A Deep Convolutional Neural Network for Brain Tissue Segmentation in Neonatal MRI

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Introduction

Brain tissue segmentation is a prerequisite for many subsequent automatic quantitative analysis techniques. As with many medical imaging tasks, a shortage of manually annotated training data is a limiting factor which is not easily overcome, particularly using recent deep-learning technology. We present a deep convolutional neural network (CNN) trained on just 2 publicly available manually annotated volumes, trained to annotate 8 tissue types in neonatal T2 MRI. The network makes use of several recent deep-learning techniques as well as artificial augmentation of the training data, to achieve state-of-the-art results on public challenge data.

Method

A fully convolutional neural network (see figure 1) with a total of 11 layers is trained to map T2-weighted images to tissue segmentations. The training data consists of just 2 axial volumes, available publicly via the neobrains12 challenge[1]. Eight different tissue-types are segmented as illustrated in figure 3 (Results).

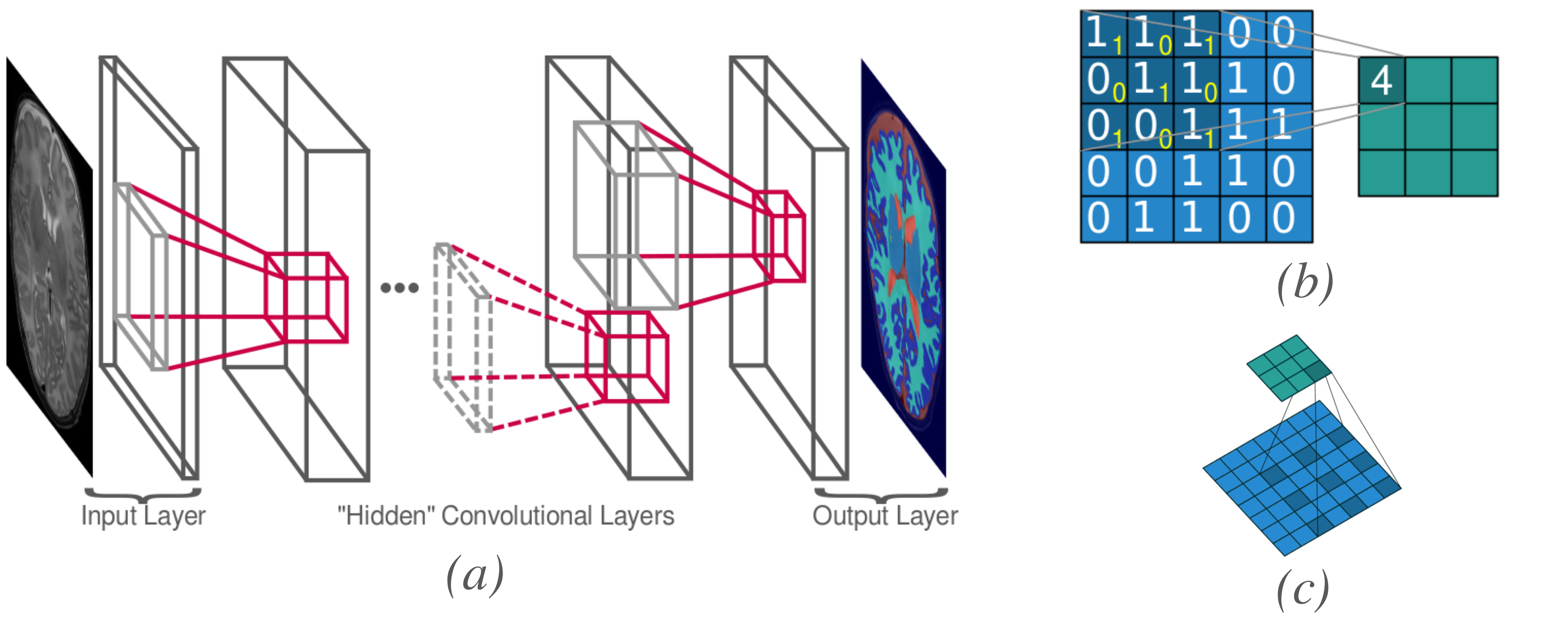

Figure 1: *(a) A schematic drawing of a fully convolutional neural network with T2-weighted MRI as input and segmentation data as output. (b) A numerical demonstration of how a convolution with input values (blue) with weights (yellow) results in output (green). (c) An illustration of how dilated convolution spans a larger region at no additional computational expense.*

Training data is augmented by applying a number of random perturbations to every slice extracted during training, as shown in figure 2. This allows the network to learn variations which may not be present in the limited training data

