

MASSIVE: Multiple Acquisitions for Standardization of Structural Imaging Validation and Evaluation

Martijn Froeling¹, Chantal M.W. Tax², Sjoerd B. Vos², Peter R. Luijten¹, and Alexander Leemans²

¹Department of Radiology, University Medical Center Utrecht, Utrecht, Netherlands, ²Image Sciences Institute, University Medical Center Utrecht, Utrecht, Netherlands

Target audience: Researchers interested in developing methods for diffusion MRI of the human brain.

Introduction: To date, investigating brain tissue with diffusion-weighted (DW) MRI remains challenging due to the complexity of the DW signal and the presence of numerous artifacts during data acquisition. Many DW MRI approaches have been proposed (DTI [1], DKI [2], DSI [3], QBI [4], CSD [5], CHARMED [6], NODDI [7], etc.) and a lot of correction procedures that address data imperfections (eddy current induced distortions, susceptibility based deformations caused by magnetic field inhomogeneities, physiological artifacts, etc. [8]) have been developed. In this context, a comprehensive evaluation of novel diffusion processing techniques or a reliable comparison between different modeling approaches is generally complicated by the lack of a genuine gold-standard (hardware phantoms can be too simplistic and simulations can be biased). In this work, we present the MASSIVE (Multiple Acquisitions for Standardization of Structural Imaging Validation and Evaluation) database, consisting of 8000 DW volumes (five shells and two Cartesian grids) and ten FLAIR, T_1 -, and T_2 -weighted images of a *single* healthy subject. This MASSIVE database provides an internal reference framework for diffusion methodology development and will be made publicly available.

Methods: All the data of the healthy subject were acquired on a 3 T system (Philips Achieva) with an 8-channel head coil. In total, the subject was scanned on 18 different occasions, where each session consisted of a 75 min MRI acquisition (total acquisition time: 22.5 h). In turn, each session comprised four DW MRI acquisition blocks, in which a unique subset of the 8000 DW volumes was acquired with a randomized ordering of the diffusion gradient orientations and the b-values to prevent an acquisition bias across sessions. In addition, B_0 -maps were acquired before and after each DW MRI acquisition block and noise maps were obtained at the end of each DW MRI acquisition block by switching off the RF pulses and imaging gradients. Additionally, In ten of the 18 sessions, FLAIR, T_1 -, and T_2 -weighted images were acquired. Note that while our main focus is on the DW MRI acquisition part, we included these more “conventional” structural MRI data as they often play an important role in diffusion MRI processing and analysis methods (e.g., [9–10]). The acquisition details were:

Structural MRI: FOV: 140x240x180 mm³; SENSE: AP/RL: 2/2; voxel size: 1x1x1 mm³; **T1:** 3D-TFE; TE/TR: 8.0/1.25 ms; TFE factor: 122; acq. time: 3.45 min. **T2:** 3D-TSE; TE/TR: 92/2500 ms; TSE factor: 124; acq. time: 2.45 min. **FLAIR:** 3D-IR-TSE; TE/TR/TI: 128/4800/1650 ms; TSE factor: 182; acq. time: 3.45 min.

Diffusion MRI: SE-EPI; FOV: 240x240 mm²; TE/TR: 105/7500ms; matrix size: 96x96; nr. of slices: 56; slice thickness: 2.5 mm; voxel size: 2.5x2.5x2.5 mm³; Gmax: 61.9 mT/m; Δ/δ : 51.6/32.8ms; SENSE: 2.5; Fat suppression: SPIR; For $b \leq 3000$ s/mm² partial Fourier: 1; BWepi: 50 Hz/pix; EPI-length: 36blips/24ms; For DSI and $b > 3000$ s/mm² partial Fourier: 0.77; BW-epi: 30 Hz/pix; EPI-length: 31blips/25ms; acquisition time for each DW MRI sub-set: 14 min and for the B_0 -map: 30 sec.

The gradient directions were defined with a positive z-direction and distributed over five shells and two Cartesian grids. The five shells contained 125, 250, 250, 250 and 300 gradient directions on the half sphere [11] with a b-value of 500, 1000, 2000, 3000 and 4000 s/mm², respectively. The two Cartesian grids were evenly spaced in half a cube, one with an even and one with an odd number of samples (8 and 9) and had a b-value of 2296 and 3000 s/mm² ($q = 0.038$ and $0.043/\mu\text{m}$) along the axes and a maximal b-value of 6890 and 9000 s/mm² ($q = 0.066$ and $0.075/\mu\text{m}$) for the corners points, respectively. They contained 365 and 256 points, respectively. Additionally, 204 $b=0$ s/mm² images were acquired, resulting in 2000 DW volumes in total with a 1:9 ratio between the non-DW and the DW volumes. The 2000 gradient directions were randomized and divided in 18 sets (8 of 120 and 10 of 104). Each set was acquired four times, i.e., with positive and negative gradient directions, thus covering the entire q-space (Fig. 1), and with anterior and posterior phase encoding direction (A+, P+, A- and P-) resulting in 8000 volumes.

