

Epidemiological implications of network structures

Animal movements modelling (SNA and ERGM)
Compartmental epidemiological model (SimInf)

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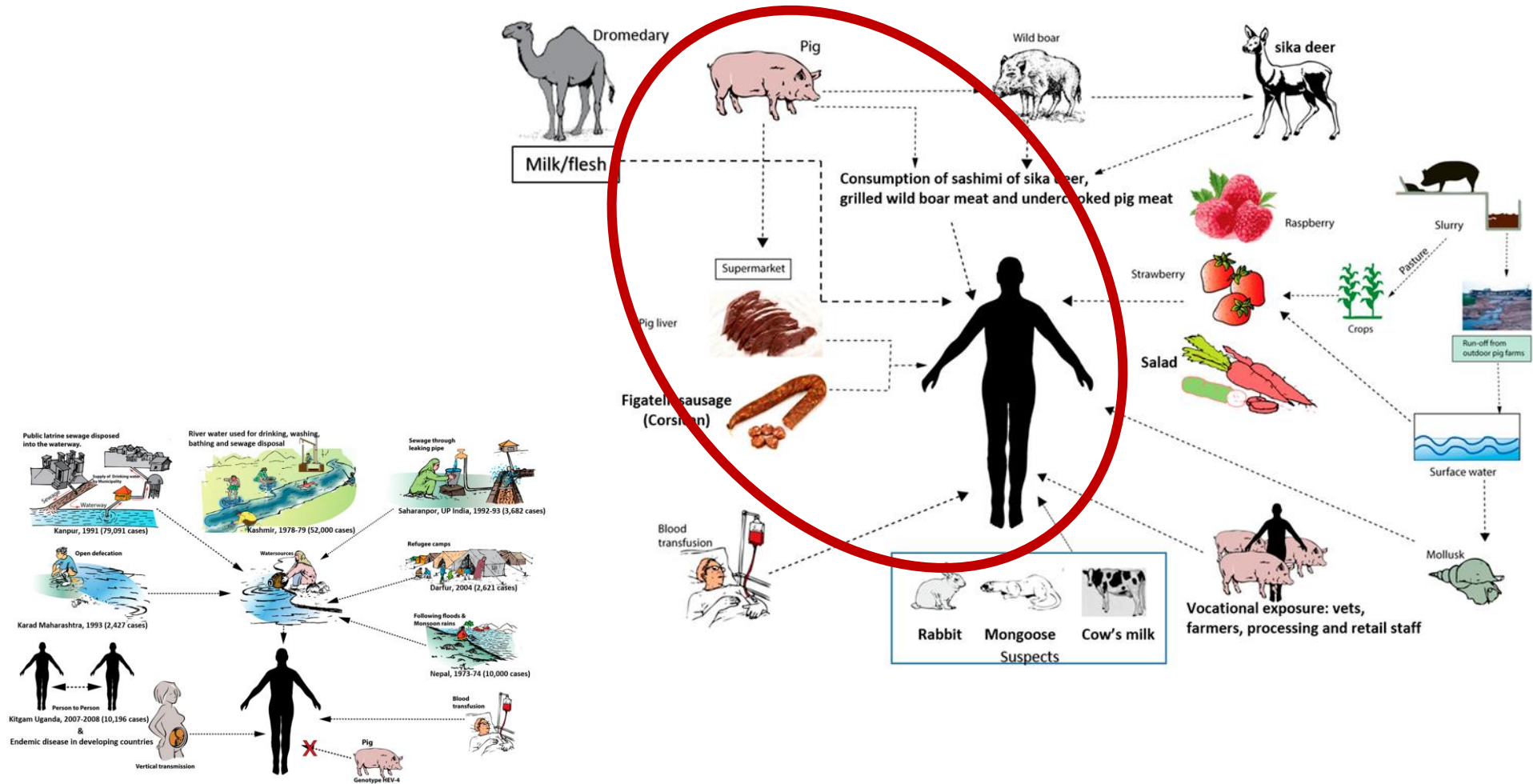
This work was supported by funding from the European Union's Horizon 2020 Research and Innovation programme under grant agreement No 773830: One Health European Joint Programme. BIOPIGEE

1 | ANSES, French Agency for Food, Environmental and Occupational Health & Safety - Epidemiology, Health and Welfare Research Unit, Ploufragan-Plouzané-Niort Laboratory, France

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3 | CIRAD, Agricultural Research for Development, Univ. Montpellier, INRAE, French National Institute for Agricultural Research, Animal, Health, Territories, Risks, Ecosystems Research Unit, Montpellier

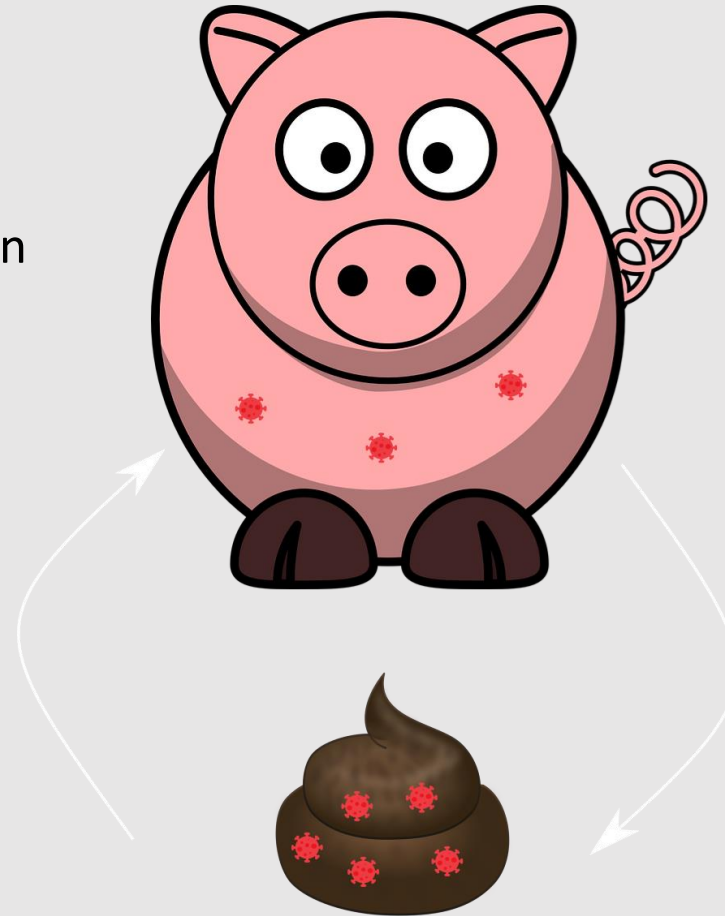
Hepatitis E Virus transmission



Khuroo, Mohammad, Khuroo, Mehnaaz, Khuroo, N., 2016. Transmission of Hepatitis E Virus in Developing Countries. Viruses 8, 253. <https://doi.org/10.3390/v8090253>

Hepatitis E Virus in swine

Asymptomatic
Detection: viro/sero
Faecal-oral transmission



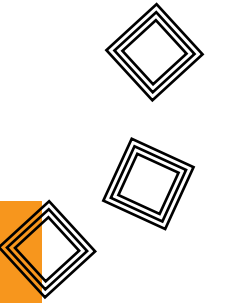
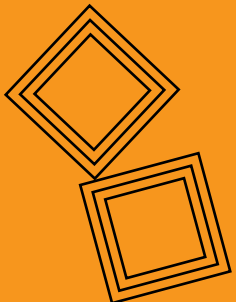
Estimate HEV prevalence in pigs sent to slaughterhouses
Assess the impact of control and surveillance activities at national scale



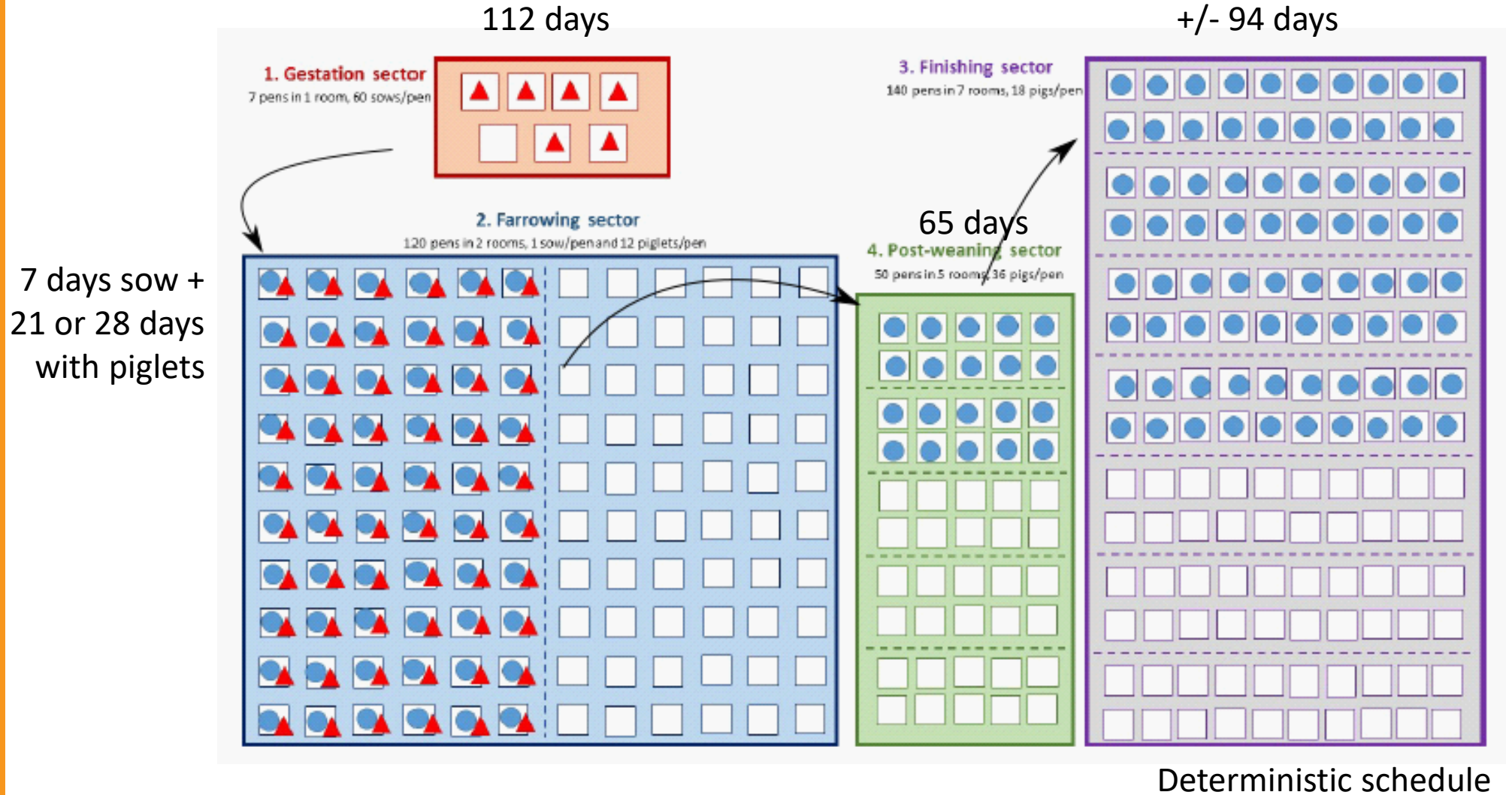
Assess national prevention, surveillance and control impact

