A Semi-Automatic Software Package for Analysis of Dynamic Contrast-Enhanced MRI Myocardial Perfusion Studies

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Abstract

Dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) is used for the detection and assessment of coronary artery disease. While myocardial ischemia may be detected visually from the MR images by trained cardiologists or radiologists, it is likely that semi-quantitative or quantitative analysis of the dynamic images can improve the accuracy of diagnoses. Such analyses have yet to be standardized and can be limited by the availability and capability of existing software.

In this work we present a modular Matlab-based software solution that can improve the analysis of DCE-MRI cardiac perfusion images. The proposed software, MPI2D (Myocardial Perfusion Imaging 2D), allows for semi-automatic processing of perfusion data to estimate kinetic parameters of myocardial perfusion.

MPI2D has been used to analyze rest and adenosine stress data in several dozen human subjects imaged at the University of Utah. The myocardial perfusion estimates obtained using MPI2D are similar to published literature values for four analysis models: 2-compartment modeling, Fermi function modeling, Model-independent analysis, and Patlak plot analysis.

One expert observer analyzed perfusion data from four subjects on two different occasions to assess the intra-user variability of MPI2D and found good correlation between perfusion estimates on both occasions (y=1.00x-0.02, r=0.98) indicating excellent reproducibility of analysis.

1. Introduction

Dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) is used for the non-invasive detection and assessment of coronary artery disease. Typically with DCE-MRI, 3-5 short-axis slices of the left ventricle (LV) are imaged every heartbeat at rest and during adenosine stress, to follow the uptake of a gadolinium-based contrast agent. While ischemia may be detected visually from the MR images by trained cardiologists or radiologists, it is likely that semi-quantitative or quantitative analysis of the dynamic images can improve the accuracy of diagnoses. Such analyses have yet to be standardized and can be limited by the availability and capability of existing software. This work aims to provide a modular Matlab-based software solution for the analysis of DCE-MRI cardiac perfusion images.

2. Methods

The software, MPI2D (Myocardial Perfusion Imaging 2D), can be run from the command line or with a graphical user interface (GUI) and takes DICOM perfusion images as input. Although this software consists of many optional stages, the backbone of the software includes four primary stages for (1) image registration, (2) image segmentation, (3) model curve fitting, and (4) display of results. Figure 1 shows a screenshot of a sample GUI used in MPI2D, depicting a segmented image of the LV myocardium and the corresponding regional enhancement curves, along with several interactive buttons.

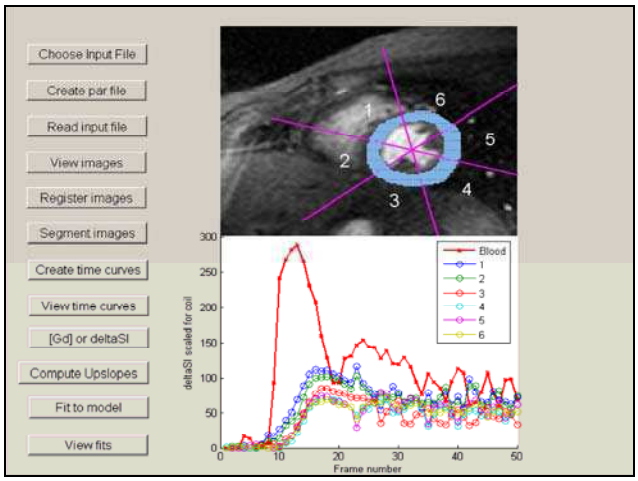

Figure 1: A screenshot of a sample GUI used in MPI2D depicting a segmented image of the LV myocardium and the corresponding enhancement curves, along with several interactive analysis buttons.

The registration stage is used to compensate for respiratory or in-plane cardiac motion and can be manual or semi-automatic. First the user manually traces the endocardial and epicardial contours of the LV myocardium to which all the image frames will be aligned. Once drawn, the user shifts each of the perfusion images in the chosen series vertically or horizontally to overlay the registration contours. Although manual registration of the perfusion images is the gold standard for perfusion analysis, MPI2D also includes an optional stage for automatically registering the perfusion images using a signal-intensity, mutual-information based algorithm or a model-based registration algorithm [1]. Individual image frames that are not well registered with the automatic registration algorithm can be manually adjusted after the stage is completed. Figure 2 depicts a single reference image from which the registration contours were drawn, along with an unregistered image frame and its corresponding manually registered image. The user-defined contours can include the right ventricle and other landmarks as well.

