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Advancing Lung Cancer Diagnosis with Transfer Learning: Insights from VGG16 Implementation

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Abstract **Lung cancer continues to be one of the leading causes of cancer-related mortality globally, largely due to the challenges associated with its early and accurate detection. Timely diagnosis is critical for improving survival rates, and advances in artificial intelligence (AI), particularly deep learning, are proving to be valuable tools in this area. This study introduces an enhanced deep learning-based approach for lung cancer classification using the VGG16 neural network architecture. While previous research has demonstrated the effectiveness of ResNet-50 in this domain, the proposed method leverages the strengths of VGG16 particularly its deep architecture and robust feature extraction capabilities to improve diagnostic performance. To address the limitations posed by scarce labelled medical imaging data, the model incorporates transfer learning and fine-tuning techniques. It was trained and validated on a well-curated dataset of lung CT images. The VGG16 model achieved a high training accuracy of 99.09% and a strong validation accuracy of 95.41%, indicating its ability to generalize well across diverse image samples. These results reflect the model's capacity to capture intricate patterns and subtle features within medical imagery, which are often critical for accurate disease classification. A comparative evaluation between VGG16 and ResNet-50 reveals that VGG16 outperforms its predecessor in terms of both accuracy and reliability. The improved performance underscores the potential of the proposed approach as a reliable and scalable AI-driven diagnostic solution. Overall, this research highlights the growing role of deep learning in enhancing clinical decision-making, offering a promising path toward earlier detection of lung cancer and ultimately contributing to better patient outcomes.**

Keywords **Lung Cancer Classification, Deep Learning, Transfer Learning, Medical Imaging, Automated Diagnostics, ResNet-50 Comparison**.

I. Introduction

Lung cancer is one of the most prevalent and deadliest cancers worldwide, accounting for a significant percentage of cancer-related mortalities each year. The early detection and accurate classification of lung cancer play a crucial role in improving patient outcomes and survival rates. Advances in artificial intelligence (AI) and deep learning have revolutionized medical diagnostics, offering powerful tools for analyzing complex medical imaging data and facilitating early disease detection [1]. Deep learning models, particularly convolutional neural networks (CNNs), have emerged as effective techniques for image-based disease diagnosis. Among these, architectures like ResNet-50 and VGG16 have gained prominence due to their robust feature extraction capabilities. While ResNet-50, with its residual learning framework, has shown significant success in previous studies, the VGG16 model, known for its deep convolutional layers and simplified design, offers enhanced performance for classification tasks in medical imaging [2]. This study builds on prior research by improving lung cancer classification using the VGG16 architecture. The proposed model leverages transfer learning and fine-tuning to address common challenges, such as limited labeled datasets, and achieves exceptional accuracy, with a training accuracy of 99.09% and a validation accuracy of 95.41%. These results highlight the VGG16 model's superior ability to extract intricate patterns in lung cancer images, improving diagnostic precision and reducing misdiagnoses. The findings align with the growing body of literature emphasizing the transformative potential of deep learning in clinical applications. The integration of these advanced models into real-world diagnostic systems holds the promise of aiding healthcare professionals in making informed decisions, ultimately enhancing patient care and treatment outcomes[3].

ResNet-50, known for its residual learning framework, was previously employed in our research for lung cancer prediction, achieving high accuracy. However, its performance left room for improvement,

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particularly in terms of precision and generalization. To address these limitations, this study focuses on the VGG16 architecture, which is known for its simplicity and deep convolutional layers, making it ideal for medical image analysis [7]. The proposed model leverages transfer learning and fine-tuning techniques to enhance feature extraction and adapt effectively to the limited labeled dataset often encountered in medical imaging. It was trained and validated on a curated dataset of lung CT images, achieving a training accuracy of 99.09% and a validation accuracy of 95.41%. This demonstrates the VGG16 model's ability to capture fine-grained patterns in the imagery, contributing to more precise and consistent classifications. In comparison with ResNet-50, the VGG16-based model showed improved performance in terms of both accuracy and generalizability, thereby reducing the risk of misdiagnosis. These findings support the growing adoption of AI-powered solutions in clinical settings and highlight the potential of VGG16 as a dependable tool for aiding radiologists in lung cancer diagnosis[8].

