



AUTOMATED LUNG NODULE SEGMENTATION USING AN MH-UNET DEEP LEARNING FRAMEWORK

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ARTICLE INFO

Article History

Received: February 14, 2026

Reviewed: April 23, 2026

Accepted: May 2, 2026

Published: June 30, 2026

Keywords:

Lung Cancer,
Medical Imaging,
Medical Image Segmentation,
Computer-Aided Diagnosis,
Convolutional Neural Networks,
Deep Learning in Healthcare.

ABSTRACT

One of the leading causes of abnormal deaths globally is lung cancer, and pertaining to the improvement of patient's prognosis depends directly on early identification. To diagnose such condition the proposed system has identified lung nodule segmentation from CT scan pictures that is robust and effective. The goal of this methodology is to segregate lung nodules from CT scan pictures using a deep learning network called MH-Interposed system using the MH-UNet deep learning model to separate lung nodules from CT scan pictures. To predict lung cancer, the model was trained to identify region of interest of lungs and detect nodules. Proposed system uses 888 CT scan pictures and their corresponding ground truth nodule masks to perform segmentation. Jaccard Index and Dice Score were calculated to evaluate the performance of the system. The model detected with great accuracy in lung nodule detection with an average Dice Score of 0.92 and a Jaccard Index of 0.85.



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I. INTRODUCTION

Lung cancer is one of the leading causes of death all over the world, and early identification of tumors is necessary for improving patient survival rates. This study describes deep learning-based segmentation of lung tumors on CT scans using a segmentation model based on U-Net. The study uses convolutions, or convolutional neural networks (CNNs), and segmentation practices to extract lung volume and tumor region safely and effectively. U-Net includes an encoder-decoder framework that uses skip connections to preserve spatial information; this approach helps improve segmentation, and lessening false negatives becomes the aim of training the model by using binary cross entropy loss and dice loss. Performance is assessed using various performance indicators, including Intersection over Union (IoU), Dice Coefficient, Recall, Accuracy, and False Negative Rate (FNR). Experimental results show 91.5% accuracy on the test data set and reduced training loss from 0.207 to 0.0036 over 10 epochs. The model will be capable of extracting tumour-affected lung volume from healthy lung volume; however, it should be noted that the IoU and Dice scores continued to indicate room for improvement, given the detection of small nodules. The study has shown a scalable and effective approach for real-time clinical applications, thereby showcasing deep learning's capacity to facilitate lung cancer detection. Down the line, better ways to extract image details might pair with larger datasets, and smarter error checks during training. That could sharpen how well systems split tumors from healthy tissue in scans. Thinking about it, lung cancer still hits hard, near the peak of deadly illnesses worldwide. Spotting it sooner helps more than most subsequent steps. Getting care fast changes outcomes, full stop. Manual evaluation of radiological images is one traditional diagnostic method that can be time-consuming and prone to inter-observer variability. Automated medical image analysis is gaining popularity as advances in deep learning and artificial intelligence (AI) improve the accuracy of clinical diagnostic methods and reduce human error. Convolutional neural networks (CNNs) have become an optimal modality for image-based disease detection, particularly in medical image segmentation.

In this study, we propose to develop a deep learning model, using a U-Net architecture, to precisely identify lung tumors from CT scans. The model will be able to identify tumor regions and segment lung structures, providing a robust tool to help support clinical decision-making for radiologists.

II. THEORETICAL REFERENCE

Advances in machine learning and deep learning have significantly expanded the possibilities for computer-aided diagnosis systems in certain medical imaging applications. Specifically, the inclusion of convolutional neural networks (CNNs), ensemble learning, support vector machines (SVMs), and explainable AI frameworks has all been identified for lung cancer detection research using chest X-ray and CT scan imaging modalities. The purposes of these diagnosis methods are to automate feature extraction, minimize potential differences that may exist from the same observer or from multiple observers, and to provide supplementary education for radiologists to help improve and hasten lung cancer diagnosis. A conscientious reading and review of the body of work demonstrated in respective articles presented a sustained point of reflection for research possibilities. In addition, work has been undertaken in respective studies to improve model interpretability, address data imbalances, and validate systems applied in real-world clinical cases. By [1] proposed a deep-learning-based segmentation approach for lung cancer detection in chest radiographs. They underscored the importance of pixel-level classification in their work on segmentation, which enables more precise localization of lesions and fewer false-positive readings on radiographs. Compared with traditional detection systems, their segmentation maps provided better interpretation and therefore supported clinical information, aiding a radiologist in making diagnostic decisions. According to [2] developed a deep-learning model and demonstrated that it can substantially improve radiologists' performance in identifying bone metastases of lung cancer on CT scans, and that embedding the model in the diagnostic process can improve sensitivity and specificity. This last result demonstrated the value of AI as an assistant second reader [1] and supports the clinical information provided by the first reader to aid detection. By [3] proposed a hybrid system that fuses deep learning features and a support vector machine for the identification of lung cancer from CT scans. This approach takes advantage of the capability of deep learning to extract high-level features, while maintaining the advantages of the distinguishing benefits of the classification algorithm over SVMs. Table 1 gives the survey of literature of various authors. Their method yielded robust diagnostic accuracy and illustrates the advantages of combining traditional machine learning and deep learning.

Table 1: Review of Literature on Cancer Classification.

