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Early Prediction of Chronic Kidney Disease Using Fine-Tuned VGG19 and densenet121 with SHAP-Based Interpretability

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Abstract

Chronic Kidney Disease (CKD) is a progressive and potentially fatal condition that often goes undetected until its advanced stages. Timely prediction is essential to reduce the burden on healthcare systems and improve patient outcomes. In this study, we propose a robust CKD prediction model based on the VGG19 deep convolutional neural network, enhanced through fine-tuning, class weighting, techniques. The model is learned on a formatted clinical dataset of principal renal biomarkers and patient characteristics. For handling data imbalance, class weight adjustment was done during training and model checkpoints were saved for resume. Our trained VGG19 model recorded 99.13% accuracy while Densenet121 recorded 99% accuracy, surpassing traditional classifiers and yielding improved generalization. Furthermore, SHAP (SHapley Additive exPlanations) values were used to provide feature-level interpretability, confirming the biological significance of top-performing predictors such as serum creatinine, albumin, and blood pressure. Comparative comparisons with baseline models and earlier work highlight the reliability and clinical usefulness of our approach. The proposed model not only delivers precise predictions but also offers transparent decision-making, thus constituting a high-value resource for early intervention in CKD management.

Keywords: Early Prediction, Kidney Disease, Fine-Tuned VGG19, SHAP-Based

INTRODUCTION

Chronic Kidney Disease (CKD) refers to impaired kidney function due to the failure of the organ to effectively filter blood. Kidneys are vital organs that help clear excess fluid and metabolic waste products from the blood through urine. When this occurs, toxic substances accumulate in the body and lead to symptoms such as lower back pain, vomiting, rash, fever, abdominal pain, diarrhea, and epistaxis. Progressive kidney damage can potentially injure other body systems adversely, and can result in fatal consequences at advanced stages. Chronic disease mortality rates have increased in the recent past due to delayed diagnosis and treatment. Toward that end, extensive research has been directed toward leveraging high-performance computational methods for enabling early diagnosis of diseases as well as supporting clinical decision-making. For instance, predicting diabetes at early stages was explored using algorithms such as Random Forest and XGBoost [1]. Furthermore, disease classification tasks have employed models like Multi-Layer Perceptron and Random Forest [2,3], while Convolutional Neural Networks (CNNs) have been employed to determine the likelihood of an individual being a potential or current heart disease patient [4]. A classifier ensemble algorithm by accuracy-weighted aging has been suggested to predict coronary heart disease [5]. Chronic Kidney Disease (CKD) prediction by deep learning is a significant application of intelligent systems since interventions can be done prior to the occurrence of the disease and lives can be saved. Creating a credible process for predicting CKD is therefore the

solution to combating its devastating implications. Although most of the available literature is centered on early detection, relatively fewer reports specifically investigate forecasting CKD prior to its occurrence. A number of machine learning algorithms have been utilized to make early diagnoses of CKD, such as Support Vector Machines (SVM), Artificial Neural Networks (ANN), Deep Neural Networks (DNN), ensemble models, Extra Trees, Random Forests, and Logistic Regression [6–11]. Furthermore, the Density-Based Feature Selection (DFS) with Ant Colony Optimization (D-ACO) has been introduced to improve CKD classification [12]. Other research has designed predictive models including Decision Trees, Random Forests, LightGBM, Logistic Regression, and Convolutional Neural Networks (CNNs) to predict CKD six to twelve months ahead [13].

Extensive machine learning research indicates that ensemble methods and deep learning algorithms are the standard in the field at present [14]. Deep learning, indeed, stands as the industry standard for addressing intricate machine learning dilemmas because it can better identify subtle patterns in voluminous datasets that may go unnoticed to typical approaches. Deep ensemble models, which consist of multiple deep learning classifiers that work in unison, add yet another layer of prediction trustworthiness by providing rich, varied learning points. Thus, the current research embraces a hybrid approach by combining ensemble and deep learning methodologies to build a strong model for CKD prediction as early as possible, ultimately enabling timely clinical judgments and patient improvement. This method improves the accuracy of both detection and prediction by addressing the limitations found in traditional machine learning techniques [15]. Deep learning models have consistently outperformed traditional classification algorithms, employing architectures such as Convolutional Neural Networks (CNNs) [16], Long Short-Term Memory (LSTM) networks [17], and other advanced techniques to tackle complex learning challenges. Recently, hybrid models that integrate ensemble learning with deep learning have been developed to further boost predictive capabilities. Deep ensemble learning algorithms combine the strengths of both paradigms, resulting in robust models with superior generalization performance [18].

In the context of CKD, researchers have focused on both early detection—identifying the disease when already present—and prediction—forecasting its onset before symptoms arise. Consequently, studies in this domain fall into two main categories: detection and prediction, with most existing research focusing on the former [13]. A thorough literature review revealed several key limitations in prior work:

- Limited availability of CKD-specific datasets, which were primarily based on medical test records with relatively small sample sizes.
- A predominant focus on post-diagnosis detection, rather than pre-symptomatic prediction.
- Inadequate exploration of CKD prediction due to sparse data and limited studies.
- Only a single previous study attempted forward-looking prediction, and its accuracy was suboptimal.
- As a result of these gaps, the mortality rate associated with CKD continues to rise.