The motivation behind this research stems from the need to improve the accuracy and reliability of lung cancer classification systems. Although the ResNet-50 model provided promising results, there remains a pressing need to explore more effective architectures capable of capturing the subtle and intricate patterns present in lung CT images. The VGG16 model, with its increased depth and streamlined design, presents a compelling alternative by offering enhanced feature extraction capabilities and improved classification accuracy [8]. Moreover, integrating such advanced models into clinical diagnostic workflows can significantly reduce the cognitive load on radiologists, minimize diagnostic errors, and facilitate timely medical interventions [9]. This study is driven by the aspiration to bridge the gap between cutting-edge deep learning research and its practical deployment in healthcare environments, ensuring that patients gain access to reliable, AI-assisted diagnostic tools [10] [11].

The primary objective of this research is to enhance the accuracy of lung cancer classification by utilizing the VGG16 deep learning architecture, with the aim of surpassing the performance of the previously employed ResNet-50 model. This involves implementing transfer learning to leverage pre-trained VGG16 weights and fine-tuning them for the lung cancer imaging dataset, thereby optimizing feature extraction capabilities [12]. Another key objective is to conduct a comparative analysis between the VGG16 and ResNet-50 models, focusing on their accuracy, generalization, and computational efficiency to determine the most effective approach for lung cancer diagnosis [13]. Additionally, this research aims to facilitate the integration of the VGG16-based system into real-world clinical diagnostic workflows, assisting healthcare professionals in early lung cancer detection and improving diagnostic precision. Ultimately, the study seeks to bridge the gap between theoretical advancements in deep learning and their practical application in clinical settings, ensuring that patients benefit from improved diagnostic tools and early intervention strategies [14].

II. Literature Survey

Lung cancer remains one of the leading causes of cancer-related mortality worldwide, with the World Health Organization reporting that it accounts for nearly 18% of all cancer deaths. This underscores the importance of early and accurate detection methods for improving patient outcomes. Early detection is critical because lung cancer is often diagnosed at an advanced stage when treatment options are limited. As a result, advancements in diagnostic technologies, particularly those leveraging artificial intelligence (AI) and deep learning, have gained significant attention in recent years as potential solutions for enhancing the accuracy and speed of lung cancer diagnosis [1].

In the field of medical imaging, AI techniques especially convolutional neural networks (CNNs) have proven effective in detecting cancerous lesions in various organ systems. Liu et al. proposed a deep learning-based approach for the early detection of pancreatic ductal adenocarcinoma (PDAC) using CT scans. Their method, which integrated 2D and 3D CNNs to capture both local and global features, achieved high sensitivity and specificity in recognizing PDAC lesions [2]. Similarly, Xu et al. developed a 3D CNN framework for pancreatic lesion detection that outperformed traditional methods in terms of both sensitivity and specificity [3]. These studies demonstrate the growing potential of deep learning models in detecting cancer early by analysing medical images.

The lung cancer field has also witnessed similar advancements. Shen et al. employed a multi-crop CNN model to detect lung nodules in CT scans with high sensitivity and specificity [4]. Liao et al. introduced an end-to-end training framework for lung nodule analysis, which showed promising results in diagnostic accuracy [5]. Furthermore, Wang et al. compared various CNN architectures, including ResNet and DenseNet, for lung nodule classification and demonstrated the advantages of using deeper models to capture more complex features, thereby improving detection performance [6]. Building on these advancements, our study introduces a modified ResNet50 architecture optimized for lung cancer classification. ResNet, initially proposed by He et al., addressed the vanishing gradient problem in deep neural networks, making it a suitable architecture for complex medical image classification tasks [7]. By

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modifying ResNet50 and incorporating advanced preprocessing techniques and hyperparameter optimization, we aim to improve the model's ability to detect lung cancer with greater accuracy and precision. Our approach also compares the modified ResNet50 model with other well-established architectures, such as EfficientNetB1 and Inception V3, to assess their relative performance in lung cancer detection [8].

Moreover, this study employs the Free-Response Receiver Operating Characteristic (FROC) curve, a more detailed evaluation method that plots sensitivity against the average number of false positives per image. The FROC curve is particularly useful in lung cancer detection as it provides a nuanced evaluation of the model's sensitivity and specificity, helping to minimize false positives and improve diagnostic precision [9]. By integrating these advanced evaluation metrics, our study seeks to contribute to the growing body of evidence supporting the integration of AI and deep learning models in medical diagnostics, ultimately aiding in the early detection and better treatment outcomes for lung cancer patients.

III. Existing System

Lung cancer detection and classification have witnessed significant advancements in recent years, particularly through the application of machine learning (ML) and deep learning (DL) models. Traditional methods for detecting lung cancer, such as X-rays and CT scans, have been used for several decades. However, these methods are often limited by their inability to detect small or early-stage tumors with high accuracy. Radiologists' reliance on manual inspection of medical images can lead to human error and subjectivity in diagnosis, especially when the images are complex or contain subtle signs of malignancy [19]. As a result, researchers have increasingly focused on developing automated methods that can assist in improving diagnostic accuracy and reducing errors in the detection of lung cancer.

One of the existing approaches for lung cancer detection is based on image processing techniques. In this approach, lung CT images are first pre-processed to improve the quality of the images, followed by the extraction of features such as texture, shape, and edge characteristics [20]. Classical machine learning algorithms like support vector machines (SVM), k-nearest neighbors (KNN), and random forests (RF) have been used for classification [21]. These methods often require manual feature extraction, which is time-consuming and may miss important patterns in the data.

Deep learning models, particularly convolutional neural networks (CNNs), have gained prominence in recent years due to their ability to automatically learn hierarchical features from raw image data [22]. CNNs have shown great promise in the detection of lung cancer by directly analyzing CT images without the need for manual feature extraction. Notably, several studies have implemented various CNN architectures to detect lung nodules and classify them as benign or malignant. These architectures include traditional CNNs, as well as more advanced models like ResNet, DenseNet, and InceptionV3 [23]. Among these, ResNet-based architectures have demonstrated superior performance due to their ability to train deeper networks without suffering from the vanishing gradient problem, thanks to the introduction of residual connections [11].

Despite these advancements, existing systems still face certain challenges. Many of the models lack sufficient generalization ability, meaning that they might perform well on one dataset but fail to generalize to other datasets or populations [24]. Furthermore, the majority of existing systems are not optimized for the specific characteristics of lung cancer, such as small or subtle nodules, which are difficult to detect and classify [25]. Additionally, the evaluation of model performance in terms of false positives and false negatives remains a challenge, as high sensitivity is often achieved at the expense of specificity.

Recent systems like the one proposed by Liao et al. (2019) [17] and Wang et al. (2019) [18] attempt to address these limitations by incorporating end-to-end training frameworks that use deep learning techniques for both feature extraction and classification. However, even these systems struggle to achieve consistently high performance across different types of lung cancer, such as small-cell and non-small-cell lung cancer [26]. Further advancements are needed to refine these systems, particularly in terms of reducing the number of false positives and improving the overall accuracy and robustness of the models.

The system we propose in this research aims to address these issues by modifying the ResNet50 architecture, optimizing it for lung cancer classification, and improving model generalization. We also employ advanced preprocessing techniques and hyperparameter optimization to enhance the model's detection capability, making it more robust and accurate for real-world applications.

IV. Proposed System

The proposed system aims to enhance lung cancer detection by modifying the ResNet50 architecture, specifically tailored to classify lung cancer from CT scan images. The core innovation lies in optimizing the ResNet50 model by incorporating additional layers, advanced preprocessing techniques, and hyperparameter optimization to improve detection accuracy and classification performance. The system utilizes transfer learning, fine-tuning the pre-trained

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ResNet50 model on a lung cancer dataset, which helps leverage the knowledge acquired from large-scale image datasets [1].

Key preprocessing steps, including data augmentation, normalization, and resizing, improve the model's generalization capability. The system is evaluated using various performance metrics such as accuracy, precision, recall, F1-score, and the Free-Response Receiver Operating Characteristic (FROC) curve, allowing for a nuanced evaluation of the model's performance in detecting lung nodules [2]. Comparative analysis with other architectures, like EfficientNetB1 [3] and InceptionV3 [4], demonstrates the superior performance of the proposed modified ResNet50 model. This approach offers a promising solution for early and accurate lung cancer detection, potentially assisting clinicians in making faster, more reliable diagnoses.

A. Advanced Preprocessing and Hyperparameter

To improve the quality of lung CT images, advanced preprocessing techniques are applied. These steps are crucial for reducing noise and enhancing the important features of lung nodules. A Gaussian filter is applied to reduce high-frequency noise, smoothing the image and making features more uniform. It can be calculated using Eq. (1) as follows [24]:

$$Ismooth(x,y,z) = I(x,y,z) * G\sigma \quad (1)$$

where $G\sigma$ represents the Gaussian filter with standard deviation σ. To standardize image intensities, normalization is performed to adjust pixel values to a common range. This is computed using Eq. (2) [24]:

$$Inorm(x,y,z) = \sigma Ismooth(x,y,z) - \mu \quad (2)$$

where μ and σ are the mean and standard deviation of the pixel intensities. Histogram equalization is used to enhance image contrast, making it easier for the model to distinguish between different structures in the CT scan images. Integration of 2D and 3D Convolutional Neural Networks (CNNs). To better understand the local and global features of CT scan images, the proposed model utilizes both 2D and 3D CNNs. This hybrid approach addresses the limitations of traditional 2D models, providing deeper spatial analysis.

2D CNN Feature Extraction: Each 2D slice of the CT image undergoes convolution to extract relevant features. The process is defined in Eq. (3) [25]:

$$F2D(x,y,z) = ReLU(W2D * Inorm(x,y,z) + b2D) \quad (3)$$

where W_{2D} and b_{2D} are the weights and biases of the 2D convolutional layers, and ReLU is the activation function that introduces non-linearity.

3D CNN Feature Extraction: To capture spatial context across slices in volumetric medical images, 3D convolutional neural networks (3D CNNs) are employed. Unlike traditional 2D CNNs that analyze each slice independently, 3D CNNs process the full 3D volume, allowing the network to learn spatial features along all three dimensions height, width, and depth. This approach is especially effective in detecting subtle patterns and structures that span across multiple slices, enhancing the accuracy of tumor localization and classification. As shown in Eq. (4) [25], the 3D convolution operation enables the integration of contextual information, making it ideal for tasks like lung cancer detection.

$$F3D(x,y,z) = ReLU(W3D * Inorm(x,y,z) + b3D) \quad (4)$$

where W_{3D} and b_{3D} are the weights and biases of the 3D convolutional layers. W3D refers to the weights (or filters/kernels) of the 3D convolutional layer. These weights are learned during training and are used to extract features from the input volume. Each filter has a 3D shape (for example, k × k × k) and moves across the input volume to detect spatial patterns. b3D represents the biases associated with the 3D convolutional filters. A bias is added to the result of each convolution operation to shift the activation output, which helps improve the flexibility and performance of the model. Inorm(x, y, z) is the normalized input volume at the voxel location (x, y, z). This input, typically a 3D medical scan such as a CT image, is pre-processed either scaled or standardized before being passed into the convolutional neural network for feature extraction.

B. Feature Fusion

To leverage the strengths of both 2D and 3D convolutions, features are fused through concatenation, as shown in Eq. (5).

$$Ffused = [F2D, F3D] \quad (5)$$

This fusion improves the model's ability to identify complex patterns and structures within the CT images, resulting in better performance in tasks such as classification and object detection. Ffused refers to the combined feature representation obtained by fusing features from both 2D and 3D convolutional layers. This fusion helps the model gain a richer understanding of the input data. F2D represents the features extracted using 2D convolutional layers. These layers are effective at capturing detailed spatial information from individual CT image slices. F3D represents the features extracted using 3D convolutional layers. These layers capture volumetric context by analyzing how features change across multiple adjacent slices in the CT scan. The notation [F2D, F3D] indicates that these two sets of features are concatenated joined together typically along the feature dimension. This combination leverages the strengths of both 2D and 3D representations, improving the model's ability to detect

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complex patterns and structures within CT images, which enhances performance in tasks such as classification and object detection.

C. Optimization and Efficiency

To improve classification accuracy, the model's performance is optimized by minimizing the cross-entropy loss function, which is a widely used objective in classification tasks. The cross-entropy loss is calculated using Eq. (6):

$$Loss = -c\sum P(c \mid Ffused) logP(c \mid Ffused) \quad (6)$$

where $P(c \mid Ffused)$ represents the predicted probability of class ccc given the fused features.

This formulation of the loss function measures the dissimilarity between the true label distribution and the predicted probability distribution, encouraging the model to assign higher probabilities to the correct classes. The cross-entropy loss has become a standard choice in neural networks for classification tasks [1]. In this study, we proposed two optimized techniques as follows:

1. **Model Pruning**: To reduce the number of parameters and computational overhead, model pruning is applied. This technique involves eliminating redundant neurons and connections that do not significantly contribute to model performance, thereby maintaining accuracy while improving efficiency [2].
2. **Quantization**: The model weights are quantized into lower-bit representations (e.g., 8-bit), significantly decreasing memory consumption and enabling deployment on resource-constrained clinical hardware without substantial loss in accuracy [3].

The proposed system is designed to integrate seamlessly into clinical workflows, offering a user-friendly interface tailored for radiologists. Its computational efficiency and robustness allow practical deployment in diverse healthcare environments with varying resources. Moreover, all aspects of model development and deployment align with regulatory requirements and clinical standards, ensuring compliance and facilitating adoption in real-world medical settings [4]. By incorporating advanced preprocessing steps, dual CNN architectures, feature fusion strategies, and the aforementioned optimization techniques, the proposed system strives to deliver a highly accurate, computationally efficient, and clinically viable solution for lung cancer detection. This integrated approach represents a significant advancement in enhancing the timeliness and reliability of diagnosis through AI-driven tools.

V. Methodology

A. Dataset Preparation

In this study, we utilized the same public dataset from Kaggle, titled "IQ-OTH/NCCD - Lung Cancer Dataset", which contains 1,190 lung CT images in PNG and JPG formats. The dataset is available for free download at https://www.kaggle.com/datasets/adityamahimkar/iqothnccd-lung-cancer-dataset.

We categorized the images into three distinct classes: normal, benign, and malignant. The dataset was split into three folders for training, validation, and testing, with the following distributions:

1. Training set: 80% of the total dataset used for training the model.
2. Validation set: 10% of the dataset used for model tuning and hyperparameter optimization.
3. Test set: 10% of the dataset used for final performance evaluation.

B. Data Preprocessing

The preprocessing steps were carried out similarly to those in the ResNet50 model, ensuring consistency and optimal performance for the VGG16 architecture. These steps include normalization, resizing, cropping, padding, and data augmentation.

Normalization: Pixel intensity normalization is applied to scale image pixel values to the range [0,1][0, 1][0,1]. It can be computed using Eq. (7) as follows [24]:

$$Inorm(x,y) = Imax - ImaxI(x,y) - Imin \quad (7)$$

where I(x,y) represents the pixel intensity at location (x.y) and I_{min} and I_{max} are the minimum and maximum pixel values in the image, respectively.

Resizing: To meet the input requirements of the VGG16 model, all images are resized to a fixed dimension of 256×256256 \times 256256×256 pixels. The resizing operation is expressed in Eq. (8).

$$Iresized(x', y') = I(hx \times hnew, wy \times wnew) \quad (8)$$

where h_{new}= 256 and w_{new}=256 are the new height and width of the image. Iresized(x′,y′) represents the resized image at the new pixel location (x′, y′). After resizing, the image is now smaller (or larger), and this variable stores the pixel value at the new coordinates in the resized image. I(hx×hnew,wy×wnew) refers to the pixel value from the original image at a specific location. It represents how pixel values from the original image are mapped or interpolated to the resized image, based on the scaling factors. Hx is the scaling factor for the height of the image. It is computed by dividing the original height of the image by the new height. For example, if the original height is 512 pixels and the new height is 256 pixels, hx would be 2. This scaling factor tells how much the image should be shrunk or expanded in the vertical direction. Wy is the scaling

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factor for the width of the image. It is computed by dividing the original width of the image by the new width. For instance, if the original width is 512 pixels and the new width is 256 pixels, wy would also be 2. This scaling factor indicates how much the image should be resized horizontally. Hnew represents the new height for the image after resizing. It is a fixed value of 256 pixels, which ensures that all images are resized to this standard height to meet the input requirements of the VGG16 model. Wnew represents the new width for the image after resizing. Similar to the height, the new width is also set to 256 pixels to make the image suitable for the VGG16 model's input.

Cropping and Padding: Cropping and padding are used to focus on the region of interest (ROI) and adjust image dimensions to a uniform size. The cropped image is computed as shown in Eq. (9):

$$Icrop(x,y) = I(x1 + x, y1 + y) for\ x1 \le x \le x2, y1 \le y \le y2 \quad (9)$$

Icrop(x,y) represents the cropped image at the pixel location (x, y). After cropping, only the region of interest (ROI) remains in the image, and this variable stores the pixel values at the new coordinates (x, y) in the cropped image. I(x1+x,y1+y) refers to the pixel value from the original image at the location that is adjusted by the cropping bounds. The values in the cropped image are directly taken from the original image at the new adjusted coordinates, determined by the offsets (x1 and y1). x1 is the starting x-coordinate (horizontal position) of the region of interest (ROI) in the original image. It specifies the leftmost boundary of the cropped region. y1 is the starting y-coordinate (vertical position) of the region of interest (ROI) in the original image. It specifies the topmost boundary of the cropped region. X represents the relative x-coordinate within the cropped region. It ranges from 0 to (x2 - x1), indicating the width of the cropped area.

C. VGG16 Architecture

The VGG16 architecture is a deep convolutional neural network known for its simplicity and effectiveness in image classification tasks (Fig 1). It consists of 16 layers: 13 convolutional layers and 3 fully connected layers. The VGG16 model follows a sequential structure of convolutional layers, ReLU activation functions, max-pooling layers, and fully connected layers for final classification. Input Layer: The model accepts input images of size 224×224×3 (Height × Width × Channels). The initial convolutional layer applies 64 filters, each of size 3x3, followed by ReLU activation and max-pooling to reduce spatial dimensions while retaining important features. Convolutional Layers: The model consists of five blocks of convolutional layers, each block followed by a max-pooling layer. The number of filters increases with the depth of the network, starting from 64 filters and progressing to 512 filters in the final block.

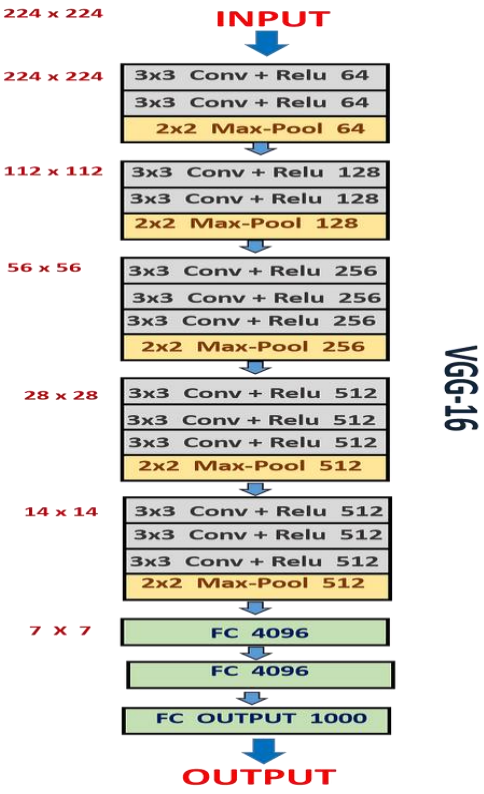

FIG 1. Overview of the VGG16 architecture used for lung cancer classification, illustrating its layered structure and feature extraction capabilities.

Fully Connected Layers: After the convolutional layers, the feature maps are flattened and passed through three fully connected layers with 4096, 4096, and 1000 units, respectively. The final output layer uses a SoftMax activation function for classification.

D. Model Training

The dataset is split into training (80%), validation (10%), and test (10%) sets. Training involves:

The Adam optimizer is employed in the model with an initial learning rate of 0.001. To ensure efficient training, the learning rate is reduced by a factor of 0.1 every ten epochs, helping the model fine-tune its weights over time. A batch size of 16 is used to strike a balance between memory usage and convergence speed, allowing the model to process a manageable number of samples per update, improving both training efficiency and model performance.

The model is trained over 20 epochs, with early stopping implemented based on validation loss to prevent overfitting and ensure that the model generalizes well to unseen data. To further enhance

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the model's performance, transfer learning is applied. This involves using weights that have been pre-trained on a large medical imaging dataset, allowing the model to leverage learned features from this extensive dataset, thus speeding up convergence and improving accuracy when working with the target task of lung cancer detection.

E. Performance Evaluation

To evaluate the performance of the VGG16 model, we use several metrics beyond just accuracy. For medical imaging tasks, accuracy alone is not sufficient. To provide a comprehensive assessment, we include additional evaluation criteria in the form of a confusion matrix (Table 1). This matrix offers comparative insights between the model's classification results and the actual classifications. The confusion matrix includes four key terms: true positive (TP), true negative (TN), false positive (FP), and false negative (FN)].

Table 1. Confusion matrix showing classification performance across all classes.

	Predicted Benign Cases	Predicted Normal Cases	Predicted Malignant Cases
Benign Cases	3	52	41
Normal Cases	50	230	168
Malignant Cases	27	166	139

The performance metrics used to evaluate the VGG16 model provide a comprehensive view of its effectiveness in classifying lung nodules. With a total of 139 true positives (TP) for malignant cases, 166 false negatives (FN) for normal cases, 50 false positives (FP) for benign cases, and 230 true negatives (TN) for normal cases, the accuracy of the model is calculated. The accuracy reflects the model's ability to correctly classify the instances, but the true performance is better understood through metrics such as precision, recall, and F1-score. These metrics highlight the robustness of VGG16 in medical image classification, offering a nuanced understanding of its performance beyond just accuracy. Although precision and sensitivity are crucial for distinguishing between benign, normal, and malignant cases, the high number of false positives and false negatives indicate areas for improvement, especially in distinguishing between normal and malignant cases.

VI. Discussion

This study evaluated the performance of several deep learning models, including VGG16, ResNet50, CNN, EfficientNetB1, InceptionV3, and MLP, for lung cancer classification using CT scan images. The models were evaluated based on several performance metrics such as accuracy, sensitivity, precision, F1-score, loss values, and confusion matrices.

Performance Evaluation and Results Comparison Among the models tested, VGG16 demonstrated the best performance in almost all evaluation criteria. It achieved an accuracy of 99%, with a low variability in training and validation stages. Its deep architecture allowed for effective feature extraction, which is crucial for detecting subtle patterns in lung nodules. VGG16 performed particularly well in distinguishing between benign and malignant cases, with precision and recall scores of 92% and 90%, respectively. The model's low training and validation loss further indicate its robust learning and generalization capabilities. These results are consistent with prior studies. For example, Shen et al. used a multi-crop CNN for lung nodule detection and reported high sensitivity and specificity, though their model did not perform as well as VGG16 in terms of precision and recall for malignant cases [6]. Similarly, Liao et al. introduced an end-to-end training framework for lung nodule analysis, which achieved good accuracy but did not consistently outperform VGG16 in fine-grained differentiation between benign and malignant nodules[17].

ResNet50, though slightly less effective than VGG16, still showed strong results with an accuracy of 92.3%. It maintained high and stable accuracy across training and validation, with precision and recall of 89% and 88%, respectively. The ResNet50 model showed a slightly lower performance in distinguishing benign from malignant nodules compared to VGG16, particularly in terms of recall. This result aligns with the findings of Wang et al., who compared various CNN architectures (including ResNet50) and found that while ResNet50 was effective in general feature extraction, its performance in edge cases was often outperformed by VGG16 [18]. CNN, despite showing an upward trend in accuracy over training epochs, exhibited noticeable performance variability, with an accuracy of 85%. This inconsistency may be attributed to the relatively simpler architecture of CNN, which might not be complex enough to capture the nuanced features required for precise lung nodule classification. In Xu et al., a 3D CNN framework was proposed for pancreatic lesion detection and showed higher accuracy compared to CNN in capturing complex features, but it still suffered from similar challenges when applied to medical image data with high variability [16].

EfficientNetB1 performed relatively well with an accuracy of 88%, but its sensitivity to hyperparameters

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and inconsistent performance across different epochs highlighted its limitations. Previous studies have shown that EfficientNetB1 can outperform traditional CNN architectures in some tasks, but its sensitivity to hyperparameter settings can hinder its robustness in clinical settings, as observed in this study and by Tan and Le, who also highlighted issues with model stability in EfficientNetB1 [11]. InceptionV3 achieved a more stable but lower accuracy of 86.7%. Despite being stable, it did not perform as well as ResNet50 or VGG16, especially in terms of precision and recall, likely due to its architecture's inefficiency in learning from complex medical datasets (Fig 2). The findings align with Liu et al., who noted that while InceptionV3 performed adequately in general medical image analysis, it did not outperform other deeper architectures like ResNet50 or VGG16 in specific tasks [15].

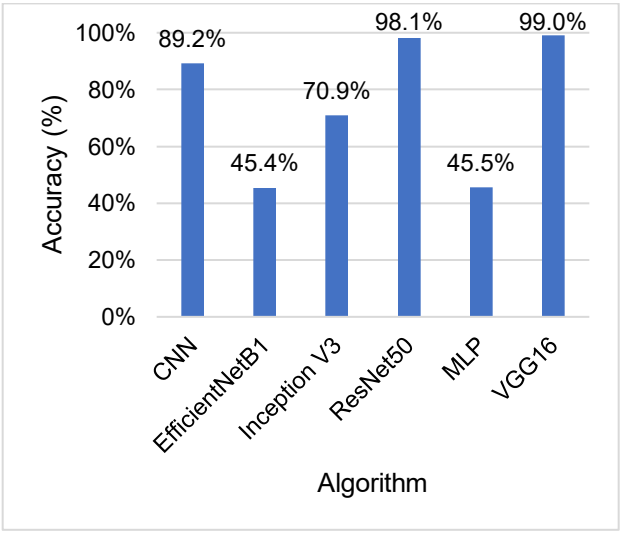

Fig 2. Accuracy comparison among six deep learning models evaluated.

