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CNN- GRU algorithm-based chronic kidney disease prediction and classification

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Abstract. Numerous disorders related to lifestyle choices and environmental factors are prevalent among humans today. Predicting and detecting these diseases early on is essential to halting their spread and severity. For physicians, accurately diagnosing illnesses can be challenging. Specifically, one of the key origins of morbidity and death from non-communicable diseases that impact 10-15% of the global population is chronic kidney disease, or CKD. Still, making medical predictions is a difficult and complex undertaking. Our proposed system uses powerful machine learning algorithms to detect and predict people with prevalent chronic conditions. These methods can enhance classifiers' ability to reliably identify chronic diseases. The dataset collected from Kaggle is a chronic kidney disease dataset, comprising 25 features. The first step is preprocessing and normalization of the dataset. PCA extracts the features of chronic disease. The k-nearest neighbour (KNN) is a feature selection method used to select features. A CNN (convolutional neural network)-GRU (gated recurrent unit) classification algorithm is used to predict disease from the dataset. The predicted result is binary, like "CKD" or "NOT CKD", The classification algorithm efficiently evaluates performance metrics, including precision, accuracy, recall, and an F1 score of 1.0.

Keywords: accuracy F1- score; chronic kidney disease; CNN-GRU; KNN; PCA; precision; recall

1. Introduction

Chronic diseases are a major problem for the healthcare system everywhere. The medical statement claims that the rising death rate among people is a result of chronic diseases. More than 70% of the patient's income is spent on therapies for this illness. Therefore, reducing the patient's risk factor that results in death is crucial. The progress in medical research facilitates the collection of health-related data. The demographics, medical analysis reports, and patient medical history are all included in the healthcare data. The diseases that result from living in different regions and ecosystems may vary. Therefore, the patient's living situation and environmental state should be included in the data collection in addition to the disease data.

CKD is a hazardous medical illness marked by a gradual loss of kidney function over time. The primary function of the kidney is to filter out excess water and waste from the blood, thereby

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maintaining a balanced concentration of minerals and salts in the blood, which is essential for various bodily functions. Efficient kidney function regulates blood pressure, activates hormones, and produces red blood cells. An imbalance, particularly a high concentration of calcium, can result in severe health issues such as bone diseases and cystic ovaries in women. CKD can also cause sudden illnesses or allergic reactions to certain medications.

Early and accurate prediction of CKD is crucial for prompt intervention and efficient disease management. Clinical tests and patient histories are often the mainstays of traditional diagnostic techniques, which can be time-consuming and may be insufficient for early detection. Recent developments in deep learning and machine learning have created new opportunities for more accurate and effective CKD prediction.

CKD is an important Convolutional Neural Network (CNN), and Gated Recurrent Units (GRU) are powerful deep learning frameworks. CNNs efficiently capture spatial features and patterns from data, while GRUs efficiently handle continuous data and capture temporal dependencies. Combining these two architectures can enhance their strengths, providing a robust framework for predicting CKD.

This paper discovers the application of a hybrid CNN-GRU model for CKD prediction. By integrating CNNs' ability to extract relevant features from medical imaging or structured data and GRUs' capability to analyze temporal patterns in patient health records, the proposed model aims to enhance CKD diagnosis prediction accuracy and reliability. Through comprehensive experiments and analysis, we determine the probable of the CNN-GRU model in transforming CKD prediction and flagging the way for improved patient outcomes.

2. Related work

(Debal *et al*. 2022) One of the main obstacles to achieving the UN's Sustainable Development Goals, mostly focused on health and wellbeing, is the prevalence of non-communicable diseases like chronic kidney disease (CKD). For early detection, machine learning approaches like RT (random forests), DT (decision trees) and SVM (support vector machines) are employed; RF outperforms SVM and DT. Higher accuracy is demonstrated by multiclass models, which achieve 82.56% for five-class datasets and 99.8% for binary classes.

(Chittora *et al*. 2021) seven classifier algorithms include Logistic Regression, Artificial Neural Networks and Logistic Regression; these algorithms are used to analyse CKD data using UCI data. The findings show that using the full-feature synthetic minority over-sampling method, LSVM can achieve a maximum accuracy of 98.86% with penalty L2. Additionally, the study contrasts the GINI coefficient, F-measure, area under the curve, recall, accuracy, and precision of several machine learning models.

(Arumugam *et al*. 2023) the multidisciplinary area of data mining for healthcare, assesses the efficacy of medicinal treatments. Diabetics who have the chronic ailment diabetes-related heart disease. Diabetic patients' heart disease cannot be predicted from available data, even with the use of data mining technologies. An ideal decision tree approach for estimating diabetes patients' risk of heart disease.

(Rashid *et al*. 2022) employed a unique method to forecast five prevalent chronic diseases: diabetes, myocardial infarction, renal disease, hepatitis, and breast cancer. It does this by combining ANN with the use of particle swarm optimization (PSO). The model outperforms existing classification methods with a 99.67% accuracy rate and requires less computation time

than methods based on random forests, deep learning, and SVMs. Tools for diagnosing chronic illnesses might be developed online using the study's findings.

(Bhatt *et al*. 2023) to enhance the accuracy of forecasting cardiovascular problems and ultimately reduce mortality rates, Huang employed k-means clustering to refine the model's classification precision. Huang achieved notable accuracy improvements by applying this approach to a real-world dataset comprising 70,000 cases from Kaggle. Among various methods tested, the multilayer perceptron with cross-validation emerged as the most effective, achieving a maximum accuracy rate of 87.28%.

(Islam *et al*. 2023) CKD examined the connection between the attributes of the target class and the data features using predictive modelling. Twelve machine learning classifiers were assessed inside a supervised learning framework. Of them, XgBoost outperformed the others in terms of multiple metrics. Specifically, the F1-score, recall, and accuracy of the XGBoost classifier are 0.98, 0.983, and 0.98, respectively.

