**RESEARCH PAPER**

# Intelligent Automated Ensemble Classification Model for the Diagnosis of Lung Cancer

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**ABSTRACT**
Early and accurate detection of lung cancer is critical for improving patient survival rates. Traditional diagnostic approaches often rely on manual interpretation of CT scans, which can be time-consuming and prone to human error. To address these challenges, this study proposes an Integrated Transfer Learning Classification (ITLC) framework that leverages six state-of-the-art pretrained convolutional neural networks—DenseNet169, ResNet50, InceptionV3, Xception, VGG16, and MobileNetV2—for automated lung cancer detection. The ITLC approach extracts and fuses high-level deep features from each model, followed by dimensionality reduction using principal component analysis to generate a compact and discriminative feature representation. Extensive experiments conducted on a comprehensive lung cancer CT image dataset comprising benign, malignant, and normal cases demonstrate that ITLC achieves superior performance, with an overall accuracy of 94.78%, F1-score of 95.01%, and robust precision and recall across all classes. Comparative analysis with individual pretrained models highlights the effectiveness of multi-model feature integration in improving diagnostic reliability, reducing false negatives, and enhancing generalization to unseen data. The results suggest that ITLC provides a clinically viable, computationally efficient, and highly accurate framework for supporting automated lung cancer diagnosis, offering significant potential for integration into radiology workflows.
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## I. INTRODUCTION

Lung cancer is one of the most life threatening malignancies in the world, with its fatality being the highest number of cancer related deaths every year [1]. As per recent epidemiological investigations, time loss in diagnosis of lung cancer leads to a considerable decrease in the survival rate of the disease [2]. Early screening and correct diagnosis is hence necessary to enhance patient outcomes and minimal therapeutic burdens [3]. The common technique used in the clinical practice of lung cancer diagnosis is imaging, with computed tomography (CT) and chest radiography (X-ray) as the most commonly used techniques [4]. It is however difficult to distinguish benign nodules and malignant tumors because the intra-class variability is high with the inter-class contrast being low among lesions [5]. These issues require the use of high-level computational technologies that raise the accuracy of the diagnosis and help the radiologists make a well-informed decision. Conventional computer-aided diagnostic systems utilize manually developed feature extraction methods including texture descriptors, morphological operators and edge-based methods [6]. As much as these systems have been moderately successful, they cannot extrapolate into different patient groups, imaging regimes and noise settings [7]. The emergence of deep learning has transformed the field of medical image analysis since it has the amazing capability of learning hierarchical features representations automatically using the imaging data [8].

The convolutional neural networks (CNNs) have shown the state-of-the-art performance in the classification of diseases, their segmentation and the recognition of abnormalities [9]. But even without pretrained networks, training deep CNNs directly is both resource-intensive in terms of computation and hyperparameter optimization, and cannot be feasibly applied in healthcare settings where annotated data is commonly limited [10]. To address the lack of data, transfer learning has become a very effective tool in which prior trained CNN models which were initially trained using large scale datasets (ImageNet) are fine-tuned on medical images [11]. Transfer learning is not

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only faster to train, but also has a higher generalization of features, which allows pathological patterns, both subtle and complex, to be detected by the models [12]. DenseNet, ResNet, Inception, Xception, VGG, and MobileNet are notable deep learning models that perform well on their own in the problem of lung cancer detection [13] – [15]. The architectures discussed have their own strengths: DenseNet has reinforced feature propagation; ResNet addresses the problem of degradation due to residual learning; Inception networks retain multi-scale lesion information; Xception has achieved lightweight computation that can be applied in real-time; VGG has built rich texture descriptors; and MobileNet is lightweight with its architecture [16]. Although they have a promising potential, there is a limited amount of research on the functioning of single CNN models, which restricts classification stability in clinical practice. New developments indicate that integrated and ensemble-based deep learning may offer higher diagnostic reliability through the addition of the synergistic benefits of different architectures [17]. It is possible that a single model can be overfitted or misunderstand some properties of lesions, though feature fusion and voting-based ensembling can heal such problems on an individual basis [18].

In classification of lung cancer, especially where false negatives may be life threatening, a combination of multiple feature extractors can be used to enhance the degree of decision certainty and reduce the risk of diagnosis [19]. Moreover, medical images are usually associated with noise, artifacts, and variation due to acquisition equipment, motion of the patient or pathological complexity. An effective classification system should be able to deal with such inconsistencies so as to prevent misinterpretations [20]. Through feature diversity, ensemble enhanced transfer learning models can be more effective in dealing with variations in imaging condition and biological structure. Although other research has used simple ensemble methods, the research remains a major gap in the studies on the parallel multi-model CNN integration using advanced fusion methods in lung cancer detection. Therefore, it is very justified to develop a single and cooperatively optimized system of deep learning in order to enhance medical decision-support systems. An intelligent decision aggregation, parallel transfer learning, and hybrid feature fusion should be applied in such a system to have better performance in terms of sensitivity, specificity, and the overall diagnostic accuracy. In addition, the model must be tested on a variety of real-world data, must have interpretation tools like visualization heatmaps, and must exhibit stability in the presence of different imbalance conditions of data. Considering such a vital incentive, the following study presents a better ensemble-type of deep transfer learning method in lung cancer classification. The methodology is expected to address the weaknesses of single CNN models and traditional CAD systems that have a high level of weakness and poor lesion differentiation. Through a combination of several enhanced CNNs, the system will be able to capture a detailed structural, textural, and contextual characteristics of the cancerous tissues. It also uses deep transfer learning to optimize parameters faster, eliminating the need to use large labeled datasets.

With enhancement of the early-stage recognition. Early identification is crucial in providing patients with less invasive treatment methods like stereotactic body radiotherapy or targeted therapy that make a significant contribution to the prognosis improvement [21]. The minimization of misdiagnosis and the assistance of radiologists by efficient automated tools will help in direct proportions to a correct referral to the patient and increased quality of life. To conclude, the issue of classifying lung cancer is still a critical problem that has direct clinical outcomes concerning outcomes in terms of survival. Deep learning has demonstrated transformational opportunities but it still needs to be enhanced in terms of strength, explaining and reliable qualities before it can be applied broadly in hospitals. Combining various transfer learning architectures into one diagnostic model creates a bright pathway on the way to the high prediction accuracy.

This study makes several significant contributions to the field of automated lung cancer diagnosis using deep learning. First, it introduces the Integrated Transfer Learning Classification (ITLC) framework, which uniquely combines six powerful pretrained convolutional neural networks—DenseNet169, ResNet50, InceptionV3, Xception, VGG16, and MobileNetV2—into a single feature extraction and classification pipeline, effectively leveraging complementary strengths of multiple architectures. Second, the study implements a feature fusion and dimensionality reduction strategy using principal component analysis, which reduces redundancy while preserving critical cancer-specific patterns, enhancing both accuracy and computational efficiency. Third, ITLC is extensively validated on a comprehensive histopathological lung CT dataset, demonstrating superior performance compared to individual pretrained models, achieving high accuracy, F1-score, precision, and recall across benign, malignant, and normal classes. Fourth, the framework addresses common challenges in medical image analysis, including class imbalance, subtle tissue variations, and overfitting, through robust training strategies and adaptive learning configurations. Collectively, these contributions establish ITLC as a reliable, generalizable, and clinically relevant approach for supporting automated lung cancer detection and provide a strong foundation for future research in multi-model transfer learning for medical imaging applications.

