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AviFluMap: An interactive tool to assess H5N1 avian influenza incursion risk in Australia via migratory birds

Tobias A. Ross [a,*], Sara Ryding [a], Simeon Lisovski [b], Joris Driessen [c], Emily Mowat [c], Stephanie Todd [c], Chris Purnell [c], Aaron Spence [d], Simone Vitali [e], Hui Yu [a], Marcel Klaassen [a]

[a] School of Life and Environmental Sciences, Deakin University, Geelong, VIC 3216, Australia
[b] Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research, Section Polar Terrestrial Environmental Systems, Potsdam 14473, Germany
[c] Birdlife Australia, Melbourne, VIC 3053, Australia
[d] School of Information Technology, Deakin University, Geelong, VIC 3216, Australia
[e] Wildlife Health Australia, Canberra, ACT 2602, Australia

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ABSTRACT

The current panzootic of clade 2.3.4.4b H5Nx high pathogenicity avian influenza (H5 HPAI bird flu) has resulted in unprecedented global impacts on both wild bird populations and poultry industries. Despite the virus' near-global circulation, Australia remains free of this strain. In response to the need for proactive biosecurity and conservation planning, we developed AviFluMap, an interactive tool that integrates global data on H5 HPAI events in birds, migratory bird pathways, species susceptibility assessments, and bird aggregation maps to evaluate the incursion risk and establishment of H5 bird flu via wild birds, with special reference to Australia. AviFluMap (https://hpairisk.deakin.edu.au) provides a transparent, data-driven platform for use by a range of stake holders such as wildlife managers, government agencies, researchers, and livestock industry, to support H5 bird flu preparedness and response planning. This article outlines the structure and functionality of AviFluMap, its data sources and methodology, and its role in informing risk-based surveillance and preparedness strategies.

1. Introduction

Since the turn of the century, H5 high pathogenicity avian influenza (HPAI) viruses have been increasingly emerging along with the increase in global poultry production. These viruses massively burden the poultry industry, and increasingly wild birds, as well as domestic and wild mammals and humans (Klaassen and Wille, 2023). The goose/Guandong lineage of HPAI H5N1 emerged in 1996 (Xu et al., 1999) and gave rise to a lineage known as H5Nx clade 2.3.4.4b (hereafter, 'H5 bird flu') currently causing a global panzootic with unprecedented impacts on wild birds and on mammals (both domestic and wild) (Bellido-Martín et al., 2025; Koopmans et al., 2024).

Assisted by the movement of migratory birds, since October 2021 H5 bird flu has spread to all continents, except Australia (Wildlife Health Australia, 2025a; Wille et al., 2024a; Wille et al., 2024b; Wille et al., 2025). Understanding the potential role of wild birds in introducing and spreading HPAI virus is an important aspect of preparedness and response planning for Australia. If this specific virus reaches Australia, it will have significant impact on Australia's unique wildlife and will cause major socio-economic consequences (Ryding et al., 2025a; Ryding et al., 2025b). The H5 bird flu incursion risk assessment for Australia (Wildlife Health Australia, 2023) includes information on the ecology and evolution of avian influenza and their avian hosts. However, the likelihood of H5 bird flu incursion to Australia via wild birds, and of its subsequent establishment and spread, is fluid and requires an information tool that provides critical and current, disease-risk related information.

Here, disease risk refers to the likelihood of H5 bird flu being introduced into Australia via wild birds, as well as the consequences if it were to arrive. That risk varies depending on where, when, and at what intensity HPAI virus is present in overseas countries neighbouring Australia, and whether migratory birds are exposed to and can bring the virus from those locations to Australia. Migratory birds relevant to this risk include shorebirds arriving from Asia or North America between August and November, and wide-ranging seabirds that return to Australia to breed around the same time of year. If H5 bird flu is absent (or circulating in low amounts) at these overseas locations from Australia, migratory birds to Australia may not get exposed and infected to H5 bird flu prior to migration to Australia (Wille et al., 2024a).

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[*] Corresponding author.
E-mail address: t.ross@deakin.edu.au (T.A. Ross).

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However, when H5 bird flu is present at overseas locations visited by birds migrating to Australia, bird species may vary in their susceptibility to exposure and infection. Moreover, any migratory bird that does get exposed and infected must stay healthy enough to successfully migrate to Australia while remaining infectious (Risely et al., 2018).

