Reducing Readout Duration in Single-Shot, Stack-of-Spirals Arterial Spin Labeling Using 2D In-plane Accelerations

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Target audience Physicians and scientists interested in the quantification of cerebral blood flow (CBF) and functional MRI (fMRI) of the brain.

Purpose Arterial spin labeling (ASL) is an established method to study brain function by imaging cerebral blood flow (CBF) (1). For the imaging portion of ASL, a fast read-out scheme capable of rapidly traversing the *k*-space is desirable to optimize sensitivity and image quality. Out of the common fast imaging strategies such as EPI, GRASE, and spiral, spiral read-out has the advantage of low sensitivities to artifact-inducing factors such as motion (2) and magnetic susceptibility difference in issues (3), and was shown to produce perfusion maps of higher SNR (4,5). 3D ASL without acceleration has required segmented acquisitions to maintain acceptable readout times. This can lower the temporal signal-to-noise ratio (TSNR), because the full *k*-space data is collected over multiple labeling periods, and increase sensitivity to motion artifacts. Further, segmented acquisitions are poorly suited to monitoring dynamic processes such as task activation or functional connectivity. Parallel imaging provides opportunities to collect whole-brain data with a single RF excitation pulse ("single-shot") by skipping significant portions of *k*-space, while maintaining image resolution and field-of-view (FOV). In this work we present single-shot, 3D background suppressed spiral ASL with 2D in-plane acceleration using non-Cartesian parallel imaging reconstruction.

Methods Study was performed on a 3T Trio Whole-Body scanner (Siemens Medical Solutions) with a 32-channel head coil. Three healthy subjects who provided written consent were imaged, two of which with both fully and under-sampled imaging, and one with only fully sampled imaging. Imaging parameters include pseudo-continuous labeling (6) and a background-suppression scheme to suppress the signal from static tissue in the brain (7). Labeling time=1.5 s, Post-labeling delay=1.5 s. Data were collected by a single-shot, a stack of uniform-density spiral read-outs (3D-RARE), 4 spiral arms. Centric partition encoding was used with a partial Fourier factor of 5/8 and an oversampling factor of 4.5%. TR/TE_{eff} = 4460/12.7 ms, FOV = 240X240X126 mm^3, resolution = 3 mm isotropic. Total read-out time = 780 ms, total scan time = 5.5 min for 36 label and control pairs. One subject was imaged with multi-shot 8 spiral interleaves and retrospectively under-sampled by a factor of 2 to evaluate the quality of 2D accelerated ASL. Acquisition acceleration and image reconstruction: 2 of the 4 spiral interleaves were acquired for each 2D plane, resulting in an acceleration factor of 2 and a total number of 56 echoes for a full 3D image set. Fully-sampled reference scans were collected in 2 segments at the beginning of the sequence for both label and control images. Images were reconstructed off-line using MATLAB. Details of corrections for gradient delays and partial *k*-space can be found in Refs. (4) and (5). After gridding, the central 1/4 portion of the *k*-space of each reference scan was used to generate the coil sensitivity maps using ESPIRiT (8). Images were then reconstructed by iteratively enforcing *k*-space data consistency and image domain sparsity (8,9). The procedure normally converged in 6 iterations. Mean-perfusion maps were generated as the difference of the magnitude images between label and control.

Results The mean perfusion maps created from the fully sampled (left) and retrospectively under-sampled (right) multi-shot images are shown in Fig. 1. Figure 2 shows an example slice from the fully-sampled reference label image (left) and the same slice of accelerated label image (right) acquired later in the same scan. The mean perfusion maps generated using all the accelerated label/control pairs are shown in Fig. 3.

Discussion We note our results at the current resolution would be nearly impossible without acceleration: the fully sampled data would require a read-out period of more than 1.5 s in a single shot sequence, well beyond the T_2 of grey matter (~100 ms (10)). The ESPIRiT-reconstructed under-sampled images show little loss of quality compared to the fully sampled images, as demonstrated in both Fig. 1 and Fig. 2. The perfusion maps generated using such acceleration strategy, as shown in Fig. 3, demonstrate resolution and quality similar to those of the multi-shot approach (11) but with potentially higher TSNR because of the reduced acquisition time over an entire image set. Future directions: Given the T_2 of the grey matter about 100 ms (10), our current read-out time of 780 ms is still long, causing signal attenuation and image blurring. The read-out time can be further reduced by combining the current scheme with acceleration along the partition direction (12), in addition to higher in-plane acceleration factors. Another challenge comes from the extended data processing time due to the iterative reconstruction procedure and the large data size. We note that there are methods that could significantly reduce data size that could potentially be helpful in speeding up the image reconstructions (13).

