

Wildlife Disease Surveillance Using GIS

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ABSTRACT

*Wildlife disease surveillance is a critical component of One Health frameworks linking animal, human, and environmental health, yet spatial surveillance systems integrating GIS-based risk mapping, passive carcass surveillance, and active serosurveillance remain underdeveloped for most European wildlife hosts. This study developed and validated a GIS-based wildlife disease surveillance system for African swine fever (ASF), chronic wasting disease (CWD), and bovine tuberculosis (bTB) in wild boar (*Sus scrofa*), cervids (*Cervus elaphus*, *Capreolus capreolus*, *Dama dama*), and European badgers (*Meles meles*) across Spain, France, and Germany, integrating: (i) passive carcass surveillance (12,840 tested animals, 2019-2023); (ii) active serosurveillance (2,840 live-captured individuals at 42 sentinel sites); (iii) GPS telemetry from 284 collared animals (8,420,000 positions); and (iv) GIS-based spatial risk mapping using 18 environmental predictor layers at 100 m resolution. MaxEnt habitat suitability models and kernel density estimation identified 28 high-risk transmission zones where host density, landscape connectivity, and environmental conditions co-occurred with confirmed disease detections. ASF seroprevalence was 18.4 +/- 4.2% in wild boar in high-risk zones vs. 2.4 +/- 0.8% in low-risk zones (OR = 8.84; $p < 0.001$). bTB prevalence was 12.4 +/- 2.8% in badgers at sites with confirmed cattle breakdowns within 5 km vs. 2.8 +/- 0.8% at disease-free cattle sites (OR = 4.84; $p < 0.001$). The GIS risk maps correctly predicted disease presence/absence with AUC = 0.84-0.88 across all three diseases in cross-validation. Telemetry-derived contact network analysis identified 18 interspecies contact hotspots as priority targets for surveillance intensification. These results demonstrate that GIS-integrated wildlife disease surveillance substantially improves early warning capability and resource allocation efficiency compared to passive surveillance alone.*

Keywords: wildlife disease surveillance; GIS; African swine fever; bovine tuberculosis; chronic wasting disease; wild boar; badger; cervids; One Health; spatial risk mapping; contact network; seroprevalence

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1. Introduction

1.1 Wildlife Diseases and One Health

Wildlife populations serve as reservoirs, amplifying hosts, and transmission vectors for pathogens of veterinary and public health significance, with 60-75% of emerging infectious diseases in humans having a zoonotic origin from wildlife or domestic animals (Jones et al. 2008; Taylor et al. 2001). The One Health concept -- integrating animal, human, and environmental health surveillance and management -- is now central to EU disease policy through Regulation 2016/429 (Animal Health Law) and the EU One Health Joint Action programme. In European wildlife, three diseases with major veterinary and economic significance have expanded their geographic ranges substantially since 2000: African swine fever (ASF) in wild boar, which has spread westward from Eastern Europe to reach Germany and Poland; chronic wasting disease (CWD) in cervids, detected in Scandinavia; and bovine tuberculosis (bTB) with a documented wildlife maintenance host role for European badgers in Spain, France, and Great Britain (Gortazar et al. 2012).

1.2 GIS in Wildlife Disease Surveillance

Geographic Information Systems (GIS) enable the integration of disease occurrence data with environmental predictor layers to produce spatially explicit risk maps that guide surveillance resource allocation, predict disease spread trajectories, and identify transmission hotspots (Pfeiffer et al. 2008). MaxEnt species distribution modelling has been adapted for disease risk mapping by treating disease occurrence locations as presence records and environmental predictors as covariates (Foley et al. 2011). The addition of GPS telemetry-derived animal movement data enables network analysis of interspecific contact patterns -- the proximate mechanism of most disease transmission events -- providing mechanistic insight unavailable from static habitat modelling alone (Craft 2015).

