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TEMPORAL GRAPH CONVOLUTIONAL NETWORKS FOR PREDICTING DISEASE OUTBREAKS IN PUBLIC HEALTH SURVEILLANCE

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ABSTRACT

Aim/Purpose	A new predictive model for disease outbreak prediction is to be developed using Temporal Graph Convolutional Networks (TGCNs).
Background	The emergence and spread of contagious diseases seriously threaten public health systems worldwide. Early diagnosis and disease outbreak prediction are necessary to implement quick solutions and reduce their impacts. Present methods often overlook the complex connections between many factors influencing disease transmission, such as population dynamics, temporal trends, and spatial proximity. To overcome these limitations, we introduce TGCNs as a novel paradigm for disease outbreak prediction.
Methodology	Temporal convolutional and graph neural networks are coupled in TGCN models to reflect spatiotemporal dependencies in disease spread. The degree of interaction between different locations is shown by edges in a graph, and this spatial relationship forms the foundation of the graph structure. Using this proposed method, temporal convolutional layers, and graph convolutional layers, TGCNs learn temporal patterns in disease incidence data and geographical representations of nodes.
Contribution	The main research problem in this research is to tackle and develop a prediction model that can accurately predict disease outbreaks based on diverse data sources, which mainly focus on the application of temporal surveillance data and geographical relationship information. In this research work, the objective is to describe the dynamics and underlying structure of disease transmission networks throughout time and to harness the capabilities of graph convolutional networks (GCN), which precisely forecast and focus on future outbreak episodes.
Findings	The TGCNs outperformed state-of-the-art methods for disease outbreak prediction using the disease surveillance datasets. Through the effective application of both temporal and spatial information strategies, TGCNs show strong performance across various disease types and geographical areas, which helps to achieve better results and accuracy on an enhanced proposed method.
Recommendations for Researchers	Investigations should prioritize the validation of the algorithm in various healthcare environments to assess its efficacy in clinical application.
Future Research	In future research, this work can be enhanced using several deep learning algorithms to achieve better accuracy and performance.
Keywords	disease, public health, temporal graph convolutional networks, spatiotemporal dynamics, prediction

INTRODUCTION

Predicting and monitoring disease epidemics are top priorities in public health. In terms of and focus on current industry 4.0 growth and global economic factors, we need to adopt several AI technologies in terms of protecting and controlling the spread of infectious diseases (L. Wang et al., 2022). It is difficult work to make accurate predictions, nevertheless, because of the complex connections between many factors influencing disease transmission dynamics (Yu et al., 2023). The intricacy of these relationships makes it challenging for conventional surveillance methods to capture them, leading to suboptimal forecast performance.

Background

Infectious diseases still endanger public health worldwide, and epidemics cause high rates of morbidity, mortality, and financial expense. Historically, the manual interpretation of disease incidence data and the passive reporting employed by surveillance systems have hindered the discovery of epidemics. Even though recent advancements in data collection technology have made large-scale spatiotemporal datasets easier to produce, it is still extremely challenging to extract meaningful insights from these data (Fritz et al., 2022).

Challenges

Considering the complex dynamics of disease spread along both temporal and spatial dimensions is one of the several challenges in disease outbreak forecasting (Siji Rani et al., 2023). Precise forecasting is challenging because disease transmission networks are dynamic and comprise components including population movements, environmental conditions, and pathogen change. Standard modeling techniques also often fail to adapt to shifting epidemiological patterns and disregard the variety of transmission routes (Ma et al., 2022).

Problem Definition

The main research problem in this research is to tackle and develop a prediction model that can accurately predict disease outbreaks based on diverse data sources, which mainly focus on the application of temporal surveillance data and geographical relationship information. In this research work, we aim to overcome the issues and challenges in the existing research work and emulate the spatiotemporal dynamics of disease transmission networks. Our main goal is to focus on and improve the prediction abilities of surveillance systems, which help to provide quick responses and reactions to reduce the impact of infectious diseases.

Objectives

The major objectives of our investigation are summed up as follows:

1. One new predictive model for disease outbreak prediction is to be developed using Temporal Graph Convolutional Networks (TGCNs).
2. The rich spatiotemporal information found in disease surveillance data is used to derive the basic dynamics of disease transmission networks.
3. To evaluate and compare the proposed model with state-of-the-art methods on real surveillance datasets.

