# A stochastic compartmental grid-based model for the “Merry Island 2020 ASF outbreak” (simulated scenario for a challenge)

Jun-Hee Han and **Matthieu Vignes**[†]

School of Mathematical and Computational Sciences
Massey University, NZ

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[†] `m.vignes@massey.ac.nz`

# Outline

- Challenge presentation
- Our modelling choice(s)
- Results
- Discussion

# Part I

# African Swine Fever INRAE modelling challenge presentation

# Motivation: The African Swine Fever (ASF) virus

## Background

- ASF, a disease in swine at the interface between wildlife and livestock
- Very high mortality rate & no vaccine. → strong impact on swine production
  [EU classification is A (immediate eradication measures)+D (strong trade restrictions)+E (mandatory surveillance protocol)]
- Recent pandemics → need for robust predictive tools to cope with health in uncertain scenarios: epidemiological assumptions, environmental changes and control strategies
- Data collection and availability is key too

# The ASF modelling challenge

## Why?

- Several models (phenomenological vs mechanistic, deterministic vs stochastic...) can represent an epidemiological situation
- *Optimal* modelling choice to address a given query?
- Comparing models is therefore essential. But difficult: models can use different data, cover different time-scale, etc.
- Lack of collaboration between modellers and decision-makers
- Be prepared to different scenarios, when real epidemics strikes
- Modelling challenges: CASP (Moult et al. 1995), GRN inference (Marbach et al. 2012), seasonal flu in the US (Reich et al. 2019), Ebola (Viboud et al. 2018), Chikungunya (Del Valle et al. 2018) and Dengue (Johanson et al. 2019)

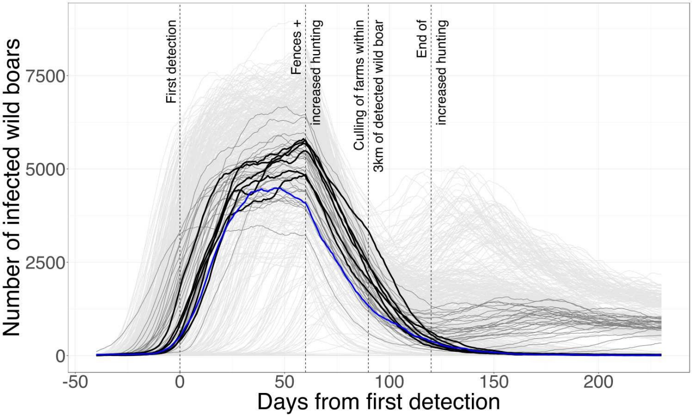
# The ASF modelling challenge on Merry Island

## Description

- Data generated from a detailed Agent-Based Model (ABM) fed with population data (spatial distribution of the host populations, movement of live pigs...) and parameterised with key transmission parameters and intervention strategies
- Land = agricultural $\cup$ forest $\cup$ urban
- First outbreak detected in a Domestic Pig (DP) farm (among $4,775$ with different characteristics) near a forest area. Wild Boar (WB, $500,000$) are present on the island
- Data = dynamics of reports of infected DP farms (assuming perfect test) and WB carcasses

# The ASF modelling challenge

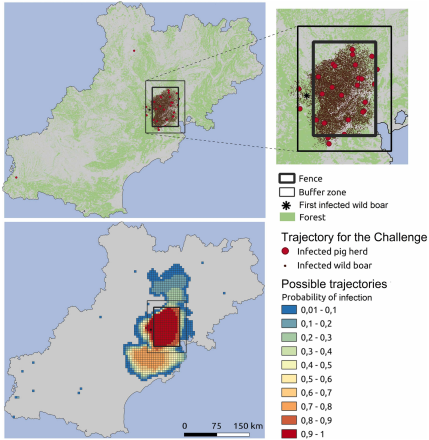
## Temporal dynamics in WB and a few control strategies



(see Picault et al. 2022)

# The ASF modelling challenge

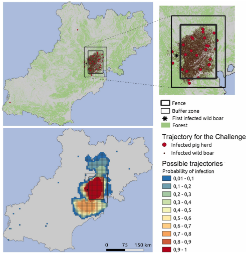
## Spatial distribution of infected units



