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Automated detection of kidney masses lesions using a deep learning approach

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ABSTRACT

Deep learning has emerged as a potent tool for various tasks, such as image classification. However, in the medical domain, there exists a scarcity of data, which poses a challenge in obtaining a well-balanced and high-quality dataset. Commonly seen issues in the realm of renal health include conditions such as kidney stones, cysts, and tumors. This study is centered on the examination of deep learning models for the purpose of classifying renal computed tomography (CT)-scan pictures. State-of-the-art classification models, such as convolutional neural network (CNN) approaches, are employed to boost model performance and improve accuracy. The algorithm is comprised of six convolutional layers that progressively increase in complexity. Every layer in the network utilizes a uniform 3x3 kernel size and applies the rectified linear unit (ReLU) activation function. This is followed by a max-pooling layer that downsamples the feature maps using a 2x2 pool size. Following this, a flatten layer was implemented in order to preprocess the data for the fully linked layers. The consistent utilization of uniform kernel sizes and activation functions throughout all layers of the model facilitated the smooth extraction of complex features, thereby enhancing the model's ability to accurately identify different kidney conditions. As a result, we achieved a high accuracy rate of 99.8%, precision is 99.8%, and F1 score of approximately 99.7%.

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1. INTRODUCTION

The human body is equipped with a pair of kidneys, which are organ structures resembling beans and located bilaterally along the spinal column [1]. The kidney assumes a vital function in the regulation of body fluid and solute equilibrium by means of metabolic waste secretion and filtration. Additionally, it is responsible for the secretion of a number of hormones and contributes to the regulation of blood pressure [2].

One of the primary pathological conditions affecting the kidney is the presence of kidney masses, which are characterised by the development of aberrant growths within the renal organ [3]. While a considerable proportion of renal tumours are found to be non-malignant, a substantial subset necessitates additional medical intervention. The anatomical features, clinical manifestations, and physical examination findings pertaining to the retroperitoneum are inadequate in terms of their ability to accurately identify renal masses.

Various imaging modalities, including computed tomography (CT), magnetic resonance imaging (MRI), and ultrasound, are employed in the diagnostic process of identifying masses [4], [5]. Renal masses can be categorised as either solid or cystic. Solid renal masses are of particular concern due to the potential presence of cancer. Conversely, renal masses diagnosed as kidney stones or renal cysts are generally considered to be less threatening [6], [7].

The development of a kidney tumor occurs when renal cells undergo a cessation of normal function and subsequently undergo rapid proliferation. Renal cell carcinoma, originating from renal cells, exhibits varying degrees of metastatic potential, ranging from indolent to very aggressive. Renal cell carcinoma often presents as a solitary neoplasm. Nevertheless, it is possible for any kidney to acquire various types of cancers [8], [9]. The incidence of kidney tumours is a significant global issue, with an annual registration of over 400,000 cases in the field. Among those, in terms of cancer prevalence, it ranks as the 9th most frequently diagnosed cancer in males and the 14th most frequently diagnosed cancer in females [4], [10].

The necessity for an automated system to reliably classify kidney cancer histopathology images is supported by the scarcity of available medical specialists, the possibility of interobserver variability, and the time-consuming procedure of kidney cancer diagnosis. Such a system might enhance the speed and accuracy of cancer diagnosis, resulting in early detection and better patient outcomes by utilising cutting-edge computer algorithms and deep learning approaches. The adoption of any artificial intelligence (AI)-based medical system in clinical practise, however, must first undergo extensive validation and testing to guarantee its safety and efficacy. This problem has been addressed successfully in the past [11]-[13].

In recent years, significant advancements in the field of AI and machine learning, particularly in the area of deep learning, have presented novel opportunities in the healthcare sector pertaining to the domains of detection and prediction. Neural networks, which are fundamental components of deep learning methodologies, have exhibited remarkable efficacy in tasks such as image recognition, feature extraction, and classification [14], [15]. The algorithms and models currently available possess remarkable capabilities, providing healthcare professionals with robust tools for analysing extensive medical data with exceptional precision and speed. Consequently, these technologies have the potential to enhance the effectiveness of medical prescriptions. Nevertheless, there are some areas that have not yet been extensively explored in the realm of AI, and one such domain is kidney masses disorders. To date, no prior research utilising AI has been conducted on this particular disease.

