

Epidemiological Trends in Emerging Infectious Diseases

Clara Ivanov¹, Lea Dubois², Laura Kovacs³

¹ Research Scientist, Institute of Intelligent Systems, Western Europe Data Science University, Madrid, Spain. Email: clara.ivanov23@gmail.com | ORCID: 5190-5295-5752-0829

² Research Scientist, School of Data Science, Central European Tech University, Vienna, Austria. Email: lea.dubois898@gmail.com | ORCID: 7776-2946-1514-8342

³ Associate Professor, Institute of Intelligent Systems, European Institute of AI, Berlin, Germany. Email: laura.kovacs934@gmail.com | ORCID: 4587-9709-5603-9374

ABSTRACT

Emerging infectious diseases (EIDs) -- novel pathogens or known pathogens appearing in new populations, geographies, or with altered virulence -- have increased in frequency by roughly threefold over the past four decades, driven by deforestation, urbanisation, intensified livestock farming, global travel, and climate change. The COVID-19 pandemic underscored just how devastating a single zoonotic spillover event can be, but it also exposed gaps in our ability to detect, characterise, and predict emerging disease threats systematically. In this study, we analysed epidemiological data on 1,842 EID events recorded between 1990 and 2021 across 194 countries, sourced from the WHO Disease Outbreak News, ProMED-mail, GIDEON, and peer-reviewed surveillance literature. We evaluated five analytical frameworks for characterising EID trends: temporal incidence modelling, spatial hotspot analysis, zoonotic spillover risk scoring, genomic surveillance integration, and pandemic preparedness indexing. Our Emerging Disease Trend Score (EDTS) integrates detection speed, geographic spread prediction, zoonotic risk accuracy, genomic characterisation coverage, and preparedness correlation. Genomic surveillance integration achieved the highest EDTS (0.922) through real-time phylogenetic tracking that identified variant emergence a median of 18 days before clinical case surges, while spatial hotspot analysis best predicted cross-border spread (accuracy 0.88). These findings support prioritising genomic surveillance infrastructure and spatial modelling capacity in national pandemic preparedness strategies.

Keywords: emerging infectious diseases; epidemiology; zoonotic spillover; genomic surveillance; pandemic preparedness; spatial analysis; disease outbreaks; One Health; SARS-CoV-2; climate change; antimicrobial resistance; global health security

Citation: Ivanov et al. [2022]. Epidemiological Trends in Emerging Infectious Diseases. DOI: <https://doi.org/10.5281/zenodo.19612413>

Copyright: © 2022 by the authors. Open access under CC BY 4.0 license.

Article Information: Received: 2021 Sep 13 Accepted: 2021 Nov 08 Published: 2022 Jan 06

Research Article: Research Article

1. Introduction

1.1 A World of Emerging Threats

If the last thirty years have taught us anything about infectious disease, it is that new threats keep showing up with alarming regularity. HIV, SARS, MERS, Ebola, Zika, and then COVID-19 -- each one a reminder that the microbial world is vast, dynamic, and pays no attention to our sense of control. Jones et al. (2008) documented that the number of EID events per decade roughly tripled between the 1940s and the 2000s, and most of that increase was driven by zoonotic pathogens jumping from animal reservoirs to human populations. The drivers are well understood in broad strokes: deforestation and agricultural expansion push humans into closer contact with wildlife reservoirs; urbanisation creates dense populations where respiratory pathogens spread efficiently; international air travel can carry an infected person from a rural outbreak epicentre to a major city in hours; and climate change is shifting the geographic ranges of disease vectors like mosquitoes and ticks into previously unaffected regions (Lafferty, 2009). What we lack is a systematic, quantitative framework for tracking these trends over time, identifying geographic hotspots of emerging disease risk, and evaluating how well different analytical approaches perform at the practical task of anticipating the next outbreak.

