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# Deep learning-based segmentation of diffuse large B-cell lymphoma in 18-FDG PET images

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## Abstract

***Background:*** *Diffuse large B-cell lymphoma (DLBCL) is a common and aggressive subtype of non-Hodgkin lymphoma. This study aimed to evaluate the effectiveness of deep learning for automatically segmenting DLBCL lesions in positron emission tomography (PET) images, which is crucial for treatment planning and monitoring.*
***Methods:*** *A 2D U-Net convolutional neural network was trained on a dataset of FDG-PET scans from 150 DLBCL patients. The model's performance was evaluated using two key metrics: the Dice similarity coefficient (DSC) and the Jaccard index.*
***Results:*** *The results showed a mean DSC of 0.71±0.13 and a mean Jaccard index of 0.62±0.12, indicating accurate identification of lymphoma lesions.*
***Conclusions:*** *These findings suggest that deep learning-based automated segmentation holds great potential for accurately detecting and delineating DLBCL lesions, thereby improving the precision and effectiveness of treatment planning and monitoring for affected individuals.*

## 1. Introduction

DLBCL is one of the most common types of non-Hodgkin lymphoma, characterized by the presence of abnormal B cells in the lymph nodes, spleen, bone marrow, or other organs. Accurate and efficient segmentation of DLBCL lesions is essential for diagnosis, treatment planning, and monitoring the response to therapy [1-3]. Traditional methods for DLBCL segmentation from 18F-FDG PET images often rely on manual delineation by expert radiologists, which is time-consuming, subjective, and prone to inter-observer variability. Recent advancements in deep learning algorithms, particularly convolutional neural networks (CNNs), have revolutionized the field of medical image analysis by automating the segmentation process [4].

Several studies have demonstrated the effectiveness of deep learning–based auto-segmentation methods for lymphoma. Blanc-Durand et al. (2024) developed a fully automatic segmentation method for diffuse large B-cell lymphoma (DLBCL) lesions on 3D FDG-PET/CT images. They employed a convolutional neural network (CNN) to predict the total metabolic tumor volume (TMV) of DLBCL lesions. The proposed method was based on the U-Net architecture, a widely used model for medical image segmentation. On the validation set, the mean Dice similarity coefficient (DSC) and Jaccard index were $0.73 \pm 0.20$ and $0.68 \pm 0.21$, respectively [5]. Semi-automated 18F-FDG PET segmentation methods for tumor volume determination in non-Hodgkin lymphoma patients were studied by Keijzer et al. (2023) [6]. Yousefirizi et al. (2024) developed a method for automated tumor delineation in lymphoma from PET/CT scans using a cascaded approach. They trained TMTV-Net, a convolutional neural network (CNN), on a large dataset of lymphoma PET/CT images from multiple centers. The network was designed to handle the variability

in image quality and patient characteristics across different institutions. The study included quantitative analysis using Dice score (DSC) and TMTV comparisons, as well as qualitative evaluation by nuclear medicine physicians. The results showed an average DSC of $0.68 \pm 0.12$ for the internal test data from the developmental dataset and an average DSC of $0.66 \pm 0.18$ on the multi-site external data [7]. Other studies have been conducted to investigate the automatic segmentation and detection of tumors using deep learning, highlighting the significance of these methods in the field [8-14].

