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Dynamic Insights into Dengue: Leveraging Spatio-Temporal Graph Convolution Networks

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Abstract: Examining the nexus between dengue fever and weather variables, this study proposes the innovative application of Spatio-Temporal Graph Convolution Network (STGCN) models to unravel complex patterns. Through extensive experimentation, our STGCN model demonstrates exceptional proficiency in capturing synthetic data patterns generated by the SEIR-SEI model, indicating its potential for real-world applications. Integrating human mobility networks and weather attributes into our approach enables more precise predictions of dengue cases. Leveraging these advanced machine learning techniques, particularly STGCN, we significantly advance our comprehension of the nuanced dynamics of disease transmission. This interdisciplinary approach represents a seminal advancement in combating vector-borne diseases, with profound implications for public health policy and decision-making.

Keywords: Dengue, Graph neural networks, Spatio-temporal convolution, Forecasting, Weather attributes

1 Introduction

The dengue virus is carried by mosquitoes and is one of the most prevalent disease. The dengue virus is spread through mosquito bites and is caused by four serotypes (DENV-1 to DENV-4) [35]. Since, the 16^{th} and 17^{th} centuries, dengue outbreaks and spread have increased continuously, particularly in the 18^{th} and 19^{th} centuries. The dengue virus became a global concern after World War II and the beginning of the 19^{th} century [8, 13]. Every year, millions of people in tropical and subtropical areas suffer from dengue due to insufficient awareness and prevention efforts [29]. More than 80% of infections are mild and asymptomatic, resulting in between 100 - 400 million infected every year around the world [35]. The presence of dengue disease in Nepal was reported in 2004 [23], and infections in people were observed in 2009 [7]. The first largest outbreak was recorded in 2019, and around 18000 people are infected in all 77 districts with low to high temperature zones [27]. Dengue disease has unpredictable transmission dynamics, and many researchers [19, 20, 24] have modeled it mathematically using yearly infected cases with constant assumptions. Seasonal behavior is the most essential aspect. Furthermore, the four seasons—spring, summer, fall, and winter—regularly follow one another. Each has its own unique seasonal light, temperature, and weather patterns. In Nepal, summer and fall are very sensitive for disease spreading to the populations [21].

Prior research has endeavored to clarify the connection between weather characteristics and the occurrence of dengue worldwide [6, 14, 25]. Nearly all studies concur that weather factors significantly affect the dynamics of dengue. However, there is a lack of consensus within the scientific community regarding the specific weather attributes and their categorization as positive or negative influencers. For instance, in the Chitawan district of Nepal, rainfall was not identified as a contributing factor to dengue [31], while it was observed to have a negative impact in Dhaka, Bangladesh [11] and Makassar [28] and a positive impact in an urbanized tropical city [9]. This highlights that while weather variables do impact dengue dynamics, the nature of this relationship varies depending on factors such as time, geographical structure, and the populations of both humans and vectors. Also, human and vector mobility play a crucial role in charismatic behaviours of dengue dynamic [30]. Consequently, it is imperative to develop a model that soundly captures the intrinsic dynamics for accurate predictions of dengue cases in advance.

Accurately predicting the dynamics of epidemics is crucial for preventing or controlling outbreaks of infectious diseases [17]. Therefore, it is not surprising that various forecasting models have been proposed globally in recent years [26, 33]. Graph-based deep learning models, especially those addressing the complexity of mobility networks in epidemic dynamics, have gained significant attention. Graph Neural Networks (GNNs) have demonstrated success in modeling epidemic disease dynamics, with examples such as cross-location attention based graph neural networks[5] for predicting influenza-like illness, Temporal Multiresolution Graph Neural networks [12], Casual Based Graph Neural Networks [32], Transformer Graph Neural Networks [18], Epidemic Graph Neural Networks [34] for COVID-19 forecasting, and Temporal Multiresolution Graph Neural Networks [2] for observing the circulation dynamics of West Nile viruses. This success has inspired us to apply graph neural networks to forecast dengue disease in Nepal, incorporating intertwined weather attributes and a random mobility network.

The paper is structured as follows: Section 2 covers the fundamental concepts of graphs and introduces the basic graph neural network used in our model architecture. Section 3 elaborates on the data preprocessing techniques employed for simulation purposes. In Section 4, we delve into the details of our model architecture and Section 5 presents the results and discussion. Finally, Section 6 concludes the paper.