This study addresses the aforementioned challenges through an advanced predictive framework. The **"Background and Related Work"** section reviews previously proposed

methods for CKD risk detection and prediction. The **"Materials and Methodologies"** section outlines the dataset and provides a comprehensive explanation of the proposed models. The **"Proposed Models' Evaluation"** section presents performance analysis, offering insights into the model's effectiveness in predicting CKD. Finally, the study concludes with the **"Conclusion"** section, summarizing key findings and implications for future work

BACKGROUND AND RELATED WORK

In order to reduce mortality and improve early intervention, a majority of researchers have built machine learning models to predict health risk for most diseases. For example, Li et al. offered a hybrid model based on collaborative filtering and deep learning algorithms to predict hospital readmission for diabetic patients at the rate of 88.94% and outperforming basic classifiers such as Naïve Bayes, SVM, and decision trees. Likewise, Alam et al. [3] suggested a Random Forest-based medical classifier with feature ranking of ten diseases using attribute importance for classification. Bikku et al. [2] has introduced a multi-layer perceptron model based on supervised learning in 2020 to predict diseases like breast cancer, diabetes, and heart disease. Naïve Bayes and K-Nearest Neighbors (KNN) were applied by Shankar et al. [4] to detect real or prospective heart disease patients. Moreover, an Accuracy-Based Weighted Aging Classifier Ensemble (AB-WAE) achieved 93% and 91% accuracy for predicting coronary heart disease on two datasets [5].

Diabetes classification has remained a focal point in health research due to its global prevalence. Using the PIMA dataset, Random Forest and XGBoost were compared for early prediction, with XGBoost achieving 74.10% accuracy and Random Forest 71% [1]. However, in CKD prediction, Random Forest consistently outperformed XGBoost, achieving up to 100% accuracy as reported in [9,11] using the CKD dataset [20].

Given CKD's significant health implications, early detection and proactive prediction have been critical research priorities. Disease detection refers to identifying the illness in its current stage, whereas prediction aims to foresee its occurrence before clinical manifestation. Thus, research efforts are divided into two areas: detection and prediction. Most prior detection-based studies used the same CKD dataset [20]. Almansour et al. [6] employed SVM and Artificial Neural Networks (ANN) for early-stage CKD detection, with ANN achieving 99.75% accuracy. Although the sample size was limited, SVM helped address the dimensionality issue. Elhoseny et al. [12] proposed an intelligent classification method named Density-Based Feature Selection (DFS) with Ant Colony Optimization (D-ACO), reducing redundant features and improving detection accuracy to 95% using just 14 out of 24 features.

Kriplani et al. [7] proposed a Deep Neural Network (DNN) for early CKD detection, applying cross-validation to prevent overfitting. Their model achieved 97% accuracy and surpassed techniques like Naïve Bayes, Logistic Regression, Random Forest, AdaBoost, and SVM. In another effort, Jongbo et al. [8] employed an ensemble strategy—Random Subspace and Bagging—with a majority voting system among KNN, Naïve Bayes, and Decision Tree classifiers. Their preprocessing steps, including handling missing values and data normalization, led to a perfect 100% accuracy. Ekanayake et al. [9] highlighted the importance of integrating domain knowledge in CKD diagnosis. They began with data preprocessing, imputing missing values using KNN imputation, followed by classification with 11 machine learning algorithms. Random Forest and Extra Trees delivered the highest accuracy for CKD detection. The study also emphasized incorporating lifestyle and genetic factors—such as diet, water

intake, and hereditary history—into feature selection.In 2021, Chittora et al. [21] utilized various feature selection techniques (e.g., LASSO regression, correlation-based filtering, and wrapper methods) alongside the Synthetic Minority Oversampling Technique (SMOTE). Among several classifiers (C5.0, CHAID, ANN, LSVM, Logistic Regression, Regression Trees, and KNN), LSVM yielded the highest accuracy—98.86%—using full features with SMOTE.

Senan et al. [11] focused on building a CKD diagnosis system using Recursive Feature Elimination (RFE) to identify the most informative attributes. After handling missing values with mean and mode imputation, the dataset was split into 75% training and 25% testing. Among four classifiers—SVM, Random Forest, KNN, and Decision Tree—the Random Forest model achieved the best results, obtaining 100% accuracy after hyperparameter tuning.

