



Department
for Environment
Food & Rural Affairs

Gamebird wild bird risk assessment tool (GWRAT) methodology

Developing a semi-quantitative risk assessment tool
to assess the impact of releasing non-native
gamebirds on or near a special protection area (SPA)

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Summary

A semi-quantitative risk assessment tool has been developed to aid risk managers in the decision-making process while granting licences for the release of non-native gamebirds around special protection areas (SPAs). The gamebird wild bird risk assessment tool (GWRAT) identifies the semi-quantitative likelihood of a series of pathways through which avian influenza can influence the risk posed to the SPA conservation objectives by release of non-native gamebird species, based on the current highly pathogenic avian influenza virus (HPAI) situation. The impact is assessed for each site, based on the likely case fatality rate of HPAI H5N1 infection in different bird species, the ability of the population to recover (which will depend on many other factors, not just disease prevalence) and this, combined with the likelihood can be used to assess the risk for each site.

Introduction

The avian influenza epizootic in Great Britain, caused by HPAI H5N1, has been extraordinary in its scale and longevity in the wild bird population. It has resulted in substantial impacts on populations of some wild species. Spill-over into the poultry sector has occurred regularly over the last 3 years. There has been a concern about the potential for infection transmission back into wildlife to occur from poultry. This is exceedingly unlikely from kept poultry, given the speed of response to outbreaks in the UK. However, for non-native gamebirds that have been released and are therefore classed as wild birds, there is a greater level of uncertainty and opportunity for wild bird contacts.

Introduction of exotic avian diseases into naive wild bird populations has resulted in large-scale outbreaks with serious economic and socio-ethical impact (OHHLEP, 2023). Hence, preparedness is warranted to prevent, detect, and control outbreaks of exotic animal diseases.

HPAI is mainly introduced into Great Britain through infected wild birds (typically ducks, geese and swans) migrating into Great Britain from northern and eastern Europe and Asia in autumn. However, over the summers of the last 2 years HPAI has been maintained in wild birds including seabirds and gull species.

Risk assessment is a useful tool to inform risk managers on potential spread of HPAI between wild bird species. Data required for such risk assessments would include:

- the distribution of diseases and potential host species
- susceptibility and infectiousness of hosts
- host to host contact rates
- contamination of and survival of pathogens in products and material
- the numbers of hosts and their movements within and between infected areas to the target regions

Risk assessments are developed as bespoke models to assess the risk for a single disease and transmission pathway.

Use of modelling in predicting risk of incursion

In recent years, several generic risk models or frameworks have been developed that can easily be applied to assess the incursion risk for multiple diseases (Havelaar and others, 2010; Roberts and others, 2011; ANSES, 2012; De Vos and others, 2016; EFSA, 2017; Kyyrö and others, 2017; Roelandt and others, 2017; Simons and others, 2019; Taylor and others, 2019).

In contrast to bespoke models, generic risk assessment (RA) tools allow for a more rapid response to a variety of newly emerging or re-emerging diseases. Generic RA tools are faced with 3 major challenges:

1. The need for extensive and real-time databases on disease presence and movements of commodities.
2. The use of algorithms to combine all input data into either a qualitative or a quantitative risk estimate.
3. The validation of results.

The International Disease Monitoring tool for risk of incursion (IDM) is a semi-quantitative RA tool developed in Microsoft Excel. that ranks diseases according to their incursion risk to the UK, based on:

- the geographical presence of disease in global regions
- the different pathways for entry (mostly associated with trade commodities)
- the mitigation measures applied at origin

The IDM tool (Roberts and others, 2011) is used for comparing different risk pathways (or trade commodities). It was first developed for the UK but has since been adapted for use in Italy (Condoleo and others 2021) and as part of a European Food Safety Authority (EFSA) programme on generic tools (EFSA, 2017). It is now used for the UK Target Operating Model to direct our border checks (in press). It will also be used as part of a Food and Agriculture Organization (FAO) project to develop a new system for low or middle income countries (LMIC)(FAO, pers.comm).

Here it has been adapted for use to consider:

- the likely presence of HPAI H5N1 across England
- the potential for spread into released gamebirds, based on the proximity in time and distance to other cases in either wild birds or captive birds
- the potential exposure to certain other bird species present, particularly birds in SPAs in the same region, through contact with gamebirds

The GWRAT uses the same concept of IDM, in that it is a pre-populated tool defining:

- geographical presence of disease
- the population at risk at origin and destination
- risk pathways based on the likelihood of inter and intra-population contacts

The pathways can be weighted and assigned a semi-quantitative score, in this case for the entry of H5Nx into gamebirds and their contact with wild birds. GWRAT can be regularly updated to take into account changes in disease presence by region, season and presence of birds. The tool is manually populated with information on disease outbreaks, wildlife cases, susceptibility of wild birds and impact on wild bird populations. All input parameters are given semi-quantitative risk scores that serve as input into the calculations.

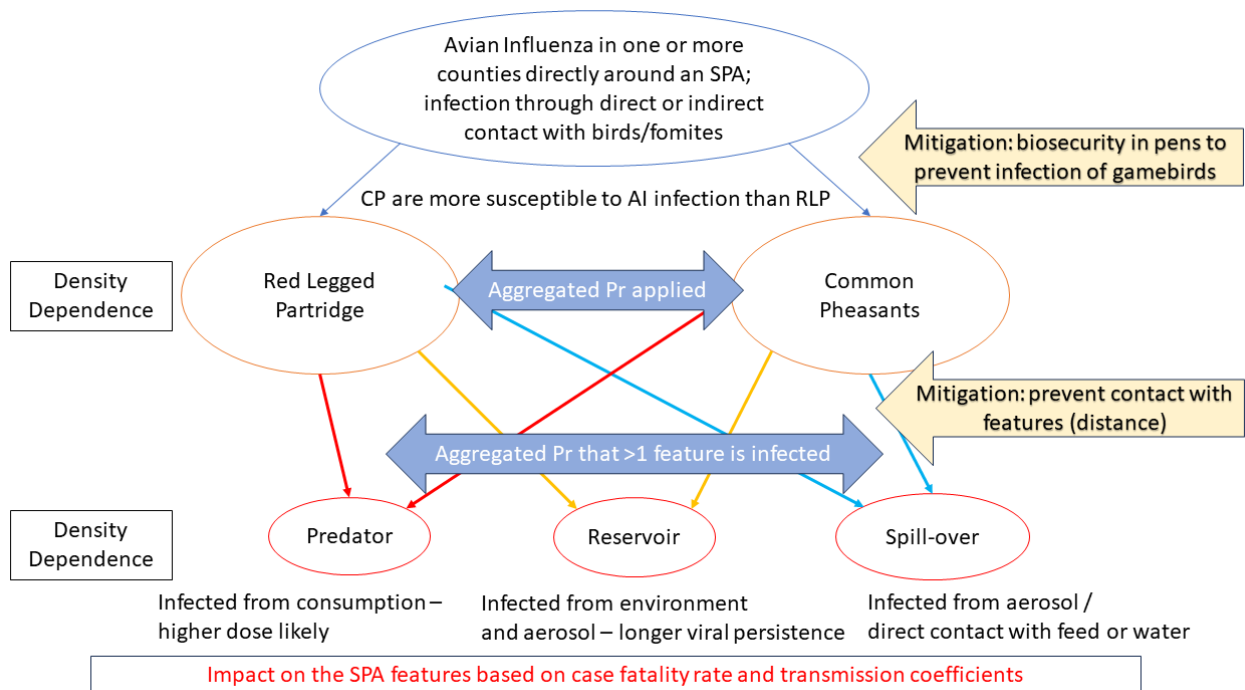


Figure 1: A schematic overview of the different steps in the GWRAT.

Figure 1 shows that:

1. HPAI presence in different counties and the potential for its spread into any given SPA in those counties is assigned a level of risk based on when and where cases occurred.
2. This risk is used to calculate an aggregated probability that common pheasants and red-legged partridges are infected. Density of gamebirds and common pheasants' higher susceptibility to HPAI than red-legged partridges are taken into account. Points at which mitigation measures such as biosecurity in pens to prevent infection can be included are shown.

3. This aggregated probability is then used to calculate a further aggregated probability that more than one species feature could be infected. Density of protected features and transmission routes to different groups of features are taken into account. Sources of infection for each species group are listed. At this point mitigation measures to prevent contact between gamebirds and species features are introduced.

4. Finally, overall cumulative impact on SPA features is calculated using the probability derived in step 3, and case fatality rates and transmission coefficients.

