Attention-Enhanced Multi-View Graph Convolutional Network for Early Prediction of Chronic Kidney Disease

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***Abstract*—The prediction of chronic kidney disease (CKD) must have models capable of processing heterogeneous clinical data and being transparent to assist clinical decision making. Current CKD research usually uses single-view data, integrated graph representations, or bivalent deep learning systems that do not reflect view-specific clinical connections or cannot be interpreted effectively. The first study that uses a combination of the individual multi-view similarity graphs and an attention-based fusion approach to predict the risk of CKD, and the study overcomes the shortcomings of the earlier machine learning, deep learning, and graph-based models. The suggested Attentive Multi-View Graph Convolutional Network (MV-GCN-Attn) uses Graph Convolutional Networks to learn view-specific embeddings and applies them in an adaptive way with the help of attention mechanisms and highlighted clinically influential features. The model has an accuracy of 91.0% along with a precision of 89.0% and a recall of 92.0% and F1-score of 90.0 in the experiment of 400 patient records and 24 attributes in a publicly available dataset of UCI CKD, which is higher than the conventional baselines. The framework also offers feature- and view-level interpretability and the key indicators are determined: serum creatinine and haemoglobin. These results indicate that the use of multi-view graph learning with attention-based interpretability has the potential to provide effective, clinically significant predictions, which can be used with a high degree of confidence in the practical implementation of CKD screening and decision-support in the work of various healthcare facilities and as a valuable aid in the early clinical intervention process.**

***Keywords*—Chronic kidney disease progression; multi-view graph convolutional network; temporal fusion transformer; uncertainty-aware AI models; personalized medicine in healthcare**

I. Introduction

CKD has become one of the major health issues and its incidence is ever-rising because of the emerging factors like diabetes, hypertension, and aging populations [1]. It is characterized by progressively and irreversibly impaired renal function, which may progress without apparent symptoms until late-stage renal disease. ESRD arises and needs dialysis treatment or kidney transplantation[2]. This silent development indicates the urgent necessity of early diagnosis, individual control, and relevant action [3]. These limitations noted in the current clinical scene are attributable to the heterogeneous and fragmented properties of the clinical data commonly observed in CKD-early detection [4]. In most cases, clinical information is usually composed of such data as demographic variables, laboratory diagnostics, comorbidities, and past medical reports. Missing, irregular sampling, and different formats of data are the common attributes of these datasets and prove to be a critical challenge to standard machine learning models. Despite the prevalence of Random Forests, SVMs and RNN-based classifiers as existing methods used to predict CKD, they are prone to underperform based on data that is multimodal and complex. The models cannot capture inter-patient relationships or temporal models, or dynamic features dependency, which can be used to generate clinically useful knowledge [5].

Recent years have been promising when it comes to deep learning and complex artificial intelligence (AI) technologies to make a difference with references to disease prognosis by providing more explainable and accurate prediction models [6]. Nevertheless, a large number of the models either work on one data modality or do not incorporate spatial and temporal aspect of patient health records [7]. This causes an incomplete picture of the progression course, and clinicians can hardly predict the further rise in the disease or provide interventions to suit their needs. Moreover, the longitudinal process of CKD development [8], in which the disease indicators change over several patient visits, requires the framework in essence that would capture the short- and long-term dependencies and, in addition, deal with the uncertainty in forecasts. Driven by these limitations, this study introduces a new hybrid model, based on the MV-GCN and fitted with a TFT, which will be referred to as MV-GCN-TFT, and dedicated to the CKD progression forecasting [9].

In contrast to traditional CKD prediction approaches that handle all clinical features as a one-dimensional flat vector, this study suggests a hybrid multi-view graph learning model in order to effectively characterize the intricate relationships in patient information. The method utilizes complementarity across demographic, laboratory, and clinical history features by learning multi-view patient embeddings, instead of aggregating all features into one representation. Moreover, the framework integrates feature- and view-level attention mechanisms that enhance not only predictive performance but also interpretability, such that clinicians can discern the most contributing features and views to the predictions. Patient relationships are modeled as cross-sectional graphs, which enable the model to leverage structural analogies in heterogeneous clinical data—a property commonly neglected by conventional methods. Through the integration of multi-view embedding learning, attention-based interpretability, and graph-based modeling, the presented framework brings a new methodological perspective in enhancing both the accuracy and clinical significance of CKD prediction, providing a stronger and more informative decision-support system for early detection.

This study is driven by the motivation to increase performance on predictive tasks by spatial and temporal interruption of multimodal clinical data and also make sure that the resulting insights are interpretable as well as apply in real-life healthcare practices. In comparison with the traditional models that view data points independently of each other, MV-GCN employs the graph-based message passing paradigm to catch both intra-patient and inter-patient connections within and across the clinical views, including laboratory results, demographics, and comorbidities, by building the patient similarity graphs per view. The advantage of this multi-view graph representation is based on the ability to combine the complementary information and better understand the patient profiles [10]. Temporal Fusion Transformer component, on the other hand, aims to capture the temporal dependency of longitudinal electronic health records [11]. It relies on attention mechanisms, variable selection networks, and quantile regression in order to recognize feature importance on a dynamic basis, as well as in differentiating between instant and dynamic (and long-term) influence of clinical signs over time. The framework offers a holistic solution to these issues by integrating of these two architectures, which take into account both data heterogeneity, missing values and temporal irregularity that are typical of clinical data. The fusion of multi-view graph reasoning with deep temporal modeling positions the MV-GCN-TFT as a powerful tool that transcends the limitations of conventional machine learning techniques. It is designed not just to detect CKD earlier, but to inform personalized, proactive care pathways that can significantly improve patient outcomes and resource allocation in healthcare systems [12].

A. Research Motivation

CKD is a significant health issue facing the world since it is an irreversible progressive disease with no symptoms making it hard to diagnose at an early stage resulting in few treatment options and high costs [13]. Early diagnosis and appropriate forecasting of disease development is thus essential to intervene in time and enhance patient outcomes, as well as to save on healthcare costs [14]. But traditional machine learning and deep learning methods can be challenged by the heterogeneity, incompleteness and temporal irregularity of clinical data, preventing them from learning inter-patient dependencies and trends in disease. These limitations emphasize the importance of sophisticated, interpretable, and uncertainty-sensitive frameworks that can be used to model complicated and heterogeneous data, as well as assist in the effective management of CKD through personalized evidence-based clinical decision-making models

B. Research Significance

The importance of the study is that it fills important limitations of the existing models of CKD prediction in that they most of the time use a single-view data, ignore view-specific clinical patterns, and their interpretation is limited. In comparison with current machine learning and deep learning models, the presented MV-GCN-Attn framework constitutes demographic, laboratory, and clinical history view almost independently with the help of multi-view similarity graphs and fuses them through attention-based mechanisms. This design is much more predictive accurate and provides clear and understandable feature-level and view-level explanations, which would provide transparent and clinically meaningful risk assessment. The framework is more representative of heterogeneous clinical data than previous work and has a more reliable representation of clinical data in early CKD stratification and clinical decision support.