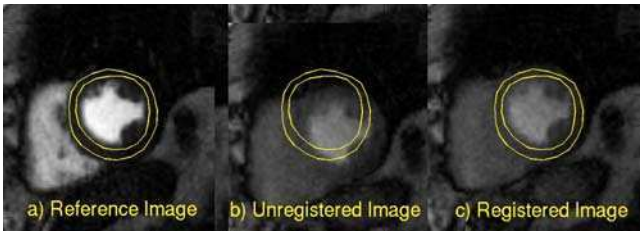

Figure 2: a) A representative "reference" image from which the registration contours were drawn using MPI2D to align the dynamic series of perfusion images. b) A typical unregistered image frame and c) the same image frame after manual registration using MPI2D.

Once the perfusion images are registered, the user manually draws contours around the endocardial and epicardial borders of the LV myocardium in a single reference image to segment the myocardium. The reference image is chosen by the user to ensure the myocardium is clearly discriminated from the LV blood pool signal and the surrounding pericardial fat signal. Because all of the image frames during the perfusion study do not overlap exactly, the contours of the myocardium are typically drawn conservatively so that only the blood and tissue signal of interest are included in the analysis. The LV blood signal—or arterial input function (AIF)—is obtained by manually drawing a region of interest in the LV blood pool, preferably in a basal diastolic slice.

Prior to curve-fitting analysis, all of the dynamic perfusion images are scaled to correct for spatial coil sensitivity variations This can be done by assuming the pre-contrast signal in the myocardium should have uniform signal intensity and scaling each region of the tissue to make this occur. Alternatively, the perfusion images can be divided by a proton density image map, which was acquired prior to the injection of contrast agent.

For regional perfusion analysis, the myocardium is subdivided into a user-defined number of radial and circumferential segments for curve fitting. Alternatively, each pixel within the segmented myocardium can be analyzed to generate a pixelwise perfusion map of the myocardium.

Figure 3 shows an example set of blood and tissue enhancement curves obtained from six equiangular regions in the LV myocardium. The tissue enhancement curves were normalized as described above, and the baseline signal was subtracted off. A reference image showing the regional segments of the myocardium from which the enhancement curves were obtained is overlaid on Figure 3.

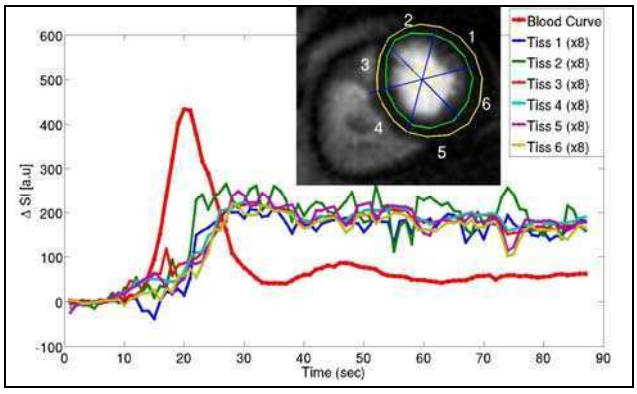

Figure 3: An example set of measured blood and tissue enhancement curves (upscaled by 8x for better visualization) obtained from the segmented image of the LV myocardium (inlaid) using MPI2D.

Once the blood and tissue enhancement curves have been generated, estimates of myocardial perfusion are computed by deconvolution of the measured AIF and tissue enhancement curves using one or more of various pharmacokinetic models that the user selects. Currently implemented choices of models include a 2-compartment model [2], the Fermi function model [3], model-independent analysis [4], Patlak plot analysis [5], and maximum upslope analysis [6].

Estimates of myocardial perfusion (and other model parameters, if applicable) are saved to a text file, once the model-based analysis is complete. For visualization of the results, MPI2D displays a color-coded perfusion map of the myocardium, along with the corresponding model-fits for each region of tissue. Figure 4 shows an example

regional perfusion map overlaid on the corresponding reference image of the myocardium.