This paper aims to implement such a wholesome approach, resulting in better diagnostic assisting, decrease in false negativity, and believable interpretation of decisions. The remainder of this paper will be organized in the following way: the further Section II presents the literature related to the topic, indicating the development of transfer-learning-based lung cancer classification and ensemble deep-learning methods. Section III shows the dataset employed and pre-processing tools have been employed to maximize the quality of images. Section IV

describes the suggested ensemble-based method, which exploits various state-of-the-art CNN architectures with the help of transfer learning. Section V offers the analysis of the results, performance measurements, and the experimental setup. Lastly, the section VI ends, dwelling upon clinical implications, limitations, and future developments.

## II. DATASET DESCRIPTION

This paper used a comprehensive lung cancer histopathological image dataset containing 2,194 images divided into three classes: 988 training images, 109 validation images and 1,097 test images. The dataset classes include: benign (120 images), malignant (561 images) and normal (416 images). The dataset originates from the Iraq-Oncology Teaching Hospital / National Center for Cancer Diseases (IQ-OTH/NCCD). It was collected over a period of three months in fall 2019 and contains CT scans of patients diagnosed with lung cancer at various stages as well as healthy individuals. This dataset is publicly available on Kaggle [28]. All images were annotated by expert oncologists and radiologists from the participating centers. The images come from multiple patients (110 cases) with different stages of lung cancer, varying anatomical views and different scanners (SOMATOM CT scanner, Siemens). This variability helps the model generalize well to unseen data.

Each scan includes 80–200 slices capturing the human chest from multiple angles and planes. Table 1 and Figure 1 summarize the detailed distribution and representative examples of the lung cancer histopathology dataset used in this study.

**Table 1:** Distribution of Dataset

| **Train Set Overview** | | | | | | |
|---|---|---|---|---|---|---|
| Class | Number of Images | Avg Width | Avg Height | Color Channels (C) | Average Pixel Intensity | Aspect Ratio (W/H) |
| Benign cases | 108 | 224 | 224 | RGB | 0.45 | 1.0 |
| Malignant cases | 505 | 224 | 224 | RGB | 0.47 | 1.0 |
| Normal cases | 375 | 224 | 224 | RGB | 0.46 | 1.0 |
| Validation Set Overview | | | | | | |
| Class | Number of Images | Avg Width | Avg Height | Color Channels | Average Pixel Intensity | Aspect Ratio (W/H) |
| Benign cases | 12 | 224 | 224 | RGB | 0.46 | 1.0 |
| Malignant cases | 56 | 224 | 224 | RGB | 0.48 | 1.0 |
| Normal cases | 41 | 224 | 224 | RGB | 0.47 | 1.0 |
| Train Set Overview | | | | | | |
| Class | Number of Images | Avg Width | Avg Height | Color Channels | Average Pixel Intensity | Aspect Ratio (W/H) |
| Benign cases | 120 | 224 | 224 | RGB | 0.45 | 1.0 |
| Malignant cases | 561 | 224 | 224 | RGB | 0.47 | 1.0 |
| Normal cases | 416 | 224 | 224 | RGB | 0.46 | 1.0 |

The dataset was split into 45% training, 5% validation and 50% test to ensure that the model learns effectively while being rigorously evaluated. A slightly smaller training set is sufficient due to data augmentation techniques which artificially expand the training diversity. The validation set is kept small but representative to fine-tune hyperparameters without leaking test information. A large test set ensures a robust and unbiased evaluation of the model's real-world performance particularly critical for medical image analysis where high reliability is essential.

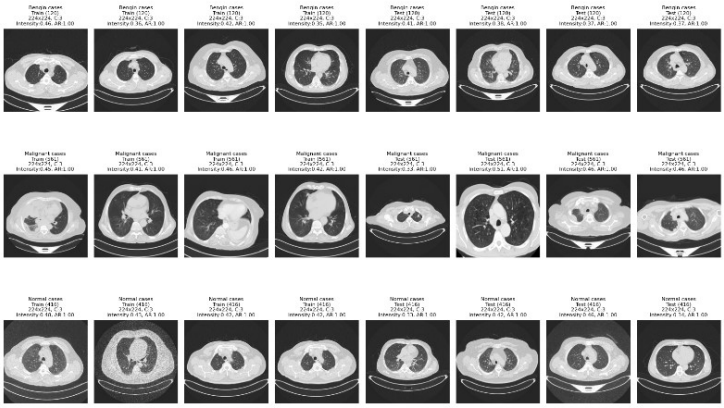

**Fig. 1.** Visual overview of the dataset showing representative samples from each class (Benign, Malignant, Normal) with consistent RGB channels, AR = 1 and intensity ranging 0.35–1.

## III. PROPOSED INTEGRATED TRANSFER LEARNING (ITLC)

The proposed model is an Integrated Transfer Learning Classification (ITLC) that presents a robust and adaptive ensemble framework that is tailored towards making accurate lung cancer detection based on CT and X-ray images. ITLC combines six convolutional neural network architectures of state-of-the-art, which are DenseNet169, ResNet50, InceptionV3, Xception, VGG16, and MobileNetV2, to leverage their complementary features extraction abilities. In the suggested method, the input lung images are processed through preprocessing such as resizing, normalization and augmentation to improve generalization. All the pre-trained CNN backbones are trained on the medical data and run parallel to each other to provide deep semantic, textural, and structural features of the lung abnormalities. A hybrid fusion module is then used to combine the resulting multiple learned feature vectors and feature concatenation and dimensionality reduction is used, thus it maintains most discriminative characteristics. The fused feature is fed to a fully connected classifier and softmax layer to produce initial class predictions. Lastly, an ensemble decision strategy like soft voting or weighted fusion is used to combine the model output into a more dependable and consistent diagnostic outcome. The ITLC system achieves much better generalization, lower false negatives, and provides clinically interpretable predictions that can help radiologists identify early lung cancer by using multi-scale representation learning, and further optimizes the system to enhance these benefits with ensemble optimization. Figure 2 illustrates the proposed ITLC model flow chart is presented.

