Dynamic Virtual Graph Significance Networks for Predicting Influenza

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Abstract—Graph-structured data and their related algorithms have attracted significant attention in many fields, such as influenza prediction in public health. However, the variable influenza seasonality, occasional pandemics, and domain knowledge pose great challenges to construct an appropriate graph, which could impair strength of the current popular graph-based algorithms to perform data analysis. In this study, we develop a novel method, Dynamic Virtual Graph Significance Networks (DVGSN), which can supervisedly and dynamically learn from similar “infection situations” in historical timepoints. Representation learning on the dynamic virtual graph can tackle the varied seasonality and pandemics, and therefore improve the performance. The extensive experiments on real-world influenza data demonstrate that DVGSN significantly outperforms the current state-of-the-art methods. To the best of our knowledge, this is the first attempt to supervisedly learn a dynamic virtual graph for time-series prediction tasks. Moreover, the proposed method needs less domain knowledge to build a graph in advance and has rich interpretabilities, which makes the method more acceptable in the fields of public health, life sciences, and so on.

Index Terms—Representation Learning, Dynamic Virtual Graph, Influenza Prediction, Time Series.

1 INTRODUCTION

With the growing emergence of graph-structured data such as social networks and biological networks [1], [2], the algorithms to analyze graph data have attracted significant attention, such as Graph Convolutional Networks (GCNs) [3], [4], [5] and Graph Attention Networks (GAT) [6], etc. The structure of graph data exerts significant impact on the performance of these algorithms, because these algorithms heavily depend on the neighborhood relationship of the graph. For example, GNNs iteratively aggregate and integrate the embedding of its neighbors to learn the node embedding of the graph. However, finding out all the influential neighbor nodes and measuring their edge weights appropriately to construct a graph are nontrivial in many cases, such as in life sciences and public health fields, which require substantial domain knowledge.

Influenza prediction is an important interdisciplinary problem between computer science and public health. Influenza circulates worldwide and places a heavy burden on people’s health. Every year [7], [8]. The strong infectivity and outbreak of influenza are estimated to result in approximately 35 million cases of symptomatic illnesses, 16 million outpatient medical visits, 490 thousand influenza-associated hospitalizations, and 34 thousand cases of deaths in the influenza season of 2018-2019 in the United States [9]. The influenza virus undergoes high mutation rates and frequent genetic re-assortment [10], [11], [12]. To help clinicians, hospitals, pharmaceutical companies, and governments better prepare for influenza in a timely manner, we need a reliable model to predict influenza trends.

There are mainly two challenges of predicting influenza. [Challenge 1] Influenza seasonality usually varies, from one season to another, in timing, severity, and duration [13], [14]. Table [1] shows the descriptive statistics of the Influenza-Like Illness (ILI) rates of influenza seasons from 2003-2004 to 2016-2017 in the United States. The rates of “standard deviation / mean” in the “Highest ILI Rate” and “Duration” are 33% and 39%, respectively. Such an irregular variation handicaps the predictive methods. [Challenge 2] Influenza pandemics occur occasionally but can totally disorder the seasonality for years. A pandemic is a serious worldwide outburst, resulting from the emergence of a new type of virus and resulting in extremely higher ILI rates, several close and consecutive peaks, and much longer duration, as the piece of the curve around 2009 in Figure [1] shows. Such a “mutated” outbreak makes the prediction more difficult.

Fig. 1: The ILI rates of influenza seasons from 2003-2004 to 2016-2017 in the United States. The ILI rate is defined as the number of ILI patients divided by the number of all-illness patients.

The existing machine/deep learning models, such as XGBoost (XGB), Temporal Pattern Attention Long Short-Term Memory (TPA-LSTM), Temporal Convolutional Networks (TCN), and Transformer, use current and historical values in a user-defined time window as input to predict...
TABLE 1: The columns illustrate the variation of influenza in timing, severity, and lasting, respectively. “Duration” counts the consecutive weeks, during which the ILI rates are all over 0.01.

| Seasons    | Peak Week (year/week) | Highest ILI Rate | Duration (weeks) |
|------------|-----------------------|------------------|------------------|
| 2003-2004  | 2003/06               | 0.0317           | 28               |
| 2004-2005  | 2003/52               | 0.0706           | 25               |
| 2005-2006  | 2005/07               | 0.0475           | 37               |
| 2006-2007  | 2005/52               | 0.0305           | 31               |
| 2007-2008  | 2007/07               | 0.0327           | 31               |
| 2008-2009  | 2008/07               | 0.0542           | 31               |
| 2009-2010  | 2009/06               | 0.0334           | 91               |
|            | 2009/21               | 0.0421           |                   |
|            | 2009/42               | 0.0762           |                   |
| 2010-2011  | 2011/05               | 0.0444           | 37               |
| 2011-2012  | 2012/11               | 0.0229           | 41               |
| 2012-2013  | 2012/52               | 0.0603           | 44               |
| 2013-2014  | 2013/52               | 0.0439           | 43               |
| 2014-2015  | 2014/52               | 0.0611           | 41               |
| 2015-2016  | 2016/10               | 0.0359           | 42               |
| 2016-2017  | 2017/06               | 0.0481           | 44               |
| MEAN       | -                     | 0.0460           | 40               |
| standard deviation (SD) | -       | 0.0152           | 16               |
| SD/MEAN    | -                     | 33%              | 39%              |

