Modelling the spread of transboundary animal disease in and between domestic and wild swine populations

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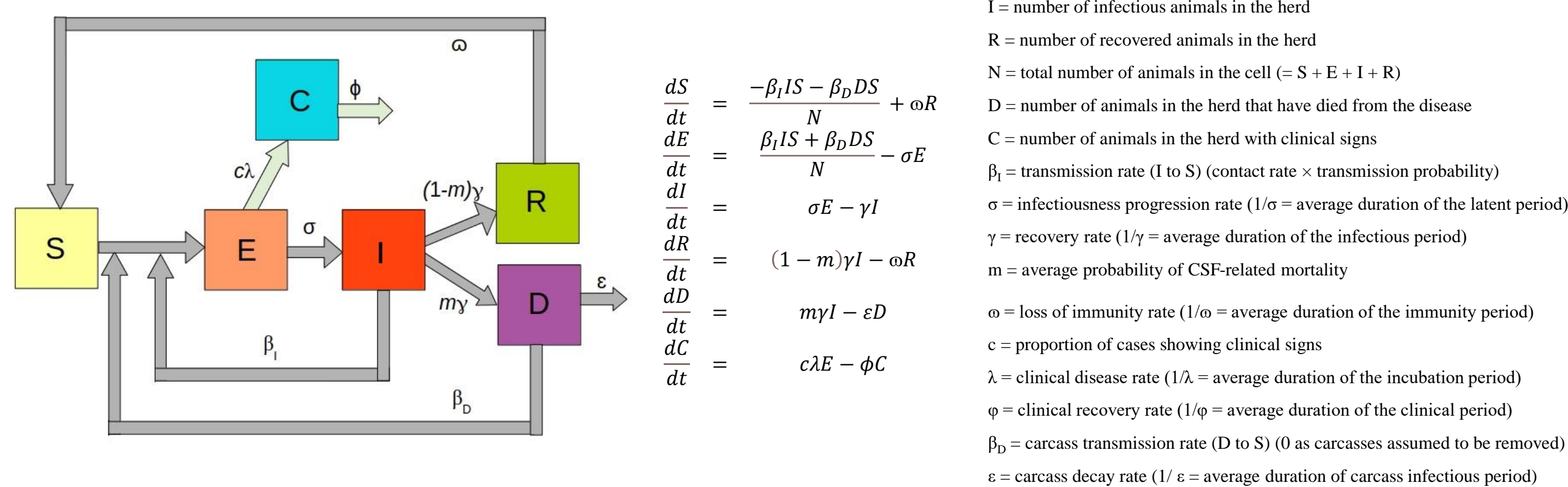
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Overview

- EuFMDiS[a] is a continental-scale model of livestock disease designed to support emergency animal disease planning in Europe. It is a multi-country adaptation (funded by the EuFMD), of the Australian Government's national-scale livestock disease model AADIS[b].

- EuFMDiS simulates the spread of livestock disease within and between countries and allows control policies to be enacted and resourced on per-country basis. It provides decision support in assessing the risk of disease introduction, establishment and spread; control approaches in terms of effectiveness and costs; resource management; and post-outbreak management issues.

- The objective of this project was to extend the EuFMDiS model to include wildlife spread pathways. The spread and control of classical swine fever (CSF) in Spanish domestic pigs and wild boar was selected as the test case. A parallel AADIS development project is underway in Australia with African swine fever in Queensland domestic and feral pigs as the test case.

## Modelling the spread and control of CSF in Spanish domestic pigs

- The EuFMDiS epidemiological unit of interest for livestock is the 'herd' − defined as a group of co-mingling animals of the same species under the same production system. Herds are categorised by 'herd type' by which the key characteristics of disease dynamics, production systems, and marketing systems can be captured.