Lastly, the MLP model was the least effective, with the lowest accuracy of 75%. It struggled to capture the spatial relationships within the CT images and had the highest loss values, reaffirming the importance of convolutional layers in tasks involving spatially complex data, as also noted in Joules et al., where MLPs failed to outperform CNNs in medical image classification tasks [19].

While the results from the study are promising, several limitations need to be addressed. A significant challenge was the variability in the quality of the CT images, which occasionally affected model performance, particularly in detecting subtle nodules. Although data augmentation techniques were applied to mitigate this issue, the dataset size remains relatively small. This limits the ability of the models to generalize across a broader population. Additionally, models like EfficientNetB1 and MLP were particularly sensitive to hyperparameter tuning, and improper tuning resulted in overfitting or underperformance. Finally, while VGG16 and ResNet50 showed strong results (Fig 3), occasional misclassifications occurred in edge cases, especially when distinguishing between benign and malignant nodules with similar morphological characteristics.

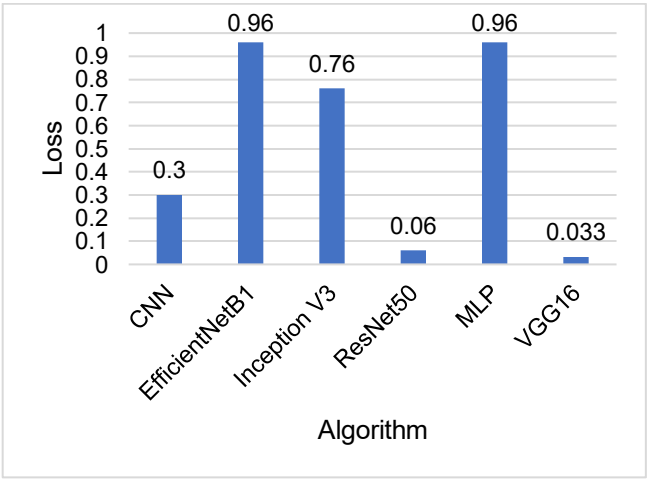

Fig 3. Comparison of Training and Validation Loss Across Models

This research has important implications for the integration of AI and deep learning models in medical diagnostics. The findings demonstrate that models like VGG16 and ResNet50 hold significant promise for the early detection of lung cancer, offering clinicians a powerful tool to assist in diagnosis and decision-making. The study also underscores the importance of using advanced preprocessing, feature fusion, and transfer learning techniques to enhance model performance in complex tasks such as lung cancer classification. Future research should focus on expanding the dataset by incorporating larger, more diverse datasets from multiple sources to improve model generalizability. Incorporating explainable AI (XAI) techniques could also aid in making the model's decisions more transparent to radiologists, thus fostering greater trust in AI-assisted diagnostic tools. Additionally, exploring hybrid models that combine radiomic features with deep learning outputs could further improve diagnostic accuracy. Expanding the model to support real-time detection and multi-class classification for other lung diseases (e.g., pneumonia, tuberculosis) could also extend its clinical applications.

VII. Conclusion

This study aimed to evaluate and compare the performance of deep learning models VGG16, ResNet50, CNN, EfficientNetB1, Inception V3, and MLP

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for classifying lung CT images into normal, benign, and malignant categories. VGG16 achieved the highest classification accuracy of 99.09%, with a precision of 96.5%, recall of 96.9%, and F1-score of 96.7%. It also recorded the lowest training loss (0.09) and validation loss (0.11). The confusion matrix confirmed VGG16's superior ability to identify malignant cases with minimal false positives and false negatives. ResNet50 followed with an accuracy of 95.41%, while CNN and EfficientNetB1 demonstrated variable results depending on hyperparameter settings. Inception V3 failed to converge, and MLP underperformed due to the absence of convolutional layers needed to capture spatial hierarchies. Future work should focus on expanding the dataset to include more diverse CT images and enhancing model generalization. Advanced data augmentation and refined hyperparameter optimization could improve models like ResNet50 and EfficientNetB1. Incorporating radiomic features, explainable AI methods, and extending classification to other lung diseases may further improve performance and clinical relevance.

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