Erice MathCompEpi 2015

Erice (Italy) August 30 2015 – September 5 2015.



Density dependent diffusion and spread of epidemics in a metapopulation model.

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Joint work with A. Avinyó, J. Ripoll and J. Saldaña

Outline

- The model: density-dependent diffusion on a metapopulation.
- Migratory flows without epidemics.
  - Heavily versus lightly populated areas.
- Early stage of the epidemic.
  - Local epidemic outbreaks.

[Ripoll, Avinyó, Pellicer, Saldaña: PRE 2015]

The model

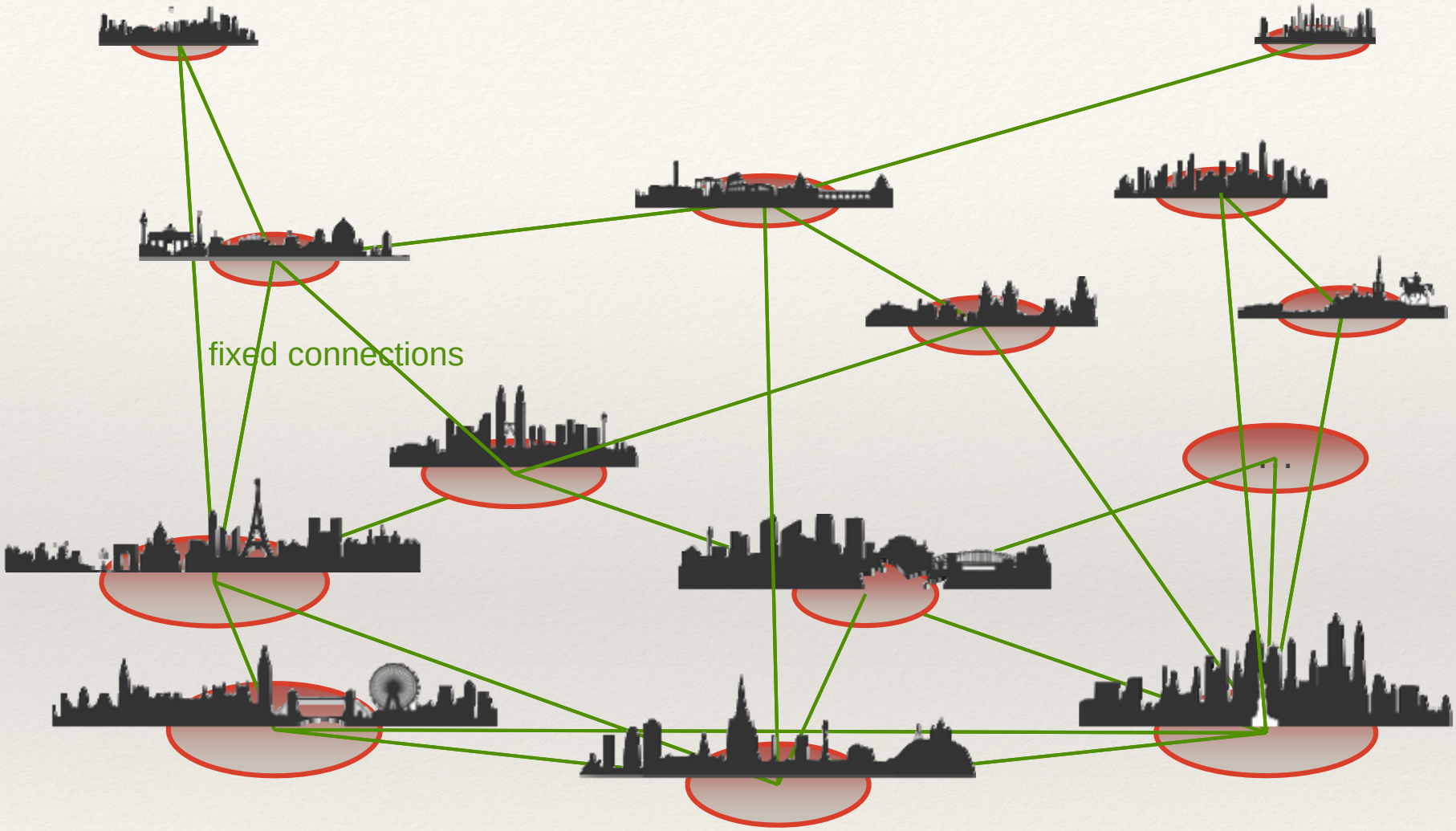
Metapopulation: complex network

- Nodes are local populations as cities (metropolitan areas) or regions or habitats in patchy landscapes, pair-wise connected by a non-trivial pattern of migratory flows.

