Quantitative proton density mapping in pathological tissue: comparison of two receiver profile correction methods

Steffen Volz¹, Ulrike Nöth¹, Alina Jurcoane², Ulf Ziemann³, Elke Hattingen², and Ralf Deichmann¹

¹Brain Imaging Center, University Frankfurt, Frankfurt, Germany, ²Department of Neuroradiology, University Frankfurt, Frankfurt, Germany, ³Department of Neurology, University Frankfurt, Frankfurt, Germany

Introduction: Mapping of the proton density (PD) in human brain tissue is usually realized by correcting the image intensity for all other contrasts like T1, T2* and the sensitivity profiles of the RF-coils used for both transmission (B1) and reception (RP). T1, T2* and B1 can be accessed directly by measurement, resulting in M0 maps that represent the product of PD, RP and a constant. Thus, mapping of RP is crucial for PD mapping. RP mapping techniques are often based on the reciprocity theorem [1]. However, this can be a problem at field strengths beyond 1.5T. Here, two new methods for RP mapping were applied and results compared: (1) RP mapping based on segmentation-based bias field correction [2] and (2) RP mapping based on calculation of pseudo PD maps [3], assuming a linear relationship between T1 and PD in white matter (WM) and grey matter (GM) [4] and subsequent interpolation to the whole brain. It has been shown that both methods yield good results in healthy subjects [2, 3]. Here, the applicability in presence of pathological changes was investigated in patients suffering from multiple sclerosis (MS), stroke and brain tumours.

Materials and Methods: All measurements were performed on a 3T whole body MR scanner (body coil transmission, 8-channel phased-array head receive coil). The measurement protocol consisted of the following sequences: (1) B1 mapping as proposed in [5] with 4 mm isotropic resolution. (2) T1 mapping with whole brain coverage and 1 mm isotropic resolution based on the variable flip angle technique [6] with a spoiled FLASH-EPI hybrid readout [7]. (3) T2*-mapping by two FLASH scans with different TE and 2 mm isotropic resolution. The total acquisition time for these scans amounted to 15min 40sec. The sequence parameters are described in detail in [2]. Additionally, for delineation of T2 hyperintense lesions a FLAIR data set was acquired with 1 mm isotropic resolution. Lesions were excluded from the pseudo PD calculation. Calculation of RP and PD using the above mentioned methods was performed according to [2, 3]. In summary, for the first method, M0 maps were subjected to a bias field correction, assuming that this removes the bias imposed by the RP profile, yielding a PD map. For the second method, pseudo PD values were calculated from the T1 map inside a mask comprising healthy GM and WM only. Thus, the quotient of M0 and pseudo PD should yield an RP map for healthy tissue which can be extended to the whole brain by polynomial interpolation.



Results The figure shows results for an MS patient (left) and a patient with a glioblastoma (right). Depicted are respectively a single slice of the FLAIR data set showing either the MS lesion or the T2 hyper-intense tumour (top images) and the PD maps resulting from the bias field correction based method (middle images) and the pseudo PD based method (bottom images). Histograms of the PD values were created by pooling all voxels in WM and GM (top histograms) and in a semi-automatically generated lesion VOI (bottom histograms). The PD maps and histograms show that there is no significant difference between both methods in the PD values for the MS patients. Similar results were obtained for the stroke patients (data not shown). However, significant differences can be observed for the tumour patient. Within the tumour the pseudo PD based method yields increased PD values (as in GM and edema), whereas the bias field correction based method yields lower PD values (as in WM). The respective histograms for healthy WM/GM are shifted to systematically lower (about 2.5%) PD values for the pseudo PD based method, probably due to the fact that CSF is used for normalizing the PD maps and ventricles extend into the tumour area.

Discussion The results show that both methods yield nearly identical PD values for healthy tissue and for patients with only small lesions (e.g. MS patients) making the bias field correction method preferable due to the less complex post processing. However, the advantage of the pseudo PD based method is the fact that pathological tissue can be excluded from the sample points, avoiding erroneous PD values in these areas. Large PD differences were found in the glioblastoma, but the results obtained with the pseudo PD based method are more plausible, as increased PD values in tumours correspond to literature results [8], in contrast to the low PD values obtained with the bias field correction based method.

References [1] Hoult, 2000, ConcMagnReson 12: 173-183. [2] Volz et al, 2012. MRM 68, 74-85. [3] Volz et al, 2012. NeuroImage 63, 540-552. [4] Gelman et al, 2001. MRM 45, 71-79. [5] Volz et al, 2010. NeuroImage 49, 3015-3026. [6] Venkatesan et al, 1998. MRM 40, 592-602. [7] Preibisch et al., 2009. MRM 62, 240-246. [8] Neeb et al., 2006, NeuroImage 31:1156-1168.