A simulation model for
highly pathogenic avian influenza
spread in Danish wild birds

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Introduction

The poultry industry and wild bird conservation are affected by highly pathogenic avian influenza (HPAI).

Wild birds are drivers of HPAI outbreaks in poultry.

It raises the need to investigate the risks of HPAI in wild birds.

Denmark has experienced several epidemics caused by HPAI H5Nx virus since late 2020.

Aim: To explore the potential role of wild birds and transmission dynamics of HPAI in Denmark using a spatiotemporal cellular automata model.

Methods

Spatial: 10 by 10 km grid cells overlayed on a map of Denmark.
Temporal: by weeks in five epi years (Oct. – Sep. as a year).
Species: Whooper Swan (WS), Barnacle Goose (BG), Mute Swan (MS), Greylag Goose (GG), Mallard (M).

Data (host populations): 1) NOVANA: nationwide mid-winter census cross-sectional data; 2) DOFbasen: citizen science data with weekly abundance changes.
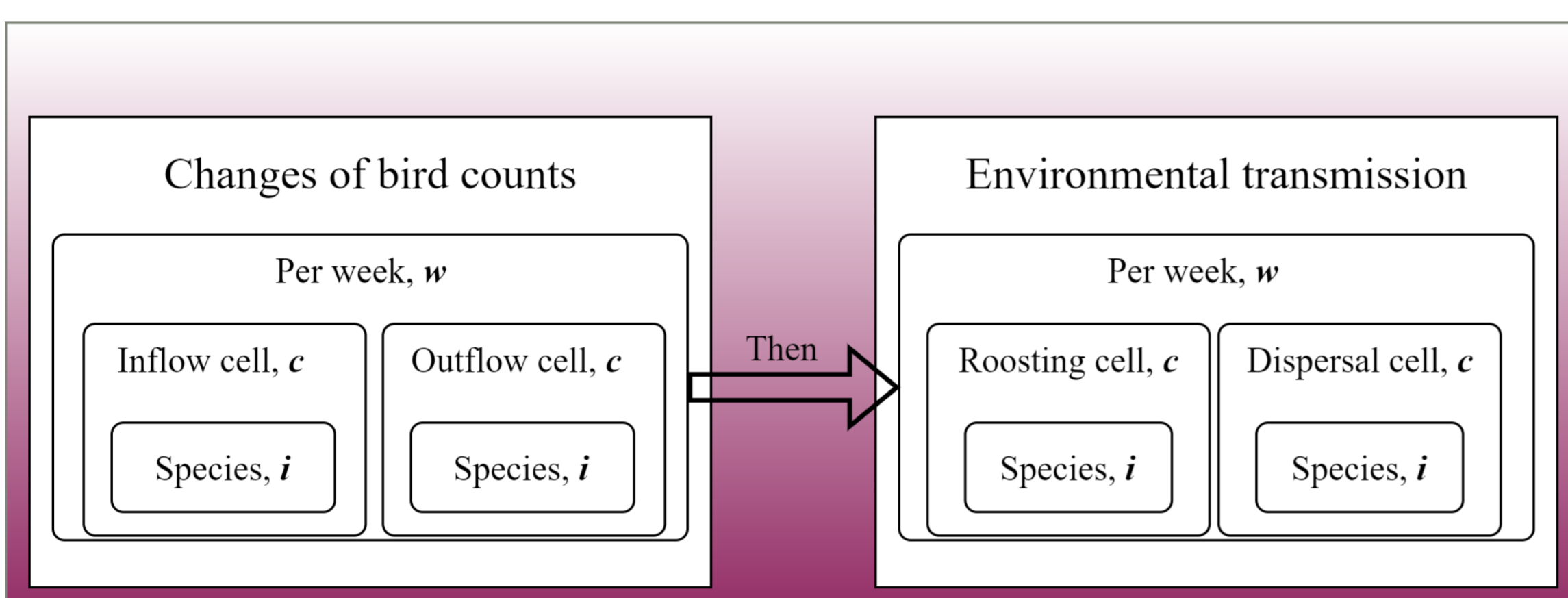

Figure 1. The workflow of the spatiotemporal model for population ecology (i.e. bird migration) and environmental transmission (i.e., spread of HPAI and local bird dispersal).

