



## Modeling of the spread and control of *Mycobacterium avium* subsp. *paratuberculosis* in a metapopulation of dairy cattle herds

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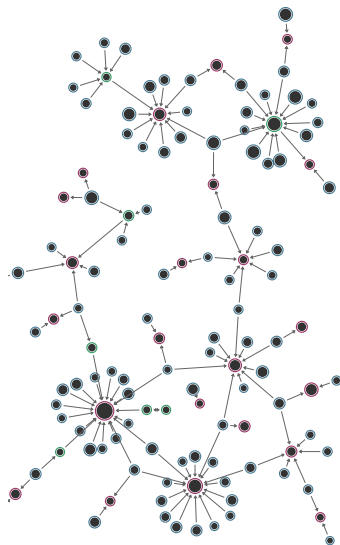
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# Motivations

- ▶ Movements of livestock form complex dynamic networks linking farms
- ▶ Many important cattle diseases spread between herds through these movements
- ▶ Paratuberculosis → introduced into farms by purchasing infected stock



# Objectives

- ▶ Study the spread of paratuberculosis in a metapopulation of dairy herds
  - ▶ build a modelling framework coupling realistic intra-herd demographic and infection dynamics and inter-herd connexions
  - ▶ integrate data on annual movements (for a French region)
  
- ▶ Assess the efficacy of control strategies based on the management of animal movements between herds

# Paratuberculosis / Johne's disease

- ▶ Chronic enteritis (bowel inflammation)
- ▶ *Mycobacterium avium subsp. paratuberculosis* (*Map*)
- ▶ Two types of transmission
  - ▶ vertical (*in-utero*)
  - ▶ horizontal (colostrum, milk, feces)
- ▶ Clinical signs
  - ▶ chronic diarrhea
  - ▶ severe weight loss and weakness
  - ▶ decline in milk production
- ▶ Significant economic impact



## Within dairy herd model (1) : main assumptions

Coupling population dynamics in a dairy herd explicitly defined with *Map* transmission

- ▶ Seasonality (housing vs. grazing)
- ▶ 5 routes of transmission :
  - ▶ *in utero*, colstrum, milk, local environnement (calf-to-calf), global environnement
- ▶ Infection occurs before **1** year only
- ▶ Heterogeneity of shedding
- ▶ Survival of *Map* in the environment

## Within dairy herd model (2) : health states

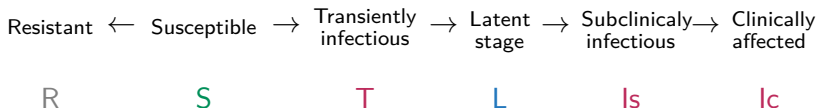
S - Susceptible

T & Is - Infected asymptomatic, shedders

L - Infected asymptomatic, non-shedders

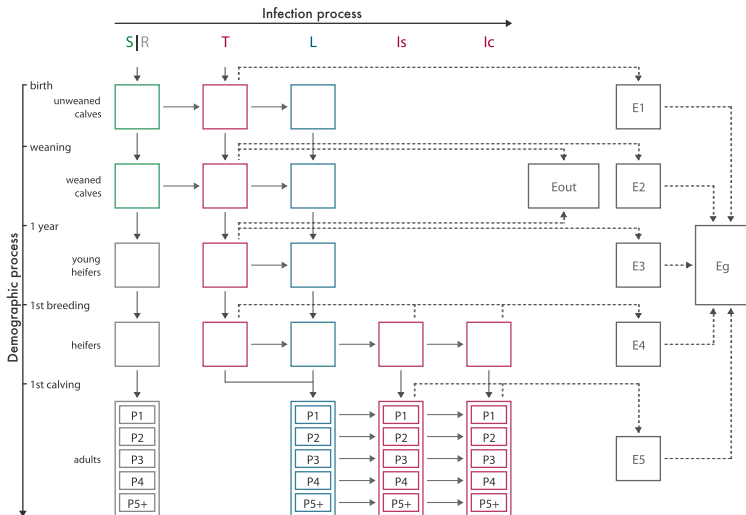
Ic - Infected symptomatic, shedders

R - Resistant



# Within dairy herd model (3)

## Disease progression + herd management



## Within dairy herd model (4) : mathematical framework

- ▶ Semi-Markov stochastic compartmental model on discrete space and in discrete time
  - ▶ 63 parameters & 495 state variables (age structure)

Examples of transitions :