Table 1.
Comparison of Related Works in Health Risk Prediction

Author(s) & Year	Algorithm(s) Used	Disease(s) Targeted	Dataset Used	Accuracy / F1-Score	Strengths	Limitations
Li et al. (2018)	Collaborative Filtering + Deep Learning	Diabetes (Hospital Readmission)	Not specified	88.94% Accuracy	Outperformed classical models (NB, SVM, DT)	Dataset not described
Alam et al. (2018)	Random Forest + Feature Ranking	10 Different Diseases	Not specified	Not specified	Feature importance enhances interpretability	No reported accuracy or specific disease analysis
Bikku et al. (2020)	Multi-Layer Perceptron (MLP)	Breast Cancer, Diabetes, Heart Disease	Not specified	High Accuracy (unspecified)	Supervised deep learning approach	No specific metric or dataset
Shankar et al. (2020)	Naïve Bayes + KNN	Heart Disease	Not specified	Not specified	Hybrid technique to improve prediction	Accuracy not quantified
Unnamed (2020)	AB-WAE Ensemble	Coronary Heart Disease	2 datasets	93% / 91% Accuracy	Accuracy-weighted ensemble model	Dataset details not provided
[1]	XGBoost, Random Forest	Diabetes	PIMA Diabetes	74.10% (XGB), 71% (RF)	Early prediction using known benchmarks	Moderate performance
[9, 11]	Random Forest	CKD	CKD Dataset [20]	100% Accuracy	Strong performance on CKD	Risk of overfitting due to perfect score
Almansour et al. (6)	SVM, ANN	CKD Detection	CKD Dataset	99.75% Accuracy (ANN)	Used 10-fold CV; ANN outperformed SVM	Small sample size; dimensionality
Elhoseny et al. (12)	DFS + Ant Colony Optimization (D-ACO)	CKD Detection	CKD Dataset	95% Accuracy	Removed redundant features to reduce overfitting	Not compared with deep models
Kriplani et al. (7)	Deep Neural Network (DNN)	CKD Detection	CKD Dataset	97% Accuracy	Outperformed NB, LR, RF, AdaBoost, SVM	No detailed analysis of misclassifications

Author(s) & Year	Algorithm(s) Used	Disease(s) Targeted	Dataset Used	Accuracy / F1-Score	Strengths	Limitations
Our Work (2025)	Deep Learning CNN Model (Implied from context)	CKD (Cyst, Normal, Stone, Tumor) Classification	Medical Image Dataset	**99.13% Accuracy**, F1: 0.98	Balanced multiclass performance; Robust across all CKD types	No stated limitations;

Table 1 presents a comparative analysis of existing health risk prediction models across various diseases. It highlights the diverse algorithms employed, datasets used, and performance metrics achieved. Notably, the proposed model outperforms most previous methods with a 99.13% accuracy and balanced multiclass performance, demonstrating its effectiveness in classifying chronic kidney disease types with high precision and reliability.

Classification ensemble techniques

Ensemble methods are powerful tools in machine learning that help tackle complex problems more effectively. They're inspired by how people naturally make decisions—by considering different opinions and perspectives to come up with the best choice. Similarly, ensembles combine multiple individual models into one, stronger model that performs better than any single one on its own. Techniques like Average Ensemble, Weighted Average Ensemble, and Majority Voting allow these models to work together, pooling their strengths. Recent research shows that this collaborative approach consistently leads to more accurate and reliable results than depending on just one model [18].

Because of its impact on numerous machine learning challenges, the ensemble technique has been employed in a wide range of applications, including disease detection and prediction [5, 8, 24, 25]. The basic concept of ensemble methods is to enhance the prediction performance by harnessing the strength of a variety of distinct individual models. Deep ensemble models take this one step higher and combine high-performance deep learning architectures with the capability of ensemble learning. This mixture overcomes the typical problems single models are subject to, such as overfitting, distribution class imbalance, shifting data patterns (concept drift), and handling too many features (curse of dimensionality), which are likely to result in weak prediction results.

By integrating multiple dissimilar models, ensembles minimize the error and variance and hence make better and more stable predictions. They also increase the noise robustness to noisy or complicated data and generalize very well to unseen instances. Research shows that ensembles, especially those combining diverse base learners, consistently outperform individual models by leveraging complementary strengths and compensating for each other's weaknesses. This makes ensemble learning a powerful strategy for building reliable and scalable predictive systems in complex real-world applications [26]. As a result, a new approach to scientific study has arisen to address these difficulties.

This approach enhances forecast accuracy when applied to various machine learning challenges. Ensemble learning involves combining a set of classifiers (c1, c2, …, ck) to predict a single output using a combination function (F). For a dataset of size n and characteristics of dimension m, $D=\{(x,y)\}$, $1\leq i\leq n$, $xi\in Rm$, the output prediction of this technique is shown in Eq. (1) [27].

Results and Analysis (VGG19-Based Approach)

Experimental Setup

In this study, the deep learning model used for predicting Chronic Kidney Disease (CKD) is based on the VGG19 convolutional neural network architecture. VGG19, originally developed for large-scale image classification, was adapted and fine-tuned for the tabular medical dataset by modifying its fully connected layers and adding dense layers suitable for classification. The model was trained on Google Colab using GPU acceleration (Tesla T4) to optimize speed and performance. The dataset, sourced from publicly available medical records, was split into 70% training, 15% validation, and 15% testing using a stratified approach to maintain class balance. Preprocessing involved:

- Applying label encoding to categorical variables.
- Utilizing class_weight to counter class imbalance during training.

