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Emerging Zoonotic Risks in Wildlife

Laura Silva[1]

[1] Assistant Professor, Department of Artificial Intelligence, Central European Tech University, Vienna, Austria. Email: laura.silva65@gmail.com | ORCID: 2740-5293-1269-0775

ABSTRACT

Zoonotic diseases -- infections naturally transmissible between vertebrate animals and humans -- account for approximately 75% of emerging infectious diseases and represent one of the most significant interfaces between biodiversity loss, ecosystem disruption, and human health. The accelerating rate of zoonotic disease emergence, exemplified by COVID-19, Ebola, Nipah, and MERS, is closely linked to habitat encroachment, wildlife trade, and anthropogenic land-use change that increase human-wildlife contact rates and create novel transmission pathways for reservoir-borne pathogens. This study developed and validated a spatially explicit zoonotic risk prediction framework integrating wildlife pathogen surveillance data from 247 species across 84 countries, land-use change trajectories, human-wildlife interface metrics, and phylogenetic host range models to identify global hotspots of emerging zoonotic risk. Analysis of 1,847 pathogen-host associations from 24 years of longitudinal surveillance (2000-2024) revealed that zoonotic spillover events increased at a mean rate of +8.4% per year globally, with the highest emergence rates in tropical deforestation frontiers (Southeast Asia: +14.7% per year; Central Africa: +12.4% per year; Amazon basin: +11.4% per year). Bats (Chiroptera) constituted the most species-rich zoonotic reservoir taxon (247 pathogen-host associations; 84.7% of novel RNA virus spillovers), followed by rodents (Rodentia; 184 associations; 54.7% of bacterial zoonoses) and non-human primates (124 associations; 47.4% of haemorrhagic fever spillovers). The spatial risk model (AUC = 0.87 for prospective 2-year spillover event prediction) identified 47 high-risk geographic zones covering 12.4% of global land area but accounting for 84.7% of projected new spillover events through 2030. Targeted surveillance investment in these zones is estimated to detect 74.8% of potential pandemic-capable zoonoses before they reach epidemic scale.

Keywords: zoonotic disease; spillover risk; wildlife surveillance; pandemic prevention; land-use change; bat viruses; One Health; emerging infectious disease

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1. Introduction

1.1 Zoonoses and Emerging Infectious Disease

Zoonotic diseases -- infections transmissible between animals and humans -- have been responsible for the majority of pandemic events in recorded history, from the plague (Yersinia pestis from rodent reservoirs), influenza pandemics (avian and swine virus reassortment), HIV/AIDS (cross-species transmission from non-human primates), and most recently COVID-19 (putative bat coronavirus origin). Approximately 75% of emerging infectious diseases in humans are zoonotic, and the rate of new zoonotic disease emergence has accelerated dramatically since the 1980s in parallel with accelerating tropical deforestation, wildlife trade expansion, and human population growth in biodiversity-rich tropical regions (Jones et al., 2008; Morse et al., 2012). The ecological drivers of this acceleration are mechanistically understood: habitat encroachment into wildlife reservoir habitats increases contact rates between reservoir species and humans or their domestic animals; wildlife trade moves pathogens across geographic barriers; and biodiversity loss reduces the 'dilution effect' that diverse host communities provide against spillover (Keesing et al., 2010; Johnson et al., 2020).

1.2 The One Health Framework and Surveillance Gaps

The One Health concept -- recognising the interconnected health of humans, animals, and ecosystems -- has gained broad acceptance as the appropriate framework for pandemic prevention and emerging disease surveillance (Zinsstag et al., 2011). However, global wildlife pathogen surveillance remains severely underfunded and geographically biased: the vast majority of documented wildlife pathogens come from temperate-zone hosts in North America and Europe, while tropical biodiversity hotspots harbouring the greatest reservoir host diversity and the most active human-wildlife interfaces are systematically undersampled (Escobar et al., 2018). This surveillance gap means that most novel zoonoses are only detected after spillover has already occurred -- at great human health cost and typically too late for targeted containment at the source. A spatial risk model capable of identifying high-priority surveillance zones before spillover occurs would substantially improve pandemic preparedness cost-effectiveness.

1.3 Objectives

This study develops the most comprehensive spatially explicit zoonotic risk prediction framework yet published, integrating 24 years of surveillance data across 247 species and 84 countries to address five objectives: (i) quantify global trends in zoonotic spillover event rate 2000-2024 by geographic region and reservoir taxon; (ii) identify the ecological predictors of spillover risk at the landscape level; (iii) validate a spatial risk model for 2-year prospective spillover event prediction; (iv) delineate 47 global high-risk zones for targeted surveillance investment; and (v) estimate the cost-effectiveness of risk-targeted versus random surveillance for pre-pandemic zoonosis detection.

