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An Efficient AGMM-Based Framework for Lung Cancer Segmentation and Severity

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Abstract

Lung cancer develops due to the uncontrolled growth of abnormal cells in the lungs and poses a significant health risk, as the lungs contain extensive blood vessels and lymphatic pathways that facilitate metastasis. Early identification and staging of lung tumors are crucial factors in improving patient survival rates. Computed tomography (CT) imaging is widely used for detecting lung abnormalities, as it provides detailed information about lung structures. Accurate medical image segmentation plays a vital role in enhancing the detection of lesion regions.

In this work, a robust image segmentation method utilizing an Adaptive Gaussian Mixture Model (AGMM) is introduced. Initially, computed tomography (CT) scans are obtained from the Lung Image Database Consortium (LIDC) dataset. To improve image quality, a Gaussian filtering technique is applied to remove noise and unwanted variations. The enhanced images are then processed using the AGMM framework to identify and segment the region of interest (ROI). To further improve segmentation accuracy, the traditional Gaussian Mixture Model is optimized using the Improved Crocodile Optimization (ICO) algorithm, which enhances parameter selection and model performance. Following the segmentation stage, the severity of lung cancer is determined based on the extent of the detected affected regions. The proposed approach is evaluated using standard performance metrics, including accuracy, sensitivity, specificity, Dice Similarity Coefficient (DSC), and Jaccard Index (JI). The entire model is implemented and tested using the MATLAB environment.

Keywords: *Segmentation, CT imaging, Gaussian Mixture Model, Improved Crocodile Optimization, Severity Assessment.*

1. Introduction

Mastitis Lung cancer is one of the leading causes of mortality worldwide and continues to pose a major challenge in the healthcare sector [1]. It develops due to the uncontrolled growth of abnormal cells in lung tissues and can spread rapidly through blood vessels and lymphatic pathways. Early detection and accurate diagnosis are essential to improve survival rates and treatment effectiveness. Computed tomography (CT) imaging is widely used for identifying lung abnormalities, as it provides detailed visualization of internal lung structures and nodules [7]. Compared to other imaging modalities such as MRI and PET, CT scans offer better clarity in detecting soft tissue variations and affected regions [8]. However, accurately identifying tumor regions from CT images remains difficult due to variations in shape, size, and intensity.

Conventional diagnostic methods such as biopsy and bronchoscopy are commonly employed for confirming lung cancer. Although these methods provide reliable results, they are invasive and may not always ensure high precision [6]. Therefore, there is a growing need for automated and intelligent systems that can assist clinicians in detecting lung cancer at an early stage with improved accuracy. In recent years, computer-aided diagnosis (CAD) systems have gained significant attention in medical image analysis. These systems utilize advanced computational techniques to enhance detection accuracy and reduce human intervention [9]. Image segmentation plays a crucial role in isolating the affected regions from CT images, which directly impacts the performance of classification and severity analysis. Deep learning techniques, particularly convolutional neural networks (CNNs), have demonstrated strong performance in medical image segmentation tasks [10]. However, these approaches require large annotated datasets and high computational resources, which can limit their practical implementation in clinical settings.

To overcome these limitations, this study proposes an efficient lung cancer segmentation and severity analysis framework based on the Adaptive Gaussian Mixture Model (AGMM). The proposed method incorporates Gaussian filtering for noise reduction, Gaussian Mixture Model (GMM) for segmentation, and the Improved Crocodile Optimization (ICO) algorithm to enhance segmentation accuracy. This integrated approach aims to provide a reliable and computationally efficient solution for lung cancer detection and analysis. The remainder of the paper is structured as follows: Section 2 presents the literature survey, Section 3 describes the proposed methodology, Section 4 discusses the experimental results, and Section 5 concludes the study.

2. Literature Survey

Recent advancements in medical image analysis have led to the development of various techniques for lung tumor detection and segmentation. These methods primarily focus on improving segmentation accuracy while minimizing computational complexity.

Kamal et al. [11] introduced a deep learning architecture known as Recurrent 3D-DenseUNet for automated lung tumor segmentation from volumetric CT images. The model incorporates recurrent connections and dense blocks to capture spatial dependencies across slices. Additionally, CONVLSTM layers are utilized to preserve contextual information. Although the method achieved improved Dice scores with reduced false predictions, further refinement is required to enhance overall performance.

Cao et al. [12] proposed a Double Branch Residual Network (DB-ResNet) for lung tumor segmentation. This approach employs convolutional neural networks to extract intensity-based features and utilizes a central intensity pooling mechanism to improve feature representation. A weighted sampling strategy is also implemented to enhance learning efficiency. Experimental results demonstrated improved segmentation accuracy; however, additional optimization is necessary for better generalization.

Singatkar et al. [13] developed a segmentation framework based on deep deconvolutional residual networks (DDRNs) for pulmonary nodule detection. The model is trained on two-dimensional CT images and focuses on preserving spatial resolution during feature extraction. While the method provides reasonable segmentation outcomes, the achieved accuracy and similarity measures indicate scope for further improvement.

Fu et al. [14] presented a multi-scale spatial attention module (MSAM) designed to enhance tumor segmentation by emphasizing relevant regions and suppressing non-tumor areas. This attention-based mechanism guides convolutional neural networks to focus on potential tumor locations. Although the model demonstrates improved segmentation performance compared to conventional approaches, its effectiveness varies across different nodule types.

Rakesh and Mahesh [15] proposed an optimization-based segmentation technique combining cuckoo search with active contour models. The method incorporates a Markov Random Field (MRF) for post-processing to refine segmentation boundaries. Despite achieving better results than several existing techniques, the method still requires improvements in accuracy and robustness.

Kumar and Raman [16] introduced a computer-aided diagnosis system utilizing a three-dimensional convolutional neural network for lung nodule segmentation. The approach improves classification performance by effectively capturing volumetric features from CT images. The model achieves a higher Dice coefficient, indicating enhanced segmentation accuracy.

Gao et al. [17] developed a CNN-based encoder–decoder architecture with deep supervision for medical image segmentation. The model enhances feature representation through pixel-wise operations and improves segmentation performance on clinical datasets. However, further refinement is needed to achieve consistent accuracy across diverse cases.

Yu et al. [18] proposed a deep learning-assisted approach for lung cancer prediction using CT images. The method integrates clustering techniques with feature extraction mechanisms based on similarity measures. Image enhancement is performed to improve segmentation quality, and the model demonstrates effective prediction capability. Nevertheless, there remains potential for improving segmentation precision and computational efficiency.

3. Proposed Framework for Lung Cancer Segmentation and Severity Assessment

This study presents an automated framework for lung cancer segmentation and severity evaluation based on the Adaptive Gaussian Mixture Model (AGMM). The overall system is structured into three major stages: preprocessing, segmentation, and severity assessment.

Initially, CT scan images are collected and prepared for analysis. These images often contain noise and intensity variations that can negatively affect segmentation accuracy. Therefore, a preprocessing step is applied to enhance image quality before further processing.

Following preprocessing, the segmentation stage is performed using an adaptive probabilistic model. The segmentation process is further refined using an optimization strategy to improve accuracy and robustness. Finally, the severity of lung cancer is determined by analyzing the segmented regions.

