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Lung and Lung Tumor Segmentation of CT Images During MWA Therapy Using AI Algorithm

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Abstract

Microwave ablation (MWA) therapy as a thermal ablation procedure is an excellent alternative to open surgery for tumor treatment. The technique is considered advantageous for patients who are not candidates for open surgery due to factors such as age, anatomic limitations, resection, etc. Computed tomography (CT) is a commonly used interventional imaging modality during MWA therapy for localizing the tumor and finalizing the tumor treatment process. However, the CT scan of the body usually includes neighboring organs that are not relevant to lung tumor MWA therapy. Therefore, the segmentation of the lung and lung tumor in CT images provides valuable information about the tumor margin. This information can assist physicians in precisely and completely destroying the tumor during the MWA procedure. To solve the aforementioned problem, deep learning (DL), in particular, achieves a higher level of accuracy in segmentation than machine learning techniques due to its composition of multiple learning layers. The immediate goal is to distinguish among the different tissue structures of the tumor, healthy tissue, and the ablated area in lung CT images using the DL method to segment the organ and cancer area. Researchers have proposed various segmentation models. However, different segmentation tasks require different perception fields. In this study, we propose a new DL model that includes a residual block based on the U-Net model to accurately segment the lung organ and lung tumor tissue. The dataset consists of lung CT images acquired during MWA therapy using a CT scanner at the University Hospital Magdeburg. Manual tumor segmentation has been performed and confirmed by physicians. The results of our proposed method can be compared with those of the U-net model with a SSIM of 90%. Furthermore, accurately determining the margin area of the tumor tissue can decrease insufficient tumor ablation, which often leads to tumor recurrence. We anticipate that our proposed model can be generalized to perform tumor segmentation on CT images of different organs during MWA treatment. Finally, we hope that this method can achieve sufficient accuracy to decrease tumor recurrence and enable dose reduction for patients in interventional CT imaging.

Keywords: Deep Learning (DL); Artificial Intelligent (AI); Lung Tumor Segmentation; Microwave Ablation (MWA) Therapy.

1. Introduction

Lung cancer is one of the diseases that causes millions of deaths each year [1]. Extensive research has been conducted in the field of lung cancer diagnosis and treatment. However, upon careful review of the published literature, we have

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identified certain gaps that need to be addressed. In recent years, MWA has gained significant attention as a minimally invasive and effective treatment technique for lung cancer. Tumor ablation, which involves using heat under image guidance, has proven to be a highly effective method for eliminating tumors in their specific locations [2]. CT is an efficient medical imaging modality commonly used in MWA therapy. However, when conducting a CT scan of the body, it often includes different neighboring organs that are not relevant to lung tumor MVA therapy. Therefore, the segmentation of the lung and lung tumor in CT images provides valuable information to physicians regarding the tumor margin. This information assists them in precisely and completely destroying the tumor during the MWA procedure [3–5]. However, lung segmentation, particularly lung tumor segmentation, poses a significant challenge is a challenging task. Deep learning, with its composition of multiple learning layers enabling automatic feature extraction, has achieved a higher level of accuracy compared to traditional machine learning techniques [7, 8]. DL in this field holds the potential to replace manual and time-consuming tasks performed by physicians based on their expertise and experience. It can assist them in their daily routine by precisely distinguishing between tumor and healthy tissue, ultimately reducing tumor recurrence.

Numerous approaches have been suggested in previous studies to accomplish the objective of segmenting lung tumors, each with its own achievements and approaches. Dutande et al. [8] incorporate various components, including a preprocessing method based on maximum intensity projection, two innovative deep learning networks (DRS-CNN1 and DRS-CNN2), and an ensemble strategy. These networks, DRS-CNN1 and DRS-CNN2, outperformed the U-net network as well as other segmentation networks, demonstrating superior performance. This method achieved a dice value of 0.649 and a mean sensitivity of 0.737. Hu et al. [9] propose a novel image segmentation approach using a parallel deep learning algorithm with a hybrid attention mechanism. It involves extracting lung parenchyma, applying a hybrid attention mechanism and DenseNet, and exploring different options for optimal performance. Experimental results show the algorithm achieves a high accuracy of 94.61% in segmenting lung tumors. He et al. [10] utilized an ANN algorithm to create a lung cancer recognition model. The model accurately identified the lung cancer lesion area using an image segmentation algorithm. Through a comparison experiment, it was verified that the model achieved an accuracy of 94.6% in identifying lung cancer.

Ait Skourt et al. [11] present a lung CT image segmentation approach utilizing the U-net architecture, a popular deep learning architecture for image segmentation. The U-net comprises a contracting path for high-level information extraction and an expanding path for information recovery. This network demonstrates superior performance, surpassing many existing methods, and achieves precise segmentation with a Dice-Coefficient index of 0.9502. Rehman et al. [12] utilized U-Net with a mean_iou of 92.82 to generate lung segments from X-ray images. Pang et al. [13] introduced a novel automatic segmentation model based on radiomics, combining handcrafted and automated features, achieving Dice similarity coefficients of 89.42% on the ILD database MedGIFT. Chen Zhou et al. [14] developed an automatic segmentation model by integrating (3D) V-Net and a spatial transform network (STN) for segmenting pulmonary parenchyma in CT images. They further analyzed the texture and features of the segmented pulmonary parenchyma regions to aid in the COVID-19 diagnosis. Mizuho Nishio et al. [15] optimized the U-Net architecture using Bayesian optimization on Japanese and Montgomery datasets, resulting in DSC scores of 0.976 and 0.973, respectively. Ferreira et al. [16] proposed a modified U-Net model for detecting COVID-19 infection on CT scans, achieving a dice value of 77.1% and an average specificity of 99.76% when trained and evaluated on the CT database of Pedro Ernesto University Hospital. Cao [17] improved the traditional U-Net architecture by incorporating a Variational Autoencoder (VAE) in each layer of the decoder-encoder, enhancing the network's feature extraction capability. Testing and training on NIH and JRST datasets, the model achieved accuracy and F1 scores of 0.9701, 0.9334, and 0.9750, 0.9578, respectively.

In this study, we aim to contribute to the current body of knowledge by focusing on the challenging task of lung tumor segmentation. While various segmentation techniques have been proposed, there is a need to further advance the field by leveraging the capabilities of deep learning. By employing deep learning in lung tumor segmentation, we aim to replace labor-intensive and time-consuming manual tasks performed by physicians, reducing both subjectivity and the potential for human error. In this context, we employ the ResLU-Net model for segmentation. Its exceptional performance in liver segmentation using interventional CT scans has motivated us to extend its application to lung tumor segmentation. Building upon the success achieved in liver tumor segmentation, we maintain optimism that the ResLU-Net model will exhibit high effectiveness in segmenting lung tumors. This advancement holds promise for both the medical community and patients, representing a significant breakthrough in medical image segmentation. Our research aims to fill the existing gap in the literature by providing a novel and effective approach to lung tumor segmentation, enhancing the precision and efficiency of tumor identification.

2. Method and Materials

The aim of this research was to gather anonymous CT scan data from 50 patients suffering from lung tumors who received MWA treatment at the University Hospital of Magdeburg, Germany. Finding the tumor in separate slices during the process is difficult, particularly for untrained observers. However, it becomes easier to locate the tumor if we examine the slices taken during the insertion of the needle during MWA therapy. We can estimate the tumor's location and size from the slices taken before the MWA procedure, using the needle's location as a reference. The block diagram of our workflow is shown in Figure 1. The diagram shows that, at first, CT images are acquired during MWA therapy. Then, image selection is performed, including the images of the lung and lung tumors. Following that, manual annotation of the lung and lung tumors is performed and confirmed by experts. To address the small dataset issue, data augmentation is conducted. Subsequently, the data is divided into three classes for training, validation, and testing purposes, using the ResLU-Net model for segmentation. The final step involves generating predicted masks, which are the outcomes of our model.

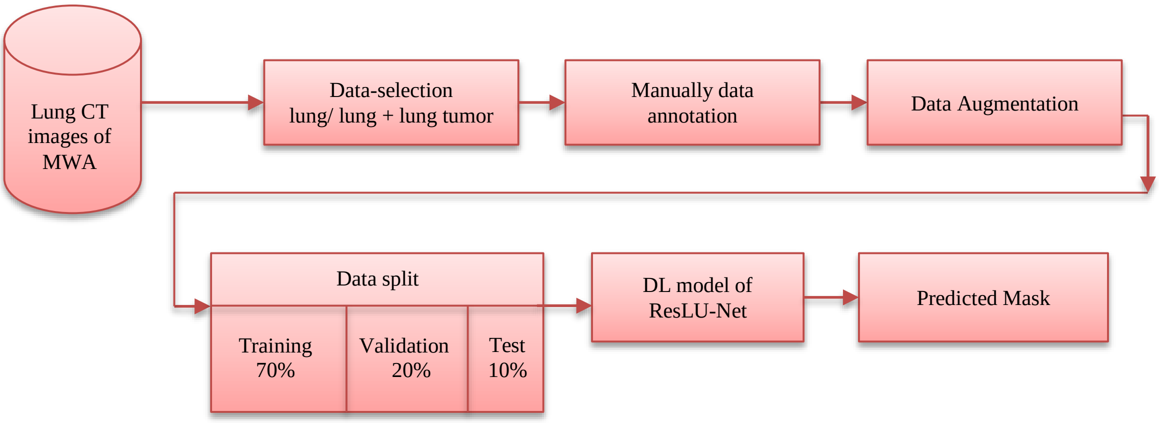
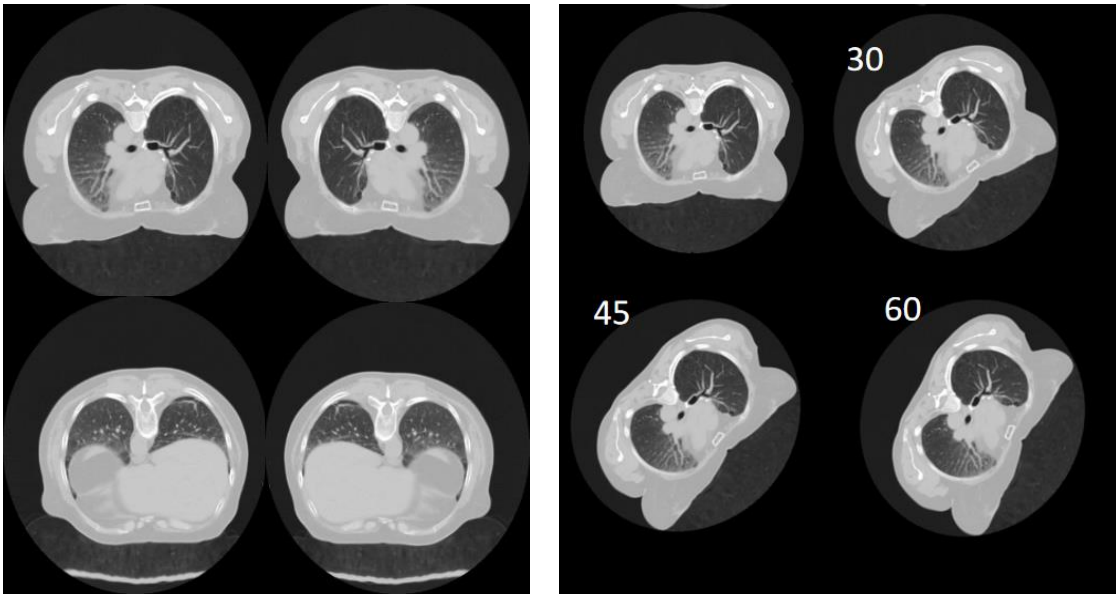


Figure 1. The workflow of Lung and lung-tumor segmentation steps

2.1. Database

Our experiments were conducted on lung CT images acquired during MWA therapy at the University Hospital Magdeburg, Germany (IRB No:66/22). The dataset consists of original and augmented images from 50 patients, with 70% of the images used for the training set, 20% for the validation set, and the remaining for the testing set. The annotations in this dataset cover the tumor region and the entire lung area, including both the right and left lungs. The dataset comprises DICOM files with a resolution of 512 x 512 pixels for CT scan slices, acquired using a Toshiba Aquilion PRIM CT scanner.

