

Review Article

Progress and challenges in infectious disease surveillance and early warning



Ying Shen^{a,b,c,1}, Yonghong Liu^{a,c,1}, Thomas Krafft^d, Quanyi Wang^{a,b,c,*}

^a Beijing Center for Disease Prevention and Control, Beijing 100013, China

^b Beijing Research Center for Respiratory Infectious Diseases, Beijing 100013, China

^c Beijing Key Laboratory of Surveillance, Early Warning and Pathogen Research on Emerging Infectious Diseases, Beijing 100013, China

^d Department of Health, Ethics and Society, Faculty of Health, Medicine and Life Sciences, Maastricht University, Maastricht, 6200 MD, the Netherlands

ARTICLE INFO

Keywords:

Infectious disease
Surveillance
One Health
Early warning model
Early warning system

ABSTRACT

The increasing incidence of emerging infectious diseases emphasizes the urgent need for timely and accurate global surveillance and early warning systems. In recent years, infectious disease surveillance has become more diversified, and early warning technologies have seen significant advancements in sensitivity and timeliness. This review outlines the evolution and application of infectious disease surveillance and focuses on the potential of the One Health approach. By integrating data across human, animal, and environmental domains, the One Health approach provides a more comprehensive and effective framework for addressing future pandemics. Furthermore, this review systematically introduces key concepts in infectious disease early warning that include the selection of warning thresholds and the categorization of warning models. This review also summarizes representative global early warning systems for infectious diseases, discusses their prospects, and offers insights for developing intelligent, multi-source data-driven monitoring and early warning systems globally.

* Corresponding author.

E-mail address: wangqy@bjcdc.org (Q. Wang).

¹ These authors contributed equally to this work.

<https://doi.org/10.1016/j.medp.2025.100071>

Received 11 December 2024; Received in revised form 3 January 2025; Accepted 17 January 2025

Available online 21 January 2025

2950-3477/© 2025 The Author(s). Publishing services by Elsevier B.V. on behalf of Science China Press and KeAi Communications Co. Ltd. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

1. Introduction

In recent years, the incidence and impact of emerging infectious diseases have increased significantly, with notable outbreaks such as the 2003 severe acute respiratory syndrome (SARS), the 2009 swine flu pandemic, the 2012 Middle East respiratory syndrome (MERS), and, most recently, the coronavirus disease 2019 (COVID-19) pandemic.¹ These events highlight the urgent need for more robust and holistic infectious disease surveillance and early warning systems that allow the timely monitoring, detection, and assessment of emerging health threats.^{2,3}

Surveillance systems made significant advancements during the COVID-19 pandemic, particularly in the use of wastewater surveillance and digital methods such as mobility tracking and infodemiology.⁴ However, notable gaps still remain. One major issue is that existing systems continue to focus primarily on human health, with hospital-based surveillance forming the backbone. However, hospital-based systems often experience delays in detecting anomalies, emphasizing the need for further enhancements to address future pandemic risks.⁵ Another challenge is the disparity in monitoring capabilities across countries. Whereas some nations have well-established infrastructures, others face barriers, including limited resources, a lack of laboratory capabilities, political instability, and inadequate data-sharing systems, which further hamper global efforts in detecting and responding to emerging infectious diseases.^{6,7} For example, since October 2024, the Democratic Republic of the Congo has been struck by an undiagnosed disease that includes symptoms of fever, headache, cough, runny nose, and body ache. However, the cause was not identified until 2 months later, in December, as an acute respiratory infection complicated by malaria, further indicating regional disparities in resources and diagnostic capabilities.

The performance of early warning systems is closely linked to the effectiveness of disease surveillance because these systems transform data into actionable insights. Early warning techniques have also evolved considerably with the expansion of data sources and advancements in computational power. Today, multi-channel surveillance data are integrated to assess factors that influence the spatiotemporal spread of diseases, expanding the range of indicators to include symptoms, risk factors (e.g., meteorological conditions, vector density, and pathogen data), population mobility, and even internet queries.⁸ Moreover, the scope of early warning has broadened to include spatial and spatiotemporal warnings, thus offering a more comprehensive view of disease dynamics.⁹ Furthermore, earlier warning techniques have relied primarily on time series models that issue real-time alerts. However, modern systems now employ a range of advanced algorithms, including machine learning and deep learning,¹⁰ to forecast trends and provide proactive alerts that enable earlier resource preparation and better allocation.

Generally, surveillance data and early warning techniques are integrated into systems such as the China Infectious Disease Automated-alert and Response System (CIDARS)¹⁰ and EPIWATCH¹¹ to support timely interventions^{12,13} and optimal resource allocation.¹⁴ With ongoing advancements in technological and computational power and data availability—including information on pathogens, animal hosts, vectors, human populations, and environmental factors—early warning systems are increasingly capable of delivering precise and proactive alerts, thus enhancing global preparedness and response to emerging infectious diseases.^{15–17}

In this review, we critically examine the current landscape of global infectious disease surveillance and early warning systems and discuss development, applications, and areas for enhancement. By integrating data across human, animal, and environmental domains, the One Health approach offers a more comprehensive and effective framework for addressing future pandemics. Furthermore, we systematically introduce key concepts in infectious disease early warning systems that include the selection of warning thresholds and the categorization of warning models. The review also provides an overview of key global early warning systems, discusses their potential, and offers insights into the development of intelligent, multi-source, data-driven monitoring and early warning systems.

2. Infectious disease surveillance

2.1. History and development of surveillance

The concept of surveillance dates back to the 14th century when the Venetian Republic made the first attempt to detect and exclude ships that carried infected individuals. As the plague spread through

London in the 17th century, parish clerks initiated the first weekly reports of deaths and their causes in the form of ‘Bills of Mortality’ to infer disease intensity and inform appropriate actions. This effort marked the formulation of basic surveillance principles, including data collection, analysis, interpretation to provide information, and the dissemination of information to guide actions.^{18,19}

In the 19th century, the practice of analyzing and interpreting data to inform public health actions was fully developed. In 1850, Lemuel Shattuck’s landmark ‘Report of the Massachusetts Sanitary Commission’ in the USA first linked living conditions to various health outcomes, including death from any cause, infant and maternal mortality, and infectious diseases. During the same period, William Farr, one of the founders of modern surveillance, focused on collecting vital statistics, used data to advance population-based surveillance and disseminated findings to guide public health interventions.¹⁹ Surveillance became more systematic and institutionalized over this period. For example, the UK established the Central Register Office in 1836 and formally introduced death registries. In 1888, Italy mandated the reporting of 11 communicable diseases and death certification.¹⁸

Surveillance practices continued to evolve in the 20th century. In 1955, Dr. Alexander D. Langmuir in the USA first defined surveillance as the collection, analysis, and dissemination of data on illness and health events.²⁰ This definition became a cornerstone for modern epidemiological practices and was integral to the newly created Communicable Disease Center, now known as the US Centers for Disease Control and Prevention (CDC).^{18,19} In 1986, the US CDC further refined the definition of surveillance as ‘the ongoing systematic collection, analysis, and interpretation of health data essential to the planning, implementation, and evaluation of public health practice, closely integrated with the timely dissemination of these data to those who need to know.’²¹ Since then, surveillance has played a crucial role in many aspects of public health and serves as its cornerstone. Former US Surgeon General Dr. David Satcher once stated, ‘In public health, we can’t do anything without surveillance. That’s where public health begins.’²² Although its most recognized use is the detection of epidemics in the population, surveillance has several other important functions, including risk factor monitoring, disease burden estimation, health intervention evaluation, guidance for research and development of vaccines and medications, disease eradication, and medical resource allocation.^{23–27}

2.2. Common surveillance systems and data sources

As the importance of public health gains increasing recognition and technological advancements persist, surveillance systems have diversified into various forms including passive versus active surveillance,²⁸ indicator-based versus event-based surveillance,^{29,30} and syndromic versus laboratory-based surveillance (Table 1).^{31,32} Each system contributes uniquely to understanding disease trends. Passive surveillance, which is based on routine healthcare reports, is widely used for its cost-effectiveness and broad coverage but is often limited by underreporting and delays in data collection. By contrast, active surveillance involves proactive data collection from healthcare providers or sentinel sites and generates more timely and accurate data but has greater resource requirements.

For example, indicator-based surveillance focuses on predefined indicators such as case counts, hospitalizations, and mortality that are essential for tracking established diseases. Conversely, event-based surveillance draws upon a broader range of formal and informal channels, including media reports and digital platforms, which are more suitable for identifying unusual health events and early outbreaks.^{29,30} The integration of these surveillance systems enhances the ability to capture a comprehensive picture of disease dynamics.

Despite these strengths, the complexity of emerging infectious diseases, particularly those with zoonotic origins, necessitates a more integrated surveillance framework. Traditional systems, although effective for specific functions, often operate in isolation and may be inadequate in detecting the early signs of emerging infectious disease outbreaks. This shortcoming highlights the need for a One Health approach to surveillance that integrates information on pathogens, hosts, environments, and socio-factors to create a comprehensive, interdisciplinary system for early detection and response.

Table 1
Common surveillance categories and their applications.

