3T DCE MRI in prostate cancer – comparison between population average and patient specific Arterial Input Function

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Introduction

A population-averaged bi-exponential Arterial Input Function (AIF) has been commonly used to fit DCE MRI data to a pharmacokinetic model [1]. It has also been shown that patient specific AIF improves fit to an adiabatic approximation model in prostate tumours [2].In this pilot study, we compared the quality of fit to the extended Kety model of the prostate DCE MRI data using population-averaged and patient specific AIF.

Methods

DCE MRI data were acquired from two subjects involved in a larger study. Both subjects had a high clinical suspicion for prostate cancer (elevated PSA and/or prostate nodule) and received no prior treatment. The subjects underwent MRI examination prior to TRUS guided biopsies. DCE MRI data were acquired on a 3T Philips Achieva MRI scanner using a 3D T_1-weighted spoiled gradient echo sequence (256x163 matrix, TR/TE = 3.4/1.06 ms, flip angle = 15^0, FOV = 24 cm, 12 slices 4 mm each, 75 dynamic scans with temporal resolution of 10.6 sec.). PD images were acquired with the same sequence but with TR/TE = 50/0.95 ms and flip angle = 4^0. Dynamic T1-weighted images were acquired following bolus injection of Gd-DTPA (Magnevist, Berlex, Canada, 0.1 mmol/kg within 10 sec. followed by 20 ml flush of saline).

Non-rigid 2D affine registration, based on a mutual information algorithm, of the dynamic time series and PD images was performed using proprietary registration toolbox (Philips PRIDE) to correct motion corruption. AIF data were extracted from voxels in external iliac or femoral arteries in the central slice for each patient [3]. Pharmacokinetic parameters (K^{trans}, extra-vascular extra-cellular space – v_e, plasma volume – v_p) were calculated by fitting the extended Kety model with population-averaged and patient specific AIF to the concentration vs. time curves for two voxels within the prostate gland defined in high and low enhancing areas in Gd-DTPA concentration maps which were calculated from the DCE MRI data acquired from one subject with biopsy proven cancer. In addition, fitting was carried out on the central slice of the DCE MRI data acquired from both subject (one subject with biopsy proven cancer and the other with negative biopsy) to generate parametric maps.

Results and Discussion

Figure1 shows the concentration vs. time curves of two voxels both from the central slice of the patient with positive biopsy with high (left) and low (right) enhancement (squares), as well as the fits of extended Kety model with population-averaged (circles) and patient specific (diamonds) AIF. It can be seen that in the voxel with high enhancement patient specific AIF provides better model fit ($\chi^2 = 0.310$) than population-averaged AIF ($\chi^2 = 0.474$). However, in the voxel with low enhancement the quality of the fit is better with the population-averaged AIF ($\chi^2 = 0.041$) than patient specific AIF ($\chi^2 = 0.215$). The K^{trans}, v_e and v_p values in high enhancing voxel were 5.331, 0.297 and 0 respectively for population-averaged AIF and 0.074, 0.100 and 0 respectively for the patient specific AIF, while for low enhancing voxel they were 0.889, 0.339 and 0.004 respectively for population-averaged AIF and 0.050, 0.140 and 0 respectively for the patient specific AIF. Figure 2 shows the K^{trans} maps generated from population-averaged AIF (left) and patient specific AIF (right) of the patient with positive biopsy. Table 1 shows the average DCE MRI parameters calculated with population-averaged AIF (Table 1(a)) and with patient specific AIF (Table 1(b)) from the central slice. Tumour (PCa) was identified as a hyperintense area (delineated with green circles in Figure 2) in K^{trans} map of central slice of the patient with positive biopsy. Average values for the normal central gland (CG) and peripheral zone (PZ) were calculated from the parametric maps of central slice of the patient with negative biopsy (not shown).

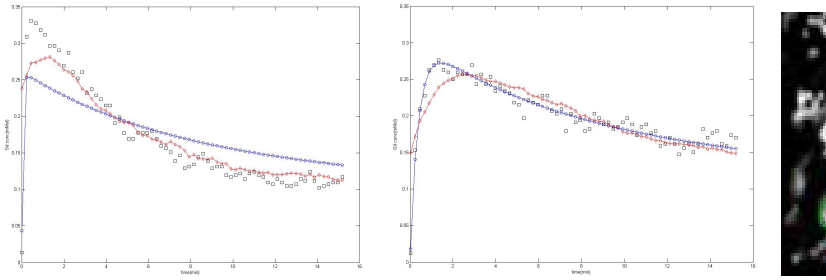

Fig.1. Gd concentration ( ) vs. time, model fitting results with population- averaged AIF (°) and with patient specific AIF (◊). The curve on the left was extracted from high enhancing region (marked as a red dot in Figure 2), and the curve on the right was extracted from low enhancing region (marked with blue dot in Figure 2).

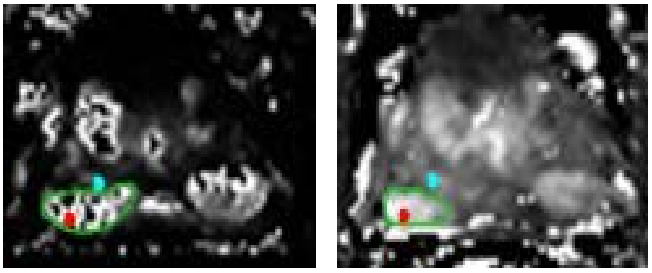

Fig.2. K^{trans} maps generated with population-averaged AIF (left) and with patient specific AIF (right) for the patient with biopsy proven carcinoma in right peripheral zone. Voxels with K^{trans} > 5.0 are displayed black.

Table 1(a). Average K^{trans}, v_e and v_p values calculated with population AIF from ROIs of tumor (PCa), central gland (CG) and normal peripheral zone (PZ)

	K^{trans} [min^{-1}]	v_e	v_p
PZ	0.148	0.209	0.006
CG	0.456	0.530	0.039
PCa	2.186	0.147	0.006

Table 1(b). Average K^{trans}, v_e and v_p values calculated with patient specific AIF from ROIs of tumor (PCa), central gland (CG) and normal peripheral zone (PZ)

	K^{trans} [min^{-1}]	v_e	v_p
PZ	0.024	0.056	0.013
CG	0.067	0.261	0.034
PCa	0.074	0.198	0.006

The results of our study show that, population-averaged AIF can provide good fitting in areas with low contrast enhancement. However in tumour region, which typically experiences high enhancement, patient specific AIF gives more accurate and reliable model output. This is because the bi-exponential AIF functional form fails to maintain the first-pass peak feature of concentration course of highly enhanced voxels. Although in this pilot study both fitting methods produced higher K^{trans} values in the tumour, as compared to the normal peripheral zone, the more accurate fit would likely result in more accurate delineation of the tumour, which is clearly visible on K^{trans} maps shown in Figure 2. This is important if this technique is to be adopted to estimate the tumour volume. Direct correlation of the DCE MRI data to histological sections of the prostate is needed to verify this hypothesis.

In conclusion, patient specific AIF provides more accurate pharmacokinetic modeling of prostate DCE MRI data in high enhancing areas than population-averaged bi-exponential AIF. Thus, patient specific AIF may result in more accurate cancer diagnosis than population-averaged AIF.

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