

Detection of MR perfusion transit time effects in pulsed arterial spin labeling using a ‘model validity metric’

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Introduction: Arterial spin labeling (ASL) is a MR imaging technique capable of measuring regional cerebral blood flow (rCBF) non-invasively in vivo. Quantification of rCBF requires several experimental and physiological parameters to be properly accounted for. Variable bolus transit time and postlabeling delay are two confounding factors that may compromise the quantitative accuracy of perfusion estimates^[1]. The widely used PICORE Q2TIPS method of pulsed ASL (PASL) with a fixed temporal width of the tagging bolus enables quantitative estimates of rCBF from a measurement at a single time of inversion (TI). However, one of the key assumptions of Q2TIPS is that TI chosen is sufficiently long for the trailing edge of the tagged bolus to have reached the imaging voxel^[2]. Empirical observations suggest that transit time can be altered in different physiological and/or pathological conditions^[1,3]. Therefore, we like to propose a novel PASL method as an extension of the standard acquisition and processing of perfusion images by introducing a “model validity metric” to reduce artifacts by prolonged bolus transit time effects.

Theory: PASL uses an inversion pulse for tagging (like PICORE, FAIR, EPISTAR methods) and a tag saturation module to define the temporal duration of the tag (e.g. QUIPSS, Q2TIPS methods), rCBF maps can be calculated using equation [1]^[4], where ΔM = signal

$$f = \frac{\lambda \Delta M}{2\alpha M_0 \tau \exp(-TI_2 / T_{1a})} \quad [1]$$

difference between label and control images, λ = blood/tissue water partition coefficient, τ = bolus cut off time(also defines bolus duration), T_{1a} = the longitudinal relaxation time of blood, α ... inversion efficiency, M_0 = acquired map of equilibrium magnetization. TI_2 = image acquisition time (transit time $w = TI_2 - \tau$). In this model as proposed by Buxton et al.^[5], different slices are measured at different inversion times TI_2^{SLICE} due to the acquisition duration of a slice using 2D fast imaging methods like EPI, so that rCBF estimates that account for different TI_2^{SLICE} can be made by applying an inverted factor $\Delta M^{\text{CORRECTED}} = \Delta M \cdot \exp(ATI_2^{\text{SLICE}} / T_{1a})$, which normalizes the different TI_2^{SLICE} for different slices to the first slice with $TI_2^{\text{SLICE-1}}$. In line with the shape of PASL kinetic curves shown by Gallichan et al^[1], after a transit time Δt , the first inverted blood spins of the bolus arrive at the slice. During the time $(\Delta t + \tau)$, the bolus accumulates in the slice and give the increase in perfusion signal ΔM according the function $\Delta M \sim t \cdot \exp(-t/TI')$. At the time $(\Delta t + \tau)$, the perfusion signal ΔM reaches a maximum. After the time $(\Delta t + \tau)$ the perfusion signal ΔM undergoes longitudinal relaxation modeled with an effective relaxation time TI' according the function $\Delta M \sim \exp(-t/TI')$. TI' is a function of TI in tissue and blood. This approach minimizes bias in rCBF values if the bolus arrives in time in all regions of the slice with minimal temporal dispersion. In brain regions with altered bolus transit times due to pathology or biological differences, the bolus transit times are larger than $(TI_2^{\text{SLICE}} - \tau)$, then the standard model calculation will underestimate the true rCBF. In this study, we introduce a novel method to acquire two consecutive PASL scans with identical parameters, one in ascending and another in descending slice order. Each slice now has two average perfusion maps with different TI_2^{SLICE} times. The two maps and corresponding TI_2^{SLICE} can be interpolated, e.g. an average $TI_2^{\text{compensated}} = (TI_2^{\text{SLICE-1,1}} + TI_2^{\text{SLICE-1,2}}) / 2$ is assumed. Then, all slices have the same average TI_2 , while signal-to-noise ratio (SNR) per unit time is preserved. No further assumptions, as in the standard model, are required, because all maps for different slices are quantified with TI_2^{average} . In addition, a model validity map can be calculated from the rCBF maps at different TI_2^{SLICE} : the experimental signal difference at different TI_2^{SLICE} is set in ratio (A / B) to the theoretical model: $\Delta M(TI_2^{\text{SLICE-1,1}}) / \Delta M(TI_2^{\text{SLICE-1,2}}) =: A$ compared to $\exp(-(TI_2^{\text{SLICE-1,1}} - TI_2^{\text{SLICE-1,2}}) / TI') =: B$.

Methods: PASL data were acquired using PICORE Q2TIPS sequence on a 3T MRI scanner (Trio, A Tim System, Siemens, Germany) with 32-ch head receive coil. To minimize the head motion artifact, inline 3D Prospective Acquisition Correction (PACE) was used during all PASL scans. Scan parameters: 16 slices, 7mm thickness no gap, matrix 64x64, FOV=24cm, TR=2000ms, TE=12ms, one scan in ascending and another one in descending slice order, $TI_1=700$ ms, $TI_2=1500$ ms, total 32 acq. pairs plus one M0 image per scan, total scan time 2:20min. As stated above, a metric analysis was applied to estimated rCBF using $TI_2^{\text{compensated}}$. The model validity map was also calculated as described above.

Results: Example images are shown in Fig. 1: an rCBF map (left) and a corresponding model validity map (right). A model validity ratio (MVR) A/B close 1 (shown in green color) indicates that maximum transit times are below TI_2^{SLICE} and that assumptions for the standard model are valid. A model validity ratio deviating from unity (showing in red color) indicates that transit times exceed $(TI_2^{\text{SLICE}} - \tau)$ and that calculated rCBF values are underestimated in corresponding voxels. In the current case, several regions with questionable estimated rCBF were found in bilateral temporal lobes, occipital lobe and orbitalfrontal lobe. Our preliminary results suggest that spatial map of “model validity ratio” can potentially serve a quality control in rCBF estimates or violation of the standard model assumption.

Discussion: The development of a robust, quantitative ASL protocol is critical for estimation of quantitative CBF in research and clinical applications. A number of studies have measured multiple TI times for the same slices and demonstrated in healthy human brain that the model provides unbiased rCBF estimates in some regions, but in other regions, considerable bolus dispersion and latency are observed^[1]. Moreover, acquisition of multiple TI acquisition will considerably increase the exam time and might not be feasible in some clinical applications. In this study, a novel PASL method was introduced using 32-ch coil to preserve SNR at clinically acceptable measurement time. Compared with the standard PASL, this new technique can provide a model validity map. Spatial deviation in the model validity map is related to differences in regional transit time providing an indicator of potential biased in rCBF estimates.

Refs: 1).Gallichan D, MRM2009,686. 2).Luh W, MRM1999,1246. 3).Bokkers R, AJNR2008,1698. 4).Wang JJ, JMRI2003,404. 5). Buxton RB, MRM(1998)383