Outputs of GWRAT are presented as semi-quantitative risk scores for each SPA and for each group of birds, according to their transmission risk. Although the GWRAT is deterministic, the uncertainty in input parameters can easily be explored by what-if analysis.

The emphasis is on the likelihood of infection being transferred to wild birds through their contact with an infected gamebird. However, the tool also considers the probability of exposure of the SPA features (the protected birds, present at the site, as either breeding or overwintering populations). This requires understanding of where the SPAs are and the location and current cases detected in wild birds. These data are factored into the tool, with weekly updates on current cases.

GWRAT outputs

There are 2 outputs from the tool:

1. A histogram of the different SPAs, by:
 - gamebird species released (such as 200 pheasants and 500 red legged partridges being released on or near a particular SPA)
 - the SPA feature species group (reservoir species, spill-over species and raptors)

There is a minimum score (or acceptable level of risk) that can be assigned by the risk managers (Figures 2a and 2b). This is a concept of acceptable level of risk, below which no action is necessary. The cut-off score is based on the year round 'very low' level of avian influenza presence in the country at any time of the year. It's driven by the likelihood of waterfowl carrying low pathogenicity avian influenza viruses.

2. An impact bar chart which identifies the SPAs at highest risk of an impact. This could be used by the risk manager (Figure 3) to consider vulnerability of certain sites, based on the species recovery (breeding capacity, number of birds present and case fatality rates).

Uncertainty is caused by:

- the unknown duration and frequency of gamebird contact with wild birds

- the susceptibility and clinical picture of infection in different species
- the impact of different H5Nx viruses, clades and genotypes
- other impacts on the recovery or decline of wild bird feature species, including predation

Therefore, the tool should be used to provide guidance about the relative risk between areas and pathways and not an absolute value. Expert elicitation has been used to inform the parameters where possible and the outcome from those questions are given in the Annex.

In this GWRAT, the number of:

- disease outbreaks (or wild bird cases) in certain counties that surround each SPA are updated on a weekly basis
- gamebirds released at each SPA have been provided by the licensing team
- SPA features at each site are based on the [Joint Nature Conservation Committee \(JNCC\) list of UK SPAs](#) and the category of bird present

Number of gamebirds released at SPAs were set as the total number across all individual licence applications received in 2023, whether the applications were successful or not.

No applications were received for gamebird releases in 2023 for 56 of the SPAs in England, however. For these SPAs, we applied an estimate for the number of gamebirds that could feasibly be released. This was set to 2,501 of each species as, based on available serological evidence, modelling indicates that transmission does not occur with any greater frequency above this number. This is therefore a precautionary measure, used to replicate a scenario of maximal HPAI transmission within a gamebird population. This maximum number was also applied to SPAs that received applications for the release of fewer than 2,501 gamebirds in 2023.

The JNCC data were last updated in September 2022. This means numbers are an approximate estimate of the composition of qualifying species.

Algorithms embedded in the tool then provide the comparable risk score for each SPA.

Wild bird surveillance and spatial prevalence of infection

The England wild bird surveillance programme is based on passive surveillance of dead wild birds testing positive for HPAI H5N1. This is not a perfect surveillance system - it is designed to provide information about the likely presence of different strains of HPAI in the target waterfowl and other likely hosts. Not every bird will be tested, and not every dead bird will be collected. However, the presence of at least one infected wild bird in a new region would suggest there is potential for further cases to be present. Birds tested include

those on the [EFSA target list](#). This lists the fifty species that consistently test positive for HPAI H5 or H7 avian influenza viruses (prevalence of over 0.4%).

The surveillance system for wild birds is not designed to detect every infected bird, but instead is designed for looking at changes in the ecology of avian influenza viruses in the population of target species. This approach enables a score to be given for each county and for the week of interest. However, to reduce strain on laboratory resources, once a bird in an area tests positive, no new birds will be collected or tested for the next 2 weeks. Therefore, infection is considered to be present for the following weeks, even if no detections are reported in that time.

If disease has been detected in a wild bird in a county:

- 4 months ago, the score is 1
- 2 months ago, the score is 2
- 1 month ago, the score is 4
- 2 weeks ago, the score is 6
- the current week, the score is 10

Additional scoring is done when:

- a bird tests positive on the SPA or in the buffer zone – the score is increased by 10
- there is an active poultry case (meaning disease control zones are still present) – the score is increased by 10
- there is a mass mortality event (more than 10 birds of the same species are found dead at the same time and in the same location) – the score is increased by 10

This is because, for these types of events, the environmental contamination is present for longer than just a 2 week period.

Therefore, the maximum score for a county is 53, and this is taken as a proportion of the maximum possible for the whole country. Because surveillance is based on either public reporting or warden reporting in conservation areas, it is not possible to consider using a finer granularity.

Gamebird susceptibility

The 2 gamebird species considered were common pheasants and red legged partridges. These 2 species have a different level of susceptibility according to some experimental data and field observations. This is taken into account in the tool (Seekings and others, 2023; Liang and others, 2022).

The difference between the 2 species was also subject to an expert elicitation. Agreement was reached that there is likely to be at least a ten-fold difference in susceptibility, with common pheasants more readily infected than red-legged partridges. This is addressed in

the tool by assigning a different 'p value' to each species. The p value shows that the probability of at least one common pheasant being infected in a group is greater than for the red-legged partridges.

Seekings and others (2023) undertook experimental work comparing infection and infectivity of HPAIV in both species. They showed:

“Intraspecies transmission to contact pheasants was successful for both viruses and associated with viral environmental contamination, while interspecies transmission to a first chicken-contact group was also efficient.

“However, further onward transmission to additional chicken contacts was only achieved with H5N1-2021. Intra-partridge transmission was only successful when high-dose H5N1-2021 was administered, while partridges inoculated with H5N8-2021 failed to shed and transmit, although extensive tissue tropism was observed for both viruses.

“Mortalities among infected partridges featured a longer incubation period compared to that in pheasants, for both viruses.

“Therefore, the susceptibility of different gamebird species and pathogenicity outcomes to the ongoing H5Nx clade 2.3.4.4b HPAIVs varies, but pheasants represent a greater likelihood of H5Nx HPAIV introduction into galliforme poultry settings.”

Other field observations have identified the risk posed by infected gamebirds to mammals that predate the carcasses (Tammiranta and others, 2023). Other H5Nx viruses have also been used to experimentally infect pheasants (Liang and others, 2022). More recently, a modelling approach for the interaction between different wild species and poultry premises has indicated a positive association between the release of gamebirds and the increase in outbreaks in poultry during August 2022 and January 2023 (Vickers and others, 2024). Therefore, the evidence is unequivocal that infected non-native free-living gamebirds pose a risk through both direct, indirect and consumption pathways for poultry, as well as other wild birds.

The evidence base for red-legged partridges shows they are susceptible (from the number of outbreaks and cases across Europe and North America). Beyond this, it shows virus can be recovered from infected birds, but a high dose is needed to infect them. Therefore, they are deemed less susceptible than common pheasants.

Wild bird features

Categories of wild birds (features) at the SPA were split into 3 types:

- reservoir (principally waterfowl)
- spill-over (passerines, ground nesting birds)
- birds of prey (raptors)

These categories are based partly on the way in which the birds are likely to become infected (principal transmission pathway). They are also based on their ability to infect each other and produce mass mortalities of wild species of conservation concern, which we consider here a substantial impact.

The most important reservoir species for HPAI are widely accepted to be wild birds from the orders of Anseriformes (ducks, geese, and swans) and Charadriiformes (gulls, skuas and wading birds). In particular, various species of dabbling ducks are considered important (Yoon, Webby and others 2014).

The susceptibility to disease of individual species for any single strain of virus ranges:

- very high (for example, chickens, turkeys)
- tolerant (for example, mallard ducks, geese and crows, which support virus replication without severe disease)
- almost entirely resistant (for example, pigeons, that can be refractory to infection)

While the majority of the evidence is circumstantial or from transmission experiments, some structural biology modelling also supports the differences in susceptibility based on receptor binding.

Categorisation of the wild bird species considered here (all features on SPAs in England) allows us to identify 3 distinct principal transmission pathways.

