Advancing Chronic Kidney Disease Detection: Improving Biomarkers and CT Imaging for Enhanced Detection(copy)

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Abstract*— Chronic Kidney Disease (CKD) is one of the major global health challenges, with millions of people suffering from this condition. This paper aims at improving the early detection and diagnosis of CKD using state-of-the-art machine learning methodologies on biomarkers and CT image data analysis. Random Forest is used for the analysis of datasets of biomarkers, and a custom-made CNN is used in the interpretation of the CT scan images. Both models are rigorously cross-validated and finely tuned to ensure robust performance with very high accuracy. Results: In the RF model, delivered accuracy of 99.4% with different methods of cross-validation, the customized CNN model revealed a validation accuracy of 99.41%. On the other hand, both models manifested very minimal overfitting. This dual approach provides a comprehensive diagnostic tool with considerably improved CKD detection. The results suggest that a combination of these innovative models would yield early and more accurate diagnosis of CKD, hence timely intervention for better outcomes in patients. Future studies should consider the integration of these models into a comprehensive diagnostic system with enhanced clinical utility and patient care.

Keywords*— Chronic Kidney Disease (CKD), Convolutional Neural Network (CNN) , Random Forest

SECTION I: INTRODUCTION

CKD is a global health problem concern, with millions affected worldwide. CKD is a characterized by any condition that causes progressive reduction in kidney function, often in association with fibrosis, tubular atrophy, and interstitial inflammation [1]. CKD is progressive; it is a process leading to the irreversible loss of functional units of kidneys, resulting in end-stage renal failure—the kidneys can not work anymore—thus dialysis or kidney transplantation is necessary for survival [2].

The prevalence of CKD is on the rise globally, partly related to increased conditions associated with it, including diabetes mellitus and cardiovascular disease. Both DM and CVD are very common comorbidities and significant risk factors for the development of CKD [3]. Estimates indicate that more than 850 million people worldwide have CKD, AKI, or require RRT. [4] In 2016, CKD ranked 13th as a cause of death globally [5] and is forecast to be the 5th leading cause of years of life lost by 2040 [6]. These estimates thereby define a pressing need for better preventive strategies, early diagnostic approaches, and effective treatment modalities for CKD.

The traditional risk factors include hypertension, smoking, diabetes mellitus, and obesity. The non-traditional factors include exposure to nephrotoxins, fetal and maternal factors, and environmental factors. A history of kidney stones can increase the risk of CKD up to 116% [10]. Common risk factors for CKD and cancer predispose people to both renal cell carcinoma and CKD [11][12]. Simple kidney cysts do not, per se, present a direct risk. Nonetheless, the presence of such cysts could be helpful in pointing out underlying conditions or ruling out inherited cystic kidney disease [13].

Many patients with early stages of CKD remain undiagnosed and require screening for risk factors. Any early interventions are associated with an improved quality of life and treatment of the underlying diseases, which include diabetes and hypertension. KEEP and KDEP enhance the early detection and treatment capabilities of patients and health professionals. Targeted screening of populations at risk allows detecting a patient early for an intervention to be possible. The management of CKD effectively requires collaboration between the primary physician and specialists [14][15].

Traditional CKD screening has issues with regard to cost-effectiveness and efficiency. There is a need for closer collaboration between primary and secondary care to avoid unnecessary testing, which is associated with anxiety for the patient and unnecessary labeling. Traditional screening methods result in false positives—unnecessary procedures—and conspicuously fail to improve outcomes for patients [16][17].

In this paper, we take a closer look at some advanced methods to improve CKD detection using biomarkers and CT imaging. Section I includes the introduction. Section II considers the background and related work, including the more recent development of machine learning for the detection of CKD. Section III outlines the methodology in detail. Section IV presents the results and evaluates the performance of our models. Finally, Section V presents our findings with respect to possible future research, and Section VI concludes the paper by summarizing key points and providing overall significance statements for our work.

SECTION II: LITRATURE SURVEY

With an ever-increasing burden of CKD, there is an urge in like proportion to get some effective tools for early

prediction of CKD. Machine learning now has the potential to bring about sea change in the diagnosis, treating, and prevention of diseases like CKD.