Objectives

- 1: Simulate animals movements within and between farms
- 2: Simulate disease spread
- 3: Test prevention, surveillance and control measures

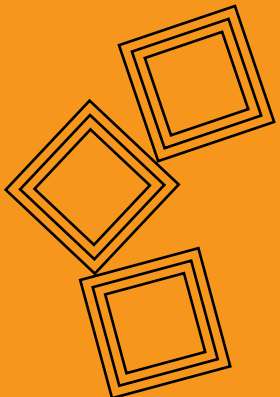
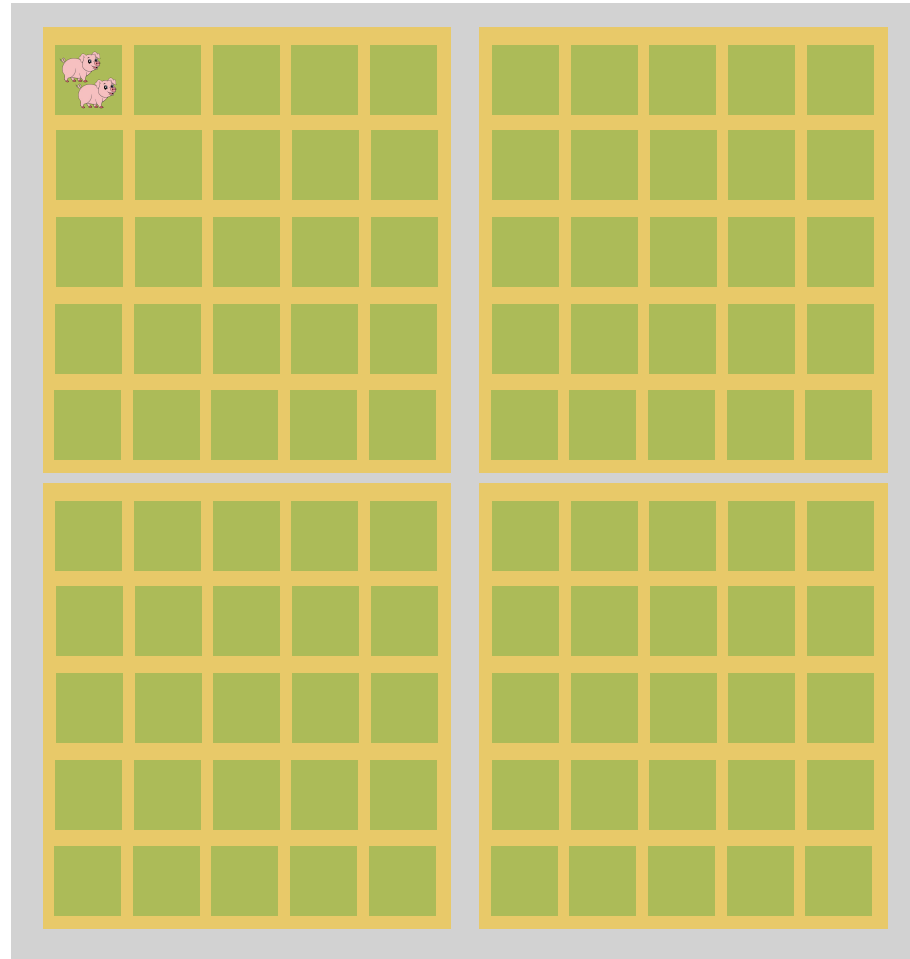


Production cycle of swine

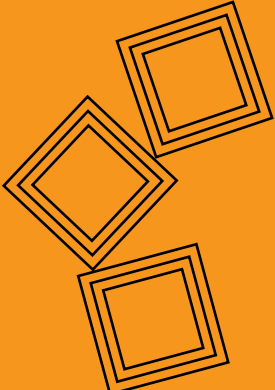
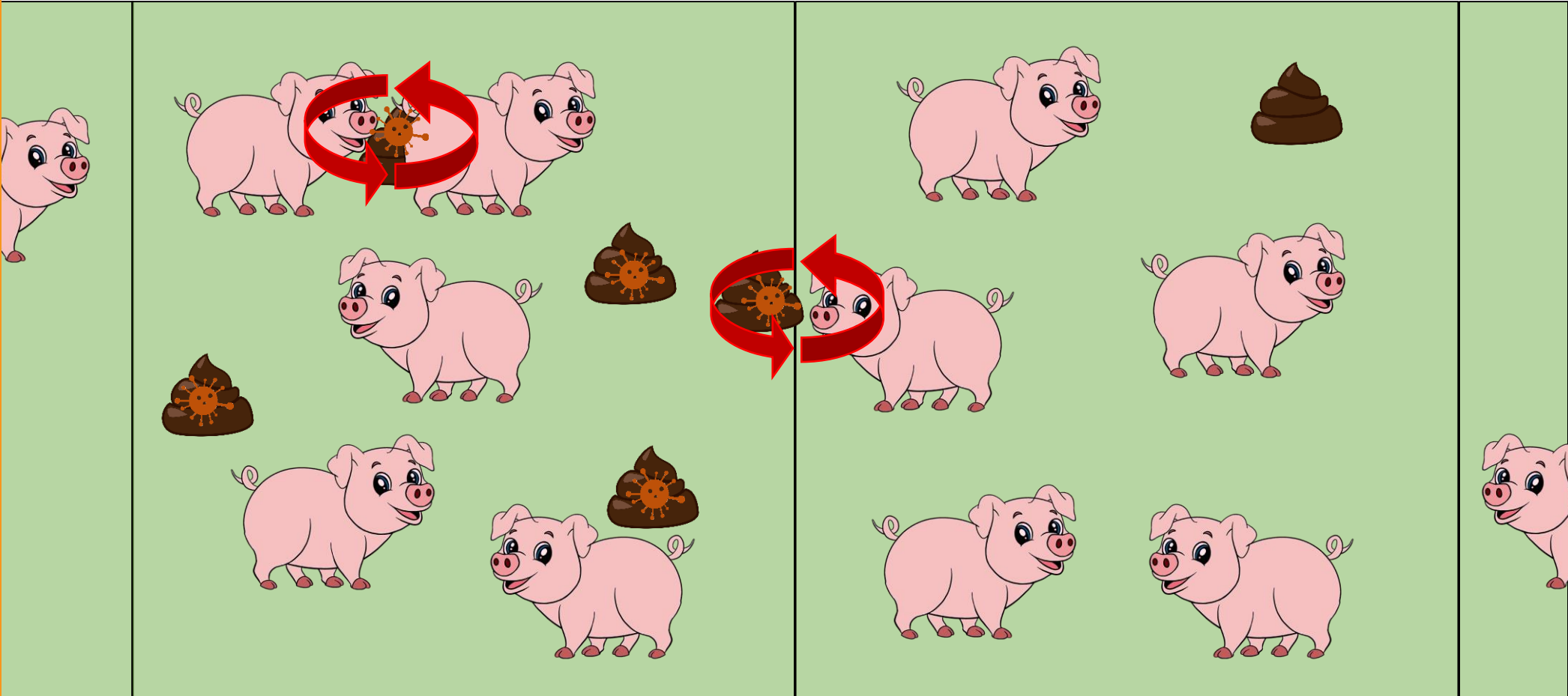


Unit structure

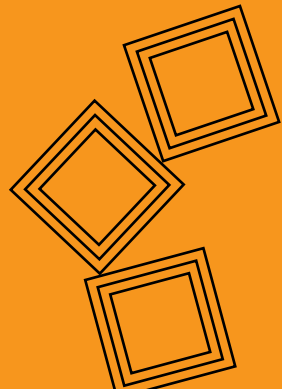
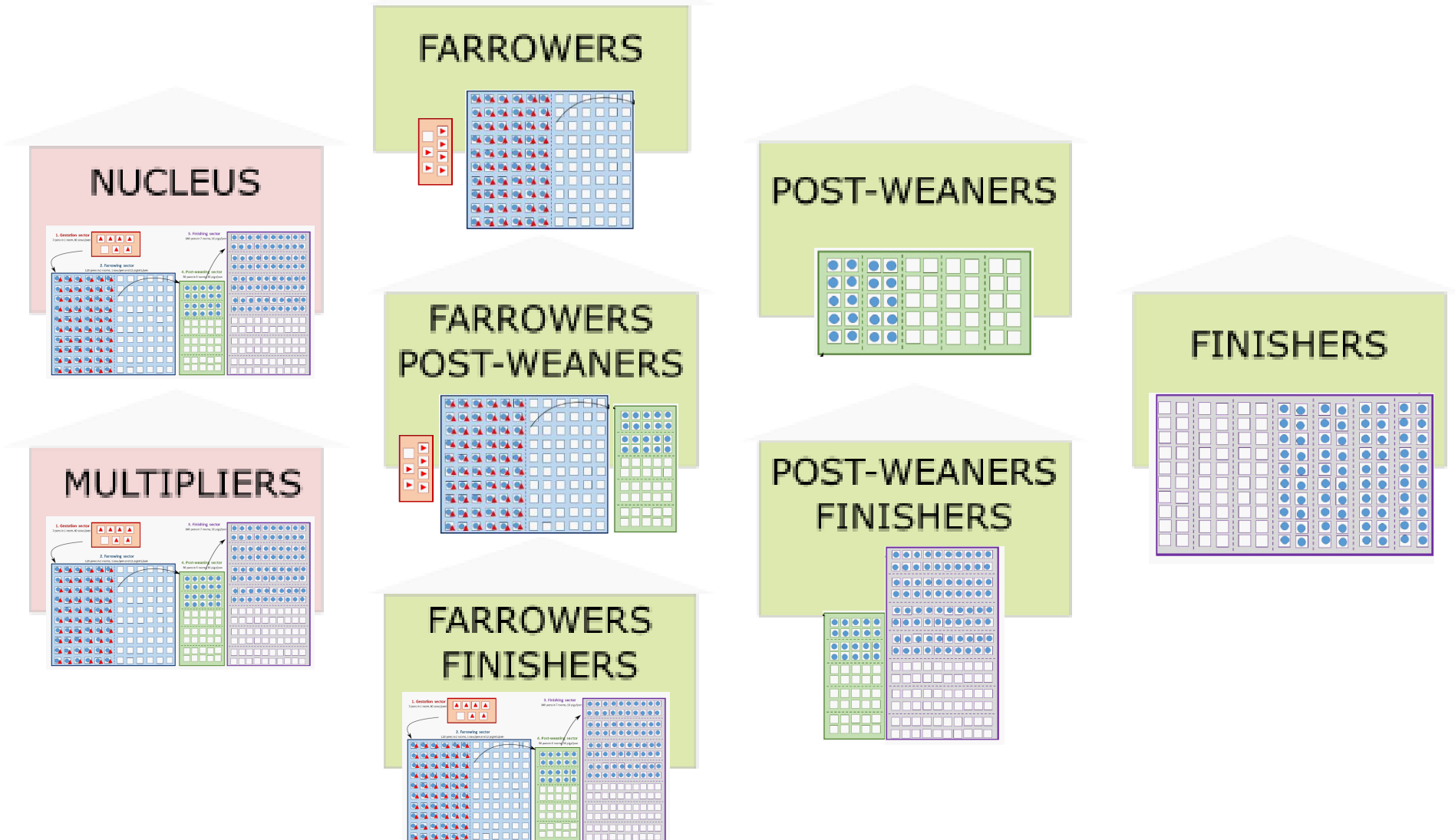
Unit Room Pen