1. Reservoir: Commonly where dense aggregations of birds share the same space (roosting or foraging) as well as extensive periods living in a highly transmissible matrix (cold water) when considering orofaecal transmission of HPAI. These conditions promote multiple and substantial direct and indirect transmission pathways.
2. Birds of prey (raptors): Direct transmission, especially from infective symptomatic birds or carcasses, where consumption of highly infective organs occurs before any significant environmental degradation has taken place. The propensity for many species to scavenge during lean or stressful periods of winter suggests significant likelihood of interaction with infective prey. This may also include consumption of small bridging species, such as passerines.
3. Spill-over: This group includes all other avian species that must be considered (not mammals). This is most difficult group to gauge susceptibility. Species are often considered to be un conducive to indirect transmission pathways where:
 - their ecology and use of habitats produces much lower likelihoods of interaction with gamebirds (for example, obligate shorebirds or cliff nesting seabirds)
 - they do not form extensive interaction networks during sensitive periods (for example, breeding passerines or nightjar)
 - their behaviour and habitats are unlikely to result in a prolonged use of shared space or direct interaction with gamebirds in largely dry, warm, terrestrial contexts

However, if these birds share space, when breeding on open moorland or inhabiting wetland areas during overwintering periods, they may come into direct contact with gamebirds. However, beak to beak contact may be required for transmission. They may act as bridging species.

These 3 groups were largely agreed by the expert elicitation. They recognised that some individual species are not normally assigned to one group or the other. However, this year has been unusual in the number of species affected with this particular virus, HPAI H5N1 clade 2.3.4.4b such that some are considered reservoirs where before they were not. Also, some birds, such as the golden plover, may be present on an SPA in the winter in wetland areas, as well as in summer on moorland breeding sites. The numbers used in the tool are based on times when the birds are counted as being features.

Not all of the birds in table 1 are features on England SPAs.

Table 1: Wild bird groups and assignment of species.

Group	Species included
Reservoir	Barnacle goose, Bewick's swan, brent goose, common eider, common goldeneye, common pochard, common scoter, common shelduck, Eurasian teal, Eurasian wigeon, gadwall, garganey, goosander, greater white-fronted goose (Greenland), Greenland white-fronted goose, greylag goose, light-bellied brent goose, long-tailed duck, mallard, mute swan, northern pintail, northern shoveler, pink-footed goose, red-breasted merganser, scaup, taiga bean goose, tufted duck, velvet scoter, whooper swan, black-headed gull, European herring gull, great black-backed gull, Mediterranean gull, mew gull, lesser black-backed gull, little gull
Birds of prey	Eurasian hobby, golden eagle, hen harrier, honey buzzard, marsh harrier, merlin, osprey, peregrine falcon, red kite, short-eared owl
Spill-over	Aquatic warbler, Arctic skua, Arctic tern, bar-tailed godwit, black-tailed godwit, black-throated diver, common greenshank, common guillemot, common puffin, common quail, common redshank, common ringed plover, common snipe, common tern, corncrake, Dartford warbler, dunlin, Eurasian whimbrel, Eurasian avocet, Eurasian bittern, Eurasian coot, Eurasian curlew, Eurasian dotterel, Eurasian oystercatcher, Eurasian spoonbill, Eurasian stone-curlew, European golden plover, European nightjar, European shag, European storm petrel, Fair Isle wren, great cormorant, great crested grebe, great Northern diver, great skua, grey plover, kittiwake, Leach's storm petrel, little egret, little tern, Manx shearwater, Northern fulmar, Northern gannet, Northern lapwing, purple sandpiper, razorbill, red knot, red-billed chough, red-necked phalarope, red-throated diver, roseate tern, ruff, sanderling, sandwich tern, Scottish crossbill, Slavonian grebe, spotted crake, turnstone, water rail, Western capercaillie, wood sandpiper, wood warbler, woodlark

Grouping here also reflects varied consequences of infection by gamebirds and the potential impact of transmission to protected features on SPAs.

Reservoir species often have substantial populations where they are close to gamebirds. They may also be in substantial and dense mixed -species aggregations. This introduces the potential for a disease-induced mass mortality of one or more features. The death of a few birds as a consequence of infection is unlikely to produce a population-level effect at the site, though there is the potential for significant impacts.

In contrast, birds of prey are often rare or very rare. The consequential death of even a few birds on a site is likely to produce a population-level effect at the site and merits special consideration.

Bridging species

Because of the complexity of bridging species interactions with susceptible species, it was not possible to consider each possible combination of pathways (Caron and others, 2015). The presence of bridging species is therefore considered to be country-wide and is included in the 'indirect transmission' pathway. The [paper by Caron and others](#), sets out in detail the ways that interactions between different bird groups (maintenance species, such as gamebirds; bridge species, such as gulls; any SPA species feature) can result in transmission of HPAI, and how disruption of these pathways through management of the relevant species can prevent this transmission.

Determining the risk score

Risk scores for individual pathways are calculated by multiplying:

- the expression of the spatiotemporal description of risk (time since and location of the last 'local' positive case of HPAI in either poultry or wild birds)
- the species of gamebird
- the category of wild bird feature

The final risk score is calculated by summing the scores for all individual pathways. It should be used as an arbitrary unit for comparison purposes and is given by:

Risk score = \sum for all pathways relevant for each SPA.

A pathway is defined as the HPAI prevalence in the area of origin as proportion of total possible prevalence \times probability (P_{CP} or P_{RLP}) of at least one gamebird being infected \times probability of at least one wild bird being infected (P_{RES} , P_{PRED} or P_{SPILL})).

For the probability (P) of at least one bird being infected, the aggregated risk equation is used:

$$P=1-(1-p)^n$$

n is the number of individuals in a group. p is the probability of one of them (either common pheasant or red legged partridge) being infected and infectious.

Where the group size is large, the probability of at least one of them being positive at any time is greater and eventually reaches unity.

The same concept is applied to the different wild bird features, where p will depend on the route for transmission, consumption, direct or indirect contact (with decreasing probability respectively).

To determine p , expert elicitation was used for each of the 5 categories (CP, RLP, RES, SPILL and PRED).

A pathway is defined for each gamebird species coming into contact with each wild bird group. Therefore, there are 6 possible combinations for each of the SPAs:

Table 2: The possible pathway combinations by which a gamebird could come into contact and transmit bird flu to a wild bird, according to its group

	Reservoir	Spill-over	Bird of prey
Pheasant (high susceptibility)	Direct or indirect contact	Direct contact	Consumption
Partridge (low susceptibility)	Indirect contact	Direct contact	Consumption

The risk score might also be reduced by applying mitigating management measures. However, this is excluded in current thinking as ranking mitigation measures is complex, requiring an understanding of their value and feasibility. This will be subject to further work.

The risk score is determined by the presence of avian influenza in the area around the SPA and this will vary from one week to the next. Because of this, the tool will be updated each week, to reflect the dynamic character of the spatiotemporal component of risk. Thus, the risk produced by planned releases of gamebirds around each SPA (each with a unique combination and population of seasonally sensitive features) can be assessed consistently. This reflects the differing risks and consequences of releasing varied numbers of common pheasants or red-legged partridges on each of the 3 groups of features (reservoir, spill-over and raptor).

