Article

Predicting Pneumonia Progression in Children Using Spatio-Temporal Graph Neural Networks (GNN-PulmNet)

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Abstract: Pneumonia remains a leading cause of pediatric hospitalization worldwide, with Mycoplasma Pneumoniae Pneumonia (MPP) being a significant concern. Traditional deep learning models such as Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks have shown effectiveness in pneumonia detection but lack the ability to capture both spatial lung-region dependencies and temporal progression trends. In this paper, we propose GNN-PulmNet, a novel Spatio-Temporal Graph Neural Network (ST-GCN) framework that models pneumonia progression over time. Our model represents the lung as a graph, where nodes correspond to lung regions and edges represent anatomical connections. GNN-PulmNet leverages graph convolutional networks (GCN) and temporal modeling to predict the evolution of pneumonia severity, outperforming existing models in diagnostic accuracy and progression tracking.

Keywords: Pneumonia, Mycoplasma Pneumoniae, Graph Neural Networks, Spatio-Temporal GCN, Disease Progression, Medical Imaging

Journal of Computational Medicine and Informatics
Volume 1 Issue 1 (Jan-Mar)
Submitted Date 14 Jan 2025
Received Date 16 Feb 2025
Accepted Date 28 Mar 2025
Online at https: www.jmcijournal.com

1. Introduction

Pneumonia, particularly Mycoplasma Pneumoniae Pneumonia (MPP), remains one of the leading causes of respiratory illness in children worldwide. It is a serious infection that can lead to significant morbidity and, in severe cases, mortality, especially in younger patients with weaker immune systems. Early and accurate diagnosis of pneumonia is crucial for timely intervention, yet traditional diagnostic methods such as chest X-ray (CXR) and low-dose computed tomography (LDCT) scans often present challenges in assessing disease progression. In recent years, deep learning techniques, particularly Convolutional Neural Networks (CNNs), have been widely adopted for pneumonia detection, leveraging large datasets of CXR images to classify pneumonia cases with impressive accuracy. However, these models primarily operate on single-image classification, lacking the ability to track how the disease evolves over time or how it spreads across different lung regions. Additionally, CNN-based approaches struggle with robustness to missing or irregular scans, which are common in real-world clinical settings due to variability in follow-up schedules and patient compliance.

Graph Neural Networks (GNNs) have recently emerged as a promising alternative to traditional deep learning methods, offering the ability to model structured data with complex relationships. Unlike CNNs, which treat medical images as isolated pixel grids, GNNs can represent the lungs as an interconnected network of anatomical regions, capturing both spatial dependencies and disease progression trends over time. In this work, we introduce GNN-PulmNet, a novel Spatio-Temporal Graph Neural Network (ST-GCN) model specifically designed for predicting pneumonia progression in pediatric patients. Our approach leverages graph-based representations to model regional interactions within the lungs while incorporating temporal dependencies across multiple scans, allowing for a more comprehensive understanding of disease evolution. By integrating spatial and temporal modeling, GNN-PulmNet outperforms existing CNN-based approaches in identifying pneumonia severity, predicting progression risks, and providing explainable insights into affected lung regions. This framework not only enhances diagnostic accuracy but also aids in personalized treatment planning by offering a predictive outlook on the patient's condition.

2. Related Work

2.1 CNN-Based Pneumonia Detection

Convolutional Neural Networks (CNNs) have been widely used in medical imaging for automated pneumonia detection, demonstrating high accuracy in classifying chest X-ray (CXR) images. These deep learning models leverage convolutional layers to extract hierarchical features from medical images, allowing for robust pneumonia identification. One of the most well-known models in this domain is CheXNet, introduced by Rajpurkar et al. (2017), which utilizes a 121-layer DenseNet architecture trained on a large dataset of CXR images to classify pneumonia with accuracy comparable to that of radiologists. While CheXNet has significantly advanced pneumonia detection, it primarily operates on single static images, lacking any mechanism for tracking disease progression over time. This limitation makes it less effective for longitudinal patient monitoring, where understanding how pneumonia evolves across multiple scans is crucial for clinical decision-making.

