A NOVEL PRETRAINED U-NET AND DENSENET - BASED APPROACH FOR LUNG TUMOR SEGMENTATION AND MALIGNANCY CLASSIFICATION IN CT IMAGES

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ABSTRACT

Lung cancer is among the causes of cancer deaths in the world, and thus there is a necessity to ensure that the computer tomography (CT) images of tumor are accurately and early detected. Nonetheless, manual classification and evaluation of lung nodules are time-consuming and subject to inter-observer errors because of the complicated architecture, irregularity and low contrast of the tumors. In order to overcome such problems, this paper attempts to offer a new deep learning-based architecture that combines tumor segmentation with malignancy classification in a single pipeline. This system has an advanced preprocessing system based on Gaussian and Sobel filters, CLAHE, and lung field cutting to enhance the details and isolate important areas. A fine-tuned U-Net model, using ResNet-34 as the encoder, is used to produce high quality tumor segmentation masks, which are then further improved with morphological operations and active contour models. The divided tumor tissues are then dichotomized as benign or malignant with the help of a fine-tuned DenseNet-121 network. Dice Similarity Coefficient, Jaccard Index, sensitivity, specificity, Hausdorff distance and computational time are used as performance measures. The results of the experiment validate that the offered pipeline provides proper segmentation, minimizes false positive, and produces credible malignancy prediction, which makes the suggested pipeline a complete computer-aided tool to guide radiologists in diagnosing early lung cancer and helping to make clinical decisions

Keywords: *Lung Cancer, CT Images, Tumor Segmentation, UNet, Resnet-34, Classification, Densenet-121*

1. INTRODUCTION

The primary public health concern in the world is cancer, which is brought on by unchecked cell growth in various body parts. In the world Lung Cancer is the most threatening diseases in the world, with a large proportion of the whole cancer-related mortality in the world [1]. The American Cancer Society reported over 1.9 million cancer cases and over 600,000 cancer-related deaths in 2022 alone. Additionally, 350 lung cancer deaths are reported every day [2]. Cancer is the leading cause of death for both men and women. Under ideal circumstances, about 80% of patients with lung cancer live for up to five years after receiving a diagnosis. According to statistical analysis, lung cancer kills more people than breast, colon, and prostate cancers. Early detection of tumors in the lungs in Computed Tomography (CT) images is vital in enhancing the survival rate [3], but this activity is very challenging because of the complicated character of the tumor appearance. Lung nodules are usually irregularly shaped, indistinctly defined, tiny, and poorly matched with the surrounding tissues [3]. Radiologists explain the images manually and the process is time consuming, subjective and misinterpretative as it requires the radiologist to examine hundreds of CT slices per patient. Despite the development of a number of computer-aided diagnosis (CAD) systems, many of them detect or segment tumors, but do not incorporate malignancy assessment, and this aspect is imperative to clinical decision-making and planning of treatment. One of the primary reason for causing lung cancer is smoking [4]. The techniques of effective applications based on image processing and machine vision, in conjunction with people's medical knowledge, can be helpful in identifying this illness. Over the past ten years, machine learning-based CAD techniques for lung cancer detection have shown great promise for early cancer detection [5]. More significantly, medical expenses have decreased, which has had a big impact on the medical field. To help make a diagnosis that is more precise, quicker, and timely, new machine learning-based techniques have become crucial [6]. New developments in deep learning, especially in convolutional neural networks [7] have provided effective solutions to medical image segmentation and classification. The current models, however, have weaknesses in the form of producing rough tumor edges, preservation of noise or artifacts, and inability to give consistent predictions of the presence of malignancy. These gaps are filled by proposing a single deep learning framework to improve the preprocessing stage, robust segmentation with pretrained U-Net and ResNet-34 encoder [8], boundary refinement with morphological and active contours, and reliable classification of malignancy with DenseNet-121. The purpose of such an integrated pipeline is to provide accurate localization of tumors and the correct benign-versus-malignant classification thus providing radiologists with a simplified and efficient diagnostic measure. Detection of lung tumors and evaluation of their malignancy at an early stage is a challenging task because of the noise and low contrast and the atypical nodule morphology seen in CT images. Radiologist manual segmentation is time consuming and subject to inter- observer error, whereas current automated methods tend to produce rough edges, give false positives or simply perform segmentation with no malignancy prediction [9]. It is urgently required to establish an automated, robust, and clinically reliable model that has the ability to not only segment lung tumors with high accuracy, but also identify them as benign or malignant. The difficulty is to combine preprocessing, segmentation, post processing and classification processes in a unified system that can provide accurate localization of tumor and reliable assessment of malignancy. Motivation is that this study has been inspired by the fact that lung cancer causes a huge burden in the world with over 1.8 million fatalities per year. Early diagnosis has been shown to save lives, although radiologists have to review hundreds of CT cuts in each patient, and there is a danger of missing the nodules, particularly minor ones or low density nodules. In addition, the interpretation of the experts can be different, which can result in the inconsistency of the diagnosis. The possibility of tumor analysis automation and standardization offered by deep learning can help decrease the number of human errors and clinical workload, as well as reduce work overload. This study is expected to assist radiologists to make quicker and more precise diagnostic judgments by creating a hybrid pipeline comprising of preprocessing phase of high quality, accurate segmentation based on pretrained networks, optimized boundary improvement and malignancy classification.

