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Connectome-like quality diffusion MRI in 13 minutes - Improving diffusion MRI spatial resolution with denoising

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INTRODUCTION: Diffusion Weighted Images (DWIs) datasets are usually acquired at a lower spatial resolution than their structural counterpart due to a decrease in the Signal-to-Noise Ratio (SNR) and increased acquisition time as the voxel size is reduced. Achieving high spatial resolution improves the specificity of reconstructed tracts and diffusion features, which might not be present at a lower spatial resolution [1]. Noisy DWIs also suffer of biased measurements due to the non-Gaussian nature of the noise [2], which prohibits high resolution acquisition if no further processing is done. The Human Connectome Project (HCP) [3] aims to provide high quality DWIs using state-of-the-art MRI sequences and image correction. While the sequences are available, their applicability on a clinical scanner is restricted due to the difference in hardware quality used by the HCP. We show that high resolution DWIs are achievable thanks to proper denoising and favorably compare to the HCP dataset, while still being feasible in 13 mins on a standard 3T clinical scanner. We qualitatively compare a high spatial resolution gold standard dataset made of 10 averaged acquisitions with 60 DWIs acquired using non-collinear diffusion gradient orientations, a full brain acquisition of the same subject, but with only 40 denoised DWIs, and one acquisition from the HCP.

METHOD: We acquired two datasets at 1.2 x 1.2 x 1.2 mm^3 from the same subject in a single scanning session. The first dataset is a full brain acquisition consisting of 40 DWIs at b=1000 mm/s^2 and one b=0 mm/s^2 image, TR/TE = 18.9 s / 104 ms, gradient strength of 45 mT/m for an acquisition time of 13 minutes on a 3T Philips Ingenia scanner with a 32 channels head coil. An in-plane parallel imaging factor of R=2 was used without multiband acceleration. The second dataset is a partial brain dataset made of 9 slices, 60 DWIs at b=1000 mm/s^2 and one b=0 mm/s^2 image, TR/TE = 3 s / 104 ms, using the same spatial resolution as the first dataset. We acquired during the same scanner session (total time of 30 minutes) and averaged 10 such datasets in order to provide a gold standard comparison against denoising the full brain acquisition. Using the full brain dataset, we first corrected the Rician noise bias by using [4]. We then applied the Non Local Spatial and Angular Matching (NLSAM) [5] with a local neighborhood of 3 x 3 x 3 voxels and 4 angular neighbors to denoise the full brain acquisition. No further processing (such as eddy current or motion correction) was applied as we wanted to compare the effects of denoising on the raw acquisition without risking introducing blurring artifacts or noise distortion due to interpolation.

