

# A stochastic SIR model on a population graph

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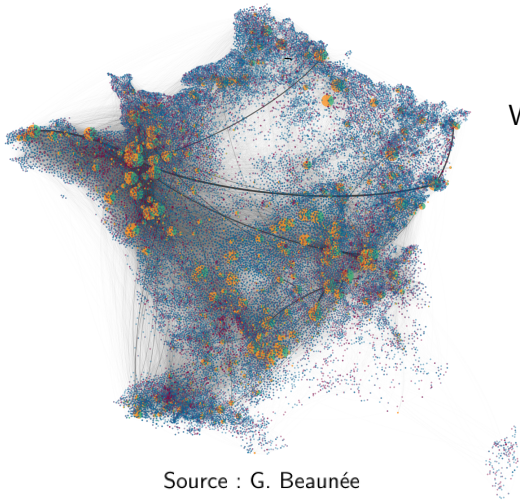
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# Motivation

Aim : predict and understand pathogen spread on a cattle trade network



Why using a network ?

- Accounts for complex contact structures
- Natural representation of a spatial object
- Abundant data make it possible to build a labelled graph

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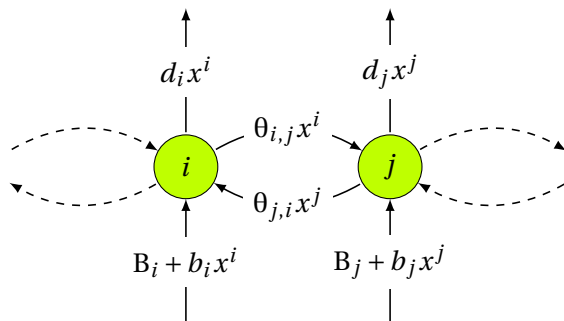
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- Epidemiological dynamics within each node
  - How can we define a major epidemic outbreak, compute its occurrence probability and quantify its amplitude ?
- Epidemic spread between nodes because of animal movements
  - Does the graph structure play a role in determining the major outbreak probability of an epidemic starting at a given node ?

# 1- The population model

- $n$  nodes standing for holdings (farms and commercial operators)
- Markovian model with discrete state space (jump process  $X = (X_t)_{t \geq 0}$  on  $\mathbb{Z}_+^n$ )
- Unitary jumps
- For a given  $x = (x^1, \dots, x^n)$  population vector :
  - Birth rate in node  $i$  :  $b_i x^i$
  - Import rate to node  $i$  :  $B_i$
  - Death (or exit to slaughterhouse) rate from node  $i$  :  $d_i x^i$
  - Transfert rate from node  $i$  to node  $j$  :  $\theta_{i,j} x^i$

Multitype branching process (BP) with immigration : independent individuals enter the system at rate  $B_i$ , give birth at rate  $b_i$ , move at rate  $\theta_{i,j}$  and die at rate  $d_i$ .

# The population model





# Stability of the population process

## Stability condition for the population process

Define

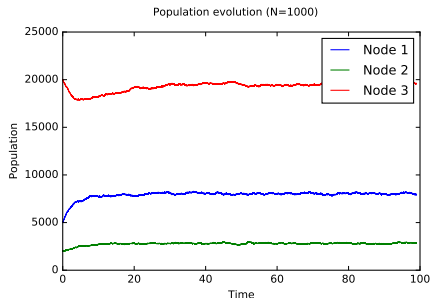
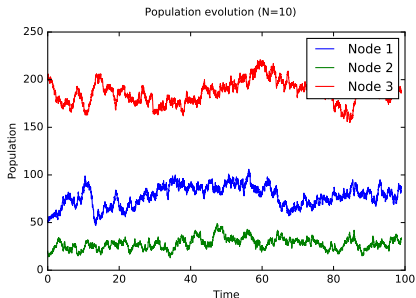
$$A = \begin{pmatrix} b_1 - d_1 - \sum_{j \neq 1} \theta_{1,j} & \theta_{2,1} & \cdots & \theta_{n,1} \\ \theta_{1,2} & b_2 - d_2 - \sum_{j \neq 2} \theta_{2,j} & \ddots & \vdots \\ \vdots & \ddots & \ddots & \theta_{n,n-1} \\ \theta_{1,n} & \cdots & \theta_{n-1,1} & b_n - d_n - \sum_{j \neq n} \theta_{n,j} \end{pmatrix}$$

and assume that all eigenvalues of  $A$  have a negative real part. Then  $(X_t)_{t \geq 0}$  is **positive recurrent** and its law converges at an exponential rate towards its unique invariant probability.