- The domestic pig population in Spain was classified according to 4 herd types:
  large-scale commercial fattening (n=14,470)
  large-scale commercial breeding (n=12,093)
  small-scale commercial (n=16,451)
  backyard (n=41,424)

- Regional differences in production and marketing systems were captured through the definition of 4 livestock regions: Extensivio, Intensivo Baleares and Canaris, Cantabrico Pirineos

- The spread of infection within a herd is represented by an SEIRDC compartmental model.

$$\frac{dS}{dt} = \frac{-\beta_I IS - \beta_D DS}{N} + \omega R$$

$$\frac{dE}{dt} = \frac{\beta_I IS + \beta_D DS}{N} - \sigma E$$

$$\frac{dI}{dt} = \sigma E - \gamma I$$

$$\frac{dR}{dt} = (1-m)\gamma I - \omega R$$

$$\frac{dD}{dt} = m\gamma I - \varepsilon D$$

$$\frac{dC}{dt} = c\lambda E - \phi C$$

S = number of animals in the herd that are susceptible
E = number of latently infected animals in the herd
I = number of infectious animals in the herd
R = number of recovered animals in the herd
N = total number of animals in the cell (= S + E + I + R)
D = number of animals in the herd that have died from the disease
C = number of animals in the herd with clinical signs
β_I = transmission rate (I to S) (contact rate × transmission probability)
σ = infectiousness progression rate (1/σ = average duration of the latent period)
γ = recovery rate (1/γ = average duration of the infectious period)
m = average probability of CSF-related mortality
ω = loss of immunity rate (1/ω = average duration of the immunity period)
c = proportion of cases showing clinical signs
λ = clinical disease rate (1/λ = average duration of the incubation period)
φ = clinical recovery rate (1/φ = average duration of the clinical period)
β_D = carcass transmission rate (D to S) (0 as carcasses assumed to be removed)
ε = carcass decay rate (1/ ε = average duration of carcass infectious period)

- The spread of ASF/CSF between herds is modelled with stochastic and spatially-explicit pathways representing direct spread (via animal movements between farms and involving markets), indirect spread, and diffusive local spread between neighbouring farms.

- After detection of the index case, control measures comprise movement restrictions, surveillance, tracing, and stamping out, and optionally pre-emptive culling and emergency vaccination.

- All control actions are costed and constrained by resource availability.

- Systemic imperfections in control are represented including false positive reports of disease leading to redundant surveillance visits, false positive & false negative test results, non-compliance with movement restrictions, and tracing inefficiencies leading to false positive tracing results.

## Representing the wild boar population in Spain

- A grid was overlaid Spain with cell size approximately 4 km². Each cell has a range of environmental attributes.

