(IJACSA) International Journal of Advanced Computer Science and Applications,
Vol. 17, No. 6, 2026

# Progression-Aware Temporal Graph Transformer for Reliable Chronic Kidney Disease Trajectory Prediction

Dr. Roshan D. Suvaris[1], Dr. Padmavathy E.[2], Dilfuza Akabirkhodjaeva[3],
Dr. T. K. Rama Krishna Rao[4], Dr. R. Sindhu[5], Farrukh Sobia[6], Elangovan Muniyandy[7], Aseel Smerat[8]
Nitte (Deemed to be University)-NMAM Institute of Technology (NMAMIT), Department of MCA, Nitte, India, 574110[1]
Assistant Professor, Department: Mathematics, Vel Tech Rangarajan Dr. Sagunthala R&D Institute of Science and Technology, Avadi, Chennai, India[2]
Department: System Analysis and Mathematical Modelling, The University of World Economy and Diplomacy, Uzbekistan[3]
Professor, Department of Computer Science and Engineering, Koneru Lakshmaih Education Foundation, Vaddeswaram, Guntur, Andhra Pradesh, India[4]
Assistant Professor, Department of Mathematics, Dr. N.G.P Arts and Science College, Coimbatore-641048, Tamil Nadu, India[5]
Department of Health Informatics, College of Public Health and Tropical Medicine-Jazan University,
Jazan, Kingdom of Saudi Arabia[6]
Department of Biosciences, Saveetha School of Engineering-Saveetha Institute of Medical and Technical Sciences,
Chennai, India - 602 105[7]
Faculty of Educational Sciences, Al-Ahliyya Amman University, Amman, 19328, Jordan[8]

***Abstract*—Chronic Kidney Disease (CKD) is a progressive and irreversible condition that requires early prediction of renal deterioration for effective clinical intervention. Existing studies based on static machine learning and conventional deep learning models fail to capture temporal dependencies, evolving biomarker interactions, and longitudinal disease progression patterns, leading to limited predictive reliability in real-world clinical settings. To address these limitations, this study proposes a Progression-Aware Temporal Graph Transformer for reliable CKD trajectory prediction using the Chronic Renal Insufficiency Cohort (CRIC) dataset comprising 5,625 patients with longitudinal clinical follow-ups and repeated biomarker measurements including eGFR, creatinine, albumin, blood pressure, glucose, and HbA1c. The proposed framework integrates a temporal transformer encoder for sequential patient representation, a dynamic biomarker graph to model evolving renal interactions, and a multi-scale temporal attention mechanism to capture both short- and long-term deterioration patterns. The model is implemented using Python with PyTorch and executed on GPU-based computational infrastructure for efficient training and inference. Experimental results demonstrate that the proposed model achieves 95.0% accuracy, 94.2% precision, 95.1% recall, and 94.6% F1-score, improving performance by approximately 2–4% over state-of-the-art baselines such as Random Forest, KNN, GNN, and 1D CNN models. Additionally, survival analysis yields a Concordance Index of 0.952, confirming strong risk-ranking capability for dialysis onset prediction. The framework also maintains robust performance under noisy and missing data conditions, demonstrating strong generalization ability. In conclusion, the proposed model provides an interpretable, scalable, and clinically reliable solution for CKD progression forecasting, enabling early intervention, personalized treatment planning, and improved renal outcome prediction in clinical decision-support systems.***

***Keywords*—Chronic Kidney Disease; temporal graph learning; disease progression prediction; longitudinal healthcare modeling; trajectory prediction**

## I. INTRODUCTION

Chronic Kidney Disease is a chronic, progressive and life threatening condition where the kidneys function over time [1]. It impacts millions of people worldwide and is a significant public health problem because of its close link with cardiovascular disease, ESRD, and higher death rate [2] [3]. Many cases of early stage CKD are not diagnosed and are not treated because they do not have any symptoms [4]. Therefore, it is important to monitor renal biomarkers like estimated glomerular filtration rate (eGFR), serum creatinine, blood pressure, glucose level and albuminuria continuously to detect progression of disease before irreversible kidney damage [5]. Early prediction of CKD progression is an important tool for improving patient outcomes by enabling timely clinical interventions, patient-tailored treatment and avoiding dialysis dependency [6].

Although significant progress has been made in the prediction of CKD using machine learning and deep learning, there remain several key limitations in the current approaches [7]. Most of the conventional models are based on the binary classification of the presence or absence of CKD, and do not account for the temporal patterns of renal deterioration. Such techniques typically analyze each clinical variable separately and fail to account for the changing relationships among the biomarkers over time for individual patients [8]. Moreover, many of the current methods are not capable of temporal reasoning, which limits their usefulness in modeling a progressive decline in kidney function over the long term [9]. Existing models also lack the flexibility to adapt to different disease states as the disease progresses, due to the use of fixed graph structures and shallow attention mechanisms [10]. Furthermore, the lack of interpretation and lack of clinical transparency decreases the trust of physicians and hampers the direct use in clinical practice.

Motivated by these challenges, this study proposes a novel framework entitled Progression-Aware Temporal Graph Transformer for Reliable Chronic Kidney Disease Trajectory Prediction. The proposed model utilises patient trajectories over time, along with the interaction of biomarkers that is dynamic, to predict future patterns of renal deterioration. The temporal transformer encoding is used to model the sequential clinical evolution, and the progression-aware graph learning models the adaptive interdependencies between biomarkers at various clinical stages. Furthermore, multi-scale temporal attention is used to boost long-term progression reasoning, and make the clinical interpretation more interpretable. The proposed framework is able to predict CKD trajectories instead of the static classification, which enables early intervention, prevents dialysis, and assists with nephrology decisions for clinical prognosis.

### *A. Problem Statement*

Existing prediction approaches for CKD are mostly static prediction of the disease stage and are not well suited to the longitudinal modelling of renal deterioration in the repeated visit of patients [11]. Traditional machine learning and deep learning methods focus on the clinical features themselves rather than dynamically evolving relationships between the biomarkers, like the interactions between creatinine, glucose, blood pressure and eGFR over time [12]. In addition, most graph-based methods use fixed graph structures, which are unable to evolve to different phases of CKD. The other major drawback is the lack of current models which can predict future renal decline, dialysis risk or disease course in advance. These constraints limit the clinical validity and early intervention potential, and underscore the importance of progression-aware temporal learning frameworks that can model evolve temporal biomarkers and long-term CKD trajectory forecasting.

### *B. Key Contribution*

- A progression-aware temporal graph transformer framework is proposed to model longitudinal clinical trajectories for reliable Chronic Kidney Disease progression prediction.
- Dynamic biomarker graph learning is introduced to capture evolving interdependencies among renal biomarkers across different stages of disease progression.
- A multi-scale temporal attention mechanism is developed to simultaneously learn short-term fluctuations and long-term renal deterioration patterns from sequential patient records.
- The proposed framework performs future trajectory forecasting by predicting estimated glomerular filtration rate decline and Chronic Kidney Disease stage transitions using longitudinal CRIC patient data.
- Extensive experimental evaluation and comparative analysis demonstrate improved predictive reliability, temporal reasoning capability, and clinical interpretability over existing machine learning and deep learning approaches for CKD prognosis.

The remainder of this study will be structured as follows: Section II will contain a summary of the study that is currently available. Section III is about the model proposed and its implementation. The Section IV entails experiments and discussion that accompanied them. Last conclusion and future work in Section V.

## II. RELATED WORKS

Lei et al. [13] performed a systematic review and meta-analysis to investigate the efficacy of ML techniques in predicting the development of kidney disease. This research involved the examination of 15 articles, where 6 studies, including 12,534 patients, were considered in the meta-analysis. According to the results, ML models had sufficient predictive performance, with an AUC of the HSROC of 0.87. The ML techniques exhibited high specificity and average sensitivity concerning the identification of disease progression. Moreover, the subgroup analysis for CKD and IgA nephropathy demonstrated a decent predictive accuracy as well.

Islam et al., [14] Examined the use of machine learning and predictive modeling in early detection of CKD. In this research, 25 different clinical variables were analyzed by means of feature selection to determine the most important predictors. This helped in reducing the data set to about 30 percent of the original features. Twelve different supervised machine learning classifiers were considered for predicting CKD. It was found that the XGBoost classifier gave the best results with accuracy, precision, recall, and F1 score of 98.3, 98, 98, and 98, respectively.

Nagawa et al., [15] proposed a new method of CKD diagnosis through ultra-wide-field fundus examination as opposed to conventional laboratory examination. They used convolutional neural networks to identify discriminative retinal features that are related to kidney disease progression. The research used a huge imaging dataset and showed a high sensitivity and specificity, which reveals a good diagnostic ability. One of the strengths is that its screening procedure is non-invasive such that CKD can be detected during eye check-ups. However, the approach depends on specialized imaging equipment and lacks integration with structured clinical data, which may restrict its scalability and applicability in resource-constrained healthcare environments.