Novelty and Contributions

Temporal modeling techniques with graph convolutional networks to represent the complex interdependencies of disease transmission dynamics are achieved. Temporal patterns in disease incidence data and detailed descriptions of the spatial connectivity between locations enable disease outbreak prediction. We have contributed a new predictive model, evaluated its performance on several datasets, and comprehended its practical applications in public health monitoring and response actions. Our work advances the state of the art in predicting disease outbreaks and supports ongoing initiatives to strengthen global health security.

Scope

The research focuses specifically on predicting disease outbreaks for infectious diseases with significant public health implications, such as influenza, dengue fever, and other contagious viral diseases. The study emphasizes leveraging temporal surveillance data and spatial relationships to model and forecast outbreaks in urban and densely populated regions where accurate and timely predictions can have the most significant impact.

LIMITATIONS

1. The predictive model is primarily validated using datasets from specific geographical regions, limiting its generalizability to regions with similar demographic, environmental, and healthcare infrastructure characteristics.
2. The accuracy of the model depends on the quality and completeness of the data. Limited access to high-resolution spatiotemporal data or missing data from underdeveloped regions may affect performance.
3. The study focuses on structured data sources such as government surveillance reports, population movement data, and climate datasets. Unstructured or real-time data sources like social media trends are not considered.
4. The model is designed to handle infectious diseases with relatively well-understood transmission dynamics and may be less effective for emerging or poorly understood diseases with complex or unknown transmission pathways.

RELATED WORKS

Many approaches have been made to address the critical role of disease outbreak prediction in public health surveillance. In this section, we review pertinent research on several aspects of disease outbreak prediction and cover machine-learning techniques, traditional statistical approaches, and current advances in spatiotemporal modeling (Du et al., 2021).

Time series analysis and autoregressive models were the main statistical models utilized in early disease outbreak prediction techniques (Y. Wang et al., 2022). Usually, based on seasonal and temporal trends, these methods use historical surveillance data to predict the occurrence of diseases in the future. Conventional statistical models, although simple and intuitive, sometimes struggle to capture the complex dynamics of networks of disease transmission and might not account for non-linear interactions or spatial dependencies (Oliveira et al., 2022).

As machine learning techniques have developed, interest in using computer models to improve disease outbreak prediction has grown. Support vector machines (SVM), random forests, and neural networks have been applied to processing surveillance data and discovering characteristics predictive of disease outbreaks (Li et al., 2022). Many data sources can be integrated, and complex connections between variables can be investigated thanks to scalable and flexible machine-learning techniques. Still, issues with class imbalance, handling high-dimensional data and ensuring the interpretability of models exist (La Gatta et al., 2021).

Recently, advances in spatiotemporal modeling have led to the development of sophisticated frameworks for disease epidemic prediction. Particularly, graph-based techniques are being utilized more and more to track the spread of infectious diseases and mimic the spatial connectivity between geographical locations (Song et al., 2023). Complex networks of disease transmission have been modeled, and future epidemic events are predicted based on temporal dynamics and spatial connections (Lv et al., 2021).

An interesting development in disease outbreak prediction is the use of clinical, environmental, and social media data. By combining information from numerous sources, researchers seek to improve the accuracy of predictive models and boost early outbreak detection (da Silva et al., 2021). The complementing character of several data modalities has been exploited to enhance prediction performance by means of ensemble learning, feature engineering, and data fusion (Liu et al., 2024).

As the area of disease epidemic prediction grows, efforts have been made to unify evaluation metrics and benchmark datasets to allow comparisons across many methodologies. Academics can evaluate their predictive models on real monitoring data and progress the development of effective forecasting systems through projects like the Global Epidemic Prediction Initiative (EPI) and Predict the Next Pandemic (PREDICT) (Liu et al., 2024).

PROPOSED METHOD

TGCN is a new framework designed to forecast disease outbreaks by integrating temporal modeling techniques with GCNs. The vast spatiotemporal information included in disease surveillance data is employed by TGCNs to record the dynamic changes in disease transmission networks (Figure 1).