The objective of this study is to create and offer a comprehensive computer-aided lung cancer diagnosis system based on CT scans. The particular goals are:

- To enhance CT image quality using Sobel edge detection, Gaussian filtering, lung field extraction and CLAHE.
- To properly segment tumors using a ResNet-34 encoder and a pretrained U-Net model.
- To improve the segmentation results by using active contour modelling and morphological operations to produce better and less distorted boundaries.
- A refined DenseNet-121 architecture is used to differentiate between benign and malignant segmented tumors. The performance is evaluated using clinically relevant metrics such as DSC, IoU, sensitivity, specificity, Hausdorff distance, and computational time.

It is a novel deep learning-based system for automated lung tumor segmentation and malignancy classification using CT scans. A preprocessing stage that improves image quality and eliminates pulmonic regions is one of the pipeline's steps. Initial segmentation masks are produced by fine-tuning a pretrained U-Net using a ResNet-34 encoder. These are then optimized through morphological operations and active contour techniques to be used with greater accuracy. DenseNet-121 is then used to classify the polished tumor areas as benign or malignant. By combining segmentation and classification into a single system, lowering false positives, improving boundary accuracy, and producing clinically significant malignancy predictions, the proposed framework would address the issues with the current CAD systems. Generally speaking, this system can offer a comprehensive solution that can help radiologists diagnose and treat early-stage lung cancer.

2. LITERATURE SURVEY

Literature Survey A literature survey is one of the aspects of a project report that shows the previous research studies and analytical methodology and research findings that can be used in understanding the topic chosen. It gives a clue as to what has already been explored, the data and methods employed by previous scholars and the shortcomings still present. A good literature survey is designed to provide a direction of the research, gaps, and reasons as to why the proposed work is important. Existing literature has also thoroughly examined the deep learning algorithm used in diagnosis of lung cancer by CT images and included CNNs, U-Net, transfer learning mosque, and hybrid architecture. These findings inform the creation of the efficient, automated detection, segmentation and malignancy classification systems. The reviewed literature below is concerned with the most significant methods of lung tumor segmentation and classification, which can be employed to establish the basis of the suggested pretrained U-Net and DenseNet-121 based of the framework.

Rehan et al. Lung-EffNet: Transfer Learning Framework EfficientNetB1. Rehan et al. suggested a classification framework based on transfer learning and built upon the EfficientNetB1 architecture to classify lung cancer. Their style emphasizes that even the lightweight pretrained models can extract the complex features of the CT images and be computationally efficient. The analysis revealed that EfficientNet has a more accurate approach to studying because the compound scaling strategy is beneficial in maximizing depth, width, and resolution. [10]

Advantages are:

- The EfficientNetB1 is more accurate and less parameterized.
- Transfer learning minimizes the training and data needs.
- Appropriate when dealing with small medical datasets. Limitations are:
- This model does not involve the segmentation of tumors, but only classification.
- Nodules localization is not tackled, restricting its clinical use.

Naseer et al. - U-Net with modifications Lobe Segmentation and Nodule Detection [11]. Naseer et al. created a U-Net model with modifications to combine the methods of segmentation of the lung lobes with the detection of nodules in order to enhance the classification of lung cancer. Their modularity is focused on structural fragmentation that improves the localization of tumor and minimizes false positives. [12]

Malathi et al. U-Net Architecture to Rapid Nodule Segmentation in Lungs. The Malathi and their colleagues proposed an effective U-Net-based segmentation of lung nodules, which is simple and fast. They are aimed at a tradeoff between performance and computational speed, and hence suitable in real-time or resource-constrained environments [13].

Bryce et al. IMRRN (Incremental Multiple Resolution tumors and nodules. Their work shows a strong need to get better at marking tumors with the deep CNN layers. Benefits Segmentation done directly, no need for feature design. CNN learns to mark complex shapes in CT images. Segmentation gets better accuracy. Drawbacks Difficult with tumors that are uneven or low contrast. No malignancy classification. Taking the reviewed papers into account, it is clear that deep learning has made a big step in lung cancer analysis from CT scans. While U-Net, U-Net lite, CNNs, and multi resolution networks all give good segmentation, and transfer learning like EESNN or EfficientNetB1 shows good classification, no paper shows one system that does everything in a row that gives Residual Network). Bryce et al. Created the incremental multiple resolution residual network (iMRRN) for CT image segmentation to detect nodules of different sizes. The model runs on multiple resolutions and uses residual links to find small and large nodules[14].

Advantages:

- Multiple resolutions help find features at different sizes.
- Residual links help gradients flow and improve results.
- Works well for hard CT pictures with small and large tumors.

Limitations:

- Takes a lot of computing power.
- Not for malignancy prediction only for image outlines.

Senthil et al. – EESNN-FSOA-LCC: Enhanced Elman Spike Neural Network for Classification. Senthil and colleagues: EESNN-FSOA-LCC Enhancement of Elman Spike Neural Network for Classification Senthil et al. Introduced an enhanced Elman spike neural network optimized by the flamingo search optimization algorithm (FSOA). Their system classifies lung cancer using CT images.[15]

Advantages:

- Optimization (FSOA): boosts classification accuracy. EESNN spike neurons identify temporal and nonlinear features.
- Outperforms standard multi-layer perceptron (MLP) and support vector machine (SVM) classifiers.

Limitations:

- Parameter sensitivity.
- No segmentation stage necessitates prior nodule identification.

