Single-Shot Whole-Brain Background-Suppressed pCASL MRI with 1D Accelerated 3D RARE Stack-Of-Spirals Readout

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Target audience: Researchers interested in ASL methods and applications, and MRI physicists.

Introduction: Arterial Spin Labeling[1] (ASL) provides repeatable, non-invasive quantification of cerebral blood flow (CBF) in physiological units of ml/min/100g of tissue. Previous work suggests that ASL fMRI could provide several advantages over Blood Oxygenation Level Dependent (BOLD) contrast as a biomarker of regional neural activity, such as superior sensitivity in low task frequency and longitudinal studies, and decreased intersubject variability[2]. However, these benefits have not been widely realized in practice due to the relatively low sensitivity of most dynamic ASL methods.

Methods to improve the signal-to-noise ratio (SNR) of ASL include pseudo-continuous ASL (pCASL)[3] to maximize labeling and 3D sequences[4,5] combined with background suppression (BS)[6] schemes that suppress the static tissue signal to improve the temporal and spatial SNR of the ASL time series data[7]. However, whole-brain coverage remains limited in 3D single-shot acquisitions due to T2 decay, resulting in typical through-plane voxel resolutions of 6-7mm. While recent work has shown the feasibility of obtaining whole-brain, high-resolution, high-SNR ASL CBF maps using segmented BS 3D sequences[8], segmented readouts require multiple RF excitations or shots to acquire the complete k-space, and thus are ill-suited for studying dynamic perfusion changes. The use of RF coil arrays and parallel imaging techniques[9] provide a means for reducing scan time and SAR deposition by utilizing the spatially localized sensitivity of each component coil to recover the non-acquired k-space data. Despite the SNR penalty in the raw images observed with increasing acceleration factors, previous work has found no quality loss in the perfusion images with twofold accelerations in 2D EPI ASL data[10] due to the increased perfusion signal achieved by the shortened TE and readout time.

In this work, parallel imaging was implemented along the partition-encoding direction in a pCASL sequence with BS and 3D RARE Stack-Of-Spirals readout **(Fig. 1)**, using an improved GRAPPA[11] approach to reconstruct the missing partitions and to achieve whole-brain single-shot imaging with 3.75mm isotropic resolution. Both non-accelerated and twofold-accelerated versions of the sequence were evaluated in 6 volunteers during a motor-photic task, and their performance was assessed in terms of temporal SNR (tSNR), GM-WM contrast, and statistical significance of the detected activation. Simulated accelerated datasets were also derived from the non-accelerated acquisitions, to assess the impact of the GRAPPA interpolation process on these parameters.

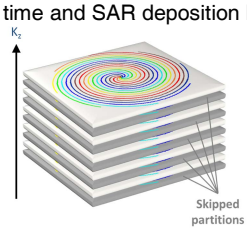

Figure 1. *3D RARE Stack-Of-Spirals with R=2 through-plane acceleration.*

Methods: 6 healthy subjects (2 F; 35 ± 10 years) participated in the study, after signing written informed consent.

Scanning protocol: The study was carried out on a 3T Siemens Trio using a 32-channel head array. First, an anatomical T1-weighed image and a Time-Of-Flight (TOF) angiogram were obtained. Then, subjects underwent 2 ASL fMRI runs of 6min duration with alternating rest and task blocks, in which they were asked to perform a right-hand finger-tapping task while looking at a flashing checkerboard **(Fig. 2)**. ASL data were acquired with the non-accelerated and accelerated sequence version, in a pseudo-randomized order. Two additional control images without BS and long TR were acquired at the end of each run for CBF quantification.

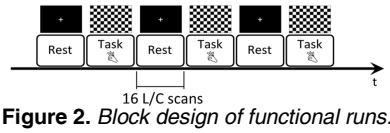

Figure 2. *Block design of functional runs.*

pCASL preparation and BS scheme: The pCASL pulse consisted of 1520 selective RF pulses with a labeling duration of 1.5s and post-labeling delay of 1.5s. The location of the inversion plane was determined individually for each subject based on the TOF angiogram, and maintained across runs. The BS scheme employed was optimized to suppress the static tissue signal to 10% of its equilibrium value. BS implementation details can be found in **(8)**.