future values. These methods lack considering similarities outside the time window. Although one can simply increase the length of the time window to include more information, there are always some timepoints outside the window. Besides, the bigger the length of the time window is, the fewer the training instances will be left, which makes the predictive model unreliable. If a method can dynamically find historical timepoints that have similar “infection situations” as auxiliary information, the model could tackle the varied seasonality and the occasional pandemics.

However, how to accurately represent the “infection situations” poses a challenge since the situation should include the information of the influenza severity, the tendency, the duration and other factors that may be beyond our knowledge.

In this study, we develop a novel method, namely Dynamic Virtual Graph Significance Networks (DVGSN), as Figure 2 illustrates. DVGSN constructs a virtual graph for influenza prediction. In the virtual graph, a virtual node represents a timepoint. The embedding of a virtual node represents the “infection situations” at the timepoint. The virtual edges connect two virtual nodes at two timepoints, and the edge weights measure the significance of the virtual edge. Since the timepoints connected by the virtual edges can be outside the time window, DVGSN can break the limitation of the time window by learning from neighbor nodes and improve the predictive accuracy.

A natural static graph defined with domain knowledge beforehand could not align well with the specific analytical task. As a result, the “neighborhood” in an “unsupervised graph” could be improper for the specific analytical task and damage the analytical outcomes. Different from a natural graph with static nodes and edges, in a dynamic virtual graph, every node and edge are supervisedly dynamically learned during the training procedure in the prediction task. Moreover, a virtual graph naturally has rich interpretabilities. For example, similar “infection situations” found by the virtual graph can provide us with clues how the virtual graph finds similarities and how the proposed method performs the prediction for pandemics. The interpretabilities make the proposed method more acceptable, especially in the fields of epidemiology and public health, in which researches usually emphasize the interpretabilities of the predictive models for further government measures, etc.

The contributions of this work are concluded as follows.

(1) To the best of our knowledge, this is the first attempt to supervisedly learn a dynamic virtual graph for time-series prediction.

(2) The proposed method need less domain knowledge to build a graph in advance and has rich interpretabilities, which are indispensable in epidemiology, public health, and the like.

(3) We carry out extensive experiments on the real-world data, and the experimental results prove that the proposed method significantly outperforms the state-of-the-art methods.
2 RELATED WORK

This section describes the previous work from the point of view of influenza prediction and graph-based deep learning.

2.1 Influenza Prediction

The machine/deep learning for forecasting influenza or other time-series data are mainly categorized into two groups. Firstly, some researchers focus on looking for effective “features”. For example, search engine query data are used for prediction influenza in Google Flu Trends [15, 16]. Twitter data are also used in other research papers [17, 18]. However, these models usually suffer from the unreliable source of huge amounts of information from such as internet searches. For example, Google’s algorithm was quite vulnerable to overfitting to seasonal terms unrelated to the flu, like “high school basketball”. This example also demonstrates the importance of model interpretability. Secondly, other researchers focus on looking for effective “models”, such as RF [19, 20, 21], Gradient Boosting [19, 21], Multi-layer Perceptron (MLP) [19, 21], Long Short Term Memory (LSTM) [19, 21, 22], Transformer (TFR) [23], and so on. Deep learning based methods, e.g. Transformer, are drawing more attention for their accuracy while most of them suffers from the poor interpretability.

Moreover, statistical models and dynamic analysis models are considered easily accessible tools for simulating patterns of infection by influenza, such as SI, SIS, SIR model and their variants [24]. However, their parameters are subject to change and the approximation of the parameters is difficult [25], such as the basic reproduction number $R_0$, population mobility etc.

2.2 Graph-based deep learning

For mining a natural graph, such as Cora [26] and Digg [27], Graph Neural Networks (GNNs) are usually used, such as GCN, GAT, and Graph Isomorphism Network (GIN) [28]. In an analytical task without a natural graph, to leverage powerful GNNs, a graph can be constructed beforehand. Researchers need to use domain knowledge, such as medicine and transportation [29], and mathematical calculation, such as Euclidean distance [30], to construct a graph beforehand. Nonetheless, all of these graphs are thought of as “unsupervised graphs” because the calculation for the construction is not updated by backpropagation for the specific analytical task. In other words, an “unsupervised graph” could NOT align with the specific analytical task. As a result, the “neighborhood” in an “unsupervised graph” could be improper for the specific analytical task and damage the analytical outcomes. In this study, we develop a method to construct a “supervised graph”, which could dynamically and supervisely learn the effective information from other instances during the training procedure in the specific analytical task.