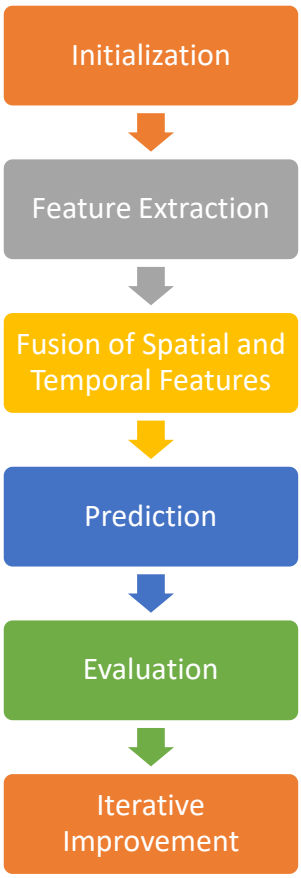

Figure 1. Proposed TGCNs method

GRAPH CONSTRUCTION

Graph Building TGCNs begin with the construction of a graph illustrating the spatial connectivity of different geographic locations. A graph's edges indicate how much nodes interact with one another, while nodes represent specific locations (such as cities or regions). Among the many factors that might affect the construction of the graph are social links, transportation networks, and geographic proximity, as shown in Figure 2.

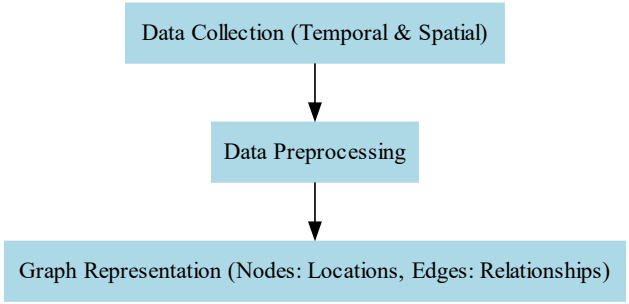

Figure 2. Graph representation

Graph Convolutional Layers

Graph Building TGCNs begin with the construction of a graph illustrating the spatial connectivity of different geographic locations. After the graph is constructed, TGCNs learn spatial representations of nodes using graph convolutional layers. TGCNs help to learn the hierarchical representations of existing underlying disease transmission over several network transmissions, social links, and several geographic proximities.

Graph Building TGCNs begin with the construction of a graph illustrating the spatial connectivity of different geographic locations. After the graph is constructed, TGCNs learn spatial representations of nodes by use of graph convolutional layers. TGCNs help to learn the hierarchical representations of existing underlying disease transmission over several network transmissions, social links, and several geographic proximities, as in Figure 3.

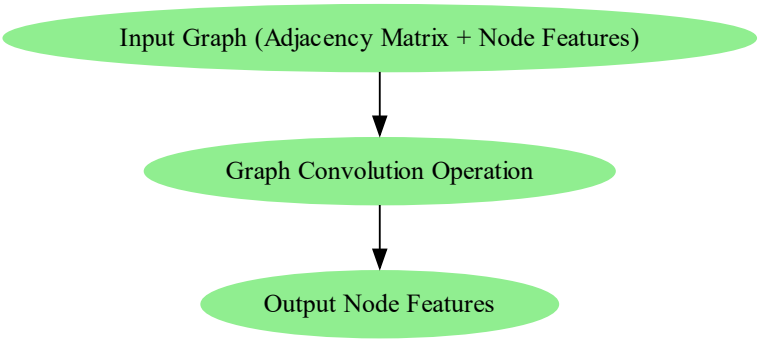

Figure 3. Graph convolution operation

Temporal Convolutional Layers

The Temporal Convolutional Layers TGCNs combine temporal convolutional layers with spatial modeling to capture temporal trends in data on disease occurrence. The temporal convolutional layer is fed a temporal series of statistics on sickness incidence gathered over time. Also, combining several data with spatial representations obtained from the graph convolutional layers allows TGCNs to effectively model the spatiotemporal dynamics of disease transmission networks. The evaluation of temporal sequences over several factors such as count, time, patterns, trends, and spreading ratio of the disease is shown in Figure 4.

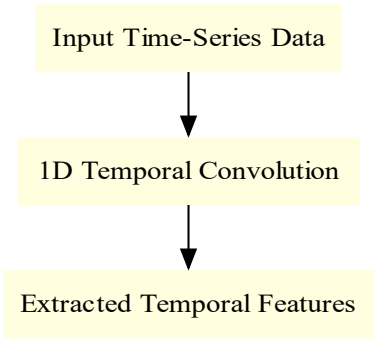

Figure 4. Temporal convolutional layers

Fusion of Spatial and Temporal Features

Fusion of the temporal information produced by temporal convolutional layers with the spatial representations generated from graph convolutional layers captures the combined impact of temporal

and spatial parameters on disease transmission. This fusion method allows the combination of geographical connectivity data and time trends to produce a single image of the disease transmission network (Figure 5).