Tawsik Jawad et al.,[16] investigated the use of XAI with the ensemble method for predictive analysis of CKD. In this study, a predictive model was created based on accurate predictions by utilizing clinical biomarkers to increase transparency in the decision-making process through XAI methods. Using the suggested framework, the most relevant features were determined, which impact the prediction of CKD, as well as the reasons for each prediction, making it possible for doctors to make informed decisions regarding treatment. The results of the investigation showed that integration of ensemble learning and XAI improves prediction accuracy and early detection of CKD.

Arif et al., [17] aimed to enhance CKD prediction with an enhanced preprocessing and feature selection pipeline.. They used the Boruta algorithm, feature relevance analysis, and anomaly detection to identify predictors that are stable and significant. The method was experimented on clinical data and found to be highly classified, which indicates the significance of preprocessing in a medical machine learning system. Nonetheless, the research has a limitation of a small sample size and lacks a wide range of population. The lack of external validation further limits its use in actual healthcare context where heterogeneity of the data is a crucial criterion.

Al-Momani et al., [18] carried out a comparative analysis to compare various machine learning algorithms in the prediction of CKD. The research analyzed Artificial Neural Networks, Support Vector Machines, and K-Nearest Neighbors using clinical data. Of these, Artificial Neural Networks had the best accuracy, and therefore they have the potential to model nonlinear relations within CKD data. The research offers good information about the performance of the algorithms, but has shortcomings in terms of limited features and absence of long-term patient outcomes. These weaknesses limit the model in terms of capturing disease progression, and impact its strength in a real-world clinical usage.

Huamg et al., [19] introduced a predictable and computationally cost effective CKD forecasting framework with an optimized XGBoost model. The approach included Bayesian optimization using Optuna and explained using SHAP. The model was tested on structured electronic health records and performed better at predicting that at a lower computational cost. One of the benefits is accuracy/interpretability balance. But the framework is heavily dependent on quality structured data, which restricts its applicability to heterogeneous or unstructured clinical settings. It also does not incorporate relational feature learning to learn biomarker interactions.

The main limitation of the literature on CKD prediction is that researchers focus on fragmented modeling approaches, considering preprocessing, feature selection, prediction and explainability as individual elements, which results in poor generalization and weak performance in conditions of noisy or imbalanced clinical data. A lot of methods are based on manual preprocessing or single-level attention and explainability is commonly post-hoc and not connected to the learning process. Scalability and other clinical feasibility limitations are also added with imaging-based and hybrid models. The proposed Progression-Aware Temporal Graph Transformer predicts future Chronic Kidney Disease progression by learning longitudinal biomarker trajectories, dynamic temporal relationships, and evolving renal deterioration patterns, enabling accurate forecasting of eGFR decline, CKD stage transition, dialysis risk, and hospitalization probability.

Table I provides a comparative study of the current CKD prediction models, their methodologies, datasets, strengths, and limitations. Although most methods are very accurate and have better interpretability, most of them have shortcomings, including inability to scale to large data sets, reliance on structured data, no relational modeling, and lack of validation in a variety of clinical settings.

TABLE I. COMPARATIVE ANALYSIS OF EXISTING CKD PREDICTION METHODS

| Author | Methodology | Advantage | Disadvantage |
|---|---|---|---|
| (Ghosh & Khandoker,[20] | GBoost with SHAP, LIME | Accurate and interpretable predictions | Small imbalanced dataset limitations |
| Iftikhar et al.,[21] | Multiple ML model comparison | Comprehensive model evaluation. | No temporal progression modeling. |
| Dritsas & Trigka, 2022b [22] | Class balancing with ML | Extremely high prediction accuracy | No temporal progression modeling |
| Jawad et al. [23] | RF-based ML model | High accuracy and explainability | Limited feature interaction modeling |
| Arif et al. [17] | Boruta + preprocessing pipeline | Stable feature selection | Small dataset, no validation |
| Al-Momani et al. [18] | ANN, SVM, KNN comparison | Strong ANN performance | Limited features, no temporal data |
| Huang et al. [19] | XGBoost + SHAP + Optuna | Efficient and interpretable | Depends on structured data |

## III. PROPOSED PROGRESSION-AWARE TEMPORAL GRAPH LEARNING FOR EARLY CKD PROGRESSION FORECASTING

The proposed methodology proposes a Progression-Aware Temporal Graph Transformer framework for forecasting the progression of Chronic Kidney Disease in the CRIC dataset. The proposed framework is distinct from traditional CKD prediction models that make a single binary classification, as it captures the renal deterioration trajectory over multiple clinical visits. Longitudinal patient records with renal biomarkers, demographics and clinical measures are preprocessed initially with missing value imputation, temporal alignment, feature normalization and progression-aware balancing. Sequential patient trajectories are then built to ensure that the disease evolution patterns are maintained visit wise. The proposed framework aims to learn the temporal biomarker dependencies and the behavior of the changes over time from repeated patient visits using a Temporal Transformer Encoder. Biomarkers are shown as dynamic graph nodes to reflect the changing nature of the physiological interactions, and clinical relationships as adaptive temporal edges. The main novelty of the study lies in this progression-aware graph construction because the interactions between biomarkers are dynamic and change throughout the different clinical stages of renal deterioration and in function of the severity of the CKD. For instance, glucose and HbA1c have a greater effect in early diabetic nephropathy, while creatinine, albumin, and eGFR dominate during the advanced stages of CKD progression. Moreover, a Multi-Scale Temporal Memory Attention mechanism is introduced to learn simultaneously both short-term fluctuations in biomarkers and long-term patterns of renal deterioration acceleration. Finally, a forecasting head forecasts future eGFR decline, CKD stage transition, dialysis onset probability and renal hospitalization risk over a number of time horizons. The proposed methodology addresses the temporal reasoning, progression consistency, adaptive biomarker learning and clinical interpretability challenges, which are not addressed by current static CKD prediction methods. Fig. 1 shows overall workflow architecture of proposed model.

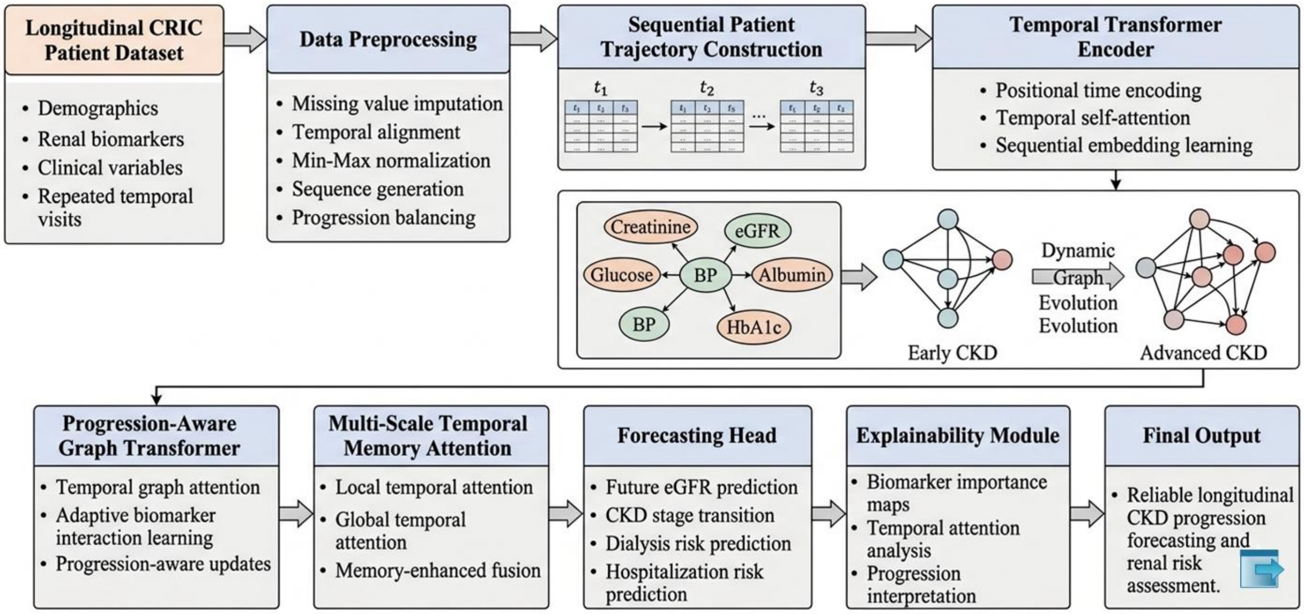

Fig. 1. Proposed progression-aware temporal graph learning for early ckd progression forecasting framework.

### A. Data Collection

The dataset analyzed in this study is the Chronic Renal Insufficiency Cohort Study (NIDDK CRC) longitudinal clinical data set from the NIDDK Central Repository [24]. The CRIC data set includes clinical data from some 5,625 patients with Chronic Kidney Disease, who have been followed longitudinally over time since 2003. The data comprises annual clinical visits as well as evaluations at 6-month intervals, offering detailed time trajectories for individual patients for renal progression analysis. There are approximately 400+ clinical variables and laboratory parameters available, such as demographic, renal biomarkers, cardiovascular parameters, medication history, lifestyle and comorbidity data.