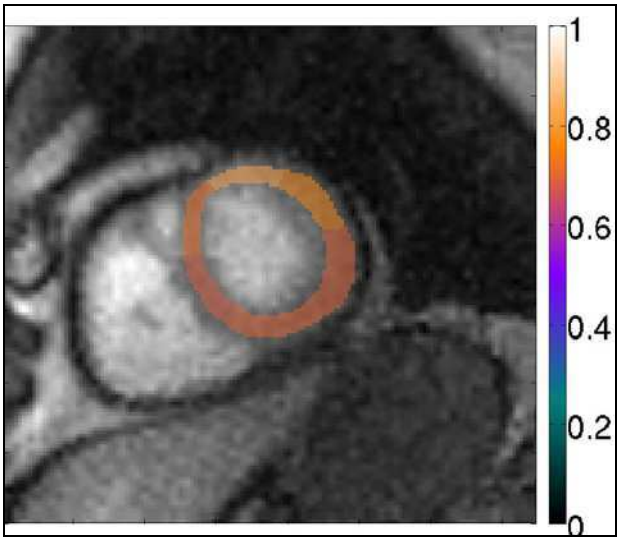

Figure 4: An example regional perfusion map overlaid on the reference image of the myocardium using MPI2D. Units are in ml/min/g.

3. Results

MPI2D was used to analyze 14 adenosine stress and rest studies acquired at the University of Utah, after the injection of a low-dose (~0.025mmol/kg) of gadolinium. The myocardial perfusion estimates were similar to published literature values and were not significantly different between the different models, except for the Fermi model at stress [7].

One expert observer processed four of these low-dose datasets with MPI2D on separate occasions to assess the intra-observer variability of perfusion estimates in AHA-defined regions. Figure 5 shows the correlation of intra-user reproducibility of perfusion estimates for these four subjects. There was good correlation between perfusion estimates (y=1.00x -0.02, r=0.98).

4. Discussion and conclusions

MPI2D is a modular Matlab-based software package used for analyzing dynamic perfusion data. It allows for the semi-automatic processing of DICOM image data to estimate kinetic parameters of perfusion with relatively low intra-observer variability. This software provides quantitative estimates of perfusion, which, when given accurate DCE-MRI data may be complementary with qualitative clinical analysis to more accurately detect perfusion deficits. MPI2D may also be used to track the progression of myocardial ischemia or to detect balanced triple vessel ischemia, which can be missed without quantitation.

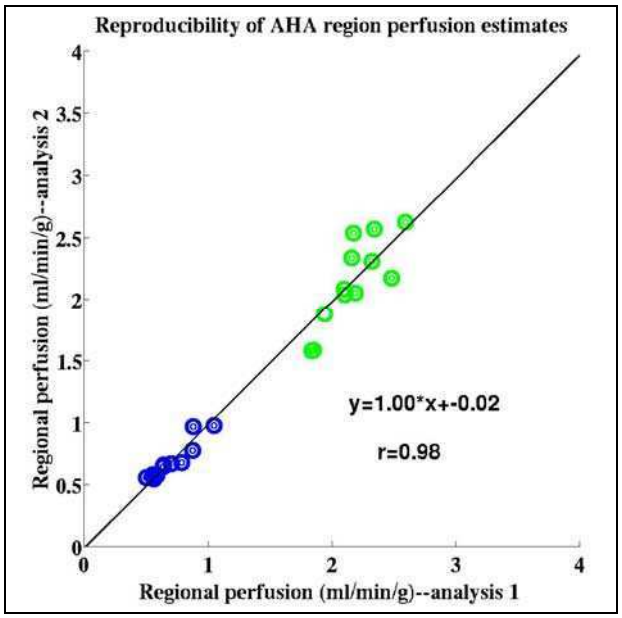

Figure 5: The intra-user correlation between AHA regional perfusion estimates in 4 subjects computed by the same expert user on two separate occasions using MPI2D. The good correlation (y=1.00x -0.02, r=0.98) suggests that perfusion results obtained using MPI2D are reproducible.

MPI2D has been used extensively to analyze cardiac perfusion data and tumor enhancement data. It is modular and additional stages for image analysis can be easily added by the user. For example, additional parameters can be added to any of the kinetic models, or a fully-automated image registration or image segmentation algorithm could be included in the analysis.

MPI2D is freely available by request for research purposes.

Acknowledgements

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