

Opinion

Using wild-animal tracking for detecting and managing disease outbreaks

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Zoonotic diseases increasingly threaten human and wildlife populations, driving a global rise in mass-mortality outbreaks, including the ongoing avian influenza panzootic in wildlife and zoonotic spillovers such as the COVID-19 (SARS-CoV-2) pandemic in humans. We introduce a new general framework for detecting and managing pathogen outbreaks using animal movement and sensory biologging data to enhance early outbreak detection, provide near-real-time updates on sentinel host health and mortality, and reveal infection-induced behavioral changes. Integrating past and near-real-time biologging with disease surveillance data also enables prospective assessments of spatiotemporal outbreak dynamics, informs management decisions, helps to mitigate spillover risks, and supports both disease control and wildlife conservation.

The threat of infectious disease to humans and wildlife

Zoonotic diseases (see [Glossary](#)) pose a growing global threat to humans and wildlife, with rising incidence over the past 20 years [1–3]. Recent examples include severe acute respiratory syndrome coronavirus (SARS-CoV-1) [4], swine flu (H1N1) [5], and the COVID-19 pandemic caused by SARS-CoV-2 [6]. The emergence of **highly pathogenic avian influenza (HPAI)** is particularly concerning, with old and new virulent **avian influenza virus (AIV)** strains causing widespread outbreaks [7–9]. The current HPAI panzootic is unprecedented, killing vast numbers of poultry, livestock, and wildlife globally – mainly birds but also mammals, including sustained transmission among dairy cattle [10] – raising concerns about increased human spillover risk, currently rated low to moderate [11,12].

Wildlife disease monitoring is shifting from reactive to preventative approaches, estimated to be 20 times more cost-effective at reducing human mortality [13,14]. Effective prevention requires integrating new tools for wildlife disease **surveillance** into disease management frameworks before spillover to humans or other **target hosts**. While **biologging** and other **movement ecology** [15] tools have been used to describe the spread of past outbreaks [16], they have seldom been applied to directly assist active outbreak detection and management. Recent advances in biologging enable fine-scale, near-real-time animal tracking [17], offering critical insights for outbreak detection and management. To advance the integration of movement ecology tools into zoonotic disease management, we present a general framework leveraging biologging data to support disease management before, during, and after an outbreak occurs in a **focal management area (FMA)** of interest.

Current approaches to managing zoonotic disease outbreaks: what are we missing?

Zoonotic disease control typically focuses on humans, domesticated animals, and animal husbandry practices, using biosafety regulations, surveillance, diagnostics, vaccines, isolation of infected individuals, and culling [18]. However, since wildlife are primary **hosts** of zoonotic diseases, early detection before spillover requires dedicated wildlife surveillance [1,19]. Despite

Highlights

Biologging enhances early detection and management of wildlife disease outbreaks by complementing existing surveillance with near-real-time outbreak alerts from sentinel species, identifying hotspots, quantifying spatiotemporal dynamics and guiding management.

We present a general framework integrating movement and sensor data for disease management through six applications, broadly relevant across zoonotic diseases and pathogen–host systems.

While upfront costs can be high, biologging offers substantial value by reducing the risk of rare but catastrophic disease outbreaks.

Biologging alone is insufficient; integrating epidemiological and environmental data, along with movement ecology theory and additional tools, provides reciprocal insights.

Formalizing biologging-based surveillance as a core disease management tool is essential and requires sustained collaboration across health, environment, and conservation sectors.

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well-established surveillance protocols for animal husbandry and international regulations on transport and trade, wildlife surveillance remains underfunded and underdeveloped globally [14,20]. It relies heavily on **passive surveillance** of incidentally collected wild-animal carcasses, while **active surveillance** programs are less frequent, short-term, and project-specific [14,21]. Consequently, even in developed regions, wildlife surveillance remains incomplete [3,14,22].

Most surveillance programs rely on reverse transcription polymerase chain reaction (RT-PCR) testing, which provides valuable epidemiological insights, particularly when followed by virus isolation, necropsy, serology, and genome sequencing [23]. However, these tools are costly, labor-intensive, and provide a snapshot of disease presence, not transmission dynamics [24]. Although biologging data have been used for **retrospective data analysis** of disease transmission (e.g., in migratory birds [25]) and their potential for disease detection and management has been noted [16], a comprehensive framework that incorporates **prospective data analysis** using near-real-time biologging data from wild animals is still critically lacking.

A general framework for integrating biologging into disease management workflows

We propose a six-component framework that leverages historical and near-real-time biologging data from tracked animals to support the detection and management of emerging and ongoing zoonotic diseases. The framework aligns with disease progression stages: before, during, and after an outbreak in the FMA (Figure 1).

