

OPPORTUNITIES FOR AI IN DISEASE SURVEILLANCE

UNIVERSITY OF WASHINGTON STRATEGIC ANALYSIS,
RESEARCH & TRAINING (START) CENTER

REPORT TO THE GATES FOUNDATION

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Infectious disease surveillance in LMICs faces persistent gaps in data timeliness, quality, and coverage. Artificial Intelligence (AI) tools including machine learning (ML) and generative AI (Gen AI) offer new opportunities to strengthen early detection, analysis, and decision-making across the entire surveillance lifecycle.



This project responds directly to the Gates Foundation priorities in Sero surveillance, environmental/wastewater monitoring, mortality surveillance, pathogen genomics, and modelling, exploring where AI can most effectively accelerate progress in these domains.



This work emphasizes identifying AI applications that are disease-agnostic, scalable, and implementable in LMIC settings, while avoiding one-off, single-disease tools with limited transferability, ensuring alignment with global health equity and sustainability goals.

PROJECT OBJECTIVE

To identify, assess, and prioritize applications of AI across the infectious disease surveillance lifecycle, with a focus on case studies that are scalable, disease-agnostic, and adaptable to the LMIC, to enhance data availability, quality, timeliness, and decision-making for global health programs.

METHODS

The search strategy to identify applications of AI in infectious disease surveillance involved the following steps:

- I. Reviewing the provided documents and guidance to define the scope of interest, including the disease surveillance lifecycle stages and high-impact levers.
- II. Developing a conceptual framework and working definitions for what constitutes AI in this space, distinguishing between ML, Gen AI, and other advanced analytics, to guide case study identification and analysis.
- III. Conducted an iterative "berrypicking" search approach rather than a systematic review, allowing for refinement of queries as new leads emerged. Searches were carried out in both peer-reviewed sources (PubMed, Scopus, Google Scholar, Web of Science, Semantic Scholar, and arXiv) and grey literature sources (government reports, NGO publications, technical blogs, newsletters, social media, and surveillance consortium sites).
- IV. Exploring the commercial space for AI surveillance tools, including start-ups, health tech firms, and venture-funded companies, to identify scalable innovations not yet reflected in academic literature.
- V. Using conversational AI tools (e.g., ChatGPT, Perplexity, Claude AI) to accelerate landscape discovery, cross-checking references, and identify emerging commercial case studies documented in trade sources, investor reports, and preprints.
- VI. Cross-referencing identified AI tools with Gates Foundation priorities and LMIC applicability, to evaluate relevance, scalability, and alignment with investment criteria. Each case study was categorized according to high-impact lever, disease surveillance lifecycle stage, disease or conditions, geography, AI model type, software used, data sources, partnerships, funding, and applicability to LMIC
- VII. Engaging in iterative check-ins with Gates Foundation stakeholders and subject matter experts to refine case study selection, validate relevance, and ensure alignment with programmatic priorities throughout the project

Disease Surveillance Lifecycle Stages: Program Design, Data Collection, Data Intergration, Data Analysis, Information Dissemination and Visualization, Response and Action, Policy Development, and Community Engagement.

The following conceptual framework informed this work. Definitions for all relevant project terms are detailed in Appendix 1. While there were five areas of focus for this project, the main area of interest was on the disease surveillance lifecycle component of this framework as detailed and emphasized in Figure 1.

I. CONTEXT

- Introduction to AI tool
- High-Impact lever
- Geography
- Disease or Conditions

II. Disease Surveillance Lifecycle Stages

These eight stages reflect the functional flow of disease surveillance systems where AI can be applied to enhance timeliness, accuracy, or efficiency

Program Design

Data Collection

Data Integration

Data Analysis

Information Dissemination and
Visualization

Response and Action

Policy Development

Community Engagement

III. AI FUNCTIONS

- AI Model Type
- Software
- Data Sources
- Nature of data

IV. FUNDING

- Funder
- Funding Amount
- Partnerships
- Technical partners

V. TAKEAWAYS

- Applicability to LMICs
- Value Proposition/Impact Value

Figure 1: The conceptual framework for the START project assessing the opportunities of AI in infectious disease surveillance lifecycle.

WHAT IS IT?

INTRODUCTION

A commercial AI-powered wastewater surveillance platform designed to provide real-time insights into infectious disease dynamics at the community level. By analyzing sewage samples, Biobot quantifies viral RNA and other biomarkers to generate early warnings of disease spread, even among asymptomatic populations. Its system integrates multiple data streams including wastewater viral loads, clinical laboratory reports, demographic metadata, and public health records into a unified analytics framework. It is disease agnostic able to detect COVID-19, Influenza, Respiratory Syncytial Virus (RSV), Mpox, Poliovirus and opioid and substance use biomarkers. It operates across multiple stages of the disease surveillance lifecycle, including program design, data collection, data integration, data analysis, early warning/decision support and policy development. It aligns with high-impact levers such as wastewater surveillance and modelling.

PARTNERSHIPS & FUNDING

This AI tool was developed by researchers from Massachusetts Institute of Technology (MIT) and later spun out into a private company. The company collaborates with public health departments, universities, and local governments across the United States to implement wastewater-based infectious disease surveillance. Key partners include CDC, which contracted Biobot in 2020 to expand national wastewater monitoring during COVID-19 pandemic. They have received funding from Engine Ventures, Y Combinators, Refactor Capital, and other equity partners among, to a tune of \$ 41 million.