Categories	Applications	Advantages	Limitations
Passive ³¹ vs. active surveillance ²⁸	Passive surveillance ³¹ depends on routine reports from healthcare providers, who identify and document diseases during regular medical care. Active surveillance ²⁸ involves proactive data collection by health authorities through contact with healthcare providers, record reviews, and sentinel sites.	Cost-effective, covers large populations. Provides more accurate and detailed data, allows early detection of outbreaks.	Prone to underreporting, delays in data collection. Resource-intensive, requires more manpower and coordination.
Sentinel ²⁸ vs. population-based surveillance ³¹	In sentinel surveillance, a prearranged sample of reporting sources agrees to report all cases of defined conditions. Population-based surveillance tracks the incidence and prevalence of diseases in the entire country (national) or a defined subnational population area.	Could indicate trends in the entire target population. Excellent for detecting major public health problems. Produces more generalizable data on incidence of disease.	May be insensitive to rare events, which may emerge anywhere in the population. Resource-intensive and may face challenges related to data quality.
IBS vs. EBS ³⁰	IBS collects data based on pre-defined specific indicators such as case numbers, hospitalization rates, and mortality. EBS gathers data from formal and informal sources such as media reports and social networks to detect unusual health events.	Tracks the status of known diseases effectively. Allows rapid identification of unusual health events and quick response to new public health threats.	Limited to predefined indicators, may miss new or emerging threats. May result in false alarms due to unverified or unreliable sources.
Syndromic ³² vs. laboratory-based surveillance ³¹	Syndromic surveillance monitors symptoms and clinical presentations to detect potential outbreaks before specific diagnoses are made. Laboratory-based surveillance involves the identification of pathogens using techniques such as PCR, serological tests, and genomic sequencing.	Enables early detection of outbreaks through pre-defined symptom tracking. Provides definitive pathogen identification, guides treatment and prevention strategies.	Lacks specificity, may result in false positives and mis-confirmed diagnoses. Resource-intensive, requires laboratory infrastructure and expertise.

EBS: event-based surveillance; IBS: indicator-based surveillance; PCR: polymerase chain reaction.

2.3. Surveillance from a One Health approach

2.3.1. Pathogen surveillance

In the context of pathogen surveillance, genomic surveillance is a critical tool for identifying and understanding the genetic structure, variations, and evolutionary changes of pathogens.³³ By sequencing pathogen genomes, researchers can monitor the emergence of new pathogens, track their transmission patterns, and detect mutations that may influence their virulence or capacity for immune evasion.^{34,35} A notable example is the initial identification of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) at the onset of the COVID-19 pandemic.^{33,36} Metagenomic RNA sequencing was employed to

uncover the cause of the unknown respiratory disease and successfully identified the novel coronavirus. This early detection was crucial and allowed for the rapid development of molecular diagnostic assays, vaccines, and therapeutic interventions.

Genomic surveillance also plays an essential role in monitoring the emergence of new pathogen variants. In the case of SARS-CoV-2, the ongoing surveillance of mutations—particularly in the spike protein and receptor-binding domains—has enabled scientists to evaluate changes in transmissibility, immune escape, and disease severity.^{37–41} This information helps forecast the predominance of specific variants and potential disease trends. Moreover, these data inform public health responses such as updating vaccine formulations to target specific variants and managing strategic reserves of antiviral medications.⁴²

Genomic surveillance is equally vital for zoonotic diseases such as avian influenza. Tracking specific mutations, such as those in polymerase basic protein 2 and sialic acid binding sites, is crucial for detecting signs of viral adaptation in mammals. Such mutations can increase the risk of human-to-human transmission and heighten the pandemic potential, as exemplified by the global spread of clade 2.3.4.4b of H5N1 in 2023–2024. Early identification of these genetic markers offers an opportunity to implement targeted control measures and prevent wider outbreaks.

The global open sharing of genomic data is fundamental to pathogen surveillance and the evaluation of pathogen characteristics.³³ International initiatives, including the World Health Organization's (WHO) International Pathogen Surveillance Network and the Global Genomic Surveillance Strategy for Pathogens with Pandemic and Epidemic Potential, 2022–2032 and the Global Initiative on Sharing All Influenza Data,^{43–45} were developed to facilitate this process. These efforts enhance the early detection of pandemic and epidemic threats and enable coordinated global responses by providing a unified platform for genomic data exchange and analysis.

2.3.2. Vector surveillance

Vectors are living organisms that can transmit infectious pathogens between humans or from animals to humans. Many vectors are arthropods such as mosquitoes, ticks, and flies that ingest pathogens from an infected host (human or animal) during feeding.⁴⁶ Once infected, the vector can transmit the pathogen to new hosts in subsequent feedings.⁴⁷ Therefore, vector-borne diseases refer to human illnesses caused by viruses, bacteria, and parasites that are transmitted by vectors.

Vector surveillance involves the systematic and continuous collection, analysis, and interpretation of vector population data such as species composition, density, and distribution and the seasonal variation of mosquitoes, rodents, flies, and other disease-carrying organisms.⁴⁸ These data are a critical resource for guiding public health authorities and disease prevention agencies in designing, implementing, evaluating, and adjusting vector control strategies. The effective surveillance of vector populations can help minimize their impact on communities, reduce economic losses, and most importantly, prevent and control the spread of vector-borne diseases. For example, in mosquito-borne diseases, warm and humid environments create favorable conditions for mosquito breeding and disease transmission.^{46,49,50} Countries such as Uganda have used satellite systems to predict heavy rainfall—a key factor in mosquito population growth—to forecast disease risk and prepare early control measures. To strengthen the global response to vector-borne diseases, the WHO launched the Global Arbovirus Initiative on March 31, 2022.⁵¹ This initiative emphasizes improved risk monitoring and disease forecasting, the reduction of outbreak risk, the enhancement of vector control and prevention, innovation in new methods, and the development of partnerships to support these efforts globally.

2.3.3. Host surveillance

Host surveillance aims to elucidate the distribution and transmission dynamics of pathogens within animal hosts in natural ecosystems. This method includes identifying transmission factors and detecting spillover events, offering early warnings for potential human infections, and supporting epidemic preparedness. Generally, host surveillance targets wildlife, domestic poultry, and livestock that often serve as reservoirs for emerging infectious diseases. For example, monitoring wild birds, especially migratory species, is critical for tracking avian influenza virus transmission.^{52,53} Migratory birds are natural reservoirs for various influenza strains, and their seasonal, transcontinental movements can introduce new viral subtypes into different regions.^{54,55} Surveillance along migratory routes and resting areas identifies

potential viral strains that could spread to domestic poultry and wildlife.^{52,56} Continuous monitoring of domestic poultry is also essential because these birds act as intermediaries between wild bird populations and human environments.⁵⁷ Infected flocks in poultry farms can lead to economic losses and elevated human exposure risk, making early surveillance in farms and markets vital for implementing rapid containment actions such as culling.

Spillover surveillance is also crucial in host surveillance. Spillover refers to the phenomenon in which pathogens cross species barriers and spread across various hosts, such as the transmission of the avian influenza virus from birds to mammals.^{58,59} Such spillover events may indicate that the virus is adapting to new hosts, thereby increasing the risk of human infection.⁶⁰ Incidents involving the highly pathogenic avian influenza virus H5N1 have highlighted the need for vigilant monitoring given that the virus spreads from wild birds or poultry to mammals, including cattle, rodents, elephant seals, and pigs, thus triggering global outbreaks.^{61–63} Monitoring spillover incidents is essential—particularly for identifying adaptive mutations in mammals such as polymerase basic protein 2 adaptation or mutations that affect sialic acid binding—and provides critical insights into the risk of human-to-human transmission.^{60,64–66}

Host surveillance systems should be customized to specific ecological and regional characteristics. For example, in urban green parks, monitoring tick, rodent, and weasel populations is essential for elucidating viral transmission in urban wildlife and allows the timely assessment of infection risk to the surrounding human populations.^{67,68} This localized approach enhances the effectiveness of host surveillance by addressing unique ecological challenges and improving public health preparedness.

2.3.4. Human surveillance

Once a pathogen establishes itself in human populations, systematic human surveillance becomes critical for monitoring its spread and public health impact. As illustrated in the infectious disease pyramid model, human surveillance encompasses various stages: initial infection, symptom manifestation, healthcare engagement, hospitalization, progression to severe cases, and mortality (Fig. 1).⁶⁹ At each stage, only a portion of infected individuals advance to the next stage, creating a stratified disease structure. For example, a pathogen may cause symptoms in 80% of infected individuals, yet only 60% may seek medical care and approximately 30% of those may require hospitalization.^{70,71} Comprehensive surveillance must thus encompass the full continuum of healthcare encounters by integrating pre-hospital behaviors such as absenteeism, self-medication, and online health inquiries with clinical visit data and treatment outcomes. By using various monitoring systems—whether passive or active, indicator-based or event-based—human surveillance could provide a more comprehensive view of the pathogen's impact on human populations, facilitating early detection and enabling prompt, targeted public health responses.

