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VGG BASED MULTICLASS CLASSIFICATION FOR LUNG CANCER

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Abstract

Abstract– Lung cancer is the most common cause of cancer-related cancer, having been estimated to claim about 9 million lives worldwide primarily owing to the diseases symptomatology often presenting itself in its advanced stage. Early detection is essential in the management of patients to enhance their wellbeing. Detecting lungs cancer is not challenging but differentiating its stages is quite difficult task. Traditional diagnostic methods, although efficient, occasionally contradict themselves as to the issue of precise and cost effective, especially at the onset of the disease. Among these, the most used technique is Computed Tomography. However, the Based on these scans, its interpretation can be difficult and sometimes may be subjective in nature which in turns creates variability in the levels of diagnosis accuracy achieved. To address these challenges, the deep learning approaches, particularly in (CNNs), have recently been used in the subsequent automation and the improvement of the analysis process of medical images. Our subsequent approach, training on VGG-Net and CT scan data to classify it into normal, benign and malignant cases. By leveraging in this model, we hope to get better accuracy and results consistency in detection of lung cancer than the previous techniques of diagnosis. Our model achieved 99. 2% accuracy, with both precision, recall, and F1 score showed value of 1. 0.

INTRODUCTION

Tobacco smoking is said to cause lung cancer, one of the most common and life-threatening diseases. Kinds of cancer in the world, contributing to the highest cancer deaths which occur annually as depicted in Fig. 1.

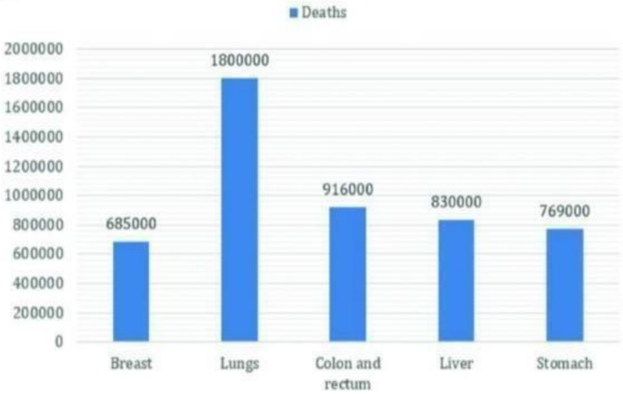


Fig. 1. Global Distribution of Caner-Related Deaths [15]

As it will be noted, timely detection and correct identification of some disorders is key positively affecting patient survival outcomes, still such patients continue to pose a great clinical challenge because the issue also stems from the fact that the disease is complex in its appearance [1]. Traditional diagnostic techniques for lung cancer for example through chest X-rays. Sputum cytology and the computed tomography scan [CT] scans are also associated with certain degree of sensitivity and specificity especially in the initial state of oncological disease [2]. In recent years, Convolutional neural networks (CNNs) belong to one of the deep learning technologies. The implementation of the learning algorithm called reinforcement learning has been particularly effective in image classification tasks because of the possession of are endowed with the capability of automatically extracting hierarchical features from raw data [3]. CNNs are developed to imitate the human's visual to process the input data and produce the desirable output processing, which makes them suitable for application with complicated patterns in medical images. In the case of Lung cancer, CNN has been used to analyze the CT scans for detection. Actively involved in the process of aiding to automate the process of detection and recognition of patterns out of the given information classifying lung nodules. This is true since one of the purpose is VGG-Net. Which is characterized by deep analysis and rather high accuracy in image classification tasks[4]. Extract features from the images by using different procedure like data augmentation in which different steps are performed. Accurately classify different stages of diseases (Benign, Malignant and normal) increase the model's resistance. And higher accuracy of model's show's model wonder-able performance. This is why VGG-Net is an ideal network for medical image analysis since it will be able to capture minimal details important in the CT scan images which include establishing a differential of lung lesion from huge amounts of data to find such details as intricate patterns which can be inaccessible to the human vision. Scans were done with the patients and obtained images were stored in the computer for comparison with other examinations pinching a nostril while blowing air inside the lungs to the maximum to receive an accurate image quality [5]. In this subject deep learning in improving the performances of the detection of lung cancer detection but more importantly, it plays a great role in providing insight in the analyses for medical image segmentation which in turn leads to the use of CNNs for medical image analysis and in the long run providing the foundation for enhanced patients' condition [6].

This paper is divided into the following sections: literature review in Section II. The dataset applied or employed results in Section III, and the architecture of VGG explained in section IV and the methodology in Section V. Experiment and results in section VI. The paper is concluded in Section VII along with the future work.

TABLE I.
LIMITATIONS OF OUR RESEARCH WORK

Limitation	Description
Dataset Size	Limited data might reduce the generalizability of the model
Model Interpretability	It is difficult to understand how the deep learning model makes decisions.
Class Imbalance	Imbalance in the number of benign, malignant, and normal cases might bias results.

