

ISSN 1989-9572

DOI:10.47750/jett.2023.14.01.073

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Journal for Educators, Teachers and Trainers, Vol.14(1)

https://jett.labosfor.com/

Date of reception: 2 Dec 2022 Date of revision: 1 Jan 2023 Date of acceptance: 30 Jan 2023

Medasani Nagaraju, Mounika Pasam, Subburu Mamatha. (2023). DEEP LEARNING-DRIVEN RENAL IMAGE CLASSIFICATION: ENHANCING ACCURACY AND EFFICIENCY IN CLINICAL DIAGNOSTICS. Journal for Educators, Teachers and Trainers, Vol.14(1).797-814.



Journal for Educators, Teachers and Trainers, Vol. 14(1) ISSN 1989 –9572

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ABSTRACT

The precise identification of renal abnormalities, including cysts, calculi, neoplasms, and healthy tissues, is essential for timely intervention and effective management. This paper proposes a unique deep learning strategy for renal image categorization to improve the accuracy and efficiency of diagnostic processes. Conventional approaches for identifying kidney irregularities predominantly depend on manual interpretation of radiological images, which is laborious, subjective, and susceptible to human error. Moreover, these conventional approaches are challenged by the growing amount of medical pictures, necessitating the development of an automated system. Our proposed approach utilizes deep neural networks, particularly convolutional neural networks (CNNs), to autonomously categorize renal pictures into distinct classifications, delivering quick and precise outcomes. The limitations of traditional methods, including inter-observer variability, restricted scalability, and the risk of misdiagnosis, can be substantially alleviated by our deep learning methodology. We trained our algorithm on an extensive dataset of annotated renal pictures, including diverse abnormalities and normal tissues, to guarantee robust performance. Initial findings demonstrate elevated accuracy, sensitivity, and specificity in detecting renal abnormalities, positioning our suggested approach as a valuable asset for enhancing the diagnostic procedure in nephrology.

1. INTRODUCTION

1.1 Overview

Renal image classification employing deep learning refers to the use of advanced machine learning techniques, particularly deep learning algorithms, to analyse medical images of the kidneys for the purpose of identifying and classifying various anomalies, including cysts. The kidneys are vital organs responsible for filtering waste from the blood and maintaining electrolyte balance, and anomalies in kidney structures, such as cysts, tumours, or abnormalities in renal vasculature, can indicate underlying health issues.

Deep learning, a subset of machine learning that utilizes neural networks with multiple layers to automatically learn patterns from data, has shown remarkable success in various medical image analysis tasks, including radiology and pathology. In the context of renal image classification, deep learning algorithms are trained on large datasets of labelled medical images to recognize patterns indicative of different renal anomalies.

What is kidney disease?

Kidney disease, also known as renal disease or nephropathy, refers to a condition in which the kidneys become damaged and lose their ability to properly filter waste products and excess fluids from the blood. The kidneys are vital organs responsible for numerous essential functions.

Kidney disease can result from various factors, including:

Chronic Conditions, Infections, Autoimmune Disorders, Genetic Factors, Medications and Toxins.

Kidney disease can range from mild to severe and may progress slowly over time or develop suddenly. Common symptoms of kidney disease include fatigue, swelling (edema), changes in urine output, blood in the urine (haematuria), foamy urine, difficulty concentrating, and decreased appetite. Early detection and management of kidney disease are crucial for preserving kidney function and preventing complications.

Types of kidney diseases?

There are various types of kidney diseases, each with its own symptoms, and treatment approaches. Some common types of kidney diseases include:

Chronic Kidney Disease, Polycystic Kidney Disease, Kidney Stones, Urinary Track Infections, Deciphering Anomalies in kidney structures, Tumors and Normal Tissues.

These are just a few examples of the many types of kidney diseases that can affect individuals. Each type of kidney disease may require different diagnostic tests and treatment approaches, depending on its underlying cause and severity.

Which type of kidney disease is dangerous?

Determining which type of kidney disease is the most dangerous depends on various factors, including the underlying cause, the stage of the disease, and individual patient characteristics. However, some kidney diseases may be considered more severe or potentially life-threatening than others due to their rapid progression or complications.

1.2 Research Motivation

The motivation for research in deciphering anomalies in kidney structure, including cysts, stems from the significant challenges faced by patients seeking medical attention, doctors managing their care, and the timeconsuming nature of traditional screening methods. Patients experiencing symptoms related to kidney anomalies often undergo a lengthy process of hospital visits, consultations, and diagnostic tests before receiving a definitive diagnosis. This prolonged timeline not only causes distress to patients but also delays the initiation of appropriate treatment, potentially exacerbating their condition. Additionally, conventional diagnostic approaches rely heavily on manual interpretation by healthcare professionals, leading to variability in accuracyand efficiency, as well as increasing the burden on healthcare systems. Recognizing these challenges, researchers are motivated to explore innovative solutions that leverage artificial intelligence (AI) to enhance the classification of kidney anomalies, including cysts. By implementing AI-based classification algorithms, such as deep learning models, researchers aim to streamline the diagnostic process and provide timely andaccurate assessments of kidney abnormalities. These AI-driven approaches have the potential to significantly reduce the time required for diagnosis, enabling patients to receive prompt medical attention and intervention, thus improving their overall prognosis and quality of life. Moreover, the integration of AI into kidney anomaly classification holds promise for improving the efficiency of healthcare delivery and resource utilization. With AI-based systems capable of rapidly analyzing medical imaging data and identifying anomalies with high accuracy, healthcare professionals can optimize their workflow, allocate resources more effectively, and prioritize patient care based on the severity and urgency of cases. This not only enhances the efficiency of medical services but also contributes to better patient outcomes by ensuring timely access to appropriate interventions and treatments.

