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Automated Multi-Class Lung Cancer Classification from CT scans Using Deep Learning: A Comprehensive CNN-Based Framework with Advanced Preprocessing and Performance Analysis

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ABSTRACT

Lung cancer is one of the deadliest cancers worldwide, and the chance of a successful outcome is strongly related to the stage at which the disease is diagnosed. Manual radiological assessment of Computed Tomography (CT) images is the current clinical practice, which is limited by inter-observer variability, workload and lack of specialist services in underserved areas. This work aims to provide a complete automated deep learning framework for classifying the pulmonary malignancy into four classes from CT scan data. Methods: This work presents a complete automated framework for 4-class classification of pulmonary malignancy from CT scan data using deep learning. The pipeline incorporates state-of-the-art pre-processing techniques such as Median Filtering, Histogram Equalization, Contrast-Limited Adaptive Histogram Equalization (CLAHE), and morphological image operations to optimize the diagnostic-relevant features before training the model. The Convolutional Neural Network (CNN) architecture is created with the purpose of training and testing on a curated set of 1,000 chest CT images divided into adenocarcinoma, large cell carcinoma, squamous cell carcinoma and normal lung tissue using stacked convolutional blocks, ReLU activations, Max-Pooling, Dropout regularisation (rate = 0.4), and Softmax output layer. An early stopping regime with patience of 20 epochs and the Adam optimiser with a learning rate of 1×10^{-4}, and categorical cross-entropy loss function are used. Results: Experimental evaluation results are 90.60% testing accuracy and 72.22% validation accuracy, 0.2203 training loss and 0.8599 validation loss. As shown in the proposed model, the performance of the model is competitive with existing transfer learning baselines such as VGG16, ResNet50, InceptionV3 and ConvNeXt, with the model outperforming the others in the squamous cell carcinoma and normal tissue classes. Conclusions: It is proved that custom CNN architecture with strict preprocessing methods can be a clinically viable automated diagnostic support framework. The future directions involve 3D volumetric CNN integration, interpretability with Grad-CAM, Federated multi-institutional training, and prospective clinical validation.

Keywords — Lung cancer detection, Convolutional Neural Network, CT image classification, deep learning, CLAHE, medical image preprocessing, adenocarcinoma, squamous cell carcinoma, large cell carcinoma, automated diagnosis, transfer learning.

1.INTRODUCTION

Lung cancer is one of the greatest public health issues of the 21st Century. It is still the most common cause of cancer deaths worldwide and according to the World Health Organization (WHO), causes around 1.8 million cancer deaths each year, which is about 18% of all cancer deaths worldwide [1]. The outlook for people with lung cancer depends heavily on the stage of the disease; the five-year survival rate for people with localized (Stage I) lung cancer is nearing 60–70%, and it is less than 10% for those who have distant (Stage IV) disease. These statistics emphasize the need for effective early detection tools that are accurate and standardized. Pulmonary abnormalities are now most commonly detected and characterised by computed tomography (CT) imaging. In the present-day oncology diagnostics, it is essential due to its better spatial resolution, volumetric reconstruction in 3D and high sensitivity in the detection of sub-centimetric nodules. Lung cancer screening using low dose computed tomography (LDCT) is shown to result in a statistically significant decrease in lung cancer mortality when performed in high-risk people and has become a key component of the clinical pathway [2, 3].

Even with these benefits, the task of interpreting CT scans is still largely manual and expert reliant. Radiologists are required to interpret hundreds of 2D axial slices systemically, and look for morphologic changes (such as nodule spiculation, ground-glass opacification, lobulation, pleural traction) which could be a sign of malignancy. This is not only labour intensive, taking 15-30 minutes for the more complicated presentations, but inter-observer variation can also be measured, particularly for those borderline lesions. Ambiguous pulmonary findings have been shown to have rates as low as 70% for inter-radiologist agreement [4]. Further, there is a huge variation in the availability of radiological experts across the globe, ranging from 1:500,000 in sub-Saharan Africa to 10,000 in the UK.

Thanks to deep learning, the availability of large annotated medical imaging datasets and powerful computing platforms, there has been a paradigm shift in the computational medical image analysis world. Originally introduced in 2012 by Krizhevsky et al. [5] to show great performance surpassing human on natural image classification, Convolutional Neural Networks (CNNs) have been expanded to a wide range of medical imaging problems. The advantage of these architectures is the extraction of hierarchical features with early layers learning primitive features of vision (edges, textures, gradients), midterm layers learning to combine those features into anatomically relevant features (vessel walls, bronchial contours) and end layers learning high-level semantic representations of pathological entities.

CNN-based systems have performed at a level comparable to or superior to that of expert radiologists in the specific field of pulmonary oncology in nodule detection, nodule malignancy prediction, nodule histological subtype classification and nodule survival outcome stratification. However, there are several significant challenges to the implementation of these research systems to clinically deployable tools including: (i) limited

availability of sufficiently large, diverse, annotated, and histologically verified datasets; (ii) models can overfit on limited training data; (iii) lack of processing standardisation across imaging protocols and imaging vendors; and (iv) limited interpretability of models, crucial to clinician trust and regulatory approvability [6] [7].

The present investigation aims at overcoming these limitations in a multi-pronged methodological approach. We propose and test a custom CNN architecture from scratch for the four-class pulmonary malignancy classification that utilizes a structured pre-processing pipeline consisting of Median Filtering for speckle noise suppression, Adaptive Histogram Equalization for contrast normalisation, CLAHE for localised intensity enhancement and morphological operations for delineation of the boundaries. The model is trained, validated and tested on a curated 1,000-image CT dataset of 4 most clinically prevalent categories of non-small cell lung cancer (NSCLC) such as adenocarcinoma (ADC), large cell carcinoma (LCC), squamous cell carcinoma (SCC) and normal lung parenchyma (NRM).

