Physical Education, Health and Social Sciences

https://journal-of-social-education.org

E-ISSN: 2958-5996
P-ISSN: 2958-5988

Renal Vision Advanced Kidney Disease Detection Using Attention-Powered Ensemble CNNs

Muhammad Nadeem Akhtar[1*], Kashif Iqbal[2], Muhammad Shoaib Abid[3]

[1,2,3] Department of Computer Science & IT, Ghazi University, Dera Ghazi Khan, Pakistan,
[1]muhammadnadeemakhtar2869@gmail.com, [2]kashifiqbal7239922@gmail.com,
[3]shoaib.jatoi.msit@gmail.com

DOI: https://doi.org/10.63163/jpehss.v3i1.114

Abstract

The kidneys eliminate waste, pollutants, and unnecessary water from the bloodstream, which helps to sustain general health. Impaired kidney functioning can have solemn effects for someone's health. Machine learning (ML) approaches have revealed to be operative tools for enlightening clinical decision-making and reducing ambiguity. However, current approaches for detecting kidney disease are frequently imprecise because to biological characteristic constraints. This study delivers a progressive machine learning model that forecasts renal illness by combining preprocessing procedures, hyper parameter optimization, feature selection and Machine Learning algorithms. To improve detection accuracy, a Convolutional Neural Network (CNN) is used in aggregation with an attention mechanism. The model identifies kidney anomalies, for example cysts, stones, and cancers, as markers of renal illness. The model was validated using k-fold cross-validation, and the dataset contained around 4000 photos (1000 in each class). The suggested CNN with concentration model has a remarkable accuracy of 99.87% in diagnosing various kidney disease kinds. This version simplifies the language and simplifies the process while leaving the important elements intact.

Keywords: Machine Learning, CNNs, the Hyperparameter Optimizing, Medical Image Analysis, and K-Fold Cross-Validation, Ensemble CNNs, Attention Model, Hybrid model.

Introduction

Chronic kidney disease, also known as CKD, is a degenerative medical disorder in which the kidneys gradually lose their capacity to filter blood, resulting in a buildup of toxins, waste products, and extra water in the body. The kidneys regulate electrolytes, keep fluids balanced, and eliminate toxic chemicals like urea and creatinine. When the renal system deteriorates, waste products accumulate in the circulation, creating serious health consequences. [1]. People are frequently faced with several common diseases including high blood pressure and other diseases like diabetes and cardiovascular that increases the chances of CKD that rises with age factor[2]. In the year 2010 the incidence of chronic kidney disease was determined as the 18th cause of death globally and as at 2013 it has caused the death of more than one million people [3]. Currently, it is estimated that about 10 percent of the world's population already has CKD, a trend likely to increase in the future given the aged population and growing risk factors such as diabetes and hypertension [4]. Despite the fact that healthcare diagnostics has improved over the years, CKD is still not detected until it is in the advanced stage making the quest for vigorous prevention quite impossible. Other methods for kidney disease detection such as blood tests and urine analyses, ultrasound and biopsies are based on biological features which have limited sensitivity

and worryingly lead to either delayed or missed diagnosis One of understanding these constraints over the recent decade has been the introduction of machine learning (ML) which has improved the accuracy of diagnosing and assisting clinicians. More recently, ML models, including Convolutional Neural Networks (CNNs), have been used to analyze medical images detecting fine details and changes that other techniques are unlikely to discern. Ovarian tumor is one of the most common tumors in human females and causes high mortality and morbidity associated with it. This cancer ranks 8th as cancer disease in women around the world with annual incidences of 295,000 new cases and 185,000 deaths due to the cancer disease.