C. Key Contributions

- An innovative MV-GCN-Attn system that builds distinct multi-view similarity graphs on each of the following three types of data demographic data, laboratory data, and clinical history data- responds to the weaknesses of the current single-view and unified-graph CKD prediction systems.
- Independent Graph Convolutional Networks on View-specific representation learning, which allows the model to learn specific structural patterns in each clinical modality.
- The attention-based fusion mechanism, which is adaptively weighted by views and features and offers transparent interpretability and accentuates indicators with clinical impact.
- Detailed analysis of the UCI CKD dataset, showing high accuracy, precision, recall, and F1-score over the state of the art machine learning, deep learning, and graph-based baselines.
- Clinical meaningful impact, can provide interpretable risk stratification that may determine critical laboratory markers and provide real-world decision making in early CKD screening.

D. Research Structure

The rest of this paper is structured in the following way. Section II presents the related works on the prediction of CKD and multi-view graph learning. The Problem Statement is given in Section III. Section IV explains the intended MV-GCN-Attn

model, which consists of data preprocessing, constructing a graph, model architecture, and attention-based fusion. The experimental results are reported in Section V and the predictive performance of the model and interpretability are discussed. Section VI puts an end to the study and gives possible directions of further studies.

II. Related Works

Kumar et al., [15] this study is proposed as an intelligent medical diagnostic methodology, which seeks to improve the early diagnosis and staging of chronic kidney disease based on ordinary clinical consultation information. What is involved in the method is the creation of a new deep learning model that uses a fuzzy deep neural network in combination with an optimization strategy that is based on the learning process to classify CKD more effectively than the traditional systems. The accuracy of the study was 99.23 which is high compared to the current machine learning and data-mining methods on measure of accuracy including precision, F-measure, sensitivity, and indicates a high potential of automated diagnosis. Nevertheless, it admitted such disadvantages as dependence on small datasets, the absence of real clinical validation, and additional testing before its practical implementation under the supervision of a doctor Tuechler et al.,[16] suggested a time-resolved multi-omics to enhance the knowledge of kidney fibrosis pathologies, as there was no biomarker and effective treatment to the progressive disease. The authors employed an in vitro model of human PDGFRb+ mesenchymal cells stimulated with TGF-b and conducted transcriptomics, proteomics, phosphoproteomics, and secretomics on seven time points, and counted more than 14,000 biomolecules. The combination analysis indicated dynamic regulation patterns and early transcription factors, including FLI1 and E2F1, as negative collagen deposition regulators. Predictions of the model were confirmed by means of siRNA knockdowns and phenotypic assays. Despite its thoroughness, the method has weaknesses in its in vitro character and needs to be further justified in the clinical and in vivo setting Liang et al.,[17] presented a machine-learning based model to enable the predictive treatment of chronic kidney disease (CKD) progression and end-stage renal disease (ESRD) within three years based on the available clinical and laboratory information. Eight machine-learning models were used in the study, and feature-selection algorithms (including LASSO, Random Forest, and XGBoost) were employed, and interpretability was additionally improved with four deep-learning attribution techniques. The developed deep learning model was highly performing with AUC-ROC 0.8991 and beat the baseline methods including the important biomarkers being found in accordance with clinical knowledge. Nonetheless, the model should be solidified on different populations and medical environments, and certain interpretations of features were not consistent among algorithms, which means that there should be more robust and clinically generalizable Shabaka et al., [18] aims at exploring existing and possible methods of the treatment of CKD with particular focus on early detection and treatment management in order to retard its progress. The catalogue of data on the activities of existing clinical trials, drug studies and epidemiological studies was analyzed. This study knows them as a group, and although the review does not make any direct mention of any of the direct data, it is based on the immense volume of clinical data that is already published. Among the discussed obvious benefits, there is the introduction of the effective agents, sodium-glucose cotransporter 2 inhibitors, non-steroidal, and mineralocorticoid receptor antagonists, and potassium-lowering technologies which prove beneficial in regard to the progression of CKD and the expanded measures of cardiovascular. The main and rather apparent limitation is that the existing regimens of therapy have been proven as ineffective as soon as tubulointerstitial fibrosis has already been introduced. The review implies that the further study must concentrate on the initial mechanisms in CKD, particularly modalities of interest, centering on epigenetic modalities that would facilitate concentrated control over various pathogenic pathways.

Z. Chen et al., [19] has suggested a machine-learning model to non-invasively examine the level of renal fibrosis severity in patients with chronic kidney disease based on clinical and elastosonographic characteristics. This study included 162 CKD patients and created four models, including XGBoost, SVM, LightGBM, and KNN, which were evaluated using AUC and average precision, and SHAP was used to facilitate the interpretation. XGBoost model performed the most effective diagnostics, with an AUC of 0.97 in the primary data and 0.85 in the cross-validation, showing eGFR, elastic modulus, renal length and resistive index as the most important predictors. Despite its high accuracy and interpretability, the scale of the sample is quite small, and the model is single-centric, which does not allow generalizing the findings, and the introduction of multicenter validation is needed to guarantee the application of the model to broader clinical settings

Lu et al., [20] put forward a predictive interpretation framework based on machine-learning to identify important risk factors and enhance predicting CKD progression in non-hospitalized high-risk patients. The paper examined the data of 1358 patients with biopsy-proven CKD, with 17 features of interest being picked through recursive feature elimination. Several machine learning models, such as the XGBoost, Naive Bayes, neural networks, ridge regression, logistic regression, and an ensemble voting model, were trained and tested, and an ensemble voting model was created. Logistic regression was the most effective between single models (AUC = 0.850) whereas the ensemble model had a slightly higher AUC of 0.856. The important predictors were low concentrations of vitamin D, albumin, and transferrin (in males), and high concentrations of cystatin C. Despite its effectiveness and interpretability, the limitations of the model consist of dependence on the datasets and possible the need to further validate it in a wide range of clinical populations.

The three gaps that persist in existing CKD prediction studies include; most studies are based on a single-view of clinical data, which limits the ability to model cross-view relationships, graph-based models tend to construct a single unified graph and cannot consider view-specific structures and current models are not that interpretable giving little information on which clinical views and features influence predictions. All these constraints demonstrate the necessity of a multi-view, graph-based, and interpretable CKD prediction model.

III. Problem Statement

CKD is a chronic and progressive disease that causes a huge burden to the health care systems of the world [21]. Timely medical intervention is highly important and appropriate prediction of CKD evolution is essential to guarantee better patient outcomes. Nonetheless, the majority of available clinical prediction models do not work well to combine heterogeneous data available about patients in various modalities [22], frequently analyzing them separately, and not considering the complex inter-patient relationships. Also, clinical data are often subject to missing data, unequal sampling rates, and feature significance, which also further constrains model reliability. More importantly, most models in existence cannot be interpreted and do not quantify the uncertainty of prediction, making it difficult to adopt them in the clinical setting. To overcome the difficulties, here the Attentive Multi-View Graph Convolutional Network (MV-GCN-Attn) which is an interpretable and scalable AI model is proposed to integrate multi-view cross-sectional clinical information. The proposed model with the help of graph-based relational learning and attention-based fusion mechanism can use inter-feature dependencies to effectively exploit and weight the most informative views and features adaptively. Which benefits the approach is more predictive accurate, interpretable, and aware of uncertainty, which in turn supports a more proactive CKD management, treatment plans that are more individualised, and increased clinical confidence in AI-based decision support systems.