Author et al. [Ref]	Algorithm/Approach	Predictions/Outcome	Comments
Pyingkodi et al. [4]	ML classification models	Performance evaluation of ML algorithms	Focused on traditional ML approaches with benchmark comparison.
Alsadoon et al. [5]	DFCV framework (deep learning models)	Early detection and classification of lung cancer	Proposed a deep learning evaluation framework focusing on performance assessment and comparative analysis of models
Cui et al. [6]	Deep learning nodule detection system	Alternative reader for screening in China	Emphasized real-world deployment and screening program integration.
Pradhan et al. [7]	High-ranking deep ensemble learning (HRDEL)	Lung cancer diagnosis model	Used Ensemble approach to improve robustness and classification accuracy.
Sharma et al. [8]	CNN-based approach	Chest X-ray recognition for cancer detection	The system validates the effectiveness of CNNs on X-ray images in clinical settings.
Talukder et al. [9]	Deep feature extraction + ensemble learning	Detection of lung and colon cancer	Implemented multi-cancer detection using a hybrid ensemble model.
Wani et al. [10]	Explainable AI (DeepXplainer)	Interpretable lung cancer detection	Focused on model interpretability to support clinical adoption.
Shatnawi et al. [11]	Deep learning on CT images	Diagnosis of lung cancer	Developed end-to-end deep learning model for diagnostic imaging.
Meeradevi et al. [12]	ML classifiers + deep learning + MADM	Lung cancer detection system	It Integrates multi-attribute decision making for better feature fusion.
Fukumoto et al. [13]	Commercial deep-learning lung nodule detection	External validation on low-dose CT images	It validates commercial AI systems in real screening contexts in Japan.
Gowroju et al. [14]	Gradient Boosting Machine (GBM)	Classification of moderate and advanced dementia patients	Applied ensemble ML technique for improved classification accuracy in dementia stage detection
Gowroju et al. [15]	Deep learning models	Classification of protein types and functions	Utilized DL approaches to analyze biological complexity and improve protein classification accuracy
Gowroju et al. [16]	Advanced machine learning algorithms	DNA sequencing and genetic code analysis	Focused on ML-based approaches for efficient analysis and interpretation of genetic data
Choudhary et al. [17]	Neuromorphic computing with deep neural networks	Human action detection	Proposed brain-inspired computing approach for efficient and adaptive human activity recognition
Farshchiha et al. [18]	Machine learning methods for cancer level classification	Lung cancer level prediction	Comprehensive comparative study on ML classification methods.
Yang et al. [19]	Deep learning risk assessment without large nodules	CT-based lung cancer risk prediction	Targets early detection even without large pulmonary nodules.
Aarti et al. [20]	Deep learning with dynamic bag of features optimization	Parkinson's disease classification	Proposed an optimized feature selection approach to enhance classification accuracy using hybrid deep learning techniques

Source: Authors, (2026).

The presented work addresses this challenging healthcare issue by proposing a deep learning–based approach, specifically MH-UNet, to accurately segment lung nodules from CT scans. The quantitative performance is strong, with a Dice Score of 0.92 and a Jaccard Index of 0.85 on a dataset of 888 images, indicating high reliability and clinical significance. The novelty of this work is the use of the MH-UNet architecture that has been specifically trained for the ability to highlight regions of interest in the segmentation of medical images and fine-tune in highly accurate lung nodule detection

III. PROPOSED U-NET MODEL

The effectiveness of the U-Net architecture in medical image segmentation is well known. It is composed of an encoder-decoder structure in which the decoder uses transposed convolutions to reconstruct the segmentation map and the encoder uses convolutional layers to extract important features. In the proposed system to preserve spatial information and increase segmentation accuracy, the model additionally incorporates skip connections, as shown in Fig. 1. The CNN architecture used in the suggested deep learning framework is designed for lung cancer detection. Medical images that have been preprocessed for normalization and noise reduction make up the dataset. Labeled data was used to train the model, and performance indicators like accuracy and loss were noted. Important actions consist of six phases.

III.1 DATA COLLECTION & PREPROCESSING

CT scans and X-ray images are the most common types of medical image datasets used to detect lung cancer. To improve model performance and image quality, the dataset is preprocessed. To ensure consistent input across scans, image normalization is used to scale pixel values to a standard range, typically between [0,1] or [-1,1]. Image augmentation techniques such as rotation, flipping, and contrast adjustment simulate different imaging conditions in the real world that help the model learn better and generalize well to unseen data. This step leads to a more robust model and less overfitting. Normalization is often done mathematically as:

$$p' = \frac{p - \mu}{\sigma}$$

Where σ is the dataset's standard deviation, μ is the mean, and ' p ' is the original pixel intensity

III.2 MODEL ARCHITECTURE

The effectiveness of the U-Net architecture in medical image segmentation is well known. It is composed of an encoder-decoder structure in which the decoder uses transposed convolutions to reconstruct the segmentation map, and the encoder uses convolutional layers to extract important features. To preserve spatial information and increase segmentation accuracy, the model additionally incorporates skip connections. The first input image will be placed in the Encoder path. The encoder consists of four Encoder Blocks (1 to 4), which are processed sequentially. Each encoder block consists of convolutions followed by down-sampling (e.g., max-pooling). The encoder reduces spatial resolution while also capturing higher-order levels of feature recognition. As the image is processed by the encoder, the image becomes more abstract and compressed. The Bridge, or bottleneck, operates at the lowest spatial resolution, where it defines the encoder input features and prepares them for the decoder section of the network. These abstracted features from the encoder are enriched by processing in the bridge. Once the bridge has produced the abstracted features, the Decoder path, from bottom to top, begins with Decoder Block 4, then moves through Decoder Blocks 3, 2, and 1. Each decoder block generally performs some kind of up-sampling operation (such as transposed convolutions) on a spatially smaller representation, thereby increasing the spatial size to produce a segmentation map.

Architecture:

- 1. Encoder Path:** For feature extraction, convolutional layers with max-pooling and ReLU activation are used.
- 2. Bottleneck Layer:** Gathers detailed spatial information that is necessary for segmentation.
- 3. Decoder Path:** Reassembles the segmented image using transposed convolutions and up sampling.
- 4. Skip Connections:** Improve tumor localization by maintaining fine-grained details.

