Study of the variability of short association bundles segmented using an automatic method applied to a HARDI database.

Edison Pardo[1], Pamela Guevara[1], Delphine Duclap[2], Josselin Houenou[2], Alice Lebois[2], Benoit Schmitt[2], Denis Le Bihan[2], Jean-Francois Mangin[2], and Cyril Poupon[2]
[1]*University of Concepción, Concepción, Concepción, Chile,* [2]*I2BM, CEA-Neurospin, Gif-sur-Yvette, France, France*

Introduction: The construction of an atlas of the human brain connectome [1, 2], in particular, the cartography of fiber bundles of superficial WM (SWM) are still an unachieved task. Two main approaches can be used for its study. First, manual ROI placement and analyses from an expert can lead to very detailed results, as in [3], where a single subject was studied using HARDI data and particular regions of the brain. Second, automatic fiber labeling can be performed, for example, using a non-linear GM/WM ROI atlas warping. This is the case of [4],where 29 SWM bundles were found in a 20 subjects DTI database. This was the first work describing several bundles but no detailed analysis was performed about the variability of the segmented fiber bundles. Other work combined an automatic fiber clustering approach with expert labeling for the construction of an atlas of 47 SWM bundles present in at least half of the population from a HARDI database of 20 subjects [5]. In this work we applied the method proposed by [4] on a HARDI high quality database, adding several processing steps in order to improve the results. Then we studied the variability of the 40 SWM fiber bundles in 12 subjects for each hemisphere, and we constructed a model of these bundles in MNI space.

Methods: *Acquisition:* Twenty healthy subjects from a high resolution HARDI database were used for this analysis. Scans were acquired on a Tim Trio 3T MRI system with a 12-channel head coil (Siemens, Erlangen), and the MRI protocol included the acquisition of a T1-weighted dataset using an MPRAGE sequence (160 slices; FOV=256mm, Phase FOV=93.8%; TH=1.10mm; TE/TR=2.98/2300ms; TI=900ms; flip angle FA=9°; matrix= 256x240; RBW=240Hz/pixel), a B0 fieldmap, and a SS-EPI single-shell HARDI dataset along 60 optimized DW directions, *b*-value= 1500s/mm2, (70 slices; FOV 220mm, Phase FOV 100%; TH=1.7mm, TE/TR=93/14ms: FA=90°; matrix=128x128; RBW=1502Hz/pixel; echo-spacing ES=0.75ms; 1 excitation; partial Fourier factor PF=6/8; parallel acceleration factor GRAPPA=2; total scan time 16min46s). *Post-processing:* the data were processed using BrainVISA/Connectomist-2.0 [6]; they were preliminary corrected for all the sources of artifacts (eddy currents, susceptibility effects, spikes, noise) and the analytical Q-ball model [7] was computed to obtain ODF fields; a streamline deterministic tractography was performed on the entire brain mask computed from [8] using a forward step of 0.1mm leading to an average of 1 million of fiber per subject. An atlas with 130 WM/GM ROIs (JHU_MNI_SS_WMPM_TypeII) [9] was warped to each subject using dual-channel (B0 and FA) non-linear LDDMM transformation [4]. Next, 40 WM fiber bundles were segmented in function of the 2 regions connecting them. We used pre-filtered data from an intra-subject clustering method [10], a fiber oversampling and a special fiber selection function in order to reduce the number of outliers. We calculated statistics of the number of fibers and volume of the bundles. For calculating the volume we used oversampled fibers and thresholded fiber density images with 2x2x2 times T2 resolution (0.8594x0.8594x0.85 mm). For a better comparison, the fiber number and volume were normalized by the brain size and multiplied by the mean brain size. Binarized bundle images from each subject where then aligned to MNI space for the construction of a model of the 40 bundles per each hemisphere.

Results and discussion: The *mean* and the *std* of the number of fibers and the volumes of all the bundles were calculated separately for the left and right hemispheres. A factor **FC**=mean/std was calculated in order to evaluate the fiber count variability, and similarly, a factor **VC** was calculated for the bundle volume. Fiber bundles were regrouped into 5 groups using FC as an index of variability. Table 1 lists the fiber bundles, and the *min*, *mean* and *max* values for FC, FV, number of subjects where bundles were found in both hemispheres (**SC**) and the difference between right and left hemisphere VC (**VD**). Bundles that were found in all the subjects in both hemispheres are in bold. Bundles described in [4] are in red and bundles described in [3] are in blue. We can verify that almost all the bundles (29) described in [4] exists in all the subjects. Figure 1 shows the bundles for each group of bundles.

