An open multi-B0-multi-B1-CEST dataset of the healthy human brain

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INTRODUCTION: Chemical Exchange Saturation Transfer (CEST) MRI is described quanzitativeley by the Bloch-McConnell (BMC) equations. Nevertheless, in vivo, a quantitative determination of the exchange rate and the relative concentrations from BMC fitting is difficult due to different issues. (i) The intrinsic non-linearity of the problem and the interaction of the different proton pools. (ii) The complex situation in vivo where also existing pool models remain under question. (iii) Different used data for the quantification with even different fitting tools. We think to address the issues an open dataset is needed that can be used by different groups so algorithms and pool models can be applied to the same data and compared between groups. Also, other quantification approaches can forward simulate our well-defined preparation to compare the resulting outcome. As exchange rates and proton pool concentrations should be field independent, a multi-B0-multi-B1 data is proposed. In this work, we share a multi-B0-multi-B1 Z-spectra dataset of human brain grey matter (GM) and white matter (WM), ready for BMC fitting and full quantification.

METHODS: Data was acquired from 1 healthy subject after written informed consent on 2 Siemens scanners, a MAGNETOM Prisma (3T) using a 1Tx64Rx head coil and a Terra.X (7T) scanner using a 8Tx32Rx head coil. For CEST data acquisition we used a conventional Spin-Lock pulse train preparation define in the Pulseq-CEST standard (10 pulses, DC = 50%, tp = 100 ms, td = 100 ms) at B1 levels of 0.6, 0.9, 1.5, 2, 2.7, 4 µT. Spin lock was used as it provides high quality spectra, while it is also possible to simulate efficiently with pulse-wise constant Bloch-McConnell matrices. Image readout was the 3D snapshot-CEST GRE [1]. For the different B1 levels the frequency offsets were equidistantly distributed between -100 and 100 ppm, while a finer sampling was used between -6 and 6 ppm with a step of 0.25 ppm for B1<4µT, and a step of 0.5 ppm for B1=4µT which was later interpolated. Exact B1 and B0 maps were measured with the WASABI method [2]. Also different normalization scans and quantitative T1 is part of the dataset. For further evaluation, we co-registered and resliced 7T data onto 3T data. To ensure simultaneously homogenous B0 and B1 values, a region-of-interest was defined, compromising ± 5% deviation from B1 map and ± 0.1 ppm deviation from B0 map. Within these regions, grey and white matter in regions were defined ensuring the aimed at offsets and B1 levels at both B0 field strengths. Total data acquisition time was 1:15 at 3T and 1.20h at 7T.

The datasets and loading codes are made publicly available at https://github.com/cest-sources/MultiB0_B1_qCEST_brain.

RESULTS: Figure 1ab shows the possible areas for homogeneous B1 and B0 in grey matter (a) and white matter (b) of the brain. The area was determined by the 7T WASABI B1 (c) and B0 (d) map. Within the matching red areas, two regions of interest (ROIs) were drawn, one in each tissue type. The mean Z-spectra for all B1 levels were calculated within these ROI's and are shown in Figure 1e-h for 3T and 7T. First BMC fitting attempts using a 7-pool CEST system were performed (data not shown, but available on the git).

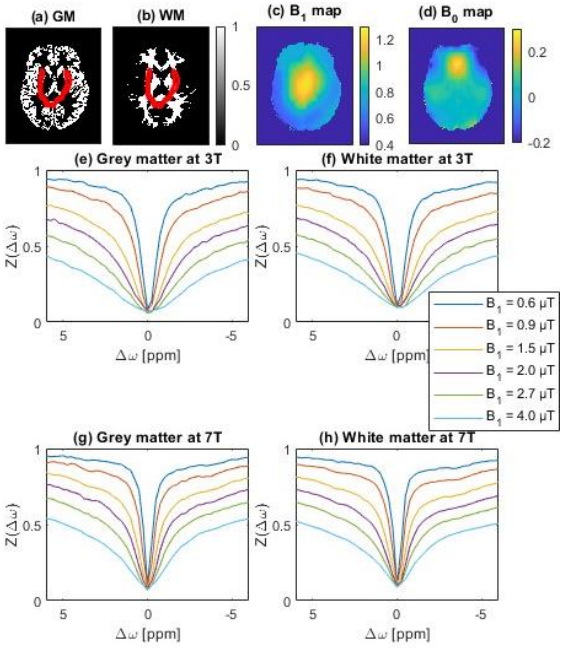

Figure 1: (a,b) Segmentation of grey matter and white matter with possible area for ROIs, determined by 7T B1 and B0 maps (c,d). The homogenous area (red) was defined in the B1 map as B1 = 1 ± 0.5 and in the B0 map as dB0 = 0 ± 0.1 ppm. Z-spectra in grey and white matter for all B1 levels at 3T (e,f) and at 7 T (g,h).

DISCUSSION: In vivo BMC quantification of the human brain was attempted previously at 7T using multi-B1 data [3], and at 3T using MR fingerprinting [4]. In this work we created quantitative CEST data of the same human brain at two different field 3T and 7T. Most importantly, we make this data publicly available together with the exact definition of its preparation and acquisition. Our aim is to perform BMC fitting on this multi-B0-multi-B1 dataset and invite other research groups to do the same. We are convinced that such a dataset will help the CEST community to sort out misunderstandings, improve fitting models, acquisition, and create deeper understanding of in vivo CEST and ultimately trigger novel discoveries.

CONCLUSION: We created and share comprehensive quantifiable CEST data of the same human brain acquired at 3T and 7T to trigger reproducible quantitative CEST and subsequent innovation.

REFERENCES:

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