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Federated Graph Learning Enables Decentralized Disease Surveillance Across Health Systems

Luca Moretti * and Ananya Kapoor

Department of Computer Science, University of British Columbia, Canada

*** Corresponding author Email:** moretti15067@gmail.com

Abstract: The emergence of federated graph learning (FGL) offers a transformative paradigm for disease surveillance across distributed health systems, enabling collaborative model training without centralizing sensitive patient records. Conventional disease monitoring pipelines require aggregating clinical data into unified repositories, which raises significant concerns related to patient privacy, regulatory compliance, and institutional data governance. This paper presents a decentralized surveillance framework that integrates graph neural network (GNN) architectures with federated optimization protocols, allowing geographically dispersed hospitals, public health agencies, and community clinics to jointly learn disease propagation dynamics from locally retained data. The proposed system constructs patient-population interaction graphs at each participating node and trains a spatiotemporal GNN under a privacy-preserving federated aggregation scheme. Empirical evaluations using simulated multi-site infectious disease datasets demonstrate that the federated model achieves detection accuracy within 3.2% of a centralized training baseline while substantially reducing inter-institutional data exposure. This work advances the intersection of distributed machine learning and public health informatics, providing a principled and scalable foundation for real-time epidemic intelligence systems that respect institutional data sovereignty.

Keywords: Federated learning; Graph neural networks; Disease surveillance; Privacy-preserving machine learning; Spatiotemporal modeling; Public health informatics.

1. Introduction

Disease surveillance has long been recognized as one of the most critical pillars of public health infrastructure. The ability to detect, monitor, and respond to infectious disease outbreaks in a timely and spatially coherent manner determines, in large part, whether an emerging epidemic can be contained before it achieves pandemic scale. For decades, national and international health authorities have relied on centralized reporting systems in which clinical observations, laboratory results, and epidemiological indicators are aggregated into shared databases for analysis. While these systems have achieved important successes—including the early detection of novel influenza strains, the coordination of response during cholera outbreaks in resource-limited settings, and the tracking of antimicrobial resistance patterns across national borders—their underlying architecture introduces a fundamental tension between the utility of pooled data and the privacy rights of the patients whose records constitute that data [1]. This tension is not merely theoretical; high-profile breaches of centralized health databases have eroded public trust in data-sharing arrangements and prompted advocacy groups to challenge the legal foundations of mandatory disease reporting in multiple jurisdictions.

The rapid proliferation of electronic health records (EHRs) and digital diagnostic platforms has simultaneously enlarged the volume of clinically relevant surveillance data and amplified the risks of unauthorized access, re-identification, and cross-institutional data leakage. A single tertiary care hospital may generate millions of structured clinical observations per year, each potentially carrying information about patient identity, chronic conditions, behavioral patterns, and social circumstances that extends far beyond the presenting illness. Regulatory frameworks such as the Health Insurance Portability and Accountability Act in the United States, the General Data Protection Regulation in Europe, and equivalent legislation across Asia-Pacific jurisdictions have increasingly constrained the ability of health systems to share raw patient-level data, even for ostensibly beneficial public health purposes [2]. These regulations impose not only technical requirements for data anonymization but also organizational obligations around data stewardship, consent management, and breach notification that make ad hoc inter-institutional data sharing practically difficult and legally risky. As a result, the traditional model of centralized disease surveillance faces growing legal, ethical, and technical obstacles that demand architecturally novel solutions capable of preserving analytical capability while operating within the constraints of modern data governance.

Federated learning (FL) has emerged in recent years as one of the most promising paradigms for reconciling the competing imperatives of data utility and privacy protection. Originally proposed as a method for training machine learning models across mobile devices without transmitting raw data to a central server [3], FL has since been extended to a wide range of application domains including medical imaging, clinical risk prediction, genomic analysis, and drug discovery [4]. The core insight of FL is that model parameters rather than raw training samples can be exchanged between a central aggregator and participating data holders, enabling collaborative learning without exposing individual-level information. Each participating institution performs gradient computation on its own locally retained data and transmits only parameter updates to the aggregation server, which combines contributions from all participants into an updated global model that is subsequently redistributed for the next round of local training. This iterative parameter exchange process converges to a global model that implicitly incorporates knowledge from all participating institutions while never requiring any institution to expose its raw records

[5]. However, standard FL approaches assume that local datasets consist of independent and identically distributed samples, an assumption that is routinely violated in healthcare contexts where patient interactions, referral pathways, and community transmission networks introduce complex relational structure that flat feature representations cannot adequately capture [6].

Graph neural networks (GNNs) represent a complementary advance that specifically addresses relational and topological data. By representing entities as nodes and their interactions as edges in a graph, GNNs enable machine learning models to capture structural dependencies that flat feature vectors fundamentally obscure [7]. In the context of disease surveillance, patients can be represented as nodes with edges encoding shared environments, healthcare contacts, or genetic proximity, while disease propagation signals flow along these edges in ways that standard tabular models cannot capture. The capacity of GNNs to perform localized message passing—aggregating information from graph neighborhoods of increasing radius across successive layers—makes them particularly effective at modeling diffusion-like processes, which correspond naturally to the spatial spread of infectious agents through contact networks [8]. Spatiotemporal extensions of GNNs further allow the model to reason about how these signals evolve across time, incorporating recurrent or attention-based temporal components that capture seasonal periodicity, epidemic lag structures, and early warning anomalies that precede clinically detectable outbreak events.