- ▶ Stochastic

$$S_{(t,a)} \longrightarrow T_{(t,a)} \sim \text{Bin} \left( S_{(t,a)}; P_{inf(t,a)}^{global} \right)$$

$P_{inf(t,a)}^{global}$  the probability of infection through the global routes depending on  $a$  (age),  $t$  (time) and  $E^g$  (global environment) :

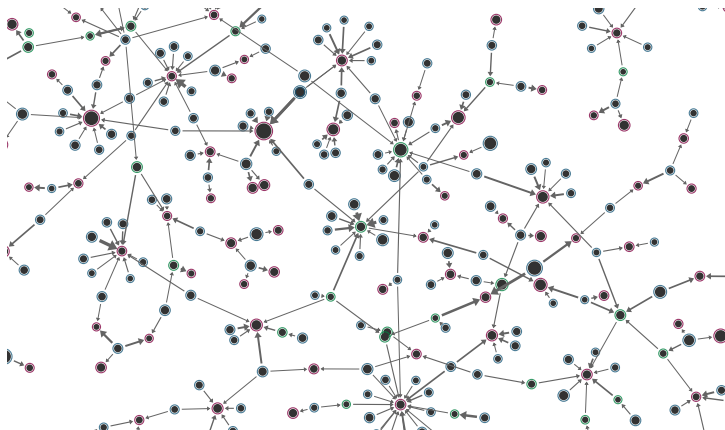
$$P_{inf(t,a)}^{global} = 1 - \exp \left( -\exp[-h(a-1)] \cdot \frac{\beta_g E_{(t)}^g}{\alpha N_{(t)}^g} \right) \quad ; \quad E_{(t)}^g = \sum_{i=1}^{i=5} E_{i(t)}$$

- ▶ Deterministic

$$S \longrightarrow R \quad \text{when age} = 1 \text{ year}$$



# Between-herd model



Coupling of within-herd dynamics through animal trade movements, based on real data.

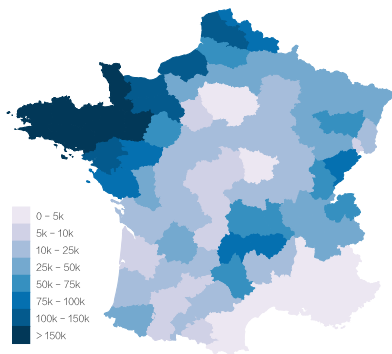
# Animal movements data (1)

- ▶ French cattle identification database (2005-2009)
  - ▶ Contains all the movements of all cattle
  - ▶ Includes data from farms, markets and assembly centers
- ▶ Informations
  - ▶ ID of animals exchanged
  - ▶ ID and type of holdings
  - ▶ type and age of animals
  - ▶ date of movements
- ▶ Here : subset of the whole network → all the dairy farms exchanging females in Brittany (region in Northwestern France)

## Animal movements data (2)

Motivation for Brittany data :

- ▶ High density of dairy cattle herds
- ▶ Longitudinal epidemiological data on *Map* available for future validation of the model



Number of dairy animals

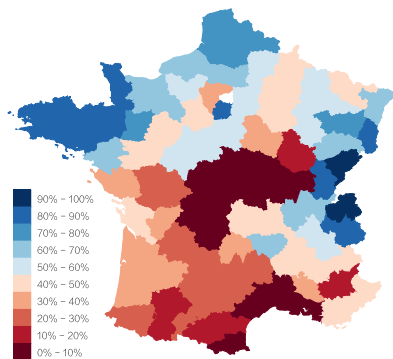
⇒ Rebuild a version of the network without markets (M) and assembly centers (AC) motivated by :

- ▶ short duration of stay in M/AC
- ▶ low risk of infection in M/AC

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Proportion of dairy animals

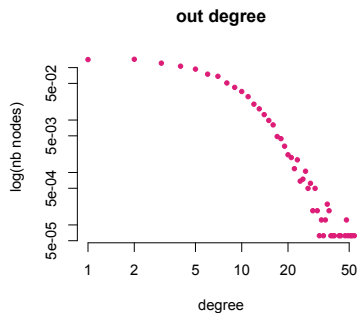
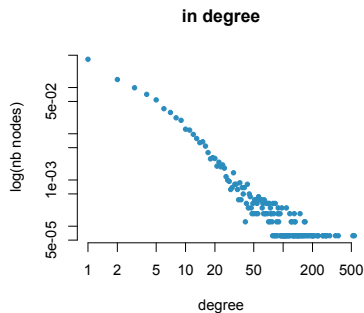
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# Network of dairy herds in Brittany (2005-2009)

