**Supplementary information**

Table S1. A list of 11 migration patterns used in the DanHPAIwild model based on combinations of activities of the five modelled bird species in Denmark.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Index | Migratory pattern | Description | Bird-outflow cells (probabilities of moving S:I:R) | Bird-inflow cells (probabilities of moving S:I:R) | Unchanged cells | Source |
| I | All cells wintering | The same population in the cell between two time steps. | All cells followed 1:1:1 | All cells follow PS(j):PI(j):PR(j)  Note: when introduction occurs, PI(j) is replaced by PI(j)+Pintro. So as following patterns.  The first week of a year always follows 1:0:0 for newly arrived birds. | No migration | We used literature-reported Danish bird phenology curves to create and assign migration patterns for each week and each species  (BG (Tombre et al., 2008), WS (Månsson & Hämäläinen, 2012), MS (Bønløkke et al., 2006), GG (Nilsson & Kampe-Persson, 2018), and M (Bønløkke et al., 2006)) |
| All cells breeding |
| All cells moulting |
| All cells resident |
| 8% of cells: wintering + 92% of cells: residence |
| All cells summering |
| II | 50% of cells: wintering + 50% of cells: staging | In half of the cells the same population stayed in the cell between two time steps (wintering), if the bird counts increase in the next time step the additional birds are susceptible, while in the other half of the cells, a new susceptible population arrives in the next time step (staging). | 50% of cells: 1:1:1 (wintering/ summering).  50% of cells: all birds were replaced with susceptible and recovered birds (staging) following PS(j):0:PR(j). | 50% of cells: PS(j):PI(j):PR(j) (wintering/summering).  50% of cells: all birds were replaced with susceptible and recovered birds (staging) following PS(j):0:PR(j) if no introduction occurs, otherwise follow PS(j):Pintro:PR(j), and then new arrived birds follow PS(j):PI(j):PR(j).  The first week of a year always follows 1:0:0 for new arrived birds. | 50% of cells: no migration (wintering/ summering).  50% of cells: all birds were replaced with susceptible and recovered birds (staging) following PS(j):0:PR(j), and if PS(j) is 0 or NA, 1:0:0 is used. |
| 50% summering + 50% staging | In half of the cells the same population stayed in the cell between two time steps (summering), if the bird counts increase in the next time step the additional birds are susceptible, while in the other half of the cells, a new susceptible population arrives in the next time step (staging). |
| III | 4% Wintering + 4% staging + 92% resident | Only 8% of cells were migratory cells where in half of these cells the same population stayed in the cell between two time steps (wintering), while the in the other half of these cells new susceptible population in the next time step (staging). The rest 92% of cells had the same population in the cell between two time steps (resident) | 96% of cells: 1:1:1 (wintering & resident).  4% of cells: all birds were replaced with susceptible and recovered birds (staging) following PS(j):0:PR(j).all birds were replaced with susceptible birds (staging). | 96% of cells: PS(j):PI(j):PR(j) (wintering & resident).  4% of cells: all birds were replaced with susceptible and recovered birds (staging) following PS(j):0:PR(j) if no introduction occurs, otherwise follow PS(j):Pintro:PR(j), and if PS(j) is 0 or NA, 1:0/ Pintro:0 is used. | 96% of cells: no migration (wintering & resident).  4% of cells: all birds were replaced with susceptible and recovered birds (staging) following PS(j):0:PR(j), and if PS(j) is 0 or NA, 1:0:0 is used. |
| IV | All cells staging | A new susceptible population in the next time step. | In all cells, all birds were replaced with susceptible and recovered birds (staging) following PS(j):0:PR(j). | In all cells, all birds were replaced with susceptible and recovered birds (staging) following PS(j):0:PR(j) if no introduction occurs, otherwise follow PS(j):Pintro:PR(j). | all birds were replaced with susceptible and recovered birds (staging) following PS(j):0:PR(j), and if PS(j) is 0 or NA, 1:0:0 is used. |
| V | First week of a new season |  | In all cells, infectious and recovered birds were replaced with susceptibles. | In all cells, infectious and recovered birds were replaced with susceptibles, and newly arrived birds are susceptible. | In all cells, infectious and recovered birds were replaced with susceptibles. |  |

Table S2. The estimated parameters for the species-specific Weibull functions by Fandos et al. (2023). They obtained ringing data for each species and fitted into several dispersal functions, where the Weibull function was selected as the best-fitting distribution by comparing the expected log posterior pointwise density. This function contains two parameters affecting the shape and scale of the distribution.

|  |  |  |
| --- | --- | --- |
| Species | Shape parameter, a | Scale parameter, b |
| Whooper Swan | 0.54 | 29.42 |
| Barnacle Goose | 0.32 | 6.57 |
| Mute Swan | 0.53 | 15.8 |
| Greylag Goose | 0.47 | 11.51 |
| Mallard | 0.4 | 3.19 |

