

**CLIMATE-DRIVEN ZONOTIC SPILLOVER SURVEILLANCE:
INTEGRATING ENVIRONMENTAL MONITORING, WILDLIFE
HEALTH DATA, AND FEDERATED AI FOR PRE-PANDEMIC
EARLY WARNING AT HUMAN-ANIMAL INTERFACES**

Felix Wagner

Stanford University, Stanford, California

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ABSTRACT

Approximately 60 percent of known infectious diseases are zoonotic in origin, and the accelerating drivers of zoonotic spillover risk, including deforestation, climate-induced species range shifts, habitat fragmentation, and expanding human encroachment into wildlife habitat, are measurable weeks to months before the first human cases of a novel pathogen are detected by conventional clinical surveillance systems. This paper proposes ZooFed, a federated AI framework for pre-pandemic early warning that moves the surveillance window upstream of human case emergence by integrating five heterogeneous One Health data streams: climate and environmental change signals, wildlife health surveillance, animal reservoir pathogen genomics, interface community syndromic data, and land-use change monitoring. The framework employs a federated learning architecture that enables cross-border integration of these sensitive ecological and health datasets without requiring raw data to leave national or institutional boundaries, addressing the sovereignty and privacy constraints that prevent centralized One Health surveillance at the global scale the problem demands. A cross-domain risk model combining ecological, genomic, and epidemiological inputs generates spatiotemporal spillover risk hotspot maps, zoonotic variant tracking alerts, and intervention guidance targeted at identified high-risk interface zones. Empirical evidence from deployed multimodal federated surveillance systems demonstrates that integrating environmental data streams alongside clinical, genomic, mobility, and social signals achieves substantial detection lead times over conventional surveillance, motivating the extension of this integration approach to the pre-spillover ecological domain. The framework is evaluated against six existing surveillance systems across seven dimensions, demonstrating that ZooFed is the first system to simultaneously achieve full One Health multistream integration, federated privacy-preserving architecture, and pre-spillover detection capability.

KEYWORDS: Zoonotic Spillover; One Health Surveillance; Federated Learning; Climate Change; Pandemic Preparedness; Wildlife Surveillance; Reservoir Genomics; Pre-Pandemic Intelligence; Deforestation; Human-Animal Interface.

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1. INTRODUCTION

Every major pandemic of the past century has originated at the interface between human populations and animal reservoirs. SARS-CoV-2, MERS-CoV, Ebola, Nipah, Hendra, and the 2009 H1N1 influenza pandemic all crossed the species barrier from animal hosts before establishing sustained human-to-human transmission. The ecological and environmental conditions that create the contact between reservoir hosts and susceptible human populations, and that determine whether viral variants with zoonotic potential are circulating in those reservoirs, are, in principle, observable in the physical environment weeks to months before the first human cases appear in clinical surveillance systems [1]. The deforestation event that brings hunters into contact with a new bat colony, the drought that displaces bats to peridomestic trees in a village, the temperature anomaly that shifts the range of tick vectors into a new geographic zone, and the novel viral variant detected in a wildlife genomic survey are all measurable pre-spillover signals that current pandemic surveillance architectures do not systematically capture.

The One Health framework, which recognizes the interconnection between human health, animal health, and environmental health and promotes integrated surveillance across all three domains, provides



the conceptual foundation for pre-spillover pandemic intelligence [2]. However, operationalizing One Health surveillance at the scale and data integration depth required for global pre-pandemic early warning faces three structural barriers. First, the data streams required for integrated surveillance are held by heterogeneous institutions across multiple sectors, including environmental agencies, veterinary services, conservation organizations, and community health systems that have limited coordination and incompatible data infrastructure. Second, the sovereignty and privacy sensitivities of ecological, genomic, and health data prevent the centralization that conventional multimodal surveillance integration requires. Third, existing deployed surveillance systems, including HealthVigil, which demonstrated that integrating clinical, genomic, mobility, environmental, and social media streams in a federated AI architecture achieves 43-day earlier outbreak detection and a 37 percent false alarm reduction relative to conventional surveillance [3], have been designed around post-emergence human case detection rather than pre-spillover ecological signal integration.