Machine Learning is a sub-branch of Artificial Intelligence dealing with the design and development of algorithms that enable a computer to predictively learn without being explicitly programmed. Either of some other healthcare applications includes predictive analytics, diagnosis, treatment, personalized medicine, clinical decision support, and population health management. In health for example, ML algorithms that are applied on data sourced from electronic health records and others can predict health outcomes, hence enabling health providers to find high-risk patients for preventive measures. It can also analyze different medical images like CT scans and x-rays for diagnosis and find the best options in treatment [30]. On top of that, it can anticipate the outcome of treatments for that matter based on features presented by a patient, including genetics and case history. These two examples alone provide insight into the profound influence that ML has on patients' lives, public health, and resource allocation [31].

A good number of studies have shown that ML is very effective in predicting and classifying CKD. For instance, in the paper from Venkatesan et al. 2023, the following ML techniques—built with datasets extracted from the Irvine ML Repository—tested: Support Vector Machine, K-Nearest Neighbors, Random Forest, Logistic Regression, and Decision Tree classifiers. Results showed Extreme Gradient Boosting with an accuracy of 98.00%, therefore being the best-performing model and showing the potential of high precision in CKD prediction. In fact, only such models can enable policymakers to project future trends of CKD, detecting it early enough, and appropriately allocating resources [32].

Qin et al. (2020) provided a method that combined logistic regression and random forest by a perceptron and reached 99.83% accuracy in the diagnosis of CKD. This approach underlined gains in the accuracy of prediction due to integration of several methods of ML. In another related study, Sobrinho et al. (2020), it tested the J48 decision tree and achieved an outcome of 95.00%. The model is widely recognized because of its interpretability, so it is suitable for developing countries [33]. However, other methods, such as random forest, naive Bayes, and support vector machine, are highly accurate but very cumbersome in the interpretation of produced results [34].

It finds further development in a system model proposed by Prasad et al. (2022), in which CT scan images and blood samples constitute the basic features for CKD detection. The image processing was done by means of edge detection techniques, while KNN algorithms were used to predict the disease from those images, thus evidencing the tight integration between imaging and machine learning for the construction of comprehensive diagnostic tools. Alnazer et al. (2021) review some techniques of medical image analysis, illustrating the potentials of AI in renal segmentation, including novel approaches for predicting CKD, like DeepMedic and VNet [35][36].

Singh et al. (2022) proposed a deep neural network model with regard to the early detection of CKD that showed an accuracy of 100%, which is very high compared to that of other classifiers. In this study, some key features have been identified that best relate to hemoglobin, specific gravity, serum creatinine, red blood cell count, albumin, packed cell volume, and hypertension using Recursive Feature Elimination. This deep learning approach may become very helpful for nephrologists in the early detection of CKD[37].

As such, most studies usually lack cross-validation and often focus on biomarker data or imaging data alone. The need for hybrid models is, therefore, realized in improving diagnosis of CKD and enabling early interventions. Cross-validation is important because it gives a good estimate of model robustness and generalization through the systematic division of data into independent training and validation sets, hence lower risks of overfitting.

CKD prediction often uses either biomarker data, which provides biochemical details, or imaging data, which gives the structural information. While these sources may be complementary, hybrid models that include both are rather rare. A hybrid approach that considers both biomarkers and imaging data could therefore deliver a very substantial improvement in diagnostic accuracy and provide the foundation for early intervention, thus enabling detailed kidney health monitoring with a view to effective treatment at the individual level.

This study will, therefore, concentrate on improving the performance of the Random Forest model for biomarkers and that of the customized CNN for computed tomography scans through rigorous cross-validation and fine-tuning. This will help to project the correct robustness and generalization capability of the models, reducing the risk of overfitting to train data, ensuring better performance on unseen data.

