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Recent Advances in Deep Learning for Detecting and Classifying Lung Cancer – A Review

Harsha G[1], Dr. Suresh M[2]

Research Scholar, Sri Siddartha Academy of Higher Education, Tumkur[1]

Professor, Department of Electronics and Communication Engineering, Sri Siddartha Institute of Technology, Tumkur[2]

Abstract: Cancer is recognized as one of the most severe health threats, causing millions of deaths worldwide each year. Among its various types, lung cancer stands out as the most aggressive, with the highest mortality rate. Hence, the development of reliable and precise methods for detecting lung cancer is critical to ensure timely and effective treatment. Designing a strong and accurate classification model is particularly important in medical diagnostics. Due to its widespread occurrence and tendency to remain hidden during the initial stages, lung cancer underscores the urgent need for efficient detection and classification techniques. Globally, it is one of the most common and deadliest cancers, making a significant contribution to cancer-related deaths. Its silent progression during early phases often leads to late diagnosis, when treatment options become less effective.

Robust classification systems can help bridge this diagnostic gap by identifying subtle and complex patterns in medical images. Positron Emission Tomography (PET) is widely applied for diagnosing and staging multiple cancers, including lung, liver, and lymphoma. Correct subtype identification is vital for tailoring effective treatment strategies. For instance, lung cancer includes subtypes such as adenocarcinoma, squamous cell carcinoma, and small cell carcinoma, while liver cancer can present as hepatocellular carcinoma or cholangiocarcinoma. Likewise, lymphoma has categories such as Hodgkin’s lymphoma and diffuse large B-cell lymphoma. Subtype classification using PET imaging, therefore, carries substantial clinical importance. However, a key limitation in real-world clinical settings is the scarcity and imbalance of subtype-specific datasets. The major challenge, then, is achieving accurate subtype classification when working with limited data.

Keywords: Lung Cancer, Positron Emission Tomography, early-stage manifestation

I. INTRODUCTION

Lung cancer poses a serious global health challenge, ranking as one of the leading causes of cancer-related deaths. The significance of early detection and precise classification cannot be overstated, as these factors directly influence patient survival and treatment strategies. This disease results from uncontrolled cell proliferation in lung tissues, leading to malignant tumour formation that can metastasize to other parts of the body. Lung cancer is generally categorized into two major types: non-small cell lung cancer (NSCLC) and small cell lung cancer (SCLC). With an estimated 2.2 million new cases reported in 2020, its worldwide prevalence highlights the urgent demand for effective control measures. Although breast cancer overtook lung cancer in 2020 as the most frequently diagnosed cancer, lung cancer still accounted for the highest mortality, with approximately 1.8 million deaths.

At present, tumour subtype classification through medical imaging can be divided into two main approaches: radiomics-based techniques and deep learning-based techniques. Radiomics methods involve the extraction of biologically and clinically relevant features from tumour regions using predefined manual feature calculation rules. These features are then processed by classifiers for subtype determination. Various tools and libraries, such as SERA, Pyradiomics, and Lifex, support radiomics feature extraction. Although interpretable, radiomics methods often suffer from poor generalizability due to the task-specific nature of the features and their reliance on expert domain knowledge.

Conversely, deep learning approaches address subtype classification by developing end-to-end networks that automatically extract and learn relevant features, thereby eliminating the need for manual feature engineering. However, these models require large volumes of annotated training data to perform effectively. In practical scenarios, subtype datasets are often limited and imbalanced, restricting the performance of deep classification networks. Moreover, traditional radiomics features, such as tumour shape, volume, and texture — which are essential for distinguishing multiple subtypes — may not always be effectively captured by deep learning models.