Major demographics like age, gender, ethnicity and body mass index (BMI) are chosen for this study. Serum creatinine, estimated glomerular filtration rate (eGFR), and urinary albumin-to-creatinine ratio (UACR), along with albumin, hemoglobin and blood urea nitrogen, are all important renal biomarkers that are used to monitor kidney function deterioration. Other clinical parameters like blood glucose, SBP, DBP, HbA1C, diabetes status and cardiovascular parameters are also included. The proposed framework is predicted to cover three important clinical outcomes: future eGFR decline, transition to CKD stage and estimation of dialysis risk. The CRIC dataset is ideal for modelling the temporal progression of the disease and predicting CKD trajectories due to repeated patient visits and longitudinal measurements of biomarkers.

### B. Data Pre-Processing

Mode imputation was used to fill in categorical features, whereas missing values for numerical biomarkers like creatinine, hemoglobin, albumin, blood pressure, and eGFR were imputed through median imputation, which involves calculating the median of the available values of each feature. In cases where a single value is missing within a longitudinal patient's trajectory, temporal interpolation is utilized to maintain temporal consistency between neighboring visits. This is stated in Eq. (1) below.

$$X_t = X_{t-1} + \frac{t-t_{-1}}{t_{+1}-t_{-1}}(X_{t+1}-X_{t-1}) \tag{1}$$

where, $X_t$ represents interpolated biomarker value at time $t$, $X_{t-1}$ and $X_{t+1}$ represent nearest available observations before and after the missing visit, respectively, and $t_{-1}$ and $t_{+1}$ denote their corresponding timestamps. This formulation performs linear temporal interpolation to estimate missing biomarker measurements while preserving the temporal continuity of longitudinal patient trajectories.

Since patient visits occur at irregular time intervals, all visits are temporally aligned and converted into ordered longitudinal sequences based on visit timestamps. This allows disease progression analysis in terms of patient-specific temporal trajectories to be constructed. To stabilize transformer training and avoid feature dominance, Min-Max normalization is applied to all numerical biomarkers as (2).

$$Z_{norm} = \frac{Z-Z_{min}}{Z_{max}-Z_{min}} \tag{2}$$

where, Z is the feature value, $Z_{min}$ is the minimum, and $Z_{max}$ is the highest of that feature. Moreover, class imbalance due to the scarcity of severe CKD progression events is corrected by introducing Temporal SMOTE, focal loss optimization and progression-aware weighting methods for better prediction of rare events in CKD progression and robust temporal generalization.

Approximately 5,000 patient trajectories were retained following the preprocessing, temporal sequence generation and the elimination of longitudinal data of patients with incomplete data. Nearly balanced longitudinal training samples were created by applying Temporal SMOTE and progression-aware resampling to overcome the progression-event imbalance in order to ensure reliable CKD trajectory forecasting.

### C. Sequential Patient Trajectory Construction

The patient trajectory construction problem in the longitudinal CRIC dataset is solved by the sequential patient trajectory construction method, which will be a structured temporal evolution sequence of diseases of patients in the CRIC that can be used for progression-aware learning. Unlike traditional CKD prediction approaches that rely on isolated clinical snapshots, this framework models continuous renal deterioration across repeated follow-up visits, enabling a more realistic representation of disease progression dynamics. Each patient $P_i$ is represented as an ordered trajectory in (3).

$$P_i = \{Xi^1, X_i^2, Xi^3, \ldots, X_i^T\} \tag{3}$$

where, $X_i^T$ denotes the biomarker feature vector recorded at visit $t$ and $T$ represents the total number of available longitudinal assessments.

Each temporal biomarker vector is defined as $Xi^{\mathrm{t}} = [Cr_{\mathrm{t}}, eGFR_{\mathrm{t}}, UACR_{\mathrm{t}}, Glucose_{\mathrm{t}}, HbA1c_{\mathrm{t}}, BP_{\mathrm{t}}, Albumin_{\mathrm{t}}, BMI_{\mathrm{t}}]$, capturing key renal, metabolic, and physiological indicators. Here, $\mathrm{Cr_t}$ represents serum creatinine, $\mathrm{eGFR_t}$ denotes estimated glomerular filtration rate, $\mathrm{UACR_t}$ indicates urine albumin-to-creatinine ratio, $\mathrm{Glucose_t}$ and $\mathrm{HbA1c_t}$ reflect glycemic status, $\mathrm{BP_t}$ captures blood pressure, $\mathrm{Albumin_t}$ represents serum albumin levels, and $\mathrm{BMI_t}$ denotes body mass index.

This structured representation retains the longitudinal dependencies and allows learning of the patterns of progressive deterioration of biomarkers associated with CKD progression. For example, rise in creatinine along with a fall in eGFR would mean a deterioration in renal function whereas rise in glucose and HbA1c would mean progression of diabetic nephropathy.

To further capture temporal dynamics, transition variations between consecutive visits are computed as $\Delta Xi^{\mathrm{t}} = Xi^{\mathrm{t+1}} - Xi^{\mathrm{t}}$, representing biomarker change over time. This formulation allows to estimate the velocity of progression, deterioration rate and trends in temporal evolution. These sequential representations are then passed to the Temporal Transformer Encoder and Dynamic Temporal Graph Learning module for the purposes of CKD stage transition prediction, future eGFR forecasting and dialysis risk assessment.

### D. Temporal Biomarker Embedding

The Temporal Biomarker Embedding stage aims to model the longitudinal renal progression behavior from a series of patient trajectories in CRIC. The proposed framework utilizes a Temporal Transformer Encoder to capture temporal dependencies, visit-wise disease progression and evolving biomarker interactions across various follow-up visits, unlike the conventional CKD prediction models, which process independent clinical records, where there is no temporal continuity. This stage will allow the model to learn the pattern of the renal biomarkers that occur over time and the nature of their contribution to the subsequent worsening of CKD. First temporal biomarker vectors are merged with positional time encoding to retain the temporal order of visits to the patient. The temporal input representation is formulated as (4).

$$Z_t = X_t + PE_t \tag{4}$$

where, $Z_t$ denotes the temporal input embedding at visit t, $X_t$ represents the biomarker feature vector at time t, and $PE_t$ denotes positional temporal encoding used to preserve visit order information. The positional encoding helps the transformer to distinguish the different observation times of the kidney, maintaining the order of the progression of renal events across the patient's history.

The Temporal Transformer Encoder is then used to calculate the contextual temporal representations based on self-attention learning. The framework is able to capture the temporal self-attention, which means it knows how past renal states affect future kidney deterioration. For instance, if a patient's creatinine and UACR continue to rise over multiple appointments and his or her eGFR continues to fall over time, the weights for these measures are larger at each visit, allowing for the accurate prediction of progression. The temporal embeddings generated capture short-term fluctuations in the biomarkers as well as long term patterns of renal decline. These learned representations are then passed to the Dynamic Temporal Graph Learning module for modelling the evolving biomarker relationships and progression-aware CKD forecasting.

### E. Dynamic Temporal Biomarker Graph Construction

Progression-Aware Temporal Graph Transformer's main contribution is the Dynamic Temporal Biomarker Graph Construction module. The proposed approach dynamically models the evolving renal interactions over the course of the disease with longitudinal clinical visits, whereas the conventional CKD prediction models assume fixed relationships between the biomarkers throughout the disease. The nodes in each time step are the individual biomarkers, and the adaptive graph edges are a model of physiological and pathological relationships between biomarkers. This allows the framework to reflect the dynamics of renal interactions that are different across disease stages in the course of CKD. At each timestamp t, the temporal biomarker graph is represented as: $R_t = (O_t, E_t)$ where $R_t$ denotes the dynamic biomarker graph at temporal visit $t$, $O_t$ represents the set of biomarker nodes, and $E_t$ denotes adaptive temporal edges representing biomarker interactions.

The renal and clinical variables included in the biomarker node set are creatinine, eGFR, glucose, blood pressure, albumin, HbA1c and UACR. Edges in the graph are the emerging physiological relationships between the biomarkers. For instance, glucose and HbA1c have more interactions in the early stage of diabetic nephropathy, and creatinine and albumin have more interactions in the later stage of renal deterioration. To model evolving biomarker relationships, temporal graph attention is computed as (5).

$$h_i^{(t+1)} = \sigma\left(\sum_{j \in N(i)} \alpha_{ij}^{(t)} W_t h_j^{(t)}\right) \tag{5}$$

where, $h_i^{(t+1)}$ denotes the updated representation of biomarker node $i$ at the next temporal state, $N(i)$ represents neighboring biomarkers connected to node $i$, $\alpha_{ij}^{(t)}$ denotes temporal attention weight between biomarkers $i$ and $j$, $W_t$ represents learnable temporal transformation weights, $h_j^{(t)}$ denotes neighboring biomarker representations, and $\sigma$ represents nonlinear activation. The adaptive graph evolution allows the framework to learn the progression-aware renal dependency patterns between the different stages of CKD. As a result, the model reflects clinically relevant deterioration processes, changing interactions between diseases, and temporal renal progression patterns better than static graph architectures.