Due to the absence of obvious behavioral features which can be traced in the early stages and assessment in the late stages, the 5-year survival rate is less than 30%, emphasizing the vital need for early identification. Traditional diagnostic approaches, such as histopathologic examination of blood samples, CA-125 blood tests, and ultrasound imaging, have drawbacks such as low sensitivity and specificity, which frequently leads to missed diagnosis and extended treatment wait periods [7]. A. Farjana et al. (2023) used the UCI CKD dataset to forecast chronic kidney disease, also called CKD, using machine learning (ML) techniques. Missing data was added with the mean value technique, and hold-out verification was used. Their findings indicated that LightGBM outperformed the other algorithms in the research. However, the study's shortcomings included complex imputation approaches, outlier management, data scaling, feature selection, and model tuning [8]. Another study used machine learning methods to predict CKD by imputing missing data using mean and mode procedures, then choosing features using recursive feature elimination and principal component analysis (PCA). However, scaling strategies and hyper parameter optimization techniques were not employed [9]. M. M. Hassan (2023) predicted the chronic kidney disease through the electronic medical records using machine learning. For missing data assumptions, predictive mean matching was used, and for grouping, K-means was applied. The XGBoost method was employed both for feature selection as well as SHAP value analysis. However, they did not include any scaling or hyperparameter optimization procedures of the study [10]. In the same manner, Kaur (2023) did a prediction analysis of chronic kidney disease application of machine learning where absence of certain data was dealt with using a little's mcar tucking. The comparative methods were employed in modeling multiple approaches, bagging was found to be the most effective. However, scaling, cross-validation and hyperparameter tuning were not conducted [11]. Thus, machine learning algorithms can be used comfortably in enhancing the precision of prediction of diseases diagnosis by improving reliability on the extensive analysis, which reduces the chances of error. The employment of the ML algorithms and classifications, as it has been observed, is one of the effective means of identifying a situation and forecasting a great number of diseases such as cardiovascular disease, diabetes, cancer and liver diseases among other conditions [12]. In one research [13], four different types of appropriate methods were leveraged to estimate the likelihood accuracy of the dataset. The gradient boosting classifier achieved the highest accuracy against other methods of 99.80% and other methods such as AdaBoost and LDA were190 to 97.91%. Another research [14] explored the opportunity of machine learning to identify CKD early by examining predictive data from an archive of 400 patients compiled by Apollo Medical Centers in India. The study used a hybrid model containing two target labels (CKD patients along with control persons) and four machine learning classifiers. In a comparable investigation, researchers revealed how several machine learning models may help healthcare practitioners detect CKD. The authors suggested a novel selection criterion to estimate CKD [15]. A performance examination of particular classifiers found that random forest classifiers outperformed Naive Bayes and artificial neural networks [16]. The authors of [17] created a strategy for predicting CKD (chronic kidney disease) by combining machine learning and deep neural network approaches. The Support Vector Machine, also known as the SVM, model outperformed all other machine learning techniques. Nevertheless, this study did not look into the correction of missing information or outliers. Despite this, every characteristic of the dataset was used to train the ML model. Another artificial intelligence CKD classifier was built in [18], and the SVM model once again performed best in

each of the test sets. Although this study took outliers into consideration during imputation, it failed to tackle data balance because it only used 12 characteristics. Additionally, no hyperparameter adjustment was conducted to improve the model's accuracy. Another study [19] described a machine learning approach for predicting CKD prognosis. In [20], the authors evaluated the efficacy of four alternative algorithms for early identification of renal disease. These AI systems were evaluated using a variety of performance criteria, including precision, precision, sensitivity, the F1-score, and Matthew's Correlation Coefficient. The study discovered that AdaBoost overall Random Forest beat gradient boost and Stochastic Gradient Descent is terms of preciseness, sensitivity, and consistency. AdaBoost and Random Forest received high marks in both MCC and Area Under the Distribution (AUC). These intelligent computer programs present an effective solution for the efficient prevention of chronic kidney diseases. The work by [21] aims to utilize past medical records, in order to predict the progress of chronic kidney disease (CKD) in patients. This study performed quality assessment, missing data treatment, and data preparation. Eleven algorithms were tried out, and indeed, out of all the tested classifiers, both Gradient Boosting and Random Forest emerged as the most accurate and unprejudiced. The study deployed collection of geographical aspects with practical aspects for data collection in predicting the disease CKD. In [22], four classification techniques were evaluated: Random Forest, Logistic Regression, K-Nearest Neighbors and SVM. The study employed 400 records from UCI repository having 25 attributes per patient. Models accuracy of 94%, 98% and 97% were recorded with a random forest classifier achieving the highest accuracy often of 100%.Acharya et al [23], when dealing with medical electronic records with disease diagnosis related datasets, improved outcome of statistical analysis. They deployed conceptual strategies using artificial reliable on the ECG dataset and CNN to achieve a classification of body images in a determination of 94% accuracy.Wasle et al. [24] examined the available chronic kidney disease dataset with different techniques of machine learning and reported that Random forest was found to be better than both Naive bayes and Decision Trees in classifying. Nithya et al. [25] have developed a K-Means based movement system for the classification and clustering of CKD data. He has also worked on predicting (artificial neural network) pictures of renal illness and achieved a classification accuracy of 99.61%. Navaneeth and Suchetha [26] also worked through the system for predicting chronic renal illness with the help of dataset and various baseline machine learning techniques with CNN and SVM . They reported good accuracy, sensitivity, and specificity at present paper describes a new way of kidney disease detection using an ensemble model of CNNs with attention mechanisms. Attention mechanisms are another area of fascinating research which have already been applied to many applications in computer vision and natural language processing, concentrates on important regions of an image and thus enhances the other regions of the image making feature extraction and classification better [7]. This method seeks to use a combination of CNN and attention to enhance the detection of cyst, and stones, and tumor of the kidneys. The model's performance is further validated through k-fold cross-validation on a dataset consisting of nearly 4000 kidney images. The proposed approach demonstrates a significant improvement over traditional methods, achieving an accuracy of 99.87% in classifying different kidney disease types. This paper is organized as follows: Section 2 discusses related work, highlighting existing methods for kidney disease detection using ML techniques. Section 3 describes the proposed methodology, including preprocessing steps, feature selection, and model architecture. Section 4 presents experimental results, followed by a discussion in Section 5. Finally, Section 6 concludes the paper and suggests potential directions for future research.