(see Picault et al. 2022)

# The ASF modelling challenge

## Spatial distribution of infected units



(see Picault et al. 2022)

- Note: only a subset of all infections were reported in the data

# The ASF modelling challenge

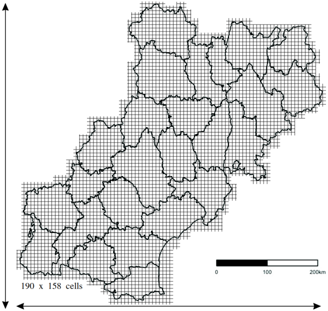
## Participant mission(s)

1. Phase 1 (50 days after first detection), teams were asked to predict the number & location of infected WB and farm outbreaks in the next 4 weeks with/without a fenced buffer zone and with/without increased hunting pressure.
2. Phase 2 (80 days after first detection) → update predictions with a buffer zone of 15km away from the fenced area and assess the effectiveness of alternative control options: culling of all DP in “protection zone”; increasing the size of an active search near detected WB from 1 to 2 km; culling of all DP in farms within 3km of detected WB; culling after movement between farms when infected <3 weeks.
3. Phase 3 (110 days after first detection) → update predictions and estimate the chance of a fade out of the epidemic 4 months later, incl. flagging a long-term risk.

# Part II
# ASF modelling challenge: Team kiwi choices

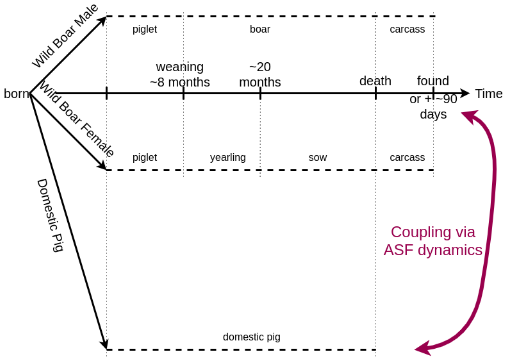
# Merry Island: a grid representation for Wild Boars (WBs)

- 190 × 158 cells, as many ∼ 10 km$^2$-habitats of WB sounders (aka family groups)
- In each cell, WB go through demographic and disease dynamics (see next slides); interactions with neighbouring WBs and DP farms



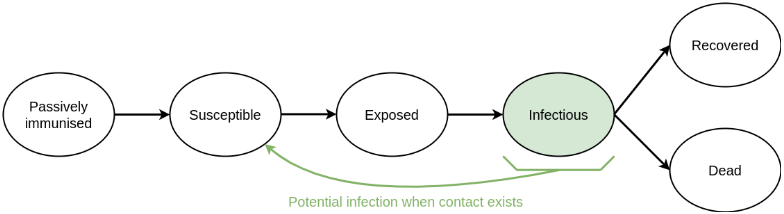
- Farms interact via trade movements only
- 150 days cycle in Merry Island animal movements; assumed it was the case in prediction periods

# Demographic dynamics



- Three tracks: Domestic pigs, Female WB and Male WB
- Time unit $= 1$ day. Year assumed to be 365 days

# ASF disease compartments


Passively immunised
Susceptible
Exposed
Infectious
Recovered
Dead
Potential infection when contact exists

- Passively immunised at birth via maternal antibody
- Exposed: infected but not infectious, $\sim$ 5 days
- Infectious $\sim$ 7 days
- 5% of infected animals recover, 95% die.
- Decay of carcasses is $\sim$ 90 days.
- (all random times are discretised $\mathrm{Exp}$ distributions unless otherwise specified)

# WB population dynamics

- For each cell: maximal WB population was estimated from the first 50 days hunting bag by kernel density
- Sows, up to $\sim 20\%$ WB population, farrow each year at random day in December (weaning)+random gestation time $\sim \mathrm{round}\left(\mathrm{N}(115, 2.5^2)\right)$; number of piglets$\sim \mathrm{round}\left(\mathrm{N}(5, 1^2)\right)$
- Total WB after hunting season assumed $= 520,000$; Hunting season (1 June $\rightarrow$ 31 Jan) had $\sim 275,000$ non-piglet WBs hunted and culled
- Natural mortality in WBs: 12% (non-piglets) and 17% (piglets), calibrated to keep population at constant size
- Male WBs' random dispersal was simulated allowing them to move up to 16 cells from starting point; unsaturated ending cell
- Female WB just weaned could split from their sounder and move up to 2 cells from their starting point; female-free ending cell