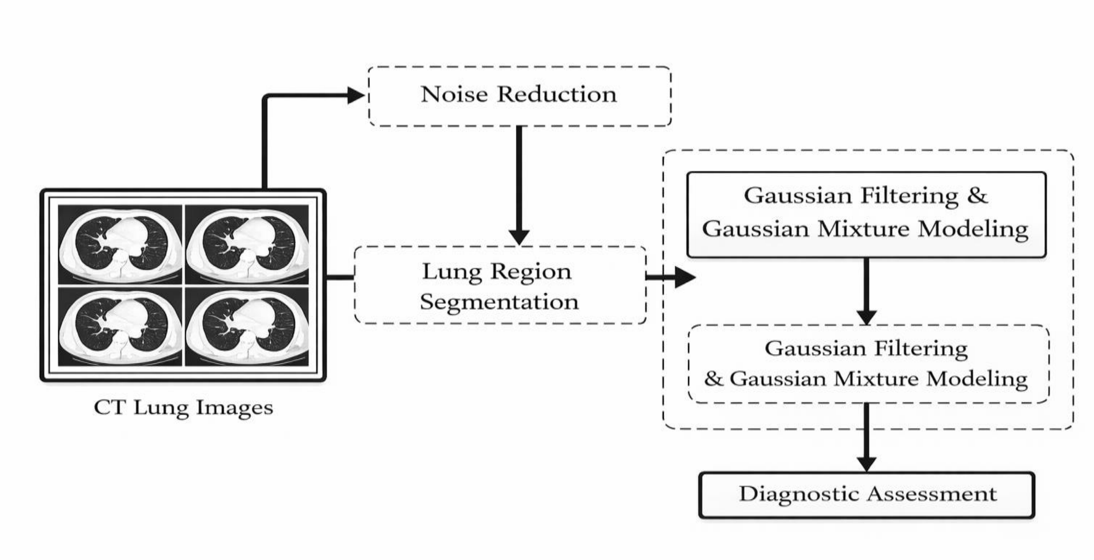


Figure 1: Proposed lung cancer severity analysis model

3.1 Image Denoising Using a Gaussian Filter

In the first stage, noise present in CT images is reduced using a Gaussian-based smoothing technique. This filtering process works by applying a weighted averaging operation to neighboring pixel values, where the weights are determined by a Gaussian distribution. The filtering operation effectively suppresses high-frequency components such as noise while preserving the essential structural information of the image. Although slight smoothing may occur at edges, the overall quality of the image is significantly improved, making it suitable for segmentation.

The degree of smoothing is controlled by a parameter that defines the spread of the Gaussian function. Proper selection of this parameter ensures a balance between noise removal and detail preservation. It is a weighted average procedure with weights defined as follows:

$$w_{a,b}\ \alpha\ \exp\left(\|y - y_b\|\right), a \neq b \tag{1}$$

The rapid decay distance is determined by the value of$w_{a,b}$.

3.2 Image Segmentation Using Adaptive Gaussian Mixture Model

After preprocessing, segmentation is carried out using the Adaptive Gaussian Mixture Model. This model treats the image data as a combination of multiple statistical distributions, where each distribution represents a specific region within the image.

The segmentation process involves grouping pixels into clusters based on their intensity values. Each cluster is characterized by parameters such as mean, variance, and weighting factor. These parameters define how the data points are distributed within each cluster. The goal of the model is to estimate these parameters in a way that best represents the underlying image structure. By doing so, the model effectively separates the region of interest (tumor area) from surrounding tissues.

To enhance segmentation performance, the model adapts dynamically based on the input data, allowing it to handle variations in image characteristics more effectively than conventional methods, the objective function of a GMM can be determined.

$$\text{Objective function} = \sum_{i=1}^{N} \log\left\{\sum_{k=1}^{K} \hat{\pi}_k \,.\, f_N\left(X_i \,|\hat{\mu}_k, \hat{\Sigma}_k\right)\right\} \tag{2}$$

Here;

$\hat{\pi}_k$→Mixture coefficient

$\hat{\mu}_k$→ Mean vector

$\hat{\Sigma}_k$→ Covariant matrix of k^{th} component

3.2.1 Parameter Optimization Using Improved Crocodile Optimization (ICO)

To further improve the segmentation accuracy, an optimization technique known as the Improved Crocodile Optimization (ICO) algorithm is integrated into the framework. This algorithm is inspired by the cooperative hunting behavior of crocodiles and is categorized under swarm intelligence methods. In this approach, a population of candidate solutions is initialized, where each solution represents a possible set of model parameters. The population is divided into two groups: search agents that actively explore the solution space and those that exploit promising regions. During the optimization process, solutions are updated iteratively based on their performance, which is evaluated using a fitness function. This function measures how well the segmentation model represents the image data. To enhance exploration and avoid premature convergence, additional strategies such as random search movements and adaptive position updates are incorporated. These mechanisms allow the algorithm to efficiently search both local and global regions of the solution space. The optimization continues until the best parameter set is identified. These optimized parameters are then used in the segmentation model to achieve improved accuracy and stability.

3.3 Disease Severity Assessment

After obtaining the segmented tumor regions, the severity of lung cancer is evaluated based on the extent of the affected area. The analysis is performed by calculating the proportion of abnormal regions within the lung. The segmented output is analyzed by counting the number of pixels corresponding to the affected region. This value is then normalized with respect to the total lung area to determine a severity index. Based on this index, the condition is categorized into different levels such as mild, moderate, severe, and critical. This classification provides useful information for clinical decision-making and helps in understanding disease progression.

4. Result and Discussion

The performance of the proposed AGMM-based segmentation framework is evaluated using CT images obtained from the LIDC dataset. The implementation is carried out using Python on a system configured with an Intel Core i5 processor, 6 GB RAM, and Windows operating system. The effectiveness of the model is assessed using standard evaluation metrics such as accuracy, sensitivity, specificity, Dice coefficient, Jaccard index, segmentation error, and average computation time.

