# Estimation of Blood Magnetization for quantification of Arterial Spin Labeling Signal

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**INTRODUCTION:** Arterial Spin Labeling (ASL) is a method used for quantitative MRI of brain perfusion, among others. From the difference of two images, control and label, the flow can be calculated using for instance the general kinetic model proposed by Buxton et al.[1]. Cerebral blood flow (CBF) quantification requires an accurate estimate of the blood equilibrium magnetization $M_{0b}$. This is often measured in the sagittal sinus, or, in case of single time-point experiments, from the tissue signal in the control images. However, partial volume effects and $R_2$* differences between arterial and venous blood influence the measured $M_{0b}$ and therefore the estimated CBF, especially at higher field strength. The goal of this study was to get an estimate of the average brain tissue magnetization $M_{0t}$ in a user-independent way, using the QUASAR [2] sequence. $M_{0b}$ is then estimated using established blood-brain partition coefficients $\lambda$ ($M_{0b}= M_{0t}/\lambda$). Monte Carlo simulations are provided in order to test the robustness of the method.

**THEORY:** The QUASAR pulse sequence uses a rapid multi-time-point sampling strategy at a small flip angles $\alpha$ and a sampling rate $\Delta TI$. The observed $T_{1t\ app,eff}$ due to this Look-Locker readout, can be described as [3]:

$$\frac{1}{T_{1app,eff}} = \frac{1}{T_{1t}} + \frac{f}{\lambda} - \frac{\ln(\cos\alpha)}{\Delta TI} \qquad \textbf{(Eq. 1)}$$

By averaging the results from the label and control experiments, the $f/\lambda$ term is cancelled out, leaving just the effective relaxation term. Knowing $\alpha$ and $\Delta TI$, $T_{1t}$ can be isolated. In the QUASAR pulse-sequence, a pre-saturation pulse is applied before the Look-Locker readout, leading to a saturation recovery behaviour of the tissue signal $S=M_{0t}\cdot(1-e^{-t/T1t})$. The effective $M_{0t}$ can be described by:

$$M_{0t,eff} = M_{0t}\cdot\left(1-e^{-\frac{\Delta TI}{T_{1t}}}\right)\cdot\left(\sum_{i=0}^{N-2}\left(\cos^{i}\alpha\cdot e^{-\frac{\Delta TI}{T_{1t}}\cdot i}\right)+\left(\cos^{(N-1)}\cdot e^{-\frac{\Delta TI}{T_{1t}}}\cdot\frac{1-e^{-\frac{TI}{T_{1t}}}}{1-e^{-\frac{\Delta TI}{T_{1t}}}}\right)\right) \qquad \textbf{(Eq. 2)}$$

**METHODS:** Label and control curves were averaged and fitted to $M_{0,eff}$ and $T_{1,eff}$. The accuracy of this fit was tested for both parameters A and B (Fit = $M_0$ (A-Be$^{-t/T1t}$)), which are equal for saturation recovery. $T_{1t}$ and $M_{ot}$ were obtained from Eq.[1] and Eq.[2] respectively from 10 healthy volunteers who had all given written informed consent participated. The scans were performed on a 3T Philips Intera scanner using the following parameters: TR/TE/$\Delta$TI/TI1=4000/23/200/50 ms, 64x64 matrix, 4 slices, FOV=240x240, $\alpha$ = 30°, SENSE = 2.5. Additional scans were performed at flip angles of 10° and 20° in three subjects. Gray and white matter segmentation was based on automatic $R_{1,appeff}$ histogram fitting to a dual Gaussian. For $M_{0b}$ estimation, the partition coefficients $\lambda_{GM}$ = 0.98 and $\lambda_{WM}$ = 0.82 [4] were used for gray and white matter, respectively. To test the robustness of the method, a series of Monte Carlo simulations was performed by solving the Bloch equations numerically using a 4th order Runge-Kutta integration.

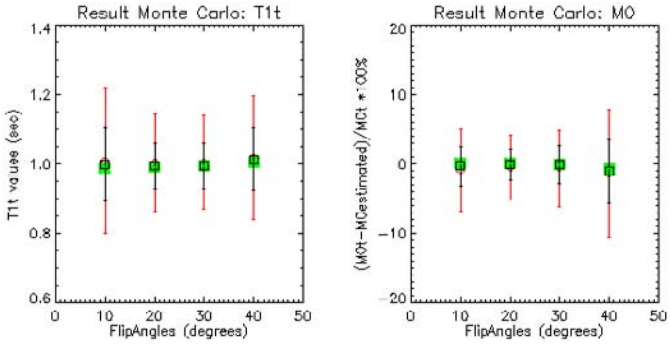


**Figure 1:** $T_{1t}$ =1.0s and $\Delta$TI=0.3s a) $T_{1t,est}$ b) $M_{0t,est}$ (SNR: ∞: green*, 100: black □, 50: red ○, number of repetitions: 1000)