2 Preliminary

A static graph featuring a temporal signal is defined as an ordered collection of tuples $D = \{(G, X_1), (G, X_2), \ldots, (G, X_T)\}$, where G = (V, E, W) represents a weighted undirected graph, and $X_t \in \mathbb{R}^{|V| \times d}$ for all $t = 1, 2, \ldots, T$ is the node feature matrix. In this context, V denotes the set of nodes corresponding to locations or regions, $E \subset V \times V$ represents the set of edges, and W is the weight matrix indicating the strength of connections between nodes.

The prediction of epidemiological target involves a common time series forecasting problem, where the goal is to predict the most probable epidemiological cases in the next M days based on the preceding K days of information. This can be expressed as:

$$\hat{X}'_{t+1}, \hat{X}'_{t+2}, \dots, \hat{X}'_{t+K} = \arg \max_{X'_{t+1}, \dots, X'_{t+K}} \log P\left(X'_{t+1}, \dots, X'_{t+K} | X_{t-M+1}, \dots, X_t\right)$$

Here, $X'_t \in \mathbb{R}^{|V|}$ represents the matrix of epidemiological cases, and $X_t \in \mathbb{R}^{|V| \times d}$ is the node feature matrix. The latter consists of d-1 weather attributes and epidemiological cases of locations in V.

Traditional convolutions designed for grid structures face challenges when applied to graphs. To overcome this limitation, spectral convolution, leveraging graph Fourier transform, is introduced to extend Convolutional Neural Networks (CNNs) to graph data. For a graph signal $x \in \mathbb{R}^n$ and a kernel Φ , the graph convolution operator [3] is defined as:

$$\Phi *_G x = U\Phi(\Lambda)U^T x,$$

where $U \in \mathbb{R}^{n \times n}$ represents the matrix of eigenvectors of the normalized graph Laplacian $L = I - D^{-\frac{1}{2}}WD^{-\frac{1}{2}} = U\Lambda U^T$, $D \in \mathbb{R}^{n \times n}$ is the diagonal degree matrix with $D_{ii} = \sum_j W_{ij}$, $\Lambda \in \mathbb{R}^{n \times n}$ is the diagonal matrix of L, and $\Phi(\Lambda)$ is a diagonal matrix.

Addressing the computational complexity of graph kernel computation, an approximation method [4] is employed using Chebyshev polynomials. These polynomials, defined by the recurrence relation $T_0(\lambda) = 1$, $T_1(\lambda) = \lambda$, and $T_i(\lambda) = 2\lambda T_{i-1}(\lambda) - T_{i-2}(\lambda)$ for $i \ge 2$, approximate the (K-1)-th order polynomial for the graph filter as:

$$\Phi *_G x = \sum_{i=1}^{K-1} \beta_i T_i(\tilde{\Lambda}) x,$$

where $\beta \in \mathbb{R}^{K}$ is a vector of polynomial coefficients, and $\tilde{\Lambda} = \frac{2\Lambda}{\lambda_{\max}} - I$ represents the re-scaled graph Laplacian matrix, transforming its eigenvalues from $[0, \lambda_{\max}]$ to [-1, 1]. The computational cost of graph convolution with Chebyshev polynomial approximation is $\mathcal{O}(kn)$, excluding the explicit computation of Laplacian eigenvectors.

3 Data Pre-processing

3.1 Graph formation

The availability of a systematic database for daily human mobility in Nepal is limited. While some previous studies [18] have employed mobile phone location data to monitor human mobility, obtaining such data from a telecommunications source for research purposes in Nepal has proven challenging. As a substitute, we employ the stochastic block model (SBM) as the most suitable approximation to capture human mobility patterns within and between the seven provinces in Nepal. The primary objective of using the SBM model, setting aside other constraints, is based on the simplifying assumption that human mobility occurs more frequently within the same province for purposes such as administrative tasks, medical services, and education, while inter-provincial movement is comparatively infrequent. Thus we consider SBM model to incorporate these administrative and geographical proximity.