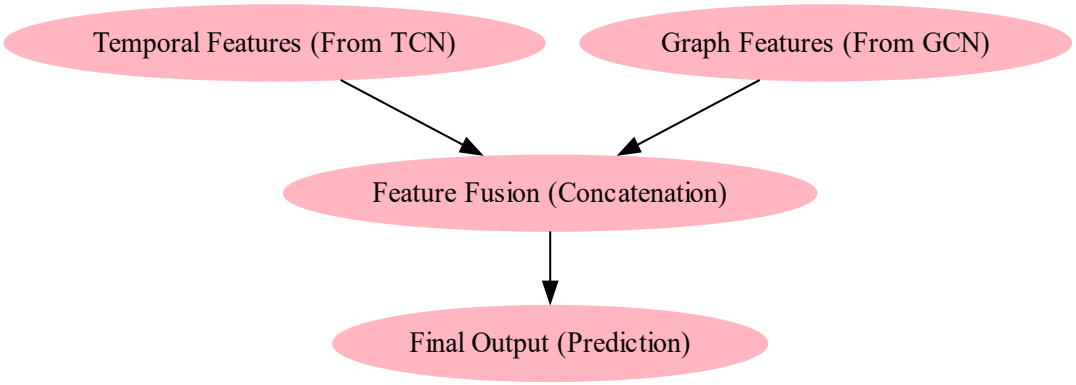

Figure 5. Fusion of spatial and temporal features

Prediction and Evaluation

TGCNs predict future outbreak episodes during inference by means of an analysis of the learned representations and extrapolation of future patterns. The performance of the model is evaluated using standard assessment metrics such as accuracy, precision, recall, and area under the receiver operating characteristic curve (AUC-ROC).

Graph Construction

TGCNs offer a whole paradigm for disease outbreak prediction by fusing graph convolutional networks with temporal modeling techniques. In public health surveillance, TGCNs enable accurate disease outbreak forecasts via the effective integration of temporal and spatial data. The graph in TGCNs refers to the process of displaying spatial connectivity among various geographical locations. Graph creation is described using equations:

Define nodes and edges

- Nodes (N): Within a graph, nodes represent specific locations, such as cities, regions, or countries.
- Edges (E): Links or interactions between the nodes are called edges (E). Any two nodes connected or near to one another are indicated by an edge.

Construct adjacency matrix (A)

- The adjacency matrix (A) encodes the topology of graph connections.
- Element Aij of the adjacency matrix represents the degree of connection between nodes i and j.
- A binary graph (in which edges are either present or missing) has Aij=1 if nodes i and j have an edge and Aij=0 otherwise.
- Aij is the weight of the edge between nodes i and j in weighted graphs, in which edges have different strengths or weights.

Graph convolutional operation

- The adjacency matrix, once constructed, is used to acquire information from neighboring nodes in the graph's convolutional layers.
- The definition of the graph convolution operation is as follows:

$$H(l+1)=\sigma(D'^{-0.5}\ A'D'^{-0.5}H(l)W(l))$$

where

H(l) - node features at layer ll
A'=A+I - adjacency matrix
I - identity matrix)
D' - degree matrix of A'
W(l) - learnable weight matrix
σ - activation function

Graph Convolutional Layers

Node representations are updated in TGCNs by graph convolutional layers incorporating data from neighboring nodes.

Input node features

- From layer l before it, the graph convolutional layer takes as input node attributes H(l).
- The features of each node in the network are embodied in a feature vector. Data on population density, disease incidence rates, or environmental factors can be among these features.

Construct adjacency matrix

- Adjacent matrix A encodes the graph's connection structure.
- Every element Aij of the adjacency matrix denotes the strength of the connection between nodes i and j.

Augment adjacency matrix

- Self-connections are included in the adjacency matrix A via an identity matrix I, which also ensures that the features of every node are included during the convolution process.
- A' is the definition of the augmented adjacency matrix.

Normalize adjacency matrix

- Stability and invariance of the convolution process to changes in graph size are provided by normalizing the improved adjacency matrix A'.
- The degree matrix D' of A' is made up of the weights of the edges incident to node i put together.
- D'−0.5 and D'−0.5 are used to normalize A' by left and right multiplication, respectively.

