Poster: Head and Neck Tumor Segmentation With Sliced 3D PET Scans

Nina Gruteser
ningru23@pds.org
Princeton Day School / SUNY Stony Brook

ABSTRACT

We present a semi-automatic 3D segmentation technique for head and neck tumors in PET Scans. First, we slice the 3D PET Scans into 2D images and separate the slices into slices with tumor and slices without tumor. The slices with tumor get segmented by a 2D U-Net. After training the U-Net for 100 epochs, the model achieved a dice score of 0.7799 and a dice loss of 0.3732.

CCS CONCEPTS

• **Applied computing**;

KEYWORDS

head and neck tumor segmentation, deep-learning

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1 INTRODUCTION

Head and neck cancer accounts for around 4% of all cancers in the US, and there are 900,000 cases and 400,000 deaths annually. Radiomics, a form of rich image analytics, promises to enhance cancer care by obtaining insights such as volume, depth, density, texture that are difficult to obtain through traditional methods. A key step in radiomics is 3D tumor segmentation, which identifies the exact 3D shape of the tumor.

So far, segmentation has typically been done manually by radiologists who encircle areas of interest. Manual segmentation, however, is very time consuming and has large variability. Recently, many deep learning-based automatic segmentation models have been studied to address these issues [1–5, 7, 8, 10]. Vallières and colleagues performed automatic segmentation using radiomic models on head and neck tumors and predicted the risk of locoregional recurrences and distant metastases [9]. Ronneberger et al. presented a form of convolutional neural network (CNN), called a U-Net, that can produce good segmentation results when trained on few medical images [8].

Most segmentation models have been trained on MRI and CT scan data. While MRI and CT scans picture organs and tissues, PET scans show how an organ functions in real time and can discover cellular changes earlier. Since PET scans can detect tumors earlier and better distinguish the metabolically active tumor from the surrounding edema [6], tumor segmentation models for PET scans are crucial.

Here, we focus on 3D PET scans and propose a semi-automatic segmentation model to increase performance by performing 2D segmentation on only the slices with tumors of each 3D PET scan. We assume that a radiologist marks the dimension of the tumor along one axis, which allows identification of the 2D slices that contain part of the tumor. We then apply a CNN, a 2D version of the U-Net architecture shown in Fig. 1, to segment each slice. Once the segmentation of each slice is done, the slices can be put back together into a 3D tumor segmentation.

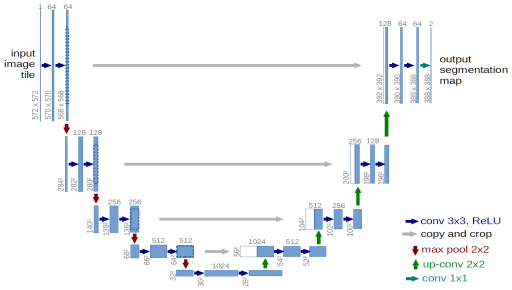

Figure 1: U-Net Architecture [8]

2 METHODOLOGY

For this project, we used the U-Net implementation from the MONAI framework [1]. Our dataset comes from 294 patients from 4 different hospitals. The dataset consists of one 3D PET scan and one 3D tumor mask for each of the patients. Figure 2 shows an example of a slice of one of the PET scans and its corresponding tumor mask.

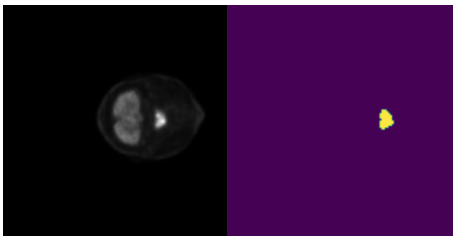

Figure 2: PET Scan Slice and Ground Truth

[1] https://docs.monai.io/en/stable/index.html

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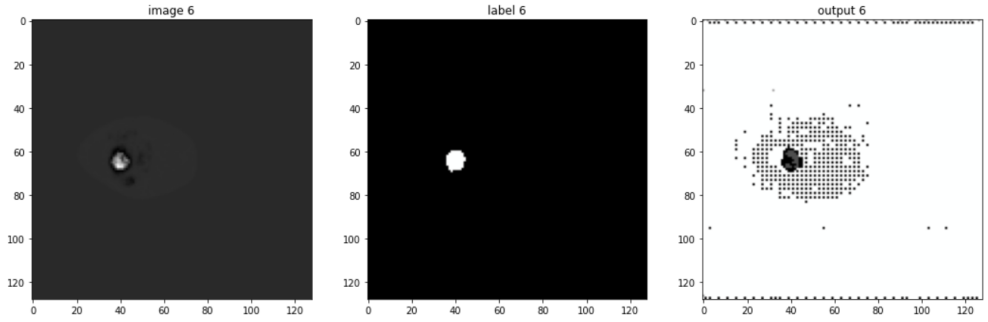

Figure 3: PET Scan Slice, Ground Truth, and Model's Prediction

All of the 294 3D PET scans contain tumors, however only 4,833 slices out of the 45,168 total 2D slices contain tumors.

To emulate the manual part of this semi-automated technique, we first sliced all of the images and labels and found which of the labels contained tumors using an algorithm that calculates the sum of each label. Labels with a sum greater than 0 contain tumor, and labels with a sum of 0 do not contain tumor. We trained the 2D U-Net using only those images.

To split the dataset, we used a 80:10:10 split for the training, validation, and testing sets. The training set ended up with 3,865 images, the validation set with 483 images, and the test set with 482 images. For data augmentations, we normalized the sizing and scaled the pixel intensity from 0-255 to 0-1 across all images. We also added a 50% random rotation augmentation to the train images. We used the Adam optimizer with a learning rate of 0.001 and a batch size of 2.

3 EXPERIMENTAL RESULTS

We evaluate the model using the dice score metric as defined below:

$$\text{Dice Score} = \frac{2 * A \bigcap B}{A + B} \tag{1}$$

where A is the set of tumor pixels in the ground truth and B is the set of tumor pixels in the model's prediction. The dice score represents 2 times the amount of overlap divided by the total number of pixels, resulting in a value between $[0, 1]$. Dice score is a better fit than pixel accuracy for segmentation tasks because, unlike pixel accuracy, it does not take true negatives into account.

After training the 2D model for 100 epochs, it achieved a dice score of 0.7799 (a dice loss of 0.3732).

To put these results in perspective, we compare with a basic 3D segmentation model using a 3D U-Net, where we fed the whole 3D PET scans into the model. After 100 epochs on the 3D model, the best dice score was 0.5031 (a dice loss of 0.4969). While the 3D model could likely be improved with further work, the results show that the semi-automatic 2D segmentation approach, where the model does not have to determine which slices have no tumors, performs significantly better than the fully automated 3D segmentation approach.

After putting the segmented 2D slices back together, our model would also produce a 3D segmentation like the 3D model.

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