If a H5 bird flu virus incursion into Australia occurs, establishment and further spread depends on where and when it arrives, whether susceptible species are present at that location in sufficiently large numbers and density to sustain ongoing transmission, and the extent of interaction between infected and susceptible birds (Lisovski et al., 2018). Understanding the role of wild birds in introducing and spreading the HPAI virus is crucial for Australia's preparedness and response planning. To provide insights in these highly dynamic processes, the AviFluMap tool (https://hpairisk.deakin.edu.au) integrates datasets on H5 HPAI outbreaks (including H5Nx clade 2.3.4.4b H5 bird flu), bird migrations, species at risk, and susceptible bird aggregations on the Australian continent. The tool will continue to evolve alongside major developments of the current global panzootic, with new data added with these developments. AviFluMap's dynamic nature enables stakeholders to better evaluate the contemporary risk and understand the potential role of wild birds to introduce and spread H5 bird flu in Australia, based on global data. While being designed to notably serve stakeholders in Australia, the unique level of data integration and presentation will be of interest to stakeholders globally.

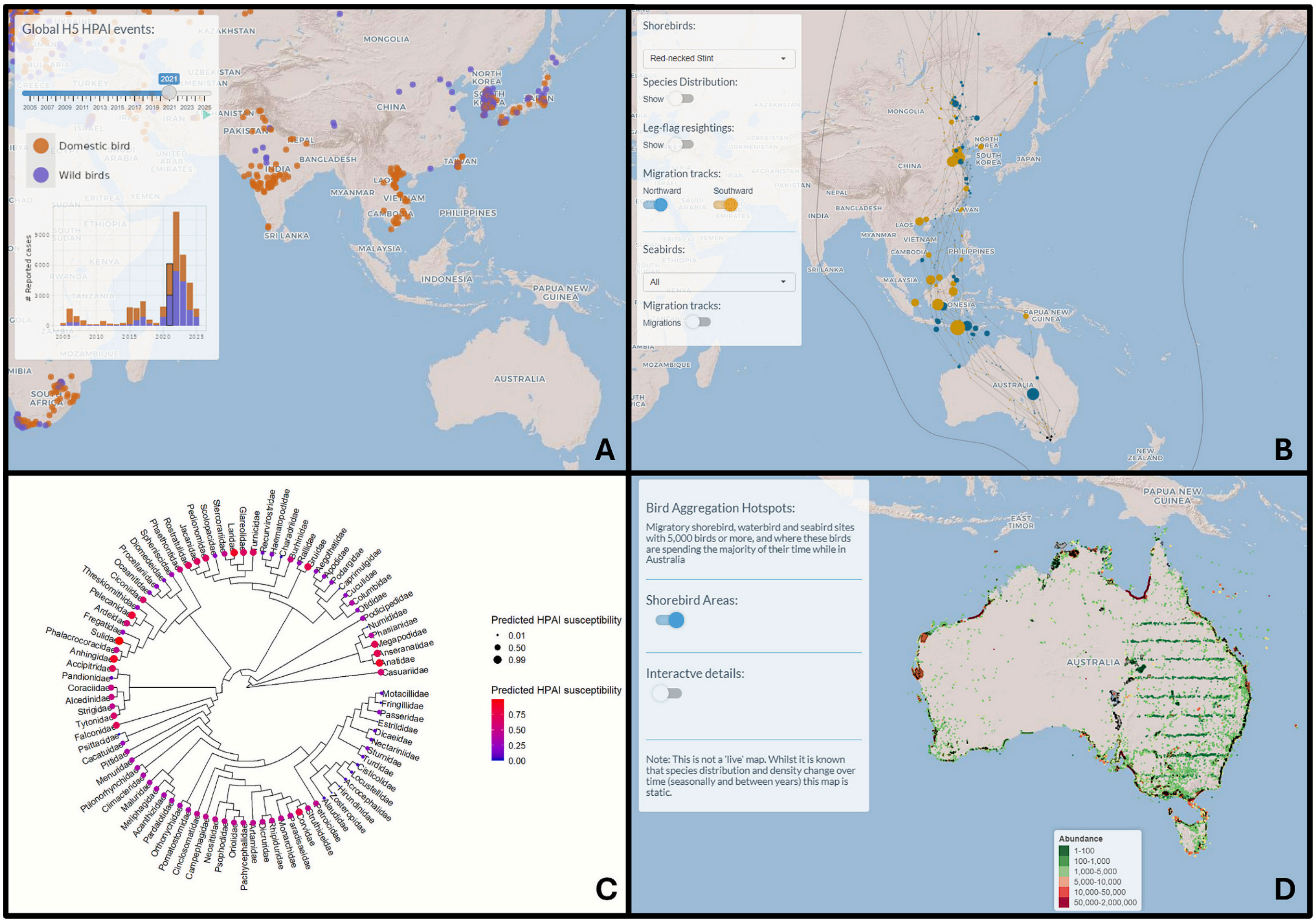
2. Methods

2.1. Data inputs and sources

AviFluMap is a web-based tool developed in the R environment, using the shiny package (Chang et al., 2025). It provides an integrative platform for exploring data on H5 bird flu events in birds, bird migration routes, species susceptibility, and high-density bird aggregation sites within Australia (Fig. 1).

2.2. H5 HPAI Event map data

The interactive, zoomable outbreak map tool (Fig. 1A) makes use of OpenStreetMap (OpenStreetMap contributors, 2025) and shows the locations of H5 HPAI events from the World Organisation for Animal Health (WOAH) World Animal Health Information System (WAHIS) (World Organisation for Animal Health, 2025). We focus on H5 HPAI events in both wild and domestic birds, using all H5 HPAI event data compiled in WAHIS since 2005. Since October 2021, the majority of H5 HPAI events captured in WAHIS relate to HPAI H5N1 clade 2.3.4.4b (H5 bird flu). Each event recorded in WAHIS includes the number of cases and deaths by species. All records are from outside of Australia, as no H5 bird flu outbreaks have been reported in Australia to date. The user can interact with the map by selecting the time period and geographic focus using simple features (sliding timescale and map zoom functions). This



Migratory shorebird, waterbird and seabird sites with 5,000 birds or more, and where these birds are spending the majority of their time while in Australia