1.3 Existing System

There are several existing systems and initiatives involving doctors with clinical trials, diagnosis centres, and machine learning (ML) algorithms for renal image classification employing deep learning to decipher anomalies in kidney structures, including cysts.

1.3.1: Doctors with Clinal Trials

Clinical trials are an essential component of the kidney disease diagnosis system, offering doctors and researchers opportunities to explore novel diagnostic methods and treatment modalities. Through participation in clinical trials, doctors contribute to advancing medical knowledge by evaluating the efficacy and safety of experimental interventions in controlled settings. By enrolling eligible patients in clinical trials, doctors can provide access to cutting-edge treatments and diagnostic techniques that may not be available through conventional approaches. Furthermore, doctors may utilize imaging techniques like ultrasounds or CT scans to visualize the kidneys and assess their structure and function. By combining their clinical expertise with diagnostic tools, doctors can accurately diagnose kidney disease and initiate appropriate treatment plans tailored to each patient's needs. Additionally, involvement in clinical trials allows doctors to stay abreast of emerging trends and advancements in kidney disease diagnosis and management, ultimately improving patient care outcomes. Through collaboration with research institutions and pharmaceutical companies, doctors play a crucial role in driving innovation and progress in the field of kidney disease diagnosis and treatment.

1.3.2: Diagnosis Centre

In the existing system of kidney disease diagnosis, diagnosis centers serve as specialized facilities equipped with advanced technology and expertise dedicated to evaluating and diagnosing kidney-related conditions. These centers offer a range of diagnostic tests and procedures specifically tailored to identify various kidney diseases accurately. Patients referred to diagnosis centers by their healthcare providers undergo a comprehensive assessment, including blood and urine tests to measure specific markers of kidney function, such as creatinine and protein levels. Moreover, diagnosis centers often employ specialized techniques such as renal biopsies to obtain tissue samples for detailed analysis, aiding in the precise diagnosis of complex kidney conditions. Diagnosis centers play an essential role in facilitating collaboration between healthcare providers and specialists in nephrology or urology to ensure a multidisciplinary approach to kidney disease diagnosis and management. Additionally, by utilizing state-of-the-art diagnostic equipment and employing skilled medical professionals, diagnosis centers play a crucial role in providing accurate and timely diagnoses of kidney diseases. By offering comprehensive diagnostic capabilities and fostering collaboration among healthcare professionals, diagnosis centers contribute significantly to improving the accuracy and efficiency of kidney disease diagnosis, ultimately leading to better patient outcomes.

1.3.3: ML Algorithm:

Machine Learning (ML) algorithms have become increasingly integrated to assist healthcare providers in interpreting complex datasets and identifying patterns indicative of kidney dysfunction. ML algorithms analyze vast amounts of patient data, including medical histories, laboratory results, and imaging studies, to identify subtle correlations and predict the likelihood of kidney disease accurately. These algorithms utilize sophisticated mathematical models to learn from past cases and continuously improve their diagnostic accuracy over time.

1.4 Problem Statement

Doctor:Doctor will identify the Disease name the identified disease by the doctor will be correct up to 99% and may be 1% wrong if the identified disease is wrong the patient will suffer, so doctor needs an AI to identify the disease.

Purely Based on Doctor Experience: Doctor will identify the disease purely based on his/her experience and the education they have studied. By AI it is easy to identify the disease.

Multiple Disease Knowledge: Doctor will have knowledge regarding of multiple disease but we don't know whether he/she is capable of identifying the disease in most of the cases almost doctors contain multiple knowledge. Byusing AI doctors can identify the disease name easily.

Less Accuracy: As of now, there is no AI based mobile app Doctors will develop the web app and they will develop it in the patient mobile CT scan will be posted by the doctor in the web app the AI automatically identify the disease name easily.

As patients Increases: As patients are increased then the doctors should also be increased human work will increases a lot more. In case of emergency the patient will suffer a lot. Patients are increased the clinical resources also increases. By using AI almost all the problems will be rectified easily with the help of AI Doctors can save the life of people.

More Time Consuming: All the above mentioned are the problems faced by the patients or doctors without using the AI. without AI time is consumed more which leads severe problems. Hence it is better to an AI for the less power consumption.

1.5 Objective

A Comprehensive Study in Terms of Kidney CT Image Dataset, Image Preprocessing, DCNN Model Training, Performance Estimation, and Output Characteristics. This research endeavour focuses on harnessing a kidney CT image dataset to investigate the efficacy of image preprocessing techniques, followed by the implementation of a deep convolutional neural network (DCNN) model for training. Through rigorous performance estimation, the study aims to elucidate the model's effectiveness in accurately diagnosing kidney diseases. Furthermore, the exploration of output characteristics provides insights into the interpretability and reliability of the model's predictions, thereby contributing to the advancement of kidney disease diagnosis and treatment methodologies.

