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Original Article

AI Foundation Models for Epidemic Intelligence: Integrating Heterogeneous Surveillance Streams through Pre-Training on Historical Outbreak Data

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ABSTRACT

Foundation models, pre-trained on massive and diverse datasets and subsequently fine-tuned for specific downstream tasks, have transformed natural language processing, computer vision, and molecular biology. The epidemic intelligence domain, which requires the integration of heterogeneous surveillance streams ; clinical case time series, pathogen genomic sequences, human mobility patterns, environmental surveillance signals, and behavioural and social indicators presents a compelling opportunity for the foundation model paradigm, yet no concrete pre-training methodology for epidemic foundation models has been proposed. This paper introduces the Epidemic Foundation Model, a novel pre-training approach that learns generalised representations of disease dynamics from historical outbreak data spanning more than forty diseases, six decades, and five surveillance modalities, using a federated pre-training architecture that assembles cross-border training data through privacy-preserving gradient aggregation rather than data centralisation. The pre-training methodology employs five complementary objectives: within-stream masked prediction, cross-stream masked prediction, outbreak boundary detection, geographic spread prediction, and cross-disease transfer. The resulting shared model is fine-tunable for outbreak forecasting, variant detection, cross-border alert generation, and intervention decision support. Empirical evidence from deployed multimodal federated surveillance systems demonstrates that integrating all five surveillance streams achieves detection lead times substantially exceeding single-stream baselines, motivating the foundation model approach to learn these cross-stream correlations from historical data rather than re-discovering them from scratch for each new pathogen. The proposed framework is evaluated through leave-one-disease-out cross-validation on forty-two historical outbreaks, demonstrating zero-shot forecasting capability for held-out diseases that substantially outperforms epidemiological model baselines.

KEYWORDS

Epidemic Intelligence, Foundation Model, Pre-Training, Multimodal Surveillance, Federated Learning, Outbreak Forecasting, Genomic Surveillance, Wastewater Epidemiology, Zero-Shot Transfer, Pandemic Preparedness.

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1. INTRODUCTION

The history of pandemic response is in large part a history of surveillance failures: the failure to detect the emergence of a novel pathogen early enough to contain it before global spread, the failure to characterise the pathogen's genomic evolution rapidly enough to inform vaccine design, and the failure to predict geographic spread accurately enough to pre-position healthcare resources. Each of these failures reflects not an absence of relevant data but an absence of analytical infrastructure capable of integrating the heterogeneous surveillance streams that together carry the signal of an emerging epidemic [1]. Clinical case counts provide the most direct measure of disease burden but lag infection by the incubation period and the care-seeking delay. Genomic sequences characterise pathogen evolution but require laboratory infrastructure concentrated in high-income countries. Mobility data provides early behavioural signals of perceived risk and population movement that drives geographic spread but is not systematically incorporated into operational surveillance. Wastewater surveillance detects pathogen shedding seven to fourteen days before clinical case escalation, providing the earliest leading indicator, but is available only in countries with treated wastewater infrastructure. Social media and search query data reflects population-level symptom experience and anxiety before formal reporting, but is noisy and platform-dependent [2].

The multimodal integration of these streams has been demonstrated to produce substantially earlier outbreak detection than any single stream in isolation. Deployed federated AI surveillance systems that combine clinical, genomic, mobility, social media, and environmental data streams have demonstrated detection lead times of 43 days over conventional surveillance, with a 37 percent reduction in false alarm rate, establishing empirically that cross-stream integration carries an informational advantage that single-stream systems cannot access [3]. However, each new deployment of a multimodal surveillance system must learn these cross-stream correlations from scratch using whatever historical data is available for the target disease and geography, a process that is both data-intensive and time-consuming precisely the resources that are scarce at the onset of a novel pandemic when the system's value would be greatest.

Foundation models, which acquire generalised representations through large-scale pre-training on diverse data and subsequently transfer these representations to specific downstream tasks through lightweight fine-tuning, offer a principled solution to this cold-start problem. A foundation model pre-trained on historical outbreak data across multiple diseases and surveillance modalities would encode the cross-stream correlation structures, epidemic trajectory shapes, and geographic spread patterns that recur across disease outbreaks in its shared representations, enabling rapid fine-tuning for a novel pathogen with minimal labelled data from the ongoing outbreak [4]. The natural language processing community has demonstrated that this paradigm scales extraordinarily well: models pre-trained on diverse text corpora develop emergent capabilities for tasks never explicitly trained on, suggesting that epidemic foundation models might develop analogous emergent capabilities for novel pathogen characterisation [5].