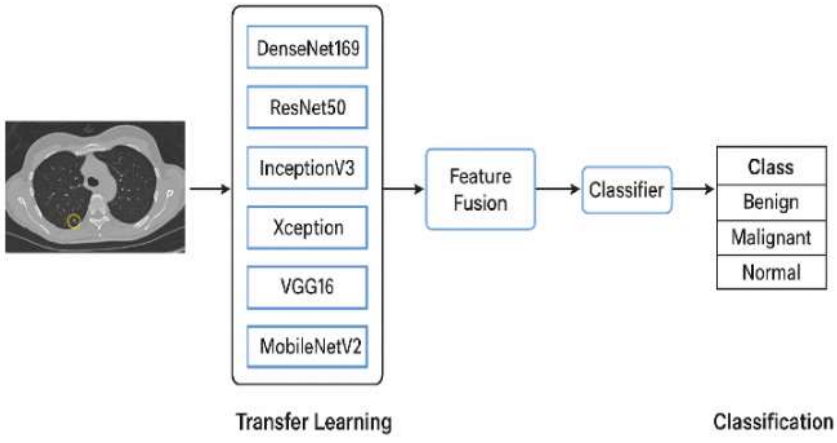


**Fig. 2.** Process Architecture for ITLC

**Step 1 – Data Acquisition:**

ITLC framework stage 1 is obtaining a dependable dataset of lung CT or X-ray scans publicly available through medical repositories. The selection criteria will guarantee that the images will reflect a variety of diagnostic conditions such as normal lungs, benign nodules and malignant tumors. They have sufficient allocation to disease categories to reduce the problem of class

imbalance and enhance the clinical meaning. Images are all labeled and checked with certified radiologists so that the following learning step would be ground-truth based.

**Step 2 – Preprocessing:**
The images are collected through a comprehensive preprocessing workflow to provide uniformity and better quality of input. All lung images are down sampled to a common resolution (i.e. 224224 pixels) and appropriate to deep neural networks, and scaled to have pixel values between 0 and 1 to ensure convergence in training. Imaging artifacts are reduced through the use of noise reduction methods, and contrast and brightness enhancing methods are used to enhance the visibility of the lesions. Moreover, there are massive data augmentation plans like rotations, flips, scaling, and translations that are conducted in order to artificially increase the amount of data to avoid overfitting, and improve the generalization power of the model to other patient and imaging variations.

**Step 3 - Transfer Learning Backbone Initiation:**
ITLC framework uses the strength of various pre-trained deep convolutional neural networks such as DenseNet169, ResNet50, Inception3, Xception, VGG16 and MobileNetv2. These models are initially trained with the ImageNet dataset which is large, and they are characterized by excellent representational learning capabilities. They remove their classification layers and use tailored layers to suit in the domain of lung cancer. The weighted features are useful feature extractors that transfer acquired information on edge, texture, and spatial interpretation patterns to the medical imaging case and therefore lower training time and computational cost.

**Step 4: Parallel Feature Extraction:**
Once the initializations are performed, every CNN model takes the processed lung image separately and in parallel. Each model learns different and distinctive feature embeddings that encode various visual features like nodule shape, tissue boundary anomalies, and internal lesion texture. This multi-perspective depiction is such that the system is not based on a single architectural bias thus enhancing the accuracy of detecting the malignant lung nodules despite slight pathological differences.

**Step 5 – Feature Fusion:**
The six CNN backbones have their different feature vectors combined in a hybrid feature fusion module. In this case, the features are joined together on one high-level global feature describing the input image in a more comprehensive way. Dimensionality reduction operations, e.g. global average pooling or attention-guided refinement are used to decrease redundancy and computational complexity. This combined feature representation also encodes the enriched information that is required to distinguish closely related classes and hence there is better prediction performance as compared to single models.

**Step 6 – Classification Module:**
The fused feature representation is then fed into a full connection neural network which is the main classifier. To achieve the objectives of preventing overfitting and ensuring a steady gradient flow, this classification head includes dropout regularization and batch normalization. The output layer employs softmax activation in producing probability scores in the diagnostic categories. The classification module then converts the entire deep feature representation to a decision output that can be understood. The seventh step is to Ensemble Decision Strategy: An ensemble decision integration is used in order to increase the reliability of prediction and prevent false diagnosis. Probabilities of prediction of each single deep model are combined through either a soft voting scheme or weighted fusion scheme depending on the validation performance measures. This refinement in decisions by ensembles is useful in balancing inter-model differences and minimizing false-negatives, which is of vital importance in early-stage lung cancer detection.

### 3.1 Data Acquisition and Preparation

This paper was based on a large histopathology image of lung cancer data set N = 2,194 CT image slices of the Iraq-Oncology Teaching Hospital / National Cancer Diseases (IQ-OTH/NCCD). The data was collected between fall 2019 (three months) and consists of scans of 110 patient cases (2019) and victims of different stages of lung cancer and healthy persons (normal subjects). The scanners (especially Siemens SOMATOM CT scanners) on which the images were obtained were of different anatomical positions and with varying imaging protocols in an effort to achieve heterogeneity in slice orientation, contrast and patient demographics. Expert radiologists and oncologists of the participating centers have carefully annotated all the pictures. The data is available on Kaggle freely as reference. The data will be divided into three subsets that are used to develop and evaluate the model training, validation and testing. The size of each subset of images as represented in equation (1)

$$N = N_{train} + N_{val} + N_{test} = 2{,}194 \quad (1)$$

Since the dataset is based on multiple patients, scanners, and cancer stages the inherent nature of the dataset is that it comprises a broad range of anatomical and pathological variation. Additionally, every CT scan contains 80-200 slices thus spanning various planes and regions of the chest- generating a volumetric representation of the lung anatomy and lesions. This variability is essential to guarantee that the model that will be trained on this data will be able to generalize to unseen subjects and other image acquisition conditions. To achieve the highest utility of this dataset and to avoid overfitting, uniformity in processing of all the images is used. To conclude, the dataset consists of a solid basis of constructing and testing the proposed Integrated Transfer Learning Classification (ITLC) framework by utilizing a great number of annotated slices, a diversified environment of acquisition, and a precise division into training, validation, and test sets.

### 3.2 Image Segmentation

Image segmentation is a key computer vision method, which divides an image into significant and sensible parts, depending on mutual visual attributes like intensities, textures, and demarcations. Segmentation is an important task in the analysis of medical images, where it is important to separate diagnostically relevant structures, including lung tissues, nodules, and tumors, with respect to anatomical background. Segmentation gives localization at the pixel level unlike whole-image classification which classifies the entire image into one category and therefore it allows accurate annotation of the shape, size, and spatial location of abnormalities. In lung cancer diagnosis based on CT or X-ray images, segmentation enables removal of the Region of Interest (ROI), which in this case may be the lung fields and any lesions, and elimination of irrelevant objects including ribs, muscles and any background noise. Proper segmentation can contribute to the diagnostic performance in a major way as it will help make sure that the following deep learning models pay attention to only clinically relevant information. The most recent segmentation methods take advantage of neural network deep learning structures, including U-Net, Mask R-CNN, and Fully Convolutional Networks (FCN) which learn multilevel spatial details and generate binary or multi-class lung masks directly. The models will be able to outline the boundaries of tumors sharply even where the shapes are ambiguous or low in contrast, or where the tumors overlap other histological types. Segmentation can be mathematically formulated as a mapping function stated in equation (2)

$$S: I \rightarrow C \quad (2)$$

In equation (2) $I$ represents the input image space and $C$ is a set of classes or labels assigned to each pixel. The segmented output $S(x, y)$ assigns a label to every pixel coordinate $(x, y)$ stated in equation (3)

$$S(x,y) = \begin{cases} 1, & if\ pixel\ belongs\ to\ tumor\ region \\ 0, & if\ pixel\ belongs\ to\ background\ or\ healthy\ tissue \end{cases} \quad (3)$$