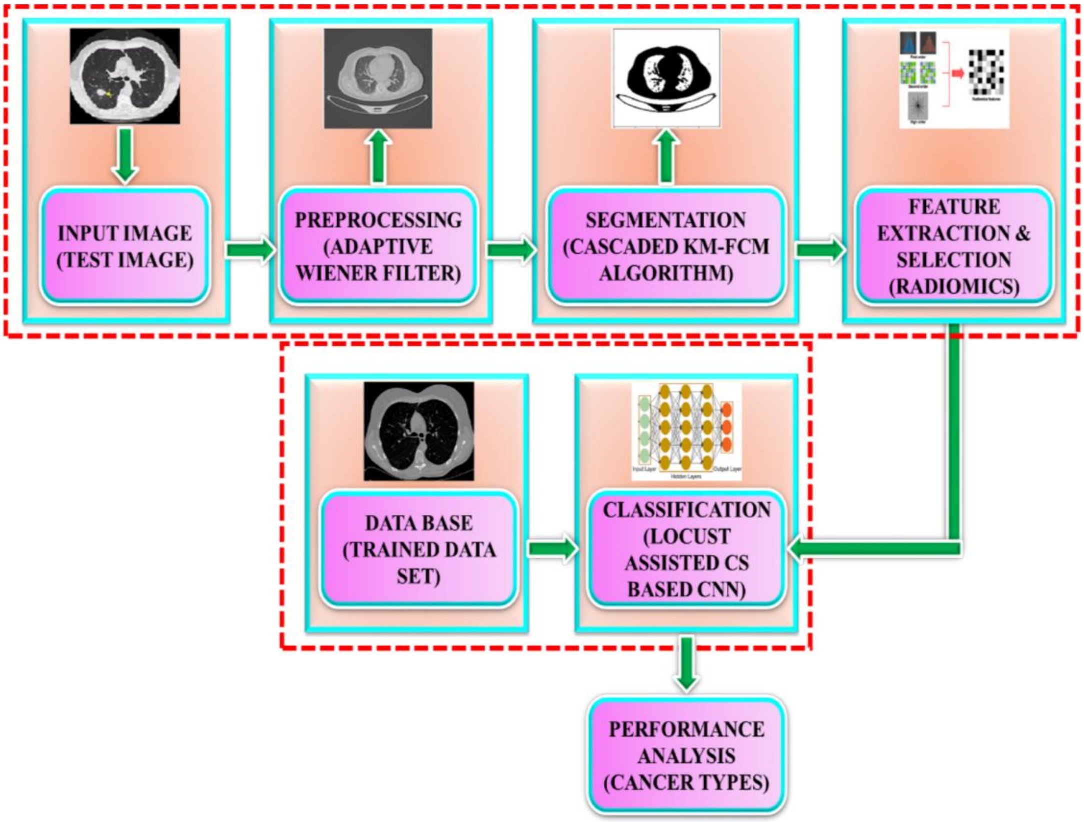

Figure 1. Proposed Block Representation.

The impact of lung cancer is far more severe than many other cancer types, as it leads to serious health complications and contributes to higher mortality rates worldwide. This deadly disease results from abnormal and uncontrolled growth of cells in lung tissues. While such malignant growth can develop in any region of the lungs, it most commonly originates from the epithelial cells lining the respiratory tract. Detecting the disease at an early stage is crucial, as it enables the identification of pulmonary nodules that develop into tumours. Unfortunately, lung cancer is often diagnosed in its advanced stages, which reduces the chances of timely intervention and lowers survival prospects. Statistically, the average five-year survival rate following diagnosis is approximately 15%. However, if lung cancer is detected early, this rate can rise dramatically to nearly 70%. This underscores the importance of early clinical detection in improving patient outcomes.

Manually measuring tumour volumes in lung tissues presents a complex and labour-intensive challenge. Radiologists are required to examine numerous CT or MRI images carefully to locate and assess tumours, a process that is both time-consuming and vulnerable to human error. By contrast, modern image processing techniques provide greater precision, reliability, and efficiency, allowing large datasets of medical images to be analyzed quickly and consistently. These technologies significantly enhance the ability to detect tumours, especially those in early or small stages, which are critical for effective treatment planning and better survival rates. Thus, the integration of image processing in medical diagnostics simplifies lung cancer detection by enhancing images and extracting relevant features that support accurate and timely identification.

II. DEEP LEARNING

Deep learning (DL), a branch of artificial intelligence, has become a powerful solution for addressing the challenges of lung cancer (LCa) detection and classification. Traditional methods rely heavily on handcrafted features and heuristic algorithms, which often fail to capture the complex and subtle patterns present in medical images. By contrast, DL models are capable of autonomously learning and extracting meaningful features directly from raw image data, enabling them to identify irregularities and structures associated with malignant growths. This ability to learn from large datasets makes DL particularly effective for medical imaging applications, where precision and detail are essential.DL models excel at capturing fine-grained and intricate features in lung scans that conventional approaches often overlook. Their proven success in other areas of medical imaging further strengthens their relevance in lung cancer diagnostics. For example, in radiology, DL has consistently demonstrated outstanding accuracy in detecting abnormalities in both X-rays and CT scans, often surpassing human performance in terms of precision and efficiency. A key advantage of DL lies in transfer learning, where pre-trained models can be refined using smaller medical datasets by leveraging knowledge from large, diverse datasets in related fields. This capability accelerates model development, improves generalization, and supports integration into medical research and clinical practice.

In lung cancer applications, DL has shown strong potential for detecting pulmonary nodules, classifying tumour subtypes, and even predicting patient outcomes. Its ability to uncover hidden patterns in CT scans enables earlier and more accurate diagnoses, leading to timely interventions. Moreover, DL models can integrate additional patient data — including medical history, genetic profiles, and clinical records — providing a more comprehensive picture of disease progression.Most lung cancer detection studies employ CT imaging due to its effectiveness in visualizing nodules. Since lung cancer often arises from a combination of genetic and biochemical abnormalities, the use of DL in analysing these imaging datasets is particularly valuable. For instance, EfficientNetB4 has shown impressive results in detecting lung disease from chest X-rays, accurately identifying affected patients. More broadly, AI-driven DL systems are increasingly effective in analysing large-scale patient datasets to support disease diagnosis. By enabling early detection, these systems significantly reduce mortality risks and improve survival rates.