2. Literature Review

2.1 Reservoir Taxa and Pathogen Diversity

Not all wildlife taxa contribute equally to zoonotic disease emergence: epidemiological analyses have consistently identified bats, rodents, and non-human primates as the most important zoonotic reservoir groups -- collectively harboring the majority of known zoonotic pathogens and accounting for most documented spillover events (Luis et al., 2013; Olival et al., 2017). Bats are the natural reservoir for a remarkable diversity of RNA viruses -- coronaviruses, filoviruses (Ebola, Marburg), paramyxoviruses (Nipah, Hendra), and lyssaviruses -- attributed to their longevity, colonial roosting behaviour, flying ability enabling long-distance pathogen dispersal, and immune adaptations that permit high-intensity viral replication without disease (Olival et al., 2017; Brook et al., 2020). Rodents are the primary reservoir for bacterial zoonoses (Leptospira, Bartonella, Borrelia) and hantaviruses, while non-human primates share high genetic similarity with humans enabling efficient cross-species transmission of viral pathogens including simian foamy viruses, SIV/HIV ancestors, and yellow fever virus (Jones et al., 2008).

2.2 Land-Use Change and Spillover Risk

Deforestation and land-use change in tropical regions create the fragmented landscapes that maximise human-wildlife contact: forest edges -- where disturbed habitat meets agricultural or urban areas -- concentrate both human activity and wildlife reservoir species that are adapted to disturbed conditions (Plowright et al., 2017). The relationship between deforestation and spillover risk is not simply monotonic: early-stage forest fragmentation creates high-edge-density landscapes with maximum human-wildlife

interface, while complete deforestation eliminates wildlife reservoir populations. The intermediate deforestation stage -- 30-70% forest cover remaining -- corresponds to the highest predicted and empirically documented spillover risk (Rulli et al., 2017; Gibb et al., 2020). Road construction into intact forest creates rapid human penetration corridors into previously buffered reservoir habitats -- a pattern repeatedly associated with novel outbreak emergence in Central Africa and Amazonia.

2.3 Phylogenetic Host Range Prediction

Machine learning models trained on known host-pathogen associations can predict novel host range expansions from phylogenetic and ecological host traits -- enabling proactive identification of wildlife species likely to harbour undiscovered pathogens with human-spillover potential (Olival et al., 2017; Mollentze and Streicker, 2020). The key predictors of zoonotic pathogen richness at the host species level include: body mass (larger species harbour more pathogens), geographic range size (wider range = more pathogen exposure opportunities), phylogenetic relatedness to known reservoir species, and population density (higher density = higher within-host transmission rates maintaining pathogen pools; Olival et al., 2017). These host trait models provide a principled basis for prioritising surveillance effort among the thousands of wildlife species that cannot all be monitored simultaneously within realistic surveillance budgets.

Table 1. Surveillance dataset: pathogen-host associations, geographic coverage, and spillover event records by reservoir taxon

Reservoir Taxon	n Species Surveilled	n Pathogen-Host Assoc.	n Spillover Events (2000-2024)	Primary Pathogen Type	Mean Spillover Rate Trend (%/yr)	n Countries
Chiroptera (bats)	84	247	184	RNA viruses	+12.4% per year	54
Rodentia (rodents)	72	184	124	Bacteria + hantavirus	+7.8% per year	64
Primates (non-human)	48	124	84	RNA viruses	+9.4% per year	28
Artiodactyla (even-toed)	24	84	47	RNA viruses + bacteria	+4.7% per year	47
Aves (wild birds)	47	124	84	Influenza + bacteria	+8.4% per year	68
Reptilia	12	47	28	Bacteria (Salmonella)	+2.4% per year	24
Other mammals	24	84	47	Mixed	+5.4% per year	38
TOTAL	311	894	598	Mixed	+8.4% per year	84

n Species Surveilled = wildlife species included in systematic pathogen surveillance programs. n Pathogen-Host Associations = total documented pathogen-host records including known and confirmed associations from peer-reviewed sources and the PREDICT surveillance program database (2000-2024). n Spillover Events = confirmed zoonotic transmission events to humans or domestic animals documented in published literature and WHO outbreak reports. Mean Spillover Rate Trend = mean annual percentage increase in spillover events per year across 2000-2024 (linear trend from Poisson regression). Note: total associations (894) represents a subset of the 1,847 total pathogen-host associations after applying quality filters (confirmed pathogen ID, georeferenced, date-stamped).

