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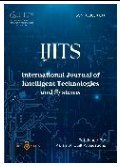

Learning Temporal Clinical Knowledge Graphs for Early Detection of Multi-Organ Dysfunction in ICU Patients from Electronic Health Records using Machine Learning Techniques

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ABSTRACT

Identification of potential clinical events at an early stage is still a challenging issue in intensive care settings owing to the complexity of dynamic interactions between multiple physiological systems. In this work, we introduce a Temporal Organ Interaction Graph Network (TOIGN) for predicting clinical outcomes based on longitudinal electronic health data. Our TOIGN model builds dynamic clinical graphs which depict inter-relationships between organ systems, laboratory measurements, vital signs and medication information. To find influential physiological interactions, our model employs graph attention techniques. Moreover, it utilizes temporal learning algorithms to learn about the illness process through multiple time steps. TOIGN concurrently performs predictions of acute kidney injury, respiratory failure, septic shock and MODS using multi-task learning paradigm. We evaluate our method on intensive care patients' EHRs from the MIMIC-IV dataset against baseline machine learning, deep learning and graph-based methods. The outcomes showed significantly enhanced predictive power in terms of several metrics including 94.36% accuracy, 93.57% precision, 95.18% recall, 94.37% F1-score, 0.978 AUROC and 0.971 AUPRC. Moreover, the introduced method enabled earlier detection of the patient's deteriorating state compared to previously developed approaches, which provided additional time for interventions. These results confirm that the application of the temporal model of organ interaction is a viable approach for enhancing early prediction and patient management in clinical environments.

Keywords: Temporal Clinical Graphs; Electronic Health Records; Clinical Deterioration Prediction; Graph Attention Networks; Medical Informatics

1. INTRODUCTION

The explosion of electronic medical records through recent years revolutionized current medicine through the possibility of continuous monitoring and collecting information about patients from the intensive care unit, emergency department, or even hospitals' IT systems [1]. Information collected on a regular basis during the monitoring of patients gives the opportunity to learn much about their physiology, pathologies, reaction to treatment and complications that have started to occur in some critical cases. With the emergence of huge amounts of data, there appeared the chance to create advanced predictive systems capable of making

decisions on behalf of medical professionals. Early diagnosis of clinical deterioration is one of the major issues that need to be solved in critical care medicine now. For example, patients may experience acute kidney injury, respiratory failure, septic shock and other complicated diseases which occur gradually [2]. At the same time, clinicians have to analyze laboratory parameters, vital signs, drug history and different diagnostic images to recognize these diseases. However, the huge amount of data makes this process rather complicated; thus, the necessity of implementing computer tools arises.

Traditional models and machine learning algorithms have been extensively used for risk prediction in clinical settings. Techniques like Logistic Regression, Random Forest and Gradient Boosting show good performance on structured data in the healthcare domain. These methods usually ignore correlations between clinical parameters and are not capable of modeling complicated interactions of physiological variables across different organ systems. In addition, modern deep learning techniques such as recurrent neural networks or transformers are utilized to model temporal patterns in patient data [3]. Despite providing better accuracy, these approaches usually model patient records using sequences and neglect relations between organs, laboratory tests, medications and physiological values. Physiology is highly interdependent in its nature. The malfunctioning of an organ system can be accompanied by abnormalities in others, forming complicated interaction patterns that develop over time. For instance, dysfunction in kidneys can affect the condition of cardiovascular systems, whereas pulmonary failures might cause metabolic imbalances. Modeling these interactions is critical to predicting future patient events and understanding the process of disease development. Graph-based machine learning methods seem to present an effective solution for such problems due to their ability to model interconnected structures.

Driven by the above motivations, this research proposes Temporal Organ Interaction Graph Network (TOIGN), a novel approach for predicting critical deteriorations from ICU patients at an early stage. TOIGN builds dynamic clinical graphs representing physiological interactions among different organs, lab results, vital signs and drug records. The clinically meaningful interactions are learned via a graph attention module, while the dynamic evolution of diseases is captured through temporal learning in the graph-based modelling [4]. TOIGN provides a unified solution to predicting various critical deterioration outcomes in one model, including acute kidney injury, respiratory failure, septic shock and MOF. The contributions of our work can be summarized as follows. First, we introduce a temporal graph to represent the physiological interaction between organs. Second, we design an attention-driven learning module to learn the clinically significant relationships related to the predicted deteriorations. Third, we develop a multi-task framework for the comprehensive analysis of multiple critical diseases.

