## Full-brain Blood Volume, Oxygenation and Hematocrit Imaging using T1 and T2 Prepared Velocity Selective Labeling

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INTRODUCTION: Blood oxygen saturation is an important parameter in the management of diseases such as stroke or cancer. In stroke, the bloods oxygen saturation is related to the Oxygen Extraction Fraction (OEF) and Cerebrovascular Reserve (CVR), both markers for the viability of the tissue. Impaired CVR results in high OEF and low oxygen saturation which is associated with an increased risk of ischemic events. In cancer patients, the treatment benefits from high oxygen saturation as oxygen is a vital component in the generation of free radicals which eventually destroy the cell's DNA. This is in particular the case in radiation therapy but it may also play an important role during certain types of chemotherapy. Therefore the assessment of oxygen saturation is important in the clinical setting. Techniques based on modeling of T2 and T2\* in a two-compartment model [1] have been developed for measuring oxygen saturation (Y) and regional OEF. To avoid possible sensitivity to field inhomogeneity and model assumptions, a more direct measurement of outflowing venous blood have been proposed in the form of the QUIXOTIC sequence [2]. While outflowing venous saturation Y<sub>v</sub> is ideal for true OEF estimation, the technique suffers from low SNR. In reality, the oxygenation levels have dropped significantly before blood even reaches the capillaries and SNR improvements can be achieved by including the entire vasculature as proposed in the recent T2-BIOS approach [3]. The sequence exploited the intravoxel incoherent motion (IVIM) in a single-slice T<sub>2</sub>-prepared DWI sequence to obtain blood volume and T<sub>2</sub>. Knowing the blood T<sub>2</sub>, Y can be estimated using previous determined relationships between T<sub>2</sub> and Y [4,5] if the hematocrit (Hct) is known. In this work we present an improved method, which allows simultaneous full brain measurement of blood-volume, oxygenation and hematocrit using a modified version of the T2-BIOS sequence.

METHODS: The sequence is shown in Fig. 1. It starts with a presaturation followed by a recovery time with options for adding a CSF suppression inversion pulse. Then the longitudinal magnetization is T2 prepared using either a standard MLEV preparation [4] or a series of B<sub>1</sub>-insensitive rotation pulses. Subsequently, a BIR-4 based velocity selective labeling sequence is played out right before a conventional multi-slice EPI readout. The sequence is repeated in groups of 4, each with different effective TE preparations in the range 0-160 ms. For each eTE, both a label and a control experiment is performed thereby allowing the separation of the vascular signal from the static tissue signal. In addition to this, the shortest eTE is repeated at different saturation times, allowing T<sub>1</sub> measurements of blood. Hematocrit is then calculated based on a previously determined T<sub>1</sub> vs. Hct relationship [6] using the fitted T<sub>1</sub> of blood from the sagittal sinus. For T2 the signal relationship follows:

$$\Delta S(eTE) = V_b \cdot M_{0b} \cdot e^{-\frac{eTE}{T_{2b}}}$$
where eTE is the effective

where eTE, is the effective MLEV echo time,  $V_b \cdot M_{0b}$  is blood volume fraction times bloods equilibrium magnetization. With appropriate knowledge of  $M_{0b}$ , e.g. from a partial volume free voxel

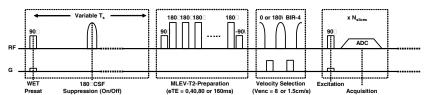


Figure 1. Sequence for measuring blood  $T_1$ ,  $T_2$ , and  $M_0$ . The sequence is repeated 4 times, each with a different  $T_2$ -preparation for each of the velocity selective label and control conditions. This result in effective TEs of 0,40,80 and 160ms used for  $T_2$  mapping. A variable saturation time  $T_s$  allows simultaneous  $T_1$  mapping of the blood.

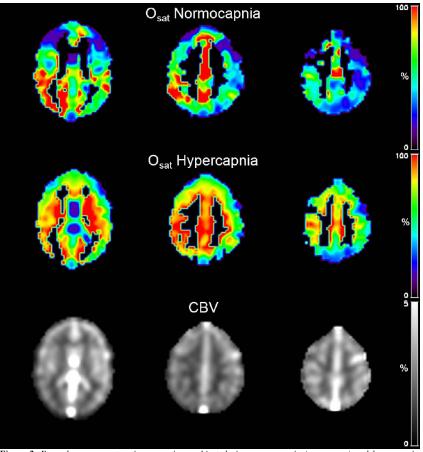


Figure 2. Example oxygen saturation maps in a subject during normocapnia (upper row) and hypercapnia (middle row). In the bottom row the corresponding CBV map is shown. The sagittal sinus region can be clearly seen in most slices and an automatic mask extracts the sagittal sinus for blood  $T_1$  and global venous  $T_2$  estimation. In the current example, the  $T_1$  of 1.73 results in a hematocrit of 0.42 and the  $T_2$  translates into a global oxygen saturation of 49.8% and 58.6% during normo- and hypercapnia, respectively.

in the sagittal sinus, a blood volume estimate can be obtained. Estimation of oxygen saturation from the fitted  $T_2$  was done by the use of eq.1 in [5]. Five healthy volunteers were scanned (3T Philips Achieva) using the modified T2-BIOS sequence according to institutional guidelines. The scan parameters were: TR/TE=7600/7ms, 40x40 matrix, FOV=240x240, flip-angle=90°, 11 slices of 7mm, SENSE=2.0, eTE=0,40,80 and 160ms,  $V_{enc}$ =0 and  $V_{enc}$ =1.5cm/s. Total scan time 6:32 min. The scan was repeated with and without a hypercapnic challenge. In 2 subjects variable saturation times were included for measuring blood  $T_1$ . In 3 subjects simultaneous oxygen saturation measurements were performed using an MR-compatible Near Infrared Spectroscopy (NIRS) device (Artinis Medical Systems, Zetten, The Netherlands).

**RESULTS and DISCUSSION:** Figure 2 show oxygen saturation maps from one volunteer. Average whole-brain normocapnia Y was  $62.7\pm5.4\%$  and hypercapnic Y was  $75.1\pm6.2\%$ . In the initial NIRS data we observed a limited increase from 66.2% to 67.6% (N=3). Global venous normocapnia  $Y_v$  was  $51.2\pm4.6\%$  and hypercapnic  $Y_v$  was  $63.1\pm7.3\%$ . Two subjects had blood  $T_1$  measured simultaneously (1.73 and 1.68s) which correspond to hematocrits of 0.42 and 0.45 respectively. This allows for the correction of the T2-Y relationship which is Hct dependent [5].

**CONCLUSION:** A full brain method for simultaneous CBV, Y and Hct mapping is proposed. Although in a preliminary phase, the initial results are promising and further validation work is ongoing in healthy subjects using a reactivity challenge while simultaneously monitoring frontal Y by NIRS.

**REFERENCES:** [1] An H et al, JCBFM 2000;20:1225-36 [2] Bolar DS et al, MRM 2011;66:1550-62 [3] Petersen ET et al. ISMRM'13 #2906 [4] Lu H et al, MRM 2008;60:357-63 [5] Lu H et al, MRM 2012;67:42-9 [6] Varela M et al, NMR Biomed 2011;24:80-8

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