Materials and Methods

Deep learning for kidney disease involves several steps that are essential to developing, training, and deploying deep learning models for clinical use (Figure.1). These steps include acquiring

data, preprocessing it, selecting a model, training, validating, and testing it, as well as evaluating and interpreting the results. Detailed explanations of each step will be provided in this section.

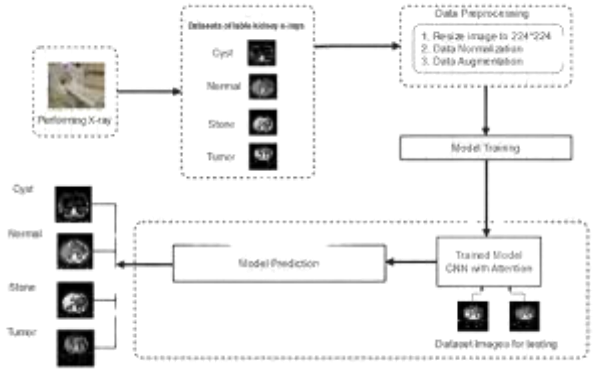

Fig. 1: Model architecture

Data Acquisition

Data acquisition involves collecting relevant and high-quality data required for model development. For this study, a dataset of kidney disease images and clinical data was sourced from [mention source or database, if applicable]. The dataset includes various types of kidney-related images (e.g., ultrasound, CT scans) and clinical parameters (e.g., blood test results, and demographic information).

In a logistic regression model aimed at detecting kidney disease, the accuracy $A(\lambda,\gamma)$ of the model is a function of two hyperparameters: the regularization parameter λ and the learning rate γ. The accuracy function $A(\lambda,\gamma)$ is given by:

$$A(\gamma,\lambda) = \left(1 - e^{-\lambda\gamma}\right) \cdot \left(1 - \frac{\lambda}{\lambda+1}\right)$$

In above equation λ and γ are positive real numbers.

(a) Find the accuracy $A(\lambda,\gamma)$ $\gamma = 0.5$ and $\lambda = 2$

(b) Compute the integral of the accuracy function over the domain $\lambda \in [1,3]$ and $\gamma \in [0.1,1]$.

To find the accuracy $A(\lambda,\gamma)$ when $\lambda = 2$ and $\gamma = 0.5$;

1. $A(2,0.5) = (1 - e^{-2\times0.5}) \cdot \left(1 - \frac{2}{2+1}\right)$

First, compute $e^{-2\times0.5} = e^{-1}$

$$e^{-1} \approx 0.3679$$

Therefore:

$$1 - e^{-1} \approx 1 - 0.3679 \approx 0.6321$$

Next, compute $\frac{2}{2+1} = \frac{2}{3}$

$$1 - \frac{2}{3} = \frac{1}{3} \approx 0.3333$$

So, the accuracy $(2,0.5)$:

$$A(2,0.5) \approx 0.6321 \cdot 0.3333 \approx 0.2107$$

(b) To compute the integral of the accuracy function over the specified domain, we set up the integral as follows:

$$\int_1^3 \int_{0.1}^1 \left(1 - e^{-\lambda\gamma}\right)\left(1 - \frac{\lambda}{\lambda+1}\right) d\gamma d\lambda$$

$$1 - \frac{2}{3} = \frac{1}{3} \approx 0.3333$$

So, the accuracy $(2,0.5)$:

$$A(2,0.5) \approx 0.6321 \cdot 0.3333 \approx 0.2107$$

(b) To compute the integral of the accuracy function over the specified domain, we set up the integral as follows:

$$\int_1^3 \int_{0.1}^1 \left(1 - e^{-\lambda\gamma}\right)\left(1 - \frac{\lambda}{\lambda+1}\right) d\gamma d\lambda$$

First, consider the inner integral with respect to:

$$\int_{0.1}^1 \left(1 - e^{-\lambda\gamma}\right) d\gamma$$

Using integration by parts for the term involving the exponential function: Let$u = \gamma$ and $dv = -e^{-\lambda\gamma} d\gamma$:

$du = d\gamma$ and $v = \frac{e^{-\lambda p}}{\lambda}$:

$$\int_a^b udv = uv|_a^b - \int_a^b vdu$$

Applying the limits $a = 0.1$ and $= 1$:

$$\left[\gamma \frac{e^{-\lambda\gamma}}{\lambda}\right]_{0.1}^1 - \int_{0.1}^1 \frac{e^{-\lambda\gamma}}{\lambda} d\gamma$$

Finally, combine the terms and integrate with respect to λ. Note, this integral may require numerical methods for exact estimation. To interpreting and integrating the accuracy function of a hyperparameter-optimized machine learning model for kidney disease detection the equation demonstrates how to apply integral calculus to make sense of the model's performance across different parameter values. A deep learning approach for kidney diseases begins with data acquisition. Developing a deep learning model typically requires a large medical image dataset. To ensure accuracy and generalizability, the data used to train the algorithm must be of high quality [28][29]. Multisource data, collected using various modalities, machines, and imaging parameters, can help reduce bias but may also affect the model's convergence [30]. Developers should be well-versed in the domain where the model will be applied and gather data from that specific domain as extensively as possible. This initial step is crucial as it lays the foundation for the subsequent stages of model development. For this study, a balanced dataset consisting of 4010 images was collected and classified into four categories: Cyst, Normal, Stone, and Tumor, as illustrated in Figure2.These datasets are available for researchers on Kaggle under the open data collection category.