Literature Review

Deep learning exceptionalities is that it has revolutionized medical visualization, which can match an accuracy in image analysis that never seen before. In a study by R. Pandian et al, the Authors The use of this gate in (CNNs) and GoogleNet for lung cancer detection/classification [7] The adopted approach that achieved 98% accuracy in terms of lung cancer detection and classification. This high performance was also illustrated by VGG-16 and GoogleNet architectures. The study of S. Katase et al. [8] gains the validation accuracy of 98.2% using VGG-based multiclass classification on the computed tomography images of the scans, showed that CNNs are effective in enhancing the classification of images tasks and thus creating the groundwork towards their implementation in medical settings. According to Hejbari Zargar et al. [9] a deep learning algorithm deep learning is a subdiscipline of machine learning that is highly dependent on artificial neural networks, cancer nodules, as the accuracy with the application is 91%. CT scans are vital in detection of Lung nodule, which can be indicative of cancer. However, what was done here was, a manual interpretation of CT scans is a process that takes a lot of time. In the review conducted by Davri et al. [10] in a study there are several important aspects that needs to be made clear achieved high sensitivity more than 97% of the lung cancer diagnosis using deep learning architectures which are based on EfficientNet-B3 lung carcinoma classification. In the context of lung cancer detection, VGG-Net architecture facilitates the possibility of extracting even further fine- grained features from CT scan images. Kumar et al. [11] in the Lung EfficientNet model employing EfficientNetB1 gave a viable automation. It achieved the level of accuracy of 99% and ROC score which ranged 0. 97 to 0. Compared with the basic PCNN model, the training accuracy and test accuracy increase to 99% on the test set. According to Another model for the classification of intraventricular atrial fibrillation is CNN model with which was developed by P. K. Ramanaiah et al. [12], CNN (VGG-19) achieved the accuracy of 93% with loss of 0. 17, and the percent of recall is also 93% at 20 epochs. After 30 iterations the model enhanced to 94% accuracy. As mentioned by S. Kumaran et al. [13] the integrated computer vision technique using a deep learning model inclusive of VGG16, ResNet50 and, I built an InceptionV3 that incurred an accuracy of 98. 18% in lung cancer detection. According to N. Sudhir Reddy et al. [14] they have developed an Intelligent deep learning algorithm an accuracy of 92% and in detection of lung cancer it has 81%, proving to be superior to classical techniques like Random Forest and Decision Trees. By using CNN model, we achieve the result, which is VGG-Net.16, it can automatically identify all kind of complicated features from CT-Scan, thus leading it to more increased reliability and uniformity classification of lung conditions. Our project achieved 99.2% accuracy with precision, recall and F1 score . By using 16 epoch only which is higher as compared to previous work .

VGGNet Architecture

In this research, the VGG-Net architecture was employed as the foundational convolutional neural network (CNN) model due to its well-known simplicity, robustness, and effectiveness in handling image classification tasks. VGG-Net, originally introduced by the Visual Geometry Group at the University of Oxford, has become a benchmark model in the field of deep learning because of its uniform architecture and its ability to extract hierarchical image features with remarkable precision. The concept of the model is elegant and is based on the notion that the combination of small convolutional filters in a series of stacked layers can attain both low-level visual features and high-level abstract features. The given feature renders VGG-Net especially applicable to areas that imply visual pattern recognition, medical image processing, and transforming EEG signals into image-like representations.

The structure of VGG-Net consists of a chain of convolutional layers that make use of small receptive fields of 3x3 that are used uniformly in the network. These small kernels allow the model to be computationally efficient and yet be able to learn intricate and discriminative spatial features. The standard versions of VGG-Net, e.g. VGG-16 and VGG-19 are composed of 16 and 19 learnable layers, respectively, which contain convolutional and fully connected layers. The convolutional operation is then of the type, and then followed by a non-linear activation function, which is usually the Rectified Linear Unit (ReLU), which introduces non-linearity into the model and enables it to estimate sharp decision boundaries.

Max-pooling layer is another important layer in VGG-Net architecture as it is placed after every set of convolutional layers. The pooling operation gradually downsizes the space of feature maps, which ultimately results in a lower computational cost and overfitting. Simultaneously, it enables the network to obtain translation invariance, as well as incorporate the spatial information at different levels of abstraction. The further the data travels in the deeper layers, the more the network shifts in data capture of simple edge and texture information to the identification of more complex and semantically significant patterns.

The VGG-Net uses fully connected (dense) layers (high level feature aggregators) after the series of convolutional and pooling operations. These layers aggregate the features that are extracted and convert them into a representation of fixed length that can be used in classification. The last architecture layer uses a softmax classifier which provides the probability distribution of the target classes, and this allows fine and interpretable classification results. This is done so that the root of the sum of probabilities on all the potential classes is one and hence, the sum of probabilities makes a normalized and probabilistic interpretation of the prediction by the model.

The VGG-Net is stronger because it can learn a rich repertoire of hierarchical features, such as the low-level syntactic structures up to the deep semantic representation. This hierarchical learning enables the network to be able to generalize on a variety of datasets and visual tasks. Besides, VGG-Net, despite its simplicity, has shown great generalization ability and frequently been used as a feature extractor or a baseline model in numerous fine-tuning-based and transfer-learning-based studies in medical imaging and signal classification applications. Thus, VGG-Net usage in the present study provides a trade-off between the simplicity and representational depth of the architecture, and thus, it is the best option to provide high performance feature extraction and classification accuracy when working with complex biomedical data settings.

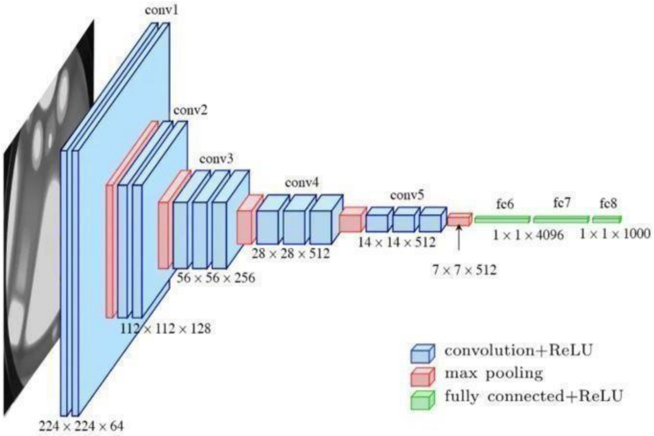


Fig. 2. VGG-16 CNN model architecture layer wise

Dataset

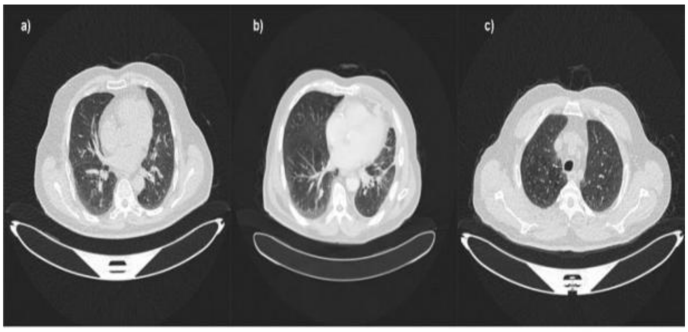
Dataset Description

The Lung Cancer Data used in this study was acquired in the first two specialized hospitals that formed a network of four hospitals found in Iraq. More specifically, the information was submitted by the Oncology Teaching Hospital and the National Cancer Diseases (IQ-OTH/NCCD) which are well-equipped in medical imaging resources and experience in studying cancer. These hospitals perform Computed Tomography (CT) scans regularly to diagnose lung cancer, which is a valid and reliable source of imaging data, and has been clinically validated. The data set, shown in Figure 3, will comprise of CT scan images of lung cancer patients at varying stages of the disease that will have a rich and representative sample of clinical variations.

The data set consists of 1,190 CT scan images of 110 patient cases all together. Out of these 40 cases were diagnosed as malignant, which were patients who had been diagnosed with lung cancer; 15 cases were benign which captured a non-cancer lesion or an abnormality; lastly, 55 cases were normal, which in this case represented normal lung structures. The CT scan of each patient is usually composed of a sequence of a multitude of image slices with each scan being comprised of 80 to 200 slices, depending on the size of the chest cavity and the CT scanning conditions. All the slices are considered as independent diagnostic images, which enable the model to be learnt through subtle anatomical variations between normal and diseased tissues.

The original raw CT images were in Digital Imaging and Communications in Medicine (DICOM)-based format which is a common medical imaging representation format that retains pixel-level fidelity and contains other important metadata such as patient demographics, imaging protocols, and slice orientation. Prior to analysis, all the identifying data was anonymized to encourage patient privacy and compliance with medical ethics. The heterogeneity of the data, both regarding pathological variability and scanning settings, has a strong basis to create automated detection systems of lung cancer that will be able to generalize to different cases and imaging equipment.

The purpose of the study was to create a unified deep learning-based screening system in lung cancer detection by combining the dataset with the VGG-Net architecture. The rationale of this strategy is based on the shortcomings of the traditional diagnostic techniques since in several cases, they heavily depend on the professionalism of radiologists and hand-over interpretation. These ways are time consuming, not to mention that they are also subject to human error and subjectivity. An alternative to this could be found in the use of a CNN-based network such as VGG-Net, which will fully automatize the feature extraction method and allow finding the malignant patterns in a prompt manner, with high accuracy, and consistency. In the end, a rich and diverse medical dataset, along with an established deep learning architecture, aims to solve current problems in the field of lung cancer diagnosis, improve clinical decision support and generally increase the use of artificial intelligence in medical imaging.



Benign Malignant Normal

Fig. 3. (a)Benign, (b)Malignant and (c)Normal

Methodology

The development of lung cancer and related pulmonary abnormalities using deep learning to identify them is a more procedural process that is geared towards ensuring the efficacy and robustness of the final model. The methodological process adopted in this paper as indicated in Figure 4 begins with the step of data acquisition followed by transition to sequence of data preprocessing, data augmentation, partitioning and classification. All these are necessary in enhancing the generalization of the models, curbing the overfitting, and enabling the deep learning model to glean meaningful features on medical imaging data..

The first source of the needed data was the Iraq Oncology Teaching Hospital and the National Center of Cancer Diseases (IQ-OTH/NCCD) which have offered a properly organized set of CT scan images in different stages of lung cancer. After gathering the raw images, an extensive preprocessing pipeline was applied to make sure that all the images were transformed to a common format and could be feed into the convolutional neural network. Some of the major operations in the preprocessing phase such as image normalization where pixel intensities are scaled to a uniform level were needed to reduce the impact of different image contrasts and brightness levels. The images were also down sampled to a fixed spatial resolution to fit the input size of the VGG-16 architecture and hence placed on the same level across all the data points.

To increase the variety and quantity of the training data, the methods of data augmentation were used. This was an important step especially since deep learning models are better when introduced to varied increase in the training data. Different perspectives and lighting conditions of the imaging were simulated by using augmentation techniques like rescaling, intensity range, and horizontal flipping. These changes assist the model to become resistant against some small differences in the image orientation and enhance its recognition of pathological patterns in various patients and scan conditions. All of these kinds of preprocessing, as well as augmentation, are aimed at enhancing the generalization capabilities of the model, to guarantee that the model works on unknown clinical data.

The dataset was then split into a training and validation set in the ratio of 80:20, after the preprocessing and augmentation processes. It means that 80 percent of the data was to be utilized in the training process, and 20 percent was to be utilized in the validation process, as a separate data that would be employed to assess the effectiveness of the model during the training process. This kind of partitioning will ensure that the learning of the model is bias free and that performance measures of the model give an accurate representation of its retention abilities of generalizing new data.

To classify the data, the study used the VGG-16 architecture which was trained on the dataset of normal and lung cancer, and it was fine-tuned to match the data peculiarities. The use of VGG-16 with a deep-layered model and small convolutional kernels was chosen because it is a proven algorithm that can be used in medical imaging when accuracy is a key factor.

The model was pre-trained on a large-scale dataset (ImageNet) through transfer learning, and this allowed the model to retain general feature extraction property whilst being re-trained on the lung CT dataset. This method had a great impact on cutting down the time of training and enhancing the convergence rate so that the model was able to classify the CT images accurately into three diagnostic categories namely normal, benign, and malignant.

The abovementioned carefully organized pipeline, (including data collection and preprocessing) model training and classification) can be effective in providing an illustration of how deep learning-based methods can render the process of identifying and classifying lung cancer automatic, thus helping clinical professionals to reach a more expedited, more reliable, and more objective diagnosis.

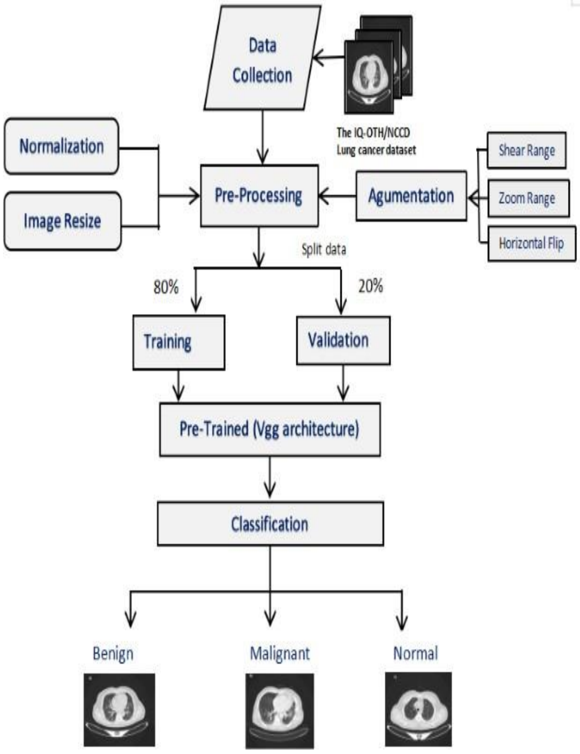


Fig. 4. General work-flow of the proposed method

Data-Preprocessing

When creating deep learning models to analyze medical images, one usually starts with the raw images and that is refined systematically because of a series of preprocessing steps that aim to make them more appropriate to the model training. The first one is normalization, which is an important method that puts the pixel intensity values of all the images in a standard range. This is done to optimize the utility of pixel information and reduce any possible discrepancies that might occur due to variations in the conditions of image acquisition, e.g. scanner sensitivity, lighting, contrast etc. Normalization also helps stabilize the gradient descent process in training and enables the neural network to converge more effectively and attain greater accuracy.

All the images are then scaled and rescaled to a common input size which fits the majority of convolutional neural network (CNN) architectures. In the paper, every picture was brought to a standardized resolution of 224 x 224 pixels, which is one of the most common benchmarks in deep learning networks including VGG-Net, ResNet, and Inception. This is done by resizing to assure uniformity in the dataset size which allows the model to manipulate each image in a standard spatial framework. Having a fixed input dimension is both an efficient means of batching in the training process and helps avoid distortion or loss of key visual data, which may impair the model to identify minute pathological features in lung CT scans, as a result.

After resizing the images, the next important thing is to perform feature extraction that requires the model to be trained, to extract and encode important visual predictors that appear within the data. They are patterns--which are usually not visible to the eye of the human being--that vary in terms of their texture, intensity, and spatial organization with indications of normal tissue, benign tissue, or malignant tissue formations. These features are learned progressively in more hierarchically higher levels, the lower levels of the hierarchy learn simple edges and gradients, and the higher levels learn the more complex and abstract representations of tumor morphology and the space around it. Such a multi-level extraction procedure is critical to making sure that the network succeeds in capturing a local and global representation of lung tissue.

Finally, the processed and feature-enhanced images are prepared for the training phase, where they are fed into the deep learning model to facilitate supervised learning. During this stage, the model iteratively updates its internal parameters to minimize classification errors and improve prediction accuracy. The entire preprocessing workflow—comprising normalization, resizing, and feature extractions visually summarized in Figure 5, which illustrates how a raw CT image is transformed into a model-ready input. This systematic approach ensures that every image contributes maximally to the training process, thereby enhancing the overall robustness, reliability, and diagnostic capability of the proposed lung cancer classification system.

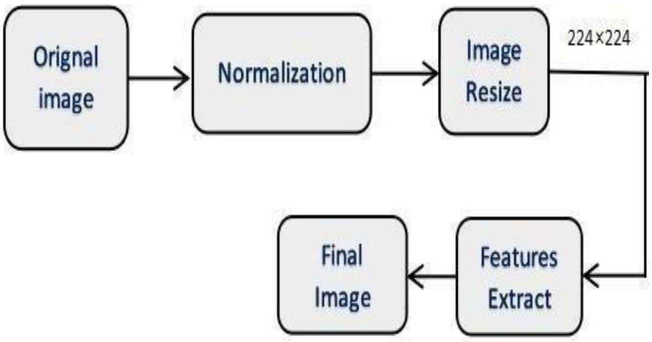


Fig. 5. Preprocessing

Data-Augmentation

ImageDataGenerator is a highly versatile and effective utility available in the Keras deep learning library that may be used to improve the training process of convolutional neural networks, especially in image classification and medical imaging. This utility allows the creation of mini-batches of real-time data of the form of a tensor image, as well as on-the-fly data augmentation, which is an important step when using a limited dataset (or one with inadequate diversity). Besides assisting to avoid overfitting which is a frequent problem when models are trained on training samples instead of learning generalizable features, data augmentation also enhances the capabilities of the model to deal with unknown or diverse input data that will occur in real-world diagnostic settings.

ImageDataGenerator was configured to have a set of parameters in the present work to optimize the process of learning the model and the generalization capacity in a systematic way. The initial parameter is rescale = 1/255 that does the pixel values normalization, this is to transform the original pixel intensity range [0 255] into [0 1]. This scaling ensures that the network receives the input values that are uniformly distributed that vastly stabilize training process with a dramatically accelerating effect on the gradient-based learning algorithms.

The second parameter, shear range = 0.2, is a shear transformation applied on the input images, which basically slants or tilts the input images along one axis to give a slightly distorted version of the original image. This transformation leads to geometrical variability, and this allows the network to acquire stronger representations of objects that may appear a bit crooked or of varying angles. With regard to lung CT scans, this step increases the performance of the model in identifying tumor characteristics even when the image orientation or anatomical view differs slightly.

Likewise, the zoom range = 0.2 parameter adds random effects of zooming in or out the image content up to 20 percent. The models variations in scale which can occur in real imaging scenarios, such as variation in patient positioning, scanner settings or slice thickness with CT scans. The introduction of this variance into the training data results in a network that is more scale-invariant, i.e. the network can correctly classify and detect cancerous regions no matter their relative size or location in the scan.

Finally, the parameter horizontal_flip = True uses random horizontal flipping on about half of the images in each batch. This operation shows the mirror image of the original data in the vertical axis producing mirror-image versions of the original data. Horizontal flipping is very effective in augmentation, in the case of medical images analysis, particularly to derive information about an organ that is symmetrical in form as seen in lungs. It enables the network to recognize the common structural and pathological appearances despite whether they appear or not in the left or right lung and, therefore, increases the generalization ability of the model across spatial orientations.

Together, such methods of augmentation, which include rescaling, shearing, zooming, and flipping, help to produce a more diverse and richer dataset that is quite similar to the imaging variability in the real world. As Figure 6 illustrates, the transformations create a sequence of augmented images based on the same original CT scan, but each one depicts a different visual condition. This dynamic augmentation pipeline not only makes the training data size effective, but it also causes the model to be more resistant to overfitting also, allowing the model to achieve additional accuracy and reliability in its predictions on unseen data in the validation and testing phases. As a result, the ImageDataGenerator of Keras is a major element in the powerful preprocessing and training process of the suggested lung cancer detector model.

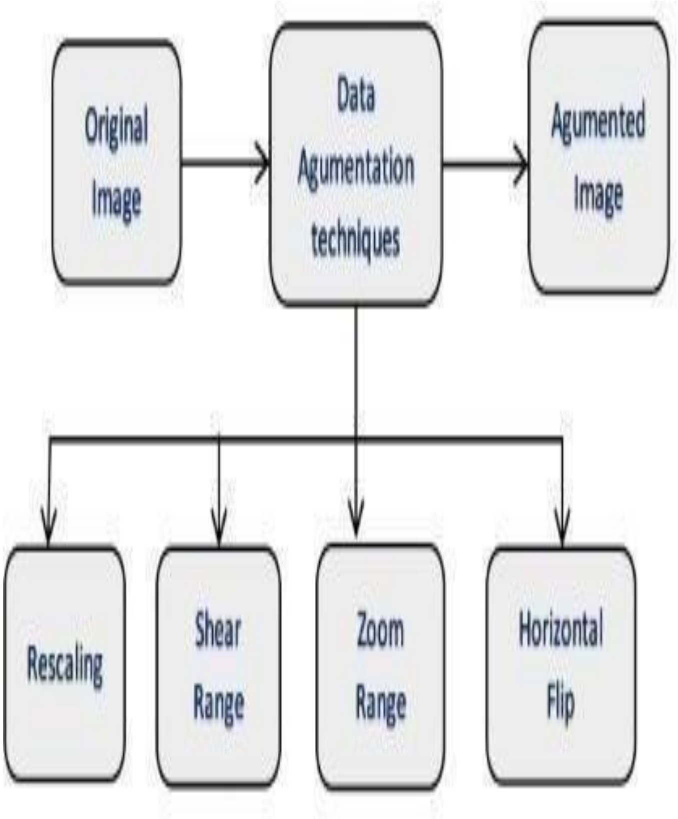


Fig. 6. Data Augmentation

Proposed Model Architecture

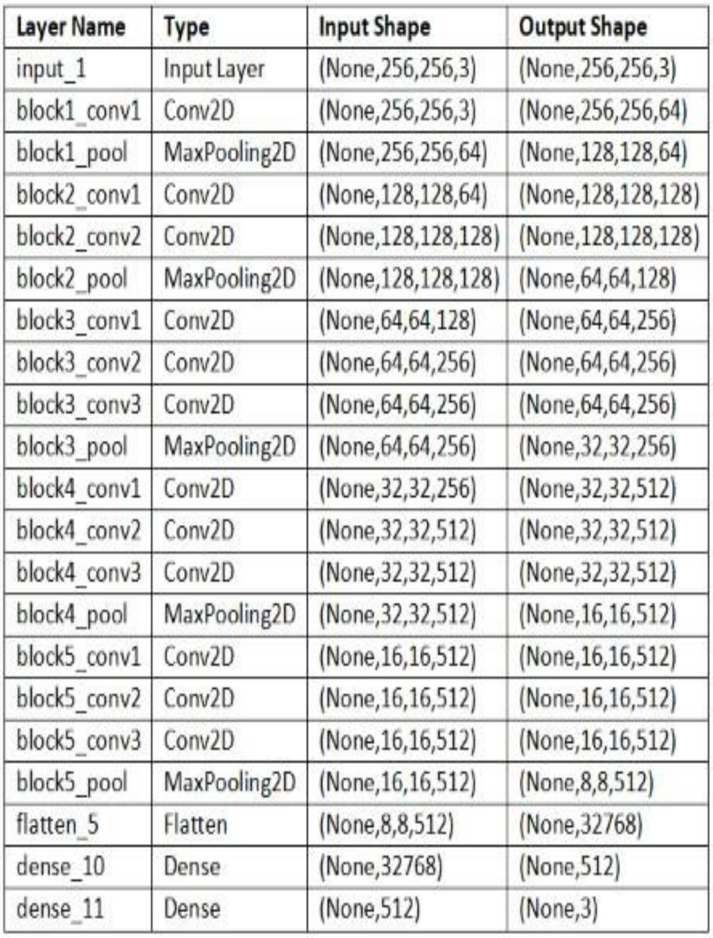
The Convolutional Neural Network (CNN) structure used in this study, to classify the lung CT scans into three diagnostic groups, including normal, benign, and malignant is more fully represented in Figure 7. The architecture was created to be very effective in capturing complex space hierarchies and structural variations within medical images and be computationally efficient and highly predictive. The basic structure of the feature extraction process consists of five convolutional blocks with subsequent max-pooling operations which make up the network. These layers progressively convert the raw pixel information to the high-level feature representations that are vital in the appropriate classification process.

The first convolutional stages are dedicated to the learning of low-level visual features, i.e. edges, corners, and simple textures that determine the overall structure of the lung tissue in CT images. The model starts to recognize more complex and abstract features, such as nodular appearances, irregular tissue edges, and different patterns of intensities because of pathological disease as the data moves through deeper convolutional blocks. Small receptive fields (e.g., 3x3 kernels) are used, and thus it becomes possible to capture even fine-grained spatial details. The max-pooling layers after each convolutional block are to downsample the feature maps, decrease the spatial dimension of feature maps, and save the most significant details.

The convolutional and pooling stages are followed by passing through the convolutional and pooling stages. the multi-dimensional feature maps that are obtained are flattened. A flattening layer is used to convert it into one-dimensional. This is a very essential change that will bridge the. convolutional section of the network-responsible of feature extraction-with the fully connected layers, which operate = high level reasoning and categorizing. The flattened output vector is then fed into two dense (fully connected) layers, in which the learned features are combined and refined. to discriminate against the various lung tissue disorders. Nonlinear decision-making is accomplished by these dense layers. learning complicated relationships between features which may not be observed directly in the spatial domain.

The last network layer uses a SoftMax activation layer which provides probability distributions among the three classes of targets, namely normal, benign, and malignant. This probabilistic approach enables the model to demonstrate its level of confidence in any given classification and hence the output of the model gives a clear interpretation that can be processed by health specialists. As an example, the malignant class has a high probability score, which means that there are high chances that the tissue has cancerous cells, and the clinicians proceed to more specific diagnostic tests.

In general, this architecture is a well-balanced design of depth, complexity, and interpretability. The convolutional and pooling operations in stages also make sure that all local and global features in the image are maintained and processed and the dense layers allow combining this information to make accurate decisions. The model, as shown in Figure 7, summarizes the full pipeline of the system including taking of images and extraction of features to the classification output and, as such, serves as the computational core of the proposed system based on deep learning to detect lung cancer in patients. Besides increasing the accuracy of the diagnosis, this hierarchical design also shows that deep learning structures can easily be scaled to the real world by analyzing clinical images.



Layer Name	Type	Input Shape	Output Shape
input_1	Input Layer	(None,256,256,3)	(None,256,256,3)
block1_conv1	Conv2D	(None,256,256,3)	(None,256,256,64)
block1_pool	MaxPooling2D	(None,256,256,64)	(None,128,128,64)
block2_conv1	Conv2D	(None,128,128,64)	(None,128,128,128)
block2_conv2	Conv2D	(None,128,128,128)	(None,128,128,128)
block2_pool	MaxPooling2D	(None,128,128,128)	(None,64,64,128)
block3_conv1	Conv2D	(None,64,64,128)	(None,64,64,256)
block3_conv2	Conv2D	(None,64,64,256)	(None,64,64,256)
block3_conv3	Conv2D	(None,64,64,256)	(None,64,64,256)
block3_pool	MaxPooling2D	(None,64,64,256)	(None,32,32,256)
block4_conv1	Conv2D	(None,32,32,256)	(None,32,32,512)
block4_conv2	Conv2D	(None,32,32,512)	(None,32,32,512)
block4_conv3	Conv2D	(None,32,32,512)	(None,32,32,512)
block4_pool	MaxPooling2D	(None,32,32,512)	(None,16,16,512)
block5_conv1	Conv2D	(None,16,16,512)	(None,16,16,512)
block5_conv2	Conv2D	(None,16,16,512)	(None,16,16,512)
block5_conv3	Conv2D	(None,16,16,512)	(None,16,16,512)
block5_pool	MaxPooling2D	(None,16,16,512)	(None,8,8,512)
flatten_5	Flatten	(None,8,8,512)	(None,32768)
dense_10	Dense	(None,32768)	(None,512)
dense_11	Dense	(None,512)	(None,3)

Fig. 7. Proposed Model Architecture

Experiment Setup and Results

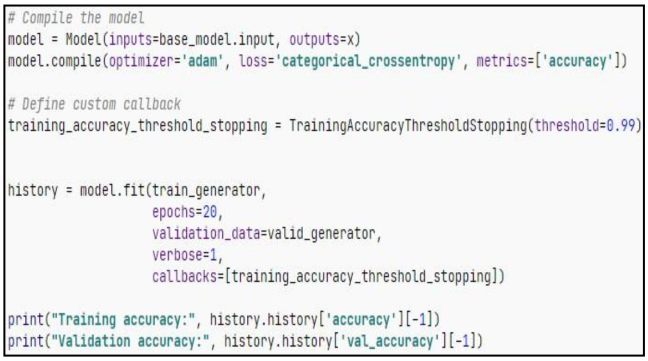
Experiment Setup

The experiments were conducted on high-performance configures in the following way:

CPU: AMD RYZEN 9 5900X
GPU: NVIDIA GEFORCE RTX 4080 SUPER 16G VENTUS 3X OC
Memory: 32 GB RAM

The Convolutional Neural Network (CNN) model was evaluated with the help of Jupyter Notebook with the support of GPU acceleration to maximize training and computational efficiency. During the experiment, it was noted that unless the concept of early stopping was adopted, the model would show indications of minor overfitting, as the training accuracy would increase and the validation accuracy would remain constant. During the first testing round, the model was trained within 20 epochs, with the overall training and validation accuracy being 98 percent and 96 percent, respectively, as shown in Table II.

To increase generalization and to avoid overfitting, additional experiments were conducted, varying the number of epochs. In the high-quality setting, the model was trained over 16 epochs holding the other hyperparameters fixed. This not only minimized the risk of overfitting, but it also increased the overall performance, and the final accuracy was 99.2. The enhancement shows that CNN has successfully learned the discriminative properties of the data set, and it has a strong balance between the efficiency of the training and generalization of the model.



```
# Compile the model
model = Model(inputs=base_model.input, outputs=x)
model.compile(optimizer='adam', loss='categorical_crossentropy', metrics=['accuracy'])

# Define custom callback
training_accuracy_threshold_stopping = TrainingAccuracyThresholdStopping(threshold=0.99)


history = model.fit(train_generator,
                    epochs=20,
                    validation_data=valid_generator,
                    verbose=1,
                    callbacks=[training_accuracy_threshold_stopping])

print("Training accuracy:", history.history['accuracy'][-1])
print("Validation accuracy:", history.history['val_accuracy'][-1])
```

Fig. 8. Process of running epochs

TABLE. II
PERFORMANCE RESULTS OF THE PROPOSED CNN WITH VGG-16

	Accuracy	Lose	Val_accuracy	Val_loss
Without earlystopping	0.9874	0.0386	0.9633	0.0654
With-earlystopping	0.9920	0.0306	0.9817	0.0527

Model Accuracy

The test can be classified according to the degree of accuracy of their diagnostic results calculated as the number of true positive and true negative instances out of total allocated to each of them as shown in Fig 9. It can be described as (1)

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

where, TP= true positive, TN= true negative, FP = false positive, FN= false negative

(1)

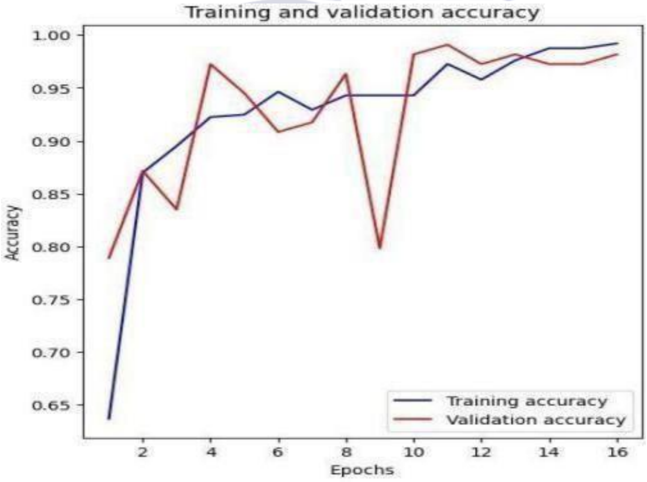


Fig. 9. Accuracy Graph

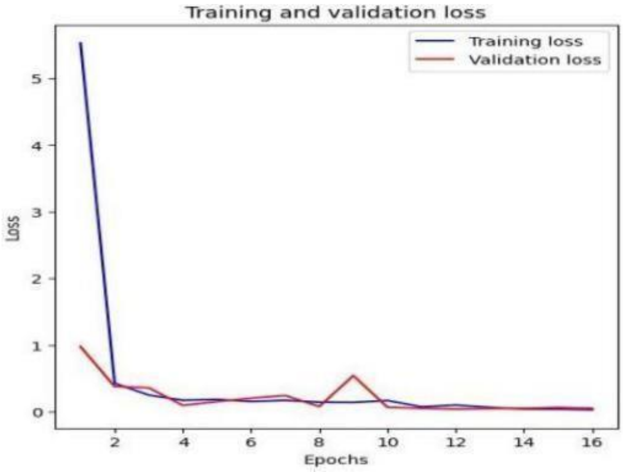


Fig. 10. Loss Graph

Fig. 11.