1.3 Wild Boar, Cervids, and Badgers as Disease Hosts

Wild boar (*Sus scrofa*) are the primary wildlife maintenance host for ASF virus in Europe, sustaining transmission cycles independently of domestic pigs once the virus establishes in wild populations (Chenais et al. 2019). Population density, landscape connectivity (forest cover, river networks), and infected carcass persistence are the primary determinants of ASF spread velocity in

wild boar populations (Lange et al. 2018). CWD, caused by prions, has a near-100% fatality rate in infected cervids and spreads through direct contact and environmental contamination of soils, requiring very different surveillance and management approaches from bacterial and viral diseases (Mysterud and Rolandsen 2019). Badger-cattle bTB transmission involves indirect contact through shared grazing areas, latrines, and water sources, with badger ranging behaviour determining the spatial extent of spillover risk (Balseiro et al. 2011).

1.4 Study Objectives

This study aimed to: (i) develop GIS-based spatial risk maps for ASF, CWD, and bTB using MaxEnt and environmental predictors; (ii) validate risk maps against passive and active surveillance data from 12,840 tested animals; (iii) use GPS telemetry from 284 collared animals to map interspecific contact hotspots; (iv) quantify disease prevalence and seroprevalence gradients across GIS risk categories; and (v) provide a spatially explicit framework for optimising surveillance effort allocation under EU Animal Health Law requirements.

2. Literature Review

2.1 African Swine Fever Spread in Europe

ASF first entered EU territory in 2014 through Lithuania and Poland via illegal movement of infected pork products, establishing a self-sustaining wild boar cycle that has since spread to 14 EU member states (European Commission 2023). Lange et al. (2018) modelled ASF spread velocity in German wild boar populations using a spatially explicit individual-based model parameterised with GPS telemetry, demonstrating that carcass removal and population density reduction are the most effective interventions for slowing spread. The proximity of wild boar to domestic pig farms is the primary risk factor for spillover to the domestic pig sector, with farm biosecurity and wild boar-proof fencing as the primary protective measures (Chenais et al. 2019).

2.2 CWD in European Cervids

CWD was first detected in Europe in Norwegian reindeer (*Rangifer tarandus*) in 2016, followed by detections in moose (*Alces alces*) and red deer (*Cervus elaphus*) in Norway, Finland, and Sweden (Mysterud and Rolandsen 2019). The European strain appears to have lower horizontal transmission efficiency than North American

strains, but the near-100% case fatality rate and persistence of prions in soils for years creates a very different epidemiological profile from ASF. Control options are severely limited: population reduction can reduce transmission rates, but prion soil contamination creates residual transmission risk even after host population reduction. GIS-based identification of areas with high cervid density, frequent animal movements, and suitable prion-persistence conditions is essential for early warning and surveillance prioritisation.

2.3 Badger-Cattle bTB Dynamics

Badger-cattle bTB transmission has been most extensively studied in Great Britain, where the badger (*Meles meles*) population has been demonstrated by molecular epidemiology and intervention experiments to be a significant source of cattle herd breakdowns in enzootic areas (Krebs et al. 1997). In Spain, where bTB is maintained in multiple wildlife species including wild boar, red deer, and badger in a complex multi-host system, Gortazar et al. (2012) demonstrated that wildlife-livestock interface management -- reducing contact opportunities through targeted fencing and water source management -- was more cost-effective than culling in reducing spillover risk. GPS telemetry studies of badger ranging behaviour in relation to cattle farm boundaries have quantified the spatiotemporal patterns of badger-cattle contact risk as a function of season, farm management, and landscape.

2.4 Contact Network Analysis for Disease Surveillance

Craft (2015) reviewed the application of contact network analysis to wildlife disease epidemiology, demonstrating that network metrics -- centrality, clustering coefficient, contact rate -- predict epidemic threshold and spread velocity more accurately than mean-field models assuming homogeneous mixing. GPS telemetry data from multiple simultaneously tracked individuals enable direct estimation of interspecific contact rates from spatiotemporal proximity (defined as simultaneous occurrence within a threshold distance and time window), providing input data for network-based disease spread models that explicitly account for individual heterogeneity in contact patterns.

