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Live animal movements

Pachka Hammami[1], Nicolas Rose[1], Vladimir Grosbois[2], Stefan Widgren[3], Andrea Apolloni[2] and Mathieu Andraud[1]

[1]ANSES, French Agency for Food, Environmental and Occupational Health & Safety Epidemiology, Health and Welfare Research Unit, Ploufragan-Plouzané - Niort Laboratory, France
[2]CIRAD, Agricultural Research for Development, Univ. Montpellier, INRA, French National Institute for Agricultural Research, Animal, Health, Territories, Risks, Ecosystems Research Unit, Montpellier, France
[3]Department of Disease Control and Epidemiology, National Veterinary Institute, Sweden

Understand trade partners choices to predict chains of contact

Background

Spread and maintenance of swine pathogens are the result of complex epidemiological processes leading to chains of contact connecting susceptible to infectious hosts. Hepatitis E virus (HEV) transmission occurs **within-farm** through direct and environmental faecal-oral routes. Because of their potential of moving infected animals from farm to farm, live animal trade is a major driver of **between farms** spread for infectious diseases of livestock such as hepatitis E.

Objectives

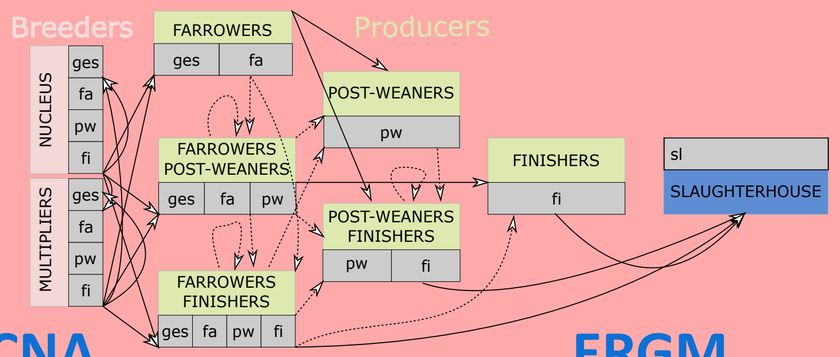
Pig movement's record became mandatory in many european coutries.

Not allowing only **tracking upstream and downsteam** the spread of pathogen in case of an outbreak, their analysis could also provide **relevant information** to improve **predictability of epidemiological models**.

This study aims to define **key drivers of trade partner choices** and to simulate **realistic networks and chains of contacts**.

Methodology

The swine production chain is composed of various facilities **interconnected by trade** of sows, pigs and piglets forming a **complex network**. Even if **structurally stable** over time, between farm **movements are changing over time**. The trade network observed at time *t* is expected to have the same topology/structure than the network observed at time *t+1* but to be composed of a different set of between farm movements.



CNA

Complex Network Analysis

Based on a descriptive analysis of 2016-2019 movements provided by the National Swine Identification Database **(BDporc)**, the network was decomposed into **relevant 6-months subnetworks with different patterns**. Drivers were selected for each subnetwork.

ERGM

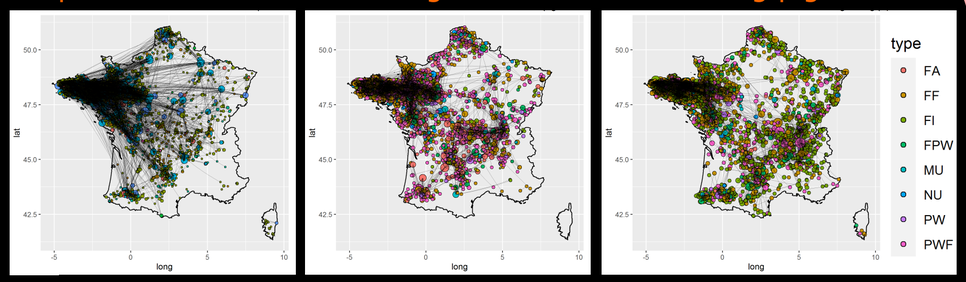
Exponential random graph models

Based on statistical analysis of network including **farm and movement characteristics and network structure**, ERGMs detect significant drivers of movements, revealing the most likely contact chains in a structured population. **Best models were chosen by AIC and goodness of fit.**

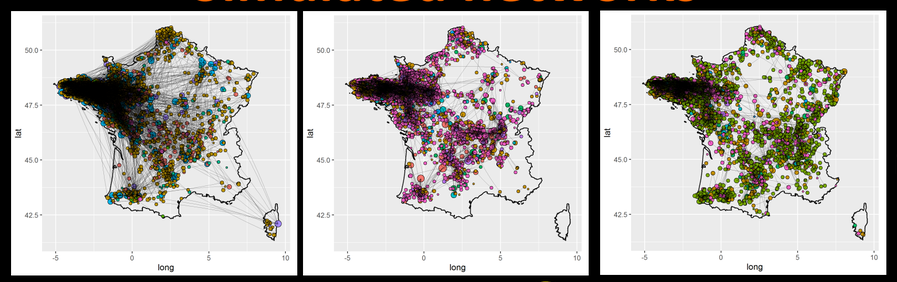
Results & discussion

Network patterns vary with the **type of transported animals**.

Reproductive sows | Piglets | Growing pigs



Simulated networks



Key drivers

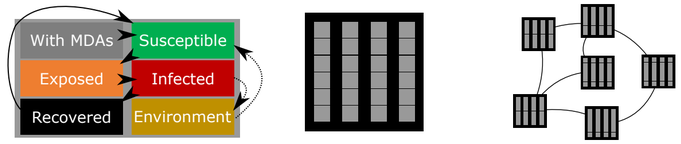
Network structure:
edges
Movements characteristics:
distance
Farm characteristics:
type, breeders or producers, company, batch rearing system, freerange status and size

Results suggest **a good adjustment of the models** allowing to simulate networks structurally similar to the observed network

Conclusion

Cross demography & virus circulation

Within pens | Within farm | Between farms



Splitting the global trade network into three subnetworks based on transported animals well captured the underlying patterns of animal flows.
Coupling probabilities of between farms contact with a demographic model would provide relevant networks to feed multilevel epidemiological models which can be implemented with SimInf.