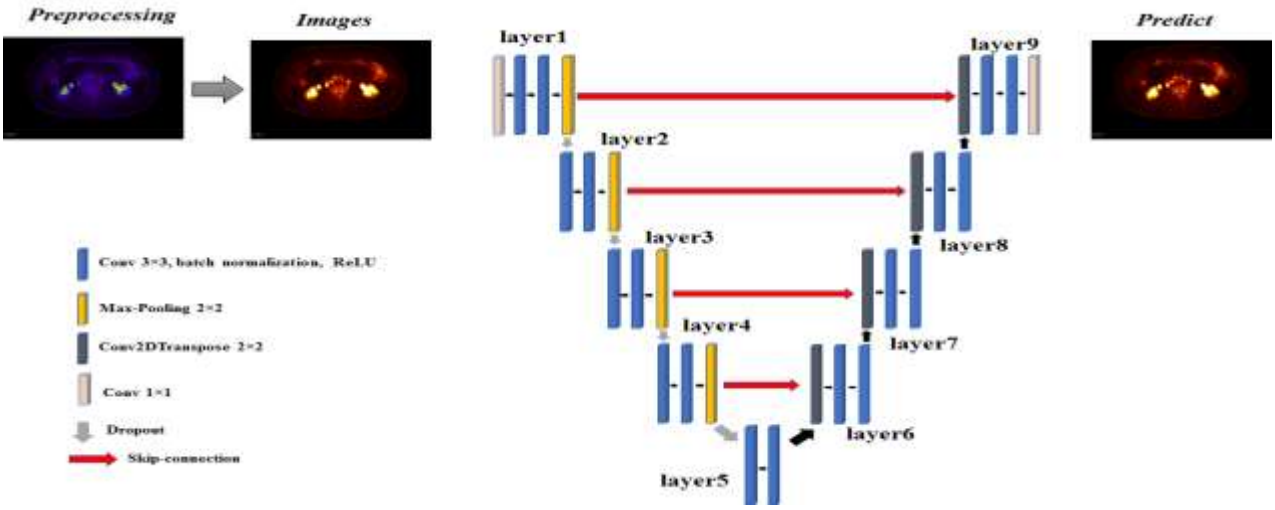


***Figure 1**. Flowchart of the study.*

In conclusion, the auto-segmentation of DLBCL from 18-FDG PET images using deep learning holds tremendous potential for improving the diagnosis and treatment of this prevalent form of lymphoma. The advancements in deep learning algorithms and the availability of large annotated datasets have paved the way for accurate and efficient DLBCL segmentation. Further research and development in this field are crucial to refine existing models, validate their clinical utility, and facilitate their integration into routine clinical practice.

In this context, the contribution of the present work is the development and evaluation of a 2D U-Net–based deep learning framework for automated segmentation of DLBCL lesions from FDG-PET images, using a dataset of 150 patients, which demonstrates the feasibility and potential of applying such methods in clinical practice

## 2. Materials and Methods

The research encompasses multiple stages. First, PET images from DLBCL patients are collected. Then, they are pre-processed and imported into a U-Net model for segmentation. Finally predicts the location and shape of lesions caused by DLBCL based on the segmented images. This process is summarized in Fig 1.

### 2.1. Dataset and preprocessing

The dataset used in this research consists of 150 [18]-FDG PET images of patients with DLBCL cancer who have visited Razavi Medical Centers in Mashhad between 2015 and 2022. These images were initially stored in NII format and were processed using 3DSlicer and ITK-Snap software for pre-processing. Subsequently, the necessary procedures such as removing patient tables, voxel size equalization, normalization, and noise removal were carried out. additionally, Data augmentation was employed to increase the diversity of the training set, reduce overfitting, and enhance the generalization ability of the deep learning model. The images, with dimensions of 128×128×z, where z represents the number of slices and varies in different patient images, were subsequently saved in NII format and incorporated into the UNet model. In collaboration with a medical specialist, the masks associate-ed with the lymph nodes of various body regions were stored as a ground truth and underwent the same pre-processing steps as previously mentioned, which were utilized for model validation.

### 2.2. deep Learning Models

The study employs a 2D-UNet architecture, as illustrated in Fig. 1. This architecture comprises three main components: downsampling, bottleneck, and upsampling. The downsampling path includes convolutional layers, pooling layers, normalization layers, dropout layers, and filters. These components

work in conjunction to extract and preserve important features from the input data. The bottleneck section acts as a bridge between the downsampling and upsampling paths, maintaining a compact and informative representation of the data. The upsampling path consists of convolutional layers, upsampling layers, and filters. In this section, the information from the downsampling path is utilized to reconstruct the image and generate predictions. Skip connections are employed between corresponding layers in the downsampling and upsampling paths, enabling the model to retain and reuse important spatial features from earlier layers. In summary, the 2D-UNet architecture initially extracts and encodes essential features during the downsampling process, and then reconstructs the image and produces predictions during the upsampling phase [15].

### *2.3. Training and Evaluation model*

Following image preprocessing, the dataset was split into a training set 80% (n=120) and a combined validation/test set 20% (n=30). Following image preprocessing, the dataset was divided into a training set (80%, n=120) and a combined validation/test set (20%, n=30). To optimize model performance, 3-fold cross-validation was applied on the training set. The final model was implemented in Python version 3.11 and executed on an NVIDIA A100 GPU with 15 GB of memory via Google Colab Pro. The model was implemented using TensorFlow 2.2 in Python. Training was performed with the Adamax optimizer, using binary focal loss as the loss function. The learning rate was set to 0.0001, the batch size to 32, and the model was trained for 100 epochs. Training was conducted on 120 datasets, each containing an average of 300 slices, while the remaining data was reserved for model evaluation. To assess the model's performance, the following metrics were calculated: Dice Similarity Coefficient (DSC), and Jaccard Index (JI).