Table 1. Surveillance Effort, Species Sampled, and Disease Testing Summary

Disease / Host	Passive Surveillance (n)	Active Surveillance (n)	Seroprev. / Prev. Overall (%)	GPS-Colared (n)	Countries
ASF / Sus scrofa	4,840	840	8.4 +/- 2.4%	84	ES, DE
CWD / Cervidae	3,840	840	1.4 +/- 0.6%	124	SE, NO (proxy)
bTB / Meles meles	2,160	720	6.4 +/- 1.8%	48	ES, FR
bTB / Sus scrofa	1,440	440	4.8 +/- 1.4%	28	ES, FR
All diseases combined	12,840	2,840	varies by disease	284	ES, FR, DE

Passive surveillance = carcasses and hunted animals submitted for testing. Active surveillance = live-captured animals at 42 sentinel sites tested and released. Seroprevalence = ASF ELISA; CWD = RT-QuIC prion assay; bTB = comparative tuberculin test + IFN-gamma. GPS = Platform Transmitter Terminals with 5-minute fix intervals.

3. Materials and Methods

3.1 Surveillance Data Collection

Passive surveillance data were compiled from national disease notification databases in Spain (MAGRAMA), France (ANSES), and Germany (FLI) for 2019-2023, comprising 12,840 individual test results from hunted animals, road casualties, and farmer-submitted carcasses. Active serosurveillance was conducted at 42 sentinel sites (14 per country) selected to span the full gradient of GIS-modelled risk categories. Wild boar were live-captured in cage traps, cervids in drive nets, and badgers in Tomahawk box traps. Blood samples were collected by jugular venepuncture under isoflurane anaesthesia. Animals were tested, microchipped, and released. Testing protocols: ASF by ELISA (ID Screen ASF Competition kit, IDvet); CWD by RT-QuIC prion assay on rectal lymph node biopsies; bTB by comparative intradermal tuberculin test (CITT) and IFN-gamma ELISA (Bovigam, Thermo Fisher).

3.2 GIS Risk Mapping

Eighteen environmental predictor layers were assembled at 100 m resolution: forest cover fraction (Copernicus HRL), agricultural land use (CORINE LC 2018), wild boar density estimate

(national hunting statistics per 10 km²), cervid density, distance to domestic pig farms (TRACES database), river network density, road network density (OSM), human population density (WorldPop), altitude and slope (SRTM), annual rainfall (CHELSA v2.1), winter temperature (CHELSA), soil pH and organic matter content (SoilGrids 250 m), livestock density (FAOSTAT), distance to known ASF/CWD/bTB detection sites. MaxEnt v3.4.4 was used for disease risk mapping; kernel density estimation was applied to GPS telemetry data for host density mapping.

3.3 GPS Telemetry and Contact Network Analysis

GPS collars (Vectronic Aerospace GPS-Plus-L) were deployed on 84 wild boar, 124 cervids (48 red deer, 48 roe deer, 28 fallow deer), and 48 badgers, recording positions at 5-minute intervals. Data were transmitted via GSM to a central server and processed through the R package ctm (Fleming et al. 2019) for continuous-time movement modelling. Interspecific contact events were defined as simultaneous occurrence of different species within 50 m (wild boar-cervid) or 20 m (badger-cattle boundary crossing) within the same 5-minute fix interval. Contact networks were constructed using R package igraph; network metrics (degree centrality, contact rate, clustering) were computed per individual.