Note: This is not a 'live' map. Whilst it is known that species distribution and density change over time (seasonally and between years) this map is static.

Fig. 1. Four information tabs from AviFluMap. A) Global H5 HPAI Event map, showing all reported cases in 2021, in both domestic and wild birds. B) Bird Migrations map, showing all Northward and Southward migration maps of the selected species Red-necked Stint. C) Species at risk tab figure, showing relative predicted HPAI susceptibility of Australian bird families. D) Bird Aggregations map, showing abundance of birds across Australia (green through to red), as well as shorebird sites (5000+ birds or more) in black (shaded) polygons. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

temporal and spatial exploration helps users to visualise the global spread of H5 viruses—how far, how fast, and along which potential routes.

2.3. Bird migrations data

Globally, migratory ducks are often considered the primary vector for transporting avian influenza. This is not the case for Australia due to a lack of long-distance waterfowl migration beyond the Australo-Papuan region (Wildlife Health Australia, 2023; Wille et al., 2022). Instead, introductions of avian influenza strains to Australia are more likely to be due to long-distance migratory shorebirds linking Australia to regions north of the continent with active influenza circulation (Wille et al., 2019). Current efforts on surveillance and risk assessment for incursion of HPAI H5 into Australia has focused primarily on these pathways of wild bird movement. Migratory seabirds are also considered a H5 bird flu incursion risk to Australia due to increasing occurrence and spread of H5 bird flu through the Antarctic continent and Southern Ocean (Clessin et al., 2025; Gorta et al., 2025; Kuiken et al., 2025). Foraging seabirds may travel between Australia and Antarctica, whilst pelagic seabirds move around the Southern Ocean; thus they may also link Australia to circulating infection, via incursion from the south.

The Bird Migrations tab's interactive map presents migration routes of selected shorebird and seabird species (Fig. 1B). Wildlife Health Australia (2023) identifies all shorebird and seabird migrants from the northern hemisphere as potential vehicles to introduce H5 bird flu to Australia. However, in our map we limited data to a few representative species, focussing on species that:

- have large Australian, non-breeding wild bird population sizes,
- are known to be susceptible to low (Wille et al., 2023) and high (Ryding et al., 2025a) pathogenicity avian influenza infection,
- suitably represent specific migration routes and strategies (Lisovski et al., 2024),
- and for which high-quality resighting or tracking data are available.