# DP population dynamics

- DP population in each farm assumed constant with no natural death
- Movements incurred repopulation in source farms by Susceptible and culling (abattoir) in target farm to keep population size constant (randomly regarless of their ASF status)

# ASF dynamics

- WB infection pressure depended on: Infectious WBs in same and neighbouring cells and of Infectious DPs in same cell farms
- DPs infection pressure depended on: Infectious DPs in same farm and density of Infect WBs in same cell (but farm detected ASF+ as soon as $\#(\mathit{Infectious}) > 0$)
- Every day, newly infected pigs was drawn from a $\mathrm{Binom}(\text{Suscept}, P_{\text{infection}})$
  - $P_{\text{infection}} = 1 - \exp(-\lambda)$ is cell-dependent and different for WB (all terms) and DP (blue terms, modified indices), with

$$\begin{aligned}\lambda_{cell} &= \beta_{WB,within}\, I_{WB\in cell} + \beta_{Carc,within}\, C_{cell}\\ &+ \sum_{j\in Neigh.cells} \beta_{WB,betw}\, I_{WB\in j} + \sum_{j\in Neigh.cells} \beta_{Carc,betw}\, C_j\\ &+ \sum_{k\in cell.farms} \beta_{WB\leftrightarrow DP}\, I_{DP\in k}\end{aligned}$$

  - We modified the force of infection to be density-dependent (phase 1) to frequency-dependent (phases 2 & 3)

# Model initialisation

- A naturally evolving population of WBs was run for 15 years to stabilise the Merry Island population
- ASF introduced at day 181 (7 days prior 8 July 2020) of year 16 on one animal in the index case farm, and 10 random WBs in this cell were “switched” to Infectious (contamination scenario hypothesis)

# Parameter estimation and predictions

## Summary strategy

- Five-parameter model
- ×200 for each of the $125 = 5^3$ parameter combinations to rank the tested parameter values
- Different parameters tuning based on monitoring different observation agreement pre-prediction phase
- Note: model over-parameterised, so fixed some values to 1
- Probabilities of events (such as farm infection) are estimated using the 200 repeats

# Part III

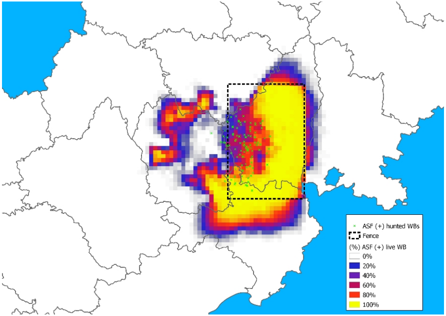
# ASF modelling challenge: Team Kiwi results

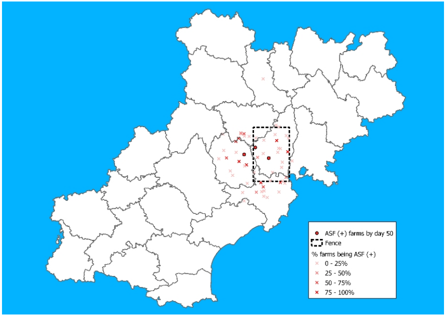
# Results phase 1: Fence only and increased hunting pressure within the fence effects

- Our model indicated that ASF is more prevalent than reports at day 50: WB and 1 or 2 unreported farms at day 50 already. We predict $\sim$ 15 infected farms by day 80 (10-20 95% PI)
- Implementation of the fence with or without the increased hunting pressure inside has an effect on ASF+ WB cases number, but is not enough to prevent the spread of the disease outside the fenced areas
- Probably overestimated the ASF spread. But not too bad

