Estimation of Pure Gray Matter Perfusion in Human Brain

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Introduction

Perfusion can be measured noninvasively with arterial spin labeling (ASL) techniques. Most of the ASL signal in the human brain is represented by gray matter (GM) due to its well-perfused nature opposed to white matter (WM). However, for absolute quantification of perfusion, it suffers from partial volume averaging effect with WM and CSF due to the fact that gray matter consists of thin layers of cortex with multiple folding of thickness ranging from 2-4mm. Most of the time imaging voxels are not fully occupied by GM. The calculated perfusion is likely to be underestimated because of mixing with other non-perfused or low perfused tissues. The most straightforward method is to use higher spatial resolution to obtain higher GM volume fraction in a voxel at the cost of SNR reduction. At a high enough spatial resolution, the measured perfusion values should reach a plateau. However, even at relatively high spatial resolution, partial volume averaging will still exist. Here we utilize a double inversion recovery (DIR) pulse sequence (1,2) to null out CSF and WM signal in order to estimate the fractional volume of GM and compare with absolute perfusion measurements from pulsed ASL techniques.

Methods

The pulse sequence for DIR consists of two selective adiabatic inversion pulses with time interval TI1 and time interval TI2 between the second inversion pulse and the excitation RF pulse for image acquisition. Here we assume CSF and WM both have a single T1 value. The TI1 and TI2 pairs were designed to suppress CSF all the time and simultaneously nulling tissues of T1 values starting from 550ms to 1800ms in a step of 50ms in order to empirically determine the best TI times for suppressing both CSF and WM. Each DIR image volume is interleaved in 3 passes to accommodate the fact that the slice-selective inversion is three-time the thickness of the imaging slice in order to compensate for flowing CSF. A total of 15 axial slices of 7mm thickness with 1mm gap were acquired in a time-multiplexed way so that a total of 5 slices was obtained in one pass. The TR is 8sec with single-shot spin-echo EPI with minimum TE of 50ms for 64x64 matrix size in 24cm FOV. The total sequence time was approximately 10min. The DIR images of the best suppression of WM and CSF were used for obtaining GM fractional volume. Assuming only GM signal was left in the DIR images, the intensity of the images was converted to GM M0 images by dividing the DIR signal according to relaxation equation (1, 2). The GM fractional volume was estimated by divide the M0 images to images obtained at the very first image acquisition without any inversion pulses equivalent to infinite TR. Images were obtained with a 3T scanner with a quadrature head coil. The T1 of CSF was first evaluated with 3 subjects with single inversion recovery with a 2mm axial slice across largest obtainable ventricular area. PICORE QUIPSS II (3) was used with TI1/TI2=700/1500ms and 2sec TR for a total of 10min acquisition of 5 axial slices coincided with the same slice locations as DIR images. ASL images were pair-wise subtracted and averaged to obtain perfusion images. The absolute cerebral blood flow (CBF) values were calculated by methods described by Wong et al. (4).

Results

Figure1 shows the DIR images and the calculated GM fractional volume maps together with the corresponding perfusion images. Strong similarity of GM structure was readily seen with DIR images and perfusion images. Figure 2 shows the scatter plot of GM volume fraction versus CBF values from ASL images of 5 slices. Although quite noisy, a general trend of correlation was observed. To convert the DIR images to GM volume fraction, a single T1 value of 1350ms for GM was used. Deviation of 10% in GM T1 will result in approximately 10% and 5% change in volume fraction if decreasing and increasing T1 values, respectively. With a typical selection of GM ROI by T1 values, the average CBF is 100 ml/100 g/min and the average GM volume fraction is on the order of 55% at current resolution with a voxel size about 100mm^3. It is consistent with PET studies around 50 ml/100 g/min in which the equivalent voxel size is on the order of 200mm^3. It is reasonable that perfusion can reach 200 ml/100 g/min in pure GM voxels.

Discussion

Many factors may contribute to the noise in the scatter plot. Assuming single T1 for WM in obtaining DIR images and incomplete suppressing of CSF and WM can lead to overestimation of GM volume fraction. Using single T1 for GM to convert DIR images to M0 images can cause both overestimation and underestimation of volume fraction. It may also be possible that for the same volume of gray matter the perfusion is different depending on the function and states of the brain location. Despite all these errors, a linear correlation of GM volume fraction and perfusion measured by pulsed ASL techniques is clearly demonstrated.

References

1. Redpath et al., *BJR* 67: 1258 (1994). 2. Bedell et al., *MRM* 39: 961 (1998). 3. Wong et al., *MRM* 39: 702 (1998). 4. Wong et al., *NMR Biomed* 10: 237 (1997).

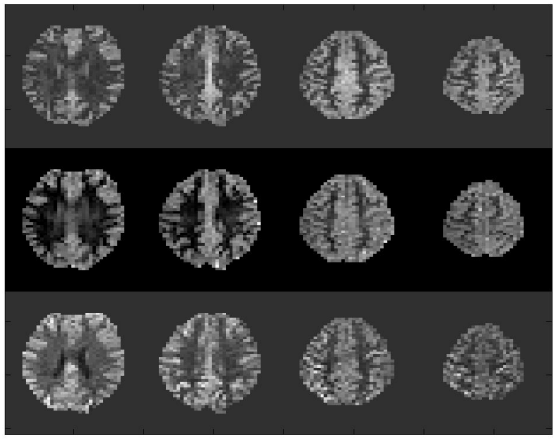

Figure 1. Top row: DIR images with WM and CSF nulling.
Middle row: estimated GM volume fraction maps.
Bottom row: QUIPSS II perfusion images.

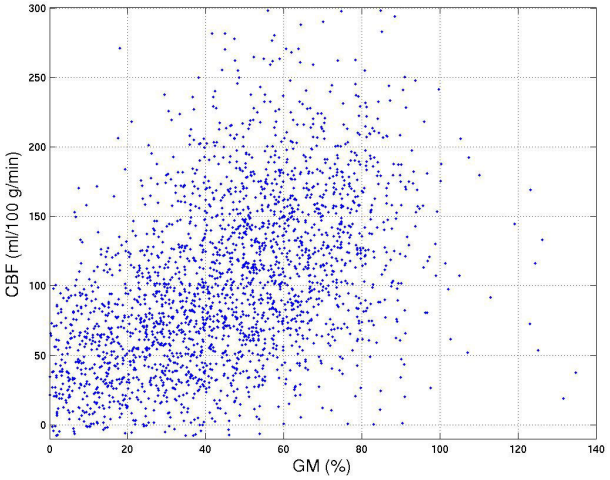

Figure 2. Scatter plot of CBF vs. GM volume fraction from voxels of all 5 slices.