Step 1. Establishing routine biologging-based surveillance and knowledge gain

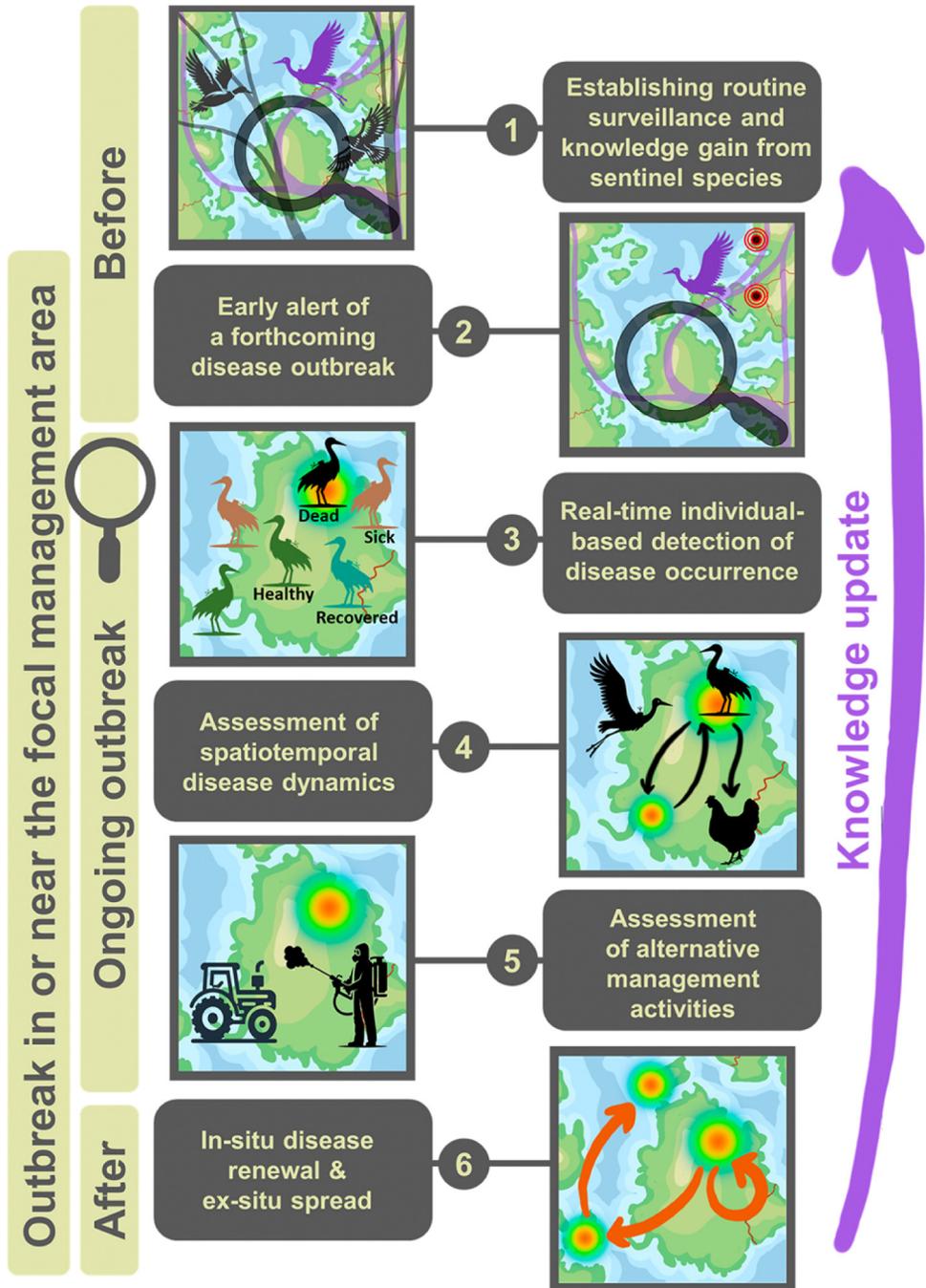
Designing a biologging-based disease-alert system begins with selecting appropriate **sentinel host species** for tracking. Sentinel species play a key role in disease surveillance (e.g., [26,27]), with selection criteria including relevance to targeted diseases and hosts, susceptibility, transmissibility, disease-symptomatic behavior, movement characteristics, abundance, life-history traits, sociality, interactions with target hosts such as humans or domestic animals, and suitability for biologging. Variation in movement syndromes (e.g., migration, foraging, and dispersal), sex, age, seasonality, and movement behavior should also be considered. For instance, variation in migration schedule, breeding and wintering locations, or other partial migration aspects should be considered. Choosing sentinel species also requires a solid understanding of disease epidemiology, ecology, transmission agents, and environmental drivers of spread. The initial assessment should determine whether sickness can be detected through movement behavior changes, followed by establishing a baseline for detecting disease-related abnormalities.

In Michigan, USA, coyotes (*Canis latrans*) were proposed as sentinels for bovine tuberculosis in white-tailed deer (*Odocoileus virginianus*), requiring 97% fewer samples and improving detection by 40% [28]. Using biologging data to identify coyotes' movement modes (e.g., 'walking', 'foraging', 'resting') [29], could further enhance detection by discriminating healthy and sick individuals. In New Zealand, bovine tuberculosis control programs targeting brushtail possums (*Trichosurus vulpecula*), considered the main **maintenance hosts**, drastically reduce tuberculosis (>95%) in livestock and in wildlife [26,30]. However, reduced possums' densities and small home ranges decreased their cost-effectiveness as sentinels, prompting the use of sentinel **bridge host** species like ferrets (*Mustela furo*), deer (*Cervus elaphus*), and especially feral pigs (*Sus scrofa*) [26]. Lessons suggest key attributes of effective tuberculosis sentinels, including bridge host function, long infection periods, and wide-ranging behavior [31].

For HPAI, migratory and resident waterfowl, especially mallards (*Anas platyrhynchos*), are key hosts [32]. Mallards are potential HPAI sentinel species for many reasons, including high infection rates, maintenance host role [32], proximity to humans, domestic ducks and other farm animals, common

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Glossary

Active surveillance: a proactive surveillance approach that systematically samples pathogens, environments, and hosts in specific species, times, and locations.

Avian influenza virus (AIV): a strain of influenza A virus that primarily infects birds.

Biologging: the use of small, animal-mounted devices to gather data on the animal's movements, behavior, physiology, and its environment. Biologging is the key data source for movement ecology research.

Bridge host: a host species or population capable of facilitating transmission between two otherwise geographically disconnected host populations (e.g., between maintenance and target hosts; see text for examples).

