Automatic Exclusion of Papillary Muscles and Trabeculae from Blood Volume Measurements in Cine Cardiac Magnetic Resonance Images

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Abstract

Short axis cine cardiac magnetic resonance is used for measuring ventricular blood volumes. Papillary muscles and trabeculae should be excluded from these volumes, despite being included by delineations that allow measurements of wall thickness. We have developed and evaluated three methods that automatically exclude the papillary muscles and trabeculae from the blood volume by classifying the interior grey values of the endocardial contours to estimate corrected areas for summation with Simpson's Rule. Classification is performed using thresholding, hard clipping and error-function clipping, respectively. An evaluation of our methods on 69 clinical data sets showed that our methods provide significantly different results for the end diastolic volume, the end systolic volume, the stroke volume and the ejection fraction, with respect to conventional methods. Furthermore, the difference between our methods was found to be not significant.

1. Introduction

Cardiac magnetic resonance (CMR) is used for evaluating cardiac function. This includes quantification of several relevant physiological properties, for which a delineation of the cardiac contours is required. Accurate measurement of wall thickness, wall motion and wall thickening requires endocardial contours surrounding the papillary muscles and trabeculae. However, these structures should be excluded from the blood pool for accurate measurement of the end diastolic volume (EDV), the end systolic volume (ESV), the stroke volume (SV) and the ejection fraction (EF) of the left ventricle. These contradicting requirements and the abundance of convenient analysis tools have made the handling of papillary muscles and trabeculae a matter of controversy. Consequently, different strategies with respect to these structures have been used in studies on ventricular volumes obtained from SA cine CMR [1, 2, 3]. In [1], papillary muscles were excluded only if they appear attached to the myocardium. In [2], additional tiny contours were drawn to delineate and exclude papillary muscle. In [3], it is proposed to include both papillary muscles and trabeculae to the blood pool, such that analysis can be done faster, despite being less accurate.

An automatic method for excluding the papillary muscles and trabeculae automatically from blood volumes starting form endocardial delineations that surround these structures eliminates the need for such pragmatic approaches. Therefore we have developed three automatic exclusion methods that classifiy the interior grey values of the endocardial contours to estimate corrected areas to be summed according to Simpson's Rule. We will describe these methods in detail in section 2 of this paper. The methods are tested on phantom data and on 69 clinical data sets. The results of these experiments are presented in section 3. We will conclude our paper with a discussion and conclusions in section 4.

2. Methods

We have developed three methods for the measurement of blood volumes based on endocardial delineations surrounding the papillary muscles and trabeculae. Each method performs a classification S of the interior voxels, to determine whether it amounts to the blood volume or not. This classification is done by using thresholding, hard clipping and error function clipping, respectively. The result of these voxel classifications can be summed to obtain the blood area in a slice (Eq. 1). These areas are then summed using Simpsons Rule to obtain blood volumes.

$$A = \sum_{I \in endo} S \tag{1}$$

The thresholding algorithm is perhaps the oldest image processing algorithm. Voxels are considered to part of the foreground (i.e. blood) if their intensity value g exceeds a certain threshold t and considered to be part of the background otherwise (Eq. 2 & 3). An appropriate threshold value can automatically be determined using Otsu's Method [4], which selects the threshold value that maximizes the class separability.

$$H(z) = \begin{cases} 1 & z \ge 0\\ -1 & z < 0 \end{cases}$$
(2)

$$S_{threshold}(g,t) = \frac{1}{2}H(g-t) + \frac{1}{2}$$
(3)

Assigning voxels to be either blood or myocardial tissue does not take into account the substantial partial volume effects present cine SA CMR slices (thickness 8-18 mm). Voxels containing more than one tissue, i.e. blood and myocardial tissue, possess intensity values equal to the sum of their intensities weighted by their quantities [5]. This suggests that hard clipping can be used to determine the fraction of a voxel being blood. Hard clipping defines a linear relation between grey level and tissue membership within a clipping range, see eq. 4 &5. The clipping range is automatically determined based using K-means clustering.

