Myocardial contour error distance metrics do not correlate with myocardial blood flow estimate errors in DCE-MRI cardiac 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. Quantification of MBF requires contours to be drawn around the left ventricular myocardium and blood pool in order to generate concentration vs. time curves from these regions. Manual contouring is prohibitively time consuming for clinical practice and is a significant barrier to the use of quantitative myocardial perfusion in clinical practice. Many automated contouring algorithms for cardiac DCE-MRI perfusion have been developed to address this issue enlisting a variety of evaluation metrics to assess their performance. This makes objective cross-comparison difficult. Often such algorithms are evaluated with some geometric distance metric, considering distances between contours with respect to some ground truth contour, or in terms of errors in estimated MBF. The aim of this study was to establish the relationship between these geometric distance metrics and MBF errors, with a view to enabling cross-comparison of algorithms from the literature.

Dice's Similarity Coefficient (DSC)	Hausdorff Distance (HD)	Partial Volume (PV)		
$DSC = \frac{2 X \cap Y }{ X + Y }$	$HD(X,Y) = \max_{x \in X} \left\{ \min_{y \in Y} d(x,y) \right\}$	$PV = \frac{X - Y}{X}$		
X represents the 'ground truth' contour, Y represents the modified contour	$d(x,y)$ is the distance between the x^{th} point in 'ground truth' contour, X , and y^{th} point in modified contour, Y .	X & Y represent the areas enclosed by the 'ground truth' and modified contours respectively.		
Table 1: Table of geometric distance metrics.				

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). A saturation recovery turbo-FLASH pulse sequence was used to acquire short axis images of the heart at mid-systole [1]. 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 of one half of the mean myocardial width for that slice. 30 iterations of random offsets were run. Signal intensities from the regions defined by the contours were converted to concentrations using the method described by [2,3] using an assumed blood $T_1(1435ms)$ [4]. This method has previously been shown to be robust to errors in the assumed T_1 value [4]. The conversion was successful in 16/17 datasets. MBF was estimated from these curves using Fermi-constrained deconvolution [5]. MBF errors were calculated as the difference between MBFs estimated from the manual and modified contours. Geometrical contour errors were evaluated in terms of two of the most commonly used and widely accepted distance metrics: Dice's similarity (i.e. contour errors passing inside and outside the myocardium are scored equally) [8], which is a distance based metric. As both of these metrics are non-directional contour errors passing inside and outside the myocardium are scored equally) a directional partial volume (PV) measure, defined as the difference in the areas of the modified and true contours divided by the true area, was also calculated. The distance metrics are summarized in table 1. Correlation between each of these distance metrics and MBF estimate was tested for using Pearson's correlation.

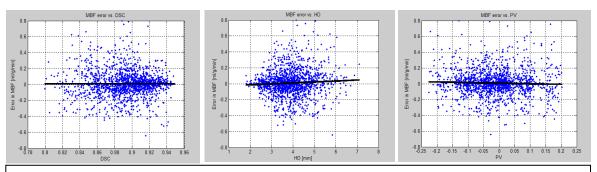


Figure 2: Distance metric vs. error in estimated MBF for DSC (R=0.002), HD (R=0.064) & PV (R=-0.042). The solid black line shows the linear least squares fit to the data.

Results: Figure 2 shows MBF error vs. distance metric plots for DSC. HD and PV. The associated Pearson's correlation Rvalues were 0.002, 0.064 and -0.042 respectively. Endocardial and epicardial contour errors in both rest and stress conditions were included into these plots. Separate consideration of each of these factors were also considered and the resulting Pearson's R-values are correlation shown in table 2.

Considering only:	MBF error vs. DSC (R-value)	MBF error vs. HD (R-value)	MBF error vs PV (R-value)
Stress Endo contour	-0.140	-0.010	-0.044
Stress Epi Contour	0.093	-0.162	0.020
Rest Endo Contour	-0.024	-0.029	0.092
Rest Epi Contour	0.050	-0.241	-0.163

Table 2: Pearson's R-values for MBF error vs. distance metric plots considering endocardium, epicardium, rest and stress cases individually.

Discussion: None of the distance metrics correlate with MBF, with all of the Pearson's R values being very low (-0.2<R<+0.2). This remained the case when stress, rest, endocardial and epicardial contour errors were considered separately. This is because the relationship between contour errors and MBF errors is not linear as has been previously shown [9], with different responses in MBF to contour invasions of the endocardium, epicardium, left ventricular blood pool and tissue outside the heart. Furthermore error response at different locations around the myocardium will yield different responses dependent on whether the erroneous contour passes into the right ventricle or surrounding tissue. Both DSC and HD are non-directional distance metrics, unable to distinguish between over and under segmentation and these two error types will have different affects on MBF error. We have shown that MBF error cannot be inferred from any of the distance metrics investigated and vice-versa thus rendering cross-comparison of automated contouring algorithms evaluated with only one of these measures impossible. Future contouring algorithms should be evaluated in terms of both MBF error and a recognised distance metric to enable objective cross-comparisons between published algorithms.

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