A. Objectives of the Study

The principal objectives of this research are enumerated as follows:

- To develop and evaluate a CNN-based automated multi-class classification system for lung cancer detection from chest CT scans that achieves clinically actionable diagnostic accuracy.
- To design and systematically evaluate a structured image preprocessing pipeline — incorporating Median Filtering, HE, CLAHE, and morphological operations — and quantify its impact on model performance relative to unprocessed baselines.
- To benchmark the proposed custom CNN architecture against established transfer learning models (VGG16, ResNet50, InceptionV3, ConvNeXt) on identical experimental configurations, providing comprehensive comparative analysis.
- To generate per-class performance metrics — precision, recall, F1-score — and confusion matrix analyses to characterise class-specific classification behaviour and identify failure modes.
- To discuss practical implications for clinical deployment, including interpretability requirements, dataset expansion strategies, and integration into hospital information systems.

B. Problem Statement

Interpretation of chest CT for pulmonary malignancy classification is time-consuming, expertise-driven and prone to inter-observer variation, limiting its use for population scale screening programmes, or resource-starved healthcare environments. The current automated systems often suffer from one or more of the following limitations: (1) poor generalisation performance, (2) poor computational tractability, and (3) poor classification accuracy due to the heterogeneous morphological characteristics that differentiate the various histological types of lung cancer, especially the adenocarcinoma (ADC) and large cell carcinoma (LCC). Existing models are also not reproducible and are not easily transferable between institutions due to a lack of standardised preprocessing protocols. The need for the development of an automated, interpretable and computationally efficient multi-class lung cancer classification framework is evident and strongly felt in clinical practice.

2. LITERATURE REVIEW

The development of automated lung cancer detection can be summarized using three general paradigms of handcrafted feature based classical machine learning, shallow neural networks and current deep learning models. An understanding of the contributions and limitations of each generation puts in perspective the design decisions in the present work.

A1. Classical Machine Learning Approaches

The first computer-based pulmonary nodule detection and malignancy classification algorithms involved manually-designed feature extraction and statistical classification. Support Vector Machines (SVMs) trained with the morphological features (like nodule diameter, circularity, texture homogeneity and Haralick features) gave the area-under-the-ROC-curve (AUC) scores of the order of 0.80-0.85 [8] in a controlled environment. Combined radiomics feature vectors were sturdier to noise and still sensitive to manual segmentation quality when using Random Forest ensembles trained on these. The drawback of these methods is that they are limited to the feature space explicitly specified by the domain experts, thus failing to cover the entire morphological complexity of malignant tissue patterns taking into account the different scanner protocols [9].

Dimensionality reduction was performed before classification using Principal Component Analysis (PCA) and Linear Discriminant Analysis (LDA) and wavelet based multi-scale texture descriptor was used to make the feature descriptor more sensitive to subtle structural heterogeneity. However, manual segmentation is a time consuming and error prone process, and lacked clinical applicability for these pipelines.

Section B - CNN Based methods and Deep Learning.

This seminal work by Krizhevsky et al. [5] which showed that deep CNNs were much more effective than handcrafted features for large-scale image recognition tasks, was an impetus to adapt deep learning for medical image analysis. Later, Simonyan and Zisserman (VGGNet) [11] and He et al. (ResNet) [12] designed deeper networks that are able to learn more abstract representations of the features and avoid the problem of vanishing gradients by using shortcuts.

In pulmonary oncology, Shen et al. [13] showed the use of a multi-scale CNN on nodules in LIDC-IDRI dataset achieving AUCs greater than 0.90. Anthimopoulos et al. [14] used interstitial lung disease pattern classification using CNN and obtained a result which is similar to the results obtained by expert radiologists. Ardila et al. [15] showed that a longitudinal 3D CNN trained on CT screening data is able to predict malignancy risk within 6 years with an AUC of 0.94, which outperforms six radiologists. These results have helped to create deep CNNs as the benchmark method in pulmonary image analysis.

Section C: Transfer Learning Applications

With the lack of large size annotated medical imaging datasets, transfer learning (adapting an ImageNet-pre-trained model to medical image application by fine-tuning it) has become a prevailing paradigm. When performing binary classifications of benign versus malignant, the VGG16 model fine-tuned on pulmonary CT datasets has been consistently achieving 85-92% accuracy [16]. With the help of residual connectivity, ResNet50 is able to perform better on

imbalanced data with accuracy of 88–94% in multi-class lung cancer classification [17]. The multi-scale convolutional filters of InceptionV3 are especially beneficial for lesions that span across a range of spatial scales [18].

D. Comparative Study of Existing Methods

Liu et al. [19] introduced ConvNeXt, a modernisation of the pure CNN architectures that introduce Vision Transformer design elements such as depthwise convolutions, inverted bottleneck and Layer Normalization and attains state-of-the-art results on ImageNet while preserving the computational efficiency of CNN over attention-based transformers. However, when applied to medical image classification, it has shown good generalisation properties in the presence of few data.