$$R(z) = \begin{cases} 1 & z \ge 1\\ z & -1 < z < 1\\ -1 & z \le -1 \end{cases}$$
(4)

$$S_{hard-clip}(g,t,r) = \frac{1}{2}R(\frac{g-t}{r}) + \frac{1}{2}$$
 (5)

Unfortunately, discrete representations of real world, continuous objects introduce more artifacts than the partial volume effect alone. As explained by [6], thresholding and hard clipping produce signals with considerable energy contributions at half the sampling frequency, which may influence the result of the measurement. Error-function clipping was introduced to produce a signal that is approximately band limited such that it should allow for more accurate measurements. In error-function clipping, the relation between the intensity value and tissue membership is defined by the error-function, which is also known as the cumulative of the Gaussian distribution, see equation 6. The relation between the image intensity value and tissue membership is defined by equation 7. The clipping range for this method is also determined automatically from the result of K-means clustering, where σ is taken from the variances within the cluster such that $\sigma = \sigma_1 + \sigma_2$.

$$\operatorname{erf}(z) = \frac{2}{\sqrt{\pi}} \int_0^z \epsilon^{-t^2} dt \tag{6}$$

$$S_{\text{erf}-clip}(g,t,\sigma) = \frac{1}{2}\operatorname{erf}(\frac{\sqrt{\pi}(g-t)}{\sigma}) + \frac{1}{2}$$
(7)

The three methods only differ in their approach towards classification of the interior grey values. Plots of the primitives used for look up are shown in 1. Furthemore, examples of the result of each approach are given in figure 2.

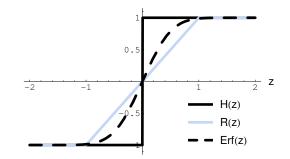


Figure 1. Graphs from equations 2,4 and 6

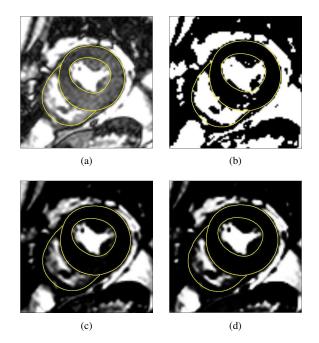


Figure 2. An example of an image from a cine SA CMR sequences including delineation (a) and resulting images after thresholding (b), hard clipping (c) and error-function clipping (d)

3. Results

The methods were first tested on a synthetic image sequence resembling SA cine CMR. In this synthetic image sequence the heart is modelled using spheres. A bright contracting sphere, modelling the blood pool, surrounded by a dark sphere of constant radius, modelling the myocardium, together modelling the heart. Inside the blood pool, two smaller dark spheres are positioned to resemble the papillary muscles. These smaller spheres appear to be floating at maximum blood volume (ED) and appear to be attached at minimal blood volume (ES). Furthermore, the images have been blurred and noise has been added to

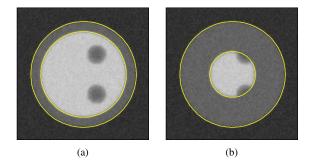


Figure 3. Slice of phantom images at ED (a) and ES (b)

make them more realistic. Example synthetic images are given in figure 3. The advantage of using these synthetic images is that we that the true blood volumes are known. The radius of the blood pool sphere is varied using a cosine function. Using simple calculus to compute volumes of spheres and there intersections (required to subtract papillary muscles), the true blood volume can be computed. These true blood volumes can compared to the volumes obtained using our methods. Averaged over all phases, we have found differences between the true blood volume and measured blood volumes of -2.1 ml (-2.0%) for method 1, -2.1 ml (-1.8%) for method 2 and -1.8 ml (-1.8%) for method 3 in the phantom experiment. This confirms theoretical arguments given in [6] that error function clipping is the most accurate approach.