Focal management area (FMA): an area of interest managed by a single authoritative entity, such as a country, state, province, supranational union, or nature reserve.

Highly pathogenic avian influenza (HPAI): a disease caused by highly pathogenic strains of AIV, including the Gs/GD H5N1 strain, which first emerged in 1996 in domestic geese and later caused mass outbreaks in wild birds and, more recently, in mammals. Although human infection is rare, the death rate is remarkably high (~52%) [89], with >450 reported deaths to date. The ongoing HPAI-H5N1 clade 2.3.4.4b outbreak is exceptional in its global extent, high wildlife mortality, and prolonged duration since 2021.

Host: a living organism that can be infected by a parasite or any other infectious agent under natural conditions. Since host classification and terminology can be complex, we focus on three key host types in multi-host zoonotic disease systems relevant to biologging-based disease management: maintenance, bridge, and target hosts.

Maintenance host: host species or population in which a pathogen can persist over time, even in the absence of transmission from other hosts (see text for examples).

Movement ecology: conceptually, this approach posits that an individual's movement path results from the interactions between its motion capacity (e.g., movement rate), navigation capacity (e.g., movement decisions), internal state (e.g., infection status), and external environment (e.g., proximity to infected individuals). Methodologically, it

Figure 1. A general conceptual framework for using biologging data from wild animals to enhance zoonotic disease detection and management. This framework encompasses six steps, organized chronologically into three phases: before, during, and after an outbreak occurs in the focal management area (indicated by the magnifying glass). Bird icons represent wild animals serving as sentinel host species.

mixture of resident and migratory populations, and suitability for biologging. However, although some studies report disease-related movement changes (e.g., [33]), mallards are typically asymptomatic [34] and face high mortality from hunting and poaching [35,36], limiting tracking duration.

Other suitable HPAI sentinels include pelagic seabirds like gannets, and migratory birds like cranes. Northern gannets (*Morus bassanus*) tracked for renewable energy studies provided crucial insights during the 2022 HPAI outbreak across the British Isles, particularly at their largest breeding colony, Bass Rock [37] (Figure 2A). Seabirds, which typically breed in large dense colonies, are highly susceptible to disease outbreaks, but their roles as bridge hosts and in pathogen reassortment remain underexplored compared to waterfowl (Anseriformes, primarily ducks) and shorebirds (Charadriiformes) [38]. Biologging, widely applied to study their extensive foraging movements, can offer valuable insights into disease dynamics [38]. For example, the recent spread of HPAI (H5N1 and H5N5) from Europe to North America – infecting numerous wild birds and causing fatal spillover to multiple mammal species – has been attributed to pelagic seabirds traversing the North Atlantic, as evidenced by biologging data [39].

Similarly, migratory common cranes (*Grus grus*) have received limited attention in disease-related research, despite their tendency to congregate and travel along HPAI hotspots. Cranes recently experienced two waves of mass HPAI-caused mortality in Israel in 2021 (Figure 2B) and another in Hungary in 2023 (Talmon *et al.*, unpublished) [40,41]. Other migratory birds were suspected to have contributed to the recent spread of HPAI from North to South America [39]. Disease-symptomatic migratory birds and non-migratory, wide-ranging seabirds could serve as sentinel species along migration flyways and across oceans, respectively. Large, gregarious and conspicuous birds sensitive to HPAI are more likely to be detected upon mortality than smaller, solitary and inconspicuous species, enabling validation of their biologging-inferred infection status (Step 3). To enhance cost-effectiveness, biologging efforts should prioritize the populations or individuals that undertake long movements, interact with bridge or target hosts, and have high potential for pathogen reassortment and disease spread.

At this early stage of biologging-based disease management, sentinel species are unlikely to be selected solely on general theoretical criteria. Instead, their selection may rely more on recent outbreak history and availability of tracking data. Notably, in both examples shown in Figure 2, the species were not initially tracked for disease research. Future efforts should integrate both theoretical considerations and outbreak data, prioritizing resources to track a sufficient number of individuals (e.g., 60 barn swallows (*Hirundo rustica*) and house martins (*Delichon urbicum*) in [42] and 34 griffon vultures *Gyps fulvus* in [43]) and focusing on key hosts and high-risk sites for active surveillance [24].

Step 2. Early alert of a forthcoming disease outbreak

Wildlife movement data have been used retrospectively to analyze disease spread [44], with one study identifying 70 movement data/disease analysis publications between 2000 and 2017 [45]. This includes HPAI spread by migrating birds [25] and wild bird overlap with poultry farms [46], swine fever in wild pigs [47], and brucellosis transmission risk from elks to livestock [48]. However, prospectively predicting disease dynamics using biologging data for active outbreaks that could expand into the FMA has yet to be implemented. Recent advances in wildlife tracking enable near-real-time data [17], allowing earlier outbreak alerts before large-scale mortality is detectable by passive surveillance. Biologging data from sentinel species could and should be coupled with concurrent disease outbreak location data to forecast disease arrival in FMAs (Figure 2B, Talmon *et al.*, unpublished).

A key requirement for biologging-based alert systems is near-real-time data acquisition, with ‘near-real-time’ defined flexibly depending on disease characteristics (e.g., transmission period),

emphasizes the need to collect data on the movement of individual organisms, their traits, the environmental factors influencing their movement, and the broader consequences (e.g., disease spread). Therefore, movement ecology provides a robust conceptual and methodological foundation for using biologging data to detect and manage infectious diseases.

One Health: an interdisciplinary approach that integrates ecosystem, animal, and human health, recognizing their interconnections in order to achieve optimal health outcomes for all.

Passive surveillance: a surveillance approach that relies on spontaneous reporting or opportunistic sampling of pathogens, hosts, and environments, without targeted efforts, typically focusing on dead or sick animals.

