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Research Article

A Generic Risk Assessment Model for Animal Disease Entry through Wildlife: The Example of Highly Pathogenic Avian Influenza and African Swine Fever in The Netherlands

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Animal diseases can enter countries or regions through the movements of infected wildlife. A generic risk model would allow to quantify the risk of entry via this introduction route for different diseases and wildlife species, despite the vast variety in both, and help policy-makers to make informed decisions. Here, we propose such a generic risk assessment model and illustrate its application by assessing the risk of entry 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 entry 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 273 (95% uncertainty interval: 254–290). 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 entry risk. On a yearly scale, the predicted entry risk for HPAI correlated well with the number of observed outbreaks. In conclusion, we present a generic and flexible framework to assess the entry risk of disease through wildlife. The model allows rapid and transparent estimation of the entry risk for diverse diseases and wildlife species. The modular structure of the model allows for adding nuance and complexity when required or when more data becomes available.

1. Introduction

Emerging and reemerging animal diseases that affect livestock can be introduced into a country or region through movements initiated by humans, such as the movement of live animals, products, and people [1]. However, many of these diseases can occur in wildlife populations as well, and thus the movement of wildlife can act as a possible entry route [2]. This movement is often complex and based on many external factors that vary between regions and time, such as availability of feed [3], variation in temperature [4], and climate change [5].

Wildlife has played an important role in the transmission of several recent emerging and re-emerging animal diseases. For example, introductions of highly pathogenic avian influenza (HPAI) into the Netherlands were mainly attributed to migrating wild birds [6]. Seasonal migration patterns seem to drive the introduction of this virus [7]. For instance, the 2005 spread of HPAI from Russia to the Black Sea basin followed the spatiotemporal pattern of duck migration from Siberia [8], which was confirmed by phylogenetic analyses [9]. In 2020, the HPAI outbreak in the Netherlands was preceded by outbreaks of the same virus strain on breeding grounds in Kazakhstan and Russia, leading to the conclusion that the autumn migration of waterfowl likely caused the introductions [10].

Similarly, for the entry of African swine fever (ASF) into European countries, wildlife plays an important role. Dispersal of wild boars is considered the highest risk for ASF introduction and spread in Europe [11, 12]. The number of ASF outbreaks in Europe has been increasing over the last decade [13, 14], as has the number of affected countries.

Where ASF virus spread by wild boar is mostly slow (approximately 50 km/year) [15], long-distance jumps have resulted in outbreaks of wild boar in the Czech Republic in 2017, Belgium in 2018, and Italy in 2022, suggesting a human-mediated introduction rather than an introduction by actively migrating wild boar [16]. The movement of wild boar has proven difficult to manage, and the persistence and reinfection of carcasses have played an important role in the continued transmission of ASF in Europe [17, 18].

Assessing the risk of introduction is the first step in the risk assessment that helps prioritize and plan preventive measures to mitigate the entry risk of emerging animal diseases and surveillance activities for early detection. Risk assessment provides an "objective and defensible method" of assessing the risk that pathogens pose to a country or region [19]. Generic risk assessment tools allow for the rapid and transparent comparison of the risk across multiple diseases. The number of pathways addressed by these tools, however, varies largely, and not all tools have incorporated wildlife movements as a pathway for disease incursion [20]. Most of these risk assessments are qualitative [21] or semi-quantitative [22–25], and some of them rely heavily on expert knowledge. Simons et al. [1] and Taylor et al. [26] tried for a more quantitative approach where the wildlife risk was based on density and habitat suitability raster maps [1, 26]. The latter assumes that the movement of wildlife is more likely to be towards raster cells where the habitat is more suitable. This approach was used to assess the incursion risk of ASF and might be appropriate for wild boar movement [26]. 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. This means that the generalizability of those models is limited, and detailed wildlife abundance data is required, which is often not available. Disease-specific risk models to assess the entry risk of HPAI via wild bird migration are mostly spatially explicit. For example, Kosmider et al. [27] assessed the entry risk of HPAI in the United Kingdom [27] using a risk score approach informed by the overlap of wild bird and poultry abundance, producing a risk map. Similarly, Martinez et al. [28] used a spatial approach to identify areas of high risk and perform risk-based surveillance [28]. These models tend to give a more detailed insight into the spatial distribution of risk, but at the expense of generalizability to other diseases.

In contrast to bespoke models, a generic risk model would allow to quantify the entry risk via wildlife movements for different diseases and wildlife species, despite the vast variety in both. Here, we describe a generic model to assess the entry risk of animal disease through wildlife and demonstrate its workings with the example of the entry of HPAI through wild birds and ASF through wild boar for the Netherlands.

2. Materials and Methods

In the risk assessment model described below, we estimate the risk of "entry" of a pathogen into a new territory through wildlife movements. We define the entry risk as the expected number of infected animals that reach the border of a territory per unit of time.

We first describe the generic model: the modelling approach, the model structure and the model calculations. We then assess the model by assessing the entry risk of HPAI through wild birds and ASF through wild boar for the Netherlands. For the two diseases, we describe the input data, parameterization, model assumptions, and validation of results.

All analyses were performed in R version 4.0.5 [29].

2.1. Modelling Approach. We considered that disease outbreaks that occur beyond the borders of a land mass or region could pose an entry risk through wildlife movements. This risk depends on geographic proximity, and the 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," "duration," and "abundance" to define different "behaviour groups," accommodating for different movement patterns ranging from, for example, home range to migratory behaviour. Multiple "behaviour groups" combined allowed us to mimic more complicated movement patterns. "Directionality" is the probability that the outbreak spreads in a certain cardinal or intercardinal direction, the directions of an 8-wind compass rose. This can be considered the direction the infected animal or group of animals decides to travel. "Distance" is the total 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. The model assumes that infected animals move in a single direction and travel in a straight line; the direction and distance may be different though in each iteration based on sampled values. "Duration" is the period (in days) over which the transmission chain or infection can persist. "Abundance" represents the monthly number of animals in each behaviour group; this parameter allows us to take into account fluctuations in abundance, for example, due to seasonal patterns. We defined the seasonal/temporal abundance within a behaviour group (monthly/temporal abundance denoted by $T_{\text{abundance}}$) relative to the month with the highest abundance (see parameterized example).