(Hassan *et al*. 2023) have directed efforts to develop more effective classification models for CKD diagnosis to identify the best features from clinical datasets. Machine learning techniques include neural networks (NN), RF, SVM, RT and Backing tree models (BTM). In contrast to the SVM, RF, and RT models, which achieved 98.75%, 96.25%, and 96.75% accuracy, respectively, the neural network model achieved 100% flawless accuracy. Compared to previous research, this method performs better in accurate diagnosis.

(Panda *et al*. 2022), the body's inability to metabolize glucose is a hallmark of diabetes mellitus, a chronic condition. This study looks into machine learning methods for diabetes prediction using SVM and KNN. The research highlights the importance of feature selection in ML models by evaluating the effectiveness and accuracy of diabetes prediction using four algorithms. Despite their best attempts to control their diabetes, many people still have symptoms.

(Silveira *et al*. 2022) used unbalanced and small-size datasets to support early prediction of CKD. Utilized data, including age, gender, glomerular filtration rate, creatinine, urea, albuminuria, diabetes, and hypertension, were taken from Brazilian medical records. Models were developed using decision trees, random forests, and multiclass AdaBoosted DTs with an oversampling technique. The DT model used SMOTE and manual augmentation and obtained the best accuracy score (98.99%).

(Bai *et al*. 2022) examined how patients with chronic kidney illness can be at risk for end-stage kidney disease (ESKD) by using machine learning (ML). The Kidney Failure Risk Eq. (KFRE) was used to comparison the performance of 5 ML algorithms that underwent training and testing. According to the study, three machine learning models demonstrated higher sensitivity and comparable predictability compared to the KFRE, indicating possible applications for patient assessments. Subsequent research endeavours should incorporate external validation and enhance models by incorporating extra predictor factors.

(Wang *et al*. 2022) A blood metabolite connected to GFR, creatinine, is essential for CKD stage identification. A study uses open-source data to build a regression model to estimate creatinine levels and assess CKD risk. Six parameters influence creatinine value in the model, which employs machine learning and ensemble learning. This approach can aid in early detection and the assessment of CKD risk.

(Yang *et al*. 2021) offer an innovative method for predicting chronic diseases using an incremental deep neural network. Over time, the system becomes increasingly accurate in forecasting diabetes by continuously assessing users' tendency to have chronic conditions. The solution uses sensor-collected user data and a Chinese diabetes dataset comprising 575 individuals.

A real-world diabetes dataset is used to assess the system, demonstrating its efficacy in tracking users and offering pre-emptive alerts for potential diabetic complications.

(Krishnamurthy *et al*. 2021) A better option in clinical datasets is to develop an ML model to predict the onset of CKD in six- or twelve months using medication and comorbidity data from Taiwan's National Health Insurance Research Database. The best model was Convolutional Neural Networks, with diabetes mellitus, age, gout, and medication being significant predictors. Policymakers may find the model helpful in anticipating changes in CKD, enabling patient-centered care, early detection, close monitoring, and better resource allocation.

(Dritsas *et al*. 2022) CKD or progressive kidney function decrease affects overall health. Inadequate diagnosis and treatment may lead to end-stage renal disease and mortality. Machine learning (ML) techniques are critical to anticipating illness. This research aims to create effective techniques that use feature ranking, class balance, and performance indicators to predict the recurrence of CKD. With a 99.2% accuracy, the RF model performs better than the other models.

(Almustafa 2021) To diagnose disorders related to CKD, this study explored various classifiers using the dataset. The J48 and Decision Table classifiers performed exceptionally well, achieving ROCs and accuracies of 99%. When feature selection techniques were applied, the performance of the Naïve Bayes and Result Table classifiers improved, reaching accuracies of 99.75%, 98.25%, and 99.25%, respectively.

(Chiu *et al*. 2020) Men are more likely than women to have CKD, which affects 63,538 people in India. Predicting the proportion of cases with and without chronic renal disease is being done utilizing machine learning algorithms. This study uses Rcode to compare the accuracy-based performance of several algorithms. The GB (gradient boosting) model produced the best detection efficiency, outperforming the multilayer perceptron algorithm (MLP) single point split, seven characteristics, and 98.4% F1 measurement. Additionally, the investigation discovered a 98.0% F1 measure that was more efficient than RF and five apps.

(Wang *et al*. 2021) A metabolite associated with GFR, creatinine, is essential for CKD stage identification. An open-source data study demonstrated a regression model that predicted creatinine value from 23 health-related characteristics. The ensemble learning approach enhanced the predictor's performance, which led to an AUC of 0.76, lowering the risk of CKD and promoting early identification.

(Yadav *et al*. 2021) This paper uses a Neural Network classifier strategy with four feature strategies to improve classification accuracy in medical data science. Several statistical methods, including Pearson Correlation, Chi-Square, Extra Tree, and Lasso regularization, were used to examine the model for chronic renal disease. After 300 tests, the model's greatest accuracy of 99.98% was attained with a lower error rate.

(Ilyas *et al*. 2021). The J48 and RF algorithms were used to create a sustainable model. J48 performed with an accuracy of 85.5%, outperforming Random Forest in every phase. Because of this enhanced performance, J48 may be employed for automated system identification of the severity of CKD.

(Kaur *et al*. 2023) ML techniques for predicting chronic kidney disease. This study seeks to provide practical tools through performance metrics, feature standardization, and class balancing. The two machine learning classifiers, decision tree and packing ensemble technique, performed best with 95% and 97%, respectively.