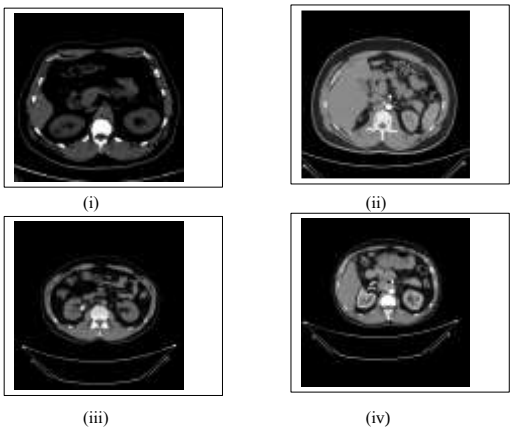

Fig. 2: Classification of datasets:(i) Cyst, (ii)Normal, (iii) Stone, (iv) Tumer

2.2 Data Preprocessing:

As the second step of deep learning, data preprocessing involves cleaning and preparing the dataset. In order to make the algorithm more accurate, it is essential to improve the quality of the data. Image normalization, image registration, and noise reduction are some of the techniques used in data preprocessing[1]. Labeling is another component of data preprocessing. In different types of learning tasks, labels come in different forms. The labeling of data involves assigning a

class or category to each image in a dataset, as in kidney disease classification [2][3]. Self-supervised learning, on the other hand, does not require an additional label for the generative model.

Data Augmentation:
Enhancements to data are another important component of data preprocessing. The process of data augmentation involves generating a series of modified versions of existing data by means such as rotation, scaling, and cropping, in order to reduce overfitting for model training. A number of generative adversarial networks have been shown to generate new synthetic images with high authenticity[4][5], demonstrating their potential for data augmentation.

Feature Extraction:
With deep learning, you can solve different shortcomings of machine learning feature extraction by utilizing the best and most reliable technique, called a CNN[6]. Knowledge is learned through layers. Data are matched and extracted using filtering mechanism.

Dataset Partitioning and Model Selection Methodology:
K-fold cross validation technique is used to partition the dataset that is divided into K values, where K + 1 has to be obtained in the next division. According to the study researcher, [8, 20] recommends a K value of 10. A total dataset of 4000 data is divided into 10. Each fold uses 400 data. K = 10 means 10-fold cross-validation. By the end of this routine activity, 0.8% of the problems have been resolved (3210 kidney images) Perform to the best of your ability, which is then trained, while the remaining 0.2% (800 kidney images) In this way, the system is validated through testing. In this model design, the first step is to acquire images from the x-ray machine. Following acquisition of the images, the data were prepared for analysis by applying preprocessing techniques. In order to extract features with neural networks using preprocessed images, preprocessed images were inserted into the Ensembled model that is CNN with attention model. Researchers used 0.25 and 0.5 dropout percentages in each layer of the experiment, and 0.5 dropout percentage produced the best results. Based on this analysis, the best extractions for representing the image are derived. Data used during training and testing for identification Extractions are based on the extracted features. Figure.1 shows how trained knowledge bases classify new images into their associated syndromes.

Results and Discussions
A variety of experiments were conducted to find an efficient model by customizing various parameters. There are five parameters to consider: A dataset's color, number of epochs, augmentation, optimizer, and dropout should all be considered. An augmented RGB colored image resulted in a 15% improvement in accuracy over a non-augmented image. This new model was trained over three epochs, 50, 100, in order to determine its performance. The model performed best on 100 epochs, however. As of the 100th epoch, training accuracy was 0.9987, which was found to be highest. Figure 2 shows the model's accuracy rates during training and validation, and Figure 3 shows the model’s loss statistics