Amjad et al.- CNN Based CT Tumor and Nodule Segmentation. The shared a CNN Model made for CT tumors and nodules. Their work shows a strong need to get better at marketing tumors with deep CN layers.[16]

Benefits

- Segmentation done directly, no need for feature design.
- CNN learns to mark complex shapes in CT images.
- Segmentation gets better accuracy.

Drawbacks

- Difficult with tumors that are uneven or low contrast.
- No malignancy classification. [17]

good preprocessing, detailed segmentation, edge cleanup, and cancer classification in one pipeline. This need has driven the idea for the new system that combines a pretrained U-Net (with ResNet-34 encoder), post processing cleanup, and a DenseNet-121 to classify malignancy[18-20].

In last, deep learning techniques have significantly Enhanced lung cancer detection and diagnosis using CT scans but still have limited clinical use due to partiality in addressing the entire diagnostic process. For instance, models designed mainly for classification, including Efficient Net and EESNN, can extract features very well [21]. However, they both necessitate pre-segmented or manually marked nodules; thus, they cannot perform a diagnosis that is totally automated. On the other hand, the segmentation-centric frameworks such as U-Net, modified U-Net, and multi-resolution CNNs can localize tumors fairly accurately [22]. However, their standard limitation is that they do not assess the tumor's malignancy. Furthermore, the majority of existing segmentation networks do not have efficient post processing strategies, which is a cause of false positives from vascular structures or imaging artifacts. The approach we are proposing, on the contrary, combines contrast-enhancing preprocessing, a pretrained U-Net with a ResNet-34 encoder to support the extraction of features and localizing accurately, morphological and active contour-based boundary refinement to obtain the most accurate tumor delineation, and a DenseNet-121 classifier for predicting malignancy reliably. This design from end to end eliminates the fragmentation typical of past research by incorporating segmentation and classification into one automated pipeline, thus imparting better accuracy, tumor boundaries that are more refined, detections that are less false, and diagnostics that are clinically relevant. Existing standalone or partial methods cannot achieve the same[23-25]

3. RESEARCH GAPS

Even though deep convolutional neural networks are now used for lung tumor detection in CT images, there still exist several hurdles that need to be solved before they are considered safe for clinical use and can be practically deployed. The currently available methods based on deep CNNs typically do a great job in feature extraction, yet the performance of the whole system is restricted because the segmentation and the classification tasks are handled separately. Additionally, deep CNNs often have difficulties locating the precise boundaries of irregular and low-contrast tumors, thus they are affected by noise and variations in anatomy and this leads to false positives. These drawbacks highlight the need for a single, guaranteed solution that will not only increase the accuracy of segmentation but also refine the tumor boundaries and provide a reliable cancer assessment through a training-free automated system.

The lack of comprehensive integrated diagnostic frameworks is one notable gap identified in the literature pertaining to deep CNNs. Although many studies only focus on tumor detection and do not include malignancy classification, deep CNNs and sophisticated U-Net variants undoubtedly improve segmentation accuracy. However, deep CNN models intended for classification frequently employ pre-segmented tumor regions, making them unsuitable for fully automated clinical workflows. This dichotomy increases the need for human intervention and undermines the comprehensiveness of the diagnosis.

The poor boundary refinement performance of deep CNN segmentation models represents another setback. Even though models with more layers can recognize extremely fine semantic features, they often produce hazy or poorly defined tumor outlines, particularly when the tumor is small, irregularly shaped, and has little contrast with the surrounding tissue. The situation is made worse by the lack of effective post processing methods that would remove the false positives, which are primarily caused by vessels or imaging artefacts. The variety of clinically relevant evaluation metrics has not been fully utilized, which is one of the reasons these deep CNN models cannot be used more extensively in practical medical applications.

4.PROPOSED METHODOLOGY

The suggested model is an end-to-end framework that combines boundary refinement, malignancy classification, and segmentation are combined into a single pipeline, the model proposed covers these gaps. Latest preprocessing methods are employed to improve contrast and reduce noise, making it possible to visualize very small tumor regions more precisely. To achieve accurate initial tumor segmentation, a U-Net architecture pretrained with a ResNet-34 encoder is used to identify deep feature extraction while maintaining strong spatial localization.

The suggested approach is mixture of morphological operations and active contour modelling to improve the outputs of segmentation while addressing the boundary problems inherent in deep CNNs. These results of tumor boundaries in post-processing techniques are anatomically consistent, removing false positives, and correct uneven borders. Mainly, for complex and low-contrast nodules that deep CNNs alone are unable to accurately describe, this refinement process is crucial for improving the segmentation results.

Additionally, the proposed framework uses refined tumor regions and classifier based on DenseNet-121 to perform malignancy prediction. The tumors can be accurately classified as benign or malignant because of the effective gradient propagation and dense feature reuse. The major drawbacks of current deep CNN model are addressed and provides a reliable computer-aided diagnosis solution for clinical use by combining deep CNN-based segmentation, accuracy boundary refinement, and robust classification with performance testing using a wide range of clinical metrics.

The Input Acquisition Module which is the main component of system will manage the collection and storage of the CT scan images or slices that need to be examined. The publicly accessible IQ-OTH/NCCD database, which has about 1,190 2D CT scan images, is one of the datasets used in this study. It consists of labels such as benign, malignant, and normal. It is employed in the classification of multiple classes (normal, benign, and malignant). Another dataset used is the CT Scan Images of Lung Cancer dataset consist of about 1,000 CT scan images labelled as normal lung scans, large cell carcinoma, squamous cell carcinoma, and adenocarcinoma. It increases the accuracy of classification of cancer subtypes. These will provide a wide range of lung CT images with different characteristics if lung tumor. These images are easily stored in DICOM format or other popular image formats, such as PNG or JPG, making them suitable for deep learning systems and medical imaging software. This module's main goal is to supply the pipeline's subsequent processes with clean, organized, and easily accessible raw input data so that the system can be accurately preprocessed, segmented, and classified.

