Towards automatic quantitative analysis of cardiac MR perfusion images

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Abstract

Magnetic Resonance Imaging (MRI) is a powerful technique for imaging cardiovascular diseases. The introduction of cardiovascular MRI into clinical practice is however hampered by the lack of efficient and reliable automatic image analysis methods. This paper focuses on the automatic evaluation of the perfusion of blood in the myocardium (the heart muscle) from cardiac MR perfusion image series, acquired using contrast-enhanced ECG-triggered MRI. We have developed a semi-automatic quantitative analysis method with which the perfusion image series can be analysed in only a few minutes. The method is described in this paper and preliminary validation results are presented. © 2001 Elsevier Science B.V. All rights reserved.

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1. Introduction

Cardiovascular diseases have become one of the major death causes in the western society. Since the population is aging, it is expected that the number of people suffering from a cardiovascular disease will increase in the coming decades. For the diagnosis and monitoring of these diseases, efficient and reliable cardiovascular imaging and image-processing methods are needed.

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Traditionally, echocardiography, nuclear medicine and X-ray angiography are used to image the heart. Recently, MRI has proven to be also a powerful cardiovascular imaging technique. The amount of anatomical detail that can be acquired with MRI is larger than what can be obtained with the conventional imaging techniques. In order to maximally benefit from this increase in detail, efficient and reliable image-processing tools are needed.

This paper focuses on the analysis of cardiac MR (CMR) perfusion images. A semi-automatic quantitative analysis method is described and preliminary validation results are presented.

2. Materials and methods/patients

2.1. CMR perfusion imaging

MR-based myocardial perfusion imaging is performed as follows. During a period of 30–60 s, one to six short-axis slices are acquired at different positions through the myocardium. The patient's electrocardiogram (ECG) is used to trigger MR scanning, typically one set of slices is acquired per one to two heartbeats at a point of time close to diastole. The result is a four-dimensional image signal $I(x, y, z, t)$, where x and y are integers that indicate the position of a pixel in an individual image, z is an integer that indicates the position of the image along the long axis of the heart (the axis from base to apex, z is usually called the slice number) and t is an integer that indicates the discrete time (i.e., the heart beat) at which the set of slices was acquired.

Fig. 1 illustrates how scanning is performed. During the first breath-holding period, so-called baseline images are acquired. These images contain the myocardium and the left ventricle without contrast agent and are later on used to correct the measured perfusion parameters for inhomogeneities in the image intensity. The patient is then allowed to take several deep breaths. Shortly before the second breath-holding period, a contrast agent is injected. During the second breath-hold, the contrast–uptake images are acquired. The arrival of the contrast agent in the myocardium results in an increase of its intensity in the MR images. Insufficiently perfused parts will have a lower and/or delayed intensity increase. Perfusion imaging is usually performed both when the patient's heart is at rest and when it is stressed [1,2].
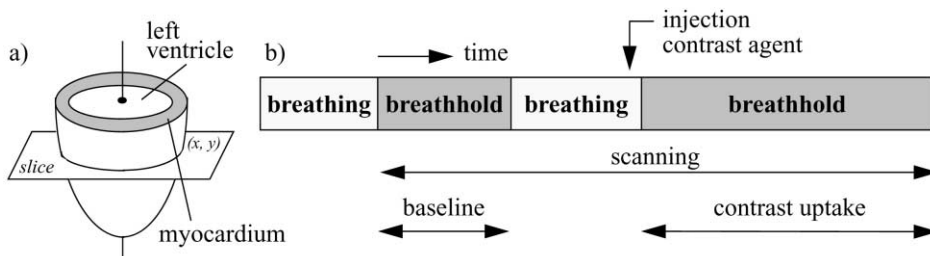

Fig. 1. Myocardial perfusion imaging: (a) position of a short-axis slice, (b) scanning as a function of time.
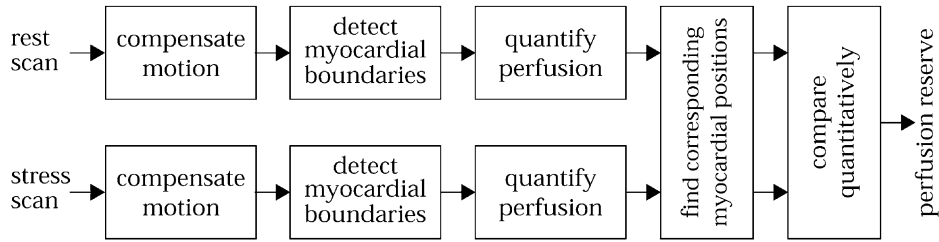
Fig. 2. The proposed quantitative perfusion analysis method.

2.2. Image-processing requirements

The perfusion images have a relatively low resolution, contain a significant amount of noise and may contain significant intensity inhomogeneities. The myocardium is usually not clearly visible in all images and may move considerably due to the fact that the patient was not able to hold his/her breath during the complete scanning period. Furthermore, the ECG triggering may sometimes fail, which can lead to the scanning of images at the wrong slice position and/or orientation (outlier images).

