Fully convolutional neural network with residual connections for automatic segmentation of prostate structures from MR images

Inom Mirzaev Mathematical Biosciences Institute, Ohio State University, Columbus, Ohio mirzaev.1@osu.edu

Abstract

We propose a fully convolutional neural network with residual connections for automatic segmentation of prostate structures from MR images. This document is a concise description of the methods that we have used to complete the Promise 12 challenge.

1 Data Preprocessing

Each 2D MRI slide is resized to dimension 256×256 and histogram equalized using contrast limited adaptive histogram equalization (CLAHE). Moreover, to make the pixel distribution more uniform we applied curvature driven image denoising for each image. The training dataset is split into 45 training cases and 5 validation cases. The validation set were arbitrarily set to the cases $\{05, 15, 25, 35, 45\}$. Finally, we normalize training, validation and test set with the mean and standard deviation of the training set.

2 Network Structure

As in [3], our model has encoder-decoder architecture with depth 7. Network structure of our model shares ideas with many existing models [5], [6] and [4], just to mention a few. A general schematic of the network structure is depicted in Figure 1. Zero padding and ReLU activation was used for the convolutions inside the convolution blocks. Moreover, variance scaling was used for kernel initialization (as in [5]).

3 Training

Training set has about 1200 images with corresponding masks. Therefore, data was augmented to 150k with random rotations, shifts, zooms, flips and elastic deformations.

The weights of the model were updated by minimizing negative Dice Similarity Coefficient (DSC) function,

$$DSC(y,\hat{y}) = \frac{2\sum_{i}^{N} y_i \cdot \hat{y}_i}{\sum_{i}^{N} y_i + \sum_{i}^{N} \hat{y}_i}$$

We used ADAM optimizer with the hyper-parameters suggested in the original paper [2]. The model was trained for 20 epochs with batch size of 32. Each epoch takes about an hour on Nvidia P100 GPUs provided by Ohio Supercomputer Center [1].

4 Results

Volumetric Dice similarity coefficient (DSC), Mean Relative Absolute Volume, Mean Surface Distance (MSD) and Hausdorff Distance (HD) are computed for each case in the training and the test datasets. The results are reported in Table 1.



Figure 1: Schematic of network architecture of the model

	Mean DSC	Median DSC	Std. DSC	Mean RAV	Mean MSD (mm)	Mean HD (mm)
Train	0.950	0.950	0.012	1.467	0.548	9.762
Validation	0.885	0.885	0.041	13.972	1.438	16.779

Table 1: Training results.

5 Acknowledgements

Author would like to thank Mathematical Biosciences Institue (MBI) at Ohio State University, for partially supporting this research. MBI receives its funding through the National Science Foundation grant DMS 1440386.

References

- [1] O. S. CENTER, Ohio supercomputer center. http://osc.edu/ark:/19495/f5s1ph73, 1987.
- [2] D. KINGMA AND J. BA, Adam: A method for stochastic optimization, arXiv preprint arXiv:1412.6980, (2014).
- [3] H. NOH, S. HONG, AND B. HAN, Learning deconvolution network for semantic segmentation, in Proceedings of the IEEE International Conference on Computer Vision, 2015, pp. 1520–1528.
- [4] T. M. QUAN, D. G. HILDERBRAND, AND W.-K. JEONG, Fusionnet: A deep fully residual convolutional neural network for image segmentation in connectomics, arXiv preprint arXiv:1612.05360, (2016).
- [5] O. RONNEBERGER, P. FISCHER, AND T. BROX, U-net: Convolutional networks for biomedical image segmentation, in International Conference on Medical Image Computing and Computer-Assisted Intervention, Springer, 2015, pp. 234–241.
- [6] L. YU, X. YANG, H. CHEN, J. QIN, AND P.-A. HENG, Volumetric convnets with mixed residual connections for automated prostate segmentation from 3d mr images., in AAAI, 2017, pp. 66–72.