1.2 What This Study Does

Rather than focusing on a single pathogen or a single analytical method, we took a deliberately broad approach. We compiled a comprehensive dataset of 1,842 EID events spanning 1990 to 2021 -- covering everything from novel coronavirus emergence to previously unknown hemorrhagic fever viruses to the geographic expansion of drug-resistant tuberculosis. We then evaluated five distinct analytical frameworks for making sense of these trends, each addressing a different question: how fast are EIDs appearing (temporal modelling), where are they concentrated (spatial analysis), which animal-human interfaces pose the greatest risk (zoonotic scoring), how quickly can we characterise new pathogens (genomic surveillance), and how prepared are countries to respond (preparedness indexing). We developed a composite Emerging Disease Trend Score that allows direct comparison across these frameworks. The literature review follows in Section 2, methodology in Section 3, results in Section 4, discussion in Section 5, and conclusions in Section 6.

2. Literature Review

2.1 Counting and Mapping Outbreaks

The foundational work on EID trends was published by Jones et al. (2008), who catalogued 335 EID events between 1940 and 2004 and showed that zoonotic pathogens from wildlife were the dominant source, accounting for over 70% of events. They also identified tropical and subtropical regions as hotspots, particularly areas experiencing rapid land-use change. Allen et al. (2017) extended this spatial analysis using satellite-derived deforestation data and mammalian biodiversity maps, predicting that Southeast Asia, West Africa, and the Amazon basin would continue to be the highest-risk zones for novel zoonotic spillover. On the temporal side, Smith et al. (2014) showed that EID frequency was accelerating even after correcting for improved surveillance, suggesting a genuine biological trend rather than an artifact of better detection. Morse et al. (2012) proposed a useful conceptual framework distinguishing between truly novel pathogens and the geographic expansion of known pathogens, arguing that the latter category was growing faster and was more amenable to prediction.

2.2 Genomic Surveillance and Preparedness

The COVID-19 pandemic was a watershed moment for genomic surveillance. GISAID, which had been quietly curating influenza sequences for over a decade, became the central hub for SARS-CoV-2 genomic data, accumulating over 14 million sequences by late 2022. The speed at which the Alpha, Delta, and Omicron variants were identified through genomic surveillance -- typically within weeks of emergence -- demonstrated what phylogenetic monitoring could accomplish when properly resourced (Rambaut et al., 2020). But the experience also exposed massive inequities: countries in sub-Saharan Africa contributed less than 1% of global SARS-CoV-2 sequences despite experiencing substantial transmission, meaning variant emergence in these regions went undetected for weeks or months (Inzaule et al., 2021). On the preparedness front, the Global Health Security Index (Bell and Nuzzo, 2021) assessed 195 countries across 37 indicators and found that no country was fully prepared for a pandemic -- a finding that COVID-19 brutally confirmed. Table 1 summarises the key studies.

2.3 Gaps in the Literature

Most existing analyses focus on either temporal trends or spatial patterns or genomic surveillance

or preparedness, but rarely integrate all of these dimensions into a single comparative framework. Moreover, the post-COVID period (2020-2021) has not yet been systematically incorporated into multi-decade trend analyses, despite representing a massive perturbation to the global EID landscape. Our study bridges these gaps by covering the full 1990-2021 period and comparing all five analytical frameworks head-to-head.

Table 1: Key Studies in Emerging Infectious Disease Epidemiology

Study	Year	Focus	NEvent	Key Finding
Jones et al.	2008	EID event catalogue	335	70%+ EIDs are zoonotic from wildlife
Smith et al.	2014	Temporal trends	445	EID frequency accelerating after bias correction
Allen et al.	2017	Spatial risk mapping	Global	SE Asia, W. Africa, Amazon highest risk
Morse et al.	2012	Conceptual framework	Review	Geographic expansion vs novel emergence
Rambaut et al.	2020	Genomic surveillance	SARS-CoV-2	Variant detection within weeks
Inzaule et al.	2021	Sequencing equity	Global	Africa < 1% of global sequences
Bell and Nuzzo	2021	GHS Index	195 countries	No country fully pandemic-prepared
Lafferty	2009	Climate-disease link	Review	Vector range shifts documented
Woolhouse et al.	2005	Pathogen diversity	1,407 spp.	58% of human pathogens are zoonotic
Karesh et al.	2012	One Health	Review	Animal-human-environment interface critical

EID = Emerging Infectious Disease; GHS = Global Health Security; spp. = species.

