Accelerated T1 Mapping for Brain MRI Perfusion Quantification

J. J. Mouannes[1], W. Shin[2], M. Shah[1], and T. J. Carroll[1,3]

[1]Biomedical Engineering, Northwestern University, Chicago, Illinois, United States, [2]National Institute on Drug Abuse, National Institute of Health, Bethesda, Maryland, United States, [3]Radiology, Northwestern University, Chicago, Illinois, United States

Introduction:

Absolute brain perfusion quantification has been proven possible with the Bookend technique [1,2], whereby a typical MR perfusion scan consists of two identical segmented, multiphase Inversion Recovery (IR) Look-Locker echo-planar imaging (LL-EPI) pulse sequences [3] one prior to and one following a single-dose injection of a gadolinium-based contrast agent One of the major hemodynamic parameters to be computed and mapped in perfusion post-processing is the cerebral blood volume (CBV) in the brain, which is essential for the diagnosis of certain brain conditions, such as the presence of a tumor or the occurrence of a stroke. Shin et al [2] report that the calculation of the latter requires an accurate mapping of T_1 relaxation times in a given imaging slice in the brain, both prior and after contrast agent injection. Currently, IR LL-EPI T_1 mapping is a time-consuming process, since it takes at least 7 minutes to compute one 128 x 128 T_1 map. Prolonged post-processing will prohibit both widespread dissemination of bookend perfusion quantification and impede its clinical use. We present here a new, accelerated T_1 mapping method which ensures a minimum acceleration factor of at 3.28 x 10^4. Our approach has been incorporated into a fully automatic reconstruction chain that eliminates user input for quantification of cerebral blood volume and cerebral blood flow.

Materials and Methods:

The current T_1 mapping process uses the *lsqcurvefit* function in MATLAB 7.0 (The MathWorks, Inc.) to fit the IR LL-EPI relaxation curve into Equation 1 to determine *A*, *B*, and T_1*, then solve for T_1 using Equation 2 [3]. The new, three-point estimation method determines the 3 unknowns in

$$M_z(t) = A - Be^{-t/T_1^*} \quad \text{(Equation 1);} \qquad T_1 = T_1^* * ((B/A) - 1) \quad \text{(Equation 2)}$$

Equation 1 without performing any fit, via solving a system of 3 equations, obtained at 3 critical time points during signal regrowth (t = 0, $t \rightarrow \infty$, and null time point, i.e. when the signal intensity is zero). The new T_1 mapping method was first tested without spatial filtering, then with Wiener filter, using MATLAB function *wiener2*, to perform a 2D adaptive noise removal filtering. The Wiener filter of varying neighborhood size ([3x3] and [5x5]) with and without Gaussian additive noise was applied. The analysis included a voxel-by-voxel regression calculation between the T_1 values calculated via fitting and the ones calculated using the three-point estimation method with each of the filtering options, for a single 128 x 128 brain slice. In addition, the percent difference in T_1 values in a white matter (WM) region of interest (ROI), in a WM mask, and in blood voxels were computed and compared for all the various fitting options of the three-point estimation method. The T_1 mapping mean computation time was also compared. This entire analysis was performed on 5 healthy volunteers' brain perfusion LL-EPI scans, done on a 3T Siemens MR scanner (Erlangen, Germany), both prior and after contrast agent injection, and the average results are reported.

Results and Discussion:

The effect of spatial filtering was negligible, and both the pre- and post-contrast analyses show a mean regression slope close to 1 (between 0.93 and 1.00), the most optimal case being when Gaussian additive noise degradation is assumed (Figure 1), which agrees with the known nature of the source of noise in the MR signal. A high correlation (ranging from 0.97 to 0.99) between the true T_1 values (from old fitting method) and the ones given by the new method is also observed. Both analyses indicate very small percent differences between the mean true and mean new T_1 values for WM ROI and WM mask (between 0.3 and 3.1%). The mean T_1 mapping computation time using the new method ranged from 5.7 ms (without filtering) to 12.8 ms (Wiener filter [5 5] with Gaussian additive noise), thereby resulting in a minimum T_1 mapping acceleration factor of 3.28 x 10^4. The percent differences between the new and true mean blood T_1 values prior to contrast injection are relatively large, even when applying the various filtering procedures (19.1 to 22.9%), which degrades the accuracy of our new T_1 mapping technique for relatively long T_1 values (1700 to 2200 ms). This error is due to the approximation made by considering the last signal value in the regrowth curve equal to the signal value as time goes to infinity (i.e. steady state). These limitations are consistent with our goal of quantification of blood volume, which requires accuracy in T1-mapping in the range 50 ms to 700 ms. While this assumption is accurate for cases when T_1 values are relatively short – the percent differences being less than 1% for the post-contrast blood T_1 values (250 to 320 ms), which allows almost complete signal recovery during the allowed repetition time, it may be violated for longer T_1 values, due to the segmented nature of the IR LL-EPI acquisition. However, by substituting another time-point to the last one in the system of equations, we expect to make the pre-contrast blood T_1 value converge to the true one.

Conclusions:

We have proven that a new, accelerated method for the quantification of cerebral blood flow, bases on rapid T1-estimations. Our T1-estimations are based on the three-point estimation which provides accurate T_1 values over a limited range of values. We have proven our approach to provide a 3 x 10^4 –fold acceleration with no loss of accuracy.

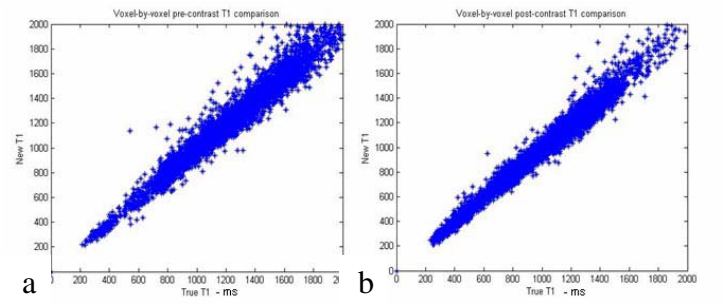

Figure 1. Voxel-by-voxel regression plots of the T_1 values obtained with the three-point estimation method with 3x3 Wiener filtering and assumed Gaussian additive noise, and the ones obtained from regular fitting (true ones), both prior to (a) and after (b) contrast agent injection, for one brain slice containing a major white matter region and a section through the sagittal sinus (blood).

References:

[1] Sakaie et al. JMRI 21:512-519 (2005).
[2] Shin et al. MRM 56:138-145 (2006).
[3] Messroghli et al. MRM 52:141-146 (2004).