

## A novel probabilistic connectivity atlas for the human connectome : the CONNECT/ARCHI atlas

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**Introduction:** Building an atlas of the human connectome is a major scientific challenge that is now reachable using large cohorts. Two ambitious projects were recently launched to reach this goal: the Human Brain Connectome [1] in the USA and the CONNECT project [2] in Europe. The ARCHI database we describe here was acquired under the framework of the CONNECT project and aims at developing a novel probabilistic atlas of the human brain structural connectivity.

### Materials and methods:

**Acquisition** - The ARCHI database involved 79 healthy subjects, aged between 18 and 40. The protocol was composed of 2 scan sessions of 1h30, on a 3T Siemens MRI system. It included anatomical T1 data with 1 mm resolution each session and one high resolution 0.75 mm T1. Diffusion-weighted (DW) MRI data were acquired thanks to two different q-space sampling, first with high angular resolution diffusion imaging (HARDI) along 60 directions for  $b=1500$  and  $3000\text{s/mm}^2$ , second with a multi-shell acquisition of 20 directions on 10 shells between  $0-3000\text{s/mm}^2$ . It also included 3 relaxometry datasets dedicated to the construction of quantitative maps of the T2, T2\* and T1 times and resting state fMRI data. This abstract focuses on the investigation of the HARDI datasets.

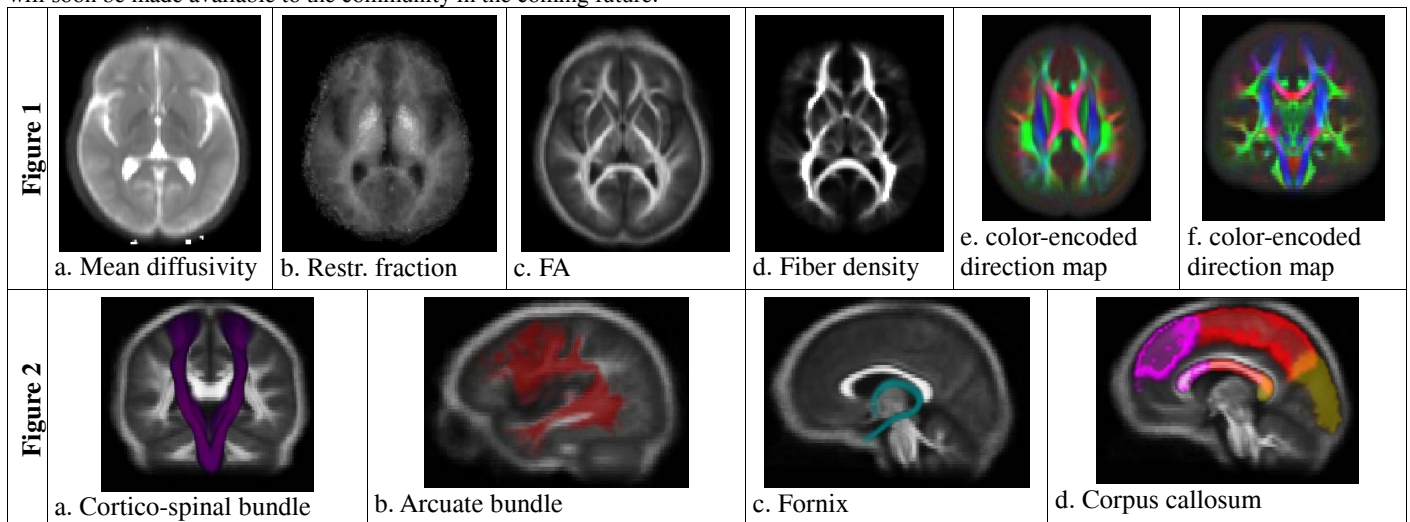
**Data processing** - The T1-weighted data were processed with BrainVISA/Morphologist [3] in order to obtain a robust mask of the brain, and the DW data were processed using BrainVISA/Connectomist [4]. The processing consisted of 5 steps including 1) the detection and correction of all the imaging artifacts (susceptibility effects, eddy current, outlier, motion), 2) the computation of individual analytical Q-ball fields to obtain orientation distribution function (ODF) maps [5], 3) probabilistic streamline tractography [6] applied to the entire brain of each individual and to provide dense tractograms, 4) the intra-subject clustering of fibers into bundles using the automatic technique of [7], 5) the automatic bundle labelling using the short and long bundle atlas of [7].

**Human brain white matter atlas** - The connectivity atlas was constructed by mapping all the subject data into the common space defined by the IXI template [8] using DTI-TK, which provides a diffeomorphic tensor-based coregistration optimized for aligning white matter anatomy [9]. This coregistration projects all the bundles to the common atlas space defined by the IXI template and enabled us to create the probabilistic density maps for 38 well-known long WM bundles as well as for 94 short WM bundles that could be found in all the 79 subjects. Average diffusion maps were also computed for the FA, the ADC, the transverse/parallel diffusivities, the restricted volume fraction from the CHARMED model [10]. Additional measures from other quantitative imaging, such as relaxometry, can be similarly included to this atlas.

### Results and discussion:

Figure 1 depicts the average a) mean diffusivity, b) restricted fraction, c) fractional anisotropy, d) fiber density, e) and f) color-encoded direction maps stemming from the novel atlas built from the 79 subjects. Thanks to the huge amount of data per subject and to the high number of subjects in the database, these quantitative maps showed a very good contrast between the various brain structures, for instance in the deep brain structures. Figure 2 provides isosurface renderings of several WM bundles after thresholding each probabilistic bundle density map to 75%. Examples are provided here for a) the cortico-spinal tract, b) the arcuate bundle, c) the fornix, and d) the corpus callosum, similar results (not shown) are found for the 38 long WM bundles and the 94 short WM bundles.

**Conclusion:** The CONNECT/ARCHI database presents a unique opportunity to build a probabilistic atlas of the human brain connectivity embedding morphometric information for each WM bundle as well as quantitative information along their centroids. We believe that this novel atlas of the brain connectivity will help making a step forward towards the inference of the human brain connectome, and analysis are undergoing to provide additional microstructural information for each bundle such as the axon diameter index [11]. This atlas of the connectome will soon be made available to the community in the coming future.



**References:** [1] The NIH Human Connectome Project, <http://www.humanconnectomeproject.org>, [2] The European CONNECT Project, <http://www.brain-connect.eu>, [3] Cointepas Y. et al, 2010, in Proc 9<sup>th</sup> HBM Vol 19(2), [4] Duclap D., 2012, ESMRMB #842 [5] Descoteaux M., 2007, MRM 58(3):497-510 [6] Perrin M., 2008, Neuroimage 39:215-22 [7] Guevara P. et al, 2011, Neuroimage, 54(3):1975-93, [8] Zhang H., WBIR 2010, [9] Zhang H., MedIA 2006, [10] Assaf Y., NeuroImage, 2005, 27(1):48-58, [11] Alexander I., 2010, Neuroimage 52(4):1374-1389.