



Research Article

Machine learning based Lung Disease Prediction Using Convolutional Neural Network Algorithm

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ABSTRACT

Lung disease prediction is a critical issue in today's world. However, in the past two years, the corona virus disease 2019 (COVID-19) has a broad range and, in a limited percentage of people, a notable effect on the lungs. In the past, the fuzzy logic method has been used to classify lung disease prediction, but it has faced challenges such as difficulties in identifying segmented regions and output inaccuracies. To solve the issue Convolutional neural networks are used in machine learning to predict lung condition. The preprocessing based weighted average filter gives greater weight to the central value, making its contribution more significant than that of other values and can regulate the degree of image blurring. The process of segmenting based on region split and merge techniques involves separating one or more areas or entities in an image according to a size of m by n at one level of a threshold value. This segmented in multiple sub-regions of the same size, indicating a fundamental representational structure, from that Image classification using convolutional neural networks (CNNs) is a type of neural network specifically designed to extract distinct characteristics from segmented data. They are often used in tasks such as lung disease prediction and recognition due to their ability to identify intricate details in clustered data. The approach was evaluated using the MATLAB tool, a novel CNN with multiple image processing technique in our experiment to efficiently classify lung illnesses under typical circumstances, the average accuracy increased up to 97%. The results of this study show significant improvement in the prognosis of lung prediction in medical filed.

1. INTRODUCTION

Lung diseases are breathing conditions that affect the various tissues and tissues complex in breathing, subsequent in disorders of lung circulation, lung tissue, and airways. Machine learning algorithms are used to diagnose and treat pneumonia. The lungs play a crucial role in the human body as they expand and contract to take in oxygen and expel carbon dioxide. A computer is equipped with a sophisticated algorithm or source code that enables it to recognize data and make predictions based on that recognition. Machine learning can help interpret the vast amount of information related to lung diseases.

Lung cancer is considered most terrifying type of cancer because it often presents with no symptoms in the early stages. However, as the disease progresses, severe symptoms may appear. Managing patients with lung cancer can be challenging, especially since the disease is often diagnosed at a later stage. The intensity of treatment and its potential negative consequences on the body may vary depending on the patient's age and immunity. In certain instances, a CT scan or other imaging test may reveal the presence of a growth, prompting doctors to consider the possibility of lung cancer. As the demand for improved diagnostic precision continues to rise, there is a growing need for automated classification methods to determine which cases warrant surgical referral. However, despite advancements in technology,

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there has yet to be a successful fully automated system for classifying intra-cardiac masses on echocardiograms. In a study by Strzelecki et al., a neural network was utilized to semi-automatically classify and differentiate between various malignant intra-cardiac masses. A completely automated classification approach typically consists of four key components.

Germ cell malignancies are typically found in the reproductive systems of both men and women, originating from reproductive cells. If they are found outside of the reproductive system, they may be referred to as extra-gonadal germ cell malignancies. In order to accurately validate these findings, it is important to divide a large dataset into training and test sets. However, due to the limited size of the training set, estimators may produce unstable and faulty methods, resulting in incorrect classification of the data. It is evident that patients with higher incomes may have a greater chance of survival, which can improve the accuracy of prediction models. To further enhance the estimation of results, classification techniques based on structured data in predetermined categories can be utilized. Machine learning classification methods aim to effectively utilize large amounts of data to achieve optimal success and productivity. Accuracy and sensitivity are essential in computer-aided heart disease prediction methods. Recent studies have shown that machine learning approaches can significantly improve the accuracy of computer-aided techniques for heart disease detection.

2. LITERATURE SURVEY

The diagnosis and prediction of heart failure are critical medical responsibilities that assist cardiologists in correctly classifying patients and treating them accordingly. Machine learning algorithms, which can identify patterns in data, have been increasingly applied in the medical field. In this study, a data set was used to analyze the relationship between gender and chronic renal disease, using a clustering method known as k-modes. The processed data was then used to train a model. By grouping continuous input into discrete groups or bins, the algorithm is able to distinguish between different classes of data [1].

The data set used in this study contained of 400 samples from the UCI Machine Learning Repository. Three machine learning classifiers were utilized: Support Vector Machine (SVM), Decision Tree (DT), and Logistic Regression (LR), the bagging ensemble approach was applied. The clusters within the dataset related to chronic renal disease were used to train the machine learning classifiers. Nonlinear characteristics and categories were also incorporated into the Kidney Disease Collection. The decision tree yielded the most accurate results [2].

Chronic kidney disease can be predicted using a predictive model. In order to forecast and diagnose illnesses, machine learning algorithms are frequently employed in medicine. However, it is important to note that false medical records are common. The Kidney Disease Collection utilizes non-linear characteristics and categories through logistic regression (LR) to accurately identify decision trees [3]. Additionally, a Diabetes Problems Prediction Model has been developed to forecast the likelihood of complications in patients with diabetes. This model serves as a tool for diagnosing diabetes in communities and conducting direct diabetes screenings, as well as providing comprehensive testing for individuals identified by the model [4].

Artificial intelligence (AI) based sickness identification has the possible to alter medicine by identifying patterns and qualities that human specialists would find difficult to identify. It does this by integrating machine learning techniques with algorithms for evaluating vast amounts of medical data. As genetic data, medical imaging, and electronic medical records become more accessible, more accurate and focused sickness detection methods are needed [5]. With corresponding values of 85.01%, 92.11%, and 87.73% for cardiovascular illness, the RF algorithm demonstrated the greatest prediction accuracy, sensitivity, and recursive operative characteristic curve. It also showed the least applicability and the lowest incidence of misclassification mistakes (8.70% and 43.48%, respectively) and these results suggest that the RF method is the most effective option for CVD classification and prediction [6].

Medical practitioners may now identify ailments more quickly and accurately thanks to the outstanding outcomes of integrating machine learning classification algorithms into healthcare facilities. Machine learning techniques and technologies assist the extraction of important information from datasets, resulting in more accurate outcomes. A hybrid model for the classification of liver and cardiac data combining the support vector machine (SVM) method with the modified particle swarm optimal perfect. The data sets originate from UCI's machine learning repository [7]. In order to achieve a 99% prediction accuracy using the random forest technique, a hybrid model was created by combining the top four models and using the UCI Chronic Kidney Disease dataset [8]. This approach is particularly effective in extracting robust features from complex medical data. Validation using various datasets has shown impressive results, with accuracy levels reaching up to 98.50%. This technique also addresses the issues with gradient descent and allows for quick model rebuilding through incremental learning. However, one limitation of BLS is its difficulty in extracting complex features from medical data [9].

The use of multi factor authentication (MFA) and granular access control in the cloud ensures secure access to patients' data. Multiple layers of data encryption are employed to prevent unauthorized access, while data anonymization and

masking are utilized to protect patient privacy. Additionally, biometric authentication is being implemented to grant safe access to medical information and to provide real-time alerting and monitoring for potential security breaches [10]. The centralization of policy-based access management enables the use of MFA and granular access control for patient data stored in the cloud. Data anonymization and masking techniques are also employed to enhance patient privacy, and multiple levels of encryption are utilized to prevent unauthorized access.

Furthermore, biometric authentication is being used to ensure secure access to medical records and provide real-time alerts and monitoring to detect potential security breaches [11]. This highlights the potential of deep learning (DL) and machine learning (ML) approaches, specifically K-nearest neighbor (KNN) methods, in predicting cardiovascular disease (CVD). However, there may be operational barriers that hinder the accuracy of these approaches at the clinician level due to insufficient conditions for model testing and training. Additionally, the surveyed publications lack clarity on the optimal threshold for accuracy. For example, while it is recommended to have an area under the curve (AUC) value of 0.96 or higher, there is also a focus on overall accuracy [12].

For the experimental findings, the real-time heart disease dataset and the UCI dataset were used. Both datasets were input into the K-Means clustering technique to remove duplicate data. The C-Bi-LSTM approach was then utilized to predict heart diseases. The effectiveness of this approach was demonstrated through comparisons with several traditional classifier techniques, such as Analysis Tree, SVM, Logistic Regression, KNN, Gated Recurrent Unit, and Ensemble. The results showed that the C-Bi-LSTM had the highest accuracy of 94.78% on the UCI dataset and a reliability of 92.84% [13]. The deep learning technology has greatly improved the forecasting of time series. The contemporary research community is no longer satisfied with short sequence time-series forecasting and is now focusing on long sequence time-series forecasting (LSTF), also known as long-term future prediction. Therefore, there is an urgent overview of methodologies, data, professionals who want to compare LSTF approaches, given the rapid growth of LSTF based on deep learning techniques [14].

