# Segmentation based registration of myocardium in cardiac perfusion images

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**Introduction:** Dynamic cardiac perfusion images often suffer from motion artifacts due to respiration. Registration and segmentation of the left ventricular myocardium in the images are important steps to extract useful qualitative or quantitative information about myocardial perfusion. The two steps can be used to improve each other. We propose a robust registration algorithm using a pixel wise minimization of mean squared difference registration method and a level set based segmentation to improve the accuracy of the registration.

**Methods:** Dynamic MR perfusion images have high potential to evaluate and characterize coronary artery disease. Contrast agent is injected and images are acquired over approximately a minute using ECG gated sequences. Breathing of patients during the scan causes motion of the heart. Registration of the left ventricular myocardium in the perfusion images is required to aid the visual analysis and to get accurate semi-quantitative or quantitative estimates of perfusion to the tissue. Many methods have been proposed to correct for motion in cardiac images [1-3]. Most methods [1, 2] register all the images to a single reference image, which may not give the best results due to changing contrast in the images. Also many of these methods use not only the myocardium but also other surrounding structures, which might not move in the same way as the myocardium, to optimize the registration cost function. Methods based on tracking of the heart [3] using statistical models require manual segmentation of a large number of training datasets. Also statistical models cannot capture the shape variability outside the range of the training datasets. In the current method, a coarse registration is first performed to aid the automatic segmentation of the left ventricular blood pool and the segmentation is then used to improve the registration of left ventricular myocardium.

In the first step a rectangular mask is defined to include the heart from all the images in the sequence. The mask is then multiplied with all the images to remove objects moving in a direction very different from the heart. Perfusion images are then registered to a reference image chosen from the temporal center of the perfusion sequence by minimizing the mean squared difference between the reference image and test image. A spatial weighting function is used to weight the squared difference more in the center region as compared to the outer regions, where the heart is usually located. The second step is based on a level set segmentation approach to improve the registration of myocardium. Level sets have proven to be promising in segmenting medical images. In this approach a curve is embedded as a zero level set of a higher dimensional function $\phi$ and the entire function is evolved as governed by a differential equation. In the current segmentation framework the governing equation for evolution of level sets is given by equation (1).

$$\frac{\partial(\phi)}{\partial t} = -\lambda_1 P(\boldsymbol{x})\left|\nabla(\phi)\right| + \lambda_2 \kappa \left|\nabla(\phi)\right| \quad - (1)$$

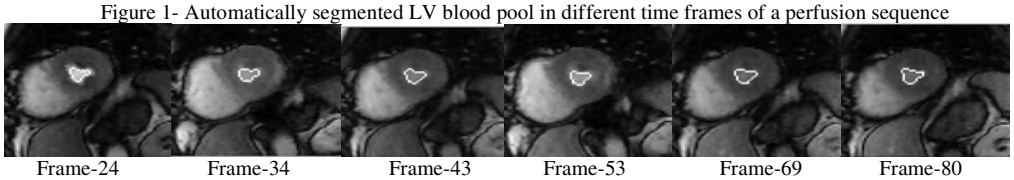
$$P(\boldsymbol{x}) = \begin{cases} g(\boldsymbol{x}) - L; \; if \; g(\boldsymbol{x}) < (U-L)/2 + L \\ U - g(\boldsymbol{x}); \; otherwise \end{cases} \quad - (2)$$

In equation (1), $P$ is the intensity based propagation term, $\kappa$ is the curvature term for smoothness of the evolving surface. $\lambda_1$ and $\lambda_2$ are the weighting factors for the propagation and curvature terms respectively. The propagation term $P$ is calculated from the input image $g$ with upper threshold $U$ and lower threshold $L$ according to equation (2). The implementation of the segmentation frame work is based on routines available in ITK [4]. A seed in the LV blood pool is automatically found by finding the peak in the variance image as proposed in [5]. The variance image is computed by calculating the temporal variance of the pixel intensities. The seed is input to the segmentation framework and LV blood pool is segmented in the frames after the contrast agent is in the blood pool. The upper and lower thresholds required are chosen as fractions of the intensity of the seed found in the LV blood pool. A high weighting on the curvature term is used to prevent the leakage of level sets into tissue in the frames where there is less contrast between the blood pool and myocardium. Figure 1 shows the segmented LV blood pool in different time frames in a typical dataset from a patient. Segmented LV blood pool masks in different frames are registered to the LV blood pool mask of the reference image using minimization of mean squared difference technique. To ensure accuracy of registration, centroids of the registered LV blood pool masks are computed and masks whose centroids differed by more than 1.5 pixels are not used for registration. It is assumed that the difference in centroids of the registered masks arose from significant change in shape of the segmented LV blood pool mask due to out of plane motion.

**Results:** The method is tested on datasets from three different patients scanned on a Siemens 3T scanner with a saturation recovery turboFLASH sequence. The reconstructed pixel size varied between 1.7 and 1.9 mm. The shifts for each frame obtained using the automatic method are compared with those from manual registration. Manual registration was done using custom software with an accuracy of 0.5 pixels. An improvement in registration is observed in the datasets. The average absolute motion per frame for a typical patient shown in Figure 1 reduced from 0.71 ± 0.93 and 2.68 ± 2.87 pixels (pixel size=1.8mm) in X and Y directions before registration to 0.61 ± 0.80 and 0.47 ± 0.51 pixels after the first step and 0.45 ± 0.67 and 0.40 ± 0.57 pixels after the second step. The method is also tested by segmenting the myocardium on a single frame and dividing into eight regions as shown in Figure 2 to estimate regional perfusion flow indices. The same regions are used over the perfusion sequence and a perfusion flow estimate for each region is obtained by fitting the average signal intensity time curves to a two-compartment model. A comparison of the flow indices before and after registration for the typical data set is given in Table 1. The average relative error in flow indices for each region reduced from 0.5301 before registration to 0.1203 after automatic registration.

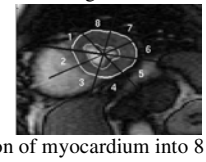
**Discussion and Conclusion:** A fast and robust method to register myocardium in cardiac perfusion images that compares well to manual registration is presented. The myocardium is not directly used for registration due to the variability in segmenting the epicardium in some of the frames. The method has the potential to accurately register the myocardium in the perfusion images during and after contrast uptake in the tissue which is important for accurate estimation of clinically useful kinetic parameters.

Figure 1- Automatically segmented LV blood pool in different time frames of a perfusion sequence



Frame-24 Frame-34 Frame-43 Frame-53 Frame-69 Frame-80

Figure 2




Division of myocardium into 8 regions

Table1-Comparison of perfusion flow indices of the tissue regions shown in Figure 2 before and after registration

| Flow index \ Region | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
|---|---|---|---|---|---|---|---|---|
| Manually registered | 0.9624 | 0.7076 | 0.8536 | 0.6678 | 1.1856 | 1.2092 | 1.0472 | 1.1010 |
| Automatically registered | 1.1334 | 0.7662 | 0.9610 | 0.5388 | 1.0776 | 1.1744 | 1.1792 | 1.2526 |
| Unregistered | 0.002 | 0.8848 | 1.5118 | 1.0558 | 1.3996 | 1.9570 | 0.8138 | 0.4200 |

**References:** [1] Gallipi et al., JCMR 2002;4:459-469; [2] Bracoud et al., FIMH, 2003, LNCS 2003;2674:215-223; [3] Stegmann et al., Med Image Anal 2005;9:394-410; [4] Yoo et al., Vol. 85, Amsterdam: IOS Press, pp. 586-592, 2002; [5] Adluru et al., Submitted to ISBI-2006