# Scaling limit for the population process

Scaling parameter  $N$  in  $X_0 = x_0 = N[\tilde{x}_0]$  (the initial population vector) and  $B = N\tilde{B}$  (the importation rates vector).

As  $N$  tends to infinity, convergence over finite time intervals of  $X/N$  towards a deterministic process solution of  $z' = Az + \tilde{B}$ .



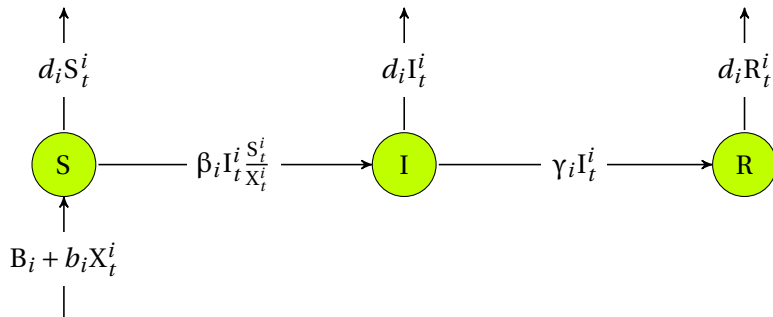
## 2- The epidemiological model

Within each node, three compartments (S, I and R) associated to three subpopulations  $S_t, I_t, R_t \in \mathbb{Z}_+^n$  such that  $S_t + I_t + R_t = X_t$ .

Define in each node  $j$  a Markov jump process SIR for which, at a given  $(s, i, r) \in \mathbb{N}^{3n}$  state :

- An additional infection occurs at rate  $\beta_j \frac{i^j s^j}{i^j + s^j + r^j}$
- An infectious individual gets removed at rate  $\gamma_j i^j$
- Individual have the same birth rate ( $b_j$ ), movement rate ( $\theta_{j,k}$ ) and death rate ( $d_j$ ) as before
- Individuals entering the system by birth or immigration are susceptible
- No infectious contact occurs between individuals that belong to different nodes

# The epidemiological model



# Comparison with a BP

Main idea : the infection rate in node  $i$  is  $\beta_i I_t^i \frac{S_t^i}{X_t^i} \approx \beta_i I_t^i$  in the first stages of the infection.

For some multitype BP  $(I'_t)_{t \geq 0}$  with birth rates  $\beta_i$ , death rates  $\gamma_i + d_i$  and movement rates  $\theta_{i,j}$ , denoting by  $\tau'$  its extinction time and  $Z'$  its final size :

## Comparison with a BP

For all  $T \geq 0$ ,

$$\mathbb{P} \left( \|I_u - I'_u\| \xrightarrow{N \rightarrow +\infty} 0 \right) = 1$$

If  $\tau^N$  is the extinction time of the epidemic and  $Z^N$  its final size, then a.s.

$$\mathbb{P} \left( \tau^N \xrightarrow{N \rightarrow +\infty} \tau' \right) = \mathbb{P} \left( Z^N \xrightarrow{N \rightarrow +\infty} Z' \right) = 1$$

$Z' < +\infty$  : minor outbreak.  $Z' = +\infty$  : major outbreak.

# Computation of $R_0$ and the major outbreak probability

Two quantities of interest :  $R_0$  (basic reproduction number) and  $\mathbb{P}(Z' = +\infty)$ .

## Definition of $R_0$

$R_0$  is the highest eigenvalue of the matrix  $(\mathbb{E}(W_{i,j}))_{i,j}$ , where  $W_{i,j}$  is the typical offspring (for  $I'$ ) in  $j$  of an individual born in  $i$ , that is, the typical number of individuals infected in  $j$  by an initial, single infective in node  $i$ .

