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# Monitoring avian influenza in mammals with real-time data

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Current bird flu outbreaks are significantly affecting various animal communities, including poultry, wild birds, and some mammals. There are ongoing efforts to identify genetic mutations in the virus that might increase its ability to spread among birds and mammals, humans included. In this context, Rabalski et al. [1] discovered that domestic cats in Poland are susceptible to the highly pathogenic H5N1 avian influenza, underscoring their potential role in the virus's transmission. This transmission to cats may occur through consuming infected wild birds or exposure to contaminated poultry products.

Mink farming poses a dual threat of pathogen spillover and spillback, with minks serving as potential reservoirs and amplifiers of viruses with pandemic potential. Adaptations in mink populations' viruses, particularly in the polymerase, resemble those observed in human cases, emphasizing the need to monitor and manage mink farming risks for global public health. Examples include outbreaks in Spain [2] and Finland [3], indicating minks' role in virus transmission. Globally, there's no confirmed transmission of H5N1 from mammals to humans, but circumstances like close contact with infected birds may pose a risk. Despite structural and immune barriers, some avian influenza viruses can infect humans [4,5].

Genetic studies revealed its reassortment with other avian influenza strains, contributing to its diversity and adaptability [6]. The history of pathogenic avian influenza viruses spans decades, marked by a series of genetic shifts and viral reassortments, but the pivotal event in this transformation was the acquisition of specific mutations that led to increased virulence in poultry and other avian species [7]. The most notorious of these strains include H5N1, H7N9, and H5N8. Originating in Asia in the late 1990s, the H5N1 strain was characterized by its high mortality rate in domestic poultry and sporadic transmission to humans, resulting in severe illness and fatalities. Genetic analysis revealed multiple clades and subclades within the H5N1 lineage, reflecting

ongoing evolution and geographic spread across continents [8]. Another significant lineage, H7N9, emerged in China in 2013, posing a dual threat by causing severe disease in humans and leading to poultry outbreaks. This strain demonstrated a capacity for genetic reassortment, allowing it to acquire genes from other influenza viruses, heightening concerns over its pandemic potential [9]. The H5N8 strain, identified in birds in 2014, swiftly spread across several continents via migratory bird routes. While primarily affecting wild birds, it occasionally caused outbreaks in domestic poultry [9]. Additionally, the H1N1 swine flu, primarily known for affecting pigs, also contains genetic elements linked to avian species. This discovery sheds light on the complex dynamics of inter-species transmission, illustrating how influenza viruses can cross barriers between different animal groups.

## Open data's crucial role in monitoring recent mammal outbreaks

A comprehensive surveillance strategy is critical to efficiently monitor and respond to outbreaks in mammalian populations, i.e. a wide range of animal species, both wild and domestic, as both play a critical role in the epidemiological landscape. The specific challenge arising from this biological diversity is addressed through a strategic approach to surveillance. Rather than attempting comprehensive, all-encompassing monitoring of all species, it is useful to focus on specific subpopulations or geographic areas at high risk. This holistic approach encompasses a range of tactics, including timely issue identification, data collection, rigorous analysis, collaborative initiatives, and a well-coordinated response. Such a strategy guarantees the prompt detection and mitigation of potential health threats, thereby safeguarding the well-being of both animal and human communities.

The COVID-19 pandemic, caused by the SARS-CoV-2 virus, manifests primarily with symptoms like fever, dry

cough, fatigue, and respiratory difficulties. Its global spread led to profound socio-economic impacts, prompting preventive measures such as social distancing, mask-wearing, and vaccination campaigns. This last pandemic has underscored the pivotal importance of open data in an unprecedented manner, offering one of the most important lessons. As the world faced an unparalleled global health crisis, the sharing of timely, accurate, and accessible data became paramount. Open data played a crucial role in tracking the spread of the virus, understanding its impact on different populations, and formulating effective response strategies. In the aftermath of the pandemic, the significance of open data persists. It not only enhances transparency but also fosters collaboration and innovation across multiple sectors. Open data enables researchers, policymakers, healthcare professionals, and the public to engage in evidence-based decision-making. By openly sharing data related to disease trends, vaccination rates, healthcare capacity, and socioeconomic impacts, nations can collectively work toward informed solutions and more resilient societies. Moreover, open data serves as a catalyst for scientific advancement. Researchers worldwide can access and analyze data, accelerating the development of medical treatments, vaccines, and other critical interventions. This collaborative approach expedites the response to emerging threats and reinforces the global health community's ability to navigate future challenges effectively. By valuing transparency, collaboration, and the unrestricted sharing of information, societies can harness the power of open data to build a more resilient and interconnected world. Indeed, a global strategy that includes open data, healthcare investment, collaboration, technology utilization, and targeted economic support is essential for effectively addressing epidemic outbreaks that cause significant economic harm. This strategy should be complemented by the implementation of targeted policies to support vulnerable economic sectors during epidemics, such as emergency plans and aid for affected businesses.