Given the massive volume of medical image data, manual analysis is both time-consuming and error-prone. Reliable DL models are therefore essential to accurately and efficiently identify lung cancer. In clinical settings, DL improves diagnostic speed and accuracy, enabling faster treatment decisions and better outcomes. Beyond lung cancer, DL has enhanced patient care in other contexts, such as breast cancer, by supporting physician decision-making and improving treatment planning. Overall, DL represents a highly promising approach for lung cancer detection and classification. Its data-driven adaptability, combined with success across diverse imaging domains, positions it as a transformative tool. By harnessing its capabilities, researchers and clinicians can advance diagnostic methods and significantly improve patient care.

III. RELATED WORKS

The proposed model utilizes the IQ-OTH/NCCD lung cancer dataset to classify cases into normal, benign, or malignant categories. The novelty of this research lies in the introduction of the MHA-DCNN, a state-of-the-art framework designed to overcome key limitations of conventional lung cancer classification models. Traditional deep learning approaches often struggle with overfitting, high computational demands, and poor generalization across heterogeneous datasets.To address these challenges, the MHA-DCNN integrates a multi-head attention mechanismwith depthwise convolutions, enabling the network to focus on the most informative regions of CT scan images while maintaining computational efficiency. This integration enhances spatial awareness and significantly reduces overfitting, a common issue in existing methods.The framework's efficiency is further strengthened through the incorporation of the EBWO algorithm for feature selection, which filters out redundant and irrelevant attributes from the extracted dataset. This process reduces computational complexity and ensures that only discriminative features contribute to classification. Additionally, AEO-based hyperparameter tuning dynamically adjusts learning parameters during training, allowing the model to adapt to diverse data distributions and achieve optimal performance.

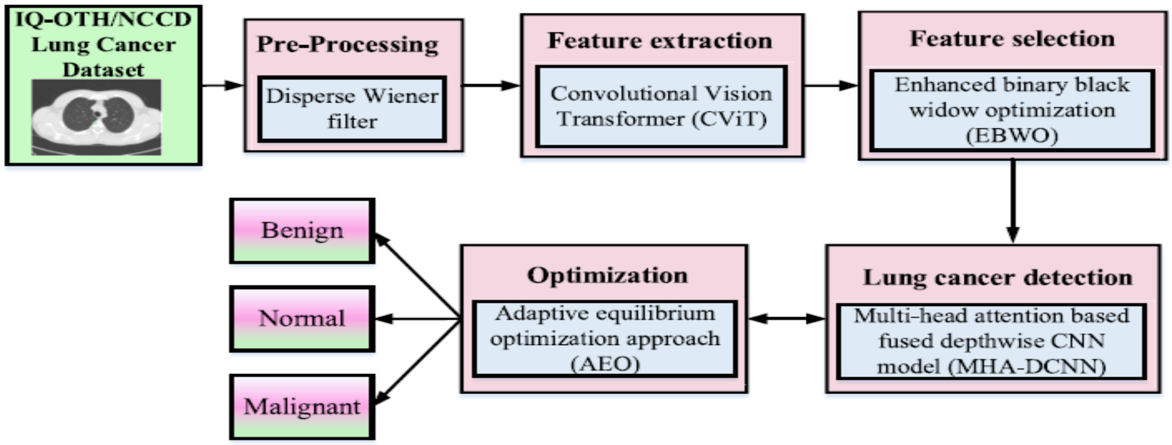

Figure 2. Graphical workflow of the proposed model (Sadam Kavitha et al., 2025).

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By combining multi-head attention, depthwise convolutions, feature selection, and adaptive optimization, the proposed MHA-DCNN delivers superior classification accuracy and robustness. It effectively addresses real-world challenges such as noise reduction, feature redundancy, and parameter optimization, thereby setting a new benchmark in lung cancer detection using CT images.Figure 2 presents a schematic of the proposed framework. Initially, CT scan data from the IQ-OTH/NCCD dataset undergoes pre-processing to eliminate noise. Next, features are extracted from the cleaned images, followed by selection of the most relevant attributes. Finally, the MHA-DCNN model classifies the cases into benign or malignant tumours based on these optimized features.

This study introduces an effective model, termed SpiLenet, for lung cancer detection. The process begins with the acquisition of CT images from a publicly available dataset, which are then subjected to pre-processing using an SG filterto minimize noise. Following pre-processing, lung lobe segmentation is performed with the help of DRINet, after which a grid-based approach is employed to identify lung nodules. From the segmented regions, a comprehensive set of features is extracted.