2.3.5. Environmental surveillance

Environmental surveillance for infectious diseases involves a comprehensive assessment of natural environmental conditions and socio-environmental factors. Natural environmental monitoring focuses

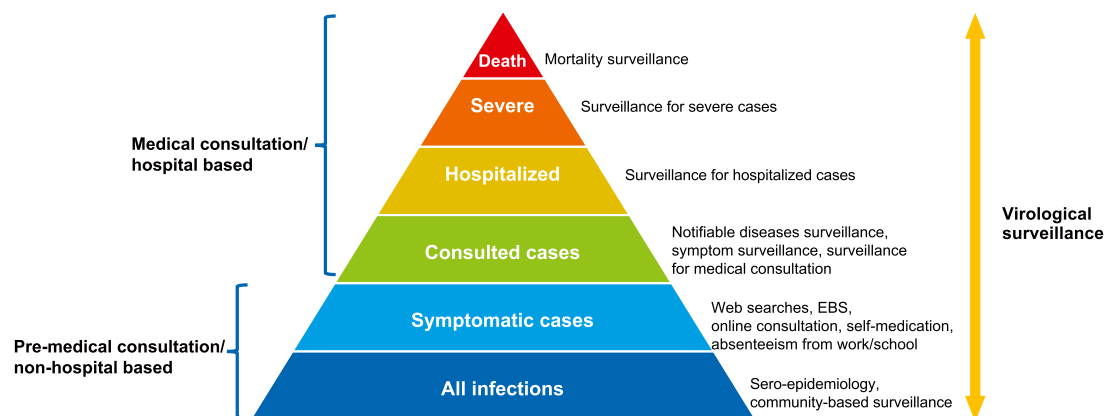


Fig. 1. Spectrum of infectious disease surveillance in humans. EBS: event-based surveillance.

on systematically observing and assessing conditions, such as water, air, soil, and climate, and is essential for understanding disease dynamics and informing control strategies.⁷² For example, meteorological data are widely used in the predictive modeling of diseases such as dengue and malaria. Studies have demonstrated that specific climate indicators—such as sea surface temperature anomalies in the tropical Indian Ocean—can correlate with the incidence of dengue, potentially allowing for earlier disease forecasts and intervention planning.⁷³

Wastewater surveillance has emerged as a highly effective tool for the early detection and monitoring of infectious agents in communities.^{74,75} This approach, which tracks RNA/DNA in sewage, was widely adopted during the COVID-19 pandemic by certain countries, including the USA, the UK, and Germany.^{76,77} By providing a cost-effective, community-wide measure of infection levels and even capturing trends among asymptomatic individuals, wastewater monitoring offers a valuable early warning system for emerging pathogens.⁷⁵ Continued advancements in sampling, detection, and amplification technologies are expected to expand the utility of wastewater monitoring in surveillance frameworks for infectious diseases.⁷⁸

Environmental changes such as land degradation, forest loss, and climate shifts also significantly impact zoonotic spillover risks.^{72,79} For example, altered migratory bird patterns and changes in virus persistence under different climatic conditions can influence the spread of avian influenza (AIV). Environmental changes have led to AIV transmission in regions that had previously remained unaffected, as evidenced by the emergence of H5N1 in Antarctica in 2023.⁶² Additionally, monitoring high-density poultry farms—where the risk of virus amplification and human transmission is high—enables the early detection of AIV and provides essential data for containment efforts.

Socio-environmental factors such as human mobility and public health events also play a critical role. Population movement restrictions, as seen early in the COVID-19 pandemic, were crucial for limiting the virus's spread.⁸⁰ Mobility data enhance predictive models for cross-border transmission of vector-borne diseases and supplement traditional surveillance systems. Furthermore, platforms such as ProMED-Mail and EPIWATCH facilitate event-based surveillance by tracking public health events for indications of outbreaks.^{81,82} Internet search trends also offer early insights into potential outbreaks and assist public health officials in detecting emerging infectious disease threats and implementing timely interventions.^{83–85}

In summary, comprehensive surveillance systems are essential for the effective monitoring and analysis of infectious disease dynamics. Integrating multi-source data—including information on pathogens, hosts, vectors, human populations, and environmental conditions—allows public health officials to detect potential outbreaks and emerging threats with increased precision and promptness. The following section examines how the integration of these surveillance systems with predictive analytics and early warning frameworks significantly enhances the capacity to respond proactively to infectious disease challenges, ultimately safeguarding public health and preventing widespread outbreaks (Fig. 2).

3. Infectious disease early warning

3.1. Basic principles of early warning

Infectious disease early warning refers to the issuance of signals before or at the early stages of an outbreak or epidemic that alert to the potential occurrence, spread, and severity of the event.⁸⁶ The fundamental principle is the use of specific analytical methods or models to detect anomalies in infectious disease surveillance data that exceed expected normal levels.⁸⁷ The early warning framework consists of six main steps (Fig. 3). First, define the purpose of the warning: Is it to signal the start of an epidemic season? To identify an unusual rise in cases? Or to determine if case numbers exceed historical averages or available resources? Second, select alert indicators based on the objectives, such as number of cases, test positivity rate, or emergency department visits. For diseases with high underreporting rates, the test positivity rate can be a particularly effective indicator.⁸⁸ Third, establish warning gold standards and thresholds. They should depend on the disease's epidemiological characteristics and public health needs, ensuring timely warnings without triggering unnecessary responses. Fourth,

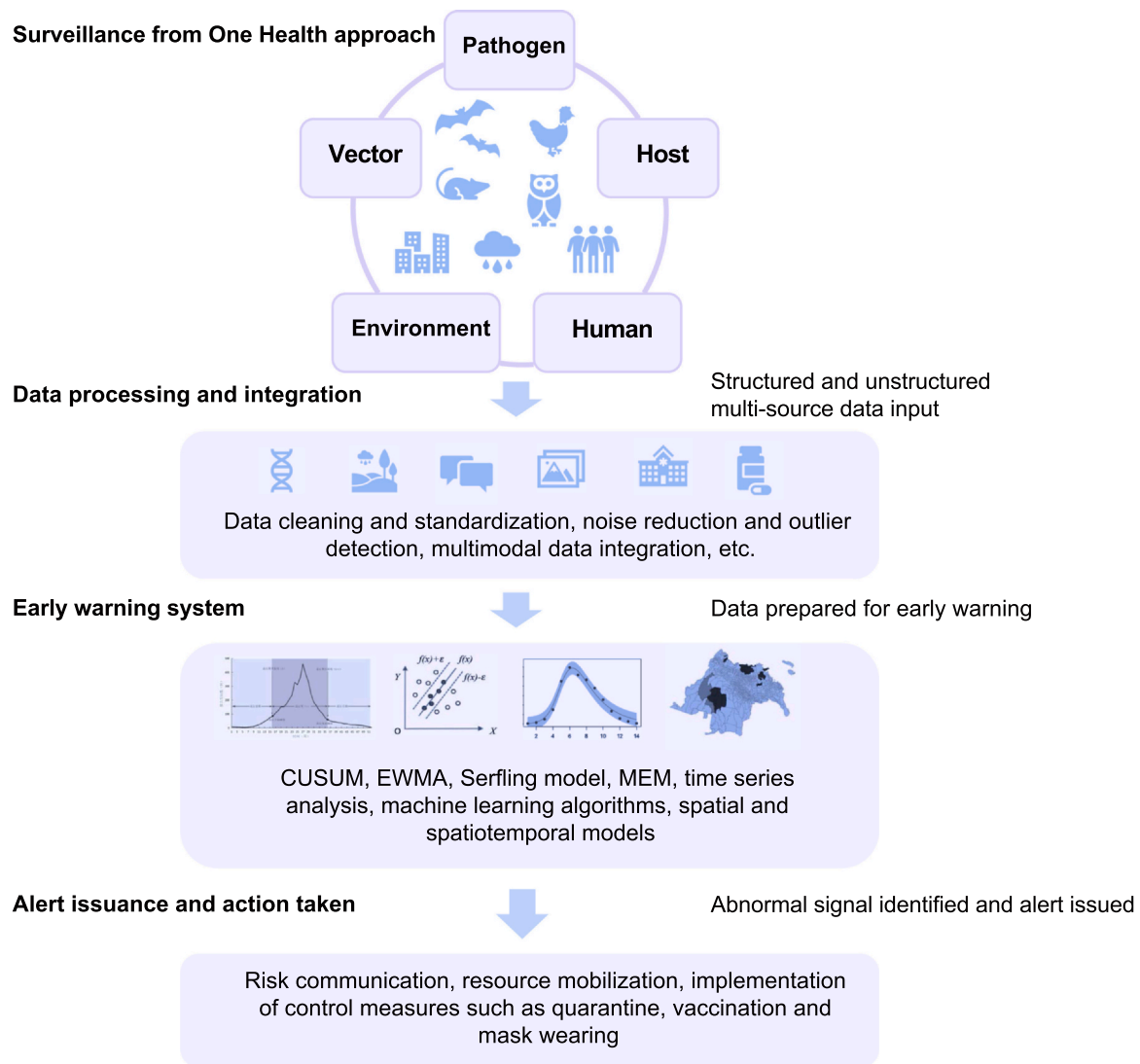


Fig. 2. Framework for infectious disease surveillance and early warning. CUSUM: cumulative sum; EWMA: exponentially weighted moving average; MEM: moving epidemic method.

determine the warning strategies and models. Two common approaches are (1) using real-time data with preset thresholds for alerts and (2) using real-time data to predict future trends and assessing whether a warning is necessary based on thresholds. Fifth, evaluate the early warning system's effectiveness, is measured by focusing on sensitivity (detecting true events), specificity (excluding non-events), and timeliness (the interval between a warning and the actual event). Finally, once objectives, indicators, thresholds, and methods are established, proactive warning signals are issued in real-time and are followed by necessary emergency responses, including pharmaceutical and non-pharmaceutical interventions, to mitigate epidemic risk.

Every step in the infectious disease early warning framework is essential. This review focuses specifically on the selection of early warning gold standards and thresholds and the classification of early warning models given that these elements are pivotal for ensuring timely and accurate alerts. Appropriate gold standards and thresholds balance the need for responsiveness with resource efficiency, whereas the choice of early warning models directly influences the reliability and precision of predictions.