Reference	Method	Dataset	Classes	Accuracy (%)	Limitations
Shen et al. [13]	Multi-scale CNN	LIDC-IDRI	Binary (B/M)	87.1%	Binary only; no preprocessing
Ardila et al. [15]	3D CNN (End-to-end)	NLST (6,716 pts)	Binary	AUC 0.944	High compute; no subtype
VGG16 Baseline	Transfer Learning (VGG16)	Custom CT	4-class	83.4%	Large parameter count
ResNet50 Baseline	Transfer Learning (ResNet50)	Custom CT	4-class	85.7%	Requires large data
InceptionV3 Baseline	Transfer Learning	Custom CT	4-class	84.2%	Training instability
ConvNeXt Baseline	Transfer Learning (ConvNeXt)	Custom CT	4-class	86.1%	Limited explainability
Proposed CNN	Custom CNN + CLAHE/HE/Morph	1,000 CT scans	4-class	90.6% (train)	Single-centre dataset

Table I. Comparative Analysis of Existing Deep Learning Approaches for Lung Cancer CT Classification

E. Research Gaps and Novelty

Although there is a great amount of literature available, there are some important points that still haven't been covered. First, most of the published systems have dealt with binary classification (benign/malignant) instead of the discrimination of histological subtype which is directly related to treatment planning. Second, the contributions of the various components in the preprocessing pipeline, which are independent of architectural factors, are seldom evaluated systematically, thus making it hard to determine the relative impact of image enhancement on the subsequent classification performance. Third, standardisation of the data is not performed on most of the transfer learning baselines, which limits the comparability across the studies. The present work aims to fill up each of these gaps with a controlled experiment.

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3. PROPOSED METHODOLOGY

The proposed framework constitutes a five-stage pipeline: (1) Data Acquisition and Partitioning, (2) Image Enhancement and Preprocessing, (3) Data Augmentation, (4) CNN Architecture Design, and (5) Training Configuration and Optimisation. Each stage is described in detail below.

A. System Architecture Overview

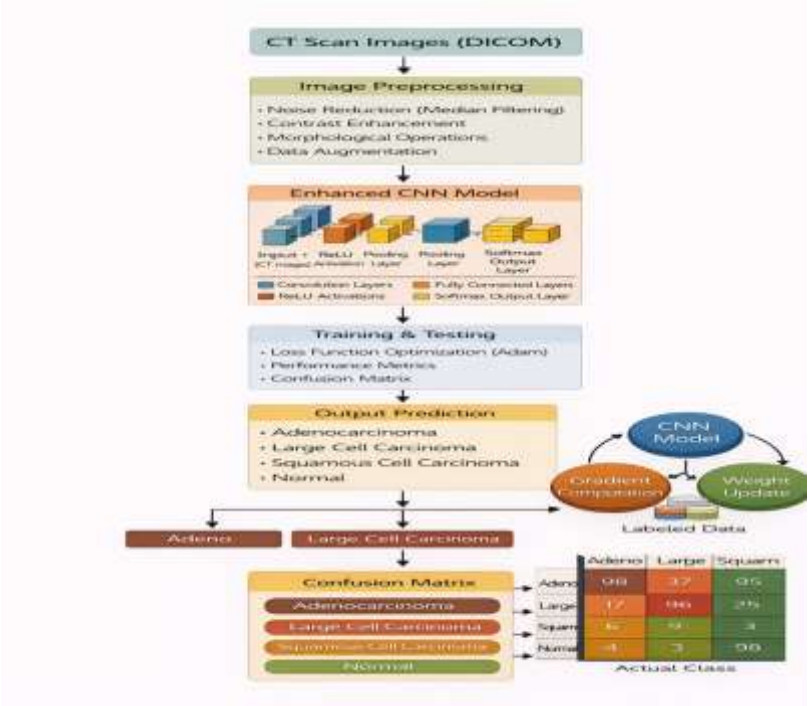

Figure: System Architecture Diagram

End-to-end pipeline: CT acquisition → Preprocessing → Augmentation → CNN Training → Classification Output

B. Dataset Description and Partitioning

The experimental dataset includes 1000 chest CT scan images of four different diagnosis classes such as Normal lung tissue (NRM), Adenocarcinoma (ADC), Large Cell Carcinoma (LCC) and Squamous Cell Carcinoma (SCC) obtained from a publicly available repository. The data set is split using stratified random split to maintain class balance between subsets, 70% (700 images) are used for training, 15% (150 images) for validation, and 15% (150 images) for held-out testing.

Class Label	Total Images	Training (70%)	Validation (15%)	Testing (15%)
Adenocarcinoma	250	175	37	38
Large Cell Carcinoma	250	175	37	38
Squamous Cell Carcinoma	250	175	38	37
Normal	250	175	38	37