Here, we would like to draw attention to the efforts of our team, which has created an open-access database available at the link https://github.com/fbranda/avian-mammals and a corresponding visualization (https://tinyurl.com/avianflu-mammals-map) designed to monitor reported cases in mammals across various countries. The dataset was created by aggregating curated data from World Animal Health Information System (WAHIS, https://wahis.woah.org/), a Web-based computer system that processes the information gathered by the Veterinary Services from World Organisation for Animal Health (WOAH, formerly the Office International des Epizooties (OIE)) Members and non-Members Countries and Territories on WOAH-listed diseases in domestic animals and wildlife, as well as on emerging and zoonotic diseases. All data are geocoded and encompass essential information, including the causal agent with serotype, outbreak details such as start/end dates, locations, detailed characterization, infection category, and the number of affected animals), diagnostic tests (including the test name and originating laboratory), and event-specific control measures. We also release the R code needed to perform visual validation of the data and a README file in which we describe the database in detail. This approach is designed to ensure the accuracy of the reported data and to provide accessibility to researchers, policymakers, and the general public. Nonetheless, in consideration of safeguarding the privacy of animal proprietors, it's important to note that the outbreak locations (specifically, city or village details) as furnished in the WAHIS reports might not precisely pinpoint the exact outbreak locations. Consequently, the provided information should be approached with caution as it may not serve as an absolute representation of the outbreak locations.

To describe the versatility and importance of our open access database, we present visual representations in Figures 1 and 2 that offer valuable insights into the global landscape of avian influenza events in mammals. Specifically, Figure 1 provides a spatial overview, addressing the fundamental question of 'Where did avian flu events in animals occur?' As of August 2023, over 300 events from 20 countries were collected (15 March 2021–30 August 2023). In addition, this spatial representation not only identifies event locations, but also highlights regions where significant hotspots and trends can be identified. Most of the outbreaks in United States of America (163), followed by Canada (50), Chile (34), Finland (33), Belgium (24), and Germany (13).