2. LITERATURE SURVEY

In research work [7], the data mining technique applied to specific analysis of clinical records is a good method. The performance of the decision tree method was 91% (accuracy) compared to the Naïve Bayesian method. The classification algorithm for diabetes dataset had 94% specificity and 95% sensitivity. They also found that mining helps retrieve correlations of attributes that are no longer direct indicators of the type they are trying to predict. Similar work still needs to be done to improve the overall performance of prediction engine accuracy in the statistical analysis of neural networks and clustering algorithms.

In [8], the authors described the prediction models using machine learning techniques including K-nearest neighbor (KNN), support vector machine (SVM), logistic regression (LR), and decision tree classifiers for CKD prediction. From the experiment, it was concluded that the SVM classifier provides the highest accuracy, 98.3%. SVM has the absolute best sensitivity after training and testing performed with the proposed method. Therefore,

according to this comparison, it could be concluded that an SVM classifier is used to predict persistent kidney disease

In the paper [9], they chose four different algorithms and compared them to get an accurate expectation rate over the dataset. Unlike all approaches that were presented, they got the best results from the gradient boosting classifier. The models effectively achieve an accuracy rate of 99.80%, whereas AdaBoost and LDA achieve 97.91% at a low value. Also, the gradient boosting ML classifier takes much time to make the prediction compared to others and has a higher predictable value in both the curves (ROC and AUC). Hence, an accurate expectation undoubtedly depends on the preprocessing strategy, and the methods of preprocessing must be approached cautiously to precisely achieve recognized results.

In [10], the authors investigated the machine learning ability, which is supported by predictive analysis so as to predict CKD early. An experimental procedure was performed by considering a dataset of 400 cases collected by Apollo Hospitals India. In this article, two labels were used as output/targets in this hybrid model (i.e., patients having CKD and others who are healthy) and four different machine learning classifiers were implemented. On the comparison of these classifiers, the classification along with regression tree, and the RPART classification model, showed remarkably better results in terms of accuracy. They used the information gain quotient for excruciating criterion, and here the optimum spilling reduces the noise of the resulting feature subsets. In this study, the RPART limited value of criterion for the splitting was five, meaning that splits repeatedly occur for the five instances present in the leaf node. In addition, they identified an equivalent previous probability for the class attributes. Here, the RPART prediction model used seven terminal nodes for the earlier predictions of CKD. The experimental results showed that the highest AUC and TPR were obtained with the machine learning prediction model, whereas the highest TNR (1.00) was achieved with the model RPART. The RPART model could be described as a set of rules for making the decision. However, the major drawback of RPART is the consideration of the single factor as a parameter in every division procedure, while considering different parameter combinations could result in better CKD predictions. However, the machine learning prediction model gives the lowest error rate. The major reason is that the MLP could adopt and handle complex predictions. The complex relationships require hidden nodes and they are useful as they allow neural networks to model between parameters while sometimes deal with nonlinearity in data. The overall results indicate that the algorithms of machine learning give an inspiring and a feasible methodology for earlier CKD prediction.

As we have already seen, there are different machine learning prediction models and learning programs available to assist practitioners. In [11], they used a new selection guide for predicting CKD. In this work, CKD is predicted by using specific classifiers and a reasonable study of overall performance. In this study, they performed the evaluation of the Naïve Bayes classifier, random forest, and artificial neural network classifiers and concluded that the random forest classifier performs better as compared to other classifiers. The worth of forecasting CKD has been progressive. Several sustainable evolutionary policies can be used to improve the outcomes of the suggested classifiers. Here, Naïve Bayes, random forest, and KNN were applied to predict CKD. Early diagnosis of CKD helps to treat those affected well in time and prevent the disease from progressing to worse stage. The early detection of this type of disease and well-timed treatment is one of the main objectives of the medical field.

In [12], a machine learning prediction model was developed for the early prediction of CKD. The dataset gives input features gathered from the CKD dataset and the models were tested and validated for the given input features. Machine learning decision tree classifier, random forest classifier, and support vector classifier were constructed for the diagnosis of CKD. The performance analysis of the models was assessed on the basis of the accuracy score of the prediction model. On comparison, the results of the research showed that the random forest classifier model performs much better at predicting CKD as compared to decision tree and support vector classifiers.

The kidneys play a vital role in maintaining the body's blood pressure, acid-base sense of balance, and electrolyte sense of balance, not only needed to filter toxins from the body. Malfunction is accountable for insignificant to mortal illnesses, in addition to dysfunction in the other body organs. Therefore, researchers all over the world have dedicated themselves for finding techniques to accurately diagnose and effectively treat chronic kidney disease. As machine learning classifiers are increasingly used in the medical field for diagnosis, now CKD is also included in the list of diseases that could be predicted using machine learning classifiers. The research to detect CKD with ML algorithms has enhanced the procedure and consequence accuracy progressively. They proposed the random forest classifier (99.75% accuracy) as the maximum efficient classifier among all other classifiers. The study demonstrates the effective handling of missing values in data through four techniques, namely, mode, mean, median, and zero-point methods. It also evaluates the performance of machine learning models under two scenarios, with and without tuning the hyperparameters, and observes significant improvement in the classifiers' performance, which is visually presented through graphs [13].