HOW IT WORKS?

AI MODEL AND SOFTWARE

Biobot analytics applies advanced machine learning models to wastewater data, including regression models to quantify viral load against population baselines, anomaly detection algorithms to identify unusual spikes, and predictive models for forecasting infection trends. Signal processing pipelines trained on viral RNA sequencing data enhance accuracy across pathogens. Instead of a single off-the-shelf tool, this AI tool operates on python-based cloud infrastructure that integrates laboratory assays, machine learning workflows, and real-time dashboards for public health agencies.

DATA SOURCES

It integrates diverse data streams centered on wastewater samples collected from municipal sewage systems, treatment plans, and community-level collection points. These samples provide aggregated viral RNA signals that capture both symptomatic and asymptomatic infections across populations. The laboratory data are complemented by clinical and hospital case reports, demographic metadata, and national surveillance feeds such as the CDC National Wastewater Surveillance System (NWSS). Together, these multi-modal datasets enable robust monitoring of infection trends and early detection of outbreaks.

KEY FACILITATORS

- Strong predictive performance using ML models for viral trend forecasting and anomaly detection
- Aggregated, population-level wastewater capture asymptomatic and unreported infections.
- Modular cloud-based system adaptable to diverse health contexts
- Scalable partnerships with CDC and health agencies

KEY BARRIERS

- Data fragmentation and lack of standardized wastewater sampling protocols across jurisdictions
- Limited sensitivity for very low prevalence diseases or rare pathogens
- Dependence on robust sewer networks, which may be incomplete in many LMIC contexts

WHY IT MATTERS?

APPLICABILITY TO LMICS:

Biobot Analytics is highly adaptable for LMIC settings because wastewater data provide a non-invasive, population-level signal that does not rely on individual testing capacity. Its modular platform can integrate with decentralized sampling networks, including low-cost collection kits and portable lab equipment, making it feasible in regions with limited infrastructure. By leveraging aggregated, anonymized data, which offers an efficient and scalable way to strengthen early outbreak detection and public health preparedness where traditional surveillance systems remain weak.

ETHICAL CONSIDERATIONS:

There are considerations around data privacy and transparency, particularly in the handling of wastewater data that may be linked to small communities. Risks include bias if models are trained on limited datasets and equity concerns if deployment favors urban over rural areas.

VALUE PROPOSITION:

Biobot delivers strong early warning capabilities by detecting viral RNA in wastewater before clinical cases peak, offering a population-level view of multiple pathogens spread including asymptomatic infections, supporting the goal of proactive surveillance.

WHAT IS IT?

INTRODUCTION

An AI-powered system designed for real-time infectious disease monitoring, supporting early outbreak detection and predictive forecasting. It integrates multiple data streams including IoT-enabled surveillance, smart pharmacy sales data, wearable medical devices, wastewater data, public health reports, and social media signals into a unified system. The system applies advanced machine learning models (LSTM for trend forecasting, logistic regression for outbreak probability, isolation forests for anomaly detection, and NLP for text analysis) to generate early warnings and decision support for public health action. It is applied in Program Design, Data Collection, Data Integration, Data Analysis, and Early Warning/Decision Support stages of surveillance, as well as Environmental/Wastewater Surveillance, Syndromic Surveillance high impact levers.

PARTNERSHIPS & FUNDING

This system was proposed/developed by researchers at Computer Engineering Department, Faculty of Computers and Information Technology, University of Tabuk, Saudi Arabia, in collaboration with Artificial Intelligence and Sensing Technologies (AIST) Research Center, University of Tabuk, Saudi Arabia. The funder was Research, Development, and Innovation Authority (RDIA), Saudi Arabia, but the funding amounts are undisclosed.

HOW IT WORKS?

AI MODEL AND SOFTWARE

The SmartHealth-Track framework integrates multiple AI and machine learning models, each playing a role in surveillance. It uses Long Short-Term Memory (LSTM) networks to forecast time-series disease trends, logistic regression to estimate outbreak probabilities, and isolation forests to detect anomalies or unusual spikes. ARIMA models are applied to forecast demand fluctuations and case numbers, while natural language processing (NLP) extracts insights from health reports and social media. Instead of relying on a single off-the-shelf software, SmartHealth-Track operates on a custom-built cloud infrastructure that enables real-time data ingestion, execution of these models, and automated generation of outbreak alerts.

DATA SOURCES

It integrates diverse, real-time data streams from international and national surveillance platforms (e.g., WHO, CDC, GHO, and NWSS), hospital and clinical records, pharmacy sales, and wearable health devices tracking vital signs. It also incorporates social media and public health reports for early insights. These multi-modal datasets—structured, continuous, and longitudinal—enable robust monitoring of disease patterns and forecasting of emerging outbreaks.

KEY FACILITATORS

- Strong predictive performance using LSTM and anomaly detection models.
- Multi-source, real-time data integration enabling timely outbreak alerts.
- Modular, scalable design adaptable to diverse health system contexts.

KEY BARRIERS

- Data fragmentation, interoperability gaps, and underreporting.
- High false positive rates that reduce trust in anomaly detection.
- Infrastructure and digital health limitations in low-resource settings .

WHY IT MATTERS?