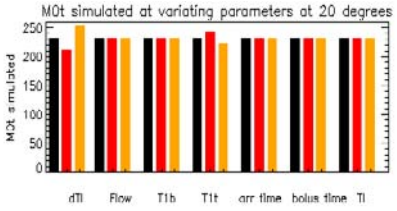


**Figure 2:** Simulation results at 20°. The standard parameters in black, -/+ (red/yellow) dTI = 0.2(-/+0.1)s, Flow = 60(-/+40) ml/min/100g, $T_{1b}$ = 1.65(-/+0.2)s, $T_{1t}$ = 1.2(-/+0.2)s, arrival time = 0.5(-0.5/+0.4)s, bolus time=1.0 (-/+0.5)s, TI = 0.05(-0.02/+0.01) s, $\lambda$=0.9

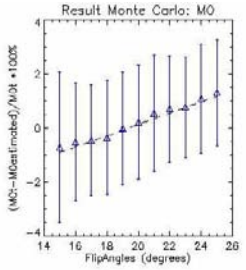


**Figure 3:** Influence on $M_{0t,est}$ of error in $\alpha$ (blue, SNR=100; Black:SNR=∞)

**RESULTS and DISCUSSION:** In the Monte Carlo simulations with SNR = ∞ and $\lambda$ = 0.9, the following parameters were varied: $\alpha$, $\Delta$TI, TI, flow, $T_{1b}$, $T_{1t}$, arrival time and duration of the bolus. The estimated $M_{ot}$ was significantly influenced by $\alpha$ (data not shown), $\Delta$TI and $T_{1t}$ (Fig. 2). The independence of $M_{0t}$ vs. $f$ proves that the addition of the label and control curves is an eligible way to exclude flow. Simulation results with noise (SNR = ∞, 100, 50) are visualised in figures 1 and 3. Fig. 1a) shows that data generated with $T_{1t}$ = 1.0 s and $\Delta$TI = 300 ms returns a $T_{1t}$ with a mean of 1.0 s for all noise levels and Fig. 1b) visualises the relative difference between $M_{0t,,est}$ and $M_{0t}$. The true $M_{0t}$ is estimated with a standard deviation of 3% compared to the real one. Further simulations (SNR = 100) showed that an error of 10% in $T_{1t,est}$ results in a $M_{0t,est}$ of 0.9+/-3.0% at 10° and 5.8+/-5.1% at 40° (data not shown). An error in the flip angle of 5° around 20° gives a $M_{0,est}$ of 1%+/-2.5% (Fig. 3). Despite the good results from the simulations, attention should be paid to errors that occur in the estimation of $T_{1t}$ or those coming from uncertain flip angles, since both factors would influence greatly the estimation of the true $M_{0t}$.

In ten subjects, a mean $T_{1t,GM}$ of 1.61 +/- 0.22 s and $T_{1t,WM}$ of 1.06 +/- 0.12 s were obtained. The $T_{1t,GM}$ is on the higher range of published values, while $T_{1t,GM}$ is in close agreement with literature values [5]. $M_{0b,WM}$ was compared to $M_{0b}$ obtained from the sagittal sinus after correction for $R_2$* effects [2]. The mean percent differences between subjects were 15% with extremes of -20% and +36%. Due to scanner optimization before each scan, $M_0$ can not easily be compared in between subjects and/or in between repetitive scans. However, the observed difference demonstrates the poor reliability of the sagittal sinus estimation and test-retest scans are needed for final validation of the technique.

**CONCLUSION:** A new approach of estimating $M_{0b}$ is proposed that is believed to be more reliable and offers a user-independent way of estimating M0b compared to traditional ROI based methods. Further tests on a larger group of volunteer and repetitive scans are needed in order to validate the method finally.

| $\alpha$ | $T_{1t,GM}$ | $T_{1t,WM}$ |
|---|---|---|
| 10 | 1.38 +/- 0.008 | 1.00 +/- 0.004 |
| 20 | 1.47 +/- 0.016 | 1.05 +/- 0.019 |
| 30 | 1.74 +/- 0.085 | 1.18 +/- 0.058 |

**Table 1:** Result for 3 subjects at 3 flipangles

**REFERENCES:** [1] Buxton et al., MRM 1998; 40:383-396 [2] Petersen et al. MRM 2005; in press [3] Günther et al., MRM 2001; 46:974-984 [4] Herscovitch et al., JCBFM 1985; 5:65-69 [5] Lu et al. JMRI 2005; 22:13–22

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