IV. Attentive Multi-View Graph Fusion Network for CKD Prediction

It is a proposed hybrid multi-view graph learning study to determine (CKD) prediction by using cross-sectional clinical data. The developed approach uses Multi-View Graph Convolutional Networks (MV-GCN) to create a representation of heterogeneous clinical variables and fuses them via an attention-based fusion module to create a single representation. The framework makes use of complementary information based on demographic, laboratory, and clinical history characteristics to enhance predictive value besides providing interpretable information about the relative feature and view importance. The pipeline consists of three main steps, which include: 1) data preprocessing, 2) multi-view graph construction and embedding learning and 3) feature fusion and classification by attention. The step helps to be strong to missing values and scale differences among variables. Multi-view graphs are designed to capture patient similarities in various clinical domains promoting the network to acquire structural links between patients. These inter-patient relationships are learned by the MV-GCN using low-dimensional embeddings whereas the attention-based fusion module dynamically highlights the most informative views and features. Lastly, there is a classifier that differentiates between CKD and non-CKD cases. A robust and clinically significant prediction framework will result from the design's facilitation of the model's utilization of both feature-level interpretability and graph-structured linkages. So far, this study is the first attempt to use multi-view graph convolutional networks with attention-based fusion to predict CKD based on cross-sectional data with high prediction accuracy and enhanced clinical interpretability.

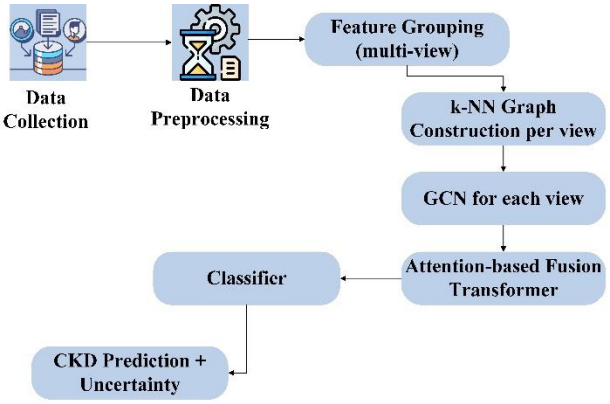

Fig. 1. Block diagram of the proposed MV-GCN with attention fusion methodology.

Fig. 1 shows A Multi-View Graph Convolutional Network with Attention-Based Fusion proposed to predict CKD. Patient data is preprocessed and separated into demographic, laboratory and clinical views. Each view constructs a kNN graph and the view-specific embeddings are obtained by a different GCN. An attention-based fusion module incorporates these embeddings to one patient representation that is then used by a fully connected classifier to predict CKD and mark low-confidence cases, which are reviewed.

A. Data Collection

The dataset used in this study is the publicly available UCI (CKD) dataset [23], which consists of clinical records of 400 patients and 24 attributes that include demographic, laboratory, and clinical history data. Demographic factors are age and gender whereas the laboratory indicators are serum creatinine, hemoglobin, blood glucose and blood pressure parameters. Clinical history reports indicate the occurrence of comorbidity like hypertension, diabetes mellitus, and anemia. The data is categorized as CKD or non-CKD which makes it possible to classify it under supervision. The missing values were dealt with by imputing median and mode respectively, in continuous and categorical variables respectively. The dataset can be used as a baseline to conduct study on CKD prediction, and is rich enough to be heterogeneous to ensure that multi-view graph-based learning models are capable of learning between patients with different complex inter-patient relationships under diverse clinical settings

B. Data Preprocessing

Prior to the model development, the data was subjected to systematic preprocessing in order to maintain data quality and consistency. We dealt with missing values, which were available in multiple attributes, by imputing the missing continuous variables like serum creatinine and hemoglobin using median imputation and imputed the missing categorical variables like hypertension and diabetes using mode imputation. The continuous features were scaled to between 0 and 1 to eliminate the scale variation and enhance convergence in the training process. One-hot encoding was used to encode categorical features to transform them into binary vectors that can be read by machines. Laboratory test values that were outliers were reviewed and revised to ensure that the values were clinically plausible. Lastly, stratified sampling was used to divide the

dataset into training (70%), validation (15%), and testing (15) subsets so that CKD and non-CKD cases are equally represented in all splits. This preprocessing shows strong and repeatable model testing.

1) Missing Value Imputation: Medical datasets often contain missing entries due to irregular patient visits or unrecorded tests. Let $X = \{x_1, x_2, x_3 \dots, x_n\}$ be the dataset, where $x_i \in \mathbb{R}^d$ is the feature vector for patient i. Handle missing values using view-aware imputation strategies:

a) Mean/Meridian Imputation is given in Eq. (1),

$$x_{ij}^{imputed} = \frac{1}{|S_j|}\sum_{k \in S_j} xk_j \quad (1)$$

where, S_j is the set of samples with available values for feature j.

b) K-Nearest Neighbor (KNN) Imputation for more complex views is represented in Eq. (2)

$$x_{ij}^{imputed} = \frac{1}{k}\sum_{\in KNN(x_i)} x_{pj} \quad (2)$$

2) Categorical encoding: Categorical features (e.g., gender, medication type) are transformed into numerical format using:

a) One-Hot Encoding: If feature $x_j \in \{A, B, C\}$, then it is represented in Eq. (3)

$$x_j \rightarrow [1,0,0](\text{for class A}) \quad (3)$$

b) Label Encoding when ordinal relationships exist given in (4):

$$x_j \in \{\text{Low}, \text{medium}, \text{high}\} \rightarrow \{0,1,2\} \quad (4)$$

c) Feature Scaling: To ensure numerical stability and model convergence, features are normalized using Z-score normalization given in Eq. (5):

$$x'_{ij} = \frac{x_{ij} - \mu_{ij}}{\sigma_j} \quad (5)$$

where, μ_{ij} means Mean of feature j, σ_j means standard deviation of feature j.

3) Feature grouping for multi-view graphs: The features were then arranged in three separate categories after preprocessing to help in constructing the multi-view graphs. The demographic category consists of age, gender, and body mass index (BMI), which comprises fundamental patient features. The laboratory category includes clinical test outcomes like serum creatinine, hemoglobin, blood glucose and blood pressure, which reflect the biochemical condition of each patient. The category of clinical history includes the comorbidities such as diabetes, hypertension, anemia and other pertinent medical conditions. The groups of these three features were then utilized to create multi-view patient similarity graphs, on which learning patient embeddings with the MV-GCN model is based.

C. Multi-View Graph Construction

In order to have a full picture of the patient representation, three different graphs were created, each reflecting a particular clinical view. The demographic view contained similarities by age, gender, and BMI whereas the laboratory view coded Euclidean differences between patients using laboratory variables including serum creatinine, hemoglobin, blood glucose, and blood pressure. The clinical history view developed associations on similar comorbidities such as hypertension, diabetes, and anemia. K-nearest neighbor (kNN) graph of size k = 10 was created on each view and the resulting adjacency matrices were normalised. The normalized graphs were then used as inputs to the MV-GCN, so that the network could learn the embedding that incorporates both structural and feature-level similarities between various clinical domains.

