

Comparison of myocardial blood flow estimates from dynamic contrast-enhanced magnetic resonance imaging with four quantitative analysis methods

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Introduction: Several quantitative analysis methods have been used in recent years to estimate myocardial blood flow from dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) perfusion studies [1-5]. Despite validation with microspheres or other imaging modalities, blood flow estimates from these and other studies have varied widely, possibly depending on what analysis method was used to analyze the dynamic perfusion data. The objective of this work was to implement and compare four quantitative analysis methods (2-compartment modeling, Fermi function modeling, model-independent analysis, and Patlak plot analysis) used for quantifying myocardial blood with DCE-MRI.

Methods: To directly compare the four quantitative analysis methods outlined in this work, each model was implemented with DCE-MRI perfusion data acquired in 20 human subjects. The subjects were imaged with Siemens MRI scanners using several different sets of SR-FLASH imaging parameters. At least three short-axis slices of the left ventricle (LV) were acquired every heart beat. Due to space constraints, further details and variations of the imaging parameters are not reported here. However, since the primary goal of this study was to compare the results from four analysis methods, identical acquisitions were not essential. All of the subjects were imaged at rest after being given low-dose (~0.02 mmol/kg) bolus injections of gadolinium (Gd), that were unlikely to have much saturation of the AIF, followed by a saline flush of 15mL, both at 5cc/s. Fourteen of these subjects were also imaged at adenosine stress (140 µg/kg/min) with similar doses of Gd.

Offline, the MR images were manually registered and segmented, and tissue enhancement curves, $C_{tis}(t)$, were obtained from six equi-angular regions in each slice of the LV and a single blood enhancement curve, $C_{bld}(t)$, was obtained from a uniform region in the LV blood cavity. The same $C_{tis}(t)$ and $C_{bld}(t)$ curves were input to all four analysis methods. For 2-compartment modeling, regional blood flow estimates were computed by constrained deconvolution of the measured $C_{bld}(t)$ and $C_{tis}(t)$ data using Eq (1) [6]. K^{trans} —an index of the extravascular blood flow estimate—was reported. For Fermi function modeling, blood flow estimates were computed by constrained deconvolution of the measured $C_{bld}(t)$ and $C_{tis}(t)$ data using Eq (2) [3]. The value of the Fermi function evaluated at $h_F(t=0)$ was reported. For model-independent analysis, the cost function shown in Eq (3) [5] was minimized to estimate $h(t)$, from which total blood flow was computed by dividing the maximum initial amplitude of $h(t)$ by the inverse of the mean sampling rate of the perfusion images: $Flow = \max[h(t)]/dt$. For Patlak plot analysis, the measured $C_{tis}(t)$ data was plotted versus the integral of the accumulated $C_{bld}(t)$ data as in [4]. Using linear regression, K^{trans} was approximated as the slope of the line of best-fit between $C_{tis}(t)$ and the integral of $C_{bld}(t)$. This value was reported as the blood flow estimate for each region of tissue. Myocardial perfusion reserve (MPR) values for each subject imaged at rest and stress were computed from the ratio of stress and rest blood flow. Analysis of variance was performed to determine whether there were significant differences in rest and stress blood flow estimates and the MPR values between each of the four quantitative analysis models.

$$C_{tis}(t) = C_{bld}(t - \Delta t) \otimes K^{trans} e^{-k_{ep}t} + V_b C_{bld}(t - \Delta t) \quad (1)$$

$$h_F(t) = \frac{F}{e^{k(t-\tau)} + 1} \otimes \delta(t - \Delta t) \quad (2)$$

$$\min_{h(t)} \left\{ \|C_{bld}(t) \otimes h(t) - C_{tis}(t)\|^2 + \lambda^2 \|\nabla h(t)\|^2 \right\} \quad (3)$$

Results:

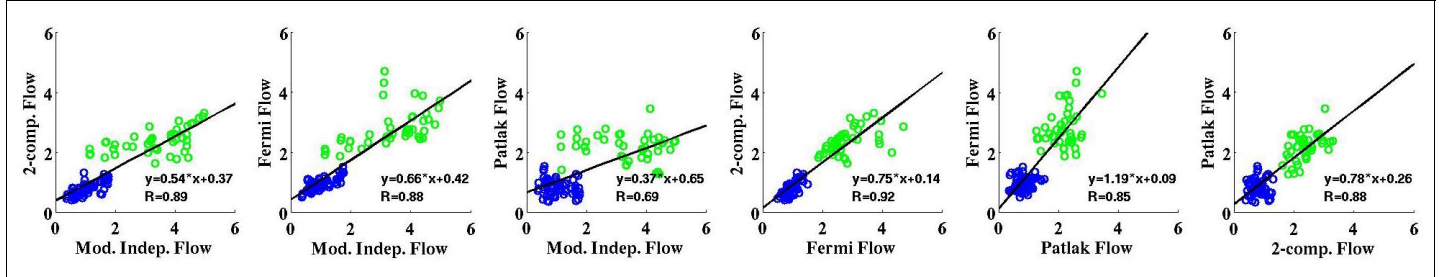


Figure 1: Scatter plots from all four quantitative analysis methods used in the study showing the comparison of mean rest (blue) and stress (green) blood flows in three coronary artery territory regions for all 20 subjects imaged at rest and all 14 subjects imaged at adenosine stress in the study (all units are in ml/min/g). The line representing the equation of best-fit for each model comparison and the R-value associated with each fit are overlaid on the plots.

Table 1: A summary of the aggregate blood flow estimates and MPR values from all 20 subjects imaged at rest and all 14 subjects imaged at adenosine stress in the study, using 2-compartment modeling, Fermi function modeling, model-independent analysis, and Patlak plot analysis.

	Rest blood flows (ml/min/g)	Stress blood flows (ml/min/g)	MPR values
2-Compartment modeling (K^{trans})	0.82±0.22	2.43±0.42	3.43±0.72
Fermi function modeling	0.97±0.25	2.82±0.71	3.35±0.64
Model-independent analysis	1.03±0.43	3.36±1.13	3.54±1.21
Patlak plot analysis (K^{trans})	0.83±0.27	2.17±0.45	3.54±1.19

Discussion and Conclusion: While there is good correlation between myocardial blood flow estimates between the four quantitative analysis models, the absolute values of rest and stress blood flow were significantly different ($p < 0.0025$ at rest, $p < 0.001$ at stress). The aggregate estimates of rest and stress blood flow were slightly lower for 2-compartment modeling and Patlak plot analysis than with Fermi function modeling and model-independent analysis. This is likely due to the fact that K^{trans} was reported from 2-compartment modeling and Patlak plot analysis, instead of total blood flow. Not surprisingly, because these two methods were derived from the same model, the aggregate K^{trans} values were not significantly different ($p = 0.79$).

Aggregate estimates of blood flow from model-independent analysis were consistently higher than the other three methods and had larger standard deviations. The larger standard deviations may be due to the larger number of parameters estimated with that method than with 2-compartment modeling and Fermi function modeling. The model-independent method also requires that the regularization weight parameter matches the CNR of the image data [5]. Despite differences in absolute rest and stress blood flow estimates between the four quantitative analysis methods, the aggregate MPR values for all four methods were not significantly different ($p = 0.94$), which suggests that systematic differences in each of the models are cancelled when the ratio of stress and rest blood flow is computed.

References: [1] Vallee J-P et al. Magn Reson Med 1998, 40:287-297. [2] Jerosch-Herold M et al. Med Phys 2002, 29(5):886-897. [3] Christian TF et al. Radiology 2004, 232(3):677-684. [4] Ishida M et al. Proc. Intl. Soc. Mag. Reson. Med. 14 (2006), #3621. [5] Pack NP et al. J Cardio Magn Reson 2008, 10:52. [6] Tofts et al. J Magn Reson Imaging 1999, 10:223-232.