- Spatial description of patches given by the connectivity distribution ***p(k)*** and **conditional probability *P(k'|k)*.**

  ⟶ *Approach based on the degree (k) of the nodes.*

- Individuals move randomly over the network at a certain diffusion rate.



Processes taking place within each node: infection, recovery and demographic turnover.
Process taking place on the network: migratory diffusion.

SIS-diffusion model

- The average number of Susceptible and Infected individuals in patches of degree k at time t: $\rho_{S,k}(t), \rho_{I,k}(t)$.

$$\rho'_{S,k} = \left(\mu - \beta c(\rho_k)\frac{\rho_{S,k}}{\rho_k}\right)\rho_{I,k} + \delta(\rho_k - \rho_{S,k}) - D_S(\rho_k)\rho_{S,k} + k\sum_{k'} D_S(\rho_{k'})P(k'|k)\frac{\rho_{S,k'}}{k'},$$

$$\rho'_{I,k} = \left(\beta c(\rho_k)\frac{\rho_{S,k}}{\rho_k} - \mu\right)\rho_{I,k} - \delta\rho_{I,k} - D_I(\rho_k)\rho_{I,k} + k\sum_{k'} D_I(\rho_{k'})P(k'|k)\frac{\rho_{I,k'}}{k'}.$$

- Local population size $\rho_k = \rho_{S,k} + \rho_{I,k}$. Density-dependent rates: contact rate $c(\rho_k)$ and diffusion rates $D_S(\rho_k)$ and $D_I(\rho_k)$.

β infection probability, μ recovery rate, and δ equal birth and death rates.

Other dispersal processes

- Gravity models (D. Brockmann (2010) , …)
- V. Colizza, A. Vespignani (JTB 2008): diffusion depending on k, k’
- …

Ours: dependence on the population density

of departure patch.

Goal:

Study the impact of these migration patterns (1 mechanism)

- on the population distribution among **heavily** and **lightly** populated areas (**HP** and **LP**) **without epidemics**.
- on the **epidemic growth**.
- on the **epidemic spreading** (contribution of each local population to the propagation of the infection)

Density-dependent diffusion

- $F(\rho) := D_S(\rho) \cdot \rho =$ **total outflow** of individuals

  Hypothesis: strictly increasing, F(0) = 0, continuous

- **Special case**: $D_S(\rho) \sim \rho^{\alpha}$ (on the **departure** patch)
  - $\alpha = 0$: **constant** diffusion rate (previous work [PRE 2009])
  - $\alpha > 0$: positive dependence or conspecific **competition**
    ➡ emigration from **heavily** populated patches
  - $-1 < \alpha < 0$: negative dependence or conspecific **attraction**
    ➡ emigration from **lightly** populated patches

Diffusion without epidemics ($\rho_I=0$)

DF or migration-driven equilibrium

★Existence and uniqueness of **DF equilibrium** ρ^*_k:

$$\rho_k^* = F^{-1}(M\,k)$$

(*M: normalizing constant such that* $\langle \rho^*_k \rangle = \rho^0$)