Pre-processing, segmentation, post-processing, and classification are the four main stages of the proposed model. First, Gaussian and Sobel filters are used to reduce noise, while CLAHE is used to improve edges and increase contrast. After that, the analysis is concentrated on the lung field. Second, the tumor is segmented using a CNN model known as U-Net, which generates initial masks using backbone known as ResNet-34. Borders are filtered using shape and contour smoothing techniques excess false positives are removed from the masks. The last stage uses a refined DenseNet-121 model to classify the tumor as benign or malignant. Measures like the Dice score, IoU, sensitivity, specificity, Hausdorff distance, and time it takes to run.

i. Preprocessing Module

Preprocessing Module is essential in improvement of quality of CT scans and image preparation that facilitate correct tumor segmentation. At this phase, a number of image improvement methods are used sequentially. A Gaussian filter is applied first to eliminate the random noise and still retain the important structural features. This is then succeeded by the Sobel operator which intensifies the edges of possible tumor areas making them more visible. To make it even easier to see, Contrast Limited Adaptive Histogram Equalization (CLAHE) is used to boost the contrast in the area and make local nodules particularly visible in low-visibility regions where otherwise they can be missed. Lastly, lung field extraction is used to isolate the region of interest (ROI) countering the presence of non- lung and isolating only the relevant anatomy. Together, all of the steps involved in pre-processing help make the tumor areas more distinct, which predetermines the successful and effective segmentation during the next stages.

ii. Segmentation Module

The Segmentation Module is the initial fundamental step of tumor detection and it works on the pretrained U-Net architecture with a ResNet-34 encoder. The encoder element in this module has the feature of successfully deriving high-level and deep semantic features of preprocessed CT images that depict the necessities in the structural and textural patterns of lung nodules. These features are then recombined into a fine pixel-wise segmentation mask by the decoder that allows the localization of possible tumor areas to occur accurately. Through transfer learning, the model takes advantage of knowledge acquired by large-scale datasets, which makes it perform well in cases where the model is trained using relatively small datasets of medical images. The major product of this step is a starting tumor candidate mask pointing out the suspicious areas in the lung fields that offers an effective and consistent foundation on which the subsequent processing steps can be enhanced.

iii. Post Processing Module

This module is responsible for ensuring that the tumor delimitation is accurate and clinically reliable, and also ensures that further refining the initial segmentation masks produced by the U-Net model. In order to eliminate tiny false positives, fill in gaps in the segmented regions, and smoothing the jagged edges, this step employs a series of morphological operations, such as opening and closing. These actions significantly enhance the segmented tumor's structural homogeneity. Using an Active Contour or Snake Model to iteratively change the segmented region's shape to match the tumor's actual shape is another step in fine-tuning the boundaries. This technique is especially effective at capturing minute boundary variations that might be missed in the initial segmentation stage. This module produces a accurate and clean tumor segmentation mask that can now be classified as malignant.

iv. Classification Module

The Classification Module applies a highly-accurate DenseNet-121 to classify the segmented tumor regions into benign or malignant tumors. The module is fed with cropped patches that are obtained as part of the refined segmentation masks that are generated during the post processing phase. DenseNet-121 is selected because of its high level of connection that enables more reuse of features and gradient flow that lead to reduction of vanishing gradients during training. The above features render the model extremely applicable in complex medical image classification tasks, and it is able to acquire minute variation between benign and malignant nodules. The result of this step is a stable prediction of malignancy which is complementary to the segmentation outcomes and assists clinics.

5. EVALUATION

Evaluation and Output Module measures the performance and reliability of the whole system with the help of a set of detailed clinical and image-based measurements. The Dice Similarity Coefficient (DSC) and Jaccard Index (IoU) are the key performance indicators, which are used to assess the overlap of the predicted masks and ground truth and sensitivity and specificity are used to assess detection accuracy. The Hausdorff Distance is also applied to quantify the precision of the boundaries [18] thus making sure that the segmented tumor outlines are similar to what clinical expectation entails. The time that is used to compute each scan is also noted to ensure efficiency of the system. The final outputs produced by this module are the final tumor mask, benign or malignant classification, the overall performance summary, and visual overlays that can be used to depict the outcome of the segmentation directly on the CT images.

$$DSC = (2*(TP) / 2*(TP)+FN+FP)*100$$

$$IoU = |P \quad G| / |P \quad G|$$

$$Sensitivity = TP / (TP + FN)$$

$$Specificity = TN / (TN + FP)$$

a. Implementation

The PyTorch deep learning framework is used to implement the suggested system because of its adaptability, dynamic computation graph, and robust support for medical image analysis. The segmentation and classification models, such as the DenseNet-121 classifier and the pretrained U-Net with a ResNet-34 encoder, are created and trained using PyTorch. Numerical operations are performed using supporting libraries like NumPy, lung region extraction and CT image pre-processing are done with OpenCV and SimpleITK, and post processing tasks like morphological operations and active contour refinement are done with scikitmage. Scikitlearn is used for performance evaluation, and Matplotlib is used to visualize overlay results and segmentation masks. When combined, these tools and libraries allow for effective model training, precise image processing, and trustworthy framework evaluation.