Numerous prior investigations have been undertaken to implement AI in order to automate the detection and classification of kidney medical images for kidney masses disorders with different features (normal, cyst, stone, and tumor). Attia *et al.* [16] introduced a computer-aided approach designed to automatically classify ultrasound kidney disorders. The study included the examination of five distinct types of images, namely normal, cyst, stone, tumour, and failure. The region of interest in each image was subjected to feature extraction, resulting in two sets of features: statistical features and multi-scale wavelet-based features. To minimise the dimensionality of the feature space, principal component analysis was conducted. The chosen attributes were employed in the development and training of a neural network classifier. The utilisation of multi-scale wavelet-based features has resulted in a classification rate of 97% that is deemed accurate [16].

Mangayarkarasi and Jamal [17] proposed a computer-assisted tool for the processing and analysis of ultrasound kidney images. The purpose of this tool is to classify renal pathologies based on the obtained results. The classification of ultrasound kidney images encompasses four distinct categories, namely normal, cyst, calculi, and tumour. The classification process involves utilising inputs from a urologist's perspective, which include scanned kidney ultrasound images and knowledge related to common pathologies. The images undergo pre-processing to eliminate speckle noise with the application of median and Gaussian filters. The utilisation of the optimal thresholding segmentation algorithm is employed to acquire the region of interest. A collection of statistical features of the first order is extracted. The aforementioned features are utilised as inputs during the training and testing phases of the probabilistic neural network classifier. The holdout approach is employed, wherein 50% of the images are allocated for training purposes, while the remaining 50% are reserved for testing. The evaluation of the classifier's efficiency is ultimately conducted. A classification accuracy of 93.5% is achieved [17].

Wu and Yi [18] offer an automated architecture for the detection of different kidney problems. This design utilises convolutional neural networks (CNN) and operates on abdominal ultrasound images. The model comprises three components. The first component is responsible for selecting suitable ultrasound images of kidneys. The second component utilises a detection model to identify the specific region occupied by the kidney within the given image. The third component employs the multifeature fusion neural network (MF-Net) to differentiate between normal and abnormal kidneys. This is achieved by analysing the presence of abnormal symptoms in the images. The performance of the detection model is enhanced by integrating it with a weighted ensemble technique. The MF-Net incorporates a multi-feature fusion layer to effectively extract distinguishing features from numerous perspectives of pictures. The three components collaborate in a synergistic manner to autonomously identify anomalies related to renal function. A comprehensive dataset of 3,722 abdominal ultrasound pictures, accompanied by classification and localization annotations, has been curated for the purpose of training and evaluating the model. The experimental findings indicate that the ensemble detection model, as presented, exhibits superior performance with an average true positive fraction of 98.0%. Additionally, the MF-Net demonstrates an average classification accuracy of 94.67% [18].

Kanauchi *et al.* [19] propose the development of a deep learning model with the capability to autonomously identify renal cysts in ultrasound images. Additionally, the model is designed to predict the precise location of a pair of significant anatomical landmarks, which is crucial for accurately measuring the size of the cysts. The detection of renal cysts was performed using a deep learning model that utilised a fine-tuned version of YOLOv5. Additionally, the prediction of saliency maps, which indicate the location of prominent landmarks, was carried out using a fine-tuned version of UNet++. The ultrasound images were utilised as input for the YOLOv5 model. Subsequently, the images were cropped within the bounding box and then recognised from the input image by the YOLOv5 model. These detected images were then fed as input to the UNet++ model and the accuracy of 86% is achieved [19].

Affan and Hussain [20] introduced a set of deep learning models designed for the purpose of classifying renal CT-scan pictures. State-of-the-art classification models such as CNNs are commonly employed in order to boost model performance and improve accuracy. Techniques such as data augmentation, normalisation, and transfer learning are utilised to achieve these objectives. The CNN architecture employed in this study is VGG-16, which is further enhanced by the development of a bespoke model for further training. In order to get a more balanced distribution of the dataset, data augmentation techniques were employed. As a result, the accuracy of the model reached 98%, with an F1 score of about 99% [20].

Even though earlier studies have conscientiously explored the utilization of AI in the identification and categorization of kidney masses, a conspicuous void remains as they have yet to explicitly tackle the exhaustive classification criteria via the analysis of CT images. This study aims to employ deep learning techniques, specifically neural networks, to facilitate the efficient and accurate diagnosis of kidney masses disorders. The suggested architecture demonstrates significant efficacy in accurately identifying kidney images, precisely localising kidneys within the images, and effectively recognising various kidney disorders.