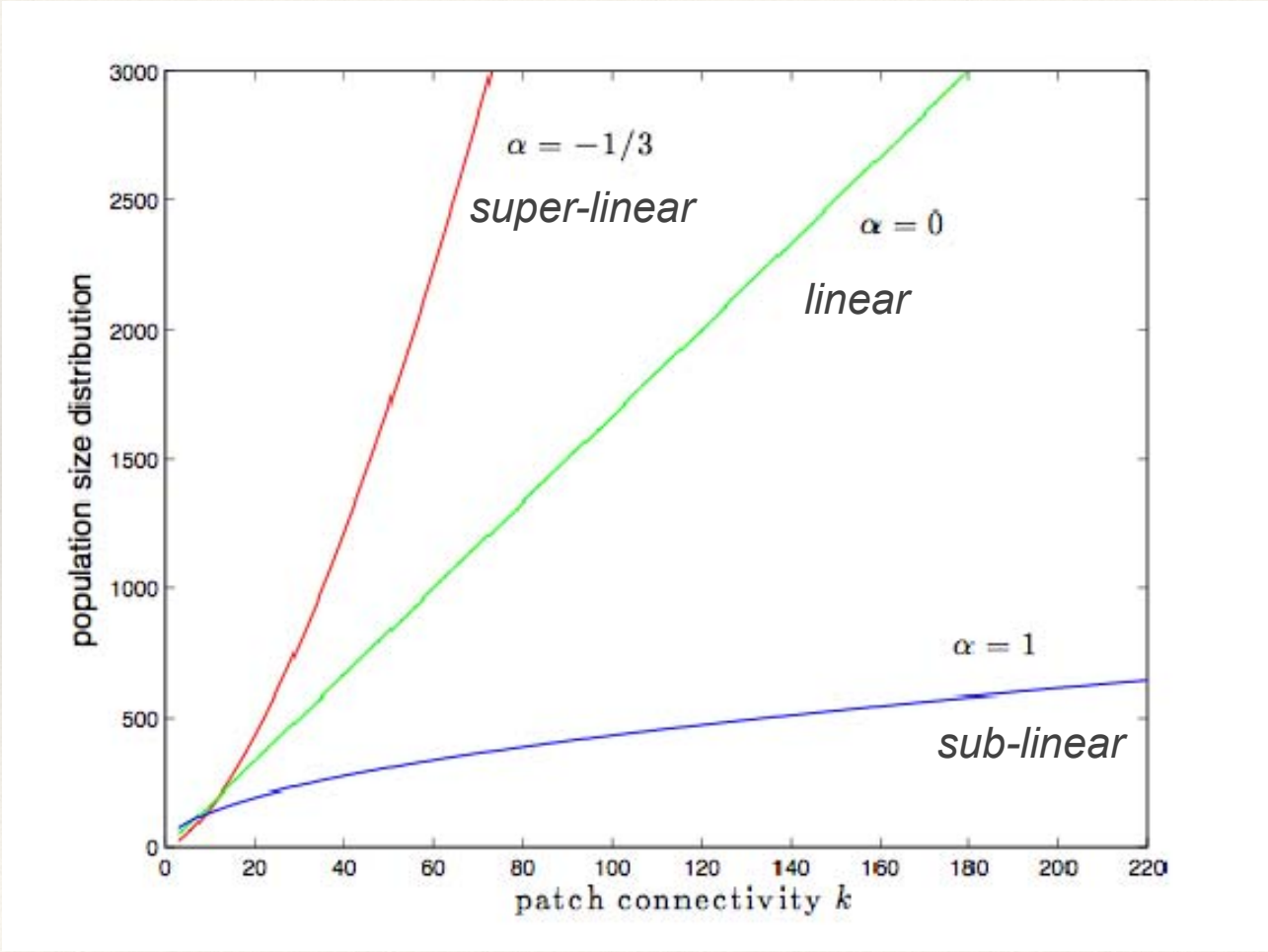
Rmks:

- ❖ Increases with k
- ❖ Independent of the network topology (driven by diffusion process)

Example: population profile when $D_S(\rho) \sim \rho^{\alpha}$

$$\text{If } D_S(\rho) = D_S^0 \left(\frac{\rho}{\rho^0}\right)^{\alpha}, \alpha > -1, \text{ then } \quad \rho_k^* = \frac{k^{1/(1+\alpha)}}{\langle k^{1/(1+\alpha)} \rangle} \rho^0.$$

Scale-free networks k_{min} =3, γ =3.



Migration exponent: -1 < **α** < 0 emigration higher in lightly pop., **α** > 0 emigration higher in heavily populated, and **α** = 0 ct. diffusion.

Heavily vs. lightly populated areas

- The sites (k) of the metapopulation are classified into:

  LP or **lightly** populated $(\rho_k \leq \rho^0)$.

  HP or **heavily** populated (otherwise)

- At equilibrium, HP patches are those with degree k

$$k > D_S(\rho^0)\rho^0/M$$

HP and LP when $D_S(\rho) \sim \rho^{\alpha}$ and scale-free network (γ)

- **% HP** $= \left(\frac{\omega}{\omega}\right)^{\omega-1}$ with $\omega = (\gamma - 1)(1 + \alpha) > 1$.

