Temporal Sampling of MRI Myocardial Perfusion Studies: Effects on Three Analysis Methods

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Abstract: The effects of different temporal samplings for contrast MRI measurement of myocardial perfusion were investigated using simulations and measured data. Flow related parameters (upslope, $K^{\text{trans}}$, from a two compartment model fit, and $F$ from a modified compartment model which has not previously been used in cardiac applications) were obtained for the original and downsampling time curves. The results imply that the upslope parameter is least robust to decreased sampling rates in real data, and that the two compartment model may be more robust than the modified model as sampling rates decrease.

Introduction: Other groups have used models to fit gadolinium bolus kinetics for myocardial perfusion and have studied the errors arising from reduced sampling rates of the time-curves [1-3]. However, much of the work did not use the clinically standard peripheral IV bolus or was not acquired rapidly enough to provide a good gold standard, and the dependence on the particular model used is not well understood. Also, a few researchers in dynamic contrast enhanced tumor imaging have begun using a modified model (here termed the Johnson-Wilson or JW model) that may provide the ability to separate extraction and flow [4-6]. This model may have different sampling requirements than the more common two compartment model or the semi-quantitative upslope parameter.

Methods: Dynamic acquisitions were performed with a fast gradient echo, multi-shot echo planar sequence on a GE 1.5T Signa. TR=7ms, TE effective=1.7ms, 132x96 acquisition matrix. One frame per heartbeat was acquired. Blood pool and tissue regions were manually selected and processed to obtain gadolinium concentration curves (Fig. 1). One set of curves was used to assist in obtaining realistic parameters for the XSIM model (nsr.bioeng.washington.edu). Parameters from [1] were used along with fits to this measured dataset to create the XSIM model which was then used as the simulation gold standard. Simulated and real curves were downsampled to create four different versions: the original, sampled only every second point, every third, and every fourth. An integer “jitter” parameter was used to change the timepoint of the starting sample; results using the starting sample that produced the greatest change in the fits (the worst case) are reported. The arterial input function was not downsampled. Three means of obtaining flow-related parameters were employed. i) Upslope was calculated using a 3 point fit. ii) A two compartment model with 3 parameters ($K^{\text{trans}}, v_e, V_p$) was used to fit the curves. iii) The JW model with an axial concentration gradient in the capillaries [5] and 4 parameters ($E, F, v_e, T_c$) was also used. Fitting with the JW model was repeated with different starting estimates to overcome problems with local minima.

Results: Fig. 1 shows the real data case with the fits from the two models. Fig. 2 shows the percent change in the upslope and in the $K^{\text{trans}}$ and $F$ parameters for the two compartment and JW models, respectively.

Discussion: The results imply that sampling every other beat introduces relatively small errors for modeling approaches but larger error for upslope calculation. Less frequent sampling can produce reasonable estimates on average but can be quite dependent on sampling start (jitter). Additional constraints for example on $v_e$ could change these results (e.g. $K^{\text{trans}}$ of the two compartment model seemed to vary most depending on $V_p$). This work assumed that the arterial input function is sampled at a higher rate than the downsampling tissue curves; this assumption is reasonable since a) the blood pool does appear in all non-apical slices, so it can be sampled more often than each slice b) there are schemes e.g. small pre-bolus contrast injections that may allow for obtaining the curve shape before the actual perfusion study, c) blind deconvolution methods are being developed that can also provide an input where none was measured [7]. Thus the focus here is on downsampling of the tissue curves. Since fewer points were available in the downsampling curves, the upslope method performed better with a 3 point fit rather than the 5 point linear regression used by [8]. The slightly larger error in the real data case with this model may be in part due to this “overfitting” of the data with the $T_c$ parameter.

References: