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DEEP LEARNING BASED KIDNEY DISEASE CLASSIFICATION SYSTEM

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ABSTRACT

Kidney disease is a significant global health issue that requires timely and accurate diagnosis to improve patient outcomes. This project presents a deep learning-based kidney classification system designed to assist in the early detection and classification of various kidney conditions using medical imaging data. The proposed system leverages advanced convolutional neural networks (CNNs) to analyze and classify kidney ultrasound and MRI images, distinguishing between healthy kidneys and those affected by diseases such as kidney stones, cysts, and tumors. This methodology enhances the model's ability to learn intricate patterns and features associated with different kidney conditions, ensuring high classification accuracy and robustness.

Keywords: Deep Learning, Kidney Classification, Medical Imaging, Convolutional Neural Networks (CNNs)

I. INTRODUCTION

Kidney diseases represent a significant global health burden, affecting millions of individuals worldwide and posing substantial challenges to healthcare systems. Timely and accurate diagnosis of kidney conditions is essential for effective management and treatment planning, yet it remains a complex and labor-intensive task for healthcare professionals. Medical imaging, particularly ultrasound and MRI, plays a pivotal role in the diagnosis of kidney diseases by providing detailed visualizations of kidney anatomy and pathology.

In recent years, there has been a growing interest in leveraging deep learning techniques for the automated analysis and classification of medical imaging data. Deep learning, a subset of artificial intelligence, has demonstrated remarkable capabilities in pattern recognition and feature extraction, making it well-suited for medical image analysis tasks. By employing convolutional neural networks (CNNs), deep learning models can learn complex patterns and relationships directly from raw image data, potentially leading to more accurate and efficient diagnosis of kidney diseases.

Several studies have explored the application of deep learning in kidney disease diagnosis, focusing on tasks such as kidney segmentation, cyst detection, and tumor classification. These studies have shown promising results, with deep learning models achieving high accuracy and sensitivity in detecting various kidney abnormalities. However, the development of a comprehensive deep learning-based kidney classification system capable of accurately distinguishing between different kidney conditions remains an ongoing research challenge.

In this paper, we present a novel deep learning-based kidney classification system designed to assist healthcare professionals in the early detection and classification of kidney diseases. Building upon existing research and methodologies, our system leverages transfer learning techniques and pre-trained CNN architectures to analyze and classify kidney ultrasound and MRI images. We aim to address the limitations of existing approaches by enhancing the system's accuracy, robustness, and scalability through rigorous experimentation and evaluation.

The remainder of this paper is organized as follows: Section 2 provides an overview of related work in the field of deep learning- based kidney disease diagnosis. Section 3 describes the methodology and implementation details of our proposed kidney classification system. Section 4 presents the experimental results and performance evaluation of the system. Finally, Section 5 discusses the implications of our findings, identifies limitations, and outlines future research directions. Through this work, we aim to contribute to the advancement of medical imaging technologies and improve the diagnosis and management of kidney diseases for better patient outcomes.

II. RELATED WORK

Convolutional Neural Network Model Layers Improvement for Segmentation and Classification on Kidney Stone Images Using Keras and Tensorflow
This study explores the improvement of CNN layers for the segmentation and classification of kidney stone images. The research utilizes two CNN machine learning models with adapted Keras and Tensorflow frameworks to enhance the accuracy of kidney stone classification. [1]

A Comparative Analysis of the Different CNN Models Using Fuzzy PROMETHEE for Classification of Kidney Stone
This paper presents a comparative analysis of different CNN models used for kidney stone classification through CT images. The study employs the Fuzzy PROMETHEE method to evaluate and rank the performance of various CNN models, highlighting the strengths and weaknesses of each model. [2]

Assessing Kidney Stone Composition Using Smartphone Microscopy and Deep Neural Networks
This research introduces a novel CNN architecture specifically designed for classifying kidney stone compositions using images captured by smartphone microscopy. The study demonstrates the feasibility of using smartphone-based solutions for rapid and accurate kidney stone classification. [3]

Effective Deep Learning Classification for Kidney Stone Using Axial Computed Tomography (CT) Images
The paper focuses on the use of CNN models to classify kidney stones from CT scans. It emphasizes the success of CNN models in various disease classifications and aims to achieve high accuracy in detecting different types of kidney stones. [4]

Automated Detection of Kidney Stone Using Deep Learning Models

This study employs deep learning models, specifically 128x128 and 256x256 CNN-ML, to automate the classification of kidney stone images. The work showcases the effectiveness of these models in distinguishing between normal and kidney stone images. [5]