For the segmentation task, two-dimensional CT slice images were employed. The challenge with medical CT images lies in the variation of shape, size, and location of the lung and lung tumor, which are the regions of interest (ROI) in our work. Additionally, the tumor size in our dataset is small and the number of images is limited, which adds complexity to the task. In order to overcome the mentioned problem, data augmentation techniques are employed, including image rotation with angles of 30, 45, and 60 degrees and horizontal flipping (see Figure 2). In the preprocessing step, the ground truth for both the lung tumor and the lung organ's annotated areas is generated using ImageJ 1.53e software.



(a) flip (b) rotation

Figure 2. An example of (a) horizontal flipping and (b) rotation with three different degrees: 30, 45, and 60

2.2. ResLU-Net Model

In this study, we present a novel and improved approach for lung CT image segmentation utilizing the U-Net model, which is widely recognized as one of the most effective segmentation models in the medical imaging domain [1]. The conventional U-Net model consists of a symmetric structure comprising a contracting path and an expanding path, where each layer incorporates convolutional and pooling operations [6]. However, despite its proven efficacy, the traditional U-Net model may not be universally suitable for all segmentation tasks. Therefore, we propose a modified version of the U-Net model that introduces slight modifications, resulting in superior segmentation performance.

Our proposed model represents a significant contribution to the field of medical image segmentation, building upon the success achieved in liver tumor segmentation using interventional CT [7]. It replaces the ReLU activation function with the Leaky rectified linear unit (LReLU) activation function, which is more suitable for preserving image details. Additionally, we incorporate a residual structure in the last convolutional layer of the down-sampling process to address the degradation problem and enhance the model's performance. Further details about the model can be found in our previous study, which focuses on liver tumor segmentation in CT MWA images [7]. In Figure 3-a, we illustrate how the ResLU-Net model, with its residual structure in the middle part, takes input lung and lung tumor CT images and generates an output mask. The contracting path in the ResLU-Net model remains the same as in the conventional U-Net architecture, with the inclusion of LReLU as the activation function (Figure 3-b).

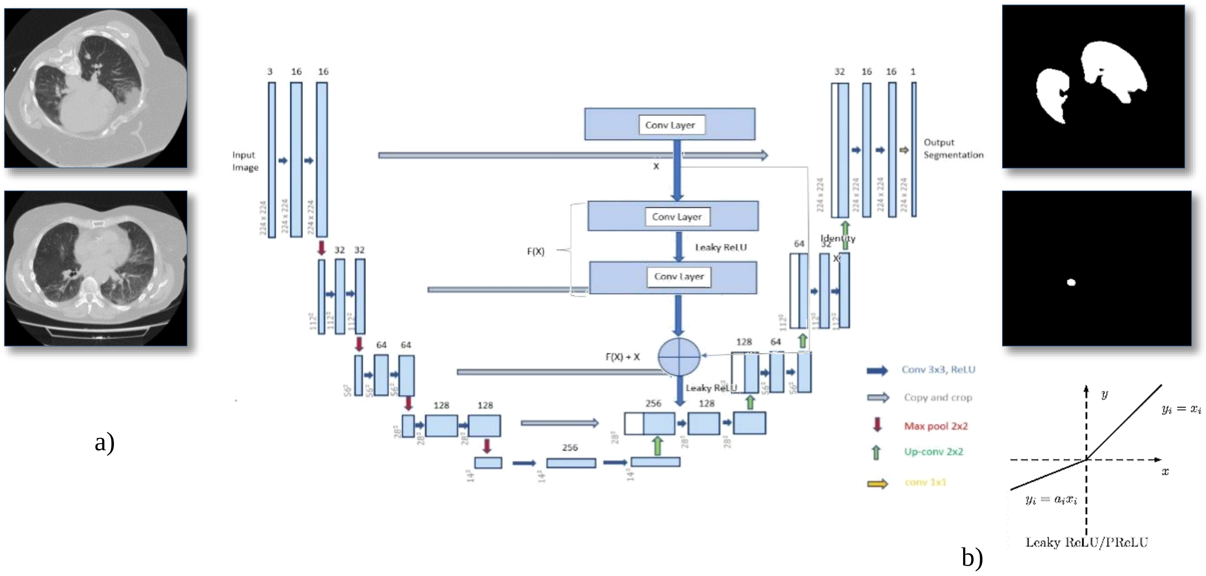


Figure 3. (a) The ResLU-Net model and an example of lung and lung tumor segmentation, and (b) the Leaky rectified linear unit (LReLU)