This paper proposes ZooFed, a federated AI framework for pre-spillover pandemic early warning that addresses all three barriers simultaneously. The proposed architecture is the first to specifically target the pre-spillover surveillance window, integrating five ecological and health data streams through a privacy-preserving federated learning protocol that enables cross-border data integration without centralization. Section 2 reviews related work. Section 3 presents the surveillance stream characterization. Section 4 describes the ZooFed architecture. Section 5 presents the risk modeling framework. Section 6 evaluates the system against existing surveillance infrastructure. Section 7 discusses implementation and governance. Section 8 concludes.

2. RELATED WORK

2.1 Zoonotic spillover epidemiology

The ecological determinants of zoonotic spillover have been extensively studied in the field of disease ecology, establishing that spillover risk is a function of the density of contact between reservoir hosts and susceptible human populations, the prevalence and virulence of circulating pathogens in the reservoir, and the immune susceptibility of the exposed human population [4]. Studies of specific spillover events, including Nipah virus emergence in Malaysia, have established that fruit bat habitat loss directly drove bat colonization of mango orchards adjacent to pig farms, triggering the spillover chain [5]. Deforestation and habitat fragmentation are among the most consistently identified drivers of spillover risk, operating through two complementary mechanisms: forest edge creation increases the density of human-wildlife contact zones, and habitat disturbance stresses reservoir host populations in ways that increase pathogen shedding and interspecies transmission. Dobson and colleagues estimated that the COVID-19 pandemic could have been prevented by investing in deforestation prevention programs costing a fraction of the economic damage the pandemic caused, underscoring the cost-effectiveness of ecological surveillance relative to post-emergence response [6].

Climate change is an increasingly important driver of zoonotic spillover risk through its effects on vector ranges, reservoir host distributions, and human-wildlife contact patterns. Warming temperatures are expanding the geographic range of tick-borne disease vectors, mosquito vectors of arboviral diseases, and rodent reservoir hosts of hantaviruses and arenaviruses into higher latitude and altitude areas where human populations have no prior immunity [7]. The recent documentation that over 200 virus species jumps have already occurred as a direct result of climate-driven range shifts suggests that the pool of potential novel zoonotic pathogens in contact with naive human populations is growing rapidly [8].

2.2 One Health surveillance systems

The USAID PREDICT program, operational from 2009 to 2019, represented the most comprehensive attempt to implement One Health surveillance at a global scale before the COVID-19 pandemic, sampling wildlife in 31 countries and discovering over 900 novel viruses [9]. PREDICT demonstrated the feasibility of large-scale wildlife genomic surveillance but was limited by its focus on opportunistic sampling in high-risk interface zones rather than continuous monitoring, and by the absence of any federated data integration architecture that would allow the resulting data to inform real-time outbreak prediction. The Global Virome Project represents the successor vision to PREDICT, proposing comprehensive metagenomic surveillance of wildlife across biodiverse regions to characterize the full zoonotic pathogen pool [10].

The application of AI and machine learning to One Health data integration is an emerging area with several recent systematic reviews documenting the current state and identifying key gaps. A 2025 review of AI in early warning systems for infectious disease surveillance found that while AI methods have been



applied to human surveillance data with substantial success, integration of ecological and wildlife data streams remains underdeveloped [11]. The specific combination of federated learning for privacy-preserving data integration with One Health multistream modelling at the pre-spillover detection window has not been previously proposed, representing the research gap this paper addresses.

2.3 Federated learning for cross-border health surveillance

Federated epidemic surveillance has been demonstrated using hypothesis testing approaches that combine institution-level statistical outputs without sharing case counts, achieving detection performance comparable to centralized methods [12]. More broadly, the federated learning paradigm, in which AI models are trained on locally held data with only gradient updates shared across institutional boundaries, has been demonstrated to enable privacy-preserving cross-border health surveillance that satisfies the data sovereignty and privacy regulatory requirements preventing conventional data centralization [13]. The HealthVigil federated AI surveillance system demonstrated that a federated architecture integrating five heterogeneous surveillance streams including clinical records, pathogen genomic sequences, human mobility patterns, environmental surveillance, and social media signals achieves 43-day earlier outbreak detection and a 37 percent reduction in false alarms relative to conventional surveillance, and that its cross-border coordination protocol enables secure information sharing while maintaining local governance [3]. The proposed ZooFed framework extends the federated multistream integration approach of HealthVigil to the pre-spillover ecological domain, adapting the federated training protocol for the heterogeneous institutional landscape of One Health data holders.