In spite of the far-from-perfect image characteristics, it is required to efficiently and reliably quantify the local uptake of the contrast agent in the myocardium. Motion of the myocardium must therefore be compensated, the myocardial boundaries have to be detected, relevant perfusion parameters have to be derived for individual locations or for small segments in the myocardium, and the perfusion parameters derived from the rest and stress scans have to be compared quantitatively. Performing these tasks manually is a very tedious job, which can easily take more than 1 hour per patient. An automatic or at least semi-automatic analysis that takes at most a couple of minutes per slice is therefore required.

2.3. The quantitative analysis method

Fig. 2 shows the block diagram of the proposed semi-automatic perfusion analysis method. Briefly summarized, it works as follows.
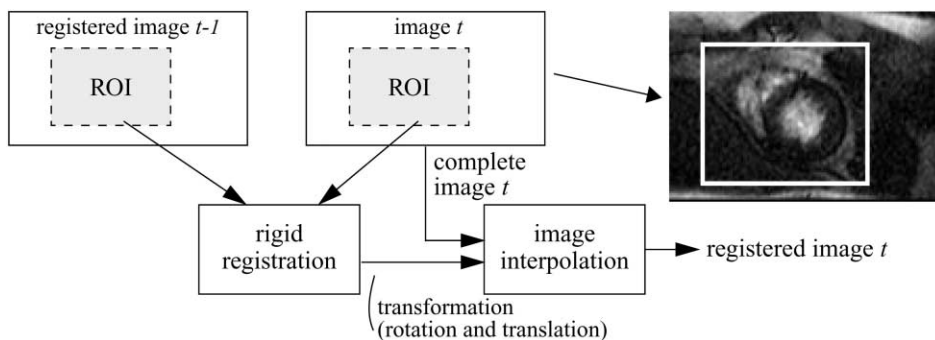

Fig. 3. The registration procedure and one image with a ROI.

Rigid image registration [3] is used to compensate for translation and rotation of the myocardium over time (i.e., through-plane motion and nonrigid deformations are neglected). The registration is applied on pairs of two successive images in the image series, considering only the information in a region of interest (ROI) including the heart. The detection of this ROI and the rigid registration itself are performed completely automatically [4,5]. The user has the possibility to modify the detected ROI or to draw it manually. Fig. 3 shows a block diagram of the registration procedure.

The boundaries of the myocardium can be manually drawn on one of the images in the series or on a so-called Temporal Maximum Intensity Projection (TMIP) of the series and can then be copied to all other images in the series. To compensate for incorrectly compensated myocardial motion, the user can manually modify the boundary position per image. We have also developed a completely automatic boundary detection method [4]. Briefly summarized, the boundaries are found by classifying the individual image pixels on the basis of their time–intensity profiles and by using constraints on the shape of the myocardium. This allows us to detect the inner and outer contours of the myocardium of the left ventricle.

The cardiologist is especially interested in the first pass of the contrast agent through the left ventricle and the myocardium. The first pass time interval is automatically detected from the average time–intensity profiles of the blood pool in the left ventricle and of the myocardium. Then, various perfusion parameters are measured from the local myocardial time–intensity profiles in the detected time interval (mean upslope, maximum upslope, time-to-peak, etc.). These parameters are visualised as colour overlays on the original images. Fig. 4 illustrates the calculation of the maximum upslope (to correct for intensity inhomogeneities, the upslopes a_{LV} and a_{MC} are divided by the average intensity which is estimated from the baseline images [5]).

Finally, the perfusion parameters derived from the rest scan are compared to those derived from the stress scan. First, corresponding positions within the myocardia of these scans (which usually have a different position and shape) are found by nonrigid registration techniques [5]. Then for corresponding positions or for small corresponding segments, the perfusion reserve is calculated, which is the ratio of the perfusion parameter derived from the stress scan and that derived from the rest scan. It has been shown that the perfusion reserve is a good indicator for the presence of a coronary–artery stenosis [1,2]. The perfusion reserve is visualised as a colour plot.
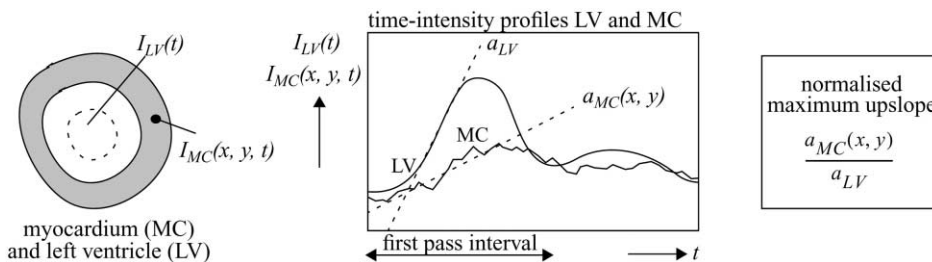

Fig. 4. Calculation of the maximum upslope.

