

Realignment strategies in ASL timeseries

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Introduction

Arterial spin labeling (ASL) is a non-invasive perfusion measurement technique that is based on the subtraction of tag and control image pairs. Due to the low SNR of ASL difference images, any misregistration between tag and control images, e.g. due to motion, may cause large errors in ASL perfusion images. Realignment of ASL timeseries is therefore necessary to ensure good-quality perfusion images both for baseline perfusion and for perfusion fMRI measurements. Realignment is typically done using a least squares (LS) algorithm with rigid body transformations. Resulting realignment parameter curves for ASL timeseries sometimes exhibit what seems like $1/(2TR)$ modulations corresponding to a systematic difference between tag and controls images. Such a difference could arise from the small perfusion-related difference between tag and control images. It is shown here that these high frequency modulations are in fact due to respiration-induced motion.

Methods

13 healthy subjects (all female) were scanned using a PICORE QUIPSS II sequence [1] on a Siemens 3T Trio MR scanner. Imaging parameters were twelve 5mm slices, $T11/T12=700/1500$ ms, $TR/TE = 2200/20$ ms, 64×64 matrix GE-EPI readout, $FOV=192$ mm, 410 reps. After the first 134 reps, a blood pressure cuff placed around the subjects' right calf was inflated and was kept at a constant pressure for the remainder of the scan. Physiological data (respiration and pulse) were recorded during the scan.

The measured ASL timeseries (before subtraction) were realigned using three methods in SPM2: 1) the standard LS alignment of all images to first tag image, 2) normalized mutual information (NMI) alignment of all images to first tag and 3) LS alignment of tag images to first tag and control images to first control and NMI coregistration of first control to first tag. The alignment parameters (3 translations and 3 rotations) were modelled using a general linear model (GLM) with 22 regressors: 10 respiration and 10 pulse RETROICOR [2] regressors, a regressor modelling tag-control differences ($[-1 \ 1 \ -1 \ 1 \ \dots]$) and a constant term. The ASL difference timeseries were then modelled using a GLM. Two models were used: a simple model including only the paradigm regressors, and a model with RETROICOR regressors to locate voxels with residual respiration and pulsation induced motion effects. Following the SPM analysis the residuals were examined for whiteness and normality using the SPM diagnosis (SPMd) toolbox [3].

Results

The realignment parameters had components related to respiration (figure 1) for 10/13 subjects ($p < 0.0001$ for methods 1 & 3 and $p < 0.002$ for method 2). Components related to pulsation were less prominent ($p < 0.007$ for 4/13 subjects using method 1 and $p < 0.003$ for 2 subjects using method 3) most likely due to the dorsal slice position. Significant tag-control differences in the realignment parameters were only found using method 2 with 12 subjects having $p < 0.00005$. The achieved realignment parameters using methods 1 and 3 were generally somewhat different with a trend of the LS realignment shifting the images in the $-z$ direction. Figure 2 shows the voxels in a representative subject with significant residual respiration induced motion effects ($p < 0.05$ FDR corrected).

Discussion

Three alignment strategies for ASL timeseries were examined. All three strategies were found to detect respiration induced motion. Using LS or NMI realignment for all images was superior to using LS alignment of tag images to first tag and control images to first control. The latter method introduced a systematic misregistration between tag and control images.

While we have confirmed previously reported [4] lack of low-frequency drift in ASL difference images, we did find significant effects of physiological noise (especially respiration). When left unmodelled especially the respiratory induced effects lead to non-white residuals in the SPMd analysis.

References

[1] E. C. Wong et al. *Magn Reson Med*, 39:702-8, 1998.

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[3] W. L. Luo and T. E. Nichols. *NeuroImage*, 19:1014-32, 2003.

[4] A. M. Smith et al. *NeuroImage*, 9:526-33, 1999.

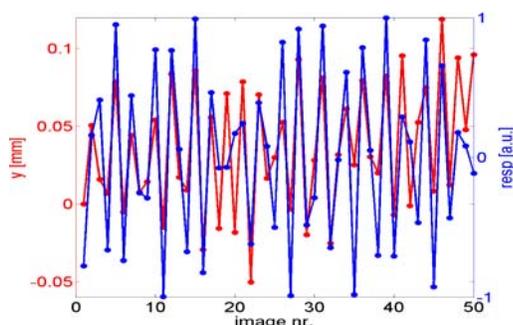


Figure 1: Realignment parameter for y-translation (red) for first 50 images and first RETROICOR respiration regressor (blue).

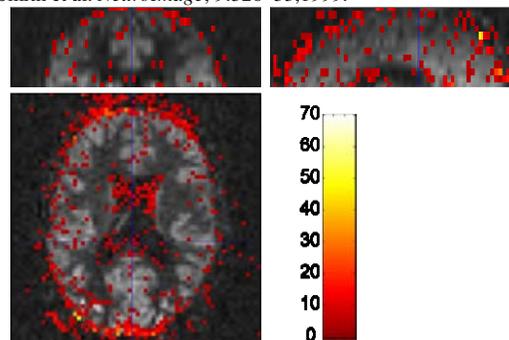


Figure 2: F-test images of RETROICOR respiration regressors ($p < 0.05$ FDR corrected) overlaid mean ASL perfusion image.