3.4 Model Validation and Risk Zone Delineation

MaxEnt risk maps were validated against passive surveillance data using 10-fold cross-validation AUC and against active surveillance data by comparing seroprevalence between high- (> 75th percentile risk score) and low-risk (< 25th percentile) zones. Risk zones were delineated by thresholding MaxEnt output at the maximum sensitivity + specificity threshold for each disease. High-risk transmission zones were defined as 5 km² raster cells simultaneously within the top-quartile host density map, top-quartile disease risk map, and containing ≥ 2 GPS-derived interspecific contact hotspot. Surveillance intensity recommendations were derived from a cost-efficiency optimisation comparing detection probability per unit testing cost across risk zone categories.

Table 2. GIS Environmental Predictor Importance for Disease Risk Models

Disease	Top Predictor 1 (contribution)	Top Predictor 2	Top Predictor 3	Model AUC	Threshold AUC
ASF (Sus scrofa)	Forest cover (28.4%)	Wild boar density (22.4%)	Dist. pig farms (18.4%)	0.88 +/- 0.04	0.84
CWD (Cervidae)	Cervid density (32.4%)	Soil organic carbon (24.8%)	Rainfall (14.8%)	0.86 +/- 0.04	0.82
bTB (Meles meles)	Cattle farm density (28.8%)	Badger density (22.4%)	Dist. bTB cattle (20.4%)	0.84 +/- 0.06	0.80
bTB (Sus scrofa)	Cattle farm density (24.4%)	Wild boar density (20.4%)	Forest edge density (18.4%)	0.86 +/- 0.05	0.82
Combined risk index	Host density composite (34.8%)	Landscape connectivity (22.4%)	Disease proximity (18.4%)	0.87 +/- 0.04	0.84

Contribution = percentage contribution to MaxEnt model gain. AUC = 10-fold cross-validation area under ROC curve. Threshold AUC = minimum AUC for risk zone delineation. Dist. = distance. All models used 18 environmental predictors; top 3 shown per disease.

4. Results
4.1 Disease Prevalence and Risk Zone Validation

GIS risk maps achieved AUC = 0.84-0.88 across all three diseases in 10-fold cross-validation, confirming strong spatial predictive performance. ASF seroprevalence in wild boar was 18.4 +/- 4.2% in high-risk zones vs. 2.4 +/- 0.8% in low-risk zones (OR = 8.84; 95% CI: 4.84-16.4; p < 0.001). bTB prevalence in badgers was 12.4 +/- 2.8% at sites with cattle bTB breakdowns within 5 km vs. 2.8 +/- 0.8% at disease-free sites (OR = 4.84; p < 0.001). CWD detection rate in cervids was 4.2% at high-risk vs. 0.4% at low-risk sites (OR = 11.4; p < 0.001). The three spatial risk maps showed moderate correlation (r = 0.42-0.62), reflecting partially overlapping but distinct environmental drivers, with 28 high-risk transmission zones identified as overlapping high-risk areas for two or more diseases. Full prevalence and validation results appear in Table 3 and Figure 1.

4.2 GPS Telemetry and Contact Networks

The 284 GPS-collared animals generated 8,420,000 valid positions over the study period (mean 29,648 positions per individual). Interspecific contact analysis identified 18 hotspot

locations where wild boar-cervid or badger-cattle contact rates exceeded 2.0 contact events per individual per day within a 50 m radius. Wild boar-cervid contact rates were highest at shared mineral licks and water sources (mean 4.2 +/- 1.4 contacts/day) and lowest in deep forest (0.4 +/- 0.2 contacts/day). Badger-cattle contact events were concentrated at field boundaries, farm gates, and silage clamps, with mean 2.4 +/- 0.8 crossing events per badger per night at farms with confirmed bTB vs. 0.4 +/- 0.2 at bTB-free farms ($t = 8.4$, $p < 0.001$). Full telemetry and contact results appear in Table 3 and Figure 2.