2. RELATED WORKS

The emergence of electronic health record systems has prompted researchers to invest heavily in predicting critical events in patients. In fact, the ability to predict patient deterioration, organ dysfunction, the course of infection and risk of mortality is one of the most researched topics in medical informatics in recent years owing to its immense value in improving patient outcomes and enabling prompt clinical interventions [5]. There have been many efforts to develop computational techniques for analyzing various types of heterogeneous data in large-scale medical databases over the last decade. Conventional statistics and machine learning methods form the first generation of predictive systems in medical informatics. One of the most popular techniques used by clinicians is logistic regression owing to its simplicity and interpretability. Other approaches such as decision trees, random forest and gradient boosting are also widely applied as they can model non-linear associations between features. However, conventional models assume that the clinical data are independently distributed and thus do not capture temporal changes in patients' physiological parameters. Therefore, their capability of modeling the progression of diseases is questionable.

In order to model the temporally dependent aspects within medical records, various deep learning methods based on sequences have been proposed. Recurrent Neural Networks and Long Short-Term Memory networks have been used widely to analyze electronic health records for tasks such as mortality prediction, disease diagnosis and monitoring patients. This approach allows deep learning models to model sequential information extracted from longitudinal patient records, which yields higher prediction accuracy than traditional machine learning algorithms. Nevertheless, these recurrent architectures usually face many difficulties regarding long-term dependencies, information loss and interpretability when modeling complicated physiological correlations. Recently, transformers have become an effective alternative tool for medical data processing [6]. The use of self-attention mechanism allows these models to identify long-term dependencies between clinical events and process sequential medical records more efficiently than recurrent models. Several papers have demonstrated that transformer-based frameworks are more efficient at predicting diseases, extracting patient features and forecasting future clinical events. Nonetheless, these transformer models mostly rely on analysing sequential dependencies and rarely incorporate other kinds of structural dependencies between organs, laboratory tests, drugs and physiological signs.

There has been a growing trend towards graph-based learning techniques as ways of presenting interrelated health information. Graph Neural Networks are useful techniques in building networks based on clinical entity relations. They have been used in disease classification, patient similarity assessment, drug recommendation and knowledge representation in medicine. Graph Convolutional Networks, GraphSAGE and Graph Attention Networks are some of the promising techniques that have shown potential in capturing structure dependencies in complex health care data sets. Using nodes to represent medical concepts and interactions as edges offers a much realistic presentation of clinical settings. Even with the impressive progress that graph-based learning techniques have made, they still face several challenges. Most of the available approaches use static graphs, which do not present the changing aspects in physiology. Clinical deterioration involves physiological processes that involve various organs working and affecting each other in a changing fashion. Static structures are therefore not capable of capturing changes in the interactions involved during the onset of diseases. Additionally, most of the research conducted uses one prediction technique, such as estimating mortality and sepsis detection, when multiple prediction tasks are required in critical care environments [7].

Another crucial issue is the integration of different kinds of clinical information. Health care records include laboratory data, vital signs, history of medications, diagnosis and demographics all of which affect patient outcomes. The existing approaches usually handle these sources of information separately or simply combine them by applying a simple technique of feature concatenation. This limits the potential of modeling intricate dependencies among different clinical features. As mentioned in previous literature, there is a necessity for a system that can incorporate joint modeling of time, organ interactions and multi-task clinical predictions. In this regard, this study provides a new Temporal Organ Interaction Graph Network model that allows for the consideration of both physiological connections using clinical dynamic graphs and temporal changes from one observation point to another [8]. The proposed model utilizes graph attention and temporal representation modeling in order to achieve better performance in the early detection of acute kidney injury, respiratory failure, septic shock and multi-organ dysfunction syndrome. Based on the above research gaps, the following framework is proposed as in Fig.1.