Change of bird counts

- An expectation-maximization (EM) algorithm with generalized linear mixed models was used to impute missing bird count data.

Environmental transmission

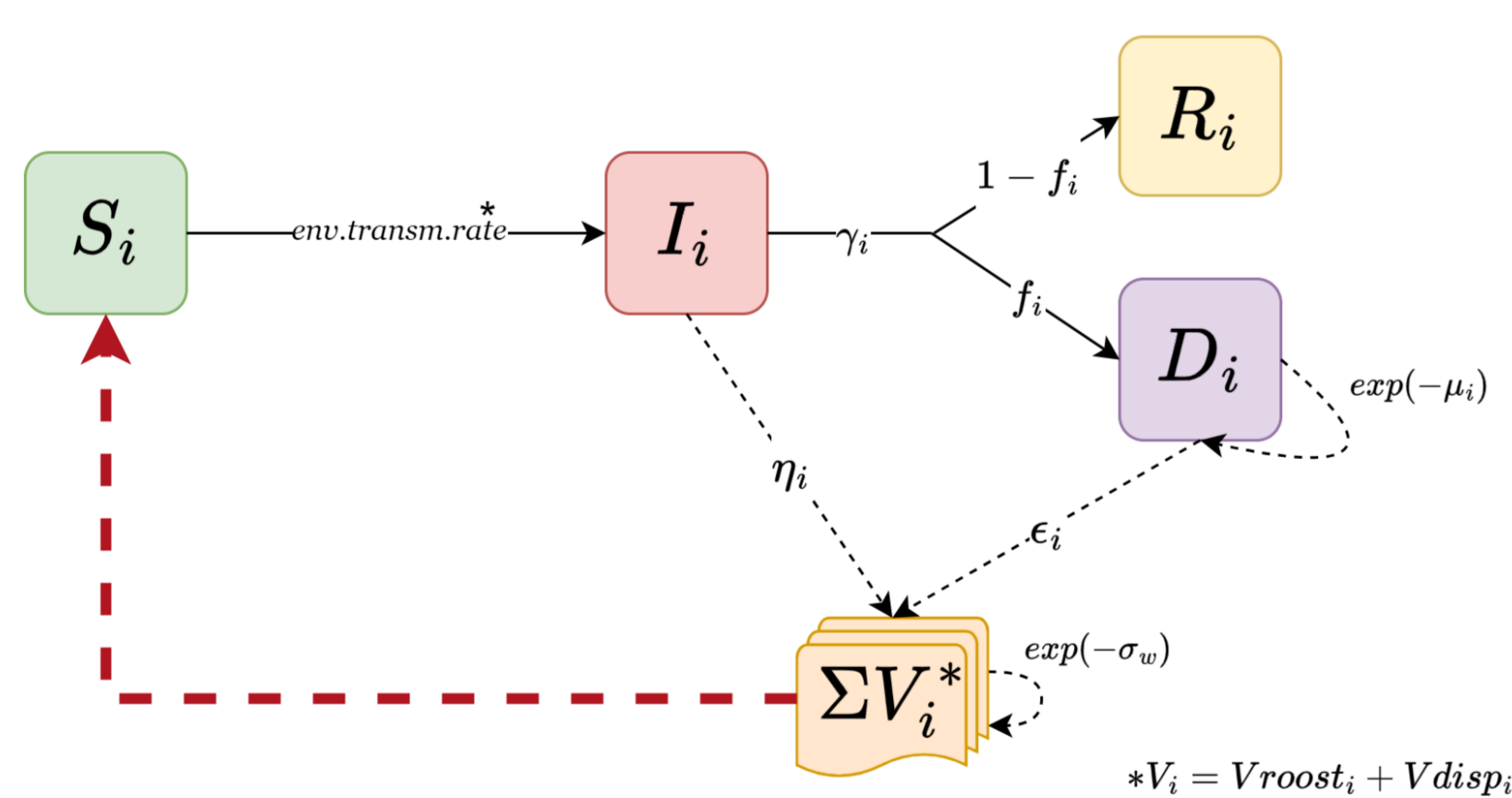- A SIDR model integrated with a dose-response model was constructed.