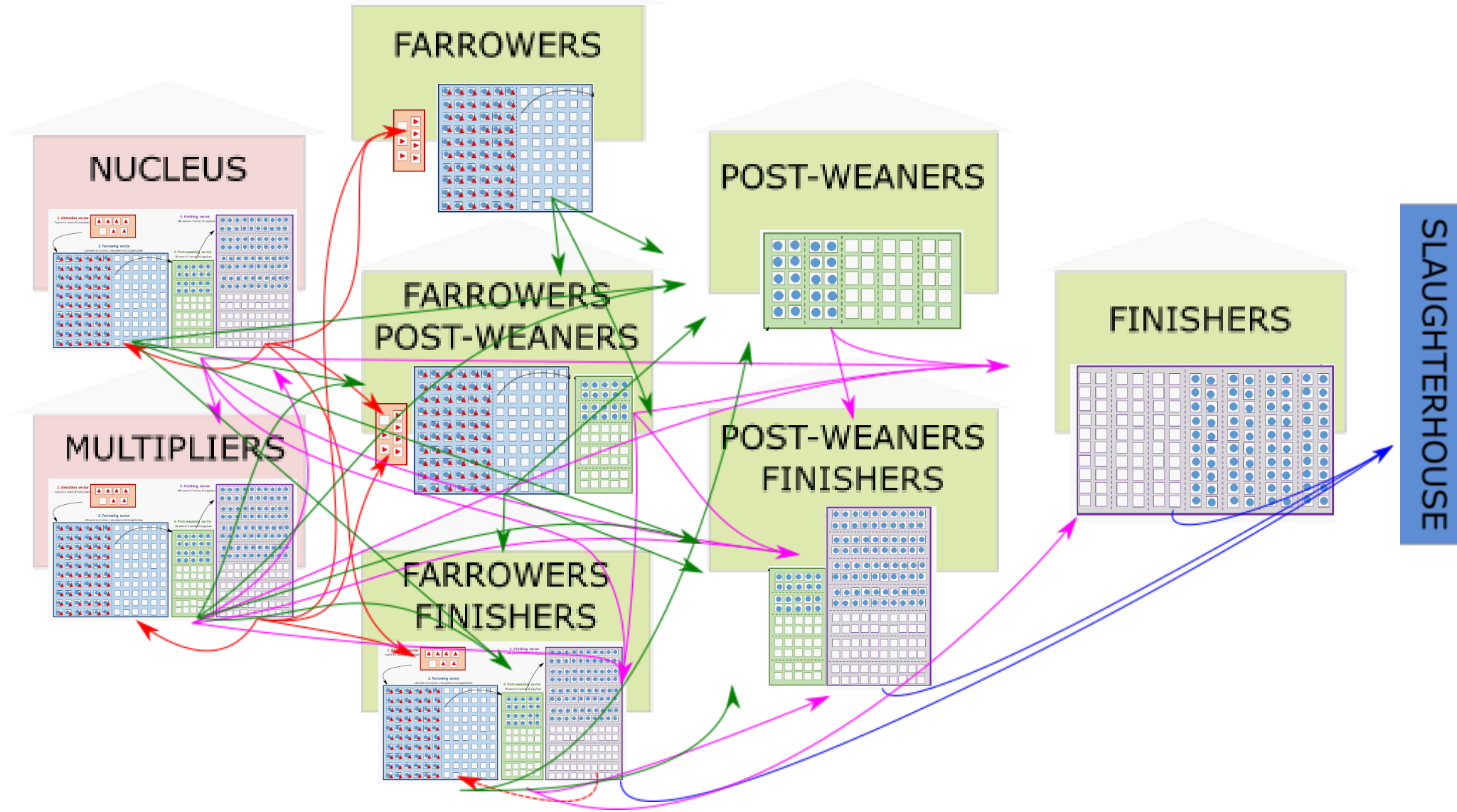
Within farm transmission



Farms structure - husbandry activity



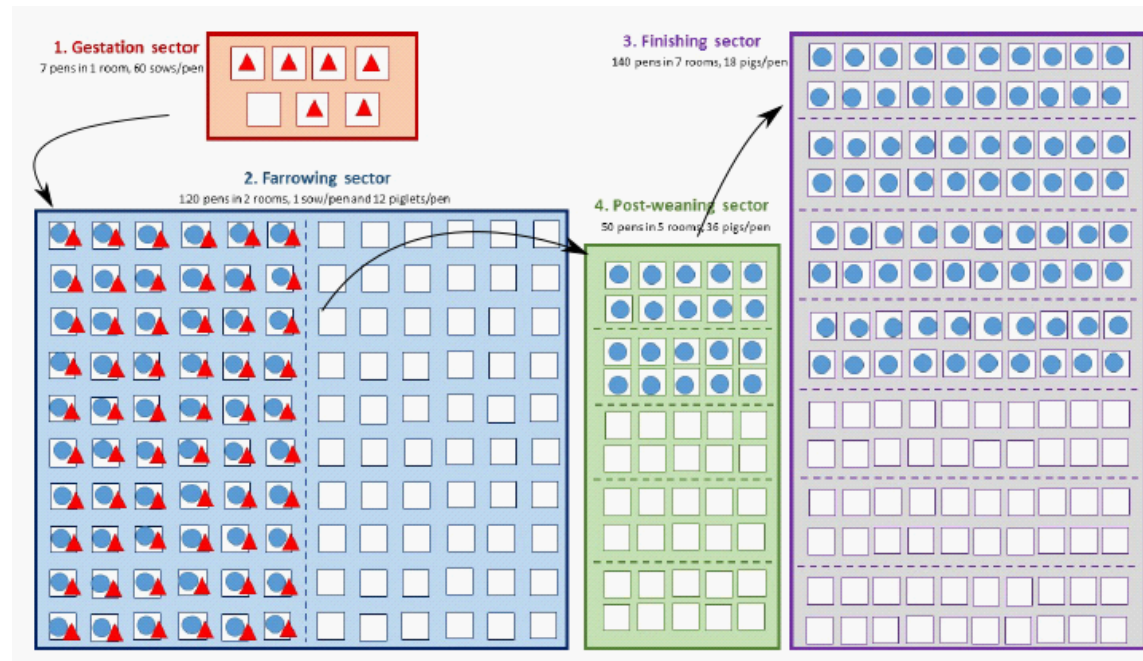
Between farm movements/spread



Salines, M., Andraud, M., Rose, N., Widgren, S., 2020. A between-herd data-driven stochastic model to explore the spatio-temporal spread of hepatitis E virus in the French pig production network. PLoS ONE 15, e0230257. <https://doi.org/10.1371/journal.pone.0230257>

Data were provided by the French national pig identification database (Bdporc)

Within farm movements

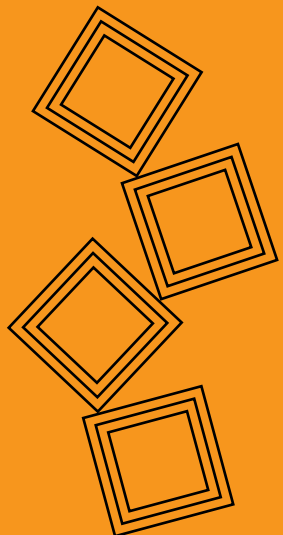


Farm variables:

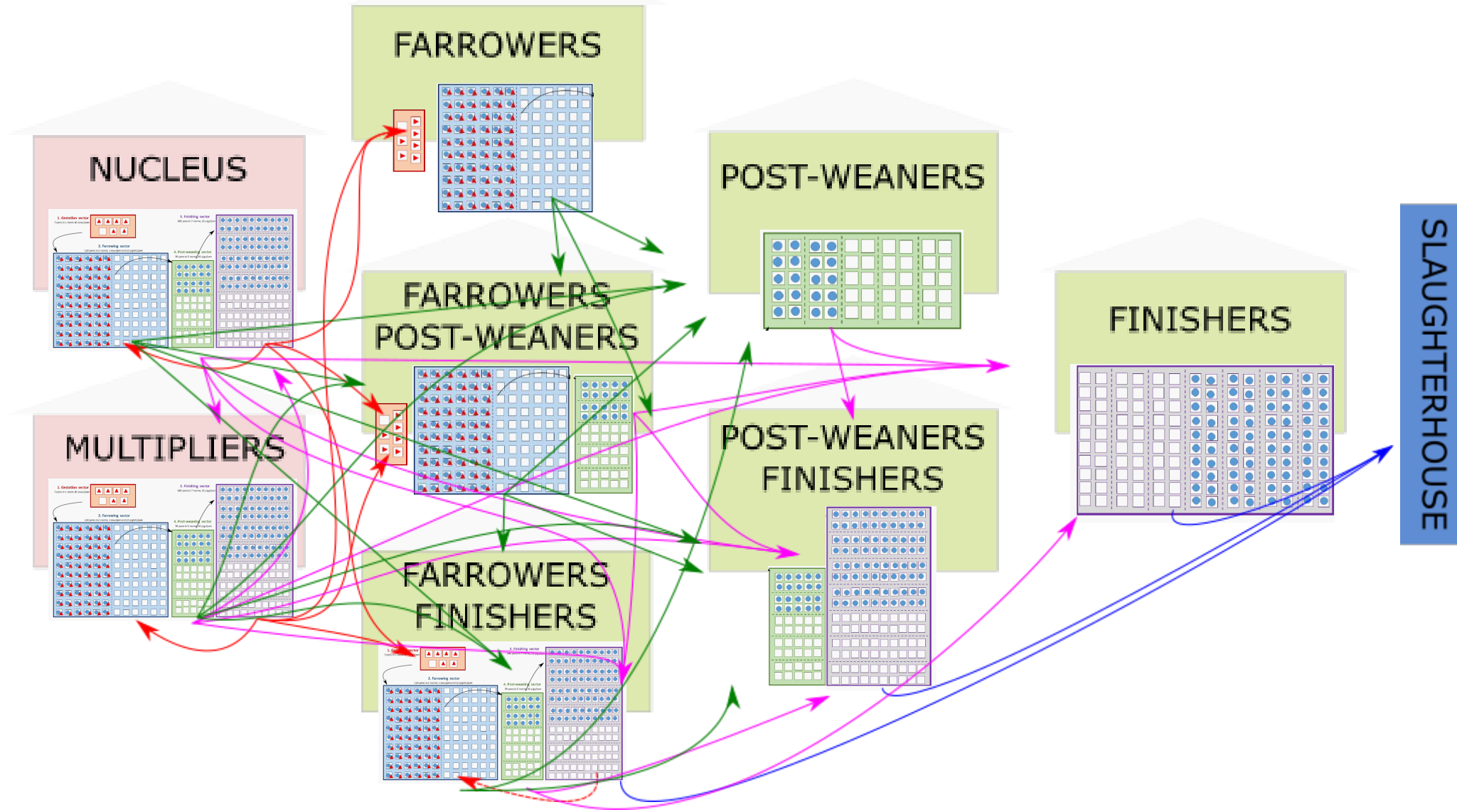
- Farm type
- Number of rooms per unit
- Number of pens per room
- Number of animals per pen
- Duration of stay in each unit
- Duration of sanitary void in each unit

New features:

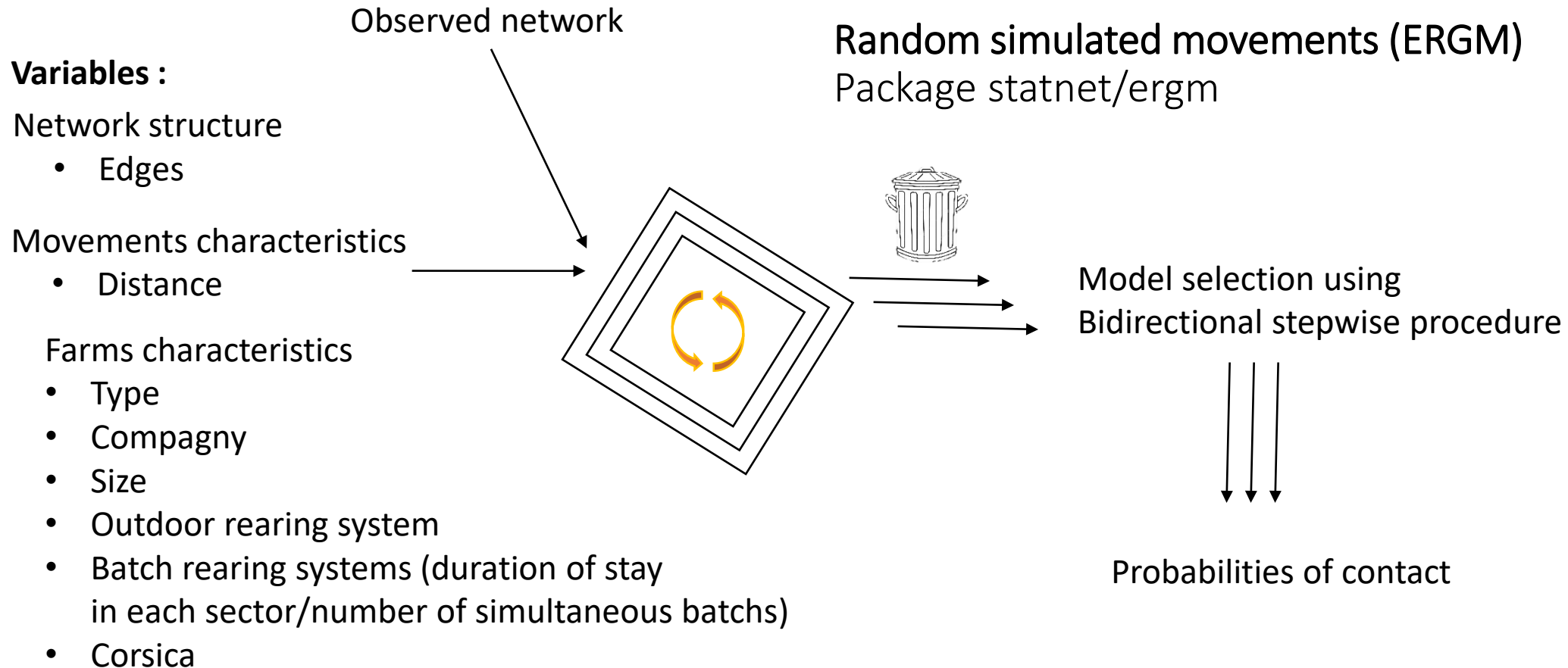
- 8 types of farms
- 5 batch rearing systems (dynamics – deterministic duration)
- Higher size variability
- Room scale



Between farms movements



Exponential Random Graph Models



Relun, A., Grosbois, V., Alexandrov, T., Sánchez-Vizcaíno, J.M., Waret-Szkuta, A., Molia, S., Etter, E.M.C., Martínez-López, B., 2017. Prediction of Pig Trade Movements in Different European Production Systems Using Exponential Random Graph Models. Front Vet Sci 4, 27. <https://doi.org/10.3389/fvets.2017.00027>

Hunter, D.R., Handcock, M.S., Butts, C.T., Goodreau, S.M., Morris, M., 2008. ergm: A Package to Fit, Simulate and Diagnose Exponential-Family Models for Networks. J Stat Softw 24, nihpa54860. <https://doi.org/10.18637/jss.v024.i03>

Salines, M., Andraud, M., Rose, N., 2017. Pig movements in France: Designing network models fitting the transmission route of pathogens. PLoS ONE 12, e0185858.

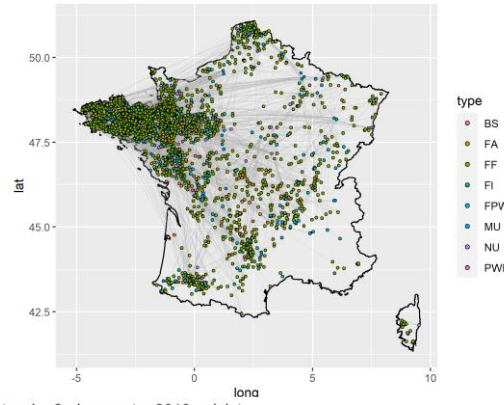
<https://doi.org/10.1371/journal.pone.0185858>

Data were provided by the French national pig identification database (Bdporc)

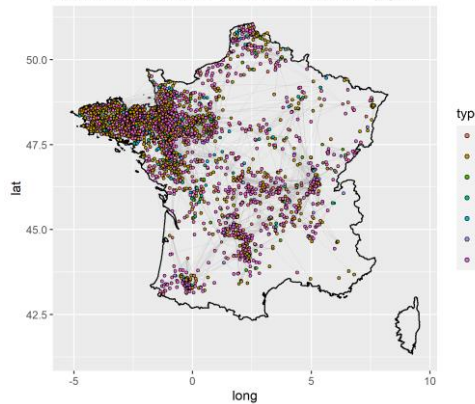
Network statistics – structural stability

Observed movements (SNA)
Package igraph

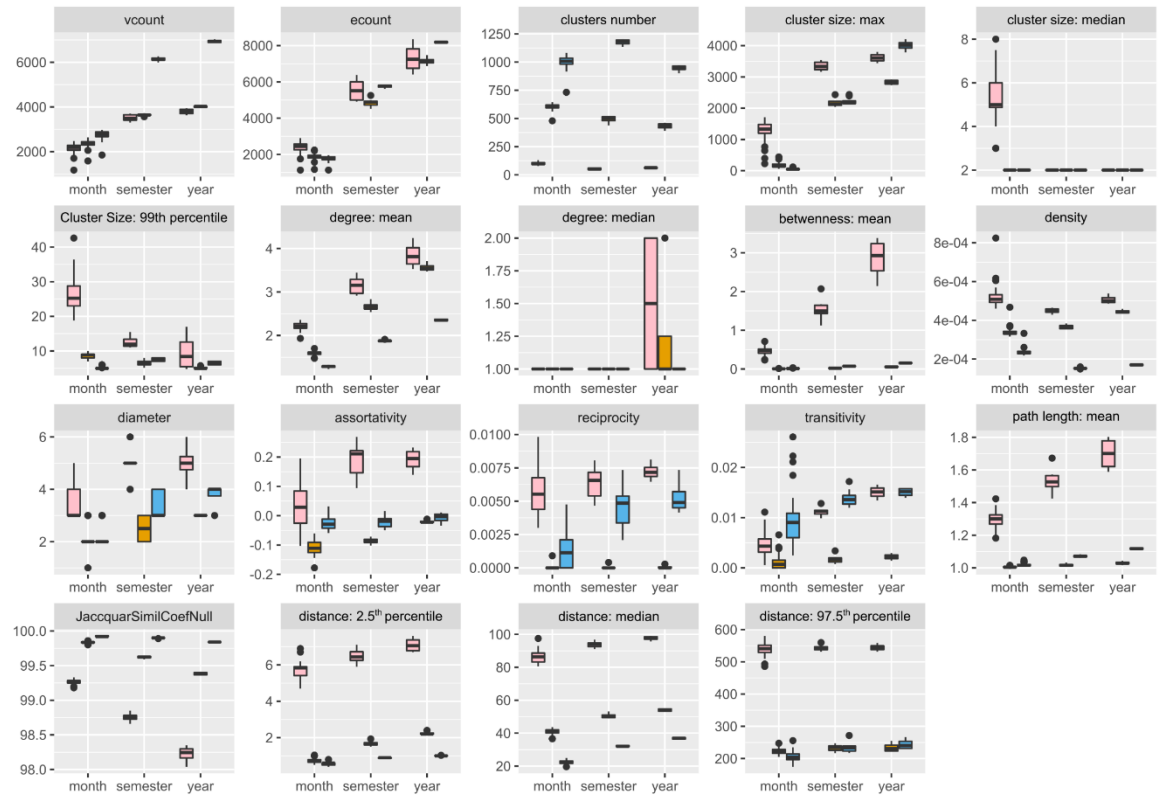
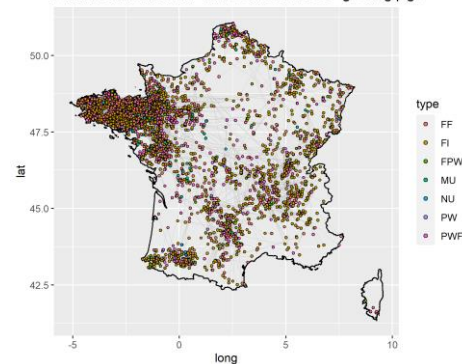
French Swine network - 2nd semester 2019 - reproductive.sows