  - decreasing in ω
  - % HP in [36.79%,100%]
    - $(\omega \to \infty)$
    - $(\omega \to 1)$
    - ω = 2: **50%** (γ=3, α=0)
    - ω > 2: **mostly LP** (γ=3, α>0)
    - ω < 2: **mostly HP** (γ=3, α<0)

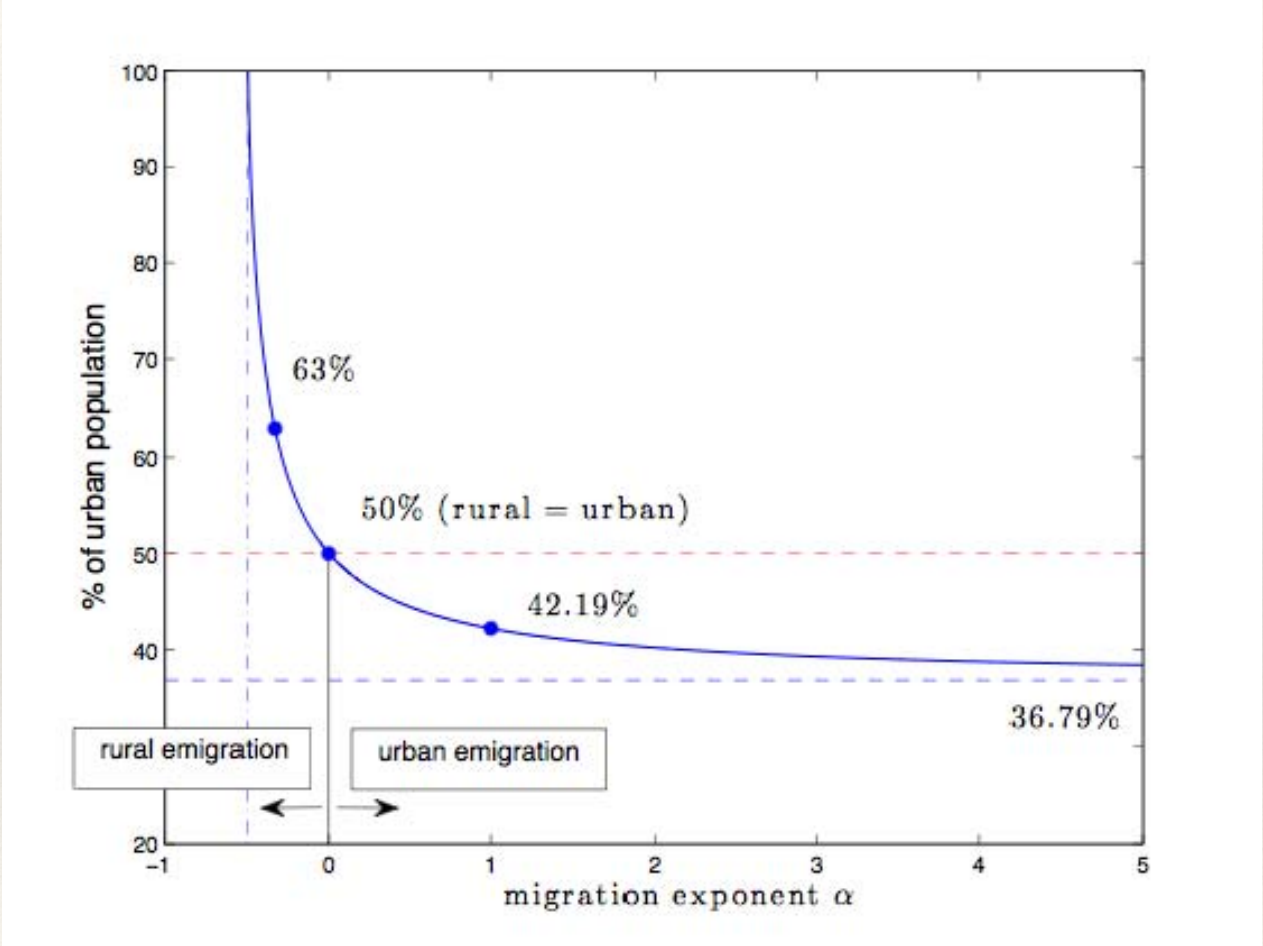
In particular, **higher α implies lower HP**

Consequences in epidemic spreading.

% of individuals of the metapopulation living in HP areas.

$D_S(\rho) \sim \rho^{\alpha}$ $p(k) \sim k^{-\gamma}$ with $\gamma = 3$

Dots: 3 different demographic scenarios.



Exponent α can be used as a tuning parameter to shape the profile to a specific % of HP population. Analogous results for other values of the γ exponent.