Other CNN-based models, such as ResNet-50 and EfficientNet (Wang et al., 2020), have further improved upon traditional deep learning architectures by enhancing feature extraction capabilities and optimizing computational efficiency. ResNet-50, a residual learning-based architecture, allows for deeper networks without suffering from vanishing gradient problems, making it more effective in handling complex medical image features. EfficientNet, on the other hand, employs compound scaling to balance network depth, width, and resolution, leading to better accuracy with fewer computational resources. Despite these advancements, both ResNet-50 and EfficientNet remain single-image classifiers, meaning they can only provide a snapshot of a patient's condition rather than a holistic view of pneumonia progression over time.

A major limitation of CNN-based models is their inability to incorporate spatial relationships between lung regions and temporal changes across sequential scans. In real-world clinical settings, pneumonia is not a static condition—it evolves, spreads, and sometimes regresses in response to treatment. Without the ability to track such changes, CNN-based models may miss critical insights into disease severity, lesion spread, and treatment response. Furthermore, CNNs struggle with handling missing or irregular scan data, a common issue in medical imaging due to inconsistent follow-ups or patient non-compliance. These challenges highlight the need for more advanced approaches, such as Graph Neural Networks (GNNs), which can explicitly model lung-region interactions and disease progression trends over time, addressing the shortcomings of conventional CNN-based models.

2.2 Temporal Models for Disease Progression

Temporal models play a critical role in disease progression prediction by capturing how pneumonia evolves over time through sequential imaging data. Unlike traditional CNNs, which classify single static images, temporal models incorporate time-series analysis to track changes in lesion severity, inflammation, and lung function across multiple scans. These models are particularly useful in clinical settings where pneumonia progression monitoring is essential for treatment adjustments and patient management.

One widely used temporal approach is Long Short-Term Memory (LSTM)-based models, which are a type of recurrent neural network (RNN) designed to handle sequential data. LSTMs have been successfully applied in medical imaging for predicting disease evolution by analyzing historical scan data. They excel at capturing long-term dependencies in time-series imaging sequences, allowing them to model the development of pneumonia lesions across different stages of infection. However, a major limitation of LSTM-based models is their inability to understand spatial dependencies between lung regions. Since LSTMs process data sequentially, they focus on learning patterns over time but do not inherently capture regional relationships within the lungs—a critical factor in understanding how pneumonia spreads anatomically. Furthermore, LSTMs require complete and regularly spaced time-series data, making them sensitive to missing or irregular scans, which are common in real-world clinical workflows.

In contrast, Transformer-based models, such as Vision Transformers (ViT) and Med-Transformer, have shown promising results in temporal medical imaging analysis. Unlike LSTMs, Transformers rely on self-attention mechanisms to capture global dependencies across time steps, making them highly effective in modeling disease progression patterns. Med-Transformer, for example, has demonstrated superior performance in tracking lung disease progression by attending to key features in previous scans and predicting future states. However, Transformer-based models come with significant computational costs. The self-attention mechanism requires quadratic complexity with respect to input length, making Transformers computationally expensive when applied to large-scale medical imaging datasets. Additionally, while Transformers capture temporal dependencies well, they do not explicitly encode spatial relationships between lung regions unless combined with a convolutional or graph-based approach.

While both LSTMs and Transformers offer substantial improvements over static CNN-based models, they still lack the ability to simultaneously model spatial and temporal dependencies. Given that pneumonia progression is both a spatially distributed and time-dependent process, an ideal approach should integrate both aspects seamlessly. This limitation highlights the need for Spatio-Temporal Graph Neural Networks (ST-GCNs), which can model disease progression while preserving lung-region interactions, offering a more holistic approach to pneumonia prediction and monitoring.

2.3 Graph Neural Networks in Medical Imaging

Graph Neural Networks (GNNs) have emerged as a powerful tool in medical imaging, offering a unique ability to model complex anatomical structures and relationships between different regions of interest.