A graph produced through a stochastic block model (SBM) [10] consists of c clusters, accompanied by a symmetric $c \times c$ matrix. The matrix, denoted as P_{ij} , signifies the probability that an edge will connect a pair of nodes (u, v) if node u belongs to cluster i and node v belongs to cluster j. The probability function we have used is

$$P(x,y) = \begin{cases} e^{-x_i} & \text{if } u, v \in C_r \\ e^{-y_i} & \text{if } u \in C_r, v \in C_r \end{cases}$$

where x_i and y_i non-negative real number such that $x_i \ll y_i$ and x, y are the districts.

3.2 Node feature selection

In the data preprocessing phase, we addressed the lack of consensus on weather attributes influencing dengue viruses by employing Karl Pearson's correlation coefficient. Focusing on Nepal's diverse geographical regions, we identified 47 districts exhibiting high dengue spread from July 17, 2019, to October 17, 2019. Given that traditional healers serve as the primary point of contact for health issues in Nepal [16], especially in rural areas, people do not go to hospitals [15] as the major hospitals are concentrated in urban regions, we hypothesized that individuals with positive dengue cases sought treatment locally.

To extract relevant weather attributes, we utilized the latitude and longitude of district headquarters, obtaining the data from NASA¹. Since dengue cases were reported across diverse districts, we focused on highly correlated weather attributes for each district. We visually represent the frequency distribution of these attributes through bar charts. From the pool of highly correlated variables, six were selected as the key weather attributes significantly impacting the dynamics of dengue spread.

Figure 1 demonstrates highly correlated weather attributes with dengue dynamics in 47 districts of Nepal with their frequencies. Among these weather attributes: PRECTOTCORR: Precipitation (mm/day) PS: Surface Pressure (kPa), QV2M: Specific Humidity at 2 Meters (g/kg), RH2M: Relative Humidity at 2 Meters (%), T2M: Temperature at 2 Meters (C), T2MWET: Wet Bulb Temperature at 2 Meters (C), TS: Earth Skin Temperature (C), WS10M: Wind Speed at 10 Meters (m/s), WS10M_MAX: Maximum Wind Speed at 10 Meters (m/s), WS10M_MIN: Minimum Wind Speed at 10 Meters (m/s), WS10M_RANGE: Wind Speed Range at 10 Meters (m/s), we selected WS10M_MAX, RH2M, WS10M, PRECTOTCORR, and PS. The preprocessing and weather attribute selection is similar to that was done in weather feature selection [1].

3.3 Data simulation

In addressing the sparse nature of the obtained data and acknowledging potential limitations in predicting real-world scenarios based on this data, we opted to generate synthetic data for each of the 47 locations. The actual data is highly sparse, with nominal dengue cases reported in some districts over the time span. While the available information on dengue cases across 47 districts is viable, it is insufficient for directly

¹https://earthdata.nasa.gov/collaborate/open-data-services-and-software/data-information-policy/ data-rights-and-related-issues



Dynamic Insights into Dengue: Leveraging Spatio-Temporal Graph Convolution Networks

Weather attributes correlated to dengue cases

Figure 1: The bar chart of frequency distribution of weather attributes highly correlated to dengue cases.

applying machine learning models. To overcome this, we generated authentic and realistic data using the SEIR-SEI model. This approach, inspired by the model proposed by Pandey et al. [22], incorporates the populations of each district as susceptible entities.

$$\frac{dS^{h}}{dt} = \mu_{h}N_{h} - b\beta_{h}\frac{S^{h}I^{h}}{N_{h}} - \mu_{h}S^{h}$$

$$\frac{dE^{h}}{dt} = b\beta_{h}\frac{S^{h}I^{h}}{N_{h}} - (\mu_{h} + \eta_{h})E^{h}$$

$$\frac{dI^{h}}{dt} = \eta_{h}E^{h} - (\delta_{h} + \mu_{h})I^{h}$$

$$\frac{dR^{h}}{dt} = \delta_{h}I^{h} - \mu_{h}R^{h}$$

$$\frac{dS^{v}}{dt} = A_{v} - b\beta_{v}\frac{S^{v}I^{h}}{N_{h}} - \mu_{v}S^{v}$$

$$\frac{dE^{v}}{dt} = b\beta_{v}\frac{S^{v}I^{h}}{N_{h}} - (\kappa_{v} + \mu_{v})E^{v}$$

$$\frac{dI^{v}}{dt} = \kappa_{v}E^{v} - \mu_{v}I^{v}$$
(1)

where $N_h = S^h + E^h + I^h + R^h$, $N_v = S^v + E^v + I^v$, $S_0^h, S_0^v > 0, E_0^h, I_0^h, R_0^h \ge 0$ and $E_0^v, I_0^v \ge 0$. Here, μ_h, η_h are birth or death, and rate of infection in human populations respectively. b, β_h, β_v are also the parameters affecting the mosquito and human populations. Here, N_h and N_v are respectively human and vector total populations of the district. The use of differential equations are vulnerable to initial conditions