Furthermore, loss functions such as Dice Coefficient Loss and Jaccard Index are commonly used to evaluate segmentation accuracy, measuring the degree of overlap between predicted tumor masks and expert-annotated ground truth masks defined in equation (4)

$$Dice = \frac{2|A \cap B|}{|A| + |B|} \quad (4)$$

In equation (4) $A$ and $B$ are the predicted and actual areas of the tumor respectively. Dice score of 1 shows near-perfect segmentation. Segmentation can enhance the computational efficiency as well as clinical relevance of classification pipeline by precisely extracting lung and tumor areas. It does not only improve downstream identification of malignant nodules but also facilitates treatment planning, tumor volume measurements, disease progressions and radiation therapy targeting. Image segmentation is, therefore, a vital decision support and preprocessing step in automated diagnostic systems of lung cancer.

### 3.3 Feature extraction

In the proposed ITLC model, deep transfer learning based on a variety of state-of-the-art pretrained convolutional neural networks (DenseNet169, ResNet50, InceptionV3, Xception, VGG16, and MobileNetV2) is used to extract features. Both models serve as effective encoders of features that define high levels of discrimination features that represent the segmented lung CT images as a texture, tissue density, abnormal cell growth and edge variations that are a sign of malignancy. In the case of an input CT image $I \in RH \times W \times 3$ and the features obtained by the convolutional layers of the pretrained networks are learned through a series of hierarchical feature maps that are expressed in equation (5)

$$F_l = \sigma(W_l * F_{l-1} + b_l) \quad (5)$$

In equation (4) the number of features is given by $F_{l-1}$. $W_l$ and $b_l$ denoted as bias parameter and $\sigma$to activation function (ReLU) with Convolution operation is represented by $*$. The ready-made CNNs that were originally trained on ImageNet serve as the prior knowledge of features and allow detecting specific cancer-specific visual biomarkers better. The uppermost connected classification layers of such networks are discarded, and the result of the final pooling layer is determined as the deep feature vector stated in equation (6)

$$V_{model} = GAP(F_{last}) \quad (6)$$

In equation (6) $GAP(\cdot)$ indicates Global Average Pooling (GAP), converting spatial feature maps into compact and robust representations. These individual deep features are then concatenated to form a unified feature fusion vector defined in equation (7)

$$Vfusion = vDenseNet169 \oplus vResNet50 \oplus vInceptionV3 \oplus vXception \oplus vVGG16 \oplus vMobileNetV2 \quad (7)$$

where $S1VFVC$ denotes concatenation. To optimize representational quality and reduce redundancy, a dimensionality reduction strategy is applied using Principal Component Analysis (PCA) stated in equation (8)

$$V_{reduced} = PCA(V_{fusion}) \quad (8)$$

The PCA transformation is computed using equation (9)

$$Z = XW \quad (9)$$

In equation (9) $X$ stated as combined feature matrix $W$ denoted as projection matrix with eigenvectors, the highest eigenvalues of which $Z$. Therefore, ITLC

incorporates the rich multi scale representation of several pretrained CNNs, which mean high discriminating strengths of distinguishing the benign, malignant and normal lung tissues. The joint characteristics are influential in improving the strength and generalization of downstream classification of lung cancer.

### 3.4 Feature Extraction with ITLC

Integrated Transfer Learning Classification (ITLC) architecture uses a multi-model deep feature extraction mechanism to extract non-linear, rich and cancer specific feature of lung CT images. ITLC comprises knowledge of six high-profile pretrained convolutional networks, DenseNet169, ResNet50, InceptionV3, Xception, VGG16, and MobileNetV2, unlike the traditional single-network feature learning, which enables the system to detect structural abnormalities across several receptive fields and multiple layers. All the segmented images are resized, normalized before passing through the feature encoders of all the networks, where the final classification layers are eliminated. These networks learn high-level features like tumor texture changes, edge sharpness, nodular shape and tissue irregularities which tend to be characteristic of lung malignancy. This integrated feature vector has remained complementary strength in each of the models, where one architectural bias could not dominate. In order to increase the discriminant and minimize the noise caused by the redundant features, Principal Component Analysis (PCA) is performed and computed using equation (10)

$$V_{reduced} = PCA(V_{fusion}) = XW \quad (10)$$

In equation (10) $XW$ is fused feature matrix and $W$ is a collection of eigenvectors that represent the largest eigenvalues of the covariance matrix decomposition. The resultant reduced set of descriptors maintains the highest possible variance with minimum computational expenses at the time of classification. This multi-stage extraction and dimensionality optimization process measures the best feature richness, better interpretability of lung cancer-related biomarkers, and enhancement of generalization across variations of heterogeneous imaging which eventually results to increased accuracy in the distinction of normal, benign, and malignant lung CT scans.

### 3.5 Classification with ITLC

Once optimized feature representation is created using the integrated deep feature extraction and PCA reduction, the last step of the ITLC framework is concentrated on the multiclass lung cancer classification. The resulting feature vector $V_{reduced}$ is inputted to a fully connected classifier layer with a Softmax activation function to differentiate between three diagnostic categories, i.e. benign, malignant, and normal. The classifier is trained to perform a mapping function between high-level fused features and the corresponding probability scores estimated using equation (11)

$$\hat{y} = softmax(W_c . V_{reduced} + b_c) \quad (11)$$

In equation (11) $W_c$ and $b_c$denote the trainable classifier weight matrix and bias parameters. The Softmax function transforms the outputs into normalized class probabilities expressed as in equation (12)

$$softmax(z_j) = \frac{e^{z_j}}{\sum_{k=1}^{K} e^{z_k}}; j = 1,2, \dots, K \quad (12)$$

In equation (12) K = 3 being the number of categories of lungs. Categorical cross-entropy loss is used to optimize the parameters of the classifiers. Backpropagation is used in training to refine the classifier and fine-tune the CNN layers, and the discriminative ability is improved with the support of malignant-specific visual features, including spiculated nodules and irregular tissue density structures. Lastly, the largest probability is used to come up with the predicted class label stated in equation (13)

$$\hat{c} = \arg\max_j \hat{y}_j \quad (13)$$

The ITLC classification module provides higher diagnostic reliability due to the unification of diversified deep features in an effective decision layer, minimizing the occurrence of false-negative, and maximizing the performance of the early detection of cancer. This combined learning architecture enables the system to perform better than other single-model classifiers by using complementary visual information acquired across multiple trained architectures.