Prospective data analysis: prospective analysis using near-real-time biologging data to forecast, detect, and manage impending or ongoing outbreaks.

Reaction norms: the pattern of phenotypic variation expressed when individuals of the same genotype are exposed to varying environmental conditions. In the context of biologging-based disease surveillance, the phenotype is movement behavior (estimated by movement metrics) and the environmental conditions are related to the presence or absence of a disease.

Retrospective data analysis: retrospective analysis uses historical biologging data to assess disease spread and connectivity in past outbreaks.

Sentinel host species: a wild-animal species monitored (in this context, through biologging) to forecast and detect disease, and to inform management decisions, through the assessment of individual health status and identification of potential health hazards to other wildlife, domestic animals, or humans.

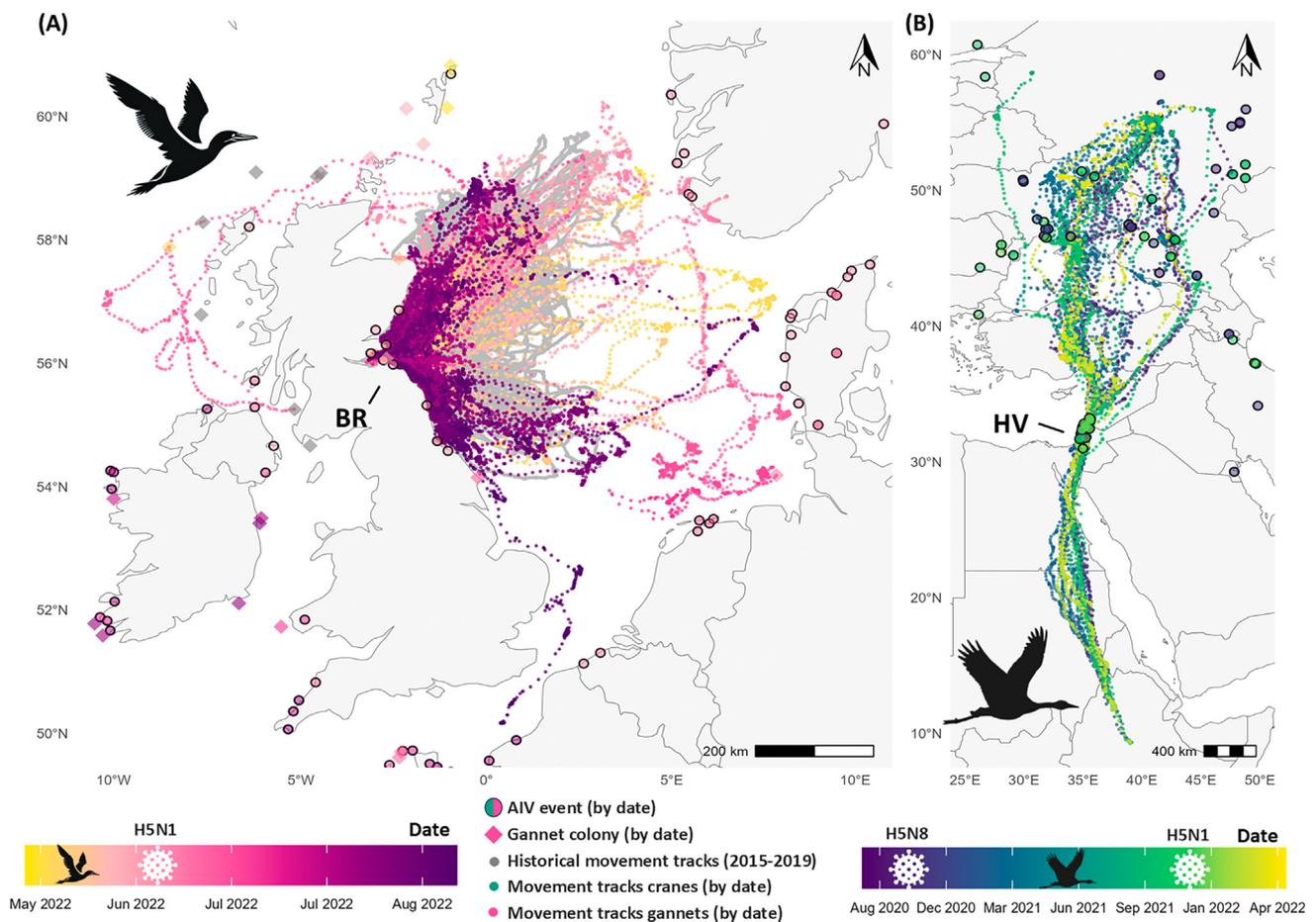
Surveillance: the collection, analysis, and interpretation of health data to detect, monitor, and mitigate disease risks.

Target host: the species or population that is the focus of disease control efforts, due to their susceptibility to the pathogen (e.g., humans, livestock, poultry, threatened wildlife species).

Virtual geofence: a designated area outlined by predefined coordinates in a biologging device. When a tracked animal enters this area, biologging

biologging constraints [17], and the response time of FMA partitioners. From a biologging perspective, early alert can range from a minute to a day or longer, depending on the biologging device used and its configuration. Most commercial GPS tags transmit data via satellites or GSM at intervals ranging from 10 min to several days, and many now feature two-way communication, allowing remote biologging adjustment (e.g., localization and data retrieval rates) without requiring recapture. GPS-GSM tags can also send short-message systems (SMS) alerts when tagged animals cross predefined **virtual geofences** for California condors (*Gymnogyps californianus*) approaching wind turbines [49], African elephants (*Loxodonta africana*) heading towards farms [50], and African lions (*Panthera leo*) nearing cattle [51]. A similar geofence in the FMA could trigger automatic alerts and adjustments or be manually adjusted based on the tracking data. Energy

settings (e.g., sampling resolution or communication rate) are adjusted according to predefined criteria. **Zoonotic diseases:** diseases transmitted from nonhuman animals and other organisms to humans, which have historically caused major outbreaks in human populations and continue to pose a substantial risk for future panzootic and pandemic outbreaks.



