Abstract: Fast MRI Whole Brain Segmentation with Fully Convolutional Neural Networks

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Whole brain segmentation from structural MRI-T1 scan is a prerequisite for most morphological analyses, but requires hours of processing time and therefore delays the availability of image markers after scan acquisition. We introduced a fully convolution neural network (F-CNN) that segments a brain scan in several seconds [1]. Training deep F-CNNs for semantic image segmentation requires access to abundant labeled data. While large datasets of unlabeled image data are available in medical applications, access to manually labeled data is very limited. To aid training of this complex network with limited data, we propose to pre-train on auxiliary labels created from existing segmentation software FreeSurfer [2]. The network is pre-trained on a large dataset with auxiliary labels and then fine-tuned with a small dataset with manual annotations [1]. The architecture consist of 3 encoder-decoder based 2D F-CNNs, segmenting slices along coronal, axial and sagittal axes. These predictions are aggregated to obtain the final segmentation. Dense connections are introduced within each encoder/decoder block to promote feature re-usability and ease of training. Apart from these, long skip connections and unpooling layers for upsampling in the decoder are used. The network is learnt by optimizing a joint loss function of weighted Logistic loss and Dice loss. The weights are set to tackle class imbalance and to encourage reliable contour estimation. In an extensive set of evaluations on several datasets that cover a wide age range, pathology, and different scanners, we demonstrated that our method achieves robust and superior performance to state-of-the-art atlas based methods, while being orders of magnitude faster. This drastic speed up greatly facilitates the processing of large data repositories and enables wide spread integration of imaging biomarkers in the routine clinical practice by making them almost instantaneously available.

References

- 1. Error corrective boosting for learning fully convolutional networks with limited data. Springer 2017.
- 2. Whole brain segmentation: automated labeling of neuroanatomical structures in the human brain. In Neuron; 2002.