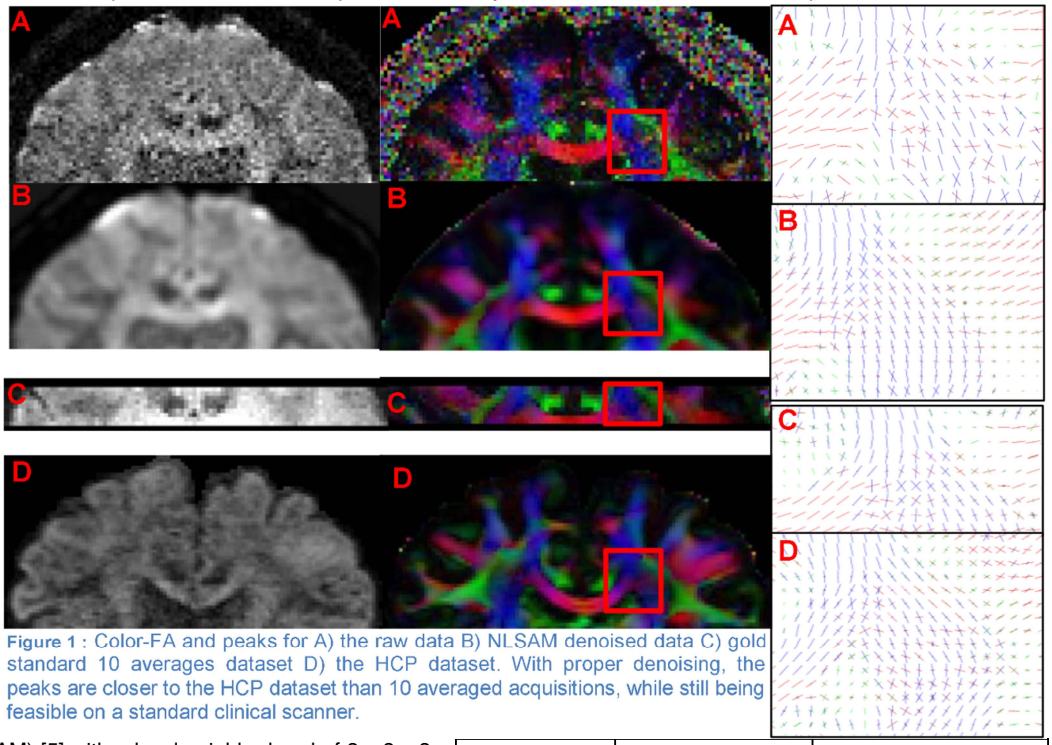

Figure 1 : Color-FA and peaks for A) the raw data B) NLSAM denoised data C) gold standard 10 averages dataset D) the HCP dataset. With proper denoising, the peaks are closer to the HCP dataset than 10 averaged acquisitions, while still being feasible on a standard clinical scanner.

DATASET: We used the 90 DWIs at b=1000 mm/s^2 and the 18 b=0 mm/s^2 DWIs from a pre-processed dataset (motion, eddy current and distortions corrections) from the HCP. The data was acquired at a spatial resolution of 1.25 x 1.25 x 1.25 mm^3 with TR/TE = 5.5 s / 89 ms, gradient strength of 100 mT/m, in-plane parallel imaging with R=2 and multiband acceleration of 3. The total acquisition time was 55 minutes for all three shells on a 3T Siemens Skyra scanner with a 32 channels head coil. Since we only use the b=1000 mm/s^2 shell, the acquisition time would be roughly 20 mins on the HCP scanner.

	Our dataset	HCP dataset
DWIs	40 DWIs + 1 B0	2x 90 DWIs + 18 B0s
Resolution	1.2 x 1.2 x 1.2 mm^3	1.25 x 1.25 x 1.25 mm^3
TR/TE	18.9 s / 104 ms	5.5 s / 89 ms
Acq. Time	13 mins	~ 18 mins
Gradient	45 mT/m	100 mT/m
Multiband	No	3x

Table 1 : Difference between the HCP and our full brain acquisition.

RESULTS: Figure 1 shows the raw data for the gradient direction closest to (0, 1, 0), color fractional anisotropy (FA) and peaks extracted from fiber orientation distribution function (fODF) computed using constrained spherical deconvolution (CSD) of order 8 [6]. Even though the raw data (Fig. 1A) suffers from noisy peaks, proper denoising (Fig. 1B) restores coherence in the junction of the corpus callosum (CC), corticospinal tract (CST) and superior longitudinal fasciculus (SLF). The denoised data (Fig. 1B) is comparable to the gold standard average of 10 acquisitions (Fig. 1C) and to the high quality acquisition from the HCP (Fig. 1D).

DISCUSSION: Even though the HCP project uses 2.5x stronger gradients, 2.25x more DWIs than our in-house acquisition and 3x fast multiband imaging (see **Table 1**), we are able to achieve a qualitatively comparable data quality. Using proper denoising, even a 3T clinical scanner can achieve in 13 minutes a diffusion MRI acquisition at a high spatial resolution, which would normally take 3-4 hours [1] for multishell data or ~ 1h15 for a comparable acquisition at b=1000 mm/s^2. This means that the diffusion MRI community could aim for higher spatial resolution DWIs, without requiring the use of costly new hardware or complicated acquisition schemes. This also means that projects such as the HCP can now acquire data at a much higher spatial resolution and include denoising in their pre-processing pipelines, enabling higher quality acquisition. This could in turn reveal new anatomical details, which are not achievable at the spatial resolution currently used in diffusion MRI.

REFERENCES: [1] Sotiropoulos & al. (2013) NeuroImage. [2] Jones & al. (2013) NeuroImage. [3] Van Essen & al. (2013) NeuroImage. [4] Koay & al. (2009) Journal of Magnetic Resonance. [5] St-Jean & al. (2014) ISMRM. [6] Tournier & al. (2007) Neuroimage.