Second, the methods are applied on clinical image data from 69 patients. SA cine CMR images were acquired consisting of 9 - 14 contiguous slices and 15 - 50 phases, were acquired using an ECG triggered BTFE protocol on a 1.5T Philips Integra scanner. All images were 256 x 256 in size, covering a field of view ranging from 350 x 350 mm up to 480 x 480 mm. The images were acquired using echo time 1.4 - 1.7 ms, repetition time 3.0 - 4.0 ms and flip angle 45 - 55 degrees. A cardiologist manually delineated these images on the ED and ES phase, positioning the endocardial contours surrounding the papillary muscles and trabeculae. We have computed the EDV, ESV, SV and EF for all patients using no exclusion and our three automatic exclusion methods. The results of this experiment are given in table 1. Relative and absolute mean difference tests have shown that automatic exclusion results in significantly different $(\alpha=0.05)$ volumes than performing no exclusion (p-value < 0.001 for all parameters using all methods). The new methods among each other differ less, but are also mostly significant (α =0.05). However, absolute and relative differences between LV EDV and LV SV values measured by the thresholding and hard clipping are not significant. Absolute differences in LV SV values measured by thresholding and error function clipping are also non-significant.

4. Discussion and conclusions

We conclude that we have developed three methods for automatic exclusion of papillary muscles and trabeculae for blood volume measurements. In a phantom experiment we have found that the approaches were accurate. In an evaluation on clinical image data from 69 patients, the methods have shown to reduce the blood volumes measured significantly. Furthermore, the differences between the new methods have shown to be not significant. Nevertheless additional development and experiments are required to come to accurate and reproducible blood volume measurements from SA cine CMR.

Unfortunately, this study will not end the long lasting debate on how to the handle the structures inside the ventricular cavity for blood volume measurements. The decisive word in this debate requires additional experiments. First of all, any approach with respect to papillary muscles and trabeculae should result in constant myocardial mass throughout the heart cycle. Furthermore, the measured stroke volumes should be compared to stroke volumes from more accurate methods such as Q-FLOW acquisitions in the proximal aorta.

We have investigated three methods for more accurate blood volume measurements from SA cine CMR that handle the papillary muscles and trabeculae appropriately and consistently. However, as shown by [7], experts frequently define the basal slice differently, causing inter-observer differences up to 19.8 ml for the LV EDV and 27.3 ml for the LV ESV. Therefore, the slice selection procedure should be standardized/automated to obtain accurate and reproducible blood volumes. Note that in our study, the basal slice contributed on average 13.4 ± 6.3 ml (18 ± 13 %) to the blood volumes and the apical slice contributed on average 1.1 ± 0.9 ml (2 ± 2 %) to the blood volumes.

As mentioned in the introduction, different approaches with respect to handling the papillary muscles and trabeculae have been used in other studies. Although appropriate, a detailed quantitative comparison between the results of these studies and our study cannot be performed. Detailed differences between the studies hamper such a comparison. Next to differences in the study populations, differences in acquisition protocols (i.e. TGE vs. SSFP) affect the outcome of volumetric measurements [2]. Differences in slice thickness and separation will influence the number of slices included for volume measurements, consequently causing large volumetric differences, as pointed out by [7]. Similarly, different inclusion criteria for the basal slice in the studies cause large differences. At last, none of the studies provides details on their algorithm used for volume computation, which can also cause differences in the outcome of volume measurements.

	LV EDV (ml)	LV ESV (ml)	LV SV (ml)	LV EF (%)
No correction	135.9 ± 50.8	66.7 ± 43.8	69.1 ± 17.2	53.6 ± 11.3
Thresholding	99.8 ± 39.0	36.8 ± 31.8	63.0 ± 14.9	66.7 ± 12.7
Hard clipping	100.2 ± 38.2	37.8 ± 31.7	62.4 ± 14.1	65.7 ± 12.5
erf clipping	100.8 ± 38.5	37.4 ± 31.9	63.4 ± 14.3	66.4 ± 12.6

Table 1. Ventricular parameters (mean \pm 1SD) measured using different methods

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