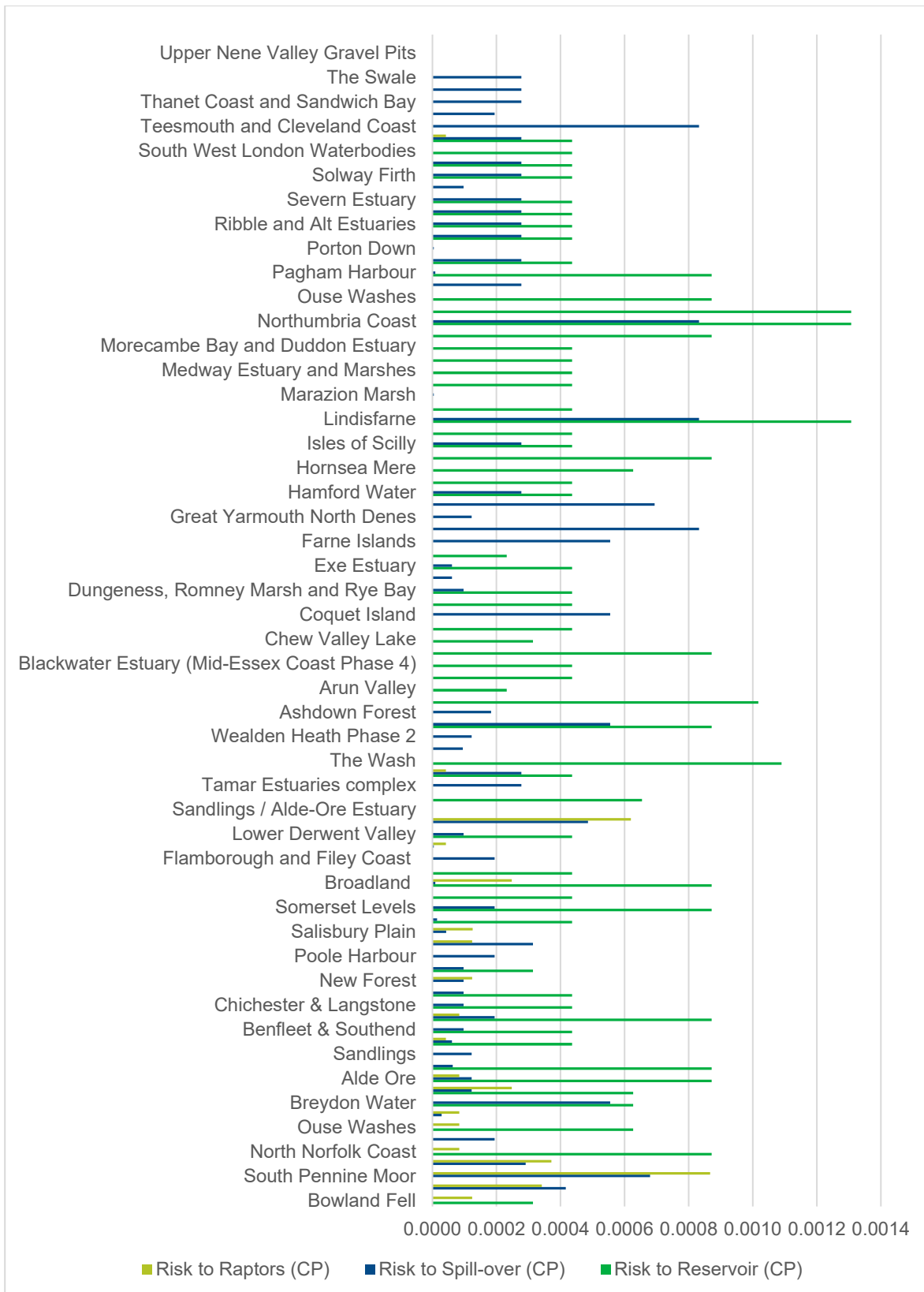


Figure 2a: Example of the relative risk score for each SPA, according to numbers of common pheasants released (as applied for in 2023). The scores assume a background level of avian influenza (the acceptable level of risk, where no additional biosecurity measures are required for poultry).

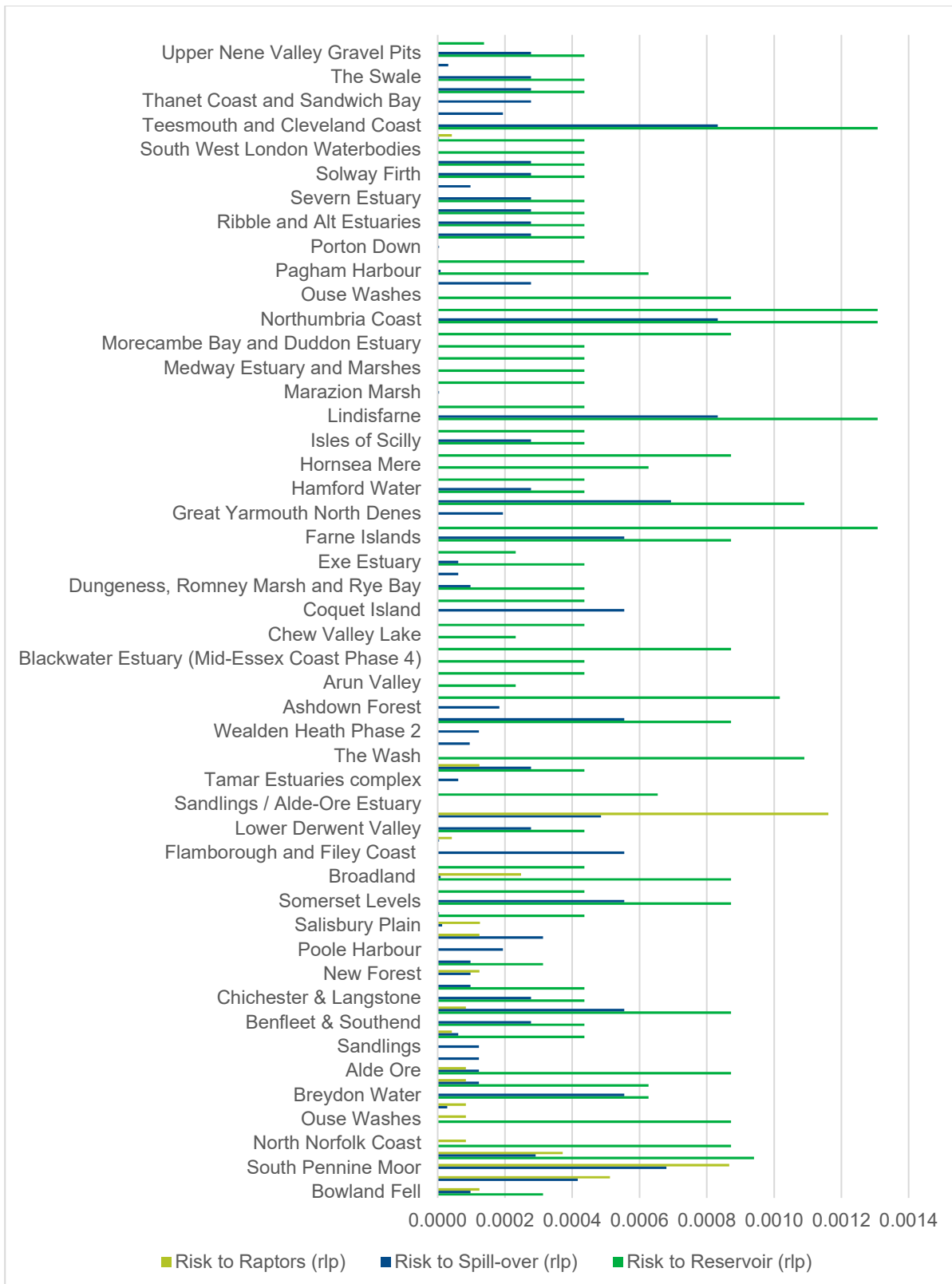


Figure 2b: Example of the relative risk score for each SPA, according to numbers of red-legged partridges released (as applied for in 2023). The scores assume a background level of avian influenza (the acceptable level of risk, where no additional biosecurity measures are required for poultry).

Numbers of gamebirds being released at a site can be changed as needed, as can the presence of feature wild birds at the site.

A regulatory risk manager can decide on the value on the x axis, above which management is needed and below which is an acceptable level of risk. If the score generated is less than 0.001 for all sites it would not be recommended to apply management at any of the sites. This would be based on a background level of risk and common pheasants or red-legged partridges being released at the numbers applied for last year (almost 40,000 birds). This score has been determined by assuming a constant level of circulation of low pathogenic avian influenza viruses in a small proportion of the wild waterfowl. This may occasionally give rise to an outbreak at any time of the year, including outside the migration season.

Using the same baseline level of 0.001 (or the acceptable level of risk), several sites would merit some risk management measures to reduce the risk. The tool weights heavily for mass mortalities and poultry outbreaks because it suggests there is a high level of environmental contamination in that area.

Figures 2a and 2b were generated on 14th June 2024, using the most recent available case data 9 the most recent case data at the time. No HPAI cases had been detected in 8 weeks, and the most recent thereafter were 11 weeks old.

Impact score

The impact has been scored without the sensitivity associated with the number of gamebirds released. The assumption is that infection is introduced into the site, and this scores the impact on the site, according to the category of species present.

The value of the combined risk score may vary with the introduction of a new strain of HPAIV and emerging evidence of any species-specific vulnerability to disease. To determine whether there would be an impact at a specific SPA if HPAI were to be introduced in the features, this would depend on:

- the anticipated rate of spread within the population
- the size of the population
- the case fatality rate
- the reproductive rate of the population

For the purpose of the tool, we presume:

- small dabbling ducks have a low case fatality rate (CFR) and can recover from infection
- large waterfowl such as geese and swans show a higher CFR (based on evidence from the Abbotsbury swannery site)

Birds of prey have a CFR of around 50%, although it is greater in younger birds.