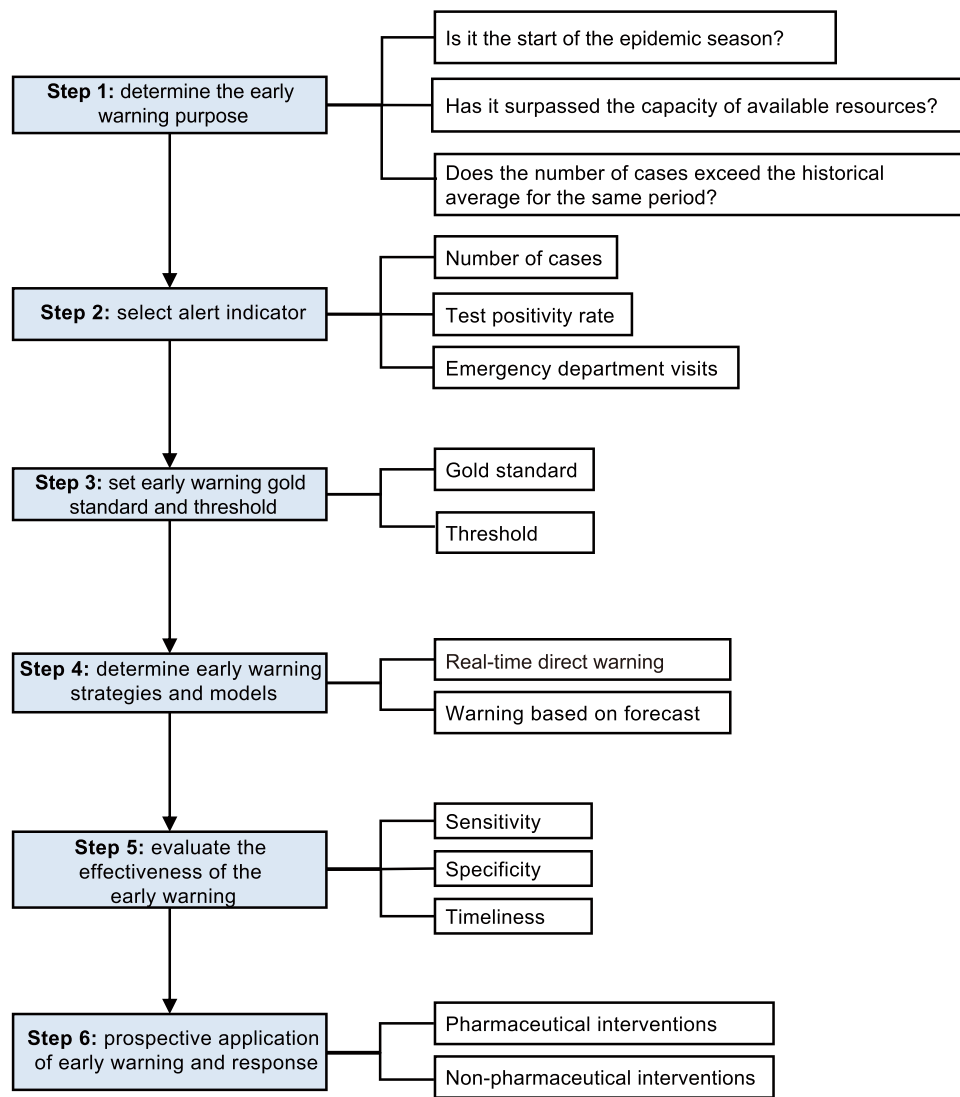


Fig. 3. The infectious disease early warning framework.

3.2. Selecting appropriate early warning gold standards and thresholds

The terms ‘gold standard’ and ‘threshold’ refer to distinct concepts. The gold standard typically refers to verified, accurate reference data or methods—such as high-quality laboratory test results—that accurately reflect the epidemic situation and serve as a benchmark for assessing the sensitivity and specificity of early warning practice. By contrast, thresholds are based on statistical models or epidemiological data to identify the timing of epidemic outbreaks as indicated by the gold standard.

The establishment of the gold standard and threshold is crucial for ensuring the timeliness and accuracy of alerts. Setting these parameters too high or too low can undermine their effectiveness. The determination of a gold standard should consider factors such as the characteristics of the pathogen, local immunity levels, and the availability of medical resources. For example, when the infectious disease in question (e.g., influenza) poses a significant public health threat, a low gold standard that increases sensitivity and helps identify more potential outbreaks may be more appropriate. Conversely, for low-impact diseases, a high gold standard may be selected to minimize the societal consequences.

The gold standard for a specific pathogen in a particular region is generally not adjusted frequently, and only substantial evolutionary changes in the pathogen warrant a revision of the gold standard. By contrast, the early warning threshold often requires adjustments in response to the actual development of an epidemic. Alerts for infectious diseases are typically categorized into three types: fixed thresholds, moving averages, and historical trends.⁸⁹ For certain diseases (e.g., Ebola infection) in which even a single case poses a potential public health risk, single-case alerts are commonly used. Trend-based alerts are frequently employed to signal the onset of seasonal infectious disease outbreaks.

CIDARS initially recommended uniform warning thresholds across all levels of China CDC. However, the practical implementation of these thresholds revealed a high false-positive rate and a substantial discrepancy between outbreak alerts and confirmed outbreaks.⁹⁰ These findings suggest that the nationally recommended thresholds may not be suitable for all CDC levels. Therefore, it is recommended that each CDC level conduct localized studies to establish thresholds that are tailored to regional infectious disease patterns.^{91,92}

3.3. Early warning models

The early warning model is a crucial component of infectious disease surveillance. In recent years, early warning methods have evolved with the expansion of monitoring dimensions and the advancement of artificial intelligence technology. Beyond traditional single-indicator models, multi-covariate approaches—such as machine learning and deep learning models—offer significant advantages in processing large datasets. Research has demonstrated the effectiveness of these approaches in capturing complex transmission dynamics.⁹³ Bayesian methods have also been applied to create disease risk maps and identify anomalies, particularly for surveillance systems that integrate data from multiple sources.⁹⁴ Model-based integrated warning systems that aim to enhance warning effectiveness and prediction accuracy by combining the strengths of multiple models have been widely applied in recent years. These methods often integrate different types of models—such as transmission dynamic models, statistical models, and machine learning models—to improve the performance of infectious disease warning systems.¹⁰ These emerging technologies not only facilitate the efficient processing and analysis of a vast amount of data but also enhance the timeliness, sensitivity, and specificity of infectious disease alerts by incorporating and analyzing data from diverse surveillance sources. Infectious disease early warning models can be classified into temporal, spatial, and spatiotemporal models based on the dimensions of analysis.

3.3.1. Temporal early warning models

Temporal early warning models focus primarily on detecting temporal changes in infectious disease data within a specified area; these models identify anomalous signals by setting threshold criteria. These methods can be classified into two categories based on their predictive capabilities (Table 2). The first category includes methods that provide real-time alerts without predictive functionality. One such method is Statistical Process Control (SPC),⁹⁵ which was originally developed by Walter Shewhart in 1924 to detect statistical shifts in process quality. SPC has since been widely adapted for disease surveillance to identify abnormal signals. Building on the principles of SPC, cumulative sum (CUSUM)⁹⁶ and exponentially weighted moving average (EWMA)⁹⁸ were developed. Both methods are particularly effective at detecting small changes in data. Another widely used approach proposed by Serfling in the 1970s⁹⁷ is the Serfling regression model, which has become a standard tool for epidemic detection and disease burden estimation based on clean historical data. Similarly, the moving epidemic method (MEM)⁹⁸ developed in Spain in 2001, is designed to detect the onset and intensity of an outbreak. The Serfling regression model and MEM rely solely on historical monitoring data and do not require a gold standard, making these methods highly applicable in infectious disease early warning systems.

The second category of temporal early warning methods involves predicting future trends before detecting abnormal signals. Common techniques in this category include classical time series models⁹⁹ such as generalized linear models, generalized additive models, logistic regression, autoregressive moving average models, and transmission dynamic models (e.g., susceptible-infectious-removed and susceptible-exposed-infectious-removed model).¹⁰⁰ In recent years, machine learning and deep learning

Table 2
Classification of infectious disease early warning models.

Categories	Early warning based on real-time data	Early warning based on forecast
Temporal early warning models	<ul style="list-style-type: none"> • SPC • CUSUM • EWMA • MEM • Serfling 	<ul style="list-style-type: none"> • Classical Time Series Models (e.g., GLM, GAM, ARIMA) • Infectious disease dynamic model (e.g., SIR, SEIR) • Machine Learning Models (e.g., RF, SVM) • Deep Learning Models (e.g., LSTM, Informer)
Spatial early warning models	<ul style="list-style-type: none"> • Moran's <i>I</i> • LISA • Getis-Ord <i>Gi</i>* 	Not applicable
Spatiotemporal early warning models	Spatio-temporal scan statistics	Bayesian spatio-temporal models

ARIMA: autoregressive moving average model; CUSUM: cumulative sum; EWMA: exponentially weighted moving average; GAM: generalized additive model; GLM: generalized linear model; LISA: local indicators of spatial association; LSTM: long short-term memory; MEM: moving epidemic method; RF: random forest; SEIR: susceptible-exposed-infectious-removed; SIR: susceptible-infectious-removed; SPC: statistical process control; SVM: support vector machine.

algorithms have also proven effective in infectious disease early warning⁹³; models such as random forest, support vector machine, long short-term memory, and Informer have demonstrated strong predictive capabilities. Importantly, time-based early warning models, although effective in capturing temporal trends, are limited because they rely solely on the temporal dimension and are unable to detect spatial anomalies.

3.3.2. Spatial early warning models

Spatial early warning models primarily focus on detecting changes in infectious disease patterns within a specific geographic area at a given time. These models compare the incidence of disease in the target area with that of the broader region or neighboring areas to identify statistically significant spatial clusters that may indicate an emerging epidemic. The application of spatial early warning models requires geographic information—such as the residential addresses of reported cases or the latitude and longitude of locations—within the surveillance data. Moran's *I*, a spatial analysis method, was introduced in the mid-20th century to determine whether the spatial distribution of a disease exhibited clustering. Other techniques, such as local indicators of spatial association¹⁰¹ and Getis-Ord *Gi**¹⁰², have been employed to identify spatial aggregation patterns. In 1997, Kulldorff developed the spatial scan statistic¹⁰³ by using a likelihood ratio to detect spatial clustering. On the basis of this approach, the SaTScan software was developed and remains widely used in spatial data analysis.⁹ More recent improvements, including the maximum clustering set-proportion¹⁰⁴ and the maximum clustering heterogeneous set-proportion,¹⁰⁵ address limitations related to parameter selection in spatial scanning statistics, particularly by incorporating prior information. However, spatial early warning models are typically used to identify spatial anomalies within specific time frames and cannot detect temporal anomalies or compare current trends with historical data.

