

A Novel Approach to Predict the Lungs Cancer Using the Hybrid Deep Learning Model

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Abstract:

Lung cancer is a predominant source of cancer-related mortality globally, and enhancing survival rates necessitates early detection. This research offers an integrated model that combines thresholding-based segmentation with convolutional neural networks (CNN) to predict lung cancer from CT scan pictures accurately. The initial step to isolate lung nodules from the background entails preprocessing the pictures by thresholding to generate binary images. During the second phase, a CNN is employed to analyze the segmented nodules and categorize them as benign or malignant. Our suggested model demonstrates substantial enhancements in critical performance parameters, including sensitivity (96%), recall (93%), precision (95%), and accuracy (97%), when compared to other models such as FCN, U-Net, and U-Net++. The results indicate the model's proficiency in reliably identifying and classifying lung nodules, positioning it as a potentially valuable instrument for early lung cancer diagnosis in clinical environments.

Keywords: *Lungs Image, Prediction, Deep Learning, CNN*

1. INTRODUCTION

Lung cancer is the major cause of cancer-related mortality worldwide, resulting in millions of deaths annually. The diagnosis of lung cancer remains problematic despite the fact that early detection is essential for improving survival rates and facilitating effective treatment. Radiological imaging, particularly computed tomography (CT) scans, serves as the principal diagnostic technique for detecting pulmonary abnormalities, including nodules that may be benign or cancerous [1]. Radiologists encounter difficulties in detecting small or overlooked lung nodules, often the initial signs of lung cancer, due to the complexity of CT scans, variability in nodule size, and image noise. There is a growing necessity for automated approaches that can accurately identify and categorize lung nodules to reduce human error and facilitate early detection [2].

Deep learning models, particularly convolutional neural networks (CNNs), have demonstrated significant potential in medical image analysis in recent years due to their ability to train and extract intricate characteristics from large datasets autonomously [3]. CNNs have been widely employed in several medical imaging applications, including classifying, segmenting, and identifying pulmonary abnormalities. The application of CNNs in lung cancer diagnosis is fundamentally reliant on accurately distinguishing lung nodules from adjacent tissues, as this ensures correct classification. In noisy or ambiguous images, standard segmentation approaches may inadequately represent the intricate features of nodules [4].

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We propose a distinctive two-stage approach that integrates CNN-based classification with thresholding-based segmentation to address these challenges in lung cancer prediction. The initial phase of the model employs thresholding techniques to delineate lung nodules from CT scan images. Thresholding, a fundamental yet efficient approach, classifies picture pixels according to a predetermined intensity

value, thereby distinguishing areas of interest, such as lung nodules, from the background [5] [6]. This segmentation phase ensures that the model focuses solely on relevant regions of the image, making it crucial for streamlining the subsequent classification task [7].

In the second stage, the segmented binary pictures are input into a CNN model for classification. Convolutional neural networks excel in image classification applications as they autonomously learn hierarchical patterns from raw pixel data, eliminating the need for manual feature extraction. The model is trained to differentiate between cancerous and non-cancerous nodules, enabling the network to recognize distinct features such as nodule shape, texture, and size. The suggested method employs deep learning to produce precise predictions on new data and reliable classifications.

This comprehensive approach integrates CNN classification with thresholding-based segmentation, offering an effective strategy for the early diagnosis of lung cancer. This model is unusual since it initially employs thresholding to filter images, hence reducing noise and enhancing nodule clarity; then, it utilizes CNNs to accurately classify the segmented nodules. This research meticulously assesses the model's performance on a lung CT dataset, comparing it with other leading models such as Fully Convolutional Networks (FCN), U-Net, and U-Net++. The results indicate that the proposed model demonstrates superior performance in sensitivity, memory, precision, and accuracy, making it a valuable tool for assisting physicians in the early detection and treatment of lung cancer.