For spill-over birds in which infection spreads via direct contact, CFR can be high. However, there is a lot of uncertainty because these birds are not often picked up or sampled in the UK surveillance programme. During the breeding period for some of these birds, unless they are colony breeding birds, there is little interaction with other birds. Therefore, to measure the impact, the tool uses risk factors (RF):

1. Immediate impact on the wild bird population.
2. Ability of a wild bird population to maintain circulating infection, thereby expanding the epizootic across seasons.
3. The recovery of the population.

Table 3: Risk factors, definitions and scoring for the impact of HPAI on wild bird species

Population dynamic Risk Factor (RF)	Population risk descriptor	Score (based on relative risk and expert opinion)	Example species at risk and other considerations
RF1: Immediate impact of disease on the species at risk	Bird has low susceptibility, with low case fatality rate, good recovery, reservoir	1	Reservoir species, for exam Anatidae and birds which overwinter in high numbers
RF1: Immediate impact of disease on the species at risk	Bird has medium susceptibility, with medium case fatality rate, uncertain recovery, not reservoir	10	Ground nesting non-reservoir species and summer colony breeding populations
RF1: Immediate impact of disease on the species at risk	Bird has high susceptibility, with high case fatality rate, no recovery, not reservoir	20	Raptors
RF2: Ro for species transmission = Extending the epizootic	Transmission within and between species with high case fatality rate	2	Short duration, little environmental contamination except around nest site
RF2: Ro for species transmission = Extending the epizootic	Transmission within and between species with medium case fatality rate	5	If little interaction between the birds then the impact is reduced

RF2: Ro for species transmission = Extending the epizootic	Transmission within and between species with low case fatality rate	20	Long duration of epizootic at the site, in winter, could be several weeks
RF3: Species recovery - "S" or "R" breeder	Species population recovery good (only young affected, large effective population breed more than 1 clutch per annum)	1	Low impact due to population recovery
RF3: Species recovery - "S" or "R" breeder	May breed more than one clutch but adults and young affected	5	Medium impact where there is a high number of offspring
RF3: Species recovery - "S" or "R" breeder	Limited number of breeding pairs, slow to breed, one clutch only	10	High impact where breeding pairs are limited

Each SPA has a unique combination of features and differing population sizes. For each, the sensitivity of the site to the introduction of disease by gamebirds can be assessed as potential impact. A bound is given, below which the impact is considered minor (see Figure 3 - SPAs that fall below this bound are colour coded orange to indicate minor impact).

It can be seen from Figure 3 that sites such as North Pennine Moors are more vulnerable to the impact because of the high number of birds of prey. Birds of prey have a slow recovery time and vulnerable young. This is in comparison to sites such as:

- Minsmere-Walberswick, where there are breeding raptors but a main population of waterfowl assemblage – the waterfowl will recover quickly (with multiple clutches of several young in one breeding season), but also act as reservoir species, extending the length of the epizootic
- the Wash, where very few gamebirds were released, even though the wild birds present would act as an efficient reservoir species and maintain circulating disease for longer

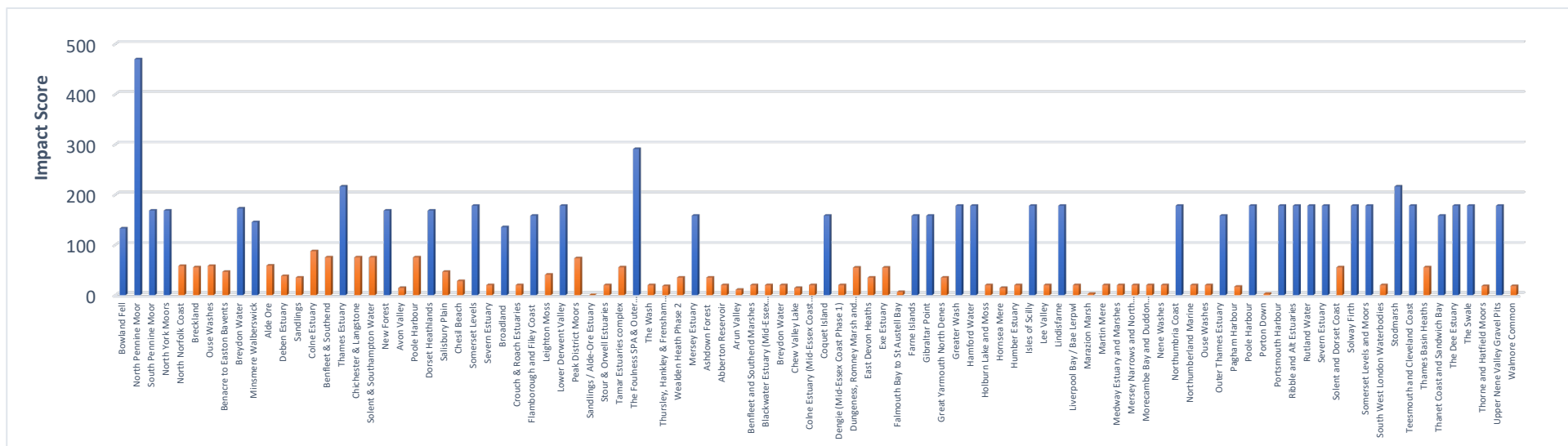


Figure 3: Vulnerability to infection of populations of features at SPAs based on their likely case fatality rate, breeding rates and population size.

It is also possible to express these 'vulnerability' scores against the prevalence or the likelihood of disease incursion given the number of gamebirds (Figure 4). For example, Peak District Moors (PDM) scores higher than North Pennine Moors (NPM) on impact. However, the likelihood of incursion is higher at NPM under current prevalence levels.

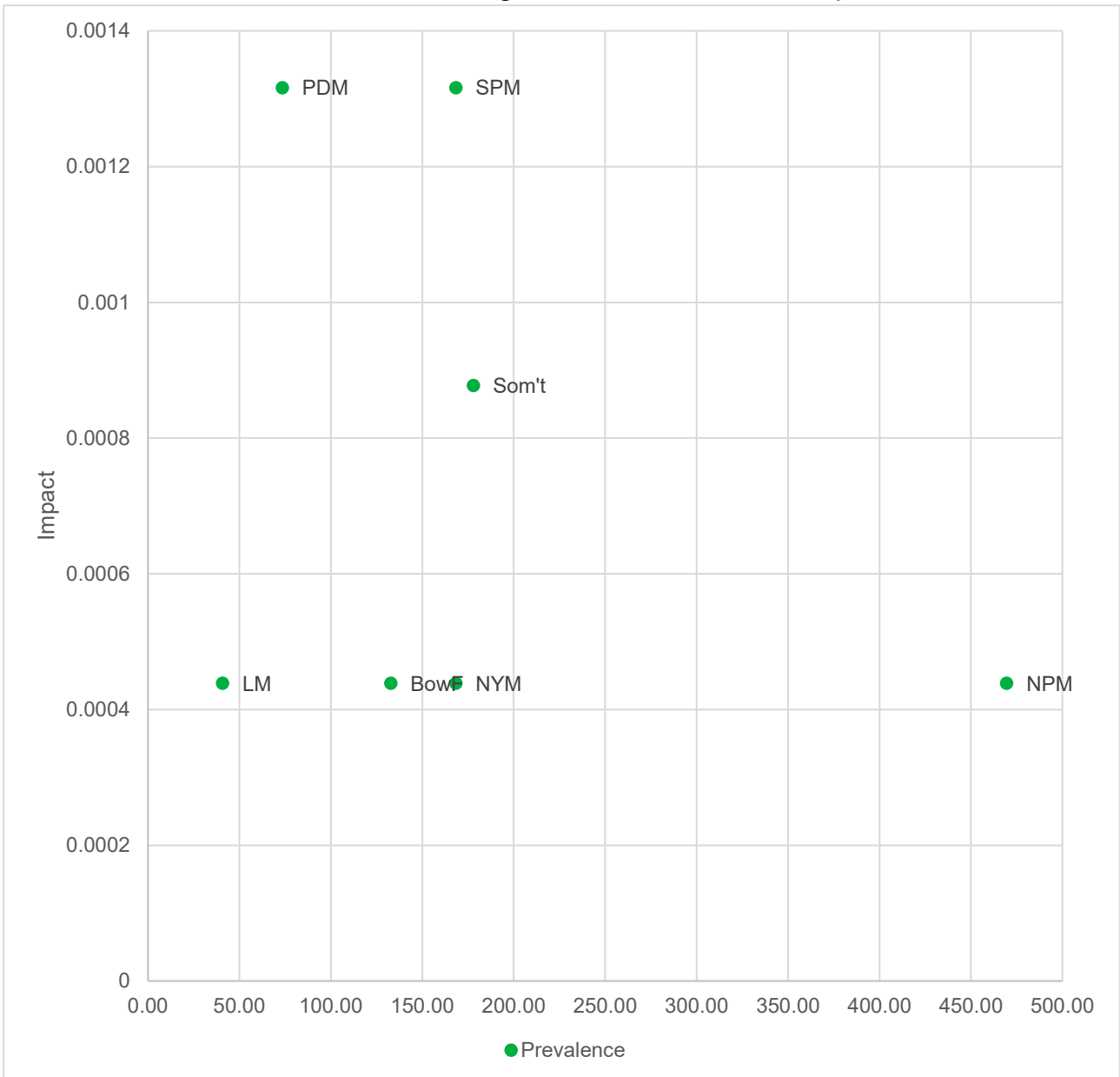


Figure 4: Prevalence of HPAI H5N1 at a reduced selection (for ease of readability) of sites, based on proximity to local cases and vulnerability score for the site.