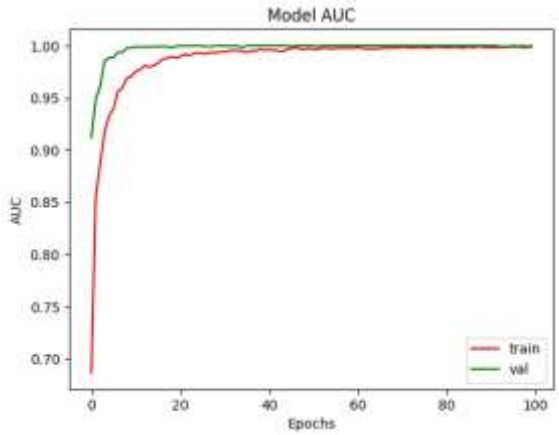

Fig. 3: Training and validation accuracy

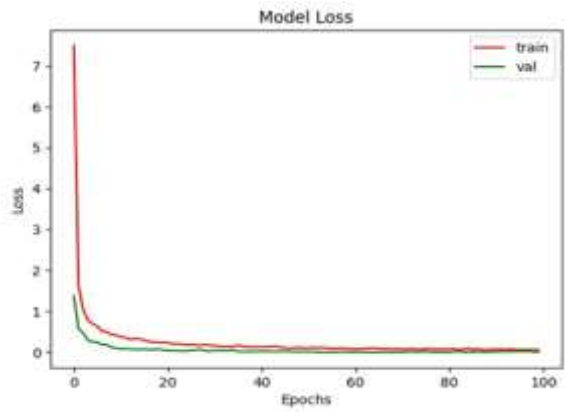

Fig. 4: Training and validation loss

Model Evaluation

Performance metrics were used in this study to evaluate the accuracy and effectiveness of the developed ML models. It was possible to gain valuable insights into the performance of the classifiers based on metrics such as accuracy, recall, precision, and F1-score. A confusion matrix, shown in figure 4, was used as the basis for the evaluation. By examining the confusion matrix, the classification results were comprehensively examined. When true positives (TP) were identified, they indicated instances correctly classified as positive, and when true negatives (TN) were identified, they indicated instances correctly classified as negative. The term false positive (FP) is used to describe a prediction that is incorrectly classified as a positive; on the other hand, the term false negative (FN) stands for a prediction that is incorrectly classified as a negative. In order to assess the model's accuracy and effectiveness in detecting kidney disease early, this evaluation approach was used.

Confusion Matrix:

Precision is a commonly used confusion Metrix in classification problems, especially for imbalanced datasets. It is defined as:

$$\text{Precision} = \frac{\text{True Positives}}{True\ Positives + False\ Positives}$$

True Positives (TP): TP use to correctly predicted the positive class.
False Positives (FP): FP use to incorrectly predicted the positive class.
Key Insight: High precision means that when the model predicts a positive class, it is often correct. Figure. 5 shows how the generated model performs efficiently in classifying data.

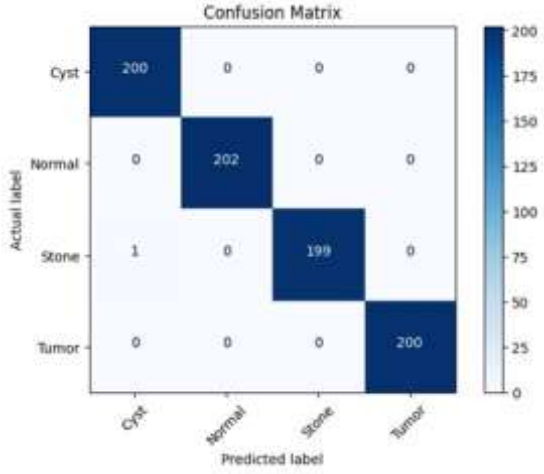

Fig. 5: Confusion matrix

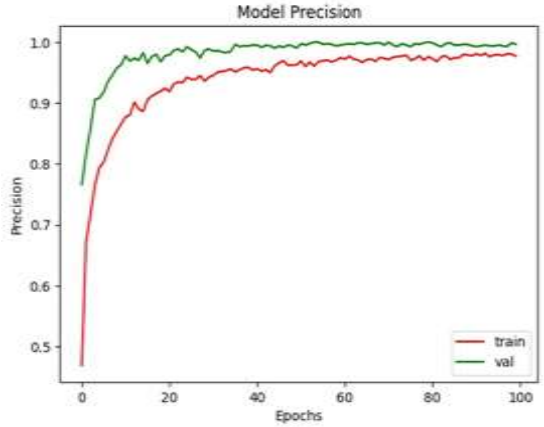

Fig. 6: Precision

Precision:

Basically, precision is a performance metric for data collection from samples. An observation that was closely predicted to be positive and one that was observed to be positive is called a fraction. Therefore, precision measures how accurate our model can predict positive results (i.e., how many are true positives). Precision of model show in figure. 5.After one-fold, the CNN model makes predictions, and we obtain the following:

True Labels	Predictions	Correctly Predicted
1	1	True Positive (TP)
0	1	False Positive (FP)
1	1	True Positive (TP)
0	0	True Negative (TN)

Recall:

A metric that determines whether the data is retrieved correctly is called recall. This is also called sensitivity, and it is the proportion of correctly predicted positives to the total amount of positives (positives) that occur. As a result, recall measures the number of actual positives (total) captured by the model. Recall of the model is show in figure.6

$$R = \frac{\text{True Positives (TP)}}{\text{True Positives (TP)} + \text{False Negatives (FN)}}$$

F1-Score:

Test accuracy is measured by this metric. Recall and precision are weighted averages of the F1 score. It makes sense even when there is uneven distribution, since it attempts to strike a balance between precision and recall.

