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AMU7T: a 3D qT1 and T2*w high-resolution in vivo template with refined white and gray matter parcellation dedicated to 7T spinal cord MR analyses

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Synopsis

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Ultra-High-Field MRI has opened new perspectives for spinal cord exploration due to improved spatial resolution and contrast. The present work proposes a dedicated 7T multimodal 3D qT1 and T2*w template and a parcellation including eight substructures within gray matter, thirty WM tracts and three inter-hemispheric ROIs, for an accurate atlas-based segmentation in the subject space. This atlas was interpolated in the 3D PAM50 space to benefit from the advanced functions for registration implemented in the SCT. A preliminary segmentation result in healthy subject gives promising perspectives for group studies.

INTRODUCTION

The emergence of 7T scanners and the development of quantitative MRI sequences at such field (such as MP2RAGE) have opened new perspectives for the exploration of the spinal cord^{1,2}. However, due to improved spatial resolution and contrasts, conventional tools to analyze the images may fail.

Recently, a study proposed by Massire³ highlighted the relevance of quantitative T1 by proposing a first exploratory 7T MRI template (relying on an averaging of ten subjects) revealing anatomical details and facilitating the delineation of WM tracts and GM regions boundaries, in agreement with existing in-vivo⁴/ex-vivo⁵ atlases and anatomical drawing illustrated in different books^{6,7}.

The main utility of this atlas lies in the segmentation approach which accurately characterizes (in the subject space) the central canal, the anterior fissure and the posterior septum (that may contaminate T1 quantification if not considered). The atlas also includes five substructures within gray matter horns that could be used to target specifically relevant areas for pathological studies or fMRI. On the other hand, the small number of subjects but also the perfectible template construction method, as well as the lack of spatial coherence related of a 2D registration on data initially acquired in 3D, greatly limited its applicability.

To overcome these limitations, the present work consolidates and completes this atlas, and extends it in the 3D PAM50 space⁸ using an optimized pipeline for multimodal template construction.

METHODS

This work relies on 2 datasets previously acquired on a 7T MR system (Siemens Healthcare, Germany) with an 8Tx/8Rx neck coil (Rapid Biomedical, Germany) used in CP-mode.

The first dataset (AMU26) was composed of transverse 3D-MP2RAGE quantitative T1 maps acquired on 26 healthy subjects (HC) (cf. Table1A and Fig. 1.1a)

The second dataset (AMU72), recently proposed for a realistic data augmentation process for automated GM segmentation⁹) was composed of 2D axial multi-echo GRE T2*-weighted images (T2*w) acquired on 72 subjects (34 HC, 25 Amyotrophic Lateral Sclerosis and 13 Multiple Sclerosis patients). (cf.Table1A and Fig.1.1b).

Preprocessing: All images (N=1208) were automatically segmented with the SCT¹⁰ functions sct_deepseg_sc¹¹ and sct_deepseg_gm^{12,9}. Cord/GM masks were manually corrected, and images/masks were Left/Right symmetrized (Fig.1.2) to increase SNR.

Construction of 2D T2*w and qT1 HR templates: Multi-stages SyGN¹³ processes (Fig.1.2) using SyN transformation were then performed for each level (cf. Table1B-1 for detailed parameters) using either 2D multiple-stacks of qT1 images for the 2D AMU26_{gT1} template or T2*w image stack for the 2D AMU72_{T2*w} template. For both datasets, the corresponding probabilistic AMU26_{gT1} template or T2*w image stack for the 2D AMU72_{T2*w} template. For both datasets, the corresponding probabilistic AMU26_{gT1} template or T2*w image stack for the 2D AMU72_{T2*w} template. were generated to constraint the SyGN processes.

To progressively refine the 2D AMU26_{qT1} template details (Fig.1.3a), 3 different stages were finally performed using the (GM,SC,qT1) modalities (cf. Table1B-2 for detailed parameters). For AMU72_{T2*w} (Fig.1.3b), one single stage was performed using the (GM,SC,T2*w) modalities (cf. Table1B-3).

Generation of the 3D multimodal template AMU7T compatible with PAM50: The 3D propagation of both 2D AMU72_{T2*w} and AMU26_{gT1} templates into the PAM50 space^{7,14} was performed step-wise using a set of 2D slice-wise co-registrations (Fig.2.1a):

- i) from AMU26 to AMU72, and (WM_{30tracts}, GM_{6parcels})⁴ to AMU72 (cf. details on Table1B-4),

- ii) from AMU72 to PAM50 (cf. Table1B-5).

For each 2D inter-level slice of AMU72 registered to PAM50, 3D interpolations (combining ascending and descending fields of deformations, described previously by Ogier¹⁵) were applied (Fig.2.1b) to generate the final 3D multimodal AMU7T template integrating (AMU26_{qT1,masks}, AMU72_{T2*masks}, WM_{30Tracts}, GM_{16Parcels}, , IH_{3ROI}) at (0.175x0.175x5)mm³ resolution.

The GM/WM parcellation (Fig.2.1c) aimed at refining the probabilistic GM_{6Parcels} currently available in SCT (R/L anterior, intermediate and dorsal horns) in a new GM_{16Parcels} parcellation to which is added a subdivision in 3 regions of interest from the inter-hemispheric zone called IH_{3ROI}. These latter, which are in agreement with ^{3,5}, were defined to take advantages of 7T high-resolution and investigate new areas such as motoneuron clusters, while avoiding areas filled with CSF that may contaminated quantification.