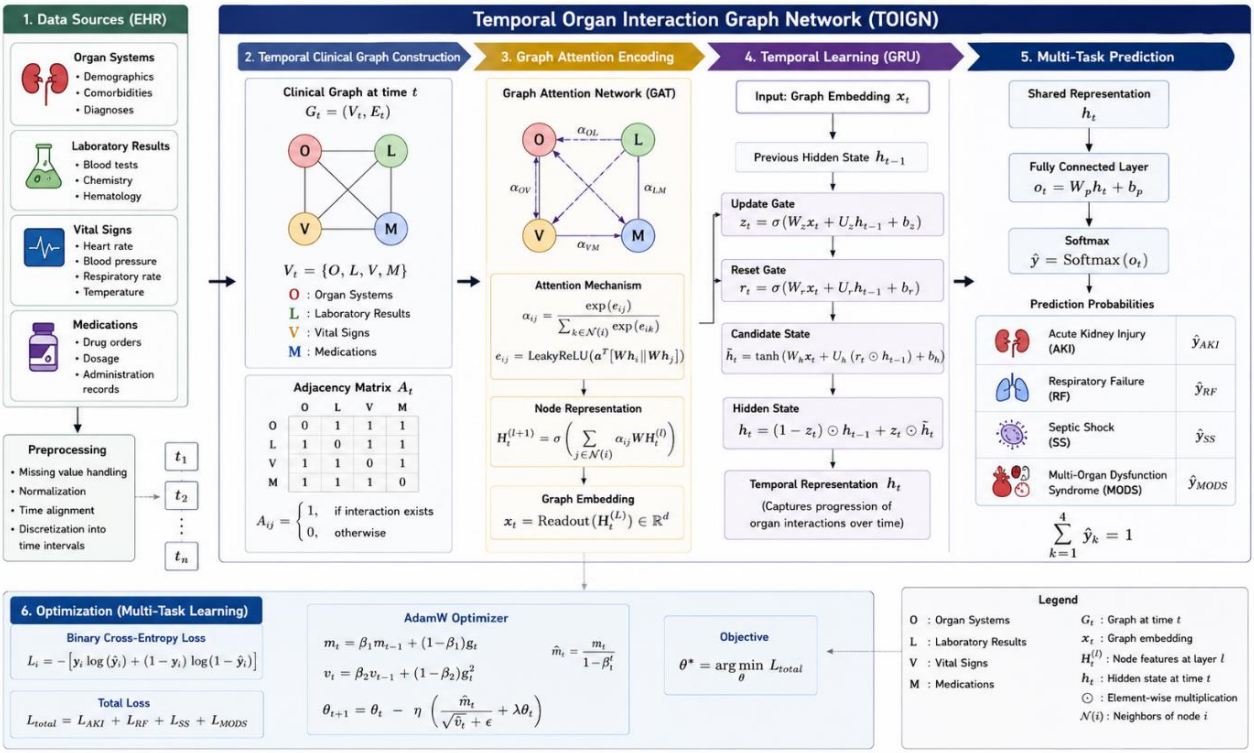

Fig.1. Architecture of the proposed Temporal Organ Interation Graph Network (TOIGN)

Architecture diagram as in Fig.1. describes an end-to-end workflow of the Temporal Organ Interaction Graph Network (TOIGN), which is used for early prediction of clinical deterioration events through long-term analysis of electronic health records gathered from ICU patients. Heterogeneous medical data is used by the TOIGN architecture to predict patient status using relationships and patterns of illness. Data acquisition starts with the gathering of information from different sources that are part of the patient's EHRs [9]. The sources can be related to patient information about organ systems, laboratory tests, vital signs and prescriptions.

After collecting all information, there are certain preprocessing steps that are carried out including dealing with missing data, normalization of data, aligning it temporally and segmenting it into consecutive time slices.

In the second step, a Graph Attention Network (GAT) learns the significance of interactions in the clinical graph using attention. In this way, the model is able to assign different weights to neighboring nodes. As a consequence, it can concentrate on those physiological relationships that have higher significance. This step results in enriched node representations and outputs a graph embedding which encapsulates the clinical information in each temporal graph. As a result of gradual onset of illness, temporal embeddings extracted at different time windows are provided to a Gated Recurrent Unit (GRU)-based temporal learning module. The GRU architecture uses two kinds of gates: the update gate and the reset gate to keep important information from the past while updating the model with current observations [10].