- EuFMDiS provides two options for estimating a wildlife population (a) a built-in species distribution model that considers habitat suitability in each cell over time, coupled with mathematical estimations of within-cell abundance, or (b) externally generated 'time slices' of population counts that leverage off specialised habitat modeling.
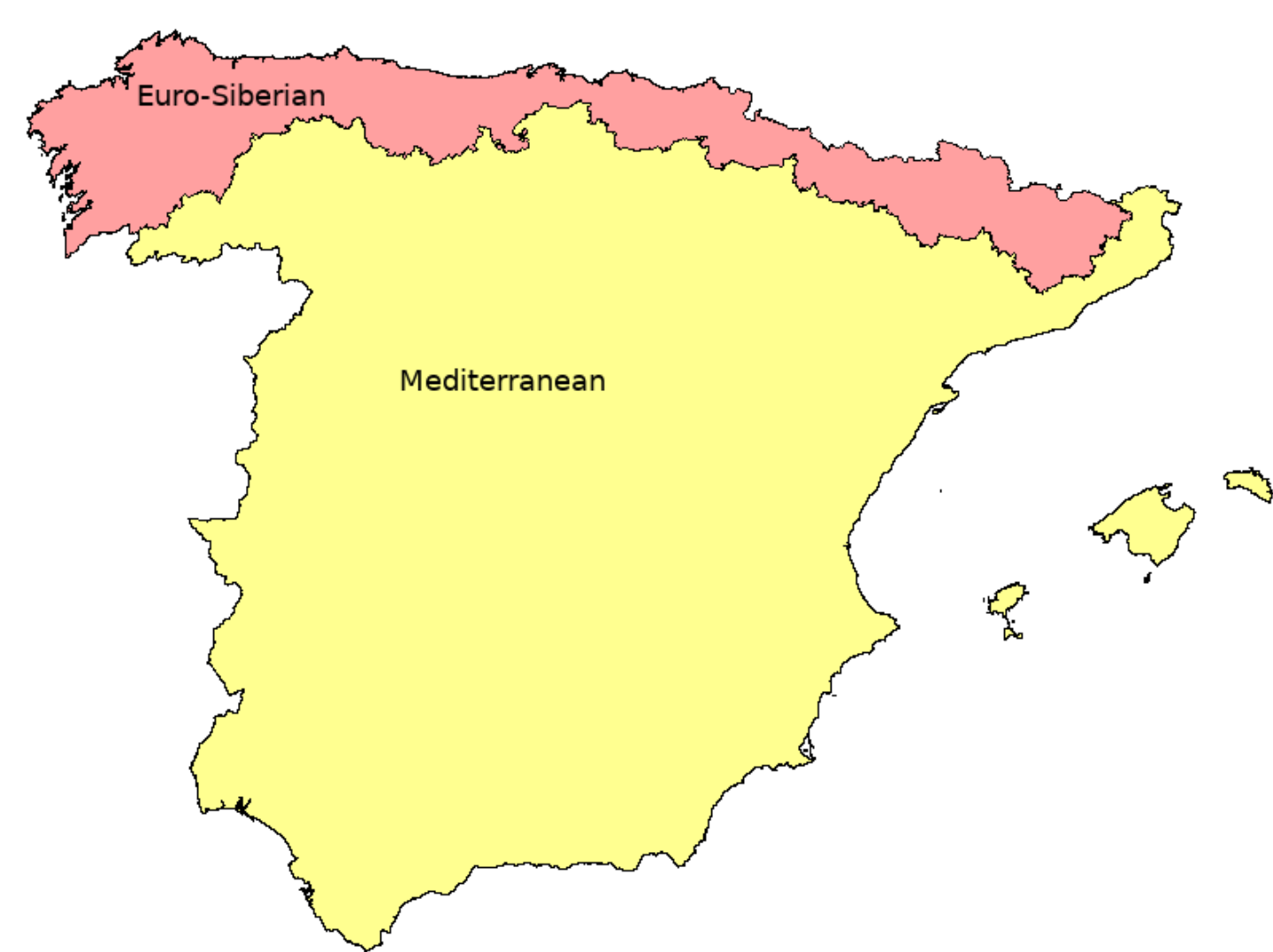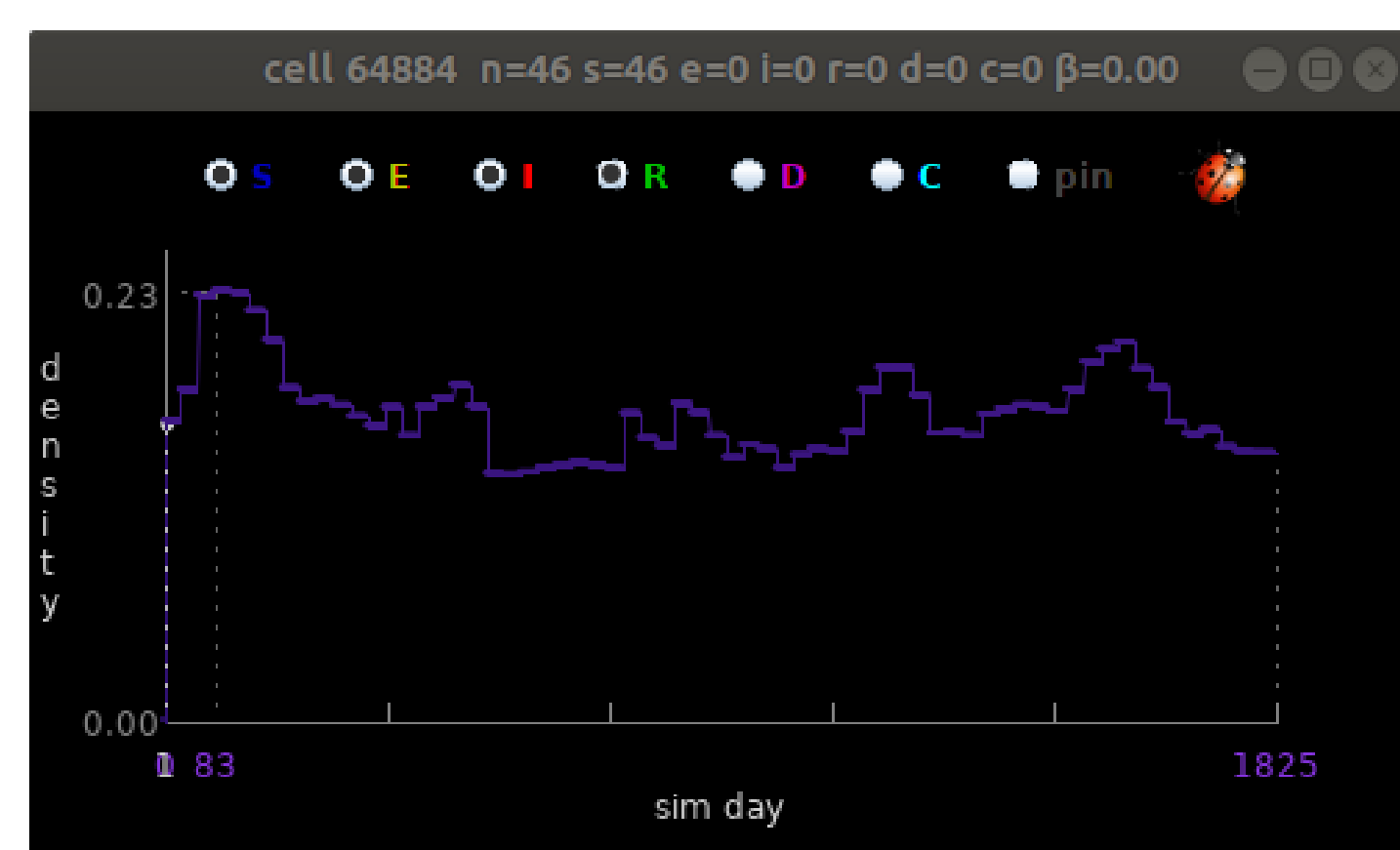
- The wild boar population count in each cell is determined by 4-weekly time slices (generated outside the model), that consider regional and seasonal heterogeneities in Spain over a 5-year time frame.