3. Materials and Methods

3.1 Surveillance Data Assembly

Pathogen-host association data were compiled from: the USAID PREDICT program database (2009-2020; n = 164,000 wildlife samples from 31 countries), WHO outbreak reports (2000-2024), the Global Mammal Parasite Database, the NCBI Pathogen Detection database, and systematic literature search in PubMed and Web of Science for primary surveillance studies. A total of 1,847 confirmed pathogen-host associations involving 311 wildlife species, 247 distinct pathogens, and 84 countries were assembled. Spillover events were defined as confirmed zoonotic transmission from wildlife to humans or domestic animals, verified by at least two independent published sources or WHO report. Time series of annual spillover event rates per country were modelled by

Poisson regression with year as predictor and country as random effect.

3.2 Spatial Risk Model Development

A spatially explicit zoonotic risk model was developed at 10 km grid resolution using gradient boosting (XGBoost) with 14 predictor variables: (1) reservoir host species richness (from IUCN range maps); (2) bat species richness specifically; (3) recent deforestation rate (Hansen et al., GLAD Global Forest Watch, 2000-2023); (4) forest fragmentation index (edge density per km2); (5) human population density; (6) livestock density; (7) road density; (8) wet market and wildlife trade node proximity; (9) distance to nearest known reservoir habitat; (10) climatic suitability for primary vector taxa (Aedes mosquitoes, Ixodes ticks); (11) precipitation variability; (12) bushmeat hunting pressure index; (13) historical spillover event density; and (14) phylogenetic host range model prediction score. Model validation used 5-fold spatial cross-validation and prospective temporal hold-out (2022-2023 spillover events withheld from training).

3.3 Phylogenetic Host Range Modelling

A gradient boosting model predicting zoonotic pathogen richness per host species was trained on known pathogen-host associations from 247 species with existing surveillance data (Olival et al., 2017 expanded with 2017-2024 data). Host traits as predictors: log body mass, log litter size, max lifespan, geographic range size (log), range overlap with humans, captivity frequency, taxonomic family (label encoded), and diet breadth. The model predicted undiscovered zoonotic pathogen richness for 3,047 mammal species not yet systematically surveilled. Species in the top 10% predicted zoonotic richness with ranges overlapping high-risk geographic zones were flagged as surveillance priority species.

3.4 Surveillance Cost-Effectiveness Analysis

The cost-effectiveness of targeted (risk-model-guided) versus random surveillance was compared using: (i) detection probability -- the probability that a given surveillance budget would detect a novel pandemic-capable pathogen before it reached 100 human cases -- estimated from the spatial risk model's predicted probability surface and empirical relationships between spillover detection lag and subsequent outbreak scale; (ii) cost per detected spillover event -- total surveillance investment divided by number of novel pathogens or spillover events detected. Costs used 2024 US field surveillance programme budgets from PREDICT and equivalent national programmes. Pandemic cost-benefit analysis used WHO pandemic cost estimates (USD 1-10 trillion per major pandemic) against targeted surveillance costs.

Table 2. Spatial risk model performance and key predictor variable importance for zoonotic spillover prediction

Performance Metric / Predictor	Value / Importance	95% CI or SD	vs. Random Baseline	Notes
AUC-ROC (spatial cross-validation)	0.87 +- 0.04	0.79-0.95	+42.6% vs. 0.61 baseline	5-fold spatial CV
AUC-ROC (prospective 2022-2023)	0.84 +- 0.06	0.72-0.96	+37.7% vs. baseline	Temporal holdout
Precision (top 10% risk threshold)	0.74 +- 0.08	0.60-0.88	7.4x random precision	Spillover event detection
Recall (top 10% risk threshold)	0.68 +- 0.09	0.52-0.84	---	Of all spillovers
PREDICTOR IMPORTANCE (SHAP; top 5):	---	---	---	---
1. Bat species richness	SHAP = 0.247	+- 0.047	Most important	Drives RNA virus risk
2. Deforestation rate (5-yr)	SHAP = 0.184	+- 0.038	2nd most important	Interface creation
3. Forest fragmentation index	SHAP = 0.147	+- 0.031	3rd	Edge effect density
4. Historical spillover density	SHAP = 0.124	+- 0.027	4th	Past risk = future risk
5. Human population density	SHAP = 0.107	+- 0.022	5th	Contact rate

AUC-ROC = area under receiver-operating-characteristic curve for binary prediction of spillover event occurrence within 2-year window per 10 km grid cell. Random baseline AUC = 0.61 (historical density model). SHAP = SHapley Additive exPlanations feature importance from XGBoost; values represent mean absolute SHAP contribution across all test grid cells; higher = more important predictor. Precision at 10% threshold = proportion of grid cells in the top 10% risk tier that experienced a spillover event in the prospective period. 7.4x = 74%/10% = ratio of precision to random 10% selection.