2.4. Validation experiments

The method was initially tested on 30 CMR perfusion scans acquired at the German Heart Institute, Berlin, Germany on a 1.5-T MR Tomograph (Philips ACS NT). Most scans consisted of three slices with $60-70$ images/slice (128^2 pixels/image), some consisted of one slice of 60 images (256^2 pixels/image).

In a subsequent experiment, we analysed CMR perfusion scans from 12 patients. Three short-axis slices at apical, mid and basal level were acquired at the German Heart Institute Berlin using a TFE–EPI sequence with 60 images/slice on a 1.5-T MR Tomograph (Philips ACS NT). The scans were acquired at rest and under pharmaceutical stress. For all patients, X-ray angiograms were available as well. The myocardial perfusion reserve of myocardial segments was measured and was compared with the percentage stenosis as observed in the X-ray angiograms.

A more thorough clinical validation will be performed in the coming months. The main purpose of this validation is: (1) to evaluate how well the initial motion compensation performs (how often are manual corrections needed), (2) to compare the results of fully manual boundary drawing with those obtained after (semi-automatic) boundary detection, (3) to evaluate the sensitivity and specificity of the method for the detection of a coronary–artery disease, (4) to study intra-and inter-observer variability (for the analysis steps that include manual corrections).

3. Results

Fig. 5 shows an example of the output produced by the analysis method. Fig. 5a shows the maximum upslope at rest represented on a gray scale from black (low upslope) to white (high upslope). The myocardium has been divided into 12 inner and 12 outer segments. Fig. 5b shows the maximum upslope for the stress scan and Fig. 5c shows the perfusion reserve on a gray scale from 1.0 (black) to 1.5 (white).

The initial test on 30 perfusion scans showed that the motion compensation is one of the most crucial parts of the analysis. Only if the rigid registration is performed sufficiently well, the automatic boundary detection works well and a fully automatic analysis can be performed. For most scans, the registration worked well for the contrast–uptake part and
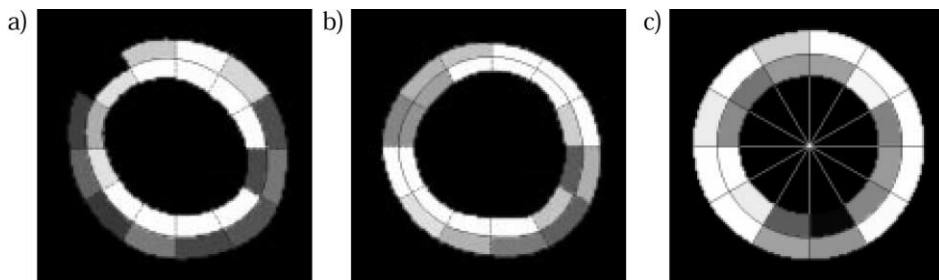

Fig. 5. (a) The maximum upslope at rest, (b) the maximum upslope at stress, (c) the perfusion reserve.

for the baseline part. In these parts, the motion is usually relatively small and smooth, so that it can be relatively easily tracked. Small misregistration can be corrected by manually shifting the myocardial boundaries after these have been detected.

For a number of the scans, it was not possible to use the baseline images for the correction of intensity inhomogeneities. This was due to that fact the shape and position of the myocardium in the baseline images differed significantly from those in the contrast–uptake images, which is probably caused by a different position of the lungs during the two breath-holding periods. Not correcting for inhomogeneities will generally significantly reduce the accuracy of the analysis [5]. In most cases, however, the first images in the contrast–uptake scan could be used for estimating the required correction factors.

The results of the preliminary clinical validation are encouraging. For 11 out of the 12 patients a good correspondence was found between the segment-based perfusion-reserve values as calculated by our method and the percentage of coronary-artery stenosis as graded from the X-ray coronary angiograms. The mean time for evaluation of one slice was about 4 minutes (range from 2.2 to 6.5 minutes).

4. Discussion

Our goal is the development of an efficient and reliable, fully automatic quantitative comparison of CMR perfusion images scanned when the heart is at rest and when the heart is stressed. The method presented in this paper is a significant step in this direction. For good quality perfusion scans, the motion compensation, the myocardial boundary detection, the estimation of perfusion parameters and the comparison of the rest and stress parameters can indeed be performed automatically in only a few minutes per slice.

The image quality of the perfusion scans can vary significantly. Patients may not be able to hold their breath sufficiently well or sufficiently long or they may move during scanning. This may result in excessive motion of the myocardium, which often cannot be compensated fully automatically. Also, the ECG triggering may sometimes fail, which may result in outlier slices. Because of the use of advanced triggering techniques (e.g., vector ECG), the latter problem is however, for the greater part, solved.

At present, scans with too low image quality can only be semi-automatically analysed. The required number of user interactions is relatively small: only the indication of outlier images that should be excluded from the analysis and the correction of the detected myocardial boundaries to compensate for misregistrations. These interactions do take some time, but the complete analysis still costs significantly less time than a fully manual analysis. We are therefore convinced that our approach is a valuable step towards the introduction of MRI-based quantitative myocardial perfusion analysis into daily clinical practice.

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