Importance of biosecurity

The integration of risk management measures can be done through reducing the:

- probability of a gamebird to be infected in the first place
- level of contact with the wild bird species

In EFSA (2017), expert elicitation was used to consider various biosecurity measures that could be applied on a poultry holding to reduce the likelihood of either entry or spread. From this process, the following conclusions were drawn.

If a poultry holding has very high biosecurity, this can have a 264-fold reduction in the risk of incursion. Very high biosecurity means the holding applies all possible biosecurity measures, including airlocks, designated clothing and footwear, housing with all vents covered by small gauge mesh and rodent control. This type of biosecurity is very costly and difficult to keep in place over the long term and therefore it is only suitable in a few instances. For example, certain commercial breeders may apply these measures.

For other poultry establishments, a combination of risk reduction measures can be used, to varying effect. It is estimated that:

- preventing access of birds to outdoor water bodies will reduce the risk by three-fold
- housing will reduce the risk by a further two-fold
- implementing other biosecurity measures, such as general care over sharing equipment, boot dips and rodent control, will reduce the risk by four-fold

This is based on reducing the incursion risk from 100 wild birds in the local environment. The following 2 diagrams are taken directly from EFSA AHAW Panel and others (2017). Taking the average gamebird establishment as having equivalent biosecurity as a backyard premises (NEEG, Personal Comment), there are several biosecurity measures considered unfeasible and not effective.

In terms of incursion, this suggests that certain biosecurity measures were seen as very difficult to apply and not effective. These include cleansing and disinfecting vehicles, disinfecting equipment, carcass disposal and waste collection. However, under the expert elicitation, these were considered partially feasible for gamebird establishments.

On the other hand, some measures were seen as feasible and effective in both the EFSA expert elicitation and this study. These include biosecurity training, restricted access, closed bedding storage, health monitoring and preventing mammal access.

Therefore, it is reasonable to consider that the fold reduction in risk of incursion and spread could be increased by implementing these measures. This is provided they are sustained throughout the period while birds are captive. However, these cannot entirely reduce the risk, even when applied regularly.

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Annex

Example text going into the HRA

'The GWRAT identifies the semi-quantitative likelihood of a series of pathways through which avian influenza can influence the risk posed to the SPA conservation objectives by release of gamebird species, based on the current HPAIV situation, as follows: For SPAs at a very low risk (background); low risk; medium risk; high risk, according to the EFSA definitions. These qualitative risk levels are applied based on the logarithm of scores generated by the GWRAT.

Annex Table 1: EFSA risk level definitions

Risk level	Definition
Negligible	Event is so rare, does not merit consideration
Very low	Event is very rare, but cannot be excluded
Low	Event is rare, but does occur
Medium	Event occurs regularly
High	Event occurs very often
Very high	Event occurs almost certainly

Specifically, the potential impact of gamebird release on the feature groups is as follows for CP: Reservoir 0.0001; Raptors 0.0000; Spill-over 0.0000; and as follows for RLP: Reservoir 0.0000; Raptors 0.0000; Spill-over 0.0000. So, with the current level of AI prevalence the risks posed by gamebird release on Leighton Moss SPA fall substantially below the 0.001 risk threshold, suggesting that no management conditions are needed.'

Expert elicitation

This project uses the EFSA process for Expert Knowledge Elicitation (EKE) using the Delphi method (written elicitation with feedback loops) [Guidance on Expert Knowledge Elicitation in Food and Feed Safety Risk Assessment](#). The goal of EKE is to produce a

probability distribution for the uncertain quantity. The guidance results in an outcome where the experts' judgements are converted to a distribution.

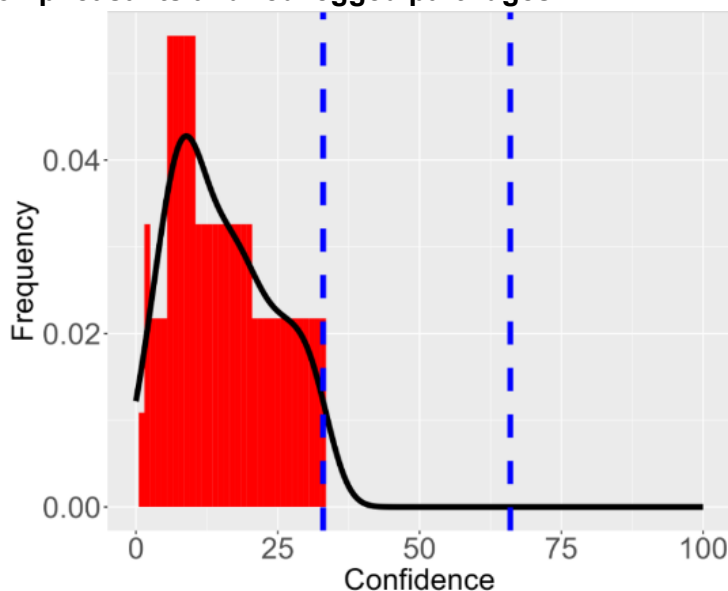
It is important to recognise that a fitted distribution implies many judgements that the expert has not been asked to make. For instance, the expert might have expressed the judgement that the probability that X is less than 2 is 25 %, while the probability that it is less than 5 is 50%. The fitted distribution will imply a probability for X being less than 3 (and indeed for every value between 2 and 5). It is good practice, therefore, to verify that the fitted distribution is a reasonable representation of the expert's views. The processes known as feedback and overfitting can be useful in this task.

A related challenge arises when judgements are elicited from multiple experts. However, as a single judgement is required, opinions must be aggregated in some way. This aggregation can be done by the experts themselves, through a process of interaction between experts that is designed to encourage them to reach a consensus view (known as behavioural aggregation).

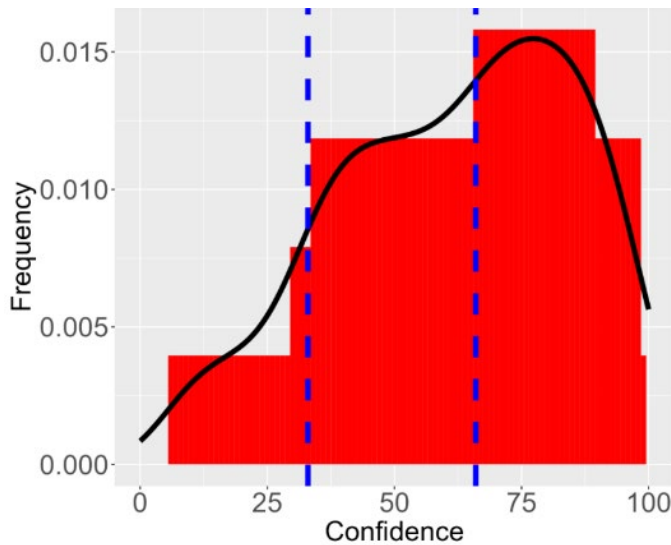
The following questions were given to a group of experts. The probability distribution is shown for the final outcome. These opinions are used to inform the parameters of the tool.