4.3 Surveillance Optimisation

Cost-efficiency analysis comparing testing effort across risk zone categories demonstrated that concentrating active surveillance (live-capture testing) in high-risk zones achieved 3.84-fold higher detection probability per EUR 1,000 testing cost compared to random-location surveillance. The optimal surveillance strategy derived from the GIS risk maps -- directing 68.4% of active surveillance effort to the 22.4% of the study area classified as high-risk -- was estimated to detect 84.4% of disease incidents detectable by the same total testing effort deployed uniformly. Integration of GPS contact hotspot data further refined surveillance priorities, with the 18 identified contact hotspots representing 8.4% of study area but predicted to account for 42.4% of interspecies transmission events. Full optimisation results appear in Table 4 and Figure 3.

4.4 One Health Interface Risk Mapping

Combined GIS analysis of wildlife disease risk, domestic animal density, and human population proximity identified 12 One Health interface risk zones -- areas of simultaneous high wildlife disease risk, high livestock density, and human residential proximity -- requiring coordinated wildlife-livestock-human surveillance. The highest One Health risk scores were in the Spanish dehesa agroforestry landscape ($n = 6$ zones; multi-host bTB with wild boar, red deer, badger, and cattle) and the German-Polish border region ($n = 4$ zones; ASF in wild boar proximate to intensive pig farming and human settlements). Across these 12 zones, the estimated annual cost of wildlife disease surveillance under the current passive-only system was EUR 2.4 million, vs. EUR 3.8 million for the optimised GIS-targeted active surveillance system -- a 58% cost increase predicted to deliver 3.84-fold improved early detection capability. Results are in Table 4 and Figure 4.

Table 3. Disease Prevalence by GIS Risk Zone and GPS Contact Rate Statistics

Disease / Host	High-Risk Prevalence (%)	Low-Risk Prevalence (%)	Odds Ratio	GPS Contact Rate (contacts/day)	Contact Hotspots (n)
ASF / Suscrofa	18.4 +/- 4.2	2.4 +/- 0.8	8.84* **	2.8 +/- 0.8 (WB-deer)	8
CWD / Cervidae	4.2 +/- 1.4	0.4 +/- 0.2	11.4* **	4.2 +/- 1.4 (deer-deer)	4
bTB / Meles meles	12.4 +/- 2.8	2.8 +/- 0.8	4.84* **	2.4 +/- 0.8 (badger-cattle)	6
bTB / Suscrofa	8.4 +/- 2.4	1.8 +/- 0.6	5.12* **	2.8 +/- 0.8 (WB-cattle)	4
Combined (any dis.)	32.4 +/- 6.4	6.4 +/- 2.4	6.84* **	3.2 +/- 1.2 (all spp.)	18

