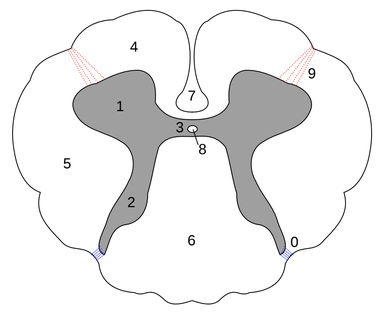
Spinal Cord Gray Matter-White Matter Segmentation on Magnetic Resonance AMIRA Images with MD-GRU

Antal Horváth[1], Charidimos Tsagkas[2], Simon Andermatt[1], Simon Pezold[1], Katrin Parmar[2], Philippe Cattin[1]

[1]Department of Biomedical Engineering, University of Basel, Switzerland
[2]Department of Neurology, University Hospital Basel, Switzerland

Introduction

In this work [4] we present an automatic method that segments the inner structures of the human spinal cord (SC) on magnetic resonance (MR) images.
The SC is embedded in cerebrospinal fluid (CSF) and consists of white matter (WM) and the inner butterfly shaped gray matter (GM), see Fig. 1. Imaging these thin and small structures (SC: $<1\,\mathrm{cm}$ of diameter) is challenging because state-of-the-art MR sequences only achieve an in-slice resolution of around $0.5\,\mathrm{mm}$ while maintaining a good signal-to-noise ratio (SNR) and a clinically feasible acquisition time.



Gray matter
1 Anterior horn
2 Posterior horn
3 Gray commissure

White matter
4 Anterior funiculus
5 Lateral funiculus
6 Posterior funiculus

Cerebrospinal fluid
7 Anterior median fissure
8 Central canal

9 Anterior root
0 Posterior root

Fig. 1: Schematic cross-section of the SC GM (*gray*) and WM (*white*).

Therefore, an accurate and precise segmentation of GM and WM in MR images under the mentioned limiting trade-off between resolution, SNR, and acquisition time also remains a challenge.

Data

In this work we use averaged magnetization inversion recovery acquisition (AMIRA) [1] images of the SC on vertebra C2 to C6 level. The AMIRA sequence consists of 8 inversion recovery (IR) images of the same anatomical slice with remarkable tissue contrast, see Fig. 2. With increasing IR times, the GM-WM contrast decreases and the CSF-WM contrast increases. The first IR image has the best GM-WM contrast and compared to the other images a negative CSF-WM contrast.

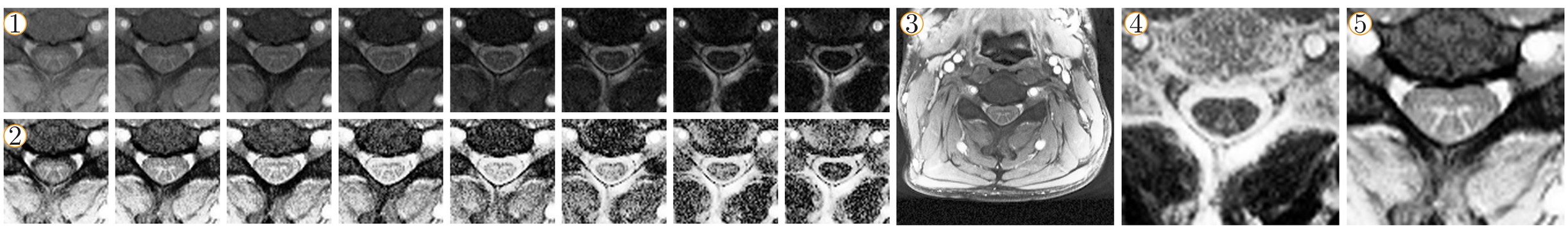


Fig. 2: AMIRA images 1 to 8 (1), histogram equalized (2); full view, sum of the first 5 (3); zoomed, optimal CSF-WM (4)and GM-WM (5)combination.