Single-shot 3D RARE Stack-Of-Spirals: TE_{Eff}=10.3ms, $TR_{non\text{-}acc}/TR_{acc}$=4.5s/4s, excitation/refocusing FA=90º/180º, resolution=3.75mm isotropic, 34 nominal partitions with 5.9% OS, centric encoding acquisition scheme, slice PF=5/8, acquired partitions (non-acc/acc)=24/12, FOV=240x240x128mm^3, matrix=64x64, 2 spiral arms, max slew rate=120mT/(m·ms), max G_{amp}=36mT/m, BW=3125Hz/px, total readout time (non-acc/acc)=779ms/397ms.

Data preprocessing and analysis (SPM8 and Matlab scripts): Images were realigned and coregistered to the anatomical dataset before subtraction of label and control. Sinc subtraction was applied to minimize any BOLD contamination. CBF maps were computed using the one-compartment model[12]. Anatomical GM, WM and whole-brain masks were created for each subject from their T1-weighted image segmented tissue maps, to extract mean GM, WM and whole-brain CBF values. The tSNR was calculated as the ratio of the whole-brain perfusion signal to its standard deviation across time. The GM-WM contrast ratio was assessed in the mean CBF maps derived from the rest blocks using the segmented GM and WM masks. Functional activation data were assessed for each run at the subject level, using the general linear model, by fitting the data into a block-design with two alternating conditions, rest and task. Individual contrast maps of the task and rest comparison were obtained for each subject and thresholded at p< 0.001 unc.

Results and discussion (Fig. 3 and 4): Group whole-brain mean CBF were 58.6 ± 6.0 and 54.8 ± 5.4 ml/min/100g for the non-accelerated and accelerated sequences, respectively. Both sequences demonstrated the ability to detect functional activation at the subject level, including cerebellar activity. The accelerated sequence showed increased GM-WM contrast and more compact-defined activation clusters, with no tSNR or activation penalty associated. This is likely a result of the increased perfusion signal level and decreased through-plane blurring achieved by the shortening of readout time. Future work will explore in-plane acceleration strategies to reach higher acceleration factors.

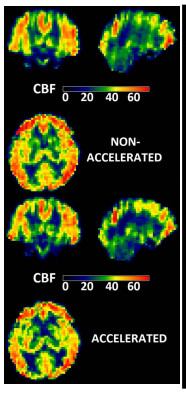

Figure 3. *Representative mean CBF maps.*

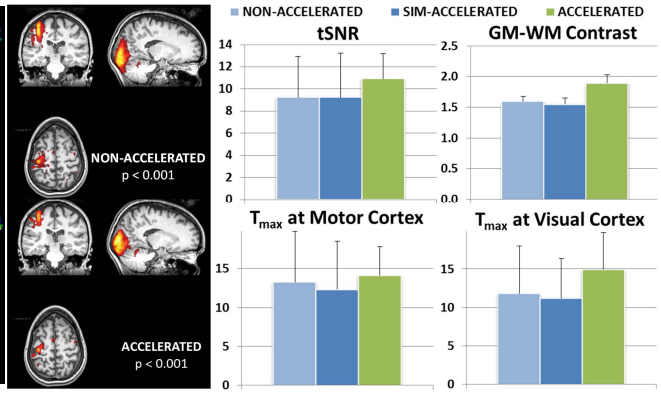

Figure 4. *Functional activation maps obtained on a representative subject (left) and mean results across the 6 subjects (right).*

References: **1.** Detre et al. MRM 1992; 23:37-45. **2.** Wang et al. MRM 2003; 49:796-802. **3.** Dai et al. MRM 2008; 60:1488-97. **4.** Guenther et al. MRM 2005; 54:491-98. **5.** Fernández-Seara et al. MRM 2008; 59:1467-71. **6.** Garcia et al. MRM 2005; 54:366-72. **7.** Vidorreta et al. NeuroImage 2013; 66:662-71. **8.** Vidorreta et al. NMR Biomed 2014; 27:1387-96. **9.** Duhamel and Alsop. Proc. ISMRM 2004; 518. **10.** Wang et al. MRM 2005; 54-732-37. **11.** Griswold et al. MRM 2002; 47:1202-10. **12.** Wang et al. Radiology 2005; 235:218-28.