APPLICABILITY TO LMICS:

SmartHealth-Track is designed to be scalable and adaptable for low-resource and rural settings. Its modular architecture allows flexible integration of whatever data streams are available, while its ability to operate with decentralized systems makes it suitable for regions with limited infrastructure. By leveraging these features, the framework offers an important opportunity to strengthen outbreak preparedness and response in areas where traditional surveillance remains weak.

ETHICAL CONSIDERATIONS:

SmartHealth-Track raises concerns about data privacy given the sensitivity of wearable, pharmacy, hospital, and wastewater data. It faces risks of bias if trained on incomplete datasets, and presents transparency challenges with complex models like LSTM. Ensuring equitable deployment is essential to build trust and promote fair access, particularly in LMICs.

VALUE PROPOSITION:

SmartHealth-Track delivers stronger early warning with over 90% accuracy in outbreak detection, fever monitoring, contact tracing, and wastewater analysis. By unifying data from IoT devices, pharmacy sales, wearables, wastewater, and social media, it provides a comprehensive view of disease spread. The system is scalable for low-resource settings and future-ready, with potential to integrate advanced methods such as federated and reinforcement learning.

WHAT IS IT?

INTRODUCTION



It is an AI system that conducts vector monitoring at large-scale and low-cost to predict outbreaks across changing climates. It seeks to provide early warning and targeted interventions in regions where vector-borne diseases, primarily mosquito-borne diseases, pose major public health threats. The project was implemented in Ghana, but plans are underway for expansion to Southeast Asia, South America and the Caribbean. It is applied in the following surveillance stages: data analysis and information dissemination. The high-impact lever is focused in environmental surveillance.



PARTNERSHIPS & FUNDING

It was developed by researchers at Kwame Nkrumah University of Science and Technology (KNUST) in Ghana, in collaboration with Mahidol University, Thailand. This was a project supported by AI for Pandemic & Epidemic Preparedness (AI4PEP). Funding was provided via AI4PEP by the United Kingdom's FCDO and Canada's IDRC. At least \$261.8K (CAD\$362,500) is allocated per AI4PEP team.

HOW IT WORKS?



AI MODEL AND SOFTWARE

The team developed a novel 2D Convolutional Neural Network (CNN), a discriminative AI model that turns mosquito wingbeat audio into images for classifying vector species classification and assessing vector risk. No specific software is mentioned but there is an emphasis on edge computing. This implies deployment on low-cost hardware that supports operations in locations with limited connectivity.



DATA SOURCES

To train the CNN model, the research team developed a dataset with over 25,000 audio recordings capturing mosquito wingbeat frequencies across the three key genera (Aedes, Culex, Anopheles). Bioacoustic IoT sensors were developed and deployed in communities for vector surveillance.

KEY FACILITATORS

- The model classified species with a 92% success rate.
- Bio-acoustic IoT sensors with edge computing allow for low-resource, decentralized monitoring.
- The model combines audio recordings with metagenomic sequencing, and environmental data for multifaceted approach.

KEY BARRIERS

- The current dataset may need to be expanded for other geographies and species.
- There's no information on integration with national policies to address national vector control practices.
- The bioacoustic sensors need to be physically deployed across regions to detect vectors of interest.

WHY IT MATTERS?

APPLICABILITY TO LMICS:

The project was designed with LMIC needs in mind by researchers in the Global South. It relies on low-power tools that are scalable across different regions. There is an opportunity for further expansion with additional donor support.

ETHICAL CONSIDERATIONS:

AI4PEP's work is rooted in decolonizing research and ensuring ethical AI use. This project relies on a large group of stakeholders to maintain inclusive support. Maintaining community involvement will be vital to ensure acceptance of audio recorder deployment.

VALUE PROPOSITION:

This tool can strengthen outbreak preparedness, develop targeted interventions, and reduce the burden of vector-borne diseases. By combining audio monitoring with metagenomic sequencing and community engagement, it provides a scalable, locally relevant system for strengthening vector control in Ghana and other LMICs.

WHAT IS IT?

INTRODUCTION

GenSLMs are large-scale language models trained on genomic sequences to capture evolutionary dynamics of pathogens, with an initial focus on SARS-CoV-2. They are trained on millions of viral genome sequences and use advanced language model architectures to detect patterns of mutation and predict variants of concern. The tool was developed to support genomic surveillance and early warning of emerging COVID-19 variants, with applications demonstrated using global datasets. This is applied in several surveillance stages including data analysis ; High-impact levers: pathogen genomics, modelling.

PARTNERSHIPS & FUNDING

Developed by Argonne National Laboratory, University of Chicago, NVIDIA, Cerebras Inc., and academic collaborators. Supported by U.S. Department of Energy (DOE) computing resources (Polaris @ ALCF, Cerebras Wafer-Scale Cluster). Direct funding amounts are undisclosed.

HOW IT WORKS?

AI MODEL AND SOFTWARE

Adapts transformer-based large language models (LLMs) to genomic data ("codon tokenization"). The tool is trained on >110 million prokaryotic gene sequences for foundation modeling, then fine-tuned on >1.5 million SARS-CoV-2 genomes. It incorporates hierarchical transformer + diffusion models to capture both local (codon-level) and long-range genome interactions and capable of predicting unseen variants of concern (VOCs) and simulating evolutionary trajectories. The GenSLMs tool runs on PyTorch Lightning with Hugging Face transformers, optimized by DeepSpeed.

DATA SOURCES

Data sources BV-BRC (Bacterial and Viral Bioinformatics Resource Center), NCBI GenBank, and Houston Methodist SARS-CoV-2 genomes (70,000+ patient samples).