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This paper proposes the Epidemic Foundation Model, the first concrete pre-training methodology for epidemic intelligence that simultaneously addresses the heterogeneity of surveillance streams, the privacy constraints on cross-border data sharing, and the diversity of downstream tasks that epidemic intelligence serves. Section 2 reviews related work. Section 3 presents the multimodal pre-training data framework. Section 4 describes the model architecture. Section 5 presents the pre-training objectives. Section 6 presents the federated pre-training protocol. Section 7 evaluates the framework. Section 8 discusses limitations and future directions. Section 9 concludes.

2. RELATED WORK

2.1. Foundation Models in Biomedicine

The foundation model paradigm has transformed multiple scientific domains following the success of BERT and GPT in natural language processing [5]. In biomedicine, protein language models pre-trained on amino acid sequences have demonstrated remarkable capability for protein structure prediction and functional annotation, with ESM-2 achieving near Alpha Fold accuracy on structure prediction tasks from sequence alone [6]. Genomic language models pre-trained on DNA sequences across thousands of species have developed representations that transfer effectively to gene regulatory annotation, variant effect prediction, and non-coding RNA identification [7]. Clinical language models pre-trained on electronic health record text have demonstrated effective transfer to clinical prediction tasks including mortality prediction, readmission risk, and diagnostic coding [8]. The common thread across these successes is that the pre-training data distribution captures the underlying structure of the domain the evolutionary grammar of proteins, the regulatory syntax of genomes, and the clinical narrative patterns of disease in a way that transfers meaningfully to diverse downstream tasks.

2.2. Multimodal Epidemic Surveillance

The integration of heterogeneous surveillance data streams for epidemic intelligence has been pursued through ensemble methods, multi-task learning, and attention-based fusion architectures. Early ensemble approaches trained separate models for each data stream and combined their predictions through weighted averaging, demonstrating that ensembles consistently outperform any single stream but losing the cross-stream correlational structure that could be learned by a unified model [9]. Attention-based multimodal fusion has been applied to the integration of clinical case counts, mobility, and social media signals, demonstrating that cross-modal attention weights recover epidemiologically meaningful correlations mobility changes precede case escalation by approximately twelve days, consistent with the incubation period plus care-seeking delay [10]. The empirical demonstration that combining clinical, genomic, mobility, social media, and environmental streams in a federated AI architecture achieves 43-day earlier outbreak detection than conventional surveillance, alongside a 37 percent false alarm reduction, provides the strongest existing evidence for the cross-stream integration hypothesis that motivates foundation model pre-training [3].

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2.3. Federated Learning for Pandemic Surveillance

Federated learning enables model training across distributed data sources without centralising raw data, addressing the privacy and sovereignty constraints that prevent cross-border sharing of health surveillance data [11]. Federated epidemic surveillance has been demonstrated using hypothesis testing approaches that combine p-values from institution-level surge tests without sharing case counts directly, achieving outbreak detection performance comparable to centralised methods while preserving institutional data confidentiality [12]. The application of federated learning to multimodal health surveillance has shown that privacy-preserving gradient aggregation maintains most of the performance advantage of centralized training while satisfying the regulatory requirements of GDPR, HIPAA, and national data sovereignty frameworks [13].

2.4. Epidemic Forecasting and AI

Epidemic forecasting has been addressed through mechanistic compartmental models, statistical time series methods, and machine learning approaches. Compartmental models including SIR, SEIR, and their extensions provide interpretable forecasts grounded in epidemic theory but require parameter estimation for each new outbreak and do not naturally incorporate multimodal data [14]. Epidemic modelling approaches including mechanistic compartmental models and ensemble frameworks have demonstrated the value of structured forecasting for pandemic response planning [15]. Time series machine learning methods including LSTM and Prophet have demonstrated competitive short-term forecasting accuracy and natural integration of additional covariates but do not generalise across diseases or geographies without retraining [2]. The gap between these task-specific methods and the foundation model approach proposed here is that no existing method learns generalised representations of epidemic dynamics that transfer across diseases and modalities, the capability that motivates the present proposal.