Results: Figure 2 shows example images for the different shells and points on the Cartesian grid (A to H) together with the anatomical scans (T_1 - and T_2 -weighted and FLAIR) and a B_0 phase map (I to L). Figure 3 shows the average SNR per acquired volume of the 72 scanned blocks of the dMRI data.

Conclusion: In this work, we have presented the MASSIVE database, which consists of ten T_1 -weighted, T_2 -weighted and FLAIR anatomical scans, B_0 field maps, noise measurements, and 8000 DW MRI data volumes of a *single* healthy subject. This unique in vivo data set of the human brain will facilitate the evaluation and development of new diffusion MRI methods and will be made publicly available.

References: [1] P.J. Basser et al. J Magn Reson B. 103 (1994) 247–254. [2] J.H. Jensen et al. Magn. Reson. Med. 53 (2005) 1432–40. [3] V.J. Wedeen et al. Magn. Reson. Med. 54 (2005) 1377–86. [4] D.S. Tuch Magn Reson Med. 52 (2004) 1358–1372. [5] J.D. Tournier et al. Neuroimage. 35 (2007) 1459–1472. [6] Y. Assaf et al. Neuroimage. 27 (2005) 48–58. [7] H. Zhang et al. Neuroimage. 61. (2012) 1000–16 [8] J.D. Tournier et al. Magn Reson Med. 65 (2011) 1532–1556. [9] H. Huang et al. Magn. Reson. Imaging. 26 (2008) 1294–302. [10] R.E. Smith et al. Neuroimage. 67 (2013) 298–312. [11] D.K. Jones et al. Magn Reson Med. 42 (1999) 515–525

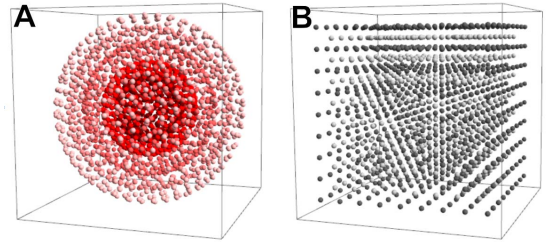


Figure 1: Schematic representation of the encoding schemes in q-space **A)** b-shells, **B)** Cartesian grids.

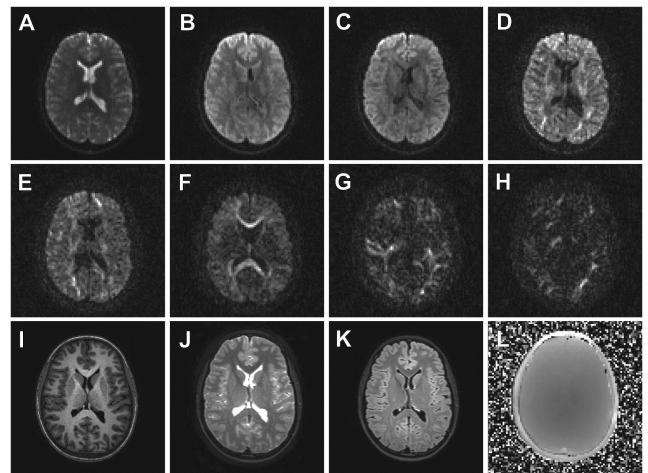


Figure 2: Example images with an applied b-value of **A)** 0 mm²/s, **B)** 500 mm²/s, **C)** 1000 mm²/s, **D)** 2000 mm²/s, **E)** 3000 mm²/s, **F)** 4000 mm²/s, **G)** 5500 mm²/s, **H)** 9000 mm²/s and anatomical images **I)** T_1 , **J)** T_2 , **K)** FLAIR, **L)** B_0 phase map.

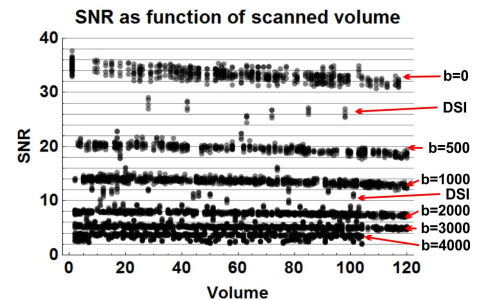


Figure 3: SNR as function of acquired volume for each of the 72 blocks (8000 volumes in total).