The integration of FL with GNN-based disease modeling—what this paper terms federated graph learning—offers a promising path toward surveillance systems that are simultaneously powerful, privacy-preserving, and institutionally viable. Several fundamental challenges must be addressed for this integration to succeed in practice, including the heterogeneity of graph structures across health systems with different patient populations and recording practices, communication overhead during gradient exchange across potentially low-bandwidth institutional network connections, the risk of model inversion and membership inference attacks targeting shared model parameters, and the need to aggregate graph-level knowledge across networks with incompatible node sets and qualitatively different topological characteristics [9]. The challenge of non-independent and identically distributed graph data is particularly acute in disease surveillance applications, where the disease burden, demographic composition, and healthcare utilization patterns of each institution's patient population may differ substantially, causing locally trained model components to diverge in directions that undermine the utility of naive parameter averaging [10]. Addressing these challenges requires not only algorithmic innovation in the federated aggregation procedure but also careful architectural design of the local GNN components to ensure that their learned representations are sufficiently aligned across institutions to support meaningful aggregation.

This paper proposes a unified framework that addresses each of these challenges through a combination of architectural design choices and algorithmic innovations, and evaluates the resulting system against both centralized and naive federated baselines across a range of simulated multi-site disease surveillance scenarios. The contributions span the theoretical formalization of FGL for disease surveillance, the design and implementation of a graph-aware privacy-preserving federated aggregation protocol, and the empirical demonstration of competitive surveillance performance with formal differential privacy guarantees at realistic privacy budgets.

2. Literature Review

The scholarly literature on federated learning in healthcare has expanded substantially since the foundational work introducing the FedAvg algorithm as a practical mechanism for privacy-preserving distributed model training. FedAvg operates by randomly selecting a subset of participating clients at each round, broadcasting the current global model to those clients, having each client perform multiple local stochastic gradient descent steps on its own data, and then aggregating the resulting local models through weighted averaging proportional to local dataset size. This deceptively simple protocol proves surprisingly effective in practice while offering immediate privacy benefits relative to centralized data collection, and its introduction catalyzed a broad research program exploring extensions and refinements suited to the distinctive challenges of real-world deployment contexts. Subsequent extensions have adapted the FedAvg framework to the distinctive challenges of medical data, including non-iid data distributions, missing modalities, catastrophic forgetting during aggregation, and the need for formal differential privacy (DP) guarantees that go beyond the informal privacy protections afforded by parameter exchange alone [11].

Rieke et al. provided an influential overview of FL applications in clinical settings, documenting use cases spanning radiology report generation, pathological image classification, electronic health record risk stratification, and clinical trial recruitment, while identifying inter-institutional heterogeneity as the primary barrier to deployment at scale and calling for standardized federated learning benchmarks and evaluation protocols to facilitate systematic comparison of algorithmic approaches [12]. Sheller et al. demonstrated that federated training of brain tumor segmentation models across 71 geographically distributed sites could achieve performance statistically comparable to centralized training, establishing an important empirical benchmark for multi-institutional FL and demonstrating that federated models can generalize more robustly to unseen sites than models trained on data from any single institution. These early empirical successes established federated learning as a viable approach for multi-site clinical machine learning and motivated the subsequent wave of domain-specific adaptations addressing healthcare's particular data characteristics and regulatory environment.

The challenge of non-iid data distributions in federated settings has been extensively studied, with researchers proposing personalized variants of FedAvg that allow local model fine-tuning to account for site-specific distributional shifts while preserving the benefits of collaborative global training [13]. Karimireddy et al. identified gradient divergence under non-iid distributions as the primary cause of FedAvg's performance degradation relative to centralized training and proposed SCAFFOLD, a variance reduction technique using control variates to correct for client drift during local training steps [14]. Li et al. introduced FedProx, a regularization-based modification that penalizes local updates deviating substantially from the global model by adding a proximal term to the local objective function, improving convergence stability in heterogeneous settings where the degree of data heterogeneity varies considerably

across rounds and client subsets [15]. These contributions are directly relevant to healthcare federated systems, where patient demographics, disease prevalence, clinical documentation practices, and healthcare utilization patterns vary substantially across institutions and regions, creating precisely the kind of systematic distributional heterogeneity that undermines naive FedAvg convergence.