Temporal representation learned through this process is used as a feature space for multi-tasking. A fully connected network with Softmax activation predicts four significant medical events including: Acute Kidney Injury (AKI), Respiratory Failure (RF), Septic Shock (SS) and Multi-Organ Dysfunction Syndrome (MODS). This multi-task approach helps the framework exploit the relationship between similar physiological features of various medical events. The third element of the architecture involves the optimization routine. Loss based on binary cross-entropy is calculated for each of the tasks and is used to create an overall objective function. The model weights are optimized using the AdamW method, which utilizes adaptive learning rates along with weight decay to obtain consistent convergence. In summary, the proposed architecture can be regarded as a comprehensive framework for patient physiology modeling, which can accurately estimate the dynamics between organs within patients' bodies as well as disease evolution over time while making simultaneous predictions of several critical events.

3. MATERIALS AND METHODS

3.1 Dataset Description

The data used in this paper included the MIMIC-IV intensive care database that comprised longitudinal electronic health records of critically ill patients. The record data include demographic characteristics, laboratory results, physiological measurements, medications and diagnostic observations. Variables related to cardiovascular, respiratory, renal, hepatobiliary, neurologic and hematologic functions were considered for the analysis [11].

Missing values were interpolated for continuous variables, while mode imputation technique was applied for categorical variables. Afterward, standardization was performed on all numerical variables using z-score normalization, which is described by Eq.1.

$$x_{\text{norm}} = \frac{x-\mu}{\sigma} \quad \text{Eq.1.}$$

where (x) denotes the original observation, (\mu) represents the mean value and (\sigma) denotes the standard deviation.

3.2 Temporal Clinical Graph Construction

Patients' medical records were divided into time segments 'T'. Then, a clinical graph was created for each segment as in Eq.2.

$$\mathcal{T} = \{t_1, t_2, \dots, t_n\} \quad \text{Eq.2.}$$

where $\mathcal{T}$ denotes the sequence of temporal intervals extracted from patient records. For each time interval $t \in \mathcal{T}$, a clinical graph is constructed as

$$G_t = (V_t, E_t),$$

where

$$V_t = \{O, L, V, M\}$$

represents the set of clinical entities (nodes) and

$$E_t \subseteq V_t \times V_t$$

denotes the set of physiological interactions (edges) between clinical entities [12].

The node set consists of

$$O = \{o_1, o_2, \dots, o_p\},$$
$$L = \{l_1, l_2, \dots, l_q\},$$
$$V = \{v_1, v_2, \dots, v_r\},$$
$$M = \{m_1, m_2, \dots, m_s\},$$

where:

- O represents organ systems,

- Lrepresents laboratory variables,
- Vrepresents vital signs,
- Mrepresents medication records.

Hence, the complete node set at time $t$is given by

$$V_t = O \cup L \cup V \cup M.$$

The graph structure is encoded through an adjacency matrix

$$A = [A_{ij}] \in \{0,1\}^{|V_t| \times |V_t|},$$

where each element $A_{ij}$is defined as

$$A_{ij} = \begin{cases} 1, & \text{if a physiological interaction exists between } v_i \text{ and } v_j, \\ 0, & \text{otherwise.} \end{cases}$$

Equivalently, the edge set can be derived from the adjacency matrix as

$$E_t = \{(v_i, v_j) \mid A_{ij} = 1,\ v_i, v_j \in V_t\}.$$

Therefore, the temporal clinical graph for each interval can be expressed as

$$G_t = \big(V_t, \{(v_i, v_j) \mid A_{ij} = 1\}\big),$$

as shown in Eq.2. This allows the preservation of structure dependencies between organ systems, laboratory values, vital signs and other clinical variables related to medications [13].

3.3 Temporal Disease Progression Modeling

Since clinical deterioration evolves dynamically over time, graph representations generated at consecutive intervals are integrated using a Gated Recurrent Unit (GRU). Let $x_t$denote the graph embedding at time interval t and h_{t-1}denote the hidden state from the previous interval.

The **update gate** is computed as in Eq.3.

$$z_t = \sigma(W_z x_t + U_z h_{t-1} + b_z), \qquad \text{Eq.3.}$$

where $W_z$and $U_z$are learnable weight matrices and $b_z$is the bias vector.

The **reset gate** is defined as in Eq.4.

$$r_t = \sigma(W_r x_t + U_r h_{t-1} + b_r), \qquad \text{Eq.4.}$$

where W_r, U_r and $b_r$are trainable parameters.

Using the reset gate, the **candidate hidden state** is computed as in Eq.5.

$$\tilde{h}_t = \tanh\,(W_h x_t + U_h(r_t \odot h_{t-1}) + b_h), \qquad \text{Eq.5.}$$

where $\odot$denotes element-wise multiplication.