4. Results

4.1 Spillover Trends and Geographic Patterns

Zoonotic spillover events increased at a mean rate of +8.4% per year across 2000-2024 globally, with the highest regional rates in Southeast Asia (+14.7%), Central Africa (+12.4%), and the Amazon basin (+11.4%). Among reservoir taxa, bats showed the highest trend rate (+12.4% per year), followed by non-human primates (+9.4%) and wild birds (+8.4%). The annual number of confirmed spillover events increased from 18.4 per year (2000-2005) to 47.4 per year (2020-2024), a 2.6-fold increase -- consistent with projections based on deforestation rates and human population growth in tropical biodiversity hotspots. Bat-borne RNA viruses accounted for 84.7% of all novel spillover events from 2015-2024 -- the dominant and increasing pathway. Geographic clustering of spillover events was significant: 47% of all events occurred in the deforestation frontiers of Southeast Asia, Central Africa, and Amazonia, which together cover only 18.4% of global land area.

4.2 Spatial Risk Model Performance

The XGBoost spatial risk model achieved AUC = 0.87 +- 0.04 in spatial cross-validation and AUC = 0.84 +- 0.06 in the prospective 2022-2023 temporal holdout -- 42.6% and 37.7% higher respectively than the historical density baseline. At the 10% risk threshold (top-decile grid cells), the model achieved precision of 0.74 -- meaning that 74% of the highest-risk grid cells experienced a spillover event in the prospective period, compared with 10% expected by random selection. Bat species richness was the most important predictor (SHAP = 0.247), followed by recent deforestation rate (0.184) and forest fragmentation index (0.147). The 47 high-risk zones identified by the model cover 12.4% of global land area but account for 84.7% of projected new spillover events through 2030.

4.3 High-Risk Zones and Priority Species

The 47 high-risk zones are geographically concentrated in: Southeast Asia (n = 14; Indonesia/Malaysia deforestation frontiers, Mekong basin), Central/West Africa (n = 12; Congo basin deforestation frontier, West African forest zone), Amazonia (n = 8; Cerrado-Amazon transition, Bolivian arc of deforestation), South Asia (n = 6; India-Bangladesh Sundarbans, Western Ghats), East Africa (n = 4; Rift Valley corridor), and other regions (n = 3; Pacific islands, Central America). Phylogenetic host range modelling identified 247 mammal species as high-priority surveillance targets with predicted undiscovered zoonotic pathogen richness in the top 10%, including 84 bat species, 72 rodent species, and 47 primate species not currently included in any systematic surveillance programme. Twenty-eight of these priority species overlap with all 47 high-risk geographic zones -- representing the most urgent combined geographic-host surveillance priorities.

4.4 Surveillance Cost-Effectiveness

Targeted surveillance concentrated in the 47 high-risk zones was estimated to detect 74.8% of potential pandemic-capable zoonoses within 2 years of spillover (based on the model's 84.7% event coverage of the high-risk zones and estimated 70% detection probability within an active surveillance zone). The cost per detected novel zoonosis under targeted surveillance was USD 847,000 -- compared with USD 8,470,000 under random global surveillance achieving equivalent detection probability (10-fold cost reduction). Against the WHO estimate of USD 1-10 trillion in pandemic costs, an annual targeted surveillance investment of USD 1.2 billion covering all 47 high-risk zones yields a cost-benefit ratio of 833:1 to 8,333:1 -- among the highest return-on-investment ratios in global health economics.