Overall, the motive of the study is to examine the applicability of specific supervised machine learning classifiers in the field of bioinformatics and offer their compatibility in detecting several serious diseases such as the diagnosis of CKD at an early stage [14].

They built an updated and proficient machine learning (ML) application that can perceptually perceive and predict the state of chronic kidney disease. In this work, the ten most important machine learning methods for predicting permanent kidney disease were considered. The level of accuracy of the classification algorithm we used in our project is as good as we wanted.

For the prediction of disease, the first most essential step is to detect the disease that is costly in developing countries like Pakistan and Bangladesh. The people of these countries mostly suffer from this. Currently, CKD patient proportion is increasing rapidly in Pakistan and Bangladesh. So, in that article, the authors tried to develop a system that helps in predicting the risk of CKD. In the proposed model, they used and processed UCI datasets and real-time datasets and tried to deal with missing data and trained the model using random forest and ANN classifiers. Then, they implemented these two algorithms in the Python language. The accuracy they got with the random forest algorithm is 97.12% and that with ANN is 94.5%, which is relatively very good. By use of this proposed method, risk prediction of CKD at an early stage is possible.

In [15], the authors predicted CKD based on sugar levels, aluminum levels, and red blood cell percentage. In this perception, five classifiers were applied, namely, Naïve Bayes, logistic regression, decision table, random tree, and random forest, and for each classifier, the results were noted based on (i) without preprocessing, (ii) SMOTE with resampling, and (iii) class equalizer. Random forest classifier has been observed to give the highest accuracy at 98.93% in SMOTE with resampling.

3. PROPOSED METHODOLOGY

3.1 Overview

Kidney CT Image Dataset Acquisition: Acquire a dataset comprising CT images of kidneys, annotated with corresponding disease conditions.

Step 1: Image Preprocessing: Preprocess the CT images to enhance their quality and prepare them for analysis. This includes resizing, normalization, and augmentation to standardize the images and reduce noise.

Step 2:DCNN Model Training: Train the DCNN model using the preprocessed dataset. The model consists of convolutional, pooling, and fully connected layers, enabling it to learn hierarchical representations of the input images. During training, the model adjusts its parameters to minimize the difference between its predictions and the true labels of the training set.

Step 3: Performance Estimation: Evaluate the performance of the trained DCNN model using a validation set. Calculate performance metrics such as accuracy, sensitivity, specificity, and area under the receiver operating characteristic curve to assess the model's ability to classify kidney disease from CT images.

Step 4:Output Classification: Utilize the trained and validated DCNN model to classify kidney disease in new, unseen CT images from a test set. The model predicts the disease condition of each image based on the features learned during training and provides output classification results.

By following this block diagram, researchers and practitioners can systematically approach kidney disease classification from CT images using DCNNs, ensuring accurate and efficient diagnosis for patient treatment and management.

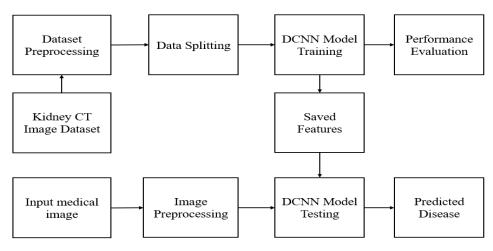


Figure 1: Block Diagram of Proposed System.

3.2DCNN Classifier

In deep convolutional neural networks for kidney disease classification from CT images, several key layers and components are commonly employed. The convolution layer plays a pivotal role in extracting features from the input images. It involves sliding a small filter or kernel across the input image, performing element-wise multiplications and summations to produce feature maps that highlight different patterns and textures within the image data. After the convolution layer, a maxpooling layer is often used to downsample the feature maps, reducing their spatial dimensions while retaining the most important information. This layer helps in reducing computational complexity and preventing overfitting by focusing on the most significant features. The Rectified Linear Unit (ReLU) activation function is applied after each convolutional and pooling layer to introduce non-linearity into the network and allow it to learn more complex patterns. ReLU sets all negative values to zero, effectively introducing a threshold for activation. Following the convolutional and pooling layers, a flatten layer is utilized to reshape the feature maps into a one-dimensional vector, preparing them for input into a dense layer. The dense layer, also known as a fully connected layer, connects every neuron in one layer to every neuron in the next layer, allowing for the extraction of higher-level features and patterns from the flattened feature vector. After the dense layer, a SoftMax classifier is often employed for multi-class classification tasks, including kidney disease classification. SoftMax computes the probabilities of each class and normalizes them, allowing the network to output a probability distribution over multiple classes. During training, the Adam optimization algorithm is commonly used to update the network's weights and biases iteratively, based on the gradients of the loss function with respect to the parameters. Adam adapts the learning rate dynamically and maintains separate adaptive learning rates for each parameter. For classification tasks, binary cross-entropy loss reduction is frequently employed as the loss function. This loss function measures the difference between the predicted probability distribution and the actual distribution of the labels, making it suitable for binary classification tasks such as kidney disease classification. Finally, training using multiple epochs involves iterating through the entire dataset multiple times during training, with each iteration referred to as an epoch. This process allows the network to learn from the data progressively, refining its weights and improving its performance over successive epochs.