By utilizing machine-learning algorithms, forecast the spread and evolution of transmissible illnesses in both space and time, aiding in the control of infectious diseases. These algorithms can identify key factors that contribute to the spread of diseases, allowing managers to make informed decisions regarding vaccination purchases, public awareness campaigns, and health training activities [15]. When the cardiac muscle is unable to meet the body's physiological demands by pumping enough blood, heart failure occurs. In order to measure physical characteristics, test findings, and symptoms, healthcare providers can access the patient's automated medical records. Convolutional neural network (CNN) algorithms are utilized in important health maintenance management to assess a patient's risk of mortality or hospitalization due to heart failure. The effectiveness of this approach is evaluated using a dataset of patients with heart disease. The accuracy of the proposed CNN approach is compared to the existing system, which utilizes SVM, and found to be higher at 85% [16].

Performance metrics were compared for the detection of heart disorders using four machine learning methods and one neural network approach. A classification system called logistic regression was employed in predictive analysis to identify the presence of cardiac diseases. The Naïve Bayes approach is a classifier algorithm that categorizes illnesses based on medical diagnosis characteristics. In supervised learning, the fuzzy KNN method is primarily used as a classifier [17].

During the preprocessing stage, the brain MR images are enhanced and the Curvelet transform is applied to convert the spatial domain image into a multi-resolution image. The modified coefficients are then used to extract statistical characteristics and texture. These characteristics are then trained and classified by the ANFIS classifier, followed by further morphological acts to accurately identify and separate tumor areas. According to published data, this method has achieved an accuracy of 98.5% in distinguishing between abnormal and normal brain MR images. The categorization design consists of five layers, each with a specific number of neurons. The ANFIS architecture is created using two fuzzy rules [18] - [19]. Through proper area and degree measurements and wound chart origin, the investigative category tests report increased repeatability and robustness, as well as metric assessment. Within this publication, it is suggested to segment wound images and classify tissues using Random Forest (RF) grouping [20].

2.1 Problem statement

- The input image of a medical lung image is complex, as it is based on a threshold value and a complex dimensional area image.
- The processing of K-Means clustering is challenging and requires a low processing time, particularly when specific detection areas need to be identified.
- The collection of data sets and generation of prediction models are more efficient when using logistic regression (LR) in image segmentation.

- However, accuracy needs to be improved, as there is low sensitivity in detecting disease-affected areas using long sequence time-series forecasting (LSTF).

2.2 Objective

Lung disease is a group of diseases that affect the lungs and associated organs. It is one of the leading causes of death in the modern world. The treatment and survival rate of patients depend on the stage at which the disease is diagnosed. Therefore, early detection is crucial for the recovery process. Data is collected and tabulated, and missing values are filled using a multi-filter and all-filter approach. Early recognition and prediction of lung disease can greatly improve the survival rate of patients. However, diagnosing the disease is a major challenge for radiologists.

3. MATERIALS AND METHODS

Early prediction of lung disease is crucial in saving lives, as individuals who have been impacted by COVID-19 may develop lung disorders. The medical field benefits from the use of machine learning (ML) and feature selection approaches, as they allow for early and accurate diagnosis of illnesses. Out of the 207 lung CT-scan images in the Indian medical field dataset, 115 images were used. Preprocessing of the images was done using a Weighted-average filter to remove any pepper and salt noise. This involved replacing the original pixel value with the median value of its neighboring pixels. The images were then segmented using a region split and merge technique, where small square sections were combined to create larger, irregular regions. However, in the pyramidal structure, adjacent regions in the image space may have different parents or be at different levels (i.e. different sizes). The process of image classification using a convolutional neural network (CNN) involves accurately classifying the segmented images into distinct classes and overall block diagram shown in Figure 1

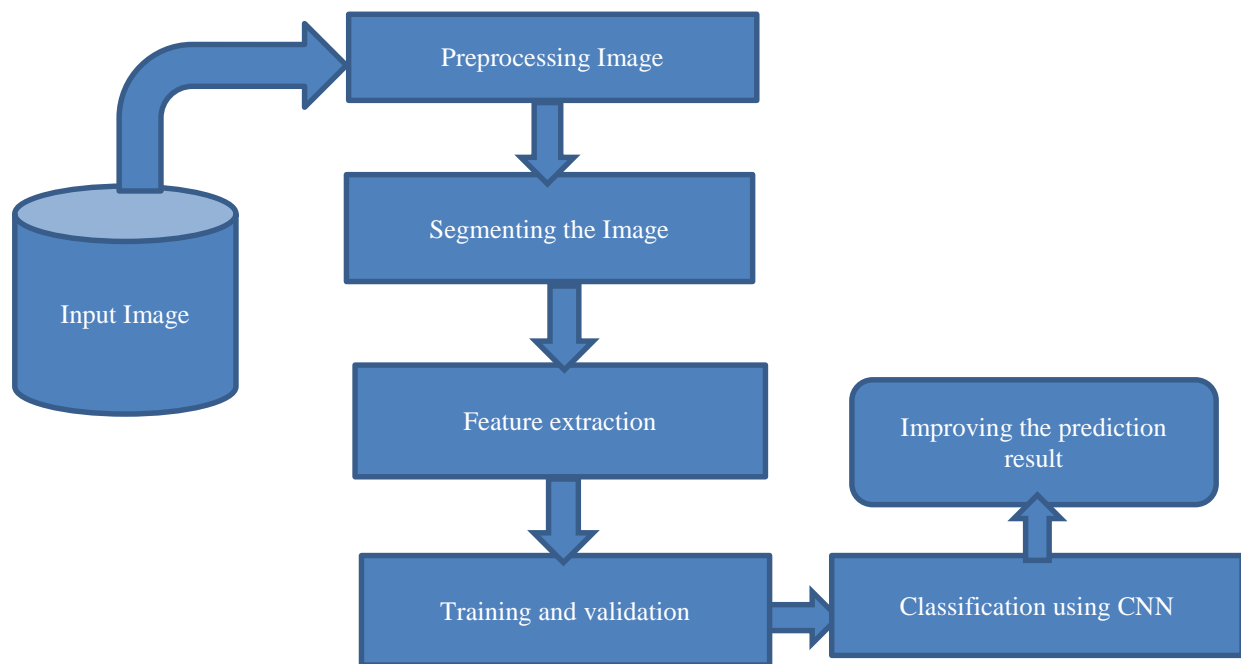


Fig. 1. Proposed block diagram

3.1 Input Image data set

Figure 2 shows the input image from Teaching Hospital/National Center for Cancer Diseases, Thoracic computed tomography images (CT) with marked-up annotated lesions are part of the Lung Image Database Consortium collection of images (LIDC-IDRI). These images are used for lung cancer screening and diagnostic purposes. During the first blinded-read stage, each radiologist examined every CT scan individually and classified groupings of lesions: "nodule <3 mm," "nodule > or =3 mm," and "non-nodule > or =3 mm". During the subsequent unblinded read phase, every radiologist evaluated their own scores and the scores of the other three radiologists on their behalf.

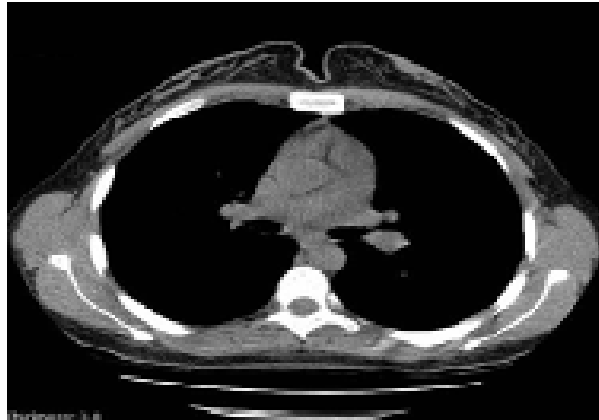


Fig. 2. Input image data set.

3.2 Preprocessing Image using Weighted-average filter

A weighted mean filtering approach has been developed to address the limitations of traditional mean filtering methods. This is necessary because noise can significantly affect the accuracy of metallographic image interpretation. The technique involves using a modified mean filter to remove noise points, followed by detecting and filtering out pulse noise points in the image. This approach has been developed in relation to patents on metallographic image processing and figure 3 shows the preprocessing image. The extreme point in the overall pixel indicates the noise point that needs to be directly filtered.

$$Q_{ij} = \{ f(i,j) \mid i,j \in 1,2, \dots, m \} \quad \dots \quad (1)$$

The filter size is $(m+2) \times (m+2)$ in order to carry on detecting until the criteria is met. Once the noise has been identified, the filter window of size $m \times m$ eliminates the identified noise pixels, leaving a residual number of non-noise pixels.



Fig. 3. Preprocessing image

3.3 Segmentation based region split and merge technique.

Figure 4 shown a region-growing step and two region-merging phases will be used to achieve segmentation. This method involves grouping nearby pixels or a group of pixels with similar characteristics into larger areas, known as region growth. The opposite approach to region growth or merging is region separation and after applying the non-maximum suppression technique, the remaining edge pixels are subjected to a thresholding process to identify the true edges of the image.

$$I(PT) = \sum_{i=1}^n IP_i - IT_i \quad \dots \quad (2)$$

Strong edge pixels are those above the high threshold, while weaker edge pixels are suppressed if they fall below the low threshold. The process begins with the entire image in one region and then divides it into smaller parts as each smaller region meets the similarity requirement. Once all sub-regions meet the requirement, the splitting process ends. If the standard deviation of the parent (merged) region is lower than the uniformity criterion and the intensity mean of the sub-regions is nearly equal, the two regions are further merged.

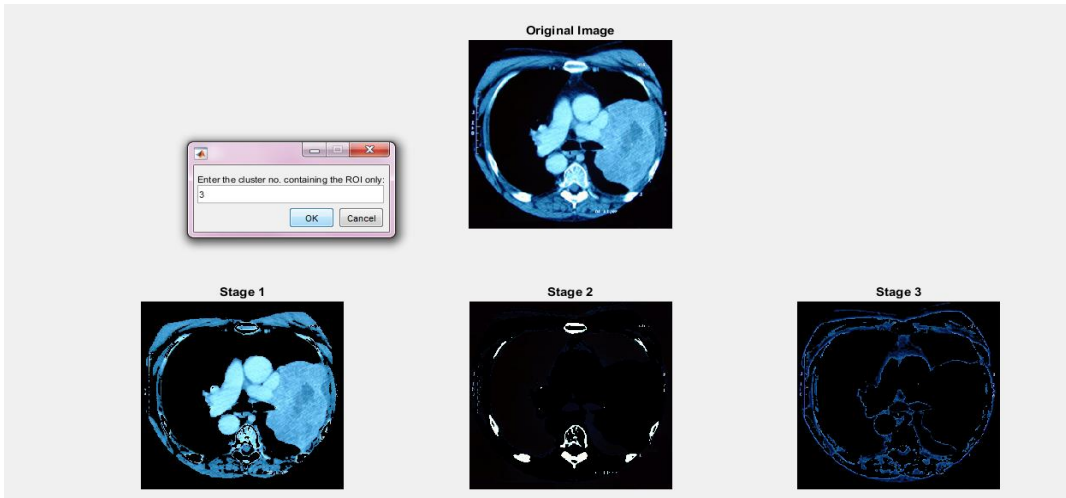


Fig. 4. Segmented Image.

3.4 Image classification using convolutional neural network (CNN)

Figure 5 shows the over working function classification technique, during the forward pass, each filter is applied to the entire input volume. The maximum value from the segmented image in the previous layer is used for max pooling. It is determined by the clusters present in the previous layer

$$y(m, n) = \sum_{q=-A}^A \omega(p, q) \times (m, p, n - q) \quad \dots \quad (3)$$

Each pixel in one layer communicates with every other layer through the completely linked layer. In feature point calculations, the average community falls within the feature point range; in maximum pooling, it falls within the feature point maximum. Mean pooling preserves background information while lowering the error brought on by the area size restriction. In this equation, w represents the convolution kernel coefficients that will be used as weights, and $y(m, n)$ represents the image sample at (m, n) in the output image.