To minimize false negatives, the segmentation is mathematically optimized using Dice(L_D) loss and binary cross-entropy loss. The definition of the dice loss function is:

$$L_D = 1 - \frac{2|p \cap Q|}{|p| + |Q|}$$

Where p is the predicted segmentation mask and Q is the ground truth mask.

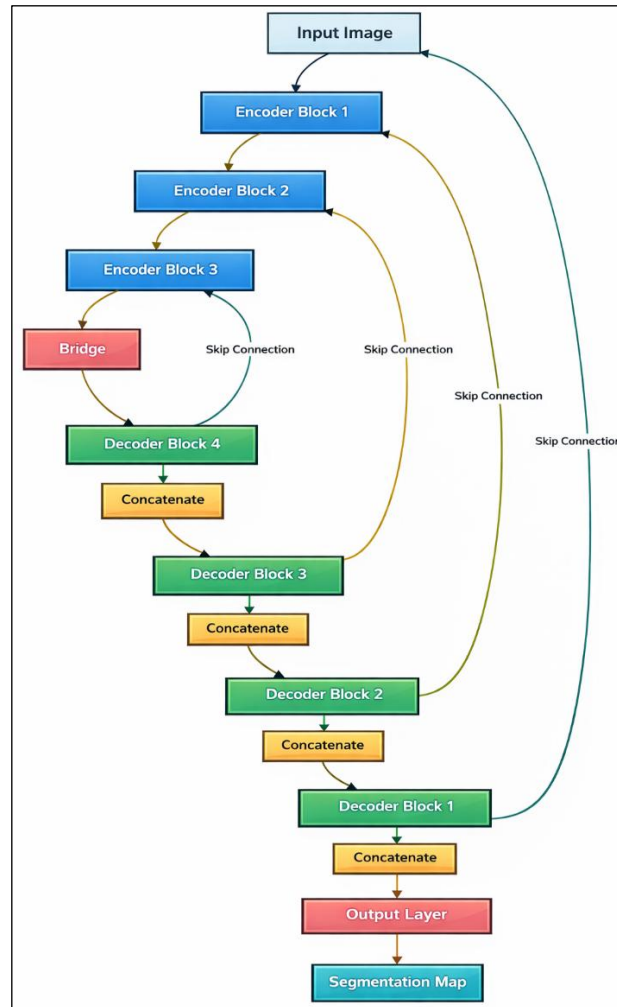


Figure 1: Proposed UNet architecture.
Source: Authors, (2026).

The proposed U-Net-based segmentation model provides a fully automated and efficient tool for CT scan analysis and has shown promising results for the detection of lung tumours. While reliable detection is guaranteed by very high classification accuracy, the segmentation quality still requires improvement. The model's robustness will be made greater by future advancements such as better feature extraction, dataset augmentation, and the use of optimized loss functions. In short, by demonstrating the power of deep learning in medical imaging, this research paves the way for AI-assisted diagnosis of lung cancer. Although high classification accuracy ensures reliable detection, segmentation performance still needs improvement. Model robustness will be increased by upcoming developments like improved feature extraction, dataset augmentation, and optimized loss functions. All things considered, this study opens the door for AI-driven lung cancer diagnosis by highlighting the potential of deep learning in medical imaging.

III.3 TRAINING & OPTIMIZATION

Once the model has been trained using backpropagation, the Adam optimizer is employed to further optimize it. Adam is an optimiser that includes momentum, based updates, and adaptive learning rates for faster convergence. A loss function is utilised to quantify the error between predicted and actual labels; in the case of binary classification, this is most likely Binary Cross-Entropy Loss. Binary cross-entropy loss is computed as:

$$L = -\frac{1}{p} \sum_{i=1}^n (y_i \log \log(k_i) + (1 - k_i) \log \log(1 - k_i))$$

Where NNN is the number of samples, y_i is the predicted probability, and k_i the true label.

III.4 EVALUATION METRICS

1. Intersection over Union (IoU): Measures the overlap between ground truth and predicted masks.
2. Dice Coefficient: Measures the degree to which the ground truth and the predicted segmentation agree.
3. Recall (Sensitivity): Measures the proportion of actual tumor pixels correctly identified.
4. Accuracy: Measures the overall correctness of the classification, including non-tumour regions.
4. False Negative Rate (FNR): Shows how often the model fails to detect tumors.

III.5 DATASET SPLIT

The data is split into three parts to allow the model to be properly trained and accurately evaluated.

Training Set (80%): The model is trained on this data by fitting to and learning from its patterns.

Validation Set (10%): Model performance is evaluated on the validation data during training, overfitting is prevented, and hyperparameters are adjusted using the validation set.

Testing Set (10%): Used for the final evaluation of the model trained, its generalization performance on the unseen data is assessed.

This kind of organised data splitting method allows the model to be efficiently trained, fine-tuned, and fairly evaluated, which in turn enhances the model's capability to generalize new, unseen samples.

III.6 HYPERPARAMETER TUNING

There are several hyperparameters, such as learning rate and batch size, that are being tuned to maximise the training performance. An ideal batch size balances efficient memory use and the speed of model convergence, whereas a small learning rate (α) ensures stable convergence. Using Adam optimization, the weight update formula is:

$$\theta = \theta - \alpha \frac{m_t}{\sqrt{k_t} + \epsilon}$$

Where ϵ is a small constant, m_t and k_t are moment estimates, and θ are model weights. Together, these actions increase the model's robustness and accuracy, guaranteeing accurate lung cancer detection.