Conclusion: To the best of our knowledge this is the first work that study the variability of SWM bundles using HARDI data in both hemispheres, as previous works reported about the existence of these fiber bundles in a population of subjects or analyzed their individual shape. We conclude that most of the studied bundles exist in most of the subjects and that bundles can be classified into different groups in function of their variability. For example, fiber bundles in group 1 have a low variability (for fiber count and volume), are present in all the subjects and their 3D shape can be better defined as shown in figure 1. Future work will be focused on the improvement of the described method and the inclusion of more subjects into the analysis. Other registration and segmentation methods will be implemented and compared, as some fiber missing can be due to registration errors.

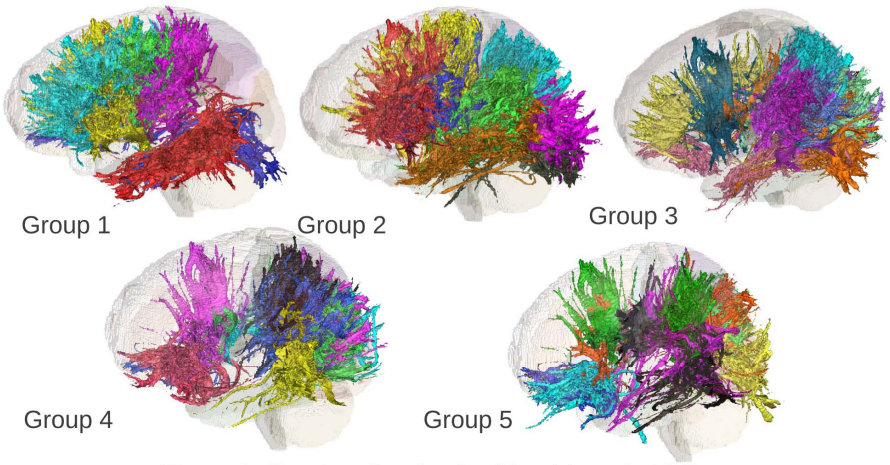

Figure 1: fiber bundles for the 20 subjects in MNI space.

group	SWM bundles (ROI1-ROI2 from [4])		FC	SC	VC	VD
1	**PrCG–PoCG** **SFG–MFG**	min	0.31	20	0.30	0.01
	SFG–IFG **MFG–PrCG**	mean	0.46	20	0.45	0.09
	LG–Fu **ITG–MTG**	max	0.55	20	0.58	0.19
2	**STG–MTG** Fu–IOG **IOG–MOG**	min	0.37	20	0.28	0.00
	SPG–AG **SFG–PrCG** **IFG–PrCG**	mean	0.54	19.8	0.47	0.1
	STG–SMG **MFG–IFG**	max	0.62	19	0.76	0.21
3	**PoCG–SMG** **Fu–MOG** **CingG–PrCu**	min	0.46	20	0.33	0.01
	Cu–LG **SPG–PrCu** CingG–SFG	mean	0.67	19.6	0.49	0.12
	AG–SMG **Cu–MOG** **SOG–MOG** Fu–PHG	max	0.75	18	0.76	0.22
4	**SPG–MOG** **SPG–MOG** **Cu–SOG**	min	0.48	20	0.42	0.02
	MTG–SMG **PoCG–AG** **AG–MOG**	mean	0.76	19.2	0.52	0.15
	IFG – LFOG	max	0.9	18	0.70	0.29
5	SPG–SMG SPG–SOG PrCG–MTG	min	0.57	8	0.42	0.03
	PoCG–MTG LFOG–MFOG LG–MOG	mean	1.13	16.8	0.71	0.40
	LG–MOG LFOG–RG PrCu–SOG SPG– CingG	max	2.12	19	1.41	0.76

Table 1: indexes for fiber count and volume variability for both hemispheres (worst value).

References: [1]The NIH Human Connectome project. [2]The European CONNECT project. [3]Catani M, Cortex 48, 2012. [4]Zhang Y, NI 52, 2012. [5]Guevara P, NI 61, 2012 [6]Duclap D, ESMRMB 842, 2012 [7]Descoteaux M, MRM 58, 2007. [8]Guevara P, ISMRM 818, 2011. [9]Oishi K, NI 43, 2008. [10]Guevara P, NI 54, 2011.