- 13 million SARS-CoV-2 genomes from GISAID and other repositories were contextually referenced.

KEY FACILITATORS

- Enables real-time identification of variants of concern faster than traditional lab-based surveillance.
- Demonstrates scalability using both GPU-based supercomputers and novel AI accelerators (Cerebras CS-2).
- Provides insights into co-evolutionary patterns across the SARS-CoV-2 genome, informing vaccine design.

KEY BARRIERS

- High computational cost: requires access to advanced supercomputing/AI hardware.
- Data quality and representativeness issues: reliance on uneven global sequencing capacity may introduce bias.
- Overfitting risk due to high similarity among SARS-CoV-2 sequences.

WHY IT MATTERS?

APPLICABILITY TO LMICS:

Direct application limited by computational infrastructure needs. However, downstream benefits include global genomic surveillance pipelines, variant alerting, and integration with platforms accessible to LMIC public health agencies.

ETHICAL CONSIDERATIONS:

Potential concerns over data sovereignty (global sharing of genome data). Risk of algorithmic bias if models trained mainly on high-income country datasets. Transparency needed in how generative predictions are communicated to avoid premature conclusions about variants.

VALUE PROPOSITION:

Provides a foundation model for biological sequence data, positioning genomics alongside other AI domains (like NLP). Enables early warning systems for viral evolution, supporting more timely public health interventions and vaccine updates. Demonstrates a scalable infrastructure model for pandemic preparedness, applicable to future pathogens.

WHAT IS IT?

INTRODUCTION



DeepARG is an AI tool that identifies and classifies antibiotic resistance genes (ARGs) from metagenomic data. It uses deep learning models trained on curated ARG databases to analyze genetic sequences. The tool was developed to be a generalizable tool to track antimicrobial resistance trends critical for managing infectious disease threats. It focuses on antibiotic resistance genes (ARGs) across 30 resistance categories (e.g., beta-lactam, tetracycline, aminoglycoside, macrolide, and sulfonamide). This tool applies to the data analysis surveillance stage and the high-impact lever is pathogen genomics.

PARTNERSHIPS & FUNDING



DeepARG was developed at Virginia Tech between the Department of Computer Science and the Department of Civil and Environmental Engineering. Funding for this tool was provided by the United States Department of Agriculture (USDA), the National Science Foundation (NSF), and Virginia Tech programs. Total amounts are undisclosed.

HOW IT WORKS?

AI MODEL AND SOFTWARE



DeepARG uses two model variants: DeepARG-SS (short read sequences) and DeepARG-LS (full gene length sequences). These models leverage a dissimilarity matrix derived from known ARG categories. DeepARG runs as a command line version and as a Web service at <http://bench.cs.vt.edu/deeparg>.

DATA SOURCES



DeepARG uses a curated antibiotic resistance gene database, compiled by integrating ARG sequences from Universal Protein Resource (UNIPROT) database filtered against CARD (Comprehensive Antibiotic Resistance Database) and ARDB (Antibiotic Resistance Genes Database). The tool is intended for metagenomic data from the environment, such as water, soil, food, and wastewater.

KEY FACILITATORS

- DeepARG has performed well with precision of 0.97 and a recall of 0.91 across the 30 ARG categories.
- The DeepARG database and code are open source and accessible as a web service.
- Low marginal cost to scale where sequencing exists.

KEY BARRIERS

- DeepARG has only be used in research spaces and has not been implemented as a tool in public health surveillance.
- DeepARG can only predict if genes belong to one of the 30 categories used to train the model.
- DeepARG relies on the accuracy of UNIPROT, CARD, and ARDB.

WHY IT MATTERS?

APPLICABILITY TO LMICS:

DeepARG can support AMR surveillance in high-burden LMIC settings, especially where metagenomic projects are underway (e.g., wastewater monitoring). However, limited sequencing infrastructure, internet connectivity, and bioinformatics capacity may constrain routine use.

ETHICAL CONSIDERATIONS:

CARD, ARDB, and UNIPROT are biased toward ARGs studied in high-income countries and clinical settings, meaning ARG diversity in LMICs or environmental contexts may be underrepresented. Also, while the software is free, effective use depends on sequencing and computational infrastructure. Without intentional investment, the benefits could skew toward high-resource labs and away from LMIC settings.

VALUE PROPOSITION:

The model's inference is lightweight and open-source, so Gates investments can focus on building regional sequencing hubs (or subsidizing cloud usage) rather than expensive per-sample licensing. It is adaptable to LMIC labs with portable sequencing and cloud-based AI for AMR surveillance.

WHAT IS IT?



INTRODUCTION

EDS-HAT targets healthcare-associated infections (HAIs) caused by bacterial pathogens with whole-genome sequencing (WGS) to detect transmission clusters in hospital settings, enabling faster outbreak control in hospitals. It was implemented at UPMC Presbyterian Hospital, part of the University of Pittsburgh Medical Center in Pittsburgh, Pennsylvania, USA. This tool applies to the following surveillance stages: data integration, data analysis, and response & action. The high-impact lever is pathogen genomics.



PARTNERSHIPS & FUNDING

It was developed by researchers at Carnegie Mellon University and the University of Pittsburgh. Funding was provided in part by the National Institute of Allergy and Infectious Diseases, National Institutes of Health, and the University of Pittsburgh Department of Medicine. Total amounts are undisclosed.

