Susceptibility-Based Analysis Of Dynamic Gadolinium Perfusion MRI

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Introduction. Perfusion-weighted imaging (PWI) performed using bolus injection of Gd-DTPA contrast agent is traditionally analyzed based on changes in brain signal relaxation times (usually T_2*, but also T_2 and T_1) associated with passage of contrast through the brain. However, there is appreciably evidence that changes in transverse relaxation times do not depend linearly on the Gd-DTPA concentration, which makes quantitative analysis difficult [1, 2]. The Gd-DTPA bolus pass also causes a localized change in tissue magnetic susceptibility $\Delta\chi(t)$, which results in a shift of the local MRI resonant frequency (the effect decreases with $1/r^3$ if r is the distance from the source). Recently, Quantitative Susceptibility Mapping (QSM) has been developed to determine local susceptibility by solving the ill-posed inverse problem of deconvolution of a field map in terms of the voxel dipole field, surrounding dipole fields and static background fields [3, 4]. The local susceptibility change induced by the presence of Gd-DTPA is expected to be linearly proportional to its concentration (molar susceptibility χ_m), and independent of intra- or extra-vascular location. In this abstract, the feasibility of dynamic QSM data reconstruction for reconstruction of cerebral blood flow (CBF) is investigated.

Methods. *Experiment.* A 68 year-old male patient without perfusion deficit was scanned at 3.0T (Philips Medical Systems) as part of his stroke workup for symptoms of blurred vision. Informed consent and IRB approval were obtained; *Scan parameters.* 20 slices, 80 dynamics, multi-slice 2D gradient echo EPI, FOV=240x240 mm^2, 256x256 matrix, 5mm slice thickness, TR/TE 1500/40 msec, 0.2 mmol/kg Gd-DTPA bolus. *Analysis.* For conventional DSC processing, maps of ΔR_2*(t) were calculated[5]. For QSM processing[6, 7], frequency maps f(t) were calculated from unwrapped phase images $\varphi(t)$, and the averaged fitted background phase of the first two pre-bolus dynamics was subtracted from all dynamics. Susceptibility calculation used deconvolution of the unit perturber field from the phase difference data using regularized least squares optimization [6]. A brain mask was generated using standard FSL routines [8]. CBF was calculated using standard DSC processing [5] with Tikhonov regularization [9], using both ΔR_2*(t) and $\Delta\chi(t)$ maps. A semi-automatically detected arterial input function (AIF) [10] was used for both DSC and QSM perfusion processing. Results for CBF=max{CBF•R(t)} are shown, where CBF•R(t) is the deconvolved concentration time curve[5] (R(t): residue function); other methods for CBF determination[10] yielded similar results. Calculations used a transverse relaxivity of Gd-DTPA r_2=5.2 L•$mmol^{-1}$•sec^{-1}[11] and molar susceptibility χ_m=0.3209•10^{-3} L•mol^{-1} [2] to reference to plasma concentrations. Tissue contrast concentration maps were calculated from $C_t(t)= \Delta\chi(t)/\chi_m$.

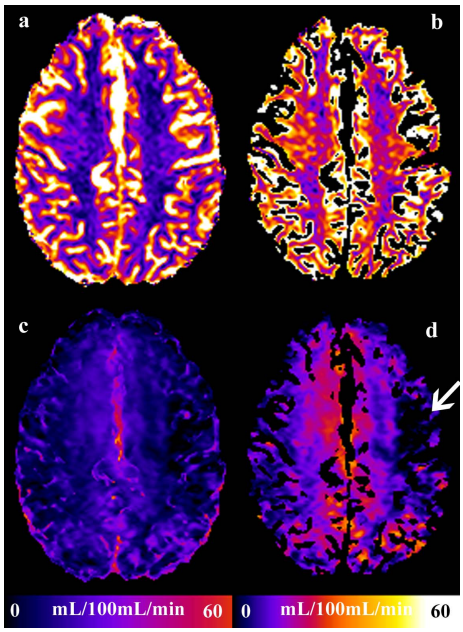

Figure 1

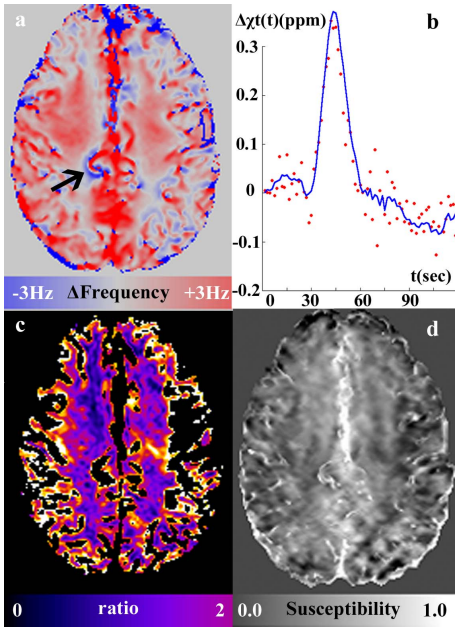

Figure 2

Results and Discussion. Fig.1 depicts a representative slice at the level of the centrum semiovale and shows qualitative agreement of ΔR_2* (a/b) and $\Delta\chi$ perfusion (c/d) images for white matter (WM). A brain mask is applied in (b) and (d) to remove high signal associated with sulcal veins, and CSF spaces. Relatively large frequency errors occur in the periphery of the brain due to the current implementation with subtraction of the averaged background gradient for phase correction, limiting assessment of cortical gray matter flow with the current approach. The peak frequency difference during the bolus is shown in Fig. 2a with strong dipolar phase changes in the cortical regions (arrow). The average susceptibility change of WM during bolus passage is shown in Fig. 2b (red: measurements, blue: 6 point sliding average). The ratio $CBF_{\Delta R2*}/CBF_{\Delta\chi}$ shows approximately two-fold lower WM CBF measurements are obtained with QSM perfusion (Fig. 2c). The susceptibility difference map during bolus peak (Fig 2d, ppm scale) shows the brain parenchymal susceptibility change clearly. An area of negative susceptibility difference in the periphery of the left hemisphere represents background removal associated phase error, causing a void in the CBF map (Fig 1d, arrow).

In summary, this pilot study demonstrates that susceptibility-based analysis of dynamic perfusion data is feasible, and can be used to reconstruct CBF maps. The optimal processing methods and a detailed comparison to conventional approaches remain to be determined. Current limitations include possible incomplete removal of dipole fields by QSM processing, and relatively large phase/frequency errors in the brain periphery which limit cortical gray matter perfusion measurements. Additional challenges include the compensation of superimposed dynamic susceptibility changes due to respiration, which are of similar magnitude to the frequency shifts associated with the Gd-DTPA bolus.

References. [1]F Calamante, et al. Magn Reson Med, 58, 2007. [2]MJ van Osch, et al. Magn Reson Med, 49, 2003. [3]W Li, et al. Neuroimage, 55, 2011. [4]F Schweser, et al. Neuroimage, 54, 2011. [5]L Ostergaard, et al. Magn Reson Med, 36, 1996. [6]L de Rochefort, et al. Magn Reson Med, 63, 2010. [7]S Wharton, et al. Magn Reson Med, 63, 2010. [8]M Jenkinson, et al. Neuroimage, 17, 2002. [9]S Sourbron, et al. Phys Med Biol, 49, 2004. [10]L Knutsson, et al. Magn Reson Imaging, 28, 2010. [11]J Pintaske, et al. Invest Radiol, 41, 2006. **Funding.** NIH P41 RR015241.