4.1 Dataset Description

The Lung Image Database Consortium (LIDC) dataset consists of a large collection of thoracic CT scans with annotated lung lesions. It includes more than 1000 cases collected from multiple medical institutions. Each scan is reviewed by experienced radiologists, who classify lung nodules into different categories based on size and characteristics. This dataset provides a reliable benchmark for evaluating segmentation algorithms.

4.2 Experimental Results

The proposed method is compared with several existing techniques, including Gaussian Mixture Model (GMM), Fuzzy C-Means (FCM), K-Nearest Neighbour (KNN), Level Set method, and Convolutional Neural Network (CNN). The comparison is carried out to validate the effectiveness of the AGMM framework in segmenting lung tumor regions.

Table 3 summarizes the quantitative performance of the proposed and existing methods. The proposed approach achieves an accuracy of 98.2%, which is higher than all the compared techniques. The improvement in accuracy demonstrates the capability of the model to correctly identify tumor regions with minimal error.

In terms of sensitivity, the proposed method records a value of 97.16%, indicating its effectiveness in detecting true positive cases. Compared to existing techniques, the model shows consistent improvement, which highlights its ability to capture tumor regions more accurately.

Similarly, the specificity value of the proposed approach is 98.24%, reflecting its efficiency in correctly identifying non-tumor regions. This reduces the possibility of false detections and improves the reliability of the segmentation process.

The graphical comparison of these metrics is illustrated in Figure 2, where the proposed method consistently outperforms other approaches across all evaluation parameters.

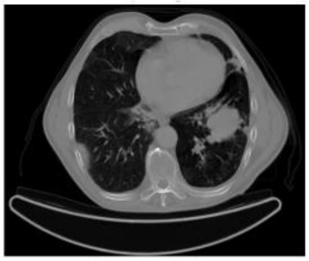
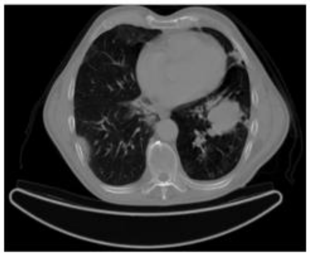
	Input image	**Preprocessed output**	**Segmented output**
Image 1			

Table 1: Comparison results of proposed and existing techniques of measurement

Dice Coefficient Analysis

The similarity between the segmented output and ground truth is evaluated using the Dice coefficient. The proposed model achieves a Dice value of 0.9, indicating a high level of overlap between predicted and actual tumor regions. In comparison, the existing methods produce relatively lower Dice scores, confirming the superiority of the proposed approach in segmentation accuracy.

Jaccard Index Analysis

The Jaccard index is also used to measure the similarity between segmented and reference regions. The proposed method achieves a value of 0.89, which is significantly higher than other techniques. This result further validates the effectiveness of the AGMM model in accurately identifying tumor boundaries.

Segmentation Error Analysis

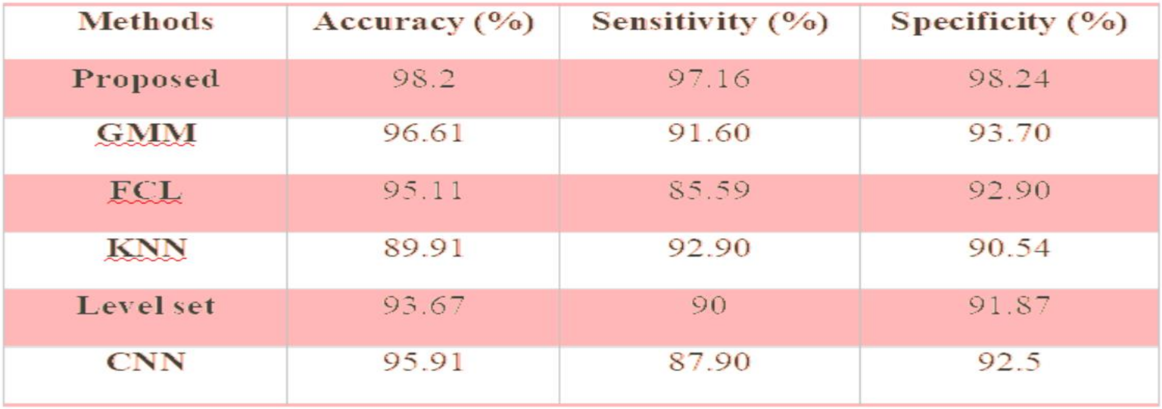
The segmentation error of the proposed model is found to be minimal compared to existing methods. The lower error rate indicates that the model produces more precise segmentation results, reducing misclassification of pixels.

