The effect of myocardial contour errors on myocardial blood flow estimates in cardiac DCE-MRI perfusion.

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Introduction: Myocardial blood flow (MBF) can be estimated from dynamic contrast enhanced magnetic resonance imaging (DCE-MRI) of the heart. Estimation of MBF requires contours drawn around the left ventricular myocardium and in the blood pool to generate concentration vs. time curves representing the arterial input function (AIF) and the myocardial tissue. Manual contouring is prohibitively time consuming for clinical practice and automated contouring has not yet been accepted into clinical use due to uncertainty over its accuracy and reliability. Understanding how accurate myocardial contours need to be for MBF estimation is important both for manual contouring and to provide a target accuracy level for automated algorithm developers. The relationship between MBF error and systematic, global contour deformations from a 'true' manual myocardial contour has been previously described [1]. Although useful for depicting the relationship between contour error and cardiac physiology systematic deviations are not realistic simulations of typical contour errors. The aim of this study was to investigate the effect of more realistic simulated contour errors on MBF and determine at what level these errors induce a significant error in MBF.

Methods: Seventeen healthy volunteers underwent cardiac perfusion DCE-MRI on a 1.5T whole body scanner (Intera Philips Medical Systems, Best, The Netherlands) under rest adenosine induced stress conditions using 2 x 0.05 mmol/kg of Gd-DTPA (Magnevist, Schering, Berlin, Germany) [2]. A saturation recovery turbo-FLASH pulse sequence was used to acquire short axis images of the heart at mid-systole. Using dedicated image analysis software (Mass 5.0, Medis, Leiden University, Leiden, The Netherlands) regions of interest depicting the myocardium and left ventricular blood pool were manually drawn. To generate random contour errors each manual contour was represented as a circular B-spline with 10 knot points whose positions were allowed to vary randomly along radial lines from the contour's centre up to a maximum deviation limit defined as a fraction of the mean myocardial width for that DCE-MRI dataset (e.g. Figure 1). 30 iterations of random offsets were run with maximum deviation limits of 0.1, 0.2, 0.3, 0.4 and 0.5 of the mean myocardial width. Signal intensities from the regions defined by the contours were converted to concentrations using the method described by [3,4] using an assumed blood T_1(1435ms) [5]. This method has previously been shown to be robust to errors in the assumed T_1 value [5]. The conversion was successful in 16/17 datasets. MBF was estimated from these curves using Fermi-constrained deconvolution [6]. MBF errors were calculated as the difference between MBFs estimated from the manual and modified contours. Errors in the endocardial and epicardial contours at rest and stress were considered separately. A statistical t-test for the difference between the MBF estimated from modified and manual contours at each maximum deviation limit was conducted for a difference in the means and an F-test for a difference in the distribution variances.

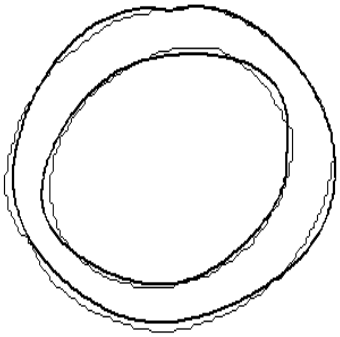

Figure 1: Manual (thin line) and modified erroneous (bold line) contours, with a maximum deviation limit of 0.2 of the mean myocardial width.