Table S3. Weekly numbers of HPAIV detected dead birds of the modelled bird species found by the passive surveillance program during the 2020/21 season, sourced from <https://ai.fvst.dk/>.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Week | Barnacle goose | Whooper swan | Mute swan | Greylag goose | Mallard | Total |
| 39/2020 | 0 | 0 | 0 | 0 | 0 | 0 |
| 40/2020 | 0 | 0 | 0 | 0 | 0 | 0 |
| 41/2020 | 0 | 0 | 0 | 0 | 0 | 0 |
| 42/2020 | 0 | 0 | 0 | 0 | 0 | 0 |
| 43/2020 | 0 | 0 | 0 | 0 | 0 | 0 |
| 44/2020 | 0 | 0 | 0 | 0 | 0 | 0 |
| 45/2020 | 12 | 0 | 0 | 0 | 0 | 12 |
| 46/2020 | 15 | 0 | 0 | 2 | 0 | 17 |
| 47/2020 | 9 | 0 | 0 | 2 | 1 | 12 |
| 48/2020 | 1 | 0 | 1 | 0 | 0 | 2 |
| 49/2020 | 0 | 0 | 2 | 2 | 0 | 4 |
| 50/2020 | 0 | 0 | 0 | 0 | 0 | 0 |
| 51/2020 | 2 | 0 | 0 | 1 | 0 | 3 |
| 52/2020 | 0 | 2 | 0 | 0 | 0 | 2 |
| 1/2021 | 1 | 1 | 0 | 0 | 0 | 2 |
| 2/2021 | 1 | 0 | 2 | 0 | 0 | 3 |
| 3/2021 | 1 | 5 | 3 | 0 | 0 | 9 |
| 4/2021 | 2 | 10 | 1 | 0 | 0 | 13 |
| 5/2021 | 4 | 2 | 2 | 0 | 0 | 8 |
| 6/2021 | 3 | 2 | 1 | 0 | 0 | 6 |
| 7/2021 | 3 | 11 | 2 | 0 | 0 | 16 |
| 8/2021 | 1 | 22 | 12 | 4 | 0 | 39 |
| 9/2021 | 2 | 3 | 8 | 2 | 0 | 15 |
| 10/2021 | 1 | 1 | 1 | 0 | 0 | 3 |
| 11/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 12/2021 | 0 | 0 | 1 | 0 | 0 | 1 |
| 13/2021 | 0 | 0 | 0 | 1 | 0 | 1 |
| 14/2021 | 0 | 1 | 0 | 0 | 0 | 1 |
| 15/2021 | 1 | 0 | 0 | 0 | 0 | 1 |
| 16/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 17/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 25/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 26/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 27/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 31/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 32/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 33/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 34/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 35/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 36/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 37/2021 | 0 | 0 | 0 | 0 | 0 | 0 |
| 38/2021 | 0 | 0 | 0 | 0 | 0 | 0 |

Model Calibration

We altered values of three model inputs to calibrate the model by comparing simulation results from 64 sets of these model inputs to real-life situations. The 64 sets of inputs comprised the original basic viral dilution factor (*NEnv*) scaled down by 109,108, 107, and 106, the median infection doses of all species scaled up by 10, 102, 103, 104, the virus decay rate scaled down by 1, 10, 20, and 30.

The model simulated each set of input values for 10 iterations, and the medians were used to be ranked in three matrices and the optimal sets should yield a minimal difference between simulated results and real-life situations. The matrices are; 1) time deviation between the simulated peak and the peak observed in surveillance, 2) difference between simulated and real weekly deaths at peak when assuming a 0.2 percent detection effort, and 3) the visual inspection of temporal trajectories between simulated and detected weekly deaths. Inspecting the ranks presented in Fig. S1, input sets 1 and 10 performed relatively well. However, the temporal trajectory of input set 1 overperformed 10, especially at the end of the simulation period.

A screenshot of a graph

Description automatically generated

Figure S1. Ranks of 64 sets model inputs in time deviation between the simulated peak and the peak observed in surveillance (left) and the difference between simulated and real detected weekly deaths at peak.

A screenshot of a graph

Description automatically generated

Figure S2. Comparisons of temporal trajectories simulated with 64 sets input values.

A screenshot of a graph

Description automatically generated

Figure S3. Comparison between the raw population and the completed population after imputation for whooper swans (WS), barnacle geese (BG), mute swans (MS), greylag geese (GG), and mallards (M) for five years (from top to bottom, the graph shows bird abundance for 2016/17, 2017/18, 2018/19, 2019/20, and 2020/21). The last panel of each graph presents the total bird abundance of five species.

An animation of HPAIV spreading indicated by the prevalence in wild birds can be downloaded from the link: <https://github.com/Yangfan0116/DanHPAIwild/blob/main/Model_scripts/03Model_runs/002%20Analyze%20model%20simulations/Figures/Prevalence_changes.mp4>.

A screenshot of a computer

Description automatically generated

A map of different countries/regions with different colored dots

Description automatically generated

Figure S4. HPAIV-infected wild birds of all species found dead in the 2020/21 season reported in passive surveillance in Denmark, described by species, counts, and distribution.

Reference list

Bønløkke, J., Madsen, J. J., Thorup, K., Pedersen, K. T., Bjerrum, M., Rahbek, C., & Fjeldså, J. (2006). *Dansk Trækfugleatlas: The Danish bird migration Atlas.*

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