(Khalid *et al*. 2023) The researchers employed a hybrid approach, selecting features using Pearson correlation and gradient boosting, decision trees, Gaussian Naïve Bayes, and random forests as base and meta-classifiers of CKD, respectively. The aim was to find the most accurate

machine learning classifier while flagging performance issues. Using the UCI chronic renal disease dataset, the study discovered that decision trees achieved 96% accuracy, random forests achieved 98%, and gradient boosting achieved 99% accuracy. Using the same dataset, the hybrid model produced 100% accurate results.

(Senan *et al*. 2021) established an ML approach for diagnosing CKD. They used a dataset comprising 400 patients and 24 characteristics. The system evaluated various algorithms, including SVM, KNN, Decision Trees, and Random Forests. The Random Forest algorithm demonstrated superior outcomes and produced an accuracy of 100%.

(Ebiaredoh-Mienye *et al*. 2022). With a sensitivity of 100%, specificity of 99.8%, and accuracy of 99.8%, the AdaBoost classifier produced remarkable results in classification. This technique can be applied to highly heterogeneous clinical datasets.

(Pal 2023) created a ML model to detect CKD at an early stage. The model increases accuracy by 3% over previous models using majority voting and baseline classifiers. The Random Forest methodology works better than SVM and ANN algorithms.

(Abdel-Fattah *et al*. 2022) to diagnose CKD, this paper suggests hybrid machine learning methods that use large data platforms like Apache Spark. In addition to six machine learning classification algorithms, GBT, DT, NB, LR, RF, and SVM, the study uses feature selection approaches, including Relief-F and chi-squared, and produced the accuracy of all these classifiers 100%.

(Singh *et al*. 2022) offered a state-of-the-art DL model for CKD prediction and early detection. The model uses SVM and KNN parameters to identify important properties, including hemoglobin, specific gravity, creatinine in the urine, the number of red blood cells, albumin, packed cell volume, and hypertension. The model achieves 100% accuracy and performs better than other classifiers.

(Gokiladevi *et al*. 2022) investigated the efficiency of many ML algorithms for the initial estimate of CKD. KNN, DT, RF, LR, and SVM are the five machine learning (ML) based classification models employed. The effectiveness of the RF model was assessed using a benchmark CKD dataset extracted from the UCI collection. With a minimum error rate of 0.012, maximum precision and F-score of 0.99, the RF model fared better than the others.

(Swain *et al*. 2023) Using readily available data to the public, the project aims to create a ML model that can predict when chronic kidney disease will manifest. The imputation of missing data points, feature scaling, and SMOTE algorithm balance are a few examples of data preparation methods. The least-required collection of related features is extracted using the chi-squared test. For model training, a variety of supervised learning approaches are employed. With test accuracy and false-negative rates of 99.33% and 98.67%, respectively, SVM and RF were the lowest applied learning techniques.

3. Proposed methodology

The proposed method for predicting CKD using a hybrid CNN-GRU model includes several key stages: preprocessing, feature extraction, feature selection, and classification, as shown in Fig. 1. This method is designed to efficiently handle and analyze the CKD dataset, which includes 25 features. The proposed CNN-GRU model aims to afford a robust and efficient framework for predicting chronic kidney disease by following this method. A combination of advanced feature extraction and temporal analysis techniques ensures that patterns and trends in CKD can be accurately identified, leading to early and reliable diagnosis.

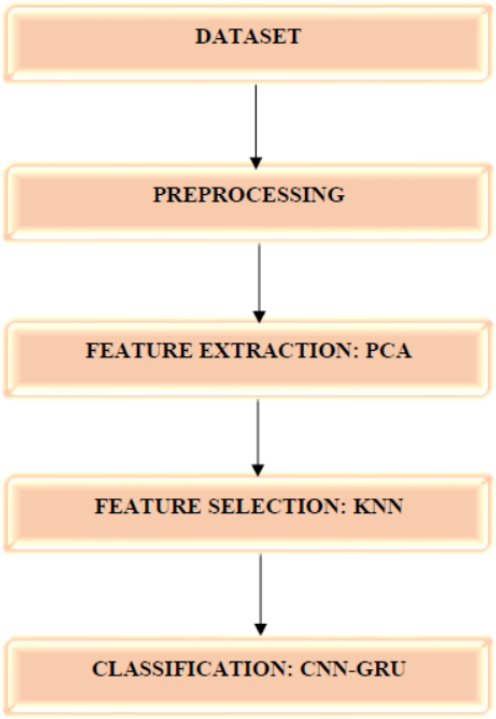

Fig. 1 Working flow of proposed methodology

3.1 Dataset

The CKD dataset was collected from patients in India over two months. CKD stands for chronic kidney disease. This dataset consists of 25 features and 400 rows. Finally, the disease can be classified as "CKD" or "not CKD."

The data must be cleaned because it contains NaNs and the numerical features must be made to float. Essentially, we were told to delete EVERY row with a NaN without any threshold. In other words, every row containing even one NaN would be removed.

The CKD dataset includes 25 clinical and demographic attributes and their corresponding medical relevance which is listed in Table 1. These include biochemical and lifestyle components and vitals which help in the right prediction of the disease. Considering the dataset's combination of analysed patient lab test results and various benchmarks concerning the medical history of the patient, the data gained is reliable and extensive, making it particularly appropriate for machine learning driven detection and classification of CKD.