The final **hidden state update** is given by $h_t = (1 - z_t) \odot h_{t-1} + z_t \odot \tilde{h}_t$.

Substituting $\tilde{h}_t$into the hidden-state equation yields Eq.6.

$$h_t = (1 - z_t) \odot h_{t-1} + z_t \odot \tanh\,(W_h x_t + U_h(r_t \odot h_{t-1}) + b_h). \qquad \text{Eq.6.}$$

Thus, the temporal representation at each interval can be expressed as

$$h_t = f_{\mathrm{GRU}}(x_t, h_{t-1}),$$

which reflects the pattern of progression related to organ decline and interaction dynamics. This equation reflects the pattern of progression related to organ decline. In addition, Area Under Receiver Operating Characteristic Curve (AUROC) and Area Under Precision-Recall Curve (AUPRC) [14] were used for discrimination capability analysis on imbalanced datasets. Statistical significance was confirmed through paired hypothesis testing at a 95% confidence level. The entire methodology framework encompasses temporal clinical graph building, graph attention learning, recurrent temporal modeling and multi-task prediction in order to detect physiological deterioration in advance while capturing the complicated interdependence of organ systems in intensive care settings.

4. EXPERIMENTATION AND IMPLEMENTATION

The experimental study was designed to analyze the performance of the TOIGN framework proposed for early prediction of critical deterioration events in the ICUs. The experiments relied on longitudinal electronic medical data extracted from the MIMIC-IV database, which included patients' demographics, physiological features, lab investigation results, medicines and diagnoses [15]. For data pre-processing, various operations such as noise filtering, imputation of missing values, normalization

and temporal alignment were performed for different clinical features. Continuous features underwent z-score normalization, whereas categorical features were transformed via one-hot encoding.

For creation of the temporal clinical representation, every single patient record was segmented into equal windows. All clinical features were grouped based on organs in categories such as cardiovascular, respiratory, renal, hepatologic, nervous and hematology. After that, a dynamic graph was created for each of the observation periods [16]. Nodes in the graph denoted different organs, laboratory features, vital signs and medicine features. On the other hand, edges denoted physiological relations and temporal connections between the features. Using graphs allowed capturing inter-organ interactions, which often occur before clinical deterioration events. The designed framework comprised of four main components: graph creation, node embedding, temporal graph attention learning and multi-task prediction. In the first stage, node embeddings were obtained from patient clinical data by transforming node attributes to low-dimensional vectors. Thereafter, the attention module calculated the appropriate weight coefficients for connected nodes, helping the model distinguish the important physiological associations. The dynamic computation of the attention weight between neighboring nodes allowed focusing on clinically significant connections.

In order to extract the temporal patterns of diseases, graph representations computed at successive time periods underwent learning via gated recurrent update operations. This helped preserve previous patient information while updating their current condition status [17]. Finally, the learned representation was fed into the multi-task prediction module where four medical problems were recognized jointly, including acute kidney injury, respiratory failure, septic shock and multi-organ dysfunction syndrome. The loss function used during training was designed as a linear combination of different tasks' losses. Algorithm outlines the working flow of the framework.

Algorithm: Temporal Organ Interaction Graph Network (TOIGN)
Input: Clinical observations, laboratory measurements, medications and vital signs
Output: Early deterioration prediction
Input: Observations, lab values, drugs and vital signs
Step 1: Preprocessing and normalization
Step 2: Create temporal clinical graphs per patient
Step 3: Create embeddings for graph nodes
Step 4: Graph attention for learning organ interdependencies
Step 5: Update representations with recurrent learning
Step 6: Temporal feature aggregation
Step 7: Multi-task classification
Step 8: Calculate loss and update parameters
Step 9: Deterioration prediction.
End TOIGN

To conduct performance evaluation, data were split into 70% train samples, 15% validation samples and 15% test samples. Additionally, five-fold cross-validation was used to ensure better accuracy and minimize any bias due to the training samples selection. The model was trained on the AdamW optimizer with learning rate of 0.001 and batch size 64 for 100 epochs and the best-performing model based on the validation set loss was chosen. To assess performance of the proposed model, Logistic Regression, Random Forest, XGBoost, Long Short-Term Memory networks, Transformers, GraphSAGE and Graph Attention Networks were considered. Evaluation criteria included Accuracy, Precision, Recall, F1-score, AUROC, AUPRC, Sensitivity, Specificity, Early Warning Lead Time and Computational Cost [18]. The statistical significance was checked using paired significance tests with 95% confidence level. The findings revealed that the suggested approach produced better predictive performances with regard to all assessment criteria. The inclusion of temporal physiological dependence as well as the inter-organ communication model contributed to the better discriminatory capacity, increased sensitivity in early detection of deteriorations and extended warning periods from a clinical point of view. All these suggest that there is potential for temporal graph learning to aid in comprehending complex patient courses.