3 THE PROPOSED MEHTOD

3.1 Influenza prediction tasks

We formally define the prediction task with the classic machine/deep learning algorithms as Formula 1:

$$\hat{y}(v,q) = [\hat{y}(v+1), \hat{y}(v+2), \ldots, \hat{y}(v+q)]^T$$

where $\hat{y}(v,q) \in \mathbb{R}^q$ is the vector to be predicted, $v$ is a given point, and $q$ is the predictive window size; $\hat{y}(v+q)$ is the predicted value of the upcoming $q$-th week, and $f_i(v)$ is a time-series model to predict the value of the upcoming $i$-th week; $\hat{y}(v,q)$ is the observed time-series values with a time lag $p$, $o_v$ is the observed value, and $o_{v-i}$ is the value of the past $i$-th week.

There are two types of time-series prediction: (a) single-step influenza prediction and (b) multi-step prediction. A single-step prediction predicts the value for one step in advance ($q = 1$ in Formula 1), and a multi-step prediction predicts the consecutive values with a bigger predictive window size ($q > 1$ in Formula 1).

As Formula 1 shows, the classic methods heavily depends on the observations in the time window but lacks considering historical similarities outside the time window. Table 2 presents the notations utilized in this work.

| Notations | Explanations |
|-----------|--------------|
| $O$       | the observed time-series data |
| $p$       | the time lag |
| $q$       | the predictive window size |
| $y_{(v,q)}$ | window size of $q$ for the node $v$ in the virtual graph |
| $\hat{y}_{(v,q)}$ | the vector of the true values of the predictive |
| $\hat{y}_{(v,q)}$ | window size of $q$ for the node $v$ in the virtual graph |
| $\mathcal{G}$ | the vector of the predicted values of the predictive |
| $\mathcal{V}$ | the virtual graph |
| $\mathcal{E}$ | the set of all virtual nodes |
| $\mathcal{F}$ | the set of all virtual edges |
| $\chi$ | the observed matrix of the ILI rates |
| $S$ | the node embedding matrix of the virtual graph |
| $T$ | the adjacency matrix of the virtual graph |

3.2 Dynamic Virtual Graph

As aforementioned in Table 1 and Figure 1, Influenza seasons that vary in timing, severity, and duration. And pandemics mutate the influenza outbreaks. Dynamically looking for similar “infection situations” instead of sticking to a fixed periodicity (roughly one year) could be a key to varied seasonality and pandemics for influenza prediction. We formally define the concept of a dynamic virtual graph.

**Dynamic Virtual Graph.** Different from a natural graph with static nodes and edges, we define a virtual graph as $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ with a set of nodes $(\mathcal{V})$ and a set of edges $(\mathcal{E})$, in which every node and edge are supervisedly or semi-supervisedly dynamically learned during the training procedure in the prediction task.

In this study each node is a function that can be trained to capture “infection situations”, and each edge describes the significance of the similarity. Figure 3 gives an image of a virtual graph to predict influenza in this study. A virtual
node \( v (v \in V) \) represents a timepoint, such as 2017/12, which means the 12th week in 2017. The embedding of the virtual node, representing the comprehensive “infection situations” at the timepoint, is denoted as \( s_v \) for the node \( v \). A virtual edge \( e (e \in E) \) connects two virtual nodes at two timepoints, and the edge weights measure the significance of the virtual edge.

### 3.3 Virtual Node Representation

The virtual node representation will be used (1) to perform “infection-situations” embedding for the subsequent representation learning and (2) to learn the significance of the similarity among the different “infection-situations”. How to define a proper function of the virtual node representation vector \( s_v \) for the node \( v \) is a pivotal problem. An “infection-situation” embedding vector needs to include comprehensive infective information, such as:

(a) the timing, severity, and duration of the infection at a given timepoint;
(b) the first-order differences (“speed”) and the second-order differences (“acceleration”) at a given timepoint;
(c) tendency (upward, downward, fluctuation, or a turning point) at a given timepoint;
(d) descriptive statistics (mean, median, maximum, minimum, variance, and the like) at a given timepoint.

Many previous researches studied how to “unsupervisedly” represent “situation” for prediction [31], [32], [33], [34]. Some use current and past values in the time-series data as input. Others use domain knowledge, such as varying lag structures at different steps [32], to present “situation” vectors. Nonetheless, these methods of “unsupervised presenting” is separate from the model training. In this study, we propose a supervised representation of “situation” to learn a more appropriate presentation for a given analytical task. Formula [2] illustrates the node representation of “infection-situations”:

\[
\begin{align*}
    s_v &= \tau(o_{v,p}; \tau) \\
    &= \tau(o_{v,p}; \theta_{\tau}) \\
    &= \sigma(W_{MLP-2}(\sigma(W_{MLP-1}O_{v,p})))
\end{align*}
\]

where \( \tau \) is a neural network, \( \theta_{\tau} \) is the parameter for \( \tau \), and \( \sigma \) is an activation function for which we use Exponential Linear Units (ELU) in this work. In this work, a two-layered Multilayer Perceptron (MLP) is adopted. \( W_{MLP-1} \in \mathbb{R}^{p \times 256} \) and \( W_{MLP-2} \in \mathbb{R}^{256 \times 256} \) are the trainable weights of the first and second layer of MLP, respectively.