Figure 2, on the other hand, focuses on the mortality rate for avian influenza in different animal species and by country. Both land and sea mammals have been affected, as evidenced by outbreaks observed in commercially bred mink in Spain, seals in the United States of America, and sea lions in Peru and Chile. Furthermore, H5N1 viruses have not spared pets either, as cases of these strains have emerged in cats and dogs in several countries. Avian influenza is generally categorized into two main forms: low pathogenic avian influenza (LPAI) and highly pathogenic avian influenza (HPAI), each having varying levels of severity and impact on birds and poultry. LPAI typically causes milder symptoms in birds compared to HPAI, which is more severe and often leads to higher mortality rates in poultry. During the current reporting period, the majority of HPAI virus detections in mammals involved the Red Fox (191), Arctic Fox (75), Harbor Seal (38), Raccoon (Northern raccoon) (21), Cats (20), American Mink, and South American Coati (19).
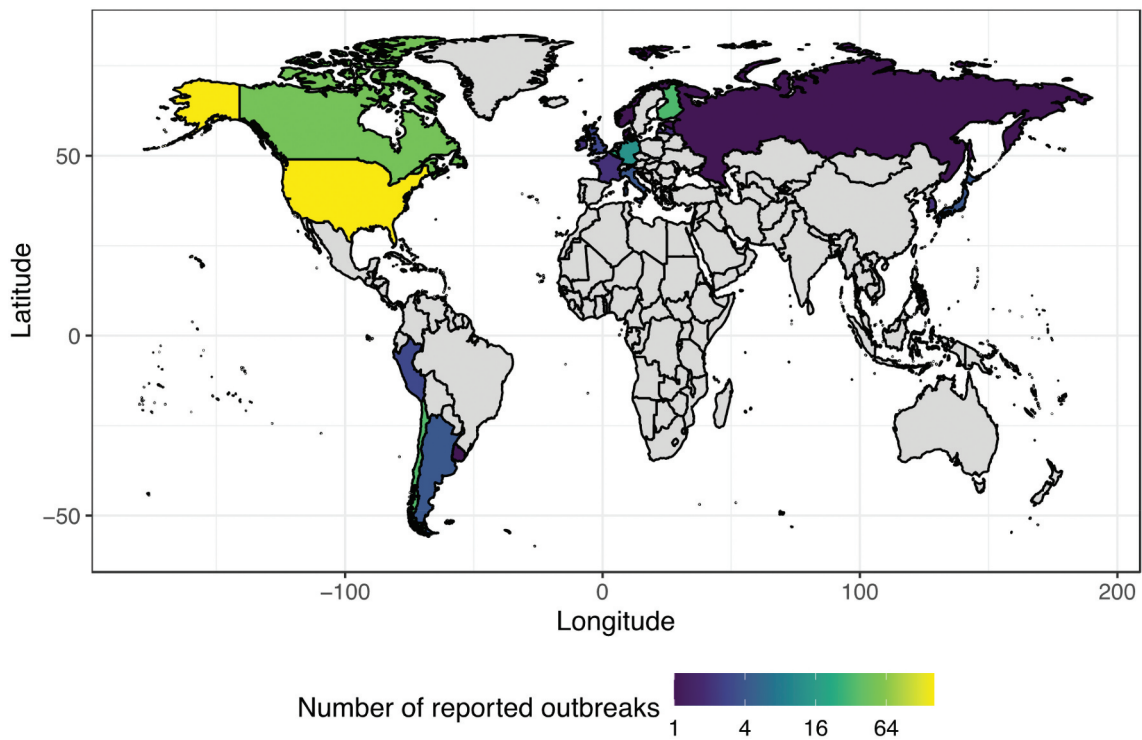
**Figure 1.** Geographical distribution of reported cases of avian influenza outbreaks in mammals.

## Fostering one health strategy awareness

Predicting pandemics has proved to be extraordinarily challenging. However, among the potential pandemic threats, influenza viruses have consistently ranked high due to their mode of transmission (air-borne) and their ability to rapidly mutate and jump species' barriers. Recent global events have underscored the necessity for proactive measures, paying urgent attention to strengthening surveillance efforts. A significant focal point is the diligent monitoring of wild animal populations. Wildlife can serve as reservoirs for novel influenza strains, making early detection crucial. Collaborative partnerships with wildlife experts and organizations are vital to identify potential viral threats among diverse species. The focal lens also extends to encompass large-scale animal farming operations, particularly those involving poultry, pigs, and mink. These settings are potential breeding grounds for influenza viruses due to the close proximity of animals, facilitating viral transmission. Moreover, animals in intensive farming systems, may experience poor care and stress. Inhumane practices and the mixing of age groups within these operations have been linked to the emergence of avian influenza [10]. Therefore, robust surveillance mechanisms within these environments are imperative, involving regular testing of animals to identify any presence of viral strains. Additionally, the health of animals should be closely monitored to swiftly recognize and address any signs of illness or unusual patterns such as elevated mortality rates.

Recognizing that disease transmission often occurs at the human-animal interface, special emphasis should be placed on individuals directly involved in animal handling and farm management. Surveillance efforts must encompass these workers, as they are at an elevated risk of contracting and potentially spreading zoonotic diseases. Providing comprehensive training on hygiene practices, proper use of protective equipment, and early symptom recognition can significantly reduce the risk of disease transmission. The importance of environmental surveillance cannot be understated. Monitoring the farm environment, including water sources, soil, and air quality, is vital to understanding the potential for viral survival and transmission. This broader perspective helps to identify possible sources of infection and routes of viral spread beyond direct animal-human interactions.