Figure 2. The SIDR model structure.

$$* Env.transm.rate = contact_i \times \left(1 - e^{-\frac{ln(2)}{ID_{50,i}} \times \frac{V_w - 1}{N_{Env,c}}}\right)$$, where $ID_{50,i}$ is the viral load required to achieve a 50% infection rate.

- Parameterization using empirical data from the literature.
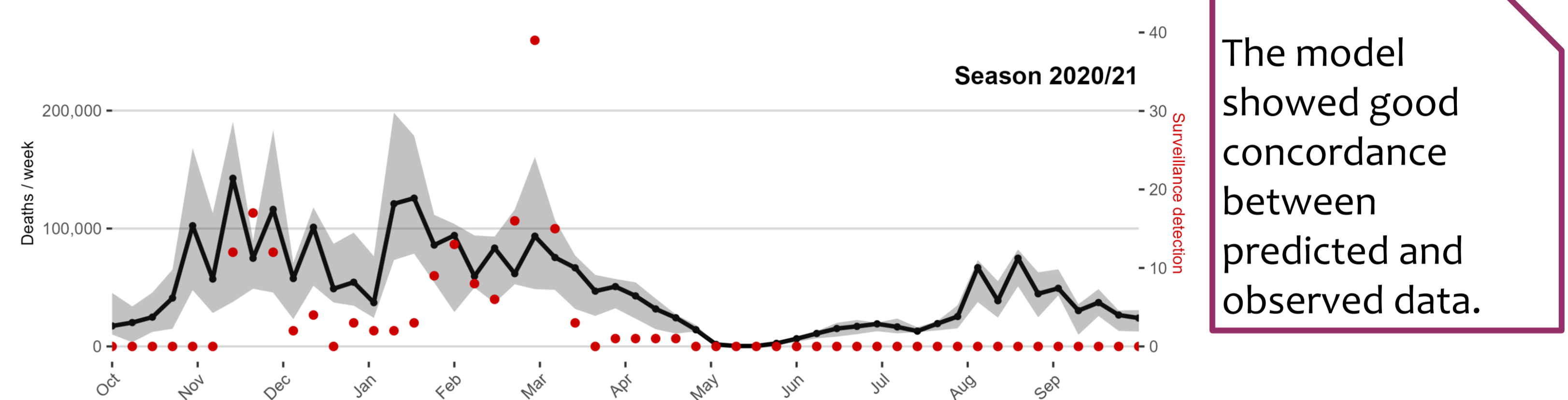
Simulation

- Initialization using the passive surveillance data for Danish wild birds in the epi **season 2020/21**. A burn-in simulation year provided environmental viral load, followed by a focal year from which we report the prediction results.
- The model was built in R. We ran 300 stochastic simulations of the model to ensure convergence.