Conclusion We demonstrated in this work that 2D in-plane accelerations can be used to significantly reduce the total read-out time for single-shot, 3D stack-of-spirals ASL.

References 1) Detre JA, et al. MRM 1992;23:37; 2) Meyer CH, et al. MRM 1992;28:202; 3) Glover GH, et al. MRM 2001;46:515; 4) Vidorreta M, et al. Neuroimage 2013;66:662; 5) Vidorreta M, et al. NMR Biomed 2014;27:1387; 6) Dai W, et al. MRM 2008;60:1488; 7) Garcia DM, et al. MRM 2005;54:366; 8) Uecker M, et al. MRM 2014;71:990; 9) Huang F, et al. MRM 2010;64:1078; 10) Wansapura JP, et al. JMRI 1999;9:531; 11) Alsop DC, et al. MRM DOI:10.1002/mrm.25197; 12) Vidorreta M, et al. ISMRM 2015 (submitted); 13) Zhang T, et al. MRM 2013;69:571

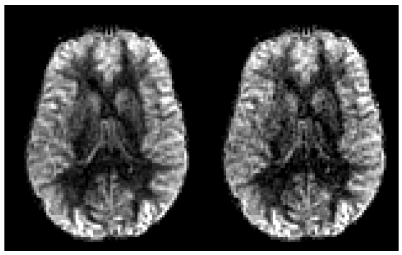

Figure 1 Mean perfusion maps from a fully-sampled data set (left) and from using only half of the spiral interleaves (right).

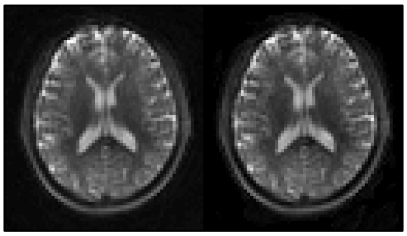

Figure 2 A fully sampled reference scan (left) and an under-sampled image of the same slice (right).

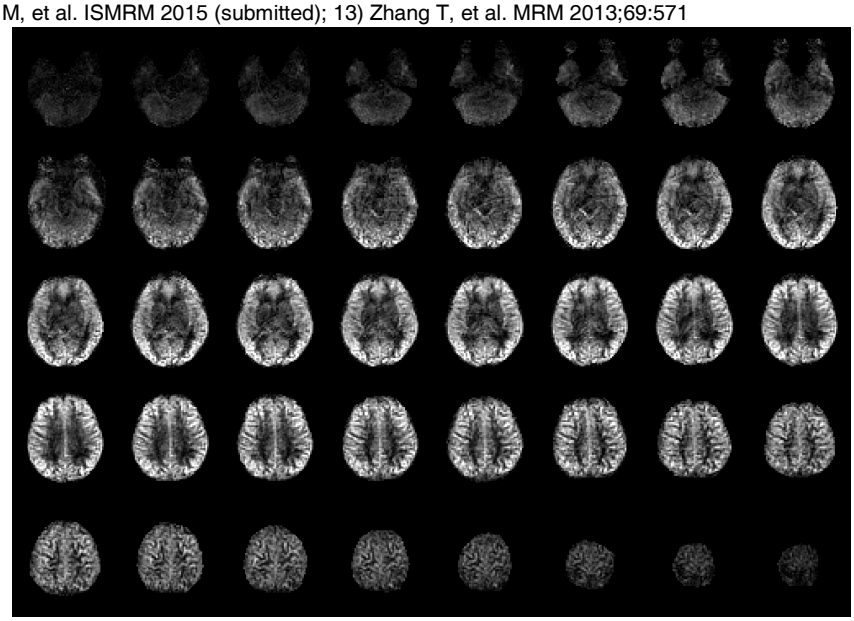

Figure 3 Mean perfusion maps generated from 36 pairs acquired using the described single-shot, 2D accelerated stack-of-spiral 3D sequence. Resolution is 3 mm isotropic.