Trends in Ecology & Evolution

Figure 2. Movement and mortality patterns of northern gannets (*Morus bassanus*) and common cranes (*Grus grus*) during highly pathogenic avian influenza (HPAI) outbreaks. (A) Movement tracks of northern gannets from Bass Rock (BR), Scotland, before, during (June 5–July 31, 2022), and after the 2022 HPAI H5N1 outbreak at the colony, with tracks color-coded by date. Gray tracks represent historical movement data from individuals tagged between 2015 and 2019. Colored circles indicate the timing of HPAI detections in gannets across the East Atlantic. Diamonds represent gannet colonies, with colors indicating the date of abnormal mortality detection; gray diamonds denote colonies where no abnormal mortality was observed. (B) Migratory tracks of common cranes before, during, and after two HPAI outbreaks: H5N8 in 2020 (shades of blue) and H5N1 in 2021 (shades of yellow), the latter causing mass mortality at a key wintering site in the Hula Valley (HV), Israel. Colored circles indicate the timing of HPAI outbreaks, and virus icons on the timeline bars (bottom) mark the start of each outbreak. Gannet movement data from [37] CC BY license (<https://s100.copyright.com/AppDispatchServlet?title=HPAIV%20outbreak%20triggers%20short-term%20colony%20connectivity%20in%20a%20seabird%20metapopulation&author=Jana%20W.%20E.%20Jeglinski%20et%20al&contentID=10.1038%2Fs41598-024-53550-x&right=The%20Author%28s%29&publication=2045-2322&publicationDate=2024-02-07&publisherName=SpringerNature&orderBeanReset=true&oa=CC%20BY#>); crane movement data from [97]; outbreak data from the EMPRES-i Global Animal Disease Information System [41]. Abbreviation: AIV, avian influenza virus.

constraints on GPS batteries, even solar-recharged ones, restrict rapid localization and communication to a few hours or days. However, this can be mitigated by confining rapid-communication geofences to high-risk areas [49] and by incorporating sensor-based on-board estimation of activity and health status.

For faster alerts (e.g., safeguarding sensitive areas or populations), reverse-GPS technologies like ATLAS [52] offer near-real-time data (typically ~45 s) but are limited to deployment areas ~30 x 30 km [17]. ATLAS could be deployed in high-risk hotspots, such as mixed-species congregations where zoonotic diseases are likely to circulate. As wildlife diseases are often structured at fine spatial scales, sometimes just a few meters [53], ATLAS's high spatiotemporal resolution is critical for understanding movement–disease interactions. Moreover, its small tags expand the range of GPS-trackable species, enabling tracking of animals as small as 7 g bats [54].

Early-alert systems should extend beyond migratory birds to include bridge hosts like migratory mammals [44] and non-migratory species. For instance, during the 2022 HPAI outbreak in the UK, northern gannets from an infected colony expanded their foraging range, increasing connectivity between distant colonies compared to baseline behavior ([37], Figure 2A). Across the Atlantic, gannets in Newfoundland (Canada) also exhibited atypical long-distance movements during the outbreak, possibly influenced by a concurrent marine heatwave [55]. Although not implemented in near-real-time, coupling GPS tracking data with epidemiological information on infected birds in such cases could have prospectively assessed disease risk across the FMA. However, seabird movements are often less directional and predictable than those of terrestrial migrants (e.g., cranes; Figure 2B), and near-real-time data retrieval is still more common in studies of terrestrial migrants.

Step 3. Near-real-time individual-based detection of disease occurrence via behavioral change

Detection of disease outbreaks within the FMA has largely relied on observations of symptomatic or dead domestic animals and wildlife, often at a late stage. However, pathogens can alter host movement patterns [56–58] and body temperature [59], hence deviations from baseline behavior of healthy individuals could help identify an individual's health status earlier, remotely, automatically, and, at least initially, without requiring sample collection (Talmon *et al.*, unpublished). Farm animal health monitoring via biologging began in the 1980s [60] and progressed with technology [61]. Although still emerging, near-real-time health assessments have shown potential for detecting injured (e.g., [50]) and sick (e.g., [33]) individuals. Accelerometers, standard in many biologging devices, can detect subtle behavioral changes through machine-learning classification [62], as applied to identify tuberculosis-infected banded mongooses (*Mungos mungo*) [63], and African swine fever-infected wild boars (*Sus scrofa*) [64]. Other sensors, such as implanted temperature loggers, have also detected disease in vervet monkeys (*Chlorocebus pygerythrus*) [44].

Step 4. Assessment of spatiotemporal disease dynamics

Once an outbreak is detected, biologging offers unique insights into its spatiotemporal dynamics that traditional monitoring cannot [47,65]. Building capacity to remotely and automatically detect disease-related behavioral changes (Step 3) can support early containment and reveal disease-related movement **reaction norms** reflecting changes in movement behavior during outbreaks or differences between infected and uninfected individuals (Figure 3).