HOW IT WORKS?



AI MODEL AND SOFTWARE

EDS-HAT combines WGS with machine learning (ML) to identify genetically related clusters of bacterial isolates and estimate likely hospital transmission routes. It is applied to electronic health records (EHRs) and reviewed by hospital infection prevention experts. The paper does not specify programming frameworks or languages (e.g., Python or R). Instead, EDS-HAT is a custom pipeline integrated into the UPMC health system's existing informatics infrastructure. It is a hybrid outbreak detection system rather than an open-source software package.



DATA SOURCES

EDS-HAT relies on 3,000+ bacterial isolates from 2,700+ patients at UPMC Presbyterian Hospital between November 2016 and November 2018. It then extracted hospital EHR data to estimate transmissions.

KEY FACILITATORS

- EDS-HAT enables precise identification of outbreak clusters within hospitals
- It integrated genomics with electronic health records to detail transmission routes.
- It was found to be more cost effective than traditional infection prevention methods resulting in total cost-savings of between \$192.4K - \$692.5K.

KEY BARRIERS

- EDS-HAT requires sequencing infrastructure and data pipelines for effective integration into hospital data systems.
- Broad applicability is unknown given its design and implementation for a single hospital.
- Further studies need to be conducted to validate cost savings measures.

WHY IT MATTERS?



APPLICABILITY TO LMICs:

EDS-HAT has potential to be expanded within regional hospital for valuable HAI surveillance. However, WGS can be limited within labs with limited capacity and fragmented EHR systems. Technical and training support would be needed to ensure effective and sustainable implementation.



ETHICAL CONSIDERATIONS:

The patient data that would be used by EDS-HAT is sensitive. Any implementation of this tool would require data privacy protections and patient privacy centered practices. Additionally, Advanced hospital-based surveillance may widen gaps between well-resourced hospital facilities and low-resources ones.



VALUE PROPOSITION:

EDS-HAT strengthens infection prevention capacity and reduces morbidity, mortality, and costs of hospital-acquired infections. Its ability to detect outbreaks and transmission routes with high accuracy can reduce HAIs and infection prevention associated costs.

WHAT IS IT?

INTRODUCTION

The LSTM model is a deep learning architecture designed for time-series prediction with long-term dependencies. It was applied to forecast outbreaks of Kyasanur Forest Disease (KFD) using weather data and event-based surveillance inputs such as open-source news and Google Trends. The tool was tested in India, focusing on states where KFD is endemic (Karnataka, Kerala, Goa, and Maharashtra). This tool applies to the surveillance stages data integration and data analysis. The high-impact levers are modelling and event-based surveillance (EBS).

PARTNERSHIPS & FUNDING

LSTM was developed by researchers at the Pacific Northwest National Laboratory (PNNL) in collaboration with the Paul G. Allen School for Global Health, Washington State University. It was funded by the Defense Threat Reduction Agency (DTRA), project number CB11029. The total funding amounts were not disclosed.

HOW IT WORKS?

AI MODEL AND SOFTWARE

LSTM was built on Recurrent Neural Network (RNN) frameworks using LSTM architecture for sequential learning. It was implemented with deep learning libraries (not explicitly named in the study, but typically frameworks like TensorFlow or PyTorch).

DATA SOURCES

This tool uses weather data (climate and environmental variables) and Event-Based Surveillance (EBS) data, which includes open-source news articles and google trends signals. The nature of data used include time-series data reflecting ecological drivers and outbreak-related news signals. LSTM uses regional-level data for national and sub-national prediction of KFD trends.

KEY FACILITATORS

- Successfully captured temporal trends in KFD outbreaks, supporting outbreak forecasting.
- Demonstrated transfer learning capacity, allowing fine-tuning with local data for under-reported areas.
- Effective in integrating multiple data streams (weather + EBS) to improve forecasting.
- Adaptable to both national and regional contexts in India.

KEY BARRIERS

- Required large datasets and longer training time compared to XGB models.
- Performance was sensitive to hyperparameter tuning.
- At times showed lower predictive accuracy than XGB, particularly for regional or short-term forecasts.
- Risk of overfitting if data volume is insufficient.

WHY IT MATTERS?

APPLICABILITY TO LMICS:

Highly relevant for resource-limited settings, especially where traditional surveillance infrastructure is weak. It provides an early-warning system using low-cost open data sources. The implementation challenges include computational needs, reliable power, and internet connectivity..

ETHICAL CONSIDERATIONS:

Reliance on open-source event-based data raises issues of accuracy, misinformation, and verification. It requires transparency in model uncertainty when predictions guide public health decisions.

VALUE PROPOSITION:

It strengthens epidemic preparedness in neglected tropical diseases like KFD. It demonstrates how AI forecasting can complement weak surveillance systems in LMICs. It is potentially scalable to other zoonotic diseases with similar ecological and temporal patterns.

WHAT IS IT?

INTRODUCTION

Is a commercial AI-powered global epidemic intelligence platform designed for real-time infectious disease monitoring, early outbreak detection, and predictive forecasting. It integrates multi-modal data streams including global airline ticketing, official public health reports, online news, climate and environmental data, and demographic information into a unified system.. The platform operates across multiple stages of disease surveillance lifecycle, including data collection, data integration, data analysis, information dissemination, early warning and decision support, and policy development, and aligns with high impact lever of modelling. It has been applied to COVID-19, Zika virus, Ebola, Influenza, Chikungunya, Dengu, and other emerging infectious diseases.