There are three reasons why we need to project the original feature space nonlinearly into a high-dimensional space as an embedding vector of a virtual node:

- **(a) To work as time-series feature extraction.**
  
  Time-series analyses usually adopt arbitrary feature engineering, such as Kalman Filtering [35], and so on. How to select effective feature engineering is non-trivial, usually experienced-based and time-consuming. Since an MLP can theoretically simulate any function [36], [37], [38], implementing MLP can perform effective representation in a high-dimensional space.

- **(b) To supervisedly and dynamically learn virtual node representations.**
  
  Since the MLP is a part of the entire end-to-end learning, the projected embedding vectors are supervisedly learned from and for a specific analytical task. Such a supervisedly-learned embedding space is supposed to work better than the original feature space, which is static and cannot be updated or learned, and thereby improve the accuracy.

- **(c) To project virtual node embedding to an appropriate space.**
  
  The high-dimensional embedding vectors of two virtual nodes will be used to define the significance of a virtual edge. A high-dimensional space that represents a variety of complex time-series characteristics can work better than the original feature space that just consists of the ILI rates of current and past few weeks.

### 3.4 Virtual Edge Significance

To a given node, different neighbors may have different similarities in “infection situations”. The significance of a virtual edge needs to be decided. In this study, we measure the significance of the virtual edge between the node \( u \) and \( v \) by performing inner product on the after linear projection and instance normalization on the high-dimensional embedding vectors of “infection-situations”, as Formula [3] illustrates:

\[
\begin{align*}
    t(v,u) &= \kappa(s_v, s_u) \\
    &= \text{inst\_norm}[W_{\text{line\_proj}}s_v] \odot \text{inst\_norm}[W_{\text{line\_proj}}s_u]
\end{align*}
\]

where \( t(v,u) \) is the the significance of the virtual edge from the node \( u \) to \( v \), \( \text{inst\_norm}() \) is the instance normalization, \( W_{\text{line\_proj}} \in \mathbb{R}^{256 \times 256} \) is the trainable weight of the linear projection and \( \odot \) is the inner product.

The significance \( t(v,u) \) of the virtual edge from the node \( u \) to \( v \) has some properties:

- **(a) \(-1 \leq t(v,u) \leq 1**
The infective information from the given timepoint, the infection situations”, and its neighbors is a function that aggregates the infective information from a model, and

\[ h_v^{(l)} = INT(h_v^{(l-1)}, AGG(h_u^{(l-1)}; \forall u \in N(v))) \]

where \( h_v^{(l)} \) and \( h_u^{(l)} \) is the representation vector at the \( l \)-th iteration/layer of the given node \( v \) and the neighbor node \( u \), respectively; \( N(v) \) is the set of neighbor nodes; \( AGG(\cdot) \) is a function that aggregates the infective information from its neighbors \( N(v) \) —the timepoints that have similar “infection situations”, and \( INT(\cdot) \) is a function that integrates the infective information from the given timepoint \( v \) itself and the aggregated infective information by \( AGG(\cdot) \) based on its neighbors \( N(v) \).

A variety of functions of \( AGG(\cdot) \) and \( INT(\cdot) \) have been proposed in the previous studies [6], [28]. In this work, we initiate and update the node representations as Formula 5 shows:

\[ h_u^{(0)} = s_v \]
\[ h_v^{(0)} = \sigma(W_{GNN-l} \cdot \sum_{u \in N(v)} (t(v,u) \cdot h_u^{(l-1)})) \]

where \( W_{GNN-l} \in \mathbb{R}^{256 \times 256} \) is the trainable weight of the \( l \)-th layer of GNNs. In this work, we adopt 2-layered GNNs.

### 3.5 Graph Significance Networks

The virtual graph, which is composed of the virtual nodes representing the “infection situation” at each timepoint and the virtual edges with the similarity significance, is input into GNNs. For a given node, the GNNs iteratively aggregate and integrate the embedding of its neighbors to learn a representation vector \( (h_v) \). Formula 6 illustrates the \( l \)-th iteration of aggregation and integration:

\[ h_v^{(l)} = INT(h_v^{(l-1)}, AGG(h_u^{(l-1)}; \forall u \in N(v))) \]

where \( h_v^{(l)} \) and \( h_u^{(l)} \) is the representation vector at the \( l \)-th iteration/layer of the given node \( v \) and the neighbor node \( u \), respectively; \( N(v) \) is the set of neighbor nodes; \( AGG(\cdot) \) is a function that aggregates the infective information from its neighbors \( N(v) \) —the timepoints that have similar “infection situations”, and \( INT(\cdot) \) is a function that integrates the infective information from the given timepoint \( v \) itself and the aggregated infective information by \( AGG(\cdot) \) based on its neighbors \( N(v) \).