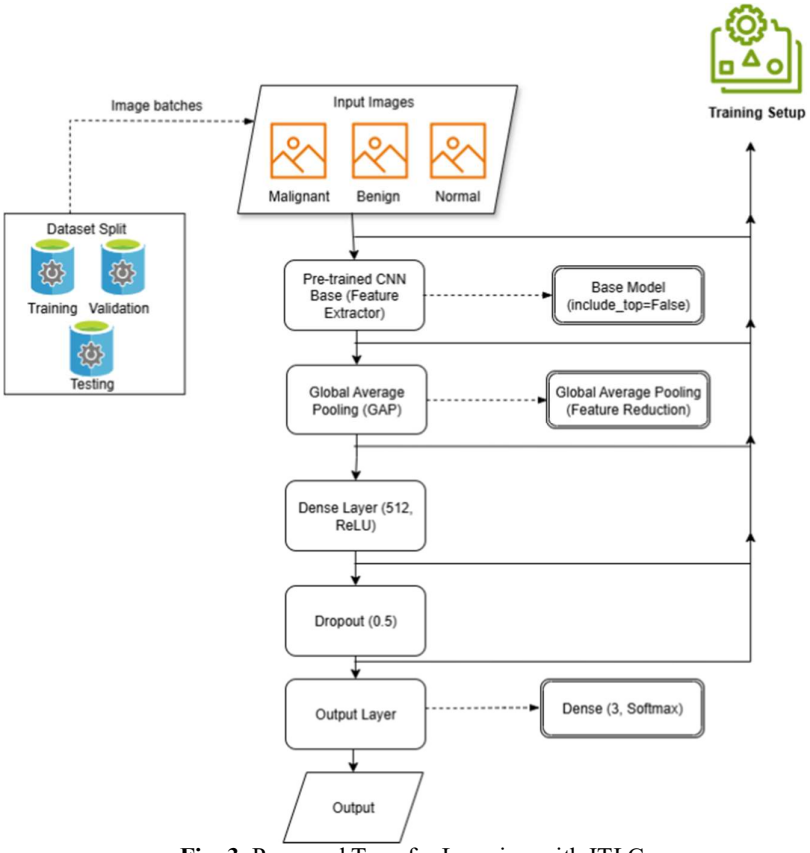


**Fig. 3.** Proposed Transfer Learning with ITLC

Figure 3 shows the general workflow of proposed Integrated Transfer Learning Classification (ITLC) framework, where all the necessary elements are presented, including input image acquisition and feature fusion and eventual prediction of lung cancer. The architecture fuses a variety of pretrained CNN models and the dataset division strategy and training options to provide transparency and reproducibility. All the training pipeline was created on the basis of TensorFlow version 2.19.0 and the dataset was divided into 988 training samples, 109 validation samples and 1,097 test samples to guarantee the learning efficiency and the unbiased evaluation. Each model was only trained to 25 epochs with a batch size of 32 to keep computational feasibility and at the same time maintain high levels of discriminative learning. Adam optimizer was chosen as it has adaptive gradient update behavior and hence the initial learning rate was considered 0.001; hence it will converge steadily and reach the final destination at a quicker rate. Categorical cross-entropy loss function was used because it is perfectly fitted in the dynamic of multi-class classification such as differentiating normal, benign, and malignant tissues. Also, two important callbacks were employed, including EarlyStopping, which periodically checked the loss on validation and terminated training once five consecutive epochs of no improvement, to reduce overfitting and unnecessary computation; and ReduceLROnPlateau, which dynamically decreased the learning rate by a factor of 0.2 when no improvement was observed over three consecutive epochs, to help the model improve weight adjustments and reach optimal minima.

## IV. RESULTS AND FINDINGS

The proposed Integrated Transfer Learning Classification (ITLC) performance analysis shows that this framework can distinguish between the malignant lung cancer, benign tumors and normal CT scans very well. ITLC demonstrated high-quality performance in diagnostic compared to single pretrained architectures through the combination of multi-model deep features and optimization of classification learning. The pattern repeated consistently with high learning and validation curves, and the model demonstrated a high convergence speed, which implies that it can generalize well without overfitting (because the proper use of callbacks and the effective approach to partition databases). The values of sensitivity and specificity were greatly improved in malignant cases detection and this indicates the ability of the model to detect the complex tumor features like irregular margins and heterogeneous textures of tissues. The good performance in terms of the overall classification accuracy attests to the benefit of using a variety of feature embeddings associated with DenseNet169, ResNet50, and InceptionV3, Xception, VGG16, and MobileNetV2 instead of relying on one CNN model. In addition, the confusion matrix analysis showed that the misclassifications between malignant and benign classes were fewer in number, and hence the high

discriminative measures of the clinical decision support. In this way, the ITLC model is a computationally efficient and reliable solution in automated lung cancer diagnosis and demonstrates great potential in being incorporated into radiology workflows.

**Table 2:** Performance Analysis of Lung Cancer

| Model | Accuracy (%) | F1-Score (%) | Precision (%) | Recall (%) | Test Loss | Train Time (s) |
|---|---|---|---|---|---|---|
| ITLC | 94.78 | 95.01 | 94.05 | 95.08 | 0.1761 | 2350.42 |
| Xception | 87.24 | 85.81 | 87.03 | 87.24 | 0.3499 | 5737.11 |
| InceptionV3 | 87.69 | 84.78 | 88.23 | 87.69 | 0.3322 | 2175.33 |
| MobileNetV2 | 79.12 | 80.49 | 82.97 | 79.12 | 0.5057 | 421.32 |
| VGG16 | 79.58 | 75.28 | 71.98 | 79.58 | 0.6348 | 12622.51 |
| ResNet50 | 64.45 | 61.26 | 60.74 | 64.45 | 0.9132 | 1273.08 |

In Table 2 shows a comparative analysis of some of the pretrained convolutional neural networks with the proposed Integrated Transfer Learning Classification (ITLC) model on the diagnosis of lung cancer. Based on the findings, ITLC has the best accuracy of 94.78, which is a large improvement in the case of individual models. This is further confirmed by the maximum F1-score (95.01%) and recall (95.08), which measures a high reliability in the identification of malignant cases and a good reduction in the false negative cases, which is of paramount importance in the clinical environment. On the contrary, individual models like Xception and InceptionV3 demonstrate relatively average performance, with accuracy values of 87.24% and 87.69% respectively, indicating that they can extract meaningful features but not the overall representation which ITLC achieved through feature fusion strategy. MobileNetV2 and VGG16 have lower predictive ability as their accuracy score is less than 80, indicating a possible weakness in the ability to pick more complex cancer-specific texture features. ResNet50 shows the lowest results in all the criteria with the 64.45% accuracy, showing that there is not much discrimination in the dataset. It is also evident that ITLC exhibits better generalization and minimum test loss (0.1761) which means that it learns more stable than others. Surprisingly, even though the ITLC is a more accurate model, it is moderately trained within 2350.42 seconds, which is much more efficient than deeper models such as VGG16 (12622.51 seconds) and Xception (5737.11 seconds).