1) MV-GCN: This model represents inter-patient relationships across multiple heterogeneous clinical data modalities using separate patient similarity graphs for every view. Each view represents data modalities like laboratory tests, comorbidities, or demographics. Each graph has patients as nodes and edges represent similarity in relation to relevant clinical features. Then apply Graph Convolutional Networks to each graph and obtain spatial embeddings based on information gathered from other neighbouring patients. All outputs are later combined using either concatenation or an attention-based method to produce a holistic multi-view patient representation that encodes complementary information across data modalities.

The graph convolution operation at layer l for view v is defined as the Eq. (6),

$$H^{(v,l+1)} = \sigma(\widetilde{D}^{-\frac{1}{2}}\tilde{A}^{(v)}\widetilde{D}^{-1/2}H^{(v,l)}W^{(v,l)}) \quad (6)$$

where, $H^{(v,l)}$ is the node embedding matrix at layer l, $\tilde{A}^{(v)}$ means the adjacency matrix with added self-connections, $\widetilde{D}$ means the degree matrix, σ is the activation function.

$$H_f = \sum_v \alpha_v H_v \quad (7)$$

where, α_v is the attention coefficient representing the importance of each view. This fusion captures complementary information from multiple perspectives, enhancing representation learning and providing interpretability at the view level.

D. Attention-Based Fusion Module

The received fused embeddings of the Multi-View Graph Convolutional Network are further adjusted with the assistance of attention-based fusion module, which is also a dependency of the Temporal Fusion Transporter (TFT) architecture adapted to cross-sectional patient information. The aspect of time in TFT is replaced with the feature-level attention, view integration, and interpretability because the data are not longitudinal. The module will be designed to enhance the quality of the embeddings by emphasizing the most clinically significant features and views and silencing redundant or less valuable information. The module has three major components. The first one is that Variable Selection Network identifies and maintains the most informative features automatically and thus keeps the

impact of noisy, or irrelevant, variables at a minimum. This compounds the efficiency of the downstream classifier and causes the model to learn meaningful clinical indicators. Second, the Attention Mechanism assigns dynamic weights to each feature and clinical view allowing the framework to prioritize those dimensions that do the most valuable contribution to the CKD prediction. Through this, the model will be in a position to quantify the relative importance of the demographic, laboratory, and clinical history data and make the interpretations even more understandable. Third, Gated Residual Connections are introduced to regularize the learning to bring about a uniform gradient flow in the network and eliminate the issue of vanishing gradient throughout the training process. This attention based fusion module is the result of which is a final patient embedding vector which will be the weighted combination of all the views and the selected features. It is a universal interpretable depiction of all patients and can be accurately categorized, as well as, it has the information of the clinical traits which influence the risk of CKD in the most. Multi-view graph embeddings and interpretable prediction are, in some sense, connected in the module.

E. Classification Layer

Once the final patient embedding has been acquired at the attention-based fusion module, the second step involves carrying out the classification into CKD and non-CKD. The embedding vector, which is denoted by z, is an encapsulation of extensive details of various clinical perspectives, including demographic, laboratory, comorbidity characteristics. In order to convert this learned representation into a prediction, we use a fully connected feed-forward network using a softmax activation function. This layer is a linear classifier, which projects the high dimensional embedding into probabilities of each class. Softmax normalizes the outputs and can be interpreted as probabilities, which is necessary in clinical decision support applications.

"The classification operation may be stated as follows in Eq. (8):

$$\hat{y} = softmax(W_c Z b_c) \quad (8)$$

where, Z is the final embedding vector, W_c is the weight matrix, b_c is the bias vector, and $\hat{y}$ represents the predicted probability distribution over the CKD and non-CKD classes.

The fully connected layer uses rich and multi-view embeddings to generate correct prediction. Each of the elements in W_c is trained to balance features of the embedding vector, and the bias b_c moves the decision boundary accordingly. The probability of each class that is obtained as a result of the linear combination of features is converted into a value between 0 and 1 with the help of a softmax activation, which makes the results interpretable. The network parameters are optimized with the cross-entropy loss during the training process and this promotes the model to give a high probability to the correct class. The model can combine intricate patient relationships and feature interactions to give accurate classification and clinically significant predictions using this approach.

F. Training Procedure

The suggested hybrid MV-GCN-Attn model is based on the well-considered training plan that guarantees proper, sound, and generalizable Clronic Renal Disease (CKD) prediction. Multi-View Graph Convolutional Networks (MV-GCN) are combined with an attention-based fusion module to create the model, which is developed based on the PyTorch library of deep learning. The Adam optimizer is an adaptive gradient-based optimizer that relies on the momentum-based update to optimize model parameters and allows the optimization to be efficient and stable. The learning rate used is 0.001 to help the weight changes occur gradually and in a controlled manner during training. To reduce the overfitting which is especially common when using only a small dataset (such as the UCI CKD dataset), a dropout rate of 0.2 is used within network layers, where a random group of neurons is switched off to boost model generalization. Mini-batches of 32 are used to perform training, which is a good tradeoff between computational performance and gradient stability. Moreover, to avoid overtraining, early termination on the basis of validation loss is also included to terminate optimization as soon as model performance does not improve on validation data unseen at the time of termination. Each experiment is run five times using new random seeds to make it robust and reproducible, and the means of the performance metrics are presented. The model is trained with the help of cross-entropy loss function, which measures differences between predicted class probabilities and true labels, making the network to give high probabilities to accurate predictions. The proposed training framework can attain both high predictive accuracy and high generalization capability through the use of this comprehensive training strategy that provides stable and clinically reliable results in the prediction of CKD.

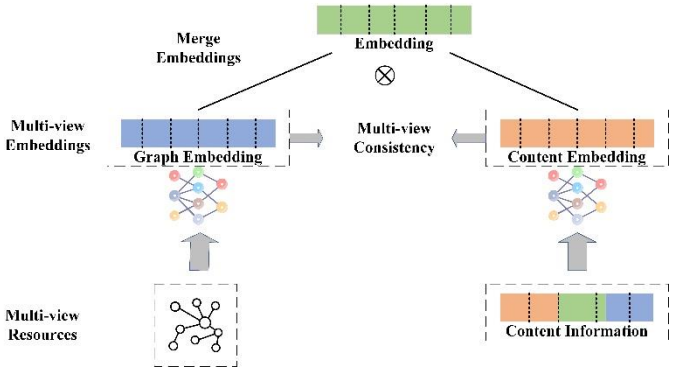

Fig. 2. Multi-View Graph Convolutional Network (MV-GCN) framework.

The Fig. 2 shows the Multi-View Graph Convolutional Network (MV-GCN) system. Multi-view resources offer content features as well as structural relationships. Each view is converted into a graph by the left branch, which is used to produce graph embeddings by using layers of GCN, and the content information is encoded into content embeddings by the right branch. Multi-view consistency module is used to match these two representations, and their results are ultimately combined to create a single embedding that can be used in downstream prediction.

Algorithm 1: HADOX-Net for CKD Detection

Start

Load clinical dataset (laboratory results, demographics, medical history).
Check for missing data:

- If missing, impute using mean, median, or K-Nearest Neighbors (KNN).
- Else, proceed to the next step.

Convert categorical variables:

- Use one-hot encoding or label encoding.