- Regional differences in the environment, wild boar behaviour, and disease dynamics were captured through the definition of two wildlife regions: Mediterranean and Euro-Siberian.

## Modelling the spread of CSF in Spanish wild boar

- The EuFMDiS epidemiological unit of interest for wildlife is the cell. If CSF is introduced into a cell, then the cell acquires an SEIRDC compartmental infection model. The within-cell infection model employs the same set of equations as the domestic herd model, except that carcasses are assumed to remain infectious in the D compartment for 1/ε days and exert infectious pressure on susceptibles at a transmission rate of β_D.

- If a cell becomes infected, then the infection model's population count is seeded with the current value in the population model. From the day of infection onwards the population count of the cell is determined by the infection model, i.e., the population model's time slices are not used.

- Once a cell population is no longer infectious it recovers gradually over a configurable period per a logistic growth model with configurable lag and gradient. At the end of the recovery period, the cell's population is once again determined by the population model time slices.
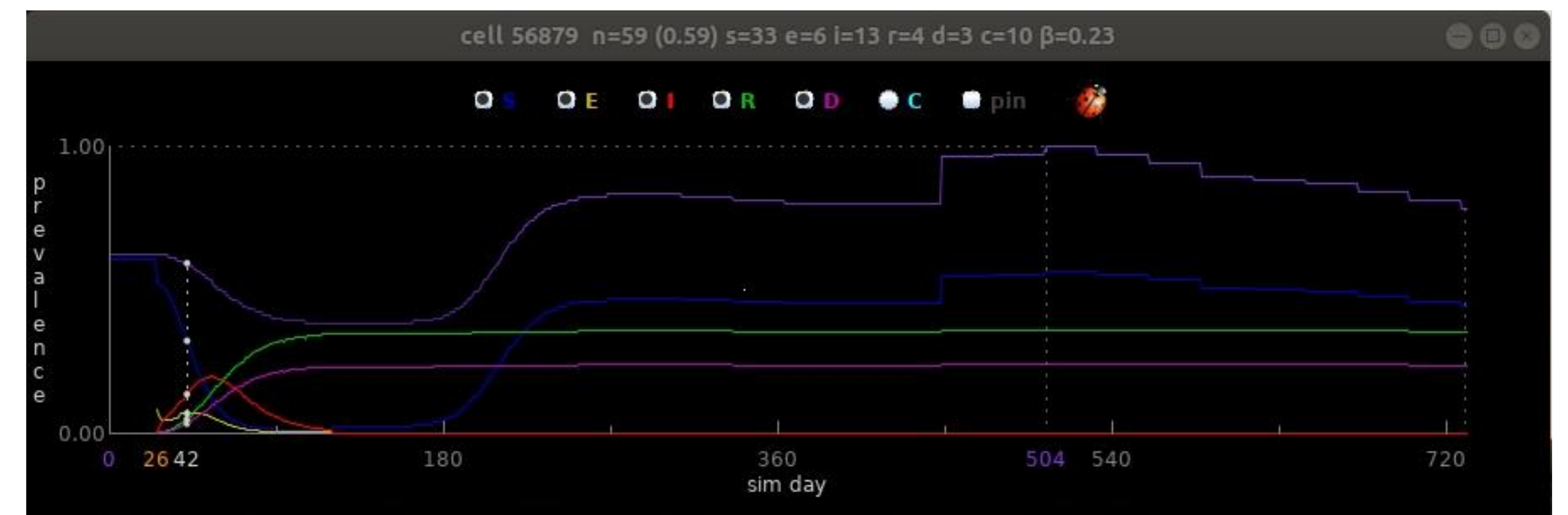
- The diffusive spread of CSF between an infectious cell and a susceptible cell is modelled by a contact rate-based spread pathway that takes into account wild boar population density and infectious prevalence, habitat suitability, and seasonal and regional influences on wild boar behaviour and virus transmissibility.

- The sporadic jumps of CSF from an infectious cell to more distant susceptible cells is modelled by a contact-rate based spread pathway that takes into account wild boar population density and infectious prevalence, habitat suitability, likely distance of the jump, and seasonal and regional influences on wild boar behaviour and virus transmissibility.

Modelling the spread of CSF between domestic pigs and wild boar

- The spread of CSF from wild boar pigs to domestic pigs is modelled with a spatial kernel-based spread pathway that takes into account wild boar population density and infectious prevalence, herd susceptibility, biosecurity measures in place at susceptible herds, proximity of herds to infectious wild boar, and seasonal and regional influences on wild boar behaviour and virus transmissibility.