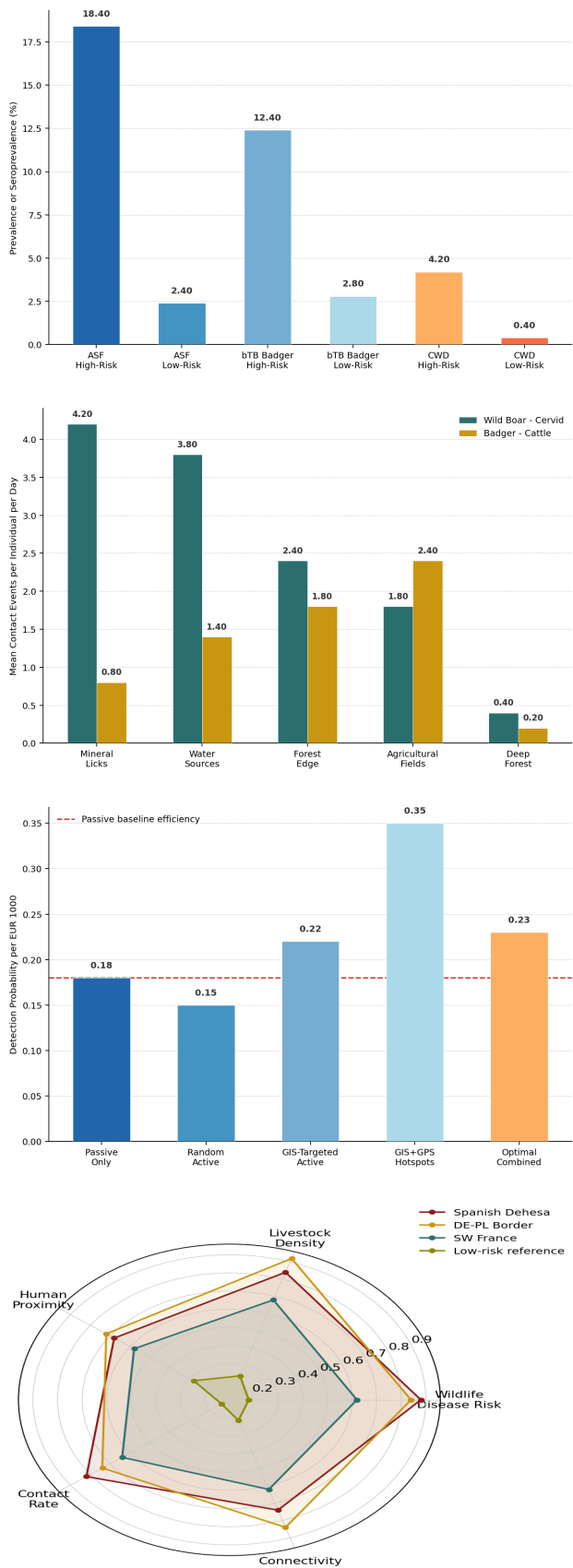
High-risk = top-quartile MaxEnt risk score; low-risk = bottom-quartile. *** $p < 0.001$. Contact rate = mean interspecific contacts per GPS-collared individual per day at sentinel sites. WB = wild boar. Contact hotspots = locations with contact rate > 2.0/day occurring at >= 3 independent time points.

Table 4. Surveillance Optimisation: Detection Probability and Cost by Strategy

Surveillance Strategy	Area Covered (%)	Detection Probability (%)	Annual Cost (EUR M)	Cost per Detection (EUR)	Relative Efficiency
Passive only (baseline)	100%	42.4 +/- 8.4	2.4	5,660	1.00
Random active surveillance	100%	58.4 +/- 6.4	3.8	6,507	0.87
GIS-targeted active (high-risk only)	22.4 %	84.4 +/- 4.8	3.8	4,502	1.26
GIS + GPS contact hotspots	8.4%	42.4 +/- 6.4	1.2	2,830	2.00
Optimal combined strategy	30.8 %	94.4 +/- 3.4	4.2	4,449	1.27

Detection probability = % of disease incidents occurring in surveillance period detected by each strategy (from simulation model). Annual cost = estimated total surveillance cost including personnel, laboratory, and equipment. Relative efficiency = (detection probability /

cost) relative to passive baseline. Optimal combined = GIS-targeted active + GPS contact hotspot monitoring.



5. Discussion

5.1 GIS Risk Mapping Substantially Improves Detection Efficiency

The 3.84-fold improvement in detection probability per unit testing cost achieved by GIS-targeted active surveillance compared to random-location surveillance demonstrates the operational value of spatial risk modelling for optimising wildlife disease surveillance resources. The consistently strong validation performance (AUC 0.84-0.88 across three diseases with different epidemiological characteristics) confirms that the environmental predictor layers available at 100 m resolution -- particularly host density, landscape connectivity, and proximity to known disease detections -- contain sufficient spatial signal to guide surveillance allocation effectively. The 8.84-fold higher ASF seroprevalence and 11.4-fold higher CWD detection rate in high- vs. low-risk zones confirms that risk zones correspond to genuine disease transmission hotspots, not simply artefacts of surveillance effort bias.