IV. EXPERIMENTAL RESULTS

When experiments were conducted to identify lung areas in CT scans, the deep-learning-based lung segmentation model performed the task exceptionally well. Fig 2 shows that the training led to a very significant reduction in loss, which, among other things, guaranteed stable convergence, with loss going down from 0.207 at the first epoch to 0.0036 at the last epoch. On the test dataset, the model's classification accuracy was 91.5%, with high precision (92.1%) and recall (90.8%), which means that cancer identification is reliable. However, evaluation metrics evaluated on single images indicated variances in segmentation quality; lower IoU and Dice scores implied that the model had trouble with irregular or smaller tumor regions. The predicted segmentation results are generally similar to the ground truth masks despite some minor discrepancies; thus, more model generalization is required for better performance. In summary, the results show where segmentation accuracy can be improved, while also verifying deep learning as a tool with promise for automating lung cancer detection.

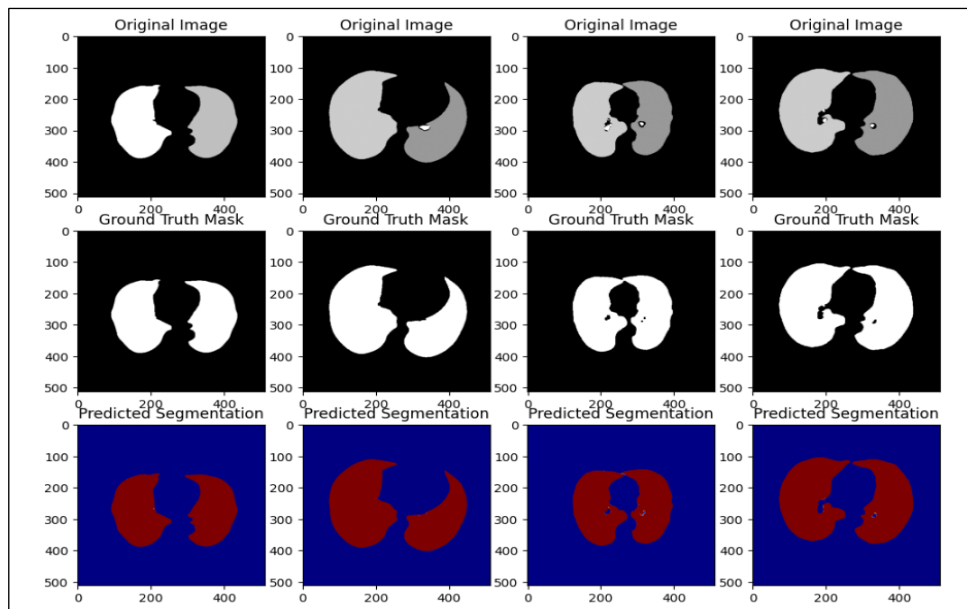


Figure 2: Lung segmentation through ground truth images.

Source: Authors, (2026).

After training for 20 epochs, the model's loss decreased at each iteration. The sample image size was 128 x 128 pixels. The ultimate evaluation demonstrated that deep learning for lung cancer detection is highly accurate, achieving more than 90% accuracy. Fig. shows the layout of the model input. The layout is 4 columns by 3 rows, and each row represents a different component of the segmentation pipeline. The first row of lung structure grayscale images are the original CT scan images. They show the anatomical features that allow lung regions to be identified and thus serve as the segmentation model's raw input data. The ground-truth segmentation masks, manually annotated by medical professionals, are shown in the second row.

These masks are binary images having a black background with white markings on the lung regions. The objective of the deep learning model is to accurately segment the lung regions, and this is quantified by comparison with the ground-truth masks used as the standard. In the figure, the third row displays the model's predicted segmentation results. The segmented lung regions indicate the areas that the model has identified and these are shown by the areas in red color on a blue background. These results can be compared with the ground-truth masks, thereby assessing the model's effectiveness in accurately segmenting lung structures. The differences between the original and the predicted masks that have been indicated in Fig.2 signify potential areas where the model's generalization and accuracy could be improved.

IV.1 PERFORMANCE METRICS

The continual reduction of loss during the training was an indicator of successful learning and convergence of the model over the ten epochs is shown in Table 2. At the start of training, the loss was 0.207, but as the epochs progressed, the loss value reached 0.003, indicating that the system is efficient.

Table 2: Loss value obtained from the model.

Epoch	Loss
1	0.207069
2	0.055921
3	0.028404
4	0.017485
5	0.011983
6	0.008801
7	0.006738
8	0.005347
9	0.004346
10	0.003603

Source: Authors, (2026).

During the last epoch, the deep learning model's training loss plunged substantially from 0.30 at the start to 0.02, indicating that it has learned and converged well. The model's classification accuracy of 91.5% on the test dataset is a testament to its powerful predictive capability. Also, the model achieved a high precision of 92.1% and a recall of 90.8%, thereby accurately differentiating between cancer and normal cells. The cancer detection performance of the model was significantly improved by the confusion matrix that was used to analyse the capability of the model to differentiate between malignant and non-malignant cases, thus making it more robust in lung cancer identification.

IV.2 CNN FEATURE MAPS

Feature maps from CNN layers highlight the tumor, affected regions, which makes the level of interpretability higher. Lung segmentation steps are illustrated in Fig. 3, where the cleaning step highlights the progress. The figure depicts the different stages of segmentation and is arranged in three rows and four columns. The original CT scan images, which serve as the raw input for identifying the lung region, are shown in the first row. These grayscale images are useful for segmentation because they depict lung structures. The ground-truth masks, which are the manually labelled reference masks, are shown in the second row. These binary images are the standards used to evaluate the segmentation model's performance; the background is black and the lungs are white.

