Atrophy computation in the spinal cord using the Boundary Shift Integral

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Synopsis

In this work, we introduce a new pipeline based on the latest iteration of the BSI for computing atrophy in the SC and compare its results with the most popular atrophy measurements for this region, mean CSA. We demonstrated for the first time the use of BSI in the SC, as a sensitive, quantitative and objective measure of longitudinal tissue volume change. The BSI pipeline presented in this work is repeatable, reproducible and standardises a pipeline for computing SC atrophy.

Introduction

Atrophy measurements obtained from structural MRI are useful biomarkers of neurodegeneration. Patients with neurological diseases commonly show higher disability with increasing brain and spinal cord atrophy[1]. Longitudinal volume changes are measured in the brain using registration-based methods like SIENA[2] or Brain Shift Integral (BSI)[3]. In the spinal cord (SC), instead, atrophy is usually quantified by measuring volume (based on 3D surface fitting) or cross-sectional area (CSA), based on 2D edge detection on serial images and subtracting the follow up measure from the former. Furthermore, CSA is obtained by computing the mean of the areas of a set of slices.

In this work, we introduce a new pipeline based on the latest iteration of the BSI in order to compute atrophy in the SC, and we compare the results with the most popular atrophy measurements for this region, the mean CSA. The current BSI formulation is generalised (GBSI) using non-binary segmentations of the baseline and repeated scans, in order to better localise and capture atrophy. The non-binary mask can be obtained either from a probabilistic segmentation (e.g. label fusion) or through a linear interpolation of the binary mask to the inter-time-point half-way space.

Methods

A new GBSI pipeline[3] was developed for SC atrophy including the steps below.

Data: In our study we included 10 healthy subjects (age: 45.5±8.9 years, gender 6F:4M) who were scanned at baseline and at 12 months on the same 3T Philips Scanner using a 16-channel neurovascular coil (which permitted coverage of the entire cervical SC). We acquired a T1-weighted MPRAGE volume (1x1x1mm^3).

Manual SC segmentation: One experienced observer manually outlined the SC between C2 and C5 at both time points for all the participants using the active surface method available with JIM6 (www.xinapse.com).

Denoising: We performed image denoising using a fast version[4] of the adaptive non-local means filter[5]. For computing the root power of the noise, we calculated the standard deviation in a ring within the cerebrospinal fluid (CSF) region and scaled the image to account for the presence of a noise floor[6] (in the MPRAGE, signal from cerebrospinal fluid (CSF) is hipointense). The ring within the CSF was built by an XOR operation between the segmented cord mask after one and after two unary dilations.

Bias field correction: Data was corrected for intensity inhomogeneity using N4 only in the region determined by the twice dilated SC mask[7]. The following parameters were used: FWHM=0.05, convergence threshold 0.0001 and maximum number of iterations 1000.

Straightening: Images were z-straightened by moving the centre of mass of the mask per each slice to the centre of the image.

Registration: A 3D symmetric and inverse-consistent rigid only (9 DOF) registration[8] to the half-way space between baseline and follow-up images was performed on both time points. Masks were resampled to the same space using linear interpolation.

Differential bias correction: Differential bias correction inside the mask area was applied to minimise global intensity differences between images.

BSI: GBSI detects atrophy at intensity changes in the vicinity of the tissue boundaries (see Figure 1), as determined by the non-binary segmentations of the aligned baseline and repeat scans[9]. This technique ensures that findings would not be biased due to the registration process. The GBSI clipping intensities were empirically set to 0.4 and 0.96 for all our SC images. A non-binary XOR region-of-interest was used.

Results and Discussion

For evaluation, we compared the results of estimating longitudinal atrophy with GBSI using the same SC mask segmentations, as outlined in the semi-automated SC segmentation, in order to enable a fair comparison between the methods (see Table 1). All results are annualised. There is no evidence of differences in performance between the two techniques ($p = 0.92$). However, BSI obtained a smaller confidence interval and coefficient of variation. Therefore, the proposed technique may require smaller cohorts in clinical trials to detect differences between groups as compared to CSA.

Conclusions

We have demonstrated for the first time the use of GBSI in the SC, as a sensitive, quantitative and objective measure of longitudinal tissue volume change. The GBSI pipeline presented in this work is repeatable, reproducible and standardises a pipeline for computing SC atrophy. Future work will focus on expanding the measurement to more subjects, including patients with a neurological disease that causes increasing SC atrophy, and introducing automatic SC segmentation and adaptively setting up the clipping window.

Acknowledgements

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Figures

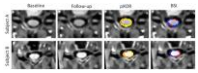

Figure 1: Example of BSI computed over two subjects. First two columns show registered baseline and follow-up images. Third column represents probabilistic XOR region where red-yellow represents range 0-1. Fourth column shows obtained atrophy voxel-wise values where blue means atrophy and orange growth.

	CSA (mm^2)	BSI (mm^2)
Mean (Std)	0.07 (1.83)	0.01 (0.13)
Confidence Interval 95%	-1.06 to 1.21	-0.07 to 0.09
Coefficient of Variation	25.16	16.15
p-test	p=0.92	

Table 1: Mean, standard deviation, confidence interval, coefficient of variation and p-test for CSA and BSI. Note that a positive BSI means lost of tissue.