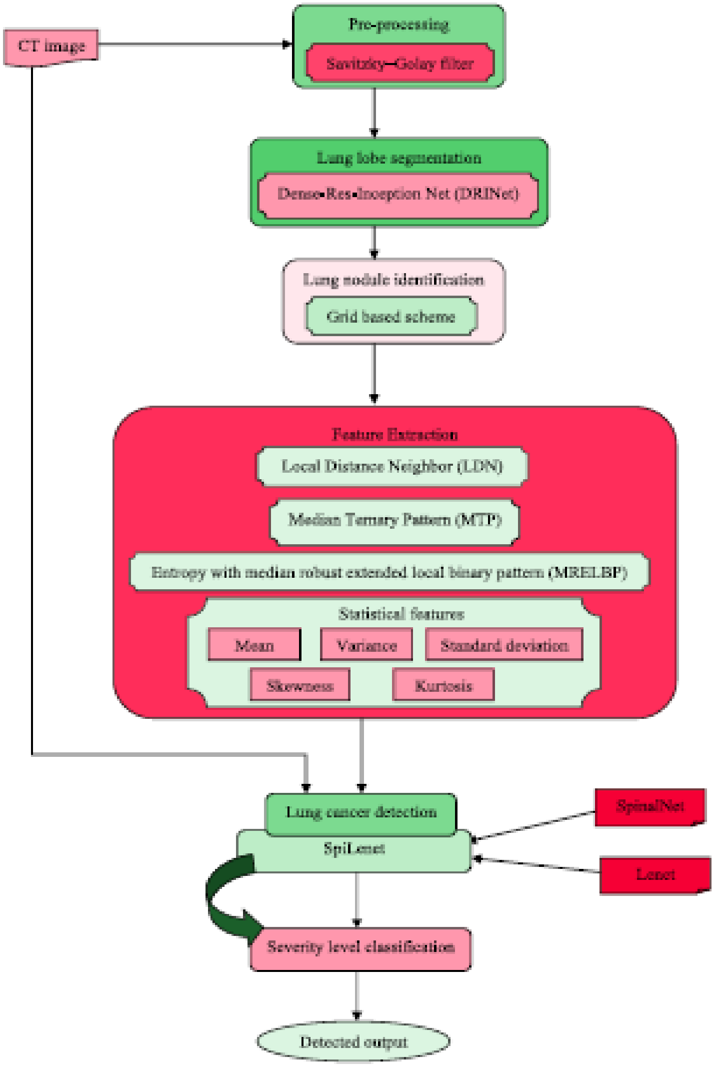

Figure 3. Diagrammatic representation of SpiLenet for lung cancer detection (LakshmanaRaoVadala et al., 2025).

These include texture descriptors such as Local Distance Neighbor (LDN), Median Ternary Pattern (MTP), and Entropy with Median Robust Extended Local Binary Pattern (MRELBP), as well as statistical measures including mean, variance, standard deviation, skewness, and kurtosis. For classification, lung cancer detection is carried out using the proposed SpiLenet architecture, which is constructed by combining SpinalNet and LeNet, with layer modifications incorporated through fuzzy logic concepts. Beyond detection, SpiLenet also facilitates the classification of cancer severity levels, thereby enhancing its clinical utility.Figure 3 illustrates the overall pipeline of the proposed SpiLenet-based lung cancer detection framework.

This study introduces a comprehensive lung cancer classification framework consisting of four key stages: feature extraction, feature reconstruction, feature selection, and classification, as illustrated in Figure 4.In the feature extraction phase, wavelet-based techniques are employed, utilizing Biorthogonal 2.2, Coiflets 2, and Daubechies 6 wavelets to capture multi-resolution features from the data. Following this, the feature reconstruction stage applies a thresholding strategy to eliminate noisy and redundant information produced during the wavelet decomposition process, thereby improving data quality.Subsequently, the feature selection stage leverages bio-inspired optimization algorithms, specifically the Dragonfly algorithm and Cuckoo Search, to identify the most relevant and discriminative gene features essential for effective classification.

