Improved correction of spatial inhomogeneities by surface coils in quantitative analysis of first pass myocardial perfusion

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Introduction: Absolute myocardial perfusion can be calculated by measuring the first pass of an MR contrast agent in the myocardium using the Fermi-model deconvolution technique [1]. To increase signal-to-noise ratio (SNR) surface coils are regularly applied. These introduce a distance-to-coil-dependent attenuation pattern [2]. However, the deconvolution technique requires a homogeneous sensitivity over the heart as one arterial input signal is applied for all segments. Therefore, corrections need to be made because of spatial inhomogeneities present. Originally, this spatial normalization is determined by using the baseline signal in the myocardium from the first pass perfusion sequence before arrival of the contrast agent [1]. As SNR within the myocardium before contrast arrival is typically low, this method introduces extra noise in the perfusion assessment. In this study we tested a pre-scan normalization method based on a separate PD-weighted pre-scan to correct for these coil inhomogeneities.

Method: 9 patients presenting at the hospital with atypical pain in the chest underwent MDCT and MRI as part of a clinical trial. In all patients coronary artery disease (CAD) could be excluded: no CAD signs on coronary angiography and a zero calcium score (MDCT), and no wall motion abnormalities, no visual infarction and no visual perfusion defects (MRI). MR was performed on a 1.5T scanner (Avanto, Siemens AG Healthcare Sector) using a 32 element surface coil (Invivo). Myocardial perfusion was assessed using with a new developed 2D saturation recovery gradient echo EPI sequence at three short-axis slices (apical, mid-ventricular and basal) at rest and during pharmacological stress (adenosine, 140 µg/kg bodyweight/min). Acquisition parameters were: TI/TR/TE: 110/5.6/1.1 ms, EPI factor 4, flip angle 18°, FOV 40x36 cm, voxel size 2.5x2.5x10 mm, TGRAPPA factor 2. The image acquisition was ECG-triggered and performed during breath-hold. The contrast agent Gd-DTPA (Magnevist, Bayer Healthcare) was administered at 0.1 mmol / kg bodyweight. A 1 ml prebolus (0.5 mol/l) was administered prior to the large bolus to reconstruct the arterial input function without limited saturation effects. Pre-scan normalization was performed as implemented by the manufacturer product (Syngo VB15, Siemens AG Healthcare Sector), using a low resolution 3D PD-weighted pre-scan within the same breath-hold. The data was reconstructed both with and without the pre-scan normalization. Additionally, the perfusion sequence was adapted such that the first two images of the regular perfusion sequence series were proton density weighted (PDW) (low flip angle and without a saturation pre-pulse) for a third normalization method. Signal-intensity time curves were obtained (Mass 5.1, Medis) for 18 segments of the myocardium (6 segments per slice) and the arterial input function at the LV blood pool (basal slice). Perfusion values were calculated by Fermi-model constrained deconvolution[1] using in-house built software (Matlab R14, The Mathworks).

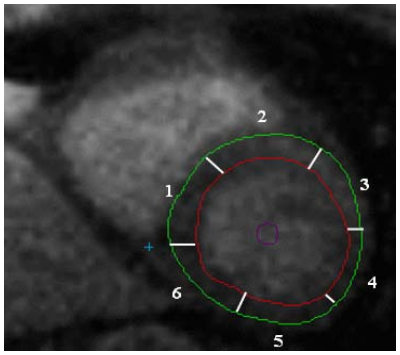

Figure 1: Short axis image showing the 6 segments per slice.

Three sets of perfusion analyses were performed: 1) regular reconstructed data with normalization using the time average of the baseline signal in the myocardium before contrast arrival, 2) regular reconstructed data with normalization using the two PD weighted images at the beginning of the time series, 3) the analysis of the pre-scan normalized reconstructed data. The first two methods assumed local linear spatial dependency of the coil sensitivity [1], both within the slice (see figure 2 and 3) and over the 3 short axis slices to reduced noise dependency.

Mean perfusion values over the subjects were calculated, and compared to baseline correction using a paired student t-test. As a measure of perfusion heterogeneity the relative dispersion was calculated as the standard deviation of perfusion over all 18 segments. The F-test was used to investigate the change in relative dispersion with a confidence level of 95%.

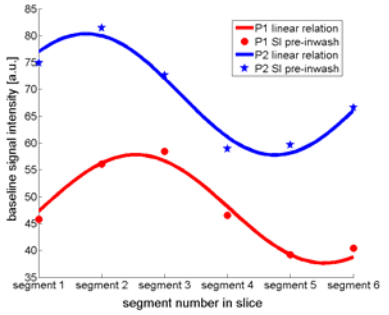

Figure 2: The linear relation before inwash of contrast agent is shown for two patients at rest. Spatial linearity in signal intensity across segments in a circle results in a sinusoid. The dots are the actual pre-inwash signal intensities of the baseline signals per segment.

Results: Mean perfusion was 0.43 ± 0.08 ml · g^{-1} · min^{-1} for baseline correction, 0.51 ± 0.11 ml · g^{-1} · min^{-1} for PDW correction and 0.49 ± 0.10 ml · g^{-1} · min^{-1} for pre-scan normalization (Figure 3), a significant change in perfusion (paired t-test, $p < 0.005$). Stress perfusion yielded 1.7 ± 0.4, 1.8 ± 0.4, and 1.7 ± 0.4 ml · g^{-1} · min^{-1} respectively (not significant, paired t-test, p=0.47). During stress, relative dispersion decreased significantly using pre-scan normalization compared to baseline correction (14% vs. 28%, respectively, F-test, p=0.04), but there was no significant difference between baseline correction and PDW correction (28% vs. 19%, F-test, p=0.12). At rest, a not-significant reduction of relative dispersion was observed. Performing the baseline correction or PDW-correction on the filtered datasets showed no reduction in dispersion.

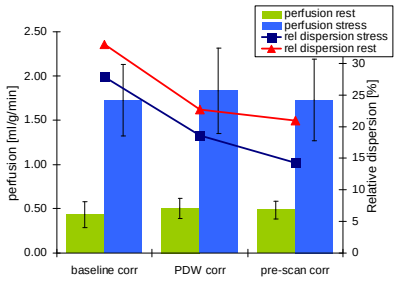

Figure 3: mean perfusion values [left axis] and relative dispersion between the segments [right axis] at rest [green, red] and during stress [blue].

Discussion: The perfusion values of these patients without CAD are expected to have a natural heterogeneity ~15% [3]. The pre-scan normalization method resulted in a perfusion heterogeneity closer to physiologically expected values compared to the perfusion calculated using baseline correction. The PDW-correction also reduced heterogeneity compared to the baseline correction. This can be explained by the better SNR properties, or suggests other spatial signal dependencies in the data such as B1 inhomogeneity, which plays less a role in PD-weighted imaging. It can be concluded that the addition of the pre-scan normalization improves quantitative analysis of perfusion. In near future, this correction method will be used to evaluate a patient population with (reversible) ischemia.

References: [1] Jerosch-Herold et al, JMRI 2004, 19:758. [2] Hoffmann et al, JMRI 2005, 21:310. [3] Beek et al, Am. J. Physiol. 1989, 257:1670.