3.3.3. Spatio-temporal early warning models

The spatiotemporal alert model integrates both temporal and spatial dimensions to detect infectious disease outbreaks. By analyzing and using temporal and spatial surveillance, this model identifies high-risk periods and geographic areas prone to outbreaks or epidemics. Common approaches include spatiotemporal scan statistics based on single indicators of case information⁹ and more complex spatiotemporal regression models that incorporate multiple risk factors. Notably, Bayesian spatiotemporal models have been widely employed for risk mapping, particularly in the context of vector-borne diseases.⁹⁴ As surveillance systems continue to evolve, these models are increasingly applied to a broader

range of infectious diseases and significantly improve the accuracy and precision of early warning systems.

4. Infectious disease early warning system

Infectious disease early warning systems are automated platforms that use analytical methods to detect anomalous data signals in real-time. The global importance of timely and efficient early warning systems was further emphasized in the aftermath of the COVID-19 pandemic. The development of infectious disease early warning systems has paralleled that of infectious disease surveillance systems. Infectious disease early warning systems are generally categorized into the following types based on the data sources on which they rely: case-based surveillance, syndromic surveillance, event-based surveillance, and pathogen surveillance.

4.1. Early warning systems that rely on case-based surveillance

Several countries have established infectious disease monitoring and early warning systems based on notifiable infectious disease data. For example, Norway¹⁰⁶ implemented in 2005 a web-based rapid alert system that is designed to issue mandatory outbreak alerts to municipal medical officials, healthcare institutions, and food safety authorities. CIDARS,¹⁰⁷ which was initiated in China in 2008, uses SPC, CUSUM, and spatial scan statistics to provide timely spatial warnings regarding 28 nationally notifiable infectious diseases. CIDARS successfully detected all dengue outbreaks with high specificity and timeliness by using the time series moving percentile method to automatically generate early warning signals when case aberrations occurred.¹⁰⁸ The computer-supported outbreak detection system,¹⁰⁹ Sweden's early warning system established in 2009, integrated the SaTScan software based on space-time scan statistics and supported four statistical detection methods—SaTScan Poisson, SaTScan space-time permutation, the Farrington algorithm, and a simple threshold algorithm—that enabled the detection of spatial-temporal anomalies in weekly reported cases for 63 infectious diseases. However, given the issues of time lags and underreporting of notifiable infectious diseases,¹¹⁰ the early warning system based on case-based surveillance requires further optimization.

4.2. Early warning systems that rely on syndromic surveillance

Individuals typically seek medical attention after symptoms have manifested for some time, resulting in a delay between symptom onset and diagnosis. As a result, symptom-based early warning systems can often detect anomalies earlier than case-based systems.¹¹¹ For example, the United States initiated the Early Aberration Reporting System¹¹² in 2000 to monitor symptoms by using the CUSUM model to identify abnormal signals. Since 2003, the United States military has been using the Early Syndrome Detection System (ESSENCE II)¹¹³ to detect potential outbreaks by analyzing data such as emergency department chief complaints, pharmaceutical sales, and school absenteeism and using the autoregressive modeling algorithm and EWMA algorithm for early warning. The CDC evaluated the effectiveness of the ESSENCE influenza-like illness (ILI) surveillance system, the CDC observed that the system failed to provide early warning or timely detection of an emerging infectious disease during a localized, single-source outbreak despite strengths in data quality, flexibility, and representativeness. In 2013, the Republic of Korea developed the Military Real-time Syndromic Surveillance System (MARSS), which gathers data from 19 military hospitals to track cases that meet the criteria for seven syndromes, including botulism, hemorrhagic diseases, fever, and influenza-like illnesses. The CUSUM algorithm is used in MARSS for early warning detection.

In the context of large-scale events, several countries have established symptom-based early warning systems to support infectious disease prevention and control. For example, the Beijing Olympic Games Infectious Disease Surveillance System (BOG-IDSS) was developed specifically for the 2008 Beijing

Olympics and uses a range of routine surveillance systems. This system effectively ensured public health security during mass gatherings.¹¹⁴ Similarly, the Emergency Department Sentinel Syndromic Surveillance System was established to enhance surveillance capabilities for the London 2012 Olympics.¹¹⁵ In recent years, advancements in artificial intelligence and wearable technology, such as smartwatches and smart rings, have enabled the detection of early signs of infection, potentially even before the manifestation of symptoms.¹¹⁶

4.3. Early warning systems that rely on event-based surveillance

With advancements in internet technology, traditional early warning systems based on notifiable cases and symptom surveillance have been insufficient for detecting the emergence of new pathogens such as SARS. Importantly, some symptomatic individuals may not seek medical attention, whereas epidemic signals often appear earlier in unstructured online sources such as social media, forums, and news outlets. Monitoring these digital sources offers significant advantages for the early detection of anomalies.

Event-based early warning systems focus on the use of unstructured health-related information that could pose serious public health risks, followed by evaluation and interpretation.¹¹⁷ ProMED-mail, one of the pioneering platforms established in 1994, supports the early identification of epidemics by disseminating outbreak information via email from its expert group to subscribers.¹¹⁸ ProMED-mail has consistently been a leading platform for the early detection and reporting of a wide range of significant and minor disease outbreaks. Notable examples include the SARS outbreak in 2003, the emergence of MERS in Saudi Arabia in 2012, and the SARS-CoV-2 outbreak in Wuhan in 2020.¹¹⁹ Developed in 2006, HealthMap is a platform for the automated real-time collection of infectious disease outbreak data and offers visual data representation.¹²⁰ EPIWATCH, launched in 2016, expands on the capabilities of ProMED-mail and HealthMap; in addition to real-time outbreak monitoring, this system provides forecasting and warning functionalities.¹¹

Platforms such as Google Flu Trend¹²¹ and the Baidu Index¹²² monitor search trends of disease-related keywords by indexing search volumes to generate time-series data that support the early warning of infectious diseases, thus contributing to epidemic monitoring and response.¹²³ In 2009, Ginsberg et al.¹²¹ developed a simple linear regression model using web search data to successfully predict the percentage of influenza-like illness cases and forecasted epidemic trends 1–2 weeks in advance. At the end of 2022, China experienced widespread community transmission of COVID-19. The notifiable surveillance systems struggled to report the total cases, whereas the Baidu Search Index, with its real-time nature and stability, assisted in epidemic curve estimation during emergencies.¹²⁴

4.4. Early warning systems that rely on pathogen surveillance

Key mutations in infectious disease pathogens can also trigger new pandemic waves, making pathogen monitoring and early warning crucial. Given the ongoing mutations of SARS-CoV-2, the WHO established the Technical Advisory Group on Virus Evolution in 2021 to support global information sharing on surveillance and research, monitor early warning signals, and assess the need for timely public health responses to emerging variants.¹²⁵ Similarly, the WHO's Global Influenza Surveillance and Response System, founded in 1952,¹²⁶ substantially contributes to global influenza pandemic control by providing a robust platform for monitoring influenza epidemiology and serving as an alert system for novel influenza viruses and other respiratory pathogens. In addition to the real-time monitoring of the distribution characteristics of pathogens, prospectively predicting the evolutionary direction of pathogens and identifying in advance mutation sites of public health are possible. By developing a model for predicting the evolutionary trends of the SARS-CoV-2 receptor binding domain under neutralizing antibody immune pressure, Cao and colleagues¹²⁷ accurately forecasted the mutation trends of various variants.

4.5. Outlook for future early warning systems

Modern infectious disease early warning systems are increasingly powered by a comprehensive data stream that spans the infection cycle—from pathogen tracking and vector monitoring to host, population, and environmental surveillance. This holistic approach enables the more precise and timely detection of emerging threats. Specifically, at the population level, data now include bio-signals that are passively measured by wearable devices (e.g., smartwatches that detect physiological anomalies), cough sounds that are captured by smart listening devices, internet search queries for viral testing sites, symptom reports that are submitted online, positive test results for viruses, social media posts about diagnoses, and even behaviors such as mask-wearing that are observed through closed circuit television.¹⁷ Each data point represents a critical aspect of infection progression and transmission.

Integrating these diverse data sources offers a unique opportunity to enhance early warning system sensitivity and responsiveness. The EpiPulse system launched by the European CDC integrates three independent monitoring systems—the European Surveillance System, the five Epidemic Intelligence Information System platforms, and the Threat Tracking Tool—to provide new functionalities and offer seamless access to data in a single platform for use by experts.¹²⁸ Similarly, China is building a national-level, provincially coordinated infectious disease monitoring, early warning, and emergency command information platform that integrates data from multiple monitoring channels to enhance early warning capabilities.^{129,130}

5. Conclusions and perspectives

The increasing incidence and impact of emerging infectious diseases highlight the critical need for a more robust global surveillance and early warning framework. As demonstrated by the global outbreaks of SARS, MERS, and COVID-19, the interconnected nature of human, animal, and environmental health requires a more comprehensive and multi-sectoral approach. This review examined the current landscape of global infectious disease surveillance and early warning systems and highlighted the transformative potential of the One Health approach, which integrates data and insights across human, animal, and environmental domains to offer a more holistic and effective response to emerging health threats.