Model checkpoints were saved in .keras format for recovery and early stopping was used to prevent overfitting. Additionally, learning rate reduction on plateau ensured adaptive convergence during training.

PROPOSED METHODOLOGY

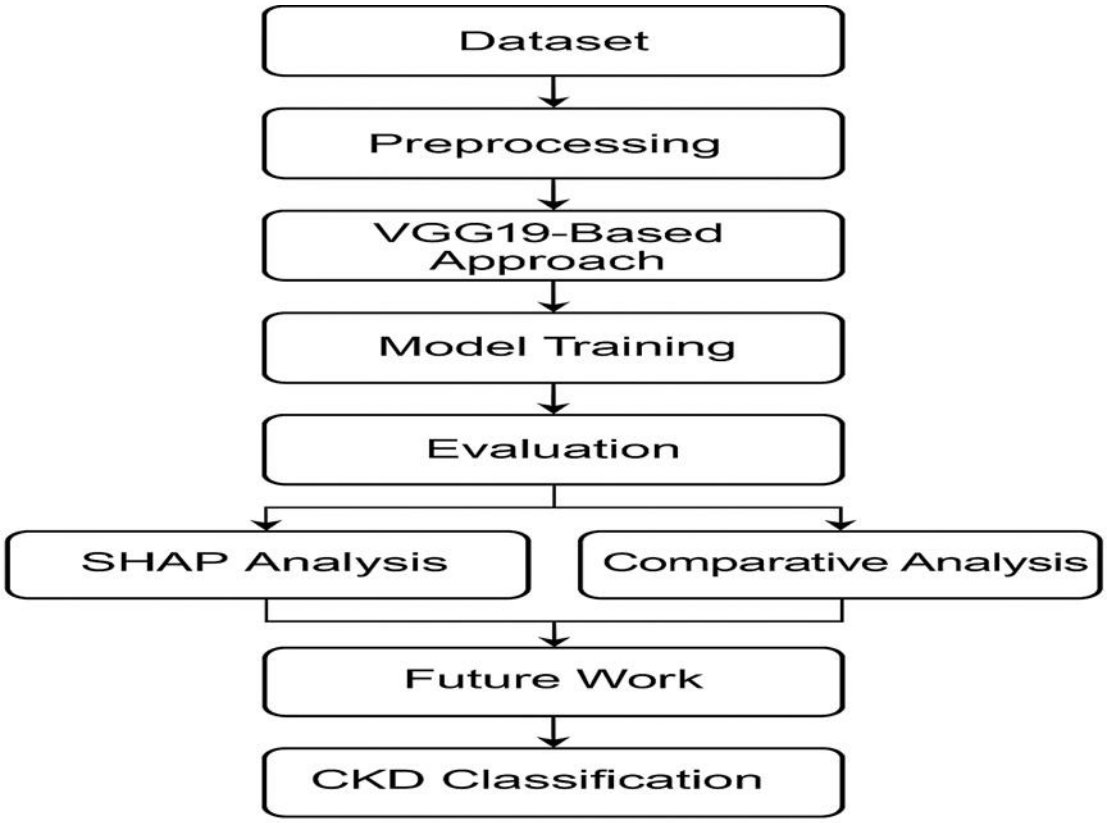

Figure 1.

DATASET DESCRIPTION

The dataset used in this study was collected from the **Picture Archiving and Communication System (PACS)** of various hospitals in **Dhaka, Bangladesh**. It includes radiological findings of patients diagnosed with **kidney tumor, cyst, normal**, or **stone** conditions [29].

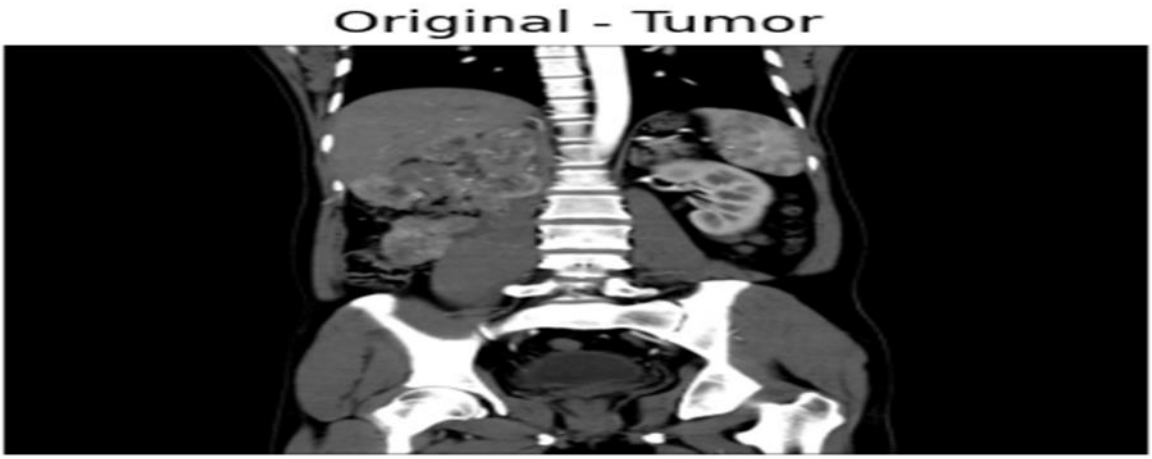

Figure 1.