Conclusion

- Early removal of carcasses could help stop HPAI from spreading, but we need more research to be sure.
- The model helps decision-makers understand risks to the environment and wild birds. It can also help decide optimal timing, locations, and species in surveillance.
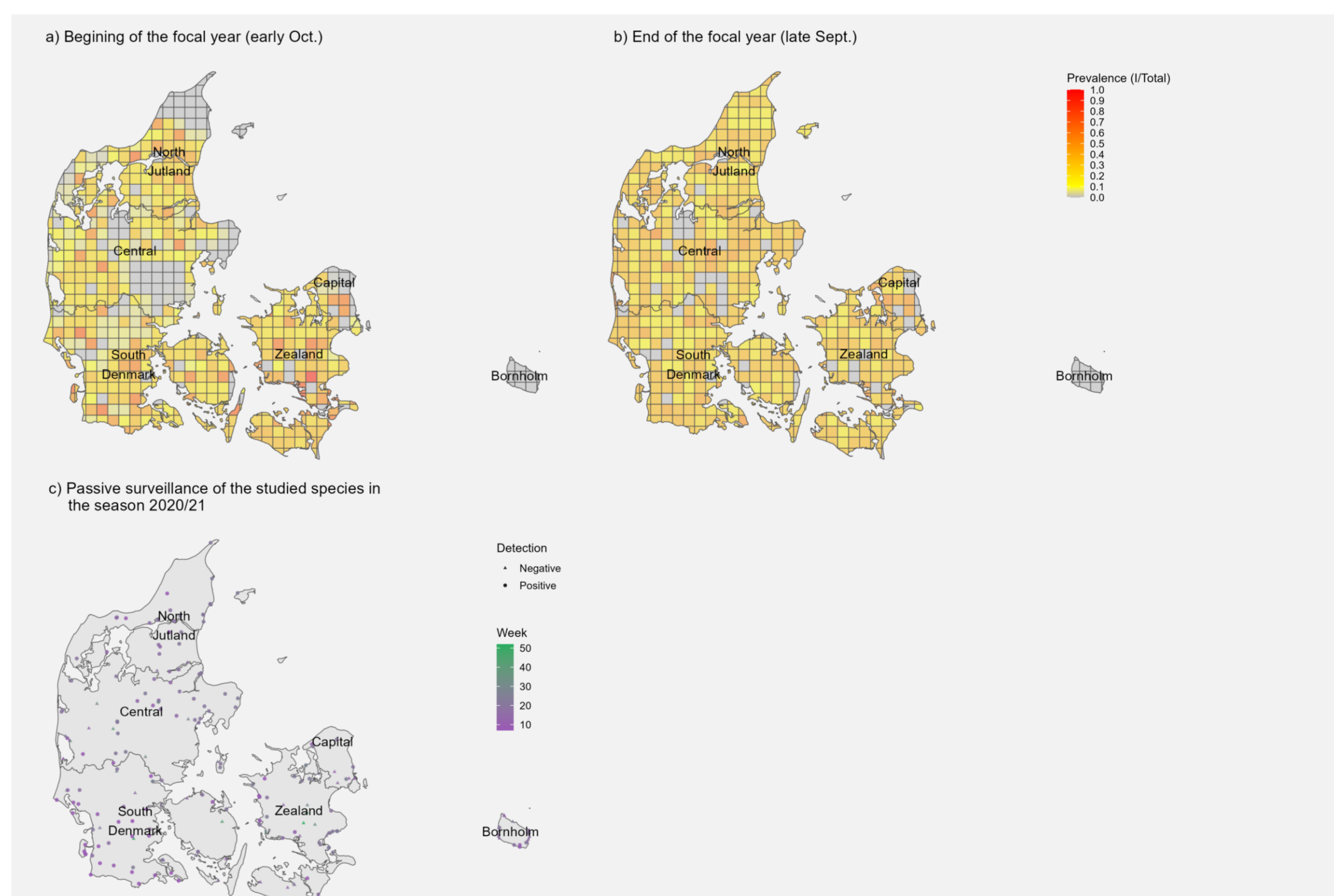
Results

Temporal transmission

The model showed good concordance between predicted and observed data.

Figure 3. Comparison between simulated total deaths per time step (medians with the 95% envelope (n = 300)) and passive surveillance detections of the five selected species in the season 2020/21..

Spatial transmission patterns

The simulation for the focal year showed, that although the expected number of cells affected by HPAI cases increased, the mean prevalence decreased from 58.6% (95% envelope: 29.3 – 70.5%) to 37.3% (95% envelope: 25.6– 39.5%).