Journal of Nepal Mathematical Society (JNMS), Vol. 7, Issue 2 (2024); H. C. Bhandari et al.

that even with small initial values these equations generate large data which does not seem to be the actual situation. Thus, to reduce dengue infection density and make more realistic, we have consider only one of the hundred fraction of the human population in the district. Also, the vector population is considered 1.5 times the human population on random.

The model parameters were estimated through a least square regression to align with the best fit curve on dengue infections in Nepal. We applied the same parameters reported in study [22], treating the districts as sample points in our synthetic data generation process. Focusing major 47 districts in Nepal, we obtained limited dengue datasets spanning 93 days from July 17, 2019, to October 17, 2019.

We have generated 93 graph snapshots, each possessing the same topology outlined by the Stochastic Block model. These graphs are augmented with node features, encompassing six weather attributes as discussed earlier, alongside simulated dengue cases modeled through the SEIR-SEI system of differential equations (1). Consequently, we now have a collection of Spatio-Temporal dynamic graphs characterized by both a static graph structure and temporal signals evolving over time.



4 Model Architecture of Graph Network

Figure 2: Architecture of Spatio-Temporal Graph Convolutional Networks (STGCN) is composed of two Spatio-Temporal Graph (STConv) blocks followed by a linear layer. Within each STConv block, the model integrates graph convolution to capture spatial information, which is interleaved with temporal gated convolution to handle temporal dynamics.

We have implemented a network architecture known as Spatio-Temporal Graph Convolutional Networks (STGCN), initially designed for traffic forecasting. In this approach, the road network serves as the graph, and the node features represent traffic density. Our objective is to enhance the model by integrating the human mobility network as the graph structure, utilizing the graph formed by the Stochastic Block Model. Refer to Figure 2 for a detailed illustration of the model architecture.

The schematic depicted in Figure 2 illustrates the comprehensive training process employed by our model. Initially, we establish the graph structure based on a stochastic block model. Subsequently, utilizing a

collection of weather attributes alongside dengue cases data, we encapsulate them as node features within the generated graph.

Following this, we propagate graph signals—comprising both the graph topology and node attributes—into a series of Spatio-Temporal Graph Convolutional Network (ST-GCN) layers, culminating in a linear layer. Through this sequence, we harness the inherent spatial and temporal dependencies present in the data.

Upon completion of this signal propagation, we acquire the refined graph topology and a subset of attributes, which serve as the labels for nodes, representing the anticipated dengue cases across target time spans.

4.1 Why graph topology for dengue prediction?

Utilizing a graph topology for dengue prediction offers a strategic advantage. Our graph, based on the stochastic block model, establishes connections between nearby regions with higher probabilities, while assigning lower probabilities for regions farther apart. This approach is grounded in the hypothesis that dengue dynamics are not independent based solely on location. Instead, the dynamics in one location are significantly influenced by those in its vicinity.

To capture the impact of human and vector mobility between locations, employing a graph structure proves to be the most effective approach. This integration is strategically positioned between two temporal gated convolutions within the STConv block, allowing the model to account for the inter connectedness of dengue dynamics across spatial regions.

4.2 Why temporal gated convolution for dengue prediction?

Employing temporal gated convolution for dengue prediction offers several advantages over other methods, such as recurrent neural networks (RNNs). While RNN-based models have demonstrated exceptional performance in temporal signal analysis, temporal gated convolution, a component of convolutional neural networks (CNNs), offers faster training and does not suffer from dependency constraints on previous time steps.

In our approach, temporal gated convolution is utilized within the Spatio-Temporal Convolution (STConv) blocks of the model. These blocks contain 1D causal convolution with a kernel size K_t along with nonlinearity. This allows the convolution operation to be applied across the entire temporal sequence without padding. The use of temporal convolution facilitates exploration of K_t neighboring time steps for each patch of graphs, progressively shortening the temporal sequence by $(K_t - 1)$ at each convolutional layer.