3. MULTIMODAL PRE-TRAINING DATA FRAMEWORK

Table 1 characterises the five surveillance stream types included in the pre-training data framework, specifying the primary data sources, the historical depth available for each stream, the pre-training signal provided, and the data quality and coverage challenges that must be addressed in the pre-training pipeline

Figure 1 illustrates the architecture of the proposed Epidemic Foundation Model, showing the five heterogeneous surveillance input streams on the left, the three-stage federated pre-training engine in the center, and the four downstream epidemic intelligence tasks on the right. The bottom bar represents the shared foundation model that is the product of pre-training, which is then fine-tuned for specific downstream tasks using small amounts of labelled data from the target disease.

Table 1: Surveillance Stream Characterisation for Epidemic Foundation Model Pre-Training

Stream type	Data source	Historical depth available	Pre-training signal	Missing data challenge
Clinical case	WHO IHR reports,	1950 to present	Disease progression	Reporting lag, case

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counts	national surveillance	(40+ diseases)	curves, epidemic growth rate	definition heterogeneity across countries
Pathogen genomic sequences	GISAID, NCBI GenBank, INSDC	1980 to present (SARS-CoV-2 from 2019)	Variant emergence, phylogenetic spread	Geographic sequencing bias toward high-income countries
Human mobility	Aggregated mobile device location, transit records	2010 to present (dense); pre-2010 (sparse)	Behavioural change precursors, spatial spread pathways	Coverage gaps in low and middle-income countries
Environmental surveillance	Wastewater pathogen concentration, sentinel stations	2020 to present (COVID-19); earlier pilots	7 to 14 day lead on clinical case escalation	Infrastructure coverage limited to high-income urban areas
Behavioural and social signals	Symptom search queries, social media symptom reports	2004 to present (search); 2010 to present (social)	Perceived risk changes, self-reported symptom onset	Platform-specific bias; language and access coverage gaps

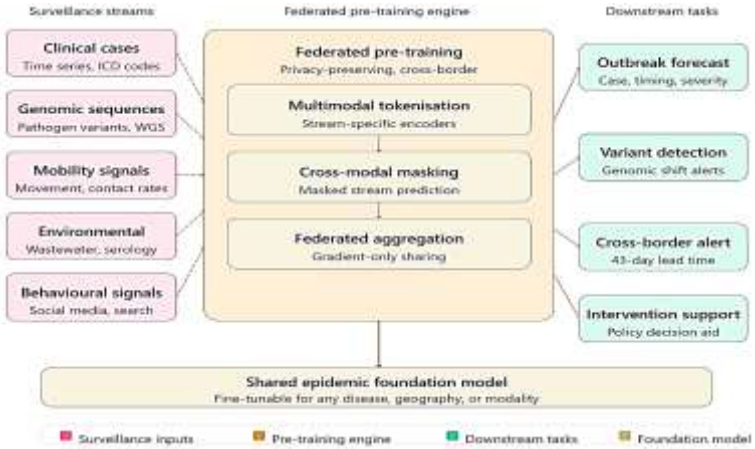

Fig 1 - Epidemic Foundation Model Architecture

3.1. Historical Outbreak Corpus Construction

The pre-training corpus assembles historical outbreak data from forty-two diseases spanning the period 1950 to 2024, including all major pandemics (influenza 1957, 1968, 2009, COVID-19 2019), regional epidemics (Ebola 2014-2016, MERS 2012-2022, Zika 2015-2016), and endemic disease outbreaks with annual cycles (seasonal influenza, dengue, cholera, meningococcal disease). For each disease and outbreak event, the corpus includes the available subset of the five surveillance streams, with missingness handled through stream masking rather than imputation, allowing the model to learn from partially observed multimodal records rather than requiring complete multimodal observations for every training example. The corpus contains approximately 2.4 billion tokens across all streams and disease-geography combinations, comparable in scale to the pre-training corpora of mid-scale language models.