Outbreak spatiotemporal dynamics are often assessed retrospectively, typically using phylogenetic analysis of the pathogen (e.g., [66]) or movement ecology tools such as agent-based models, step-selection functions, and landscape resistance maps, all derived from animal movement data. For instance, data from two GPS-tracked Canadian deer species enabled identifying landscape connectivity as a key driver of chronic wasting disease risk, guiding surveillance to river valleys surrounded

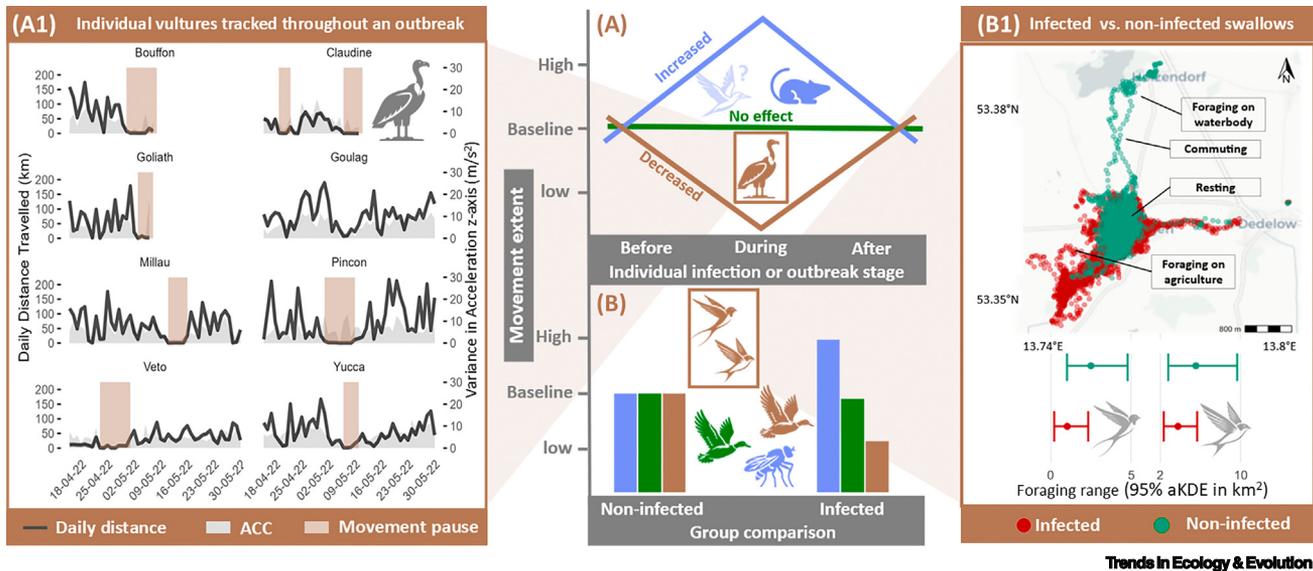


Figure 3. Two types of disease-related movement reaction norms. (A) Changes in movement before, during, and after an individual becomes infected, or in relation to an outbreak at the focal management area, illustrate three distinct reaction norms: increased movement followed by a decrease (blue), decreased movement followed by an increase (brown), and no change (green). Symbols represent empirical examples: mice (*Mus musculus*, blue) infected with a rabies-derived peptide [98]; Griffon vultures (*Gyps fulvus*, brown) infected with avian influenza virus, further detailed in panel A1 on the left (ACC = acceleration) [43]. The gannet symbol (light blue, with a question mark) highlights cases where biologging data require validation with epidemiological evidence, as tracked birds from infected colonies may not be individually infected, and observed movement changes could reflect altered habitat quality rather than a direct health response [37]. (B) Comparison of movement between infected and noninfected individuals reveals three different reaction norms: infected animals may exhibit increased (blue), decreased (brown), or comparable (green) movement relative to noninfected conspecifics, which serve as the baseline. Examples include common fruit flies (*Drosophila melanogaster*, blue) infected with multiple bacteria [99]; mallards (*Anas platyrhynchos*, green and brown) infected with avian influenza virus, showing either no change [34] or decreased movement [33]; two swallow species (*Hirundo rustica* and *Delichon urbicum*, brown) infected with blood parasites [42], further detailed in panel B1 on the right (aKDE = autocorrelated kernel density estimator).

by agriculture in an aspen parklands [67]. Retrospective biologging-based analysis also revealed outbreak dynamics within a metapopulation, highlighting roles of host sex, age, and infection status [58].

Beyond retrospective assessments, biologging enables prospective risk assessment by predicting transmission pathways in sentinel species (Step 1) using near-real-time movement data, helping forecast spillover risk to farms [16,68] and wildlife and improving early detection and targeted surveillance. Biologging is also critical for detecting subclinical infections, which persist without obvious signs, particularly through high-throughput tracking revealing subtle adverse behavioral changes otherwise missed. For example, ATLAS data from 60 birds of two swallow species revealed that parasite-infected birds had smaller foraging area, used lower-quality habitats, and had lower survival probability compared to uninfected ones ([42]; Figure 3A1). These findings highlight the hidden costs of subclinical infections and the power of advanced biologging in detecting them, even for small animals (~20 g).

While large sample sizes improve representativeness, long-term tracking of even a few individuals can reveal rare behavioral abnormalities. Examples include infected wild waterfowl disproportionately visiting particular poultry [68], and a small subset of tagged common cranes consistently preferring specific habitats in their wintering grounds [69]. Combining biologging with field observations can link large-scale migratory movements with local behavior, such as wild geese foraging alongside domestic ones [70]. However, biologging alone is insufficient for comprehensive disease assessment. Integrating movement and behavioral data with epidemiological data from live, dying or dead animals, as well as environmental samples, is essential. This integration helps assess outbreak dynamics and

long-term impacts of both clinical and subclinical infections. Integration should be bidirectional: epidemiological data can guide high-resolution tracking in infection hotspots and validate biologging-based disease dynamics and movement reaction norms, while biologging data can inform sampling locations and rates to refine active surveillance, and identify high-risk hotspots such as wintering or stopover sites with mixed-species congregations.