The final question (12) is the outcome of a baseline question. This shows there was a variation in the answers to what was expected to be a simple question that would be answered with a narrow distribution

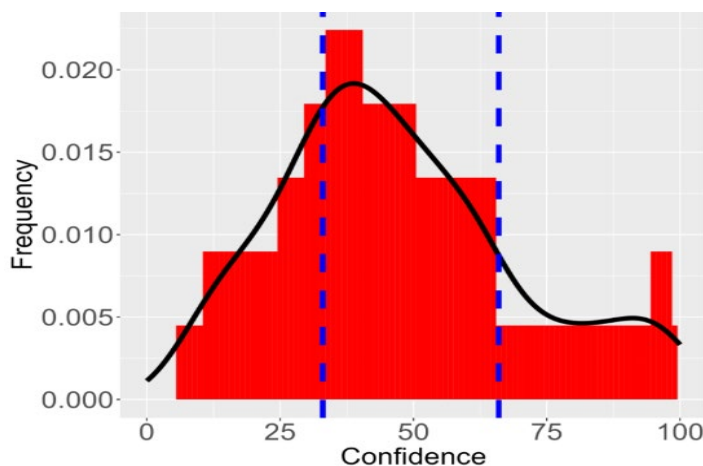
Annex Figure 1: How certain are you that there is no difference in the infection rate of common pheasants and red legged partridges?



Annex Figure 2: How certain are you that there is a five-fold difference in the infection rate of common pheasants compared to red legged partridges?

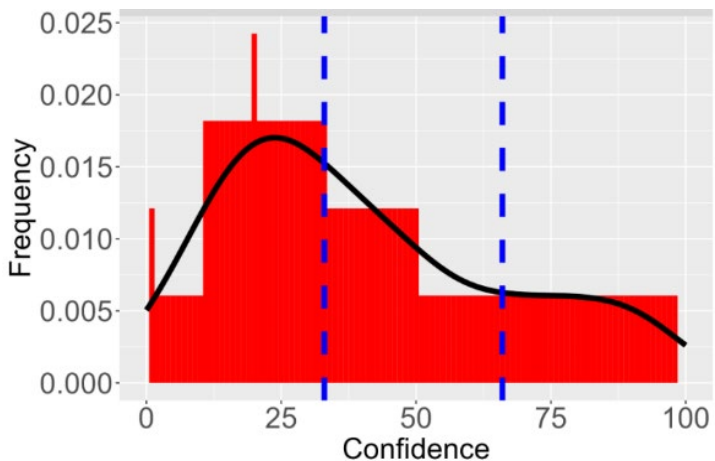


Annex Figure 3: How certain are you that there is a ten-fold difference in the infection rate of common pheasants compared to red legged partridges?

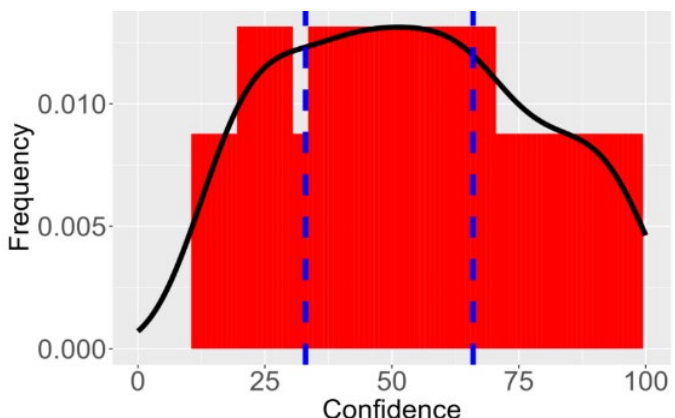


Annex Figures 1 to 3: Responses to questions regarding difference in infection rate between common pheasants and red-legged partridges. Peak confidence in there being no difference between the 2 species was 10%. Peak confidence in there being a five-fold difference in infection rate in pheasants compared to partridges was approximately 75%. Peak confidence in there being a ten-fold difference was approximately 40%. Therefore, we can conclude that expert opinion agreed there was difference between the infection rate of pheasants and red-legged partridge. The difference could be between 5 and 10 times higher rate of infection in pheasants than partridges.

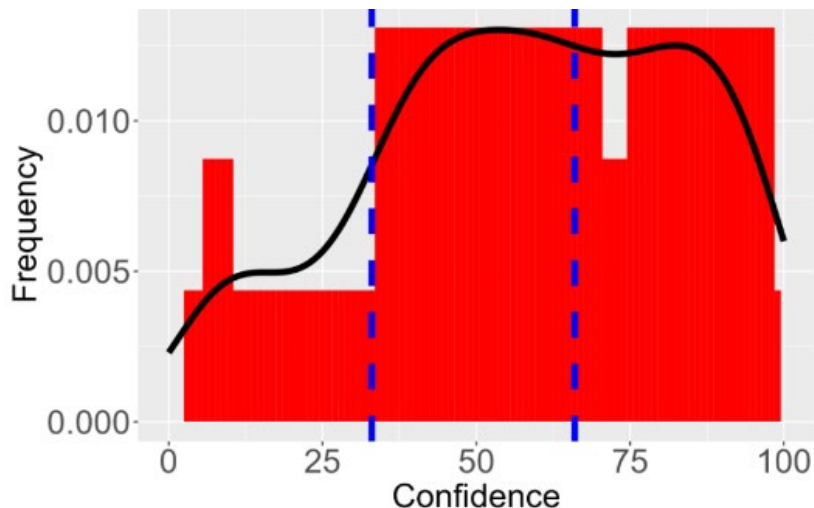
Annex Figure 4: How certain are you that a predator bird (such as hen harriers and peregrines), which comes into contact with an infected bird by consuming it, is as likely to become infected as a reservoir bird (waterfowl) which comes into contact an infected bird via a contaminated environment?



Annex Figure 5: How certain are you that a predator bird (such as hen harriers and peregrines), which comes into contact with an infected bird by consuming it, is 5 times as likely to become infected as a reservoir bird (waterfowl) which comes into contact an infected bird via a contaminated environment?

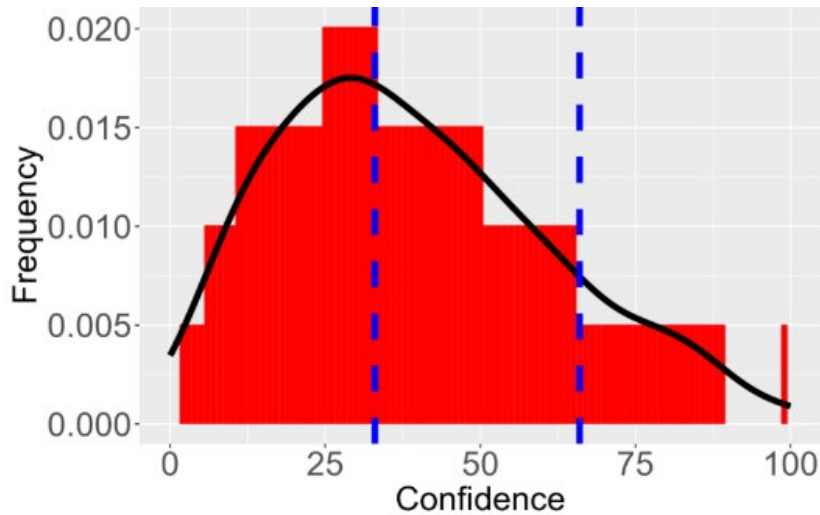


Annex Figure 6: How certain are you that a predator bird (such as hen harriers and peregrines) which comes into contact with an infected bird by consuming it is 10 times as likely to become infected as a reservoir bird (waterfowl) which comes into contact an infected bird via a contaminated environment?

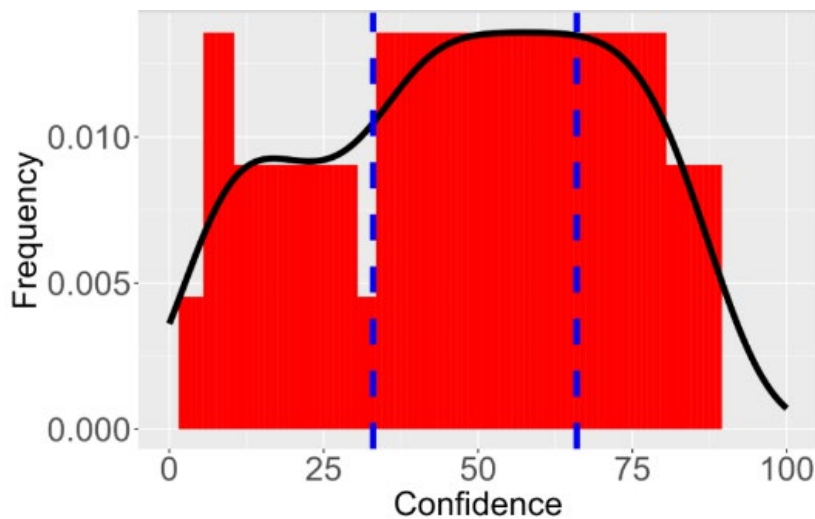


Annex Figures 4 to 6: Responses to questions regarding difference in likelihood of infection of birds of prey vs reservoir species. Peak confidence in there being no difference between the likelihood of birds of prey being infected by consuming infected prey and reservoir species being infected by coming into contact with the virus in the environment or from another bird via close aerosol contact was approximately 25%; peak confidence in there being a five-fold difference in infection rate in birds of prey compared to reservoir species was between 25% and 65%; peak confidence in there being a ten-fold difference was between 50% and 80%. Therefore, we can conclude that a predator is more likely to become infected through eating an infected bird, than waterfowl through contact with the contaminated environment. However, consensus was not reached on the difference (5 or 10 times more likely) therefore 2 to 3 times as likely is used as the parameter.