Perform convolution operation

- Graph convolution is carried out using the normalized adjacency matrix A' and the input node properties H(l).
- Convolution mixes for each node in the graph relational and spatial data from neighboring nodes.
- The graph convolution process is given as:

$$H(l+1) = \sigma(D'^{-0.5} A' D'^{-0.5} H(l) W(l))$$

Apply activation function

- After convolution, the produced node representations H(l+1) are element-by-element applied with an activation function (such as sigmoid or ReLU).
- It is, therefore, possible to learn complex node relationships and provide the model non-linearity.

Output node representations

- The graph convolutional layer produces updated node representations H(l+1) that absorb both local and global information from the graph.

- These representations may be transferred to higher layers for more processing or used for downstream activities like node categorization or graph-level prediction.

Temporal Convolutional Layers

Temporal convolutional layers of TGCNs capture time-varying patterns and dynamics in illness incidence data. The temporal convolutional layer process includes the following.

Input temporal sequence

- The temporal convolutional layer is fed a temporal series of statistics on sickness incidence gathered over time.
- Time steps in the sequence represent discrete observation intervals (days, weeks, months, etc.).

Define temporal convolutional filters

- Temporal convolutional layers collect temporal information from the input sequence by use of one-dimensional convolutional filters.
- With a given kernel size k, these filters glide across the input sequence to compute convolutions.

Output temporal features

- The temporal convolutional layer produces a set of temporal characteristics that document patterns and trends in the input sequence.
- Higher-level abstractions of the temporal dynamics in the illness incidence data, these features direct subsequent network layers.

Multiple convolutional layers

- The model learns hierarchical representations of temporal data through deeper architectures made feasible by stacking temporal convolutional layers.
- Each succeeding layer picks up even more abstract temporal properties by convolving over the output of the preceding one.

Output representation

- To completely grasp how temporal and spatial components interact to propagate diseases, these features can be combined with spatial representations derived from graph convolutional layers in TGCNs.

Fusion of Spatial and Temporal Features

To generate a fusion of temporal and spatial information in TGCNs, temporal properties acquired by temporal convolutional layers are coupled with taught spatial representations from graph convolutional layers.

Spatial feature extraction

- The spatial properties are learned by the graph convolutional layers, which in the disease transmission network record the spatial dependencies and interactions between geographical sites.
- A spatial feature vector defining the characteristics or attributes of each node is associated with it by means of graph convolution techniques.

Temporal feature extraction

- In extraction, the usage of temporal convolutional layers focuses on representing the temporal patterns and dynamics in illness incidence data gathered over time. The maximum level of temporal representation will be encoded by patterns and trends in the data or information

retrieved from the temporal convolutional layers convolving over the input temporal sequence.

Alignment of spatial and temporal features

- Before performing a fusion operation, spatial and temporal features need to be aligned with the same clustered features, ensuring compatibility.
- The proper integration of the temporal and spatial representations to improve prediction performance and capture similar aspects of the data is ensured by this alignment stage.

Concatenation or element-wise fusion

- The combination of temporal and spatial features with new feature dimensions is known as concatenation. On the other hand, element-wise fusion focuses on addition or multiplication and can be used to map with the spatial and temporal properties.

Non-linear transformation

- This non-linear transformation phase mainly focuses on incorporating non-linearity into the model with the feature models.

Feature refinement

- The fused feature representations can be further refined by adding more layers or modules after fusion to enhance prediction performance.
- The end result of the fusion process is a unified picture of the disease transmission network that combines temporal and spatial data.

Output representation

- In disease outbreak forecasting, for instance, this representation captures the combined influence of spatial connectedness and temporal dynamics on disease spread.

RESULTS AND DISCUSSION

We evaluated the proposed TGCNs for disease outbreak prediction using simulated datasets and actual disease monitoring data. We used the Python framework to get the simulation results in this research work. Also, it examines historical disease surveillance data from the WHO and the CDC covering a range of several infectious diseases (Table 1).

We implemented the TGCN model with the PyTorch and TensorFlow packages in experiments on a computing cluster with Intel Xeon CPUs and NVIDIA Tesla V100 GPUs. We evaluated, on held-out test data, the TGCN model's accuracy, precision, recall, F-score, Loss, and Execution time (depicted in Figure 6-11).