# Probability of having >1 infectious WB (left) and Probability of infected farm (right)

## Fence & increased hunting pressure scenario

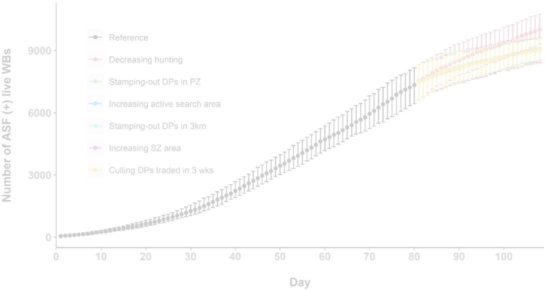


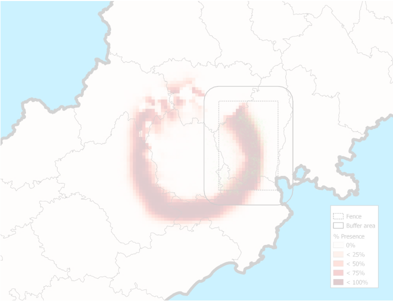


# Results phase 2: different control options

- Clear transmission west and south-west of initial zone
- Implemented proposed controlled measures have a limited effect on the spread
- Suspected index case farm west of the first 3 reported farms: “spatial wave” (see next slide)
- Implementation issue in linking grid to model?

# Total number of infectious WB by implemented control scenario (left) and Probabilistic spatial distribution cells with >1 infectious WB at the end of period 2 (right)





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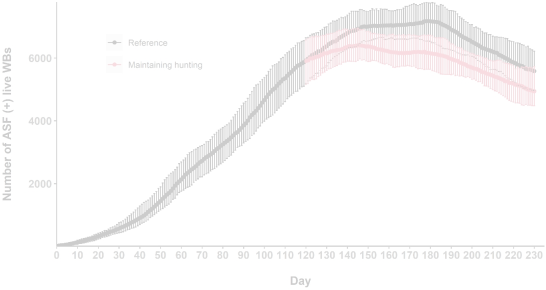
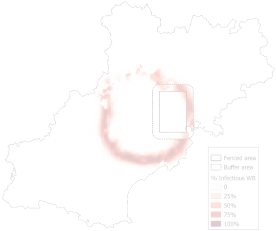
# Results phase 3: to hunt or not to hunt?

- ASF spread beyond the fenced area
- ASF endemic in WB population
- Epidemic curve seems to indicate a decline before day 230
- Yet, unless different control measures are applied, a second wave could be observed in the future

# Total number of infectious WB (left) and and Probabilistic spatial distribution cells with >1 infectious WB at the end of period 3 under maintained hunting pressure (right)

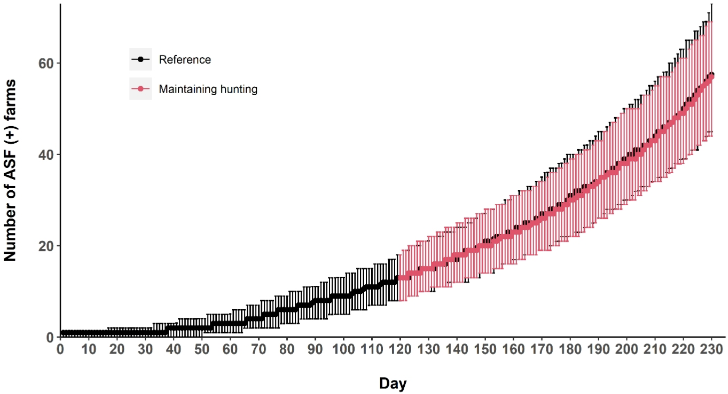




# (mini) Part IV
# ASF modelling challenge: Team Kiwi discussions

# Our model is pessimistic for farmers

The number of infected pig farms does not seem to stabilise...



# Discussion and conclusive remarks

- Parameter estimation is an issue!
- Key parameter (sensitivity analysis): reduction in 'between cell' transmission (overestimated in phase 2, less so in phase 3)
- Surprisingly not so much variability in runs
- Jaccard index choice for parameter selection questionable: MCMC was tried but extremely long running times (doable on real data from South Korea, but $\Delta t = 1$ week)
- Land cover (not used by our model) redundant with hunting bag?
- Issue in the C library we used? (any random number $< \frac{1}{37267}$ set to 0 in Windows?!)

Thank you for your attention

Questions welcome!