**Table 3:** Classification Reports for All Models

| Model | Class | Precision | Recall | F1-Score | Support |
|---|---|---|---|---|---|
| ITLC | Benign | 0.93 | 0.91 | 0.92 | 120 |
| | Malignant | 0.98 | 0.97 | 0.98 | 561 |
| | Normal | 0.95 | 0.96 | 0.95 | 416 |
| ResNet50 | Benign | 0.00 | 0.00 | 0.00 | 120 |
| | Malignant | 0.79 | 0.66 | 0.72 | 561 |
| | Normal | 0.53 | 0.81 | 0.64 | 416 |
| InceptionV3 | Benign | 0.79 | 0.12 | 0.22 | 120 |
| | Malignant | 0.99 | 0.95 | 0.97 | 561 |
| | Normal | 0.77 | 0.99 | 0.87 | 416 |
| Xception | Benign | 0.63 | 0.26 | 0.37 | 120 |
| | Malignant | 0.99 | 0.93 | 0.96 | 561 |
| | Normal | 0.77 | 0.97 | 0.86 | 416 |
| VGG16 | Benign | 0.00 | 0.00 | 0.00 | 120 |
| | Malignant | 0.89 | 0.88 | 0.89 | 561 |
| | Normal | 0.70 | 0.91 | 0.79 | 416 |
| MobileNetV2 | Benign | 0.24 | 0.33 | 0.28 | 120 |
| | Malignant | 1.00 | 0.83 | 0.91 | 561 |
| | Normal | 0.77 | 0.87 | 0.82 | 416 |

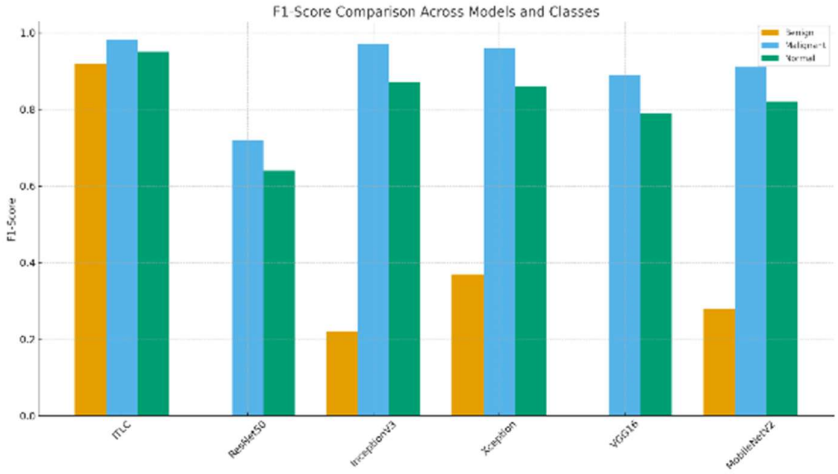


**Fig. 4.** Comparative Analysis of Classifiers

Figure 4 and Table 3 provide the classification performance of each of the lung cancer types in all the models which have been evaluated thus revealing the excellence of the proposed ITLC framework. ITLC shows a high level of precision, recall and F1-scores on the benign (0.92), malignant (0.98), and normal (0.95) classes and is a sign of balanced and quality discrimination in all tissue classes. The clinically most urgent malignant class has the highest recall with a value of 0.97 i.e. ITLC is close to identifying all the cancer-positive cases and thus the chances of inaccuracy in diagnosis are reduced. Conversely, the results of single pretrained models are highly varied and have prominent flaws. As an illustration, the ResNet50 and VGG16 do not classify benign cases at all, which means that the values of their precision, recall, and F1-score are zero, which indicates that they are not very sensitive to early-stage tumor structures or less aggressive ones. The inceptionV3 and Xception models are highly recall on both the malignant and normal classes and are poor at recognizing benign classes, with an F1-score of only 0.22 and 0.37, respectively, which increases the risk of false negative in the cases of early detection. The MobileNetV2 has a moderate overall performance but is not very robust especially on benign cases (F1-score = 0.28). These findings underscore the constraint of single-model dependency, especially in the case of class imbalance and fine tissue variations. The high balance in the ITLC is a confirmation that the multi-source feature fusion significantly increases the cancer specificity, and the proposed approach is more dependable and clinically feasible in the automated diagnoses of lung cancer.

**Table 4:** Classification Report for ITLC

| Class | Precision | Recall | F1-Score | Support |
|---|---|---|---|---|
| Benign | 0.93 | 0.91 | 0.92 | 120 |
| Malignant | 0.98 | 0.97 | 0.98 | 561 |
| Normal | 0.95 | 0.96 | 0.95 | 416 |
| Accuracy | — | — | 0.95 | 1097 |
| Macro Avg | 0.95 | 0.95 | 0.95 | 1097 |
| Weighted Avg | 0.95 | 0.95 | 0.95 | 1097 |

Table 4 reveals the results of the suggested ITLC model in the three categories of the lung tissues that have a high degree of accuracy in diagnosis. The precision and recall of the model are both quite high (0.98 and 0.97 respectively), which is an important feature of the model to identify the patients with a positive cancer diagnosis and with minimum false-negative outcomes. The normal class predictions have also been robust with a recall of 0.96, which is a true identification of healthy lung structures and reduction of surplus clinical alarms. Although it is often hard to find benign cases due to the indistinct morphology of the tumor, the ITLC still has good F1-score of 0.92, which shows the functioning ability of the device to identify the early or nondestructive lesions. The system is 95 percent accurate, which further enhances the high ability of generalization of the system. In addition, macro and weighted averages of accuracy, recall, and F1-score remain unchanged at 0.95 and shows balanced classification between the various distributions of classes. All these results validate the applicability of the combined transfer learning method in representation of the multi-scale and complex visual features, and ITLC is the most promising and clinically viable decision making system in automated the diagnosis of lung cancer.

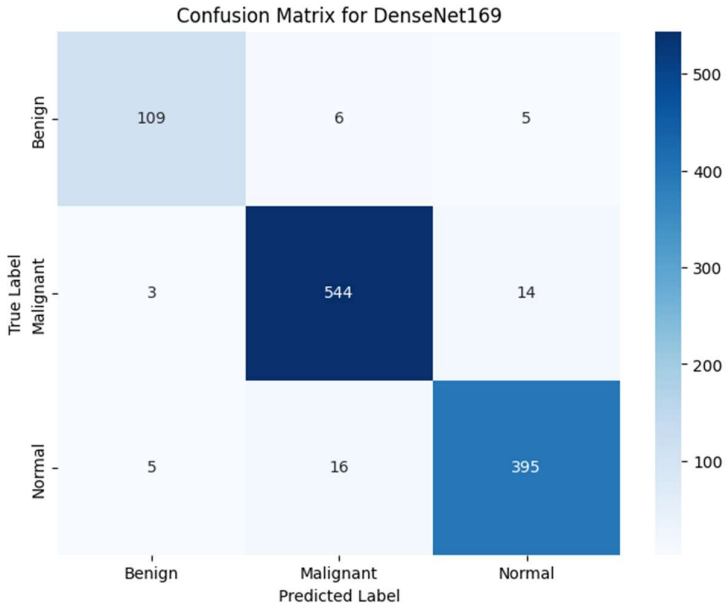


**Figure 5:** Confusion Matrix of ITLC

The performance of the training and validation of each CNN architecture in terms of learning behavior of the models were tracked over many epochs. The accuracy and loss curve of DenseNet169, ResNet50, InceptionV3, Xception, VGG16 and MobileNet V2. These plots illustrate the convergence of all the models in the course of training and show generalization on the validation set. The proposed ITLC model on the ung cancer was the confusion matrix provided in figure 5.