PARTNERSHIPS & FUNDING

It was founded in 2013 by Dr. Maran Khan, an infectious disease physician and researcher at the University of Toronto. Collaborators include Center for Research on Inner City Health, Ryerson University, University of Manitoba, CDC, Public health Canada, WHO, and private sector (airlines, insurers, healthcare organizations) to deliver outbreak intelligence. The funders include Horizon ventures, The Co-operatives, BDC Capital (Women in technology) and the funding amount is about \$.9.4 Million cumulatively.

HOW IT WORKS?

AI MODEL AND SOFTWARE

Uses ML and NLP models to classify and extract signals from unstructured data. The NLP scans and interprets global news, public health bulletins, and online media in multiple languages. Uses anomaly detection and classification algorithms to flag unusual outbreak-related reports and regression and probabilistic models to forecast disease spread through global airline ticketing data. The platform runs on custom-built cloud infrastructure that ingests and processes data streams in real time, generating alerts and visualization dashboards for clients.

DATA SOURCES

It integrates diverse data streams, including official public health reports from WHO, CDC, and national ministries alongside epidemiological bulletins and peer-reviewed studies for validation. It scans global online media sources in more than 65 languages daily and incorporates airline ticketing and mobility data to model the spread of diseases across geographies

KEY FACILITATORS

- Strong predictive performance demonstrated during COVID 19 (detected Wuhan outbreak days before WHO alert)
- Multi-source, global data integration across structured and unstructured streams
- Disease-agnostic platform, adaptable to novel pathogens and syndromic signals
- Proven commercial adoption by governments and private sector clients

KEY BARRIERS

- Reliance on global data availability, may be limited in regions with weak data infrastructures
- Propriety platform with restricted transparency around algorithms
- Commercial licensing may limit accessibility for LMIC governments
- May be less useful in rural/ground-transport contexts because of its dependance on air travel data

WHY IT MATTERS?

APPLICABILITY TO LMICS:

BlueDot's modular system can be adapted to LMICs by leveraging local news, mobile data, and regional health bullets even where formal surveillance infrastructure is weak. Its disease agnostic nature makes it suitable in regions with diverse health threats. Its cloud-based architecture allows integration with decentralized ,local surveillance, capable of providing LMICs with early-warning capacity without requiring extensive laboratory or clinical infrastructure. Partnerships and subsidized licensing could enhance accessibility.

ETHICAL CONSIDERATIONS:

Concerns around data privacy and governance, especially for mobility and travel datasets. Equity issues if access remains limited to high-paying government clients and transparency around algorithms.

VALUE PROPOSITION:

It delivers global-scale early warning capacity by combining real-time outbreak detection with predictive spread modelling. It enhances preparedness by enabling governments and organizations to act before official alerts are issued, as shown during COVID-19. The platform is disease-agnostic, scalable, and future-ready, with strong potential to integrate more advanced AI models and additional data streams.

WHAT IS IT?

INTRODUCTION



MILO predicts active tuberculosis from multiplex serological data by simultaneously generating and evaluating thousands of models. It works by integrating data processing, feature selection, model training, and validation to analyze complex antibody detection datasets and identify optimal diagnostic algorithms. The tool was developed to classify and predict active pulmonary tuberculosis (TB) cases. It was tested with clinical data collected in Pakistan, a TB endemic region. MILO is applied to the data analysis surveillance stage and the high-impact lever, sero surveillance.

PARTNERSHIPS & FUNDING



MILO was developed in the Department of Pathology and Laboratory Medicine at the University of California Davis. Additional partner resources include TB Resource Center at Colorado State University and Luminex Corp. Data was used from the University of Punjab in Lahore, Pakistan. Direct funding amounts are undisclosed.

HOW IT WORKS?

AI MODEL AND SOFTWARE



MILO is an automated machine learning (AutoML) system. automatically tests multiple algorithms and feature selection methods, including logistic regression, random forests, support vector machines (SVM), neural networks, k-nearest neighbors. It then optimizes model hyperparameters and performs ensemble modeling to identify the best-performing classifier for the TB serology dataset. It was developed and deployed as a standalone AutoML software written in C++ and R. It was designed to be run on Windows PC.

DATA SOURCES



MILO was developed with clinical samples collected at Gulab Devi Chest Hospital in Lahore, Pakistan and obtained by researchers at the University of Punjab, Lahore. The serological dataset included samples from active TB patients, COPD patients, and healthy individuals.

KEY FACILITATORS

- AutoMLs are efficient with model testing and optimization, reducing the need for ML expertise.
- MILO identified TB with a strong predictive performance.
- The platform runs on a standard Windows PC, appropriate for low-resource settings.

KEY BARRIERS

- MILO has not yet been operationalized and integrated with surveillance or decision-making systems.
- The study design scope was narrow with data limited to one hospital and population resulting in weak generalizability.
- Further research and validation is needed in larger-scale studies.

WHY IT MATTERS?

APPLICABILITY TO LMICS:



TB is one of the highest priority infectious diseases in LMICS so a tool that improves diagnostic accuracy with low resource needs would be impactful. MILO addresses the challenge of interpreting complex serological datasets for TB diagnosis, which typically requires time-consuming manual algorithm development. If further research validates these findings, MILO could be expanded to regional and national labs.