### *F. Progression-Aware Graph Transformer and Temporal Attention Mechanism*

Proposed framework for the longitudinal prediction of CKD progression is based on the Progression-Aware Graph Transformer, which is the core learning architecture. The aim of this module is to learn dynamically the evolving relationship between biomarkers and detect clinically important patterns of renal deterioration along patient's temporal trajectories. The proposed transformer dynamically updates the graph attention to reflect the severity and progression rate of CKD and the temporal evolution of the disease, whereas the conventional graph neural networks make the static assumption of biomarker relations. This allows focusing on increasing biomarker levels and accelerating renal decline patterns that are very likely to impact future kidney decline.

The temporal attention coefficient is a dynamic measure of clinical relevance of the interactions between the biomarkers throughout the disease progression. Thus, during the early stages of CKD, glucose, HbA1c and BP are given more priority because of the renal effects of diabetes and hypertension. In advanced stages of CKD, greater emphasis is placed on UACR progression, deterioration of albumin, eGFR decline, and creatinine, as these markers reflect severe renal impairment.

The proposed attention mechanism also captures the progression velocity and temporal deterioration acceleration by highlighting the fast deterioration of biomarker trajectories at the different visits. This learning is progression aware, which allows the framework to identify patients who are improving from those who are getting worse quickly. Thus, the resulting graph representations maintain clinically meaningful patterns of temporal progression, improve the ability to predict long-term graph trajectories, and increase the accuracy of the prediction of future eGFR decline, progression to CKD stage and the risk of dialysis. Fig. 2 shows Progression-Aware Graph Transformer architecture.

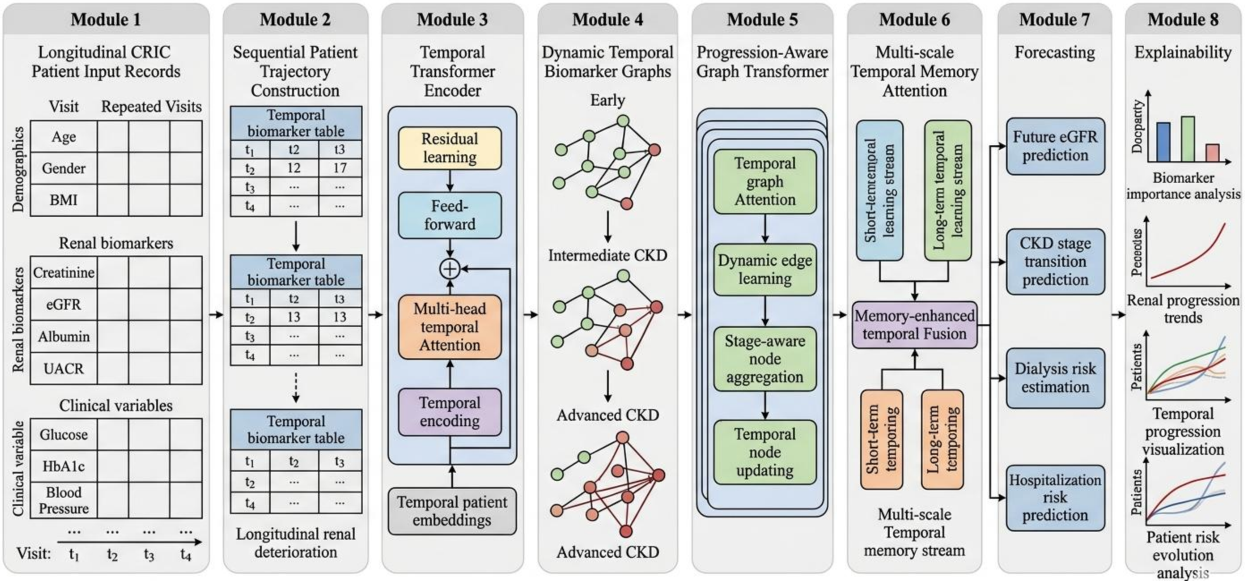

Fig. 2. Progression-aware graph transformer architecture.

### *G. Multi-Scale Temporal Attention and Memory Learning*

The Multi-Scale Temporal Attention module aims to detect short-term biomarker fluctuations and identify long-term renal deterioration patterns from longitudinal trajectories of patients in the CRIC dataset. This module is a novel aspect of the proposed framework as CKD progression is a process that occurs over a long period and is accompanied by sudden deterioration events. In traditional temporal and sequential models, the learning of the local variations and the global evolution trends of the diseases are not performed simultaneously. To overcome this shortcoming, the proposed model combines local temporal attention, global temporal attention and memory-enhanced transformer blocks to enhance the progression-consistent CKD forecasting.

The local temporal attention first learns short-term fluctuations of the biomarkers between neighboring visits. This allows the model to detect abrupt renal deterioration signals like rapid decrease in eGFR, rise of creatinine, albuminuria, and abnormal changes in blood pressure. Simultaneously, the global temporal attention mechanism is able to learn long-term disease development patterns from the entire disease history, allowing for robust modelling of chronic renal decline patterns. The multi-scale temporal attention mechanism is formulated as (6).

$$M_t = \lambda L_t + (1 - \lambda) G_t \tag{6}$$

Where $M_t$ denotes the final multi-scale temporal memory representation, $L_t$ represents local temporal attention features capturing short-term variations, $G_t$ denotes global temporal attention features representing long-term progression behavior, and $\lambda$ represents adaptive weighting used to balance local and global temporal information. The memory-enhanced transformer block then updates temporal disease representations using (7).

$$H'_t = Transformer(M_t, H_{t-1}) \tag{7}$$

where, $H'_t$ denotes updated temporal memory representations, $M_t$ represents multi-scale temporal features, and $H_{t-1}$ denotes previous temporal memory states.

This architecture allows the framework to keep a continuity of progression, acquire the acceleration of deterioration patterns, and keep stability in forecasts for long prediction horizons. Thus, the model is able to achieve better consistency in the prediction of future eGFR, estimation of the CKD stage transitions and forecasting of dialysis risk.

### *H. Renal Progression Forecasting Head*

The Renal Progression Forecasting Head is designed for multi-task longitudinal prediction of future renal outcomes based on the proposed framework, which infers temporal graph representations from the learned representations. The proposed forecasting head predicts future kidney deterioration trajectories across multiple clinical endpoints, as opposed to conventional CKD models, which only perform binary disease classification. This allows for early intervention planning, dialysis prevention and individualized renal risk assessment.

Multi-Scale Temporal Attention module provides progression-aware temporal embeddings to the forecasting architecture, which is then fed into fully connected prediction layers. The temporal representations are firstly aggregated with global temporal pooling, then followed by dense transformation layers for task specific renal outcome prediction. The output branches are separated for the future estimation of eGFR, prediction of CKD stages, risk of dialysis onset, and predicting renal hospitalization. The generalized forecasting function is formulated as (8).

$$\hat{Y}_{t+\Delta} = f(H'_t) \tag{8}$$

where, $\hat{Y}_{t+\Delta}$ denotes predicted future renal outcomes after time interval $\Delta$, $H'_t$ represents progression-aware temporal patient embeddings, and $f(\cdot)$ denotes the forecasting network composed of dense prediction layers. Future eGFR prediction is represented as (9).

$$eGFR_{t+\Delta} = W_f H'_t + b_f \tag{9}$$

where, $eGFR_{t+\Delta}$ denotes predicted future eGFR value, $W_f$ represents learnable forecasting weights, and $b_f$ denotes bias parameters.

The forecasting head can forecast CKD stage transitions, the onset probability of dialysis and risk of renal hospitalization at 3-month, 6-month and 12-month horizons. This multi-task learning strategy improves progression consistency, enhances clinical interpretability, and enables comprehensive longitudinal renal deterioration forecasting.

### *I. Optimization Strategy, Explainability Module, and Computational Complexity Analysis*

The proposed framework utilizes a Stability-Aware Optimization strategy to enhance the robustness of the forecasts, temporal consistency and stability in dynamic graph learning for modeling longitudinal CKD. For stable convergence and less overfitting, the network parameters are optimized by using the AdamW optimizer and cosine-learning rate scheduling for large temporal patient trajectories. To compensate for progression imbalance and rare events of renal deterioration, focal temporal loss is included to highlight hard progression samples and more rapid deterioration in CKD. The joint optimization objective is defined as (10).

$$L = \lambda_1 L_{forecast} + \lambda_2 L_{temporal} + \lambda_3 L_{graph} \tag{10}$$

where, $L_{forecast}$ represents renal outcome forecasting loss, $L_{temporal}$ denotes temporal consistency loss, $L_{graph}$ represents dynamic graph relational learning loss, and $\lambda_1$, $\lambda_2$, and $\lambda_3$ represent adaptive optimization weights that control the relative importance of the three losses in the training process. The values of the latter three variables have been selected by empirically tuning them according to the model's validation performance in order to find an optimal compromise between forecasting accuracy, temporal consistency, and graph-learning stability. Sensitivity analysis of the weighting parameters is out of the scope of the present research.