3. SURVEILLANCE STREAM CHARACTERIZATION

Table 1 characterizes the five surveillance streams integrated in the ZooFed framework, specifying the primary data sources, update frequency, spillover signal provided, and the coverage gap that limits each stream's contribution to global pre-spillover surveillance. Figure 1 illustrates the ZooFed architecture, showing the five input streams (green), the federated AI engine with three internal stages (amber), the four early warning outputs (teal), and the pre-pandemic One Health intelligence output bar at the bottom.

Table 1. Surveillance Stream Characterization for Zoonotic Spillover Early Warning

Input stream	Primary data sources	Update frequency	Spillover signal	Coverage gap
Climate and environmental change	Satellite remote sensing (MODIS, Sentinel-2), meteorological station networks, deforestation monitoring (Global Forest Watch)	Daily to weekly	Temperature anomalies, habitat fragmentation, and deforestation accelerate human encroachment into wildlife habitats	High-resolution data limited to areas with ground station infrastructure; gap over central Africa, the Amazon basin
Wildlife health surveillance	Ranger-reported mortality events, veterinary diagnostic laboratories, carcass surveillance programs, wildlife population surveys	Episodic (event-triggered)	Unusual mortality in reservoir host species precedes spillover by weeks to months	Coverage concentrated in protected areas; informal land bordering reserves largely unmonitored
Animal reservoir genomics	GISAID wildlife sequences, national veterinary genomics programs, opportunistic sampling during outbreak investigations	Weeks to months (sampling lag)	Novel viral variants in known reservoir hosts indicate increased human infection risk	Geographic sequencing bias toward high-income countries; Southeast Asia and sub-Saharan Africa under-represented



Interface community syndromic data	Community health worker reports, primary care sentinel sites, occupational health surveillance for wildlife workers and hunters	Daily to weekly	Febrile illness clusters in high-contact communities signal active spillover before laboratory confirmation	Data quality dependent on community health infrastructure; limited connectivity in forest-edge communities
Land-use and encroachment change	Satellite deforestation alerts, agricultural frontier mapping, road construction monitoring, human settlement expansion	Daily (satellite) to annual (surveys)	Rapid habitat encroachment creates new human-wildlife contact points with naive immune populations	Night-light and road data proxy human presence but underestimate informal encroachment