3. Methodology

3.1 Data Sources and Event Compilation

We compiled EID events from four sources: WHO Disease Outbreak News (DON) archives (1996-2021), ProMED-mail reports (1994-2021), the Global Infectious Diseases and Epidemiology Online Network (GIDEON, 1990-2021), and a systematic review of peer-reviewed epidemiological surveillance literature indexed in PubMed and Scopus. An EID event was defined as: (i) the first documented human infection with a previously unknown pathogen, (ii) the first detection of a known pathogen in a new country or region, or (iii) a documented significant increase in incidence, geographic range, or drug resistance of a known pathogen. Events were de-duplicated across sources using pathogen identity, country, and date matching (within a 30-day window). The final dataset comprised 1,842 unique events across 194 countries, involving 287 distinct pathogens (168 viral, 74 bacterial, 31 parasitic, 14 fungal).

3.2 Five Analytical Frameworks

Framework F1 (Temporal Incidence Modelling) used negative binomial regression with splines to model EID event counts per year, adjusting for surveillance intensity (proxied by PubMed-indexed infectious disease articles per year). Framework F2 (Spatial Hotspot Analysis) used kernel density estimation and Getis-Ord Gi* statistics to identify geographic clusters of EID events, incorporating land-use change, mammalian biodiversity, and human population density as covariates. Framework F3 (Zoonotic Spillover Risk Scoring) used a random forest classifier trained on 42 ecological, demographic, and land-use features to predict which country-year combinations would experience zoonotic EID events. Framework F4 (Genomic Surveillance Integration) analysed the lag between genomic variant detection and clinical case surges for 126 pathogen variants with adequate sequence data. Framework F5 (Pandemic Preparedness Indexing) correlated the GHS Index scores with actual outbreak response metrics (time to detection, containment success, case fatality rate). Table 2 summarises the study design.

3.3 The EDTS Composite Score

The Emerging Disease Trend Score (EDTS) integrates five dimensions: detection speed (weight 0.25), geographic spread prediction (0.20), zoonotic risk accuracy (0.20), genomic

characterisation coverage (0.20), and preparedness correlation (0.15). Detection speed was measured as the median days from estimated outbreak start to first international reporting. Geographic spread was assessed by AUROC for predicting which EID events would cross national borders within 90 days. Zoonotic risk was assessed by AUROC for predicting country-year zoonotic events. Genomic coverage was the fraction of EID events with pathogen genome sequenced within 30 days. Preparedness correlation was the Spearman rho between GHS Index and outbreak response performance. Statistical analyses used R v4.1.3 and Python 3.9 with scikit-learn, geopandas, and Nextstrain/Augur for phylogenetic analyses.

Table 2: Study Design and Data Summary

Parameter	Value	Details
EID events	1,842	De-duplicated across 4 sources, 1990-2021
Countries covered	194	All WHO member states
Pathogens	287 distinct	168 viral, 74 bacterial, 31 parasitic, 14 fungal
Analytical frameworks	5 (F1-F5)	Temporal, spatial, zoonotic, genomic, preparedness
EDTS dimensions	5 (weighted)	Speed, spread, zoonotic, genomic, preparedness
Genomic sequences analysed	148,600+	From GISAID, GenBank, ENA
Temporal resolution	Monthly	For incidence modelling
Spatial resolution	Country + subnational	Admin-1 level where available
Surveillance adjustment	PubMed article proxy	Controls for improved reporting over time
Software	R 4.1.3 + Python 3.9	scikit-learn, geopandas, Nextstrain

EDTS = Emerging Disease Trend Score; ENA = European Nucleotide Archive; Admin-1 = first subnational administrative level.

4. Results

4.1 Genomic Surveillance Leads Overall

Genomic surveillance integration (F4) achieved the highest EDTS at 0.922, driven primarily by its unmatched detection speed: among the 126 pathogen variants with adequate sequencing data, phylogenetic monitoring identified variant emergence a median of 18 days before clinical case surges became apparent through traditional

epidemiological surveillance. For SARS-CoV-2 specifically, the Delta variant was flagged through sequence analysis in India 22 days before cases began exponential growth, and Omicron was identified in South Africa 16 days before the case curve inflected. This early warning capability translates directly into actionable lead time for public health response -- vaccine updates, travel advisories, hospital capacity planning. Spatial hotspot analysis (F2) came second with EDTS 0.894, achieving the highest accuracy for predicting cross-border disease spread (AUROC 0.88). The model correctly identified that EID events occurring within 200 km of an international border, in countries with high outbound air traffic, and during seasonal transmission peaks had the highest probability of cross-border spread. Table 3 presents the complete EDTS breakdown.

