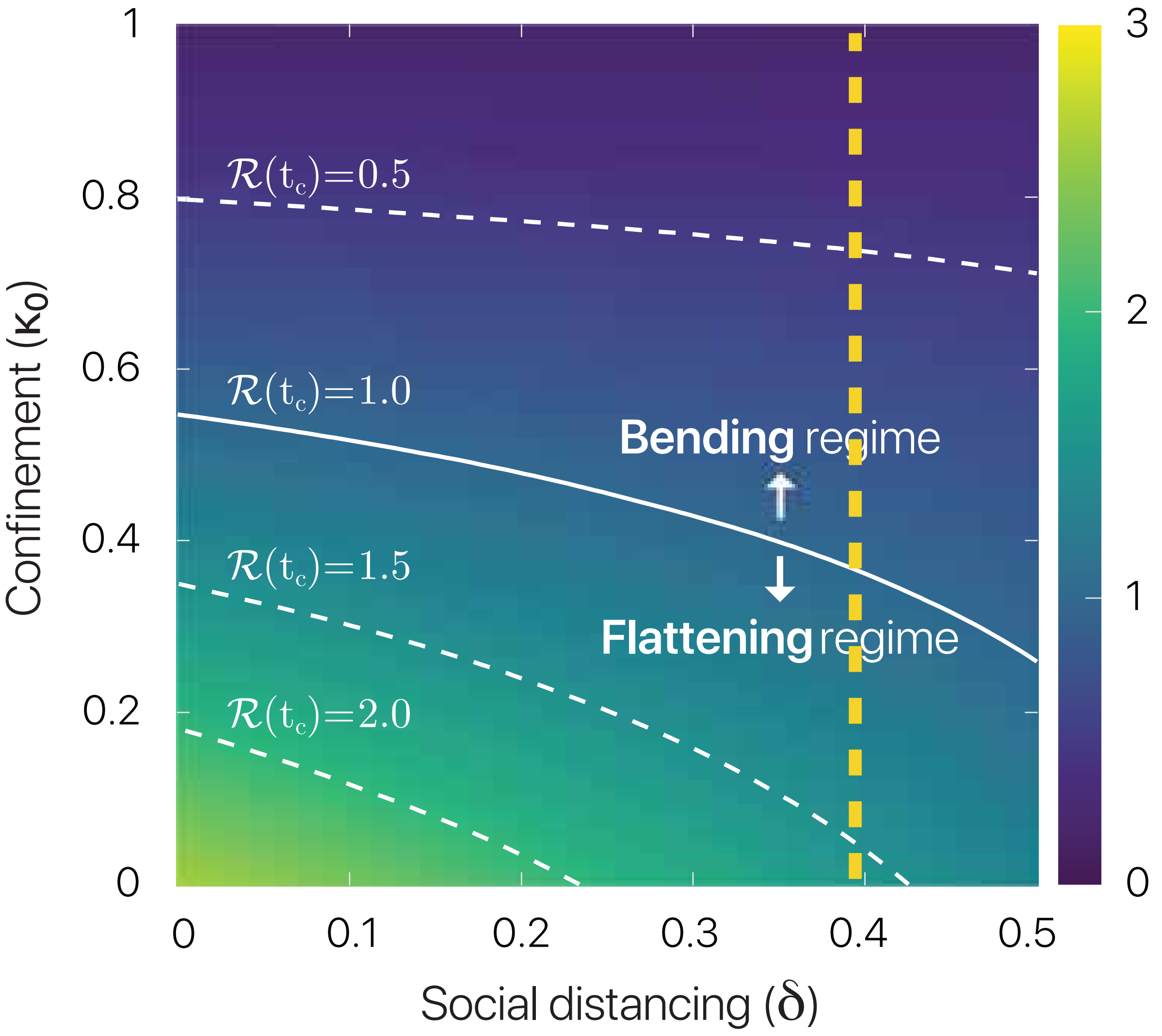
- Neglect heterogeneities among subpopulations
- The pool of susceptible remains constant during the intervention

