Clustering and Pixelwise Methods for Improved Parametric Analysis of Dynamic Contrast MRI Studies

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Introduction: Quantitative or semi-quantitative analysis of dynamic contrast MRI data is often done by uniformly dividing each slice of the organ or tumor of interest into a set number of regions to reduce noise when estimating kinetic parameters. Such regions can suffer from partial volume effects. Alternatives to this approach include pixel-wise fitting and a pre-fitting step of clustering the data into "optimal" homogenous regions. Here we investigate and compare a method for producing clusters and compare to pixelwise fitting of both unfiltered data as well as data denoised by principal component analysis (PCA) and by anisotropic diffusion in space and time. Fitting is done with a two compartment model and with maximum upslope found by regression.

Methods: Two cardiac patients – one with ischemia and one with infarction - were imaged with dynamic contrast MRI, 0.07 mmol/kg (6.5 cc/sec injection rate), adenosine stress, 6-7 slices every other heartbeat. A fast gradient echo sequence with echo train readout (FGRET) was used on a 1.5T GE Signa Lx8.4 (TR/TE 7/1.4, ETL=4). 70 time frames were acquired for each slice. The dynamic frames were registered automatically using a signal intensity matching method; manual registration was used in one case for 4 initial pre-contrast frames where the automatic registration failed. Endocardial and epicardial contours were then traced on a mid-ventricular slice in a selected time frame (see Fig. 1). Within the myocardium, signal intensity was converted to gadolinium concentration by assuming a normal T1 value for the tissue and blood pre-contrast to generate a set of scaling factors and then mapping signal intensity to 1/T1 by using a reference set of 20 vials with differing gadolinium concentrations.
The maximum upslope (normalized by the left ventricle input function upslope) was computed for each pixel, as was washin (K^{trans} in a two compartment model that included parameters for blood spillover and time delay between the input and the tissue). Figure 2 shows an example of a fitted curve. The pixelwise analysis was compared to also performing anisotropic diffusion (filtering in both space and time) [1] or principal component analysis (PCA) [2] on the initial dynamic data. As well, the registered original signal intensity time curves were sent to a k-means clustering algorithm [3] set to produce 5 clusters within the selected myocardial contours. The curves were normalized such that scaling did not affect the clustering. The mean curves of each of the clusters was converted to gadolinium concentration and fit. Alternatively, the myocardium was divided into 8 equi-angular azimuthal regions and the average curve of each region was fit.

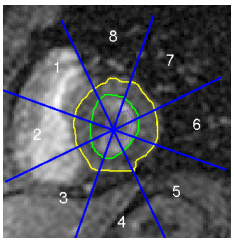


Figure 1: Diagram showing "standard" division of left ventricle into 8 regions.

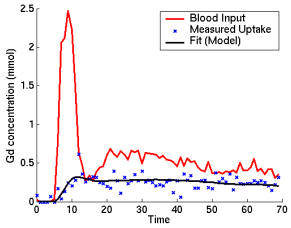
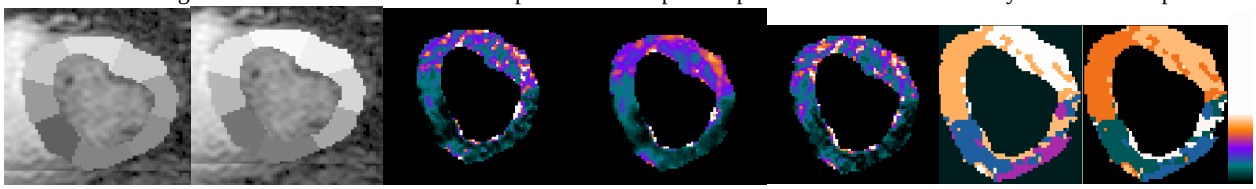


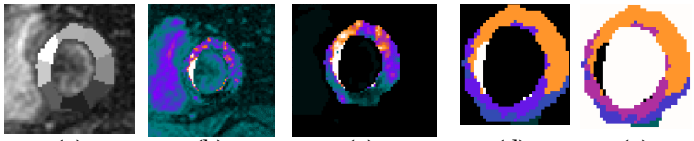
Figure 2: Example of single voxel data fit with the compartment model.

Results and Discussion:
Figures 3 and 4 show the results from the methods. Note the slightly higher contrast (signal difference from brighter normal region) in the washin parametric images compared to the upslope images. The clustered images also provide greater contrast than the 8 region results. In Fig. 4, the bright area in the septal wall (left side) is due to very high spillover from the left ventricle due to some motion that was not completely resolved with registration. The clustering provides advantages over region-wise fitting, especially with regard to partial volume effects. Pixelwise fits also appear useful, especially with pre-processing by PCA or anisotropic diffusion; the anisotropic diffusion results gave the lowest noise and high contrast. These methods show promise for improved parameter estimates from dynamic cardiac perfusion data. In particular, sub-endocardial defects are more likely to be identified since partial volume effects will play less of a role. These approaches are also likely applicable to other dynamic contrast studies that undergo parametric analyses.



(a) (b) (c) (d) (e) (f) (g)

Figure 3: Each region or pixel is given a signal intensity according to its washin or upslope parameter. (a) Upslope parameters from 8 regions. (b) Washin parameters from 8 regions. (c) Washin parameters from pixelwise fits. (d) Pixelwise washin estimates with use of anisotropic diffusion. (e) Pixelwise washin estimates with use of PCA. (f) Clusters with upslope parameters (g) Clusters with washin parameters.



(a) (b) (c) (d) (e)

Figure 4: Results from patient with inferior wall ischemia. Signal intensity corresponds to washin. (a) Washin parameters in 8 regions. (b) Pixelwise fits from unfiltered data, shown with background signal intensities from a single frame. (c) Pixelwise fits after anisotropic diffusion. (d) Clusters with washin parameters. (e) Clusters with arbitrarily assigned signal intensities is used to better show the different clusters.

References

1. Perona and Malik "Scale –space and edge detection using anisotropic diffusion", *IEEE PAMI 12:629-639, 1990.*
2. Riabkov, DiBella, and Sinusas, "Denoising of the dynamic sequence of images for cardiac perfusion studies", *ISMRM Proc., p.953, 2003.*
3. DiBella and Sitek, "Time curve analysis techniques for dynamic contrast MRI studies" *IPMI Proc. LNCS 2082:211-217, 2001.*