Magnetic Resonance Quantification of Myocardial Perfusion with a Minimally Constrained Deconvolution Model

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INTRODUCTION: Dynamic contrast enhanced magnetic resonance imaging (DCE-MRI), coupled with tracer kinetic analysis has shown to be capable of quantitative cardiac perfusion analysis [1,2]. In this study we introduce a novel contrast enhanced perfusion analysis method – minimally constrained deconvolution (MCD) – to estimate myocardial perfusion. We have demonstrated previously the numerical stability and accuracy of MCD at clinical noise levels using Monte Carlo simulations [3]. In this study we demonstrate its performance, relative to two well-known perfusion methods, in a population of 10 patients diagnosed with hypertrophic cardiomyopathy. The evaluation compares the perfusion estimates from MCD alongside two previously validated perfusion analysis techniques, Fermi function modelling [1] and 2 compartment modelling (2-Comp) [2].

THEORY: MCD estimates myocardial blood flow from a tissue impulse response function, h(t), that is obtained by deconvolving the dynamic signal intensity in the arterial blood supply, $C_{ART}(t)$, from the dynamic signal intensity in the tissue of interest, $C_{TIS}(t)$. The maximum of the h(t) yields an estimate of the myocardial blood flow. The uniqueness of this method lies in that the shape of the response curve has only two constraints: (i) h(t) must be >=0 at its beginning and end; (ii) and h(t) has only a single local maximum. Since deconvolution is numerically unstable and very susceptible to noise, current deconvolution techniques have more rigid constraints on their response curves to improve numerical stability but this may compromise overall accuracy [4]. The 2-Comp perfusion estimates were computed using constrained deconvolution of the measured $C_{TIS}(t)$ and $C_{ART}(t)$ using equation 1 to obtain K^{trans} (an index of extravascular blood flow) [2]. The Fermi response $h_f(t)$ was computed using constrained deconvolution of the $C_{TIS}(t)$ and $C_{ART}(t)$ and equation 2. The flow was then calculated by evaluating h(t=0)[1].

$$C_{TIS}(t) = C_{ART}(t-\Delta t) \otimes K^{trans} e^{-K_{ep}t} + V_b C_{ART}(t-\Delta t) \quad (1)$$

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

METHODS: The MCD, Fermi, and 2-Comp perfusion analysis techniques were implemented using first pass DCE-MRI data obtained from 10 human subjects undergoing cardiac MRI scans for hypertrophic cardiomyopathy (1 female, 9 male, between 50-61 years of age, mean age of 58 years). Subjects were imaged using a Siemens Verio System at 3T, and an ECG-triggered SR-turboFLASH pulse sequence. The following imaging parameters were used; TR/TE = 2.16/1.08 ms, TI =120 ms; flip angle = 12°; FOV= 270 x 360 mm; slice thickness = 8 mm; matrix size = 144 x 192. At least three short axis slices of the left ventricle were acquired for every heart beat. All subjects were imaged at rest and at stress (after dipyridamole injection). Each subject received bolus injections of Gd-DTPA (0.05 mmol/kg) followed by a 40 cc saline flush both delivered at 3.5ml/s. Each series of cardiac MR images were corrected for motion and manually segmented into 16 regions of interest (6 equi-angular basal, 6 mid-ventricular, 4 apex). The regions of interest were used to obtain the $C_{TIS}(t)$. A single $C_{ART}(t)$ for each series was obtained from a uniform region in the left ventricle cavity of the basal slice. The same $C_{TIS}(t)$ and $C_{ART}(t)$ were input into each of the three models. The perfusion estimates were separated into two groups; (i) rest group (ii) stress group. All perfusion estimates were then plotted, and a linear regression was used as a measure of correlation between the models.

RESULTS: are presented in four scatter plots, below; "PLOT A" demonstrates correlation between MCD and Fermi at rest in terms of a line-of-best-fit, and a Pearson correlation coefficient (R^2). PLOTS B, C and D show, respectively, correlations between MCD and 2-Comp at rest, MCD and Fermi at stress, and MCD and 2-Comp at stress; In addition Pearson correlation coefficient between Fermi and 2-Comp were found to be; R^2= 0.931, slope=0.905 and R^2=0.644, slope=0.664 for rest and stress respectively (plots not shown).

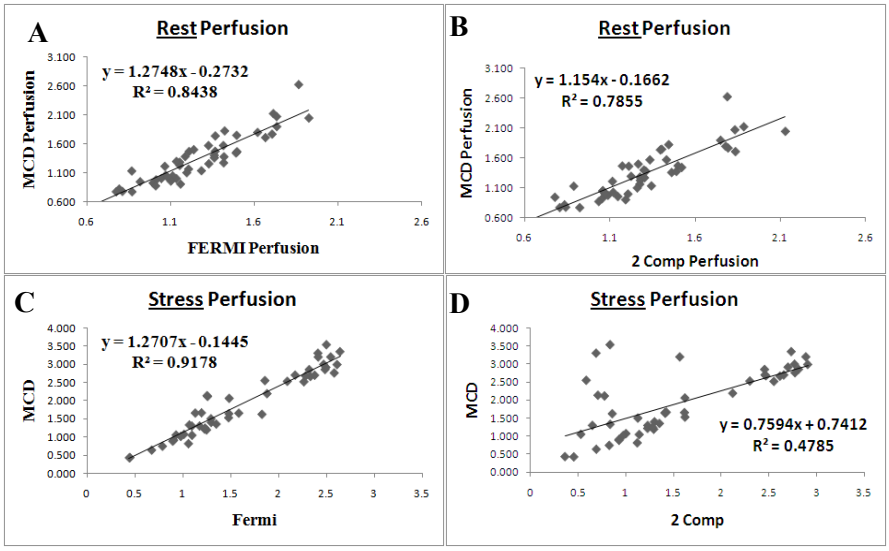

Figure 1: Scatter plots from the three quantitative methods used in the study comparing rest and stress perfusion estimates (all units are in ml/min/g). The linear equation and the R-value are overlaid on the plots

DISCUSSION: In general, the MCD technique correlates more closely with the Fermi perfusion model than with the 2-Comp perfusion model. MCD estimates of perfusion are similar to the Fermi model and the 2-Comp model correlate at rest. At stress there is increased discordance between MCD and the 2-Comp model but strong correlation with the Fermi technique. MCD appears to overestimate perfusion at both stress and rest in comparison to the Fermi model. This study also implies that variations exist between the two standard perfusion techniques especially during dipyridamole stress. At both stress and rest the 2-Comp model is overestimating perfusion in comparison to the Fermi model. Future work could focus on validating MCD against the gold standard, radioactive microspheres [5].

REFERENCES: [1] Jerosch-Herold M et al. *Med Phys* 1998, 25(1):73-82 [2] Tofts et al. *J Magn Reson Imaging* 1999, 10:223-232 [3] El-Sherif et al. *ISMRM Proceedings* 2009, 1779 [4] Goldstein, et al.. *Magn Reson Med.* 2008, 59(6): 1394-1400[5]Tong et al, *Magn Reson Med* 1993, 30:332-336