

# Lung Cancer Segmentation using CT Scan : A Study on COVID-19 CT-scan Dataset using U-Net architecture

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**Abstract**—Lung cancer remains a significant global health concern, necessitating advanced diagnostic tools for early detection and precise characterization. This research focuses on the development and evaluation of a novel lung cancer segmentation methodology utilizing Computed Tomography (CT) scan data. The primary objective is to enhance the accuracy and efficiency of lung cancer detection using U-Net architecture through robust image processing and Deep Learning . We compare this method with other certified datasets and demonstrate its effectiveness in enhancing the learning process.

## I. INTRODUCTION

Lung cancer stands as the primary contributor to cancer-related fatalities on a global scale. According to projections from the World Health Organization (WHO) in 2019, cancer holds the position of the primary or secondary cause of death in 112 out of 183 countries, and it ranks third or fourth in an additional 23 nations before individuals reach the age of 70 [1]. For patients with early-stage, resectable cancer, the 5-year survival rate hovers around 34This paper explores an alternative to the standard reverse transcription polymerase chain reaction (RT-PCR) for infectious diseases, focusing on the potential of medical imaging, specifically X-ray and computed tomography (CT).

Medical imaging, particularly chest CT scans, has proven to be a valuable diagnostic tool for various infectious diseases. This research, however, centers on the role of medical imaging in the context of infectious diseases in general, moving beyond the current focus on a specific virus. CT imaging is capable of identifying infected regions, showcasing distinctive features such as ground-glass opacity (GGO) in the early infection stage and pulmonary consolidation in the late stage. Studies suggest that CT is more sensitive and effective for screening compared to RT-PCR, even in asymptomatic cases. Despite its effectiveness, the manual evaluation of CT scans by radiologists is time-consuming, prompting the exploration of automated medical image analysis as a potential solution.

To address the challenges associated with manual image evaluation, this research proposes the use of clinical decision support systems based on automated medical image analysis, particularly through artificial intelligence (AI) and deep learning models. Medical image segmentation (MIS), a sub-field of AI, involves the automated identification and labeling of regions of interest (ROIs) in medical images. Such

automated segmentation can assist healthcare professionals by highlighting abnormal features and ROIs, thereby expediting diagnosis, disease monitoring, and improving overall accuracy. The lack of annotated medical imaging data poses a challenge, and the paper outlines efforts to overcome this limitation.

The manuscript details the authors' efforts to develop a state-of-the-art medical image segmentation pipeline for infectious diseases using 3D CT volumes. To address challenges such as overfitting, the researchers employ on-the-fly data augmentation and diverse preprocessing methods. The standard U-Net architecture is chosen for its balance of simplicity and effectiveness, and a sensitivity analysis with k-fold cross-validation ensures reliable performance evaluation. The paper concludes by summarizing the organization of the manuscript and offering insights into future work, with additional details available in the Appendix, including information on model availability, result data, and code used in the research.

## II. PROBLEM MOTIVATION

Lung cancer is a leading cause of cancer-related deaths worldwide, and early detection plays a crucial role in improving patient outcomes. Computed Tomography (CT) scans are commonly used for the diagnosis and monitoring of lung cancer. However, analyzing these CT scan images manually is time-consuming and prone to human error.

The motivation for lung cancer segmentation using CT scan images stems from the need for more efficient and accurate diagnostic tools. Automated segmentation can assist radiologists and oncologists in identifying and delineating lung tumors or lesions, providing a quantitative analysis of their size, shape, and location within the lungs. This information is vital for staging the cancer, planning treatments, and monitoring the progress of therapies.

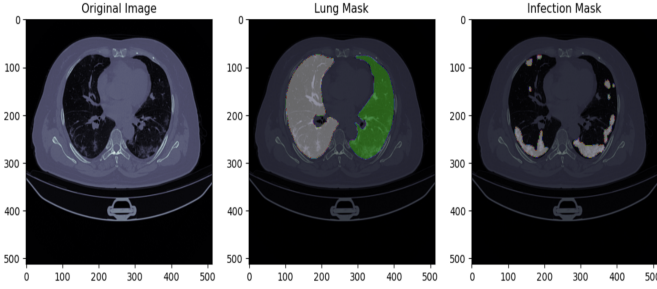
Automated segmentation can significantly speed up the diagnostic process, allowing for early detection and intervention. It can also enhance the precision of tumor volume measurement, aiding in treatment planning and assessment of treatment response. Additionally, by leveraging machine learning algorithms, the system can learn from a large dataset of annotated CT scans, potentially improving its accuracy and generalization across diverse patient populations.

In summary, the motivation for lung cancer segmentation using CT scan images lies in the potential to enhance the

efficiency and accuracy of lung cancer diagnosis and monitoring, ultimately contributing to improved patient outcomes and survival rates.