Technological advancements offer significant opportunities for enhancing surveillance and early warning systems. For example, large language models, such as PandemicLLM developed by Yang et al.,¹³¹ offer promising capabilities by integrating diverse data sources in real-time to analyze epidemiological, genomic, and policy data. However, further optimization is needed to improve the computational efficiency and interpretability of these models. Furthermore, in 2023, China launched a community-based novel surveillance system that uses a mobile app for ordering testing kits; samples are collected and transported for polymerase chain reaction testing. Results are delivered within hours, reducing the burden on clinics and improving efficiency during outbreaks.¹³² Additionally, wearable devices such as smartwatches and smart listening tools can detect biosignals such as health metrics and cough patterns and offer promising opportunities for the early detection of abnormal signals.¹⁷

Despite these strengths, significant challenges remain. Resource limitations in underserved regions, which often lack the infrastructure and capacity for effective surveillance, are a major concern. Given their weak public health systems, these areas are potential sources of emerging pandemics. Because laboratory-based methods are often impractical in these settings, symptom-based monitoring and a focus on common clinical signs such as fever, cough, or diarrhea are cost-effective alternatives that enable early outbreak detection. For example, integrating syndromic surveillance systems such as Kenya's Animal Biosurveillance System¹³³ facilitates rapid data transmission and enhances monitoring across human and animal health sectors. Engaging community health workers, animal health workers, and wildlife rangers is also essential in ensuring broader geographic coverage and leveraging local knowledge to improve data accuracy.¹³⁴ Moreover, strengthening diagnostic capacity through field-based rapid tests, portable sequencing technologies, and regional laboratory networks is crucial for the timely identification of and response to emerging threats. In addition, comprehensive training in One Health practices for clinicians and frontline workers can further enhance interdisciplinary collaboration.

Ultimately, sustained funding and the engagement of stakeholders, including government and international organizations, are critical to ensuring the scalability and long-term durability of these surveillance efforts.^{135–137}

Importantly, the widespread use of digital technologies—especially those for contact tracing—during the COVID-19 pandemic raised significant issues regarding data privacy and the protection of sensitive health information. Establishing transparent and standardized data-sharing frameworks is crucial for overcoming privacy concerns and ensuring data access and reliability.^{2,17} The WHO's Global Digital Strategy (2020–2025), which sets high standards for data privacy, security, and governance, is an important step toward achieving this goal.³

Looking ahead, the integration and optimization of surveillance and early warning systems are expected to support health authorities in shifting from reactive to proactive responses. Prioritizing the development of these systems is expected to enhance the global community's ability to detect, assess, and mitigate infectious disease threats, ultimately improving global health security and preparedness for future pandemics.

CRediT authorship contribution statement

Ying Shen: Writing – original draft, Visualization, Validation, Project administration, Data curation. **Yonghong Liu:** Writing – original draft, Visualization, Validation, Software, Methodology, Data curation. **Thomas Krafft:** Validation, Supervision, Methodology, Conceptualization. **Quanyi Wang:** Resources, Project administration, Methodology, Funding acquisition, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

This work was supported by the Beijing Science and Technology Planning Project of Beijing Science and Technology Commission (Z241100009024047) and the High Level Public Health Technical Talent Training Plan (lingjunrencai-01-02).

References

1. Baker RE, Mahmud AS, Miller IF, et al. Infectious disease in an era of global change. *Nat Rev Microbiol.* 2022;20(4):193–205.
2. Moeti M, Gao GF, Herrman H. Global pandemic perspectives: public health, mental health, and lessons for the future. *Lancet.* 2022;400(10353):e3–e7.
3. World Health Organization. Future surveillance for epidemic and pandemic diseases: a 2023 perspective. <https://iris.who.int/bitstream/handle/10665/374992/9789240080959-eng.pdf>. Accessed Nov 6, 2024.
4. Clark EC, Neumann S, Hopkins S, et al. Changes to public health surveillance methods due to the COVID-19 pandemic: scoping review. *JMIR Public Heal Surveill.* 2024;10(1):e49185.
5. Williams BA, Jones CH, Welch V, et al. Outlook of pandemic preparedness in a post-COVID-19 world. *NPJ Vaccin.* 2023;8(1):178.
6. Zhou S, Feng X, Hu Y, et al. Factors associated with the utilization of diagnostic tools among countries with different income levels during the COVID-19 pandemic. *Glob Heal Res Polic.* 2023;8(1):45.
7. Han AX, Toporowski A, Sacks JA, et al. SARS-CoV-2 diagnostic testing rates determine the sensitivity of genomic surveillance programs. *Nat Genet.* 2023;55(1):26–33.
8. Yuan M, Boston-Fisher N, Luo Y, et al. A systematic review of aberration detection algorithms used in public health surveillance. *J Biomed Inf.* 2019;94:103181.
9. Coleman M, Coleman M, Mabuza AM, et al. Using the SaTScan method to detect local malaria clusters for guiding malaria control programmes. *Malar J.* 2009;8(1):68.

10. Tsang TK, Du Q, Cowling BJ, et al. An adaptive weight ensemble approach to forecast influenza activity in an irregular seasonality context. *Nat Commun.* 2024;15(1):8625.
11. MacIntyre CR, Lim S, Quigley A. Preventing the next pandemic: use of artificial intelligence for epidemic monitoring and alerts. *Cell Rep Med.* 2022;3(12):100867.
12. Pascucci M, Royer G, Adamek J, et al. AI-based mobile application to fight antibiotic resistance. *Nat Commun.* 2021;12(1):1173.
13. Bastani H, Drakopoulos K, Gupta V, et al. Efficient and targeted COVID-19 border testing via reinforcement learning. *Nature.* 2021;599(7883):108–113.
14. Dantas LF, Peres IT, Bastos LSL, et al. App-based symptom tracking to optimize SARS-CoV-2 testing strategy using machine learning. *PLoS One.* 2021;16(3):e0248920.
15. Alavi A, Bogu GK, Wang M, et al. Real-time alerting system for COVID-19 and other stress events using wearable data. *Nat Med.* 2022;28(1):175–184.
16. Cho A. AI systems aim to sniff out coronavirus outbreaks. *Science.* 2020;368(6493):810–811.
17. Brownstein JS, Rader B, Astley CM, et al. Advances in artificial intelligence for infectious-disease surveillance. *N Engl J Med.* 2023;388(17):1597–1607.
18. Declich S, Carter AO. Public health surveillance: historical origins, methods and evaluation. *Bull World Health Organ.* 1994;72(2):285.
19. M'ikanatha NM, Lynfield R, Beneden CAV, et al. *Infectious disease surveillance.* 2nd ed., UK: John Wiley & Sons; 2013.
20. Langmuir AD. The surveillance of communicable diseases of national importance. *N Engl J Med.* 1963;268(4):182–192.
21. Thacker SB, Berkelman RL. Public health surveillance in the United States. *Epidemiol Rev.* 1988;10(1):164–190.
22. Thacker SB, Qualters JR, Lee LM, et al. Public health surveillance in the United States: evolution and challenges. *MMWR Suppl.* 2012;61(3):3–9.
23. Maes EF, Diop OM, Jorba J, et al. Surveillance systems to track progress toward polio eradication—worldwide, 2015–2016. *Morb Mortal Wkly Rep.* 2017;66(13):359–365.
24. Zhang M, Wang L, Wu J, et al. Data resource profile: China chronic disease and risk factor surveillance (CCDRFS). *Int J Epidemiol.* 2021;51(2):e1–e8.
25. GBD 2021 Causes of Death Collaborators. Global burden of 288 causes of death and life expectancy decomposition in 204 countries and territories and 811 subnational locations, 1990–2021: a systematic analysis for the Global Burden of Disease Study 2021. *Lancet.* 2024;403(10440):2100–2132.
26. Samarasekera U. 50 years of the Expanded Programme on Immunization. *Lancet.* 2024;403(10440):1971–1972.
27. GBD 2021 Risk Factors Collaborators. Global burden and strength of evidence for 88 risk factors in 204 countries and 811 subnational locations, 1990–2021: a systematic analysis for the Global Burden of Disease Study 2021. *Lancet.* 2024;403(10440):2162–2203.
28. Nsubuga P, White ME, Thacker SB, et al. Public health surveillance: a tool for targeting and monitoring interventions. In: Jamison DT, Breman JG, Measham AR, eds. *Disease control priorities in developing countries. 2nd ed. Washington (DC): The International Bank for Reconstruction and Development/The World Bank.* New York: Oxford University Press; 2006:997–1016.
29. Crawley AW, Mercy K, Shivji S, et al. An indicator framework for the monitoring and evaluation of event-based surveillance systems. *Lancet Glob Heal.* 2024;12(4):e707–e711.
30. World Health Organization. A guide to establishing event-based surveillance. https://iris.who.int/bitstream/handle/10665/207737/9789290613213_eng.pdf?sequence=1. Accessed Nov 6, 2024.
31. Murray J, Cohen AL. Infectious disease surveillance. In: Quah S, Cockerham W, eds. *International encyclopedia of public health.* 2nd ed., Amsterdam: Academic Press; 2017:222–229.
32. Colón-González FJ, Lake IR, Morbey RA, et al. A methodological framework for the evaluation of syndromic surveillance systems: a case study of England. *BMC Public Heal.* 2018;18(1):544.
33. Lo SW, Jamroz D. Genomics and epidemiological surveillance. *Nat Rev Microbiol.* 2020;18(9) 478–478.
34. Li J, Lai S, Gao GF, et al. The emergence, genomic diversity and global spread of SARS-CoV-2. *Nature.* 2021;600(7889):408–418.
35. Robishaw JD, Alter SM, Solano JJ, et al. Genomic surveillance to combat COVID-19: challenges and opportunities. *Lancet Microbe.* 2021;2(9):e481–e484.
36. Wu F, Zhao S, Yu B, et al. A new coronavirus associated with human respiratory disease in China. *Nature.* 2020;579(7798):265–269.
37. Kaku Y, Okumura K, Padilla-Blanco M, et al. Virological characteristics of the SARS-CoV-2 JN.1 variant. *Lancet Infect Dis.* 2024;24(2):e82.
38. Yang S, Yu Y, Xu Y, et al. Fast evolution of SARS-CoV-2 BA.2.86 to JN.1 under heavy immune pressure. *Lancet Infect Dis.* 2024;24(2):e70–e72.
39. Kaku Y, Yo MS, Tolentino JE, et al. Virological characteristics of the SARS-CoV-2 KP.3, LB.1, and KP.2.3 variants. *Lancet Infect Dis.* 2024;24(8):e482–e483.
40. Kaku Y, Uriu K, Okumura K, et al. Virological characteristics of the SARS-CoV-2 KP.3.1.1 variant. *Lancet Infect Dis.* 2024;24(10):e609.
41. Kaku Y, Uriu K, Kosugi Y, et al. Virological characteristics of the SARS-CoV-2 KP.2 variant. *Lancet Infect Dis.* 2024;24(7):e416.
42. Munnink BBO, Worp N, Nieuwenhuijse DF, et al. The next phase of SARS-CoV-2 surveillance: real-time molecular epidemiology. *Nat Med.* 2021;27(9):1518–1524.