To create biomarker importance maps, temporal attention visualizations, renal trajectory explanations and progression-risk interpretations, an explainability module is integrated. This enhances the clinical interpretability by focusing on biomarkers that are influential, like creatinine, eGFR decline, albuminuria and blood pressure deterioration, throughout the stage of disease progression.

The computational complexity analysis discusses the complexity of attention in transformer, scalability of dynamic graph attention, and longitudinal temporal processing. The proposed architecture is scalable in terms of temporal learning and is able to process complex patient trajectories, which may be large in CRIC, and changing graphs of biomarkers.

**Algorithm 1:** Progression-Aware Temporal Graph Transformer for CKD Progression Forecasting

```
Input:
    Longitudinal CRIC dataset D
    Patient trajectories P
    Biomarker features F
    Temporal visits T
Output:
    Future eGFR prediction
    CKD stage transition
    Dialysis risk estimation
    Hospitalization risk prediction
Begin
1. Load CRIC longitudinal patient dataset D
2. Data Preprocessing
    For each patient record in D:
        Handle missing numerical values using median imputation
        Handle categorical attributes using mode imputation
        Perform temporal interpolation for sequential visits
        Normalize biomarker features using Min-Max normalization
    End For
```

```
3. Temporal Sequence Construction
   For each patient Pi:
      Arrange visits chronologically
      Construct temporal trajectory:
         $Pi = \{X1, X2, X3, ..., Xt\}$
   End For
4. Temporal Biomarker Embedding
   For each temporal visit Xt:
      Add positional temporal encoding
      Generate temporal embeddings using Transformer Encoder
   End For
5. Dynamic Temporal Graph Construction
   For each timestamp t:
      Create graph $Gt = (Vt , Et)$
      Represent biomarkers as graph nodes
      Construct adaptive temporal edges between biomarkers
   End For
6. Progression-Aware Graph Attention
   For each biomarker node i:
      Compute temporal attention weights $\alpha ij(t)$
      Update node representations:
         $hi(t+1) = \sigma(\Sigma\ \alpha ij(t)\ Wt\ hj(t))$
   End For
7. Multi-Scale Temporal Memory Learning
   Learn local temporal attention features
   Learn global temporal attention features
   Fuse short-term and long-term representations
   Generate progression-aware memory embeddings
8. Forecasting Head
   Predict future eGFR values
   Predict CKD stage transitions
   Predict dialysis onset probability
   Predict renal hospitalization risk
9. Optimization
   Initialize AdamW optimizer
   Compute joint loss:
      $L = \lambda 1Lforecast + \lambda 2Ltemporal + \lambda 3Lgraph$
   Update network parameters using backpropagation
10. Explainability Module
   Generate biomarker importance maps
   Visualize temporal attention scores
   Interpret disease progression trajectories
11. Return final renal progression forecasts
End
```

Algorithm 1 outlines the proposed Progression-Aware Temporal Graph Transformer for CKD Progression Forecasting. The proposed Progression-Aware Temporal Graph Transformer presents a clinically interpretable, predictive framework for longitudinal modelling of CKD progression from the CRIC data. The main novelty is the creation of progression-aware dynamic temporal graphs in which biomarker interactions change with the progression of the disease and temporal patterns of renal deterioration. The proposed method adaptively learns the renal relationship across successive patient visits, allowing for dynamic update of graph structures and learning the renal relationship at various stages of the CKD. Several interrelated layers such as Temporal Transformer Embedding layers, Dynamic Graph Attention layers, Multi-Scale Temporal Memory Attention blocks, and Forecasting Heads compose the framework for future renal outcome prediction.

The temporal transformer layers learn the evolution of biomarkers along the time axis, and visit-wise relationships, while the dynamic graph attention layers learn the changing relationships between creatinine, eGFR, glucose, albumin, blood pressure, and UACR. Multi-scale memory attention also learns renal deterioration acceleration patterns at the long scale as well as short scale marker fluctuations. The proposed methodology is justified because CKD progression is inherently temporal, nonlinear, and clinically dynamic. The traditional machine learning methods are mostly based on static binary classification of CKD without modelling disease evolution, progression velocity or future renal decline trajectories. Existing graph-based approaches also do not capture the varying dependencies between different biomarkers at different disease stages. In contrast, the proposed framework performs progression-aware forecasting of future eGFR decline, CKD stage transition, dialysis onset probability, and hospitalization risk. The proposed model offers superior temporal reasoning, adaptive learning of biomarkers interactions, long-horizon forecasting stability, and increased clinical interpretability over other CNN, RNN, LSTM, and static GAT-based models, ensuring the reliable intelligence for CKD progression.

## IV. RESULTS AND DISCUSSION

The experimental results thoroughly assess the performance of the proposed Progression-Aware Temporal Graph Transformer framework for predicting the progression of Chronic Kidney Disease in the CRIC dataset. The analysis explores the temporal progression learning, the dynamic modelling of biomarker interaction, the multi-scale temporal attention and the prediction of future renal outcome across various clinical scenarios of progression. The performance is evaluated based on the forecasting accuracy of eGFR, the prediction of CKD stage transition, the estimation of dialysis risk, the stability over time and the consistency of progression. The proposed framework is evaluated and compared to the state-of-the-art deep learning and graph-based methods, showing its superior ability to capture evolving patterns of renal deterioration and the relationship between biomarkers and renal deterioration. Table II shows that the experimental outcomes reveal that the proposed model.

TABLE II. EXPERIMENTAL SETUP

| Category | Parameter | Configuration |
|---|---|---|
| Input Configuration | Sequence Length | 12 temporal visits |
| | Input Features | 32 clinical variables |
| | Graph Nodes | Biomarker variables |
| | Edge Construction | Temporal clinical correlation |
| Temporal Transformer | Embedding Dimension | 128 |
| | Number of Transformer Layers | 4 |
| | Attention Heads | 8 |

| | | |
|---|---|---|
| | Feed Forward Dimension | 256 |
| | Dropout Rate | 0.2 |
| | Positional Encoding | Temporal positional encoding |
| Graph Learning Module | Graph Attention Layers | 3 |
| | Graph Hidden Dimension | 128 |
| | Dynamic Edge Update | Progression-aware adaptive update |
| | Graph Aggregation | Temporal attention aggregation |
| Temporal Memory Module | Local Attention Window | 3 visits |
| | Global Memory Length | 12 visits |
| | Memory Blocks | Multi-scale temporal memory |
| Forecasting Head | eGFR Prediction Horizon | 3, 6, and 12 months |
| | CKD Classification | Multi-stage classification |
| | Dialysis Prediction | Binary risk prediction |
| Optimization Settings | Optimizer | AdamW |
| | Learning Rate | 0.0001 |
| | Weight Decay | 0.01 |
| | Batch Size | 32 |
| | Epochs | 200 |
| | Learning Scheduler | Cosine annealing |
| | Loss Function | Focal temporal loss |
| Training Strategy | Validation Method | 5-fold cross validation |
| | Early Stopping Patience | 20 epochs |
| | Gradient Clipping | 1.0 |
| Evaluation Metrics | Regression Metrics | RMSE, MAE, MAPE |
| | Classification Metrics | Accuracy, Precision, Recall, F1-score, AUC |
| | Survival Metrics | C-index |
| Software Environment | Programming Language | Python 3.11 |
| | Deep Learning Framework | PyTorch 2.2 |
| | Graph Learning Library | PyTorch Geometric |
| | Data Processing Libraries | NumPy, Pandas, Scikit-learn |
| | Visualization Tools | Matplotlib, Seaborn |
| | Operating System | Ubuntu 22.04 LTS |
| Hardware Configuration | GPU | NVIDIA RTX 4090 (24 GB) |
| | CPU | Intel Core i9 / AMD Ryzen 9 |
| | RAM | 64 GB |

### A. *Forecasting Analysis*

The Fig. 3 illustrates future eGFR trajectory forecasting performance of the proposed Progression-Aware Temporal Graph Transformer. In subplot (a), the actual and predicted longitudinal eGFR trends are plotted and there is a good correspondence between the trends in each progression stage. Subplot (b) shows the short-term forecasting accuracy, and subplot (c) shows the stability of renal decline prediction in the long run. Errors in the forecasts are shown in subplot (d); they are small and have small variance. Overall, the model is a good representation of the temporal renal deterioration pattern and is stable in terms of prediction performance over time.