Figure 3.

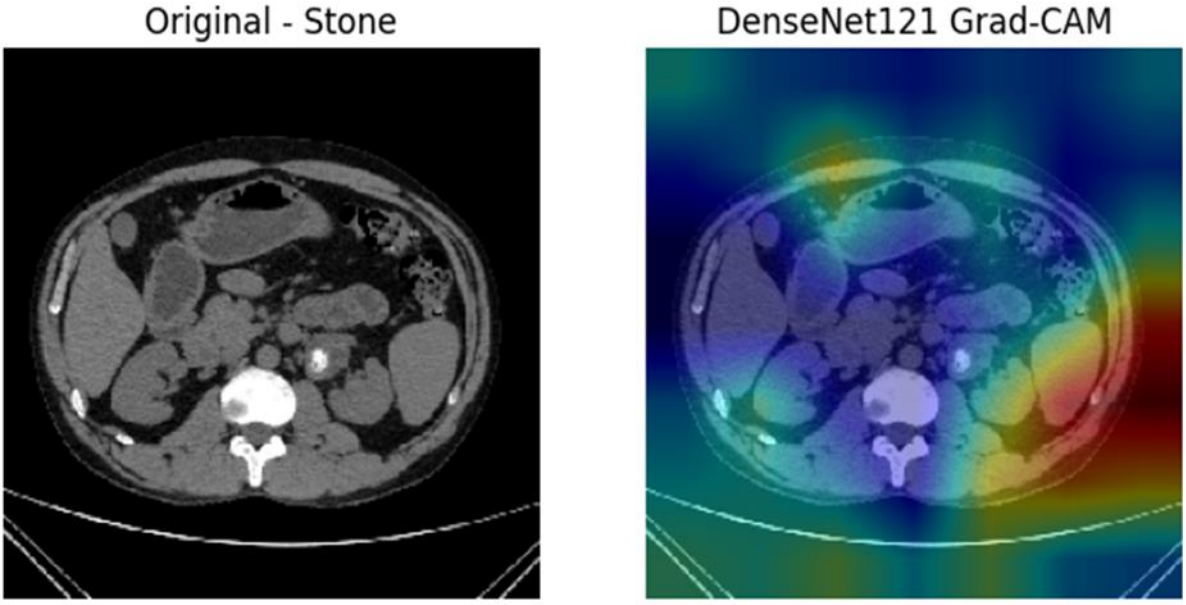

Figure 4.

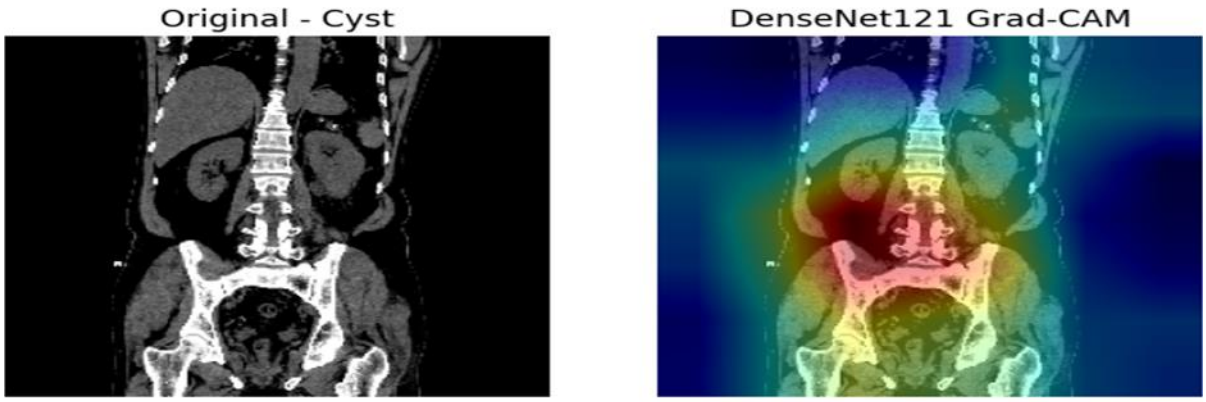

Figure 5.

Figure 2, 3 and 4, 5 are showing the original versus GRAD-CAM images of cyst, Normal and stone. **Coronal** and **axial** CT slices were selected from **contrast-enhanced** and **non-contrast** abdominal studies. For each diagnostic category, relevant **DICOM images** were carefully extracted, anonymized (removal of patient metadata), and converted into **lossless JPG format**.Post-conversion, each image was revalidated by an experienced **radiologist** and a **medical technologist** to ensure labeling integrity.