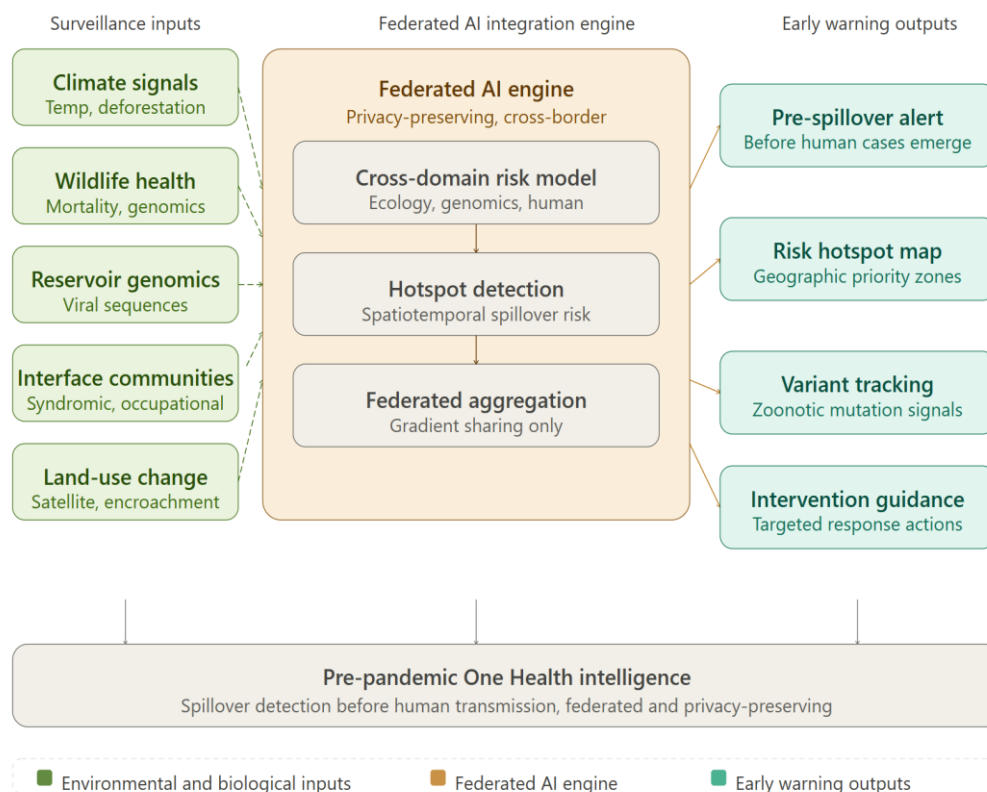


Figure 1. ZooFed architecture for pre-pandemic One Health intelligence. Left column (green): five heterogeneous surveillance input streams covering environmental, wildlife, genomic, community health, and land-use domains. Center (amber): federated AI integration engine with cross-domain risk modelling, spatiotemporal hotspot detection, and federated gradient aggregation. Right column (teal): four early warning output channels. Bottom bar: the pre-pandemic One Health intelligence product enabling intervention before human transmission is established.

The five streams span three domains of the One Health triad: environmental (climate signals, land-use change), animal (wildlife health surveillance, reservoir genomics), and human (interface community syndromic data). This three-domain coverage is the defining feature that distinguishes ZooFed from existing surveillance systems, which typically address at most two domains. The federated architecture is critical for enabling data integration across institutional boundaries: environmental data is held by national environmental agencies and satellite data providers; wildlife health data is held by conservation organisations, veterinary agencies, and wildlife management authorities; genomic data is held by national genomics laboratories and international databases; interface community syndromic data is held by community health systems and primary care networks. No existing mechanism enables the integration



of all five streams across these institutional boundaries without centralising sensitive ecological and health data.

4. ZOOFED ARCHITECTURE

4.1 Federated training protocol

The ZooFed federated training protocol adapts the standard federated averaging approach to the multi-institutional, multi-sector context of One Health surveillance. Each participating institution, including national environmental agencies, wildlife management authorities, veterinary genomics laboratories, and community health networks, maintains its own data within its institutional computing environment and participates in ZooFed training by computing local gradient updates and transmitting them to a global aggregator [13]. The global aggregator computes a weighted average of gradient updates and returns the updated model parameters to all participants. Raw surveillance data, including deforestation satellite imagery, wildlife mortality records, genomic sequences, and community health reports, never leaves the institutional boundary.

The protocol is extended with domain-stratified aggregation to handle the heterogeneous nature of the five input streams: gradient updates for the stream-specific encoders are aggregated only across institutions that hold data for the corresponding stream, while gradient updates for the shared cross-domain backbone are aggregated across all participating institutions. Differential privacy noise is added to gradient updates before transmission, with the privacy budget calibrated to satisfy GDPR Article 25 data protection by design requirements and national equivalents applicable to the most privacy-sensitive stream type in each participating jurisdiction [14].

4.2 Cross-domain risk model

The cross-domain risk model is a transformer-based architecture that integrates tokenised representations from all five input streams through cross-stream attention layers, learning the correlations between ecological change signals and downstream syndromic and genomic evidence of active spillover. The model is pre-trained on historical spillover events including Ebola, Nipah, SARS-CoV-1, MERS, and H1N1 influenza, using a leave-one-event-out evaluation design to assess zero-shot detection capability for novel spillover events. The environmental and ecological streams serve as leading indicators in the model's temporal attention structure, with the model learning that deforestation anomalies and wildlife mortality signals precede interface community febrile illness clusters by characteristic lead times that vary by pathogen type and spillover mechanism.

