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SCROLLING 2D U-NET FOR THE 3D SEGMENTATION OF SMALL VESSELS ON 7T MAGNETIC RESONANCE ANGIOGRAPHY

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1. INTRODUCTION

Advancements in 7T MRI have allowed for higher spatial image resolution and better signal-to-noise ratio for the visualization of small vessels in the brain. Given the current availability of data, most segmentation techniques in the field have focused on large blood vessel segmentation as opposed to small blood vessel extraction. Thus, there is a need to train effective small vessel segmentation tools with minimal data. In this paper, we propose a scrolling 2D U-Net that integrates information regarding the 3D volume while performing 2D segmentation. This approach was compared to the nnUnet – the state-of-the-art in segmentation models.

2. PROPOSED METHOD

2.1. Dataset

The challenge dataset consisted of 14 MRAs acquired at 7T MRI (dimension [480,640,163]). Annotations provided as part of the challenge were extracted using semiautomatic methods, such as the Frangi filter. The dataset was split into 8, 3, and, 3 for training, validation, and testing, respectively.

2.2. Training procedure

The training procedure is outlined under Algorithm 1. We have trained the model by sliding it along anatomical directions and extracting a stack of $N_{channels} = 10$ slices of the image. The model was trained for 1000 epochs using a batch size of 8, an Adam optimizer, and an initial learning rate of 0.001. The average of the Dice loss and the binary cross Entropy (BCE) was used as the loss function. Images were randomly flipped along all dimensions with a probability of 0.5.

2.3. Inference

Images are processed through the model in all $N_{dirs} = 6$ anatomical directions: AP, PA, LR, RL, IS, and SI. All outputs are summed and normalized by a factor $N_{channels} \times N_{dirs}$. After visual inspection, we decided on a threshold of 0.3 to consider a voxel as detected (roughly, this means it was detected at least through scrolling in one direction).

2.4. Implementation details

The segmentation model uses a modified 2D U-Net [1] with group normalization, "Leaky ReLu", and up-sampling. The model has 16 filters at the first convolution block output and

performs three downsampling steps using average pooling with 10 channels as input.

Algorithm 1 Training during 1 epoch, on IS direction					
$\overline{X \leftarrow pad_N(Batch_{image})} \qquad \triangleright (E$	$\overline{B}, 1, 480, 640, 163 + 2N)$				
$Y \leftarrow pad_N(Batch_{mask})$					
$C \leftarrow (DiceLoss() + BCE())/2$					
for $i = [N:510 + N]$ do					
$x \leftarrow reshape(X[,i:i+N])$	$\triangleright(B, N, 480, 640)$				
$y_{gth} \leftarrow reshape(Y[,i:i+N])$					
$y_{pred} \leftarrow model(x)$					
$L \leftarrow C(y_{gth}, y_{pred})/510$	▷ gradient accumulation				
Backpropagate L					
end for					
Step the optimizer					

3. RESULTS

Table 1 summarizes performances obtained on the three testing subjects. Results are reported as mean \pm standard error (SE). Obviously, mean and SE can be unreliable for such small samples but we were constrained by the challenge dataset. The proposed model performs comparably to the 3D nnUnet.

Method	Dice	Jaccard	MI	AvgHaus	AVER
nnUnet	0.81 ± 0.04	0.69 ± 0.07	0.77 ± 0.03	0.60 ± 0.15	0.17 ± 0.11
proposed	0.81 ± 0.05	0.68 ± 0.07	0.75 ± 0.04	0.64 ± 0.1	0.21 ± 0.08

Table 1. Summary of performance metrics4. CONCLUSIONS

The proposed method performs comparably to 3D state-ofthe-art methods like nnUnet [2]. The method has the advantage of being less computationally expensive owing to its 2D architecture.

5. REFERENCES

- Olaf Ronneberger and et al, "U-net: Convolutional networks for biomedical image segmentation," in *MICCAI*, 2015, pp. 234–241.
- [2] Fabian Isensee and et al, "nnu-net: a self-configuring method for deep learning-based biomedical image segmentation," *Nature Methods*, vol. 18, no. 2, pp. 203–211, Feb 2021.