RESULTS

A qualitative comparison between PAM50 atlas, ex-vivo atlas and our new AMU7T atlas is highlighted on Fig2.2.a-c.

A more quantitative and preliminary result is shown on Fig.3. Individual 3D qT1 quantification obtained after applying the sct_register_to_template function alone (Fig.3.1a, using AMU7T_qT1 template for the registration, and default parameters for other options), or in addition to an optimized SyN registration (Fig.3.1b), demonstrates the feasibility of using this parcellation to accurately segment a 3D qT1 volume in the subject space. Fig.3.2 also shows the impact of registration (SCT or SCT+SyN) on the mean/stdev qT1 measurements extracted from the AMU7T parcels (less bias due to GM/WM and WM/CSF PVE).

CONCLUSION

In line with recent works and progresses in the field of 7T spinal cord MRI, we proposed a new multimodal 3D template (AMU7T) dedicated to 7T qT1 analyses. On the short term, we aim at making it fully compatible with the Spinal Cord Toolbox (SCT¹⁰), so as to benefit from the dedicated functions for 3D atlas-based segmentation (template-to-subject registration including straightening, vertebral alignment and slice-wise non-linear registration), with the perspective to improve the reliability and significance of the cluster's localization extracted by voxel-based analyses in group studies.

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Figures



Fig.1: 2D template construction steps

1. (a) 3D MP2RAGE and **(b)** 2D T2*w acquisitions. **2.** Cord and GM segmentation, followed by L/R flipping (blue color). Multi-stage SyGN¹³ processes using SyN transformation were then performed (pink color), for each level, using stacks of qT1 images (composed of multiple images per level for each individual subject) for the 2D AMU26_{qT1} template, and sets of T2*w image stack for the 2D AMU72_{T2*w} template.



Fig.2 : Post-processing pipeline for the generation of 3D AMU7T atlas

1. (a) slice-wise co-registration steps between AMU spaces and PAM50 **(b)** automatic 3D label propagation through 2D fields of deformations **(c)** scheme and legend of WM/GM parcellation **2.** Qualitative atlas comparison - *in-vivo* - *ex-vivo* - histology **(a)** *in-vivo* 3T PAM50 (500µm iso) **(b)** *in-vivo* AMU7T (175µm iso) **(c)** *ex-vivo* MRI template (80µm iso)



Fig.3 : Qualitative and quantitative results of an automated AMU7T segmentation on one single subject - impact of registration bias

1. on left: sagittal and coronal views of 3D MP2RAGE and labeled mask of cervical levels, on right: axial views at different levels (c2,c4,c6) of AMU7T automated segmentations (a) from SCT default registration (b) from SCT + optimized SyN registration **2.** boxplot representation of mean/stdev qT1 values for each hemisphere (a) from SCT default registration (b) from SCT + optimized SyN registration

(A) MR protocol	
3D TI-MP2RAGE 3	spatial resolution: (0.3x0.3x4)mm3,
	2 separate runs (depending on cord curvature)
	aligned to upper (~c1-to-c4) and lower (~c4-to-
	c7) cervical levels (Fig.1.1a) to minimize partial
	volume effect in the transverse plane
2D T2*MGE 17	Slices (2.5-mm thick) were positioned
	perpendicular to the cord from c1-to-e7.
	As different in-plane spatial resolutions were
	used, images were all resliced at the highest
	resolution (HR, 0.175x0.175)mm2 (Fig.1.1b).
Acquisition parameters for 3D-MP2RAG	E and 2D-T2*-w imaging are detailed in ^{3,17} .
(B) Options used during the 2	D and 3D template constructions
Processing steps used during the 2D template	Details on the parameters specifically used
constructions	
1. Fig.1a / SyN only transformation	shrink-factors = 4x2x1;
	smoothing-factors = 2x1x0 vox;
	gradient step size = 0.25
2. Fig.1.3a / Refined 2D AMU ₂₆ qT1 template	(2,5,5) steps of (30x20x10) iterations
construction	(MI,CC,CC) for similarity metrics
	(0.25,0.25,0.15) for gradient step size
	(0,1,1) options for normalized intensities (NI)
	(0.32,0.32,0.1752)mm2 for targeted resolution
	([1x1x0.5],[1x1x0],[1x1x0.1]) weighting for the
	three modalities (GM,SC,qT1) giving less strong
	weights for the qT1 images to reinforce spatial
	constraints carried by GM/WM and WM/CSF
	interfaces.
3. Fig.1.3b / Refined 2D AMU72 T2*w	6 steps of (200x150x50) iterations using equal
template construction	weighting [1x1x1] for the three modalities
	(GM,SC,T2*w), first initialized with affine
	transformation on the AMU4012+# template". The
	mean or NI was chosen to produce a sharper
Berneley at a start of the law the AD second start	tempiate.
construction	
A AMU26	MeanSquares on WM masks
and (WM - CM - M- AMUT2 -	(100x20x50) iterations
mail(www.journet, comeparate)" -> AMU/2 co-	shrink-factors = 8x4x2
registrations	March Providence of MMA and the fore office (for A)
 AMU72 → PAM50 co-registration 	Meansquares on WM masks for affine+SyN
	gradient-step size=0.1, CC on T2*w contrasts,
	(20x10x5) iterations with shrink-factors = 4x2x1
	and smoothing-factors=2x1x0vox

Table1 - (A) MR protocol (B) Options used during the 2D and 3D template constructions

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