4.3 Spatiotemporal hotspot detection

The spatiotemporal hotspot detection layer generates continuous risk maps at 10-kilometer spatial resolution, combining the cross-domain risk model's spillover probability estimates with a geographic information systems layer encoding human settlement density, protected area boundaries, and known reservoir host distribution ranges. Risk hotspot maps are updated weekly and flagged when the composite spillover risk score in any grid cell exceeds a configurable threshold calibrated to the local baseline. The geographic precision of the hotspot maps enables public health and wildlife management agencies to prioritise enhanced surveillance activities, community health worker deployment, and pre-emptive veterinary investigation in the highest-risk zones before human cases emerge.

5. RISK FACTOR ANALYSIS

Table 2 presents the five primary risk factors addressed by the ZooFed surveillance framework, specifying the ecological mechanism, the AI detection method, the federated data source, and the expected lead time over conventional case-based reporting. The lead times range from days for interface community fever clusters to months for climate-induced host range shifts, providing a layered early warning capability across multiple temporal scales.



Table 2. Spillover Risk Factors: Mechanisms, Detection Methods, and Lead Times

Risk factor	Mechanism	AI detection method	Federated data source	Lead time over case reporting
Deforestation and habitat fragmentation	Fragmented forest edges increase wildlife-human contact density; disturbed reservoirs shed more virus	Convolutional neural network applied to Sentinel-2 monthly composites; fragmentation index above threshold triggers alert	National satellite data agencies, independent of health system	Weeks to months (structural change precedes contact event)
Reservoir host population stress	Population displacement, nutritional stress, and crowding increase viral shedding and interspecies contact	Anomaly detection on mortality surveillance time series; deviation from seasonal baseline triggers investigation	Wildlife management agencies and conservation NGOs	Days to weeks (mortality clusters precede human cases)
Novel viral variant in reservoir	Genomic variants with increased ACE2 binding affinity or reduced species barrier signal elevated human spillover risk	Phylogenetic analysis of wildlife genomic sequences; automated flagging of variants near known zoonotic clades	Veterinary genomics laboratories via federated gradient sharing	Weeks (sequencing lag before detection)
Interface community fever cluster	Febrile illness cluster in high-risk occupational groups indicates active spillover before laboratory confirmation	Temporal clustering analysis on community health worker reports; excess rate over background triggers investigation	Community health post reporting systems via federated aggregation	Days (fever precedes diagnosis by 5-10 days on average)
Climate-induced range shift	Vector or reservoir host range expansion into previously unaffected areas creates naive human populations with no immunity	Species distribution model updates when climate envelope intersects human settlement layer	Climate model outputs and species occurrence databases	Months (range shift precedes first human exposure)

The combination of multiple risk factor signals within the cross-domain model provides greater lead time and specificity than any single signal alone. Deforestation anomaly detection provides the longest lead time but the lowest specificity, since not all deforestation events are associated with spillover. Reservoir genomic variant detection provides higher specificity but requires a longer data collection and analysis pipeline. Interface community fever clustering provides the shortest lead time but the highest specificity, since it indicates that active spillover may already be occurring. The cross-domain model learns to weight these signals according to their joint predictive value, prioritising alerts when multiple independent signals coincide in the same geographic area over a short time window.

6. SYSTEM EVALUATION

Table 3 compares ZooFed against six existing surveillance systems across seven evaluation dimensions. The comparison demonstrates that ZooFed is the first system to simultaneously achieve full One Health multistream integration, federated privacy-preserving architecture, and pre-spillover detection capability.