## *3. Results and Discussion*

The predictive performance of the proposed model for lymph node segmentation in DLBCL patients is summarized in Table 1. The model achieved a Dice Similarity Coefficient (DSC) of 0.71 and a Jaccard Index (JI) of 0.62, indicating a moderate degree of spatial overlap between the predicted and ground truth segmentations. However, the DSC and JI values indicate that there remains potential for improvement, particularly in the precise delineation of lesion boundaries.

In addition to the quantitative evaluation, the predicted segmentation masks were visually compared with the original input images. This visual inspection allows a straightforward assessment of the model's ability to localize and delineate the regions of interest. As shown in Figure 2, the predicted masks demonstrated a high degree of consistency with the ground truth, enabling an intuitive verification of the model's performance.

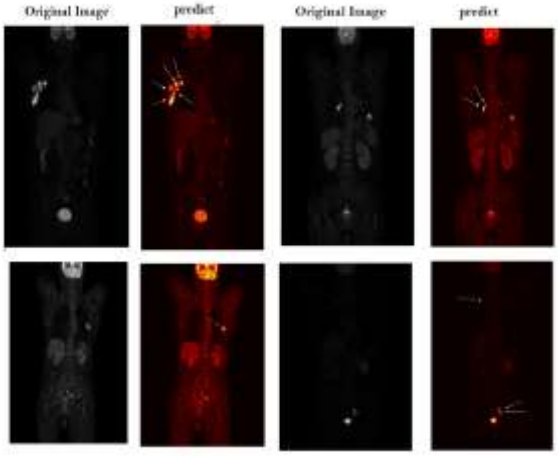


***Figure 2:*** *Visual comparison of the predicted segmentation masks and original images, demonstrating the model's performance in localizing lymph node regions.*

To contextualize these results, Jiang et al. (2022) employed a 3D U-Net architecture on a dataset of 414 DLBCL patients and reported average DSC and JI values of $0.78 \pm 0.25$ and $0.69 \pm 0.26$, respectively[16]. Their stronger segmentation performance can be attributed to the use of a larger dataset and a more complex 3D architecture.

Similarly, Yousefirizi et al. (2024) applied a semi-supervised learning strategy for DLBCL segmentation in 292 patients, achieving DSC values between 0.69 and 0.73 and a JI of up to 0.58[17]. These findings highlight the potential of hybrid and semi-supervised approaches, especially when labeled data is limited.

In summary, while the proposed model shows promising performance especially in classification accuracy and training efficiency there remains potential for improvement to improve segmentation accuracy. Future directions may include incorporating more diverse training data, adopting advanced architectures, and exploring semi-supervised or self-supervised learning frameworks to further enhance the model's generalization and spatial accuracy.

| Model name | Dice coefficient | Jaccard coefficient | p-value vs random baseline |
|---|---|---|---|
| **Fold 1** | 0.58 | 0.50 | < 0.001 |
| **Fold 2** | 0.72 | 0.63 | < 0.001 |
| **Fold 3** | 0.83 | 0.73 | < 0.001 |
| **Mean** | 0.71 ± 0.13 | 0.62 ± 0.12 | < 0.001 |

For a more comprehensive evaluation, we report the segmentation performance across all patients as mean ± standard deviation: DSC = 0.71 ± 0.13, Jaccard index = 0.62 ± 0.12. A paired t-test showed that the Dice score of our model was significantly higher than a random baseline segmentation ($p < 0.001$). These results confirm the robustness and statistical significance of our approach.

## 4. Conclusion

In conclusion, the auto-segmentation of diffuse large B-cell lymphoma (DLBCL) from 18-FDG PET images using deep learning techniques has demonstrated promising performance. The results indicate that the model is capable of accurately identifying DLBCL lesions; however, there remains room for improvement, particularly in enhancing segmentation precision. Future work could focus on further optimizing the model by incorporating larger and more diverse datasets, as well as exploring alternative or hybrid segmentation architectures. Overall, deep learning-based auto-segmentation of DLBCL has the potential to significantly enhance the accuracy and efficiency of clinical diagnosis and treatment planning in oncology.

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There is no conflict of interest between the authors.

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