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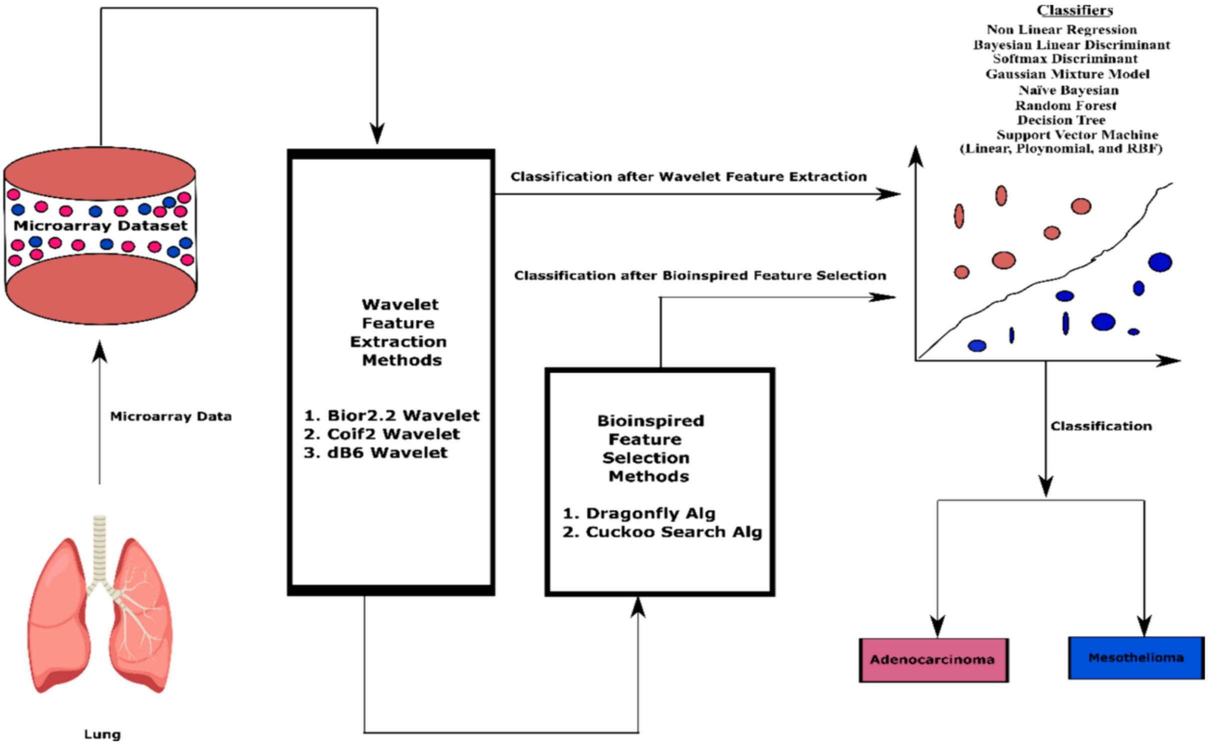

Figure 4. The Lung Cancer Classification Framework Involving Wavelet Feature Extraction and Bio-inspired Feature Selection (M.S. Karthika et al., 2024).

Next, in the feature selection stage, two bio-inspired optimization algorithms—Dragonfly and Cuckoo Search—are utilized to identify the most relevant and informative gene features, ensuring that only discriminative attributes are passed to the final phase.Finally, the classification stage employs a diverse set of classifiers to evaluate performance and ensure robustness. These include Nonlinear Regression (NR), Bayesian Linear Discriminant (BLD), Softmax Discriminant (SD), Gaussian Mixture Model (GMM), Naïve Bayes (NB), Random Forest (RF), Decision Tree (DT), and Support Vector Machine (SVM) with linear, polynomial, and Radial Basis Function (RBF) kernels.

Classification of lung cancer plays a crucial role in disease evaluation and treatment planning, as therapeutic decisions strongly depend on cancer type and stage. Although multiple imaging modalities are available for detection, Computed Tomography (CT) is most widely used owing to its high image quality and the advantage of avoiding ionizing radiation.In recent years, Deep Learning (DL), a subfield of machine learning, has demonstrated remarkable performance in medical image analysis, particularly in classification and segmentation tasks. The overall architecture of the proposed model is illustrated in Figure 5.

