Data-driven dynamic coil-bias correction for segmented myocardial perfusion images.

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Introduction: Accurate myocardial perfusion measurements by cardiac MRI are dependent on acquiring high quality images. Unfortunately, due to the heart's shape and its oblique position, coil-bias notoriously contaminates the images despite vendors' correction methods. Perfusion abnormalities in the most affected areas (closest to and furthest from coil receiving elements) can be misinterpreted leading to misdiagnosis or inconclusive results. To correct for those signal intensity discrepancies the most commonly correction method is proton density [1]. This involves acquiring an additional scan - proton density (which is neither T_1 or T_2/T_2*-weighted with shorter TE than T_2/T_2* and longer TR than T1 of myocardium). We propose an alternative method based on dynamic data-driven correction map extraction. Dynamic coil-bias correction (DCBC) does not require any additional scans and can be applied retrospectively to any segmented myocardial perfusion dataset. **Acquisition Methods:** 12 healthy volunteers and 3 patients with suspected myocardial perfusion abnormalities gave a written consent in accordance with the local ethics committee. Cardiac MRI perfusion images were acquired on a Philips Achieva 3T (TX) system, equipped with a 32-channel cardiac phased array receiver coil (Philips, Best, the Netherlands). First pass perfusion imaging consisted of a high-resolution *kt*-BLAST turbo-gradient echo sequence (imaging parameters: shortest TE=1.35-1.54ms, shortest TR=2.64-3.12ms, 50° flip angle, 90° saturation pre-pulse with 120ms delay, voxel size 1.2x1.2x10mm). Three short-axis slices (basal, mid and apical) were acquired. *Stress* imaging preceded *rest* imaging by 14±2 min. For *stress* imaging, 140 µg/kg/min of adenosine was administered intravenously for 4 min. Imaging commenced 3 min into the infusion and continued for 1 min during the acquisition of the images. Perfusion data were acquired during first pass injection of 0.075 mmol/kg Gadobutrol (Gadovist, Schering, Germany) at 4 ml/minute followed by a 20ml saline flush. A dual bolus contrast agent scheme was used to correct for signal saturation [2]. **Analysis:** The DCBC algorithm is based on the assumption that the signal intensity from the healthy myocardium at *rest* is uniform. After accurate respiratory motion correction and myocardial contour delineation, myocardial signal intensity curves were sampled using bilinear interpolation at a grid of 60 angular positions and 10 transmural layers, for a total of 600 segments per slice (Philips View Forum) [3]. The DCBC algorithm analyses the inflow of the contrast agent across the left ventricle (LV) myocardium, which corresponds to dynamics of the highest contrast-to-noise ratio. Data-driven correction maps were modelled for each slice by searching for the minimum of image inhomogeneities within a slice and across all the dynamics. Standard deviation of signal intensities in each slice were calculated and averaged across all dynamics providing us with the measurement of the uniformity. The correction maps were then applied to *rest* and adenosine *stress* perfusion series to normalise the first-pass signal intensities. The DCBC algorithm was initially developed in healthy volunteers and then applied in patients. **Results:** Figure 1 shows examples of coil-bias correction maps created by the DCBC algorithm and the more established proton density approach. Figure 2 consists of flattened myocardial intensities slices for averaged data across all dynamics. Each panel represents (from the left) uncorrected, proton density corrected and DCBC corrected images. The DCBC algorithm indicates an improvement of image uniformity of 19±13% compared with uncorrected data in the training dataset (healthy volunteers). In the patients group, where also proton density images were acquired, we could compare the DCBC algorithm with the proton density correction. The DCBC algorithm shows a 16±8% image improvement compared with a -2.5% (2.5% reduction in image uniformity) in corrected images by using the proton density approach. The latter comes with a 20% standard deviation due to this method being unreliable as the separate scan can be a subject to additional and unaccounted for artefacts. Typically it is the apical slice that the proton density-based correction fails (Fig.2). **Conclusions:** We have shown that by applying a data-driven dynamic coil bias correction (DCBC) algorithm, we can significantly reduce the affects of coil bias and improve the quality of myocardial perfusion images. We have also shown that this method seems to be superior to the more established used proton density-based correction and has the key advantage of being applicable to retrospective datasets, where proton density images were not acquired. Future work will require application of this method in larger group of patients, including subjects with left ventricular perfusion abnormalities or scars.