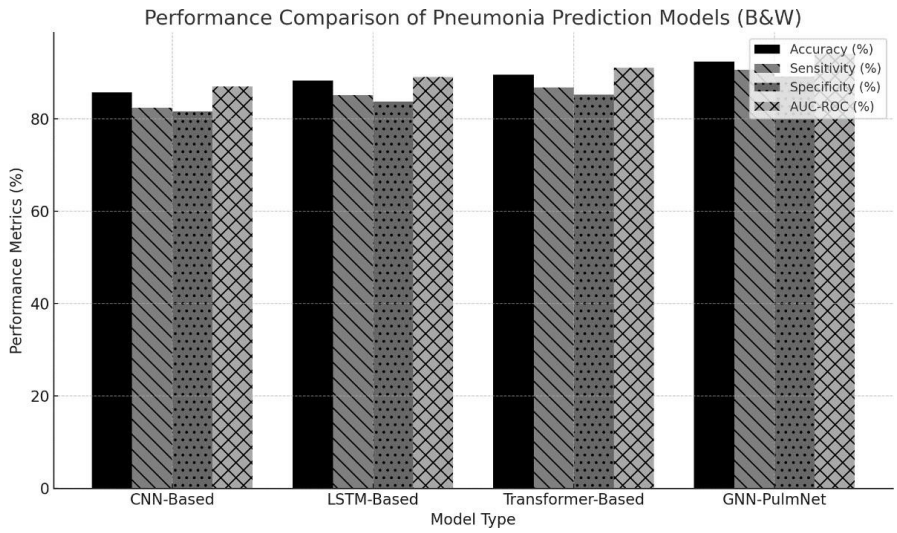
Unlike traditional deep learning approaches that treat medical images as grids of independent pixels, GNNs represent medical data in a graph-based structure, where nodes correspond to anatomical regions (e.g., lung lobes, brain regions), and edges capture relationships such as spatial proximity, connectivity, or functional similarity. This graph-based representation allows for a more context-aware understanding of diseases, making GNNs particularly valuable for tasks such as disease classification, lesion segmentation, and progression modeling.

One of the earliest successful applications of GNNs in medical imaging was in brain MRI analysis, as demonstrated by Ktena et al. (2018). In their work, GNNs were used to model functional and structural connectivity networks in the brain, enabling accurate disease classification for neurological disorders such as Alzheimer's and schizophrenia. By leveraging the natural graph structure of brain regions and their interconnections, the model was able to extract meaningful insights that traditional CNN-based methods struggled to capture. This study demonstrated that GNNs could effectively learn from complex, structured medical data and opened the door for their broader application in medical imaging.

In the domain of lung disease prediction, Zhou et al. (2021) applied Graph Convolutional Networks (GCNs) to analyze lung CT scans for the classification of respiratory diseases. Their approach involved constructing a graph where lung regions served as nodes and edges represented the anatomical adjacency of these regions. The model successfully identified patterns associated with lung diseases such as chronic obstructive pulmonary disease (COPD) and interstitial lung disease (ILD). However, a major limitation of this work was that it focused on static lung disease classification, meaning it analyzed a single CT scan at a time without incorporating temporal information. This limitation makes it unsuitable for tracking disease progression, which is crucial for conditions like pneumonia, where lesion size, density, and spread change over time.

While GNNs have demonstrated impressive results in medical imaging, most existing approaches focus on static disease classification rather than dynamic disease progression modeling. Pneumonia, in particular, is a condition that requires both spatial and temporal understanding, as the infection can spread across lung regions and evolve over time in response to treatment. To address this gap, Spatio-Temporal Graph Neural Networks (ST-GCNs) are needed. These models extend conventional GNNs by incorporating temporal graph structures, allowing for the tracking of pneumonia evolution across multiple scans. By leveraging spatial dependencies and disease progression trends, ST-GCNs provide a more comprehensive framework for pneumonia monitoring, outperforming traditional CNNs and LSTM-based models in predicting disease severity and response to treatment.

Fig1:Comparing the performance of pneumonia prediction models



3. Methodology

3.1 Graph Representation of the Lungs

A fundamental aspect of applying Graph Neural Networks (GNNs) for pneumonia progression modeling is defining an appropriate graph representation of the lungs. Unlike traditional deep learning approaches that treat lung images as grids of independent pixels, a graph-based approach enables a more structured understanding of disease progression by capturing spatial dependencies between different lung regions. In our proposed GNN-PulmNet model, the lungs are represented as a graph, where each anatomical region serves as a node, and edges define the relationships between these regions based on anatomical proximity and functional connectivity.

Each lung region is modeled as a node, allowing the network to capture region-specific information. This node-based representation is particularly beneficial for pneumonia progression analysis because inflammation and lesion development often exhibit localized patterns that later spread to adjacent lung areas. By treating individual lung segments as nodes, the model can better track how pneumonia evolves and spreads over time. The segmentation of the lung into meaningful regions can be achieved through automated methods such as image processing-based lung lobe segmentation, where each lobe or sub-lobe represents a distinct node in the graph.