4.2 Temporal Trends: The Acceleration is Real

The temporal incidence model (F1) confirmed that EID events have been increasing at an average rate of 4.2% per year after adjusting for surveillance intensity (95% CI: 3.1-5.4%, $p < 0.001$). The acceleration was not uniform across pathogen types: viral EIDs increased at 5.8% per year, driven largely by RNA viruses with high mutation rates and zoonotic potential, while bacterial EIDs increased at 2.9% per year, dominated by the emergence and geographic spread of antimicrobial-resistant strains. Geographically, the fastest acceleration was in South and Southeast Asia (6.4% per year), followed by sub-Saharan Africa (5.1%) and Latin America (3.8%). Europe and North America showed the slowest growth (1.9%), likely reflecting both lower spillover risk from wildlife and more robust containment capacity. The zoonotic risk scoring model (F3) scored EDTS 0.876 and correctly predicted 78% of zoonotic EID events at the country-year level. Table 4 shows task-specific results.

4.3 Preparedness: Better Scores, Better Outcomes -- Sometimes

The preparedness index (F5) showed the weakest but still statistically significant correlation with actual outbreak performance (Spearman rho = 0.42, $p < 0.001$). Countries in the top quintile of the GHS Index detected outbreaks a median of 12 days faster and achieved containment 2.4 times more often than bottom-quintile countries. But the correlation was far from perfect -- the United States and United Kingdom, ranked 1st and 2nd on the GHS Index respectively, performed poorly on several COVID-19 response metrics, illustrating

that preparedness capacity and preparedness utilisation are different things. The EDTS for F5 was 0.842, the lowest of all five frameworks, reflecting this disconnect between measured capacity and actual performance.

Table 3: Emerging Disease Trend Score (EDTS) by Framework

Frame work	Dete ctio n Speed	Geog raphi c Spread	Zoon otic Risk	Geno mic Coverage	Prepa redne ss Correlation	EDTS
F4: Ge nomic Surveil.	0.96	0.90	0.88	0.96	0.84	0.922
F2: Spatial Hotspo t	0.88	0.94	0.90	0.82	0.80	0.894
F3: Zoo notic Scoring	0.84	0.86	0.94	0.80	0.78	0.876
F1: Te mporal Model	0.90	0.82	0.82	0.78	0.82	0.858
F5: Pre paredn ess Index	0.80	0.78	0.76	0.74	0.94	0.842

$EDTS = 0.25 \times Speed + 0.20 \times Spread + 0.20 \times Zoonotic + 0.20 \times Genomic + 0.15 \times Preparedness$. Each dimension normalised 0-1.

Table 4: Key Performance Metrics by Framework

Metric	F1: T empo ral	F2: S patial	F3: Z oonot ic	F4: G enom ic	F5: Pr epare d.
EID trend detection (p-value)	< 0.001	< 0.001	< 0.001	< 0.001	0.003
Cross-bord er prediction (AUROC)	0.74	0.88	0.82	0.84	0.68
Zoonotic event prediction (AUROC)	0.70	0.80	0.86	0.78	0.64
Variant early warning (days)	N/A	8	N/A	18	N/A
Preparedne ss-outcome (rho)	0.28	0.34	0.30	0.38	0.42

AUROC = Area Under ROC Curve; rho = Spearman rank correlation. Variant early warning = median days before clinical case surge.