Computation Time Analysis

The average running time of the proposed model is lower than that of other techniques, as shown in Figure 4. This demonstrates that the model is not only accurate but also computationally efficient, making it suitable for real-time clinical applications.

Overall Discussion

From the experimental evaluation, it is evident that the proposed AGMM-based framework provides superior performance in terms of accuracy, reliability, and computational efficiency. The integration of Gaussian filtering, probabilistic segmentation, and optimization techniques contributes to improved results compared to traditional and deep learning-based methods.



Methods	Accuracy (%)	Sensitivity (%)	Specificity (%)
Proposed	98.2	97.16	98.24
GMM	96.61	91.60	93.70
FCL	95.11	85.59	92.90
KNN	89.91	92.90	90.54
Level set	93.67	90	91.87
CNN	95.91	87.90	92.5

Table 3 summarizes the performance comparison between the proposed method and existing segmentation approaches using key evaluation metrics such as accuracy, sensitivity, and specificity. The proposed AGMM model achieves an accuracy of 98.2%, outperforming other techniques. Specifically, the accuracy is higher by 1.59% compared to GMM, 3.09% compared to FCL, 8.29% compared to KNN, 4.53% compared to the level set method, and 2.29% compared to CNN. In terms of sensitivity, the proposed approach records a value of 97.16%, showing noticeable improvement over existing methods. The sensitivity increases by 5.56% over GMM, 11.57% over FCL, 4.26% over KNN, 7.16% over the level set method, and 9.26% over CNN. Similarly, the specificity of the proposed model reaches 98.24%, indicating better performance in correctly identifying negative cases. This represents improvements of 4.54%, 5.34%, 7.7%, 6.37%, and 5.74% over GMM, FCL, KNN, level set, and CNN methods, respectively.The graphical representation corresponding to these results is illustrated in Figure 2.

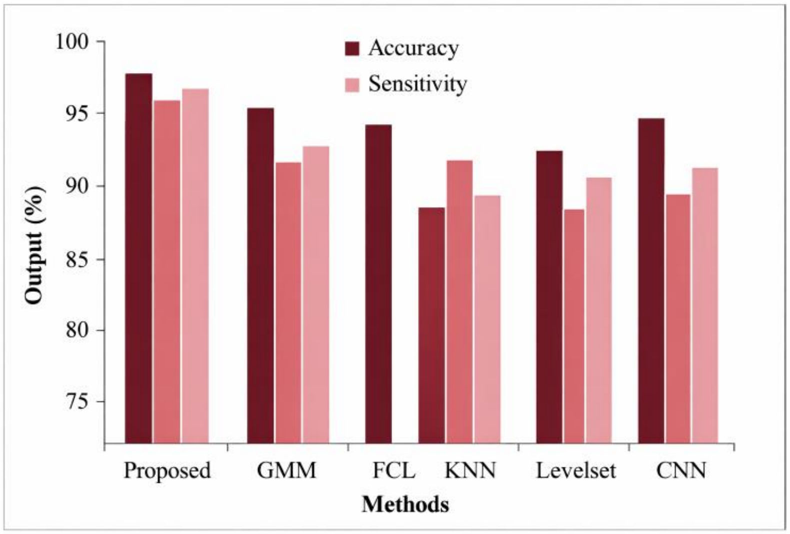


Figure 2: Comparison of metrics for the proposed technique with existing techniques

Figure 3 illustrates the comparison between the proposed method and existing approaches based on the Dice coefficient. The Dice coefficient is a statistical measure used to evaluate the similarity between two datasets, producing values in the range of 0 to 1. A value closer to 0 indicates minimal similarity, whereas a value closer to 1 represents a high degree of overlap. The proposed technique achieves a Dice coefficient of 0.9, indicating strong agreement between the segmented and reference regions. In comparison, the existing methods yield lower values, with GMM at 0.81, FCM at 0.63, KNN at 0.74, Level Set at 0.79, and CNN at 0.86.