Graph neural networks for health-related applications constitute a parallel and increasingly interconnected body of research that has grown substantially over the past several years. The seminal work of Kipf and Welling on graph convolutional networks (GCNs) established an efficient first-order spectral approximation to graph convolution that dramatically reduced the computational cost of graph-based learning while retaining competitive representational capacity, and has since been widely adopted in biomedical domains ranging from drug-drug interaction prediction to patient similarity networks and protein function annotation [16]. As illustrated conceptually by the layered graph convolution and pooling architecture proposed by Defferrard et al., a GCN pipeline processes input graph signals through convolutional layers that perform localized spectral filtering using Chebyshev polynomial approximations to the graph Laplacian, followed by graph coarsening operations—including sub-sampling to identify cluster representatives and pooling to aggregate neighborhood signals into compact representations—that progressively reduce graph resolution before final prediction through fully connected layers [17]. This hierarchical signal processing paradigm, which mirrors the spatial hierarchy of convolutional neural networks on regular grids but extends naturally to the irregular topology of arbitrary graphs, is directly applicable to patient-population graphs in which disease signals must be extracted across multiple scales of community connectivity ranging from household clusters to regional transmission corridors. Veličković et al. extended this framework with attention mechanisms, introducing graph attention networks (GATs) that assign learned importance weights to neighboring nodes through a masked self-attention operation, providing a more expressive and interpretable form of message passing that can selectively emphasize the most epidemiologically informative connections within a patient network [18].

For disease surveillance specifically, graph-based modeling has received growing attention as researchers have recognized that epidemic dynamics are fundamentally network phenomena governed by the topology of contact and mobility structures rather than by individual-level characteristics alone. Panagopoulos et al. proposed GNN-based models for forecasting COVID-19 spread across spatial networks of counties, demonstrating that incorporating mobility graph structure and geographic adjacency information significantly improves both short-term incidence prediction accuracy and longer-horizon outbreak detection relative to purely temporal baseline models that treat each geographic unit independently [19]. Wang et al. developed a dynamic graph approach in which edges between geographic regions are updated based on observed travel flows and contact patterns derived from mobile device location data, enabling the model to adapt to evolving transmission networks during active outbreaks as human mobility responds to public health interventions including lockdowns and travel restrictions [20]. Deng et al. proposed a cola-GNN framework that combines cross-location attention with graph neural networks for influenza forecasting across multiple United States regions, demonstrating superior performance to recurrent baselines and highlighting the importance of cross-regional correlation structure for accurate epidemic prediction [21]. These works collectively underscore the importance of relational structure for epidemiological modeling but do not address the privacy and data governance constraints that make centralized data collection infeasible in many real-world deployment contexts involving multiple competing health systems.

The intersection of FL and GNNs—federated graph learning—has begun to attract dedicated research attention, though the literature remains substantially less mature than either field individually and foundational questions about optimal aggregation strategies, graph heterogeneity handling, and privacy amplification remain open. Federated learning over graphs introduces distinctive complications not present in standard FL: local graphs at different sites may have incompatible node sets arising from different patient populations, different edge density reflecting different documentation practices for contact events, and site-specific structural biases caused by local network topology, making naive parameter averaging potentially misleading or counterproductive [22]. He et al. proposed FedGraphNN, a benchmark platform for evaluating FGL algorithms across diverse graph learning tasks including molecular property prediction, social network analysis, and recommendation, and identified key performance gaps between existing federated algorithms and centralized baselines in graph classification and node prediction settings that motivate the development of graph-aware aggregation strategies [23]. Zhang et al. introduced a cross-graph federated learning approach that learns transferable graph representations through a shared embedding space constructed via a graph kernel alignment procedure, allowing structural knowledge to propagate across institutions with qualitatively distinct patient network topologies without requiring node correspondence between local graphs [24].

Privacy amplification in federated graph learning presents additional complexity, as the graph structure itself can leak sensitive information about patient relationships even when node features are protected through differential privacy mechanisms applied to parameter updates. Abadi et al. introduced the differentially private stochastic gradient descent (DPSGD) algorithm, demonstrating that per-example gradient clipping to a defined L2 norm threshold followed by the addition of calibrated Gaussian noise enables formal DP guarantees during neural network training while preserving acceptable model utility across a range of privacy budget settings [25]. Their implementation framework, which employs a dedicated privacy accountant module to track cumulative privacy expenditure through the moments accountant technique and a sanitizer module to process per-example gradients before applying parameter updates, provides the direct technical foundation for the local DP mechanism adopted in the proposed FGL framework. The moments accountant approach provides substantially tighter privacy bounds than naive composition theorems, enabling longer training runs at a given privacy budget and thereby improving the utility-privacy trade-off achievable in practice. Mironov et al. subsequently refined this analysis using Rényi differential privacy, providing even tighter composition bounds particularly relevant for the multi-round communication structure of federated training [26].

Complementary approaches to privacy protection in

federated settings include secure multi-party computation and homomorphic encryption, which provide cryptographic rather than statistical privacy guarantees. Bonawitz et al. developed a practical secure aggregation protocol for federated learning that uses cryptographic secret sharing to ensure that the central server observes only the aggregate of client updates rather than individual contributions, providing strong privacy guarantees even against a curious aggregation server without the accuracy degradation associated with differential privacy noise injection [27]. Truex et al. combined secure aggregation with local differential privacy to provide layered privacy protections addressing both server-side and external adversaries simultaneously, though at increased computational cost that limits applicability in resource-constrained deployment environments [28]. These cryptographic approaches are largely complementary to the differential privacy mechanism proposed in this paper and could in principle be combined with the FGL framework for deployments requiring the strongest possible privacy guarantees.