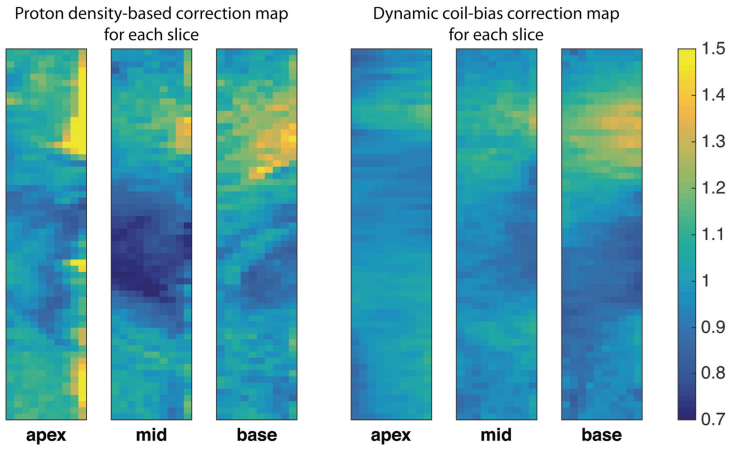

Figure 1. Correction maps for three myocardial slices created with proton density (left side) and data-driven dynamic coil-bias correction algorithm (right side).

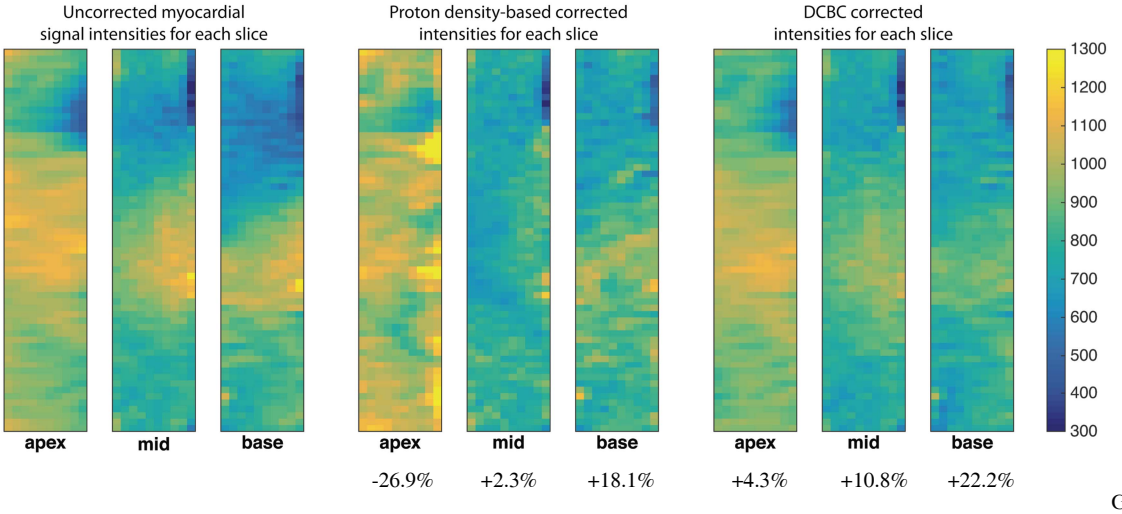

Figure 2. An example of segmented, averaged myocardial signal intensity across all dynamics for each slice; from the left: uncorrected, proton density and DCBC-corrected data. Values under corrected slices indicate the percentage improvement of the image uniformity (negative value indicates diminished image quality).

References: [1] F.P.P.J.Kremers et al. JMRI **31**:227-233 (2010); [2] M.Ishida et al. JCMR **13**:28 (2011); [3] G.L.T.F.Hautvast et al. MRM **66**:1477-1487 (2011).