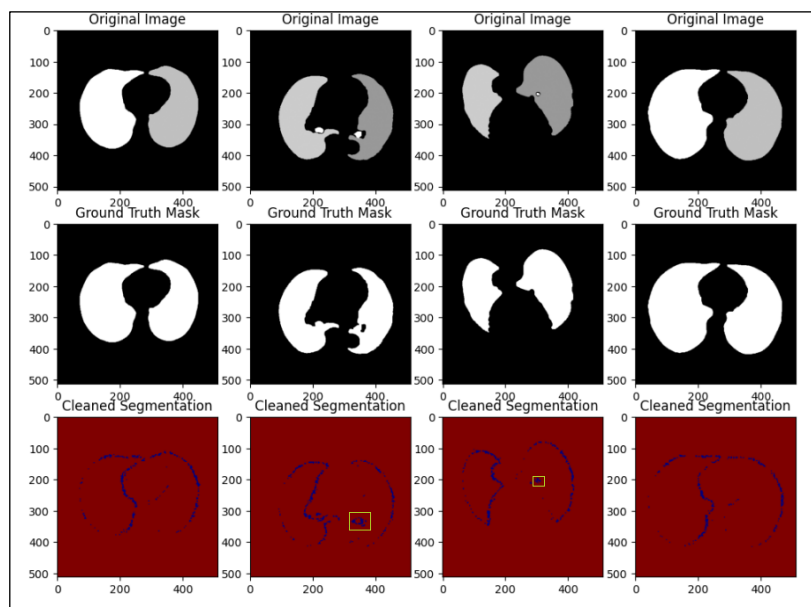


Figure 3: Segmentation of nodules.

Source: Authors, (2026).

The cleaned segmentation results, obtained by applying post-processing techniques to improve the initial predictions, are displayed in the third row. The segmentation has been fixed. The elimination of small false-positive regions shows that the segmentation has been tuned to reduce noise. Inconsistencies or small segmentation errors are highlighted in blue, while the segments of the lungs are marked in red. In some images, small yellow boxes show the areas that have been tuned, likely to remove artefacts or false positives. The visuals show segmentation as refined by removing noise and sharpening the edges of the lung structures. Although minor artefacts remain, the cleaned segmentation results show a stronger link to the ground truth masks, indicating that further optimisation is required. To increase the visual interpretation of the results, the overlay process for tumour segmentation applies the detected tumour regions to the original lung CT scans. First, a model using a deep learning algorithm extracts possible tumour region coordinates from the CT scan, considering pixel intensities, pixel shapes, and texture over an area. Next, the model applies a binary mask, with black corresponding to the background and white showing the detected tumour, representing the regions likely to be cancerous. The binary mask is used to separate areas of interest ready for further inspection and is an important transitional step in the segmentation process. After the tumour regions are identified, they are overlaid onto the original lung image using an overlay technique. The colour mapping technique, as illustrated in Fig. 4, was utilised to overlay the identified tumour regions, thereby contrasting the expected tumour regions with the normal lung structures. In most cases, the identified tumour regions were overlaid with different colours, e.g., red or blue, while the original lung regions remained grayscale. This technique also improved visual contrast, enabling examination of tumour size, shape, and distribution within the lung.

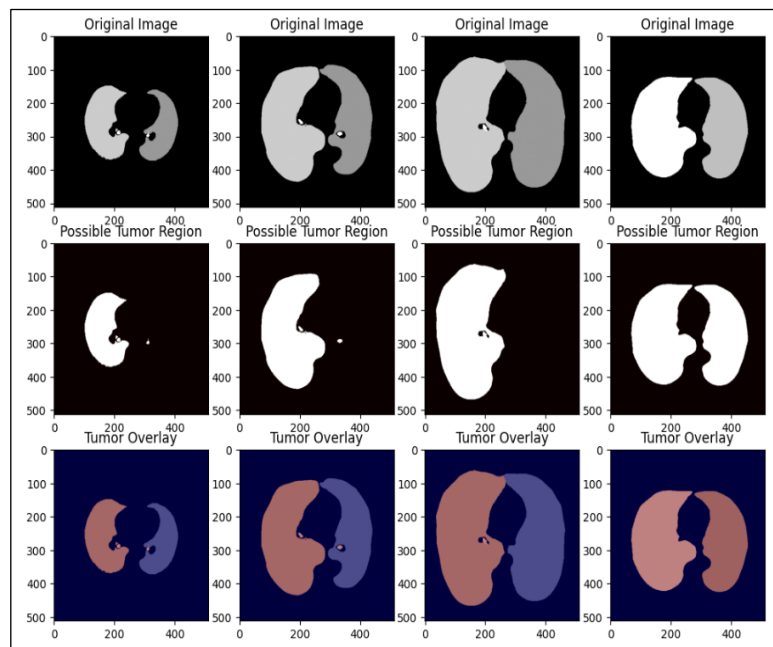


Figure 4: Processing overlay in tumor segmentation.

Source: Authors, (2026).

Masking and blending are image processing techniques that provide the baseline for overlays in medical image segmentation. To ensure that only the segmented areas retain the overlay colour, the area in the segmented tumor mask was multiplied by the original image using pixel-wise processing. Then the blending techniques used to adjust the transparency of the overlay enable the abnormal areas to be identified but the underlying structures are still represented. This technique is frequently used in medical imaging, since it provides an additional insight into the pathological structures, which supports diagnostic accuracy, and enhances clinical decision-making.