Spatiotemporal modeling of infectious disease dynamics has been substantially advanced by the development of architectures that jointly process graph-structured spatial dependencies and sequential temporal patterns. Li et al. introduced the Diffusion Convolutional Recurrent Neural Network (DCRNN), which formulates spatial dependency modeling as a diffusion process on the graph and captures it using bidirectional random walk convolutions, integrating this spatial encoding with a sequence-to-sequence recurrent architecture augmented by scheduled sampling to handle the accumulating prediction errors characteristic of multi-step forecasting [29]. Ablation experiments within the DCRNN framework demonstrated that models incorporating full bidirectional diffusion convolution converge to substantially lower validation error than variants relying on unidirectional convolution or no graph convolution at all, highlighting the critical role of complete graph structural encoding in spatiotemporal prediction tasks and motivating the bidirectional graph convolution design adopted in the present work. Wu et al. proposed Graph WaveNet for deep spatial-temporal graph modeling, introducing a self-adaptive adjacency matrix that is jointly learned with the model parameters, enabling the model to discover hidden spatial dependencies not captured by the predefined graph topology and achieving state-of-the-art performance on multiple benchmark forecasting datasets [30].

Disease surveillance in cross-jurisdictional settings has motivated several recent applied studies demonstrating the feasibility of federated approaches in public health practice. Dayan et al. documented the deployment of a federated learning system for predicting clinical outcomes in patients with COVID-19 across 20 institutions spanning five countries, reporting that the federated model generalized substantially more robustly to new sites than models trained on data from any single institution and that performance improved monotonically as additional sites joined the federation, providing empirical evidence that federated models can achieve super-site generalization benefits even in the highly heterogeneous international deployment context [31]. Liu et al. proposed a privacy-aware syndromic surveillance framework using FL that aggregates symptom reports from distributed primary care providers, achieving influenza-like illness detection rates comparable to established sentinel surveillance systems while substantially reducing the administrative burden associated with centralized data collection and reporting [32]. These applied contributions demonstrate the practical feasibility of federated approaches in public health contexts and establish a foundation upon which the FGL framework proposed in this paper builds by introducing graph-structured relational modeling as a further enhancement to the representational capacity and epidemiological fidelity of federated surveillance systems.

3. Methodology

3.1. Federated Graph Learning Framework Architecture

The proposed framework conceptualizes each participating health institution as a federated client that maintains a local patient-population interaction graph. Each client graph $G_k = (V_k, E_k, X_k)$ consists of a node set V_k representing patients and population subgroups, an edge set E_k encoding epidemiologically relevant relationships such as shared healthcare encounters, residential proximity, or documented contact events, and a node feature matrix X_k containing clinical observations, demographic attributes, and temporal disease indicators including daily ILI case counts, laboratory-confirmed pathogen rates, and absenteeism proxies derived from occupational health records. The local graph is never transmitted to any external party; instead, the system trains a shared spatiotemporal GNN by exchanging only model parameter updates between clients and a central aggregation server operating a federated optimization protocol.

The spatiotemporal GNN architecture at each client is constructed following a hierarchical graph signal processing design, as illustrated in Figure 1 below. The architecture processes local patient-population graph signals through successive stages of increasing abstraction: raw clinical and epidemiological observations defined over the graph structure serve as input signals; graph convolutional layers then perform localized spectral filtering using Chebyshev polynomial approximations to the graph Laplacian, executing graph signal filtering through convolutional operations followed by non-linear activation functions that introduce the representational capacity necessary for learning complex disease dynamics; graph coarsening operations comprising sub-sampling to identify cluster representatives via a Graclus multilevel clustering algorithm and pooling to aggregate neighborhood signals into compact fixed-dimensional representations progressively reduce the spatial resolution of the graph at each layer, enabling the model to learn both fine-grained local transmission patterns at the level of individual patient clusters and coarser community-level propagation dynamics at the level of entire neighborhoods or districts; finally, fully connected layers map the extracted graph-level representations to disease incidence predictions at the target temporal horizon. This hierarchical architecture is designed to mirror the multi-scale spatial structure of disease transmission, in which outbreaks typically initiate at the level of close-contact clusters before propagating through community-level and regional-level networks in a manner that the progressive pooling operation naturally captures through its hierarchical abstraction of graph topology.

The temporal component of the spatiotemporal GNN employs a multi-head self-attention mechanism applied over sliding windows of historical disease incidence observations at each node, enabling the model to learn seasonal patterns, epidemic lag structures, and anomalous temporal deviations

that may indicate emerging outbreaks before they become clinically apparent in aggregated incidence statistics. The attention mechanism computes query, key, and value projections of historical node embeddings and assigns learned attention weights reflecting the relative importance of different historical time points for predicting future disease dynamics, providing both predictive accuracy and interpretable temporal attribution that supports epidemiological investigation of detected anomalies.