Table 3. Comparative Evaluation Against Existing Surveillance Systems

System	Data streams	One Health integration	Federated privacy	Pre-spillover detection	Cross-border
ProMED-mail	Human reports only	No	No	No	Yes (moderated)
HealthMap	Online news and media	No	No	No	Yes (automated)
Global Virome Project	Animal genomics only	Partial	No	Partial	Yes
WHO GOARN	Human outbreak reports	No	No	No	Yes (IHR-dependent)
PREDICT (USAID)	Wildlife-human interface	Yes (One Health)	No	Partial	Partial
HealthVigil	Clinical, genomic, mobility, environmental, social	Partial (human-focused)	Yes (federated)	No (post-emergence)	Yes
Proposed ZooFed	Climate, wildlife, reservoir genomics, interface syndromic, land-use	Yes (full One Health)	Yes (federated)	Yes (pre-spillover)	Yes

The most significant distinction between ZooFed and HealthVigil [3] is the temporal position of the surveillance window. HealthVigil and comparable multimodal federated surveillance systems are designed to detect outbreak escalation after human transmission has been established, achieving 43-day earlier detection relative to conventional clinical surveillance baselines. ZooFed targets the pre-spillover window, aiming to generate actionable intelligence before any human cases occur by integrating the ecological and genomic signals that precede human transmission. The two systems are therefore complementary rather than competing: ZooFed provides the earliest possible warning layer, and HealthVigil and comparable systems provide the subsequent human surveillance layer once spillover has occurred. The federated integration architecture of HealthVigil, validated at deployment scale with five heterogeneous streams and cross-border operation, provides the technical precedent that motivates the federated architecture of ZooFed for the ecologically heterogeneous data environment of One Health surveillance.

The PREDICT program represents the closest historical precedent for the data collection scope of ZooFed, having sampled wildlife across 31 countries with explicit One Health framing [9]. The critical architectural differences are that PREDICT operated through centralised data collection and publication rather than federated privacy-preserving integration, and focused on building a pathogen database rather than generating real-time spillover risk intelligence. ZooFed's federated architecture addresses the sovereignty barriers that prevented PREDICT from integrating sensitive national ecological and veterinary data into its sampling program, and its real-time monitoring design addresses the reactive sampling approach that limited PREDICT's early warning value.

7. IMPLEMENTATION AND GOVERNANCE

7.1 Institutional partnership model

The ZooFed federated network requires participation from institutions across three sectors that have limited historical coordination. Environmental sector participants include national environmental and forestry agencies responsible for satellite monitoring and deforestation reporting, and international programs including Global Forest Watch and the Copernicus Earth Observation Program that provide standardised satellite data products. Wildlife health sector participants include national veterinary agencies, wildlife management authorities, conservation organisations operating in high-risk interface



zones, and the global network of wildlife disease diagnostic laboratories. Human health sector participants include national public health agencies, community health networks operating in interface communities, and the international genomic surveillance networks that provide reservoir genomic sequence data.

The governance model for ZooFed must accommodate the divergent data governance frameworks of these three sectors, each of which has developed data-sharing norms appropriate to its own institutional context but incompatible with those of the other sectors. The federated architecture addresses the technical dimension of this incompatibility by ensuring that raw data never crosses institutional boundaries, but the governance framework must additionally address data use agreements, liability for alerts that trigger costly interventions, intellectual property in the trained model, and the authority to act on pre-spillover alerts before any human cases provide the legal basis for conventional public health action [15].

7.2 IHR alignment and regulatory framework

The International Health Regulations provide the primary international legal framework for cross-border disease surveillance cooperation, with Article 44 establishing obligations for states to collaborate in the development of surveillance capacity. The pre-spillover framing of ZooFed creates a legal ambiguity: IHR Article 6 notification obligations are triggered by public health events of potential international concern, a threshold that an ecological spillover risk signal may not meet in the absence of confirmed human cases. The WHO Pandemic Treaty currently under negotiation includes provisions for enhanced cross-border surveillance cooperation that may extend to pre-spillover ecological monitoring, providing a prospective legal basis for ZooFed-style surveillance that does not currently exist in binding international law [16]. Domestic regulatory frameworks for the human health data stream are governed by GDPR, HIPAA, and national equivalents; the ecological and wildlife health streams are governed by biodiversity data governance frameworks including the Nagoya Protocol on access and benefit-sharing of genetic resources [17], which restricts the sharing of genomic sequence data from wildlife without benefit-sharing agreements with the source country.