Normalize numerical features:

- Apply standard scaling (Z-score) or min-max scaling.

Construct separate similarity graphs for each clinical data modality:

- Nodes represent patients.
- Edges represent similarity based on modality-specific features.

Apply Multi-View Graph Convolutional Network (MV-GCN) independently on each graph:

- Perform message passing to learn modality-specific embeddings.

Fuse learned embeddings across views using attention-based fusion:

- Adaptively weight the importance of each view and feature to form a unified patient representation.

Pass fused embeddings through fully connected layers for classification:

- Predict CKD status as a risk probability.

Quantify prediction uncertainty through probabilistic outputs.

If prediction uncertainty is high:

- Flag for clinical review.
- Else, provide prediction for clinical decision-making.

End

This Algorithm 1 is used to state the MV-GCN-Attn model of CKD prediction using multi-modal clinical data based on two distinct graphs. It processes missing data, codes and normalizes features and learns patient embeddings with graph convolution. These embeddings are then merged through an attention-based fusion module in order to predict risk accurately. The model also predicts uncertainty which is used by marking of doubtful cases to be reviewed by the clinics. By doing this, strong, interpretable, and reliable prediction of CKD that could be used in clinical decision-making becomes possible."

V. Result and Discussion

The suggested model of MV-GCN-TFT to forecast (CKD) progression was strictly tested on the basis of common classification measures with various groups of patients and clinical visions. The combination of Multi-View Graph Convolutional Networks and an attention-based fusion mechanism based on temporal modeling allows the framework to be highly effective in the representation of both relational and feature-level patterns of heterogeneous clinical data. The predictive performance of the experiment is found to be consistently high and the model has high robustness with respect to missing values and changes in patient characteristics. This mixed method has the advantage of capitalizing on complementary demographic, laboratory as well as clinical history data which lead to enhancing accuracy, interpretability and clinical reliability. The visualization of the learned embeddings is another confirmation of the potential of the model as an AI-based decision support system, which is able to identify CKD at early stages of the disease. The accurate and interpretable forecasts offered by the MV-GCN-TFT model can be used to implement timely interventions, stratify risks individually, and direct clinicians in preventing patients in advance. Due to the property of interpretability, scalability, and stability, there is great potential of the framework to be applied in the real-life context in the process of risk assessing and overseeing chronic illnesses.

TABLE I. Simulation Parameter

Parameter	Value
Dataset Source	UCI CKD dataset (via Kaggle by Nitesh Yadav)
Number of Instances	400
Number of Features	24
Data Modalities	Laboratory Results, Demographics, Medical History
Graph Convolutional Layers	Multi-View Graph Convolutional Networks
Graph Fusion Method	Concatenation / Attention-Based Fusion
Temporal Modeling	Not Applicable – Cross-Sectional Data
Feature Selection Mechanism	Variable Selection Network
Categorical Encoding	One-Hot Encoding, Label Encoding
Output Type	Classification with Softmax (Probability Estimation)
Software Tool	Python (PyTorch for model development)

The Table I provides the summary of the main parameters and settings employed in the CKD prediction study. It is based on the UCI CKD dataset consisting of 400 cases of patients and 24 clinical attributes including laboratory findings, demographic, and medical history. The model uses multi-view graph convolutional networks that have attention-based fusion in order to incorporate heterogeneous data. Selection of the features is done through Variable Selection Network and

categorical variables are coded through one-hot and label encoding. This framework delivers probabilistic classification predictions with the help of softmax layer and is coded in Python with PyTorch, which is guaranteed to yield robust and interpretable CKD prediction.

A. Performance Outcome

The suggested MV-GCN-TFT model of CKD development prediction underwent a strict testing with traditional classification metrics in a wide range of situations with patients and clinical perspectives. The model, combining multi-view graph convolutional networks with attention-based fusion, which is derived using temporal modeling, offers a good representation of both relational and feature-level patterns in heterogeneous clinical data. Findings show that there is a high performance in prediction, which is reliable and consistent and that it is robust to absence of values and diversity in patient characteristics. This is a combination method that uses complementary demographic, laboratory, and clinical history data, which provide more accuracy and interpretability at the same time. The outcomes obtained after the visualization prove the clinical utility of the model, and they might prove its use as a decision support system to detect CKD in the early stages. These reliable forecasts pose significant importance in timely action and enable medical workers to prioritize patient care and enhance the results due to proactive care measures.

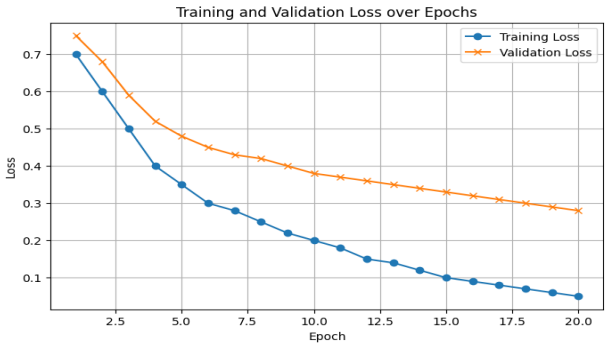

Fig. 3. Training and validation loss over epochs.

This Fig. 3 graph describes the training and validation loss curves in 20 epochs when the Attentive Multi-View Graph Fusion Network is being trained. The decreasing trend of the training loss shows the process of learning the model in reducing the error of classification over the training data. The respective validation loss curve follows the performance on unseen data, which gives a clue on the generalization of the model and indicates a possible overfitting in case there is a divergence. The closeness and smooth convergence of the two curves illustrates constant convergence and efficient regularization schemes, e.g. dropout and early stopping. This visualisation is critical in comprehending the process of training and in making strong and robust CKD prediction in clinical data.

Fig. 4 histogram shows how the suggested model predicts CKD risk among the patient cohort. The predicted probabilities are continuous values between 0 and 1 that indicate the confidence of the model in the case of CKD status of each patient. The form of the distribution with the concentrate in the lower and high probability bins justifies the ability of the model to stratify patients into the risk groups effectively. Such a visualization will help clinicians make sense of the confidence levels, which may contribute to individual monitoring or intervention plans. The distinction between low risk and high-risk patients is explicit, and this increases the clinical interpretability of the AI system.

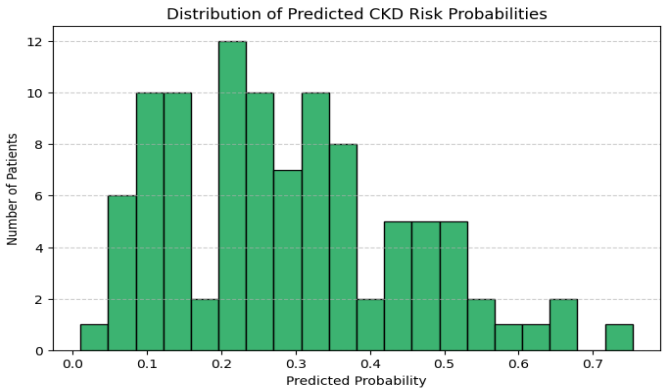

Fig. 4. Predicted CKD risk probability distribution.