Step 5. Assessment of alternative management activities

Biologging-enabled early alerts (Step 2) allow stakeholders to adjust protocols ahead of outbreaks. As an initial measure, stakeholders can close the FMA or specific disease hotspots to visitors, minimizing spillover risks and spread beyond current hotspots. Biologging data can also assist stakeholders in choosing between alternative management actions aimed at limiting disease spread. For instance, in areas where wild animals are fed to divert them from crops, reducing or halting supplementary feeding may lower animal densities and transmission risk, with biologging verifying animal responses [60]. Alternatively, maintaining food supply in a disease hotspot could prevent spread to non-infected areas or livestock, with biologging verifying outcomes. Movement data from elk (*Cervus canadensis*) in Yellowstone, for example, showed how supplementary feeding separated them from livestock during peak brucellosis transmission [71]. Where roads act as corridors for rabies or canine distemper transmission, biologging can guide targeted vaccination [72]. Biologging data can also help reduce reliance on ethically contentious mass culling to contain zoonoses [73].

Step 6. *In situ* disease renewal and *ex situ* spread

Modeling *in situ* disease renewal and *ex situ* spread of zoonotic diseases has largely focused on retrospective analyses [65,74], despite a recognized need for prospective approaches [45]. Combining ongoing and past biologging data can help construct models to project potential disease resurgence from new or existing sources (e.g., infected soil) and its broader spread [75]. Emerging disease-spread modeling approaches such as MoveSTIR (Movement-driven modeling of spatiotemporal infection risk) [47] use biologging data to for this purpose. Derived from epidemiological first principles, MoveSTIR decomposes disease transmission into key processes, such as contact formation and duration, pathogen deposition and acquisition, and host movement and behavior. It integrates diverse animal movement data and an individual-based continuous-time movement model to prospectively quantify transmission risk and disease dynamics at fine scales across heterogeneous landscapes. MoveSTIR thus provides an empirically-guided generalizable framework for understanding and predicting disease spread across host–pathogen systems, supporting theoretical and applied advances at the intersection of movement and disease ecology. Additional modeling approaches can also be combined with biologging data to assess how habitat loss [76] and global warming [77] affect disease dynamics.

Synthesis: opportunities and challenges of biologging-based zoonotic disease surveillance

Zoonotic outbreaks are rising in frequency and severity [2,3], a trend expected to intensify as climate and environmental changes elevate disease risks for both humans and wildlife [78]. Wildlife are now recognized as major pathogen hosts, with outbreaks threatening species and populations [11,12]. Although global health organizations such as the World Health Organization (WHO), the Food and Agriculture Organization (FAO), and the World Organization for Animal Health (WOAH) have long acknowledged the importance of wildlife surveillance for disease control, efforts remain limited compared to those targeting domestic animals. Similarly, while the utility of biologging for disease management was recognized two decades ago [79], it remains absent from recent wildlife surveillance guidelines [20]. We propose formalizing biologging-based disease surveillance programs as management tools and urge collaboration among stakeholders, biologging experts, health authorities, environmental agencies, and conservation practitioners [80].

Current wildlife disease surveillance methods require substantial resources and often deliver only retrospective information, underscoring the urgent need for cost-effective approaches that enable near-real-time outbreak management [81]. To confront this challenge, we present a framework highlighting six complementary ways biologging data can uniquely contribute to disease detection and management. We advocate prioritizing investment in biologging-based disease surveillance with targeted sentinel hosts regularly tagged and tracked for this purpose. While the upfront costs of biologging-based disease surveillance may be high, they are negligible compared to the economic, ecological and health consequences of rare but catastrophic 'black swan' disease outbreaks.

Implementing biologging-based surveillance faces some key challenges. Asymptomatic individuals, even of otherwise suitable sentinel host species, may not exhibit detectable behavioral changes (Steps 1 and 3), complicating inference particularly for subclinical infections (Step 4). This limitation could be addressed by integrating physiological sensors (e.g., heart rate, body temperature) or immunological biomarkers to detect subtle physiological responses indicative of infection [31]. Empirically validating biologging-inferred infection status (Step 3) is also challenging, but can be achieved through coordinated field efforts, including targeted serological surveys, improved molecular diagnostics, and computational approaches such as machine-learning algorithms that incorporate contextual data (e.g., weather conditions, habitat characteristics) to filter out confounding factors to distinguish true behavioral signals from environmental noise. Further technological innovations, including improved battery efficiency, relay stations, and technologies such as LoRaWAN-based transmission [82], will enhance data retrieval in remote areas, supporting early outbreak detection (Step 2), near-real-time data streaming (Step 3) and informed decision-making during outbreaks (Steps 4 and 5). Finally, broader movement ecology theory and complementary tracking tools (Box 1) can extend the reach of biologging-based surveillance, particularly for small-bodied species.

Box 1. Beyond biologging: incorporating broader movement ecology theory and tools

Biologging offers powerful capabilities for disease surveillance, particularly by providing near-real-time, high-resolution data on host movements. However, two main limitations constrain its broader application. First, biologging is restricted to relatively large animals. To minimize impacts on tracked animals, devices are typically limited to 1–5% of the animal's body mass, with stricter thresholds for flying rather than nonvolant animals, and for birds than for bats [90,91]. GPS devices with remote data retrieval, essential for near-real-time applications, are heavier than some biologging devices that lack remote data retrieval capacity, such as GPS loggers and geolocators. Lightweight ATLAS tags offer an exception but have limited coverage (Step 2). Consequently, biologging-based surveillance is currently feasible only for animals weighing approximately 20 g or more. Second, tagging requires capturing wild animals, a labor-intensive and often impractical task for many species.

