A generic risk assessment model for animal disease incursion through wildlife

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Summary

Animal diseases can be introduced into countries or regions through wildlife. A generic risk model would allow to quantify this incursion risk for different diseases and wildlife species, despite the vast variety in both. Here, we propose such a generic risk assessment model and illustrate its workings by assessing the incursion risk of African swine fever (ASF) through wild boar and highly pathogenic avian influenza (HPAI) through wild birds for the Netherlands between 2014-2021. We used disease outbreak data and abstracted movement patterns to populate a stochastic risk model. We found that the incursion risk of HPAI fluctuated between the years with a peak in 2021. In that year, we estimated the number of infected birds to reach the Dutch border by wild bird migration at 261 (95% uncertainty interval: 248-278). The probability that ASF outbreaks that occurred between 2014 and 2021, reached the Dutch border through wild boar movement was very low throughout the whole period; only the upper confidence bound indicated a small incursion risk. On a yearly scale, the predicted incursion risk for HPAI correlated well with the number of observed outbreaks. In conclusion, we present a generic and flexible framework to assess the incursion risk of disease through wildlife. The model allows rapid and transparent estimation of the incursion risk for diverse diseases and wildlife species. The modular structure of the model allows to add nuance and complexity, when required or when more data becomes available.

Keywords

Incursion risk, African swine fever, avian influenza, risk modelling, wildlife, The Netherlands

Introduction

Emerging and re-emerging animal diseases that affect livestock can be introduced into a country or region through movements initiated by humans, such as movement of live animals, products and people (Simons et al., 2019). However, many of these diseases can occur in wildlife populations as well, and thus movement of wildlife can act as possible entry route (Smith et al., 2017). This movement is often complex and based on many external factors that vary between regions and time such as availability of feed (Morelle et al., 2015), variation in temperature (Klinner & Schmaljohann, 2020) and climate change (Visser, Perdeck, van Balen, & Both, 2009).

Wildlife has played an important role in the transmission of several recent emerging and re-emerging animal diseases: Introductions of highly pathogenic avian influenza (HPAI) into the Netherlands were mainly attributed to migrating wild birds (Engelsma, Heutink, Harders, Germeraad, & Beerens, 2022). Seasonal migration patterns seem to drive the introductions of this virus (Xu, Gong, Wielstra, & Si, 2016). The HPAI outbreak in 2020 was preceded by outbreaks of the same virus strain on breeding grounds in Kazakhstan and Russia, leading to the conclusion that autumn migration of waterfowl likely caused the introductions (Beerens et al., 2021). Similarly for African swine fever (ASF), wildlife plays an important role. Dispersal of wild boars is considered an important driver for spatial transmission and introduction risk (De la Torre et al., 2015). The number of ASF outbreaks in Europe has been increasing over the last decade as with the outbreak in Belgium in 2018-2019 (European Food Safety Authority et al., 2020; Linden et al., 2019). Where this outbreak was successfully contained, and the country regained its disease free status by the end of 2020, ongoing circulation in for example, Germany and Poland are far from contained (European Food Safety Authority et al., 2020).

Existing risk tools have attempted to incorporate wildlife as a pathway in different ways (de Vos et al., 2020; Simons et al., 2019; Taylor et al., 2020). Some have assessed the risk semi-quantitatively (European Food Safety Authority, 2017; Kyyrö, Sahlström, & Lyytikäinen, 2017), and others have tried for a more quantitative approach where the wildlife risk was based on density and habitat suitability raster maps (Simons et al., 2019; Taylor et al., 2020). The latter assumes that the movement of wildlife is more likely towards raster cells where the habitat is more suitable. This approach might be appropriate for wild boar movement (Taylor et al., 2020). However, bird migration is hard to capture in a similar way, since their flight paths span over larger distances, and there are large seasonal fluctuations in their behaviour.

Here, we describe a generic model to assess the incursion risk of animal disease through wildlife as standalone tool or as additional pathway to the Rapid Risk Assessment Tool (RRAT) (de Vos et al., 2020) applied to the Netherlands for the years 2014-2021.

Materials and methods

The model proposed below, uses a generic framework to infer the incursion risk of animal disease through wildlife. We demonstrate the model by assessing the incursion risk of HPAI through wild birds and ASF through wild boar. We define the incursion risk as the expected number of infected animals that reach the border of the Netherlands per unit of time.

Below we describe 1) the model inputs: The outbreak data, infection and animal behaviour parameters, 2) the model structure and calculations, 3) the model outputs and interpretation, and 4) the sensitivity analysis. All analyses were performed in R version 4.0.5 (R Core Team, 2021).

Outbreak data

We retrieved data on disease outbreaks from the Food and Agriculture Organization's (FAO) Emergency Prevention System (EMPRES-I) (available from: https://empres-i.apps.fao.org/). In this database, disease outbreaks and a minimal set of characteristics are indexed by the FAO. Of the indexed outbreaks, the geolocation (latitude, longitude), the observation and reporting date, and the size of the outbreak and affected species are reported. We extracted all reported ASF and HPAI outbreaks between January 1, 2014 and December 31, 2021. We considered outbreaks that were labelled as 'wild' in the species description to have occurred in wildlife.

Infection and animal behaviour into parameters

We considered that disease outbreaks that occur outside the Netherlands could pose an incursion risk through wildlife movements. This risk depends on geographic proximity and properties of the disease, such as duration of infectiousness, and the behaviour of the animals carrying the disease. We abstracted these complex disease and behaviour properties into a simple, generic set of variables: 'directionality', 'distance', and 'duration'. We defined different combinations of parameterizations of these variables as 'behaviour groups', accommodating for a wide range of different movement patterns ranging from, for example, home range to migratory behaviour. Multiple 'behaviour groups' combined allowed us to mimic more complicated patterns.

'Directionality' is the probability that the outbreak spreads in a cardinal or intercardinal direction, the directions of an 8-wind compass rose. 'Distance' is the distance an infection can travel via wildlife. This is not limited to a single animal or group of animals; it also allows for unobserved transmission chains in the wildlife population. 'Duration' is the period over which the transmission chain or infection can persist. We defined per disease a number of these 'behaviour groups' and corresponding variables, based on literature and expert opinion. The relative probability of occurrence of these behaviour groups, allowed to capture patterns that fluctuate over time, or 'seasonality'. We took disease outbreaks as a starting point and used a probabilistic model to decide according to which behaviour group the incursion risk resulting from each outbreak is calculated. Below we discuss the parametrization for HPAI and ASF.

Highly pathogenic avian influenza

To model the incursion risk of HPAI through wild birds, we defined two behaviour groups: 1) a short range movement that occurs year round without a preferential direction, and 2) seasonal migration where an influx of birds into the Netherlands peaks in autumn (Figure 1, and Supplement 1 for additional details). For the first, we assumed that infections through wild birds can pose a risk for 15 days (duration), and can travel 30 kilometres per day (assumed to be normally distributed with a standard deviation (sd) of 5 km), resulting in a maximum median distance of 450 km (distance). For the second, the migrating birds, the majority originate from a North, North-east and East direction (directionality). Their flight range can span up to 5000 km (sd=750 km) (distance) and we assumed that they can pose a risk over 25 days (duration), taking into account the persistence of infection within a transmission chain. In Supplement 1, we provide an overview of the selected bird species and their behaviours that led to the abstraction described above. The relative abundance of migratory birds changes due to seasonal migration patterns (Figure 1). The October migratory peak population was taken as reference value (100%) to calculate the relative abundance of migratory birds for other months. We assumed that the relative abundance of the 'short range' birds was constant at 5% of the October migratory peak population. The relative abundances were used to set the relative probability of the behaviours over time

(Figure 3D). The relative probability of the migratory behaviours was thus calculated as the relative abundance of each behaviour group divided by the relative abundance of both behaviour groups.

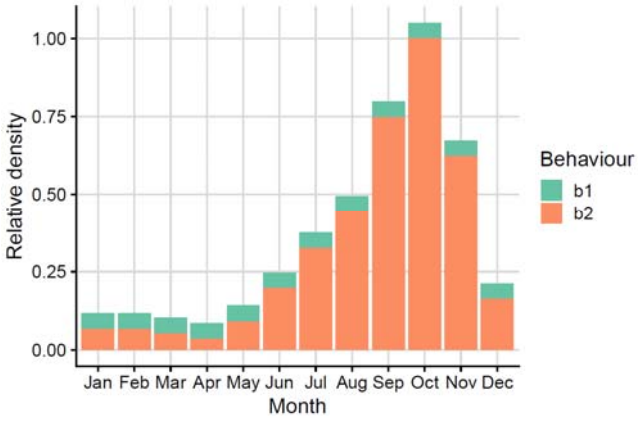

Figure 1. The relative abundance of the number of birds arriving in the Netherlands by month for short range birds (b1) and migratory birds (b2).

To account for unobserved transmission within the overlap of flyways via the shared breeding sites in Russia, we imputed outbreaks in Russia based on outbreaks in South East Asia (Figure 2, red rectangle) that occurred between February and April. Outbreaks that occurred there, were transposed in space and time: They were randomly placed within a region in Russia (Figure 2, purple rectangle). Outbreaks were shifted into the future by an average of 90 days to mimic duration of the breeding season. The imputed outbreaks were considered to pose 10% of the risk of observed outbreaks.

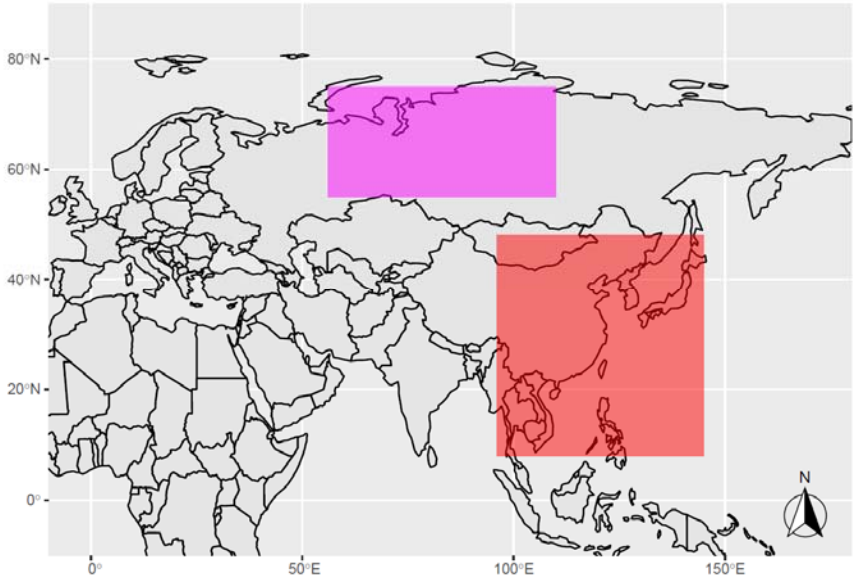

Figure 2. Imputed outbreaks to mimic crossing of shared breeding grounds. Outbreaks occurring in red rectangle (longitude range: 96-145; latitude range: 8-48) are transposed within the purple rectangle (lon: 56-110; lat: 55-75) (World Geodetic System 84, EPSG 4326 coordinates). Cases are assigned a random point within the purple rectangle according to a uniform distribution.

African swine fever

To model the incursion risk of ASF through wild boar, we defined three behaviour groups: 1) short range movement, 2) young animal dispersal movement, and 3) 'long jumps'. We defined the latter as outbreaks that occurred more than 250 km from a previous outbreak. For all behaviour groups we assumed that their directionality is uniformly distributed, i.e. the probability that the behaviour is in one of eight cardinal or intercardinal directions is 0.125. The short range movement is most likely, with an average probability of 0.85, the young animal movement is less likely, with an average probability of 0.149, and a seasonal influence (Simons et al., 2019); based on expert input, the peak of this behaviour is when young animals disperse, 1-1.5 year after birth. However, the exact moment at which this occurs varies between years, dependent on factors such as availability of resources, which is reflected in the model by the distribution over time (Figure 4A). The long jumps are rare (probability of 0.001, based on historic observations, see Supplement 2). We parameterised the distance travelled as exponential distributions with parameters that are 1/mean distance of 2, 5, and 500 km, for the three behaviour groups. The first two were based on the diameter of the home ranges of wild boar (Jerina, Pokorny, & Stergar, 2014; Morelle et al., 2015; Truvé & Lemel, 2003), whereas the distance of the long jumps was based on historical data of ASF in Europe and Russia (Supplement 2). We considered the long jumps as wildlife movements although they are likely to be human-mediated (Guberti, Khomenko, Masiulis, & Kerba, 2019). The relative abundance of wild boar is assumed to be constant over the year (with a value of 1 for all months for all behaviour groups). We assumed that all behaviours would pose a risk over the period of 10 days (duration).

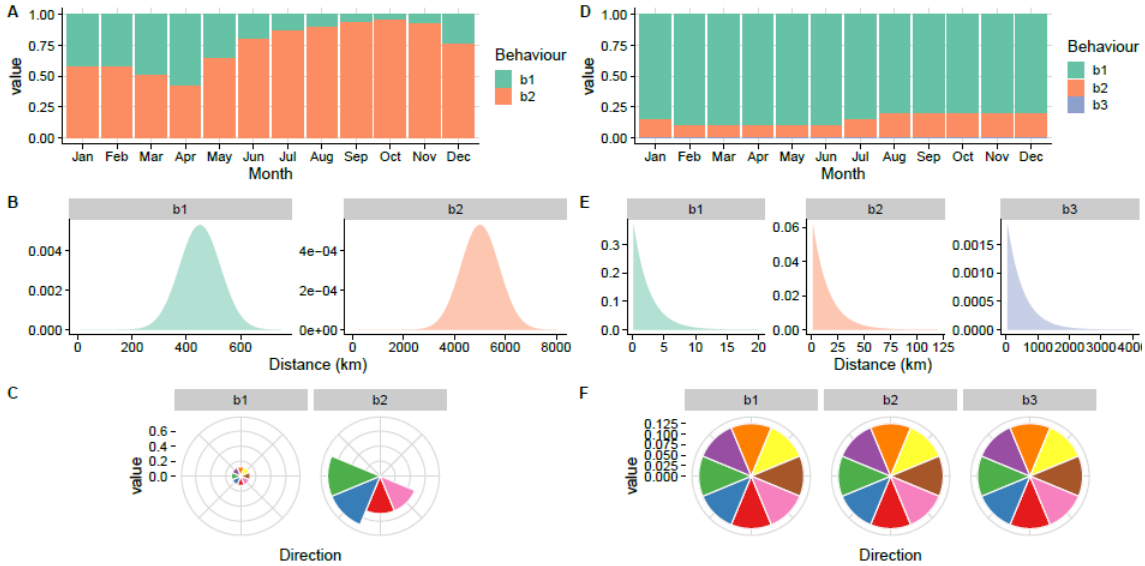

Figure 3. Behavioural parameterisation for highly pathogenic avian influenza (A,B,C) and African swine fever (D,E,F). A+D. Relative probability for each behaviour by month (The probability for b3 for African swine fever is 0.001, and thus not visible in this panel). **B+E.** Effective distance travelled by the infection (a combination of animal movement distance and persistence of transmission chains). **C+F.** Probability that an animal or infection from that cardinal direction 'moves towards the Netherlands, from the perspective of the origin. The top slice (orange) corresponds with the direction 'North'. Behaviour groups (bn): African Swine Fever (ASF) b1: short range movement, b2: young animal dispersal movement, b3: rare 'long jumps'; Highly Pathogenic Avian Influenza (HPAI): b1: short range movement, b2: long distance seasonal migration.

Model structure

The model considered the incursion risk of every individual outbreak. First, from the geolocated reported disease outbreak, we calculated the distance to the closest border point of the Netherlands and the heading in degrees for the shortest straight line from the outbreak to that border point (Figure 5) using the *geosphere* package (Hijmans, 2019). The direction was then reduced to one of eight cardinal or intercardinal directions. Second one of the behaviour groups was sampled using the probability distribution of the month in which the outbreak is observed (Figure 3 panel A and D). The behaviour group provided the probability distribution of the effective distance (Figure 3 panel B and E), the probability distribution of the cardinal and intercardinal direction (Figure 3 panel C and F) and a fixed value for the 'duration'. Third, the distance and direction were sampled from these distributions. If the sampled direction corresponded with the direction in which the closest border point is located and the sampled distance was larger than the distance to that point, we considered that the outbreak reached the border. Last, we calculated the daily incursion risk. The incursion risk ( ) by outbreak (*i*) and time (*t*) is the product of the outbreak size (*size*) and the abundance (*abundance*) of the sampled behaviour group, divided by the duration (*duration*) in days over which the transmission can take place (equation 1).

(1)

Thus, we considered the outbreak to pose an incursion risk from the observation date until the end of the infectious duration. The total daily risk ( ) of all outbreaks (*n*) is the sum of the risk of each outbreak per day(equation 2).

(2)

To calculate the monthly or yearly risk, we summed the daily risk over the number of days per month or year. Because of the stochastic nature of the model, we run 100 iterations of the model and collected the median, and 95% uncertainty interval of the incursion risk.

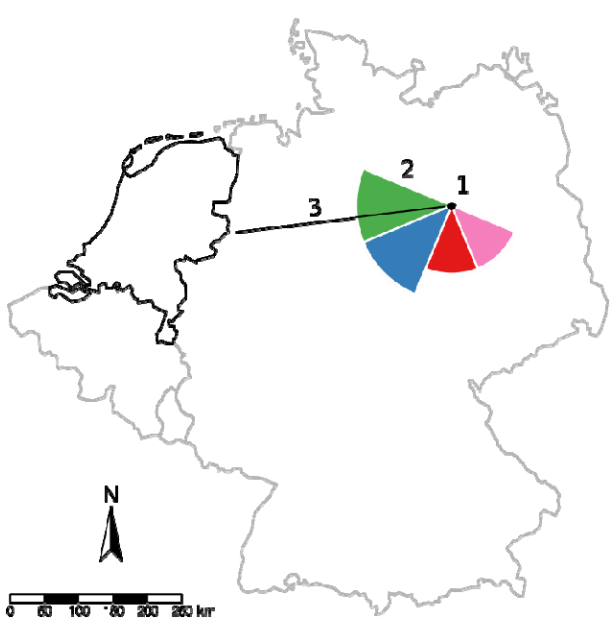

Figure 4. Model structure. An example for a hypothetical HPAI outbreak in March in Germany. From the hypothetical outbreak (1), the direction (2) and the shortest distance to the border (3) of the Netherlands were determined. In this case, the direction was West and the distance was 325 km. Then, the behaviour was sampled (Figure 3D) with the probability distribution of March. In this example, behaviour b2 was sampled, which represents long distance seasonal migration. Only when subsequently a westward direction and an effective travel distance larger than (3) are drawn, the outbreak is considered to have reached the Netherlands.

Model outputs

From the model, we collected the following outputs: 1) The number of animals reaching the border of the Netherlands per month and year. 2) The individual contributions of a) 'Behaviour groups', and b) Countries and/or imputed regions.

Model assumptions

In the model, we made several assumptions. We considered each outbreak to be of the same size (size = 1), due to a large proportion of outbreaks with missing information on the number of infected animals. In the baseline model, we made no distinction between outbreaks in 'wild' and 'domestic' animals, nor did we distinguish between different species or virus strains. We considered that domestic occurrences of HPAI can be a result of undetected circulation in wild birds, or pose a risk for spill over to wild birds again. Similarly, the occurrence of ASF in domestic pigs is likely to be a result from wild boar cases (detected or undetected). Outbreaks are assumed to be representative of disease occurrence, despite known data issues such as heterogeneity in detection/reporting efforts and quality, resulting in underreporting, and bias. An exception are the Russian breeding grounds, where we imputed outbreaks to mimic spread through crossing fly-ways for HPAI. There, we assumed that a fraction (0.1) of outbreaks in south-east Asia cause infection on the Russian breeding grounds.

By assuming travel in a cardinal or intercardinal direction, we assumed that travel occurred in a straight line and we did not consider any barriers on the path. Similarly, the distance only influenced whether a case can 'reach the border' or not; it did not, for example, affect the probability of introduction success, for example, we did not assume the loss of infection during migration.

Validation of results and sensitivity analysis

For HPAI, outbreaks in the Netherlands have been observed in the period 2014-2021. Thus, comparison of our model-predicted incursion risk with all the observed outbreaks (both in wild and domestic birds in the Netherlands) allowed us to validate the model predictions. We calculated the root-mean-square error (RMSE) to quantify the discrepancy between observed and predicted values. Additionally, we challenged the effect of two of the assumptions we made: 1) considering the relative size of imputed cases to be one hundred (model 1) or zero percent (model 2) of the observed outbreaks, instead of ten percent (baseline model); and 2) restricting the prediction to outbreaks that have been marked as 'wild' (model 3), instead of considering all outbreaks (baseline model).

Results

Highly pathogenic avian influenza

We assessed the risk of HPAI incursion into the Netherlands of the 17,718 HPAI outbreaks that were reported in EMPRES-I worldwide in both wild-life and domestic animals between January 1, 2014 and December 31, 2021. We found that the modelled HPAI incursion risk strongly varied between the years (Figure 5); for 2021, we found that a median of 261 outbreaks (95% uncertainty interval (UI): 248-278) was expected to reach the Dutch border by wild bird migration, for 2019 this was only the case for 1.3 outbreaks (95% UI: 0.6-1.8). The majority of incursion risk was due to the long range migration behaviour (b2, 97.8%); the short range flights (b1) contributed to the remaining 2.2% of the risk. The ten countries/regions that contributed the most to the risk (ranked by contribution), were Germany, Russia, Denmark, The United Kingdom, Poland, Sweden, Finland, imputed outbreaks from South East Asia, Estonia, and Kazakhstan; Ninety-seven percent of the total incursion risk came from these ten countries/regions (Supplement 3).

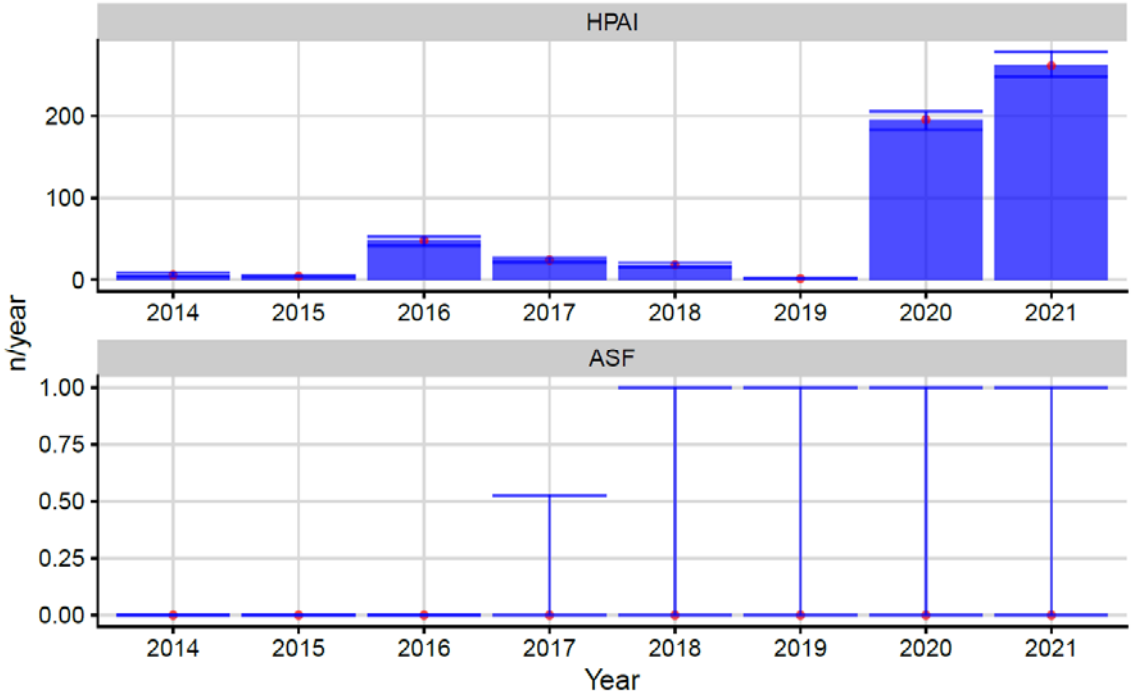

Figure 5. Median yearly risk of incursion of highly pathogenic avian influenza (HPAI) and African swine fever (ASF) through wildlife (bar and point). The error bar provides the 95% uncertainty interval.

When we compare the estimated yearly risk against the observed number of outbreaks in the Netherlands, for the period 2014-2021 (Figure 6), we find the same pattern. However, on a monthly scale, the incursion risk does not always correlate well with the observations.

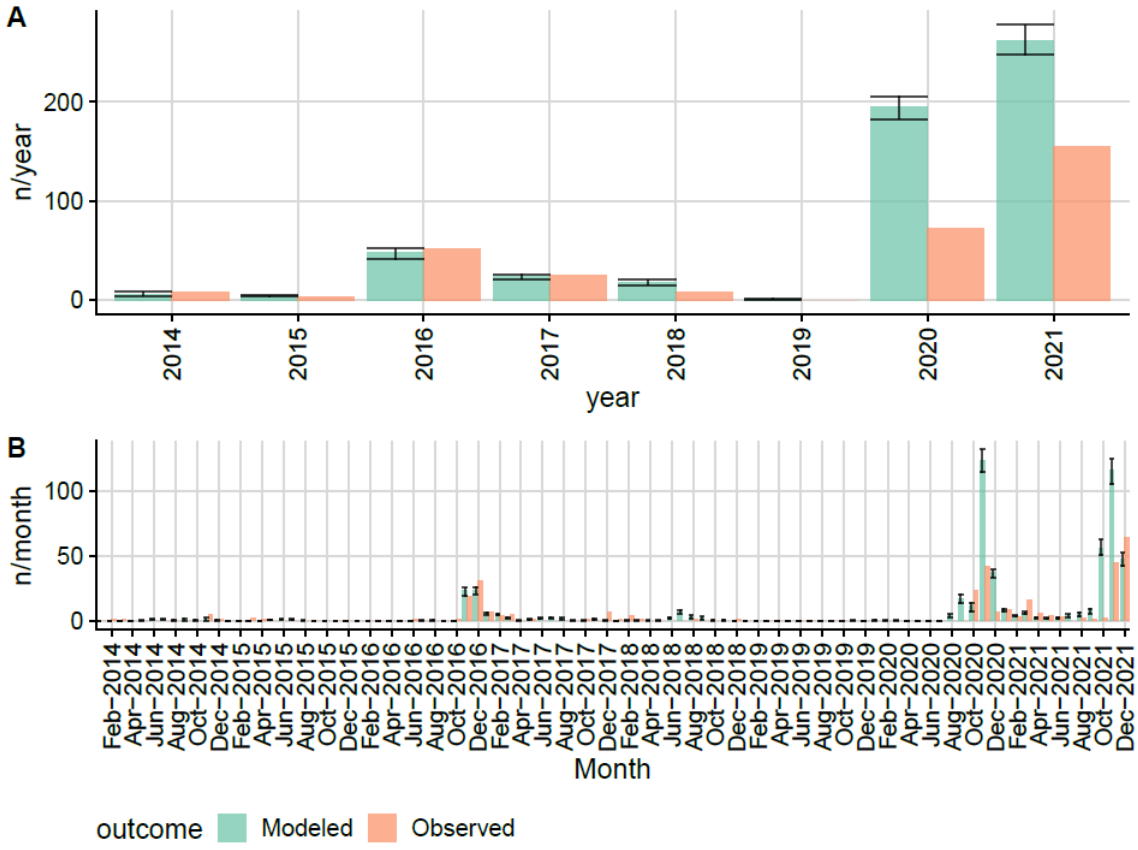

Figure 6. Modelled and observed outbreak risk for Highly Pathogenic Avian Influenza between 2014-2021. The observed outbreaks are the (wild and domestic) outbreaks that were reported in the Netherlands during that time period, by year (A) and by month (B).

African swine fever

We assessed the incursion risk for the Netherlands of 30,854 ASF outbreaks that occurred between January 1, 2014 and December 31, 2021. The yearly risk for ASF incursion was low. The median risk was zero for all years, however, the upper 95% uncertainty interval was 1 for 2018 to 2021. All of the incursion risk was a result of the 'long jumps' (b3). During this period, no outbreaks were observed within the Netherlands.

Sensitivity analysis

HPAI: observed versus predicted. When we assumed the imputation of outbreaks to be similar in size as actual outbreaks (model 1), we overestimated the incursion risk in most years (Figure 7, Table 1). The model in which we did not impute outbreaks (model 2), performed similar to the baseline model (model 0). The model in which we only considered wildlife outbreaks (model 3), outperformed the baseline model, in which we considered all outbreaks, based on RMSE (Table 1). However, that model underestimated the risk for the years 2014-2018. The improved performance was based on the prediction for years 2020 and 2021, where the other models showed a larger discrepancy between observed and predicted.

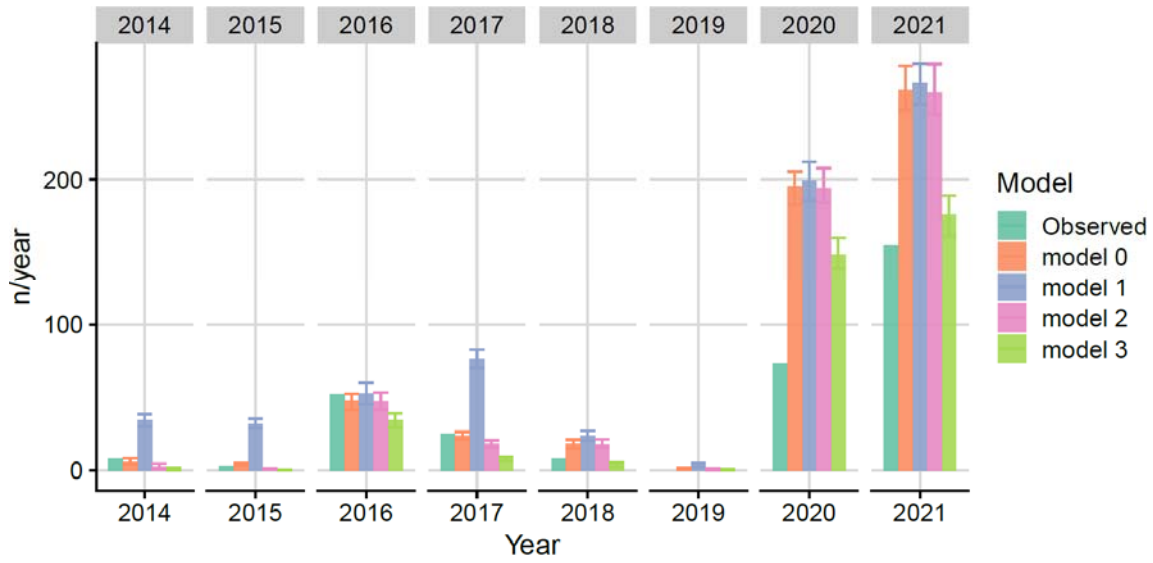

Figure 7. Comparison of different models and observed cases for Highly Pathogenic Avian Influenza between 2014-2021. See table x for model characteristics.

Table 1. Comparison of different models

Model name	Included data/assumptions	RMSE
Observed	Observed number of outbreaks (wild + non-wildlife) in the Netherlands	Ref.
Model 0 (baseline)	Wildlife + non-wildlife outbreaks, imputation size = 0.1	57.5
Model 1	Wildlife + non-wildlife outbreaks, imputation size = 1	63.9
Model 2	Wildlife + non-wildlife outbreaks, imputation size = 0	56.7
Model 3	Wildlife outbreaks only, imputation size = 0.1	29.1

Discussion

Summary of findings. Here, we estimated the incursion risk of HPAI through wild birds and ASF through wild boar for the Netherlands between 2014 and 2021. We found that the risk of HPAI fluctuated between the years with a peak in 2021. The risk of ASF was very low throughout the whole period, only the upper confidence bound indicated a small incursion risk. On a yearly scale, the predicted incursion risk for HPAI correlated well with observed outbreaks in the Netherlands.

Interpretation. The difference in risk between HPAI and ASF is driven by the probability that animals reach the Dutch border. Wild boar from ASF outbreaks that occurred between 2014 and 2021 were too far away to pose a risk and the 'long jumps' that are the result of human interference were rare; wild birds, through long distance migration, were more likely to reach the border and thus introduce HPAI. We should interpret the results semi-quantitatively: The model provides an indication of the relative incursion risk over different years rather than a prediction of the absolute number of incursions. We should also put the results in perspective of the limitations of the data used. We departed from observed outbreaks of disease, where heterogeneous underreporting and changes in what is reported in time and space is likely. We lack prevalence data, which would allow a more reliable quantitative estimation. We

also showed that imputation of outbreaks is a feasible approach to formalize unobserved outbreaks. However, the model with imputed outbreaks did not outperform the model without imputation.

Strengths and limitations. Our approach has several strengths. First, the model is generic. We managed to capture the dispersal patterns of HPAI and ASF by wildlife in the same model, despite differences in disease and susceptible species. Second, the model is balanced in its complexity, yet captures the most important patterns that seem to have driven the incursion of previous outbreaks. Thus it allowed us to formalize these patterns without the need for a complex model for which data for parametrisation are lacking. Our model has several limitations as well. We had to make several assumptions that have resulted in an oversimplification of the reality. These assumptions might hold true in the context we applied the model, but this might not be the case in other settings. For example, the current parametrisation of HPAI might overestimate the effect outbreaks in neighbouring countries have. Migrating birds are now considered to depart from any location within the distance and direction specified. This means, for example, that autumn occurrence of outbreaks in Germany pose a large risk, where these might be at end points of migration routes; whereas our model considers these as departure points. Some of the infections in neighbouring countries might even have originated from the Netherlands, rather than posing a risk for incursion. Additionally, if migration movement in reality is not predominantly in a single direction, the model, by design, fails to capture that pattern. Another limitation is that for ASF, since no outbreaks occurred in the Netherlands in 2014-2021, we could not evaluate the performance of the model. In regions where ASF does occur the comparison of predicted incursion risk with observed outbreaks might not be appropriate either, since the first outbreaks are likely to originate from introductions, but subsequent outbreaks mostly seem a result of local persistence. This also holds true for HPAI. Some of the observed outbreaks in the Netherlands will have resulted from local circulation of the virus rather than new incursions. This also demonstrates the limitation of the definition of 'outbreak' as reported in the EMPRES dataset; many of these events are likely a continuation or re-emergence of an existing event.

Comparison with other work. There are a number of comparable generic quantitative risk models that include wildlife. Simons et al. (2019) presented a generic model that considers wildlife as a pathway (Simons et al., 2019). They apply their model to infer the incursion risk of ASF, classical swine fever, and rabies through wildlife. They model dispersal behaviour of wildlife over a spatial grid, where habitat suitability drives the direction of dispersion. This requires that reliable wildlife density maps are available, which is not always the case. Contrary to our model, they do not apply the model to disease transmitted by birds. However, they do mention that a future extension is possible to include wild birds and also model avian influenza. Taylor et al. (2020) apply a similar approach to Simons, where movement depends on habitat suitability (Taylor et al., 2020). Mur et al. (2014) use a generic pathway model, where, amongst others, wildlife is considered (De la Torre et al., 2015; Mur et al., 2014). At that time, wild boar were considered an ASF incursion risk for Estonia, Finland, Bulgaria, Latvia, Lithuania, Poland, Romania, Greece, Hungary and Slovakia. Of those countries so far, only Finland did manage to keep ASF out. Semi-quantitative risk model by de la Torre (2013), used both distance to previous outbreaks and habitat suitability to estimate the risk of ASF introduction for EU countries at the eastern border of the European Union.

Disease-specific risk models for avian influenza are often spatially explicit and depart from the habitat suitability for wild birds and their overlap with poultry. For example, Kosmider et al (2016) assessed the incursion risk of HPAI in the United Kingdom (Kosmider et al., 2016). They used a risk score approach

informed by the overlap of wild bird and poultry abundance, producing a risk map. Similarly, Martinez et al. (2011) used a spatial approach to identify areas of high risk, to perform risk-based surveillance (Martinez et al., 2011). These models tend to give a more detailed insight in the spatial distribution of risk, but are less generalizable to other diseases.

Future improvements. Since models are as good as the data that is put into them, many of the improvements lie in the realm of improving input data. We need to improve the understanding of migration and dispersal patterns. For example, now, migration patterns are based on ringing of birds and retrieval of rings, which is very much dependent on the number and quality of observations, where heterogeneity and underreporting is likely. This results in biased data. Bias that is likely propagated in the models that rely on this data. Translating reliable migration data into probabilities of birds' departure and arrival would facilitate risk estimation. Additionally, considering the role of landscape and appropriate foraging and resting sites for birds could help to reveal more nuanced migration patterns as well as specific areas at risk. Similarly, extending the model to allow for barriers to be taken into account, and allowing non-linear paths, would allow for a more reliable prediction of predominantly land-based movement. The framework allows extension of the number of behaviours considered, thus allowing the incursion risk to be estimated in more detail, for example by bird species or by disease strain or subtype. We also need to improve the understanding of disease occurrence. The notification and reporting of disease occurrence is sensitive to differences in reporting across time and space. The probability of a case being detected and reported differs between regions. For ASF, e.g., we see large areas where reporting is absent. Estimation of prevalence of disease would improve the estimation of risk.

A logical extension of the model, is to predict beyond incursion. Here, we have only considered outbreaks until the point they reach the Dutch border. Extending the model with the probability of transmission and establishment will give policymakers more insight in the spatial and temporal risk, but requires a better understanding of the movement and behaviour of animals once they have crossed the border. Similarly, will the transmission success from wildlife to livestock depend on their proximity and interaction. For HPAI, extending the model to predict local outbreaks will allow a more reliable comparison with the observed outbreaks as well.

Conclusion

Here, we presented a generic and flexible framework to assess the incursion risk of disease through wildlife. Movement of wildlife is complex and based on many external factors that vary between regions and time. However, we believe that for the level of detail required here, the simplification of the movement patterns is justified. This also allowed for a one-size-fits-all modelling approach, where parameters are based on 'behaviour groups'. The model allows rapid and transparent estimation of the incursion risk for diverse diseases and wildlife species. The modular use of 'behaviour groups' allows to add nuance and complexity, when more data becomes available.

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