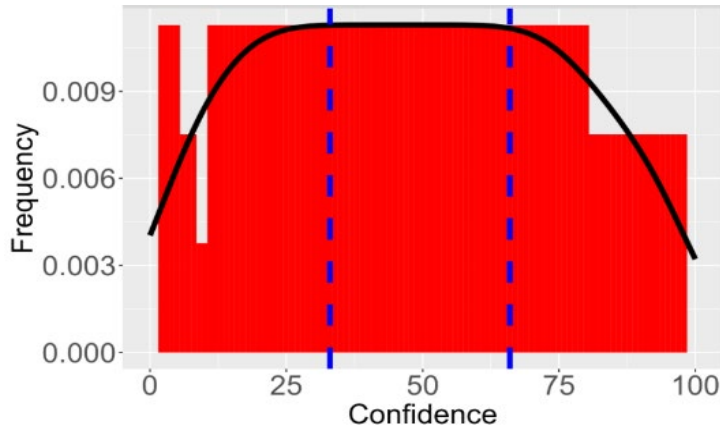
Annex Figure 7: How certain are you that a reservoir bird (waterfowl) which comes into contact with an infected bird via a contaminated environment or aerosol, is as likely to become infected as a spill-over bird (non-waterfowl; non-predator) which comes into contact with a bird via close aerosol contact?



Annex Figure 8: How certain are you that a reservoir bird (waterfowl) which comes into contact with an infected bird via a contaminated environment or aerosol, is 5 times as likely to become infected as a spill-over bird (non-waterfowl; non-predator) which comes into contact with a bird via close aerosol contact?

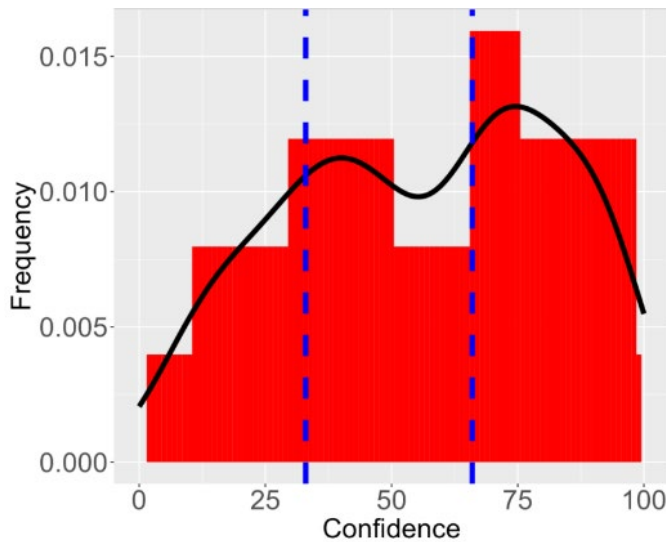


Annex Figure 9: How certain are you that a reservoir bird (waterfowl) which comes into contact with an infected bird via a contaminated environment or aerosol, is 10 times as likely to become infected as a spill-over bird (non-waterfowl; non-predator) which comes into contact with a bird via close aerosol contact?



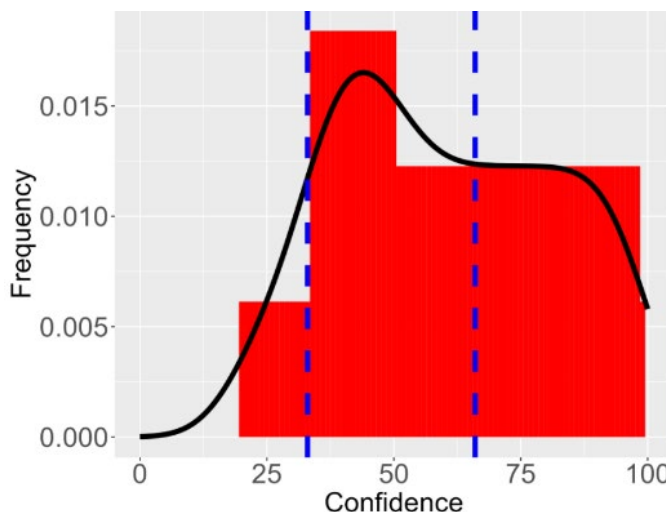
Annex Figures 7 to 9: Responses to questions regarding difference in likelihood of infection of reservoir species vs spill-over species. Peak confidence in there being no difference between the likelihood of reservoir species being infected by coming into contact with the virus in the environment or another bird via close aerosol contact and spill-over species being infected by another bird via close aerosol contact was 30%. Peak confidence in there being a five-fold difference in infection rate in reservoir species compared to spill-over species was between 50% and 60%. Peak confidence in there being a ten-fold difference in infection rate in reservoir species compared to spill-over species was between 25% and 65%. Therefore, we can conclude that a reservoir species (waterfowl) is less likely to become infected through contact with the contaminated environment, than a bird which is in direct contact with an infected bird. However, consensus was not reached on the difference (5 or 10 times more likely) therefore 2 to 3 times as likely is used as the parameter.

Annex Figure 10: How certain are you that the case fatality rate is higher in birds of prey than waterfowl or than spill-over species?



Annex Figure 10: Response to a question about fatality rates in birds of prey compared with the other species groups. Consensus could not be reached on the difference in case fatality rate between birds of prey, waterfowl and spill-over species, with separate peaks in certainty at approximately 38% and approximately 73%. During the discussion, several experts pointed out the high CFR of swans and geese at certain sites and the absence of data for spill-over species.

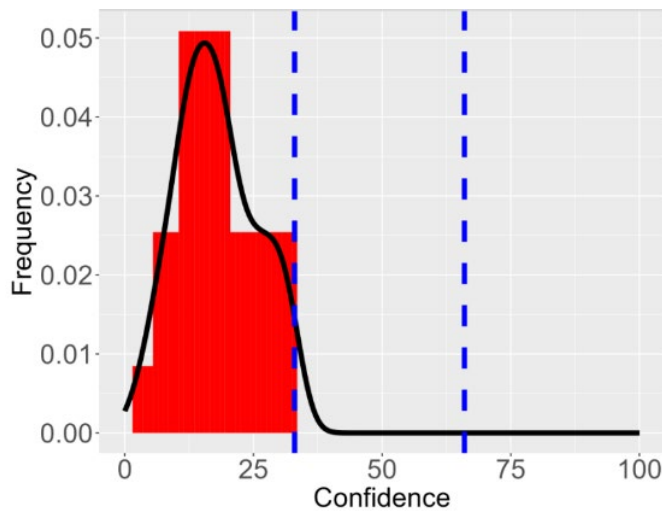
Annex Figure 11: How certain are you that differences in the likelihood of infection of SPA features are suitably represented by the 3 categories: reservoir species, spill-over species and predator species?



Annex Figure 11: Response to a question about the suitability of the species categories used to represent the difference in infection likelihood between species features. Peak confidence is at approximately 42% but the majority of votes were for between 50% and 100%. The group was reasonably confident that 3 categories could be used, but

discussion highlighted that there was a large variation in the species in each group which was provided to them for evidence, and that some of the species, such as certain sea birds, should probably be considered as reservoir species not spill over species.

Annex Figure 12: How certain are you that farmed domestic ducks and geese are as likely as farmed domestic chickens and turkeys to show a very high case fatality rate following infection with H5Nx?



Annex Figure 12: Response to a baseline question. Certainty peaked at approximately 15%. Consensus for the baseline question was reached, but there was still quite a wide distribution for what was expected to be a narrow probability.