Accuracy and precision of DCE-MRI parameters estimated by AATH and mTK models: Evaluations with MMID4 simulation and clinical NPC datasets

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Introduction

Dynamic contrast-enhanced (DCE) MRI combined with the pharmacokinetic model is widely applied in recent years to assess the physiological characteristics of tumor status in oncology. Uncertainty analysis including accuracy and precision evaluation is crucial for the pharmacokinetic modeling. Previous studies have used T1-weighted time series acquisitions and quantify the accuracy of physiological parameters measurement in DCE-MRI (3). When comparing uncertainties of different models, it is essential to use the same, thus neutral method for generating the simulated time series. However, to the best of our knowledge, only few studies have attempted to direct compare the commonly used modified Tofts and Kermode (mTK) (4) and the adiabatic approximation to the tissue homogeneity (AATH) (5) models using neutrally simulated data (1). In the particular study, Buckley compared the accuracy between the two models using the multiple path, multiple tracer, indicator dilution, 4 region (MMID4) model for data generation (1). The study aimed to extend the previous work to investigate the precision of physiological parameters with noise added to the time series and to apply the mTK and the AATH models in nasopharyngeal carcinoma (NPC) for comparison.

Methods

For computer simulation, the tissue uptake curves were simulated using the MMID4 model running under JSim (6), by adjusting input parameters including blood flow (F), capillary permeability surface area product (PS), interstitial volume (Ve) and capillary plasma volume (Vp). Following the study by Buckley, two different conditions were simulated. The first condition was represented to breast tumor with the true values : F＝0.57 (ml/g/min), PS＝0.33 (ml/g/min), Ve＝0.45 (ml/g) and Vp ＝0.06 (ml/g) (*1*) . The second condition was represented to meningioma with the true values : F＝1.2 (ml/g/min), PS＝0.34 (ml/g/min), Ve＝0.40 (ml/g) and Vp＝0.08 (ml/g). In each case points were calculated with a sampling interval of one acquisition per second over a total sampling period of 300 sec. The tissue uptake curves were then converted to signal time curves following the SPGR signal equation. Four levels of Gaussian noise, corresponding to SNRs of 100, 50, 20 and 10, were added to the signal time curves, with 1000 iterations each. These noisy curves then were converted back to the concentration time curve for fitting the mTK and the AATH models. The arterial input function (AIF) from Parker et al. (*2*) was used as an input to the model. Two NPC datasets of DCE-MRI studies were performed on a 3T clinical MRI scanner using a dedicated head and neck coil. A 3D SPGR sequence with varied flip angles was applied to obtain the T_1 maps before the contrast injection. The sequence was used for the T_1-weighted DCE-MRI with TR/TE = 4.9/1.3ms, flip angle = 30 degrees, field-of-view = 256 mm x 256 mm, and matrix size = 256 x 128, ASSET = 2, slice thickness = 6 mm. Sixty dynamic measurements were acquired during a total acquisition time of 234 s, with a sampling interval of 3.9 sec. For each patient, the averaged tumor signal time curve was obtained from a tumor ROI, determined by an experienced radiologist, and The analyzed by fitting with AATH and mTK models. The fitting procedure of AATH was repeated while tau from 0.6 sec to 90 sec with an increment of 0.6 sec.

Results

Table 1 list the accuracy results from the simulation with SNR = 100.In general, AATH provided better accuracy, which agreed with the literature (1). Table 2 shows the results obtained from the NPC patients. The The AATH model gave smaller Ktrans and Ve, and larger Vp values, as compared to mTK model, which agreed with the simulation data. The figure 1 shows the coefficient of variance (CV) of common parameters by both models,where the mTK resulted in superior precision than AATH, and greater CV was found with smaller SNR in all cases. Figure 2 shows the fitting curves of one NPC patient, which demonstrated better fitting with the AATH model especially at the first pass peak.

Table 1

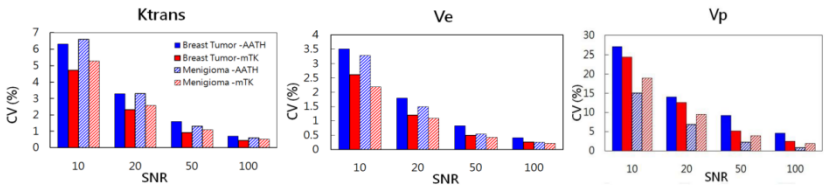
	Breast Tumor				Meningioma			
	AATH		mTK		AATH		mTK	
parameter	Mean	% error	Mean	% error	Mean	% error	Mean	% error
Ktrans	0.25	-0.92	0.28	11	0.29	-2.4	0.36	-1.6
Ve	0.46	2.0	0.48	7.1	0.4	-0.0023	0.44	9.7
Vp	0.45	-24	0.018	-70	0.069	-13	0.028	-65
F	0.54	-4.8			0.83	-30		
E	0.46	4.1			0.35	41		
PS	0.33	0.72			0.35	4.3		
τ	5.0	-20			5	25		

Unit: Ktrans (1/min), F (1/min), PS (1/min), tau (s)

Table 2

	Patient 1		Patient 2	
	AATH	mTK	AATH	mTK
Ktrans	0.062	0.27	0.10	0.48
Ve	0.11	0.37	0.24	0.86
Vp	0.024	0.013	0.046	0.043
F	0.13		0.24	
E	0.49		0.43	
PS	0.085		0.14	
tau	11.4		11.4	

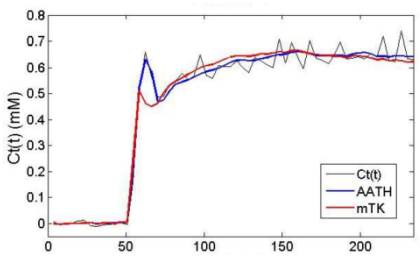
Figure 1



Conclusion

Using the MMID4 model for data simulation, this work found that the AATH model resulted in more accurate but less precise estimates of physiological parameters as compared to the mTK model. Results from the analysis of clinical NPC data were consistent with the computer simulation.

Figure 2



References

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