# Improving Quantitative Accuracy and Spatial Resolution of Parametric Imaging Using a Dual-Temporal-Resolution DCE MRI Technique

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## INTRODUCTION

Mapping kinetic parameters with high spatial resolution is desirable where lesions are small or where there is significant heterogeneity, but protocol design is limited by the performance of MRI scanners. Most studies compromise spatial resolution in order to obtain high temporal resolution necessary for accurate measurements of an arterial input function, necessary for calculation of pharmacokinetic parameters, such as the fractional plasma volume, $v_p$, transfer constant, $K^{trans}$, and the fractional volume of extravascular extracellular space, $v_e$. Conventional DCE-MRI uses a single temporal resolution (STR) method, i.e., the AIF and the tissue concentration-time ($C(t)$) curves are sampled at the same rate. Recent studies have suggested the use of a dual-temporal resolution (DTR) technique [1], where the AIF is sampled much more frequently than the tissue $C(t)$ curves. Using Monte Carlo Simulation we have found that the critical minimum time resolution for measurement of the tissue residue curve is $\Delta t \approx 10$ s for STR and 20 s for DTR. These results have been presented elsewhere. Here we propose a method for kinetic data analysis that combines the DTR strategy with an AIF in a theoretical function form[2]. In vivo data were used to validate the new approach.

## MATERIALS AND METHODS

*The proposed kinetic analysis method*

AIF was simulated using a function form described by Horsfield et al[2]. The fit parameters in the AIF model may be adjusted according to individually measured AIF. The DTR kinetic analysis method can be summarized as follows:

**1)** Calculating the theoretical $C(t)$ curves using the modified Kety model [3,4] with the simulated AIF in a time step of 1 s.

**2)** Estimating the bolus arrival time (BAT) of the experimental tissue concentration-time curves using a Linear-Linear (L-L) model proposed by Cheong et al[5], and calculating the time list of the tissue concentration-time curves by subtracting the BAT from the experimental measurement times;

**3)** Obtaining the theoretical tissue concentration values corresponding to the time list of the experimental tissue concentration-time curves (step 2) from the theoretical $C(t)$ curves (step 1) using a linear interpolation algorithm;

**4)** Fitting the theoretical tissue concentration values to the experimental data by adjusting $K^{trans}$, $v_e$, and $v_p$ in calculation of the theoretical $C(t)$ curves (step 1), and by adjusting the linear-interpolation extracting time points with a time shift value.

In this way, the tissue BAT values were first estimated by an independent method, the Cheong L-L method, which provides a preliminary BAT estimates that restricted to integer values of the sample time points, and then fine adjusted during the model fit. However, comparing with the commonly-used model-dependent approach of adding BAT as a free parameter in a simple model fit [6,7], which could result in larger confounding errors by introducing a further degree of freedom to a model[8], the new method adjusts the BAT in a separate step (step 4, the linear-interpolation step) from the modeling step (step 1). The impact of the temporal jitter uncertainty[1], as well as the confounding errors were thus minimized.

*In vivo studies*

DCE-MI data were acquired from two health volunteers and a patients with acoustic neuroma. Four consecutive 3D fast gradient recalled echo (GRE) acquisitions with an array of flip angles, typically 2°, 10°, 20° and 30°, were performed to allow calculation of T1 maps of whole brain with a matrix size of 240x240x70. The 20° sequence was then repeated ($n = 60$) to produce T1W dynamic series, the DCE-MRI, with a time resolution ($\Delta t$) of 10.7 s. Contrast (0.1 mmol/kg of Gadoterate Meglumine, Dotarem, Geurbet S.A) was given as an intravenous bolus injection with rate of 3ml/sec and 20 ml saline flush, following the seventh dynamic scan. Dynamic MR signal intensities were converted to CA concentrations. $K^{trans}$, $v_e$, and $v_p$ maps were calculated using the new DTR method and compared with those from STR method. DCE-MRI data with a $\Delta t$ of 21.4 s were generated by extracting every the other dynamic frames from the original data. Tumor regions of interest over all slices were drawn based on the DCE-MRI scan data.