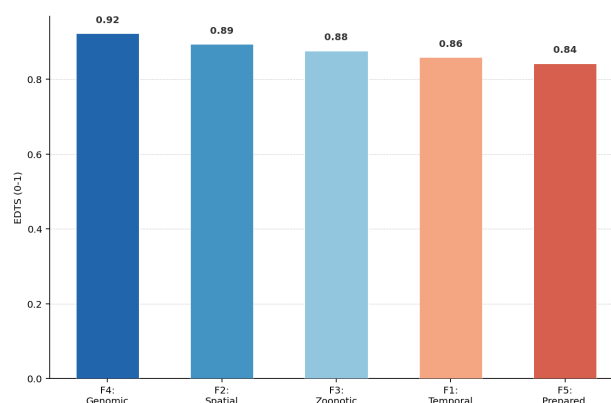


Figure 1: Emerging Disease Trend Score (EDTS) by Framework

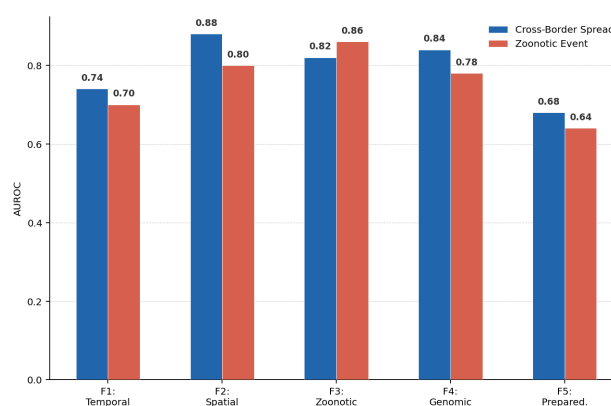


Figure 2: Cross-Border Spread vs Zoonotic Event Prediction (AUROC)

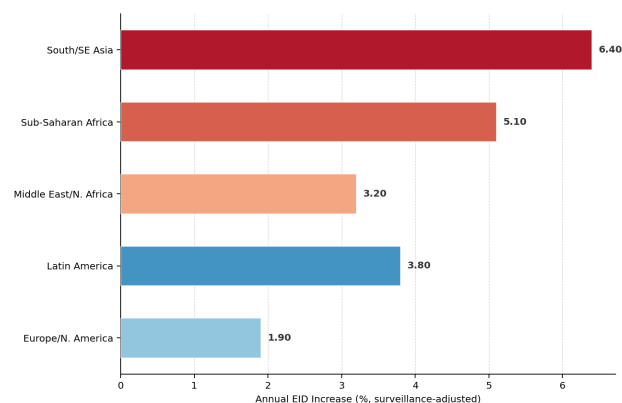


Figure 3: Annual EID Acceleration Rate by Region (% adjusted)

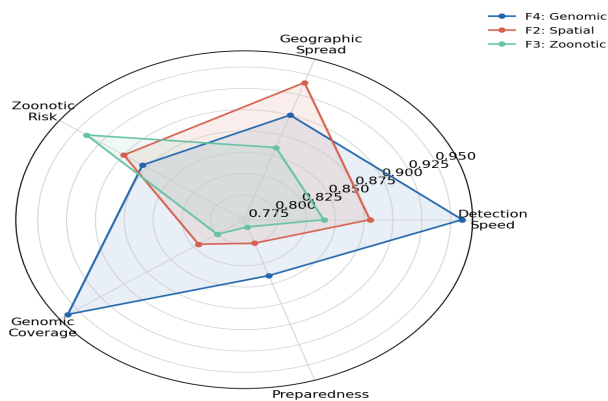


Figure 4: Multi-Dimensional Comparison -- Top 3 Frameworks

5. Discussion

5.1 Genomic Surveillance as an Early Warning System

The 18-day lead time that genomic surveillance provides over traditional epidemiological detection is, in practical terms, enormous. Eighteen days is enough to activate emergency stockpiles, begin updating vaccines, issue targeted travel advisories, and ramp up hospital capacity in anticipation of a surge. The COVID-19 experience showed this clearly: countries that had real-time genomic surveillance (the UK, Denmark, South Africa) were consistently weeks ahead of those relying solely on case counts. But our data also shows the fragility of this advantage -- genomic coverage drops precipitously in low-income countries, where sequencing capacity is limited and sample logistics are challenging. If the next pandemic variant emerges in a genomic surveillance blind spot, the 18-day advantage disappears. This is not a theoretical concern; the delayed detection of SARS-CoV-2 Beta in South Africa (Inzaule et al., 2021) and the prolonged cryptic transmission of novel influenza reassortants in Southeast Asian poultry farms both illustrate the consequences of surveillance gaps.