- Remark: the total population of each group depends on **migration pattern** $D(\rho) \sim \rho^{\alpha}$ and **topology** $p(k) \sim k^{-\gamma}$

- α (also γ) can be used as a **tunning** parameter

Early stage of the epidemic

Early stage of the epidemic

- The initial epidemic growth is governed by the dominant eigenvalue λ_1 of the **Jacobian matrix** at the DF equilibrium:

$$J = \begin{pmatrix} (\mathcal{C} - Id) \cdot \mathrm{diag}\left(F'(\rho_k^*)\right) & -\mathrm{diag}\left(\beta c(\rho_k^*) - \tilde{\mu}\right) \\ 0 & (\mathcal{C} - Id) \cdot \mathrm{diag}\left(D_I(\rho_k^*)\right) + \mathrm{diag}\left(\beta c(\rho_k^*) - \tilde{\mu}\right) \end{pmatrix}$$

- Epidemic outbreak when $\lambda_1 > 0$, and it is determined by the 4th block.
- Equivalent approach. Epidemic outbreak when the *basic reproduction number* $R_0 > 1$, and it is computed as the spectral radius of the **next generation matrix**:

$$K = \mathrm{diag}\left(\beta c(\rho_k^*)\right)\left(\tilde{\mu}\, Id + (Id - \mathcal{C}) \cdot \mathrm{diag}\left(D_I(\rho_k^*)\right)\right)^{-1}$$

Epidemic threshold: $\lambda_1 = 0 \leftrightarrow R_0 = 1$.

Meaningful condition

(c(ρ) density dependent)

- A sufficient condition to have an epidemic outbreak in the metapopulation is $\max_k\{\beta c(\rho_k^*) - \tilde{\mu} - (1 - P(k|k))D_I(\rho_k^*)\} > 0$ or, equivalently,

$$\max_k \frac{\beta c(\rho_k^*)}{\tilde{\mu} + (1 - P(k|k))D_I(\rho_k^*)} > 1$$



- Interpretation of the ratio: basic reproduction number of populations in patches of degree k neglecting the immigration from patches $k' \neq k$. So, it is an estimation (lower bound) of the actual $R_{0,k}$.
- Local epidemic outbreaks will undoubtedly take place in those sites of connectivity k such that the estimation is larger than one.

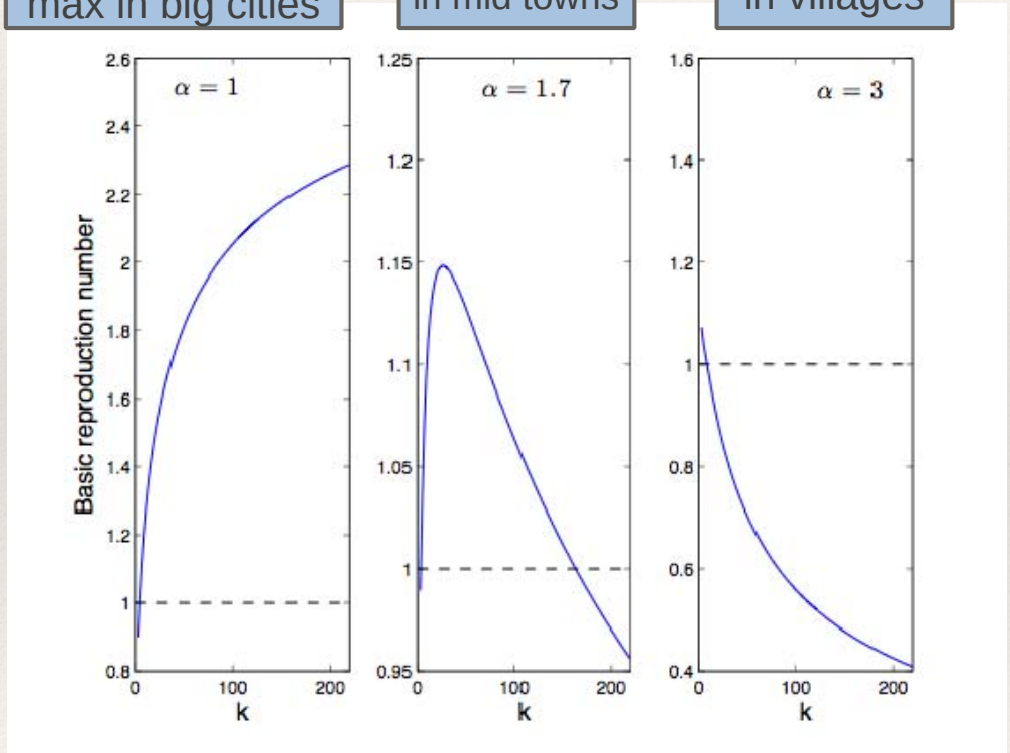
This formula is general.