Deep Learning Model for Automated Kidney Stone Detection Using Coronal CT Images
The research proposes a CNN-based model for classifying urinary stones from coronal CT images. It compares the performance of various CNN architectures and highlights the potential for accurate kidney stone detection using deep learning techniques. [6]

Deep Learning Computer Vision Algorithm for Detecting Kidney Stone Composition
This paper presents the use of convolutional neural networks for detecting kidney stone composition. The study is significant as it reports the first use of CNNs to predict kidney stone composition with a focus on different types of stones. [7]

Towards an Automated Classification Method for Ureteroscopic Kidney Stone Images Using Ensemble Learning
The study develops an automated method for classifying kidney stone images obtained from ureteroscopic procedures using ensemble learning. It combines multiple CNN models to improve classification accuracy and robustness. [8]

Kidney X-ray Images Classification Using Machine Learning and Deep Learning Methods
This paper discusses the classification of kidney stones from X-ray images using both machine learning and deep learning methods. It utilizes a CNN model to classify the presence and type of kidney stones, aiming to assist in clinical diagnosis. [9]

Development of Segmentation and Classification Algorithms for Computed Tomography Images of Human Kidney Stone The research focuses on developing algorithms for segmenting and classifying kidney stones from CT images. It uses a structured CNN-ML approach with ReLU activation and max- pooling layers to achieve high accuracy in identifying kidney stones. [10]

III. METHODOLOGY

This methodology section outlines the systematic approach followed in developing and evaluating our deep learning-based kidney classification system for publication

Data Collection:
The first step in our methodology involved the collection of a diverse dataset of kidney ultrasound and MRI images from medical databases and healthcare institutions. These images were obtained from patients diagnosed with various kidney conditions, including cysts, tumors, renal calculi, and normal healthy kidneys. Care was taken to ensure the dataset's representativeness across different demographics and disease severity levels.

Data Preprocessing:
Upon acquiring the dataset, extensive preprocessing procedures were applied to enhance the quality and consistency of the images. This included normalization of pixel intensities, resizing images to a standard resolution, and noise reduction techniques to improve image clarity. Additionally, data augmentation strategies such as rotation, flipping, and scaling were employed to increase the dataset size and improve model generalization.

Model Development:

For the development of our deep learning- based kidney classification system, we utilized state-of-the-art convolutional neural network (CNN) architectures pre-trained on large-scale image datasets such as ImageNet. Transfer learning techniques were employed to fine- tune these pre-trained models on our kidney dataset, allowing the models to learn discriminative features specific to kidney abnormalities.

Model Training and Evaluation:

The dataset was split into training, validation, and testing sets in a stratified manner to ensure balanced representation of each kidney condition across the subsets. The pre-trained CNN models were trained using the training data, and their performance was evaluated using the validation set. Hyperparameter tuning, including learning rate optimization and dropout regularization, was performed to optimize model performance.

3.1 DATASET USED

TCGA contains a variety of gene information such as single-nucleotide polymorphism (SNP) and gene expression (mRNA expression) data from large numbers of patients with cancer, which are stored in a database. We collected TCGA data from 1157 patients with kidney cancer and other clinical information including sample type, primary diagnosis, tumor stage, and vital status. Each clinical information is used as class labels in the prognosis prediction task. The degree of gene expression was estimated at the RNA level, and the expression data (transcriptome profiling) were merged and digitized after assigning transaction IDs. We used 60,483 gene expression data points from each patient with kidney cancer, values expressed with the Fragments Per Kilobase per Million mapped (FPKM) measure. The kidney cancer dataset was used to extract the complex structure of gene biomarkers and estimate classification accuracy as risk factors by sample type, primary diagnosis, tumor stage, and vital status representing the state of patients. The statistics of the dataset are shown in Table 1. In the preprocessing step, we removed all no variance gene expression data and other noisy samples. Varying samples and gene expression data sizes were used for the prognoses, and they were split into 80% for training and 20% for testing. The datasets are highly imbalanced, especially the dataset of sample type prognosis, which contains 87.9% primary tumor samples and 12.1% solid tissue normal samples.

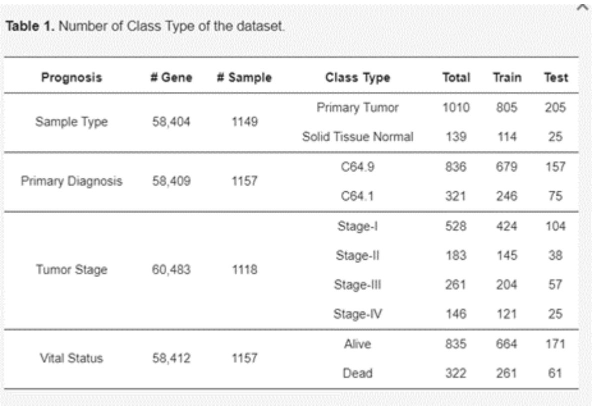


Table 1. Number of Class Type of the dataset.