By intensifying surveillance of wildlife, large-scale livestock, human operators, and the environment, we take proactive steps to prevent, detect, and mitigate viral threats that may emerge from the complex interactions between species and their environment. Managing contact with wild birds, especially within free-range systems, where livestock interacts more freely with their environment, the risk of exposure to wild birds is heightened. This dynamic scenario presents inherent challenges due to the dynamic nature of avian movements and the difficulty in regulating such interactions and requires a nuanced approach, acknowledging the benefits of free-range systems for animal welfare while addressing the
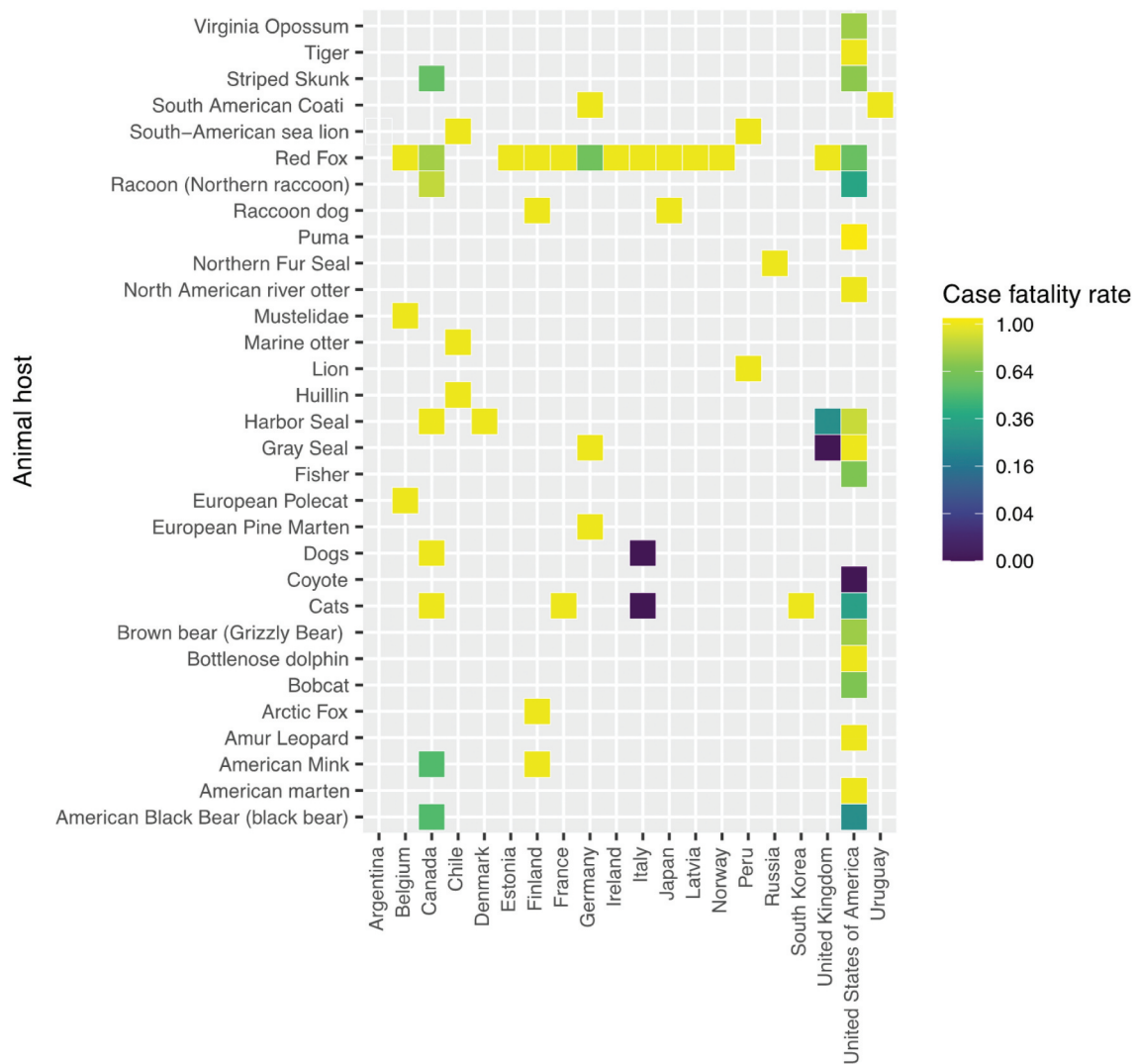
**Figure 2.** Avian flu case fatality rate per animal host and country.

challenges in minimizing contact with potential carriers of viral pathogens. A proactive stance is then imperative not only for animal health but also for safeguarding public health, considering the interconnectedness of ecosystems and the potential for zoonotic transmission.

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