Spinal cord template and a semi-automatic image processing pipeline

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INTRODUCTION: Spinal cord MR imaging is important for assessing non invasively pathological events in neurodegenerative diseases and traumas. Recently, it has been shown that changes in magnetization transfer ratio, diffusion-weighed imaging and atrophy measurements based on cord cross-sectional area correlate with clinical scores of disability and provide complimentary information useful for prognosis of functional rehabilitation (1). What is currently lacking in the field is a common template that can be used to register patient populations, compare groups and conduct quantitative analyses, as been done for the brain (2). In this work we apply existing techniques to create a spinal cord template and a semi-automated image processing pipeline that registers new subjects to it.

METHODS: Subjects and Image Acquisition: Data from 17 healthy volunteers without neurological disease were acquired on a 3T MRI system using receive-only 4channel neck and 24-channel spine coils. Anatomical scans were completed with a T2-weighted 3D turbo spin echo sequence with slab selective excitation pulses (SPACE) with the following parameters: sagittal orientation, 52 slices, FOV=280 mm, TR=1500 ms, TE=120 ms, voxel size = $0.9 \times 0.9 \times 0.9 \text{ mm}^3$, flip angle= 140° , parallel acquisition (R=3), phase encoding direction: head-foot, phase oversampling 80%, slice oversampling 7.7%, bandwidth = 744 Hz/Pixel, turbo factor = 6, acquisition time ~6 min. Image pre-processing: automatic non-uniformity correction N3 (3) was applied as a first stage of data processing. Spinal cord Template: was constructed by (i) performing rigid body co-registration between 9 subjects' scans with manually identified anatomical landmarks (most posterior midline aspect of each intervertebral disk, from C2 to C7) (ii) performing inter-subject linear intensity scaling based on histogram matching (iii) creating an unbiased anatomical average, as described in (2) see Fig. A. Spinal cord Straightening: was performed by combining ideas from (4) and (5) using k-means clustering to segment the cerebrospinal fluid (CSF) surrounding the spinal cord, followed by selecting largest connected component; straightening was achieved by warping the smoothed centerline of the segmented CSF to a straight line using thin plate splines, see Fig. B. <u>Registration to the Template</u>: A new subject is registered to the template using the following steps: (i) intensity non-uniformity correction using N3 (3), (ii) linear intensity normalization using histogram matching to the template, (iii) spinal cord straightening using the procedure explained above, (iv) linear registration to the space of straightened spinal cord template using rigid body transformation (6) with initialization provided by approximate manual identification of C1, C2 and C3 vertebrae, (v) non-linear registration to the same template using ANTS algorithm with crosscorrelation cost function (7), (vi) deformation-based morphometry analysis. The output of the registration pipeline is a non-linear transformation mapping each voxel from the original image to the template space. This template can be used for automatic identification of anatomical features (e.g., vertebral levels, nerve roots, etc...); inter-subject comparison of the shape and density of the spinal cord using techniques such as voxel-based morphometry (8), deformation based morphometry (DBM) (9) and automated analysis of diffusion-weighted, MTR and functional MRI data.

<u>RESULTS</u>: Fig C shows the output of each stage of the pipeline, from left to right: (ii) raw data after non-uniformity correction, (iii) straightening (iv) rigid-body alignment, (v) non-linear alignment. Column (vi) shows DBM-style results of the local volume difference between a subject and average anatomical template, where purple shows a relative 50% reduction in volume compared to the template, green shows no difference, and white shows a 50% increase in volume compared to the template.



A. Average template from 17 subjects.



at levels c1-c6, central sagittal slice, & coronal slice. Red

outline shows CSF space, green outline, the cord.



C. Result of the pipeline run on one subject. Red/green contours in (v) are as in Fig. B. Colour bar units are in % volume difference between subject and template in (vi).

DISCUSSION: We have created an initial template for the spinal cord that can serve as a standard space for analysis, like the Talairach space for brain. We also presented a semi-automated pipeline for spinal cord image processing which makes it possible to analyze large datasets of images with minimal manual intervention. The method is implemented using publicly available minc tools (www.bic.min.mcgill.ca/ServicesSofware). The method could be further automated by integrating automatic vertebra identification such as (*10*). The current implementation provides useful output for the analysis of spinal cord atrophy using the DBM technique. Straight-forward extension to include other modalities (Diffusion Weighted Imaging, MTR, etc) is possible.

ACKNOWLEDGEMENTS: We thank H. Benali and M. El Mendili for helping with data acquisition and M. Tuznik for helping with landmark identification.

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