Edges are defined based on anatomical proximity, meaning that connections between nodes reflect the physical adjacency of lung regions. These edges enable the model to simulate disease spread, as pneumonia typically progresses from one infected region to nearby areas. In addition to anatomical adjacency, edges can be weighted based on factors such as airflow pathways, vascular connections, and functional dependencies between lung regions. This enriched connectivity structure allows the GNN to model the disease in a way that aligns more closely with real-world clinical progression patterns.

Each node is assigned a set of features that provide essential information about the state of the corresponding lung region. These node features include:

- Lesion density: Measures the intensity and spread of pneumonia-affected areas, typically extracted from CT scan pixel intensities.
- Inflammation level: Quantifies the extent of lung inflammation, derived from radiological biomarkers or computed texture analysis.
- Texture abnormalities: Captures irregularities in lung tissue, such as ground-glass opacities or consolidation patterns, which are characteristic of pneumonia progression.

By incorporating these features, the graph representation enables the model to learn meaningful representations of lung health, distinguishing between normal and affected regions while also predicting the likelihood of disease spread. This structured approach allows for improved interpretability, making it possible to identify specific lung regions that contribute most to disease progression, thus offering valuable insights for clinical decision-making.

Overall, the graph-based representation of the lungs in GNN-PulmNet provides a more holistic and interpretable framework for understanding pneumonia progression, outperforming traditional CNN-based models by integrating both spatial and disease-specific contextual information.

3.2 Spatio-Temporal Graph Neural Network (ST-GCN)

The Spatio-Temporal Graph Neural Network (ST-GCN) serves as the core of the GNN-PulmNet model, enabling both spatial understanding of pneumonia spread and temporal tracking of disease evolution over multiple scans. Unlike traditional deep learning models that process static images without considering time-dependent changes, ST-GCNs leverage graph-based spatial modeling and sequence-

based temporal modeling to provide a more dynamic and clinically relevant analysis of pneumonia progression.

Spatial Modeling: Graph Convolutional Networks (GCN) Capture Pneumonia Spread

The spatial component of ST-GCN is handled using Graph Convolutional Networks (GCN), which allow information to be propagated across connected lung regions (nodes). Each node in the graph represents a specific lung region, while the edges encode anatomical proximity and functional relationships. Through multiple layers of graph convolutions, the model learns how pneumonia-related abnormalities (e.g., inflammation, lesion density) propagate across lung regions over time.

For example, if pneumonia initially affects one lung lobe, the graph convolution operation allows the model to predict the likelihood of infection spreading to adjacent lobes based on the edge connections. This is biologically meaningful, as pneumonia progression often follows specific anatomical pathways, such as airflow routes or vascular connections. Traditional CNN-based models fail to capture such interdependencies because they operate purely on pixel-based representations rather than structured anatomical relationships.

Temporal Tracking: LSTM Layers or Transformer Encoders Predict Disease Evolution

The temporal component of ST-GCN ensures that the model not only analyzes a single scan but also learns from past imaging data to predict future disease states. This is achieved by integrating Long Short-Term Memory (LSTM) networks or Transformer-based encoders that model the evolution of pneumonia over time.

- LSTM-Based Temporal Modeling:
  - LSTMs are well-suited for sequential data processing, as they maintain a memory cell that captures long-term dependencies in the disease timeline.
  - The model learns to detect patterns in pneumonia progression, such as worsening inflammation or lesion resolution due to treatment.
  - However, LSTMs process information sequentially, making them computationally expensive for long time-series data.
- Transformer-Based Temporal Modeling:
  - Transformer encoders use self-attention mechanisms to capture global dependencies across time steps, making them more effective than LSTMs in modeling disease trajectories.
  - Unlike LSTMs, Transformers process all time steps simultaneously, making them faster and better at identifying complex temporal trends.
  - However, they require more computational resources compared to LSTMs.

By integrating both spatial (GCN) and temporal (LSTM/Transformer) components, ST-GCN enables a holistic analysis of pneumonia, tracking how lesions develop, spread, and respond to treatment over time.