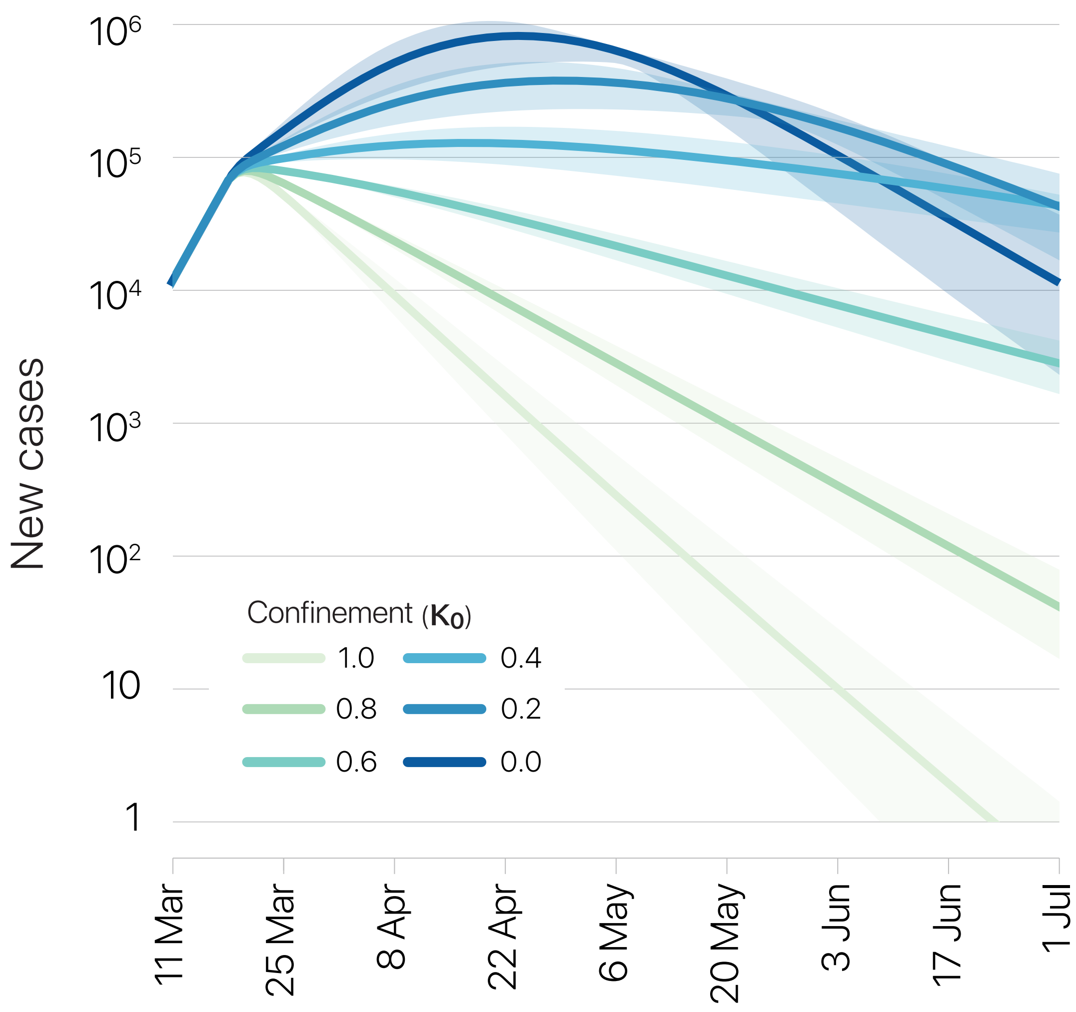
$$\mathcal{R}^g(t_c) = (\beta_A\tau_A+\beta_I\tau_I)\,\left(1-\kappa_0(1-\phi)\right)\left(\kappa_0\, k^g_{home} + (1-\delta)(1-\kappa_0)\, k^g_{home+work}\right)\sum_{h=1}^{G} C^{gh}\langle\rho^{S,h}(t_c)\rangle$$

The dependence of R(t) on the confinement $\boldsymbol{\kappa_0}$ is quadratic, confinement will force a phase transition in the incidence curve