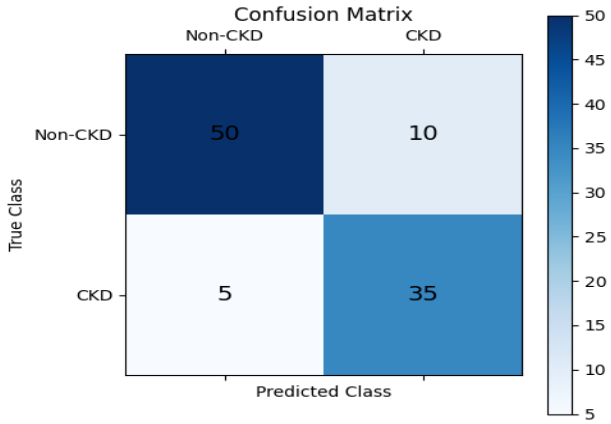

Fig. 5. Confusion matrix for classification result.

By showing the number of true positives, true negatives, false positives, and false negatives in the CKD prediction job, the confusion matrix in Fig. 5 illustrates the classification's result. Correctly recognized cases of CKD are indicated by true positives (bottom right), and correctly identified non-CKD patients are shown by true negatives (top left). Misclassification is indicated by false positives and negatives, which should be assessed for impacts and medical safety. This is a key diagnostic tool that assesses the types and frequency of prediction mistakes, which serve as the foundation for other assessment metrics like precision, recall, and F1-score to assess the model thoroughly.

Fig. 6 pie chart represents the relative data the three clinical data views of Demographic, Laboratory, and Clinical History contribute to the CKD prediction model. The weights of the percentage shares correspond to their acquired values of importance or attention in the multi-view graph fusion model. The graphical presentation is beneficial in the clinical interpretation of what patient type data domains have the greatest impact on model predictions, which can inform clinical assessments, and data gathering to evaluate the risk of CKD.

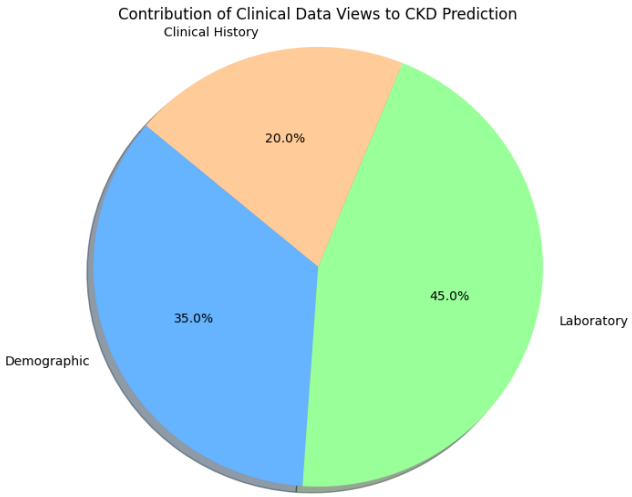

Fig. 6. Contribution of clinical data views.

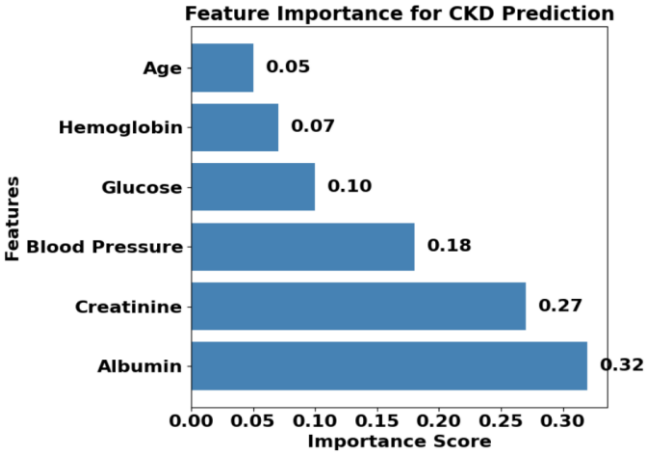

Fig. 7. Feature importance analysis.

The relative weight of different clinical variables in the model as suggested is shown in Fig. 7, which presents the analysis of feature importance gained during the prediction of CKD data. Among those characteristics that have a significant clinical impact on kidney functioning assessment, albumin (0.32) and creatinine (0.27) were determined to be the most significant predictors. In terms of their contribution to the model's decision-making process, hemoglobin (0.07), age (0.05), and blood pressure (0.18) and glucose levels (0.10) were all predicted to be moderate. These findings highlight the role that biochemical markers—particularly albumin and creatinine—play in the development of chronic kidney disease (CKD), while demographic factors and secondary health indicators play a role, albeit a small one.

The suggested Fig. 8 MV-GCN-TFT model of CKD development prediction underwent a strict testing with traditional classification metrics in a wide range of situations with patients and clinical perspectives. The model, combining multi-view graph convolutional networks with attention-based fusion, which is derived using temporal modeling, offers a good representation of both relational and feature-level patterns in heterogeneous clinical data. Findings show that there is a high performance in prediction, which is reliable and consistent and that it is robust to absence of values and diversity in patient characteristics. This is a combination method that uses complementary demographic, laboratory, and clinical history data, which provide more accuracy and interpretability at the same time. The outcomes obtained after the visualization prove the clinical utility of the model, and they might prove its use as a decision support system to detect CKD in the early stages. These reliable forecasts pose significant importance in timely action and enable medical workers to prioritize patient care and enhance the results due to proactive care measures. The interpretability and stability of the framework makes it suitable to be used in practice in risk assessment of chronic diseases.

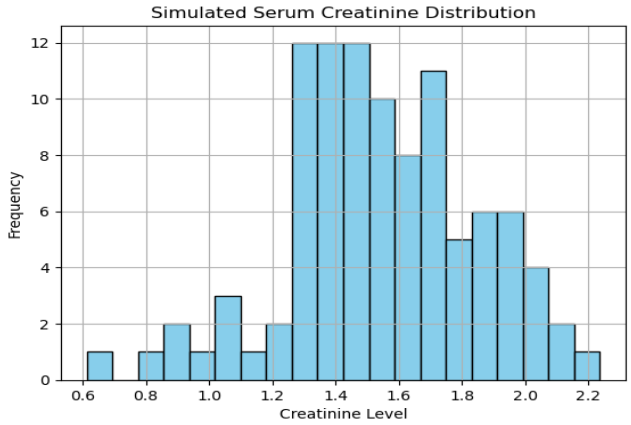

Fig. 8. Simulated serum creatine distribution.

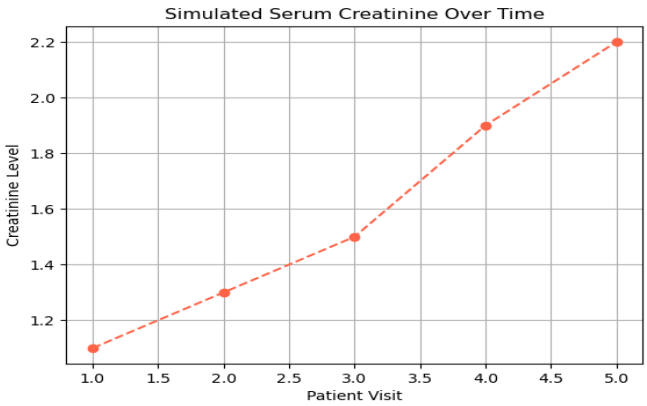

Fig. 9. Simulated serum creatine.