3.2 Preprocessing

To establish proper data standards for model training on the CKD dataset, a rigorous data preprocessing approach was adopted. Most notably, the removal of rows with missing and NaN values was maintained to ensure data quality. Although imputation via the mean or KNN could be justified, it was not used here. The features Age, BP, and SC were subjected to ordinal re-scaling

Table 1 Attributes of Chronic Kidney Disease (CKD) Dataset

Feature	Description
Age	Age of the patient; CKD risk increases with age.
Blood Pressure (BP)	High BP damages kidneys and worsens CKD.
Specific Gravity (SG)	Urine concentration; abnormal values show impaired kidney function.
Albumin (AL)	High albumin in urine indicates protein leakage due to kidney malfunction.
Sugar (SU)	High sugar levels link to diabetes, a leading CKD cause.
Red Blood Cells (RBC)	Abnormal RBC count in urine suggests kidney damage.
Pus Cell (PC)	High count indicates urinary infection affecting kidneys.
Pus Cell Clumps (PCC)	Presence shows severe infection in urinary tract.
Bacteria (BA)	Presence indicates urinary tract infection (UTI).
Blood Glucose Random (BGR)	Random blood sugar; high levels show diabetes risk.
Blood Urea (BU)	Increased levels reflect poor kidney filtration.
Serum Creatinine (SC)	Key biomarker; higher values mean kidney dysfunction.
Sodium (SOD)	Electrolyte balance; abnormal levels stress kidney function.
Potassium (POT)	Abnormal potassium affects both kidney and heart function.
Hemoglobin (HGB)	Low hemoglobin is common in CKD due to anemia.
Packed Cell Volume (PCV)	Blood concentration level; low values show CKD-related anemia.
White Blood Cell Count (WBC)	High or low WBC indicates infection or inflammation.
Red Blood Cell Count (RBC Count)	Low RBC count reflects anemia in CKD patients.
Hypertension (HTN)	Presence of high BP, a major CKD risk factor.
Diabetes Mellitus (DM)	Diabetes is the primary contributor to kidney disease.
Coronary Artery Disease (CAD)	Heart disease often co-exists with CKD patients.
Appetite (APPET)	Poor appetite is a symptom of worsening CKD.
Pedal Edema (PE)	Swelling due to fluid retention; strong CKD indicator.
Anemia (ANE)	Reduced red blood cells, common in CKD patients.
Class (Target Attribute)	Indicates final label: CKD or Not CKD.

for Min-Max normalization. The features RBC, PC, HTN, and DM were numerically classified for input into the machine learning model. Standardization using z-scores was performed on continuous features to facilitate convergence and improve training speed. The dataset was examined for class imbalance between patients with CKD and those without CKD. If classification was predominant, SMOTE was used to balance the bias. The workflows depicted above represent processes designed to eliminate unnecessary noise and enhance the credibility and consistency of the CNN-GRU prediction model.

3.3 Feature Extraction: Principal Component Analysis (PCA)

PCA identifies linear combinations of original features that capture the most variation in the data. For chronic diseases, identifying relevant features is crucial. These features might include demographic data (age, sex), lifestyle factors (diet, exercise), medical history (previous

conditions), and biomarkers (blood pressure, cholesterol levels).

Chronic diseases often involve a multitude of risk factors. PCA helps by reducing the dimensionality of the feature space while retaining meaningful information. This can streamline the model training process and improve performance by focusing on the most informative components.

The primary premise here is that the fundamental process these freshly formed components drive leads to the assumption that the variables in the data set correlate. The objectives are to use observed data to explicitly characterize an underlying process, decrease a large number of known variables to a minor number of elements, and find correlations among seen variables. It assumes x_t where t= 1, 2…M are stochastic m dimensional input data records with mean (μ). Eq. 1.

$$\mu = \frac{1}{M}\sum_{t=1}^{M} x_t \tag{1}$$

The definition $x_t$of the covariance matrix of is, Eq. 2.

$$C = \frac{1}{M}\sum_{t=1}^{N} (x_t - \mu)(x_t - \mu)^T \tag{2}$$

The following Eq. 3, eigenvalue issue of covariance matrix C is resolved via PCA.

$$C_{vi} = \lambda_i v_i \tag{3}$$

where the associated eigenvectors are $v_i(i = 1,2,\ldots.,m)$ and the eigenvalues are $\lambda_i(i = 1,2,..,n)$. We simply need to calculate the m eigenvectors, also known as primary directions, corresponding to those m highest eigenvalues (m\n) to represent data records with low dimensional vectors. It is commonly known that the variance of the input data projections in the principal direction is higher than that of the projections in any other direction.

Let,

$$\varphi = [v_1, v_2, \ldots., v_m],\ A = diag[\lambda_1, \lambda_2, \ldots\ldots, \lambda_m] \tag{4}$$

Then

$$C\Phi = \Phi A \tag{5}$$

For the following relation to hold, the value v indicates the approximation precision of the m greatest eigenvectors.

$$\frac{\sum_{i=1}^{m} \lambda_i}{\sum_{i=1}^{n} \lambda_i} \geq v \tag{6}$$

The low dimensional feature vector of a new input data set, x, is found using the two Eq.s 4, 5 and 6 above to find the number of eigenvectors that can be chosen and given a precision value, v, as shown in below Eq. 7.

$$x_f = \Phi^T x \tag{7}$$

3.4 Feature selection: k- nearest neighbour (KNN)

One of the most widely used non-parametric models for feature selection in clinical diagnostics

is KNN. The K-nearest neighbor method assumes that patients with similar health measures and symptoms may have similar diagnoses to identify CKD.

The probability that a given patient, x, has CKD can be estimated using the percentage of training patients near x diagnosed with CKD. To classify a patient, either a majority vote or the similarity degree sum of a specified number (k) of adjacent patients can be used. The diagnosis that most likely classifies x is the one with the biggest proportion of patients when a majority vote is utilized. Each diagnosis's points in the neighbourhood are added together. The similarity degree total assigns x to the diagnosis with the highest similarity score based on the K-nearest patients, which is used to calculate each health metric's similarity score. It is used more frequently because majority voting is less susceptible to outliers than the similarity degree sum.