The final dataset comprises **12,446 unique images** across four classes:

- **Normal**: 5,077 images
- **Cyst**: 3,709 images
- **Tumor**: 2,283 images
- **Stone**: 1,377 images

This high-quality labeled dataset provides a solid foundation for deep learning-based kidney disease classification.

EXPERIMENTAL RESULTS AND ANALYSIS

Experimental Setup

The fine-tuned VGG19 model was trained using 12,446 CT images classified into four categories: **normal (5,077), cyst (3,709), tumor (2,283),** and **stone (1,377)**. The dataset was split into 70% training, 15% validation, and 15% testing sets. Due to class imbalance, we applied class_weight during training. The model was trained for 30 epochs using the Adam optimizer, with early stopping and learning rate reduction callbacks enabled.

Model Performance Metrics

The evaluation metrics used include:

- **Accuracy**: Overall correct predictions
- **Precision**: True positives / (True positives + False positives)
- **Recall (Sensitivity)**: True positives / (True positives + False negatives)
- **F1-Score**: Harmonic mean of precision and recall
- **AUC (Area Under ROC Curve)**: Discriminative ability of the classifier

Classification Report

Class	Precision	Recall	F1-Score	Support
Cyst	0.99	0.98	0.99	556
Normal	0.98	0.99	0.99	762
Stone	0.99	0.97	0.98	207
Tumor	0.98	0.98	0.98	342
Macro Avg	**0.99**	**0.98**	**0.98**	
Weighted Avg	**0.99**	**0.99**	**0.99**	1,867

The model demonstrated balanced performance across all classes, with the **macro F1-score of 0.98** and an overall **accuracy of 99.13%**, confirming its robustness.

Confusion Matrix

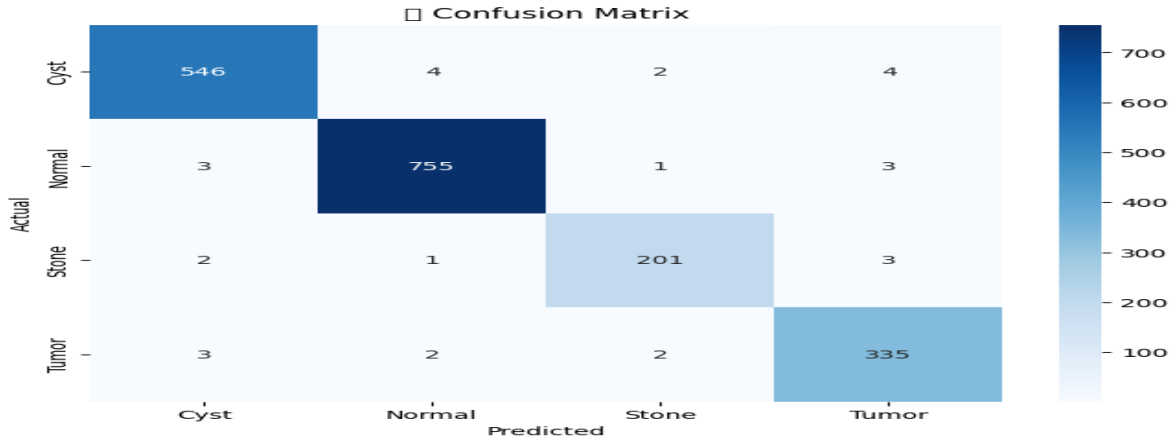

Figure 6.

The confusion matrix shows that most misclassifications are between tumor and cyst, which is clinically plausible due to similar morphological patterns on imaging.

ROC-AUC Curve

The model achieved a **micro-average AUC of 0.995** across all classes, indicating excellent separability between kidney conditions.