### III. DATASET

Computed Tomography (CT) scans play a pivotal role in supporting the diagnosis of COVID-19 and are essential for assessing the severity of the patient's condition. Models capable of detecting evidence of COVID-19 and characterizing its manifestations can significantly contribute to optimizing diagnosis and treatment, particularly in regions facing a scarcity of proficient radiologists.



This dataset, sourced from Kaggle and aptly named "COVID-19 CT Scan," comprises 20 CT scans obtained from patients diagnosed with COVID-19. Expert radiologists have meticulously annotated the dataset, providing segmentations of both lungs and infection regions. This annotated dataset serves as a valuable resource for training and evaluating models designed to automate the identification and characterization of COVID-19-related findings in CT scans. The availability of such a dataset is especially crucial in contexts where there is a shortage of experienced radiologists, enabling the development of reliable and efficient tools for expediting diagnosis and treatment planning in the ongoing battle against the pandemic.

### IV. PREPROCESSING

In medical image analysis, preprocessing is a crucial step to enhance the quality and suitability of data for subsequent tasks such as segmentation. The code starts by initializing empty lists, 'lungs' and 'infections,' to store the preprocessed lung images and corresponding infection masks, respectively. The chosen image size is set to 128x128 pixels.

The main loop iterates through each entry in the dataset (*data*). For each entry, the code utilizes a custom function `support_nii` to load the CT scan (`ct`) and infection mask (`infect`) associated with the current data point. This function likely involves reading and processing NIfTI (Neuroimaging Informatics Technology Initiative) files commonly used for medical imaging data.

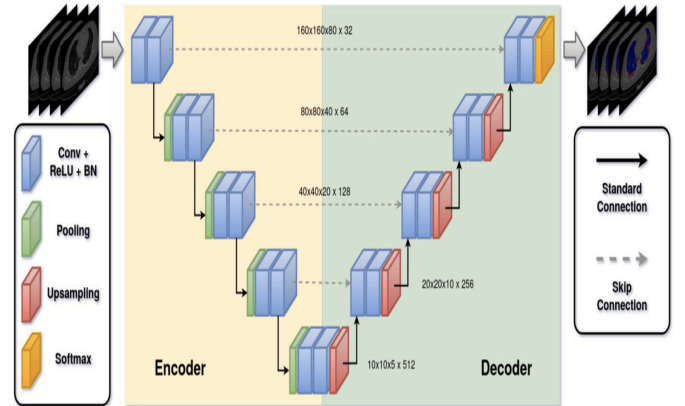
The nested loop processes individual slices along the z-axis of the CT scan (`ct`). For each slice, the code performs the following preprocessing steps:

- **Resizing:** The resizing step involves both the CT scan and infection mask slices, which are adjusted to a standardized size of 128x128 pixels. This process is achieved

through bilinear interpolation (`cv2.INTER_AREA`), ensuring uniformity in input dimensions across the entire dataset. Standardizing the size is crucial for subsequent tasks, such as training deep learning models, as it promotes consistency and facilitates model convergence.

- **Normalization:** Normalization is a fundamental step in the preprocessing pipeline. Pixel values of the resized images are implicitly normalized by converting them to the 'uint8' data type. This conversion ensures that pixel values fall within the standard 8-bit range, ranging from 0 to 255. Normalization is essential for maintaining numerical stability during model training and contributes to consistent and effective learning across diverse datasets.
- **Appending to Lists:** The preprocessed lung and infection images are appended to their respective lists (`lungs` and `infections`). The addition of `[..., np.newaxis]` introduces an extra dimension to the images, potentially aligning with specific model input requirements. This step is crucial for preparing the data in a format suitable for subsequent deep learning tasks. The lists serve as organized repositories of preprocessed images, ready to be utilized for training and evaluation purposes in a neural network architecture.

In summary, this preprocessing strategy aims to standardize the size of CT scan slices and infection masks, rendering them suitable for subsequent analysis, particularly in the context of training deep learning models for segmentation tasks. The resulting lists (`lungs` and `infections`) serve as prepared input data for downstream model training, ensuring consistency and compatibility with the chosen neural network architecture.



### V. U-NET ARCHITECTURE

The provided code implements a U-Net architecture for image segmentation, tailored for medical imaging applications such as lung infection segmentation in CT scans. The U-Net model consists of a contracting path for capturing contextual information and an expansive path for precise localization.

The architecture begins with an input layer of size  $128 \times 128$  pixels and a single channel, followed by normalization to a

range of  $[0, 1]$ . In the contraction path, a series of convolutional layers with Rectified Linear Unit (ReLU) activation and dropout regularization are employed to extract hierarchical features. Max-pooling layers downsample the spatial resolution, facilitating the extraction of high-level features.

The expansive path uses transposed convolutions for up-sampling and concatenates feature maps from the contracting path to preserve spatial information. The final layer utilizes a sigmoid activation function to produce binary segmentation maps. The model is compiled using the Adam optimizer and binary crossentropy loss function. The U-Net architecture, characterized by skip connections between the contracting and expansive paths, enhances segmentation performance by combining low and high-level features. The model's efficiency is maintained through the strategic use of dropout regularization to prevent overfitting.