Method

We use a recurrent neural network (RNN) with multi-dimensional gated recurrent units (MD-GRU) [2] to train new models that segment GM and WM slice-wise. We added a generalized dice loss (GDL),

$$L_{\mathrm{GD}} = -\frac{2\sum_{l\in\mathcal{L}}\omega_l\sum_{x\in X}p_{lx}\,r_{lx}}{\sum_{l\in\mathcal{L}}\omega_l\sum_{x\in X}p_{lx}+r_{lx}},$$

to the MD-GRU's cross entropy loss (CEL) with the image domain X, labels $\mathcal{L}$, predictions p, raters r, and class weights

$$\omega_l = \frac{1}{1+\left(\sum_{x\in X}r_{lx}\right)^2}.$$

Conclusion

We believe that the presented pipeline is a candidate for longitudinal clinical studies.

Acknowledgements

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References

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[2] S. Andermatt et al., MICCAI DLMIA 2016
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Experiments and Results

24 healthy subjects were scanned 3 times in a scan-rescan fashion, with and without repositioning, where each scan consists of 12 slices between C2 and C6 level. One experienced rater provided manual ground truth segmentations.
Adding GDL to the MD-GRU's CEL produces sharper probability maps, see Fig. 3, and improves the segmentation scores.

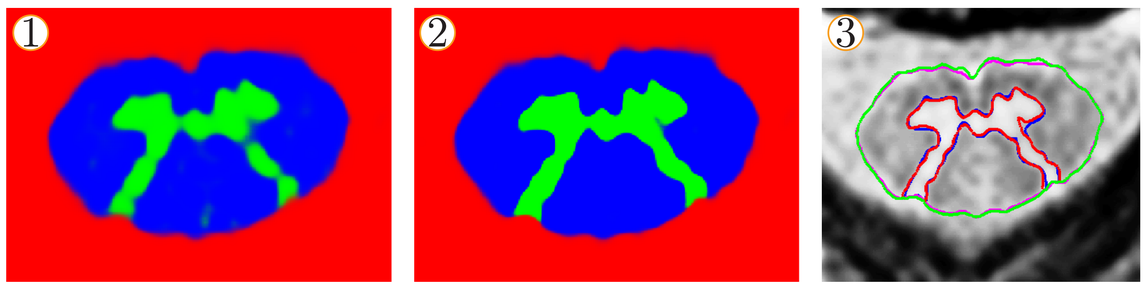

Fig. 3: Probability maps of CEL (1)and GDL (2). GM-WM and CSF-WM contours of GDL (*red*, *green*) vs manual (*blue*, *magenta*) (3).

The proposed method shows accuracte and precise segmentations of the AMIRA data, see Tab. 1, and also scored best in the SC GM segmentation challenge [3], see Tab. 2.

Tab. 1: AMIRA accuracy and precision results

		MD-GRU	Proposed	Manual
Accuracy	DSC	0.90 ± 0.04	0.91 ± 0.03	0.85 ± 0.07
	HD	0.68 ± 0.43	0.56 ± 0.33	0.62 ± 0.30
Intra-session	DSC	0.89 ± 0.03	0.88 ± 0.03	0.86 ± 0.03
	HD	0.71 ± 0.46	0.58 ± 0.32	0.67 ± 0.24
	RSD	3.22 ± 2.87	2.93 ± 2.63	5.55 ± 4.11
Inter-session	DSC	0.88 ± 0.04	0.88 ± 0.03	0.85 ± 0.03
	HD	0.70 ± 0.43	0.61 ± 0.35	0.71 ± 0.27
	RSD	3.65 ± 3.97	3.86 ± 3.49	6.27 ± 4.70

Tab. 2: SC GM segmentation results

	Perone et al.	MD-GRU	Proposed
DSC	0.85 ± 0.04	0.87 ± 0.03	**0.90** ± 0.03
MD	0.36 ± 0.34	0.30 ± 0.31	**0.21** ± 0.20
HD	2.61 ± 2.15	2.14 ± 1.20	**1.85** ± 1.16
SHD	0.85 ± 0.32	0.85 ± 0.36	**0.71** ± 0.28
SMD	**0.36** ± 0.17	0.40 ± 0.20	0.37 ± 0.17
TPR	94.97 ± 3.50	93.93 ± 3.85	**96.22** ± 2.69
TNR	99.95 ± 0.06	**99.98** ± 0.03	**99.98** ± 0.03
P	77.29 ± 6.46	82.04 ± 5.42	**85.46** ± 4.96
J	0.74 ± 0.06	0.78 ± 0.05	**0.82** ± 0.05
C	64.24 ± 10.83	70.90 ± 9.06	**77.46** ± 7.31