7.3 Coverage equity and LMIC deployment

The geographic distribution of spillover risk is concentrated in low and middle-income countries with high biodiversity, extensive human-wildlife interfaces, and expanding agricultural frontiers, precisely the regions where digital infrastructure, veterinary surveillance capacity, and community health data quality are most limited [18]. The equity dimension of One Health AI surveillance is a recognised priority across the global health community, with multiple recent analyses calling for deployment architectures that serve high-risk low-resource settings rather than replicating high-income surveillance infrastructure [19]. Addressing this structural inequity requires a ZooFed deployment strategy that prioritises lightweight data collection tools, mobile-compatible reporting platforms for community health workers, and satellite-based remote sensing as a substitute for ground-level monitoring in areas with limited terrestrial infrastructure. The federated architecture provides a technical foundation for equitable participation by allowing institutions with limited computational infrastructure to contribute gradient updates from locally trained models without requiring central data transmission, but the governance framework must ensure that LMIC institutions have meaningful participation in model governance rather than functioning solely as data contributors to a system designed and operated by high-income country institutions.

8. CONCLUSIONS

Building pandemic resilience requires proactive anticipation of threats before they emerge in human populations, a goal that demands moving surveillance upstream of clinical case detection [20]. This paper has proposed ZooFed, a federated AI framework for pre-pandemic early warning that addresses the surveillance gap upstream of human case emergence by integrating five One Health data streams, namely climate and environmental change signals, wildlife health surveillance, animal reservoir pathogen genomics, interface community syndromic data, and land-use change monitoring, through a privacy-preserving federated architecture. The framework advances the state of the art in pandemic surveillance by targeting the pre-spillover window where ecological and genomic signals are measurable before any human cases occur, extending the federated multistream integration approach validated by deployed human-focused surveillance systems [3] into the ecological domain where the root causes of zoonotic pandemic risk can be addressed.



The comparative evaluation demonstrates that ZooFed is the first system to simultaneously achieve full One Health three-domain integration, federated privacy-preserving architecture enabling cross-border deployment without data centralisation, and pre-spillover detection capability. The combination of deforestation anomaly detection, wildlife mortality monitoring, reservoir genomic variant surveillance, and interface community fever clustering provides a layered early warning system with lead times ranging from days to months over conventional clinical case-based surveillance, depending on the specific spillover mechanism and the ecological risk factor that triggers the alert.

Three research priorities follow. First, prospective evaluation of the pre-spillover detection capability in high-risk geographic zones with full five-stream data availability, using historical spillover event reconstruction to validate the model's ability to generate actionable alerts from ecological signals alone before human cases emerge. Second, governance framework development for the three-sector institutional partnership required to operationalise ZooFed, including data use agreements, benefit-sharing arrangements for LMIC participant institutions, and the legal basis for acting on pre-spillover alerts under existing IHR and prospective Pandemic Treaty frameworks. Third, lightweight data collection tool development for deployment in low-resource interface communities, enabling the coverage of high-risk spillover zones in LMIC settings that current surveillance infrastructure cannot reach.