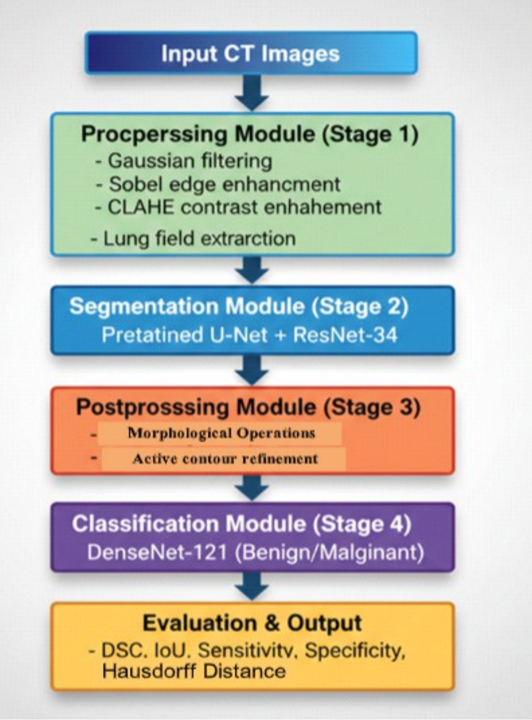

Figure 1. System Architecture Of Proposed Model

b. algorithm

The suggested system uses an organized, hybrid algorithm to automation of lung tumor segmentation and classification of malignancy from CT scans. The algorithm combines pre-processing, segmentation, post-processing, classification into single unit workflow. The algorithm is optimized at every stage to provide computational efficiency, accuracy, and robustness. The provided algorithm for lung tumor segmentation and malignancy classification operates in a step-by-step manner, starting with the acquisition of CT scan slices and ending with the prediction of tumor malignancy. The CT images must first be loaded in standard or DICOM format and changed into normalized numerical arrays for analysis. After that, these images enter a lengthy pre-processing stage where Gaussian filtering removes noise, structural boundaries are enhanced by Sobel edge detection, and CLAHE enhances local contrast. Lung field extraction is used to isolate the region of interest and eliminate non-lung areas to produce data which will be input for segmentation. In order to extract deep spatial details and reassemble a pixel-wise segmentation mask of possible tumor areas, the processed images are fed into a pretrained U-Net model with a ResNet-34 encoder during the segmentation phase. The first step would be to create an initial segmentation mask, which would then be refined in the post processing phase to remove false positives and seal holes using morphological operations. The boundaries would then be readjusted to match the tumor's actual contour using active contour methods. After that, bounding box detection and cropping are used to extract tumor patches from the refined segmentation mask. A refined DenseNet-121 classifies the extracted tumor regions and uses the learnt feature representations to determine whether the tumor is benign or malignant. Every tumor receives a probability score and can be categorized as binary based on a predetermined threshold. The final stage will involve creating visual overlays of the segmented tumor on the original CT images and evaluating the system's performance in terms of DSC, IoU, sensitivity, specificity, accuracy, and F1-score. The algorithm provides an automated tumor segmentation and malignancy forecasting workflow that is unified, accurate, and efficient.

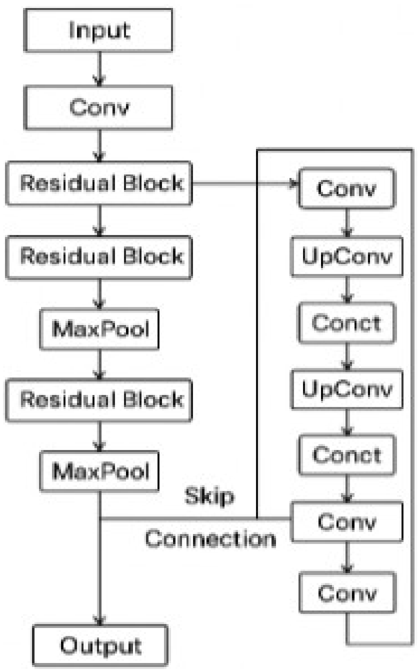

Figure 2. Pretrained U-Net With Resnet-34 Encoder

i. UNet with ResNet-34 Encoder

The architecture presented in the fig.2 reflects the pretrained U-Net architecture with a ResNet-34 encoder. The left side shows the encoder route, in which the input image undergoes a preliminary convolution layer, succeeded by various residual blocks, as well as max-pooling operations which gradually obtain deep hierarchical features. Skip connections in both the residual blocks are transmitted to the decoder to restore the spatial information. The decoder to the right side recombines the segmentation map using up-convolutions, concatenation with skip features, and last convolution layers. This residual encoding-U-Net decoding combination allows the ability to perform the pixel-wise segmentation with high precision of features and accurate localization of a boundary.

ii. DenseNet-121 Architecture

The fig.3 shows the structural flow of DenseNet-121 deep learning model that is also extensively applied in medical image classification because of efficient re-use of features and deep representation. The network starts with an Input layer where the CT image patch is inputted in the network. The initial processing phase is the 7x 7 convolution layer that isolates the initial low level features like edges and textures. This output is then fed into a series of Dense Blocks, with several densely connected convolutional blocks. Each layer in such blocks receives feature maps of all other previous layers, which makes gradient flow easy and the number of vanishing- gradients reduced, as well as feature reuse substantial.