Precision

Precision is the proportion of correct positive results, and is calculated by (2).

$$Precision = \frac{TP}{TP + FP} \tag{2}$$

Recall

It is the measure of the proportion of the positive cases that have been correctly classified to the overall values and it is determined by (3)

$$Recall = \frac{TP}{TP + FN} \tag{3}$$

F1-Score

Average proportionate that helps in moderating the measurements of precision and recall. It represents the deep learning models with precision, recall and F1-score res ults as shown in table. 5 and is calculated by (4)

$$F1Score = 2 \times \frac{Precision \times recall}{Precision + recall} \tag{4}$$

ROC

ROC curve: The graph shows the performance of a classification model at each threshold in Fig 11. ROC is based on two parameters. i. e. True Positive Rate (TPR) and False Positive rate (FPR) as mentioned in (5) & (6)

$$TPR = \frac{TP}{TP + FN} \tag{5}$$

$$FPR = \frac{FP}{FP + TN} \tag{6}$$

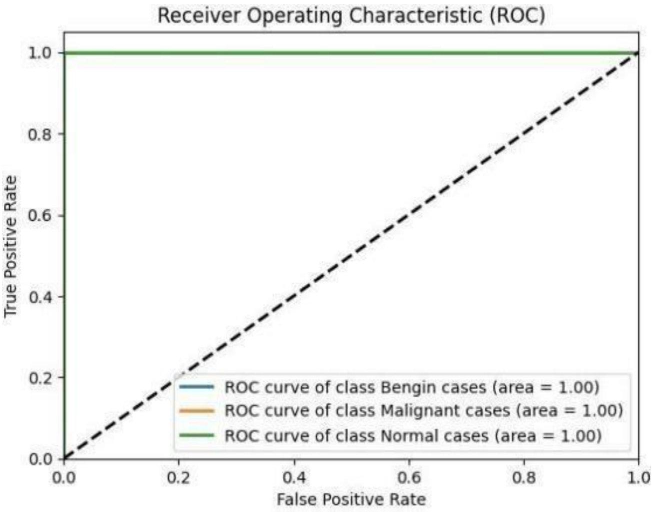


Fig. 12. Receiver Operating Characteristic(ROC)

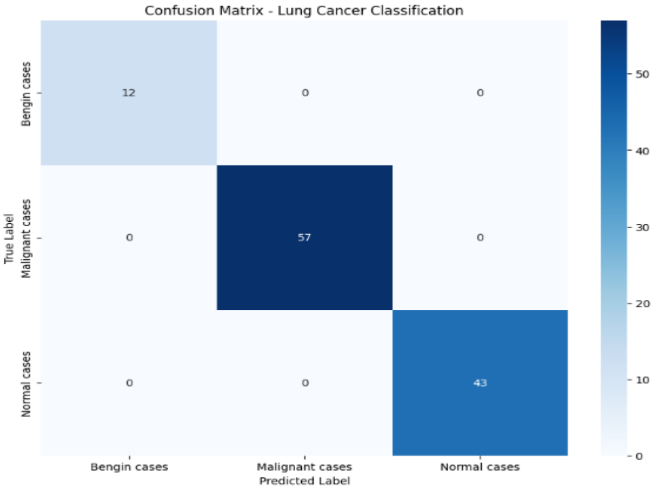


Fig. 13. Confusion Matrix

Fig. 14.

In Figure 12 Confusion matrix can be defined as summarized form of predicted result to enhance operating efficiency which aids to assess other evaluation indicators such as accuracy, recall, precision etc. By prediction of each class, it summarized the performance of the model.

TABLE. III

THE PROPOSED DEEP LEARNING MODEL'S PRECISION, RECALL AND F1- SCORE

	Precision	recall	F1-score	support
Benign cases	1.00	1.00	1.00	12
Malignantcases	1.00	1.00	1.00	57
Normal cases	1.00	1.00	1.00	43
Accuracy			1.00	112
Macro avg	1.00	1.00	1.00	112
Weighted avg	1.00	1.00	1.00	112

Conclusion and future work

We analyzed VGG-Net, a deep learning-based CNN for the detection of lung cancer using computed tomography with high generality in differentiating between normal, benign, and malignant conditions. The extent of how this model can extract details and the features of an object from medical images proves that there is great opportunity in promoting the area of early diagnosis and proper identification of lung cancer. This approach, therefore, has the potentiality of enhancing the efficiency and accuracy of lung cancer detection and minimizing human mistakes. Future research could discuss activities that can potentially improve the existing VGG-Net model through model fine-tuning parameters and additionally expanding new advanced CNN such architectures like ResNet50 or DenseNet121 and also apply transfer learning methods to improve the effectiveness of the approach even more on small datasets for medical specialty based fields. Moreover, as successfully applied in clinical practice these models.

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