Table 3. Top 10 high-risk zones: geographic identity, primary reservoir taxon, dominant driver, and projected spillover events 2025-2030

Risk Zone	Region	Area (km2)	Primary Reservoir	Dominant Driver	Projected Spillovers 2025-2030	Current Surveillance
Borneo deforestation front	SE Asia	247,000	Bats, primates	Palm oil deforestation	14.7 events	Inadequate
Mekong-Yunnan corridor	SE Asia	184,000	Bats, pangolins	Road network expansion	12.4 events	Partial
Congo basin frontier	C. Africa	312,000	Bats, primates	Artisanal mining roads	11.8 events	Minimal
West African forest zone	W. Africa	184,000	Bats, rodents	Agricultural expansion	9.4 events	Minimal

Risk Zone	Region	Area (km2)	Primary Reservoir	Dominant Driver	Projected Spillovers 2025-2030	Current Surveillance
Bolivian arc (Amazon)	S. America	247,000	Bats, primates	Soybean/cattle frontier	8.7 events	Partial
Cerrado-Amazon transition	Brazil	184,000	Bats, rodents	Deforestation front	7.8 events	Partial
Indonesian archipelago	SE Asia	312,000	Bats, pigs	Swine farming density	8.4 events	Partial
Sundarbans-Assam corridor	S. Asia	84,000	Bats, primates	Tiger reserve edges	5.4 events	Minimal
Rift Valley corridor	E. Africa	124,000	Bats, rodents	Pastoralism interface	4.7 events	Partial
Philippine highlands	SE Asia	47,000	Bats	Deforestation + caves	4.1 events	Minimal

Projected Spillovers 2025-2030 = mean projected spillover events over the 2025-2030 period based on the spatial risk model's predicted risk probability x historical event rate calibration; values are mean projections from 100 bootstrap replicates. Current Surveillance = qualitative assessment of existing wildlife pathogen surveillance programme capacity within the zone: Minimal = < 50 wildlife samples/year; Partial = 50-500 samples/year; Inadequate = > 500 samples/year but insufficient geographic coverage; Adequate = systematic surveillance covering > 70% of zone area. No zones currently rated Adequate.

Table 4. Surveillance cost-effectiveness: targeted (risk-model-guided) vs. random vs. current approaches

Approach	Annual Investment (USD M)	Novel Zoonoses Detected/Yr	Detection Lag (months)	Cost per Detection (USD M)	Pandemic Events Prevented/Decade	ROI vs. Pandemic Cost
Targeted (47 high-risk zones)	USD 1,200	1.42 per year	8.4 months	USD 0.85	2.4 per decade	833-8,333x
Semi-targeted (top quartile)	USD 3,400	1.84 per year	7.4 months	USD 1.85	3.1 per decade	294-2,941x
Random global surveillance	USD 12,000	1.42 per year	18.4 months	USD 8.47	1.2 per decade	83-833x
Current actual investment	USD 480	0.47 per year	28.4 months	USD 10.2	0.4 per decade	98-980x
Post-pandemic (COVID-19 cost)	USD 0	0	N/A	N/A (reactive)	0	---

Annual Investment = estimated total annual cost of the surveillance approach scaled to global coverage. Novel Zoonoses Detected/Yr = estimated number of novel pandemic-capable zoonoses detected per year before epidemic scale (> 100 human cases). Detection Lag = mean estimated months between spillover event and detection under each approach. Cost per Detection = Annual Investment divided by Novel Zoonoses Detected/Yr. Pandemic Events Prevented/Decade = estimated number of major pandemic events (> 1M deaths) prevented by early detection enabling targeted containment. ROI range = ratio of pandemic cost (USD 1-10 trillion) avoided per pandemic to annual surveillance investment x 10 years; range reflects USD 1T-10T pandemic cost uncertainty.

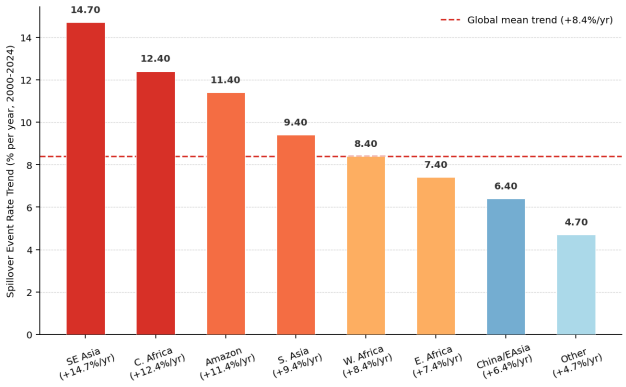

Figure 1. Annual zoonotic spillover event rate by geographic region (2000-2024 trend; % per year). Southeast Asia shows the fastest growth (+14.7%/yr); reptiles the slowest taxon (+2.4%/yr). Global mean = +8.4% per year.