The interactive map depicts resighting data from leg-flagged shorebirds and other marks, sourced from the BirdMark portal (www.birdmark.net; Deakin University, 2025), as well as tracking data from several shorebird species, primarily from light-level geolocators (collected by the Australasian Wader Studies Group, Global Flyway Network, Queensland Wader Study Group, and Victorian Wader Study Group; for data sources, see Lisovski et al., 2024; Victorian Wader Study Group, 2025) and two common species of shearwater (pers. comm. John Arnould, Deakin University). Collectively these data detail when and where these birds visit Australia from locations within the East Asian-Australasian Flyway, as well as movement to and from Antarctic waters.

The phenology or timing of migrations in this interactive map is of specific relevance, as it identifies the austral spring as a high-risk period for HPAI incursion risk. This corresponds with the arrival of migratory birds to Australia (Wille et al., 2024a). Because of increasing spread of H5 bird flu across the Antarctic and sub-Antarctic Islands (Clessin et al., 2025), the tracking data of shearwaters and notably short-tailed shearwater (*Ardenna tenuirostris*) is of particular relevance. Short-tailed shearwaters breed in their millions along Australia's southeastern shores and often feed in (sub-) Antarctic waters. Although Procellariiform species such as short-tailed shearwaters appear not particularly susceptible to HPAI infection (Ryding et al., 2025a), given their sheer numbers they could still have a potential bridging function in bringing H5 bird flu to Australia when they arrive in late spring from the south (Kuiken et al., 2025).

Users can interact with the map by selecting specific shore- and/or seabird species, and choosing whether to display species' distributions, re-sightings, and tracking data including both north- and southward migration tracks. This offers a dynamic visualisation of when and where potential incursion risk may be elevated based on bird movements.

2.4. Species at risk data

The “Species at risk” model (Fig. 1C) demonstrates how family-level phylogeny and ecological traits influence HPAI infections, to then infer susceptibility of Australian birds to HPAI infection (see Ryding et al., 2025a). The results are based off a phylogenetic analysis of HPAI infections reported to the WOAH WAHIS database since 2021, which carries in it some inconsistencies in reporting (Klaassen and Wille, 2023). However, while imperfect, WAHIS provides the most comprehensive resource of global HPAI events, and thus enabled us to investigate the impact of ecology and phylogeny and predict onto Australian species much more comprehensively than if we had used a more local sample. Furthermore, by investigating HPAI infections at a family-level, we were able to avoid biases associated with missing species that are specific to certain regions, while families are more likely to be captured even when considering underreporting in certain regions. More details on the analysis and interpretation can be found in (Ryding et al., 2025a). Australian families of ducks and geese, gannets and boobies, and gulls and terns were predicted to have some of the highest susceptibility to HPAI H5N1. In the context of AviFluMap, the term “HPAI susceptibility” refers to the likelihood that a given bird species will become infected with H5 bird flu and subsequently develop disease due to infection, act as a reservoir for its maintenance, and/or assist in the spread of the virus. Susceptibility is rescaled to go from one to 80, to allow for more intuitive visualisation of the results – detailed results on susceptibility can be found in Ryding et al., 2025a. The degree to which species within a family are susceptible to infection and sickness/death may vary, as evidenced by recent research suggesting that Australian Black Swans (*Cygnus atratus*) may be more susceptible to HPAI infection than other swan species (Karawita et al., 2023). This within-family detail is difficult to predict, so instead the modelling assumes that all species within a family will have the same level of susceptibility. While this assumption might be problematic for certain cases, like the Australian Black Swan, the high phylogenetic signal indicates that susceptibility is conserved among related birds. Because the majority (~98 %) of H5 bird flu wild bird events in the WAHIS database since October 2021 report deaths for the species recorded, AviFluMap assumes that a species' predicted susceptibility to infection is closely linked to a species' predicted likelihood of experiencing sickness and death. Based on the events in WAHIS, there have been over 13,000 events relating to H5 bird flu in wild birds, involving approximately 135,000 individuals, across 20 orders and 390 species of birds, since the start of the panzootic (1 October 2021 to 1 July 2025). However, due to biases outlined in Klaassen and Wille (2023) and also evidenced by meticulous analyses of published material to date (Knief et al., 2025), these data are an indication only and the true numbers are likely much higher, and in the millions.