To determine whether patients are neighbors, the distance between each patient and x should be calculated in the most training set for feature selection in clinical diagnosis. Any distance function can indicate which of the two patients is closer to the model patient. The most popular distance metric for determining who is K-NN is the Euclidean distance between training fs and testing ft set points. Each having n attributes (e.g., blood pressure, serum creatinine level, glomerular filtration rate, etc.), may be found using the following formula: 8

$$d = [(f_{t1} - f_{s1})^2 + (f_{t2} - f_{s2})^2 + \cdots + (f_{tn} - f_{sn})^2]^{1/2} \tag{8}$$

In this context, features like age, blood pressure, blood urea, serum creatinine, and others specific to CKD diagnosis are considered. This tailored application ensures the KNN algorithm accurately reflects the patterns and proximities relevant to chronic kidney disease detection.

3.5 Classification: hybrid CNN (convolution neural network) – GRU (gated recurrent unit)

A. CNN (convolution neural network)

Natural language processing, signal processing, computer vision, and other domains have all been transformed by CNNs. CNNs are adaptable and extensible to other forms of sequential data, such as time series or one-dimensional signals, while frequently linked with image data. When identifying patterns in sequential data while maintaining local dependencies, CNNs do remarkably well. Convolution serves as CNN's primary function. To create a feature map, convolution entails swiping a filter or kernel over the input signal, multiplying the filter's weights by the corresponding input values, and summing the results. This technique captures local patterns or features in the input signal. Eq. (9) provides the following expression for the convolution process at each step,

$$y[i] = \sum_{k=0}^{k-1} x[i+k]X\, w[K] + b \tag{9}$$

In neural networks, the convolution operation is illustrated by Eq. (9). To produce the output $y[i]$ the model calculates the weighted sum of the input elements $x[i+k]$within a specific range defined by the kernel size K. Each input is assessed with the weight $[k]$, and these results are combined in a summation. A bias term b is then added in order to shift the output. This operation captures local patterns in the input sequence allowing the neural net to learn spatial or temporal features efficiently. This is the first step in feature extraction for models such as CNNs.

This formula shows how the output at each point is calculated by adding a bias term to the filter weights' dot product and the input signal's corresponding portion.

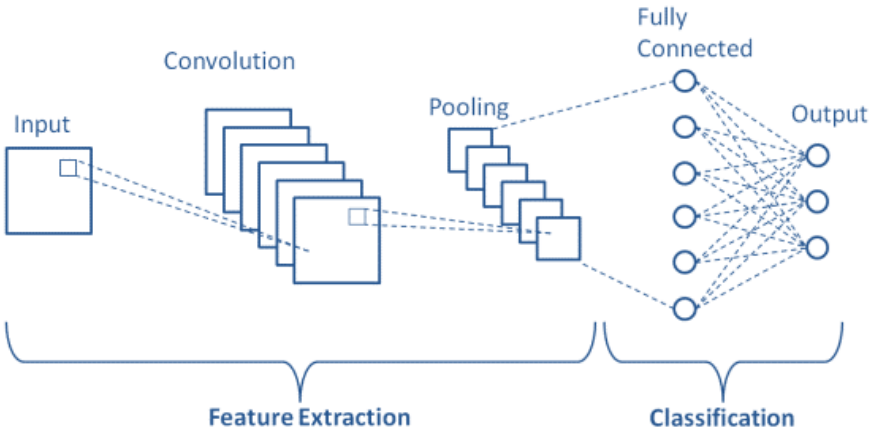

Fig. 2 CNN architecture

B. GRU (gated recurrent unit)

A GRU (gated recurrent unit) is a one of the RNN (recurrent neural network) to solve the gradient problem and to improve the long-term dependencies of sequential data. A GRU consists of update gate, hidden gate and resnet gate to regulate the flow of information within a network. As the network processes the current time step, these gates decide how much data from the previous time step should be kept or removed. Mathematically, the computations within a GRU cell can be represented as follows below Eq. 10-13.

The update gate expressed the mathematical Eq.,

$$z_t = \sigma(W_z.[h_{t-1}, x_t] + b_z) \tag{10}$$

This includes the Eq. 10 of an update gate in a Gated Recurrent Unit (GRU) network. zt defines the proportion of the hidden state $ht{-}1$ to be carried forward to the next state. The vector of $ht{-}1$ as well as the current input xt is concatenated, multiplied by the matrix of weights wz, and the bias bz is added. The sigmoid activation function σ ensures zt is confined to the 0-1 range, hence retaining the necessary old information in addition to new information to learn the sequence.

The reset gate expressed below,

$$r_t = \sigma(W_r.[h_{t-1}, x_t] + b_r) \tag{11}$$

The Eq. (11) represents a reset gate in a Gated recurrent unit (Gru) network. Reset gate $r\ t$ R Tea Controls back hidden position $h\ t$, 1 H T - 1 The candidate should be ignored while calculating the hidden state. Back hidden position $h\ t$, 1 H T - 1 And current input $x\ t$ X Tea Weight multiplied by matrix $W\ r$ and added to bias $b\ r$ B R, applies sigmoid activation σ σ Ban $r\ t$ R Tea Between 0 and 1, GRU allows the previous information to select the previous information to capture relevant temporary dependence.

The hidden state expressed below,

$$\widetilde{h_t} = \tanh\,(W.[r_t \odot h_{t-1}, x_t] + b) \tag{12}$$

This Eq. represents the candidate hidden state $\widetilde{h_t}$ in a GRU network. It computes a potential new hidden state based on the current input x_t and the previous hidden state h_{t-1},

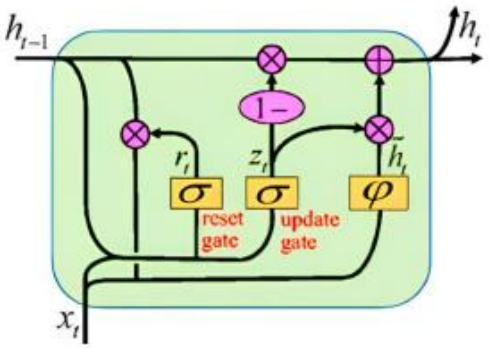

Fig. 3 GRU architecture

modulated by the reset gate r_t through element-wise multiplication. The concatenated vector $r_t \odot h_{t-1}, x_t$ is multiplied by weight matrix W and added to bias b. Applying the tanh activation ensures values are in the range [−1,1], enabling the GRU to capture non-linear temporal dependencies effectively.