METHODOLOGY (BIOMARKER MODEL)

A. Data Acquisition and Description

This dataset from the UCI Machine Learning Repository, greatly used in CKD detection, contains demographic information, physiological measures, and biochemical markers. The samples taken number 400, all having 25 features: age, gender, blood pressure, specific gravity, albumin, blood urea, serum creatinine, and hemoglobin. This includes numerical data like age and blood pressure and nominal data like edema and blood glucose classification.[18]

B. Data Preprocessing and Splitting

Several cleaning and preprocessing measures have been taken to guarantee the quality of the CKD dataset. Such steps are of vital importance in preparing the data for appropriate machine learning model training and evaluation.

- Imputation: The missing numerical values shall be replaced by mean or median imputation.[19]
- Remove the features that have more than 30% missing values; remove rows that have excessive missing values.[20]
- Standardization of numerical features by standard scaling. SelectKBest with ANOVA F-value method for feature selection of the top features.
- One Hot Encoding: Multi-category features like rbc, pc, pcc, ba, htn, dm, cad, appet, pe, ane. Label encoding for binary categorical features.

The data set is split into both training and testing sets so that the model is trained on one set and its performance evaluated on another 'unseen' set. An 80-20 split ratio is used for training and testing respectively.

C. Model Selection and Training

Depending on the type of biomarker dataset and purpose of identification of CKD presence, the models which were to be considered included:

1. Random Forest: This is another instance of ensemble learning in which several decision trees combine to make decisions. That makes it quite suitable for classification tasks, which include CKD detection due to its resilience in high-dimensional data with features that avoid overfitting.
2. XGBoost (Extreme Gradient Boosting): This is a gradient boosting algorithm, very famous for its high speed and high performance. It builds trees sequentially, where the predictive accuracy is optimized with every iteration [26]
3. SVM: A supervised learning model applied to problems of classification. This finds an optimal hyperplane that separates classes best by maximizing the margin between them [27]

By default, the models were instantiated with default parameters; SVM was set up to output probabilities by setting probability=True. The models were trained on the training data. Random Forest was trained using the RandomForestClassifier from scikit-learn. XGBoost was trained using the XGBClassifier from the library XGBoost. SVM was trained using the SVC from scikit-learn, also with probability estimates enabled.

The testing set was used to evaluate the predictive performance. Predictions were generated against the test data, and accuracy was calculated for each of the trained models below:

- Random Forest: 1.0
- XGBoost: 1.0
- SVM: 1.0.

In this case, all models realize high accuracy scores, which may by themselves hint at robust performance.

These results should, however, be taken cautiously: sometimes, perfect accuracy may mean potential issues like overfitting or data leakage. Further techniques for validation using cross-validation and hyperparameter tuning were employed in order to ensure generalizability.

VALIDATION METHODS

Machine learning algorithms evaluated in order to determine which of these algorithms best detects CKD.

Stratified K-Fold Cross-Validation

This divides the dataset into K folds, making sure to have the same class distribution. In the case of this scenario, it is especially useful when dealing with datasets like medical datasets, which have imbalanced classes.

- Random Forest: Average accuracy of 99.4%.
- XGBoost: Average accuracy of 99.4%.
- SVM: Average accuracy of 95.6%.

Leave-One-Out Cross-Validation

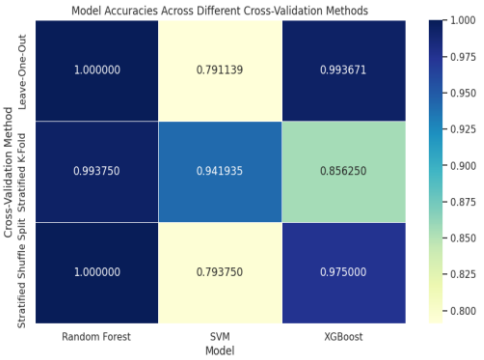
This is almost the same as K-Fold cross-validation but with each fold containing only one instance. It becomes very useful in small datasets where it's highly demanded to use available data as much as possible for training and validation.

- Random Forest: The accuracy was perfect at 100%.
- XGBoost: Somewhat lower in accuracy than Random Forest, the average was at 99.4%.
- SVM: The average accuracy was around 79.1%.

Stratified Shuffle Split Cross-Validation

This takes ideas from both stratified sampling and random splitting. It shuffles the dataset and then splits it into train/test sets while maintaining class distribution.