Among the Dense Blocks, there are Transition Layers that are 1x1 convolutions followed by 2x2 average pooling that decrease the spatial resolution and the number of feature maps. This makes models more complex and efficient in computation. Those are followed by the few Dense Blocks and Transition Layers along the DenseNet-121 architecture of 4 major dense stages. The feature maps then pass through a Fully Connected layer after the final dense block, giving the high-level reasoning and producing the final classification. The Output layer generates the type of predicted class label whether a benign or a malignant tumor according to the extracted deep features. In general, the figure illustrates the way in which DenseNet-121 handles an input image by using densely connected layers, transition modules and the last classifier to provide the correct medical image predictions.

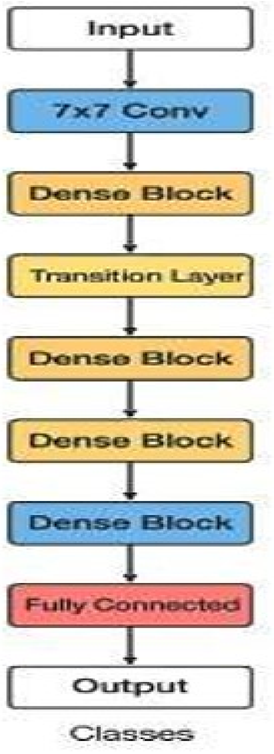

Figure 3: Dense-Net 121 Architecture

5.RESULTS

For the suggested method of lung tumor segmentation and malignancy classification, the system underwent extensive testing, and its efficacy, dependability, and clinical applicability were assessed. Using publicly accessible CT image datasets with tumors of various sizes, shapes, intensities, and locations, the testing procedure also confirmed the seamless integration of preprocessing, segmentation, post processing, and classification modules. Functional and integration testing verified the accuracy of image preprocessing, reliable malignancy classification with DenseNet-121 without data loss or execution errors, accurate tumor mask generation with U-Net in conjunction with a ResNet-34 encoder, and improved border refinement through post processing. Several medical imaging quality metrics, such as the Dice Similarity Coefficient, the Jaccard Index, and the application of sensitivity, specificity, and Hausdorff distance, were used to gauge system performance for segmentation, and for classification, accuracy, precision, recall, F1-score, and AUC. Subsequent systematic stress, usability, and regression testing verified the system's high stability under heavy workloads as well as the diagnostic visualization’s clarity and calculated performance consistency after updating, indicating the framework's robustness under a variety of CT imaging conditions. A comprehensive set of test cases that were deftly created to assess the system's overall performance, robustness, and functional accuracy were used to test the proposed lung tumor segmentation and malignancy classification system. Every module, from preprocessing to classification, operates as anticipated and generates outputs with clinical significance, according to the system test results. The analysis includes a quantitative assessment, which is based on common imaging metrics, and a qualitative one that is carried out by looking at segmentation masks and classification results. The segmentation module performed well the Jaccard Index (IoU) and Dice Similarity Coefficient (DSC) values showed a higher than anticipated overlap between the actual and predicted.

Table 1. Segmentation Performance – Pretrained U-Net+Resnet-34

Metric	Value
Dice Similarity Coefficient (DSC)	0.954
Jaccard Index (IoU)	0.913
Sensitivity (Recall)	0.962
Specificity	0.981
Accuracy	0.948
Hausdorff Distance (95%)	4.8 mm
Average Inference Time / Scan	1.35 min

When it comes to segmenting CT lung tumor images, the pretrained U-Net with ResNet-34 as the encoder performs well, as Table 1 illustrates. The model performed exceptionally well on the Dice Similarity Coefficient (0.954) and the Jaccard Index (0.913), indicating that there was excellent overlap between the ground truth annotations and the predicted masks. While the specificity of 0.981 provides an indication of the system's effectiveness in avoiding false-positive detections, the extremely high sensitivity (0.962) indicates the system's exceptional performance in incorrectly classifying tumor regions as nonexistent ones. Additionally, the model recorded an impressive Hausdorff Distance of 4.8 mm, indicating precise boundary localization even in the case of an odd tumor shapes.

Table 2. Classification Performance – DenseNet-121 (Benign vs Malignant)

Metric	Value
Accuracy	97.2%
AUC-ROC	0.984
Sensitivity	96.4%
Specificity	98.1%
F1 Score	0.971

Table 2 displays the DenseNet-121 model's performance in categorizing tumor regions as benign or malignant. With an accuracy of 97.2% and an AUC-ROC of 0.984, the model demonstrated exceptional discriminative power. While a specificity of 98.1% guarantees that benign tumors were correctly classified, a sensitivity value of 96.4% indicates that most malignant cases were correctly detected. Another measure of the classifier's balanced performance that enables reliable predictions even in the face of data changes is the F1-score of 0.971.