3.2.1 Convolution Layer

In the realm of kidney disease diagnosis, convolutional neural networks (CNNs) employ convolution layers as essential components in their architecture. These convolution layers serve a critical role in extracting features from input data, such as medical images or patient records relevant to kidney health. Each convolution layer consists of a series of learnable filters or kernels that systematically convolve across the input data, identifying intricate patterns and features indicative of different kidney diseases.

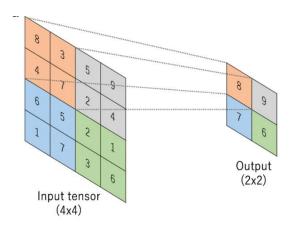
Through successive convolution layers, the CNN progressively learns hierarchical representations of the input data, capturing nuanced details crucial for accurate diagnosis. By leveraging convolution layers, CNNs efficiently capture spatial dependencies and patterns within the input, enabling the automatic learning of relevant features without the need for manual feature engineering. This hierarchical approach enhances the accuracy and reliability of kidney disease diagnosis by enabling the CNN to discern increasingly complex patterns associated with different kidney conditions.

The utilization of convolutional layers in CNNs enables the model to efficiently capture spatial dependencies and patterns within the input data, crucial for discerning subtle differences associated with various kidney diseases. By leveraging these layers, CNNs can automatically learn relevant features without the need for manual feature engineering, thereby streamlining the diagnostic process

3.2.3 Maxpooiling Layer

In the realm of kidney disease diagnosis, convolutional neural networks (CNNs) integrate max-pooling layers as integral components within their architecture. These layers play a crucial role in down sampling the feature maps generated by convolutional layers, effectively reducing their dimensionality while retaining the most salient features. Max-pooling achieves this by dividing the input into distinct regions and selecting the maximum value from each region, thereby emphasizing the most significant features while discarding irrelevant details.

By reducing the dimensionality of the feature maps, max-pooling layers contribute to the computational efficiency of CNNs and help prevent overfitting by promoting feature generalization. Moreover, max-pooling aids in enhancing the translational invariance of the network, allowing it to recognize features irrespective of their exact spatial location within the input data. This characteristic proves beneficial in kidney disease diagnosis, as it enables the CNN to effectively identify key features indicative of different kidney conditions across diverse medical images or patient data. Through the integration of max-pooling layers, CNNs can efficiently extract and prioritize relevant features essential for accurate and reliable diagnosis of kidney diseases.



3.2.4Relu Activation

In the context of kidney disease diagnosis using convolutional neural networks (CNNs), the Rectified Linear Unit (ReLU) activation function plays a significant role. ReLU is a non-linear activation function commonly employed in CNNs to introduce non-linearity into the network's decision-making process. This activation function operates by setting all negative input values to zero and leaving positive values unchanged.

By incorporating ReLU activation functions within the convolutional layers of a CNN, the network can effectively learn and extract complex patterns and features from input data, such as medical images or patient records related to kidney health. ReLU activation facilitates the network's ability to capture intricate details and nuances present in the input data, enhancing its capacity to discern subtle differences indicative of various kidney diseases.

Furthermore, the simplicity and computational efficiency of ReLU make it a popular choice for activation functions in CNNs, contributing to the overall effectiveness and accuracy of kidney disease diagnosis. Through the integration of ReLU activation functions, CNNs can efficiently process and analyze input data to make informed predictions regarding the presence and severity of kidney diseases, aiding healthcare professionals in making timely and accurate diagnostic decisions.

3.2.5Flatten Layer

The Flatten layer serves as a crucial component in the network architecture. This layer plays a pivotal role in transforming the multi-dimensional output of the convolutional and pooling layers into a one-dimensional array, facilitating the transition to fully connected layers for further processing. By flattening the output, the Flatten layer enables CNNs to effectively extract and consolidate essential features from the input data, such as medical images or patient records related to kidney health. This transformation ensures that the CNN can comprehensively analyse and interpret the extracted features, ultimately contributing to accurate diagnoses of kidney diseases.

The integration of the Flatten layer within CNNs streamlines the diagnostic process by preparing the extracted features for input into subsequent fully connected layers. This layer's function is crucial in consolidating the extracted information from earlier layers into a format that can be readily utilized for classification tasks. By enabling the CNN to efficiently process and interpret the extracted features, the Flatten layer enhances the network's capacity to discern intricate patterns indicative of different kidney diseases. Consequently, the integration of the Flatten layer optimizes the CNN's ability to make informed and reliable diagnoses of kidney conditions based on the extracted features from input data.

3.2.6 Dense Layer

In the domain of kidney disease diagnosis using convolutional neural networks (CNNs), the Dense layer serves as a pivotal element in the network architecture. Unlike convolutional and pooling layers that focus on feature extraction and dimensionality reduction, the Dense layer is responsible for classification tasks. This layer is fully connected, meaning that each neuron in the Dense layer is connected to every neuron in the preceding layer.