- Random Forest: Perfect accuracy, thus 100%.
- XGBoost: Its average accuracy remained at about 97.5%, a bit lower than that of Random Forest, indicating very good generalization.
- SVM: It gave an average accuracy of about 93.1%, which is good but relatively less robust performance compared to ensemble methods.



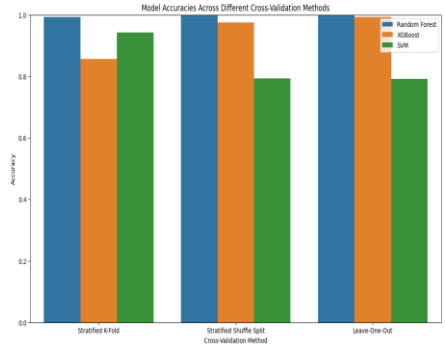
Conclusion

Stratified K-Fold: Random Forest was able to return a very high accuracy, approximately 99.4% for all subsets.

Leave-One-Out: Random Forest returned an accuracy of 100%, thus proving excellent generalization when trained on almost all instances except one. This could turn out crucial for small instances but very critical data points.

Stratified Shuffle: Random Forest's accuracy remained at 100%, thus further proving the consistency and hence the robustness in the shuffle subsets.

Random Forest's performance in all cross-validation methods was steady; hence, the algorithm is highly reliable for the detection of CKD in this study.



METHODOLOGY (IMAGING MODEL)

Data Processing

This work was done on the dataset entitled "CT KIDNEY DATASET: Normal-Cyst-Tumor and Stone" downloaded from Kaggle.[38]

In this regard, image preprocessing was performed using a custom watershed segmentation algorithm in order to enhance the discriminative features of the images and reduce noise interference. After this step, the dataset was divided according to the following subsets: training, validation, and testing sets following a 70-15-15 ratio; each subset was stored for ease of handling.

It was noticed that data augmentation could be done through Keras' ImageDataGenerator to increase model generalization and prevent overfitting by adding artificial diversity with random geometric and photometric

transformations. Configurations for different generators kept for each partition of the dataset ensured smooth data flow during training and evaluation.

Model Selection and Training

We have proposed a customized CNN model for the detection of CKD in CT images, as per the work entitled "Kidney Disease Detection from CT Images using a Customized CNN Model and Deep Learning" [39]. This model has been used in the light of its high-performance metrics compared to models like ResNet50 and EANet.

Below is the effectiveness of model customized CNN with comparative analysis according to the referenced study:

- ResNet50 worked well on cysts, normal tissues, and tumors to the tune of 87.92%.
- EANet: 83.65% strikes, nearly the same as ResNet50; it works really hard to detect stones.
- CNN model : Testing accuracy is 98.66%. Does well for all classes but biased toward stone detection.

That is to say, our developed CNN model outperformed ResNet50 and EANet with the higher accuracy in our quest for CKD detection.

a) Model Architecture

The proposed convolutional neural network (CNN) architecture consists of a series of convolutional, pooling, and fully connected layers in Figure 1. The network is designed to extract relevant features from input images and classify them into four categories.

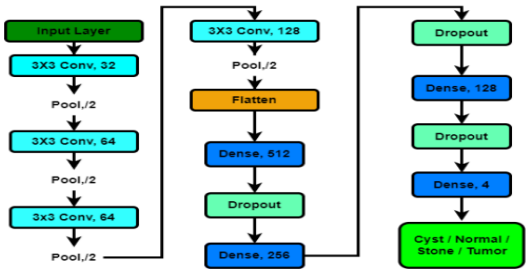


Fig. 1 CNN Model Architecture[39]