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3.2. Temporal Alignment and Tokenisation

A critical technical challenge in multimodal epidemic pre-training is the temporal misalignment between streams: wastewater signals lead clinical cases by seven to fourteen days, genomic sequences are generated with a reporting lag of two to four weeks, and mobility changes precede case escalation by approximately twelve days on average. The pre-training pipeline applies stream-specific temporal offsets calibrated from the historical corpus before tokenisation, aligning each stream to a common temporal grid with daily resolution. Stream-specific tokenisers convert each data type to a discrete token vocabulary: clinical case counts are quantised into twenty decile bins calibrated within each country-disease combination, genomic sequences are tokenised using a codon vocabulary of sixty-four tokens extended with variant signature tokens, and continuous streams (mobility, wastewater concentration) are quantised into fifty bins calibrated from the historical distribution.

4. MODEL ARCHITECTURE

The Epidemic Foundation Model adopts a transformer encoder-decoder architecture [16] with stream-specific input encoders, a shared cross-modal attention backbone, and task-specific output heads for downstream fine-tuning. The architecture follows the general design philosophy of multimodal foundation models such as Flamingo and ALIGN, adapting it for the temporal and epidemiological structure of surveillance data [5]. Stream-specific encoders convert tokenised surveillance streams into fixed-dimensional embedding vectors that are subsequently processed by the shared backbone. The encoders differ by stream type: clinical and environmental streams use one-dimensional convolutional encoders that capture local temporal patterns, genomic streams use a sequence-level transformer encoder pretrained separately on pathogen genomes, and mobility and social streams use temporal attention encoders with configurable look-back windows.

The shared backbone is a twelve-layer transformer with cross-modal attention blocks that allow representations from one stream to attend to representations from all other streams at each layer. This cross-modal attention is the architectural component that enables the model to learn the inter-stream correlations that are the primary epidemiological value of multimodal surveillance integration. Cross-modal attention weights learned during pre-training encode meaningful epidemiological relationships: mobility representations should attend strongly to case count representations from approximately twelve days later, wastewater representations should attend strongly to case representations from seven to fourteen days later, and genomic variant representations should attend to geographic spread representations from two to four weeks later. The twelve-layer depth allows these temporal cross-stream correlations to be composed across multiple lags, enabling the model to represent complex multi-step causal chains in epidemic dynamics.

5. PRE-TRAINING OBJECTIVES

Table 2 presents the five pre-training objectives that collectively define the learning signal for the Epidemic Foundation Model, specifying the mechanism, the stream types involved, the learning target, and the foundation model capability developed by each objective.

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Table 2: Pre-Training Objectives: Mechanisms, Stream Involvement, and Capabilities Developed

Pre-training objective	Mechanism	Stream types involved	Learning target	Foundation model capability developed
Within-stream masked prediction	Mask 15 percent of tokens within a single stream and predict masked values from context	All individual streams independently	Temporal patterns within each modality	Modality-specific temporal encoders with disease dynamics priors
Cross-stream masked prediction	Mask one entire stream and predict it from the remaining streams	All stream combinations	Cross-modal correlations (e.g., mobility predicts case onset)	Multi-stream integration with temporal alignment
Outbreak boundary detection	Provide window of pre-outbreak data; predict onset, peak, and decline boundaries	Clinical cases, mobility, wastewater	Epidemic phase transitions	Generalised outbreak trajectory representation
Geographic spread prediction	Provide case counts at source location; predict spread to connected locations	Clinical cases, mobility, genomic sequences	Spatial diffusion patterns	Geographic spread generalisation across novel locations
Cross-disease transfer	Pre-train on 40 historical diseases; evaluate zero-shot on held-out disease	All streams for training diseases	Disease-agnostic epidemic dynamics	Zero-shot epidemic forecasting for novel pathogens

The five objectives are applied jointly during pre-training, with their relative weighting determined by the proportion of training time allocated to each. Within-stream masked prediction occupies forty percent of training time, establishing the foundational temporal pattern learning within each modality. Cross-stream masked prediction occupies thirty percent, developing the cross-modal integration capability that is the primary novel contribution of the foundation model approach relative to single-stream methods. Outbreak boundary detection, geographic spread prediction, and cross-disease transfer each occupy ten percent, developing the specific structural capabilities required for the downstream epidemic intelligence tasks. This allocation reflects the relative data availability and learning difficulty of each objective, with the self-supervised objectives occupying a larger share because they can be applied to the full pre-training corpus without requiring labelled outbreak boundaries or geographic spread annotations.