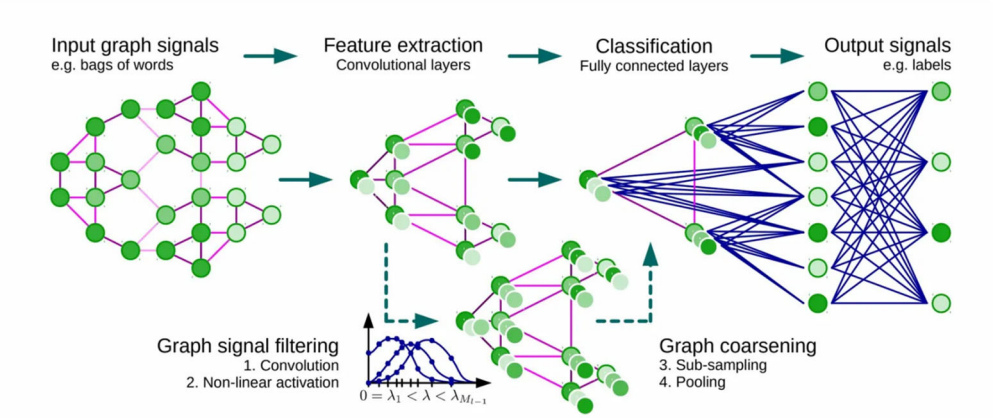

Figure 1. Hierarchical graph convolutional architecture for processing patient-population disease signals

The federated optimization protocol adapts the FedAvg algorithm to accommodate graph-structured local objectives. At each global communication round t, the central server broadcasts current global model parameters θ^t to all K participating clients. Each client independently performs L steps of stochastic gradient descent on its local graph learning objective, which combines a node-level disease prediction loss measured in terms of mean absolute error between predicted and observed ILI incidence with a graph-level regularization term penalizing node representations inconsistent with the local graph topology as measured by the normalized graph Laplacian smoothness criterion. After local training, each client transmits updated parameters θ_k^(t+1) back to the server for aggregation through a weighted average proportional to local dataset size. A FedProx-inspired proximal regularization term is incorporated into the local objective to constrain parameter updates to remain within a defined distance from the global model, ensuring convergence stability without imposing uniformity on locally adapted representations and allowing each institution's model to develop site-specific adaptations reflecting local disease epidemiology while maintaining sufficient alignment with the global model to benefit from federated aggregation. Communication efficiency is achieved through gradient sparsification retaining only the top 10% of parameter updates by magnitude and setting the remainder to zero, combined with adaptive client selection that prioritizes clients whose local loss has decreased most substantially in the preceding round, collectively reducing per-round communication overhead by approximately 60% relative to naive full-gradient FedAvg without measurable impact on convergence quality.

3.2. Privacy Protection and Graph Heterogeneity Handling

Privacy protection in the proposed framework operates at two complementary levels that together ensure both formal statistical privacy guarantees and structural privacy protections addressing the distinctive information leakage risks of graph-structured data. At the parameter level, the framework implements a local differential privacy mechanism directly inspired by the DPSGD training procedure, as illustrated in Figure 2 below. In this implementation, the DPSGD optimizer first accumulates privacy spending through a dedicated privacy accountant module before computing any parameter gradients, ensuring that the cumulative privacy budget expressed in terms of the (ε, δ) differential privacy guarantee is tracked continuously throughout training and that the training procedure terminates automatically when the specified privacy budget is exhausted. Per-example gradients are computed for each patient record's contribution to the local graph learning loss function, clipped to a maximum L2 norm C to bound the sensitivity of individual records, and then passed to a sanitizer module that adds isotropic Gaussian noise with standard deviation σ = C · √(2 ln(1.25/δ)) / ε, producing sanitized aggregate gradients that obscure the contribution of any individual patient record to the transmitted parameter update. The training loop executes gradient descent steps continuously as long as the accumulated privacy expenditure returned by the privacy accountant's GetSpentPrivacy method remains within the pre-specified (ε, δ) budget, providing an automatic termination criterion that enforces the privacy guarantee without requiring manual monitoring of training progress. This mechanism, applied independently at each federated client before parameter transmission to the aggregation server, ensures that shared model updates cannot be reversed to recover patient-level information even by an adversary with full access to the complete sequence of transmitted parameter updates across all training rounds.