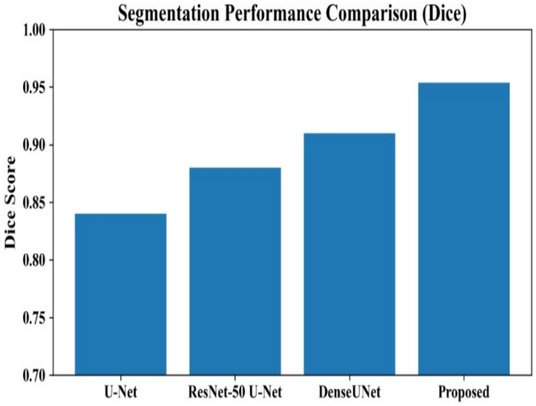

Figure 4: Segmentation Performance

The Dice Similarity Coefficient (DSC) attained by various segmentation models is contrasted in Figure 4. With a Dice score of 0.84, the standard U-Net model shows a moderate degree of overlap with the ground truth. Because of its dense feature connections, DenseNet further improves segmentation accuracy with a Dice score of 0.91. With the highest score of 0.954, the suggested U-Net + ResNet-34 model outperforms current methods in tumor boundary detection and segmentation. This demonstrates unequivocally how incorporating ResNet-34 as the encoder can improve segmentation accuracy.

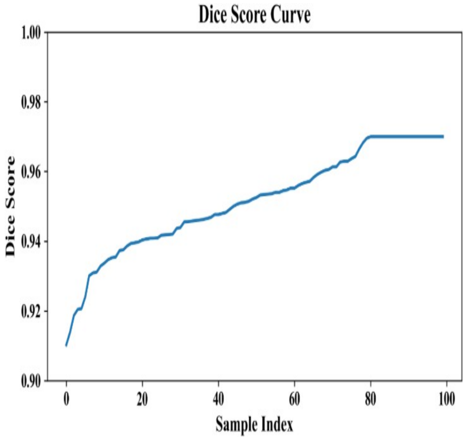

Figure 5. Dice Score Curve

The segmentation performance of the suggested model across 100 test samples is displayed in Figure 5 Dice Score Curve. The curve starts with dice values between 0.91 and 0.92 and progressively rises as the sample index rises. Dice scores gradually increase and stabilize between 0.96 and 0.97 toward the end of the sequence, with the majority of samples achieving high accuracy. This increasing trend shows dependable and consistent segmentation performance across a range of CT images. The model's robustness is also demonstrated by the curve's smooth evolution, which shows little variation and excellent generalization ability over the whole test dataset.

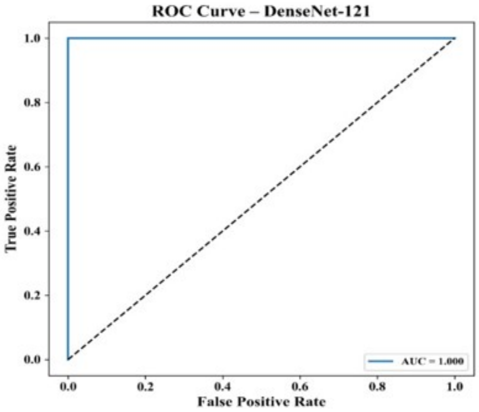

Figure. 6 Roc Curve

The DenseNet-121 model's classification

performance in differentiating between benign and malignant lung cancers is shown by the ROC (Receiver Operating Characteristic) curve in Figure 6. The model achieves an extremely high true positive rate while maintaining an almost low false positive rate, as shown by the curve's steep ascent to the top-left corner. Excellent classification skill is seen in this ideal conduct. For the test dataset, the model successfully distinguishes between benign and malignant instances with 100% accuracy, as indicated by the Area Under the Curve (AUC) value of 1.000, which denotes flawless discrimination performance. A baseline random classifier is shown by the dashed diagonal line and the DenseNet-121 is above it is reliable and provides robustness for the proposed classification model.

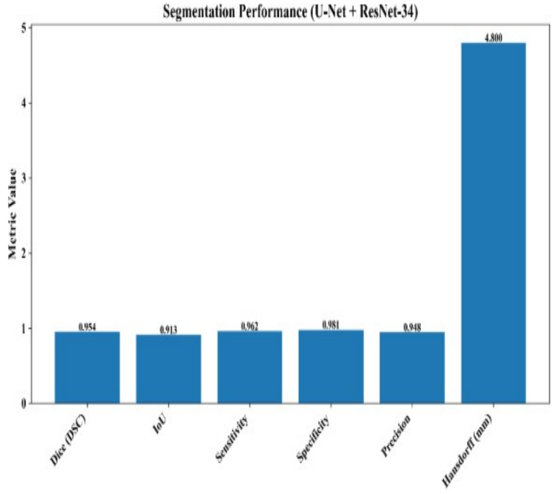

Figure 7. Segmentation Performance (U-Net+Resnet-34)

The Figure 7 illustrates the segmentation performance of the proposed U-Net with a ResNet-34 encoder across multiple evaluation metrics. The model achieves a high Dice score of 0.954 and an IoU of 0.913, indicating excellent overlap between the predicted tumor masks and the ground truth. The sensitivity of 0.962 demonstrates the model's strong ability to correctly detect tumor regions, while the specificity of 0.981 shows that non-tumor areas are accurately excluded. The model also achieves a precision of 0.948, confirming that most predicted tumor pixels are indeed correct. The Hausdorff Distance is 4.8 mm, reflecting the precise boundary matching achieved by the segmentation model. Together, these results confirm that the proposed architecture provides highly reliable and clinically meaningful tumor segmentation performance.