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### 3.6 Regressive Layer

The sum of the initial virtual node representation \( (h_v^0) \), the representation vector after the first GNN layer \( (h_v^1) \), and the second GNN layer \( (h_v^2) \) is input into a regressive layer (implemented by a linear layer) to achieve the final prediction, as Formula 6 shows:

\[ \hat{y}_{(v,q)} = W_{regr}(h_v^0 + h_v^1 + h_v^2) \]

where \( W_{regr} \in \mathbb{R}^{256 \times q} \) is the trainable weight of the final regressive layer.

### 3.7 Loss Function

The loss function is defined as Formula 7 shows:

\[ L = \frac{1}{n \times q} \sum_{v \in V} \|y_{(v,q)} - \hat{y}_{(v,q)}\|^2 + \lambda \|T\|^2_F \]

where \( \frac{1}{n \times q} \sum_{v \in V} \|y_{(v,q)} - \hat{y}_{(v,q)}\|^2 \) is the predictive loss in Mean Square Error (MSE) \( (n \) is the number of virtual nodes), \( y_{(v,q)} \) and \( \hat{y}_{(v,q)} \) are the vectors of the true and predicted values, respectively. \( T \) is the adjacency matrix of the virtual graph, and \( \|T\|^2_F \) is the penalty term to limit the complexity of the virtual graphs and improve the robustness of the model, and \( \| \cdot \|_F \) represents the matrix Frobenius norm; and \( \lambda \) is an adjustable hyper-parameter to balance the two parts of losses.

The entire algorithm of the proposed methods is shown in Figure 4 and Algorithm 1.

![Fig. 4: The structure of the proposed DVGSN.](image)
Algorithm 1 The proposed DVGSN.

Input:
The observed time-series data: O,
The time lag: $p$,
The predictive window size: $q$,
The training epochs: $I$,
The adjustable hyperparameter of levels: $\lambda$.

Output:
The predictive model for influenza in United States.
1: Prepare the observed matrix: $X = [O_{v,p}], \forall v \in V$;
2: Prepare the target matrix: $Y = [y_{v,p}], \forall v \in V$;
3: Calculate the number of virtual nodes: $n = |O| - p - q + 1$;
4: for $l = 1, 2, \ldots , I$ do
5: $S \leftarrow \text{elu}(1d_{conv} (\text{elu}(1d_{conv}(X))))$;
6: $T \leftarrow \text{inst} \_\text{norm}(1d_{conv}(S))(\text{inst} \_\text{norm}(1d_{conv}(S)))^T$;
7: $H^0 \leftarrow S$;
8: $H^1 \leftarrow \text{GNN}(S, T)$;
9: $H^2 \leftarrow \text{GNN}(H^1, T)$;
10: $\hat{Y} = \text{regressive \_layer}(H^0 + H^1 + H^2)$;
11: $L = ||Y - \hat{Y}||^2 + \lambda \times ||T||^2$;
12: Perform back propagation and update parameters;
13: end for

the observed values $(O_{v,p})$ in the user-defined time window with the time lag $(p)$. Inputting all the observed time-series data $(O)$ can capture similar “infection situations” from all the timepoints instead of sticking to the fixed static nodes and edges.

(b) Other differences
The virtual nodes and virtual edges in DVGSN are supervisely learned during the training procedure in the specific prediction task while the other existing GNNs-based methods use a static graph defined beforehand. Another difference lies in the $AGG(\cdot)$ function in Formula 4. The algorithm of the $t$-th layer of iteration in the attentive GNNs (such as GAT) and DVGSN is illustrated as Formula 9 and Formula 10 shows, respectively:

$$h^{(t)}_v = \sigma(W \cdot \Sigma_{u \in N(v) \cup \{v\}}(\alpha_{v,u} \cdot h^{(t-1)}_u))$$

$$\alpha_{v,u} = \frac{\exp(\sigma(a^T[W h^{(t-1)}_u || W h^{(t-1)}_v])}{\Sigma_{k \in N(v)}\exp(\sigma(a^T[W h^{(t-1)}_u || W h^{(t-1)}_k])}$$

where $\alpha_{v,u}$ is the normalized attention coefficient, $(\cdot)^T$ represents matrix transposition, and $||$ is the concatenation operation.

$$h^{(t)}_v = \sigma(W_{GNN-t} \cdot \sum_{u \in N(v) \cup \{v\}}(t_{v,u} \cdot h^{(t-1)}_u))$$

$$t_{v,u} = \text{inst} \_\text{norm}(W_{line \_\text{proj} s u}) \odot \text{inst} \_\text{norm}(W_{line \_\text{proj} s u})$$

In GAT, the input $(\alpha_{v,u} \cdot h^{(t-1)}_u)$ is a mean (precisely a weighted mean) of the embedding vectors in the neighborhood since $\sum_{u \in N(v)} \alpha_{v,u} = 1$ regardless of the graph structure. Comparatively, in DVGSN, the aggregation function $\sum(t_{v,u} \cdot h^{(t-1)}_u)$ is a sum of the embedding vectors in the neighborhood on condition that $-1 \leq t_{v,u} \leq 1$ holds. Theoretically, the expressive power of mean based aggregators is weaker than sum aggregators because sum captures the full multiset while mean captures the proportion / distribution of elements of a given type.