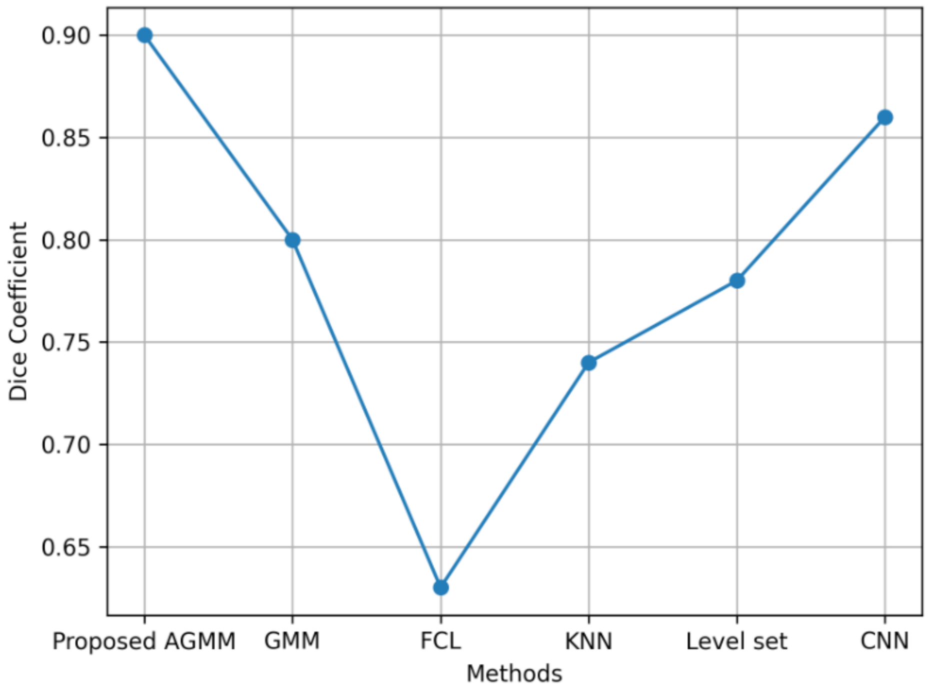


Figure 3: Comparison of Dice coefficient of the proposed and existing techniques

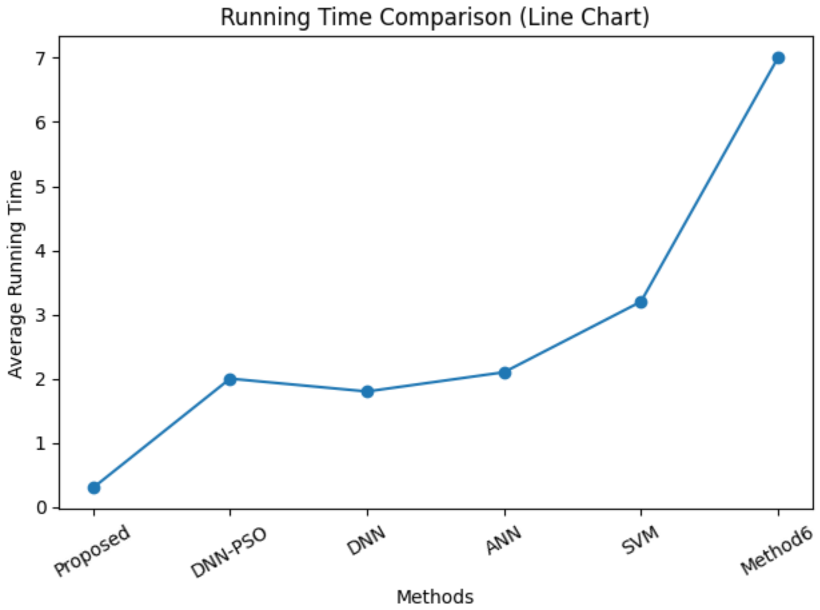


Figure 4: Comparison of segmentation average running time of the proposed and existing techniques
Through the above analysis, it is proved that our proposed AGMM based segmentation achieves better results.

5. Conclusion

This study presents an efficient framework for lung cancer segmentation and severity analysis using the Adaptive Gaussian Mixture Model. The proposed method integrates noise reduction, probabilistic segmentation, and optimization techniques to improve the accuracy of tumor detection. The experimental results demonstrate that the model achieves high performance across multiple evaluation metrics, including accuracy, sensitivity, specificity, Dice coefficient, and Jaccard index. The ability of the model to accurately segment tumor regions while maintaining low computational complexity highlights its practical applicability. Furthermore, the severity assessment mechanism provides additional clinical insights by categorizing the extent of disease progression. This feature can assist healthcare professionals in making informed decisions regarding diagnosis and treatment planning. Overall, the proposed approach offers a reliable and efficient solution for lung cancer analysis. Future work can focus on extending this framework to handle multi-class classification and integrating it with real-time clinical systems for improved healthcare outcomes.

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