- The spread of CSF from domestic pigs to wild boar is modelled with a spatial kernel-based spread pathway that takes into account herd size and infectious prevalence, wild boar population density, biosecurity measures in place at infectious herds, proximity of wild boar to infectious herds, and seasonal and regional influences on wild boar behaviour and virus transmissibility.
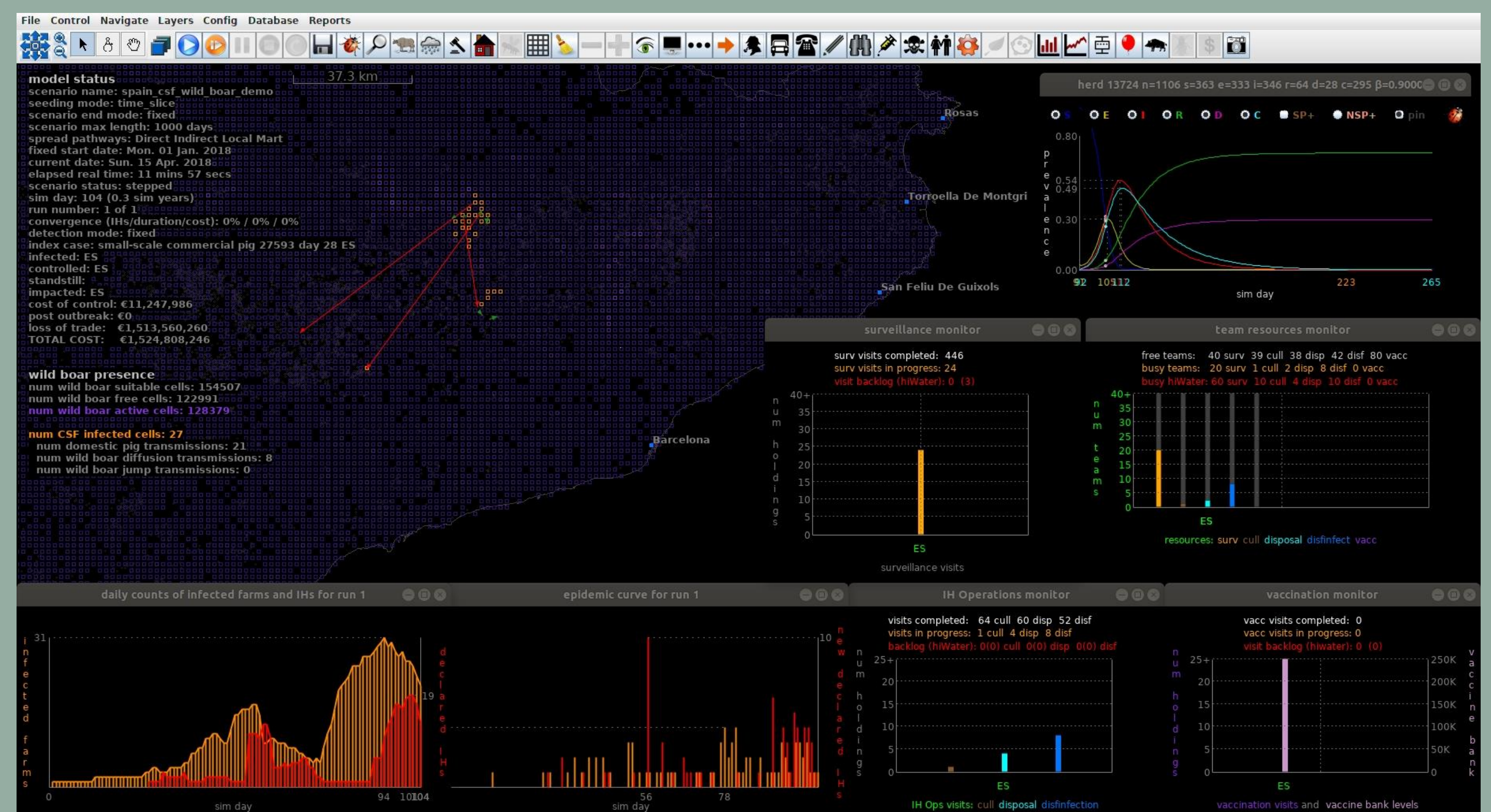
Conclusions & further work

- The key aspects of disease transmission between domestic herds and cellular populations of wild swine (within-herd, between-herd, within-cell, between-cell and between herds and cells) and domestic pig control measures have been implemented in the EuFMDiS model.

- Wild boar control measures have not yet been implemented but will include options for vaccination, selective thinning of the population, and fencing.

- The model is still being parameterised and is yet to be validated.

- The project has successfully fused an agent-based livestock disease model with a new cellular-automata-based wildlife disease model.

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