Broader movement ecology theory and alternative tracking tools can complement biologging. Theoretically, the movement ecology framework offers generalizable guidelines for disease research by dissecting complex spatiotemporal disease dynamics into key measurable components (see Glossary and [15,92]). It supports empirical studies, mechanistic modeling (Step 6), and investigation of host–pathogen feedbacks [92,93]. Practically, alternative animal tracking tools can support retrospective analyses of host movements. For small-bodied hosts, stable isotope analysis has inferred migratory connectivity in monarch butterflies (*Danaus plexippus*), revealing lower parasite infection rates in migratory than resident populations, and highlighting how tropical milkweed planting disrupts migration and worsens parasite impacts (reviewed in [93]).

Other complementary tools include data mining from social media and citizen science observations, analyzed by artificial intelligence and other digital technologies [94]. A prime example is the near-real-time modeling of COVID-19 spread using data from health agencies, social media and other sources [95]. While useful, these approaches primarily address communicable diseases and human infection reports rather than wildlife movement, making them complementary to biologging. A notable integrative approach is BirdFlow, a probabilistic model inferring bird migration and connectivity from weekly relative abundance estimates at 3 km x 3 km resolution based on eBird, the world's largest biodiversity-related citizen science database [96]. BirdFlow's forecasts align well with GPS tracks across several species, suggesting that eBird population-level data can approximate individual-level migratory movements [96]. Such frameworks can be combined with biologging, epidemiological, and human/livestock distribution data to assess transmission risks of emerging zoonotic diseases.

Cost-benefit considerations are crucial, as biologging tags are relatively expensive (~US\$2K for a GPS unit) and animal trapping requires substantial efforts. Establishing baselines for non-infected sentinel animals (Step 1) may require years of tracking and environmental data collection, while low disease prevalence demands large sample sizes (Step 4). However, advances in wildlife tracking technologies enable increasingly cost-effective high-throughput data acquisition (Step 2), supported by visualization tools and global databases like Movebank [83] and associated environmental databases [84], which can help to elucidate the environmental drivers of disease dynamics (Step 6). Such advancements not only improve understanding of animal movements and disease dynamics [17] but also support applications in human–wildlife conflict mitigation [51], wildlife conservation [85], and legal enforcement [86]. Resources invested in biologging-based disease surveillance can therefore yield broad benefits, from mitigating wildlife mortality from wind turbines or poisoning to reducing human–wildlife conflicts and supporting regulatory actions. Conversely, leveraging biologging data originally collected for non-disease-related purposes – combined with targeted sampling during outbreaks and Bayesian modeling to enhance statistical power – can improve cost-effectiveness, particularly when tracked animals are near outbreak sites, as shown in studies of gannets and cranes (Step 1).

Concluding remarks

With wildlife mass-mortality outbreaks increasing, effective disease detection and management strategies are essential within the **One Health** framework [81]. Our proposed biologging-based disease surveillance aligns with growing recognition of the importance of using movement data from wild animals to address major environmental, health, and conservation concerns. This recognition has led to international initiatives such as Move BON [87], which aim to guide the translation of animal movement data into policy decisions. A recent example is the development of a new movement-based framework for ecological connectivity, designed to support efforts to protect species and maintain ecosystem services [88]. We hope our framework and examples will inspire research and encourage practical applications of biologging to enhance zoonotic diseases detection and management (see [Outstanding questions](#)).

Author contributions

R.N. conceived the study. I.T., R.N., and S.P. wrote the initial draft. All authors discussed, reviewed, and edited the manuscript. R.N. supervised and acquired funding.

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Declaration of interests

No interests are declared.

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Outstanding questions

How can biologging data be integrated into existing wildlife disease surveillance programs? Addressing this question requires evaluating the benefits and costs of integration (see the section Synthesis). Particular attention should be given to complementary actions that reduce overall costs and increase benefits, such as using biologging to guide epidemiological sampling in potential infection hotspots, leveraging epidemiological data to validate biologging-based estimates, and developing automated near-real-time data analysis protocols.

What are the most effective sentinel species for zoonotic disease surveillance? Further research is needed to clarify the relative importance of different theoretical criteria (e.g., symptomatic behavior, sociality) and key axes of variation (e.g., sex, season) discussed in Step 1, drawing on growing evidence from tracked species experiencing disease outbreaks. Both epidemiological experiments in captivity and natural experiments on free-ranging animals (e.g., comparing movement behavior between infected and non-infected individuals, [Figure 3](#)) can help to refine selection criteria and identify key determinants.

How can biologging technologies be optimized for near-real-time disease surveillance? Technological innovations should focus on extending battery life, improving spatiotemporal resolution, minimizing tag size, shortening data retrieval intervals, reducing costs, and automating on-board behavioral classification, data processing, analysis and communication with disease management practitioners.

How can international multipurpose biologging projects be recruited to support disease management? Within a One Health collaborative framework, biologging projects, including those not originally designed for disease management, can be proactively enlisted to aid the detection and management of active outbreaks globally. Existing international biologging and epidemiological datasets should be integrated with shared capacity-building efforts to improve data flow and insights into outbreak dynamics.

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How can international health and conservation organizations help promote the adoption of biologging-based wildlife disease surveillance? Global health and conservation organizations and networks – such as WHO, FAO, WOA, World Wildlife Fund (WWF), and the International Union for Conservation of Nature (IUCN) – can play a pivotal role in mainstreaming biologging-based disease surveillance. They can proactively incorporate recent technological and methodological advances (as highlighted in this article) into international guidelines, funding priorities, and cross-sectoral One Health initiatives.

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