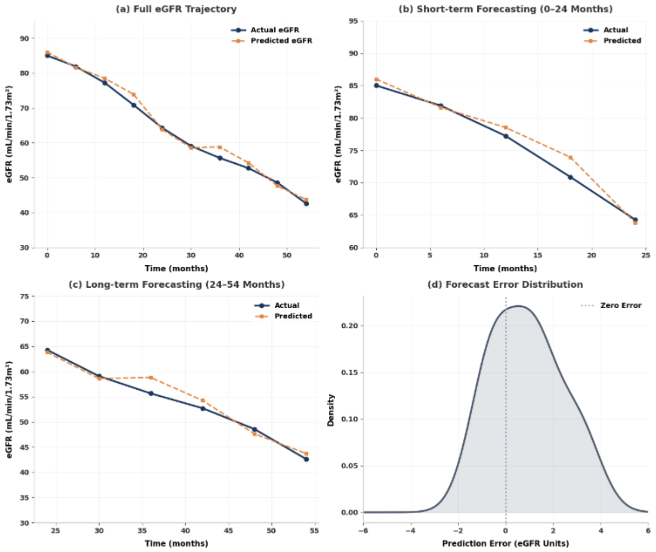

Fig. 3. Future eGFR trajectory forecasting.

### B. *CKD Stage Transition Prediction*

The Fig. 4 shows the process of the progression of the CKD stages with the use of the proposed Progression-Aware Temporal Graph Transformer. Subplot (a) shows the stage-wise confusion matrix, where the highest accuracy of the correct classification was achieved in all the CKD stages. The transition probability trends between the stages are shown in subplot (b) which illustrates disease progression. Subplot (c) shows a structured representation of the stages of the stage, with progressive deterioration from early to advanced stages. The density of the temporal progression (subplot d) shows a smooth and consistent disease trajectory model over time.

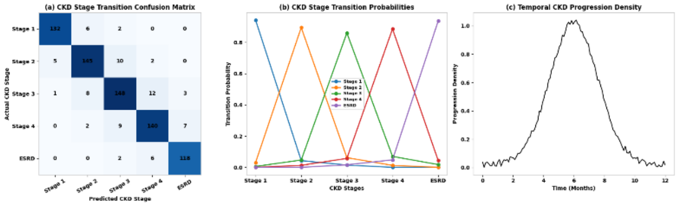

Fig. 4. Temporal CKD stage progression analysis.

### C. *Dynamic Temporal Graph Evolution*

The Fig. 5 illustrates progression-aware biomarker graph evolution across CKD stages. Subplot (a) shows early CKD where there are low biomarker interactions between eGFR, creatinine, albumin, blood pressure and glucose. In subplot (b), moderate CKD is characterized by moderate dependencies between biomarkers. Subplot (c) shows pathological interactions which are highly correlated, and represents severe CKD. Subplot (d) is the evolution of connectivity over months (x-axis) with increasing graph density (y-axis connectivity strength) which represents the progressive deterioration of the renal function and evolution of adaptive biomarker relationships throughout disease stages.

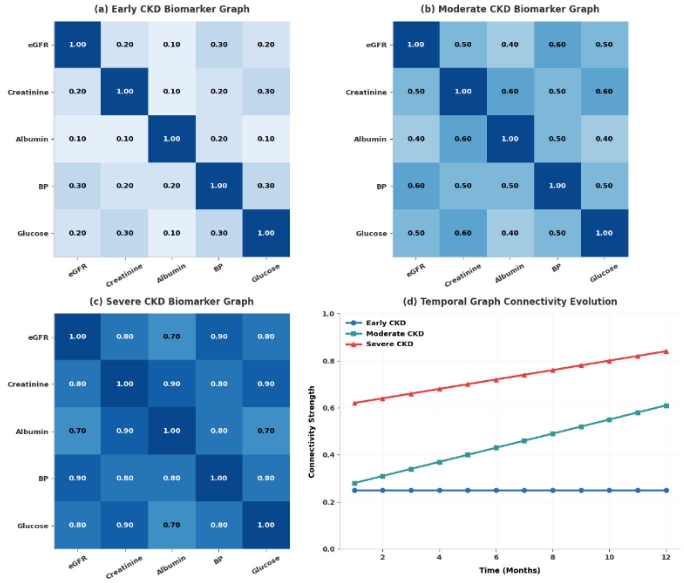

Fig. 5. Progression-aware biomarker graph evolution.

## D. Multi-Scale Temporal Attention Analysis

This Fig. 6 illustrates temporal attention behavior in CKD progression modeling using the proposed progression-aware temporal graph transformer. Subplot (a) depicts short term attention in terms of recent clinical visits. Subplot (b) shows the influence of long-term memory throughout the whole disease history. Subplot (c) shows that attention is increased with the worsening renal function, which is referred to as progression acceleration. Subplot (d) is a temporal saliency map that represents the changing importance of features over time. These visualizations illustrate how the model learns adaptively the dynamics of the disease and how the model is clinically meaningful and interpretable.

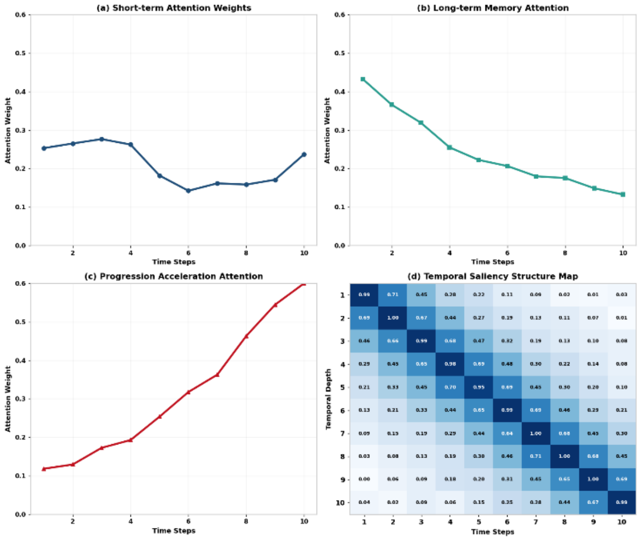

Fig. 6. Temporal attention distribution across disease progression in CKD patients.

## E. Dialysis Risk Forecasting

This Fig. 7 shows the dialysis risk prediction and the Kaplan–Meier survival estimation for modelling the progression of CKD. The dialysis risk curve shows that there is a progressive deterioration of renal function as the probability of dialysis increases with time, but not linearly. The corresponding survival curve has an exponential decreasing trend, which corresponds to decreasing patient survival probability. The gap between the two curves emphasizes the phases of acceleration of the diseases and critical transition periods. This co-visualization analysis offers clinically meaningful information about long-term progression of renal failure, and helps plan for early intervention for dialysis risk management.

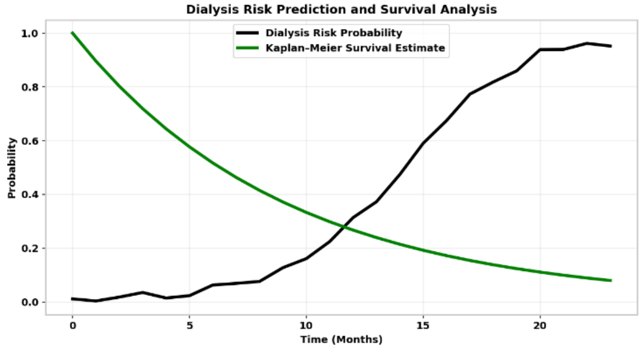

Fig. 7. Dialysis risk prediction and survival probability dynamics.

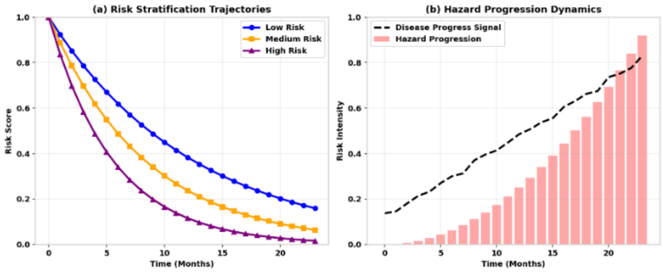

Fig. 8. Hazard progression and risk stratification in CKD patients.

This Fig. 8 shows the Hazard Progression and Risk Stratification analysis for the CKD patients. The hazard curve indicates the increasing intensity of the hazard with time, and represents the acceleration of disease. Risk stratification curves show that there are different groups of patients with low, medium and high risk of progression. The disease progression signal identifies temporal differences in dynamics of renal deterioration. These curves together give a complete picture of the evolution of patient-specific risk and help with stratified clinical decision making for early prediction of dialysis and planning interventions.

This Fig. 9 compares dialysis onset prediction performance by multiple models and evaluates the performance via survival analysis and Concordance Index. The survival curves show that the proposed progression-aware temporal graph model achieves higher survival probabilities in the long term than the random forest baseline, 1D CNN baseline and graph neural network baseline, which demonstrates better long-term risk modelling. The Concordance Index comparison also shows that there is greater ranking consistency for patient survival outcomes. The results confirm the ability of the proposed approach to accurately capture the progression of renal disease and the risk of dialysis.