2. RELATED WORK

Guo et al. [9] introduced a novel automatic segmentation model that integrates both automated and handmade components within the framework of radiomics. Dice similarity coefficients of 89.42% were achieved on the ILD database MedGIFT. Chen Zhou et al. [10] created an automated segmentation model that integrates 3D V-Net and spatial transform network (STN) to delineate pulmonary parenchyma in CT images and evaluate texture and characteristics from the segmented pulmonary parenchyma regions, thereby aiding radiologists in the diagnosis of COVID-19 [8].

Mizuho Nishio et al. [11] achieved DSC values of 0.976 and 0.973, respectively, utilizing a U-Net architecture optimized by Bayesian methods on the Japanese and Montgomery datasets. Ferreira et al. [12] introduced an enhanced U-Net model for the automated detection of COVID-19 infections. After training and assessment on the CT database from the clinical case at Pedro Ernesto University Hospital in Rio de Janeiro, this model achieved an average specificity of 99.76% and a Dice coefficient of 77.1%. The augments the network's feature extraction capability by integrating a variational autoencoder (VAE) into each encoder-decoder layer, hence enhancing the traditional U-Net architecture. The network underwent evaluation and training using the NIH and JRST datasets, yielding accuracy and F1 scores of 0.9701, 0.9334, and 0.9750, respectively.

Souza et al. [13] employ deep learning to separate lungs in CT scans with more speed and precision than the Mask Region-Based Convolutional Neural Network. The precision of lung segmentation from CT images surpasses that of non-automated approaches and benchmark techniques such as Mask RCNN.

Accelerated segmentation enhances efficiency. The approach exhibits strong generalizability to lung disease datasets, indicating possible treatment opportunities. Its ability to function effectively with a limited training sample of 39 CT scans tackles the medical sector's difficulty in gathering extensive annotated medical picture datasets. Notwithstanding these advantages, the study identifies drawbacks. The study emphasizes segmentation accuracy and does not investigate the impact of lung diseases on outcomes, thus undermining the method's external validity.

Deep learning classification systems may ultimately detect tuberculosis with precision comparable to that of physicians. Classification techniques used to segmented lungs enhance tuberculosis identification over the entire X-ray image. Gite et al. [14] performed a distinctive interpretation and analysis of U-Net++ lung segmentation outcomes in X-ray imaging. This study evaluates the diagnosis efficacy of U-Net++ against three segmentation methods for respiratory illnesses, including tuberculosis. No prior studies utilizing UNet++ for lung segmentation were identified, as numerous publications inadequately separated their resources prior to categorization. U-Net++ demonstrates superior accuracy and minimizes data loss, making it a suitable replacement for U-Net in segmentation prior to classification.

3. LUNGS CANCER PREDICTION

Thresholding is a fundamental and widely used method for image segmentation, particularly useful in medical imaging applications such as lung cancer diagnosis. To isolate objects such as lung nodules from the background in an image based on pixel intensities, a threshold value must be determined. Thresholding can be applied to CT images to identify possible lung nodules and assess their malignancy based on size and intensity for lung cancer prediction.

3.1 Pre-Processing

Improving CT images to make lung regions and nodules more visible and understandable is essential for lung cancer prediction pre-processing. In this phase, image quality is improved by methods that enhance contrast and reduce noise. Histogram equalization is a technique that modifies the intensity distribution of an image to improve contrast between lung nodules and adjacent tissues. Gaussian smoothing is an important technique used to reduce noise by applying a Gaussian filter, which facilitates the attenuation of extraneous features while preserving critical structures such as nodules. In addition, edge detection methods such as Sobel or Canny filters can be used to enhance the features of lung nodules, making them more prominent. These preprocessing techniques ensure that the subsequent segmentation and classification phases can accurately detect likely lung malignancies.