## Major outbreak probability

$\mathbb{P}(Z' = +\infty) > 0$  iff  $R_0 > 1$ , and the major outbreak probability for an epidemic started at node  $i$  by a single infectious individual is  $1 - q^i$ , where  $q$  is the unique fixed point of some explicit, contractant function  $G$  (the generating function of the  $W_{i,j}$ ).

### 3- Application to the Finistère trade network

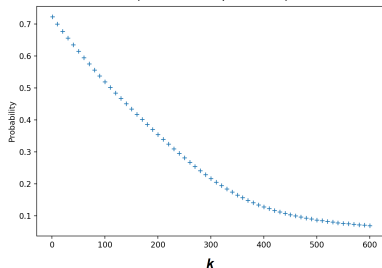
2015 Finistère trade network (BDNI data) :

- 4,163 farms, 3 markets, 17 assembly centers
- 118,311 animals exchanged within Finistère
- 55,325 animals received from outside of Finistère
- 241,747 animals sent to slaughterhouses or outside of Finistère
- Average population over the year : 424,385 animals

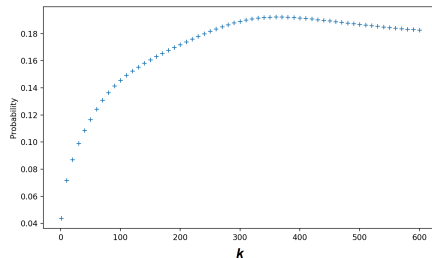
For BVD :  $\beta \approx 0.67 \text{ days}^{-1}$ ,  $\gamma^{-1} \approx 5.5 \text{ days}$ . For these values of the epidemiological paramets, the major outbreak is very close to 0.733 for most node (less than 1% of nodes are associated with values below 0.670).

# Application to the Finistère trade network

Mean major outbreak probability for an epidemic with parameters  $\beta_i/k$  and  $\gamma_i/k$



Standard deviation of the major outbreak probability for an epidemic with parameters  $\beta_i/k$  and  $\gamma_i/k$



Mean and standard deviation of the  $p^i = 1 - q^i$  for various nodes (2015 Finistère trade network) according to an epidemic slowing parameter  $k$ .

High  $p^i$  are associated to nodes from which individuals cannot exit the system, that is, that have low  $d^i$  and are poorly connected to nodes with strong  $d^i$ .



## 4- The final size of the epidemic

Dynamical system ( $\mathcal{S}$ ) defined by :

$$\begin{cases} \dot{s}_k = B_k + b_k(s_k + i_k + r_k) - d_k s_k + \sum_{j \neq k} \theta_{k,j} s_k - \sum_{j \neq k} \theta_{j,k} s_j - \beta_k i_k s_k \\ \dot{i}_k = \beta_k i_k s_k - d_k i_k - \gamma_k i_k + \sum_{j \neq k} \theta_{k,j} i_k - \sum_{j \neq k} \theta_{j,k} i_j \\ \dot{r}_k = \gamma_k i_k - d_k r_k + \sum_{j \neq k} \theta_{k,j} r_k - \sum_{j \neq k} \theta_{j,k} r_j \end{cases}$$

Heuristics : above a given threshold, the normalized epidemic process looks (over a finite time interval) like the solutions of this dynamical system. If there exists an attractive endemic equilibrium for ( $\mathcal{S}$ ), the process stays close to it for a time that is exponential in  $N$ .

### Final size of the epidemic in the stable endemic case

If  $\tilde{x}_0 = z^*$  and if ( $\mathcal{S}$ ) admits a stable endemic equilibrium, then **the final size  $Z^N$  of the epidemic is greater than  $e^{aN}$  for some  $a$  and all  $N$**  with high probability in case of major outbreak.

- Determine a condition for the existence and attractivity of the endemic steady state
- Derive an upper bound on the final size of the epidemic in the attractive endemic case
- Define a more realistic model (epidemiological specification, endogeneous movements,...)
- Study the quasi-stationary distribution of  $I$  and the extinction time of the epidemic

Thank you for your attention !