2. METHOD

2.1. Dataset

The dataset was collected from various hospitals in Dhaka, Bangladesh, utilizing the picture archiving and communication system (PACS). The patients included in the dataset had previously received diagnoses of kidney tumors, cysts, normal conditions, or the presence of kidney stones. Both the coronal and axial sections were chosen from both contrast-enhanced and non-contrast investigations following a technique for imaging the whole abdomen and urogram. The Dicom study was meticulously chosen, with a focus on one diagnosis at a time. From these selections, a collection of Dicom photos pertaining to the specific region of interest for each radiological finding was generated. Subsequently, the patient-specific data and meta data were removed from the Dicom photos, and the Dicom images were then transformed to a lossless jpg image format. Following the conversion process, each picture discovery underwent subsequent verification by both a radiologist and a medical technologist in order to reaffirm the accuracy of the data. The dataset that was generated consists of 12,446 distinct data points, categorized as follows: 3,709 for cyst, 5,077 for normal, 1,377 for stone, and 2,283 for tumor [21].

2.2. Artificial intelligence-based detection methods

2.2.1. Preprocessing phase

The preprocessing phase plays a pivotal role in preparing the data for the model. In our kidney disease classification project, we conducted several important preprocessing steps to ensure the data was suitable for feeding into our neural network. First, the dataset was organized using a ratio-based split using the splitfolders library to create training, validation, and test sets. This resulted in a stratified division of the data into 90% for training, 5% for validation, and 5% for testing. This approach facilitated the creation of distinct subsets for training, validation, and testing. Importantly, the split was stratified to maintain class balance across subsets, thus mitigating the risk of bias during model training.

The data was then preprocessed for the model. Images were resized to a consistent resolution of 200x200 pixels to ensure uniformity in the input data and reduce computational complexity [22]. Additionally, images were converted to grayscale to reduce the computational load. The images were organized into batches for efficient training using the ImageDataGenerator from the Keras library. These batches were configured for rescaling pixel values to the range [0, 1] [23]. These batches were not only instrumental in efficient data handling during training but also facilitated the implementation of data augmentation techniques such as rotation, scaling, and flipping. By augmenting the training data, we augmented the diversity of the dataset, thus enhancing the model's ability to generalize to unseen examples.

2.2.2. Model architecture

The model architecture employed for the kidney disease classification entails a sequential CNN structure [24]. The network consists of six convolutional layers sequentially increasing in complexity, with 32, 32, 64, 64, 128, and 128 filters, respectively. Each layer employs a consistent 3x3 kernel size and rectified linear unit (ReLU) activation function. Using 3x3 filters in the CNN architecture enables efficient hierarchical feature extraction, maintaining spatial information, and facilitating translation invariance for effective pattern recognition with parameter efficiency [25]. The filters are followed by a max-pooling layer utilizing a 2x2 pool size to downsample the feature maps [26]. This downsampling process aids in reducing the spatial dimensions of the feature maps while retaining essential information. Consequently, computational overhead is minimized, and the network's robustness is enhanced. Subsequently, a flattened layer was introduced to transform the multi-dimensional feature maps into a one-dimensional array. This step prepares the data for input into the subsequent dense layers (fully connected layers). The network also integrated a dense layer with 512 units, maintaining the ReLU activation function, and culminated in an output layer with four units, employing softmax activation to compute the probability distribution across classes, thereby enabling multi-class classification with confidence scores [27]. This uniformity in the kernel size and activation function across all layers facilitated the seamless extraction of intricate features, contributing to the model's robust performance in accurately identifying various kidney conditions.

3. RESULTS AND DISCUSSION

Over the course of five training epochs, the model demonstrated notable performance improvements. The accuracy of the training and validation dataset is shown in Figure 1. The accuracy of the training dataset rose significantly, starting at 52.83% and reaching an impressive 97.82% by the final epoch. In addition, the validation dataset validated the model's robustness and generalizability, achieving an exceptional accuracy of 99.92%. The precision scores of training and validation datasets shown in Figure 2 experienced a substantial increase, peaking at 97.93% in the training dataset and 99.92% in the validation dataset, underlining the model's capability for precise classification. Meanwhile, the recall values remained consistently high as shown in Figure 3, confirming the model's competence in identifying relevant instances of kidney diseases and achieving a recall of 97.71% at the end of training and in the validation dataset 99.92%.