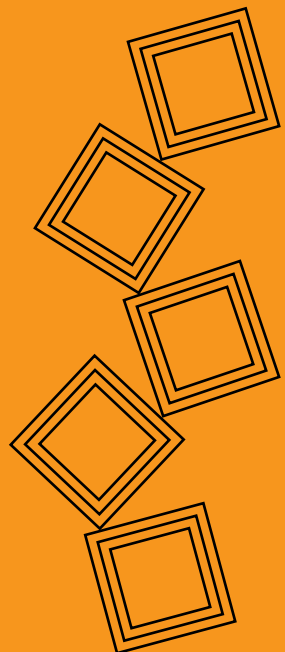
French Swine network - 2nd semester 2019 - piglets



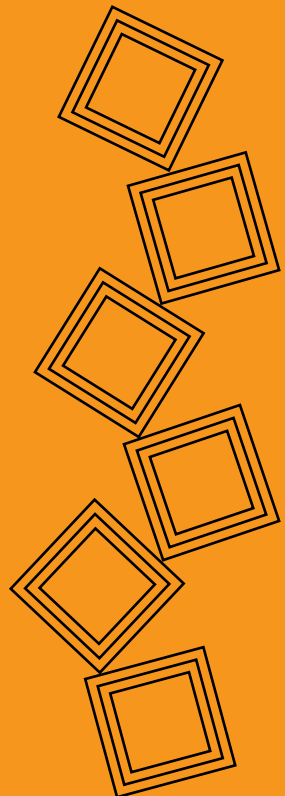
French Swine network - 2nd semester 2019 - growing.pigs