4 EXPERIMENTS

4.1 Data
We scrape the influenza data of the United States from 2003/30 to 2017/30 in the “FluView Interactive” [39], a website of Centers for Disease Control and Prevention, National Center for Immunization and Respiratory Diseases. The weekly ILI rates are calculated and used for this work. Figure 1 illustrates the time-series plot of the ILI rates. The piece of the curve around 2009, which has three consecutive peaks, is a pandemic in 2009. Table 1 summarizes the descriptive statistics of the influenza seasons from 2002-2003 to 2016-2017. The “mean ± standard deviation” of the column of “The Highest ILI Rate” is 0.0460 ± 0.0152. Besides, the standard deviation (0.0152) is around 33% higher than the value of mean (0.046), presenting a considerable variance in severity. The “mean ± standard deviation” of the column of “Duration” is 40 ± 16. The standard deviation (16) is around 40% of the mean (40), presenting a considerable variance in lasting. Moreover, the column of “The Peak week” demonstrates the timing of influenza seasons varies year by year.

4.2 Baseline
In this work, the baseline models include a variety of state-of-the-art models. We do not compare with the SI-based models because it is difficult to obtain the values of the parameters such as the number of susceptible and infected individuals.

- **Autoregression (AR).** An AR model is a statistical method that uses observed values from current and past time steps as input and implements a linear regression to predict future values.

- **$k$-Nearest Neighbors ($k$-NN).** The regression of $k$-NN examines the values of a chosen number $(k)$ of data points surrounding a target data point, and uses the mean of the values as prediction. The $k$-NN regression can be used for time-series prediction [40].

- **Random Forest (RF).** A RF model is an ensemble of decision trees trained with the “bagging” method, which leverages a combination of learning models and thereby increases the overall performance [41].

- **XGB.** The XGB regression implements the framework of Gradient Boosting by providing a parallel boosting, which consists of iteratively learning weak regressors with respect to a distribution and adding them to a final strong regressor [42].

- **Multilayer Perceptron (MLP).** An MLP is a neural network, in which each node in a layer is fully connected to every node in the adjacent layers and fit a non-linear function. The MLP can be used for time series analyses by mapping current and past values to one or multiple future predictive values [43].

- **TPA-LSTM.** The TPA-LSTM uses a set of filters to extract time-invariant temporal patterns. The extraction is similar to transforming time series data into its “frequency domain” for forecasting [44].
show that the proposed DVGSN significantly outperforms the group of experiments is 0.01.

To evaluate the robustness of the model, we also test each algorithm with a longer period. The loss functions of all the models average the predictive MSEs of the future weeks. To evaluate the predictive ability in a longer period, we set the predictive window size to 3 and 6 respectively to test the predictive ability in a short period prediction, and set the value to 1 to do a short period prediction.

4.4 Results

To perform a comprehensive comparison, we perform three series of experiments. We set the the predictive window size to 1 to do a short period prediction, and set the value to be 3 and 6 respectively to test the predictive ability in a longer period. The loss functions of all the models average the predictive MSEs of the future weeks. To evaluate the robustness of the model, we also test each algorithm with a time lag of 6, 9, and 12, respectively. The value of $\lambda$ in this group of experiments is 0.01.

Table 3 presents the results of all the models. The results show that the proposed DVGSN significantly outperforms all the baseline methods in all the prediction tasks with the predictive window size being 1, 3 and 6 respectively, which proves that DVGSN can satisfy both the short and long period prediction tasks.

Time lag. DVGSN shows a slight advantage with the time lag being 9. The results shows that it is better enough to construct the virtual graph node and reflect the current trend with the recent 9 historical data. A longer time lag may offer no help since the virtual graph can learn the similar historical situation by itself. The result also shows that the selection of the hyperparameter time lag for DVGSN is relatively easy.

The other baseline methods, including KNN, RF, XG, MLP, and TPA-LSTM shows a better performance with a short time lag 6 for the short period prediction as the predictive window size is 1, while a bigger time lag 12 is better for a longer period prediction task in which the predictive window size is 3. A longer time lag could offer more support for the longer prediction task. However, as we have introduced previously, the time lag is limited and a longer one can reduce the training space.

The situation of TCN, TFR, GAT and GIN is more like a compromise between the above two cases. They show a better performance with a short time lag 6 for the short period prediction while a slight advantage with the time lag being 9 for the longer prediction task. The graph-based solutions could reduce their dependence on the time lag. At the same time, the fact that they cannot benefit from a longer time lag for the short prediction may be caused by their fixed static graph mode.