The candidate hidden state is,

$$h_t = (1 - z_t) \odot h_{t-1} + z_t \odot \widetilde{h_t} \tag{13}$$

This Eq. represents the final hidden state h_t in a GRU network. The update gate z_t determines the balance between retaining the previous hidden state h_{t-1} and adopting the candidate hidden state $\widetilde{h_t}$. Specifically, $(1 - z_t) \odot h_{t-1}$ preserves relevant past information, while $z_t \odot \widetilde{h_t}$incorporates new information from the current input. The element-wise addition combines these two contributions, allowing the GRU to selectively update its memory, efficiently capturing long-term dependencies in sequential data.

4. Result and discussion

The CNN-GRU technique employs a dataset with 25 distinct characteristics to discourse the vanishing gradient problem and correctly categorize long-term dependency in continuous data as either CKD or not. This method effectively uses the complementing properties of Hybrid CNN-GRU to describe the complicated patterns in the dataset. It has been developed in the Google Colab environment using Python. Performance metrics for this technique include accuracy, precision, recall, and F1 score, which are listed below:

4.1 Performance metrics

Accuracy

This indicator calculates the percentage of accurate predictions that the model produced. Greater accuracy numbers indicate better model performance, indicating more correct classifications, as below Eq. 14.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{14}$$

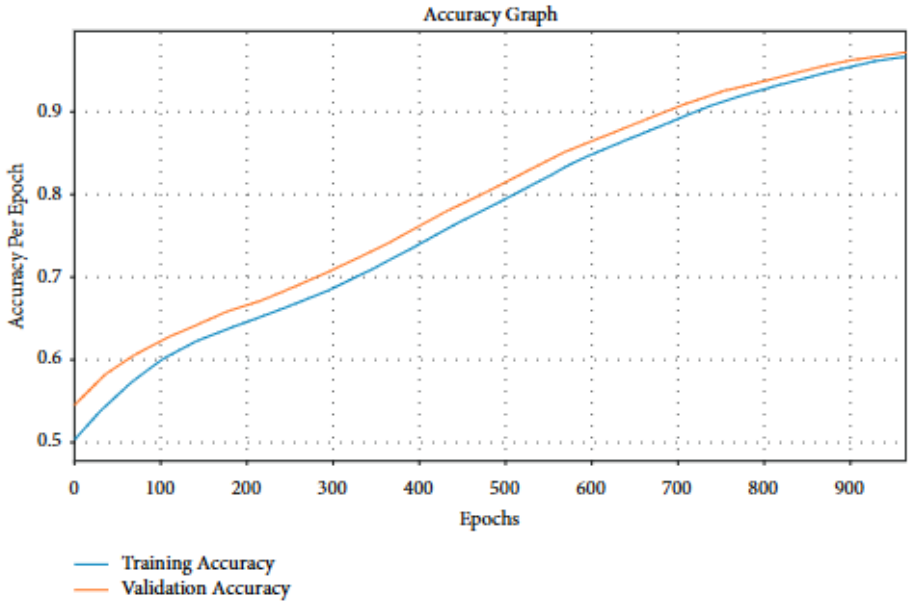

Fig. 4 Trained and validation accuracy of CKD using CNN-GRU

Precision

Precision is a measure used to evaluate the performance of a classification model. It measures the accuracy of positive predictions made by the model. Specifically, accuracy is the ratio of true positive predictions (correctly identified positive events) to the total number of positive predictions (both true positives and false positives), as below Eq. 15.

$$precision = \frac{TP}{TP + FP} \tag{15}$$

Recall

This metric calculates the percentage of true positive predictions among all true positive cases. A lower number of false-negative errors is indicated by higher recall values, demonstrating the model's ability to detect positive events correctly, as below Eq. 16.

$$Recall = \frac{TP}{TP + FN} \tag{16}$$

F1 score

F1-score, generated from the harmonic mean of precision and recall, accurately assesses the model's effectiveness. Higher F1-score values indicate an enhanced model that balances recall and precision, as below Eq. 17.

$$F1 - score = 2 * \frac{precision * recall}{precision + recall} \tag{17}$$

The CNN-GRU method's accuracy analysis on the test dataset is shown in Fig. 4. The results