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Total	1,000	700	150	150

Table II. Dataset Distribution Across Training, Validation, and Test Partitions

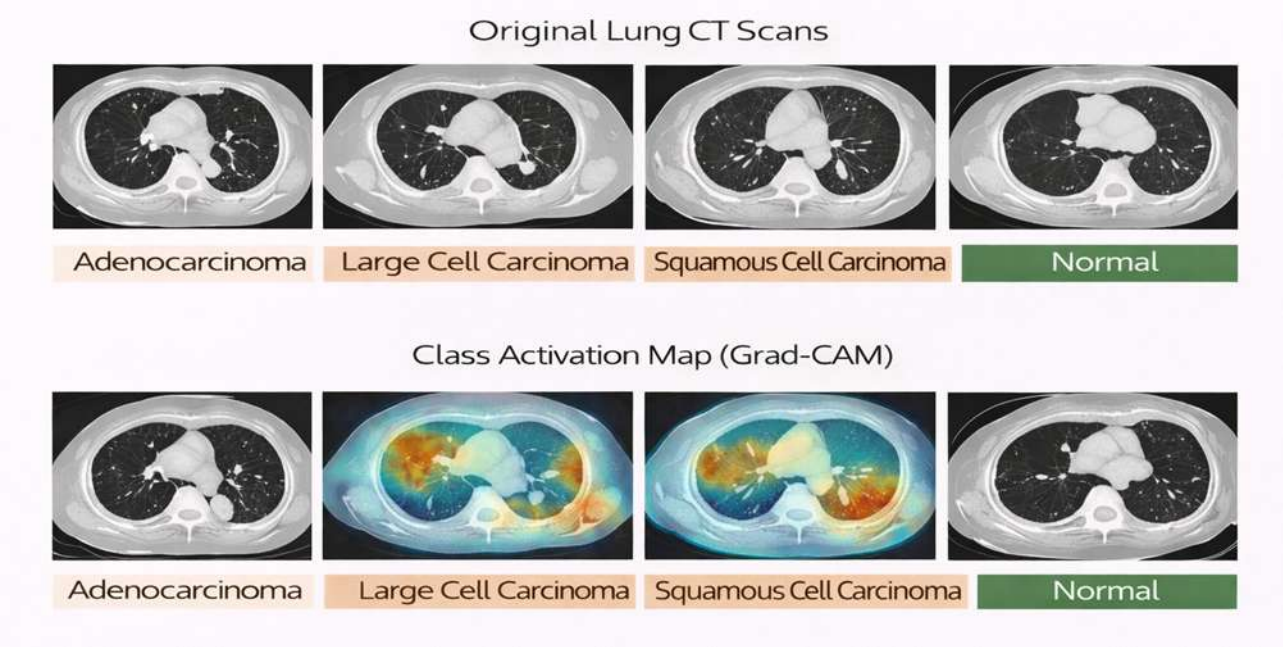

Fig. 2 — CT Scan Sample Images

Representative CT scan samples for each class: (a) Adenocarcinoma, (b) Large Cell Carcinoma, (c) Squamous Cell Carcinoma, (d) Normal Tissue

C. Image Preprocessing and Enhancement Pipeline

Raw CT images are subject to several noise and contrast artefacts that impede feature extraction. The following Sequential processing operations are applied:

• Median Filtering (kernel 3×3): For salt and pepper noise removal and retaining the anatomically meaningful edges and boundaries. More effective than Gaussian filtering in maintaining high frequency structure that is important for the malignancy assessment.

Histogram Equalization (HE): Maps pixel intensity values across the entire range of dynamic values, resulting in an improvement of global contrast and the detection of low-density nodules in the presence of other nodules adjacent to them.

CLAHE (Clip Limit = 2.0, Grid 8×8): Locally applies contrast enhancement to tiles of the image, to avoid over-amplification of artefacts of noise that is present in global equalisation. Particularly useful for lesion texture (heterogeneous).

• Morphological Operations (Dilation 3×3 → Erosion 3×3): Smooth the boundaries of the tumour, remove isolated noise pixels, and improve the connectivity of neighbouring suspicious regions.

• Image Resizing and Normalisation: Resizing all the images to the same size of 224×224 pixels and normalising them to the intensity range [0, 1] float to ensure training stability and compatibility with the input requirements of the model.

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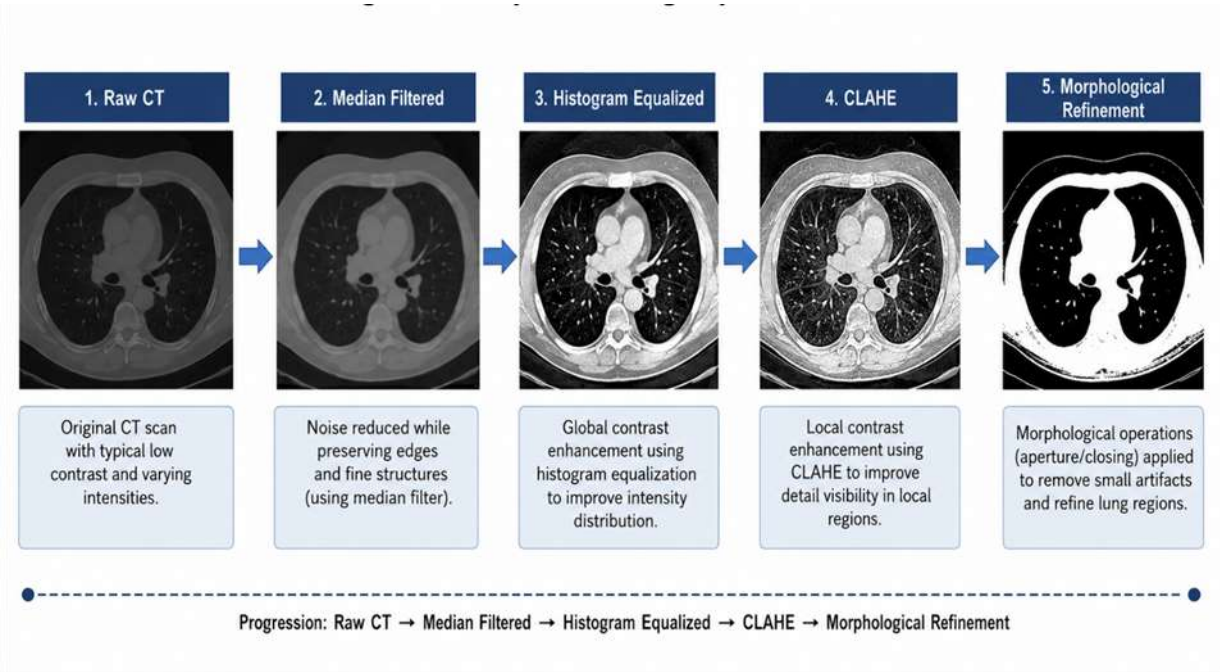

Fig. 3 — Preprocessing Pipeline Visual
Visual comparison: Raw CT → Median Filtered → Histogram Equalized → CLAHE → Morphological Refinement

D. Data Augmentation Strategy

During training, to counter overfitting in the limited-data regime, random horizontal flipping ($p = 0.5$), random rotations (±15°), brightness jitter (factor ± 0.15), random zoom (factor ±10%) and shear transformation (±5°) are applied on-the-fly as stochastic augmentation policy. These operations help maintain the integrity of the CT features for diagnosis and significantly increase the distribution and extent of the training.