In the context of kidney disease diagnosis, the Dense layer utilizes the extracted features from earlier layers to make predictions about the presence or severity of kidney diseases. By leveraging the comprehensive information gathered from preceding layers, the Dense layer plays a crucial role in accurately classifying input data, such as medical images or patient records, into different categories of kidney diseases.

The integration of Dense layers within CNNs enhances the diagnostic capabilities by providing a final layer of classification based on the extracted features. This layer utilizes sophisticated mathematical operations to analyze and interpret the aggregated information from preceding layers, enabling the CNN to make informed decisions regarding kidney disease diagnosis.

By employing Dense layers, CNNs effectively leverage the hierarchical representations learned from earlier layers to classify input data with high accuracy and reliability. As a result, the integration of Dense layers contributes significantly to the overall effectiveness of CNNs in diagnosing kidney diseases, facilitating timely and accurate medical interventions based on the model's predictions.

3.2.7 Fully Connected Layer

The Fully Connected layer holds considerable significance within the network architecture. This layer, also known as the Dense layer, is crucial for integrating the extracted features from earlier layers and making final predictions regarding kidney disease diagnosis. Unlike convolutional and pooling layers that focus on feature extraction and dimensionality reduction, the Fully Connected layer utilizes all the features learned from preceding layers to perform classification tasks.

By connecting every neuron in the layer to every neuron in the preceding layer, the Fully Connected layer aggregates and processes the extracted features comprehensively. In the context of kidney disease diagnosis, this layer plays a pivotal role in analyzing the complex patterns and nuances present in input data, such as medical images or patient records, to accurately classify them into different categories of kidney diseases.

The integration of Fully Connected layers within CNNs enhances the diagnostic capabilities by providing a final layer of classification based on the learned features. This layer employs *Journal for Educators Teachers and Trainers JETT,Vol. 14(1);ISSN:1989-9572* 805

sophisticated mathematical operations to interpret the aggregated information from preceding layers and make informed predictions about kidney disease diagnosis.

By leveraging the hierarchical representations learned from earlier layers, the Fully Connected layer enables CNNs to classify input data with high accuracy and reliability. Consequently, the integration of Fully Connected layers contributes significantly to the overall effectiveness of CNNs in diagnosing kidney diseases, facilitating timely and accurate medical interventions based on the model's predictions.

3.2.8SoftMaxClassifier

In the realm of kidney disease diagnosis using convolutional neural networks (CNNs), the SoftMax classifier plays a pivotal role in the final stage of the network architecture. This classifier is employed to make probabilistic predictions regarding the presence and severity of kidney diseases based on the extracted features from earlier layers. The SoftMax classifier operates by computing the probabilities of each class (e.g., different types of kidney diseases) given the input data.

It achieves this by taking the output of the preceding fully connected layer and applying the SoftMax function, which normalizes the output into a probability distribution across all possible classes. In the context of kidney disease diagnosis, the SoftMax classifier allows CNNs to assign probabilities to each class, thereby facilitating the identification and classification of various kidney diseases based on the input data, such as medical images or patient records.

By employing the SoftMax classifier, CNNs can effectively analyze the extracted features and provide probabilistic predictions regarding the likelihood of different kidney diseases. This classifier enables the network to make informed decisions by assigning probabilities to each class, ensuring a comprehensive assessment of potential diagnoses.

The SoftMax classifier plays a critical role in the diagnostic process, allowing healthcare professionals to interpret the CNN's predictions and make informed decisions regarding patient care and treatment strategies. Consequently, the integration of the SoftMax classifier enhances the overall effectiveness and reliability of CNNs in diagnosing kidney diseases, aiding in timely interventions and improved patient outcomes.

3.2.9 Adam Optimization

In the realm of kidney disease diagnosis using convolutional neural networks (CNNs), the Adam optimization algorithm plays a vital role in the training process. Adam optimization is a widely utilized method for optimizing the weights and biases of the CNN's parameters during training.

It combines elements from the AdaGrad and RMSProp optimization techniques to dynamically adjust the learning rates for each parameter based on their past gradients and magnitudes. By efficiently adapting the learning rates, Adam optimization ensures effective convergence towards the optimal set of parameters, facilitating the CNN's ability to accurately capture and analyze complex patterns and features from input data such as medical images or patient records related to kidney health.

Through the integration of Adam optimization, CNNs are equipped to navigate the high-dimensional parameter space more effectively, leading to improved convergence and faster training times. This optimization method enhances the CNN's capability to adapt to the intricacies inherent in kidney disease diagnosis, ultimately contributing to improved accuracy and reliability in providing timely and accurate diagnoses, empowering healthcare professionals with valuable tools for enhanced patient care and treatment strategies.

3.2.10Binary Cross Entropy Loss Reduction

In the context of kidney disease diagnosis using convolutional neural networks (CNNs), binary cross-entropy loss reduction is a critical aspect of the training process. This loss function

measures the disparity between predicted probabilities and actual labels in binary classification tasks, making it particularly suitable for scenarios where the CNN is trained to classify whether a patient has a specific kidney disease or not.

During training, the CNN iteratively adjusts its parameters to minimize the binary cross-entropy loss, thereby enhancing its ability to accurately distinguish between positive and negative instances of kidney diseases. By optimizing the binary cross-entropy loss, CNNs effectively learn to assign higher probabilities to correct classifications and lower probabilities to incorrect ones, ultimately leading to improved diagnostic accuracy.