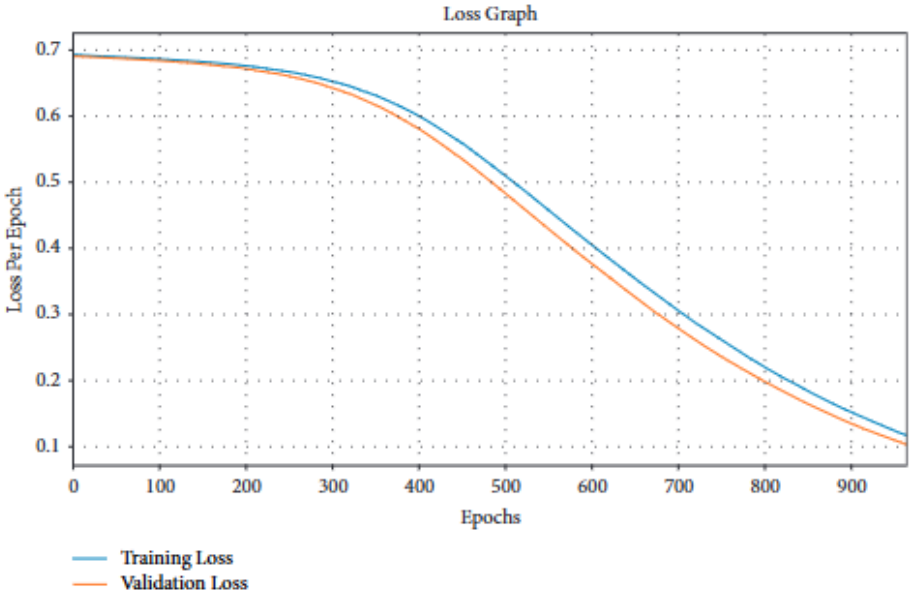

Fig. 5 Trained and validation loss of CKD using CNN-GRU

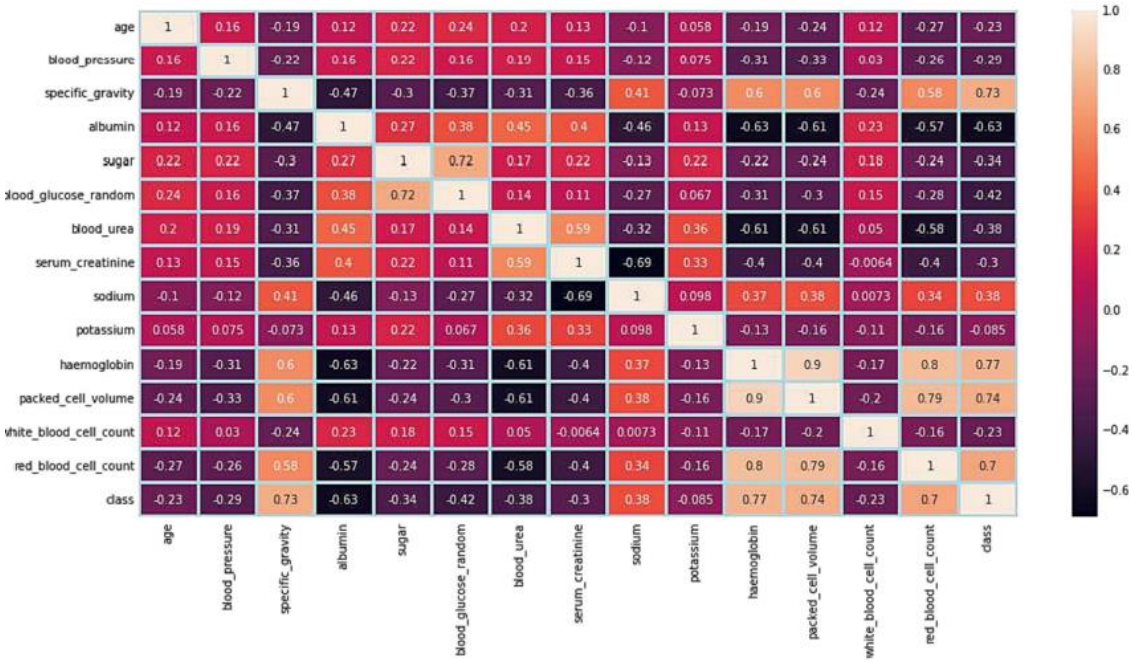

Fig. 6 Heat map with correlation data

showed that the CNN-GRU algorithm has achieved better performance with higher accuracy in both training and validation. It is evident that the CNN-GRU method has improved validation accuracy relative to training accuracy.

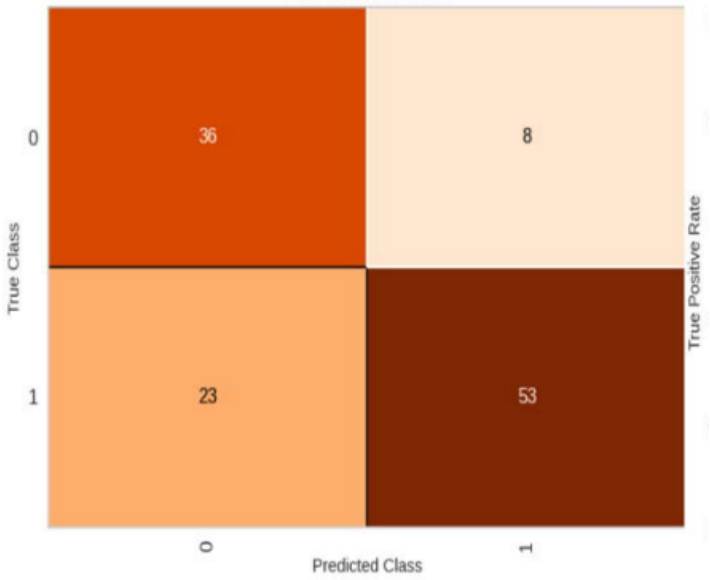

Fig. 7 confusion matrix

Table 2 Performance analysis

Methods	Precision	Recall	Accuracy	F1- score
LSTM	1.0	0.88	0.98	0.98
GRU	1.0	0.87	0.97	0.99
CNN-GRU	1.0	1.0	1.0	1.0

The CNN-GRU approach's loss analysis on the test dataset is shown in Fig. 5. The CNN-GRU system produced a good result with the least amount of training and validation loss, according to the results. In comparison to the training loss, the CNN-GRU system has provided a smaller validation loss.

The absolute values of the correlations between the class label and characteristics in the heat map Fig. 6 demonstrate that there are positive relationships between blood pressure, specific gravity, albumin, sugar, blood urea, serum creatinine, blood glucose random, and sodium. Conversely, there are negative correlations between hemoglobin, potassium, white blood cell count, and red blood cell count. The relationships between the characteristics may be seen by looking at the data heatmap in Fig. 6.