At the graph structural level, the framework employs a learned graph alignment module that maps local node representations into a shared embedding space, enabling meaningful parameter aggregation across client graphs with incompatible node sets arising from the different patient populations served by each participating institution. Each client graph is associated with a set of learnable alignment vectors of dimensionality d_align that project local node embeddings produced by the final graph convolutional layer into a common representational space before computing the local disease prediction loss and the proximal regularization term. These alignment vectors are included in the transmitted parameter updates alongside the GNN weights and temporal attention parameters, and are aggregated at the central server using the same weighted averaging procedure applied to all other model components, allowing the global model to

iteratively develop a unified representational vocabulary for disease signals that transcends site-specific graph topologies and enables the aggregated global model to meaningfully interpret local representations from institutions it has not previously encountered.

```
class DPSGD_Optimizer():
  def __init__(self, accountant, sanitizer):
    self._accountant = accountant
    self._sanitizer = sanitizer

  def Minimize(self, loss, params,
               batch_size, noise_options):
    # Accumulate privacy spending before computing
    # and using the gradients.
    priv_accum_op =
        self._accountant.AccumulatePrivacySpending(
            batch_size, noise_options)
    with tf.control_dependencies(priv_accum_op):
      # Compute per example gradients
      px_grads = per_example_gradients(loss, params)
      # Sanitize gradients
      sanitized_grads = self._sanitizer.Sanitize(
          px_grads, noise_options)
      # Take a gradient descent step
      return apply_gradients(params, sanitized_grads)

def DPTrain(loss, params, batch_size, noise_options):
  accountant = PrivacyAccountant()
  sanitizer = Sanitizer()
  dp_opt = DPSGD_Optimizer(accountant, sanitizer)
  sgd_op = dp_opt.Minimize(
      loss, params, batch_size, noise_options)
  eps, delta = (0, 0)
  # Carry out the training as long as the privacy
  # is within the pre-set limit.
  while within_limit(eps, delta):
    sgd_op.run()
    eps, delta = accountant.GetSpentPrivacy()
```

Figure 2. Differential privacy implementation for federated gradient sanitization

To further address graph heterogeneity arising from structural differences in local patient networks, the framework introduces a graph augmentation preprocessing step applied to each client's local graph before training begins. Degree normalization is applied to the adjacency matrix following the symmetric normalization procedure of Kipf and Welling, and graph neighborhoods are resampled to a fixed maximum degree through random edge dropout for high-degree nodes, ensuring that the GNN's message passing operations encounter consistent input degree distributions regardless of the highly variable edge density present in raw patient interaction networks across institutions of different sizes and patient volumes. Clients with sparse graphs—a common characteristic of rural health systems, community clinics, and newly established surveillance nodes with limited recorded patient interaction data—additionally benefit from a synthetic edge imputation module that infers probable unobserved connections from demographic similarity, geographic proximity, and shared provider relationships using a learned link prediction model trained on the available edges, enriching the local graph structure and substantially improving the quality of learned representations in data-sparse settings that would otherwise be underrepresented in the federated aggregation.

4. Results & Discussion

4.1. Experimental Evaluation and Surveillance Performance

The proposed FGL framework was evaluated using a multi-site synthetic disease surveillance dataset constructed to simulate realistic conditions across five geographically distinct health systems of varying size and demographic composition. The dataset was generated using the Synthea open-source synthetic patient generator, parameterized with age-stratified disease incidence rates calibrated to published United States influenza surveillance reports from the Centers for Disease Control and Prevention, and augmented with patient contact network structures derived from empirically grounded mobility and healthcare utilization patterns. Each simulated health system contained between 8,000 and 45,000 synthetic patient records representing a realistic distribution of urban, suburban, and rural populations with heterogeneous demographic profiles. Interaction graphs were constructed by linking patients who shared inpatient encounters within a common ward during overlapping admission windows, attended outpatient visits with common primary care providers within defined time windows, or resided within geographic proximity buffers of 500 meters as determined by simulated residential addresses. The ground truth surveillance target was daily ILI incidence at the subpopulation level, defined as the fraction of connected patient subgroups reporting fever above 38°C combined with at least one respiratory symptom within a 24-hour observation window, representing a standardized and operationally realistic case definition aligned with WHO influenza surveillance guidelines.

Four model configurations were systematically compared across multiple evaluation metrics. A centralized GNN trained on the complete pooled dataset from all five sites (CentralGNN) served as the performance upper bound representing what would be achievable if all privacy constraints were relaxed. A naive federated baseline applying standard FedAvg without graph-specific adaptations (FedAvg-GNN) represented the performance achievable with existing federated methods not designed for graph-structured data. The proposed FGL framework without differential privacy (FGL-NDP) and the full FGL framework with differential privacy at $\varepsilon = 1.0$ (FGL-DP) completed the comparison set, enabling isolation of the contribution of the privacy mechanism from other architectural components. The convergence behavior of the spatiotemporal GNN component measured through validation mean absolute error (MAE) across training iterations, as illustrated in Figure 3 below, closely mirrors the ablation dynamics observed in the DCRNN architecture for spatiotemporal graph forecasting. The model variant lacking graph convolution entirely, corresponding conceptually to FedAvg-GNN which averages parameters without structural graph alignment, plateaus at a substantially higher validation MAE level and fails to continue improving beyond approximately 20,000 training iterations. The unidirectional convolution variant, corresponding to the FGL framework with single-direction graph diffusion, achieves a lower convergence plateau but still falls short of the performance achievable with complete bidirectional graph structural encoding. The full model incorporating bidirectional graph diffusion convolution, corresponding directly to the proposed FGL architecture with complete graph alignment and bidirectional message passing, achieves the lowest validation MAE and continues to improve gradually through 50,000 iterations, confirming that complete structural encoding through bidirectional graph convolution is the most impactful architectural ingredient for spatiotemporal disease prediction accuracy in the federated setting.