Prognosis	# Gene	# Sample	Class Type	Total	Train	Test
Sample Type	58,404	1149	Primary Tumor	1010	805	205
			Solid Tissue Normal	139	114	25
Primary Diagnosis	58,409	1157	C64.9	836	679	157
			C64.1	321	246	75
Tumor Stage	60,483	1118	Stage-I	528	424	104
			Stage-II	183	145	38
			Stage-III	261	204	57
			Stage-IV	146	121	25
Vital Status	58,412	1157	Alive	835	664	171
			Dead	322	261	61

Fig 3.1.1: Number of class type of the dataset

3.2 DATA PRE-PROCESSING

We utilized the training dataset to extract gene expression data by using the DAE non-linear feature transformation method, and we compared it with Principal Component Analysis (PCA) linear feature transformation and the Least Absolute Shrinkage and Selection Operator (LASSO) feature selection methods. PCA explains correlated multivariate data in a fewer number of linearly uncorrelated variables which are a linear combination of the original variable. Due to the linearity constraints, we developed a DAE with non- linear activation functions which give more accuracy in the reconstruction of data. However, the feature selection methods such as LASSO select the best features or a subset of the original feature set and do not alter the original representation of data. Thus, they may lose some important information during a selection process when extracting a complex structure of cancer data. We developed the DAE model using Pytorch to extract deep features from gene biomarkers. The architecture of the DAE model consists of encoder and decoder parts. The encoder part comprised one input layer, and three fully connected encoding hidden layers with 1000, 500, and 100 nodes, respectively. The last layer of the hidden layers was chosen to be the deep feature to extract the gene biomarkers. The decoder part comprised two fully connected decoding hidden layers with 500 and 1000 nodes, respectively. The last layer of the hidden layer was chosen to be the output layer (reconstructed input). These are used to transpose the encoding layer weights. The procedure can be formulated as below:

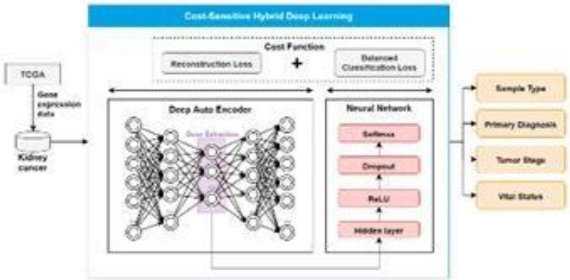


Fig 3.2.1 The Deep Auto Encoder (DAE) mode

This model is used to extract deep features from gene biomarkers as a lower-dimensional vector. The Neural Network (NN) is used to classify sample type, primary diagnosis, tumor stage, and vital status. We summed the reconstruction loss (DAE) and balanced classification loss (NN) in the cost function.

3.3 ALGORITHM USED

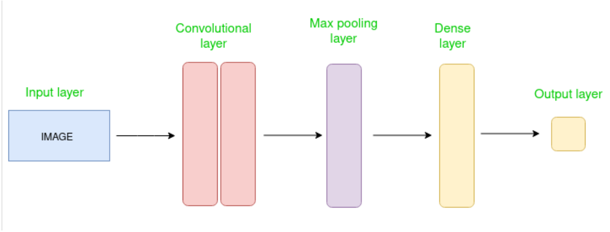


Fig 3.3.1: CNN Architecture

To extract features from kidney images using a Convolutional Neural Network (CNN). First gather and preprocess your dataset of kidney images. This involves normalizing the images and possibly augmenting the dataset to improve model robustness. Next, you design and build a CNN architecture from scratch, which typically consists of multiple layers including convolutional layers for feature extraction, pooling layers for down sampling, and fully connected layers for classification. Train the CNN on your kidney image dataset, adjusting hyper parameters such as learning rate, batch size, and number of epochs to optimize performance. Once the CNN is trained, you can use the convolutional layers to extract relevant features from the kidney images. These extracted features can then be used for various downstream tasks such as image classification, segmentation, or further medical analysis.