5 Ablation Study

To verify the effectiveness of the constructed dynamic graph, we designed a variant, denoted as “DVGSN(fixed)”, in which the virtual edges are fixed instead of being learned. A given node is connected to the nodes at the timepoints one week ago and one year (52 weeks) ago, considering the periodicity and time series of influenza. Other preprocesses are the same as those in the proposed method. We also adjust the hyperparameter $\lambda$ to demonstrate the effectiveness of the penalty term in the loss function.

Fig. 5: The average MSEs by the different $\lambda$s.

Comparison between the fixed and dynamic graph. Table 5 compares the performance of the fixed and dynamic graph. In 8 of 9 cases, the dynamic graphs perform better.
### 6 Model Interpretation

This section explains how the proposed method works.

#### 6.1 How does DVGSN learn the significance of the similarity?

Figure 6 illustrates the similarity that the virtual graph learns. The X-axis represents the time series from the past 11th week to the future 3rd week ($p = 12$ and $q = 3$). The $Y$-axis represents the ILI rate. The date in the format of “year/week” above each column of the subfigures is the “current” timepoint. The model predicts the ILI rates of the “future” timepoints. The ILI rates of the current and past 11 weeks (on the left side of the red dash line) are projected to a high-dimensional space to calculate the significance of the similarity (the green float in each subfigure). As a result, the blue curves in the top two subfigures are the most positively similar “infection situations” that the virtual graph finds; and the blue curves in the bottom two subfigures are the most negatively similar “infection situations” that the virtual graph finds.

#### 6.2 How does DVGSN learn for the varied seasonality?

This section explores whether DVGSN can deal with the varied influenza seasonality. Figure 7 gives two examples. The X-axis represents the time series from the past 9th week to the future 3rd week ($p = 9$ and $q = 3$). The red curves represent the “infection situations” of the given timepoints; the blue curves in the top two subfigures are the most positively similar “infection situations” that the virtual graph finds; and the blue curves in the third row of the subfigure are the most negatively similar “infection situations” that the virtual graph finds.

### TABLE 3: The MSEs in all the models. The bold font indicates the best performance in each test.

| $p$ | $q$ | AR  | KNN | RF  | XGB | MLP | TPA-LSTM | TCN | TRF | GAT | GIN | DVGSN |
|-----|-----|-----|-----|-----|-----|-----|----------|-----|-----|-----|-----|-------|
| 6   | 1   | 0.0796 | 0.1177 | 0.0897 | 0.1071 | 0.0795 | 0.0774 | 0.0794 | 0.0867 | 1.2326 | 1.1891 | 0.0749 |
| 6   | 3   | 0.2750 | 0.2223 | 0.2586 | 0.2106 | 0.2103 | 0.2101 | 0.2254 | 1.2228 | 1.2959 | 0.1765 |
| 6   | 6   | 0.4258 | 0.3723 | 0.3875 | 0.2976 | 0.3296 | 0.2801 | 0.3984 | 1.2239 | 1.2858 | 0.2770 |
| 9   | 1   | 0.0787 | 0.1996 | 0.0978 | 0.1138 | 0.0868 | 0.0806 | 0.0884 | 0.0995 | 1.2286 | 0.9772 | 0.0696 |
| 9   | 3   | 0.3512 | 0.2183 | 0.2523 | 0.2171 | 0.1965 | 0.2112 | 0.2512 | 1.2264 | 1.2056 | 0.1692 |
| 9   | 6   | 0.4942 | 0.3330 | 0.3743 | 0.2982 | 0.4093 | 0.3081 | 0.3422 | 1.2231 | 3.3885 | 0.2542 |
| 12  | 1   | 0.0778 | 0.2113 | 0.0844 | 0.0916 | 0.0878 | 0.0799 | 0.0840 | 0.0930 | 1.2299 | 1.2733 | 0.0691 |
| 12  | 3   | 0.3625 | 0.1839 | 0.1985 | 0.2116 | 0.1944 | 0.2099 | 0.2706 | 1.2282 | 1.4313 | 0.1692 |
| 12  | 6   | 0.4880 | 0.2941 | 0.3239 | 0.2878 | 0.3850 | 0.3209 | 0.3262 | 1.2085 | 1.6453 | 0.2695 |

* The $p$ and $q$ refers to the time lag and the predictive window size, respectively.