2.5. Bird aggregations data

Aside from species susceptibility to H5 bird flu infection (Ryding et al., 2025a), the incursion, establishment and spreading risk are also importantly determined by the number of H5 bird flu arrivals and their pattern in space and time. Thus, where dense concentrations of susceptible species reside in Australia is also of critical importance (Lisovski et al., 2018). The interactive Bird Aggregations map (Fig. 1D) incorporates static data on high-density bird areas, identified from five national databases. Relevant data for 30 families of shorebirds, seabirds and waterbirds inhabiting the Australian mainland and off-shore islands was consolidated from Birdlife's Birdata database, Australian Shorebird Monitoring Project, Colonial Nesting Birds Project (Birdlife Australia, 2025a), the Colonial Waterbird database and Eastern Australian Waterbird Survey (UNSW Sydney, 2025), and the Australian Seabird Colony Register. Given the methods for data collection and spatial referencing vary between these databases, it is difficult to reliably ascertain the true footprint of a particular population or habitat utilised. For example, a datapoint may represent a survey of birds in a 20,000 ha wetland complex or a 20 ha component of that complex. For this reason, a grid style data representation was employed. Each square in the map symbolises the maximum recorded bird abundance in a given 5 km^2 area in the last 15 to 25 years (shorebird and waterbird aggregations: 15 years; seabirds and waterbird breeding colonies: 25 years). This approach also allows representation of habitat at a scale relevant to management.

For databases utilising independent identifiers for sites, data points were aggregated at the 5 km^2 grid scale to determine an overall abundance. For databases with non-standardized site networks, the maximum for each 5 km^2 grid cell was used. Each grid cell in Australia was attributed the maximum abundance recorded from each of the five databases. The maximum of these numbers (100–⟩50,000 individuals) was then represented on the map as one of six categories along a colour gradient. Where breeding colonies were identified, each neighbouring grid cell was ascribed the next lowest category to accommodate the colony's likely minimum foraging footprint beyond the 5 km^2 grid. Maximum counts derived from the Australian Shorebird Monitoring Project were replicated across the extent of mapped "Shorebird Areas" identified by BirdLife (Weller et al., 2020). The map can be interacted with to zoom into specific regions and show mapped extent of shorebird habitat where birds that might bring H5 bird flu to Australia may congregate. Furthermore, the map can show interactive details such as maximum counts of birds at each survey location, and the breakdown of bird families represented in these counts.

3. Results

3.1. Uses of AviFluMap

AviFluMap is designed to provide support to a wide range of stakeholders involved in wildlife health, biosecurity, and environmental management. Below are several example use cases illustrating how the tool can inform planning, risk assessment, and conservation responses to H5 bird flu.

3.2. Policy and wildlife disease surveillance programs

Wildlife disease surveillance program managers (e.g., Wildlife Health Australia), can use the various components of the tool (particularly bird migration, species susceptibility and bird aggregation layers) to guide the design of the sampling framework for a targeted avian influenza surveillance program in wild bird populations, adapted from those that have been previously conducted in Australia for H5 bird flu specifically by Wille and Klaassen (2023), Wille et al. (2024a), and the National Avian Influenza Wild Bird Surveillance Program (Wildlife Health Australia, 2025b). It also has the potential to support general surveillance (e.g. monitoring and investigation of sick and dead wildlife) by identifying higher-risk locations for virus incursion and spread through understanding overlays between arrival of migratory shorebirds and seabirds, bird aggregations and species susceptibility. Thus, AviFluMap is especially suited to aid early warning and risk-based targeting, which involve prioritising certain species and regions where incursion of the disease is most likely, thereby maximising surveillance efficiency. Other forms of surveillance such as prevalence detection after incursion may require complementary approaches, such as additional longitudinal monitoring alongside the dashboard. Nevertheless, these surveillance measures, coupled with other tabs in AviFluMap, could support national and state biosecurity agencies (e.g., Department of Agriculture, Forests, and Fisheries [DAFF], state environment departments) in assessing seasonal and spatial risk of H5 bird flu incursion into Australia and being best prepared for rapid detection and response.