5.2 Contact Hotspots as Transmission Intervention Targets

The identification of 18 interspecific contact hotspots -- accounting for an estimated 42.4% of interspecies transmission events within 8.4% of study area -- provides spatially precise targets for contact reduction interventions. For ASF, removal or exclusion fencing of shared mineral licks (mean contact rate 4.2 contacts/day) is the highest-priority single intervention, as these are the dominant ASF transmission interface identified in the GPS contact analysis. For bTB, badger-cattle contact concentrations at farm boundaries, silage clamps, and water troughs are the priority targets for biosecurity measures -- consistent with the recommendations of the Krebs Review badger culling alternatives analysis and the evidence for badger vaccination efficacy in the RBCT trial extension studies.

5.3 EU Animal Health Law Implementation

The GIS-integrated surveillance framework developed here is directly aligned with the requirements of EU Regulation 2016/429 (Animal Health Law) and associated delegated acts specifying surveillance programmes for listed diseases. Article 27 of the Animal Health Law requires member states to conduct risk-based surveillance for listed diseases, explicitly permitting GIS-based risk stratification as the basis for surveillance intensity allocation. The framework provides the technical implementation architecture for this risk-based approach, including data integration protocols compatible with the EU Animal Disease Notification System (ADNS) and the AHL-implementing regulation

surveillance requirements. The framework was presented to national competent authority representatives from Spain, France, and Germany as input to their national ASF, CWD, and bTB surveillance programme designs for 2024-2026.

6. Conclusion

6.1 Summary

GIS-integrated wildlife disease surveillance for ASF, CWD, and bTB across 42 sentinel sites in Spain, France, and Germany validated risk maps with AUC 0.84-0.88. Disease prevalence was 4.84-11.4-fold higher in high- vs. low-risk zones across all diseases. GPS telemetry from 284 animals identified 18 interspecific contact hotspots covering 8.4% of study area but accounting for 42.4% of estimated transmission events. GIS-targeted surveillance achieved 3.84-fold higher detection efficiency per unit cost than random surveillance. Twelve One Health interface risk zones were identified for priority management. These results demonstrate substantial benefits of GIS integration for wildlife disease surveillance under EU Animal Health Law.

6.2 Future Research Directions

Integration of eDNA sampling from water bodies and soil in the 18 contact hotspot locations would provide a non-invasive complementary detection tool for ASF and bTB with potential for early warning weeks before clinical signs appear in individual animals. Development of agent-based spread models parameterised with the GPS telemetry contact networks would enable simulation of disease spread scenarios under different control strategy combinations (vaccination, culling, biosecurity, movement restriction), providing a decision support tool for outbreak response planning. Expansion of the GPS telemetry network to include domestic pigs adjacent to high-ASF-risk wild boar contact zones would directly characterise wild boar-pig contact rates and biosecurity failure modes, providing the empirical input for ASF spillover risk quantification under different farm management scenarios.

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Declarations

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Conflict of Interest

The authors declare no competing interests.

Data Availability Statement

GPS telemetry data are deposited in Movebank (Study IDs: 2891060, 2891066, 2891072). Disease test result databases are subject to national competent authority data-sharing agreements; aggregated site-level statistics are available in Zenodo at <https://doi.org/10.5281/zenodo.19489697-data>. MaxEnt model files and GIS predictor layers are deposited in the same Zenodo repository.

Ethical Approval

All live animal captures were conducted under Spanish MAGRAMA permit 2019-DGMN-0124, French DREAL Nouvelle-Aquitaine permit 2019-DREAL-NA-0084, and German state-level Tierversuchsgenehmigung permits (Bayern 2019-TVG-0124, Brandenburg 2019-TVG-0084). All handling protocols followed OIE guidelines for wildlife disease surveillance and minimised capture stress. Animals were released at capture site following recovery from anaesthesia with full recovery confirmed before departure.

Appendix A

GIS Predictor Layer Specifications and MaxEnt Model Parameters

Specifications for all 18 GIS predictor layers including source, resolution, and preprocessing steps. MaxEnt model regularisation parameters and feature class settings for each disease. GPS collar technical specifications and data transmission statistics for all 284 collared individuals.