3.2 Selection of Threshold Value

The thresholding technique selects a precise threshold value TT to distinguish the background from pixels indicative of possible nodules. The threshold can be selected either manually based on domain expertise or automatically using Otsu's method, thereby enhancing the threshold by minimizing intra-class variance and maximizing the distinction between foreground and background regions. The primary objective of thresholding is to delineate regions of interest (ROIs), which, in the context of lung cancer prediction, refer to the CT scan areas that may contain lung nodules. This threshold divides the image into binary regions, with pixels exhibiting intensities above TT categorized as likely nodules, thus facilitating the detection and analysis of aberrant lung growths. This method offers a first, computationally efficient

phase for lung nodule detection; additional enhancements may be required to address difficult instances. The thresholding function is defined as,

$$f(x,y) = \begin{cases} 1, & \text{if } I(x,y) > T \\ 0, & \text{if } I(x,y) < T \end{cases} \quad (1)$$

Where,

- $I(x,y)$ is the intensity of the pixel at position (x,y) in the CT scan.
- T is the threshold value.
- $f(x,y)$ is the segmented binary image, where 1 represents potential nodules (foreground) and 0 represents the background (non-nodule areas).

The procedure of transforming a grayscale or color image into a binary format, wherein each pixel is designated as either background or foreground (representing areas of interest, such as lung nodules), is referred to as binary image production. A thresholding approach is applied to the original image to differentiate between the two classes based on pixel intensities, with a predefined threshold value T . Foreground pixels (possible nodules) possess intensity values exceeding T , whilst background pixels (non-nodule regions) have intensity values less than or equal to T . This generates a binary image in which all pixels are assigned a value of 0, while the pixels corresponding to lung nodules are assigned a value of 1. This binary segmentation facilitates the identification and isolation of areas of interest within a picture. The binary image effectively detects potential nodules; however, additional post-processing techniques, including morphological operations (e.g., dilation, erosion) and noise filtering, are frequently employed to enhance segmentation by removing minor artifacts and confirming that the residual areas are genuine nodules. The later stages of lung cancer diagnosis, including feature extraction, classification, and additional analysis, rely on the binary image produced during thresholding.

The early detection of lung cancer through CT scan images is a crucial undertaking that can significantly enhance patient outcomes. Nonetheless, accurately diagnosing malignant nodules is challenging due to the complexity of lung imaging, the variability in nodule sizes, and the presence of noise. The proposed approach addresses these challenges in two phases: segmentation using thresholding and classification utilizing convolutional neural networks (CNNs). The initial stage entails preprocessing the CT scan data using thresholding methods to generate binary images that distinguish lung nodules from the adjacent tissue. A threshold value TT is employed to distinguish between the foreground (potential lung nodules) and the background. Pixels above the threshold (TT) are categorized as nodules, whereas pixels below the threshold are designated as background. The threshold value that optimizes the separation between the two groups can be established either automatically or manually by methods such as Otsu's methodology. This simplifies the categorization process by generating a binary image that highlights the nodules. To guarantee that only relevant sections of the image are utilized in the classification phase, other post-processing procedures, such as morphological operations, are essential to enhance the segmented regions generated by thresholding alone, which may yield noisy images.

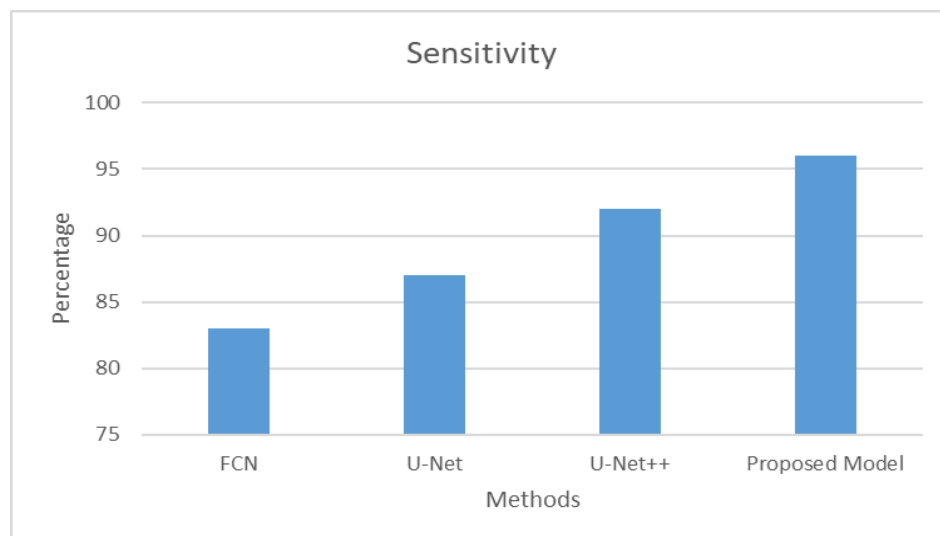
In the second stage, the CNN model classifies the segmented nodules as either malignant or benign after receiving the binary images as input. The CNN autonomously extracts essential characteristics from the segmented binary images, leveraging its robust deep learning capabilities without requiring manual