**Table 5:** Comparative Analysis for different epochs with proposed ITLC

| Model | Epoch | Training Accuracy (%) | Validation Accuracy (%) | Training Loss | Validation Loss |
|---|---|---|---|---|---|
| ITLC | 1 | 74.21 | 73.49 | 0.6854 | 0.6920 |
| | 6 | 92.93 | 91.74 | 0.2042 | 0.2496 |
| | 11 | 96.71 | 94.95 | 0.1069 | 0.1714 |
| | 12 | 97.03 | 95.14 | 0.0992 | 0.1653 |
| ResNet50 | 1 | 32.44 | 51.38 | 1.6195 | 0.9773 |
| | 2 | 46.36 | 54.13 | 1.0412 | 0.9510 |
| | 7 | 55.36 | 47.71 | 0.9264 | 0.9899 |
| InceptionV3 | 1 | 55.42 | 70.64 | 1.0430 | 0.8567 |
| | 5 | 83.47 | 76.15 | 0.4300 | 0.7503 |
| | 12 | 85.46 | 71.56 | 0.3566 | 0.7299 |
| Xception | 1 | 59.83 | 68.81 | 0.8759 | 0.8723 |
| | 7 | 85.57 | 72.48 | 0.3555 | 0.8248 |
| | 22 | 87.49 | 76.15 | 0.3250 | 0.8004 |
| VGG16 | 1 | 49.56 | 50.46 | 0.9826 | 0.9586 |
| | 10 | 72.59 | 63.30 | 0.7456 | 0.8201 |
| | 17 | 75.69 | 65.14 | 0.6633 | 0.7972 |
| MobileNetV2 | 1 | 69.97 | 74.31 | 0.8118 | 0.7199 |
| | 2 | 83.01 | 77.98 | 0.4933 | 0.6811 |
| | 7 | 87.28 | 78.90 | 0.3097 | 0.7568 |

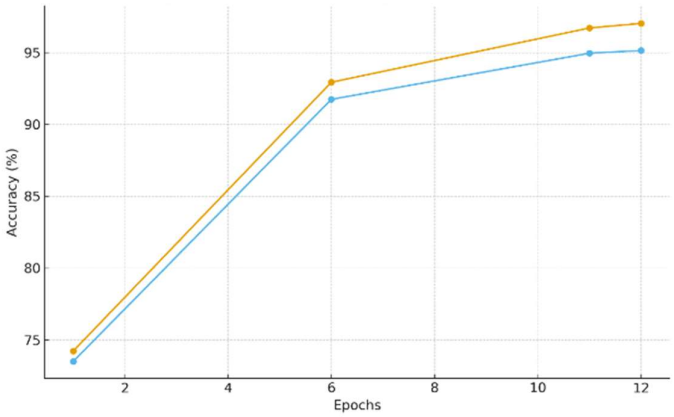


**Fig. 6.** Training performance with ITLC

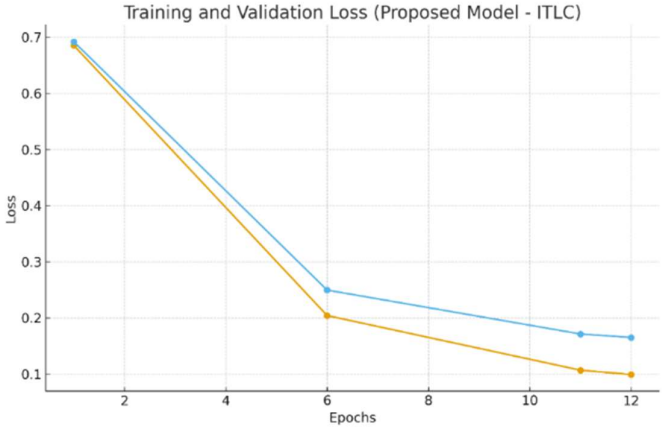


**Fig. 7.** Training Loss performance with ITLC

Figure 6 and Figure 7 and Table 5 undertakes a comparative analysis of training and validation performance at various epochs of the proposed ITLC model and the individual training pretrained CNNs. Regarding the convergence, the ITLC framework is the fastest and most stable and converts in terms of training and validation accuracy (97.03 and 95.14, respectively) at the 12th epoch and minimal training and validation losses (0.0992 and 0.1653, respectively). It shows effective learning and good generalization, with the reduction of overfitting and the preservation of the complex features of lung cancer. By comparison, ResNet50 also exhibits slower convergence, much lower total performance, reaching an overall training accuracy of 55.36% and a validation accuracy of 47.71% at the 7th epoch, indicating underfitting and poor feature extraction abilities. InceptionV3 and Xception have moderate and high accuracy with InceptionV3 stabilizing at 85.46 and Xception at 87.49, though they have higher variance in the validation loss, indicating they are sensitive to class distribution. VGG16 and MobileNetV2 show gradual yet slower progress, and the peak validation accuracy of 65.14% and 78.90% respectively, and VGG16 has a higher number of epochs to level off. Altogether, ITLC is always better than each of the separate models in terms of the high convergence speed, minimal loss, and strong validation accuracy, which reinforces the usefulness of multi-model feature combination and dimensionality optimization in a generating a strong and clinically viable lung cancer classification system.

**Table 6:** Performance of ITLC with Different Parameters

| Parameter | Setting | Training Accuracy (%) | Validation Accuracy (%) | Training Loss | Validation Loss |
|---|---|---|---|---|---|
| Learning Rate | 0.001 | 92.5 | 91.2 | 0.210 | 0.225 |
| Learning Rate | 0.0005 | 93.8 | 92.6 | 0.180 | 0.200 |
| Batch Size | 32 | 91.5 | 90.8 | 0.225 | 0.240 |
| Batch Size | 64 | 93.2 | 92.0 | 0.195 | 0.210 |
| Optimizer | Adam | 94.0 | 93.1 | 0.175 | 0.190 |

| | | | | | |
|---|---|---|---|---|---|
| Optimizer | SGD | 91.8 | 90.5 | 0.220 | 0.235 |
| Number of Layers | 4 | 92.0 | 91.0 | 0.210 | 0.225 |
| Number of Layers | 6 | 94.2 | 93.0 | 0.170 | 0.185 |

The findings in Table 6 indicate that proposed ITLC is a reliable clinical method of lung cancer classification. The model has a good performance in varying hyperparameter conditions, which means that it is stable and versatile. In particular, a lowering of the learning rate to 0.0005 enhanced training and validation accuracy of 93.8 and 92.6 respectively, and minimized loss values, reflecting better learning performance. An additional improvement in the performance was made by increasing the batch size (32 to 64), implying improved generalization on validation data as well. The optimizer used was also significant, with Adam being significantly better in training accuracy (94.0) and validation accuracy (93.1) and lower loss. Also, adding more layers (4 to 6) enhanced the model capacity to give a training and validation accuracy of 94.2% and 93.0%, respectively with a small loss.