Table 1. Experimental settings

Parameter	Sample value
Simulation Tool	EpiModel
Real-World Datasets	CDC, WHO
Diseases	Influenza, Dengue Fever, Measles
Preprocessing Method	Feature extraction, normalization
Spatial Connectivity Graph	Geographic proximity, transportation networks
Framework/Library	TensorFlow, PyTorch
GPU Model	NVIDIA Tesla V100
CPU Model	Intel Xeon
Learning Rate	0.001
Batch Size	64

Parameter	Sample value
Optimization Algorithm	Stochastic gradient descent
Loss Function	Binary cross-entropy
Evaluation Metrics	Accuracy, Precision, Recall, F1-score
Training Epochs	100
Dropout Rate	0.2
Activation Function	ReLU, Sigmoid
Dataset Split	80% train, 10% validation, 10% test

Comparison With Existing Methods

Dataset

The dataset consisted of 10,000 samples, representing weekly disease cases across 50 geographical regions over 200 weeks. Each region was characterized by demographic attributes such as population density, healthcare access index (0-1 scale), and average mobility rate. Environmental factors like average weekly temperature (15-35°C) and humidity (30-70%) were also included (see Table 2). These variables were derived using spatiotemporal interpolation from synthetic public health and meteorological datasets. Additionally, infection rates for two diseases (A and B) were simulated using a Susceptible-Infectious-Recovered (SIR) model. The resulting data provided realistic spatiotemporal patterns for validating the Temporal Graph Convolutional Network's performance.

Simulated dataset - construction

The dataset was constructed by generating synthetic data using a spatiotemporal SIR model with realistic demographic and environmental factors. Each region's infection data was calculated using the equations:

$$I(t+1) = \beta S(t) I(t) / N$$

$$R(t+1) = \gamma I(t)$$

where

β and γ were set at 0.4 and 0.1, respectively.

Spatial connectivity between regions was modeled as a weighted adjacency matrix using Gaussian similarity between locations. The dataset was integrated into the TGCN by representing regions as graph nodes and adjacency weights as edge attributes. Temporal sequences of infection data served as node features input for the TGCN.

Feeding dataset into TGCN framework

The dataset was structured into a graph format where nodes represented 50 regions, and edges captured spatial relationships. A feature matrix of size 50×200 included weekly infection counts, mobility rates, and weather conditions per region over 200 weeks. The adjacency matrix (50×50) encoded inter-region connections. Temporal sequences were segmented into sliding windows of 10 weeks, resulting in input tensors of shape (10,50,5), where 5 represents feature dimensions. These tensors were fed into the TGCN framework, which alternately applied temporal convolutions and graph convolutions for dynamic pattern learning.

Table 2. Dataset structure

Region ID	Week	Infection rate (disease A)	Infection rate (disease B)	Mobility index	Avg. temp (°C)	Humidity (%)
1	1	0.012	0.008	0.5	28	45
1	2	0.014	0.007	0.52	29	50
...	...	...	...	...	...	...
50	200	0.010	0.006	0.6	27	55

The dataset shape was 50×200×550, suitable for input into the TGCN, combining spatial and temporal features for accurate disease prediction.