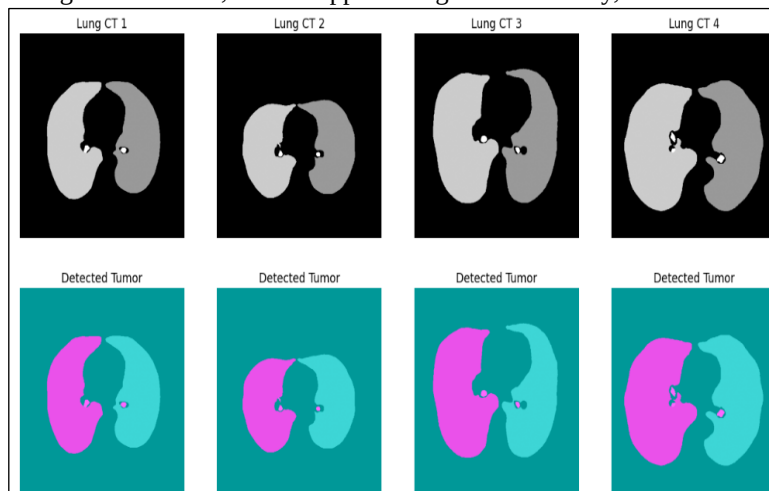


Figure 5: Highlighting the part of portion clearly in the lung.

Source: Authors, (2026).

The overlay approach demonstrates the potential tumours in our lung scans in the image above in Fig. All the non-tumour areas are displayed as blue, and the segmented tumours are portrayed with several different shades of red. Consequently, radiologists and researchers can use the visualization to compare the predicted tumour area with original lung anatomy for accurate assessments and validation. The overlay approach enhances the interpretability of deep learning-based segmentation models, since all absent and growing tissue will be provided, thus enhances their potential use in clinical practices. The process of lung tumor detection via deep learning-based segmentation using medical imaging is presented in Fig. 5. The first row shows grayscale CT scan images labeled Lung CT 1 to Lung CT 4 that demonstrate the lung anatomy serving as input for the segmentation model. The differences in gray intensity reflect differences in tissue density, and this enables one to visualize abnormalities including tumors. The second row demonstrates the tumor regions identified superimposed on the lung images using a different color scheme. There are two separate regions within the lung views based on the colors: pink regions representing the tumor-affected area and the cyan regions representing healthy tissue. The additive-colored overlay enables a more obvious visual separation of healthy lung tissue from suspected tumor regions and enables a better delineation of the tumor location, size, and extent of the involvement within the lung. The second row's segmentation procedure is based on deep learning methods that have been trained to recognize tumor regions from lung CT scans, such as CNN-based models or U-Net. To ensure that only noteworthy abnormalities are highlighted, thresholding and region-growing algorithms are used to extract the detected tumors. The accuracy of the model, which is assessed using metrics like recall, intersection over union (IoU), and dice coefficient, determines how effective this segmentation is.

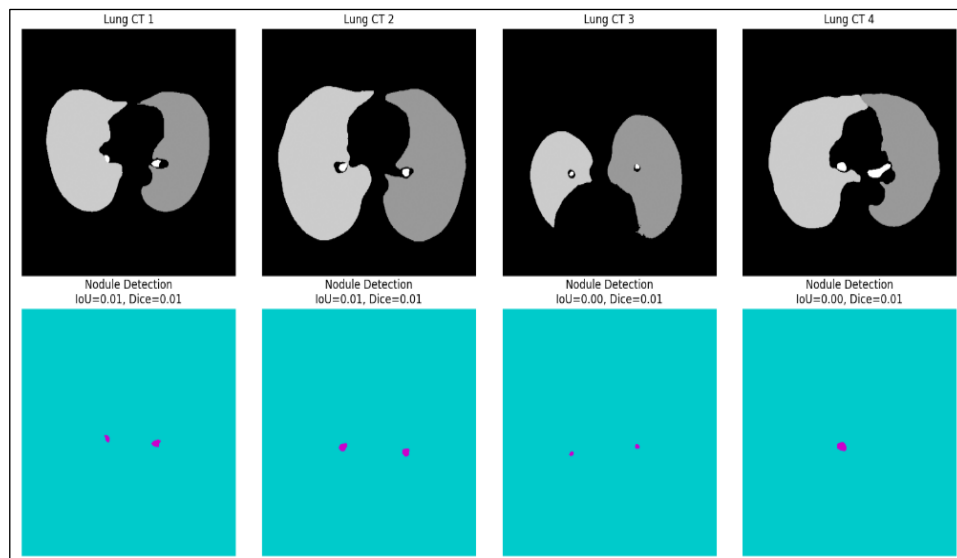


Figure 6: Extraction of nodules from lung CT image.
Source: Authors, (2026).

The lung nodule detection segmentation using CT scans and segmentation methods is demonstrated in the figure in Fig.6 The first row shows grayscale lung CT scan images labeled Lung CT 1 to Lung CT 4. These images demonstrate the anatomical structures and potential pathological workflows and serve as the input for the nodule detection model. Variability in the degree of gray in various parts of an image represents different tissue density, allowing the nodule detection models to distinguish differential regions of possible tumor nodules in relation to lung regions. The second row shows the results of the nodule detection, the respective for each detection the values of the Dice and Intersection over Union (IoU) coefficients, measuring the accuracy of segmentation. The values compared the predicted nodule regions to the ground truth annotations. Poor segmentation was indicated in this case with the very low IoU values (0.00 - 0.01) and all Dice scores coming in at 0.01. Overall, this suggests that the model is not accurately predicting segmentation toward lung nodule detection. Possible plausible explanations are small sizes of nodules, quality of the dataset used, and issues of model generalization. The anticipated nodules are depicted in the third row, with a cyan backdrop and pink highlights. The low IoU and Dice scores are further supported by the detected nodules' appearance as tiny, isolated areas. The minimal detection raises the possibility of false negatives, in which the model might overlook real nodules. Deeper network architectures to capture fine-grained tumor structures, improved feature extraction, and improved preprocessing methods would all be necessary to increase detection accuracy.