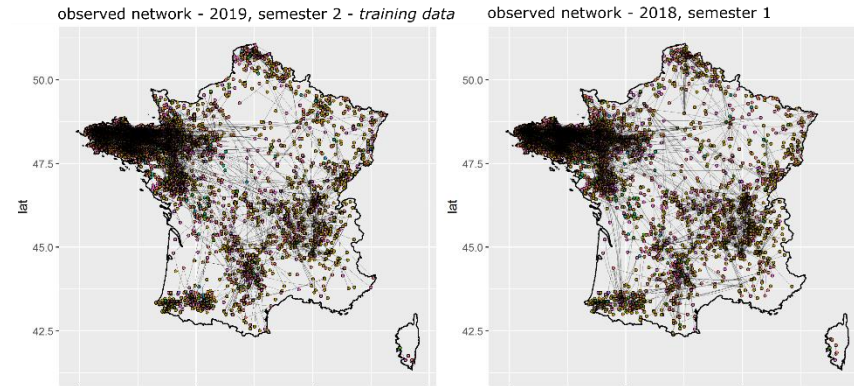
Transported animals



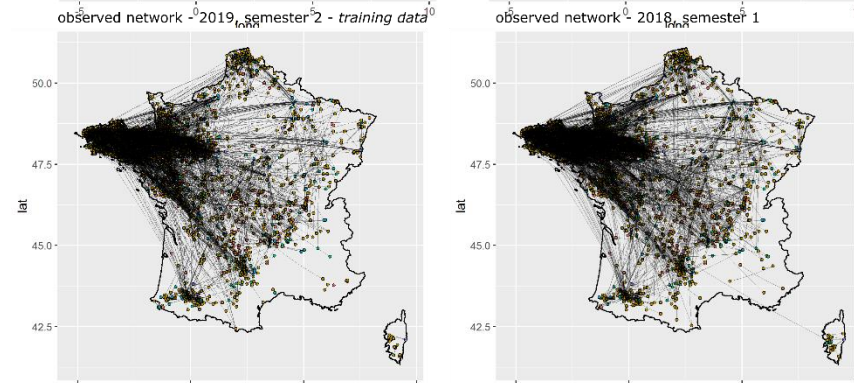
Visual validation



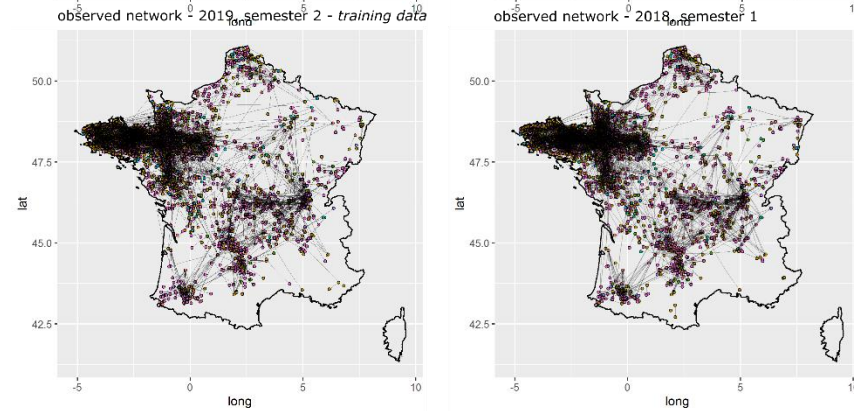
Growing pigs



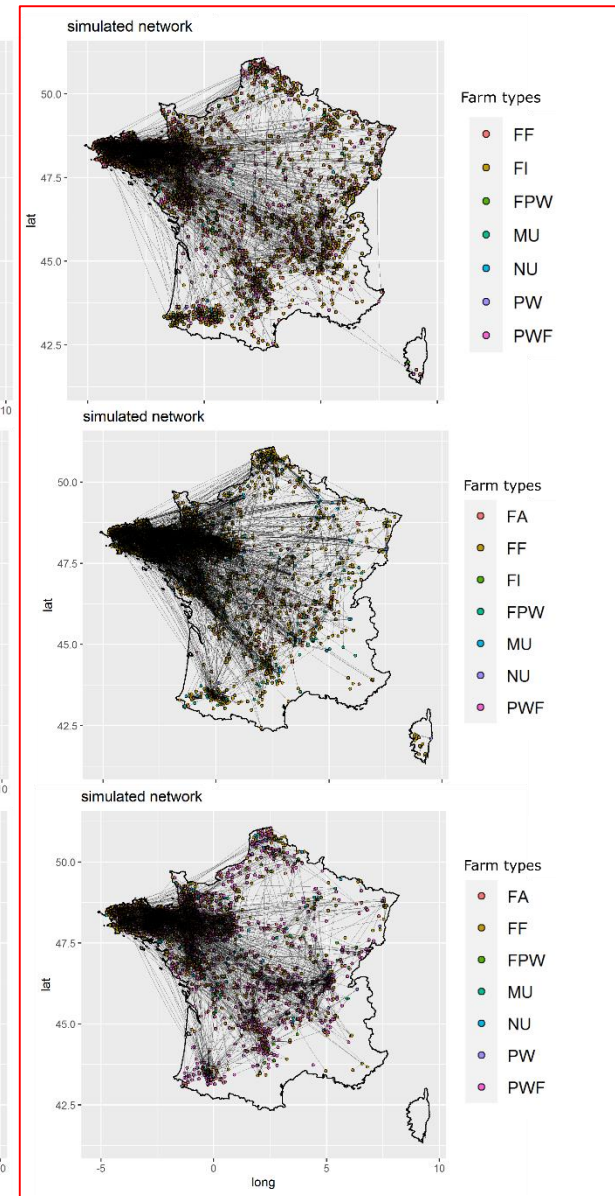
Piglets



Breeding Sows

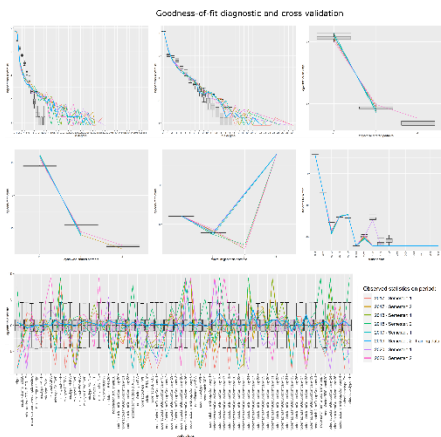


Simulated networks

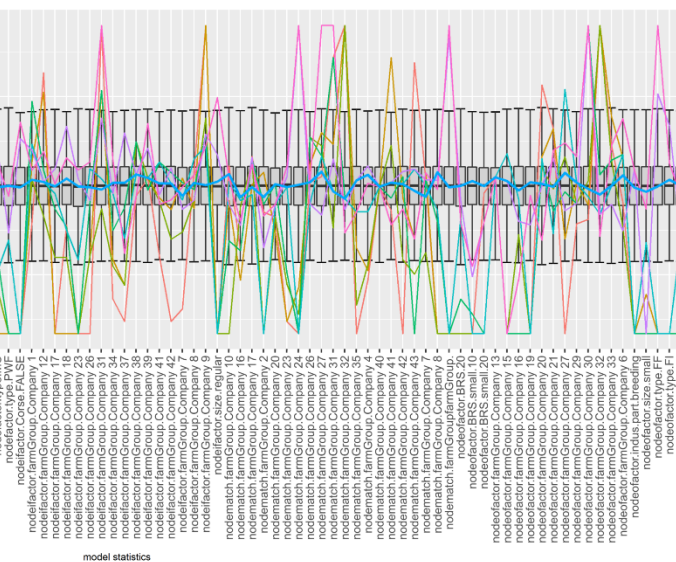
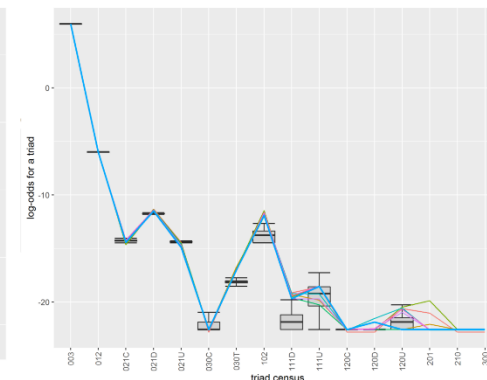
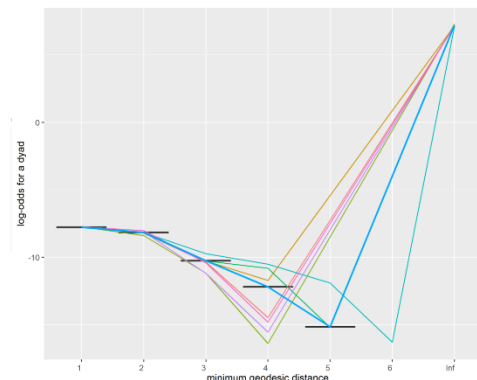
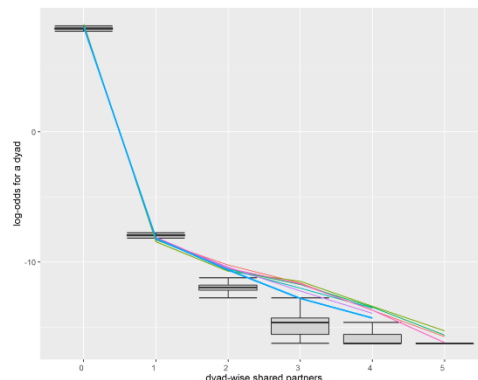
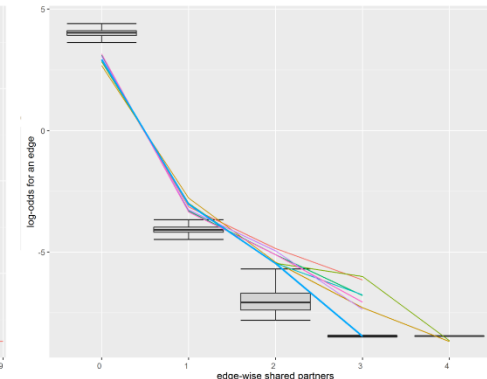
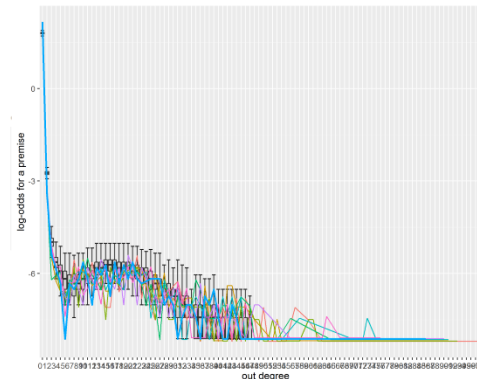
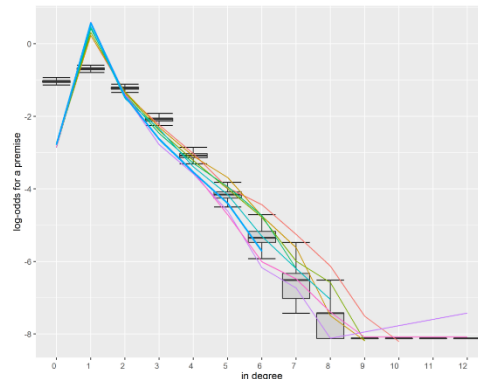
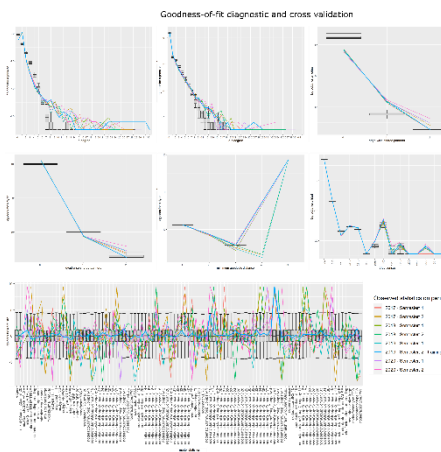


Goodness of fit

Piglets



Growing pigs



Breeding Sows

Observed statistics on period:

- 2017 - Semester: 1
- 2017 - Semester: 2
- 2018 - Semester: 1
- 2018 - Semester: 2
- 2019 - Semester: 1
- 2019 - Semester: 2 - training data
- 2020 - Semester: 1
- 2020 - Semester: 2

Demographic model

Farm structure

- n Units
- Rooms / unit
- Pens / room
- Animal / pen

Farms batch rearing systems

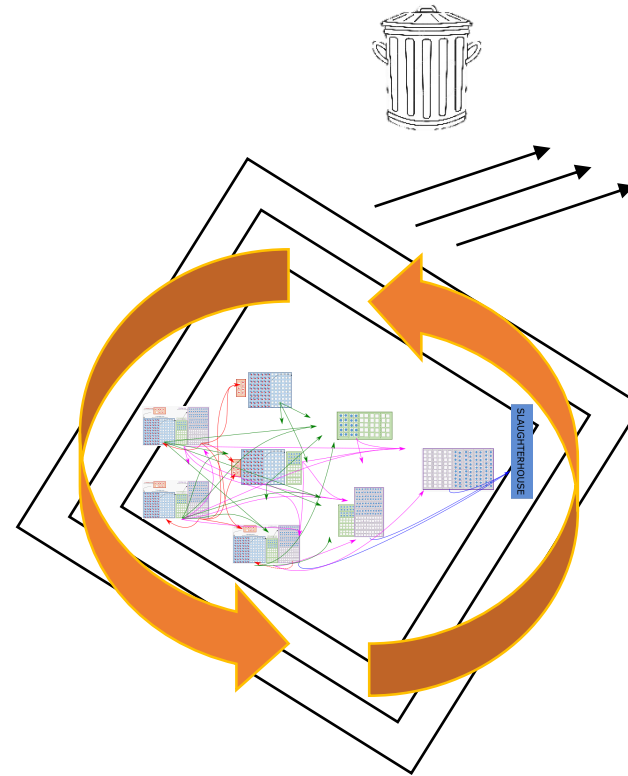
- Duration of stay in each sector
- Number of simultaneous batches

Deterministic schedule

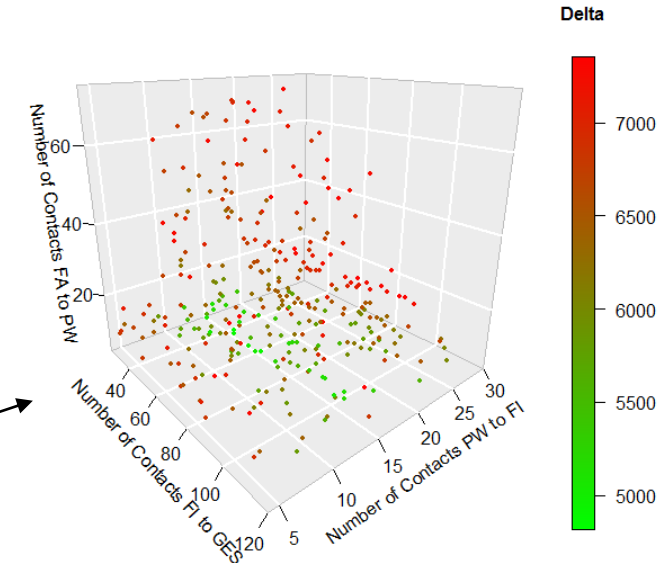
Farm contacts per type of animals

- Contact IDs
- Associated probabilities

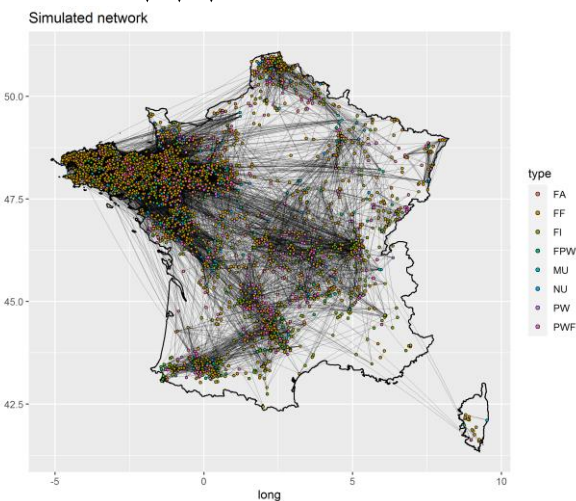
Stochastic destinations



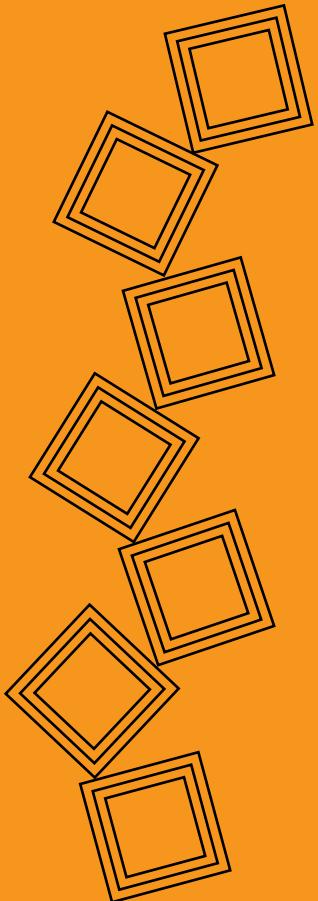
Parameters estimation incomplete sampling plan



