Robust Kinetic Model Fitting for Motion Corrupted DCE-MRI Data

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Introduction: During Dynamic Contrast-Enhanced (DCE) MRI, contrast agent (CA) is introduced into the bloodstream of a subject and passes out of the blood vessels into the interstitial spaces of the tissues at a rate which can be modelled using a characteristic uptake curve. During the acquisition of a dynamic sequence of MR images, this uptake of CA is reflected in the signals obtained. If the subject were completely stationary during the scanning process, the uptake model could be fitted accurately to the signals from a single voxel throughout the sequence (voxel profile). The parameters of the fitted model give some indication of the microvascular functional characteristics of the tissue(s) located at the voxel position, and classification is therefore possible. However, it is extremely unlikely that the subject will remain completely immobile, especially in abdominal studies, unless the dynamic series is very short. At the very least the subject will be breathing, and there may be more severe movements induced by coughing or reaction to discomfort. This means that the tissue content of a single voxel will change over time, giving a corrupt profile, potentially leading to inaccurate parameter estimation and tissue classification. On the other hand, if it is assumed that a large proportion of the images are in correct alignment, then there will be some underlying structure in the time series data. We propose a model fitting process which capitalises on the presence of underlying structure to give good estimates of the model parameters. This uses the median absolute deviation (MAD) from the curve as goodness of fit (GOF) instead of the more standard sum of squared differences (SSD).

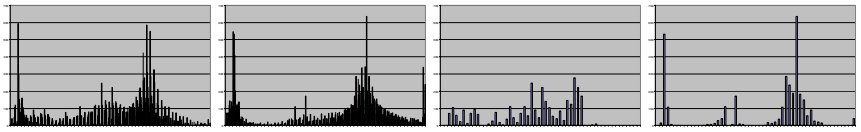
Data: In order to test the accuracy of parameter estimation, artificial dynamic series were generated with known parameter values [1]. The uptake process was simulated by using the extended Tofts model [2], and the CA concentration in the blood was simulated using the estimated population arterial input function (AIF), as developed by Parker et al [3]. These uptake curves were then converted to signal intensity curves using the standard spoiled gradient echo relationship [4]. Four data sets were generated from a static series and corrupted with Gaussian noise at various levels: Noise free; SNR 20; SNR 10; and SNR 5. Four others were generated from a motion corrupted series using the same noise levels. The motion was applied using a varying sinusoidal rhythm which approximately simulates the kind of movement obtained during an actual scan. Finally the signals were truncated to short integers to mimic standard scanner data. A typical slice through an uncorrupted volume is shown in Fig 1.

Method: The downhill simplex optimisation method [5] was used to fit an uptake curve to each enhancing voxel profile of the dynamic series in the region of the tumour. This generated estimated values of K^{trans}, v_e, and v_p for each voxel. Two GOF measures were tested: SSD and MAD. The model was fitted first to the static uncorrupted series to establish reliability of the method, and then was applied to the other series to assess performance in the presence of noise and motion. This was done by comparing the histograms of K^{trans} within and between methods using the correlation coefficient (CC).

Results: Table 1 shows the actual parameter values used to generate the phantom in the areas of tumour rim and core, and the values estimated by the model fitting on the uncorrupted phantom, using SSD and MAD. It also indicates the model fitting error as average signal intensity per voxel. It can be seen that the fitting process provides good parameter estimates, allowing for the small fitting error, which is probably due to the truncation to short integers. This indicates the best values we can expect using this model and data. The results from the remaining data sets were assessed using parameter maps of K^{trans} over the region of the tumour. Figure 2 shows some histograms generated from these maps. Ideally one would like to see 2 clear peaks indicating rim and core tissue. Tables 2 and 3 show the CC's calculated when comparing the distributions (highest values highlighted), and finally, Figure 3 shows a comparison of the model fits on typical voxel profiles from the noise free motion corrupted series.

Location	Parameter	Actual	SSD Fit	MAD Fit
Tumour Rim	K^{trans}	0.15	0.150606	0.152513
	v_e	0.30	0.300035	0.302076
	v_p	0.04	0.044820	0.043814
Tumour Core	K^{trans}	0.01	0.010312	0.010254
	v_e	0.4	0.279792	0.279747
	v_p	0.0005	0.000607	0.000857
Sig vox $^{-1}$	Fit Error		0.256286	0.329691

Table 1. Parameters estimated from uncorrupted series



a. SSD All Series b. MAD All Series c. SSD Motion Only d. MAD Motion Only

Figure 2. Histograms showing the estimated values of K^{trans} using different GOF measures

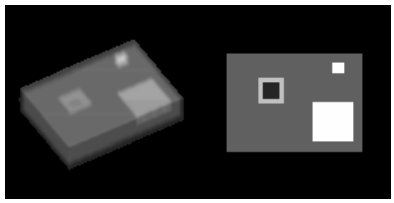


Figure 1 (a&b). Artificial volume. b: Left = Tumour Core surrounded by tumour rim; Top Right = Aorta; Bottom Right = Fat; Bkground = Muscle;

	Ssnr20	Ssnr10	Ssnr5	Mnf	Msnr20	Msnr10	Msnr5
Snf SSD	0.633	0.484	0.367	0.315	0.291	0.217	0.085
Snf MAD	0.542	0.383	0.198	0.792	0.462	0.340	0.180

Table 2. CC matrix for corrupted vs noise free (nf) results within method

Ssnr20	Ssnr10	Ssnr5	Mnf	Msnr20	Msnr10	Msnr5
0.939	0.952	0.590	0.363	0.367	0.277	0.200

Table3. CC's for SSD vs MAD results. S = Static, M = Motion

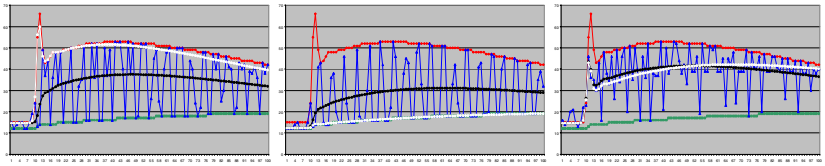


Figure 3 (a-c). The results of fitting the uptake model to voxel profiles through motion corrupted data using different GOF measures. SSD in black, MAD in white. The actual profiles for tumour rim (red) and core (green) are also shown

Conclusions: Figure 3 illustrates that the SSD fitting method does not capitalise on the underlying structure present in the phantom data that has been motion corrupted. The model fit does not follow the actual data if there is disruption in the profile. The MAD fit on the other hand comes much closer to the underlying tissue curve. The fit shown in Figure 3c is due to partial volume effects from resampling during the application of motion. This partial volume can also be seen in the histograms of Figures 2b and 2d. From the histograms it can be seen that MAD performs most consistently at separating the tissues over all series. Closer inspection combined with the statistics showed that at low noise levels with no motion the two methods were comparable. SSD performed better as noise increased but when motion was introduced MAD was considerably and consistently better. It is clear that, for data with motion corruption of the type collected in dynamic series acquisition, that MAD fitting can provide more reliable estimates.

References: **1** Buonaccorsi GA, Parker GJM. Proc ISMRM 4:795, 2006. **2** P. S. Tofts. *J. Mag. Res. Imag.* 7:91-101, 1997. **3** Parker *et al. Mag. Res. Med.* 56:993-1000, 2006. **4** Haase A. *Mag Res Med* 3:77-89, 1990. **5** Press *et al. Cambridge University Press*; 1992.

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