Abundance was also used to define the relative probability of behaviour groups by month based on their relative contribution to the combined abundance of all behaviour groups (behaviour group abundance denoted by $B_{\text{abundance}}$; See parameterized example below). This, together with the seasonal fluctuations of animal numbers over time ($T_{\text{abundance}}$) allows to capture "seasonality" or temporal changes over the year. Behaviour groups can represent different species, different age classes, or other properties that require a distinction into different behaviour groups.

2.2. Model Structure and Calculations. The model considered the entry risk of every reported disease outbreak outside the area for which the risk assessment is performed. First, from

the geolocated outbreak, we calculated the distance to the closest border point of the area of interest (The Netherlands in the parameterized example) and the heading in degrees for the shortest straight line from the outbreak to that border point (Figure 1) using the *geosphere* package [30]. The direction was then reduced to one of eight cardinal or intercardinal directions.

Second, one of the behaviour groups was sampled using the relative probability/abundance of behaviour groups in the month in which the outbreak was observed ($B_{\text{abundance}}$). The behaviour group then provided the probability distribution of the effective *distance*, the probability distribution of the cardinal and intercardinal *directions*, and fixed values for the *duration* and the temporal abundance ($T_{\text{abundance}}$). 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 had reached the border. Last, we calculated the daily entry risk. The entry risk ($R_{i,t}$) by outbreak (i) and time (t) is the product of the outbreak size, i.e., the number of infected animals reported in the outbreak (*size*) and the monthly relative abundance ($T_{\text{abundance}}$) within the sampled behaviour group, divided by the duration (*duration*) in days over which the transmission can take place (equation).

$$R_{i,t} = \frac{\text{size} \times T_{\text{abundance}}}{\text{duration}}. \quad (1)$$

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

$$R\_\text{overall}_t = \sum_{i=1}^{n} R_{i,t}. \quad (2)$$

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 ran 100 iterations of the model and collected the median and 95% confidence interval of the entry risk.

From the model, we collected the following outputs: (1) The number of infected animals reaching the border of the Netherlands per month and year. (2) The individual contributions of (a) "Behaviour groups" and (b) source countries to the monthly and annual entry risk.

2.3. Model Input 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. For the indexed outbreaks, the geolocation (latitude and longitude), the observation and reporting date, the size of the outbreak, and the affected species are reported. We considered outbreaks that were labelled as "wild" in the species description to have occurred in wildlife. The database

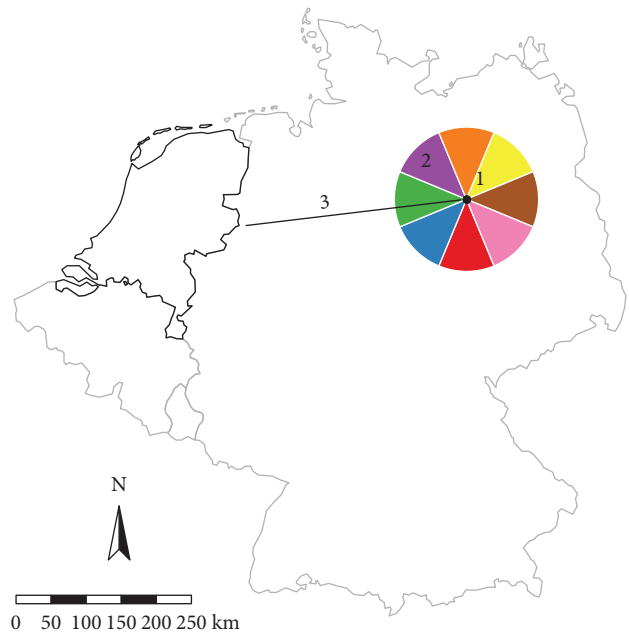


Figure 1: Model structure. An example of a hypothetical outbreak in March in Germany. From the hypothetical outbreak (1), the direction (2) and the shortest distance to the border (3) of the Netherlands were calculated. In this case, the direction was west and the distance was 325 km. Then, the behaviour was sampled based on the March probability distribution. From the sampled behaviour, distance and direction were sampled. Only when subsequently a westward direction and an effective travel distance larger than 325 km are drawn, the outbreak is considered to have reached the Netherlands.

provides outbreak data starting from 2005. We extracted all reported ASF and HPAI outbreaks between January 1, 2014, and December 31, 2021. We opted for this period since, in the period 2005–2014, few HPAI outbreaks were reported in the Netherlands. Similarly, during that period, ASF was mainly circulating in Russia, and introductions in the European Union (Poland) only started in 2014. As described above, for all disease outbreaks, we calculated the distance to the border of the Netherlands and the cardinal or intercardinal direction. In the baseline model, we considered both outbreaks that were reported in wildlife as well as outbreaks reported in domestic animals. Furthermore, we considered all outbreaks to be of the same size (size = 1), due to the large proportion of outbreaks with missing information on the number of infected animals.

2.4. Infection and Animal Behaviour Parameters

2.4.1. Highly Pathogenic Avian Influenza. To model the entry 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 2(d), 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

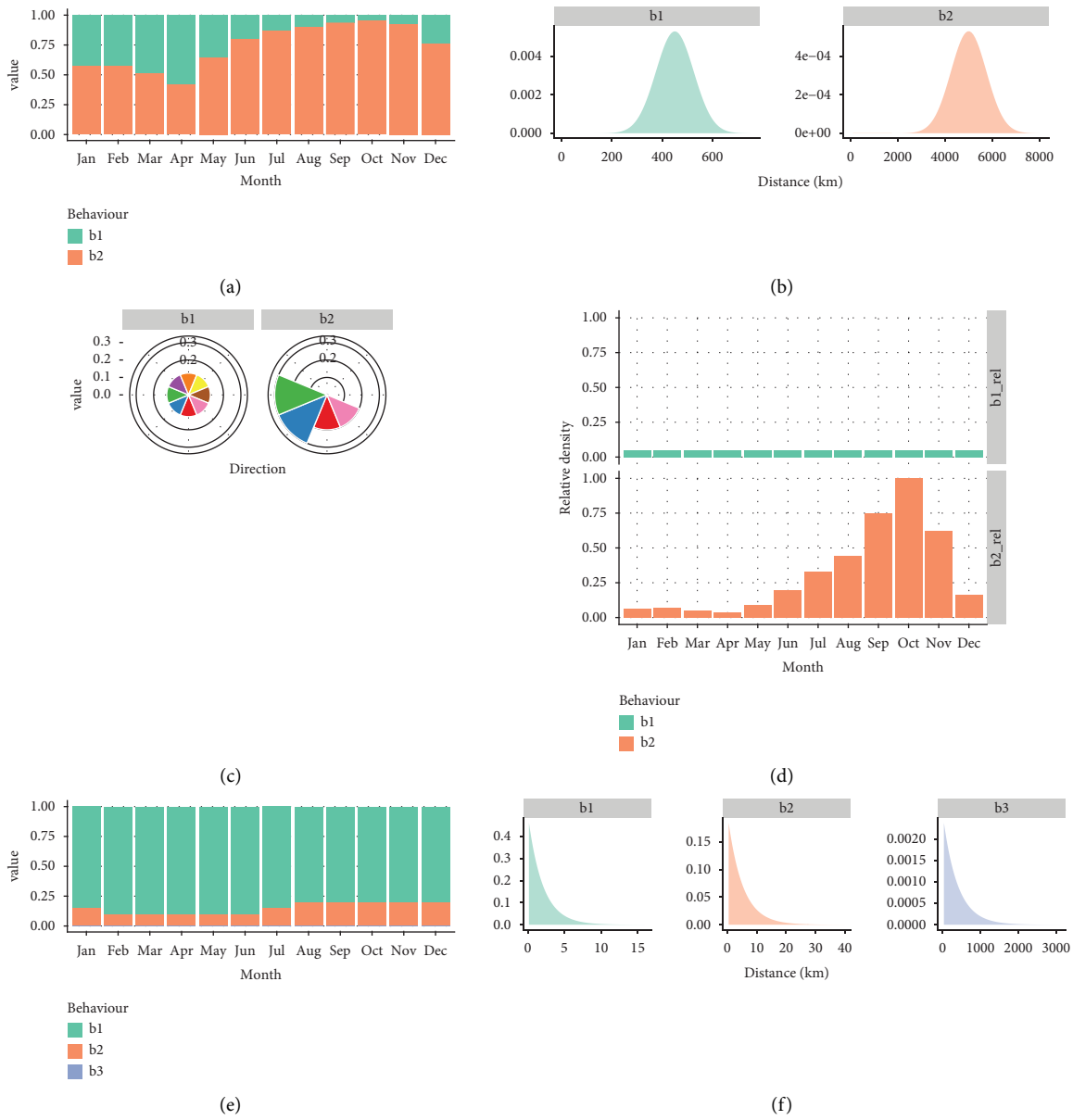
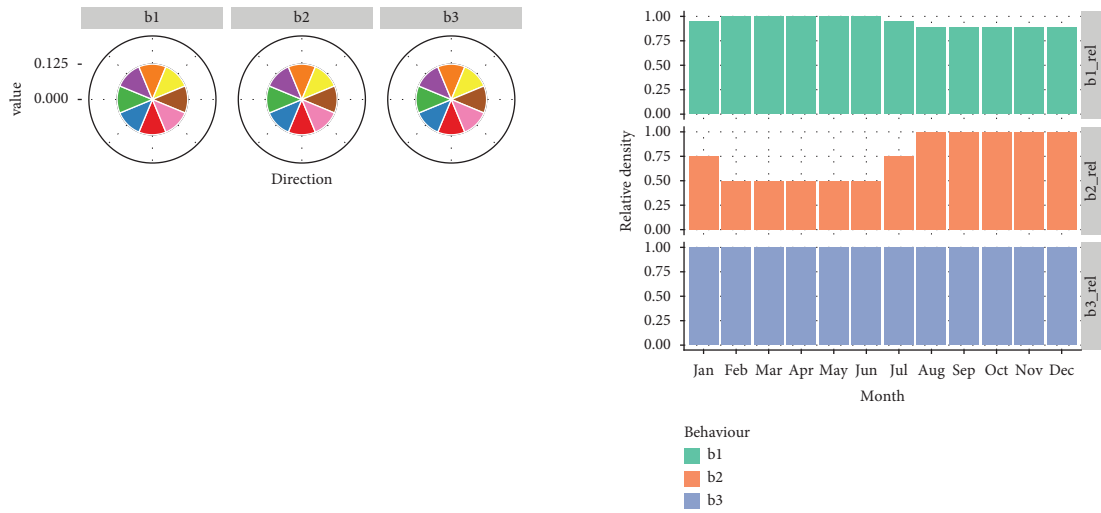


Figure 2: Continued.



(g) (h)

FIGURE 2: Behavioural parameterization for highly pathogenic avian influenza (a), (b), (c), (d), and African swine fever (e), (f), (g), (h). (a) + (e). Relative probability between each behaviour group by month ($B_{abundance}$) (the probability for b3 for African swine fever is 0.001, and thus not visible in this panel). (b) + (f). Effective distance (*distance*) travelled by the infection (a combination of animal movement distance and persistence of transmission chains). (c) + (g). Probability that an animal or infection "moves" from the outbreak location towards the Netherlands using this cardinal direction (*direction*). The top slice (orange) corresponds with the direction "North"; colours provide distinction between the directions. (d) + (g). Temporal abundance within behaviour groups ($T_{abundance}$). Highly pathogenic avian influenza (HPAI); swine fever (ASF); behaviour group (b).

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*, Figure 2(b)). For the second, the migrating birds, we considered 13 bird species of the Anatidae family to be relevant for the introduction of HPAI in the Netherlands, i.e. the Greater White-fronted Goose (*Anser albifrons*), Eurasian Wigeon (*Anas penelope*), Gadwall (*Anas strepera*), Common Teal (*Anas crecca*), Mallard (*Anas platyrhynchos*), Northern Pintail (*Anas acuta*), Garganey (*Anas querquedula*), Northern Shoveler (*Anas clypeata*), Red-crested Pochard (*Netta rufina*), Common Pochard (*Aythya ferina*), Tufted Duck (*Aythya fuligula*), Common Coot (*Fulica atra*), and the Brant Goose (*Branta bernicla*) [31]. Except for the Garganey, which spends winters in Africa, the majority of the birds originate from breeding grounds in a north, northeast, and east direction from the Netherlands (*directionality*, Figure 2(c), based on the Migration Mapping tool (https://euring.org/research/migration-mapping-tool) and expert input). Their flight range can span up to 5000 km (assumed to be normally distributed with a SD = 750 km) (*distance*), and we assumed that they can pose a risk over a duration of 25 days (*duration*), taking into account the persistence of infection within a transmission chain. In Supplement 1, we provide additional details on the selected bird species and their behaviours that led to the abstraction mentionedabove. The number of migratory birds changes due to seasonal migration patterns, which are reflected in the temporal abundance ($T_{abundance}$) (Figure 2(d)). The October migratory peak population was taken as a reference value (100%) to calculate the temporal abundance of migratory birds for other months. Based on expert input, we assumed that the abundance of the "short-range" birds was constant at 5% of the October migratory peak population. The relative abundances of both behaviour groups were used to set the relative probability of the behaviours over time (Figure 2(a)). The relative probability of the behaviour groups ($B_{abundance}$) was thus calculated as the relative abundance of each behaviour group divided by the relative abundance of both behaviour groups.

2.4.2. African Swine Fever. To model the entry 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 (between behaviour groups' probabilities based on $B_{abundance}$, Figure 2(e)). The young animal movement is less likely, with an average probability of 0.149 and a seasonal influence [1]. Based on expert input, the peak of this behaviour is when young animals disperse, 1–1.5 years after birth. However, the exact moment at which this occurs varies between years, dependent on factors such as the availability of resources, which is reflected in the model by the distribution over time (Figures 2(e) and 2(g)). The long jumps are rare (constant probability of 0.001, based on historic observations, see Supplement 2). We parameterized the *distance* travelled as exponential distributions with parameters that are 1/mean

distance of 2, 5, and 388 km for the three behaviour groups (Figure 2(f)). The first two were based on the diameter of the home ranges of wild boar [3, 32, 33], whereas the distance of the long jumps was based on historical data of the ASF in Europe and Russia (Supplement 2). We considered the long jumps as wildlife movements, although they are likely to be human-mediated [34]. The temporal abundance ($T_{\text{abundance}}$) of wild boar within the behaviour groups is fairly stable over the year and only affected by the temporal fluctuation of the number of young dispersing animals as described above (Figure 2(g)). We assumed that all behaviours would pose a risk over the period of 10 days (*duration*) [26].

2.4.3. Model Assumptions. In the model, we made several assumptions. We considered each outbreak to be of the same size (size = 1), due to the large proportion of outbreaks with missing information on the number of infected animals. This means that now the number of animals is equal to the number of outbreaks, and the overall risk (R_overall_t) could also be interpreted as the number of outbreaks reaching the border per time unit. In the baseline model, we made no distinction between outbreaks in "wild" and "domestic" animals, nor did we distinguish between different (bird) 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, and as such are also an indication of the infection pressure in wild birds. Similarly, the occurrence of ASF in domestic pigs is likely to be a result of 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, which result in underreporting and bias.

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 could "reach the border" or not; it did not, for example, affect the probability of introduction success, for example, we did not assume the probability of contact with susceptible animals in the Netherlands.

2.4.4. Validation. For HPAI in the period 2014–2021, outbreaks in the Netherlands have been observed. Thus, comparison of our model's predicted entry risk with all the observed outbreaks (both in wild and domestic birds in the Netherlands) allowed us to validate the model's predictions. We calculated the root-mean-square error (RMSE) to quantify the discrepancy between observed and predicted values. Additionally, we challenged the effect of one of the assumptions we made: restricting the prediction to reported outbreaks that have been marked as "wild" (Model 1) instead of considering all reported outbreaks (Baseline Model).

Validation of results for ASF was not feasible, as no ASF outbreaks were observed in the Netherlands in the period 2014–2021. We therefore also assessed the entry risk of ASF for Belgium and Germany, two countries in which outbreaks did occur. In Belgium, the ASF outbreak started in September 2018 [35]; in Germany, the first case was detected in September 2020 [36]. We ran the model with the same parameters as mentionedabove, assuming that wild boar behaviour did not differ between countries. The distance and direction to the border from the geolocated outbreaks were calculated for Belgium and Germany.

3. Results

3.1. Highly Pathogenic Avian Influenza. We assessed the risk of HPAI entry into the Netherlands for the 17,914 HPAI outbreaks that were reported in EMPRES-I worldwide in both wildlife and domestic animals between January 1, 2014, and December 31, 2021. We found that the modelled HPAI entry risk strongly varied between the years (Figure 3); for 2021, we found that a median of 273 outbreaks (R_overall_t, 95% uncertainty interval (UI): 254–290) was expected to reach the Dutch border by wild bird migration, whereas for 2019, this was only the case for 1.3 outbreaks (95% UI: 0.6–1.8). The majority of entry risk was due to long-range migration behaviour (b2, 97.8%); short range flights (b1) contributed to the remaining 2.2% of the risk. The ten countries that contributed most to the risk (ranked by contribution) were Germany, Russia, Denmark, the United Kingdom, Poland, Sweden, Finland, Estonia, Kazakhstan, and the Czech Republic; 97% of the total entry risk came from these ten countries (Supplement 3).

3.2. African Swine Fever. We assessed the entry risk for the Netherlands for 31,451 ASF outbreaks that occurred between January 1, 2014, and December 31, 2021. The yearly risk for ASF entry was low (Figure 3). The median risk was zero for all years, however, the upper 95% confidence interval was 1 for 2018-2021. All of the entry risk was a result of the "long jumps" (b3).

3.3. Validation

3.3.1. HPAI: Observed versus Predicted. When we compare the estimated yearly risk against the observed number of outbreaks in the Netherlands for the period 2014–2021 (Figure 4), we find the same pattern. Based on RMSE, the model in which we only considered outbreaks reported in wildlife (model 1; RMSE of 30.1) outperformed the baseline model (model 0; RMSE of 59.5), in which we considered all reported outbreaks (Table 1). However, the alternative model (model 1) underestimated the risk for the years 2014–2018. The improved performance of this model was based on the predictions for 2020 and 2021, where the baseline model showed a larger discrepancy between observed and predicted.

3.3.2. ASF: comparison The Netherlands, Germany, and Belgium. The entry risk for ASF in Germany started to increase from 2019 on from 0.15 (0.0–2.0) in 2019 to 7.0 (2.0–13.0) in 2021 (Figure 5); In Belgium, the modelled risk was low throughout the whole period. When we compared the model results between The Netherlands, Germany and

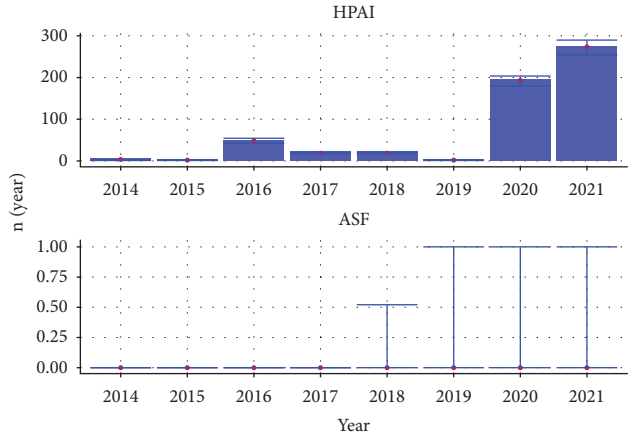


FIGURE 3: The median yearly risk of entry ($R\_overall_t$, or the number of outbreaks (n) that reach the border per year) of highly pathogenic avian influenza (HPAI) and African swine fever (ASF) through wildlife (bar and point). The error bar provides the 95% uncertainty interval.

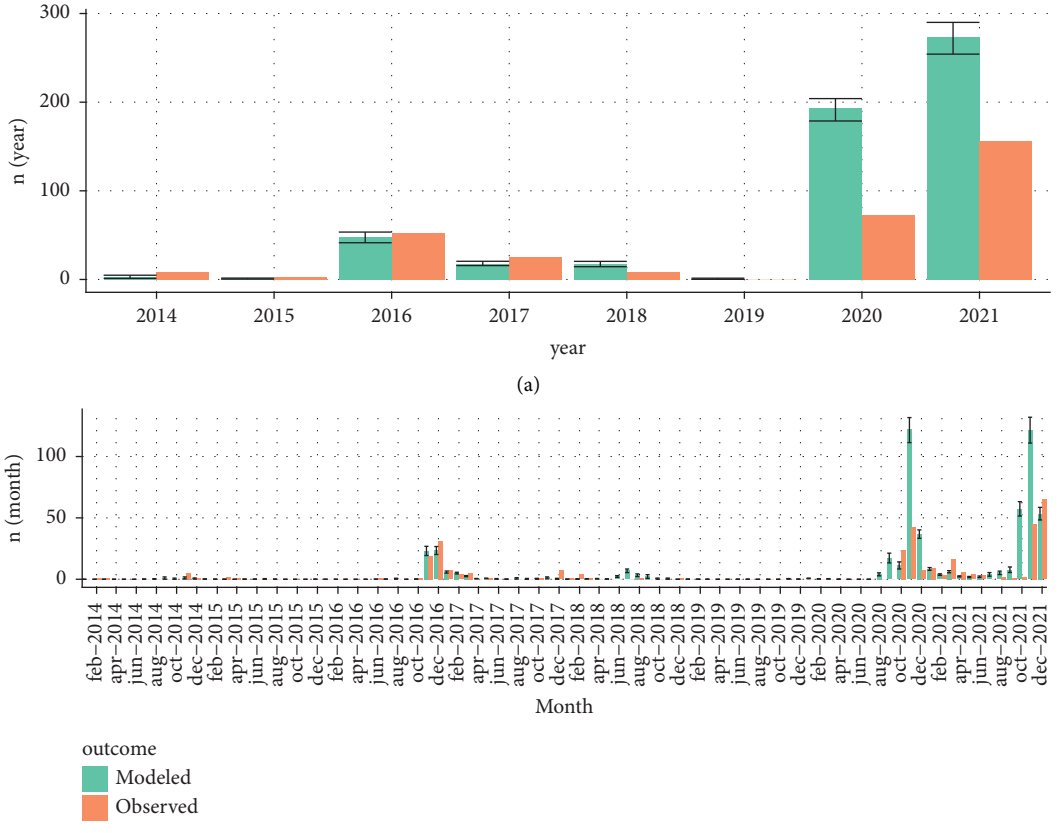


FIGURE 4: Modelled and observed outbreak risk ($R\_overall_t$) for highly pathogenic avian influenza between 2014–2021. The observed outbreaks are the (wild and domestic) number of outbreaks (n) that were reported in the Netherlands during that time period, by year (a) and by month (b).

TABLE 1: Comparison of different models.

Model name	Included data/assumptions	RMSE
Observed	Observed number of outbreaks (wild + nonwildlife) in the Netherlands	Ref
Model 0 (baseline)	Wildlife + nonwildlife outbreaks	59.5
Model 1	Wildlife outbreaks only	30.1

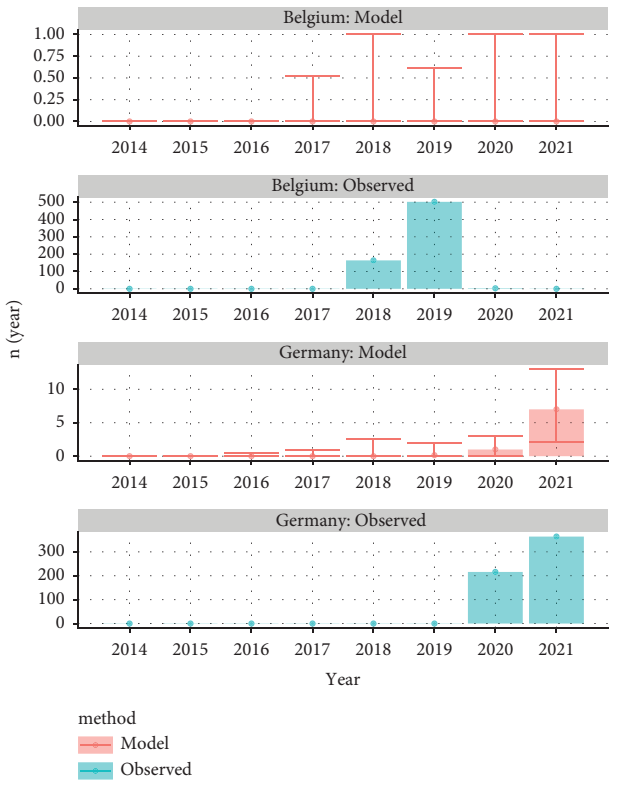


FIGURE 5: The modelled median yearly entry risk for African swine fever in Belgium and Germany compared to the observed number of outbreaks (n). The error bar provides the 95% uncertainty interval of the modelled risk.