$$F^{1} = 2 \cdot \frac{P \cdot R}{P + R}$$

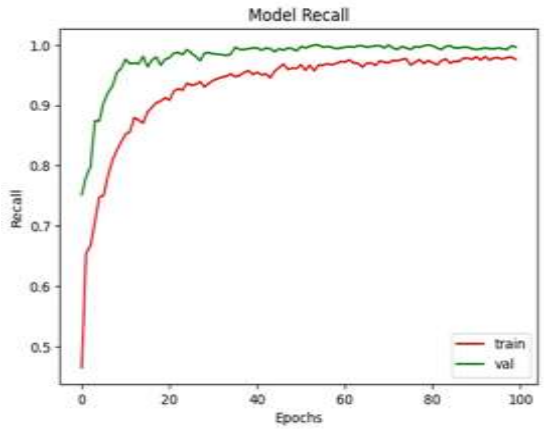

Fig. 7: Recall

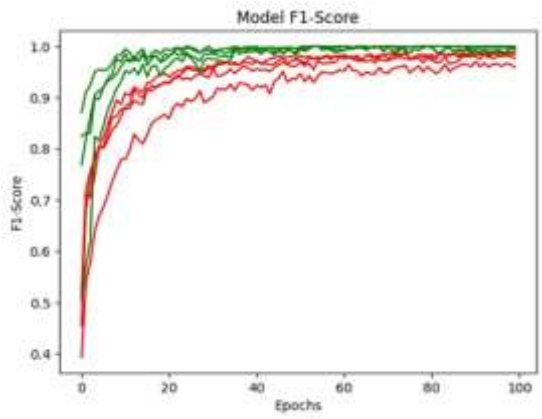

Fig. 8: F1-Score

Table 1 describe the data that is used to collect and analyze data in order to assess the success of our CNN with attention model in identifying patients with kidney disease. It demonstrates accuracy of 99.87%, meaning it accurately predicts all cases of kidney disease in patients. A harmonic mean of the accuracy and recall values was calculated to evaluate the model's effectiveness based on precision versus memory. F1 score of the suggested model is perfect as show in figure.7. In addition, she achieved a perfect 100 percent on her last exam.
Whether or not a predicted outcome is supported is determined by the number of outcomes or responses within each class.

	Precision	Recall	F1-score	Support
Cyst	0.995025	1.000000	0.997506	200.000000
Normal	1.000000	1.000000	1.000000	202.000000
Stone	1.000000	0.995000	0.997494	200.000000
Tumor	1.000000	1.000000	1.000000	200.000000
accuracy	0.998753	0.998753	0.998753	0.998753
macro avg	0.998756	0.998750	0.998750	802.000000
weighted avg	0.998759	0.998753	0.998753	802.000000

Table 1: Model evaluation report table

The results of the study prove the benefits of the ensemble CNN approach for carrying out medical image analysis, in particular, the detailed performance metrics. This strategy lays out a sound basis for the inclusion of the model in actual diagnosis process, which is important in improving kidney image analysis and effective diagnosis of the disease in practice. The optimal dropout rate of 0.5 achieved increasing the model by preventing overfitting which was crucial in improving the generalizations of the model. In the context of kidney image analysis, these findings, coupled with the K-fold cross validation evaluation metrics clearly demonstrate the efficiency, reliability and validation of the convolutional neural network (CNN) model. The model was able to achieve good coverage and completeness across these metrics, which correspond to its ability to analyze kidney images with accuracy high enough to useful the end users.

Conclusions

In this study, we present a new method to classify ovarian cancer and retinal damage on the basis of histopathology images caused by glomerulus damage. The study employs advanced segmentation techniques and deep transfer learning models, including CNN with attention, in order to obtain promising results in terms of accuracy, loss, root mean square error, precision,

recall, and F1 score. Optimization of the results was also accomplished with Adam optimizers. The best model is CNN with attention, as it performed 99.87% accurately in validation tests. As a first step, a thorough analysis of the use of a deep learning model for detecting and classifying kidney disease must be conducted. Diagnosing kidney disease should not be the sole focus of this approach. Further, the limited training dataset suggests a greater data set is needed to improve the models' applicability. For future model performance to be stronger and more reliable, it is essential to expand the dataset. Obtaining larger and more comprehensive datasets will require collaboration with medical institutions

Acknowledgements
We would like to express our deepest gratitude to Ghazi university Dera Ghazi. Khan, Pakistan for facilitating the publication of this article. Special thanks go to Dr. Hafiz Gulfam Ahmad Umar for their technical assistance and valuable discussions, which greatly enriched our work. Finally, we appreciate the support and encouragement of our friends and family, who have been a constant source of motivation.

Data Availability:
Data is publicly available on Kaggle,
https://www.kaggle.com/datasets/nazmul0087/ct-kidney-dataset-normal-cyst-tumor-and-stone
Conflicts of Interest:
The authors declare no conflicts of interest.