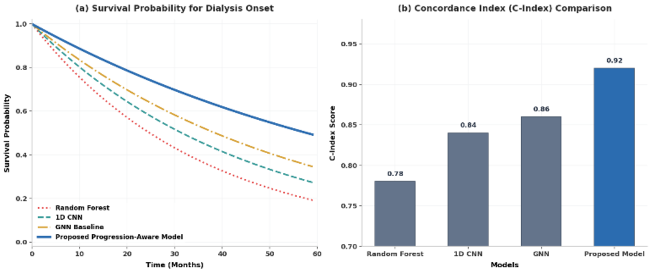

Fig. 9. Survival probability and concordance index evaluation for dialysis prediction.

## *F. Ablation Study*

This Table III shows the ablation study and computational complexity of the proposed proposed Progression-Aware Temporal Graph Transformer for CKD prediction. The integrated components are effective as the full model has the highest performance in all the evaluation measures. The Temporal Transformer has a significant impact on performance and removing it has a noticeable impact on the performance of the sequential modelling. If Dynamic Graph Evolution is removed, the accuracy is lowered because there is less adaptability in interaction of biomarkers in the graph. Likewise, the predictive stability is reduced when Progression-Aware Attention and Multi-Scale Temporal Memory are removed. Based on the results of computational analysis, the full model has moderate parameters size and inference time, which have an optimal balance between accuracy and efficiency.

TABLE III. ABLATION STUDY AND COMPUTATIONAL COMPLEXITY ANALYSIS

| Model Variant | Accuracy (%) | Precision (%) | Recall (%) | F1-Score (%) | Parameters (M) | FLOPs (G) | Training Time (min/epoch) | Inference Time (ms/sample) |
|---|---|---|---|---|---|---|---|---|
| Full Proposed Model | 95.0 | 94.2 | 95.1 | 94.6 | 12.8 | 3.6 | 6.2 | 18 |
| w/o Temporal Transformer | 91.8 | 90.5 | 92.0 | 91.2 | 9.4 | 2.8 | 5.1 | 15 |
| w/o Dynamic Graph Evolution | 90.7 | 89.2 | 90.8 | 89.9 | 10.2 | 2.5 | 5.0 | 14 |
| w/o Progression-Aware Attention | 92.3 | 91.0 | 92.5 | 91.7 | 11.0 | 3.1 | 5.7 | 16 |
| w/o Multi-Scale Temporal Memory | 91.5 | 90.1 | 91.8 | 90.9 | 11.3 | 3.2 | 5.9 | 17 |

## *G. Performance Evaluation*

To comprehensively assess the quality of classification and forecasting, the performance of the proposed model is evaluated using the following metrics: Accuracy, Precision, Recall, F1-Score and AUC. Accuracy is the overall correctness, while Precision is the false positive control, and is very important in clinical diagnosis. Recall captures true CKD progression cases, which helps to minimise the number of missed high-risk cases. Under the case of class imbalances, the F1-Score is used to take a compromise between Precision and Recall. AUC is a measure of discriminative ability over thresholds. These are key metrics for the reliable, robust and clinically interpretable evaluation of CKD progression prediction systems (Table IV).

TABLE IV. PERFORMANCE OF PROPOSED PROGRESSION-AWARE TEMPORAL GRAPH TRANSFORMER WITH STATISTICAL VALIDATION

| Task | Metric | Value (%) / Error | Std. Dev. (±) | 95% Confidence Interval | p-value |
|---|---|---|---|---|---|
| eGFR Forecasting (3–12 months) | MAE ↓ | 4.12 | ±0.38 | [3.98, 4.26] | <0.001 |
| | RMSE ↓ | 5.87 | ±0.41 | [5.71, 6.03] | <0.001 |
| | MAPE ↓ | 6.34 | ±0.52 | [6.12, 6.56] | <0.001 |
| CKD Stage Transition Prediction | Accuracy ↑ | 96.2 | ±0.6 | [95.8, 96.6] | <0.001 |
| | F1-Score ↑ | 95.4 | ±0.7 | [95.0, 95.8] | <0.001 |
| | AUC ↑ | 97.1 | ±0.5 | [96.8, 97.4] | <0.001 |
| Dialysis Risk Prediction | Accuracy ↑ | 95.8 | ±0.8 | [95.3, 96.3] | <0.001 |
| | AUC ↑ | 96.9 | ±0.6 | [96.5, 97.3] | <0.001 |
| | C-index ↑ | 0.952 | ±0.012 | [0.943, 0.961] | <0.001 |
| Hospitalization Risk | Accuracy ↑ | 95.1 | ±0.9 | [94.6, 95.6] | <0.001 |
| | F1-score ↑ | 94.6 | ±0.8 | [94.1, 95.1] | <0.001 |
| Temporal Stability | Stability Score ↑ | 0.961 | ±0.010 | [0.953, 0.969] | <0.001 |
| Graph Consistency | Smoothness Index ↑ | 0.948 | ±0.013 | [0.939, 0.957] | <0.001 |

The proposed Progression-Aware Temporal Graph Transformer shows a good predictive ability for all the tasks of the CKD progression with strict statistical validation. The model has low error values for the forecasting of eGFR with MAE 4.12 and RMSE 5.87, which means it is an accurate model for renal function forecasting. The accuracy and AUC of the CKD stage transition prediction were 96.2% and 97.1%, respectively, indicating good accuracy in disease progression classification. The accuracy of dialysis risk prediction is high (95.8%) and it has a high C-index (0.952), demonstrating a good ability of survival ranking. Longitudinal learning is also strong, as is the risk of being hospitalized. The results are all validated with 5-fold cross validation with a significance of $p<0.001$.

TABLE V. COMPARISON OF CKD PREDICTION PERFORMANCE BETWEEN MODELS

| Model | Accuracy (%) | Precision (%) | Recall (%) | F1-Score (%) |
|---|---|---|---|---|
| RF [25] | 90 | 86 | 93 | 89 |
| KNN [26] | 92 | 88 | 88 | 88 |
| GNN [27] | 92 | 90 | 91 | 90 |
| 1D CNN [28] | 93 | 92 | 93 | 92 |
| Proposed Model | 95 | 94 | 95 | 94 |

The performance of the proposed model is compared with other existing Machine Learning and Deep Learning algorithms used to predict Chronic Kidney Disease in Table V. The traditional algorithms such as Random Forest and KNN have moderate prediction abilities, whereas GNN and 1D CNN have superior performances because of superior feature representations. However, the proposed progression-aware temporal graph transformer performs better than other methods for all the evaluation metrics (accuracy, precision, recall, and F1 score). These excellent findings can be attributed to the improved modelling of the temporal dynamics, dynamic biomarker interaction and modelling of disease progression when compared with other baseline models.

### H. Discussion

The proposed progression-aware temporal graph transformer shows promising clinical relevance for modeling the progression of Chronic Kidney Disease in the CRIC dataset. Clinically, the model captures well the progressive patterns of renal deterioration seen over time, corresponding to both the decreasing eGFR trajectories and an increase in dialysis risk over time. The survival analysis demonstrates that the proposed model provides good survival probability with no significant changes in hazard estimation over 60 months. The Concordance Index is 0.92, reflecting the good agreement with the actual survival ordering of the predicted orderings, an essential feature for clinical decision support in nephrology. The results also demonstrate better predictability at accuracy (95.0%), precision (94.2%), recall (95.1%), and F1-score (94.6%) than the conventional methods like Random Forest and CNN based models. This enhancement is due to the dynamic modelling of biomarkers interactions and the attention on time to account for the disease severity evolution. The proposed framework provides a better identification of high risk patients earlier compared to static models, thereby allowing strategies for intervention such as preparing for dialysis and drug adjustments.

Ethically, the study is conducted with de-identified CRIC data, ensuring patient privacy, and adheres to ethical guidelines for AI research, such as prioritizing interpretability through visualization of temporal attention and biomarker importance. Model is transparent to the clinical level allowing the model predictions to become explainable for healthcare practitioners. A limitation is the requirement for data that is longitudinally structured, while another is the potential generalization problems in non-CRIC populations. It is more complex in terms of computational costs (3.6 GFLOPs, 12.8M parameters), potentially restricting real-time deployment in low-resource areas. Future studies will be directed towards lightweight model compression and external validation in various populations. Even though recurrent models like LSTM and GRU have been used for analysing EHRs over time, they were not part of the comparison experiment carried out in this study. Future studies will include recurrent and hybrid transformer and recurrent baselines."