- Convolutional Layers:
  Four convolutional layers are used, all of which have 3x3 kernels and the ReLU activation function. This progressively increases the number of filters from 32 to 128, making the network capture increasingly complicated features of the images..
- Pooling Layers:
  To enhance translation invariance and reduce computations, the model incorporates max-pooling with a kernel size of 2x2 and a stride of 2 between convolutional layers to downsample feature maps and thereby lower computational cost.
- Fully Connected Layers:
  A flatten layer is added to convert the output of the convolutional layer into a one-dimensional vector.
  Then dense layers are used with 512, 256, and 128 neurons, respectively, with ReLU activation to learn complex patterns in the extracted features.
  Dropout layers are added after each dense layer with a dropout rate of 0.3 to avoid overfitting by randomly dropping out neurons during training
- Output Layer:
  A final dense layer with four neurons and softmax activation is used for multi-class classification, producing probability distributions for each of the four output classes

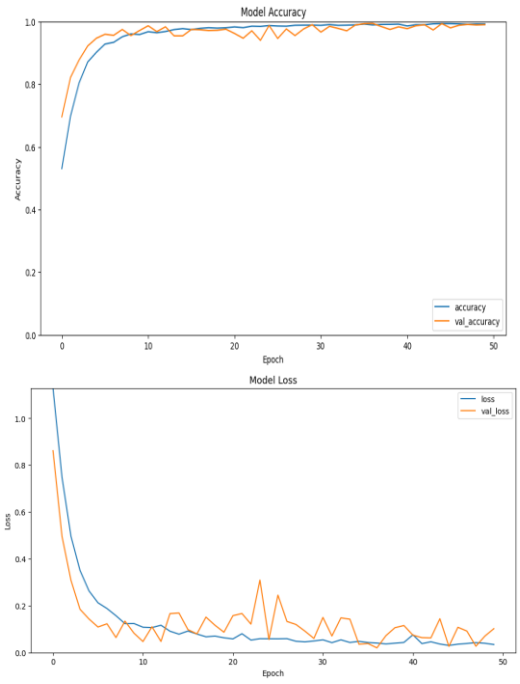
Given the demonstrated effectiveness of the proposed CNN model, we have implemented this model in our research. Our approach includes:

- **Model Implementation**: We have implemented the proposed architecture of the CNN model, and it on our dataset.
- **Fine-Tuning**: We have tuned the model based on freezing the initial layers and training the last few layers to adapt to our dataset.
- **Cross-Validation**: We have used k-fold cross-validation that will make our model more robust and generalized. This technique thus helps to estimate the performance of the model on different subsets of a dataset and avoids overfitting.

b) Model Compilation and Training

It was trained with the RMSProp optimizer, and the categorical cross-entropy loss was utilized. The number of epochs used in training was 50, with training data and validation performed on a different set. In the course of training, both training and validation losses and accuracies were tracked to be sure of effective learning.

•The Initial Epochs: Fast drop in the training and validation loss. Huge increase in the training and validation accuracy for both.
• Mid Epochs: Steady improvement but with an occasional fluctuation in the metrics of validation—a very common characteristic in model training.
• Final Epochs: A high validation accuracy, peaking at 99.41%.
Low validation loss, which evidences that there is effective learning with minimal overfitting.



The model performed extraordinarily well; validation accuracy increased linearly with a decreasing trend in validation loss during training. At the end of the final epoch, validation accuracy was at 99.41%, while validation loss remained low, hence model fit.

Fine-tuning & Cross Validation

To avoid interfering with the feature extraction capability of the CNN, only the early layers were frozen. The latter are responsible for low-level detection, like edges and textures, among others. Fine-tune the last few layers in charge of high-level feature extraction and classification to recognize specific features in our dataset. At this stage, fine-tuning is done with a lower learning rate, and to avoid overfitting, early stopping stops training when there is no substantial improvement in validation accuracy.

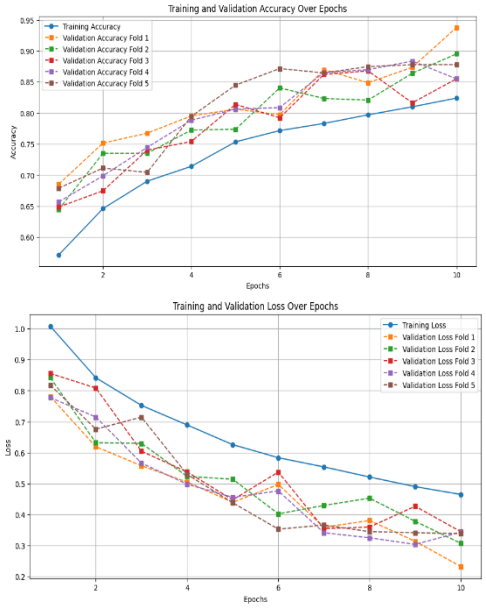
To avoid biases and ensure generalizability of the model, we have used K-fold cross-validation for projecting model performance on the following manners:

• The dataset is divided into 5 folds where each fold contains representative samples from the classes Cyst, Normal, Stone, and Tumor.

• Tenfold cross-validation in this study means training the model on the training subset and testing it on the validation subset. It does this five times. For every fold, such metrics of performance as accuracy, precision, recall, the F1 score, and loss were computed, while the average performance was used in evaluating the model.

Cross-validation showed quite consistent performance across folds, the validation accuracy ranging from 85.51% to 93.77%. This is evidence of how reliable and strong the model is with respect to the task at hand, in generalization on unseen data. This low variation in the accuracy agrees with the stability of the model and further suggests it was pretty well-tuned for this dataset.

It created high performance of the CNN model through fine-tuning and cross-validation. The parameters have been fine-tuned to very fine levels, hence optimizing the accuracy of classification for CT kidney images. By this method, high accuracy and reliable performance on different subsets of the dataset made the CNN model very suitable for this task.



II. Future Work:

Theoretical Framework for Model Integration

Future research should focus on creating or acquiring datasets that integrate biomarker and CT scan data. Collaborative efforts with medical institutions or the use of large-scale health data repositories could facilitate this goal. Empirical validation of the integrated model on real-world data is necessary to confirm its theoretical benefits. Such evaluations could establish the model's efficacy in clinical applications.

McDonald et al. (2015) evidence developing better prediction of CKD progression by integrating biomarker data and imaging results. While the RF model works well in analyzing the biomarker data for early detection of CKD, the CNN model interprets images from CT scans to identify structural abnormalities like stones, cysts, and tumors[40] . Silverman et al. (2009) point out the advantages of CT and MRI in the diagnosis of CKD. The RF model is combined with a CNN model to exploit the former's early diagnosis capabilities with biomarker data and the latter's expertise in CT scan analysis. As the abnormalities in CT scans directly affect the conditions of CKD, this combination becomes very essential[41].

The main drawback in the implementation of a hybrid model is the unavailability of a dataset that contains both biomarker and CT scan data for carrying out empirical validation of the integrative approach. The collection of multi-modal data sets involving heterogeneity of data, collection procedures, and patient's privacy issues are some of the important aspects to be taken care of while collecting data sets in the future.

Conclusion

Our research underlined how robust the performance of the Random Forest model is in detecting CKD using biomarker analysis to a very great accuracy. Likewise, it showed that a Convolutional Neural Network model was effective in pointing out structural abnormalities in CT scans, proving the strength of this technique in image analysis. While the RF model works well in explaining intricate, tabulated data with key parameters relevant for early detection of CKD, the CNN model contributes to the meaningful correlation extracted from CT imaging that identifies abnormalities such as stones, cysts, and tumors. Hence, both models borrow from the other's special strengths to contribute greatly toward CKD diagnosis and analysis of progression. An RF-CNN integrated model is likely to bring in sea change in the detection and management of CKD. While empirical evidence on this integrated dataset is lacking, theoretical advantages are huge. The results gave vent to a combined system with an RF model that was competent in biomarker data and a CNN model strong in CT scan analysis to provide an integrated diagnostic framework driven by improved accuracy, risk assessment, and early intervention strategies.

Integrating such high-accuracy models, we foresee further steps in CKD diagnosis and the optimization of strategies concerning the management of patients with CKD, hence much more personalized and effective treatments. Such a combined approach will hugely enhance patient outcomes and drive innovation in medical diagnostics. Further work in this area is required to overcome current limitations in data so that a robust and integrated model can be built that brings unprecedented levels of precision into CKD detection and management, hence improving patient care and eventually healthcare practices.

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