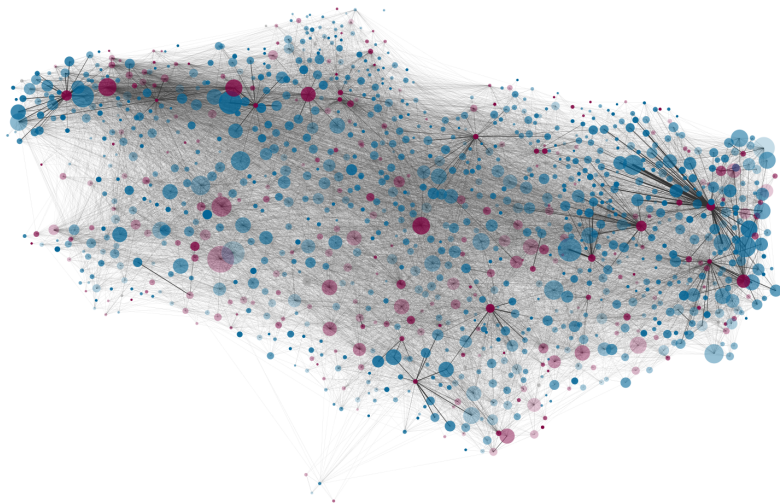
Number of active farms (nodes) : **16076**

Number of movements (links) : **680 929**  
including **150 568** within the metapop.



Age of animals exchanged : mostly calves (<10 weeks, 32.7%) and adult (> 2.5 years, 53.8%)

# Network of dairy herds in Brittany (2005-2009)



Network aggregated by communes : red - rather buyer, blue - rather seller, size weighted by the number of animals, link weighted by the number of exchanges

## Between-herd model

Coupling of stochastic within-herd dynamics through trade movements

Observed movements are explicitly modeled

- ▶ date, origin, destination and age of the animal → deterministic
- ▶ animal health status → stochastic (selected according to the herd specific prevalence)

Assign the animal health status for each movement from herd  $i$  to herd  $j$  :

$$X_{i \rightarrow j}^a = \text{Multinomial} \left( N_{i \neq lc}^a, p_i^a \right)$$

$$p_i^a = \left( p_i^{a,S/R}, p_i^{a,T}, p_i^{a,L}, p_i^{a,Is} \right) \text{ with } \sum_{X \in (S/R, T, L, Is)} p_i^{a,X} = 1$$

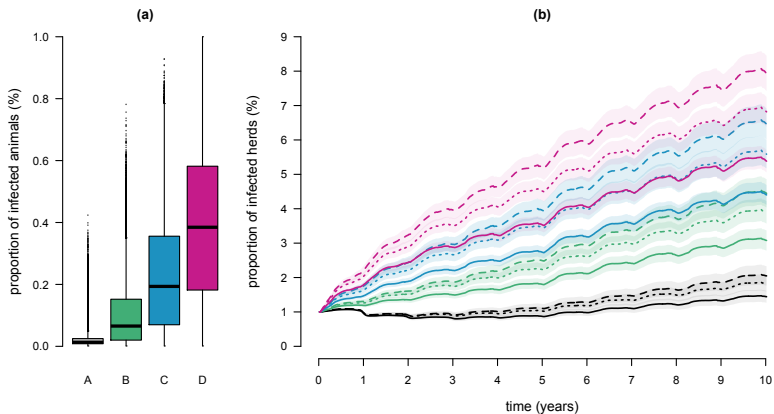
Animals  $lc$  are not allowed to move

# Simulation settings

- ▶ Number of runs per scenario : 1000
- ▶ Parameters chosen according to the litterature and expert knowledge
- ▶ Number of initially infected herds : 1% with one *Is* heifer
- ▶ Outputs : nb of infected herds, probability of infection, type of herd at risk for propagation
- ▶ Scenarios :
  - ▶ Different intra-herd prevalence at the start of between-herd dynamics
  - ▶ Different way to choose initially infected herds (at random)
    - ▶ uniformly
    - ▶ based on out-degree distribution
    - ▶ based on out-flow distribution