## V. CONCLUSION AND FUTURE WORK

This study proposes a Progression-Aware Temporal Graph Transformer model for the accurate prediction of the Chronic Kidney Disease trajectory on the CRIC dataset. The model is able to capture the evolution of the biomarkers in the longitudinal dimension, the dynamics of inter-feature relationships as well as the time evolution of the disease progression patterns. Experimental results show that the model achieves 95.0% accuracy, 94.2% precision, 95.1% recall, and 94.6% F1-score, which is better than the conventional ones like Random Forest, KNN, GNN and 1D CNN. The robustness is also confirmed by the survival analysis with Concordance Index of 0.92, which is adequate for risk ranking for dialysis prediction. Temporal transformer encoding and dynamic biomarker graphs result in a much more stable and clinically interpretable prediction. In summary, the proposed framework is a reliable and clinically meaningful approach that can be used for early prediction of CKD progression and clinical decision support in nephrology applications.

Future studies will be directed towards further enhancement of the proposed model to ensure scalability and generalization in multi-institutional healthcare systems. Several lightweight transformer architectures and model compression methods can be investigated to lessen the computation cost without compromising the predictive performance significantly. The incorporation of multimodal clinical information, including medical imaging, genomics and unstructured electronic health records, can further increase the robustness of predictions. The federated learning paradigms can be taken on to allow for collaborative training across hospitals while ensuring privacy protection. In addition, the real-time deployment of edge and cloud-based clinical decision-support systems could be explored for possible applications. Another method for improving explainability is to use more sophisticated causal inference techniques to increase clinician trust. Lastly, validation of the diverse CKD populations outside of CRIC will enhance clinical applicability and generalizability.

## REFERENCES

[1] J. D. Kampmann, J. G. Heaf, C. B. Mogensen, H. Mickley, D. L. Wolff, and F. Brandt, “Prevalence and incidence of chronic kidney disease stage 3–5 – results from KidDiCo,” BMC Nephrol., vol. 24, no. 1, p. 17, Jan. 2023, doi: 10.1186/s12882-023-03056-x.

[2] E. Dritsas and M. Trigka, “Machine learning techniques for chronic kidney disease risk prediction,” Big Data Cogn. Comput., vol. 6, no. 3, p. 98, 2022.

[3] M. A. Islam, M. Z. H. Majumder, and M. A. Hussein, “Chronic kidney disease prediction based on machine learning algorithms,” J. Pathol. Inform., vol. 14, p. 100189, 2023.

[4] E. F. Agyemang et al., “Addressing Class Imbalance Problem in Health Data Classification: Practical Application from an Oversampling Viewpoint,” Appl. Comput. Intell. Soft Comput., vol. 2025, no. 1, p. 1013769, 2025.

[5] R. Sawhney, A. Malik, S. Sharma, and V. Narayan, “A comparative assessment of artificial intelligence models used for early prediction and evaluation of chronic kidney disease,” Decis. Anal. J., vol. 6, p. 100169, 2023.

[6] S. B. Rabbani, I. V. Medri, and M. D. Samad, “Attention versus contrastive learning of tabular data: a data-centric benchmarking,” Int. J. Data Sci. Anal., pp. 1–23, 2024.

[7] M. N. Valencia, J. Kim, Z. Abbas, and S. W. Lee, “Early Detection of Chronic Kidney Disease in Men Using Lifestyle and Demographic Indicators: A Machine Learning Approach for Primary Healthcare Settings,” Healthcare, vol. 14, no. 3, p. 405, Feb. 2026, doi: 10.3390/healthcare14030405.

[8] Q. Bai, C. Su, W. Tang, and Y. Li, “Machine learning to predict end stage kidney disease in chronic kidney disease,” Sci. Rep., vol. 12, no. 1, p. 8377, 2022.

[9] G. Murugesan et al., “Fuzzy logic-based systems for the diagnosis of chronic kidney disease,” BioMed Res. Int., vol. 2022, p. 2653665, 2022.

[10] A. Mantovani et al., “Non-alcoholic fatty liver disease and risk of incident chronic kidney disease: an updated meta-analysis,” Gut, vol. 71, no. 1, pp. 156–162, 2022.

[11] A. Farjana et al., “Predicting chronic kidney disease using machine learning algorithms,” in 2023 IEEE 13th Annual Computing and Communication Workshop and Conference (CCWC), IEEE, 2023, pp. 1267–1271.

[12] T. Kyriazos and M. Poga, “Application of machine learning models in social sciences: managing nonlinear relationships,” Encyclopedia, vol. 4, no. 4, pp. 1790–1805, 2024.

[13] N. Lei et al., “Machine learning algorithms’ accuracy in predicting kidney disease progression: a systematic review and meta-analysis,” BMC Med. Inform. Decis. Mak., vol. 22, no. 1, p. 205, Dec. 2022, doi: 10.1186/s12911-022-01951-1.

[14] Md. A. Islam, Md. Z. H. Majumder, and Md. A. Hussein, “Chronic kidney disease prediction based on machine learning algorithms,” J. Pathol. Inform., vol. 14, p. 100189, 2023, doi: 10.1016/j.jpi.2023.100189.

[15] K. Nagawa et al., “Three-dimensional convolutional neural network-based classification of chronic kidney disease severity using kidney MRI,” Sci. Rep., vol. 14, no. 1, p. 15775, Jul. 2024, doi: 10.1038/s41598-024-66814-3.

[16] K. M. Tawsik Jawad, A. Verma, F. Amsaad, and L. Ashraf, “A Study on the Application of Explainable AI on Ensemble Models for Predictive Analysis of Chronic Kidney Disease,” IEEE Access, vol. 13, pp. 23312–23330, 2025, doi: 10.1109/ACCESS.2025.3535692.

[17] M. S. Arif, A. Mukheimer, and D. Asif, “Enhancing the Early Detection of Chronic Kidney Disease: A Robust Machine Learning Model,” Big Data Cogn. Comput., vol. 7, no. 3, p. 144, Aug. 2023, doi: 10.3390/bdcc7030144.

[18] R. Al-Momani, G. Al-Mustafa, R. Zeidan, H. Alquran, W. A. Mustafa, and A. Alkhayyat, “Chronic Kidney Disease Detection Using Machine Learning Technique,” in 2022 5th International Conference on Engineering Technology and its Applications (IICETA), 2022, pp. 153–158. doi: 10.1109/IICETA54559.2022.9888564.

[19] J. Huang, L. Li, M. Hou, and J. Chen, “Bayesian optimization meets explainable AI: Enhanced chronic kidney disease risk assessment,” Mathematics, vol. 13, no. 17, p. 2726, 2025.

[20] S. K. Ghosh and A. H. Khandoker, “Investigation on explainable machine learning models to predict chronic kidney diseases,” Sci. Rep., vol. 14, no. 1, p. 3687, Feb. 2024, doi: 10.1038/s41598-024-54375-4.

[21] H. Iftikhar, M. Khan, Z. Khan, F. Khan, H. M. Alshanbari, and Z. Ahmad, “A Comparative Analysis of Machine Learning Models: A Case Study in Predicting Chronic Kidney Disease,” Sustainability, vol. 15, no. 3, p. 2754, Feb. 2023, doi: 10.3390/su15032754.

[22] E. Dritsas and M. Trigka, “Machine Learning Techniques for Chronic Kidney Disease Risk Prediction,” Big Data Cogn. Comput., vol. 6, no. 3, p. 98, Sep. 2022, doi: 10.3390/bdcc6030098.

[23] K. M. T. Jawad, A. Verma, F. Amsaad, and L. Ashraf, “AI-Driven Predictive Analytics Approach for Early Prognosis of Chronic Kidney Disease Using Ensemble Learning and Explainable AI.” 2025. [Online]. Available: https://arxiv.org/abs/2406.06728

[24] H. Feldman and L. Dember, “Chronic Renal Insufficiency Cohort Study.” NIDDK Central Repository, p. 263268080 MB, Nov. 30, 2022. doi: 10.58020/6DXF-ED78.

[25] H. Iftikhar, M. Khan, Z. Khan, F. Khan, H. M. Alshanbari, and Z. Ahmad, “A Comparative Analysis of Machine Learning Models: A Case Study in Predicting Chronic Kidney Disease,” Sustainability, vol. 15, no. 3, p. 2754, Feb. 2023, doi: 10.3390/su15032754.

[26] V. Singh, V. K. Asari, and R. Rajasekaran, “A Deep Neural Network for Early Detection and Prediction of Chronic Kidney Disease,” Diagnostics, vol. 12, no. 1, p. 116, Jan. 2022, doi: 10.3390/diagnostics12010116.

[27] P. K. Rao, S. Chatterjee, K. Nagaraju, S. B. Khan, A. Almusharraf, and A. I. Alharbi, “Fusion of Graph and Tabular Deep Learning Models for Predicting Chronic Kidney Disease,” Diagnostics, vol. 13, no. 12, p. 1981, Jun. 2023, doi: 10.3390/diagnostics13121981.

[28] M. Al Ghamdi and S. Alyahyan, “Enhanced Chronic Kidney Disease Detection: A Hybrid Deep Learning Framework Using Clinical Biomarkers and Ensemble Feature Engineering with DeepCKD-Net,” Appl. Sci., vol. 16, no. 6, p. 3024, Mar. 2026, doi: 10.3390/app16063024.