Random networks

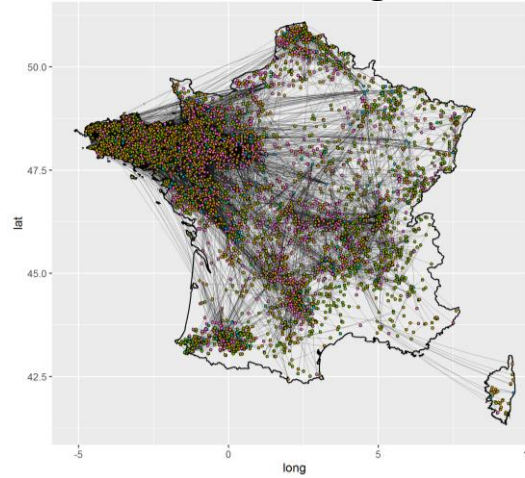


Pen scale
Daily time step



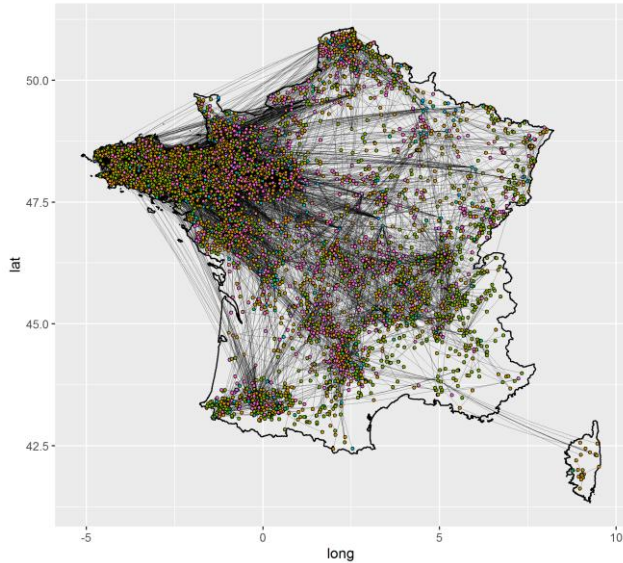
Visual validation

2019 – training data

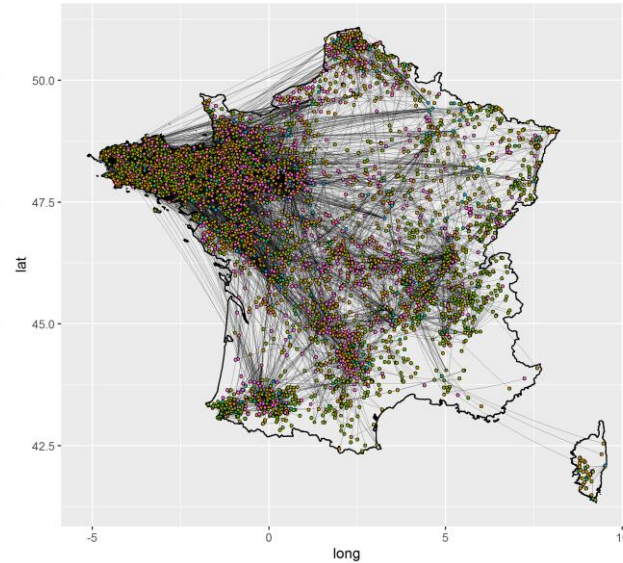


Cross-validation

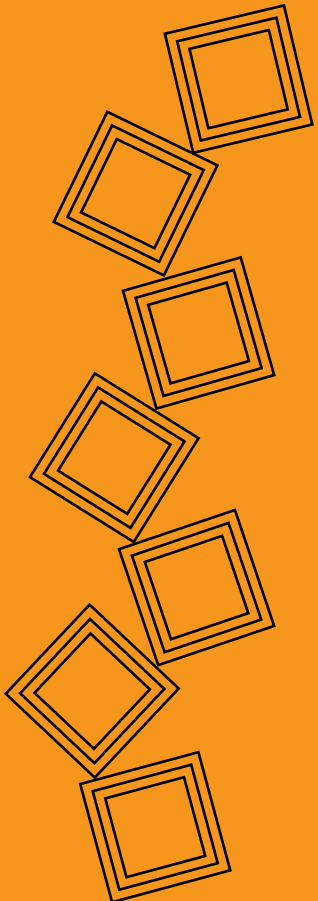
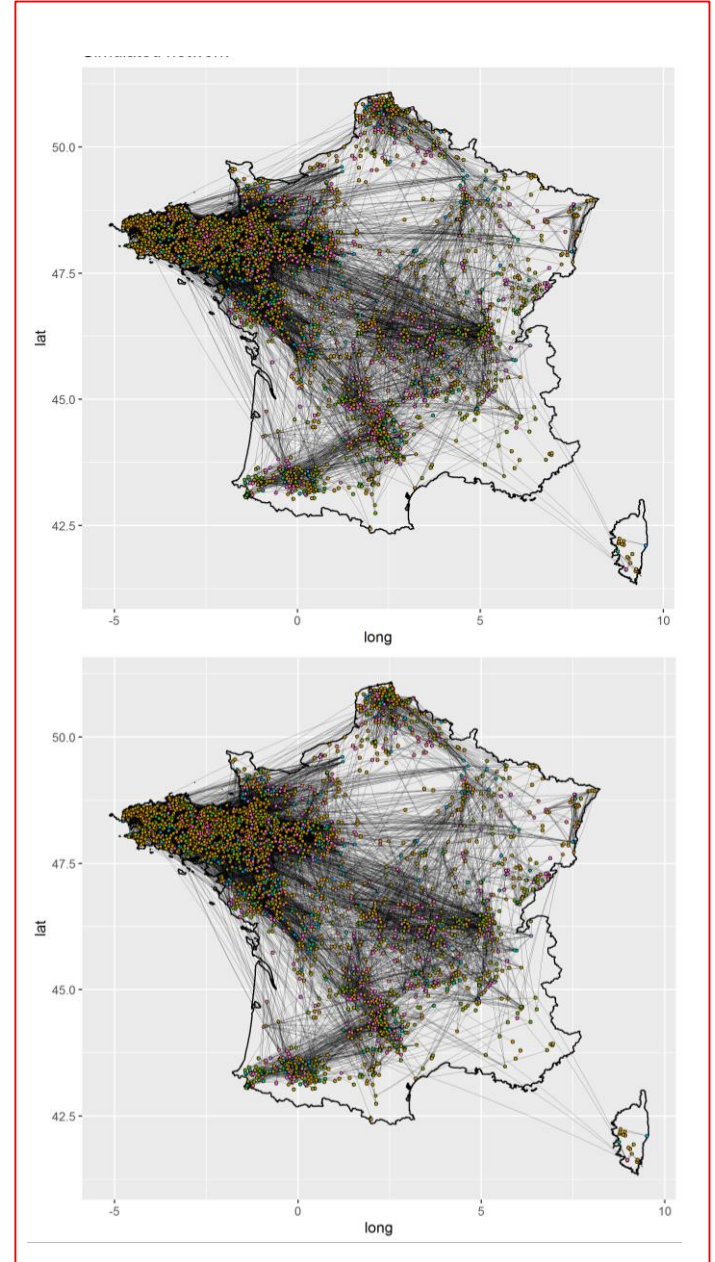
Observed network 2017



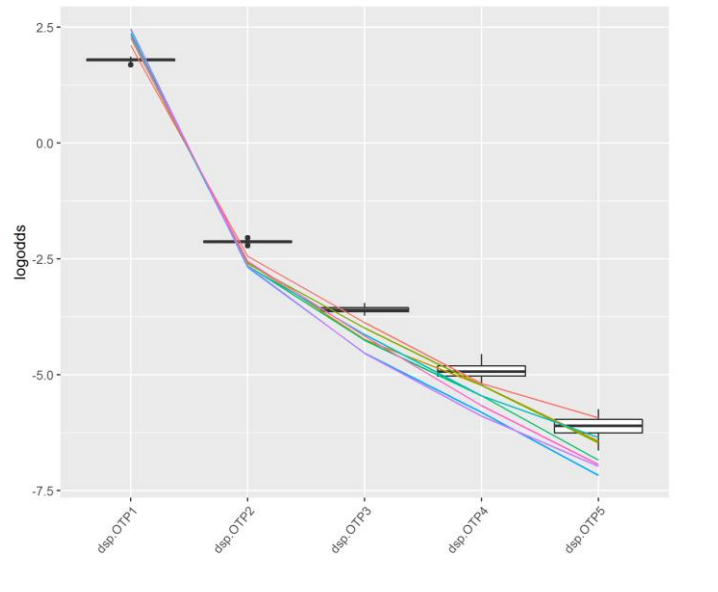
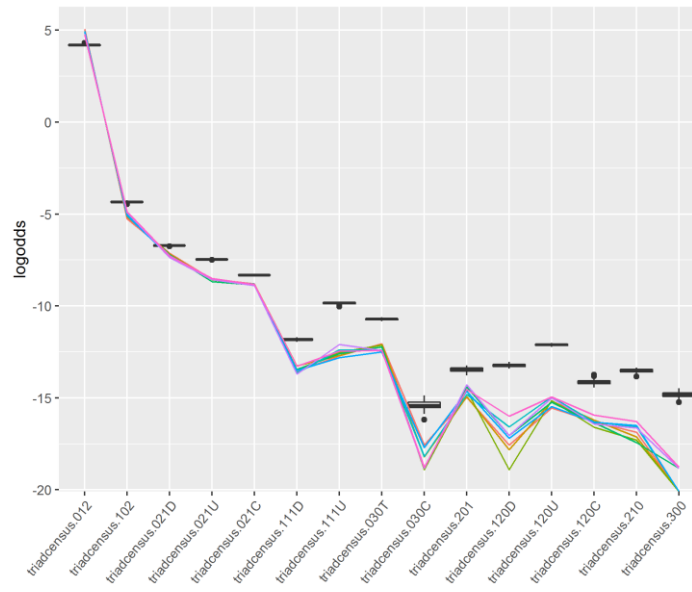
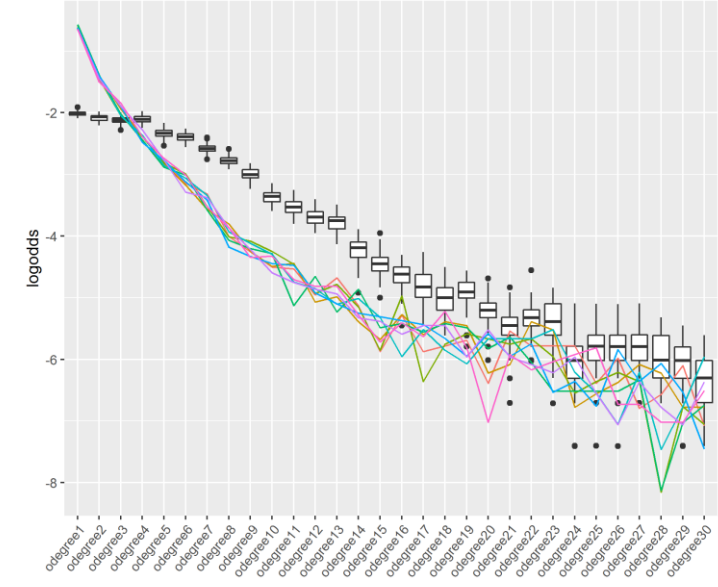
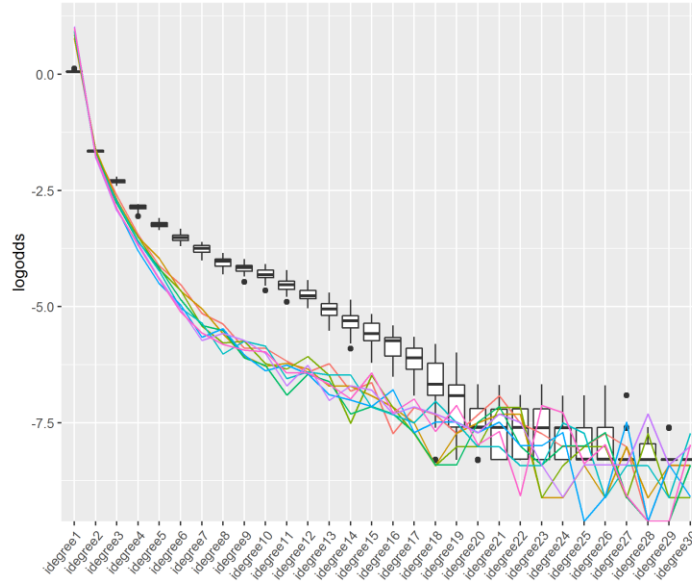
Observed network 2020