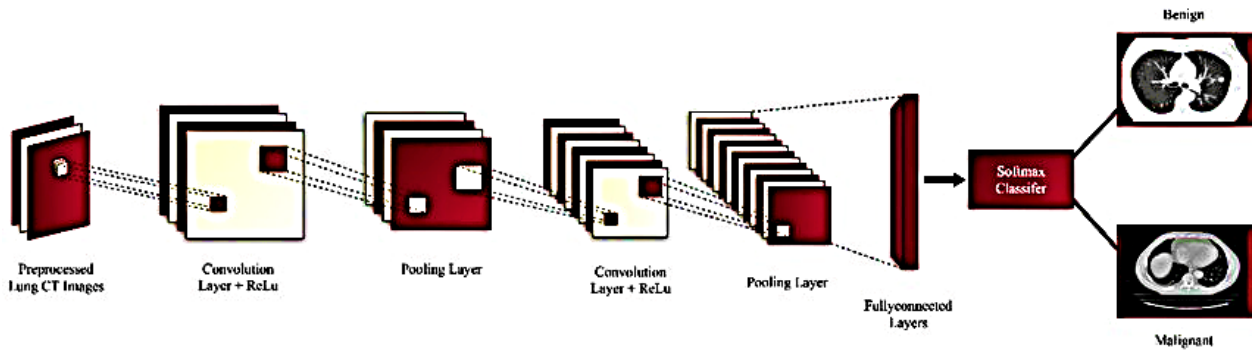


Fig. 5. Architecture of Convolutional Neural Network (CNN) for lung image classification.

4. RESULT AND DISCUSSION

This Machine learning based current work lung disease prediction and classification using Convolutional Neural Network (CNN), which is the contribution of the work is prediction of lung diseases. The input data set were selected characteristics they were evaluate in every prior work that was examined. Seven variables make up the: lung sickness kinds, image types, features, segmentation and classification methodologies, filter technique neural network classifiers and the mat lab simulation output are shown in figure 6.

Table I. Valuation of the image's examination area's contents.

Name of the lunge image taken	Number of images taken	Calculating method
Iraq-Oncology Teaching Hospital/National Center for Cancer Diseases (IQ-OTH/NCCD)	100	Confusion matrix