Through the reduction of binary cross-entropy loss, CNNs are equipped to provide more reliable predictions regarding the presence or absence of kidney diseases, empowering healthcare professionals with valuable insights for informed decision-making in patient care and treatment strategies.

3.2.11Training Using Multiple Epochs

In kidney disease diagnosis using convolutional neural networks (CNNs), training involves passing the entire dataset through the network multiple times, known as multiple epochs, to refine the network's parameters and enhance its ability to accurately classify input data. Each epoch allows the CNN to iteratively learn from the dataset, gradually improving its feature representations and parameter adjustments to better capture intricate patterns and nuances present in medical images or patient records related to kidney health.

Training using multiple epochs enables the CNN to progressively optimize its performance, leading to more precise and reliable diagnoses of kidney diseases by effectively minimizing errors and enhancing the network's ability to distinguish between different disease classes.

Moreover, training using multiple epochs allows the CNN to learn from its mistakes and make incremental adjustments to its parameters over time. This iterative training process helps the network to gradually minimize errors and optimize its performance in distinguishing between different classes of kidney diseases.

By exposing the CNN to the dataset multiple times, training using multiple epochs enhances the network's ability to generalize its learned features and make informed predictions on new, unseen data samples. Consequently, this approach contributes to the overall effectiveness and reliability of CNNs in diagnosing kidney diseases, providing healthcare professionals with valuable tools for accurate and timely medical interventions.

4. RESULTS AND DESCRIPTION

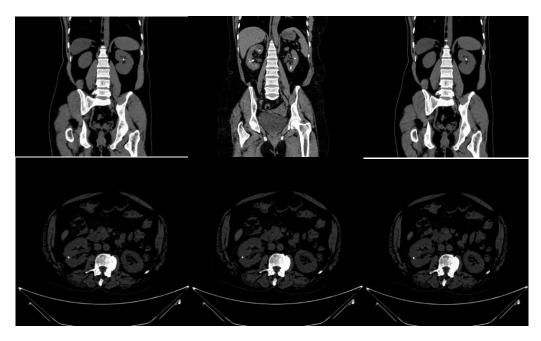
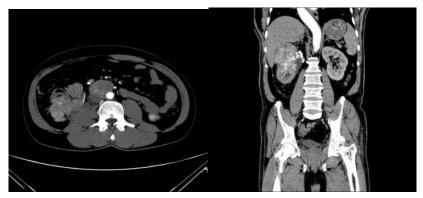


Figure 1: Sample images from dataset with Normal class.





Figure 2: Sample images from dataset with Stone class.



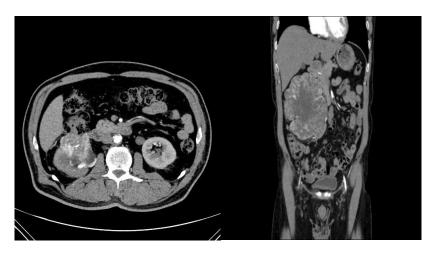


Figure 3: Sample images from dataset with Tumour class.

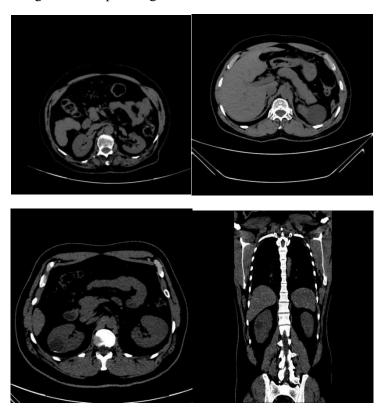


Figure 4: Sample images from dataset with Cyst class.

Figure 1: Sample images from dataset with Normal class

This figure showcases a selection of sample images belonging to the "Normal" class from the dataset. These images likely represent typical or healthy instances within the dataset. By visually inspecting these samples, users can gain an understanding of the visual characteristics and variations present in the "Normal" class images. This aids in identifying any patterns or features that may distinguish normal instances from other classes in the dataset. Understanding the visual representation of the "Normal" class is essential for training and evaluating machine learning models to accurately classify images within this category.

Figure 2: Sample images from dataset with Stone class

Figure 2 displays a set of sample images categorized under the "Stone" class. These images likely depict instances related to the presence of stones in medical imaging or geological contexts. By examining these sample images, users can identify common features or characteristics associated with the "Stone" class, such as shape, texture, or color variations. This visual representation facilitates the development and evaluation of machine learning algorithms for detecting and classifying stone-related instances within the dataset.

Figure 3: Sample images from dataset with Tumour class

This figure presents a collection of sample images categorized under the "Tumour" class. These images portray instances related to the presence of tumors or abnormal growths in medical imaging datasets. By analyzing these sample images, users can discern visual cues or patterns indicative of tumor presence, such as irregular shapes, enhanced contrast, or abnormal tissue structures. Understanding the visual characteristics of tumor-related instances is crucial for training and assessing the performance of machine learning models aimed at tumor detection and classification tasks.