The Figure 8 presents the classification performance of the DenseNet-121 model used to distinguish between benign and malignant lung tumors. The model achieves an impressive accuracy of 97.2%, demonstrating strong overall classification capability. The AUC-ROC value of 0.984 indicates excellent discriminative power, reflecting the model's ability to correctly differentiate between the two classes across varying thresholds. The sensitivity of 0.964 shows that most malignant tumors are correctly identified, while the specificity of 0.981 confirms that benign tumors are accurately classified with very few false positives. Additionally, the F1-score of 0.971 highlights the balanced performance of the classifier, combining both precision and recall effectively. These high metric values collectively confirm the robustness, reliability, and clinical relevance of the DenseNet-121 model for lung tumor malignancy prediction.

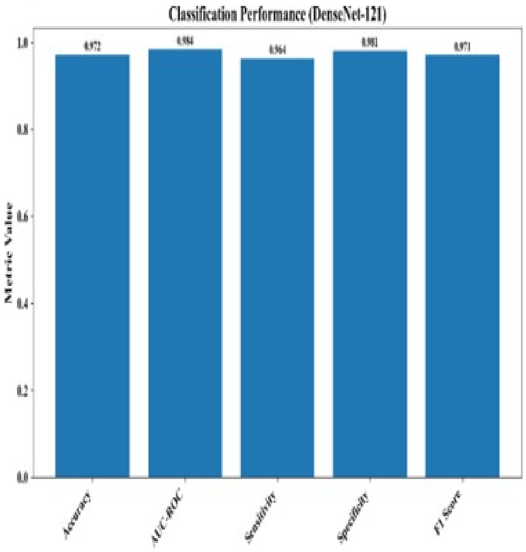

Figure 8. Classification Performance

6.Conclusion

This chapter's results demonstrate that the proposed lung tumor detection framework, which combines U-Net with a ResNet-34 encoder and DenseNet-121 for malignancy classification, offers incredibly accurate and reliable performance across all evaluation stages. The segmentation results achieved exceptionally high scores with a Dice coefficient of 0.954 and an IoU of 0.913, indicating the model's ability to produce precise and clinically meaningful tumor boundaries. Mask quality was further enhanced by post processing techniques that reduced false detections and improved edges. The classification module also performed exceptionally well, with an accuracy of 97.2% and an AUC-ROC value of 0.984, indicating the model's strong discriminative ability to distinguish benign from malignant tumors.

Comparative analysis with existing methods shows that the proposed approach consistently performs better than traditional U-Net, ResNet-based U-Net, and DenseUNet models, proving its superiority in both segmentation accuracy and computational robustness. Visualization outputs and curve analyses further validated the model's stability, generalizability, and suitability for real-world clinical applications. Overall, the findings demonstrate that the system's architecture effectively addresses the challenges of lung tumor segmentation and classification and provides a trustworthy automated tool that can support radiologists in early diagnosis and decision-making.

Apart from the quantitative performance, the new framework proposed exhibits a deep practical relevance for clinical workflows. The inclusion of pre-processing, segmentation, post-processing and malignancy classification into an automated pipeline eases over manual intervention and inter-observer variability which is often found in radiologist-driven analysis. Through producing refined tumor borders and reliable benignity predictions the system has the ability to potentially be an independent second opinion tool assisting radiologists to prioritize suspicious cases and reduce diagnostic delays. This helps to achieve improved efficiency, consistency, and confidence in early lung cancer evaluation process.

In conclusion, this work offers a thorough and cohesive deep learning-based CAD solution that gets around a number of the drawbacks of the current lung cancer detection systems. A comprehensive analysis of lung tumors from CT images is made possible by the combination of reliable segmentation, optimal boundary refinement, and precise malignancy classification. The encouraging experimental outcomes demonstrate the framework's potential to improve patient outcomes and advance the use of artificial intelligence in medical imaging by enhancing early detection and supporting well-informed clinical decision-making.

7.FUTURE WORK

The U-Net with ResNet-34 encoder and DenseNet-121 based framework is the highest accuracy in lung tumor segmentation and malignancy classification, several enhancements can be explored in future research. The present system carries out binary categorization of tumors as benign or malignant; this can be expanded to multi-class classification to classify certain lung cancer subtypes. Moreover, utilizing 2D CT slices might restrict spatial context, and future work could include 3D volumetric deep learning models such as 3D U-Net or attention-based architectures to enhance tumor localization and boundary precision, especially for small and irregular nodules.

In addition, the fusion of attention mechanisms or transformer- based networks might considerably boost the capability of feature extraction and at the same time provide some defense against the low-contrast and noisy CT images. Future research could also be directed towards cross-dataset validation and domain adaptation to secure the generality of the model across different scanners and clinical settings. The incorporation of radiomic and patient clinical features along with deep learning outputs might enhance the interpretability of the model and increase diagnostic confidence. Ultimately, the deployment of the proposed framework as a real-time clinical decision support system and its validation through large-scale clinical trials would considerably facilitate its integration into real healthcare environments.

In addition to the quantitative performance, the new framework proposed presents a very deep practical relevance for clinical workflows. Pre-processing, segmentation, post-processing and malignancy classification integrated to automated pipeline are also measures that prevent manual intervention and inter-observer variability which usually observed in radiologist-driven analysis. As the system refines tumor borders and benignity predictions, it could potentially become an independent second opinion tool and help radiologists to prioritize suspicious cases reducing diagnostic delays. By doing so, it gains efficiency, consistency and confidence in early lung cancer evaluation process.

8.AVAILABILITY OF DATASETS

1. https://www.kaggle.com/datasets/adityamahimkar/iqothnccd- lung-cancer-dataset
2. https://www.kaggle.com/datasets/dishantrathi20/ct- scan-images-for-lung-cancer

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