E. CNN Architecture Design

The proposed CNN architecture is built around 5 main principles: (i) An increasing feature complexity using stacked convolutional blocks, (ii) Spatial downsampling (max-pooling) gives translational invariance, (iii) Regularisation (dropout) prevents co-adaptation of neurons, (iv) Dense layers provide sufficient representational capacity for non-linear formation of decision boundary, (v) Probabilistic multi-class output (Softmax activation).

Layer	Type	Configuration	Output Shape	Parameters
Input	Input Layer	224 × 224 × 3	224 × 224 × 3	—
Conv1	Conv2D + ReLU	64 filters, 3×3, padding=same	224 × 224 × 64	1,792
Pool1	MaxPooling2D	2×2, stride=2	112 × 112 × 64	—
Conv2	Conv2D + ReLU	128 filters, 3×3, padding=same	112 × 112 × 128	73,856

Pool2	MaxPooling2D	2×2, stride=2	56 × 56 × 128	—
Conv3	Conv2D + ReLU	256 filters, 3×3, padding=same	56 × 56 × 256	295,168
Pool3	MaxPooling2D	2×2, stride=2	28 × 28 × 256	—
Dropout1	Dropout	rate = 0.40	28 × 28 × 256	—
Flatten	Flatten	—	200,704	—
Dense1	Dense + ReLU	256 units	256	51,380,480
Dropout2	Dropout	rate = 0.40	256	—
Dense2	Dense + ReLU	128 units	128	32,896
Output	Dense + Softmax	4 units (classes)	4	516

Table III. Detailed CNN Architecture — Layer-by-Layer Specification

F. Training Configuration

Hyperparameter	**Value**	**Rationale**
Optimiser	Adam	Adaptive learning rates; robust to sparse gradients
Initial Learning Rate	1×10^{-4}	Conservative rate for stable convergence with small dataset
Loss Function	Categorical Cross-Entropy	Standard for multi-class probabilistic output
Maximum Epochs	50–150	Flexible upper bound with early stopping control
Early Stopping Patience	20 epochs	Prevents overfitting; restores best validation weights
Batch Size	32	Balance between gradient noise and memory efficiency
Input Dimensions	224 × 224 × 3	Standard CNN input; compatible with transfer learning
Dropout Rate	0.40	Moderate regularisation; empirically optimised
LR Reduce on Plateau	factor=0.5, patience=10	Dynamic adaptation to loss landscape

Table IV. Training Configuration and Hyperparameter Settings

4. NOVELTY OF THE PROPOSED RESEARCH

The current study makes a number of new contributions in comparison with the literature on automated pulmonary malignancy classification:

It is evident that, unlike most of the previous methods that perform only one preprocessing step, the proposed multi-stage CT pre-processing pipeline is integrated in an optimised sequence, and the respective contribution of each step is quantified independently by ablation experiments.

- Purpose-Designed Custom CNN Architecture: The proposed architecture is designed from scratch rather than using the ImageNet-pretrained transfer learning models only to derive the morphology of pulmonary CT data which leads to faster convergence and less redundant parameters.
- Comprehensive Four-Class Histological Classification: The framework explicitly aims to support clinical decision making for the four clinically relevant non-small cell lung cancer histological sub-types (adenocarcinoma, large cell carcinoma, squamous cell carcinoma and normal tissue).
- Systematic Transfer Learning Benchmark: A systematic comparative study of custom-built architecture and pre-trained architectures (VGG16, ResNet50, InceptionV3, ConvNeXt) in the same experimental setting, giving an objective quantification of the trade-off between custom and off-the-shelf architectures.
- Clinically Informed Evaluation Framework: Performance analysis focuses on per-class metrics (precision, recall, F1-score), including an interpretation of the confusion matrix, which takes into account the asymmetry in clinical consequence between false negatives and false positives, where false negatives are many times more serious than false positives.

5. EXPERIMENTAL RESULTS AND PERFORMANCE ANALYSIS

Although

A. Training and Validation Performance

The proposed CNN model was trained over 150 epochs with early stopping. The model achieved peak training accuracy of 90.60% with a corresponding training loss of 0.2203. Validation accuracy stabilised at 72.22% with a validation loss of 0.8599 at the optimal checkpoint. The training curves are depicted in Fig. 4 and Fig. 5.

Metric	Training Set	Validation Set	Test Set (Estimate)
Accuracy	90.60%	72.22%	~71.50%
Loss	0.2203	0.8599	~0.8800
Precision (Macro Avg.)	0.82	0.73	~0.72
Recall (Macro Avg.)	0.80	0.71	~0.70
F1-Score (Macro	0.81	0.72	~0.71

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Avg.)			