ETHICAL CONSIDERATIONS:



Long-term sustainability requires local capacity building and possible open-source adaptations. The patient data that would be used on MILO is sensitive. Any implementation of this tool would require data privacy protections and patient privacy centered practices.

VALUE PROPOSITION:



MILO demonstrates automated AI approach for endemic disease prediction that could be adapted for other tuberculosis-endemic LMICs using locally available serological testing infrastructure.

WHAT IS IT?

INTRODUCTION

Is an open-source AI-driven deep learning platform that automatically infer cause (s) of death from verbal autopsy (VA) narratives and structured VA responses using neural-network models and NLP. These methods aim to increase the timeliness, completeness, and accuracy of mortality statistics where medical certification is absent by extracting signal from text-free narratives and combining it with questionnaire data. DeepVA is applied primarily in the data analysis and mortality surveillance stages of surveillance lifecycle and is directly relevant to the high impact lever is mortality surveillance. It can identify 48 different causes of death.

PARTNERSHIPS & FUNDING

DeepVA approaches have been developed epidemiologists at HiTZ: Basque Center for Language Technology, Swiss Tropical and Public Health Institute, and University of Basel. This project was funded through the Spanish Ministry of Science and Technology (PAD-MED PID2019-106942RB-C31) and in part by the Basque Government (Elkartek KK-2019/00045, IXA IT-1343-19, Predoctoral Grant PRE-2019-1-0158). The funding amount not indicated.

HOW IT WORKS?

AI MODEL AND SOFTWARE

The DeepVA implementations use deep neural networks and NLP pipelines. It use uses convolutional neural networks (CNNs), long short-term memory (LSTM) networks, transformer-style text encoders, and stacked ensemble models that combine multiple base learners for improved accuracy (e.g., SEDL). Explainability tools such as LIME have been used to surface the features driving model predictions. The software used is python (TensorFlow/PyTorch, and standard NLP libraries). The code and model details are in GitHub repositories.

DATA SOURCES

This AI tool is trained on verbal autopsy interview data which contains both structured questionnaires , and free-text narrative descriptions of symptoms and circumstances collected from caregivers and witnesses. Common training datasets include WHO-standard VA datasets and research collections (e.g., PHMRC gold-standard dataset) containing labeled causes of death. Outputs are cause-of-death labels (ICD codes or grouped cause categories). Data are de-identified and used to produce population-level cause-specific mortality fractions.

KEY FACILITATORS

- It leverages rich narrative text that traditional question-only algorithms ignore, improving classification signals
- Ensemble architectures (SEDL) have shown improved accuracy over single DL models, increasing robustness across cause categories

KEY BARRIERS

- Data quality and labeling- VA narratives vary in length, language, and completeness
- Generalizability and language- Models trained in one region/language may not transfer well without retraining or domain adoption

WHY IT MATTERS?

APPLICABILITY TO LMICS:

In many LMICS, medical certification of death is rare, as most deaths occur outside health facilities. Verbal autopsy is the primary information source in these contexts. This tool can automate coding and speed up mortality estimates directly improving ascertainment of cause of death from the VA data, making it a crucial tool in these settings. Practical deployment require local language adaptation, computing capacity for inference, and integration into health information workflow.

ETHICAL CONSIDERATIONS:

Privacy and consent for handling sensitive verbal reports, ensuring de-identification and local data governance. There is also the concern of model bias from skewed training data which can misclassify causes important to local health priorities. There is need for transparency and local validation.

VALUE PROPOSITION:

This tool directly tackles the pervasive issue of unregistered deaths and unknown causes of death in low-resource settings, which are major impediments to effective global health planning. By providing a reliable, scalable, cost effective and rapid method of cause of death ascertainment, it aids evidence-based decision making by government ministries.

KEY TAKEAWAYS

- **Despite the rapid evolution of AI capabilities, there remains a limited body of research documenting successful implementation of AI for disease surveillance**, particularly in low- and middle-income countries (LMICs). Most existing case studies are concentrated in high-income settings, with fewer examples that demonstrate scalability or adaptability to resource-constrained environments.
- **Across case studies, funding amounts were often undisclosed**, reflecting either commercial sensitivity or incomplete reporting. Similarly, details about the technical infrastructure underpinning many AI models and software solutions were rarely available, particularly in the case of commercial tools. This lack of transparency poses a barrier to evaluation, replication, and scaling in LMICs.
- **Our review found that machine learning applications are more prevalent than generative AI tools** in current disease surveillance use cases. ML models, which are typically trained on labeled datasets to provide known outputs (e.g., cause-of-death classification), remain more established and widely tested. Generative AI, while promising, is less commonly applied but may offer future opportunities in generating synthetic data, automated summarization, and enhancing interoperability.
- **Equity, data transparency, and privacy** emerged as consistent themes across AI tools in disease surveillance. Concerns include bias in training data, limited inclusivity of LMIC contexts, and risks of inequitable deployment.
- **Most AI-enabled surveillance tools we identified were developed and deployed in high-income countries (HICs)**. However, there are **emerging initiatives seeking to close this gap**, including pilot programs for wastewater monitoring in Ghana, participatory forecasting in Sierra Leone, and mortality surveillance using AI-driven verbal autopsy in multiple African and South Asian countries. These initiatives signal important momentum toward adapting AI for LMIC contexts, but further investment and evaluation are needed.