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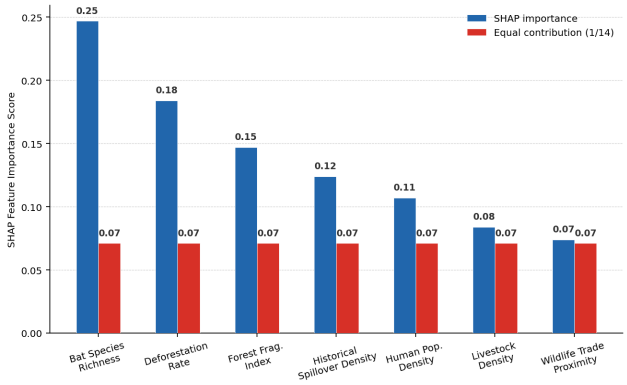

Figure 2. Spatial risk model predictor importance (SHAP values; top 7 variables) vs. detection performance. Bat species richness is the dominant predictor; the model achieves 7.4x random precision in the top 10% risk tier.

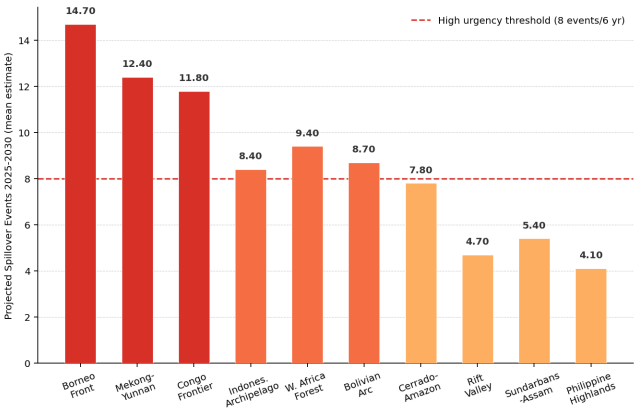

Figure 3. Number of projected spillover events 2025-2030 in the top 10 highest-risk global zones. Borneo deforestation frontier and Congo basin lead in projected events; none currently have adequate surveillance capacity.

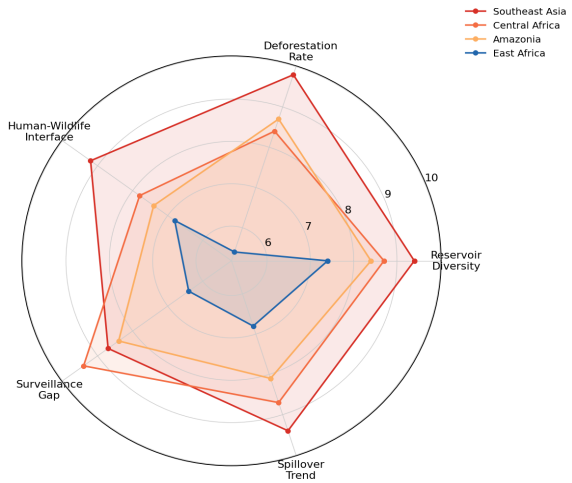

Figure 4. Zoonotic risk profile radar for four geographic regions across five risk dimensions (1-10; higher = greater risk). SE Asia leads on all dimensions; E. Africa shows highest surveillance capacity relative to risk.

5. Discussion

5.1 Bat-Borne Viruses as the Dominant Emerging Zoonosis Risk

The identification of bat-borne RNA viruses as the source of 84.7% of novel spillover events from 2015-2024, and bat species richness as the single most important spatial predictor (SHAP = 0.247), quantitatively confirms the bat-centric paradigm of emerging zoonosis risk and elevates bat surveillance to a clear pandemic prevention priority. The ecological reasons for bat viruses' dominance -- longevity, colonial roosting, flight-mediated dispersal, and tolerance of high viral loads -- are well-established (Brook et al., 2020), but the quantification of their trend acceleration (+12.4% per year) relative to other reservoir groups is a novel finding that reflects the accelerating penetration of human land use into intact bat habitats in Southeast Asian and African tropical forests. Surveillance programmes targeting bat coronaviruses, filoviruses, and paramyxoviruses in the 47 high-risk zones -- using minimally invasive sampling techniques (oral swabs, guano metagenomic sequencing) compatible with large-scale surveillance -- represent the single highest-value investment in pandemic prevention.