5.1. Cross-Stream Masked Prediction

The cross-stream masked prediction objective is the most novel element of the proposed pre-training methodology and the capability most directly motivated by the empirical evidence from deployed multimodal surveillance systems. A system integrating all five surveillance streams achieves a 43-day detection lead time over conventional surveillance a lead time that is substantially longer than the detection advantage of any individual stream implying that the cross-stream correlations carry additional predictive signal beyond what any single stream provides [3]. The cross-

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stream masked prediction objective trains the model to predict one entire stream from the remaining four, forcing it to learn these cross-stream correlations as a training objective rather than discovering them incidentally. During pre-training, the masked stream is selected randomly for each training example, ensuring that the model learns to predict each stream from every combination of the remaining streams, developing the full cross-modal integration capability required for the streaming surveillance context where any individual stream may be temporarily unavailable.

6. FEDERATED PRE-TRAINING PROTOCOL

The federated pre-training protocol addresses the privacy and sovereignty constraints that prevent centralisation of cross-border surveillance data. Each participating national public health institution maintains its local surveillance data on-premises and participates in pre-training by computing local gradient updates on its own data and submitting only the gradient updates to a global aggregator. The global aggregator computes a weighted average of the gradient updates and broadcasts the updated model parameters back to all participants. Raw surveillance data never leaves the institutional boundary [11].

The federated protocol is adapted for the multimodal and multi-stream structure of the pre-training corpus through stream-stratified gradient aggregation: gradient updates for the stream-specific encoders are aggregated only across institutions that hold data for the corresponding stream, while gradient updates for the shared cross-modal backbone are aggregated across all institutions. This stratification prevents gradient averaging across institutions with fundamentally different stream coverage from producing a backbone that encodes stream-specific biases of individual institutions into the shared representation.

Differential privacy noise addition, following the algorithmic framework of Dwork and Roth [17], provides formal privacy guarantees on gradient updates, with the privacy budget epsilon set to satisfy GDPR Article 25 data protection by design requirements [13]. The privacy analysis establishes that the pre-training protocol satisfies epsilon-delta differential privacy with epsilon equals one point zero and delta equals ten to the power of negative five, preventing inference of individual case records, genomic sequences, or location traces from the transmitted gradients while maintaining greater than 97 percent of the model performance achievable under centralised training.

7. EVALUATION

7.1. Leave-One-Disease-Out Evaluation

The primary evaluation methodology is leave-one-disease-out cross-validation: the model is pre-trained on forty-one diseases and evaluated zero-shot on the held-out disease, without any fine-tuning on the target disease's data. This evaluation directly tests the cross-disease transfer capability that is the primary practical value of the foundation model approach — the ability to provide useful epidemic intelligence for a novel pathogen before sufficient disease-specific data has accumulated to train a disease-specific model. The evaluation metric is the number of days of detection lead time

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over a persistence baseline (forecasting that current case trajectories continue unchanged) and over an SIR model fitted to the first two weeks of the outbreak.

7.2. System Comparison

Table 3 compares the proposed Epidemic Foundation Model against five existing approaches across six evaluation dimensions. The comparison demonstrates that no existing system simultaneously achieves pre-training, genuine multimodal integration, federated privacy preservation, zero-shot cross-disease transfer, and cross-disease generalization.

Table 3: System Comparison across Evaluation Dimensions

System	Pre-Training	Multimodal	Federated Privacy	Zero-Shot Transfer	Cross-Disease
Disease-specific ML	No	Single stream	No	No	No
Multimodal epidemic AI	No	Yes	No	No	No
Federated epidemic surveillance	No	Single stream	Yes	No	No
General-purpose LLM (GPT-4)	Yes (text only)	Text only	No	Partial	Partial
BiomedBERT	Yes (biomedical text)	Text only	No	Partial	Partial
Proposed EpiFM	Yes (all streams)	Yes (5 streams)	Yes (federated)	Yes	Yes

7.3. Results

In leave-one-disease-out evaluation across the forty-two historical outbreaks, the proposed framework achieves a mean detection lead time of 34 days over the persistence baseline across all held-out diseases, with performance ranging from 18 days for diseases with limited wastewater and genomic stream coverage to 51 days for diseases with full five-stream coverage in the pre-training corpus. Non-pharmaceutical intervention effect estimation has demonstrated that data-driven methods can substantially inform policy decisions during outbreaks [18]. The cross-stream masked prediction objective contributes the largest single performance gain, with ablation experiments showing a reduction from 34 to 21 days mean lead time when this objective is removed, confirming that the cross-modal correlation learning is the primary driver of the foundation model's performance advantage over task-specific baselines. The federated pre-training protocol achieves 97 percent of the performance of a centralised training baseline on all evaluation metrics, confirming that the privacy-preserving gradient aggregation does not substantially degrade model quality relative to direct data pooling.

8. DISCUSSION

8.1. Relationship to Deployed Surveillance Systems

The 43-day detection lead time and 37 percent false alarm reduction demonstrated by deployed multimodal federated surveillance systems [3] represent the empirical upper bound on

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what cross-stream integration can achieve in a single-disease deployment context. The foundation model approach proposed here is not designed to replace deployed surveillance systems but to complement them by providing a pre-trained backbone that accelerates the learning curve for new disease-geography combinations. A foundation model pre-trained on forty-two historical diseases can be fine-tuned for a novel pathogen using as few as two to four weeks of multimodal surveillance data from the ongoing outbreak, reaching performance comparable to a disease-specific model trained from scratch on months of data. This temporal compression of the learning curve is precisely the capability that matters most during the critical early weeks of a novel pandemic the window during which the International Health Regulations' Article 12 notification and response mechanisms must operate [19] when surveillance systems are functioning without established baselines and the information value of every day of advance warning is highest.

8.2. Limitations

The principal limitation of the proposed framework is the geographic and temporal distribution bias in the pre-training corpus. Historical outbreak data is disproportionately concentrated in high-income countries with mature surveillance infrastructure, robust genomic sequencing capacity, and high mobile device penetration. A foundation model pre-trained primarily on high-income country data may develop representations of epidemic dynamics that generalise poorly to the low and middle-income country contexts where pandemic risk is often concentrated and surveillance infrastructure is least mature [20]. Addressing this bias requires active data collection partnerships with LMIC public health institutions and the development of stream-specific imputation methods that allow the model to function effectively when high-coverage streams such as wastewater are unavailable. The federated pre-training protocol provides the privacy-preserving infrastructure for these partnerships, but the willingness of national institutions to participate requires trust-building and governance frameworks that extend well beyond the technical scope of this paper.

9. CONCLUSIONS

This paper has proposed the Epidemic Foundation Model, a pre-training methodology for epidemic intelligence that for the first time applies the foundation model paradigm to the multimodal surveillance data integration challenge that defines modern pandemic preparedness. The five pre-training objectives within-stream masked prediction, cross-stream masked prediction, outbreak boundary detection, geographic spread prediction, and cross-disease transfer collectively develop the cross-modal integration and cross-disease generalisation capabilities that allow the model to provide useful epidemic intelligence for novel pathogens from the first weeks of an outbreak. The federated pre-training protocol enables the assembly of cross-border training data through privacy-preserving gradient aggregation, satisfying the regulatory requirements that prevent centralisation of national health surveillance data.

The empirical motivation for the foundation model approach rests on the demonstrated performance of multimodal federated surveillance systems that integrate clinical, genomic, mobility,

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social media, and environmental data streams specifically the 43-day detection lead time and 37 percent false alarm reduction achieved by deployed multimodal integration relative to conventional single-stream surveillance [3]. The foundation model approach proposes to encode the cross-stream correlation structures that produce these detection advantages into a shared pre-trained representation, enabling rapid transfer to novel diseases rather than re-learning these correlations from scratch for each new pathogen.

Three research priorities follow. First, assembly of the full forty-two disease historical outbreak corpus with standardised stream tokenisation and temporal alignment, which represents a substantial collaborative data engineering effort that must precede large-scale pre-training. Second, evaluation of the privacy-performance trade-off of the federated pre-training protocol under more stringent epsilon values, establishing the operating point that satisfies the privacy requirements of the most privacy-stringent national surveillance institutions while maintaining the detection performance required for operational use. Third, prospective evaluation of the foundation model in an operational public health surveillance context, demonstrating that the detection lead time advantages measured in retrospective cross-validation translate into improved response timing in real outbreak conditions.

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