References

1. "National Kidney Foundation Inc. How Your Kidneys Work. ." Accessed: Jun. 22, 2024. [Online]. Available: https://www.kidney.org/kidneydisease/howkidneyswrk
2. "National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK). Chronic Kidzney Disease (CKD)." Accessed: Jun. 22, 2024. [Online]. Available: https://www.niddk.nih.gov/health-information/kidney-disease/chronic-kidney-disease-ckd
3. V. Jha et al., "Chronic kidney disease: global dimension and perspectives," Lancet, vol. 382, no. 9888, pp. 260–272, Jul. 2013, doi: 10.1016/S0140-6736(13)60687-X.
4. "Over 35,000 develop kidney failure in Bangladesh every year | The Daily Star." Accessed: Jun. 22, 2024. [Online]. Available: https://www.thedailystar.net/city/news/18m-kidney-patients-bangladesh-every-year-1703665
5. "Kidney Failure Risk Factor: Gender (Sex) | National Kidney Foundation." Accessed: Jun. 22, 2024. [Online]. Available: https://www.kidney.org/content/kidney-failure-risk-factor-gender-sex
6. Z. Momenimovahed, A. Tiznobaik, S. Taheri, and H. Salehiniya, "Ovarian cancer in the world: epidemiology and risk factors," Int. J. Womens. Health, vol. 11, pp. 287–299, 2019, doi: 10.2147/IJWH.S197604.
7. A. Hassan and A. M. H. A. Al Moaraj, "The Role of Artificial Intelligence in Entrepreneurship," Lect. Notes Networks Syst., vol. 423 LNNS, pp. 530–542, 2022, doi: 10.1007/978-3-030-93464-4_52.
8. A. Farjana et al., "Predicting Chronic Kidney Disease Using Machine Learning Algorithms," 2023 IEEE 13th Annu. Comput. Commun. Work. Conf. CCWC 2023, no. March, pp. 1267–1271, 2023, doi: 10.1109/CCWC57344.2023.10099221.
9. 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, no. January, p. 100189, 2023, doi: 10.1016/j.jpi.2023.100189.
10. M. M. Hassan et al., "A Comparative Study, Prediction and Development of Chronic Kidney Disease Using Machine Learning on Patients Clinical Records," Human-Centric Intell. Syst., vol. 3, no. 2, pp. 92–104, 2023, doi: 10.1007/s44230-023-00017-3.
11. C. Kaur, M. S. Kumar, A. Anjum, M. B. Binda, M. R. Mallu, and M. S. Al Ansari, "Chronic Kidney Disease Prediction Using Machine Learning," J. Adv. Inf. Technol., vol. 14, no. 2, pp. 384–391, 2023, doi: 10.12720/JAIT.14.2.384-391.

12. M. Kavitha, G. Gnaneswar, R. Dinesh, Y. R. Sai, and R. S. Suraj, “Heart Disease Prediction using Hybrid machine Learning Model,” Proc. 6th Int. Conf. Inven. Comput. Technol. ICICT 2021, pp. 1329–1333, Jan. 2021, doi: 10.1109/ICICT50816.2021.9358597.
13. M. A. Abdel-Fattah, N. A. Othman, and N. Goher, “Predicting Chronic Kidney Disease Using Hybrid Machine Learning Based on Apache Spark,” Comput. Intell. Neurosci., vol. 2022, 2022, doi: 10.1155/2022/9898831.
14. “Optimization of Prediction Method of Chronic Kidney Disease Using Machine Learning Algorithm | Request PDF.” Accessed: Jun. 22, 2024. [Online]. Available: https://www.researchgate.net/publication/345143713_Optimization_of_Prediction_Method_of_Chronic_Kidney_Disease_Using_Machine_Learning_Algorithm
15. Scottish Intercollegiate Guidelines Network, “Diagnosis and management of chronic kidney disease - A national clinical guideline,” Scottish Intercoll. Guidel. Netw., pp. 1–57, 2008, [Online]. Available: www.sign.ac.uuk
16. M. S. Başarslan and F. Kayaalp, “Performance analysis of fuzzy rough set-based and correlation-based attribute selection methods on detection of chronic kidney disease with various classifiers,” 2019 Sci. Meet. Electr. Biomed. Eng. Comput. Sci. EBBT 2019, Apr. 2019, doi: 10.1109/EBBT.2019.8741688.
17. P. Chittora et al., “Prediction of Chronic Kidney Disease - A Machine Learning Perspective,” IEEE Access, vol. 9, pp. 17312–17334, 2021, doi: 10.1109/ACCESS.2021.3053763.
18. C. Kaur, M. S. Kumar, A. Anjum, M. B. Binda, M. R. Mallu, and M. S. Al Ansari, “Chronic Kidney Disease Prediction Using Machine Learning,” J. Adv. Inf. Technol., vol. 14, no. 2, pp. 384–391, 2023, doi: 10.12720/jait.14.2.384-391.
19. “(PDF) Increasing Accuracy of C4.5 Algorithm by Applying Discretization and Correlation-based Feature Selection for Chronic Kidney Disease Diagnosis.” Accessed: Jun. 22, 2024. [Online]. Available: https://www.researchgate.net/publication/339972964_Increasing_Accuracy_of_C45_Algorithm_by_Applying_Discretization_and_Correlation-based_Feature_Selection_for_Chronic_Kidney_Disease_Diagnosis
20. Nikhila, “Chronic kidney disease prediction using machine learning ensemble algorithm,” Proc. - IEEE 2021 Int. Conf. Comput. Commun. Intell. Syst. ICCCIS 2021, pp. 476–480, Feb. 2021, doi: 10.1109/ICCCIS51004.2021.9397144.
21. I. U. Ekanayake and D. Herath, “Chronic Kidney Disease Prediction Using Machine Learning Methods,” MERCon 2020 - 6th Int. Multidiscip. Moratuwa Eng. Res. Conf. Proc., pp. 260–265, Jul. 2020, doi: 10.1109/MERCON50084.2020.9185249.
22. D. A. Debal and T. M. Sitote, “Chronic kidney disease prediction using machine learning techniques,” J. Big Data, vol. 9, no. 1, Dec. 2022, doi: 10.1186/S40537-022-00657-5.
23. “The impact on the classification performance of the combined use of different classification methods and different ensemble algorithms in chronic kidney disease detection | IEEE Conference Publication | IEEE Xplore.” Accessed: Jun. 22, 2024. [Online]. Available: https://ieeexplore.ieee.org/document/7851881
24. M. Fatima and M. Pasha, “Survey of Machine Learning Algorithms for Disease Diagnostic,” J. Intell. Learn. Syst. Appl., vol. 09, no. 01, pp. 1–16, 2017, doi: 10.4236/jilsa.2017.91001.
25. B. Gudeti, S. Mishra, S. Malik, T. F. Fernandez, A. K. Tyagi, and S. Kumari, “A Novel Approach to Predict Chronic Kidney Disease using Machine Learning Algorithms,” Proc. 4th Int. Conf. Electron. Commun. Aerosp. Technol. ICECA 2020, pp. 1630–1635, Nov. 2020, doi: 10.1109/ICECA49313.2020.9297392.
26. M. A. Islam and M. T. A. Shampa, “Convolutional Neural Network-based Marine Cetaceans Detection around the Swatch of No Ground in the Bay of Bengal,” Int. J. Comput. Digit. Syst., vol. 12, no. 1, pp. 877–893, 2022, doi: 10.12785/IJCDS/120173.
27. G. Tomasila and A. W. Rahardjo Emanuel, “MRI image processing method on brain tumors: A review,” AIP Conf. Proc., vol. 2296, 2020, doi: 10.1063/5.0030978.