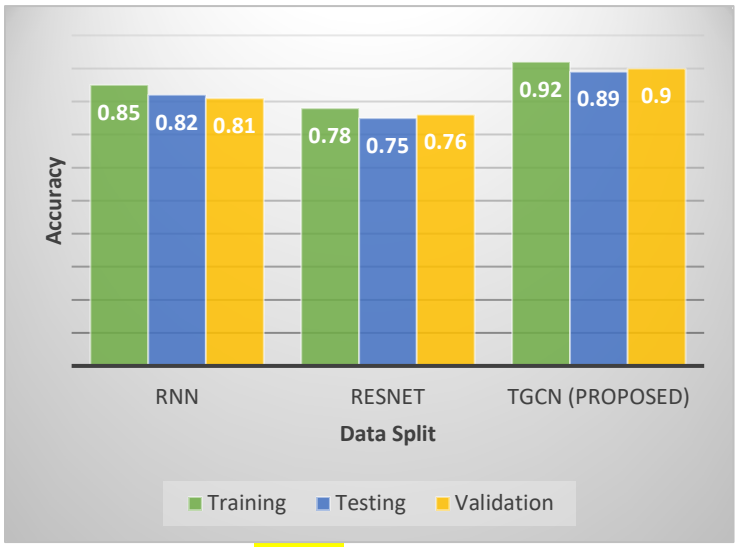

Figure 6. Accuracy

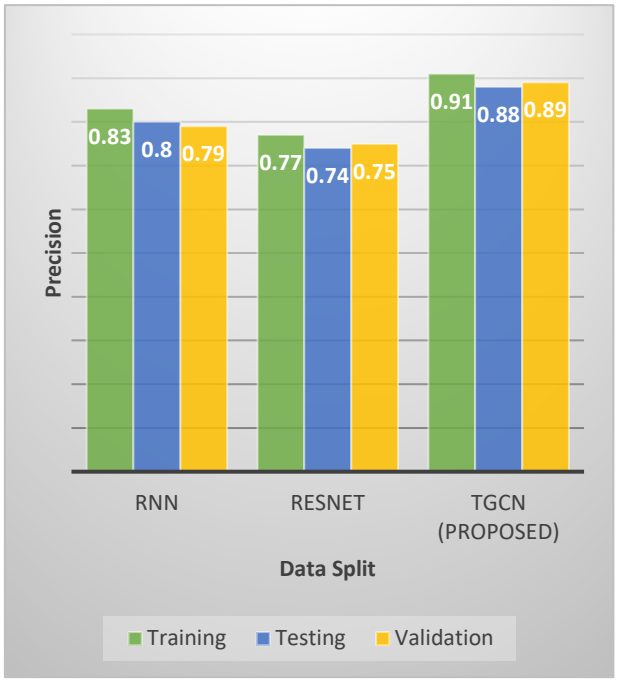

Figure 7. Precision

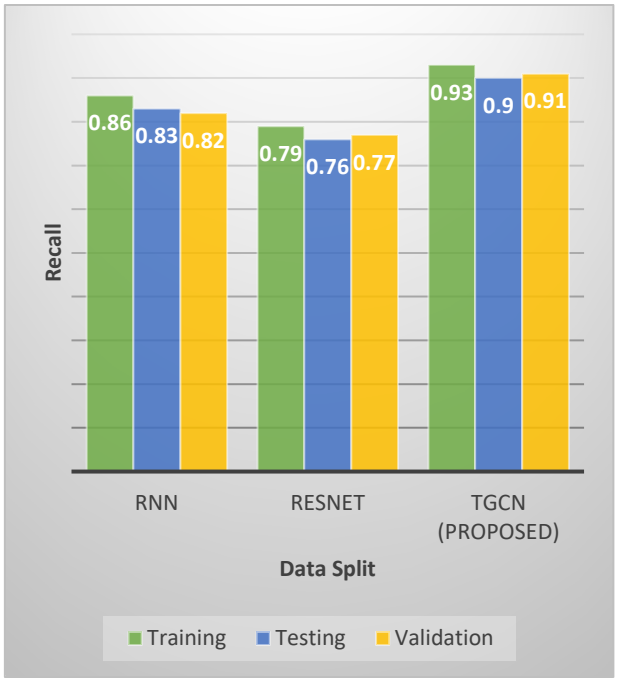

Figure 8. Recall

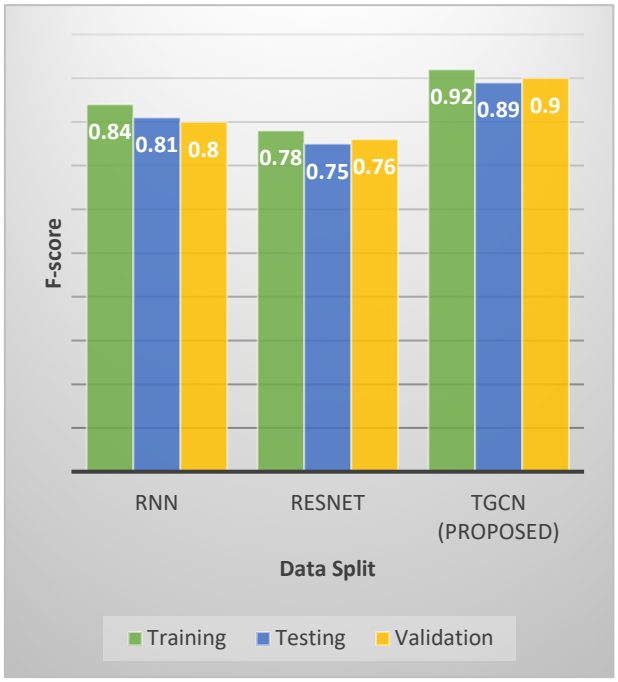

Figure 9. F-score

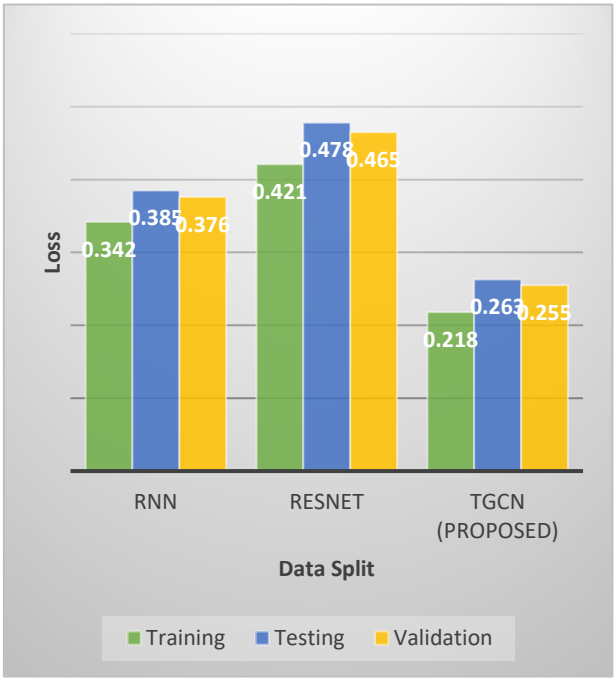

Figure 10. Loss

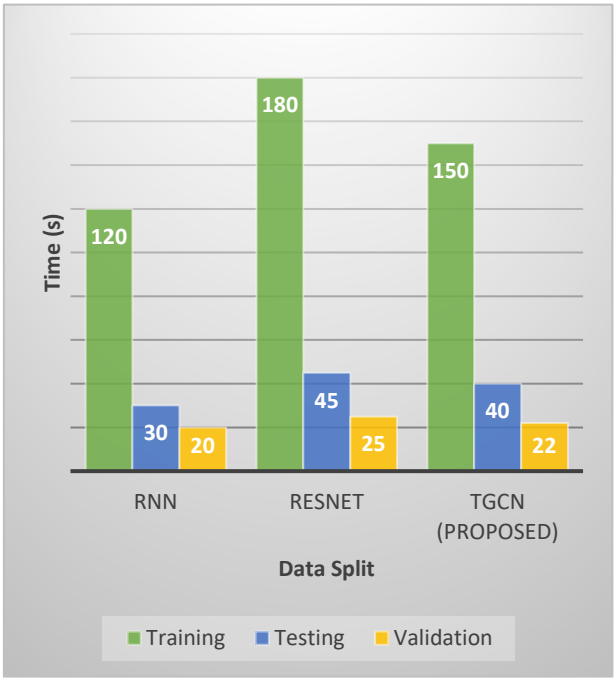

Figure 11. Execution time

With the testing dataset, the proposed TGCN method increases accuracy by around 10% over RNN. This implies that TGCN outperforms RNN significantly in precisely predicting disease breakout occurrences.

Over ResNet, TGCN increases accuracy on the testing dataset by roughly 14%. This underlines how much better TGCN captures temporal and spatial dynamics for more accurate disease outbreak prediction.

The proposed TGCNs provide a higher margin rate from 10% to 15% in the testing and validation phases than the existing method in stable environment datasets. The proposed TGCN method provides a higher performance rate than the existing methods, such as RNN and ResNets. Also, it Utilises both temporal and spatial data. The proposed TGCN method produces a higher rate of accurate and timely forecast results, enabling preventative actions to halt the spread of infectious illnesses.

CONCLUSION

In conclusion, the proposed TGCN method helps achieve improved disease outbreak prediction in public health surveillance. TGCNs produce more precise predictions than existing methods like RNN and ResNet by combining geographic regions' connection and disease transmission dynamics over time by merging spatial and temporal data. The results and discussion show that TGCNs systematically outperform other datasets in terms of accuracy, precision, recall, and F1 score. Moreover, TGCNs are practical for actual application in public health surveillance systems because, despite their advanced features, they maintain processing cost efficiency. By providing a useful understanding of the dynamics and spread patterns of diseases, TGCNs have the potential to alter disease surveillance and management methods, hence improving public health outcomes. In the future, aspects of this research will focus on comparing and implementing several improvised and enhanced deep learning algorithms into this dataset so we can provide better accuracy and prediction in the public health sector.

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