B1 mapping of the breast with a reference tissue method

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Target audience: MRI physicists and Radiologists interested in quantitative breast imaging

Purpose: Small errors in B1 can lead to large errors in T1 and the calculation of contrast media concentration in DCEMRI experiments. For example, an error of 5% in B1 can lead to an error of 50% or greater in contrast media concentration. This can result in significant errors in diagnosis and quantitative analysis of DCEMRI data. Here we report on a new post-processing/acquisition B1 mapping method for breast MRI, based on a reference signal approach using a tissue with a known T1.

Methods: Differences between the T1 of a voxel estimated with a variable flip angle (VFA) gradient echo signal and the actual T1 of this tissue can be attributed to an inhomogeneous transmit or B1 field and resulting deviations in the actual flip angle with respect to the nominal angles prescribed at the scanner console. A proportionality factor ('A') between the actual and nominal flip angles (proportional to the local B1 field) is defined as follows:

$$A = \cos^{-1}\left(e^{-TR/T_{1t}}\right) \Big/ \cos^{-1}\left(e^{-TR/T_{1m}}\right) \quad (1)$$

Where T1t and T1m are the actual and the measured T1 from the VFA data, respectively. Fat in the breast has a homogeneous T1, low inter-patient variability[1], and it surrounds the tissues of interest in breast. This makes it an ideal choice for a reference tissue in the breast. In this method 'A' is found for every fat voxel in the field-of-view. Then the values in the missing voxels (corresponding to parenchyma) are interpolated using an inverse distance weighted scheme. Images were acquired on a Philips Achieva 3T-TX scanner using a 16-channel bilateral breast coil. Four patients were scanned under an IRB approved. VFA (TR/TE = 10/2.4 ms, FA's = 5,10,15,20°) and inversion recovery (TR/TE = 5000/32 ms, TI's: 50,150,300,600,1000,3000 ms) sequences were acquired, and T1 maps generated for each one. In addition, a single voxel spectroscopic inversion recover (PRESS-IR) sequence was acquired in voxels containing mostly fat and the measured T1 was used as the 'gold standard' T1 for fat – additionally PRESS-IR data were acquired on 10 patients to assess inter-patient variability. B1 maps were generated for each case based on the values of A in the fat voxels, and these maps were used to correct the VFA data. This method was evaluated by comparing the uncorrected and B1-corrected VFA T1 maps to the IR maps.

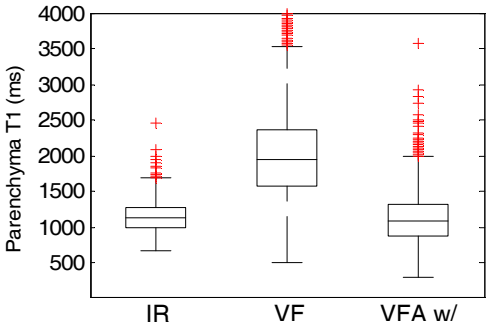

Figure 1. Boxplot of T1 values of all parenchymal voxels in the ROI's measured in four patient scans

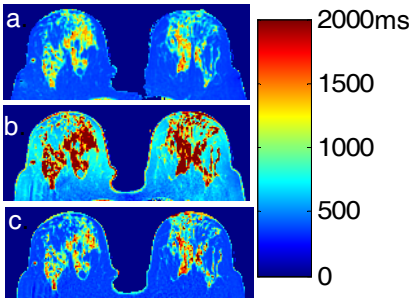

Figure 2. T1 maps for one patient scan: a. Inversion Recovery; b: VFA; c: VFA w/B1 correction

Results: Tests in a flood phantom with 'simulated' fat demonstrated that a linear inverse distance weighted interpolation accurately recovered the full B1 map. The mean T1 of breast fat measured in ten patients with the spectroscopic IR sequence was 341.3 ± 31 ms. Use of reference tissue flip angle corrections significantly reduced the difference between VFA and IR T1 values in breast parenchyma from 58% ± 21% ($p<0.05$) before correction to 3% ± 11% ($p>0.05$) after correction (Fig. 1). Average (± s.d.) T1's of parenchyma were: 1077 ± 104ms from IR; 1719 ± 267ms from VFA; 1146 ± 105ms from VFA with B1 correction. Figure 2 shows an example of T1 maps in one patient scan before and after B1 correction.

Discussion: The B1 maps generated with this method significantly reduced differences in the T1 values in parenchyma between VFA and IR measurements. The relatively low standard deviation in T1 of fat suggests a low inter (n=10) and intra (n=4) patient variability, making fat an excellent reference tissue. This method could be used in other regions of the body where an appropriate reference tissue is available.

Conclusions: We present a new approach to measurement of the B1 field in breast MRI, using a fat as a reference tissue.. The method is robust and can be easily implemented on any scanner. This method was successful in reducing differences between T1 maps generated with a VFA and IR sequences and therefore has the potential to significantly increase the accuracy of pharmacokinetic parameters generated from DCEMRI, as well as diagnostic accuracy and standardization of routine clinical practice.

References: [1] R. Rakow-Penner, et al. JMRI 2006; 23:87-91