Local epidemic outbreaks

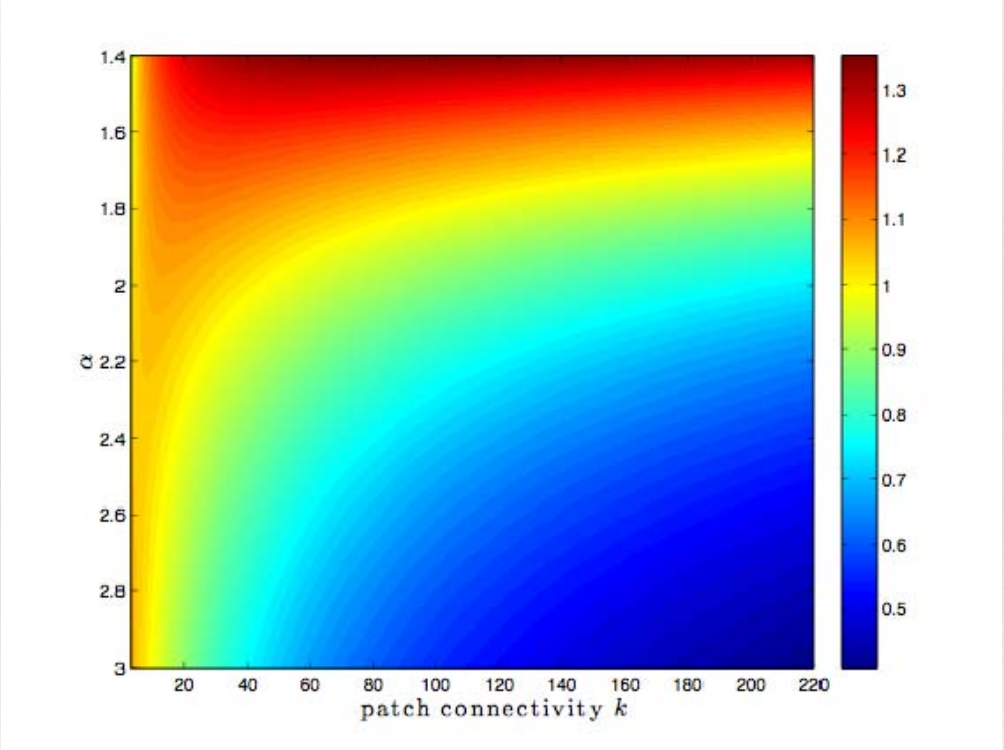
$$D_I(\rho) = \tau D_S(\rho) \sim \rho^{\alpha}, \quad c(\rho) = c_0 \rho$$ **uncorrelated scale-free network (γ=3)**

α = 1 α = 1.7 α = 3

max in big cities | in mid towns | in villages



3 different migration exponents showing 3 different epidemic scenarios.



Filled contour plot showing that the maximum in the ratio ★ decreases as the migration exponent increases.

Results

- **Our analytical approach reveals that:**
  - DF equilibrium determined by the diffusion process $D(\rho)$
  - Depending on the migration pattern ($D(\rho) \sim \rho^{\alpha}$) we get different population profiles distribution:

    Higher α ⇨ lower % HP
  - The early stage of the epidemic may be triggered by either large populations (small α), intermediate or even small ones (large α).
  - Higher α ⇨ lower epidemic growth

    (when density-dependent contact rates)

Conclusions

- Our results are based on one main assumption: *the total flow of individuals leaving a site is increasing in its population size*.
- Migration patterns play a crucial role in the spread of infectious diseases:
  - Migration patterns determine where epidemic outbreaks take place. Outbreaks do not always happen in big cities, as expected, but rather in mid-size towns or small villages.
  - The strengthening of the emigration from large population areas to small villages can contain the infection at the early stage.

Thank you for your attention.

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References

- J.Ripoll, A.Avinyó, M.Pellicer, J.Saldaña. *Impact of nonlinear migration flows on epidemic outbreaks in heterogeneous metapopulations. Phys. Rev. E (2015).*
- D.Juher, J.Ripoll, J.Saldaña. *Analysis and Monte Carlo simulations of a model for the spread of infectious diseases in heterogeneous metapopulations.Phys.Rev.E* 80, 2009.
- J. Saldaña. *Continuous-time formulation of reaction-diffusion processes on heterogeneous metapopulations. Phys. Rev. E* 78, 2008.