## RESULTS

Fig. 1 shows parametric maps from the patients with acoustic neuroma generated using the DTR and STR methods with $\Delta t$ of 10.7 and 21.4 s. The tumor morphology displayed from the parametric maps generated using the DTR method with $\Delta t$ of 10.7 and 21.4 s, and the STR method with a $\Delta t$ of 10.7 s were similar to each other, but considerably different from those obtained using the STR method with $\Delta t$ of 21.4 s. Table 1 compares mean and SD of $K^{trans}$, $v_e$, and $v_p$ over the whole tumor volume with the two methods and two time resolutions. The $K^{trans}$ and $v_e$ values using $\Delta t$ of 21.4 s were slightly less than those with $\Delta t$ of 10.7 s while using the DTR method. There was considerable underestimation of $K^{trans}$ and $v_e$ values with $\Delta t$ of 21.4 s compared with $\Delta t$ of 10.7 s while using the STR method. The mean $v_p$ showed a 0.022 higher with $\Delta t$ of 21.4 s than that with $\Delta t$ of 10.7 s while using the DTR method. The mean $v_p$ showed a 0.033 higher with $\Delta t$ of 21.4 s than that with $\Delta t$ of 10.7 s while using the STR method.

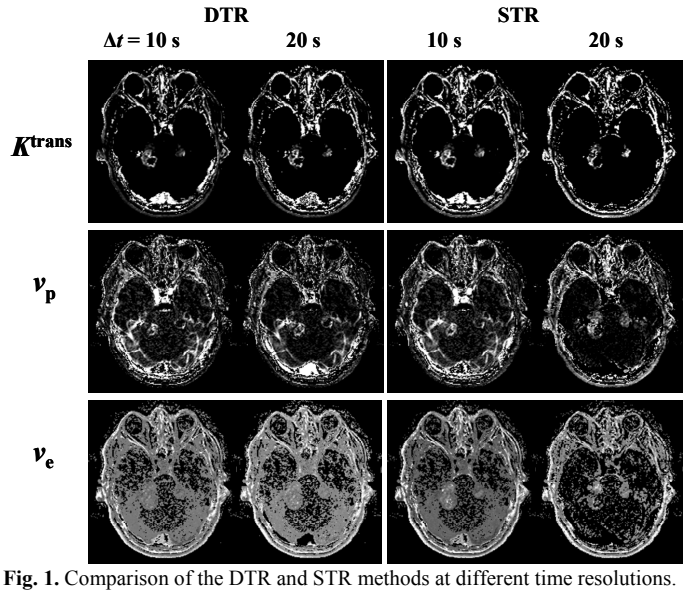


**Fig. 1.** Comparison of the DTR and STR methods at different time resolutions.

**Table 1.** Mean and SD of $K^{trans}$, $v_e$, and $v_p$ over the whole tumor volume

| mean±SD: | $K^{trans}$ (min$^{-1}$) | $v_e$ | $v_p$ |
|---|---|---|---|
| DTR | | | |
| $\Delta t$=10.7s | 0.098±0.088 | 0.34±0.12 | 0.024±0.025 |
| $\Delta t$=21.4s | 0.083±0.084 | 0.33±0.11 | 0.046±0.049 |
| STR | | | |
| $\Delta t$=10.7s | 0.094±0.084 | 0.41±0.17 | 0.043±0.038 |
| $\Delta t$=21.4s | 0.067±0.071 | 0.37±0.17 | 0.077±0.046 |

## DISCUSSION AND CONCLUSION

Clinical applications of the new DTR approach with optimized scan parameters based on a previous Monte-Carlo simulation (The results have been presented elsewhere) providing accurate pixel-by-pixel measurements of $k^{trans}$, $V_p$ and $V_e$, can be made at high spatial resolution with voxel size of 1.2 x 1.2 x 2 mm, covering whole brain. With an accurate measured AIF from the pre-bolus series, a relatively low temporal resolution could be used at $\Delta t = 21.4$ s whilst accurate characterization of tissue $C(t)$ could be preserved for the high spatial resolution.

**REFERENCES:** 1 Henderson and Lee. Magn ResonImaging 1998;16(9):1057-1073, 2. Horsfield et al. Phys Med Biol 2009;54(9):2933-2949. 3. Tofts PS. J Magn Reson Imaging 1997;7(1):91-101. 4. Tofts et al. J Magn Reson Imaging 1999;10(3):223-232. 5. Cheong et al. Phys Med Biol 2003;48(5):N83-88. 6. St Lawrence and Lee. J Cereb Blood Flow Metab 1998;18(12):1365-1377. 7. Koh et al. Phys Med Biol 2001;46(5):1519-1538. 8. Kershaw and Buckley. Magn Reson Med 2006;56(5):986-992.