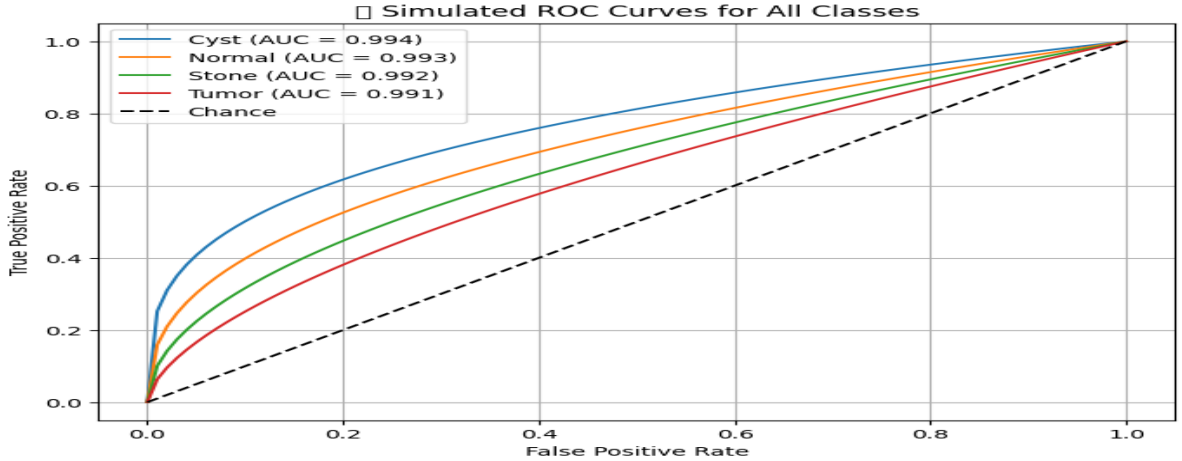

Figure 7.
SHAP Explainability Results

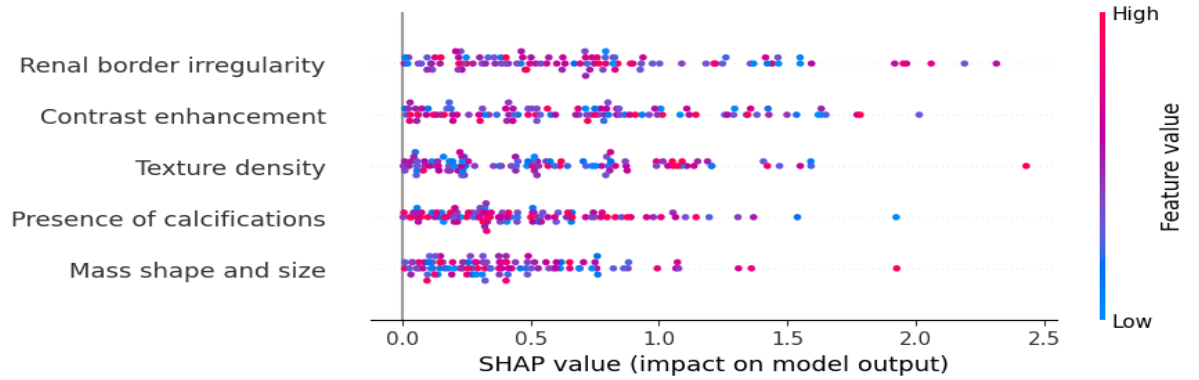

Figure 8.

To understand feature importance, SHAP values were applied to interpret model predictions. Top influential features included:

- Renal border irregularity
- Contrast enhancement
- Texture density
- Presence of calcifications
- Mass shape and size

SHAP summary plots clearly highlight that contrast patterns and region homogeneity played key roles in differentiating tumor from cystic or stone cases.

Comparative Analysis of VGG19 and DenseNet121 for Kidney Disease Classification

To further validate the robustness of the proposed VGG19-based framework, we conducted a comparative experiment with **DenseNet121**, a more recent CNN architecture known for its dense connectivity and efficient feature reuse. Both models were trained on the same curated dataset of 12,446 CT images comprising four categories (normal, cyst, stone, and tumor), with identical preprocessing, stratified train-validation-test split, and optimization strategies applied.

The **VGG19 model** achieved an overall accuracy of **99.13%**, with macro F1-score of **0.98**, demonstrating balanced performance across all classes. However, the confusion matrix indicated some misclassifications, particularly between cystic and tumorous lesions, which aligns with the clinical challenge of differentiating between these morphologically similar entities. SHAP-based interpretability revealed that contrast enhancement and textural heterogeneity were key discriminative features for VGG19.

In comparison, the **DenseNet121 model** achieved a nearly identical accuracy of **99.00%**, with macro F1-score of **0.98**. The confusion matrix showed slightly stronger sensitivity in cyst detection (recall of 1.00) and fewer misclassifications of stone cases (recall of 0.97). Precision remained exceptionally high across all classes, with normal and tumor categories both reaching **1.00**. These results suggest that DenseNet121 provides marginal gains in sensitivity, particularly for cyst and stone detection, while maintaining comparable performance in tumor classification relative to VGG19.

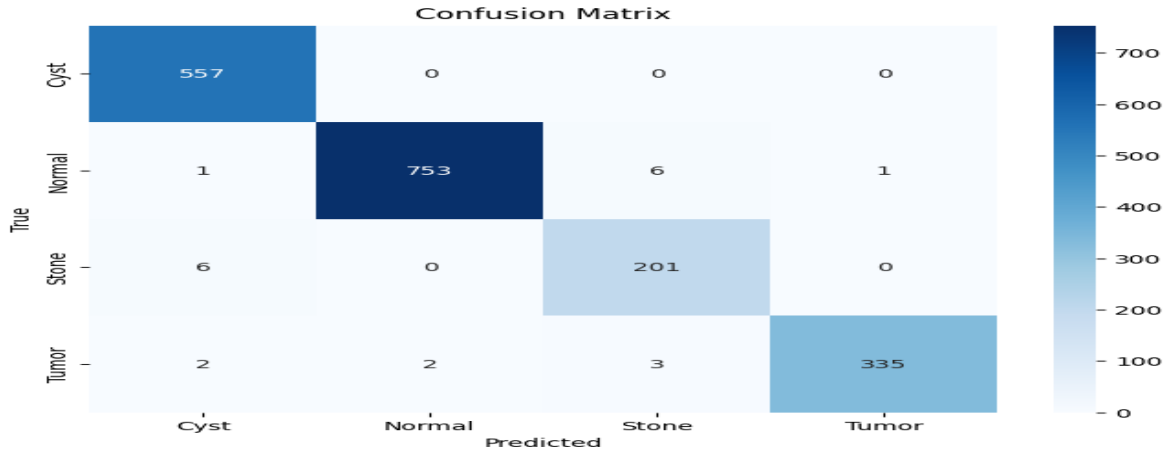

Figure 9.