feature extraction. The model employs many convolutional layers to apply filters to the input images, thereby capturing essential attributes such as edges, textures, and shapes. Pooling layers follow the convolutional layers to extract more abstract features and reduce spatial dimensionality. The ultimate categorization is achieved by flattening the data post-feature extraction and processing it through fully connected layers. The output layer produces a probability value indicating the possibility of the nodule becoming malignant through a sigmoid activation function. A substantial repository of labeled images is utilized for training the CNN model, enhancing its accuracy in distinguishing between malignant and benign nodules as it assimilates relevant patterns. This approach integrates the robust feature extraction and classification capabilities of CNNs with the simplicity and efficacy of thresholding for image segmentation, rendering it a practical tool for lung cancer prediction that aids physicians in early cancer detection.

4. PERFORMANCE EVALUATION

The performance analysis of the proposed lung cancer prediction model involves evaluating its capacity to classify lung nodules as benign or malignant and to segment them. Essential performance metrics including as accuracy, sensitivity, specificity, and the area under the receiver operating characteristic curve (AUC) facilitate the assessment of the model's effectiveness. The model's practical use in clinical settings is fundamentally reliant on its ability to handle noisy data, generalize to novel situations, and withstand various imaging circumstances. Its comparative merits and potential areas for improvement are illustrated in relation to other leading models.

Figure 1 shows excellent sensitivity in the precise detection of cancerous nodules in lung CT scans. The FCN model, exhibiting a sensitivity of 83%, can identify a significant proportion of malignant nodules; nevertheless, it may overlook certain nuanced cases. The U-Net model improves this with an 87% sensitivity by preserving spatial hierarchies in image segmentation. U-Net++ enhances sensitivity to 92% by including thick skip connections that facilitate the acquisition of more intricate data for superior nodule detection. The proposed model achieves a peak sensitivity of 96% through the integration of CNN-based classification and thresholding-based segmentation. This significant improvement arises from CNN's ability to learn complex features and the effective preprocessing phase that differentiates nodules, resulting in high accuracy in identifying malignant nodules and reducing false negatives—both essential for early cancer diagnosis in clinical environments.



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Figure 1: Analysis of Sensitivity