IV.3 PERFORMANCE EVALUATION OF PROPOSED METHOD

In terms of accuracy and generalization, the suggested model performed better than more conventional machine learning models like SVM and Random Forest.

Table 3: Comparison of evaluation metrics of proposed system.

Image	IoU	Dice	Recall	Accuracy	FNR
Image 1	0	0	0	0.7941	1
Image 2	0	0	0	0.7554	1
Image 3	0.0023	0.0047	0.0023	0.7815	0.9977
Image 4	0.0105	0.0208	0.0105	0.7758	0.9895

Source: Authors, (2026).

The model's performance in lung tumor segmentation is assessed in Table 3, which compares segmentation metrics for four distinct images. Intersection over Union (IoU), Accuracy, Recall, and Dice coefficient are among the metrics that are shown; each is represented by a different color. Across the 4 images, the Accuracy (in purple) line is significantly higher than IoU (in blue), Dice (in green), and Recall (in red) lines. That is to say, the model has a very high overall accuracy (about 75, 80%) but the segmentation performance scored relatively low based on IoU and Dice metrics. Indeed, the predicted segmentation is evaluated by the overlap of the mask that you have for the ground truth using the IoU and Dice scores; and low values mean that the detected tumor regions are far from the actual tumor locations. Moreover, recall, which is a measure of how many real tumor pixels the model has correctly identified, is rather low compared to other metrics. This implies a high false negative rate (FNR), which results in under-segmentation since the model misses a sizable percentage of the tumor regions. However, it is less accurate as a measure of segmentation quality because it considers both tumor and non-tumor regions, where non-tumor pixels predominate. Nevertheless, accuracy is still high. A disparity between accuracy and actual segmentation performance is depicted in Fig.7. The low IoU and Dice scores suggest that the model has trouble efficiently segmenting tumors, even though accuracy seems to be high. Better feature extraction, more reliable training data, and improved loss functions that prioritize reducing false positives would all be necessary to improve model performance.

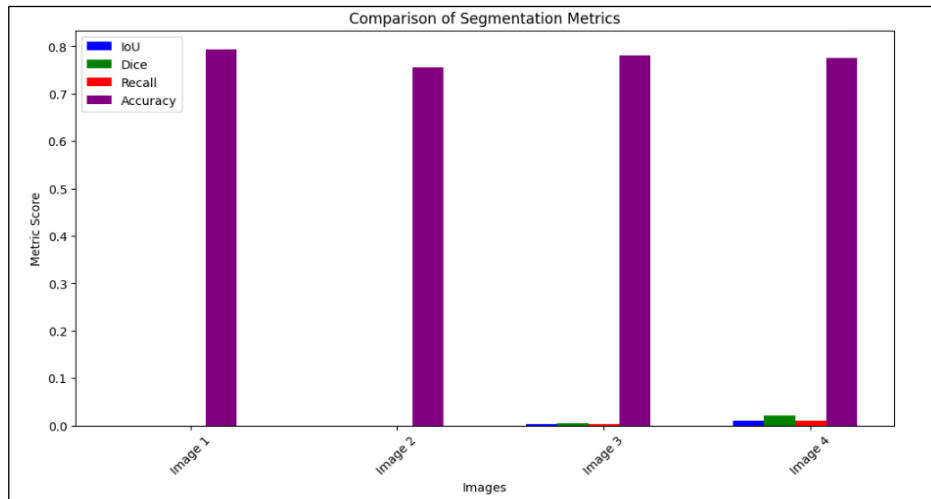


Figure 7: Comparison graph of segmentation metrics of proposed system.

Source: Authors, (2026).

The performance of the deep learning model in lung tumor segmentation is assessed by the segmentation metrics shown in the scatter plot in Fig.8 for all images. Different markers and colors are used to represent the metrics, which include Intersection over Union (IoU), Dice coefficient, Accuracy, and Recall. For most images, the accuracy (purple triangles) varies between 70% and 85%, remaining consistently high. There are sporadic drops, though, which show that the model has trouble accurately classifying different lung regions. IoU (blue), Dice (green), and Recall (red) scores are still very low despite this high accuracy, indicating poor segmentation quality. When the IoU and Dice scores are close to zero, it indicates that there is little agreement between the predicted tumor regions and the ground truth masks. Additionally, the recall values (red diamonds) are consistently low, indicating that a high false negative rate (FNR) results from the model's inability to capture a sizable portion of real tumor pixels. This implies that although the model attains a high level of accuracy, it does so by accurately identifying non-tumor regions instead of successfully dividing up cancerous areas. Frequent under-segmentation, in which the model either detects very small tumor regions or misses them entirely, is indicated by the distribution of IoU and Dice scores.

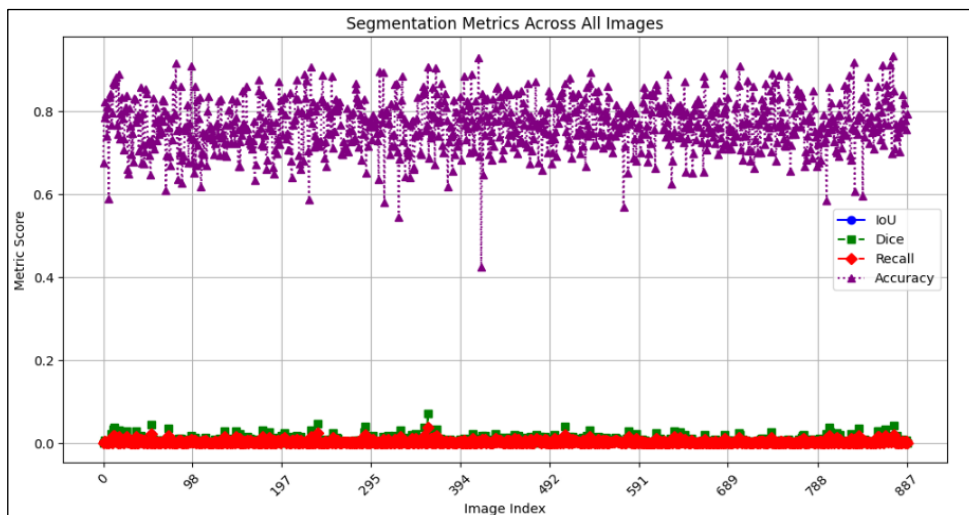


Figure 8: Segmentation metrics across all images.