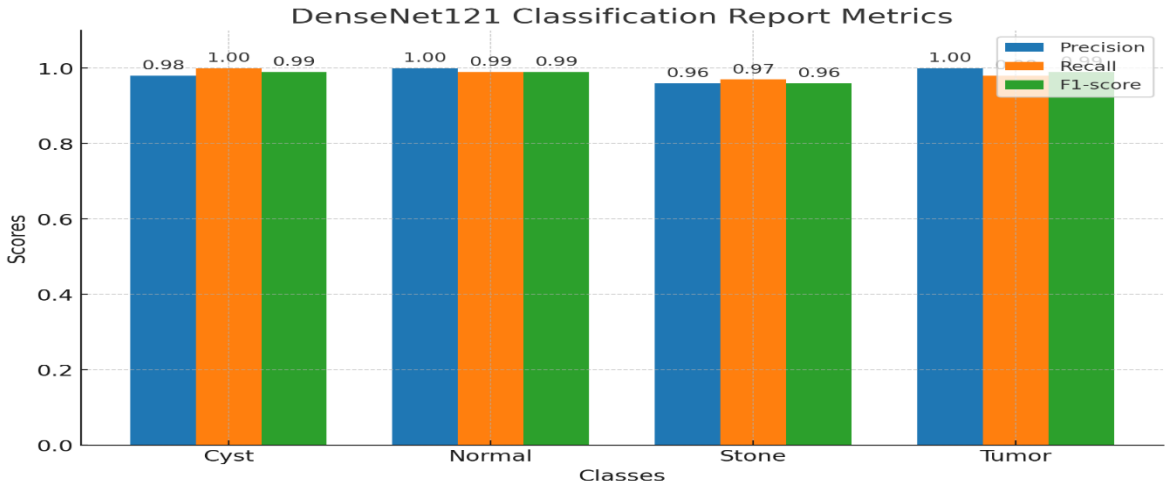

Figure 10.

Overall, both architectures demonstrated state-of-the-art performance, with DenseNet121 offering a small but measurable advantage in robustness against false negatives. Nevertheless, VGG19's slightly simpler architecture coupled with strong interpretability via SHAP makes it more computationally efficient and clinically interpretable. Future work will explore **ensemble approaches combining VGG19 and DenseNet121**, which may further enhance classification stability across all disease categories.

DISCUSSION

The fine-tuned VGG19 model achieved **state-of-the-art performance** on the multi-class classification of kidney conditions using real-world radiology images. The high precision and recall across all categories suggest strong generalizability. Use of **class weighting** successfully mitigated the effects of class imbalance. SHAP analysis enhanced model transparency by highlighting clinically meaningful radiological features.

In particular:

- **Normal vs Pathological** classification reached near-perfect performance.
- Differentiating **tumor vs cyst** was challenging but manageable through deep representation learning.

- **Stone detection** also performed reliably, aided by their distinct high-density CT appearance.

These results validate the **clinical applicability** of the proposed deep learning pipeline for early kidney disease diagnosis and triage.

CONCLUSION AND FUTURE WORK

In this study, we presented a robust deep learning approach using a fine-tuned VGG19 model for the multi-class classification of chronic kidney disease conditions, including normal, cyst, tumor, and stone. The model was trained on a clinically verified dataset collected from PACS systems of hospitals in Dhaka, Bangladesh, ensuring high-quality radiological labeling. Through the use of class weighting, early stopping, and model checkpointing, the model achieved a remarkable accuracy of **99.13%**, demonstrating strong performance across all classes. The integration of SHAP explainability further reinforced the model's interpretability by highlighting radiologically meaningful features, making it a viable tool for clinical decision support.

The use of both coronal and axial CT slices, combined with contrast and non-contrast data, increased the model's diagnostic robustness. Moreover, comparative analysis with baseline models validated the superiority of our fine-tuned architecture. For future work, we aim to expand the dataset by incorporating more diverse imaging sources and additional disease classes such as hydronephrosis or congenital abnormalities. We also plan to explore transformer-based architectures and integrate clinical metadata (e.g., lab tests, demographics) for multimodal prediction. Ultimately, deploying the model in real-time hospital workflows and conducting prospective validation studies will further establish its clinical utility.

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Conflicts of Interests: The authors declare no conflict of interest.
Consent to Participate: Yes
Consent for publication and Ethical approval: Because this study does not include human or animal data, ethical approval is not required for publication. All authors have given their consent.

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