28. G. Litjens et al., “A survey on deep learning in medical image analysis,” Med. Image Anal., vol. 42, pp. 60–88, Dec. 2017, doi: 10.1016/J.MEDIA.2017.07.005.
29. N. Tajbakhsh et al., “Embracing Imperfect Datasets: A Review of Deep Learning Solutions for Medical Image Segmentation Computer-aided breast cancer detection using mammograms View project Embracing Imperfect Datasets: A Review of Deep Learning Solutions for Medical Image Segmentation,” researchgate.net, Accessed: Jun. 22, 2024. [Online]. Available: https://www.researchgate.net/publication/340424108
30. X. Zhuang et al., “Evaluation of algorithms for Multi-Modality Whole Heart Segmentation: An open-access grand challenge,” Med. Image Anal., vol. 58, p. 101537, Dec. 2019, doi: 10.1016/J.MEDIA.2019.101537.
31. F. Ma, T. Sun, L. Liu, and H. Jing, “Detection and diagnosis of chronic kidney disease using deep learning-based heterogeneous modified artificial neural network,” Futur. Gener. Comput. Syst., vol. 111, pp. 17–26, Oct. 2020, doi: 10.1016/J.FUTURE.2020.04.036.
32. F. Zabihollahy, N. Schieda, S. Krishna, and E. Ukwatta, “Automated classification of solid renal masses on contrast-enhanced computed tomography images using convolutional neural network with decision fusion,” Eur. Radiol., vol. 30, no. 9, pp. 5183–5190, Sep. 2020, doi: 10.1007/S00330-020-06787-9.
33. T. Tanaka et al., “Differentiation of Small (≤ 4 cm) Renal Masses on Multiphase Contrast-Enhanced CT by Deep Learning,” Am. J. Roentgenol., vol. 214, no. 3, pp. 605–612, Jan. 2020, doi: 10.2214/AJR.19.22074.
34. G. Müller-Franzes et al., “Using Machine Learning to Reduce the Need for Contrast Agents in Breast MRI through Synthetic Images,” Radiology, vol. 307, no. 3, May 2023, doi: 10.1148/RADIOL.222211/ASSET/IMAGES/LARGE/RADIOL.222211.FIG6.JPEG.
35. Y. Shin, J. Yang, and Y. H. Lee, “Deep generative adversarial networks: Applications in musculoskeletal imaging,” Radiol. Artif. Intell., vol. 3, no. 3, May 2021, doi: 10.1148/RYAI.2021200157/ASSET/IMAGES/LARGE/RYAI.2021200157.FIG10.JPEG.
36. A. Chaudhary, K. S. Chouhan, J. Gajrani, and B. Sharma, Deep learning with PyTorch. 2020. doi: 10.4018/978-1-7998-3095-5.ch003.