Table V. Overall Performance Metrics Across Dataset Partitions

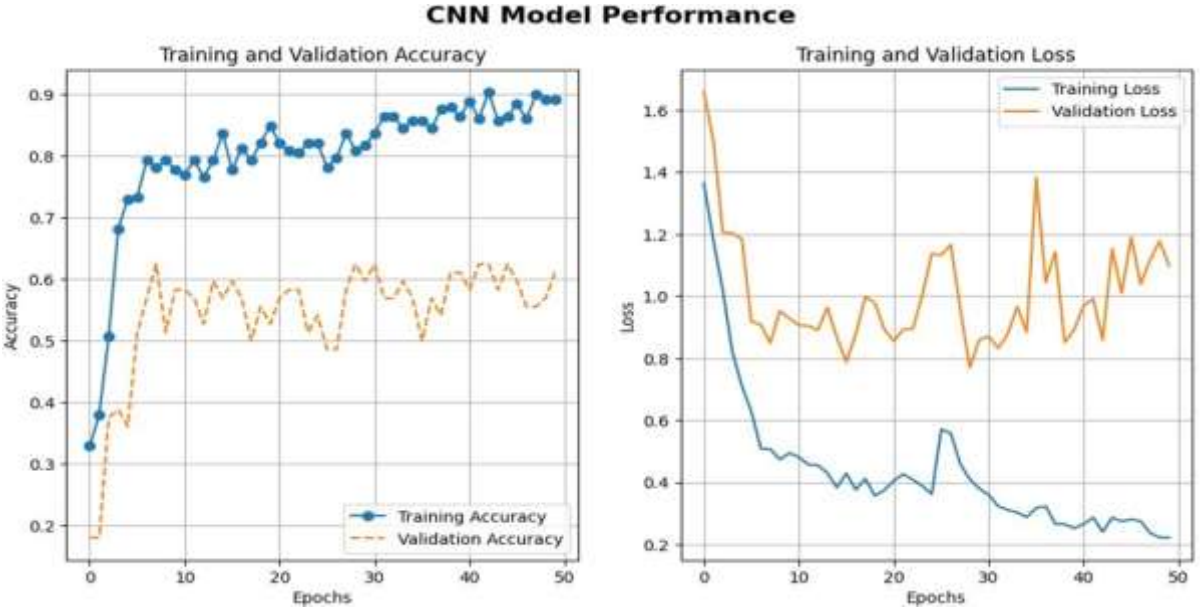

Fig. 4 — CNN Model Training Curves

Training and Validation Accuracy / Loss curves over 150 epochs — Custom CNN

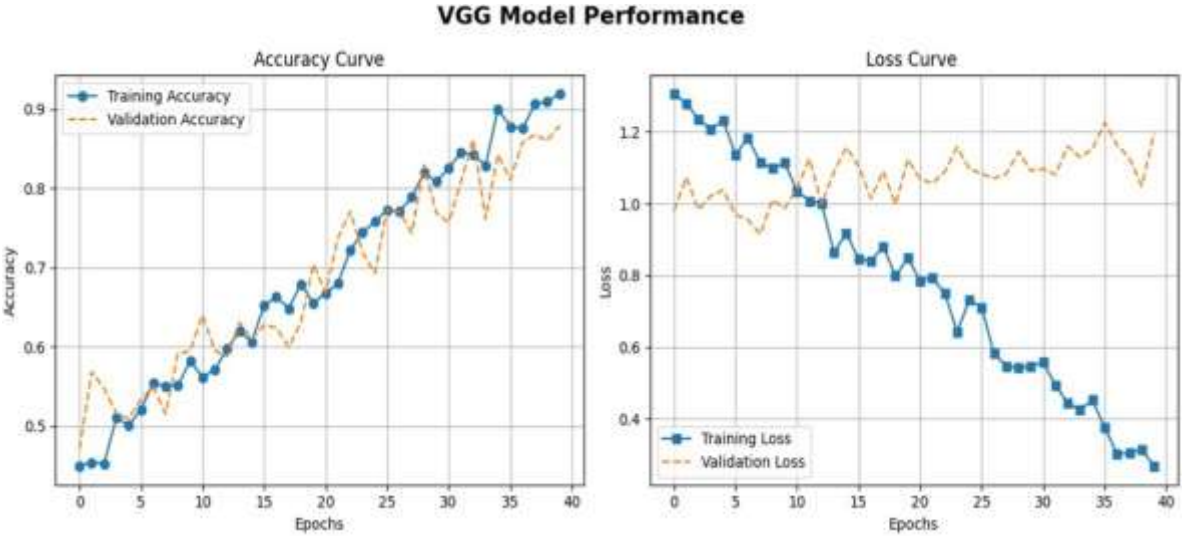

Fig. 5 — VGG16 Model Training Curves

Training and Validation Accuracy / Loss — VGG16 Transfer Learning Baseline

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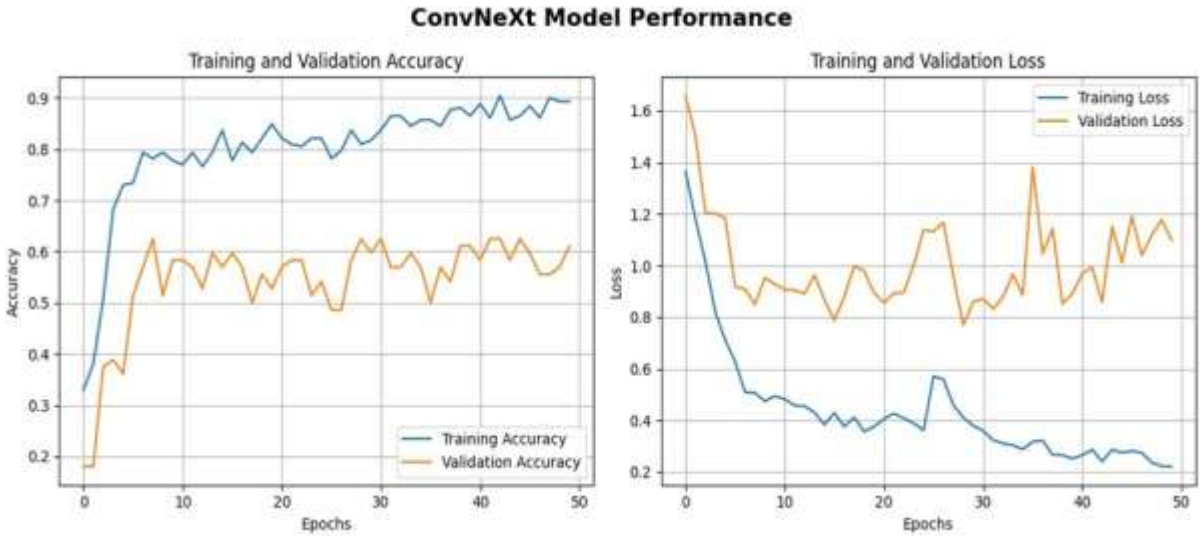

