Inline Perfusion – a new approach for fully automated generation of semi-quantitative parameter maps integrated into image reconstruction

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Introduction

The clinical use of first-pass MR myocardial perfusion imaging has shown a significant increase over the last years due to improved image quality and overall increased sequence performance in terms of spatial resolution and speed [1]. Several studies have demonstrated an at least equivalent if not superior sensitivity and specificity of MR perfusion over SPECT and PET [2] for the detection of myocardial ischemia. But one remaining advantage of nuclear myocardial perfusion is its capability to obtain quantitative and semi-quantitative results easily, whereas this is a labor intensive process for MR perfusion data today. Semi-quantitative or quantitative analysis of perfusion images usually requires significant user interaction [3] and expertise that results in prohibitive long times to evaluate myocardial perfusion images. Therefore it is mainly used in a research environment and has not entered the clinical routine yet.

The goal of this work was therefore to implement and test a framework for inline perfusion analysis which completely eliminates the need for user interaction and presents semi-quantitative parameter maps immediately after the scan together with the reconstructed images. The framework was tested on volunteers and patients undergoing stress and rest first pass perfusion. The feasibility of a fully automated perfusion analysis was demonstrated for the first time.

Material and Methods

Sequence Design

A multi-flavor perfusion sequence has been implemented on a clinical 1.5T scanner (Magnetom Espree and Avanto, Siemens Medical Solutions, Erlangen, Germany) that supports the common reported readout strategies (TurboFLASH, TrueFISP, hybrid Gre-EPI) as well as the acquisition of proton density (PD) weighted images for surface coil correction. TGRAPPA and TSENSE are supported to accelerate the data acquisition per slice [4-5]. The image analysis of the data was integrated in the framework of the scanner's image calculation environment (ICE, Siemens, Erlangen, Germany) [6].

Perfusion analysis- Inline processing

A semi-quantitative perfusion analysis was fully integrated into ICE based on recently described algorithms [7].

The analysis can be divided into seven steps: 1. Automatic detection of the heart bounding box 2. Image registration across time frames 3. Surface coil correction 4. Myocardial segmentation 5. Automated detection of foot and peak points 6. Calculation of parameter maps (upslope, area-under-curve and peak amplitude) 7. Output of parameter maps as DICOM image together with original image data. Details of the algorithms implemented in step 1.-2., 4.-6. are described in [7-8].

The surface coil correction was performed by dividing all time frames by estimated coil sensitivity map. The coil sensitivity was estimated by spatial median-filtering the PD images (kernel size: 7); regions without detectable MR signal have been replaced with interpolated values from surrounding tissue to prevent noise amplification in surface coil corrected images.

Patient Study

The inline perfusion algorithm was tested on 8 volunteers under rest acquiring 3-4 slices depending on heart rate. One patient (male, 45 years old) underwent stress and rest perfusion imaging on a 1.5T scanner (Magnetom Espree). Saturation prepared TrueFISP images (TE/TR = 1.3ms/2.7ms) were acquired during first pass of contrast agent (0.05 mmol/kg, Magnevist, Schering AG, Berlin, Germany) using a dedicated 8-channel cardiac receiver coil (Nova Medical, Wilmington, MA). TGRAPPA acceleration (factor 2) was utilized and additional PD images have been acquired.

Results

The inline calculation of the semi- quantitative maps was successful in 74% of all acquired slices (37 out of 50 slices). The patient results of the automatically generated maps are shown in Fig. 1. The inline analysis was successful for all three slices.

The PD images yielded a signal variation across the heart of 30% (linear fit) due to the inhomogeneous coil profile of the phase array receiver coil (Fig. 1a) and were used as an estimation to correct the inhomogeneous coil sensitivity (Fig 1b-c). Subsequently, the myocardium was segmented (Fig 1d) and semi-quantitative parameter maps generated (Fig. 1e-g) clearly depicting a perfusion defect involving the anterior wall (arrows).

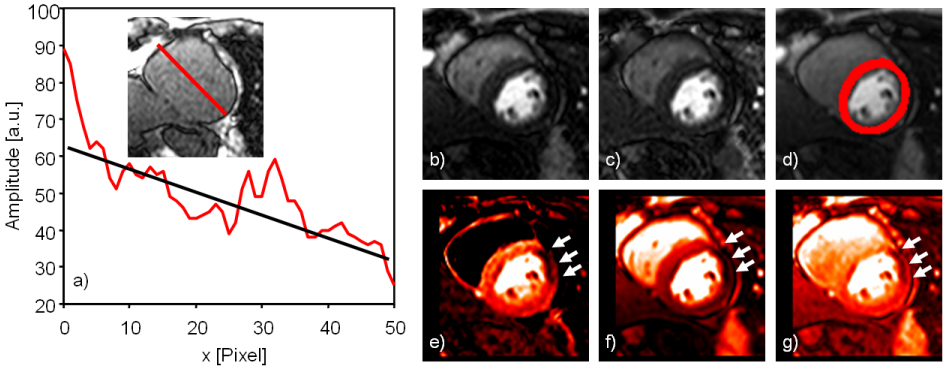

Fig.1: *Patient results:*
Inline generation of semi-quantitative perfusion maps without user interaction (1 out of 3 slices).

(a) Proton density image used for surface coil correction . The received MR signal varied significantly (30%, linear fit) across the heart.

Original (b) and surface coil corrected (c) image. Segmentation of the myocardium (d) and semi-quantitative perfusion parameter maps (e-f: up slope, area-under-curve and peak amplitude).
A perfusion defect in the anterior wall is depicted in the parameter maps (arrows).

Discussion

This study demonstrates the feasibility of fully integrated semi-quantitative myocardial perfusion analysis as part of the image reconstruction directly at the scanner without the need for any user interaction. The registration and segmentation of the images is a crucial initial step. Depending on the perfusion protocol, and patient size perfusion images exhibit a wide range of signal-to-noise, contrast-to-noise, and image artifacts such as aliasing limit the robustness of the currently implemented approaches. Further studies are required to be able to improve the performance of the algorithms and make it a reliable clinical tool.

References

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