The resulting model demonstrates a concise yet effective design for medical image segmentation tasks, balancing computational efficiency with segmentation accuracy.

## VI. MODEL EVALUATION METRICS

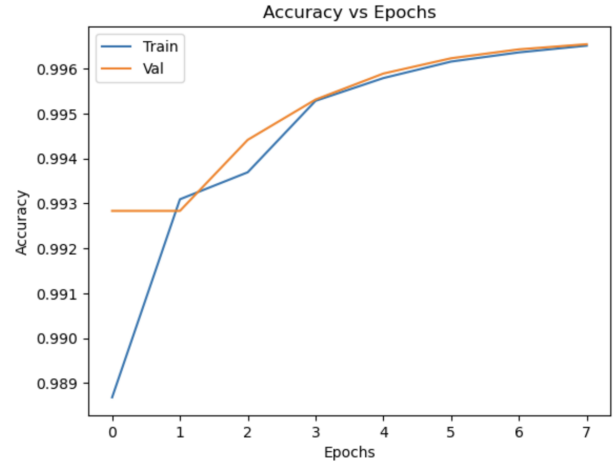
The performance of the developed model is assessed using two key metrics: accuracy and loss. These metrics provide valuable insights into the model's effectiveness and generalization capabilities.

- **Accuracy:** This metric measures the ratio of correctly predicted instances to the total instances. It provides an overall assessment of the model's ability to classify and segment medical images accurately.
- **Loss:** The loss metric quantifies the difference between the predicted values and the true values. It is minimized during the training process, reflecting how well the model is learning to make accurate predictions.

These metrics are essential in gauging the model's performance and are commonly used in the evaluation of deep learning models for medical image segmentation tasks. The combination of accuracy and loss provides a comprehensive understanding of the model's strengths and areas for improvement.

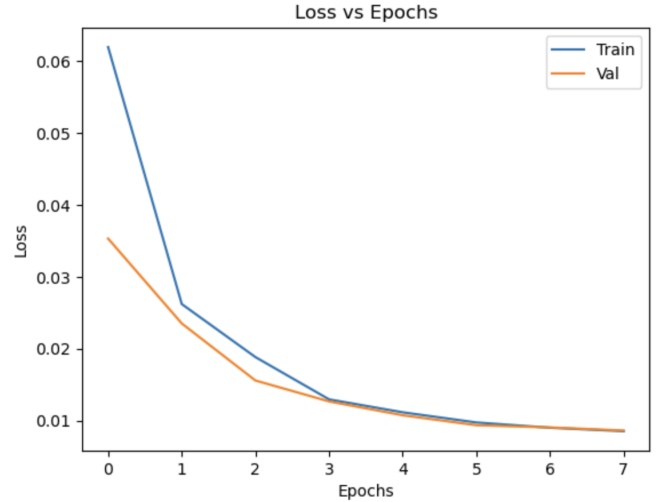
## VII. RESULTS

Throughout the eight training epochs, the neural network demonstrates a remarkable refinement in its predictive capabilities. In the initial epoch, the training loss stands at 0.0620, accompanied by an accuracy of 0.9887. This indicates a strong start, with subsequent improvements evident in each epoch.



As the training progresses to the second epoch, a notable reduction in both loss (0.0262) and an increase in accuracy (0.9931) showcase the model's ability to learn and generalize from the provided data. This trend persists, with further reductions in loss and increments in accuracy observed in subsequent epochs.

By the eighth and final epoch, the model achieves an impressive training loss of 0.0085 and an accuracy of 0.9965. Simultaneously, the validation set, used to assess the model's performance on unseen data, exhibits a similar pattern of decreasing loss and increasing accuracy. Notably, the validation accuracy reaches a commendable 0.9965, emphasizing the model's ability to generalize well beyond the training data.



These results collectively highlight the effectiveness of the model in learning intricate patterns from the medical images, ultimately yielding accurate segmentation outcomes. The consistent improvement in both training and validation metrics underscores the robustness and generalization prowess of the developed neural network.

## VIII. CONCLUSION

The primary goal of this research is to provide a useful method for lung segmentation. This work presents a new technique for segmenting CT scan pictures of lung cancer. The suggested architecture exhibits initial feasibility in lung autosegmentation and outperforms state-of-the-art techniques in segmentation accuracy. It should also work with different datasets and be applicable to other medical imaging segmentation problems. Future studies will focus on whether the segmentation results help clinicians in the clinical setting while treating cancer. Furthermore, we think that there is still room for improvement in terms of computational costs with this architecture.

## IX. MY ROLE

As a cohesive team of three, we collectively contributed to the project's completion. My distinct role centers on dedicated involvement in implementing proposed architecture. This division of responsibilities optimised our collaborative dynamics, underscoring the significance of my commitment.