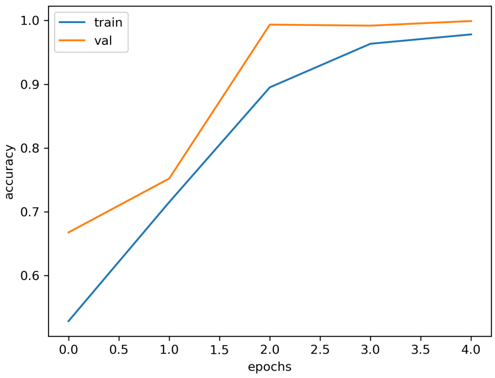

Figure 1. Training and validation accuracy

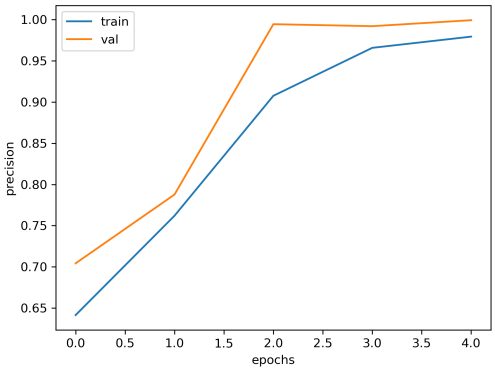

Figure 2. Training and validation precision

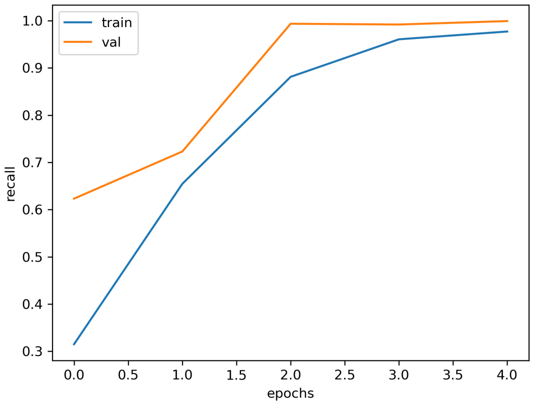

Figure 3. Training and validation recall

The test dataset results reinforced the model's efficacy, showing an accuracy of 99.76%, precision exceeding 99.77%, recall surpassing 99.66%, and an F1 score of 99.72%. The confusion matrix as shown in Figure 4 offered a comprehensive view of the model's classification performance across various kidney conditions, highlighting its accuracy in correctly identifying the classes with minimal misclassifications. These outcomes emphasize CNN's proficiency in accurately diagnosing kidney diseases, suggesting its potential application in clinical settings for precise and timely interventions.

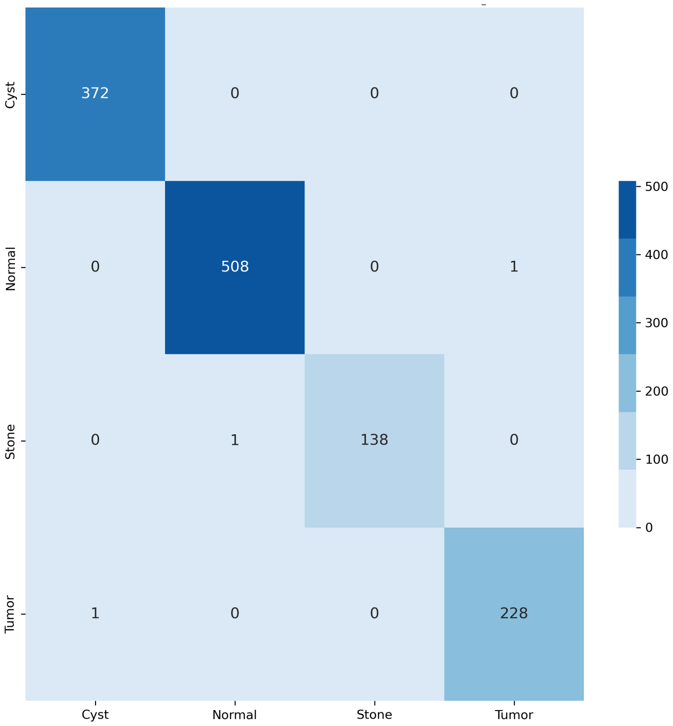

Figure 4. The confusion matrix

The receiver operating characteristic (ROC) curves in Figure 5 provide additional evidence of the model's classification performance. The macro-average ROC curve exhibited an area under the curve (AUC) of 1.0, indicating the model's remarkable ability to discriminate between different kidney conditions with precision. The model exhibited an exceptionally elevated capacity for the classification of kidney disorders, yielding a substantial abundance of true positives coupled with a minimal occurrence of false negatives. Moreover, the model demonstrated a commendable level of accuracy and precision, characterized by a minimal occurrence of false positives. These findings offer valuable insights into the robust performance of the model, particularly in its ability to accurately calcify kidney disorders.