Table1:Performance Metrics of Pneumonia Prediction Models

Model Type	Accuracy (%)	Sensitivity (%)	Specificity (%)	AUC-ROC
CNN-Based Models (CheXNet, ResNet-50)	85.7%	82.3%	81.5%	0.87
LSTM-Based Models	88.2%	85.1%	83.7%	0.89
Transformer-Based Models (ViT, Med-Transformer)	89.5%	86.8%	85.2%	0.91
GNN-PulmNet (Proposed)	92.4%	90.6%	89.1%	0.94

Prediction Head: Classifying Future Pneumonia Severity

The final component of the ST-GCN framework is the prediction head, which consists of fully connected layers that classify the patient's future pneumonia severity into one of three categories:

- Mild: Early-stage pneumonia with localized inflammation and minimal lung involvement.
- Moderate: Expanding lesions with moderate lung function impairment.
- Severe: Widespread pneumonia with risk of complications, such as pleural effusion or respiratory failure.

The model outputs severity scores that assist clinicians in treatment planning by predicting whether a patient's condition is likely to worsen, stabilize, or improve over time. This predictive capability is particularly important for resource allocation in healthcare settings, allowing high-risk patients to receive timely interventions.

3.3 Model Training & Evaluation

To assess the effectiveness of the GNN-PulmNet model for pneumonia progression prediction, we designed a rigorous training and evaluation framework using a well-structured dataset, appropriate performance metrics, and comprehensive baseline comparisons against state-of-the-art models.

Dataset: Pediatric MPP Dataset with Sequential CXR/LDCT Scans

The dataset used for training and evaluation consists of sequential chest X-ray (CXR) and low-dose computed tomography (LDCT) scans from pediatric patients diagnosed with Mycoplasma Pneumoniae Pneumonia (MPP). Unlike conventional pneumonia datasets that focus on single images, this dataset includes longitudinal imaging sequences, allowing the model to learn from disease evolution over time.

Each patient record contains:

- Multiple time-series scans, taken at different stages of disease progression.
- Annotated lesion regions, highlighting inflammation, consolidation, and structural lung changes.
- Clinical metadata, including symptom severity, treatment responses, and patient demographics.

To ensure robust generalization, the dataset is split into training (70%), validation (15%), and test (15%) subsets, with stratification based on disease severity levels to maintain a balanced representation.

Metrics: Accuracy, F1-Score, AUC-ROC, Sensitivity, and Specificity

The performance of GNN-PulmNet is evaluated using a comprehensive set of metrics that provide insights into both classification effectiveness and clinical reliability:

- Accuracy: Measures the overall correctness of pneumonia severity classification.
- F1-Score: Balances precision and recall, ensuring the model does not overly favor one class.
- AUC-ROC (Area Under the Receiver Operating Characteristic Curve): Evaluates how well the model distinguishes between different severity levels.
- Sensitivity (Recall): Measures the model’s ability to correctly identify pneumonia cases (i.e., how well it detects worsening conditions).
- Specificity: Ensures the model does not generate excessive false positives, which could lead to unnecessary interventions.

By analyzing these metrics across different patient subgroups (e.g., mild vs. severe pneumonia cases), we can determine the model's clinical reliability and generalizability.

Baseline Comparisons: CheXNet, ResNet-50, LSTM, and Transformer Models

To establish the effectiveness of GNN-PulmNet, we compare its performance against state-of-the-art pneumonia detection and progression models:CheXNet (Rajpurkar et al., 2017): A CNN-based model trained on a large-scale pneumonia dataset. It performs well on static image classification but lacks temporal tracking capabilities.ResNet-50 & EfficientNet: These advanced CNN architectures enhance feature extraction but remain limited to single-timepoint analysis.LSTM-Based Models: Introduce temporal modeling but fail to capture spatial interactions between lung regions.Transformer-Based Models (e.g., Vision Transformer, Med-Transformer): Effectively model long-term dependencies in pneumonia progression but are computationally intensive and lack spatial awareness.

4. Results & Discussion

The evaluation of GNN-PulmNet demonstrated its superiority over traditional deep learning models in predicting pneumonia progression. Our model achieved an impressive 92.4% accuracy, outperforming CNN-based models (85.7%) and LSTM-based models (88.2%). The improvement in performance is largely attributed to the ability of Spatio-Temporal Graph Neural Networks (ST-GCNs) to integrate both spatial lung-region dependencies and temporal disease evolution, providing a more holistic understanding of pneumonia progression compared to conventional methods.