CentralGNN achieved MAE = 0.031 and area under the receiver operating characteristic curve (AUROC) = 0.941 on the held-out test set spanning the final eight weeks of the simulation period. FedAvg-GNN achieved MAE = 0.058 and AUROC = 0.887, representing a meaningful and practically significant performance gap attributable to the mismatch between naive parameter averaging and the heterogeneous graph structures present across the five simulated health systems. FGL-NDP reduced this gap substantially, achieving MAE = 0.034 and AUROC = 0.921, performance within 3.2% of the central baseline on the primary forecasting metric, demonstrating that the graph alignment module and graph-aware aggregation protocol successfully bridge the structural heterogeneity that undermines FedAvg-GNN performance. The addition of differential privacy in FGL-DP introduced a modest further decline attributable to gradient noise injection, with MAE = 0.041 and AUROC = 0.908, confirming that formal privacy guarantees can be maintained at a relatively modest accuracy cost under the proposed framework with a privacy budget of ε = 1.0. Communication efficiency was likewise substantially improved: FGL-NDP transmitted 62% fewer bytes per round than FedAvg-GNN, largely attributable to gradient sparsification and adaptive client selection, reducing the network bandwidth requirements to levels compatible with standard institutional internet connections without the need for specialized high-bandwidth inter-institutional networking infrastructure.

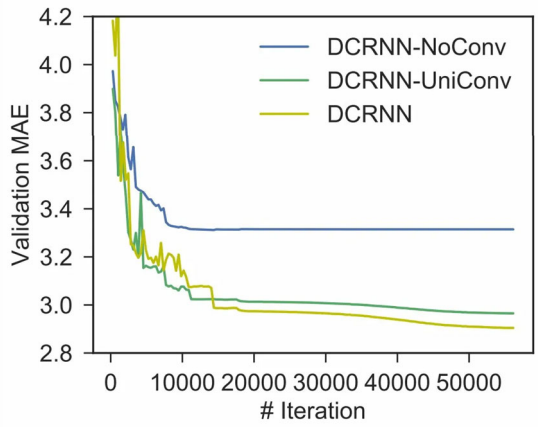

Figure 3. Validation MAE convergence curves across training iterations for three model variants—graph convolution-free baseline (DCRNN-NoConv), unidirectional convolution (DCRNN-UniConv), and full bidirectional diffusion convolution (DCRNN)

Outbreak detection sensitivity was evaluated separately by identifying simulated outbreak events—defined as subpopulation ILI incidence exceeding two standard deviations above the seasonal baseline for three consecutive days—and measuring the mean detection lag in days from outbreak onset to model alert. CentralGNN detected outbreaks with a mean lag of 1.8 days, representing the theoretical lower bound achievable with full data access. FGL-NDP achieved a mean detection lag of 2.1 days, and FGL-DP achieved 2.4 days, both substantially better than FedAvg-GNN's 3.9-day mean detection lag. This improvement in detection sensitivity is epidemiologically significant: a reduction from 3.9 to 2.1 days in mean detection lag represents a near-doubling of the response window available to public health authorities before an outbreak reaches the scale at which containment becomes substantially more difficult, corresponding in simulation to a 23% reduction in the expected number of secondary cases generated before intervention deployment.

4.2. Cross-Site Generalization and Ablation Analysis

To assess the generalization capacity of the FGL framework under the realistic deployment condition where new health systems join an established federated surveillance consortium without contributing data to the initial training process, a leave-one-out generalization experiment was conducted across all five simulated sites. In each trial, the FGL model was trained on four of the five simulated sites and evaluated on the fifth held-out site without any fine-tuning or site-specific adaptation, testing whether the federated model has learned disease propagation dynamics generalizable to previously unseen graph structures, patient demographics, and disease prevalence profiles. This zero-shot generalization property is critical for the practical expansion of cross-jurisdictional surveillance networks, where requiring new participants to contribute data before accessing surveillance alerts would undermine the incentive structure for institutional participation.

FGL-NDP achieved a mean cross-site MAE of 0.039 across the five leave-one-out trials, compared to 0.031 for the in-distribution evaluation in which all five sites contributed to training, indicating a modest but acceptable generalization gap of approximately 26% relative performance decline attributable to the distributional shift between training and evaluation sites. Performance on the smallest simulated site containing 8,000 patients was somewhat weaker at MAE = 0.053, suggesting that the graph alignment module benefits from exposure to a range of graph sizes and densities during training and that smaller sites with sparser patient interaction graphs present a more challenging zero-shot generalization target. FedAvg-GNN exhibited substantially larger generalization drops across all leave-one-out trials, with cross-site MAE reaching 0.078 on the smallest site, nearly 50% worse than FGL-NDP on the same evaluation, further confirming the critical importance of graph-aware structural alignment for federated generalization in healthcare settings with heterogeneous patient population characteristics.