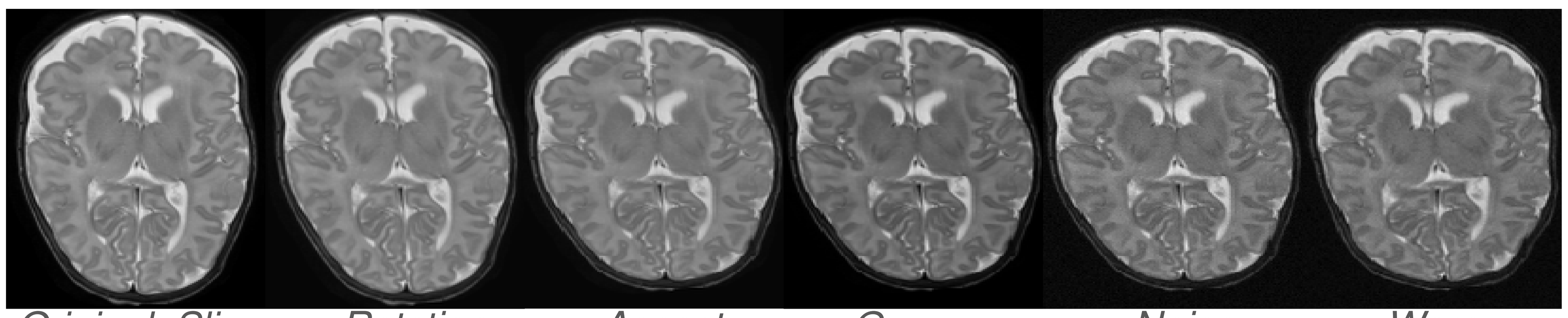

Figure 2: *A demonstration of how training data is augmented by adding subtle random variations to the original data.*

Network technical details: The network uses batch-normalization, dilated convolutions and stacked residual layers. The Adam optimizer is used and loss is calculated by cross-entropy.

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References

1. neobrains12.isi.uu.nl

Isgum et al, Evaluation of automatic neonatal brain segmentation algorithms: The NeoBrainS12 challenge, Medical Image Analysis, 2015.

Results

The trained network was used to segment tissue types on a further 5 axial T2-weighted scans which are provided by the neobrains12 public challenge[1]. Evaluation was performed independently by the challenge organisers and the reference standard is never seen by participants. Compared to other participating algorithms, our method obtained the highest median Dice Coefficient across various tissue types (figure 3). The median value for Mean-Surface-Distance was second highest, being surpassed only by a participant who had access to additional related training data. Figure 4 shows sample results on test data from the challenge.