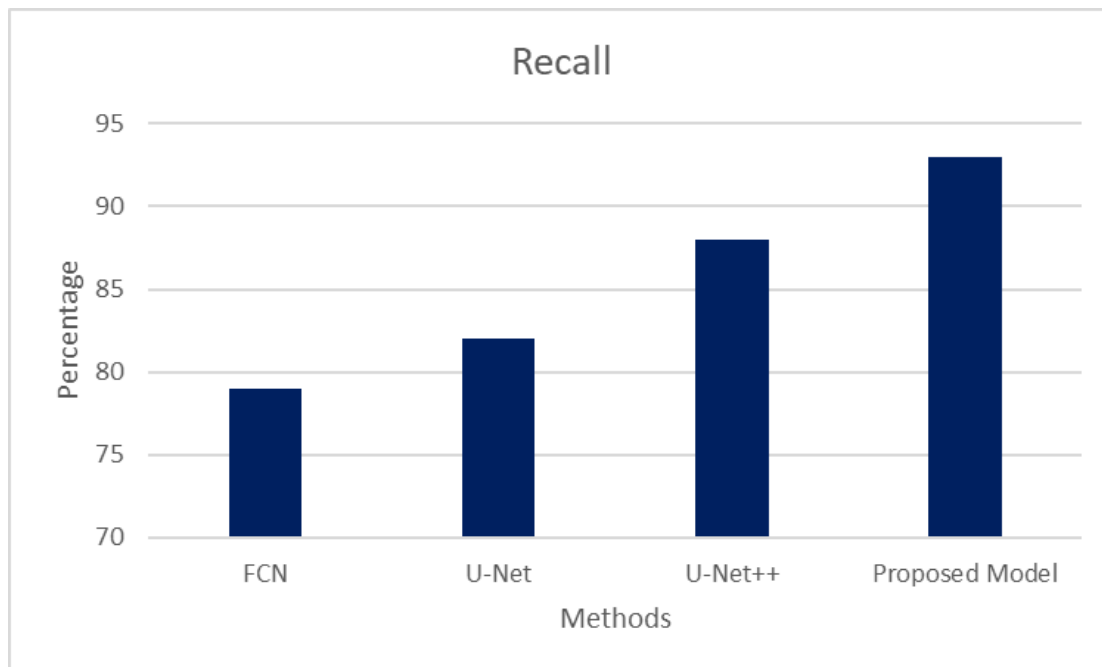


Figure 2: Analysis of Recall

Recall scores for various models indicate their efficacy in accurately identifying true benign nodules, hence minimizing false negatives shown in Figure 2. The FCN model may properly identify 79% of authentic malignant nodules with a 79% recall; nevertheless, it may overlook a significant portion, potentially leading to misdiagnosis. The U-Net model demonstrates exceptional performance, elevating recall to 82% through its refined segmentation technique for more accurate nodule identification. U-Net++ enhances recall to 88% by using more skip connections that refine the segmentation process and discern more complex patterns inside the image. The proposed model attains a maximum recall of 93% by thresholding for efficient segmentation and employs a CNN for classification. This significant rise can be attributed to its efficient preprocessing and deep learning methodology, which ensures the model consistently identifies a higher percentage of malignant nodules, hence reducing false negatives and enhancing the model's reliability for early lung cancer diagnosis.

The accuracy metrics for the various models indicate their efficacy in identifying malignant nodules while avoiding the erroneous classification of benign ones, as shown in Figure 3. The FCN model accurately identifies eighty-one percent of the anticipated malignant nodules, while nineteen percent are false positives. The U-Net model enhances the segmentation process, yielding more precise predictions and surpassing the prior model with an accuracy of 84%. U-Net++ enhances accuracy to 91% by utilizing denser skip paths for more effective detection and capture of nodules. The proposed model attains 95% accuracy by integrating CNN-based classification with thresholding-based segmentation. The model is exceptionally reliable for clinical application in accurately identifying genuine cancer cases while minimizing predictive errors due to its outstanding ability to segment nodules effectively, hence reducing false positives and correctly classifying malignant nodules.