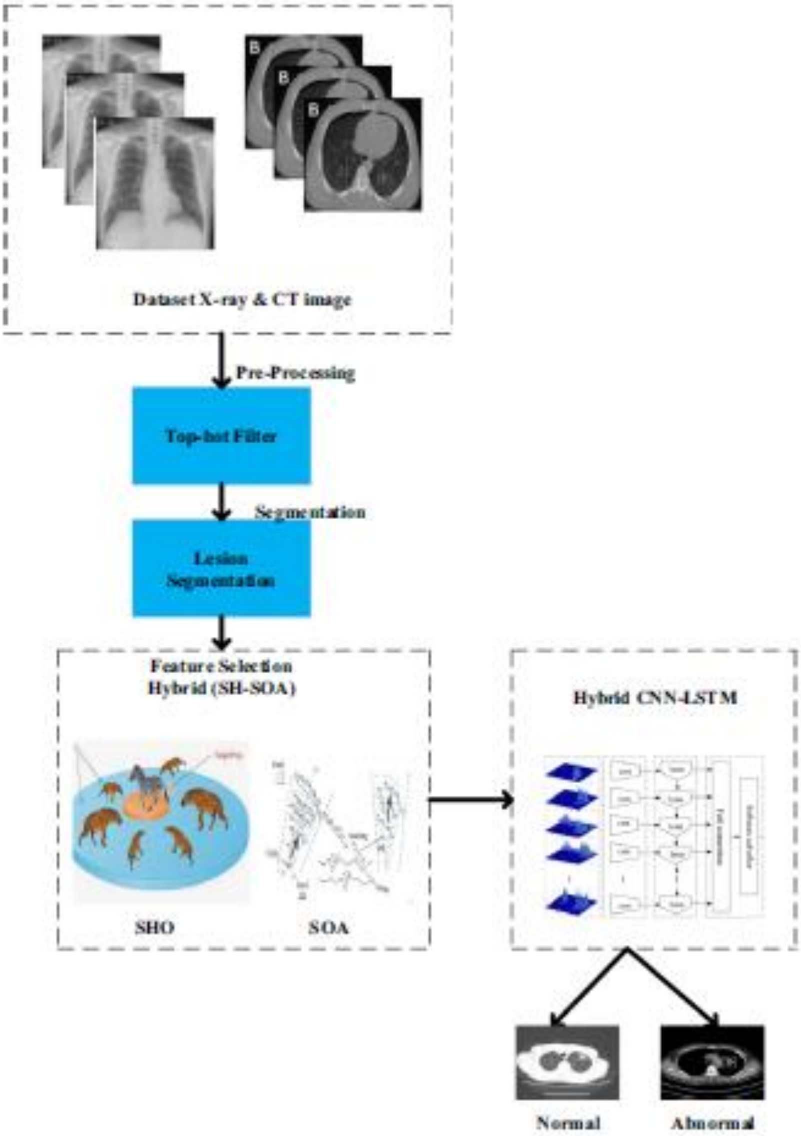

Figure 5. Proposed methodology for improved lung cancer diagnosis through feature selection and classification (Umesh Prasad et al., 2023)

The framework for lung cancer prediction and classification is organized into four major phases: pre-processing, segmentation, feature selection, and classification. Initially, lung CT images are acquired and passed through the pre-processing stage, where top-hat filtering techniques are applied. This approach enhances image contrast by suppressing background noise and emphasizing critical structural details.Following pre-processing, the segmentation phase isolates the region of interest from the CT scans with the aid of lesion segmentation, ensuring that subsequent analysis focuses on the most relevant lung regions for accurate cancer detection.

After completing the segmentation process, the resulting output is subjected to a feature selection (FS) phase. For this purpose, a novel hybrid optimization technique, SH-SOA, is proposed. This algorithm integrates the strengths of the Spotted Hyena Optimization (SHO) and the Seagull Algorithm (SOA), offering a unique and effective strategy for selecting the most relevant features.

By eliminating redundant attributes and retaining only discriminative ones, SH-SOA enhances the efficiency of the subsequent classification stage.The refined feature set is then passed to the classification phase, where an automated diagnostic framework is employed. Specifically, a Long Short-Term Memory (LSTM)-based approach is utilized to extract and learn high-level feature representations for accurately distinguishing between normal and abnormal lung conditions.The integration of SH-SOA for feature selection with an LSTM-based classifier significantly improves the model's overall performance, leading to higher classification accuracy and robust detection of lung cancer abnormalities.

Lung cancer is considered the most lethal form of cancer, with a high mortality rate compared to other types. Early-stage detection is crucial, as it greatly improves treatment effectiveness and increases patient survival rates. Several diagnostic methods are commonly employed, including Computed Tomography (CT), biopsy, blood tests, and X-ray imaging. However, pulmonary nodule detection remains a challenging task due to the wide variations in size, shape, location, and density of nodules.To address these challenges, computational intelligence techniques have been increasingly adopted for timely and accurate detection of lung cancer. The proposed model is structured into three main phases: lobe segmentation, candidate nodule extraction, and lung cancer classification.