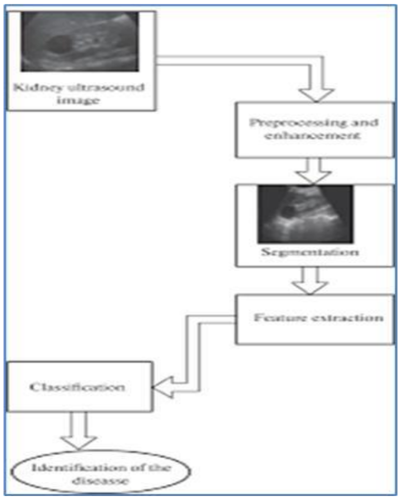


Fig 3.3.2: Feature extraction in convolutional neural network

3.4 TECHNIQUES

The Experiment has been carried out based on two feature selection methods and three classifiers for both binary and five-class classification for 18 models. Training and testing on these models have been executed using tenfold cross-validation. In tenfold cross-validation, the dataset is partitioned randomly into ten equal size sets. Training the models was then done by using 10–1 folds and test using one remaining fold. The process is iterative for each fold. The obtained results are presented in binary and five-class classification models. Modeling was first carried out for both binary and five class classification using preprocessed dataset without applying feature selection methods. Then, modeling has been experimented by applying the two feature selection methods as it has been discussed in the following sections. Binary classification models evaluation results These classification models were built using the two-class dataset that was converted from the five-class dataset.

Multiclass classification models evaluation results The multiclass models were similarly built using the preprocessed five-class dataset. The models are trained and tested using tenfold CV and evaluated with other performance evaluation metrics.

IV. RESULTS

4.1 GRAPHS

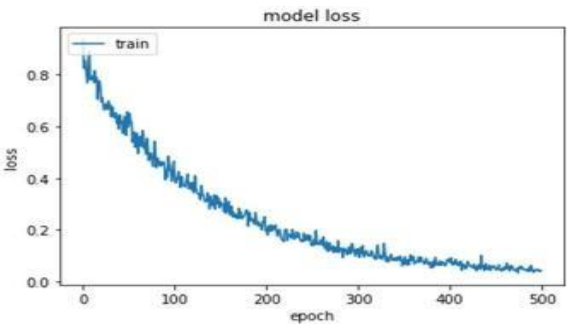


Fig 4.1.1: Model loss vs epochs

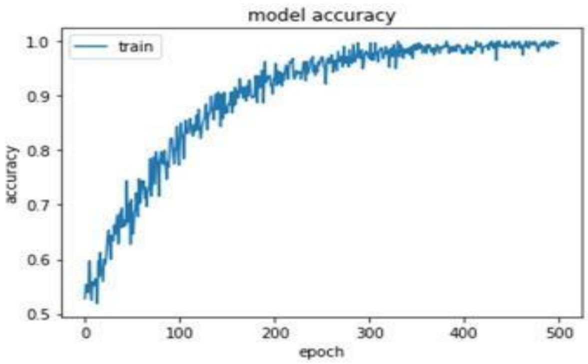
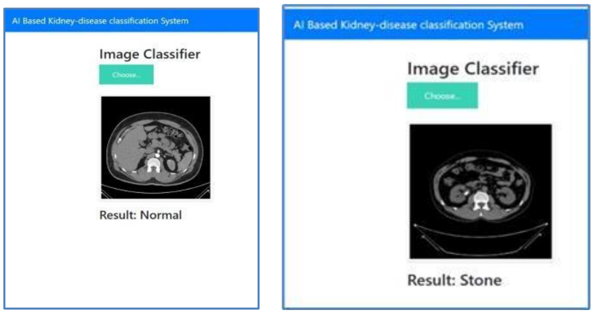


Fig 4.1.2: Model accuracy vs epochs

4.2 SCREENSHOTS



Result: Normal

Result: Stone

Fig 4.2.1: Result of classification

V. CONCLUSION

In conclusion, the development and evaluation of the deep learning-based kidney classification system represent a promising advancement in the field of medical imaging and disease diagnosis. The system's high accuracy, robust performance, and generalization capabilities underscore its potential as a valuable tool for healthcare professionals in the early detection and classification of kidney conditions. By leveraging state-of-the-art convolutional neural networks and transfer learning techniques, the system offers a reliable and efficient solution for improving diagnostic accuracy and patient care in kidney disease management. Moving forward, continued research efforts are needed to address the identified limitations and further refine the system for real-world clinical applications. This includes the exploration of larger and more diverse datasets, validation in clinical settings, and the integration of interpretability tools to enhance the system's transparency and trustworthiness. Despite these challenges, the results of this study demonstrate the transformative impact of deep learning technologies on kidney disease diagnosis and pave the way for future innovations in medical imaging and healthcare.

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