### TABLE 4: Comparison between the fixed and dynamic graph. The bold font indicates the better performance in each pair of comparison.

| $q$ | $\lambda = 0$ | $\lambda = 0.0001$ | $\lambda = 0.0005$ | $\lambda = 0.001$ | $\lambda = 0.005$ | $\lambda = 0.01$ | $\lambda = 0.05$ | $\lambda = 0.1$ | $\lambda = 0.5$ | $\lambda = 1$ |
|-----|----------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|
| 6   | 0.0712         | 0.0773           | 0.0709           | 0.1817           | 0.1749           | 0.1780           | 0.3043           | 0.2699           | 0.2749           |                 |
| 9   | 0.0696         | 0.0691           | 0.1765           | 0.1692           | 0.1692           | 0.2770           | 0.2542           | 0.2695           |                 |                 |
| 6   | 0.0796         | 0.0691           | 0.1765           | 0.1692           | 0.1692           | 0.2770           | 0.2542           | 0.2695           |                 |                 |

### TABLE 5: Comparison among different $\lambda$ in DVGSN. The bold font indicates the better performance in each pair of comparison.

| $p$ | $q$ | $\lambda = 0$ | $\lambda = 0.0001$ | $\lambda = 0.0005$ | $\lambda = 0.001$ | $\lambda = 0.005$ | $\lambda = 0.01$ | $\lambda = 0.05$ | $\lambda = 0.1$ | $\lambda = 0.5$ | $\lambda = 1$ |
|-----|-----|----------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|
| 1   | 6   | 0.0734         | 0.0763           | 0.0800           | 0.0700           | 0.0696           | 0.0749           | 0.0714           | 0.0705           | 0.0765           | 0.0710           |
| 1   | 9   | 0.0699         | 0.0657           | 0.0792           | 0.0751           | 0.0713           | 0.0696           | 0.0710           | 0.0735           | 0.0685           | 0.0698           |
| 1   | 12  | 0.0676         | 0.0898           | 0.0709           | 0.0712           | 0.0684           | 0.0691           | 0.0792           | 0.0759           | 0.0771           | 0.0775           |
| 3   | 6   | 0.1900         | 0.1874           | 0.1804           | 0.1875           | 0.1795           | 0.1765           | 0.1790           | 0.1772           | 0.1789           | 0.1888           |
| 3   | 9   | 0.1742         | 0.1777           | 0.1752           | 0.1779           | 0.1672           | 0.1692           | 0.1771           | 0.1739           | 0.1750           | 0.1708           |
| 3   | 12  | 0.1750         | 0.1873           | 0.1787           | 0.1699           | 0.1788           | 0.1692           | 0.1760           | 0.1727           | 0.1758           | 0.1777           |
| 6   | 6   | 0.2777         | 0.2758           | 0.2745           | 0.2964           | 0.2797           | 0.2770           | 0.2824           | 0.2765           | 0.3035           | 0.3082           |
| 6   | 9   | 0.3330         | 0.2797           | 0.2729           | 0.2626           | 0.2664           | 0.2542           | 0.2759           | 0.2767           | 0.2746           | 0.2962           |
| 6   | 12  | 0.2381         | 0.2376           | 0.2702           | 0.2531           | 0.2507           | 0.2695           | 0.2509           | 0.2875           | 0.2702           | 0.2618           |
two most similar “infection situations”. We find the two most similar timepoints do not correspond to the same week of the previous years, which demonstrates DVGSN can tackle varied influenza seasonality instead of sticking to the periodicity of 52 weeks.

6.3 How does DVGSN learn for the pandemic?

This section explores how DVGSN learns from the historical “infection situations” and predicts the pandemic. We present five examples in the 2009 pandemic in Figure 8. The X-axis and Y-axis represent time series from 2002/40 to 2017/30 and the ILI rates, respectively. In each subfigure, the red piece represents the “infection situations” of the given timepoints in the pandemic. The timepoints in the five subfigures are 2009/07, 2009/13, 2009/37, 2009/51, and 2010/11 respectively, which represent a rising, a falling down, a rebound after reaching a bottom, a drop after reaching a peak, and fluctuations after a huge dropping in the 2009
Fig. 7: The illustrative examples how DVGSN deals with the varied seasonality. The X-axis represents from the past 9th week to the upcoming 3rd week ($p = 9$ and $q = 3$). The “infection situations” of the given timepoints are represented by the red curves; and the most two similar “infection situations” are represented by the blue and green curves. The number after “w:” in the figure legend is the significance of the similarity.

Fig. 8: This figure illustrates how DVGSN learns from the historical “infection situations” and predicts the pandemic. The X-axis represents time series from 2002/40 to 2017/30. The two yellow pieces in the curves represent two of the most similar “infection situations” that DVGSN learns. The number after “w:” in each figure legend is the significance of the similarity. By comparing the past “infection situations” and future tendency between the red pieces and the two yellow pieces in the five examples, we conclude that DVGSN can find and learn the similar “infection situations” outside the pandemic and thereby make a reliable model for the influenza prediction.

7 CONCLUSION

In this work, we proposed a method—DVGSN. DVGSN can find similar “infection situations” outside the time window and therefore improve the predictive accuracy for influenza. The extensive experiments on real-world influenza data demonstrate that DVGSN significantly outperforms the current state-of-the-art methods. Besides, the proposed method has rich interpretabilities, which provide us clues how the model perform prediction for influenza. Another strong point of the proposed method lies in that it need less domain knowledge to build a graph in advance, which may be very difficult in the medical science related fields. As all the deep learning based methods the proposed method also depends on enough data to train the model. Hopefully, this method can help us better prepare for influenza outbreaks, and work on other public health related analytical tasks well.

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