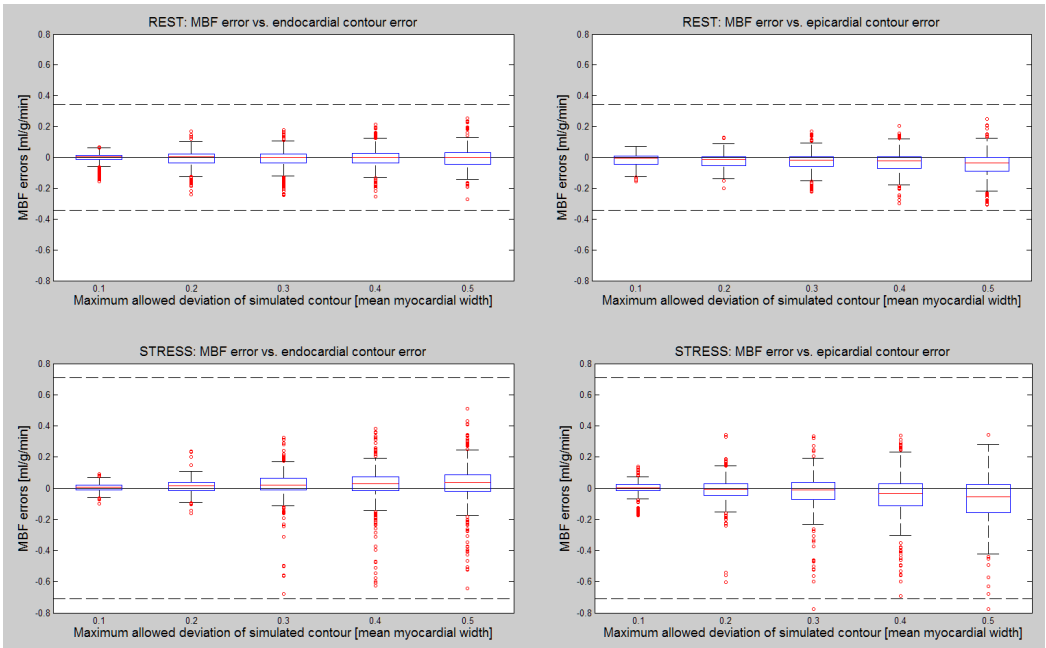

Figure 2: Boxplots (median, interquartile range and 95% confidence interval) of MBF errors vs. maximum contour deviation limit (expressed as a fraction of the mean myocardial width) in the rest endocardial contour (top left) rest epicardial contour (top right), stress endocardial contour (bottom left) and stress epicardial contour (bottom right).

Results: Using the 'true' manual contours MBF (mean ± SD) for rest and stress were 1.24 ± 0.35 ml/g/min and 3.48 ± 0.67 ml/g/min respectively. Figure 2 shows boxplots depicting the median, interquartile range and 95% confidence interval of MBF errors for each maximum contour deviation limit. The four plots correspond to endocardial and epicardial contour errors at rest and stress. The dashed black lines depict ± one standard deviation of the MBF values obtained with the manual contours. F-tests and t-test for differences in variance and mean MBF error were non-significant ($p>0.05$) in all cases except a maximum contour deviation of 0.5 of the mean myocardial width in the resting epicardium (t-test: $p=0.03$).

Discussion: The spread of MBF values we obtained from our manual contours is comparable with those found by other groups (Rest: 0.89 ± 0.32 ml/g/min; Stress 2.25 ± 0.94 ml/g/min weighted average from [7-10]). Contour errors up to a maximum deviation limit of 0.4 of the mean myocardial width did not cause a statistical shift in mean MBF. This is expected as both interior and exterior contours were allowed causing both under and overestimates of MBF. The increase in spread of MBF values with contour error is expected but F-tests did not show this to be significant even at 0.5 of the mean myocardial width. The 95% CI for MBF errors did not exceed the one standard deviation line of 'true' MBFs up to 0.5 of the mean myocardial width. This shows that the contour errors simulated did not induce a statistically significant change in the distribution of MBFs. This work implies that the variance induced in MBF estimates from contour errors is not significant compared to the natural variance of MBF within the healthy population suggesting that a relatively low target accuracy for automated contouring algorithms is acceptable.

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References: 1. Biglands J.D. et al, JCMR 2010, 12(Suppl 1):235 **2.** Radjenovic A, MRM 2010, DOI: 10.1002/mrm.22538 **3.** Larsson H.B.W. et al, MRM 1996 35:716-726. **4.** Fritz-Hansen et al, MRM 1996 36:2 225-231. **5.** Biglands J.D. et al, ISMRM Stockholm, 2010. **6.** Jerosch-Herold M., Med. Phys. 1998; 25(1):73:84. **7.** Pack N.A. JCMR 2008; 10:52. **8.** Fritz-Hansen T. JMRI 2008; 27:818-824. **9.** Icihara T., MRM 2009; 62:373-383, **10.** Vallee J.P., JMRI 1999; 9:197-203.