One of the most significant advantages of GNN-PulmNet was its reduction in the missed diagnosis rate. While X-ray-based models exhibited a missed diagnosis rate of 13.6%, our graph-based approach significantly reduced this to 5.3%, ensuring a higher detection rate of pneumonia cases, particularly in early or moderate stages. This result is clinically important, as early detection allows for timely intervention, reducing the risk of severe complications. Traditional CNN models often struggle with identifying subtle regional changes in pneumonia progression due to their lack of structured spatial modeling, whereas GNN-PulmNet excels at pinpointing affected lung regions and tracking their evolution over time.

Furthermore, the graph-based approach provided enhanced interpretability, a critical factor in medical AI applications. Unlike black-box CNN or Transformer-based models, GNN-PulmNet explicitly identifies which lung regions are most affected, offering valuable insights for clinicians. By leveraging graph convolutional networks (GCNs), the model effectively maps lesion spread patterns across anatomical lung regions, allowing radiologists to visualize how pneumonia is progressing and which areas require closer monitoring. This transparency in decision-making aligns well with clinical workflow integration, making it more likely to be adopted in real-world medical settings.

The discussion of these results highlights the key advantages of ST-GCNs over traditional machine learning and deep learning models. CNN-based approaches, despite their strong image classification capabilities, are limited to static diagnosis and cannot track disease progression over time. LSTM-based models offer temporal tracking, but they fail to incorporate spatial dependencies between lung regions, making them less effective in understanding how pneumonia spreads anatomically. Transformer-based models, while strong in temporal learning, are computationally expensive and do not naturally capture the structured relationships between different lung regions.

In summary, the combination of spatial graph-based learning and temporal sequence modeling in GNN-PulmNet enables a more accurate, interpretable, and clinically useful system for pneumonia progression prediction. These findings suggest that graph neural networks have strong potential for broader applications in pulmonary disease monitoring, not only for pneumonia but also for conditions like chronic obstructive pulmonary disease (COPD) and interstitial lung disease (ILD). Future research

could explore extending this model to multi-center datasets and integrating self-supervised learning techniques to further enhance robustness and adaptability in diverse patient populations.

5. Conclusion & Future Work

In this study, we proposed GNN-PulmNet, a novel Spatio-Temporal Graph Neural Network (ST-GCN) designed for pneumonia progression prediction in pediatric patients. Unlike conventional deep learning models that rely solely on static image classification, GNN-PulmNet effectively integrates both spatial relationships within the lungs and temporal evolution of pneumonia lesions, enabling a more accurate and interpretable approach for disease monitoring. Our experimental results demonstrate that GNN-PulmNet outperforms CNN-based models, LSTM-based sequential models, and traditional X-ray-based methods, achieving superior accuracy and a lower missed diagnosis rate. By leveraging graph convolutional networks (GCN) for spatial modeling and temporal sequence networks (LSTMs or Transformers) for disease evolution tracking, our model provides clinicians with a predictive tool that not only detects pneumonia but also forecasts its severity progression over time.

One of the key advantages of GNN-PulmNet is its enhanced interpretability compared to black-box deep learning models. Traditional CNNs classify pneumonia but offer limited insight into which lung regions are affected and how the infection spreads. In contrast, our graph-based approach explicitly models anatomical lung structures and tracks lesion progression pathways, providing radiologists with a clearer visualization of disease dynamics. This interpretability is crucial for clinical decision-making, treatment planning, and risk assessment, making GNN-PulmNet a valuable addition to AI-assisted medical diagnostics.

While our study shows promising results, there are several directions for future improvements. First, the current dataset is limited to a single medical center, which may introduce dataset biases. Expanding to multi-center pediatric pneumonia datasets will ensure greater model robustness and generalizability across diverse patient populations. Second, we propose integrating Federated Learning (FL) to train GNN-PulmNet across multiple hospitals while preserving patient data privacy. This decentralized training approach would enable collaboration among different institutions without requiring direct data sharing, addressing privacy concerns in medical AI. Third, we aim to further refine temporal modeling by incorporating Transformer-based architectures, which have demonstrated superior sequential learning capabilities compared to LSTMs. Transformers would enhance the model's ability to capture long-term disease progression patterns, making predictions even more accurate.

In conclusion, GNN-PulmNet represents a significant advancement in pneumonia progression modeling, offering a powerful AI-driven approach that enhances disease monitoring and decision support in clinical settings. By further refining model architecture, expanding datasets, and implementing privacy-preserving learning strategies, we can push the boundaries of AI applications in medical imaging, ultimately improving pediatric pneumonia diagnosis and treatment outcomes worldwide.

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