Simulated networks

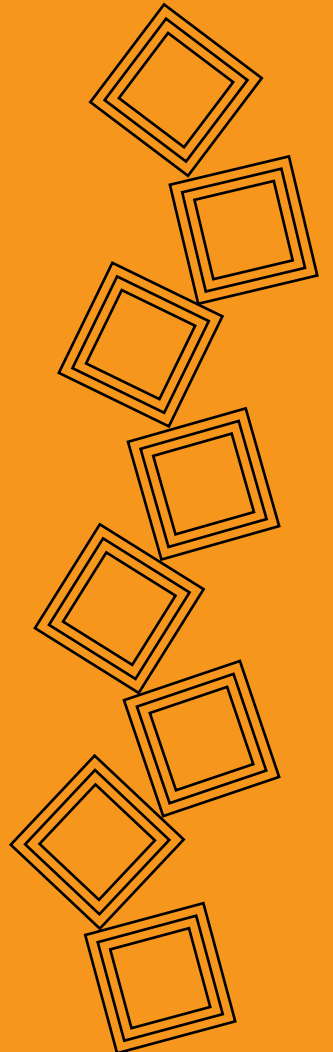


Goodness of fit



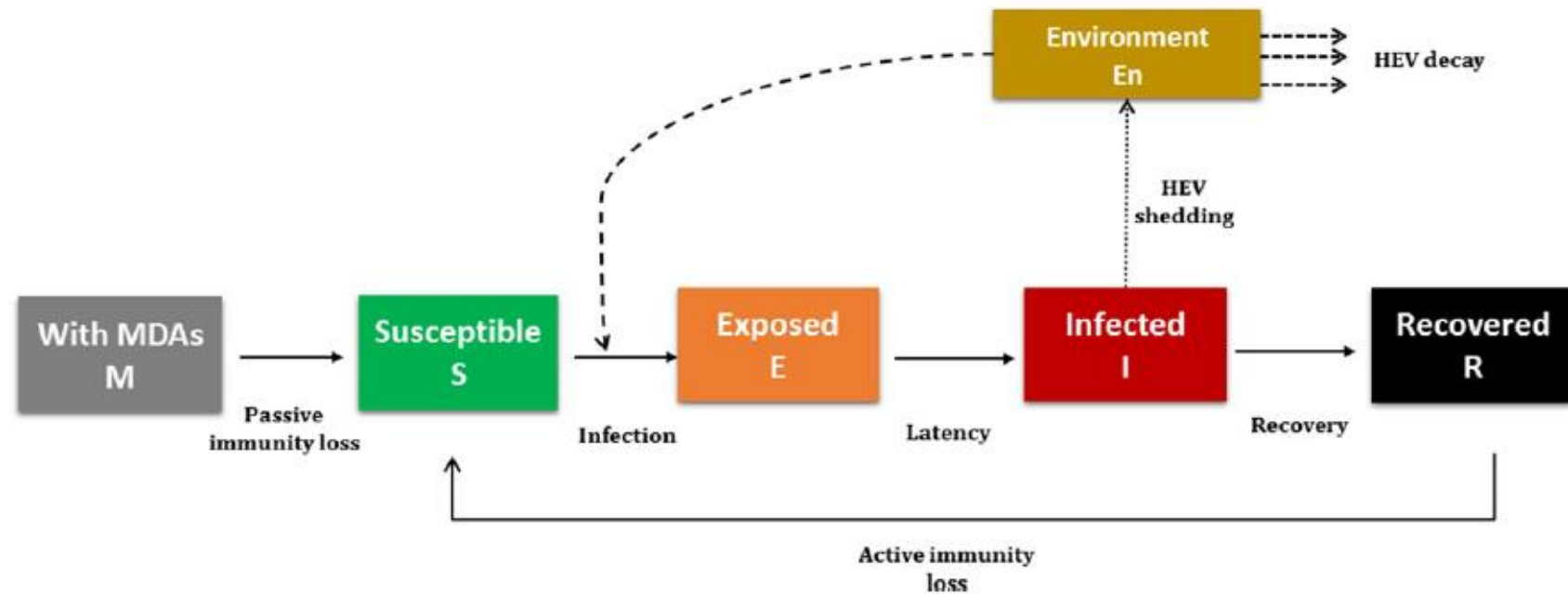
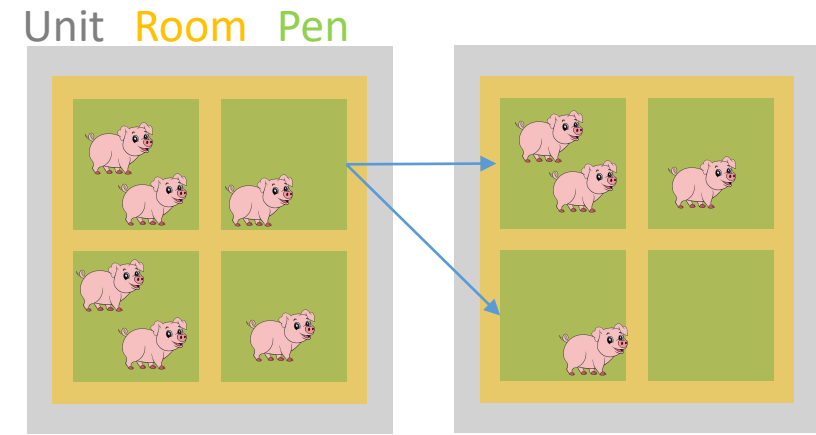
+ Average number of slaughtered pigs per year

- 2017_1
- 2017_2
- 2018_1
- 2018_2
- 2019_1
- 2019_2
- 2020_1
- 2020_2



Epidemiological model

MSEIR-En model -SimInf



Direct transmission within pen between susceptible and infectious pigs

Indirect fecal-oral transmission through environment – within pen and with neighboring pens

Epidemiological model

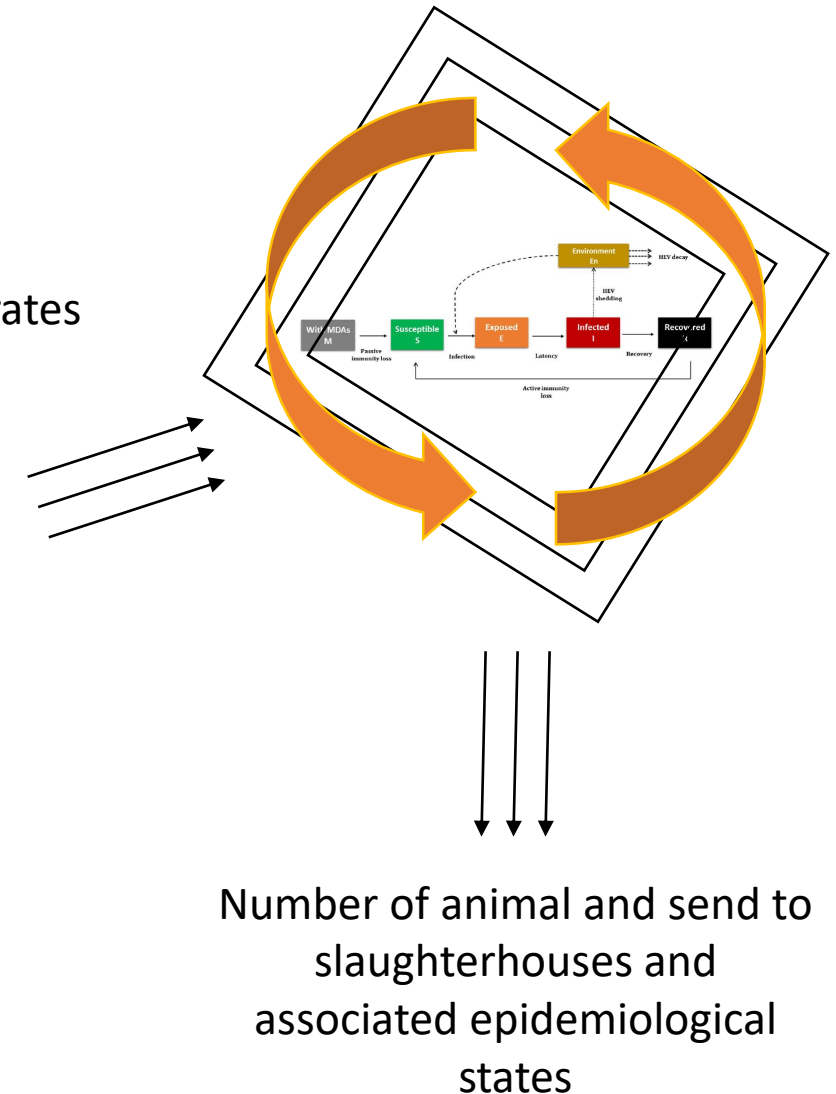
Farm-Unit level

- Direct
- Within-pen environmental transmission rate
- Between-pens environmental transmission rates
- External biosecurity level
- HEV Latency duration (days)
- HEV Infectious period (days)
- Cleaning rate

General variables

- Quantity of faeces/pig/day
- Quantity of faeces/sow/day
- Duration of maternal antibodies
- ...

Random networks



Take home messages

Flexible tool to simulate population dynamics and disease spread

Simulation of pig movements between pens

Deterministic: based on duration of stay in each unit

Stochastic between farms movements based on contact probabilities (ERGM)

Simulation of disease spread using SimInf

Continuous-time Markov chains using the Gillespie stochastic simulation algorithm

Direct contact within pens

Environmental viral charge neighboring pens

