Improved automated lesion segmentation in whole-body FDG/PET-CT via Test-Time Augmentation

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Abstract. In various areas of oncology research, the quantification of metabolically active tumors through techniques like positron emission tomography (PET) and computed tomography (CT) has been extensively conducted. F-fluorodeoxyglucose-positron emission tomography (FDG-PET) is commonly used in clinical practice and drug research to identify and measure metabolically active cancerous growths. The assessment of tumor size through manual or computer-assisted segmentation of FDG-PET images is widely practiced, and deep learning algorithms have shown promising results in this field.
However, there's a need to enhance the performance of a pre-existing deep learning network when modifications to the network are not feasible. We've introduced a novel framework that incorporates multilevel and multimodal techniques for tumor segmentation, allowing for the simultaneous consideration of PET and CT data.
n our study, we employed nnU-Net and SwinUnetr models to predict tumor masks within these two categories. To enhance the accuracy of our predictions, we utilized an ensemble approach that combines the outputs of these two models. Additionally, we incorporated Test-Time Augmentation (TTA) techniques to further improve our segmentation results. This ensemble technique, coupled with TTA, allowed us to refine our predictions and achieve improved segmentation performance. Ultimately, our objective was to enhance segmentation performance while maintaining a fixed model.
For access to our code, please visit the following URL:
https://github.com/sepidehamiri/autoPET2023.gitautoPET2023

Keywords: Test-Time Augmentation · nnU-Net · PET-CT · Swin U-Netr.

1 Introduction

For computer-assisted cancer detection and treatment, automatic tumor segmentation from medical images is a crucial step. Deep learning has recently been effectively used for this problem, improving performance [1]. However, most deep learning segmentation techniques currently in use are limited to one imaging

modality. Today's clinics frequently use PET/CT scanners, which combine PET and CT into one device and deliver metabolic and anatomical data. The particular challenge of lesion segmentation in FDG-PET resides in the fact that healthy organs, such as the brain, bladder, etc, can have high FDG uptake, making it challenging to avoid false positive segmentations, which can be seen in Fig 1. Various studies have been proposed to segment tumors in PET/CT scans autonomously. To get constant segmentation masks, between PET and CT, Song et al. created an adaptive context term for the target function [2]. In order to get object seeds, Ju et al. adopted a random walk approach as an initial preprocessing. After that, a graph cut method was applied to segment lung tumors on PET/CT images [3]. Based on the Markov Random Field optimization issue, Han et al. developed a PET/CT segmentation formulation [4]. All of the aforementioned studies showed that integrating the data from multiple imaging modalities might produce tumor segmentation results that are more precise than the segmentation results obtained from a single image modality.

2 Methods and Materials

2.1 Dataset

We used an annotated oncologic PET/CT data set in this study. Between 2014 and 2018 at the University Hospital Tübingen, 501 consecutive whole-body FDG-PET/CT data sets of patients with malignant lymphoma, melanoma, and non-small cell lung cancer (NSCLC) and 513 data sets without PET-positive malignant lesions (negative controls) were studied [5]. Additionally, 60 minutes after receiving an I.V. injection of 300–350 MBq 18F-FDG, a full-body FDG-PET scan was performed for each patient. PET data were rebuilt using the ordered-subset expectation maximization (OSEM) technique, which had a gaussian kernel of 2 mm, 21 subsets, and two iterations on a 400 x 400 matrix. Fig. 1 shows an example of fused whole-body FDG-PET/CT data.

2.2 Preprocessing

The used dataset already had pre-processing, including normalized and resampled (CT to PET imaging resolution; same matrix size) (PET converted to standardized update values; SUV). By converting image units from activity counts to standardized uptake values, PET data were made uniform (SUV). We also applied intensity scaling with a minimum of 100 and 0 and a maximum of 250 and 15 for CT and PET, respectively. To reduce the model's memory and computation requirements during segmentation, we cropped the images' foreground based on the CT.

Augmentation In the training phase, we used several data augmentation models, including random flip with the spatial axis of 1, 2, and 3, random rotation with the probability of flipping 10%, and random shift intensity with the probability of flipping 50% and offset range of 10%.

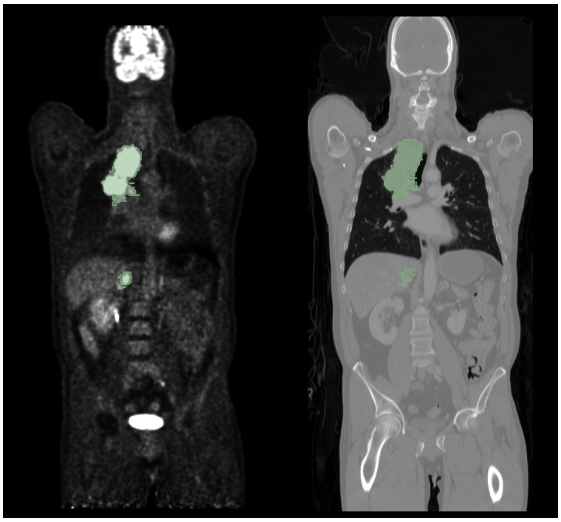

Fig. 1. An illustration of fused whole-body FDG-PET/CT data. The manually segmented malignant lesions are shown in the green sections.

2.3 Implementation Details

The configuration of the device used to implement this study is NVIDIA GeForce RTX 3080 GPU with Python 3.8.10 and Torch 1.9.0+cu111. We used patch-based U-Net and Swin U-Netr [6] with patch sizes of 96, 96, and 96 in 30000 iterations. Our method was implemented on the nnU-Net [7] code and MONAI library [8]. The batch size is 2 for training and 1 for testing. We used an Adam optimizer with a weight decay of 1e-5, and the learning rate is set as 1e-4. In the first step, we separated 12% of the total data for evaluation, 10% for testing, and 78% for learning.

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