Model free bolus arrival time estimation for dynamic contrast MR studies

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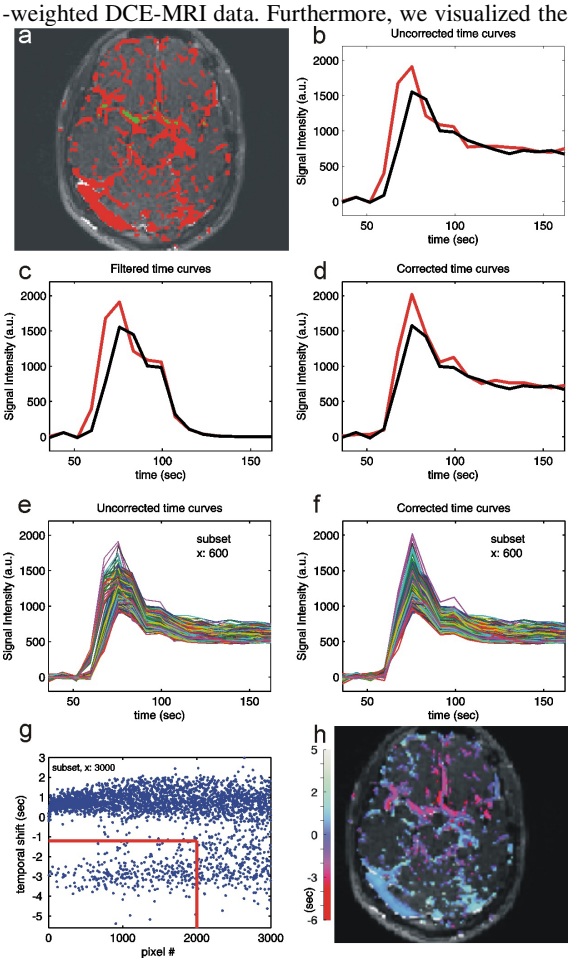
Introduction: quantitative analysis of bolus arrival time (BAT) is important in many ways for the assessment of brain when dynamic contrast MR studies are performed. Pharmacokinetic analysis of T_1-weighted or T_2-weighted dynamic studies (DCE / DSC) requires knowledge of the arterial input function (AIF), which can be estimated by selecting pixels that have an early BAT. Furthermore, the arrival time delay may provide information about blood circulation and separation between the arterial and venous bed. Several suggestions have been made in literature to estimate bolus arrival time, but these are model dependent and estimate BAT on a pixel by pixel basis[1,2]. In this paper we describe a model independent method that uses singular value decomposition (SVD) and linear regression to estimate and correct for bolus arrival time. We show that this technique can be used to select a subset of pixels that estimate the AIF in T_1 -weighted DCE-MRI data. Furthermore, we visualized the BAT in the arterial and venous bed.

Methods: 3D T_1-weighted DCE-MRI data were collected from brain (144x144x25, Δt=7.9 sec, 50 dyn.) using an Intera 3.0 Tesla MR system (Philips Medical Systems, The Netherlands). For fast initialization a mask was constructed that contained 20% of the pixels having the largest Area Under the signal intensity Curve (AUC, normalized to have 0 signal intensity at t=0). To calculate the relative BAT for each pixel, the approach of [3] was adapted to only correct for temporal shifts on signal intensity (SI) curves with magnitude information. First, the average maximum intensity time point of all SI curves was located and each SI curve was exponentially filtered starting three time points after this time point. This is done to focus on the early rising part of the SI curves, which have an assumed common lineshape. Then, SVD was applied on the covariance matrix of the SI curves. Then, each SI curve was approximated by a linear combination of the first principal component, and its first derivative. With the classical least-squares solution the coefficients of the linear regression are obtained within one calculation step. It can be proven (under the assumption of a common lineshape function $f(\omega)$ and its expansion in a Taylor series[3]) that the relative delay of each SI curve can be approximated by division of the second regression coefficient with the first one. Finally, the unfiltered SI curves are corrected in the frequency domain using inverse FFT and the Hilbert transform. Optionally, the procedure can be iterated until the eigenvalue of the first principal component is converged to a maximum.



Results: Fig. a shows in red and green the mask (107055 pixels in the 3D volume) of the slice that intersects with the Circle of Willis. In Fig. b two example curves are shown that clearly deviate in BAT. The filtered curves are shown in Fig. c and the corrected curves are shown in Fig. d. Uncorrected and corrected subsets with 600 curves are shown in Fig. e and f. In Fig. g, the 3000 sorted points with largest AUC are shown, plotted against their temporal shift (with early arrivers negative). After setting thresholds (red lines in Fig. g) the pixels in the lower left area are identified, and colored green in Fig. a. Note that the selected pixels in Fig. g are distributed over the whole volume. In Fig. h each pixel in the masked area is color coded with respect to its temporal shift relative to the mean BAT.

Discussion / conclusion: a model free correction method for estimation of bolus arrival time of dynamic MR data is discussed. The method uses the common lineshape of the data estimated with SVD. The correction provides sub-pixel time shift values, which after correction results in similarly shaped SI curves - due to equivalent sampling - that have identical starting point and optimum. This suggests that error due to dispersion is not significant. Fig. g shows that there is a very clear discrimination between a group of pixels with an early BAT and the bulk of pixels with a late BAT. The pixels with early BAT and high AUC correlate very well with the area of the internal carotid artery and the anterior cerebral artery and can be used as AIF (green in Fig. a). Since the SI curves of the selected pixels are corrected, the resulting mean AIF will have less dispersion due to averaging. The color coded overview in Fig. h shows that a quantitative representation of bolus arrival time (in seconds) is possible. This may provide relevant information about blood circulation. The time for the contrast agent to travel from the artery to the tissue of interest is also an important parameter that must be measured for pharmacokinetic analysis to be accurate. If the proposed technique can also be applied on SI curves of pathologic tissue (need for a common lineshape), it might be possible to bring the AIF curve in sync with each SI curve from which pharmacokinetic parameters need to be estimated.

References: [1] Cheong, Phys Med Biol 48, N83–N88(2003), [2] Ibaraki, J Cereb Blood Flow Metab 25(3), 378-90(2005), [3] Witjes, JMR 144, 35-44(2000)