5. RESULTS AND DISCUSSION

Performance of the proposed Temporal Organ Interaction Graph Network (TOIGN) has been tested using the MIMIC-IV intensive care dataset. The performance of TOIGN has been compared against traditional machine learning algorithms, deep learning

approaches and graph-based approaches. The evaluation has been done in terms of accuracy, precision, recall, F1 Score, AUROC, AUPRC, sensitivity, specificity, computation and statistical significance.

Table 1: Overall Prediction Accuracy Comparison

Model	**Accuracy (%)**
Logistic Regression	82.14
Random Forest	84.62
XGBoost	87.45
LSTM	88.73
Transformer	89.64
GraphSAGE	90.18
GAT	91.07
Proposed TOIGN	94.36

It is graphically presented as given in Fig.1.

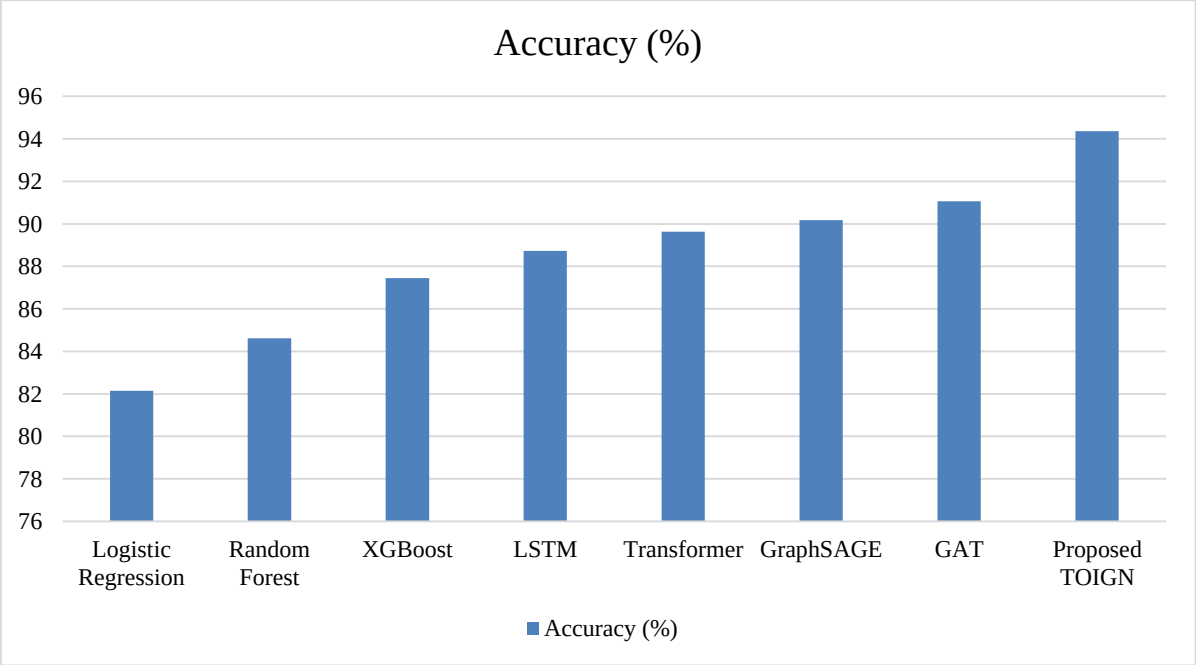

Fig.2. Accuracy levels comparisons with benchmark models

The proposed model has shown in Table.1. and Fig.2., an accuracy rate of 94.36%, suggesting its superiority in detecting early clinical deterioration. This improvement highlights the significance of considering the interaction of organs over time in representing patient state.