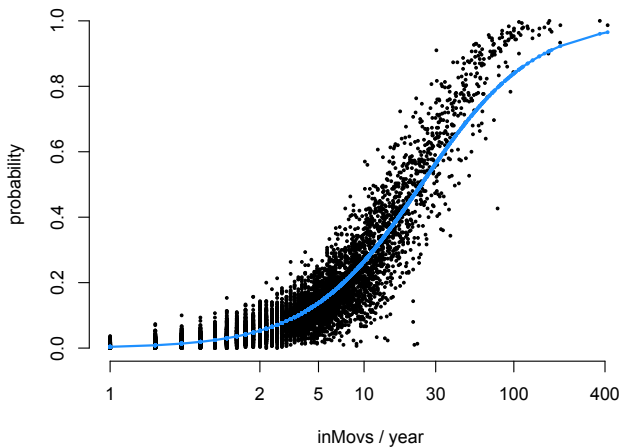


# Between-herd model : results of simulations (1)



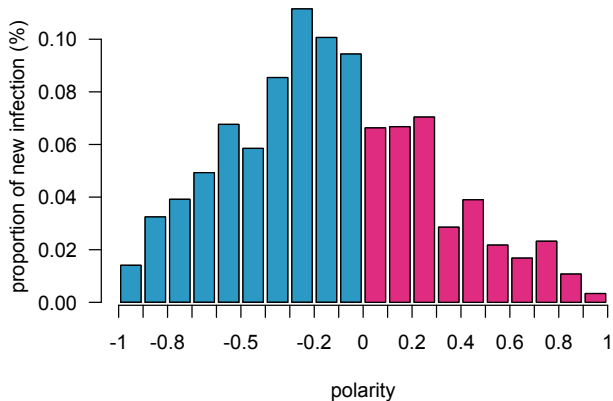
Proportion of infected herds over time

## Between-herd model : results of simulations (2)



Probability of having been infected at least once

## Between-herd model : results of simulations (3)



Risk of spreading infection by initially uninfected herds

## Test of animals status at purchase : settings

Accounting for the characteristics of the test of animals status, sensitivity ( $Se$ ) and specificity ( $Sp$ ) :

for  $S$  or  $R \Rightarrow Bernoulli(Sp)$ ; for  $T$ ,  $L$  or  $Is \Rightarrow Bernoulli(Se)$

Scenarios		Se for $T$	Se for $L$	Se for $Is$	Sp
Without test		–	–	–	–
ELISA	real	0.15	0.07	0.75	0.95
	hyp.	0.9	0.9	0.9	0.95
PCR	real	0.57	0	0.75	0.95
	hyp.	0.9	0	0.9	0.95

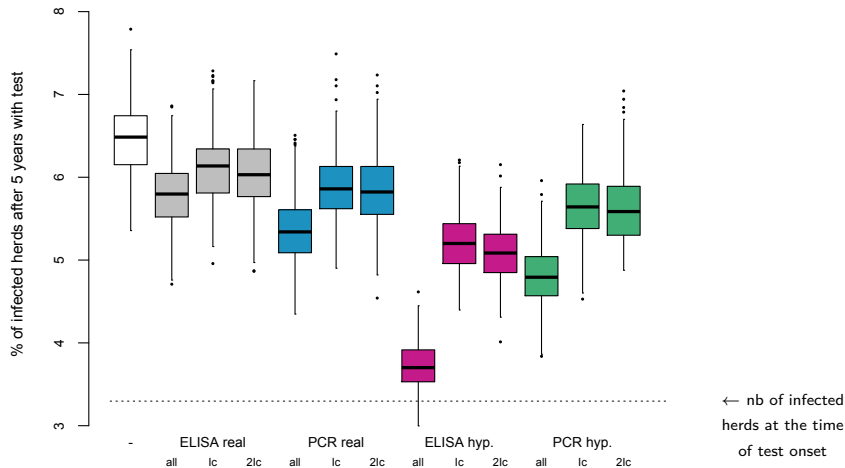
Targeted movements : 3 procedures

- ▶ all animals exchanged tested
- ▶ only movements from herds with at least one  $lc$  at movement time
- ▶ only movements from herds with at least two  $lc$  found in the past

Tests implemented after 5 years of infection spread and performed during 5 years

# Test of animals status at purchase : results

Number of infected herds 5 years after the onset of the test at purchase



## Conclusion and perspectives

- ▶ Generic modelling framework for infection dynamics in a metapopulation of cattle herds connected by animal movements
- ▶ Herds are not all equal and limited efficiency for strategies involving tests at purchase
- ▶ Assess combinations of measures (movements + internal biosecurity)
- ▶ Use of animal movement data for a larger period
- ▶ Use of epidemiological data for validation / estimation

Thanks !

MiHMΣS

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