Comparison of perfusion analysis in DCE-MRI of brain tumors with and without T1-quantification

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Introduction

Quantification of tissue perfusion and permeability parameters from DCE-MRI bolus-tracking data requires a measurement of the tracer concentration. If the concentration is low enough, a linear relationship between signal intensity and concentration can be assumed. For higher concentrations, the signal intensity becomes nonlinear [4], particularly in the arterial input function (AIF) where contrast agent concentration is highest. When the linearity assumption is made in this regime, arterial concentration may be underestimated and tissue blood flow accordingly overestimated. In general, the concentration can be estimated using a measurement of the pre-contrast tissue relaxation rate [1,4]. This does, however, require additional measurement- and post-processing time. The aim of this study was to evaluate the effect of T1-quantification of dynamic contrast enhanced (DCE)-measurements in brain metastases, and compare it to a simple approach based on relative signal enhancement.

Materials and Methods

DCE-measurements in ten patients with known brain metastases were retrospectively evaluated. Images were acquired on a 3T-Scanner (Magnetom Trio, Siemens Medical Solutions, Germany). Precontrast T1-maps were calculated from 17 2D-SR-turbo-FLASH-images with different recovery times T_{REC} (70ms to 5s) at four slice positions in the tumor and one at a slice position containing the internal carotid artery. The same sequence with a fixed T_{REC} of 120ms was used for DCE monitoring at the same slice positions as before. A total of 320 datasets were consecutively acquired every 1.3 s. Gd-DTPA (Magnevist, Bayer Schering Pharma, Germany) was injected with a total standard dose of 0.1mmol/kg, splitted in two equal bolus injections 60s apart to avoid signal saturation at peak concentration in the artery. Before modeling, the relative signal enhancement (SE) curves (S-S0)/S0 were deconvolved with the arterial input function to produce basic maps of plasma flow (F_P), volume of distribution (V_D) and mean transit time (T_D) for lesion identification. Then ROIs were manually selected in suspicious lesions as described in [2]. The change in relaxation rate $\Delta R1(t)$ was obtained for each time point as described in [4], and subsequently, an uptake model [2,3] was fitted to the relative-SE- and $\Delta R1$-ROI-curves to yield the parameters plasma flow F_P, plasma volume V_P, plasma transit time T_P, extraction flow (EF) and extraction fraction into the interstitial space ($E=EF/F_P$). V_P was scaled with the blood volume determined in the sinus sagittalis, and F_P and EF were scaled accordingly to correct for partial volume effects in the AIF.

	5Perc.	Median	95 Perc.
FP	0.91	1.57	2.23
TP	0.97	1.01	1.06
VP	0.88	1.63	2.2
EF	1.01	1.73	2.53
E	1.01	1.07	1.22

Table 1: Ratio of the fit parameters with and without T1-quantification

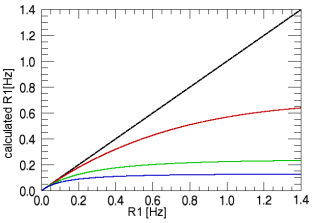

Figure 3: Dependence of calculated R1 of the effective flip angle a_{eff}. black: $a_{eff}=a_{nom}$, red: $a_{eff}=0.99a_{nom}$, green: $a_{eff}=0.95a_{nom}$, blue: $a_{eff}=0.9a_{nom}$

Results

A total of 37 lesions was investigated, typical tissue- and AIF-curves are shown in figure 1 along with a model fit. Note the two distinct peaks resulting from the double shot injection, and the good model fit. Although the SE- and $\Delta R1$-curves are very similar, the calculated values from the two fits differ in most cases, resulting from a different relative scaling of the AIF with and without T1-quantification. The flow- and volume parameters of the two approaches differed by factors from 0.9 to 2.5 (see Table 1). The extraction fraction E and the plasma transit time are only slightly affected using T1-quantification, whereas F_P, EF and V_P are lower in the analysis without T1-quantification (see Figure 2 and Table 1).

Discussion

With the double bolus injection scheme, the model yields higher flow and volume values when T1-quantification was used. This is unexpected, since T1-quantification is designed to correct for overestimations in the perfusion parameters F_P, V_P and EF caused by non-linearities in the AIF. Thus, parameters calculated with T1-quantification were expected to be similar or, in presence of high tracer concentrations in the AIF, lower as without quantification.

A possible explanation of the effect is a difference between nominal and actual flip angle. Such differences may arise, particularly at 3T, due to B1-inhomogeneities, or due to the effect of flowing blood in the artery [5]. Simulation results show that dynamic T1-quantification is very sensitive to errors in the flip angle (Figure 3) and smaller effective flip angles lead to an underestimation of $\Delta R1$. Therefore, the calculated tracer concentration in the AIF is underestimated, which accounts for the overestimation of F_P, V_P and EF.

We conclude that T1-quantification does not necessarily improve the accuracy of a perfusion analysis using 2D data acquisition. If the flip angle is not known with high accuracy and precision, the approach may even introduce additional errors in the perfusion parameters.

References:

[1] Brix(2004), MRM52:420-429, [2] Sourbron (2007), ISMRM Workshop “Cerebral Perfusion an Brain Function”, Brazil, [3] Bazelaire (2005), EurRadiol15:2497–2505, [4] Wiart (2005), MRM 56:340-347, [5] Mikkelsen, ISMRM 15(2007), 3501

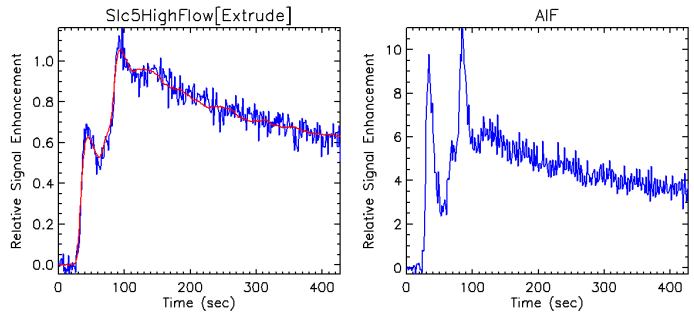

Figure 1: Left: ROI curve of a lesion (blue) and model fit(red), right: corresponding arterial input function

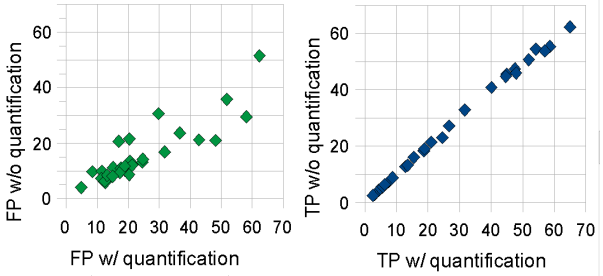

Figure 2: Comparison of either FP or TP calculated with or without T1-quantification