Improving White Matter Hyperintensities Segmentation on Unseen Scanners via Unsupervised Domain Adaptation

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1 Data Preparation

The released training set including three subsets named *Utrecht*, *Singapore* and *GE3T* respectively, are used as the training set. Each of them contains 20 subjects. Data preparation includes three steps, following the same procedure in our previous work [1,3]. Preprocessed datasets and the codes are available ⁴.

2 Unsupervised Domain Adaptation

The main focus of this submission is to perform test-time unsupervised domain adaptation on the target unseen data distribution which is different from the one that the segmentation model trained on. During the test stage, for the data from the seen scanners (i.e. *Utrecht*, *Singapore* or *GE3T*), we directly perform prediction using our previous top-performing model [1]; for the data from **unseen** scanner, we perform unsupervised domain adaptation in a *subject-wise manner* due to the container setting. For more details on the adaptation process, please check our latest work [2]. Codes will be released soon.

3 Computation Complexity

We train the domain adaptation model with 250 epochs with a batch size of 30. When using a Nvidia Titan Xp GPU with 12GB, it take less than one hour for the adaptation process. When running it with an Intel i5-8400 CPU (six cores, 2.8GHz), it takes around six hours.

 $^{4 \}text{ } https://github.com/hongweilibran/wmh_ibbmTum}$

References

- 1. Li, H., Jiang, G., Zhang, J., Wang, R., Wang, Z., Zheng, W.S., Menze, B.: Fully convolutional network ensembles for white matter hyperintensities segmentation in mr images. NeuroImage 183, 650–665 (2018)
- 2. Li, H., Loehr, T., Wiestler, B., Zhang, J., Menze, B.: e-uda: Efficient unsupervised domain adaptation for cross-site medical image segmentation. arXiv preprint arXiv:2001.09313 (2020)
- 3. Li, H., Zhang, J., Muehlau, M., Kirschke, J., Menze, B.: Multi-scale convolutional-stack aggregation for robust white matter hyperintensities segmentation. In: International MICCAI Brainlesion Workshop. pp. 199–207. Springer (2018)