Our model incorporates two STConv blocks, each with its respective K_t kernel sizes. By setting the kernel sizes to K_t^1 and K_t^1 , the temporal signal is effectively reduced by $2(K_t^1 - 1) + 2(K_t^1 - 1)$. For instance, in our model, we utilize an input window of 11 days, with $K_t^1 = 3$ and $K_t^1 = 2$ for the respective kernel sizes, resulting in a forecast output spanning 5 days.

This approach ensures that our model can effectively capture temporal dependencies and patterns in dengue dynamics, leading to accurate predictions.

4.3 Why spatial graph convolution for dengue prediction?

In our model, we employ Chebyshev graph convolutional networks for spatial convolution within each temporal graph. This process involves updating the information for each node based on its (k - 1)-hop neighbors. We effectively leverage the dengue dynamics observed in neighboring locations, which are influenced by mobility networks, to enrich the information available at the central node.

Chebyshev graph convolutional networks offer a powerful mechanism for aggregating information from neighboring nodes in a graph structure. By considering multiple hops of neighbors (up to k - 1 hops), we can capture a broader context of spatial relationships and dynamics. This allows our model to better understand the interplay between dengue dynamics in different locations and incorporate this knowledge into the prediction process.

By exploiting the mobility networks that govern the movement of individuals and vectors, we can enhance the predictive capabilities of our model. This approach enables us to account for the interconnected nature of dengue transmission and make more accurate predictions by incorporating information from neighboring locations.

5 Results and Discussions

Our investigation into the dynamics of dengue fever, particularly in relation to weather variables, has yielded promising insights. Our machine learning model demonstrated significant progress, with both training and validation loss steadily decreasing up to 120 epochs (Figure 3). This trend underscores the efficacy of our model in learning the underlying patterns within the data.



Figure 3: Training and validation loss curves.

To mitigate the risk of overfitting, a common concern in machine learning tasks, we implemented an early stopping scheme. Beyond the 120th epoch, as the validation loss began to rise, early stopping intervened, halting further training (Figure 3). This strategic approach ensures improved generalization to unseen data, safeguarding against overfitting and enhancing the overall effectiveness of our model.

Our model achieves a Mean Squared Error (MSE) of 0.089, a Mean Absolute Error (MAE) of 0.2361, and a coefficient of determination (R^2) of 0.5621. Although the results are moderate, we believe that with access to a larger and more comprehensive dataset, the model's performance could be significantly improved. Synthetic data, while invaluable for initial model assessment, may not accurately reflect the intricate relationship between weather attributes and dengue dynamics in real-world scenarios.

Our primary objective in this study is to present an alternative approach to the investigation of dengue dynamics. By focusing on the interplay between weather variables and dengue cases, we aim to offer a novel perspective that complements existing research in this field. Through the development and evaluation of our model, we have laid the groundwork for further exploration and refinement of predictive techniques in dengue fever forecasting.

6 Conclusion

In conclusion, the impact of weather conditions on dengue dynamics remains a contentious issue, with no unanimous consensus on which attributes exert positive or negative influences. To address this uncertainty, we propose the utilization of a spatio-temporal graph convolutional neural network (GCNN) based model. Our approach has shown significant promise in analyzing dengue dynamics, as evidenced by its success in effectively capturing patterns in synthetic data generated from the SEIR-SEI model.

Furthermore, with the integration of real and extensive dengue case data alongside accurate human movement information, our GCNN model presents a powerful tool for resolving not only dengue cases but also similar public health challenges. By leveraging the intricate relationships between spatial, temporal, and environmental factors, our model offers a comprehensive framework for understanding and predicting the spread of dengue fever and potentially other infectious diseases. In essence, our study underscores the potential of advanced machine learning techniques, particularly spatio-temporal GCNNs, in enhancing our understanding of complex disease dynamics and informing proactive strategies for disease prevention and control. While we have incorporated an SBM-based mobility scheme, the inclusion of real human mobility data remains a limitation of our study and a focus for future work.

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Journal of Nepal Mathematical Society (JNMS), Vol. 7, Issue 2 (2024); H. C. Bhandari et al.

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Dynamic Insights into Dengue: Leveraging Spatio-Temporal Graph Convolution Networks

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