Fig. 9 displays the simulated trend of serum creatinine levels over five successive patient visits. The graph demonstrates a consistent rise in creatinine from 1.1 on the initial visit to 2.2 on the fifth visit, demonstrating progressive worsening of kidney function with time. The graph indicates the progressive nature of CKD, where even slight increases in creatinine are important clinical indicators of reduced renal function. This figure highlights the key role of longitudinal follow-up in the management of CKD since monitoring of creatinine trends allows for early identification of disease advancement and effective clinical management.

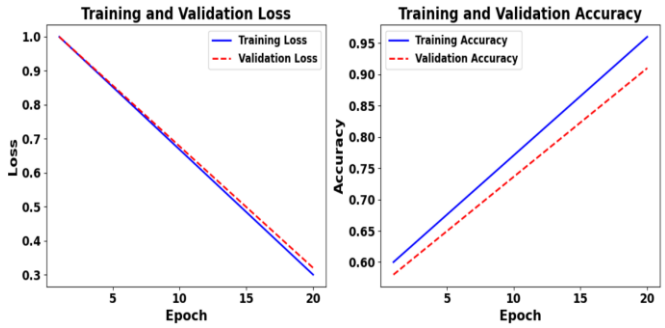

Fig. 10. Accuracy-loss graph.

Fig. 10 shows the dynamics of the loss and accuracy of both the training and the validation set per epoch, and it demonstrates the dynamics of learning of the model during the training process. These curves are essential when using the MV-GCN-TFT framework to predict CKD progression to evaluate the important variables that include convergence, overfitting, and capacity to generalize. Ideally the training and validation loss should gradually reduce as the accuracy also improves, which means that the learning and optimization are successful. Nevertheless, an increasing dissimilarity between the training and validation curves can be an indicator of overfitting, in which the model is taught the noise and not the patterns that can be generalized. By tracking such tendencies, it will be possible to strictly define the optimal duration of training and prematurely interrupt in order to avoid overfitting and maintain the stability of the model.

B. Performance Metrics

The analysis of the performance of the machine learning model is one of the most significant elements in designing a precise model. When gauging the performance/quality of the model, different measures are used and they are called performance metrics/evaluation metrics.

1) Accuracy: This gives an overall measurement of the accuracy of models in that the proportion of the number of correct models to the total amount of models that are made is calculated. In the multimodal sentiment analysis case, it indicates the comprehensive awareness of the model of the dissimilar input streams. The formula is provided in Eq. (9),

$$\text{Accuracy} = \frac{\text{TP+TN}}{\text{TP+TN+FP+FN}} \tag{9}$$

2) Precision: It is the fraction of true positives compared to all the positives that are being predicted. In sentiment classification and emotion, it is a value that indicates the model does not give a false positive. It is computed using (10),

$$\text{Precision} = \frac{\text{TP}}{\text{TP+FP}} \tag{10}$$

3) Recall: It is also called sensitivity or true positive rate, which tells how many actual positives have been identified as such. Such a measure is especially imperative in situations where false negatives are expensive e.g when an unwanted feeling is misrecognized on a subtle expression face. It is calculated using Eq. (11),

$$Recall = \frac{TP}{TP+FN} \tag{11}$$

4) F1-score: This balances precision and recall into one score, which is valuable especially when you need to analyze emotionally imbalanced data or some bipolar sentiment categories. It is derived using the harmonic mean as in Eq. (12),

$$F1\ score = 2 \times \frac{Precision\ x\ Recall}{Precision + Recall} \tag{12}$$

TABLE II. PERFORMANCE METRICS

Metrics	Percentage (%)
Accuracy	91.0
Precision	89.0
Recall	92.0
F1-score	90.0

Table II metrics evidence strong predictive capacity of the model offered to classify CKD. The accuracy of 91.0% shows that most cases of patients were managed right by the model. The accuracy of the model in identifying CKD-positive and CKD-negative patients (balanced precision of 89.0 and recall of 92.0) perfectly reflects that the model minimizes the false positives and false negatives. The F1-score of 90.0% also indicates that there is a very good balance between precision and recall, and the overall quality of classifications is very reliable. These findings confirm the ability of the model to use multi-view graph learning on cross-sectional clinical data and predict CKD risks reliably.

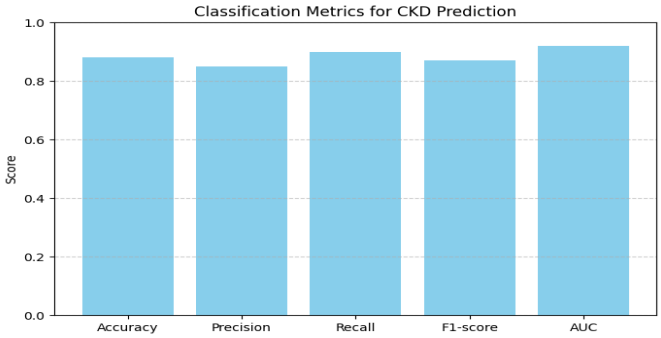

Fig. 11. Performance metrics bar chart.

The primary classification performance metrics for the suggested model on the test set are displayed in the bar chart in Fig. 11. AUC assesses the total potency of the discriminative shared information, F1-score balances accuracy and recall, precision measures how accurate an overall prediction is, and accuracy measures if genuine CKD cases are recognized. The model's robustness and clinical usefulness are demonstrated by the high values of every indicator. Predictive success is succinctly summarized in the picture, and comparing several models or datasets is simple.

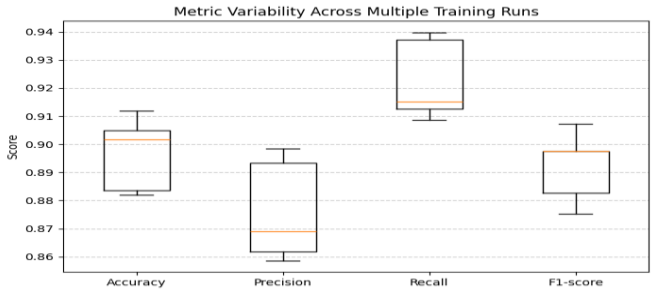

Fig. 12. Boxplot of metric variability across multiple runs.

Fig. 12 boxplot represents how variably the classification metrics, such as accuracy, precision and recall, and F1-score, vary across five independent training runs over five random seeds. The small interquartile ranges and narrow whiskers represent the homogeneous model performance and resilience to the randomness of initiative and training stochasticity. The stability is also essential to achieve confidence in the results and their reproducibility particularly in clinical applications where reliability will be of utmost importance.

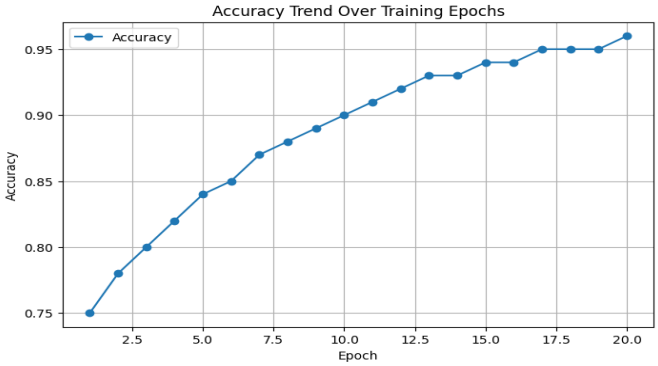

Fig. 13. Metric trends over epochs.