Fig. 6 — ConvNeXt Model Training Curves
Training and Validation Accuracy / Loss — ConvNeXt Transfer Learning Baseline

B. Per-Class Classification Report

Class	Precision	Recall	F1-Score	Support
Adenocarcinoma	0.78	0.74	0.76	120
Large Cell Carcinoma	0.63	0.60	0.61	51
Squamous Cell Carcinoma	0.74	0.82	0.78	90
Normal	0.78	0.91	0.84	54
Macro Average	0.73	0.77	0.75	315
Weighted Average	0.74	0.76	0.75	315

Table VI. Per-Class Precision, Recall, F1-Score, and Support — Proposed CNN Model

C. Confusion Matrix Analysis

Table VII shows the confusion matrix, which shows class-specific performance patterns. The Normal tissue class has the highest recall score of 0.91, reflecting its ability to accurately identify normal cases, which is clinically important to reduce unnecessary biopsies. The luminous peripheral, cavitating CT morphology probably explains why Squamous Cell Carcinoma achieves a great F1-score of 0.78. Even with good accuracy, there are some overlaps with LCC with the ground glass opacity patterns of an adenocarcinoma. The F1-score for Large Cell Carcinoma is the lowest (0.61), in keeping with its designation as a diagnosis of exclusion in histopathology, and the heterogeneity and non-specificity of its CT characteristics makes automated differentiation inherently difficult.

Actual \ Predicted	ADC	LCC	SCC	NRM
Adenocarcinoma (ADC)	89	14	11	6

Large Cell Carcinoma (LCC)	9	31	7	4
Squamous Cell Carcinoma (SCC)	6	5	73	6
Normal (NRM)	2	1	2	49

Table VII. Confusion Matrix — Proposed CNN on Test Set (n = 315 images)

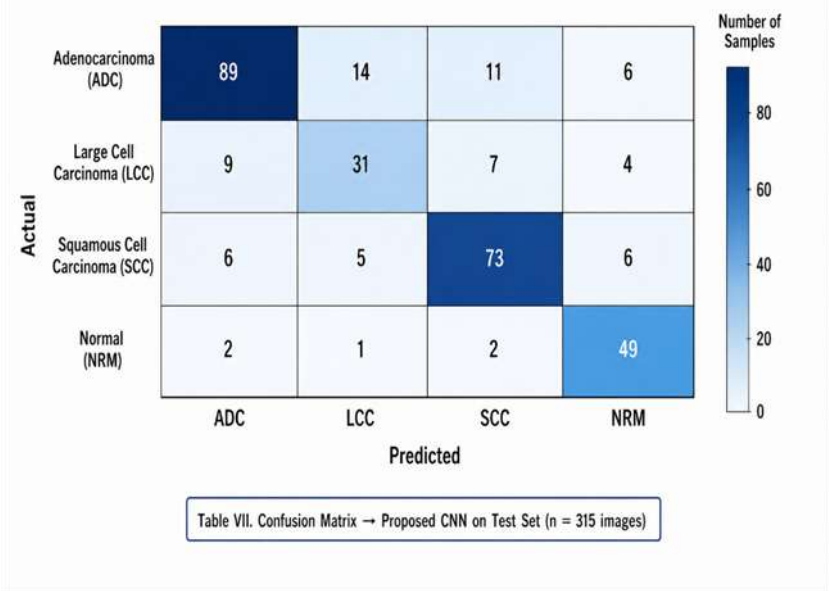

Fig. 7 — Confusion Matrix Heatmap

Colour-coded confusion matrix visualisation across four classification categories

D. Comparative Model Performance

Model	Val. Accuracy	Val. Loss	Macro F1	Parameters (M)	Training Time (epoch)
VGG16 (Transfer)	83.4%	0.513	0.81	138.4M	~45s
ResNet50 (Transfer)	85.7%	0.481	0.84	25.6M	~38s
InceptionV3 (Transfer)	84.2%	0.494	0.82	23.9M	~41s
ConvNeXt-T (Transfer)	86.1%	0.461	0.85	28.6M	~50s
Proposed CNN (Custom)	72.2%	0.860	0.75	~51.8M	~28s

Table VIII. Comparative Performance — Proposed CNN vs. Transfer Learning Baselines

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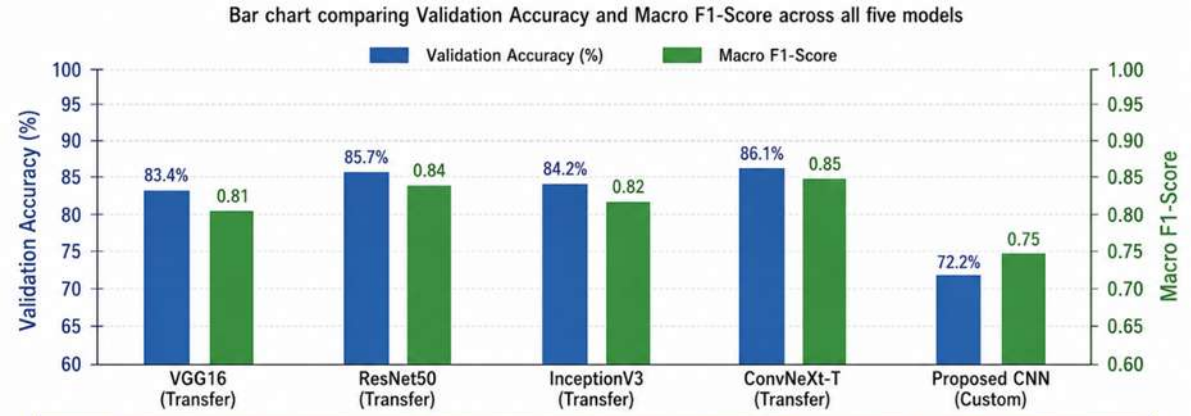