Figure 4. The evolution of median (n = 300) HPAI prevalence (I/total) from the beginning (a) to the end (b) of the focal year and passive surveillance detections (c) in the 2020/21 season.
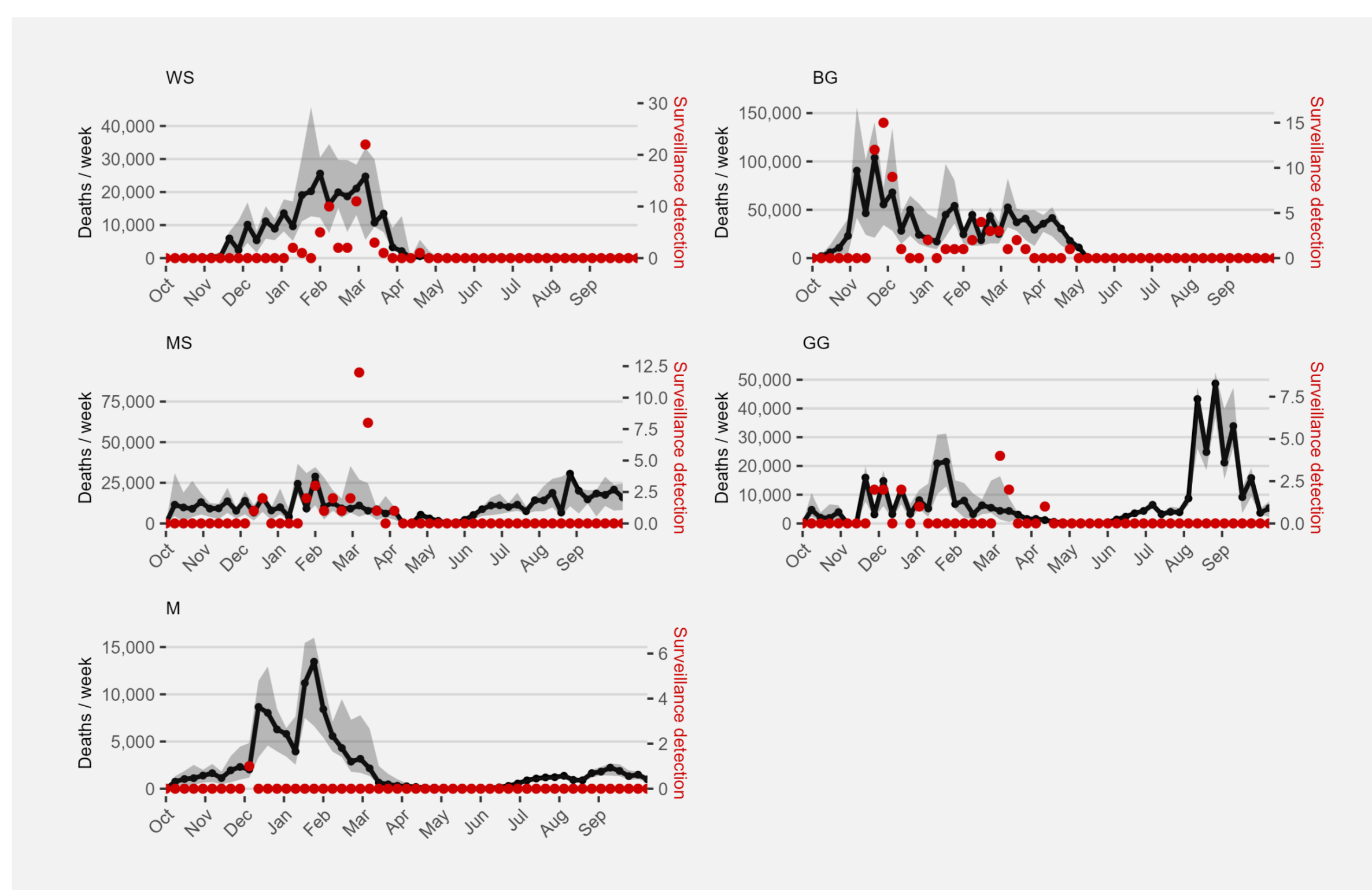
Species-specific transmission

Barnacle geese were the most numerous species (45%) during the year. Greylag geese were the main contributors to HPAI transmission in the summer.

Figure 5. Simulated bird deaths and surveillance data per species.

Sensitivity analysis

Altering most selected parameter values did not result in apparent changes in the number of bird deaths. However, we identified an obvious effect of removing carcasses on reducing HPAI transmission.

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