Belgium, we saw that the outbreaks in Germany that started late 2020, were preceded by a period of increased risk; the 2018-2019 outbreak in Belgium did not correlate with the predicted risk. During this period, no outbreaks were observed within the Netherlands.

4. Discussion

4.1. Summary of Findings. Here, we present a generic entry risk assessment model that provides a flexible and generic solution to estimate the entry risk of animal disease through wildlife movements. We demonstrated that the complexities of animal movements can be reduced to a set of parameters that can be parameterized to mimic animal "behaviour groups." With this, we managed to reach a level of complexity that was necessary to capture the key patterns of wildlife movement while maintaining flexibility and transparency.

To demonstrate the application of the model, we assessed the entry 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 entry risk. On a yearly scale, the predicted entry risk for HPAI correlated well with observed outbreaks in the Netherlands.

4.2. 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 probability of "long jumps," which are most likely the result of human interference, was very low; wild birds, through long distance migration, were more likely to reach the border and thus introduce HPAI. This is in line with the recent findings from Engelsma et al. [6] that describe HPAI outbreaks in the Netherlands as separate introductions originating from wild birds [6].

If we consider the entry risk for ASF into Belgium and Germany, we found that for Germany, the proximity of outbreaks in Poland close to the border caused an increased entry risk before outbreaks were indeed observed. For Belgium, our model did not indicate an elevated entry risk in the time period that the outbreaks of wild boar in Belgium occurred. Previous analyses of these outbreaks confirm that the outbreaks in Germany were likely the result of multiple entries of infected wild boar, whereas the outbreak in Belgium originated from a point-source introduction [36]. The latter is harder to predict due to the stochastic nature of the event.

We should interpret the results semiquantitatively: the model provides an indication of the relative entry risk over different years rather than a prediction of the absolute number of entries. We should also put the results in perspective given 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.

4.3. Strengths and Limitations. Our approach has several strengths. First, the model is generic and transparent. 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 entry 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 other assumptions that have resulted in an oversimplification of reality. These assumptions might hold true in the context in which we applied the model, but this might not be the case in other settings. For example, if migration movement in reality is not predominantly in a single direction, the model, by design, failed to capture that pattern. Also, 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 outbreaks might actually 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 in the Netherlands rather than posing a risk for entry. This could explain why we saw an increase in the modelled number of infected birds that reach the border in 2020 and 2021, as in recent years, the local circulation of HPAI in Europe has increased, causing the model to predict an increased risk originating from neighbouring countries. Similarly, some of the observed outbreaks in the Netherlands will have resulted from local circulation of the virus rather than new entries. This also demonstrates the limitation of the definition of "outbreak" as reported in the EMPRES-I dataset; many of these events are likely a continuation or reemergence of an existing event, but the reported outbreaks are not classified as "primary" and "secondary" outbreaks.

Indeed, if we look at the countries that the model predicted were most contributing to the entry risk of HPAI, some might not be in line with the assessment of the phylogenetic trees. Beerens et al. [10] noted that the "incursion was not related to viruses detected in eastern Europe, Germany, and Bulgaria earlier in 2020 but was probably associated with the fall migration of wild birds to wintering sites in the Netherlands." Although no HPAI viruses or deaths were reported at wild bird breeding sites in northern Russia, HPAI H5N8 viruses were reported in southern Russia and northern Kazakhstan in September 2020 [10]. However, due to the selective and limited sequencing of cases, this might also not provide a complete picture of transmission chains.

Endemicity of disease will result in a higher infection risk in the country than accounted for by our model, since the model, as it is parametrized here, only takes into account new introductions and not local circulation. Recently, during 2022, outbreaks of HPAI have occurred outside of the bird migration season, indicating the local establishment of the disease in many European countries, including the Netherlands [37]. Due to the endemicity of HPAI, many of the observed outbreaks are hypothesized to be the result of local circulation rather than new introductions. These changed dynamics will result in an underestimation of the risk by the current model. However, the model might still be able to predict the number of introductions, although these become less relevant when local circulation is abundant.

4.4. Comparison with Other Work. There are a few generic quantitative risk models that include wildlife as a pathway for disease entry. Simons et al. [1] applied their generic risk model to infer the entry risk of ASF, classical swine fever, and rabies through wildlife. They modelled the 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 did not apply the model to diseases 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. [26] applied a similar approach to Simons et al. [1], where the movement of wild boar depends on habitat suitability. The approaches of Simons et al. [1] and Taylor et al. [26] are more demanding than ours with respect to spatial data on susceptible wildlife host populations, which have to be collected for each species separately. The generic framework developed by Taylor et al. [38] can provide results at different spatial scales, varying from animal holding to country [38]. Our approach is at the country level but could relatively easily be adapted to other regional levels as long as file shapes are available. Although we used a quantitative approach to estimate the entry risk posed by wildlife, results should be used for prioritisation rather than prediction, similar to some of the semiquantitative generic tools that have been developed in recent years [22, 24]. By calculating the entry risk over multiple years, trends in risk can be observed, allowing for horizon scanning and early warning. Our model has been designed such that it can be easily updated when new disease outbreak data become available. It was originally developed as an extension of RRAT, a rapid risk assessment tool to assess the incursion risk of emerging and reemerging diseases for the Netherlands [20]. RRAT only addresses the incursion risk related to human activity, including legal trade in animals and animal products and animal products illegally carried by travellers, whereas for diseases such as ASF and HPAI, the incursion risk by wildlife might be more important. A next step would be to merge this tool with RRAT and apply both tools for the same diseases to enable comparisons of the entry risk across pathways and diseases.