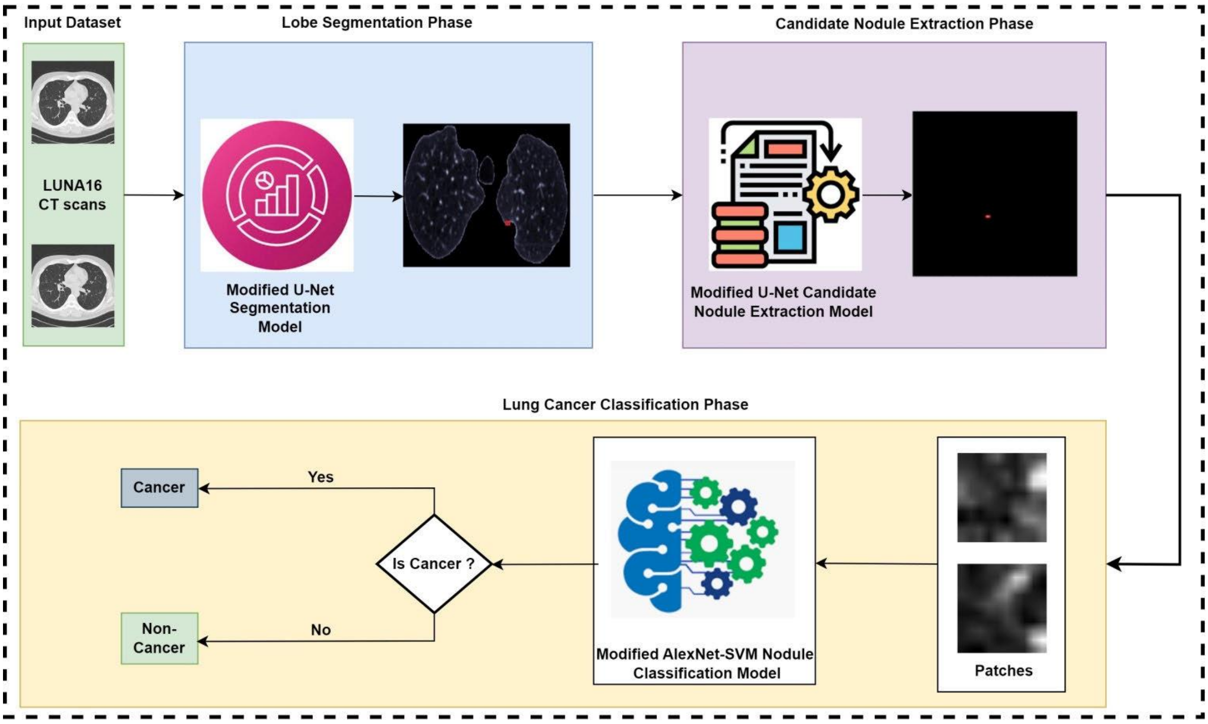

Figure 6. Proposed lung cancer classification using modified U-Net-based lobe segmentation and nodule detection model (IFTIKHAR NASEER et al., 2023)

In the lobe segmentation phase, a modified U-Net architecture is employed to segment the input CT scans, producing the individual lung lobes as output. In the subsequent candidate nodule extraction phase, the predicted lobes serve as input to another modified U-Net model, which is specifically adapted for the accurate extraction of candidate nodules.Finally, in the classification phase, patches of the extracted candidate nodules are processed using a hybrid model that combines a modified AlexNet with a Support Vector Machine (SVM). This approach leverages the deep feature extraction capability of AlexNet and the robust classification power of SVM, enabling the system to effectively classify nodules as either cancerous or non-cancerous.

The general workflow of the proposed methodology is depicted in Figure 7. Initially, CT scan slices from the dataset are loaded, followed by a series ofpre-processing steps to enhance image quality and prepare the data for analysis. Given the challenges in obtaining large volumes of annotated medical images for training, data augmentation is employed to artificially expand the dataset, thereby improving model generalization and reducing overfitting.

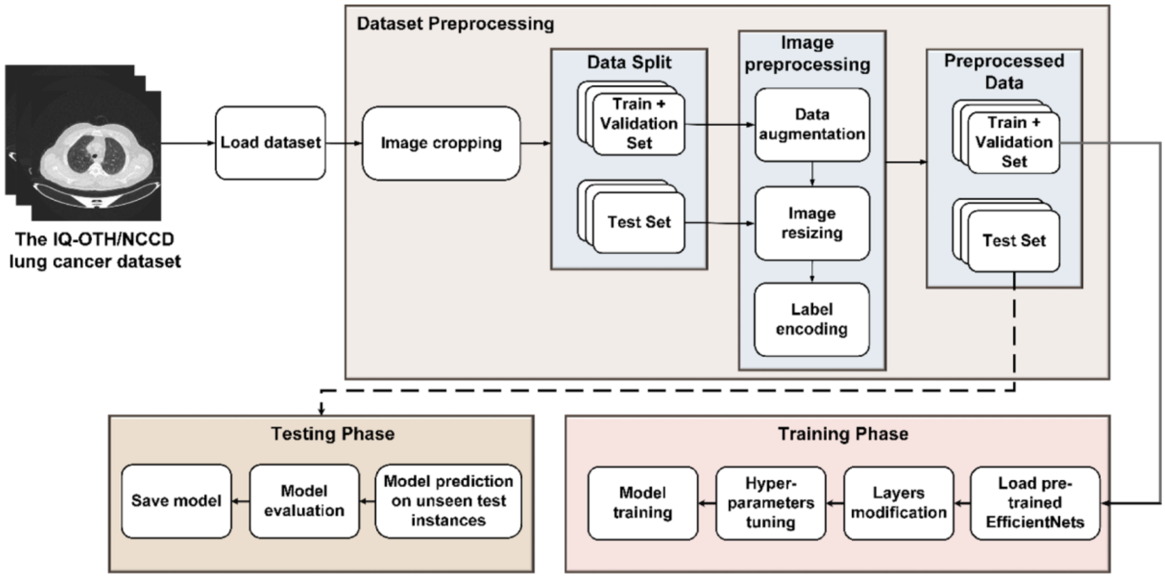

Figure 7. The general workflow of the proposed method (Rehan Raza et al., 2023).

The core of the proposed framework is built on a transfer learning strategy that leverages different variants of EfficientNet. These pre-trained models are fine-tuned for the multi-class classification of lung cancer into three categories: benign, malignant, and normal. By combining the strengths of EfficientNet with transfer learning, the methodology achieves efficient feature representation while minimizing computational cost.