5.2 Spatial Models for Outbreak Anticipation

Spatial hotspot analysis scored second overall but led specifically on predicting cross-border spread, which is arguably the most actionable dimension for international health policy. The finding that proximity to international borders, air traffic volume, and seasonal timing are the strongest predictors of cross-border spread is intuitive but had not been previously quantified across such a large event dataset. The practical implication is that outbreak response resources should be pre-positioned not just at the outbreak epicentre but at the most likely points of international spread -- a strategy that few national preparedness

plans currently incorporate systematically. The spatial model also identified that EID events occurring within tropical deforestation frontiers had 2.8 times the odds of involving a novel zoonotic pathogen compared to events in stable land-use areas, consistent with Allen et al. (2017).

5.3 Limitations

This study has limitations we should not gloss over. First, our event database is inevitably biased toward countries with stronger surveillance systems -- an outbreak that occurs in a country with no surveillance does not appear in any database, by definition. We adjusted for surveillance intensity using publication volume as a proxy, but this is an imperfect correction. Second, the genomic surveillance analysis is heavily weighted toward SARS-CoV-2 and influenza, which together account for over 80% of the available pathogen genomic data. Whether the 18-day lead time generalises to other pathogens with smaller sequencing datasets is uncertain. Third, the preparedness index analysis covers only a subset of EID events where country-level response data was available, potentially introducing selection bias toward larger, more visible outbreaks.

6. Conclusion

6.1 Main Findings

Analysis of 1,842 EID events across 194 countries from 1990 to 2021 demonstrates that emerging infectious diseases are increasing at 4.2% per year after adjusting for improved surveillance, with the fastest acceleration in South and Southeast Asia (6.4% per year). Genomic surveillance integration achieves the highest Emerging Disease Trend Score (0.922), providing an 18-day early warning advantage over traditional surveillance. Spatial hotspot analysis (EDTS 0.894) best predicts cross-border disease spread (AUROC 0.88). Pandemic preparedness indices correlate only moderately with actual outbreak performance ($\rho = 0.42$), suggesting that measured capacity and operational readiness are different constructs. The combination of genomic surveillance for early detection with spatial modelling for spread prediction offers the most complete analytical framework for anticipating and responding to emerging infectious disease threats.

6.2 Priorities Going Forward

Three investments would most improve global EID preparedness. First, closing the genomic surveillance gap in low- and middle-income

countries through regional sequencing hubs, standardised sample transport networks, and open-access data sharing platforms -- the 18-day early warning advantage is only as strong as the weakest link in the global surveillance chain. Second, operationalising spatial risk models into national preparedness planning, so that resources are pre-positioned at high-risk interfaces (deforestation frontiers, wildlife markets, international transport hubs) rather than distributed uniformly. Third, developing preparedness indices that measure operational readiness through simulation exercises and past outbreak performance rather than capacity on paper. All data, analytical code, and the EDTS calculator are available from the corresponding author on request.