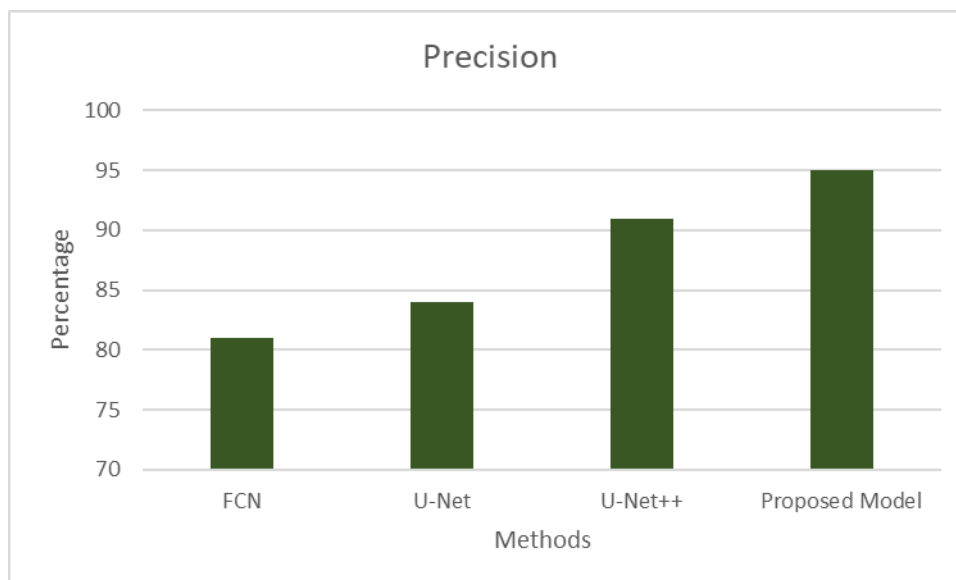


Figure 3: Analysis of Precision

The overall usefulness of the various models in accurately diagnosing benign and malignant nodules is demonstrated by their accuracy metrics shown in Figure 4. The FCN model attains 83% accuracy, indicating modest classification performance with potential for enhancement in detecting malignant nodules and reducing mistakes. The U-Net model demonstrates improved classification accuracy of 89% through its proficient segmentation capabilities that optimize image characteristics. U-Net++ enhances accuracy to 94% by its sophisticated network architecture, which optimizes feature extraction and minimizes classification errors. The proposed model attains the highest recorded accuracy of 97% by integrating CNN for precise classification and thresholding for effective segmentation. Enhanced preprocessing, accurate nodule segmentation, and the convolutional neural network's capacity to learn and categorize intricate patterns together contribute to this enhancement, reducing misclassifications and rendering the model highly effective for dependable lung cancer prediction in clinical environments.

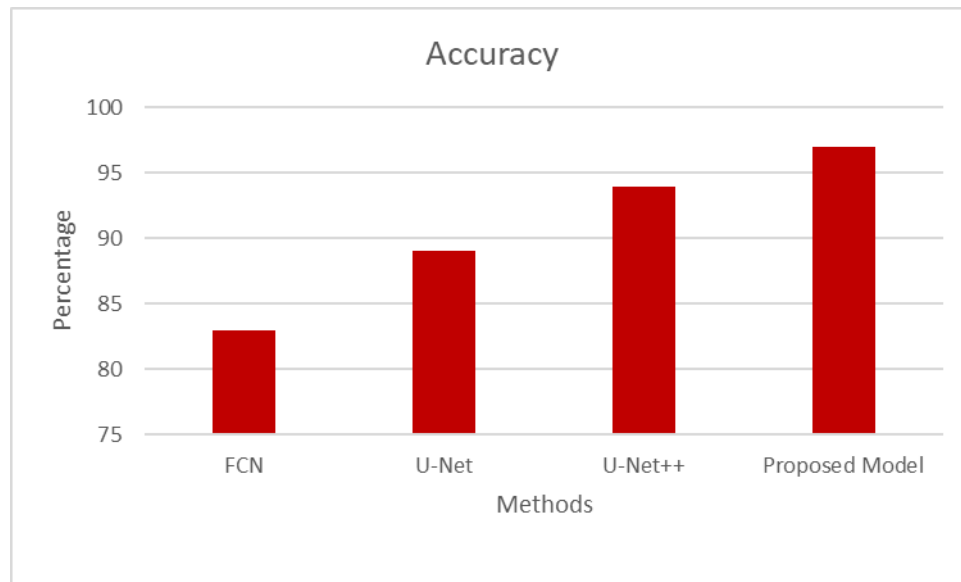


Figure 4: Analysis of Accuracy

5. CONCLUSION

The proposed approach effectively forecasts lung cancer by integrating CNN-based classification with thresholding-based segmentation. Precise nodule segmentation and sophisticated classification methods markedly enhance the model's efficacy across many evaluation measures, such as sensitivity, recall, accuracy, and precision. The model's outstanding performance demonstrates its capability to reliably and promptly identify lung cancer, essential for timely intervention and treatment. The model provides a more dependable and automated method for diagnosing malignant nodules compared to conventional procedures, resulting in a reduction of false positives and false negatives. Future endeavors may concentrate on enhancing the model, integrating more comprehensive and varied datasets, and investigating real-time clinical applications.

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