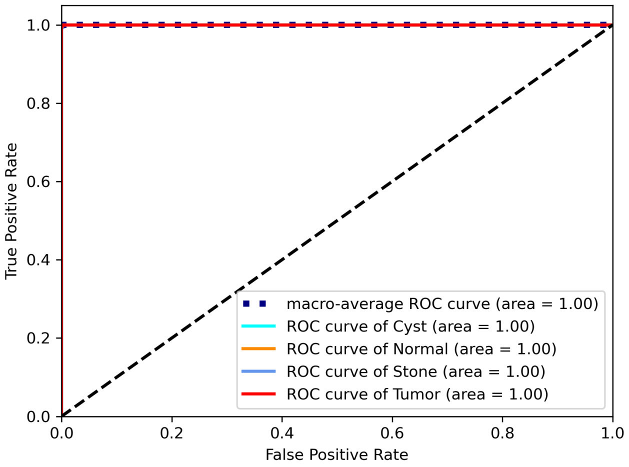

Figure 5. The ROC curves and AUC

Our study suggests that the high level of accuracy and precision observed in the classification of kidney disorders is intricately linked with outstanding performance in meeting kidney disorders treatment criteria. The proposed method stands to gain substantial advantages from the perspective of medical experts, as it offers a robust framework that aligns with their viewpoints, all the while ensuring minimal disruption to patients' therapy plans. Table 1 presents a comparison between our proposed kidney disorders detection and classification models and the existing approaches, utilising accuracy as the parameter of evaluation.

Table 1. A comparison between our proposed kidney disorders detection and classification models and the existing approaches

Reference	Technique	Accuracy (%)
[16]	CNN	97
[17]	PNN-based model	93.5
[18]	MF-Net	94.7
[19]	the UNet++ model	86
[20]	VGG-16	99
Proposed study	EfficientNetB3	100

4. CONCLUSION

Deep learning has developed as a powerful technology that may be utilized for a variety of tasks, including the classification of images. However, there is a lack of data in the medical field, which makes it difficult to acquire a dataset that is both well-balanced and of a high quality. In order to effectively train algorithms and improve their performance, deep learning models are extremely reliant on having access to a considerable amount of data. Conditions such as kidney stones, cysts, and tumors are examples of problems that are frequently seen in the field of renal health. The primary focus of this research is on the investigation of deep learning models for the purpose of image classification using renal CT scans. It is common practice to apply cutting-edge classification models, such as those based on CNN techniques, in order to increase the accuracy and performance of models. The network is made up of six convolutional layers, each of which is more complicated than the one that came before it. These layers each have a filter size of 32, followed by 64, then 128 and finally 128, in that order. Each layer of the network makes use of the ReLU activation function and employs a kernel size that is consistently 3 by 3, making it uniform throughout. After this comes a max-pooling layer, which uses a pool size of 2x2 to perform a downsampling operation on the feature maps. After this, a flatten layer was built in order to preprocess the data for the completely linked layers. This was done after the previous step. In addition to this, the network had a densely connected layer that was composed of 512 units and activated using the ReLU. After this, there was a four-unit output layer that used the softmax activation function to make multi-class classification easier. This came after the previous step. The smooth extraction of intricate features was made possible by the model's consistent use of regular kernel sizes and activation functions across all of its layers. This helped the model get better at properly identifying a variety of kidney diseases. As a consequence of this, we were able to accomplish a high accuracy rate of 99.8%, with precision at the same level, and an F1 score of roughly 99.7%. In the future, there is anticipation for the detection of precise lesions through the utilization of segmentation techniques. This approach can aid in identifying the specific location of damage within the kidney. The precise location of the tumor, cyst, or stone within the kidney is unknown. This tool has the potential to aid physicians in making prognoses.

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