A suggested approach would be for agencies to consult the Global H5 bird flu Event Map tab to track H5N1 activity since October 2021 along migratory flyways connected to Australia, then identify when high-risk migratory species may move through these regions and arrive in Australia (e.g. in austral spring) using the Bird Migrations tab. The Bird Aggregations tab allows for identification of locations where predicted susceptible species (Species at risk tab) congregate in large numbers — ideal sites for targeted surveillance and biosecurity measures alongside sick and dead wildlife monitoring, which can facilitate an early warning system. Conservation management can also be informed by using Species at risk and Aggregations tabs to identify locations where likely-infected/susceptible species and endangered species overlap, and in turn support prioritisation of species- and site-specific preparedness and surveillance plans. Regions where disproportionate harm to vulnerable species may occur when the disease arrives can have awareness campaigns, enhanced surveillance, and mitigation planning put in place prior to incursion to Australia.

3.3. Habitat management

Managers of Ramsar wetlands, national parks, and other key bird habitats can identify when and where large aggregations of predicted susceptible species occur. This can support planning for access, disturbance minimization during higher-risk periods, or biosecurity protocols at managed sites. Such biosecurity protocols may be particularly relevant in locations where hunting or human activity overlaps with high bird densities. For example, peak abundances (Aggregation tab) of susceptible species (Species at risk tab), coupled with arrival of migratory species (Migration tab) can help flag windows of heightened risk to both the wildlife of the region, and people using it. These can then inform proactive planning such as restricting access to people and implementing hygiene measures during these vulnerable periods.

3.4. Research and communication

Ecologists and epidemiologists can use the map to explore potential links between migratory connectivity, outbreak origins, and local species presence. Researchers can use the platform to generate risk models and inform publications or grant proposals, by providing an accessible interface for stakeholders to interact with complex datasets. Furthermore, the platform can be used in science communication with key stakeholders, supporting relevant authorities and other users to communicate the relevance of bird aggregation and migratory behaviours and highlight major risk pathways to Australia, thus the need for coordinated responses to potential H5 bird flu incursions.

3.5. International conservation agreements

AviFluMap can support reporting and collaboration under international frameworks (e.g., Ramsar Convention on Wetlands of International Importance, Convention on Migratory Species), and bilateral agreements. By providing regularly updated information (notably after major outbreak developments) on migratory species, outbreak proximity, and aggregation sites, the tool can be used to facilitate coordinated regional responses. AviFluMap not only highlights the ecological connectedness of nations along the flyway (underscoring the need for coordinated conservation and biosecurity action) but also provides a data-driven tool to support that coordination. The tool also demonstrates the value of integrating ecological, epidemiological, and movement data to address international conservation challenges, and reinforces the importance of sustained monitoring and collaboration across countries in the East Asian-Australasian Flyway.

3.6. Other uses

Government, industry bodies or veterinary practitioners can use AviFluMap to assess the proximity of predicted susceptible species to domestic poultry operations (Species at risk and Bird Aggregations tabs), species of cultural significance, or rare and valuable captive populations such as zoological collections or breeding facilities, to help local understanding of biodiversity risks and guide biosecurity measures on the ground. For the general public, the tool offers an accessible way to understand how and when migratory birds arrive in Australia (Migrations tab), increasing awareness of avian influenza risks and promoting informed community engagement in disease prevention and bird conservation.

4. Discussion

AviFluMap provides an example of how multiple sources of animal data can be integrated to provide support to situational awareness and risk communication in biosecurity and wildlife health. We integrate disease notifications with species ecology to visualise the spatial risk of exposure and infection posed to Australian species. Comparable efforts to our application include the United States Department of Agriculture - Animal and Plant Health Inspection Service (2025) surveillance dashboard of HPAI in wild birds, University of Minnesota's DashFLUboard tracker (2025), and the European Food Safety Authority's dashboard of HPAI detection in Europe (2025) to name a few. While these dashboards present disease notifications in the northern hemisphere, often combining multiple databases, AviFluMap takes this a step further for Australia. Our application combines elements often treated separately in dashboard-only visualisation or in modelling-only studies (An et al., 2024; Dupas et al., 2024; University of Minnesota College of Veterinary Medicine, 2025), showing not just disease notifications and wild bird movements, but integrating aggregation data and predictive modelling for wild bird susceptibility to HPAI. AviFluMap thus fills a vital need to identify connectivity in migratory networks and how these affect virus exposure and spread.

