Towards a super-resolution CONNECT/ARCHI atlas of the white matter connectivity

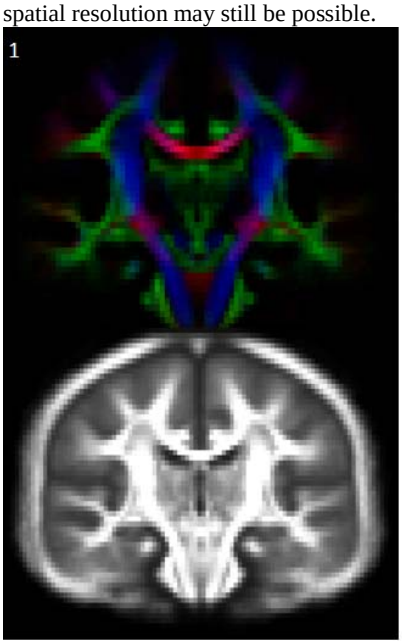
Delphine Duclap[1], Benoit Schmitt[1], Alice Lebois[1], Pamela Guevara[2], Hui Zhang[3], Clarisse Longo Dos Santos[1], Denis Le Bihan[1], Jean-François Mangin[1], and Cyril Poupon[1]

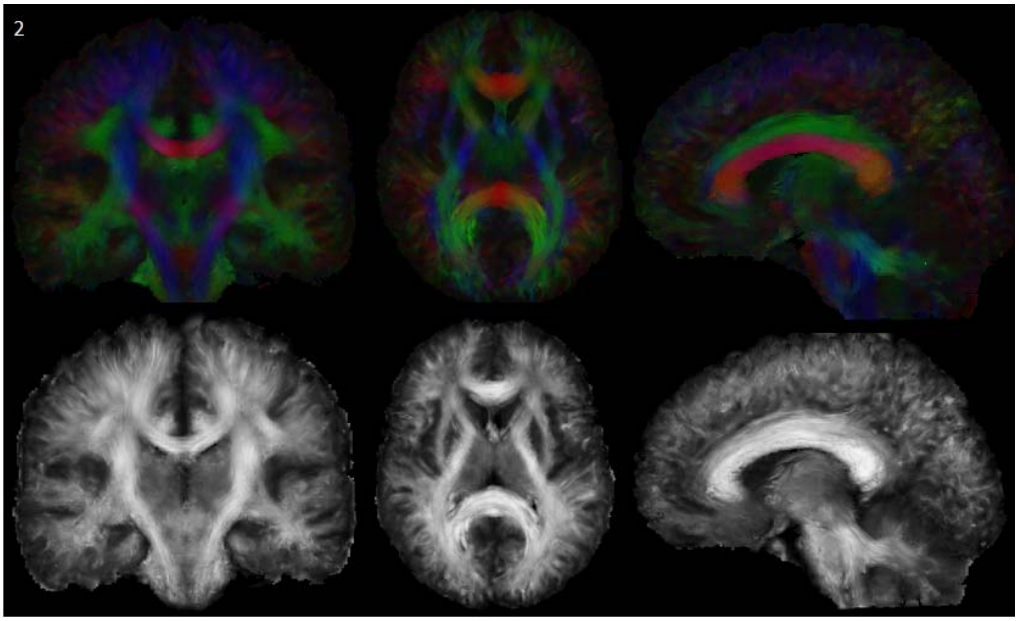
[1]I2BM, CEA NeuroSpin, Gif-sur-Yvette, France, [2]University of Concepción, Concepción, Chile, [3]Department of Computer Science and Centre for Medical Image Computing, University College London, London, United Kingdom

Introduction – Diffusion-weighted MR imaging suffers from limited spatial resolution. Although it is now possible to achieve higher resolution (1mm isotropic) with high field MRI systems (7T), such systems are not widely available. However, any diffusion signal information can be projected to a much better resolved space using dense streamline tractography techniques [1]. In this work, we propose to take advantage of super-resolution techniques to develop a novel half-millimeter isotropic resolution atlas of the white matter connnectivity.

Material and methods – *Acquisition :* Data were collected on a population of 79 healthy young subjects (CONNECT/ARCHI database), under the framework of the European connectome project (CONNECT), on a Tim Trio 3T MRI system with a 12-channel head coil (Siemens, Erlangen), and the MRI protocol included the acquistion 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; FA=9°; matrix 256x240; RBW=240Hz/pixel), a B0 fieldmap to correct for susceptibility artifacts, and a single-shot EPI single-shell HARDI dataset along 60 optimized diffusion directions at a b-value of 1500s/mm² (70 slices; field of view 220mm, Phase FOV 100%; Slice thickness 1.7mm; TE=93ms; TR=14s; flip angle FA=90°; matrix 128x128; read bandwidth 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 [2]; they were first corrected for all the sources of artifacts (eddy currents, susceptibility effects, spikes, noise) and the analytical Q-ball model [3] was computed to obtain ODF fields for all the subjects; a streamline probabilistic tractography was performed on the entire brain mask computed from [4] using a step size of 0.1mm and a dense sampling leading to, on average, 30 millions of fibers per subject. The fibers and the various diffusion maps (ADC, FA, transverse diffusivity, parallel diffusivity, restricted volume fraction, probabilistic density mask of automatically white bundles automatically segmented using [5]) of all the subjects were realigned using the diffeomorphic tensor-based registration technique provided in DTI-TK [6]. The super-resolution technique described in [1] was extended from a single subject strategy to a multiple subject strategy and was applied to the population of the ARCHI database matched to the IXI template to create a 500µm isotropic resolution atlas of the white matter connectivity.

Results & discussion – Figure 1 depicts the fractional anisotropy and color-encoded maps of the CONNECT/ARCHI atlas obtained from a similar processing but without making use of the super-resolution technique, and will be used as the low resolution gold standard. Figure 2 depicts the same diffusion maps including the super-resolution step and clearly shows the net contribution of super-resolution to improve the level of anatomical details revealed in the images. Furthermore, it creates a texture within the image adding some information about the directionality of the underlying tissue that can help a qualitative analysis of the atlas. Furthermore, the final resolution is only limited by the streamlining step size, thus even higher spatial resolution may still be possible.





Conclusion – We have demonstrated the feasibility of combining a super-resolution technique with an automatic bundle segmentation technique to provide a high 500µm isotropic resolution atlas of the human brain white matter connectivity. Because DWI is naturally embedded in a high dimensional space, densely sampled tractograms enable the resampling of any diffusion information in this diffusion inherited high dimensional space. This is more attractive than the alternative strategies, such as [7], based on non local means similarity criteria that are less natural and require longer data acquisition.

References – [1] Calamante, 2012, NI, 59(3), 2494-503 [2] Duclap, 2012, ESMRMB #842 [3] Descoteaux, 2007, MRM 58(3) : 497-510 [4] Guevara, 2011, 19th ISMRM, #818 [5] Guevara, 2012, NI, 61(4) : 1083-99 [6] Zhang, 2006, MedIA, 10(5) : 764-85 [7] Scherrer, 2012, MedIA, 16(7) : 1465-76