3. Results

The output of the ResLU-Net model is shown in Figure 4. The figure shows an example of lung segmentation on the first row and lung tumor segmentation on the second row. In order to provide accurate lung segmentation, the model undergoes training using lung CT images along with their corresponding masks (Figure 4, first row, columns (a) and (b)). During the testing phase, the model takes lung CT images as input and generates predicted masks as outputs, as illustrated in Figure 4 (first row, columns (c) and (d)). For lung tumor segmentation, the model is trained using lung CT images that contain tumor regions along with their corresponding masks (Figure 4, second row, columns (a) and (b)). The predicted mask is then generated as the model's output, as shown in Figure 4 (second row, columns (c) and (d)).

For a qualitative evaluation, we compare the performance of our ResLU-Net model with that of the conventional U-Net model. The observation of the predicted mask of lung segmentation (see Figure 4, the first row) shows that the ResLU-Net model has a better segmentation results than the U-Net model. Additionally, Figure 4's second row shows the lung tumor segmentation results, highlighting the superior performance of our model over the U-Net model (see Figures 4-c and 4-d).

All the selected slides from the patients were analyzed using the proposed model. To quantitatively evaluate the performance of our model, we utilize two measurement metrics: the dice coefficient index (Dice) and the structural similarity index (SSIM). Our model demonstrates remarkable performance in both lung and lung tumor segmentations, achieving an average Dice of 94% and 93%, as well as an average SSIM of 97% and 95% for lung and lung tumor segmentations, respectively. This result can be compared with results from the liver tissue, which used the ResLU-Net model.