AviFluMap depends on the availability and accuracy of international outbreak data, which varies in quality and timeliness (Watsa, and Group, W. D. S. F, 2020), and these sources of reporting heterogeneity must be critically evaluated. Additionally, there is uncertainty in the true susceptibility of some species due to reporting biases; some may be more frequently encountered or observed than others, and therefore more easily reported (Lawson et al., 2015). Improving this situation will require better reporting tools, coupled with both greater integration of citizen science observations, and better data-sharing between wildlife health networks and official surveillance systems, but implementing these changes remain complex. For these reasons, we currently offer explicit disclaimers around the usage of the data presented in the tool. As a precautionary approach, decisions on wildlife risk mitigation strategies should be based on an understanding of this uncertainty, especially when considering species for which there are currently low or no reported cases of H5 bird flu, and where the risk may be underpredicted. When interpreting the presented data, it should also be noted that the WAHIS data relies on reporting by countries that may differ markedly in their level of screening and reporting of HPAI in domestic and wild birds. Species and geographic regions may be over- or underrepresented depending on the wild bird HPAI event reporting processes of the responsible country (Klaassen and Wille, 2023). This is also an issue for Antarctica, which does not fall under any one national jurisdiction and is particularly data deficient. As such, the H5 Outbreak data tab lacks comprehensive data for certain regions, and the predictive “Species at risk” model for Australia may be less accurate in predicting susceptibility to infection in rarer bird families, those families endemic to Australia, or those that occur in regions of the world where reporting of wild bird events is less structured.

Currently, AviFluMap is set up in a use-case for Australia, however, its structure and data integration is implementable globally. The dashboard is well-supported by Deakin University and collaborating partners such as Wildlife Health Australia to ensure its continued accessibility into the future. The tool was built by a diverse team of academic and industry partners, with feedback from partners in NGOs (BirdLife), government (Department of Climate Change, Energy, the Environment and Water) and wildlife surveillance organisations (Wildlife Health Australia), meaning the functionality of the tool reflects priorities by scientists and ecosystem health practitioners alike. As new data becomes available, these will be incorporated on a continued periodic basis and the dashboard will remain hosted on Deakin servers. Furthermore, interest in the tool has been growing, with referring sites including the Department of Agriculture Fisheries and Forestry (2025) and BirdLife Australia (2025b). Future improvements may include automated data updates, dynamic risk forecasting based on seasonal bird movement patterns, and expansion of these tools beyond the current limit of the Australian continent, such as to incorporate the length of the East Asian-Australasian Flyway. We will also work to include further connectivity data (e.g. from bird banding efforts) to highlight the interface between wild and domestic birds. Feedback from users and collaborators (e.g. Wildlife Health Australia) for bug fixes and other functionality improvements have been considered through consultations during the development phase. Continued feedback will continue to be considered post-launch via provided contact addresses on the dashboard, so that we may continue to improve user experience. Funding bids are underway to support ongoing maintenance, and to facilitate broader adoption and community contributions to the application. Even prior to future improvements, AviFluMap represents a practical application of disease notification data to a pressing wildlife and biosecurity challenge. By integrating outbreak data with avian ecology, it helps stakeholders examine incursion risks and inform their response strategies. Ongoing development and collaboration are essential to ensure its relevance and impact.

CRediT authorship contribution statement

Tobias A. Ross: Writing – review & editing, Writing – original draft, Methodology, Investigation. **Sara Ryding:** Writing – review & editing, Visualization, Methodology, Investigation, Formal analysis. **Simeon Lisovski:** Writing – review & editing, Visualization, Validation, Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Joris Driessen:** Writing – review & editing, Investigation, Data curation. **Emily Mowat:** Writing – review & editing, Investigation, Data curation. **Stephanie Todd:** Investigation, Data curation. **Chris Purnell:** Writing – review & editing, Supervision, Methodology, Investigation, Data curation. **Aaron Spence:** Writing – review & editing, Visualization, Software, Methodology, Investigation. **Simone Vitali:** Writing – review & editing, Resources, Project administration, Conceptualization. **Hui Yu:** Writing – review & editing, Visualization, Methodology, Investigation. **Marcel Klaassen:** Writing – review & editing, Writing – original draft, Visualization, Supervision, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Data availability

Data will be made available on request.

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