43. World Health Organization. Global genomic surveillance strategy for pathogens with pandemic and epidemic potential, 2022–2032. <https://www.who.int/publications/i/item/9789240046979>. Accessed September 12, 2024.
44. World Health Organization. International pathogen surveillance network (IPSN). <https://www.who.int/initiatives/international-pathogen-surveillance-network>. Accessed September 12, 2024.
45. GISAID. Global initiative on sharing all influenza data. <https://gisaid.org/>. Accessed September 12, 2024.
46. Souza WM de, Weaver SC. Effects of climate change and human activities on vector-borne diseases. *Nat Rev Microbiol*. 2024;22(8):476–491.
47. Barillas-Mury C, Ribeiro JMC, Valenzuela JG. Understanding pathogen survival and transmission by arthropod vectors to prevent human disease. *Science*. 2022;377(6614):eabc2757.
48. Braks M, Schaffner F, Medlock JM, et al. VectorNet: putting vectors on the map. *Front Public Heal*. 2022;10:809763.
49. Rocklöv J, Dubrow R. Climate change: an enduring challenge for vector-borne disease prevention and control. *Nat Immunol*. 2020;21(5):479–483.
50. Thomson MC, Stanberry LR. Climate change and vectorborne diseases. *N Engl J Med*. 2022;387(21):1969–1978.
51. World Health Organization. Global arbovirus initiative: preparing for the next pandemic tackling mosquito-borne viruses with epidemic and pandemic potential. <https://www.who.int/initiatives/global-arbovirus-initiative>. Accessed November 5, 2024.
52. Yang Q, Wang B, Lemey P, et al. Synchrony of bird migration with global dispersal of avian influenza reveals exposed bird orders. *Nat Commun*. 2024;15(1):1126.
53. Global Consortium for H5N8 and Related Influenza Viruses. Role for migratory wild birds in the global spread of avian influenza H5N8. *Science*. 2016;354(6309):213–217.
54. Xie R, Edwards KM, Wille M, et al. The episodic resurgence of highly pathogenic avian influenza H5 virus. *Nature*. 2023;622(7984):810–817.
55. Blagodatski A, Trutneva K, Glazova O, et al. Avian influenza in wild birds and poultry: dissemination pathways, monitoring methods, and virus ecology. *Pathogens*. 2021;10(5):630.
56. Sullivan JD, Takekawa JY, Spragens KA, et al. Waterfowl spring migratory behavior and avian influenza transmission risk in the changing landscape of the East Asian-Australasian flyway. *Front Ecol Evol*. 2018;6:206.
57. Duan C, Li C, Ren R, et al. An overview of avian influenza surveillance strategies and modes. *Sci One Heal*. 2023;2:100043.
58. Plowright RK, Ahmed AN, Coulson T, et al. Ecological countermeasures to prevent pathogen spillover and subsequent pandemics. *Nat Commun*. 2024;15(1):2577.
59. Ellwanger JH, Chies JAB. Zoonotic spillover: understanding basic aspects for better prevention. *Genet Mol Biol*. 2021;44(1 Suppl 1):e20200355.
60. Plowright RK, Parrish CR, McCallum H, et al. Pathways to zoonotic spillover. *Nat Rev Microbiol*. 2017;15(8):502–510.
61. Banyard AC, Bennison A, Byrne AMP, et al. Detection and spread of high pathogenicity avian influenza virus H5N1 in the Antarctic Region. *Nat Commun*. 2024;15(1):7433.
62. Peacock T, Moncla L, Dudas G, et al. The global H5N1 influenza panzootic in mammals. *Nature*. 2024;1–2.
63. Caserta LC, Frye EA, Butt SL, et al. Spillover of highly pathogenic avian influenza H5N1 virus to dairy cattle. *Nature*. 2024;634(8034):669–676.
64. Lagan P, McKenna R, Baleed S, et al. Highly pathogenic avian influenza A(H5N1) virus infection in foxes with PB2-M535I identified as a novel mammalian adaptation, Northern Ireland, July 2023. *Eurosurveillance*. 2023;28(42):2300526.
65. Gu C, Maemura T, Guan L, et al. A human isolate of bovine H5N1 is transmissible and lethal in animal models. *Nature*. 2024;636(8043):711–718.
66. Long JS, Mistry B, Haslam SM, et al. Host and viral determinants of influenza A virus species specificity. *Nat Rev Microbiol*. 2019;17(2):67–81.
67. Gu XL, Su WQ, Zhou CM, et al. SFTSV infection in rodents and their ectoparasitic chiggers. *PLoS Negl Trop Dis*. 2022;16(8):e0010698.
68. Stephen C. Evolving urban wildlife health surveillance to intelligence for pest mitigation and monitoring. *Front Ecol Evol*. 2018;6:127.
69. Woodward M. *Epidemiology, study design and data analysis*. 3rd Ed. London: CRC Press; 2013.
70. Shen Y, Li S, Huo D, et al. Economic burden of hand, foot, and mouth disease—Beijing municipality, China, 2016–2019. *China CDC Wkly*. 2023;5(43):953–957.
71. Zhang L, Zhang Y, Duan W, et al. Using an influenza surveillance system to estimate the number of SARS-CoV-2 infections in Beijing, China, weeks 2 to 6 2023. *Eurosurveillance*. 2023;28(11):2300128.
72. Grange ZL, Goldstein T, Johnson CK, et al. Ranking the risk of animal-to-human spillover for newly discovered viruses. *Proc Natl Acad Sci USA*. 2021;118(15):e2002324118.
73. Chen Y, Xu Y, Wang L, et al. Indian Ocean temperature anomalies predict long-term global dengue trends. *Science*. 2024;384(6696):639–646.
74. Diamond MB, Keshaviah A, Bento AI, et al. Wastewater surveillance of pathogens can inform public health responses. *Nat Med*. 2022;28(10):1992–1995.
75. Grassly NC, Shaw AG, Owusu M. Global wastewater surveillance for pathogens with pandemic potential: opportunities and challenges. *Lancet Microbe*. 2024;6(1):100939.
76. Singer AC, Thompson JR, Filho CRM, et al. A world of wastewater-based epidemiology. *Nat Water*. 2023;1(5):408–415.