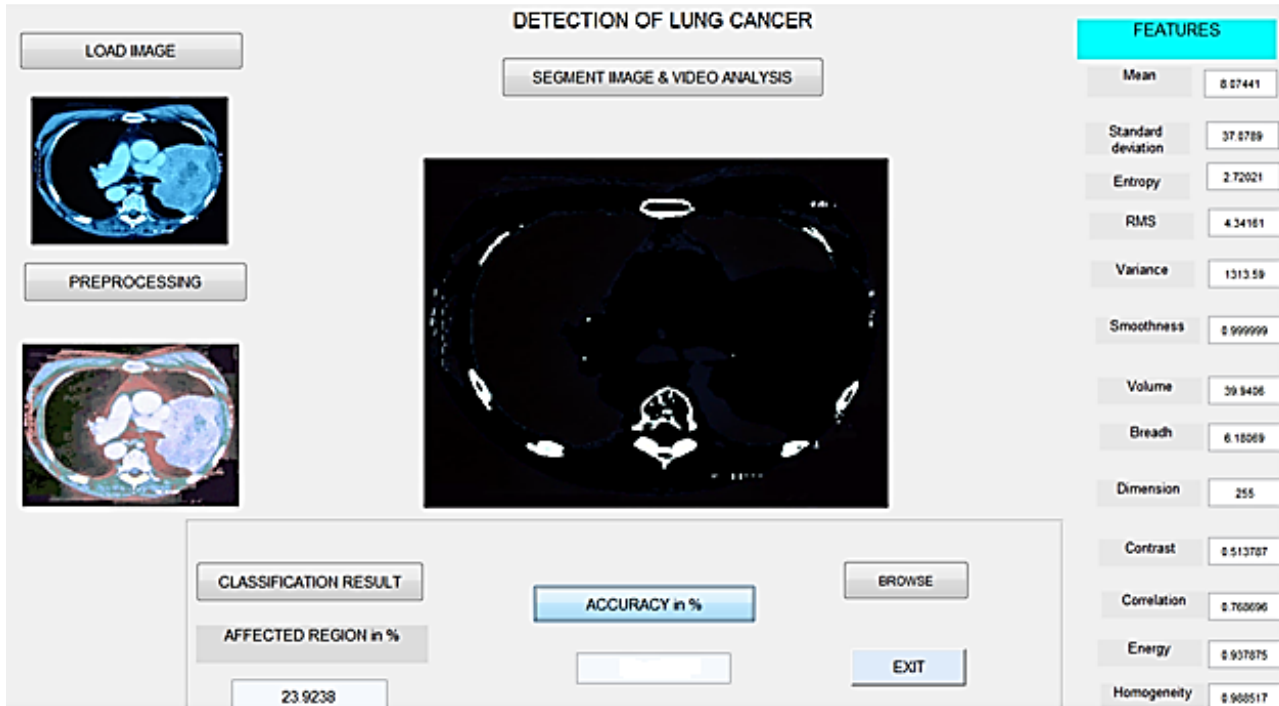


Figure 6. Simulink outcome result of CNN lung disease prediction

The accuracy of the classification output of the Convolutional Neural Network (CNN) can be calculated as follows: $(50+50) / (50+51+1+2) = 100/104 = 0.97 \times 100\% = 97.66\%$. This yields an accuracy of 97.66 %, which is achieved by the CNN. It is important to note that the accuracy may vary depending on the specific dataset and parameters used.

$$\text{Accuracy} = (\text{TP} + \text{TN}) / (\text{TP} + \text{TN} + \text{FP} + \text{FN}) \quad \dots \quad (4)$$

Table II. Exploration of Accuracy (%) from various classification techniques

Categories of classification types	Accuracy (%)	Recall (%)	Precision (%)
Logistic Regression [17]	81.86	84.32	80.06
Fuzzy K-NN [17]	87.33	87.9	82.6
Convolutional Neural Network (CNN)	97.66	96.47	95.51

Table 2 displays the accuracy performance analysis of the proposed algorithm, the existing algorithm Logistic Regression with 81.86%, and Fuzzy K-NN with 87.33%. The proposed Convolutional Neural Network (CNN) algorithm has a performance level of 97.66%, which is significantly higher. This algorithm was used to analyze different steps and accurately classify tumors from collected images, taking into account accuracy, sensitivity, and specificity.

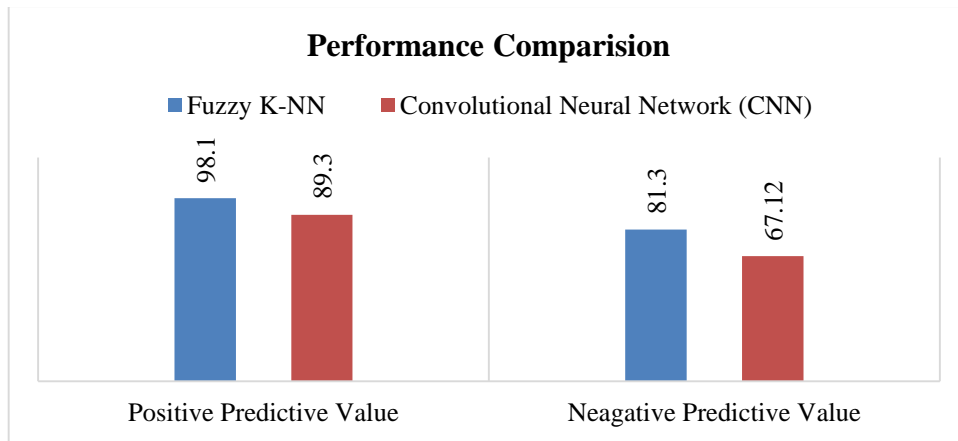


Figure 7. Graphical depiction of several assessment measures for both suggested and current approaches

The figure 7 displays a graphical representation of the evaluation metrics for our proposed Convolutional Neural Network (CNN), including a Positive Predictive Value of 98.1% and a Negative Predictive Value of 81.3%. This graph clearly demonstrates the superior accuracy of our CNN in predicting lung disease from images, as compared to the existing Fuzzy K-NN method, which also achieved a Positive Predictive Value of 98.1% and a Negative Predictive Value of 81.3%.

5. CONCLUSION

In this study, a convolutional neural network (CNN) was utilized to develop a classification model for lung cancer CT scans. The CNN was specifically designed to process datasets related to lung cancer and accurately classify the gathered information. Based on experimental data, our model demonstrated superior performance in classifying CT images for disease prediction, with a test accuracy of 97.66%. Our approach to lung cancer image classification has the potential to improve diagnostic accuracy, streamline radiologist treatment, reduce incidence rates, and simplify the overall process. To further enhance the identification of lung cancer, plan to incorporate more high-quality CT scans, which will further improve the accuracy of the network.

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Conflicts Of Interest

The author's disclosure statement confirms the absence of any conflicts of interest.

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