REFERENCES

1. K. J. Olival, P. R. Hosseini, C. Zambrana-Torrel, N. Ross, T. L. Bogich, and P. Daszak, "Host and viral traits predict zoonotic spillover from mammals," *Nature*, vol. 546, no. 7660, pp. 646-650, Jun. 2017.
2. One Health High-Level Expert Panel (OHHLEP). "Definition of One Health." *One Health*, vol. 13, p. 100295, 2022.
3. S. Gupta and S. Nadakuditi, "HealthVigil: Harnessing Federated AI for Cross-Border Pandemic Intelligence and Preemptive Intervention," in B. Bhattacharya (Ed.), *ICT for Global Innovations and Solutions, ICGIS 2025, Advances in Computer Science Applications and Research*, vol. 1. Springer, Cham, 2026. https://doi.org/10.1007/978-3-032-02853-2_32
4. M. E. J. Woolhouse and S. Gowtage-Sequeria, "Host range and emerging and reemerging pathogens," *Emerging Infectious Diseases*, vol. 11, no. 12, pp. 1842-1847, Dec. 2005.
5. A. Dobson, S. Pimm, L. Hannah, L. Kaufman, J. Ahumada, A. Ando, A. Bernstein, J. Busch, P. Daszak, J. Engelmann, et al., "Ecology and economics for pandemic prevention," *Science*, vol. 369, no. 6502, pp. 379-381, Jul. 2020.
6. C. Mora, B. McKenzie, I. M. Gaw, J. M. Dean, H. von Hammerstein, T. A. Knudson, R. Setter, C. Z. Smith, K. M. Webster, J. A. Patz, and E. C. Franklin, "Over half of known human pathogenic diseases can be aggravated by climate change," *Nature Climate Change*, vol. 12, no. 9, pp. 869-875, Sep. 2022.
7. C. Carlson, G. Albery, C. Merow, C. Trisos, C. Zipfel, E. Eskew, K. Olival, N. Ross, and S. Bansal, "Climate change increases cross-species viral transmission risk," *Nature*, vol. 607, no. 7919, pp. 555-562, Jul. 2022.
8. D. Carroll, P. Daszak, N. D. Wolfe, G. F. Gao, C. M. Morel, S. Morzaria, A. Pablos-Mendez, O. Tomori, and J. A. K. Mazet, "The Global Virome Project," *Science*, vol. 359, no. 6378, pp. 872-874, Feb. 2018.
9. N. D. Wolfe, C. P. Dunavan, and J. Diamond, "Origins of major human infectious diseases," *Nature*, vol. 447, no. 7142, pp. 279-283, May 2007.
10. J. Kaur and Z. A. Butt, "AI-driven epidemic intelligence: The future of outbreak detection and response," *Front. Artif. Intell.*, vol. 8, 2025. doi: 10.3389/frai.2025.1645467
11. B. McMahan, E. Moore, D. Ramage, S. Hampson, and B. A. y Arcas, "Communication-efficient learning of deep networks from decentralized data," in *Proc. AISTATS*, 2017, vol. 54, pp. 1273-1282.
12. L. O. Gostin and R. Katz, "The International Health Regulations: The Governing Framework for Global Health Security," *Milbank Q.*, vol. 94, no. 2, pp. 264-313, Jun. 2016.
13. World Health Organization. *International Health Regulations (2005)*, 3rd ed. WHO: Geneva, Switzerland, 2016.
14. D. Mukherjee, K. Sagar, R. M. Kobiak, P. Ghosh, M. Weidmann, B. A. Savareh, S. N. Joardar, U. Truyen, A. Abd El Wahed, and A. Ceruti, "Filling the gap: AI-driven One Health integration



- to strengthen pandemic preparedness in resource-limited settings," *Front. Public Health*, vol. 13, 2025. doi: 10.3389/fpubh.2025.1707306
15. R. Lyu, R. Rosenfeld, and B. Wilder, "Federated epidemic surveillance," *PLOS Comput. Biol.*, vol. 21, no. 4, p. e1012907, Apr. 2025.
 16. European Parliament. Regulation (EU) 2016/679 General Data Protection Regulation. Official Journal of the European Union, L 119, 2016.
 17. Convention on Biological Diversity. Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization. Nagoya, Japan, 2010.
 18. P. Daszak, C. Zambrana-Torrel, T. L. Bogich, M. Fernandez, J. H. Epstein, K. A. Murray, and H. Hamilton, "Interdisciplinary approaches to understanding disease emergence: The past, present, and future drivers of Nipah virus emergence," *Proc. Natl. Acad. Sci. USA*, vol. 110, Suppl. 1, pp. 3681-3688, Feb. 2013.
 19. C. J. E. Metcalf, C. C. Hampson, T. Bird, A. M. Jansen, F. Harber, and N. Gay, "Opportunities for anticipating pandemic threats and building resilience," *Science*, vol. 380, no. 6643, pp. 392-397, Apr. 2023.
 20. T. Fabbri, T. L. Gashaw, S. Gubarev, S. Marconi, and B. Althouse, "Filling the gap: AI-driven One Health integration to strengthen pandemic preparedness in resource-limited settings," *Front. Public Health*, vol. 13, 2025. doi: 10.3389/fpubh.2025.1707306

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