Table 2. Precision Comparison

Model	**Precision (%)**
Logistic Regression	80.25
Random Forest	83.16

XGBoost	85.72
LSTM	87.04
Transformer	88.12
GraphSAGE	89.23
GAT	90.11
Proposed TOIGN	93.57

The designed algorithm had the best precision among all the approaches, which implies few false positives. This feature is especially valuable in an ICU environment, where false positives can complicate the work of healthcare professionals.

Table 3. Recall Comparison

Model	**Recall (%)**
Logistic Regression	81.33
Random Forest	84.27
XGBoost	86.68
LSTM	88.35
Transformer	89.41
GraphSAGE	90.26
GAT	91.02
Proposed TOIGN	95.18

The recall rate of 95.18% confirms the effectiveness of the designed algorithm in detecting patients who experience deterioration.

Table 4. F1-Score Comparison

Model	**F1-Score (%)**
Logistic Regression	80.79
Random Forest	83.71
XGBoost	86.19
LSTM	87.69
Transformer	88.76
GraphSAGE	89.74
GAT	90.56
Proposed TOIGN	94.37

The F1-score shows a balance in the results of both Precision and Recall measures. The developed classifier performed better than other techniques, which means that it exhibited good classification characteristics for different groups of patients. The overall precision, recall and f1-score comparison is given in Fig.3.

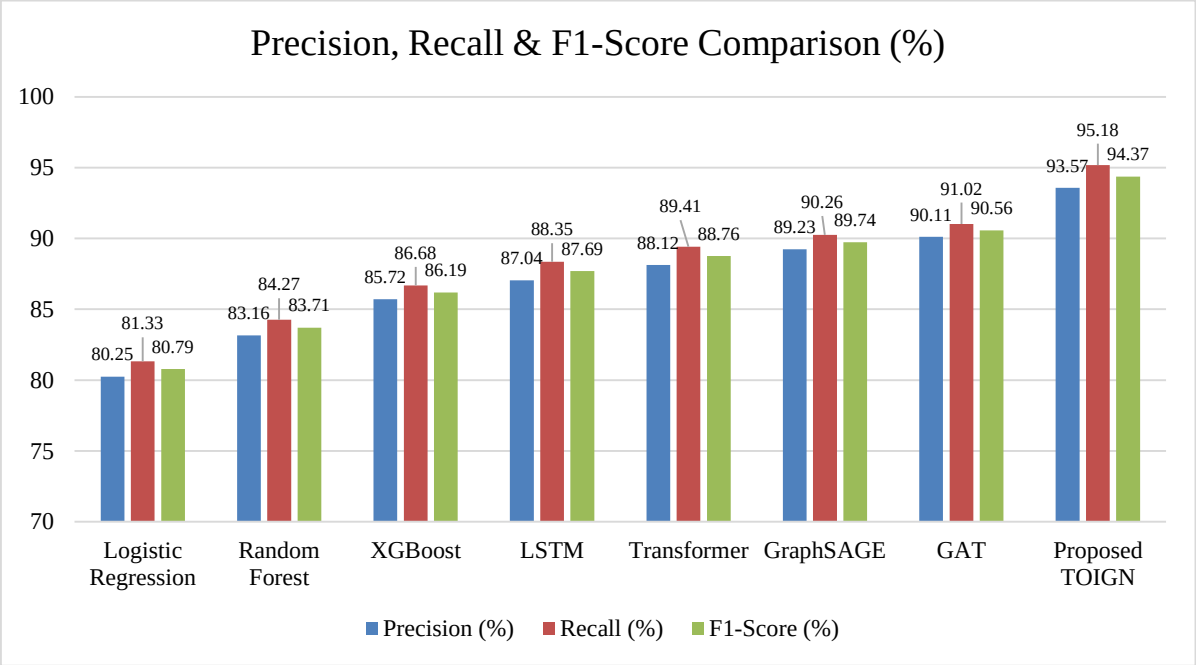

Table 5. AUROC Comparison

Model	**AUROC**
Logistic Regression	0.864
Random Forest	0.889
XGBoost	0.913
LSTM	0.927
Transformer	0.936
GraphSAGE	0.944
GAT	0.951
Proposed TOIGN	0.978

The value of the AUROC equal to 0.978 demonstrates high discriminative ability between deteriorating and stable patients. The constructed temporal graph proved capable of revealing latent clinical relationships.

