Generation of MR Myocardial Perfusion Maps Without User Interaction

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Introduction: Due to the requirements for rapid imaging on the order of 100-150 ms per image required for MR myocardial perfusion imaging, the resulting images are compromised by low SNR and relatively poor spatial resolution relative to the size of potential ischemic regions. To assist in semi-quantitative evaluation of the images, parameters related to myocardial blood flow such as upslope, peak intensity, and area under the curve are often calculated on a sector by sector basis, but at decreased sensitivity to small ischemic areas. To improve sensitivity and thus potentially clinical utility, several groups have proposed methods for parametric map generation of perfusion-related parameters [1-2]. However, these methods still require significant user interaction for registration or segmentation steps. We hypothesized that the remaining steps requiring user input could be automated, and thus provide a method for completely automatic myocardial perfusion parametric map calculation.

Methods: Analysis of myocardial perfusion from dynamic Gd-DTPA-enhanced imaging can be divided into several steps (1) preprocessing of the images including region of interest (LV) selection and registration, (2) coil correction of intensity variation, (3) determination of relevant timing landmarks such as start and end of the baseline, foot and peak of tissue time-intensity curves, and (4) calculation of parametric maps. Automation of the various steps was achieved as follows:

(1) We first implemented a 'heart finding' algorithm to determine a bounding box around the heart to be used as input to the registration algorithm. The algorithm is based upon first finding a range of frames with good contrast using assessment of temporal intensity variation. For each selected frame, a threshold for the blood is set through Gaussian clustering, and a binary image is obtained by thresholding. After removing small connected components, we compute three shape features for each remaining component and look for the one that is least eccentric, most circular, and most convex [4]. The winner corresponds to the LV blood pool, and its frame number is the reference frame, which is in turn used to estimate the thickness of the myocardium. This together with the LV bloodpool defines a bounding box region. We then applied a rigid registration algorithm to register the time series to the reference frame [5].

(2) A segmentation algorithm was developed to detect the endo- and epicardial boundaries of the myocardium. The algorithm initializes the contours using the LV blood pool and myocardial thickness estimates from step 1. Segmentation is formulated as an energy minimization problem. Since the intensity-time profiles for pixels in the LV, RV and myocardium are quite different, we introduce an energy functional that exploits the difference in the dynamics of the temporal signals associated with distinct pixels. The proposed energy-based image segmentation algorithm uses the correlation information among pixels in the same image as well as the temporal correlation across the images in the sequence [3]. It also exploits prior shape information and anatomical constraints. After segmentation, linear coil correction was applied to the images using a plane fit to the region of interest defined by the epicardial border of the left ventricle, based on images obtained pre-contrast arrival.

(3) The images were then filtered with a 5-point temporal filter, and the determination of the arrival of contrast (foot), and peak of the contrast-enhancement in the myocardium (averaged over the segmented myocardium found in step #2) was found using analysis of the temporal derivative of the averaged signal-intensity-time curve defined as $t_{foot\text{-}avg}$ and $t_{peak\text{-}avg}$,

(4) The average foot and peak found in step #3 were then used to derive parametric maps of slope (average slope from $t_{foot\text{-}avg}$ and $t_{peak\text{-}avg}$), area under curve from $t_{foot\text{-}avg}$ and $t_{peak\text{-}avg}$, and signal intensity at $t_{peak\text{-}avg}$. A standard nuclear medicine look up table was used for display, mapping minimum and maximum values to the full color range.

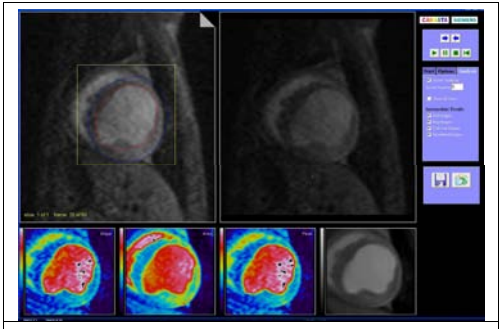

Figure 1. UI showing automatically determined bounding box, endo and epicardial borders, and resulting parametric maps.

Six patients with known coronary artery disease were evaluated at rest and during stress, and 3 dogs were imaged at rest 1 and 4 weeks post myocardial infarction (total of 18 studies). Typical imaging parameters were as follows: saturation recovery TurboFLASH, matrix 192x109, reconstructed resolution 1.9 x 1.9 mm, slice thickness 8 mm, flip angle 16, 3 images per heartbeat in diastole (acquisition window 190-220 ms), for 60 heartbeats. Images were obtained during breath hold to minimize respiratory motion. A single slice per study was assessed.

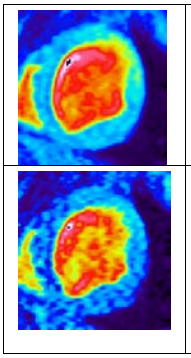

Figure 2. Clockwise from bottom left – slope, area under curve, and peak parametric maps in this subject without ischemia.

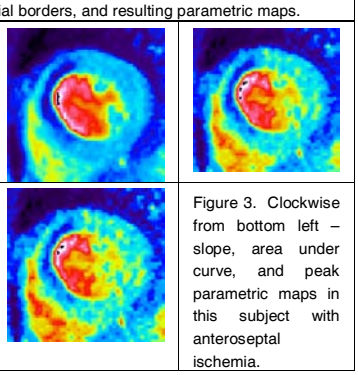

Figure 3. Clockwise from bottom left – slope, area under curve, and peak parametric maps in this subject with anteroseptal ischemia.

Results: Total processing time per series was approximately 4 seconds on a standard PC. Registration was accurate in all 18 studies as assessed visually in all but 2-3 frames per series, often late after the first pass of the bolus had dissipated and contrast was poor. The heart finding algorithm succeeded to find the LV in all 18 studies. Segmentation was sufficient in all cases for determination of coil correction and mean foot and peak, but would require finer adjustment for regional myocardial analysis of the generated parametric maps. The current UI is shown in Figure 1, and sample parametric map images are shown in Figures 2 and 3 for a case without ischemia and with ischemia, respectively.

Discussion

The method described is a compact method of visualizing the temporal dynamics of first pass myocardial perfusion imaging, with relatively high SNR, preservation of underlying spatial resolution and most importantly no user interaction. Applications could include increasing confidence in interpretation due to elimination of transient artifacts and development of tissue classification methods to separate ischemic, infarcted and normally perfused tissue. The approach could also potentially be extended to quantitative estimates of myocardial blood flow as well.

References

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