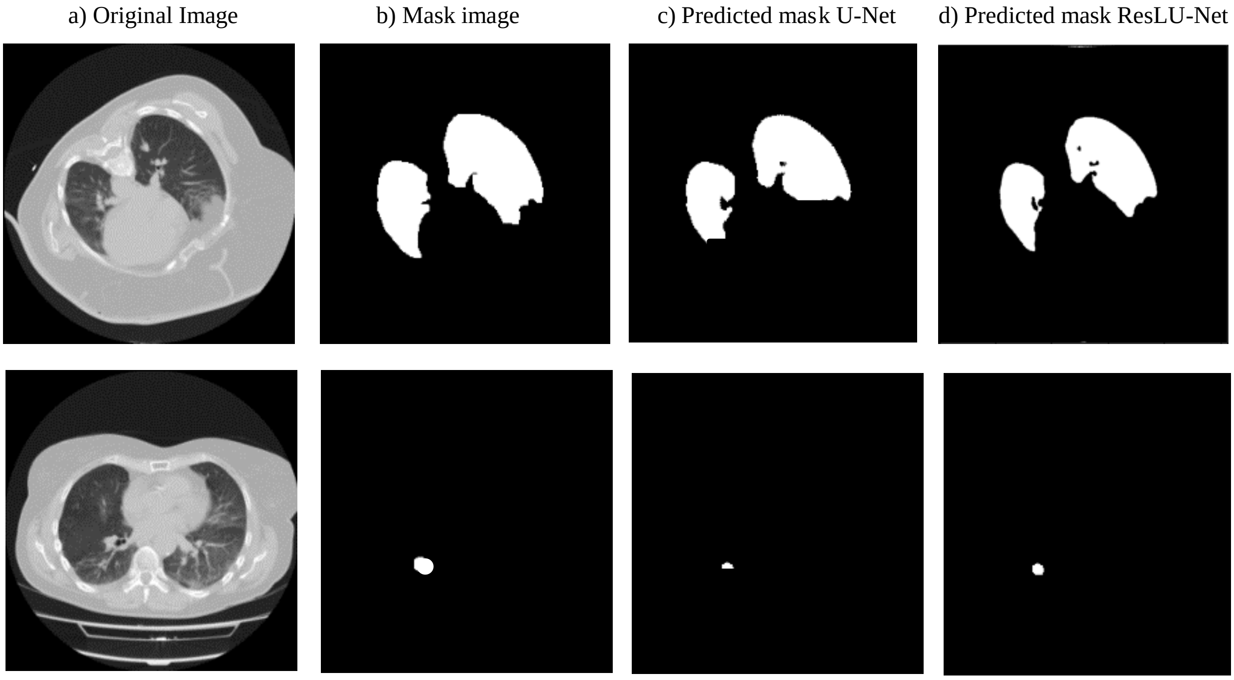


Figure 4. Illustrates an example result using U-Net and ResLU-Net segmentation models for the lung (first row) and lung tumor (second row). The first column of (a) illustrates the original CT images, the second column (b) shows the generated ground truth mask, and the last two columns of (c) and (d) show the predicted mask results from U-Net and ResLU-Net models.

The results of the study provide compelling evidence supporting the efficacy of the proposed method in accurately segmenting lung and lung tumor tissues. Detailed outcomes are presented in Table 1, where the results obtained from applying the proposed method to both the lung and liver CT image datasets acquired during MWA therapy are showcased. Notably, the ResLU-Net model exhibited superior performance compared to the conventional U-Net model across both datasets. Specifically, the liver and liver tumor segmentation achieved impressive SSIM values of 0.99 and 0.96, respectively, indicating high structural similarity between the predicted and ground truth masks. Moreover, the Dice coefficient, serving as a measure of overlap accuracy, yielded a remarkable value of 0.92 for liver segmentation. These findings highlight the robustness and effectiveness of the proposed method in accurately delineating lung and liver structures, paving the way for potential advancements in clinical applications and treatment planning. By achieving accurate and reliable segmentation results, our ResLU-Net model contributes to the growing body of knowledge in medical imaging and holds promise for enhancing the diagnosis and treatment of lung diseases.

Table 1. The results of segmentation for both liver and lung CT image datasets

Datasets:	**Liver**		**lung**		**Liver-Tumor**	**Lung-Tumor**
Measurement factors:	**SSIM**	**Dice**	**SSIM**	**Dice**	**Dice**	**Dice**
U-Net	0.94	0.84	0.93	0.88	0.86	0.85
ResLU-Net	0.99	0.92	0.97	0.94	0.92	0.93

4. Conclusion

In this study, we utilized a newly developed model called ResLU-Net, which is based on the U-Net architecture, to successfully segment both lung tissue and lung tumors. Our results indicate that the model achieves a high degree of accuracy in lung tissue segmentation. We conducted a comparative analysis with the conventional U-Net model, revealing a marked improvement in segmentation accuracy of 6% and 4% for Dice and SSIM, respectively. Furthermore, our proposed model demonstrates its capabilities beyond lung tissue segmentation by successfully applying it to the segmentation of tumors in CT images of various organs during MWA treatment. This showcases the model's potential for broader clinical applications and highlights its utility as a tool for medical image segmentation. These findings have significant implications for the medical community and hold great promise for improving patient outcomes through accurate and efficient segmentation of medical images.

5. Declarations

5.1. Author Contributions

Conceptualization, N.M. and Y.Y.; methodology, N.M.; software, N.M.; validation, N.M., Y.Y. and Z.Z.; formal analysis, N.M., H.T., M.S., M.G., and M.P.; writing—original draft preparation, N.M.; writing—review and editing, N.M., H.T., M.S., M.G., M.P., and C.H.; supervision, C.H. All authors have read and agreed to the published version of the manuscript.

5.2. Data Availability Statement

The data presented in this study are available on request from the corresponding author.

5.3. Funding

The authors received no financial support for the research, authorship, and/or publication of this article.

5.4. Institutional Review Board Statement

The study was conducted in accordance with the Declaration of Helsinki and was approved by the Ethics Committee of Otto-von-Guericke-Universität's Medical Faculty and the University Hospital Magdeburg, under protocol code 66/22 on May 20th, 2022.

5.5. Informed Consent Statement

Patient consent was waived due to the EU General Data Protection Regulation (GDPR) and the restrictions imposed by medical confidentiality, which exclude the delivery of complete patient files for monitoring.

5.6. Declaration of Competing Interest

The authors declare that there is no conflict of interests regarding the publication of this manuscript. In addition, the ethical issues, including plagiarism, informed consent, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancies have been completely observed by the authors.

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