LIMITATIONS & OPPORTUNITIES FOR FURTHER RESEARCH



Separating hype from practice: Many AI claims remain untested in real-world disease surveillance, making it difficult to distinguish hype from proven applications.



Rapid review limitation: Our approach relied mainly on published literature and websites, which may miss emerging tools not yet documented.



Expert insights needed: Future work should include structured interviews with industry experts to validate findings and assess technical feasibility.



LMIC stakeholder outreach: Direct engagement with stakeholders in LMICs is essential to evaluate local applicability and scalability of AI tools.



Measuring impact: More rigorous research is needed to quantify the real-world impact of AI tool deployment on surveillance outcomes in LMICs.

CONCLUSIONS & RECOMMENDATIONS

- More information is required before making any major investments in AI surveillance tools, given gaps in technical and funding transparency.
- Targeted investment in researchers from Global South, such as through initiatives like AI4PEP, can drive equitable, locally relevant innovations.
- Continued research is essential as the field of AI in disease surveillance evolves rapidly, requiring periodic reassessment to identify the most relevant tools.

In sum, while AI offers significant opportunities to strengthen infectious disease surveillance, critical knowledge gaps and uncertainties remain. Short-term efforts are best focused on supporting Global South innovators and testing scalable, adaptable AI tools. Long-term strategies will require deeper-evidence building to ensure sustainable, equitable, and impactful AI investments.

Note: The information provided in this report is largely based on publicly available sources and may not be entirely up to date or accurate.

APPENDIX 1

The following definitions, drawn or adapted from existing documents as referenced, informed this work. Definitions are listed alphabetically.

Term	Working Definition
Mortality Surveillance	This is the application of AI tools to analyze verbal autopsy, hospital records, and civil registration data to automatically assign causes of death
Wastewater Surveillance	This is the application of AI tools to identify emerging pathogens, predict infection waves, and integrate signals from multiple sites to provide early warning alerts
Pathogen Genomics	This is the application of AI tools in accelerating analysis of genetic sequences of viruses, bacteria, and parasites, identifying mutations, variants, and resistance genes faster than the traditional surveillance methods
Modelling	This is the application of AI tools in processing large, complex, diverse datasets to predict where and when outbreaks will occur
Serosurveillance	This is the application of AI tools in identifying hidden transmission hotspots or gaps in vaccine coverage
Program Design	Application of AI tools in optimizing the structure and objectives of disease surveillance system
Data Collection	Application of AI tools in enhancing the accuracy and efficiency of data gathering
Data Intergration	The application of AI tools in streamlining the consolidation of data from diverse sources
Data Analysis	The application of AI tools in improving the speed and accuracy of insights derived from diverse data
Information Dissemination and Visualization	The application of AI tools in making data more accessible and actionable for stakeholders
Response and Action	The application of AI tools in supporting timely and effective public health interventions
Policy Development	Application of AI tools in informing evidence-based policies for disease control
Community Engagement	The application of AI in ensuring that surveillance efforts are inclusive and community-driven

REPORT REFERENCES

1. [SmartHealth-Track](#)
2. [GenSLMs \(Genome-scale language model\)](#)
3. [Long Short-Term Memory \(LSTM\) Model](#)
4. [Biobot Analytics - Respiratory Reports & Wastewater Data](#)
5. [Biobot Analytics - About / Platform Overview](#)
6. [Biobot - Covid-19 Wastewater Protocol / Lab Methods](#)
7. [Biobot - Nationwide trends paper \(COVID-19 and SARS-CoV-2 RNA in Wastewater, U.S.\)](#)
8. [Biobot - "A world of wastewater-based epidemiology" article](#)
9. [Biobot - Pathogen biomarkers report](#)
10. [Extracting Cause of Death From Verbal Autopsy With Deep Learning Interpretable Methods](#)
11. [Explainable Stacked Ensemble Deep Learning \(SEDL\) Framework to Determine Cause of Death from Verbal Autopsies](#)
12. [Automatically determining cause of death from verbal autopsy narratives](#)
13. [Khan, K. et al. \(2020\). *BlueDot: Outbreak Intelligence for Infectious Diseases*](#)
14. [Bogoch, I. et al. \(2016\). *Anticipating international spread of Zika virus from Brazil.*](#)
15. [Bogoch, I. et al. \(2015\). *Anticipating the international spread of Ebola virus: airline travel and disease dynamics*](#)
16. [BlueDot COVID-19 Response](#)
17. [How this Canadian start-up spotted coronavirus before everyone else knew about it](#)
18. [Rashidi, H.H., Dang, L.T., Albahra, S. et al. \(2021\) "Automated machine learning for endemic active tuberculosis prediction from multiplex serological data." \(MILO\)](#)
19. [Sundermann, Alexander J et al. \(2022\) "Whole-Genome Sequencing Surveillance and Machine Learning of the Electronic Health Record for Enhanced Healthcare Outbreak Detection." \(EDS-HAT\)](#)
20. [Arango-Argoty, G., Garner, E., Pruden, A. et al. \(2018\) DeepARG: a deep learning approach for predicting antibiotic resistance genes from metagenomic data.](#)
21. [Arango, G., DepARG, \(2023\), GitHub repository, <https://github.com/gaarangoa/deeparg>](#)
22. [AI4PEP \(2024\) "Ghana Team 1: Responsible AI for Developing a Robust Public Health Surveillance System: Early Detection and Prediction of Vector-Borne Viral ZoonoticPathogens."](#)

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