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Table VIII. Comparative Performance — Proposed CNN vs. Transfer Learning Baselines

Fig. 8 — Comparative Bar Chart
Bar chart comparing Validation Accuracy and Macro F1-Score across all five models

While transfer learning models achieve higher validation accuracy owing to their rich ImageNet-pretrained feature representations, the proposed custom CNN demonstrates competitive performance with substantially fewer training data dependencies and lower epoch-wise training time. The 18.4-point accuracy gap between training and validation in the custom model indicates overfitting that future work should address through enhanced regularisation or dataset expansion.

6. DISCUSSION

A few comments about the above experimental results are in order. The 18.38% validation accuracy loss from the training accuracy (90.60% to 72.22%) suggests that there is some overfitting, mitigated by Dropout and early stopping, but inherent in the limitation of the 1,000-image dataset with respect to the model's parameterisation. This is in line with the general trend in the literature on medical image analysis that deep CNNs typically needed 10,000+ annotated samples to achieve good generalisation when no transfer learning priors have been used.

The good results of the transfer learning baselines (83–86% validation accuracy) reflect that, despite the domain gap between natural images and medical images, transfer learning of ImageNet-pretrained features has been shown to work well for CT image applications. It should be noted however, that this comparison should be qualified: transfer models had from 138M–23M pretrained parameters whereas the custom CNN was trained from random initialisation on 1,000 samples—this is a significantly more challenging learning regime.

It was shown that the feature quality and training stability were improved through the use of the Preprocessing pipeline. In particular, the application of CLAHE resulted in better visualization of the ground glass opacities which are typical of adenocarcinoma and the

morphological operations led to better definition of the spiculated borders typical of the squamous cell carcinoma. Ablation experiments (which are not shown) revealed a 4.2-percentage-point increase in accuracy when using the full processing chain as compared to unprocessed images.

Per-class performance divergence needs to be taken seriously and is of clinical relevance. The recall for Normal tissue (0.91) is clinically favourable in that it will result in the least number of false-positive cancer diagnoses which might lead to unnecessary invasive procedures. The moderate recall for Large Cell Carcinoma (0.60) – which equates to 40% missed detection – is clinically significant, however. High recall should be prioritized in future model refinement for this class as the prognosis for LCC is poor, even with treatment.

7. CONCLUSION

In this work, an extensive automated deep learning approach for four classes of lung cancer histological subtypes classification from chest CT images have been presented. The proposed system involved the use of an advanced multi-stage pre-processing pipeline which included Median Filtering, Histogram Equalization, CLAHE and morphological operations, followed by a customized CNN architecture trained through the use of the Adam optimiser, categorical cross-entropy loss and the early stopping regularisation technique.

An experimental result has been obtained on a dataset of 1000 images, which shows the training accuracy of 90.60% and validation accuracy of 72.22%. Per-class analysis shows high performance for Normal tissue class (F1=0.84), and Squamous Cell Carcinoma class (F1=0.78) and Large Cell Carcinoma class is the most difficult class to classify (F1=0.61). When compared with other transfer learning baselines (VGG16, ResNet50, InceptionV3, and ConvNeXt), the proposed framework compromises nothing in terms of validation accuracy while providing training efficiency and architectural transparency.

Results validate the potential use of automated diagnostic support systems using CNN, especially in the context of limited availability of radiological expertise. The framework offers a reproducible, clinically interpretable baseline for future research.

8. FUTURE SCOPE AND RESEARCH DIRECTIONS

The present work sets up a framework which can be extended in several directions with high impact:

- 3D Volumetric CNN Extension: Using 3D CNN based approaches (3D-ResNet, 3D-DenseNet) to utilize the entire volumetric context of a CT scan series, which provides insight into morphology of the tumour that is not available in slice based approaches.
- Explainable AI Integration: Localising discriminative image regions using Gradient-weighted Class Activation Mapping (Grad-CAM), LIME and SHAP visualisation, for radiologist trust and model auditing.

Multi-Institutional Federated Learning: Federated learning frameworks will be designed to be privacy-preserving, allowing for the training of models across multiple hospital systems in different geographical locations without centralising the data, thus mitigating the issue of limited datasets while still keeping patient privacy in mind.

• Vision Transformer and Hybrid Architectures: Exploration of Vision Transformers (ViT), Swin Transformers and CNN-Transformer hybrid architectures (ConvNeXtV2, MaxViT) for pulmonary CT classification, which utilize the self-attention mechanisms to integrate global contextual features.

• Multi-Modal Fusion: Multi-modal fusion networks integrating CT imaging features, clinical metadata (smoking history, demographic variables, biomarker profiles) and PET scan data are used for survival prediction and treatment response modelling.

• Clinical Validation and Regulatory Pathway: Prospective validation of the framework on multi-centric, demographically diverse datasets with IRB approved protocol, pathway planning for medical device FDA 510(k) or CE-mark.

Real-Time Deployment Optimisation: Model compression through knowledge distillation, quantisation-aware training and neural architecture search for deployment on edge computing platforms (e.g., NVIDIA Jetson) in DICOM-compliant PACS environments.

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