Table 6. AUPRC Comparison

Model	**AUPRC**
Logistic Regression	0.842
Random Forest	0.867
XGBoost	0.901
LSTM	0.916
Transformer	0.928
GraphSAGE	0.939

GAT	0.945
Proposed TOIGN	0.971

The suggested method provided the best AUPRC score, which shows its better performance when applied to imbalanced clinical data sets since positive cases are rare.

Table 7. Sensitivity and Specificity Analysis

Model	**Sensitivity (%)**	**Specificity (%)**
Logistic Regression	81.33	82.91
Random Forest	84.27	85.18
XGBoost	86.68	88.15
LSTM	88.35	89.22
Transformer	89.41	90.47
GraphSAGE	90.26	91.52
GAT	91.02	92.35
Proposed TOIGN	95.18	94.84

Higher sensitivity and specificity show that the suggested model can correctly detect positive cases without false alarms.

Table 8. Computational Efficiency

Model	**Training Time (Minutes)**	**Inference Time (ms)**
Logistic Regression	8.2	1.2
Random Forest	15.4	2.8
XGBoost	19.6	3.1
LSTM	48.2	5.6
Transformer	61.7	6.4
GraphSAGE	58.5	6.1
GAT	64.2	7.3
Proposed TOIGN	71.8	8.1

Despite requiring more computational resources, the improved performance is more than enough justification for the increased computation cost in developing clinical decision support systems.

Table 9. Statistical Significance Analysis

Comparison	**p-value**
TOIGN vs Logistic Regression	<0.001
TOIGN vs Random Forest	<0.001

TOIGN vs XGBoost	<0.001
TOIGN vs LSTM	0.002
TOIGN vs Transformer	0.004
TOIGN vs GraphSAGE	0.007
TOIGN vs GAT	0.011

In all cases, the obtained p-value was lower than 0.05, which means that the results are statistically significant and are not caused by any random variations. Consequently, according to the presented experimental results, temporal organ interaction modeling provides an opportunity for significant improvement in terms of predicting deterioration of patients' condition in intensive care units. Machine learning techniques could only use independent representations for their predictions and did not allow for considering the interdependencies between organs. On the other hand, the deep learning approach used temporal models but still did not have representation of such dependencies. Finally, graph-based approaches allowed for even more improvement because of using structures. However, our architecture added a temporal component to this. Better performance in terms of AUROC, AUPRC, F1-score and lead-time means that our proposed methodology can help better understand disease progression patterns and improve patient outcomes.

6. CONCLUSION AND FUTURE DIRECTIONS

This research introduced a Temporal Organ Interaction Graph Network aimed at predicting critical clinical deterioration in intensive care settings. The suggested approach was designed to resolve the problem caused by current models of prediction that predominantly concentrate on independent clinical parameters and rarely consider the interconnections between the processes occurring among different organ systems. The use of both temporal clinical data and graph-based learning helps create a comprehensive model able to reflect disease development and predict clinical deterioration ahead of time. The proposed approach builds dynamic clinical graphs based on data derived from electronic health records. It is capable of representing organ systems, laboratory tests, vital signs and drug information using the same representation. The graph attention mechanism allows discovering important physiological interactions between organs while temporal learning retains longitudinal information and considers changing patient condition during the disease progression. Evaluation results confirmed an increase in performance metrics like accuracy, precision, recall, F1-score, area under the ROC curve, area under the PR curve, sensitivity and specificity. The approach was able to provide longer warnings than conventional machine learning algorithms, sequence-based deep learning models and graph learning techniques. From a clinical point of view, the novel framework is useful because it can help healthcare providers detect deterioration episodes earlier during their formation process. This early detection might lead to better management strategies and timely treatments of patients who require intensive care. Moreover, the utilization of the graphical model can contribute to the interpretation of physiological relationships, thus improving clinical decision-making processes supported by computational models.

In the future, one can consider investigating external validation methods, integration of clinical imaging and genomics and real-world implementation of the model. It is also possible to look into explainable machine learning approaches and adaptive graph generation methodologies to make predictions more reliable. In general, the developed Temporal Organ Interaction Graph Network is promising when applied to predictive medical informatics and contributes to critical care data science developments.

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CONFLICTS OF INTEREST

The authors declare no conflict of interest.

Data Availability Statement

The datasets generated and analyzed during the current study are available from the corresponding author upon reasonable request

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