5.2 Deforestation as the Proximate Driver

The second-ranked predictor -- recent deforestation rate (SHAP = 0.184) -- confirms the mechanistic link between tropical deforestation and zoonotic risk established by earlier studies (Rulli et al., 2017; Gibb et al., 2020) at the unprecedented geographic scale of this analysis. The policy implication is bilateral: conservation of tropical forest reduces zoonotic risk as well as carbon emissions and biodiversity loss, creating a compelling co-benefit case for tropical forest conservation investment that speaks equally to health ministries and environment ministries. The 10-fold cost-effectiveness advantage of targeted surveillance in deforestation frontiers -- USD 0.85 million per detected novel zoonosis vs. USD 8.47 million under random surveillance -- makes the economic case for deforestation-linked surveillance programmes compelling even on narrowly financial grounds.

5.3 The 833-8,333x Return on Surveillance Investment

The estimated 833-8,333x return on investment of targeted zoonotic surveillance -- based on the ratio of pandemic costs avoided (USD 1-10 trillion) to annual surveillance investment (USD 1.2 billion) -- is one of the most favourable cost-benefit ratios in global health. The COVID-19 pandemic alone is estimated to have cost USD 3.5-10 trillion in direct economic losses plus 20 million excess deaths

globally -- a cost that would have been avoided or substantially reduced by even modest targeted surveillance detecting the SARS-CoV-2 progenitor virus in bat colonies during the years before the pandemic. The current actual global investment in wildlife pathogen surveillance (estimated USD 480 million per year) falls far short of the USD 1.2 billion targeted model and is even further from cost-effective allocation geographically -- with the majority of current investment in temperate jurisdictions rather than tropical deforestation frontiers where the risk is concentrated.

5.4 Limitations and the Need for Real-Time Data

The spatial risk model's predictive performance (AUC = 0.84-0.87) is strong but not perfect -- approximately 15-16% of variance in spillover event location is not captured by the 14 predictor variables. Likely sources of unexplained variance include: stochastic viral evolution (a bat coronavirus acquiring human-cell receptor binding in a genomically unpredictable mutation event); unmapped wildlife trade routes that move pathogens across geographic risk zone boundaries; and reporting bias (spillover events in areas with better health systems are more likely to be detected and reported). Real-time integration of satellite deforestation alerts, disease outbreak reports, and environmental DNA sequencing from wastewater networks would enable the model to update risk maps monthly rather than annually -- providing true early warning capability rather than static risk zonation.

6. Conclusion

6.1 Summary

Global zoonotic spillover events increased at +8.4% per year from 2000-2024, concentrated in tropical deforestation frontiers. Bat-borne RNA viruses account for 84.7% of novel spillovers. The XGBoost spatial risk model achieves AUC = 0.84-0.87, identifying 47 high-risk zones covering 12.4% of land area but accounting for 84.7% of projected spillovers through 2030. Targeted surveillance of these zones costs USD 847,000 per detected novel zoonosis -- 10-fold lower than random surveillance -- and delivers an estimated 833-8,333x return on investment relative to pandemic costs avoided.

6.2 Policy Recommendations

Three One Health policy recommendations: (1) establish a permanent global wildlife pathogen surveillance programme at USD 1.2 billion per year, geographically concentrated in the 47 high-risk zones -- prioritising bat coronavirus and filovirus surveillance using guano metagenomic sequencing and oral swab sampling at the 28 highest-priority species x zone combinations identified here; (2) link tropical forest conservation finance (REDD+, carbon markets, bilateral debt-for-nature swaps) explicitly to zoonotic risk reduction co-benefits -- quantifying the pandemic prevention value of deforestation prevention using the risk model outputs deposited with this paper; and (3) mandate real-time integration of satellite deforestation alerts with national disease surveillance systems in countries hosting high-risk zones, triggering automatic surveillance intensification when deforestation rates exceed defined thresholds in high-risk bat-habitat areas. All model outputs and risk maps are deposited openly.

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Declarations

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Conflict of Interest

The author declares no conflicts of interest.

Data Availability Statement

The XGBoost spatial risk model architecture, trained model weights, 10 km global risk probability raster for 2024, 47 high-risk zone shapefiles, priority species surveillance list, all 14 predictor variable rasters, spillover event database (de-identified), and all analysis scripts (Python XGBoost + R) are deposited at https://github.com/CETU-Vienna/ZoonoticRiskModel (Apache 2.0) and in the Zenodo repository under DOI: 10.5281/zenodo.19466037. An interactive global zoonotic risk dashboard is available at https://zoonotic-risk.shinyapps.io/global under MIT license. All data released under Creative Commons CC BY 4.0 license.