4.5. Future Improvements. Since models are only as good as the data that is put into them, many of the improvements lie in improving the input data. We need to improve our understanding of migration and dispersal patterns. For example, now, migration patterns are based on the ringing of birds and retrieval of rings, which is very dependent on the number and quality of observations, where heterogeneity and underreporting are likely. This results in biased data. There is 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 the 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 include barriers such as roads and rivers, and allowing travel across nonlinear paths, would refine the prediction of predominantly land-based movement. The framework allows for an extension of the number of behaviours considered, thus enabling the entry risk to be estimated in more detail, for example by bird species or by disease strain or subtype. For example, a more detailed parametrisation of different HPAI strains (as different diseases) and different bird species (as different behaviour groups) could increase the accuracy of the model but would require more detailed outbreak and transmission data. We also need to improve our understanding of disease occurrence. The notification and reporting of disease occurrences are 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. An estimation of the prevalence of disease would improve the estimation of risk.

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

5. Conclusion

The movement of wildlife is complex and based on many external factors that vary between regions and over time. To assess the entry risk of diseases transmitted by wildlife, we described animal movement patterns using a limited number of variables. Each set of parameterized variables represents a "behaviour group" and more nuance and complexity can be added to the model by defining additional "behaviour groups" when more data becomes available. With this approach, we were able to build a generic and flexible framework to assess the entry risk of diseases in wildlife that could be used for both terrestrial animals (illustrated by ASF) and birds (illustrated by HPAI). The model thus enables rapid and transparent estimation of the entry risk for diverse diseases and wildlife species.

Data Availability

All data are available online (https://doi.org/10.7910/DVN/LZUJKS).

Ethical Approval

The authors confirm that the ethical policies of the journal, as noted on the journal's author guidelines page, have been adhered to. No ethical approval was required as this is a review article with no original research data.

Disclosure

Note: A preprint has previously been published [39].

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Authors' Contributions

Conceptualization, methodology, modelling, data curation, writing-original draft preparation was performed by MJC,: interpretation, data curation, visualization, writing-reviewing and editing was done by RR, investigation, validation, interpretation was conducted by EGMK,. and conceptualization, methodology, interpretation, writing-reviewing and editing was done by CV.

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Supplementary Materials

Supplement 1: bird migration and parametrisation of highly pathogenic avian influenza. Supplement 2: long jumps African swine fever. Supplement 3: contribution by country. (*Supplementary Materials*)

References

[1] R. R. L. Simons, V. Horigan, S. Ip et al., "A spatial risk assessment model framework for incursion of exotic animal disease into the European Union Member States," *Microbial Risk Analysis*, vol. 13, Article ID 100075, 2019.

[2] K. M. Smith, C. M. Machalaba, H. Jones et al., "Wildlife hosts for OIE-Listed diseases: considerations regarding global wildlife trade and host-pathogen relationships," *Veterinary medicine and science*, vol. 3, no. 2, pp. 71–81, 2017.

[3] K. Morelle, T. Podgórski, C. Prévot, O. Keuling, F. Lehaire, and P. Lejeune, "Towards understanding wild boar Sus scrofa movement: a synthetic movement ecology approach," *Mammal Review*, vol. 45, no. 1, pp. 15–29, 2015.

[4] T. Klinner and H. Schmaljohann, "Temperature change is an important departure cue in nocturnal migrants: controlled experiments with wild-caught birds in a proof-of-concept study," *Proceedings of the Royal Society B: Biological Sciences*, vol. 287, no. 1936, Article ID 20201650, 2020.

[5] M. E. Visser, A. C. Perdeck, J. H. van Balen, and C. Both, "Climate change leads to decreasing bird migration distances," *Global Change Biology*, vol. 15, no. 8, pp. 1859–1865, 2009.

[6] M. Engelsma, R. Heutink, F. Harders, E. A. Germeraad, and N. Beerens, "Multiple Introductions of Reassorted Highly Pathogenic Avian Influenza H5Nx Viruses Clade 2.3.4.4b Causing Outbreaks in Wild Birds and Poultry in The Netherlands 2020-2021," *Microbiol Spectr*, vol. 45, Article ID e0249921, 2022.

[7] Y. Xu, P. Gong, B. Wielstra, and Y. Si, "Southward autumn migration of waterfowl facilitates cross-continental transmission of the highly pathogenic avian influenza H5N1 virus," *Scientific Reports*, vol. 6, no. 1, Article ID 30262, 2016.

[8] M. Gilbert, X. Xiao, J. Domenech, J. Lubroth, V. Martin, and J. Slingenbergh, "Anatidae migration in the western palearctic and spread of highly pathogenic avian influenza H5N1 virus," *Emerging Infectious Diseases*, vol. 12, no. 11, pp. 1650–1656, 2006.

[9] A. M. Kilpatrick, A. A. Chmura, D. W. Gibbons, R. C. Fleischer, P. P. Marra, and P. Daszak, "Predicting the global spread of H5N1 avian influenza," *Proceedings of the*

National Academy of Sciences of the U S A, vol. 103, no. 51, pp. 19368–19373, 2006.

[10] N. Beerens, R. Heutink, F. Harders et al., "Incursion of novel highly pathogenic avian influenza A(H5N8) virus, The Netherlands, october 2020," *Emerging Infectious Diseases*, vol. 27, no. 6, pp. 1750–1753, 2021.

[11] A. De la Torre, J. Bosch, I. Iglesias et al., "Assessing the risk of african swine fever introduction into the European union by wild boar," *Transbound Emerg Dis*, vol. 62, no. 3, pp. 272–279, 2015.

[12] A. de la Torre, J. Bosch, J. M. Sanchez-Vizcaino et al., "African swine fever survey in a European context," *Pathogens*, vol. 11, no. 2, p. 137, 2022.

[13] European Food Safety Authority EFSA, B. Anette, B. Anette et al., "Epidemiological analyses of african swine fever in the European union (november 2018 to october 2019)," *EFSA Journal*, vol. 18, no. 1, Article ID e05996, 2020.

[14] A. Linden, A. Licoppe, R. Volpe et al., "Summer 2018: African swine fever virus hits north-western Europe," *Transbound Emerg Dis*, vol. 66, no. 1, pp. 54-55, 2019.