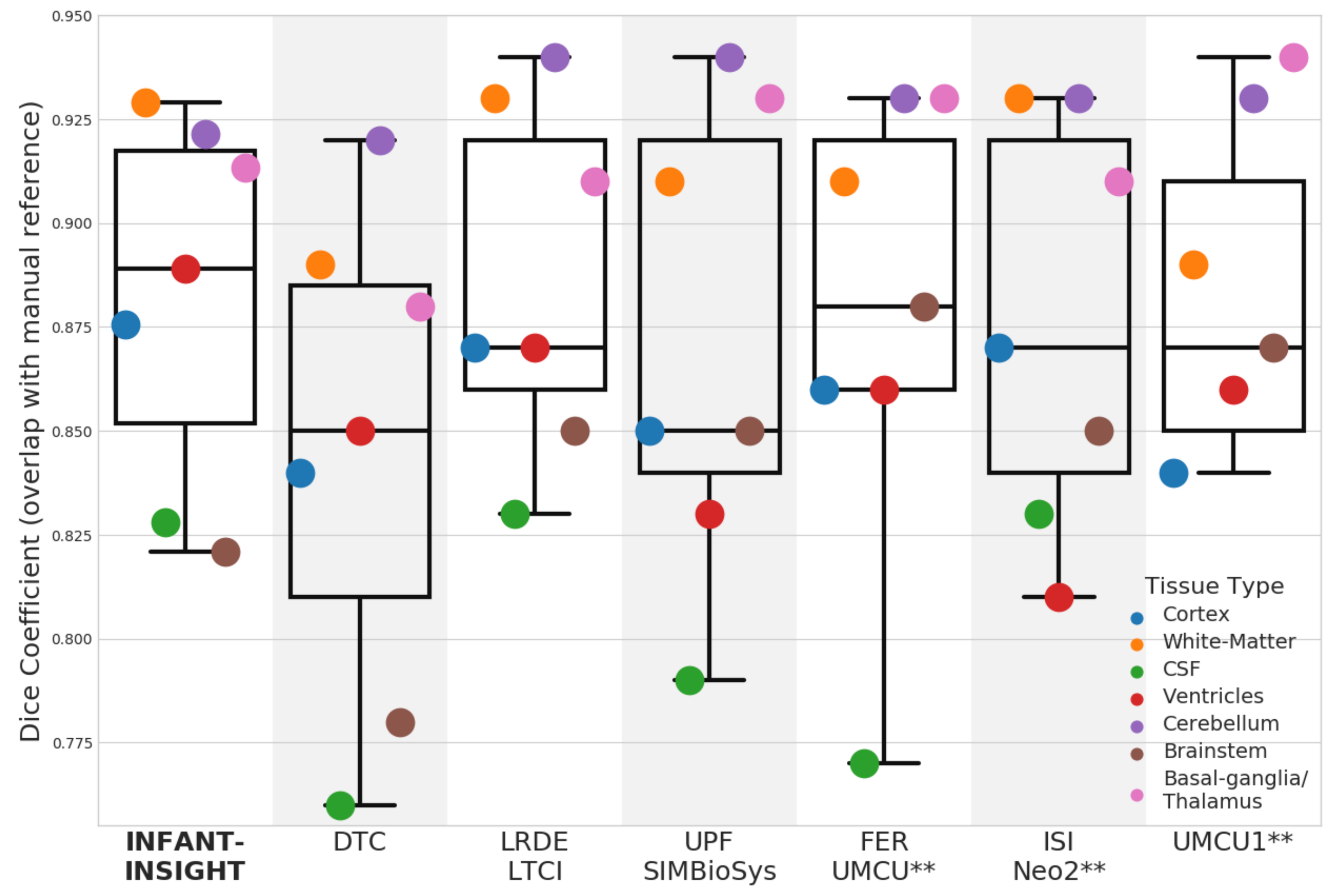

Figure 3: *Plots showing how the presented method (left) performs against comparable methods in the neobrains12 challenge[1] in terms of Dice Coefficient for overlap. Coloured points show mean performance for each tissue type, while box-plots summarise this data. **Indicates participants with access to related additional data*

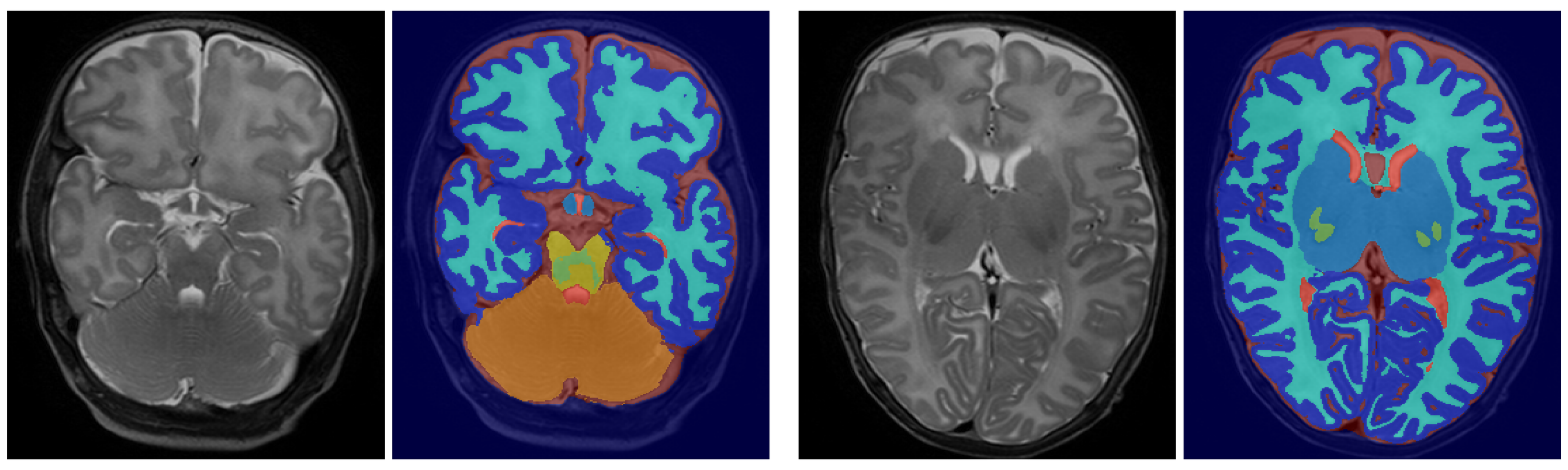

Figure 4: *Sample network segmentation results on neobrains12 [1] test data. Tissues are cerebellum (orange), cortex (darkest blue), white-matter (lightest blue), cerebro-spinal fluid (dark red), ventricles (light red), brain-stem (yellow), basal-ganglia/thalamus (mid blue), myelination (light green)*

Conclusion

Deep learning using the appropriate network architecture and data augmentation techniques have enabled state-of-the-art segmentation results using minimal training data. The presented method performs better than others which had access to additional related training scans. This is a promising result for deep learning in the medical imaging domain where a shortage of training data is typically a significant issue.

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