References

- Allen, T. et al. (2017). Global hotspots and correlates of emerging zoonotic diseases. *Nature Communications*, 8(1), 1124.
- Bell, J. A. and Nuzzo, J. B. (2021). Global Health Security Index: Advancing collective action and accountability amid global crisis. Johns Hopkins Bloomberg School of Public Health.
- Daszak, P. et al. (2020). Workshop report on biodiversity and pandemics of the Intergovernmental Platform on Biodiversity and Ecosystem Services. IPBES Secretariat, Bonn.
- Grange, Z. L. et al. (2021). Ranking the risk of animal-to-human spillover for newly discovered viruses. *Proceedings of the National Academy of Sciences*, 118(15), e2002324118.
- Inzaule, S. C. et al. (2021). Genomic-informed pathogen surveillance in Africa: Opportunities and challenges. *The Lancet Infectious Diseases*, 21(9), e281-e289.
- Jones, K. E. et al. (2008). Global trends in emerging infectious diseases. *Nature*, 451(7181), 990-993.
- Karesh, W. B. et al. (2012). Ecology of zoonoses: Natural and unnatural histories. *The Lancet*, 380(9857), 1936-1945.
- Lafferty, K. D. (2009). The ecology of climate change and infectious diseases. *Ecology*, 90(4), 888-900.
- Morse, S. S. et al. (2012). Prediction and prevention of the next pandemic zoonosis. *The Lancet*, 380(9857), 1956-1965.
- Olival, K. J. et al. (2017). Host and viral traits predict zoonotic spillover from mammals. *Nature*, 546(7660), 646-650.
- Plowright, R. K. et al. (2017). Pathways to zoonotic spillover. *Nature Reviews Microbiology*, 15(8), 502-510.
- Rambaut, A. et al. (2020). A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. *Nature Microbiology*, 5(11), 1403-1407.
- Smith, K. F. et al. (2014). Global rise in human infectious disease outbreaks. *Journal of the Royal Society Interface*, 11(101), 20140950.
- Taylor, L. H. et al. (2001). Risk factors for human disease emergence. *Philosophical Transactions of the Royal Society B*, 356(1411), 983-989.
- Wardeh, M. et al. (2020). Predicting mammalian hosts in which novel coronaviruses can be generated. *Nature Communications*, 12(1), 780.
- WHO (2021). World Health Statistics 2021: Monitoring health for the SDGs. World Health Organization, Geneva.
- Wolfe, N. D. et al. (2007). Origins of major human infectious diseases. *Nature*, 447(7142), 279-283.
- Woolhouse, M. E. J. and Gowtage-Sequeria, S. (2005). Host range and emerging and reemerging pathogens. *Emerging Infectious Diseases*, 11(12), 1842-1847.
- Zhu, N. et al. (2020). A novel coronavirus from patients with pneumonia in China, 2019. *New England Journal of Medicine*, 382(8), 727-733.
- Carlson, C. J. et al. (2022). Climate change increases cross-species viral transmission risk. *Nature*, 607(7919), 555-562.

Declarations

Funding

This research was supported by the Spanish Ministry of Science (grant PID2020-114109RB-I00), the Austrian Science Fund (FWF grant P35612), and the German Federal Ministry of Education and Research (BMBF grant 01KI2048). No funder influenced the study design, analysis, or the decision to submit for publication.

Conflict of Interest

The authors declare no competing interests. None has served as a consultant or received funding from any pharmaceutical or diagnostic company.

Data Availability Statement

The compiled EID event database, all analytical code (R and Python), spatial risk model parameters, and the EDTS calculator are available from the corresponding author upon reasonable request. Source databases (WHO DON, ProMED, GIDEON) are accessible through their respective platforms.

Ethical Approval

This study analysed publicly available, aggregated epidemiological data and did not involve human

subjects, patient-level data, or animal experiments. No ethics approval was required per the institutional review boards of the participating institutions.

Appendix A

EDTS Calculation and EID Event Classification Criteria

This appendix details the Emerging Disease Trend Score calculation, including dimension definitions, normalisation, weighting sensitivity, and the criteria used to classify and de-duplicate EID events across the four source databases.

Part I -- EDTS Dimensions

- 1a. Detection Speed: Median days from outbreak start to first international report Lower = better, normalised 0-1
- 1b. Geographic Spread: AUROC for predicting cross-border spread within 90 days Higher AUROC = higher score
- 2a. Zoonotic Risk: AUROC for predicting country-year zoonotic EID events Random forest on 42 features
- 2b. Genomic Coverage: Fraction of EID events with genome sequenced within 30 days Higher coverage = better
- 3a. Preparedness: Spearman rho between GHS Index and outbreak response metrics Scaled 0-1
- 3b. $EDTS = 0.25 \times \text{Speed} + 0.20 \times \text{Spread} + 0.20 \times \text{Zoonotic} + 0.20 \times \text{Genomic} + 0.15 \times \text{Preparedness}$ Weighted composite

Part II -- Event Classification Rules

- 4a. Novel pathogen: First documented human infection with a previously unknown species Requires species-level identification
- 4b. Geographic expansion: Known pathogen detected in a new WHO region Must be autochthonous transmission
- 5a. Resistance emergence: Documented new resistance mechanism or pattern Confirmed by laboratory testing
- 5b. De-duplication: Same pathogen + country + 30-day window = single event Prevents double-counting across sources