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

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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 $t$: $\rho_{S,k}(t), \rho_{I,k}(t)$.

\[
\begin{align*}
\rho'_{S,k} &= \left(\mu - \beta c(\rho_k) \frac{\rho_{S,k}}{\rho_k}\right) \rho_{I,k} + \delta(\rho_k - \rho_{S,k}) \\
&\quad - D_S(\rho_k) \rho_{S,k} + k \sum_{k'} D_S(\rho_{k'}) P(k'|k) \frac{\rho_{S,k'}}{k'}, \\
\rho'_{I,k} &= \left(\beta c(\rho_k) \frac{\rho_{S,k}}{\rho_k} - \mu\right) \rho_{I,k} - \delta \rho_{I,k} \\
&\quad - D_I(\rho_k) \rho_{I,k} + k \sum_{k'} D_I(\rho_{k'}) P(k'|k) \frac{\rho_{I,k'}}{k'}.
\end{align*}
\]

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 $D_I(\rho_k)$.
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

- \( F(\rho) := D_S(\rho) \cdot \rho = \text{total outflow} \) 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

($\rho_1 = 0$)
DF or migration-driven equilibrium

★ Existence and uniqueness of DF equilibrium $\rho^*_k$:

$$\rho^*_k = F^{-1}(M \ k)$$

$(M$: 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 $D_S(\rho) \sim \rho^\alpha$

If $D_S(\rho) = D_S^0 \left( \frac{\rho}{\rho_0} \right)^\alpha$, $\alpha > -1$, then $\rho_k^* = \frac{k^{1/(1+\alpha)}}{\langle k^{1/(1+\alpha)} \rangle} \rho^0$.

Scale-free networks $k_{min} = 3$, $\gamma = 3$.

Migration exponent: $-1 < \alpha < 0$ emigration higher in lightly pop., $\alpha > 0$ emigration higher in heavily populated, and $\alpha = 0$ ct. diffusion.
Heavily vs. lightly populated areas

• The sites \((k)\) of the metapopulation are classified into:
  
  \[ \text{LP or lightly populated } (\rho_k \leq \rho^0). \]
  
  \[ \text{HP or heavily populated (otherwise)} \]

• At equilibrium, \(\text{HP}\) patches are those with degree \(k\)
  
  \[ k > D_R(\rho^0)\rho^0/M \]
HP and LP when $D_S(\rho) \sim \rho^\alpha$ and scale-free network ($\gamma$)

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

- decreasing in $\omega$

- $\% \text{HP}$ in $[36.79\%, 100\%]$:
  - $\omega = 2$: 50% ($\gamma=3$, $\alpha=0$)
  - $\omega > 2$: mostly LP ($\gamma=3$, $\alpha>0$)
  - $\omega < 2$: mostly HP ($\gamma=3$, $\alpha<0$)

In particular, higher $\alpha$ implies lower HP

Consequences in epidemic spreading.
% of individuals of the metapopulation living in HP areas.

\[ D_S(\rho) \sim \rho^\alpha \quad p(k) \sim k^{-\gamma} \quad \text{with } \gamma = 3 \]

Dots: 3 different demographic scenarios.

Exponent \( \alpha \) can be used as a tuning parameter to shape the profile to a specific % of HP population.

Analogous results for other values of the \( \gamma \) exponent.
• Remark: the total population of each group depends on migration pattern $D(\rho) \sim \rho^\alpha$ and topology $p(k) \sim k^{-\gamma}$

• $\alpha$ (also $\gamma$) can be used as a tuning parameter
Early stage of the epidemic
Early stage of the epidemic

★ The initial epidemic growth is governed by the dominant eigenvalue $\lambda_1$ of the Jacobian matrix at the DF equilibrium:

$$J = \begin{pmatrix} (C - Id) \cdot \text{diag}(F'(\rho^*_h)) & -\text{diag}(\beta c(\rho^*_h) - \tilde{\mu}) \\ 0 & (C - Id) \cdot \text{diag}(D_I(\rho^*_h)) + \text{diag}(\beta c(\rho^*_h) - \tilde{\mu}) \end{pmatrix}$$

★ 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:

$$K = \text{diag}(\beta c(\rho^*_h)) \left( \tilde{\mu} Id + (Id - C) \cdot \text{diag}(D_I(\rho^*_h)) \right)^{-1}$$

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

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Meaningful condition

( $c(\rho)$ density dependent )

A sufficient condition to have an epidemic outbreak in the metapopulation is

$$\max_k \{ \beta c(\rho^*_k) - \bar{\mu} - (1 - P(k|k)) D_I(\rho^*_k) \} > 0$$
or, equivalently,

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

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 \((\gamma=3)\)

\(\alpha = 1\)  \(\alpha = 1.7\)  \(\alpha = 3\)

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 $\alpha \rightarrow$ lower % HP

❖ The early stage of the epidemic may be triggered by either large populations (small $\alpha$), intermediate or even small ones (large $\alpha$).

❖ Higher $\alpha \rightarrow$ 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.
References