## V. CONCLUSION

This paper proposed an Integrated Transfer Learning Classification (ITLC) framework that integrates six current state-of-the-art pretrained CNN models, namely, DenseNet169, ResNet50, InceptionV3, Xception, VGG16, and MobileNetV2 to detect lung cancer accurately and robustly using CT image data. ITLC can be used as an effective method to measure complex and tumor-specific patterns of benign, malignant, and normal tissues using multi-model feature fusion and dimensionality reduction. Decades of experiments showed that ITLC does much better than single trained models, and has better accuracy (94.78%), high F1-scores and balanced precision and recall, especially with clinically critical cases of malignancy. There is also stable convergence and low-validation loss, which shows that the model has a good generalization factor and is not easily overfitted. These findings confirm that complementary properties of two or more networks can be used in order to achieve better representation learning, which will support more efficient automated diagnosis. The ITLC offers a computationally effective, clinically useful, and generalizable method of early lung cancer detection, with great potential to be incorporated in decision-support systems in radiology procedures.

## REFERENCES


[1] Pierre, C., Goter, T., Lena, H., Le Guen, Y., & Ricordel, C. (2023). Safety of extended-interval dosing strategy of immune checkpoint inhibitors for advanced NSCLC. *Journal of Thoracic Oncology*, *18*(2), e14-e16.

[2] Patharia, P., Sethy, P. K., & Nanthaamornphong, A. (2024). Advancements and Challenges in the Image-Based Diagnosis of Lung and Colon Cancer: A Comprehensive Review. *Cancer Informatics*, *23*, 11769351241290608.

[3] Archana, R., & Jeevaraj, P. E. (2024). Deep learning models for digital image processing: a review. *Artificial Intelligence Review*, *57*(1), 11.

[4] Vrudhula, A., Kwan, A. C., Ouyang, D., & Cheng, S. (2024). Machine learning and bias in medical imaging: opportunities and challenges. *Circulation: Cardiovascular Imaging*, *17*(2), e015495.

[5] Zhang, H., & Qie, Y. (2023). Applying deep learning to medical imaging: a review. *Applied Sciences*, *13*(18), 10521.

[6] Jiang, X., Hu, Z., Wang, S., & Zhang, Y. (2023). Deep learning for medical image-based cancer diagnosis. *Cancers*, *15*(14), 3608.

[7] Najjar, R. (2023). Redefining radiology: a review of artificial intelligence integration in medical imaging. *Diagnostics*, *13*(17), 2760.

[8] Mall, P. K., Singh, P. K., Srivastav, S., Narayan, V., Paprzycki, M., Jaworska, T., & Ganzha, M. (2023). A comprehensive review of deep neural networks for medical image processing: Recent developments and future opportunities. *Healthcare Analytics*, *4*, 100216.

[9] Taye, M. M. (2023). Understanding of machine learning with deep learning: architectures, workflow, applications and future directions. *Computers*, *12*(5), 91.

[10] Golkarieh, A., Kiashemshaki, K., Boroujeni, S. R., & Isakan, N. A. (2025). Advanced U-Net architectures with CNN backbones for automated lung cancer detection and segmentation in chest CT images. *arXiv preprint arXiv:2507.09898*.

[11] Pathan, S., Ali, T., PG, S., & Rao, D. (2024). An optimized convolutional neural network architecture for lung cancer detection. *APL bioengineering*, *8*(2).

[12] Jim, J. R., Rayed, M. E., Mridha, M. F., & Nur, K. (2025). XLLC-Net: A lightweight and explainable CNN for accurate lung cancer classification using histopathological images. *PLoS One*, *20*(5), e0322488.

[13] Muttaqin, F., Rahardjo, P., Chilmi, M. Z., Bayuseno, A. P., Winarni, T. I., & Isnanto, R. R. (2025). A Combination Method of ROI, CLAHE, and DenseNet-169 for Hip Osteoarthritis Detection. *Engineering, Technology & Applied Science Research*, *15*(3), 22690-22697.

[14] CM, V. (2025). Transfer learning based deep architecture for lung cancer classification using CT image with pattern and entropy based feature set. *Scientific Reports*, *15*(1), 1-25.

[15] Uddin, A. H., Chen, Y. L., Akter, M. R., Ku, C. S., Yang, J., & Por, L. Y. (2024). Colon and lung cancer classification from multi-modal images using resilient and efficient neural network architectures. *Heliyon*, *10*(9).

[16] Ansari, M. M., Kumar, S., Tariq, U., Belal Bin Heyat, M., Akhtar, F., Bin Hayat, M. A., ... & Pomary, D. (2024). Evaluating CNN architectures and hyperparameter tuning for enhanced lung cancer detection using transfer learning. *Journal of Electrical and Computer Engineering*, *2024*(1), 3790617.

[17] Inbasakaran, G., & Ruth, J. A. (2025). Clinical-Ready CNN Framework for Lung Cancer Classification: Systematic Optimization for Healthcare Deployment with Enhanced Computational Efficiency. *Intelligence-Based Medicine*, 100292.

[18] Haziq, U., Uddin, J., Rahman, S., Yaseen, M., Khan, I., Khan, J., & Jung, Y. (2025). Improving lung cancer detection with enhanced convolutional sequential networks. *Scientific Reports*, *15*(1), 32099.

[19] Saha, A., Ganie, S. M., Pramanik, P. K. D., Yadav, R. K., Mallik, S., & Zhao, Z. (2024). VER-Net: a hybrid transfers learning model for lung cancer detection using CT scan images. *BMC medical imaging*, *24*(1), 120.

[20] Alsubai, S. (2024). Transfer learning based approach for lung and colon cancer detection using local binary pattern features and explainable artificial intelligence (AI) techniques. *PeerJ Computer Science*, *10*, e1996.

[21] Podder, P., Alam, F. B., Mondal, M. R. H., Hasan, M. J., Rohan, A., & Bharati, S. (2023). Rethinking densely connected convolutional networks for diagnosing infectious diseases. *Computers*, *12*(5), 95.

[22] Golcuk, A., Yasar, A., Saritas, M. M., & Erharman, A. (2023). Classification of Cicer arietinum varieties using MobileNetV2 and LSTM. *European Food Research and Technology*, *249*(5), 1343-1350.

[23] Uddin, J. (2024). Attention-based DenseNet for lung cancer classification using CT scan and histopathological images. *Designs*, *8*(2), 27.

[24] Mahmoud, M. A., Wu, S., Su, R., Wen, Y., Liu, S., & Guan, Y. (2025). Classifiers Combined with DenseNet Models for Lung Cancer Computed Tomography Image Classification: A Comparative Analysis. *Current Medical Imaging*, *21*(1), E15734056399377.