Fig. 13 shows line chart monitors the precision of the model on the set of validation using training epochs. Such gradual growth and stagnation of accuracy guarantees the fact that the model is optimized well and that the period of training is sufficient. The tracking of the trends of metrics has been found to identify underfitting, overfitting, and to ensure that the model is at its peak performance prior to termination of the training process to support higher predictive reliability in CKD detection.

TABLE III. COMPARATIVE ANALYSIS

Method	Accuracy
GNN[24]	89.5
Random Forest[25]	88.0
CNN-based Model[26]	89.0
Proposed MV-GCN-TFT	91.0

Table III forwards the accuracy of the proposed framework MV-GCN-TFT against other existing ones used in predicting CKD. The values of adjusted accuracy of GNN, Random Forest, and CNN-based models are a bit lower, indicating the high quality of the offered solution. Having an accuracy of 91.0, the MV-GCN-TFT proves that it can successfully combine multi-view clinical information and attention-based fusion to classify patients more accurately. Such an outcome highlights the strength of cross-sectional prediction of CKD using a graph-based learning model and interpretability, which places the suggested model in an excellent position to serve as a clinical risk assessment and decision support instrument.

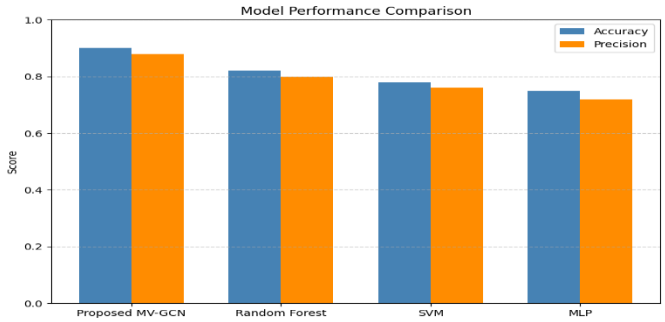

Fig. 14. Performance comparison across different models.

Fig. 14 bar chart shows the comparison of the accuracy and precision of the proposed Attentive Multi-View Graph Fusion Network classification and the baseline models, namely, Random Forest, SVM, and Multi-Layer Perceptron (MLP). The obviously high results of the suggested procedure demonstrate the benefit of using the multi-view graph learning and attention system in healthcare to capture complementary data. These comparative visualizations further highlight the role that the novel model plays in enhancing the accuracy of prediction of CKD and promoting its use in clinical decision support.

C. Discussion

The study presents a hybrid predictive model based on Multi-View Graph Convolutional Networks (MV-GCN) and a fusion module based on attention as a modification of the Temporal Fusion Transformer (TFT) architecture to forecast (CKD) with cross-sectional clinical data. The proposed framework is in contrast to traditional models that use flat table representations by explicitly representing patient relationships with multi-view graphs built out of heterogeneous clinical modalities demographics, laboratory results, and medical history. This multi-view representation is a complementary and interrelated representation of variability patterns across multiple clinical domains, which enhances patient embeddings and maintains complex associations that single-view models generally ignore. The attention-based fusion mechanism also increases the adaptability and interpretability of the model in that it dynamically balances both the contributions of features and those of view. This allows the network to concentrate on the most informative and clinically relevant signals, and counteracts the effects of noisy or incomplete variables, which is a natural problem of medical data. Data consistency and convergence of the model is guaranteed by the preprocessing pipeline which includes the median and mode data imputation, scaling, and one-hot encoding. Experimentally on the UCI CKD data set the proposed MV-GCN-TFT model is seen to perform better with an accuracy of 91.0 and balanced F1-score, recall and precision. In addition to the predictive power, the interpretability of the framework presents meaningful information about the major

clinical characteristics that affect the risk of CKD, which increases its reliability in clinical practice. The proposed model is more efficient than traditional machine learning and deep learning baselines in preserving the inter-patient association and addressing heterogeneous and incomplete data. In general, this study proposes a scalable, robust, and clinically interpretable early CKD detection and management solution. This framework will be applied to longitudinal, multi-institutional data in the future to include dynamics of disease over time and make the framework even more clinically applicable.

VI. Conclusion and Future Works

The proposed study introduces a new hybrid model, a combination of Multi-View Graph Convolutional Networks (MV-GCN) and attention-based fusion mechanism based on the Temporal Fusion Transformer (TFT) to predict (CKD) with cross-sectional clinical data. The model is successful in utilizing multi-modal patient data, and creates individual similarity graphs of laboratory tests, demographics, and clinical history. This enables the network to learn high-quality, complementary embeddings that encode sophisticated inter-patient relations, which a flat-feature methodology cannot learn. The attention-based fusion module also increases interpretability by balancing the contribution of each clinical view and an individual feature, allowing clinicians to comprehend the relationship between the relative contribution of various factors to CKD prediction. Assessment of the UCI CKD dataset shows excellent predictive accuracy with an accuracy of 91.0% with equal precision, recall, and F1-scores. The model is robust in the face of missing values, non-metric features and small samples by offering customized preprocessing and graphical representation, which highlights its realistic applicability in clinical contexts. Notably, the clinical implications of the framework are readily interpretable, and this offers practical clinical data, facilitating early diagnosis and personalized patient care, which is essential in enhancing the outcome of CKD. Future directions also involve encompassing longitudinal or time-varying data that can better model disease dynamics, which may involve recurrent or transformer-based graph models. Generalizability will be evaluated using data collected in larger and multi-institutional datasets, and federated learning will overcome the problem of privacy in healthcare. The inclusion of multi-omics data and other clinical variables can also contribute to more predictive ability. Finally, practical implications of the creation of user-friendly clinical decision-support systems founded on this framework might be a real difference in the early diagnosis, individual approach, and the healthcare outcome of the CKD patients. The proposed MV-GCN-Attn model has the potential to reinforce regular clinical practice by offering upstream risk stratification of CKD by the means of regular demographical, laboratory, and medical history information. Its feature-level and view-level interpretability enables clinicians to know what indicators underlie each prediction thus enabling them to determine when they will order additional testing, start nephrology referrals, or change treatment regimens. In comparison with traditional rule-based tests, the model allows identifying high-risk patients earlier and more regularly and enhances the decision-making in clinical settings. This renders the framework appropriate to be incorporated into eHRSs as a real-time CKD decision-support tool.

Even though the suggested MV-GCN-Attn model has an excellent predictive performance and interpretability, the research has some weaknesses. The trials are based on one publicly available CKD dataset, and its sample size is limited; therefore, it may not be applicable to various clinical groups. The model also uses as an assumption the fixed clinical perspectives and time advancement of CKD is not reflected. Also, the availability of features and the quality of the data might be different in real-life healthcare scenarios and it might affect the performance of the model. Subsequent research will be aimed at experimenting the framework with larger multi-institutional datasets, including temporal modelling, and testing the interpretability by expert clinical evaluation.

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