77. Morvan M, Jacomo AL, Souque C, et al. An analysis of 45 large-scale wastewater sites in England to estimate SARS-CoV-2 community prevalence. *Nat Commun.* 2022;13(1):4313.
78. Shaw AG, Troman C, Akello JO, et al. Defining a research agenda for environmental wastewater surveillance of pathogens. *Nat Med.* 2023;29(9):2155–2157.
79. Morse SS, Mazet JA, Woolhouse M, et al. Prediction and prevention of the next pandemic zoonosis. *Lancet.* 2012;380(9857):1956–1965.
80. Tian H, Liu Y, Li Y, et al. An investigation of transmission control measures during the first 50 days of the COVID-19 epidemic in China. *Science.* 2020;368(6491):638–642.
81. Yu VL, Madoff LC. ProMED-mail: an early warning system for emerging diseases. *Clin Infect Dis.* 2004;39(2):227–232.
82. MacIntyre CR, Lim S, Quigley A. Preventing the next pandemic: use of artificial intelligence for epidemic monitoring and alerts. *Cell Rep Med.* 2022;3(12):100867.
83. Hu Q, Mou YL, Yin RY, Tang L, Zhang F. Using the Baidu index to understand Chinese interest in thyroid related diseases. *Sci Rep.* 2022;12(1):17160.
84. Huo D, Zhang T, Han X, et al. Mapping the characteristics of respiratory infectious disease epidemics in China based on the Baidu Index from November 2022 to January 2023. *China CDC Wkly.* 2024;6(37):939–945.
85. Wang D, Lang JC, Chen YH. Assessment of using Google Trends for real-time monitoring of infectious disease outbreaks: a measles case study. *Sci Rep.* 2024;14(1):9470.
86. Yang WZ. *Early warning of infectious disease theory and practice.* Beijing: People's Medical Publishing House; 2012.
87. Buckeridge DL, Okhmatovskaia A, Tu S, et al. Understanding detection performance in public health surveillance: modeling aberrancy-detection algorithms. *J Am Méd Inf Assoc.* 2008;15(6):760–769.
88. Fasina FO, Salami MA, Fasina MM, et al. Test positivity–Evaluation of a new metric to assess epidemic dispersal mediated by non-symptomatic cases. *Methods.* 2021;195:15–22.
89. World Health Organization. *Early warning alert and response in emergencies: an operational guide.* Geneva: World Health Organization; 2023.
90. Kuang J, Yang WZ, Zhou DL, et al. Epidemic features affecting the performance of outbreak detection algorithms. *BMC Public Heal.* 2012;12(1):418.
91. Li Z, Lai S, Buckeridge DL, et al. Adjusting outbreak detection algorithms for surveillance during epidemic and non-epidemic periods. *J Am Méd Inf Assoc.* 2012;19(e1):e51–e53.
92. Wang X, Zeng D, Seale H, et al. Comparing early outbreak detection algorithms based on their optimized parameter values. *J Biomed Inf.* 2010;43(1):97–103.
93. Yang L, Yang J, He Y, et al. Enhancing infectious diseases early warning: a deep learning approach for influenza surveillance in China. *Prev Med Rep.* 2024;43:102761.
94. Lowe R, Lee SA, O'Reilly KM, et al. Combined effects of hydrometeorological hazards and urbanisation on dengue risk in Brazil: a spatiotemporal modelling study. *Lancet Planet Heal.* 2021;5(4):e209–e219.
95. Shewhart WA. *Economic control of quality of manufactured product.* New York: Van Nostrand; 1931.
96. Page ES. Continuous Inspection Schemes. *Biometrika.* 1954;41(1-2):100–115.
97. Serfung RE, Sherman IL, Houseworth WJ. Excess pneumonia-influenza mortality by age and sex in three major influenza A2 epidemics, United States, 1957–58, 1960 and 1963. *Am J Epidemiol.* 1967;86(2):433–441.
98. Alonso TV, Alonso JEL, Lejarazu RO de, et al. Modelling influenza epidemic—Can we detect the beginning and predict the intensity and duration? *Int Congr Ser.* 2004;1263:281–283.
99. Chen S, Wang X, Zhao J, et al. Application of the ARIMA model in forecasting the incidence of tuberculosis in Anhui during COVID-19 pandemic from 2021 to 2022. *Infect Drug Resist.* 2022;15:3503–3512.
100. Shaman J, Karspeck A. Forecasting seasonal outbreaks of influenza. *Proc Natl Acad Sci USA.* 2012;109(50):20425–20430.
101. Anselin L. Local indicators of spatial association—LISA. *Geogr Anal.* 1995;27(2):93–115.
102. Getis A, Ord JK. The analysis of spatial association by use of distance statistics. *Geogr Anal.* 1992;24(3):189–206.
103. Kulldorff M. A spatial scan statistic. *Commun Stat - Theory Methods.* 1997;26(6):1481–1496.
104. Ma Y, Yin F, Zhang T, et al. Selection of the maximum spatial cluster size of the spatial scan statistic by using the maximum clustering set-proportion statistic. *PLoS One.* 2016;11(1):e0147918.
105. Wang W, Zhang T, Yin F, et al. Using the maximum clustering heterogeneous set-proportion to select the maximum window size for the spatial scan statistic. *Sci Rep.* 2020;10(1):4900.
106. Guzman-Herrador B, Vold L, Berg T, et al. The national web-based outbreak rapid alert system in Norway: eight years of experience, 2006–2013. *Epidemiol Infect.* 2016;144(1):215–224.
107. Yang W, Li Z, Lan Y, et al. A nationwide web-based automated system for early outbreak detection and rapid response in China. *West Pac Surveill Response.* 2011;2(1):10–15.
108. Zhang H, Li Z, Lai S, et al. Evaluation of the performance of a dengue outbreak detection tool for China. *PLoS One.* 2014;9(8):e106144.
109. Cakici B, Hebing K, Grünwald M, et al. CASE: a framework for computer supported outbreak detection. *BMC Méd Inf Decis Mak.* 2010;10(1):14.
110. Ed Brabazon, O'Farrell A, Ca Murray, et al. Under-reporting of notifiable infectious disease hospitalizations in a health board region in Ireland: room for improvement? *Epidemiol Infect.* 2007;136(2):241–247.
111. Güemes A, Ray S, Aboumerhi K, et al. A syndromic surveillance tool to detect anomalous clusters of COVID-19 symptoms in the United States. *Sci Rep.* 2021;11(1):4660.

112. Hutwagner L, Thompson W, Seeman GM, et al. The bioterrorism preparedness and response Early Aberration Reporting System (EARS). *J Urban Heal*. 2003;80(1):i89–i96.
113. US Center for Disease Prevention and Control. Assessment of ESSENCE performance for influenza-like illness surveillance after an influenza outbreak – U.S. Air Force Academy, Colorado, 2009. *MMWR Morb Mortal Wkly Rep*. 2011;60(13):406–409.
114. Pang X, Wang X, Wang Q, et al. Infectious disease surveillance and early warning system during Beijing Olympic Games. In: Yang W, ed. *Early warning for infectious disease outbreak: theory and practice*. Amsterdam: Academic Press; 2017:163–180.
115. Elliot AJ, Hughes HE, Hughes TC, et al. Establishing an emergency department syndromic surveillance system to support the London 2012 Olympic and Paralympic Games. *Emerg Med J*. 2012;29(12):954.
116. Brownstein JS, Rader B, Astley CM, et al. Advances in artificial intelligence for infectious-disease surveillance. *N Engl J Med*. 2023;388(17):1597–1607.
117. World Health Organization. Early detection, assessment and response to acute public health events: Implementation of early warning and response with a focus on event-based surveillance. <https://www.who.int/publications/i/item/WHO-HSE-GCR-LYO-2014.4>. Accessed September 26, 2024.
118. Yu VL, Madoff LC. ProMED-mail: an early warning system for emerging diseases. *Clin Infect Dis*. 2004;39(2):227–232.
119. Carrion M, Madoff LC. ProMED-mail: 22 years of digital surveillance of emerging infectious diseases. *Int Heal*. 2017;9(3):177–183.
120. Nelson R. HealthMap: The future of infectious diseases surveillance? *Lancet Infect Dis*. 2008;8(10):596.
121. Ginsberg J, Mohebbi MH, Patel RS, et al. Detecting influenza epidemics using search engine query data. *Nature*. 2009;457(7232):1012–1014.
122. Dai S, Han L. Influenza surveillance with Baidu index and attention-based long short-term memory model. *PLoS One*. 2023;18(1):e0280834.
123. Goel S, Hofman JM, Lahaie S, et al. Predicting consumer behavior with Web search. *Proc Natl Acad Sci USA*. 2010;107(41):17486–17490.
124. Zhang T, Yang L, Han X, et al. Methods on COVID-19 epidemic curve estimation during emergency based on Baidu search engine and ILI traditional surveillance in Beijing, China. *Engineering*. 2023;31:112–119.
125. Subissi L, Gottberg A von, Thukral L, et al. An early warning system for emerging SARS-CoV-2 variants. *Nat Med*. 2022;28(6):1110–1115.
126. Ziegler T, Moen A, Zhang W, et al. Global influenza surveillance and response system: 70 years of responding to the expected and preparing for the unexpected. *Lancet*. 2022;400(10357):981–982.
127. Cao Y, Jian F, Wang J, et al. Imprinted SARS-CoV-2 humoral immunity induces convergent Omicron RBD evolution. *Nature*. 2023;614(7948):521–529.
128. European Centre for Disease Prevention and Control. EpiPulse – The European surveillance portal for infectious diseases. <https://www.ecdc.europa.eu/en/publications-data/epipulse-european-surveillance-portal-infectious-diseases>. Accessed December 23, 2024.
129. National Disease Control and Prevention Administration. Guidelines for the establishment and improvement of an intelligent multi-point trigger infectious disease surveillance and early warning system. https://www.gov.cn/zhengce/zhengceku/202408/content_6971481.htm. Accessed December 23, 2024.
130. Yang W, Lan Y, Lyu W, et al. Establishment of multi-point trigger and multi-channel surveillance mechanism for intelligent early warning of infectious diseases in China. *Chin J Epidemiol*. 2020;41(11):1753–1757.
131. Yang HF, Du H, Zhao J, et al. Advancing real-time pandemic forecasting using large language models: a COVID-19 case study. arXiv: 2404.06962. 2024.
132. Sun Y, Dai L, Shan Y, et al. Pathogen characteristics of respiratory infections in the season after the COVID-19 pandemic between August and December 2023: evidence from direct-to-consumer testing-based surveillance in Guangzhou and Beijing, China. *Int J Infect Dis*. 2024;147:107195.
133. Njenga MK, Kemunto N, Kahariri S, et al. High real-time reporting of domestic and wild animal diseases following rollout of mobile phone reporting system in Kenya. *PLoS One*. 2021;16(9):e0244119.
134. Hassell JM, Zimmerman D, Fèvre EM, et al. Africa's nomadic pastoralists and their animals are an invisible frontier in pandemic surveillance. *Am J Trop Med Hyg*. 2020;103(5):1777–1779.
135. Haldane V, Jung AS, Foo CD, et al. Strengthening the basics: public health responses to prevent the next pandemic. *BMJ*. 2021;375:e067510.
136. Williams BA, Jones CH, Welch V, et al. Pandemic preparedness requires collaboration between governments, funders and pharma. *Nat Med*. 2023;29(12):2999–3001.
137. Worsley-Tonks KEL, Bender JB, Deem SL, et al. Strengthening global health security by improving disease surveillance in remote rural areas of low-income and middle-income countries. *Lancet Glob Heal*. 2022;10(4):e579–e584.