Table 1: Comparison among state – of – the – art Lung Cancer detection Methods

Ref.	Year	Pre-processing	Methods	Datasets	Results
(SadamKavitha et al., 2025)	2025	feature selection, and hyper parameter optimization	MHA-DCNN framework	Q-OTH/NCCD lung cancer dataset	The method can detect 99.51 % lung cancer on Q-OTH/NCCD lung cancer dataset
(LakshmanaRaoVadala et al., 2025)	2025	feature extraction, feature reconstruction, feature selection	SpiLenet	medical imaging datasets	The method can detect 92.10 % lung cancer on medical imaging datasets
(M.S. Karthika et al., 2024)	2024	Wavelet-based feature extraction and bio-inspired feature selection	Cuckoo Search Algorithm (CSA)	microarray gene expression dataset.	The method can detect 97.23% lung cancer on microarray gene expression dataset.
(Umesh Prasad et al., 2023)	2023	Image filtering, Contrast enhancement and Data augmentation	The SH-SOA, a novel hybrid algorithm	LIDC/IDRI dataset	The method can detect 99.6% lung cancer on microarray gene expression dataset.
(IFTIKHAR NASEER et al., 2023)	2023	Lobe segmentation	U-Net architecture	LUNA16 dataset	The method can detect 97.98% lung cancer on LUNA16 dataset
(RehanRaza et al., 2023)	2023	data augmentation	transfer-learning approach using different variants of EfficientNet	IQ-OTH/NCCD lung cancer dataset	The method can detect 99.10% lung cancer on IQ-OTH/NCCD lung cancer dataset

IV. DISCUSSION AND ANALYSIS

This paper focuses on the application of deep learning techniques, particularly Convolutional Neural Networks (CNNs), for the detection and classification of lung cancer. The central premise is to harness the capability of deep learning to analyze medical images—especially CT scans—to identify subtle patterns indicative of lung cancer that may not be easily recognized by human observers. This, in turn, has the potential to enable earlier and more accurate diagnoses. The paper provides an overview of the methodologies, architectures, and evaluation strategies employed in this domain.

Key Aspects Addressed in the Paper

1. Deep Learning for Lung Cancer Detection

The study discusses how deep learning, and CNNs in particular, can be applied to automate the detection and classification of lung nodules from CT scans. These models are trained on large annotated datasets to differentiate between cancerous and non-cancerous nodules by recognizing complex imaging patterns.

2. CNN Architectures

Different CNN architectures tailored for lung cancer detection are reviewed. These include 3D-CNNs for processing volumetric CT data as well as hybrid approaches, such as 3D-CNNs combined with Recurrent Neural Networks (RNNs), which capture both spatial and sequential information from medical images.

3. Image Pre-processing and Augmentation

Pre-processing methods, such as image enhancement and segmentation, are highlighted as essential for improving image quality and isolating regions of interest. Furthermore, data augmentation techniques are discussed as a means to artificially increase dataset size and diversity, thereby improving model generalization.

4. Evaluation Metrics

The review outlines the evaluation criteria commonly employed for assessing model performance. Metrics include accuracy, sensitivity, specificity, and the area under the receiver operating characteristic curve (AUC), which together provides a comprehensive understanding of diagnostic reliability.

5. Challenges and Future Directions

The paper emphasizes existing challenges in deploying deep learning for lung cancer detection, such as the requirement for large, high-quality annotated datasets, the heterogeneity of lung nodules, and the difficulty of generalizing models across diverse datasets. Future directions may include developing more robust and computationally efficient models, exploring multimodal imaging approaches (e.g., PET/CT), and integrating deep learning systems into clinical decision-making workflows.

6. Comparison with Traditional Methods

Finally, the review contrasts deep learning-based methods with traditional diagnostic techniques, highlighting improvements in accuracy, efficiency, and automation. This comparison underscores the transformative potential of deep learning in medical imaging.

V. CONCLUSION

Deep learning (DL) techniques hold substantial potential for advancing lung cancer detection and classification, thereby enabling earlier and more accurate diagnoses. Although current research has demonstrated high accuracy in tasks such as lung nodule detection and classification, several challenges hinder clinical translation. These include issues of reproducibility, generalizability, and the persistent requirement for large, diverse datasets.

Future research should prioritize the following directions:

Designing robust and adaptable DL architectures capable of handling variations in lung cancer presentation. Expanding and diversifying datasets to improve training and validation, ensuring broader applicability across populations. Exploring hybrid DL approaches that combine the strengths of multiple architectures for improved performance. Developing automated annotation techniques to reduce dependency on time-consuming and error-prone manual labelling. Focusing on clinical integration, ensuring that DL models can be seamlessly incorporated into existing diagnostic workflows. Extending DL applications beyond detection to include treatment planning, prognosis, and outcome prediction.

By addressing these challenges and pursuing these research directions, DL can significantly strengthen its role in lung cancer diagnosis and management, ultimately contributing to improved patient outcomes.

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