[15] J. Bosch, A. Rodriguez, I. Iglesias et al., "Update on the risk of introduction of african swine fever by wild boar into disease-free European union countries," *Transbound Emerg Dis*, vol. 64, no. 5, pp. 1424–1432, 2017.

[16] K. Schulz, F. J. Conraths, C. Staubach et al., "African swine fever: why the situation in Germany is not comparable to that in the Czech Republic or Belgium," *Transbound Emerg Dis*, vol. 67, no. 5, pp. 1816–1819, 2020.

[17] J. Cukor, R. Linda, P. Vaclavek, K. Mahlerova, P. Satran, and F. Havranek, "Confirmed cannibalism in wild boar and its possible role in African swine fever transmission," *Transbound Emerg Dis*, vol. 67, no. 3, pp. 1068–1073, 2020.

[18] G. Woźniakowski, Z. Pejsak, and A. Jabłoński, "Emergence of african swine fever in Poland (2014–2021). Successes and failures in disease eradication," *Agriculture*, vol. 11, no. 8, p. 738, 2021.

[19] World Organisation for Animal Health, *Terrestrial Code - Chapter 2.1. Import Risk Analysis*, World Organisation for Animal Health, Paris, France, 2021.

[20] C. J. de Vos, R. Petie, E. G. M. van Klink, and M. Swanenburg, "Rapid risk assessment tool (RRAT) to prioritize emerging and re-emerging livestock diseases for risk management," *Frontiers in Veterinary Science*, vol. 9, Article ID 963758, 2022.

[21] European Food Safety Authority, "Webinar: rapid risk assessment tools for animal disease outbreaks," 2017, https://www.efsa.europa.eu/en/events/event/171127.

[22] R. Condoleo, R. A. Taylor, R. R. L. Simons, P. Gale, Z. Mezher, and H. Roberts, "A semi-quantitative model for ranking the risk of incursion of exotic animal pathogens into a European Union Member State," *Microbial Risk Analysis*, vol. 18, Article ID 100175, 2021.

[23] J. Kyyrö, L. Sahlström, and T. Lyytikäinen, "Assessment of the risk of African swine fever introduction into Finland using NORA—a rapid tool for semiquantitative assessment of the risk," *Transboundary and Emerging Diseases*, vol. 64, no. 6, pp. 2113–2125, 2017.

[24] H. Roberts, M. Carbon, M. Hartley, and M. Sabirovic, "Assessing the risk of disease introduction in imports," *The Veterinary Record*, vol. 168, no. 17, pp. 447-448, 2011.

[25] S. Roelandt, Y. Van der Stede, B. D'Hondt, and F. Koenen, "The assessment of african swine fever virus risk to Belgium early 2014, using the quick and semiquantitative pandora screening protocol," *Transbound Emerg Dis*, vol. 64, no. 1, pp. 237–249, 2017.

[26] R. A. Taylor, T. Podgorski, R. R. L. Simons et al., "Predicting spread and effective control measures for African swine fever-Should we blame the boars?" *Transbound Emerg Dis*, vol. 68, no. 2, pp. 397–416, 2021.

[27] R. Kosmider, J. Smith, S. Gillings et al., "Updated risk of H5N1 HPAI incursion to poultry in Great Britain via wild birds," *The Veterinary Record*, vol. 179, no. 18, p. 464, 2016.

[28] M. Martinez, A. M. Perez, A. De La Torre, I. Iglesias, J. M. Sánchez-VizcaÍNo, and M. J. MuÑOz, "Evaluating surveillance in wild birds by the application of risk assessment of avian influenza introduction into Spain," *Epidemiology and Infection*, vol. 139, no. 1, pp. 91–98, 2011.

[29] RCoreTeam, *R: A Language and Environment for Statistical Computing*, 2021, https://www.R-project.org/.

[30] R. J. Hijmans, "Geosphere: Spherical Trigonometry. R Package Version 1.5-10," 2019, https://CRAN.R-project.org/package=geosphere.

[31] F. C. Velkers, T. T. M. Manders, J. C. M. Vernooij, J. Stahl, R. Slaterus, and J. A. Stegeman, "Association of wild bird densities around poultry farms with the risk of highly pathogenic avian influenza virus subtype H5N8 outbreaks in The Netherlands, 2016," *Transbound Emerg Dis*, vol. 68, no. 1, pp. 76–87, 2021.

[32] K. Jerina, B. Pokorny, and M. Stergar, "First evidence of long-distance dispersal of adult female wild boar (Sus scrofa) with piglets," *European Journal of Wildlife Research*, vol. 60, no. 2, pp. 367–370, 2014.

[33] J. Truvé and J. Lemel, "Timing and distance of natal dispersal for wild boar Sus scrofa in Sweden," *Wildlife Biology*, vol. 9, no. 1, pp. 51–57, 2003.

[34] V. Guberti, S. Khomenko, M. Masiulis, and S. Kerba, *African Swine Fever in Wild Boar - Ecology and Biosecurity*, FAO, Rome, Italy, 2019.

[35] S. Dellicour, D. Desmecht, J. Paternostre et al., "Unravelling the dispersal dynamics and ecological drivers of the African swine fever outbreak in Belgium," *Journal of Applied Ecology*, vol. 57, no. 8, pp. 1619–1629, 2020.

[36] C. Sauter-Louis, J. H. Forth, C. Probst et al., "Joining the club: first detection of African swine fever in wild boar in Germany," *Transbound Emerg Dis*, vol. 68, no. 4, pp. 1744–1752, 2021.

[37] European Food Safety Authority, European Union Reference Laboratory for Avian Influenza, C. Adlhoch et al., "European Centre for disease prevention control, European union reference laboratory for avian influenza, adlhoch, Cavian influenza overview March - june 2022," *EFSA journal. European Food Safety Authority*, vol. 20, no. 8, Article ID e07415, 2022.

[38] R. A. Taylor, A. D. C. Berriman, P. Gale, L. A. Kelly, and E. L. Snary, "A generic framework for spatial quantitative risk assessments of infectious diseases: lumpy skin disease case study," *Transbound Emerg Dis*, vol. 66, no. 1, pp. 131–143, 2019.

[39] M. J. Counotte, R. Petie, E. van Klink, and C. J. de Vos, "A generic risk assessment model for animal disease incursion through wildlife," *bioRxiv*, vol. 2022, Article ID 489353, 2022.