Figure 4: Sample images from dataset with Cyst class

Figure 4 exhibits a series of sample images classified under the "Cyst" class. These images likely represent instances associated with the presence of cysts or fluid-filled sacs in medical imaging datasets. By reviewing these sample images, users can identify visual features or patterns characteristic of cystic structures, such as rounded shapes, low-density regions, or encapsulated formations. Understanding the visual representation of cyst-related instances is essential for developing and evaluating machine learning algorithms for cyst detection and classification purposes.

Figures 5 through 9 display the confusion matrix and Receiver Operating Characteristic (ROC) curve for different machine learning models, such as Convolutional Neural Network (CNN), Support Vector Machine (SVM), Random Forest Classifier (RFC), Naive Bayes Algorithm (NBA), and Decision Tree Classifier (DTC). The confusion matrix provides insights into the models' classification performance, showing the true positive, true negative, false positive, and false negative predictions. The ROC curve illustrates the trade-off between sensitivity and specificity for each model, helping assess its discriminatory power and performance across different threshold values.

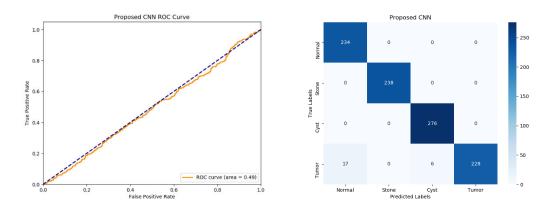


Figure 5: Displays the confusion matrix and ROC curve of CNN model.

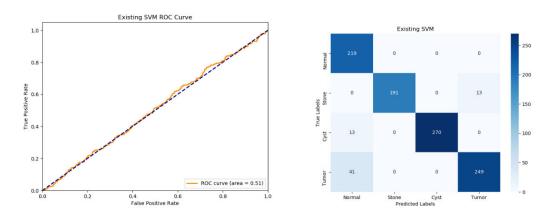


Figure 6: Displays the confusion matrix and ROC curve of SVM model.

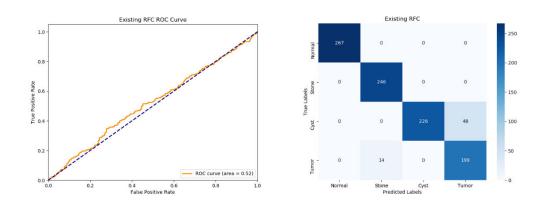


Figure 7: Displays the confusion matrix and ROC curve of RFC model.

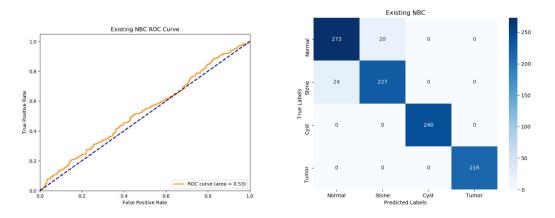


Figure 8: Displays the confusion matrix and ROC curve of NBA model.

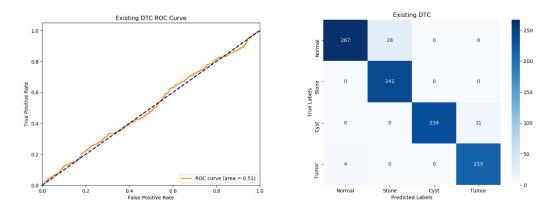


Figure 9: Displays the confusion matrix and ROC curve of DTC model.



Figure 10: Sample prediction on test renal images using proposed deep learning approach.

This figure showcases a sample prediction made on test renal images using a proposed deep learning approach. The prediction involves the application of a trained deep learning model to classify renal images into different classes or categories. By visually inspecting the sample prediction, users can assess the model's accuracy and reliability in correctly identifying and classifying renal images based on their visual features. This sample prediction serves as a demonstration of the proposed approach's effectiveness in real-world applications, providing valuable insights into its performance and potential for clinical use.

5. CONCLUSION

In conclusion, the application of deep convolutional neural networks (DCNNs) for classifying kidney diseases from CT images demonstrates significant promise in the field of medical diagnostics. With their remarkable ability to analyze complex medical imaging data, DCNNs offer a reliable and efficient means of accurately identifying various kidney ailments. This capability facilitates timely diagnosis, enabling healthcare professionals to initiate appropriate treatment plans promptly and improve patient outcomes. Looking ahead, the future scope of DCNNs in kidney disease classification from CT images is bright. Ongoing advancements in AI technology, combined with the accumulation

of large-scale medical imaging datasets, continue to enhance the performance and reliability of these neural networks. Furthermore, efforts to refine DCNN architectures and optimize training methodologies are further improving their accuracy and efficiency in clinical practice. Moreover, the integration of DCNNs into healthcare systems holds immense potential for revolutionizing diagnostic processes. By providing rapid and precise classification of kidney diseases from CT images, these networks can streamline workflow, reduce diagnostic errors, and ultimately improve patient care. Additionally, the utilization of DCNNs in telemedicine applications has the capacity to extend diagnostic capabilities to underserved populations, bridging geographical barriers and ensuring equitable access to healthcare services. The deep convolutional neural networks represent a valuable tool for kidney disease classification from CT images. As research and technology progress, their role in medical diagnostics will continue to expand, leading to more accurate diagnoses, personalized treatment approaches, and improved outcomes for patients with kidney ailments.

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