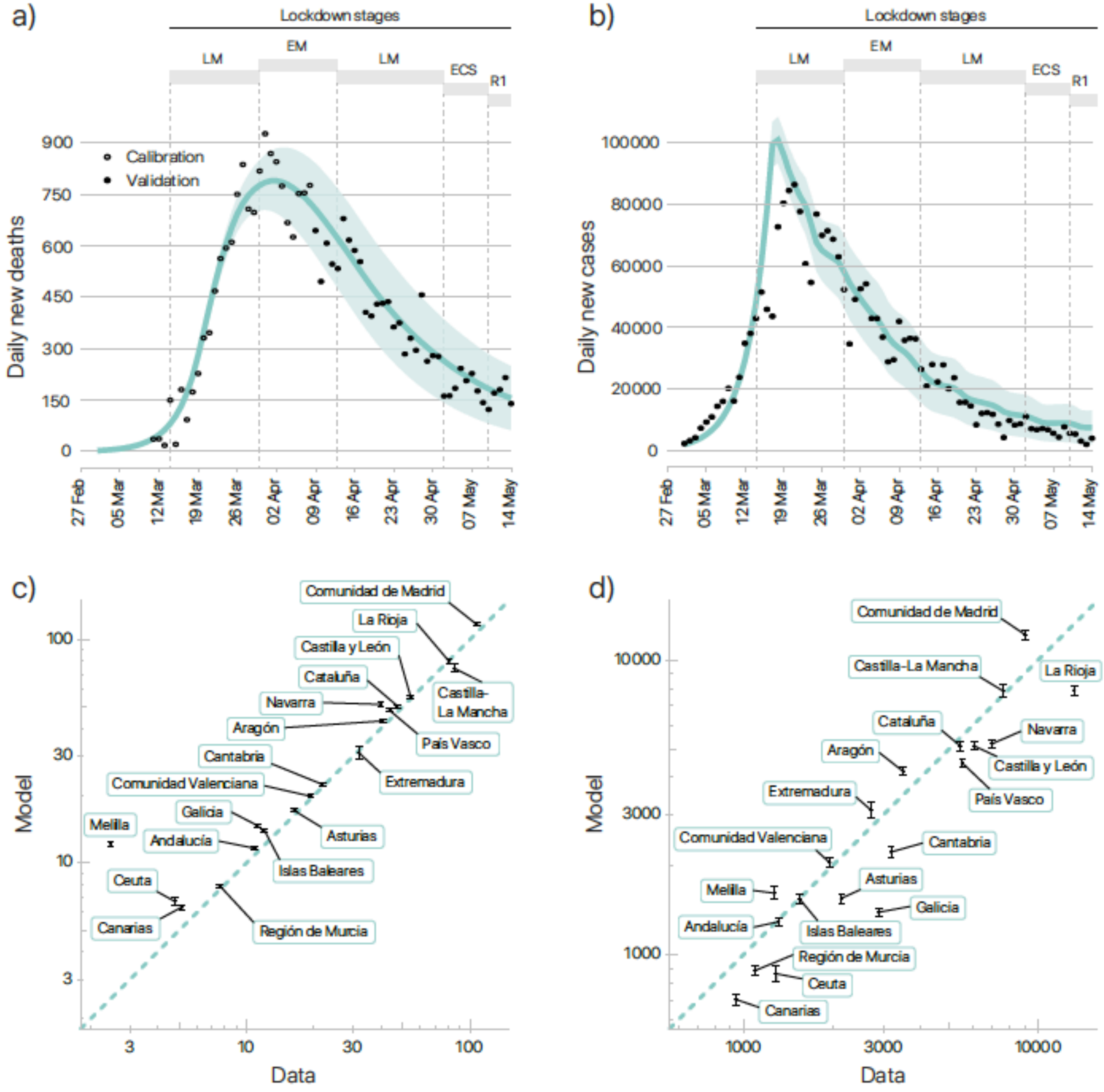
Modelling COVID

$$\mathscr{R}(t) = \frac{\sum_{i=1}^{N}\sum_{g=1}^{G}\left[\rho_i^{S,g}(t-1)-\rho_i^{S,g}(t)\right] n_i^g\, \mathscr{R}_i^g(t)}{\sum_{i=1}^{N}\sum_{g=1}^{G}\left[\rho_i^{S,g}(t-1)-\rho_i^{S,g}(t)\right] n_i^g}$$





Results modelling COVID in Spain



Conclusions

HIGHLIGHTS

- The model is suitable for monitoring the evolution of an epidemic outbreak, specially in the acceleration part.
- Gives accurate information about the geographical spread, pinpointing regions at risk.
- Useful to project scenarios evaluating the degree of lockdown needed to bend the curve.

LIMITATIONS

- Mean-field approach within patches.
- Indistinguishability of individuals.
- International mobility not included so far

Thanks to my main collaborators

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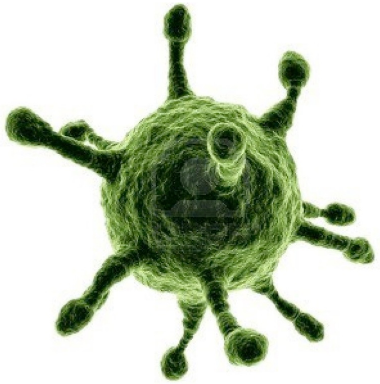
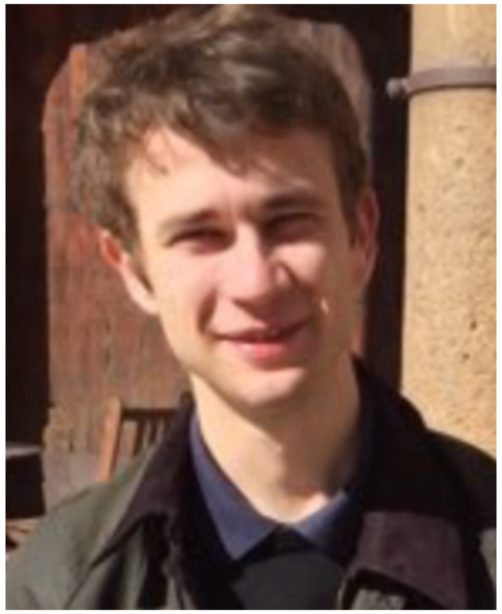
Clara Granell



David Soriano-Panos

Benjamin Steinegger



Joan Matamalas

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