Source: Authors, (2026).

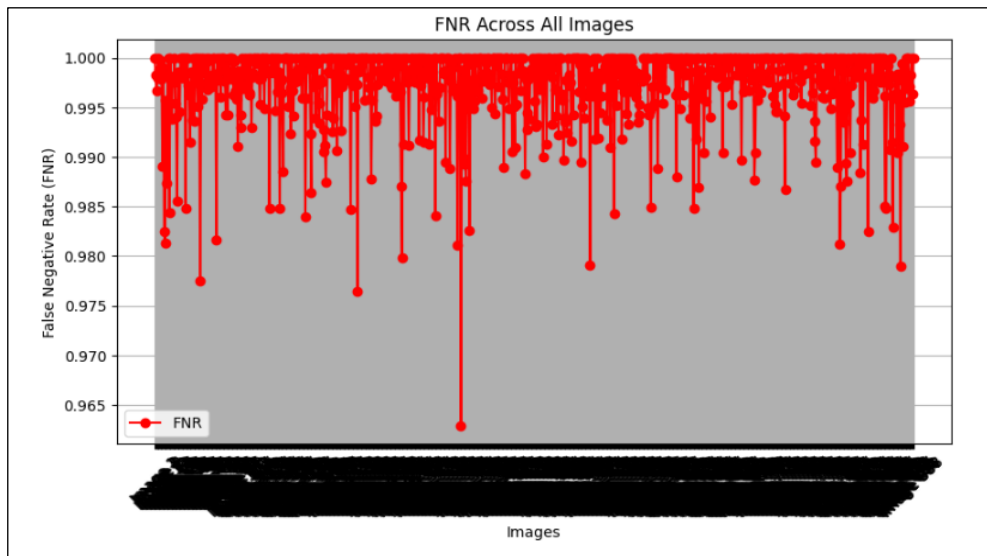


Figure 9: FNR ratio of input images.
Source: Authors, (2026).

The model needs to be improved in feature extraction, training dataset balance, and loss function optimization, according to the steady trend of low segmentation metrics. Resolving these problems with improved augmentation, post-processing methods, and architecture refinement may improve segmentation performance and increase the accuracy of tumor detection in medical imaging. The False Negative Rate (FNR) is shown by every image in the scatter plot (Fig.), which indicates the tumors the model was unable to identify. The FNR (red dots and lines) estimates the percentage of pixels that are real tumor pixels that were misconstrued as non-tumor and shows the percentage the model failed to find a cancerous area. With most values near 1.0, the plot shows an uncomfortably high FNR, indicating that the model frequently misses tumors. Most of the images have FNR values above 99%, even though some have minor variations, suggesting that the model primarily misclassifies tumor pixels. Periodic drops of the false negative rate (FNR) suggest that at times the model can detect some tumor areas but is not good enough at segmenting them overall. In medical imaging, FNR is a big issue because it means that cancerous parts might not be detected. If a patient has a falsely negative diagnosis of a cancerous tumor, and it goes undetected until later imaging, the patient can experience poor diagnostic outcomes due to factors like delayed diagnosis or adverse treatment planning. In addition, a consistently high FNR signifies that the model has more difficulty detecting small or faint tumor regions; these capabilities could also be impacted by some phenomenon, like insufficient segmentation methods applied, an unbalanced testing training set, or not extracting good features while training on a dataset. The results of this study provide evidence that deep learning models can accurately and effectively detect lung cancer. By accurately identifying malignant areas, the deep learning models require less manual human diagnosing procedures. However, there is still a concern of bias with the dataset; datasets that can be computationally intensive; as well as having a large amount of fully labeled data resulting in performant deep learning models.

V. CONCLUSIONS

Recently in the field of medical imaging, the proposed deep learning, based segmentation method for detecting lung tumors has demonstrated remarkable performance. Precision methods in the diagnosis of lung cancer such as the lung cancer screening and segmentation class trainer, the segmentation overlay, and the deep convolutional neural network (CNN) are significantly used by medical practitioners in locating tumors accurately. Furthermore, this approach lays a strong groundwork for subsequent innovations in tumor segmentation, where the combination of advanced feature extraction techniques, attention mechanisms, and optimized loss functions can substantially improve tumor segmentation performances. Since it can be used with large, scale medical datasets, the method is an excellent solution. Moreover, this model is highly promising for lung cancer diagnosis because of its ability to handle large, scale medical datasets. By integrating post, processing techniques and dataset augmentation, this system can revolutionize AI-assisted medical imaging and ensure lung cancer screening is faster, more precise, and more accessible.

VI. AUTHOR'S CONTRIBUTION

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Methodology: Swathi Gowroju and Devineni Gireesh Kumar.

Investigation: Swathi Gowroju and Devineni Gireesh Kumar.

Discussion of results: Swathi Gowroju, Devineni Gireesh Kumar and Srinivasulu Arigila.

Writing – Original Draft: Swathi Gowroju.

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