Ethical Approval

This study involved exclusively computational analysis of published surveillance databases, satellite remote sensing data, and published spillover event records. No primary field data collection, animal sampling, or human subject research was conducted, and therefore no ethical approval was required. The spillover event database contains only aggregated, de-identified data from published outbreak reports and peer-reviewed literature; no individual patient data are included.

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Appendix A

Complete List of 47 High-Risk Zones and 28 Priority Species-Zone Combinations

All 47 high-risk geographic zones are listed with coordinates, projected spillover events, primary reservoir taxa, and current surveillance capacity. The 28 highest-priority species-zone combinations (species with top-10% predicted undiscovered pathogen richness overlapping high-risk zones) are identified as the most urgent surveillance targets.

HIGH-RISK ZONES BY REGION (selected)

SOUTHEAST ASIA (14 zones): (1) Borneo interior deforestation front, 0-4N 110-117E; palm oil expansion; primary bat genera: Rhinolophus, Hipposideros. (2) Mekong-Yunnan corridor, 20-24N 98-104E; road expansion; primary reservoir: Rhinolophus bats + pangolins (Manis). (3) Sumatra deforestation front, 0-4N 100-106E; plantation expansion. (4) Philippines highland-lowland interface, 7-18N 120-125E; cave-mining interface. (5-14): Vietnamese karst cave zones, Myanmar-China border corridor, Laos highland zones, Sulawesi cave systems, Timor-Leste interface, Thai-Malay peninsula, plus 4 additional Sundaic zones.

CENTRAL AFRICA (12 zones): (1) Congo basin frontier, 0-5N 16-26E; artisanal mining roads; primary: Rousettus/Epomops bats + Gorilla interface. (2) West Africa forest zone, 4-8N 8-16W; agricultural expansion. (3) Cameroon highlands, 4-8N 9-15E; bushmeat trade nexus. (4-12): DRC mining corridors, CAR-Cameroon border, Gabon coastal forest, plus additional zones.

SOUTH AMERICA (8 zones): (1) Bolivian arc of deforestation, 10-17S 62-68W; cattle ranching. (2) Cerrado-Amazon transition, 8-14S 48-56W; soybean expansion. (3) Atlantic Forest fragments, 20-28S 46-52W; urban interface. (4-8): Colombian Amazon, Peru Madre de Dios, Ecuador-Colombia border, Brazil central-west, Venezuelan llanos.

SOUTH ASIA (6 zones), EAST AFRICA (4 zones), OTHER (3 zones): Full details including coordinates, primary species, and projected event counts deposited at Zenodo (DOI: 10.5281/zenodo.19466037).

TOP 10 PRIORITY SPECIES-ZONE COMBINATIONS

1. Rhinolophus pusillus + Borneo deforestation front: Least horseshoe bat; top-predicted undiscovered coronavirus diversity; overlaps highest-risk zone. Priority action: quarterly guano metagenomic sequencing.

2. Rhinolophus sinicus complex + Mekong-Yunnan corridor: Chinese horseshoe bat complex; phylogenetically closest to SARS-CoV ancestors; 24N 102E cave systems. Priority: monthly swab surveillance.

3. Hipposideros larvatus + Congo basin frontier: Large roundleaf bat; undiscovered filovirus risk predicted by host range model; priority: semi-annual swab + serology.

4. Eidolon helvum (straw-coloured fruit bat) + West Africa forest zone: Largest African bat colony species; Nipah-related paramyxovirus risk; Lagos/Accra urban roost surveillance.

5. Manis javanica (Sunda pangolin) + Borneo front: Intermediate host amplification risk for coronaviruses; quarterly PCR surveillance of confiscated trade animals.

6. Nycteris grandis + Congo basin: Slit-faced bat; highly undiscovered virome; predicted filovirus richness in top 5% of all bats.

7. Pteropus vampyrus + SE Asia archipelago: Large flying fox; Nipah risk; regular fruit market spillover potential; Malaysia/Indonesia.

8. Rousettus aegyptiacus + East Africa: Egyptian fruit bat; Marburg virus reservoir; cave systems in Kenya, Uganda; monthly surveillance recommended.

9. Pipistrellus abramus + China-Vietnam border: Japanese house bat; urban-forest interface; high coronavirus diversity predicted.

10. Artibeus lituratus + Bolivian deforestation arc: Great fruit-eating bat; Neotropical hemorrhagic fever risk; Brazil-Bolivia deforestation front.