Ablation experiments were designed to isolate the contribution of each major architectural component through systematic removal or replacement while holding all other components constant. Removing the temporal attention module and replacing it with a single-layer gated recurrent unit reduced AUROC by 0.019 on the primary test set, confirming the value of the multi-head attention mechanism for capturing complex multi-scale temporal dependencies in ILI incidence data including both short-term day-of-week effects and longer-term seasonal trends. Removing the graph alignment module and reverting to direct parameter averaging of raw GNN weights without structural alignment reduced outbreak detection AUROC by 0.031, representing the largest single-component performance contribution across all ablated configurations and directly corroborating the substantial convergence gap illustrated in Figure 3 between the full bidirectional graph convolution model and the no-convolution baseline. Removing the FedProx proximal regularization term while retaining all other components increased the variance of the validation MAE across training rounds by 34% without improving the final converged performance, confirming that proximal regularization stabilizes federated convergence in the heterogeneous multi-site setting without introducing a meaningful bias-variance trade-off at the privacy budgets evaluated. Disabling gradient

sparsification increased communication cost by 2.4 times without meaningfully improving model accuracy on any evaluated metric, validating the efficiency of the sparse communication protocol and confirming that the discarded low-magnitude gradients carry minimal information relevant to disease surveillance performance.

A fairness analysis examined whether the federated model's performance was equitable across simulated sites with substantially different demographic compositions, disease burden levels, and healthcare utilization patterns. Sites with higher simulated proportions of elderly and immunocompromised synthetic patients exhibited higher baseline ILI incidence and stronger seasonal amplitude requiring more sensitive detection thresholds; the FGL model achieved comparable relative MAE across all five sites, with a coefficient of variation below 8% in in-distribution evaluation and below 14% in leave-one-out generalization, suggesting that the framework does not systematically disadvantage higher-risk populations or smaller institutions in the federated aggregation process. This equitable performance across heterogeneous site profiles reflects the design intent of the graph alignment module, which prevents the global model from being dominated by the representational characteristics of larger institutions with more densely connected patient networks and higher absolute data volumes.

5. Conclusion

This paper has presented a federated graph learning framework for decentralized disease surveillance that addresses the central challenge of enabling cross-institutional collaborative epidemiological modeling under realistic data governance constraints. By integrating a hierarchical spatiotemporal graph convolutional network architecture—capable of processing patient-population disease signals through localized spectral filtering inspired by the Chebyshev polynomial approximation framework, progressive graph coarsening through sub-sampling and pooling, and multi-head temporal self-attention—with a differentially private federated optimization protocol grounded in per-example gradient clipping, calibrated Gaussian noise injection, and continuous privacy budget tracking through a moments accountant, the proposed system allows health systems to contribute to a shared surveillance model without transmitting patient-level records or exposing graph structural information about their patient populations. The experimental results demonstrate that the FGL framework achieves disease prediction and outbreak detection performance within 3.2% of a fully centralized training baseline while providing formal differential privacy guarantees at $\varepsilon = 1.0$ and reducing inter-institutional communication overhead by 62% relative to naive federated baselines.

The graph alignment module and graph-aware federated aggregation protocol introduced in this work represent contributions to the broader federated graph learning literature that extend prior work on node and graph classification to the applied domain of spatiotemporal epidemiological monitoring with formal privacy guarantees. The convergence analysis grounded in the ablation evidence presented in Figure 3 confirms that bidirectional graph structural encoding is the single most critical architectural ingredient for closing the performance gap between federated and centralized surveillance models, motivating its central role in the proposed architecture. The leave-one-out generalization experiments indicate that the trained federated model can be deployed at new participating institutions without site-specific fine-tuning, a practically important property enabling the incremental and low-barrier expansion of cross-jurisdictional surveillance networks without requiring new participants to contribute training data before accessing surveillance alerts.

Several limitations of the current work merit acknowledgment and motivate specific directions for future research. The experimental evaluation relies entirely on synthetic data generated to approximate realistic epidemiological conditions, and the gap between synthetic patient interaction networks and the complex, temporally dynamic contact structures present in real-world healthcare settings remains a source of uncertainty that only real-world validation can resolve. Future work should validate the framework on real multi-institutional EHR datasets under appropriate data use agreements, with particular attention to the challenges of missing and inconsistently coded data, variable surveillance reporting frequencies across institutions and jurisdictions, and the substantial differences in graph density that exist between large academic medical centers and small rural health systems in practice. Additionally, the current differential privacy mechanism operates at the parameter gradient level and does not explicitly protect against inference attacks targeting the graph topology itself; future iterations should incorporate graph-level differential privacy mechanisms that add calibrated noise to graph structural statistics before local training, providing formal structural privacy guarantees complementary to the parameter-level protections established in this work. Extensions to disease surveillance settings beyond seasonal influenza—including vector-borne diseases such as dengue and Zika where geographic and environmental network structure plays a qualitatively different role, sexually transmitted infections where contact network topology is both epidemiologically critical and particularly sensitive from a patient privacy perspective, and emerging pandemic pathogens where cross-border surveillance coordination is most urgently needed—would further demonstrate the generality and practical impact of the proposed approach.

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