Fig. 7 shows the CNN-GRU model's confusion matrix for predicting chronic kidney disease, which contrasts the real and predicted class labels depending on the performance of the trained model. True positives, false positives, true negatives, and false negatives across the test dataset are highlighted in this matrix, which graphically depicts the model's classification abilities.

The CNN-GRU model was used to categorize CKD; precision, recall, Accuracy and F1-score values were produced from this model and compared to GRU and Long Short-Term Memory (LSTM), two other classification algorithms. The performance metrics for the CNN-GRU, LSTM, and GRU models are shown in Fig. 8. This comparison demonstrates the better precision, recall, Accuracy and F1-score of the CNN-GRU under the 10 epochs steps.

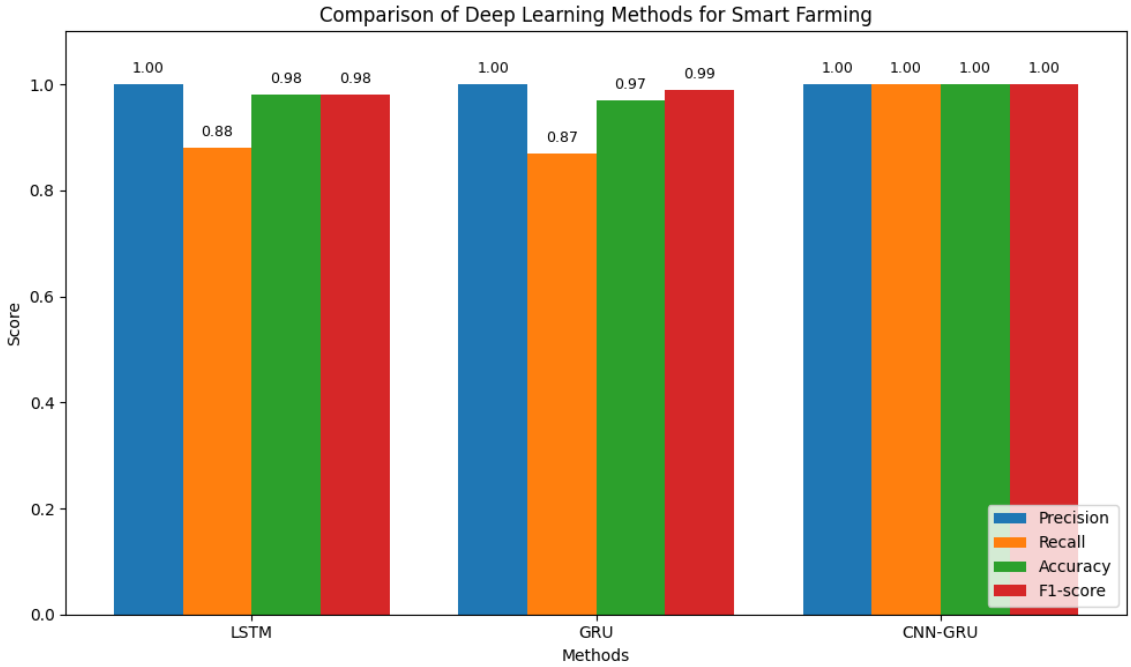

Fig. 8 Precision comparison of CKD

```
sample_data = pd.DataFrame({
    'age': [65, 45],
    'bp': [80, 70],
    'sg': [1.020, 1.015],
    'al': [1, 2],
    'su': [0, 0],
    'bgr': [150, 120],
    'bu': [36, 18],
    'sc': [1.2, 1.0],
    'sod': [140, 135],
    'pot': [4.5, 4.0],
    'hemo': [13.5, 14.0],
    'pcv': [44, 40],
    'wc': [8000, 7600],
    'rc': [4.9, 5.1]
})
```

Fig. 9 Sample data of the patient

```
1/1 [==============================] - 1s 688ms/step
['ckd positive', 'ckd negative']
```

Fig. 10 Classification resultg

The medical input characteristics of two individuals used to predict chronic kidney disease are shown in Fig. 9. In order to classify each patient as either CKD-positive or CKD-negative, the CNN-GRU model processes these characteristics.

The CNN-GRU model's classification findings are displayed in Fig. 10, which demonstrates how it divides patient input characteristics into CKD-positive and CKD-negative groups. Based on patterns learnt from clinical input data, this output shows how well the model can detect the existence or absence of chronic kidney disease.

5. Conclusions

In this paper, we introduce a hybrid model for predicting chronic kidney disease (CKD) that integrates a CNN-GRU. The CNN + GRU architecture combines the strengths of both architectures: CNNs are capable of extracting patterns and geographic features of structured information, whereas GRUs process sequential information and can extract temporal features. We conducted tests to determine that the CNN-GRU model was more successful compared to complete deep learning models and traditional machine learning methods in terms of prediction accuracy and reliability. By effectively extracting and analyzing the geographical and temporal variables of patients, the hybrid model proved to be an effective tool in early CKD diagnosis and detection. These results demonstrate the ability of high-tech, deep-learning tools to enhance patient outcomes. Early and accurate diagnosis of chronic kidney disease (CKD) may lead to early treatment, improved disease management, and better patient outcomes. Moreover, the methodology of this study can be applied to other clinical scenarios where it is essential to analyze spatial and temporal data. To generalize the model in the future, larger and more diverse datasets from multi-centered hospitals can be utilized to reaffirm the model's performance when applied to different populations. The CNN-GRU model can be integrated with clinical decision support systems to enable real-time monitoring of CKD risks for physicians. Additionally, it is possible to incorporate multimodal data, such as medical imaging and genomic biomarkers, to further enhance the accuracy of prediction. A framework of explainable AI (XAI) needs to be adopted to enhance interpretability and foster clinical trust, which in turn would facilitate the practical implementation of this framework in medical practice.

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