Template-based analysis of multi-parametric MRI data with the Spinal Cord Toolbox

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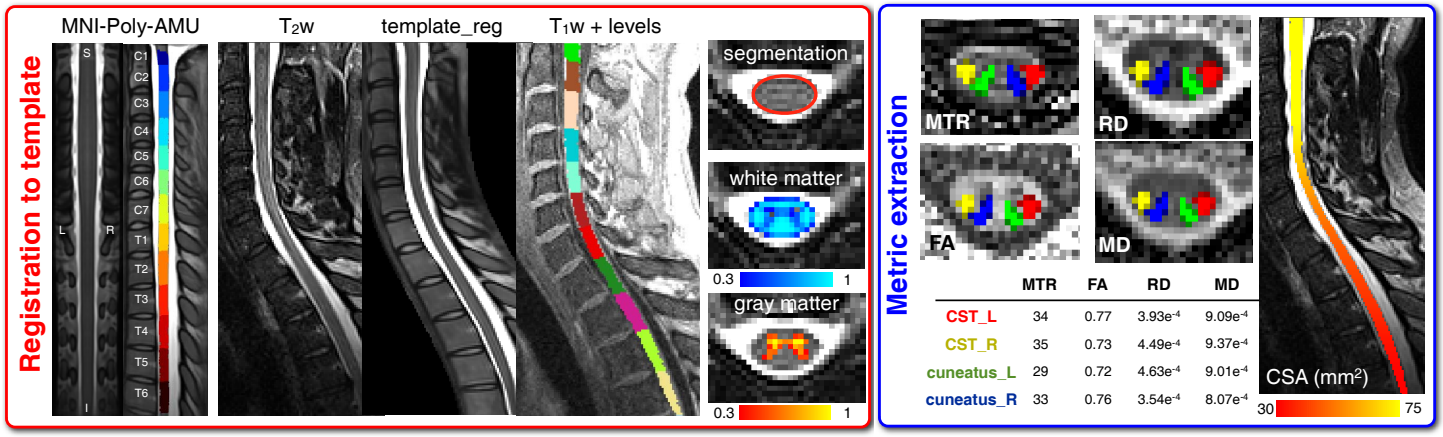
Target audience. Scientists and clinicians interested in template-based analysis of spinal cord MRI data.

Purpose. Multi-parametric MRI of the spinal cord has the potential to improve diagnosis/prognosis in various diseases and to provide objective markers for drug development. However, processing of spinal cord MRI data is hampered by the lack of standard guidelines and the need for manual intervention when quantifying multi-parametric data (e.g., manual regions of interest, ROI). The current state-of-the-art is to rely on brain software packages, which are not adapted for spinal cord segmentation, motion correction, multi-modal registration, template-based analysis and anatomical parcellation[1]. We propose the first comprehensive and open-source spinal cord MRI software package: the Spinal Cord Toolbox (http://sourceforge.net/projects/spinalcordtoolbox/), which gathers state-of-the-art methods for preprocessing and analyzing multi-parametric MRI of the spinal cord.

Methods. *Spinal cord segmentation* is performed using fully automatic method based on the propagation of a deformable model[2]. Outputs are cross-sectional area (CSA) measures along the spinal cord, binary segmentation and spinal cord centerline. *Template-based analysis*. The centerline is used for straightening the spinal cord, followed by non-rigid deformation[3] to the MNI-Poly-AMU template[4]. The only manual step is the creation of two landmarks at given vertebral levels (e.g., C2 and T2). Next, any multi-parametric data is registered to the subject's anatomical image[5]. Outputs of the whole registration procedure are forward and backward warping fields that enable to (*i*) warp subject's data to the template space and to (*ii*) warp template objects onto subject's multi-parametric space. Template objects include: cord and CSF masks, probabilistic atlas of white and gray matter[6], atlas of white matter tracts[7] and probabilistic location of spinal levels[8]. Quantification of metrics is done automatically by specifying the label to use (e.g., left corticospinal tract), the metric (e.g., fractional anisotropy) and the vertebral levels (e.g., C2 to C7). Metrics are calculated by taking into account the partial volume effect (weighted average), yielding more accuracy than binary ROI methods. *Validation*. An adult subject was scanned at 3T (Siemens Healthcare) using the following sequences: 3D T_2-weighted fast spin echo, 3D T_1-weighted MPRAGE, gradient echo FLASH with and without magnetization transfer, diffusion-weighted EPI (b-value = 800 s/mm^2) and gradient echo EPI sequence typical for fMRI protocols. Acquisition parameters are described in [4]. Processing included segmentation, registration to template, motion correction using slice-by-slice registration regularized along z and metrics extraction. A batch script that runs all processing automatically is available at: https://github.com/neuropoly/spinalcordtoolbox/blob/master/batch_processing.sh.

Results. The left panel of the figure below shows the registration of the MNI-Poly-AMU template to the T_2w and T_1w data (with overlay of vertebral labeling), as well as white and gray matter warped to the subject's anatomical space. Right panel shows magnetization transfer ratio (MTR), fractional anisotropy (FA), radial diffusivity (RD) and mean diffusivity (MD) with overlay of spinal tract atlas (here, the lateral corticospinal tracts and the cuneatus were selected out of 30 tracts). The table shows the mean values within these tracts. The sagittal image shows the CSA value from the segmentation overlaid on the spinal cord. Numerical values of CSA can also be output in text format at given vertebral levels.



Discussion. We presented a pipeline for processing multi-parametric spinal cord data. The procedure does not rely on manual intervention (except for the vertebral labeling, which takes about 30 seconds) and hence can be applied to large study population without user bias. Alternatively to running the toolbox on a local station, a web interface has also been developed. Data upload/download and script management is done with Javascript. Visualization is made using the BrainBrowser engine[9]. The web version of the toolbox is available at www.spinalcordtoolbox.org.

References. **1.** Wheeler-Kingshott CA, et al., NeuroImage, 2014;84:1082-93. **2.** De Leener B, et al., NeuroImage, 2014;98:528-36. **3.** Avants BB, et al., Medical image analysis, 2008;12(1):26-41. **4.** Fonov VS, et al., NeuroImage, 2014;102P2:817-827. **5.** Avants BB, et al., Frontiers in neuroinformatics, 2014;8:44. **6.** Taso M, et al., Magma, 2014;27(3):257-67. **7.** Benhamou M, et al. ISMRM. 2014. **8.** Cadotte D, et al. ISMRM. 2014. **9.** Sherif T, et al. HPCS. 2014.

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