MNI-Poly-AMU average anatomical template for automatic spinal cord measurements

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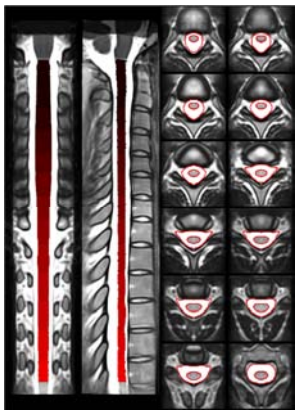
TARGETED AUDIENCE: Scientists and clinicians interested in spinal cord template-based analysis and multi-parametric MRI.

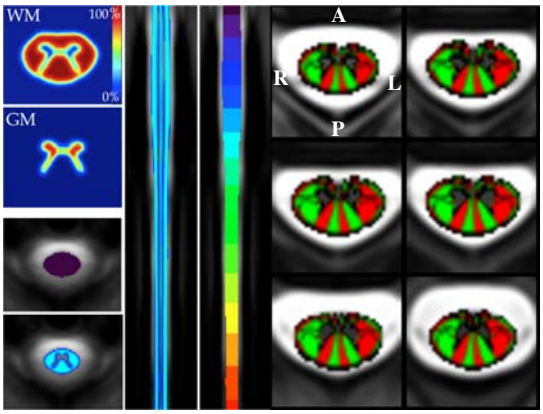
PURPOSE: MRI imaging of the spinal cord (SC) is important for the diagnosis and prognosis of neuroinflammatory and neurodegenerative diseases and posttraumatic changes, and useful for evaluation in drug development. Recently it was shown that multi-parametric MRI provides several biomarkers sensitive to white-matter integrity and neuronal function [1]. Our work is further development of the template creation methods [2,3,4].

METHODS: ***Subjects and Image Acquisition***: Data from 17 healthy volunteers without neurological disease were acquired on a 3T MRI system using receive-only 4-channel 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 = 0.9×0.9×0.9 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:*** (i) intensity non-uniformity correction using N3 [5], (ii) linear intensity normalization using histogram matching to the same subject, (iii) spinal cord straightening using linear registration between adjacent slices, with rough linear registration to the common space using a manually identified landmark at the interface between C1 and C2 and inter-slice intensity normalization by calculating intensity of CSF detected at each slice using Otsu's threshold. ***An unbiased symmetric SC template:*** was constructed using hierarchical group-wise image-registration method described in [3] followed by manual identification of the CSF and vertebral levels within SC and straightening of the resulting model using B-Splines (Fig. A) producing Montreal Neurological Institute - Ecole Polytechnique de Montreal (MNI-Poly) T2* template. ***SC tissue segmentation priors*** were created from T2*-weighted images acquired from 15 separate volunteers at 3T. Images were manually segmented into three classes (CSF, WM and GM) and a 4-DOF affine co-registration was applied as described in [6] to build a 2D multi-slice probabilistic atlas of WM and GM structures termed the Aix-Marseille Université (AMU) template (Fig. B, left). All probability maps were then symmetrized and a 3D version of the probabilistic atlases was generated by interpolating intermediate slices through each vertebral level. This method provides a 3D straightened SC probabilistic atlas, compatible with the MNI-Poly T2* template (fig. B, bottom left and middle). The resulting probability maps were then semi-automatically co-registered with the MNI-Poly T2* template and resampled into the same coordinate system at 0.5 mm isotropic resolution. A ***white-matter tract atlas*** (WMTA, Fig. B, right) was created based on manual tracing of the known human anatomy [7]. The atlas was first warped to the AMU white and gray matter probabilistic template at the corresponding vertebral level. Then, the atlas was warped and interpolated to match all levels of the MNI-Poly T2* template, from C1 to T6. The WMTA atlas consists of 30 different spinal tracts, with values ranging from 0 to 1 to account for partial volume effects. ***Semi-Automatic image processing pipeline:*** A new subject is registered to the template using the following steps: (i) same preprocessing as described above, (ii) non-linear registration to the MNI-Poly T2* template using ANTS with cross-correlation cost function [8], (iii) warping of the segmentation priors back into the native space of the subject. The output of the registration pipeline is a series of 3D volumes representing classification of each voxel into gray matter, white matter, CSF, identification of the white-matter tracts and position within spinal cord relative to the vertebral level. These segmented structures can be used as ROIs for multiparametric MRI techniques (e.g., diffusion imaging, magnetization transfer, functional MRI). Also, the pipeline produces continuous measurement of the spinal cord cross-section and proportion of white and gray matter.

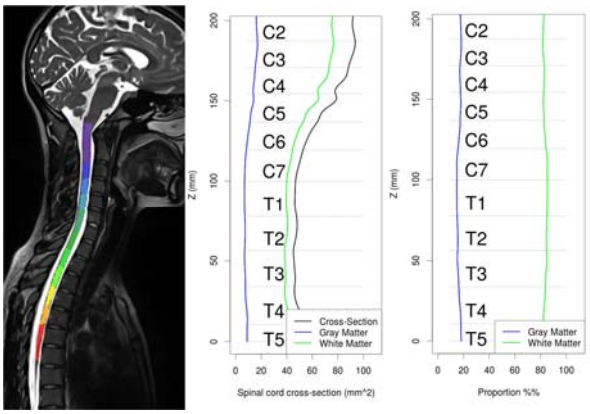
RESULTS: Fig C shows the output of the pipeline, from left to right: raw data after non-uniformity correction, overlaid with segmented spinal cord; spinal cord cross-section measurement of white matter, gray matter and the total and the proportion for grey and white matter.



A. Average anatomical template from 17 subjects.



B. Tissue segmentation priors (left), white-matter tract atlas that includes 30 regions (right).



C. Result of the pipeline run on one subject.

DISCUSSION: We created an unbiased average anatomical template of the human spinal cord, as well as a semi-automatic image processing pipeline that can be used to analyze data from new subjects – MNI-Poly-AMU template version 1. The procedure is robust and reduces variability associated with manual segmentation. The resulting images and image processing software will be available at http://www.bic.mni.mcgill.ca/Services web site for use by the community.

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