Analyzing perfusion in human gray matter

W-C. Wu[1,2] and E. Wong[2,3]

[1]Laboratory for Structural NMR Imaging, Department of Radiology, University of Pennsylvania School of Medicine, Philadelphia, Pennsylvania, United States, [2]Center for Functional MRI, Department of Radiology, University of California, San Diego, La Jolla, California, United States, [3]Department of Psychiatry, University of California, San Diego, La Jolla, California, United States

Introduction

In quantitative MRI, a lot of effort has been made to develop robust techniques to measure local cerebral blood flow (CBF), or perfusion. In human brains, CBF variation exists between white matter (WM) and gray matter (GM), and within regions of GM as well (1). Nevertheless, mean GM-CBF is commonly used as an index for technique validation. However, the extraction of GM is usually not explicitly addressed. A simple, yet objective, method to generate a GM mask is therefore desirable. Here we compare three methods that are based on longitudinal relaxation time (T1), anatomy, and CBF, respectively, on perfusion maps acquired by arterial spin labeling (ASL).

Materials and Methods

Three healthy volunteers were included. All imaging protocols were approved by the institutional review board and performed on a 3T GE EXCITE scanner. Perfusion images were acquired using PICORE QUIPSS (2,3) ($TR/TE/TI_1/TI_2$ = 2000/2.9/700/1400 ms, NEX = 40). CBF was calculated following the procedure proposed Wong et al (3). T_1 maps were generated by a series of inversion recovery scans with following parameters: TE = 2.9 ms, TI = {30, 80, 150, 300, 600, 1000, 1500, 2000, 3000, 5000}ms, TR = TI+15 s. At last, FLAIR technique was used to eliminate CSF signal while the contrast between GM and WM was optimized (TR/TE/TI = 2530/2.9/1041 ms, NEX = 10, T_1 = 3500/1330/830 ms for CSF, GM and WM, respectively (4)). All images were collected from three 5mm axial slices (FOV = 22 cm, matrix size = 64x64) with spiral gradient-echo readout. In-plane intracranial region was manually defined on the average ASL image (voxel number denoted as N). Mean CBF was then obtained over the GM masks generated by methods described as follows (Fig 1). Method 1: Intracranial pixels were sorted in an ascending order according to their T_1. GM pixels were extracted using a window (W) and an offset (δ). The W was varied to cover {10, 15, 20, …, 50}% of N after skipping a δ equal to {0, 2, 4, …, 20}% of N. δ started from the T_1 of 1100ms. Method 2: Intracranial pixels were sorted in an ascending order based on their image intensity. W and δ were defined as above but adjusted along image intensity. δ started from the intensity of 0. Method 3: Intracranial pixels were sorted in a descending order according to CBF. δ started from the highest CBF. The choice of 50% was based on the volume fraction of GM in intracranial volume (5).

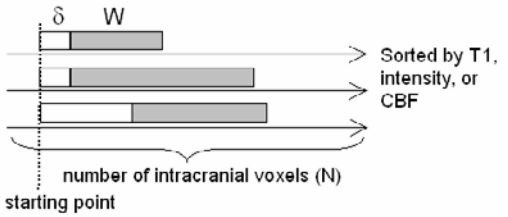

Fig 1. Examples of the combination of δ and W. For each case, a mask is generated over the voxels falling in the range of W and mean CBF is calculated.

Results and Discussion

Fig 2 shows part of GM masks obtained from a representative subject. In method 1, GM can be better distinguished from WM and CSF as opposed to method 2 that can include substantial CSF contamination to GM as δ is small. Large δ+W in method 2, on the other hand, can lead to CBF underestimation due to the inclusion of WM. Mean CBF obtained by methods 1 and 2 are shown in Fig 3 (mean CBF is 69.4+/-2.0 and 68.7+/-2.5 ml/100ml/min respectively, using the masks marked in Fig 2). In method 3, a δ of 2-5% is necessary to exclude the signal from large vessels. As W = 40-50%, mean CBF is 67.5+/-3.1 ml/100ml/min. In conclusion, three methods provide comparable GM-CBF. Calculating GM-CBF based on CBF or ASL signals usually raises the concern of circular data analysis. Many studies therefore resort to T1 map or anatomic image of high resolution as an independent reference for GM segmentation, which requires extra scan time and/or registration to account for different readout and matrix size. The present study demonstrates that CBF map (or ASL signal) can be used as a simple and objective method for GM-CBF calculation.

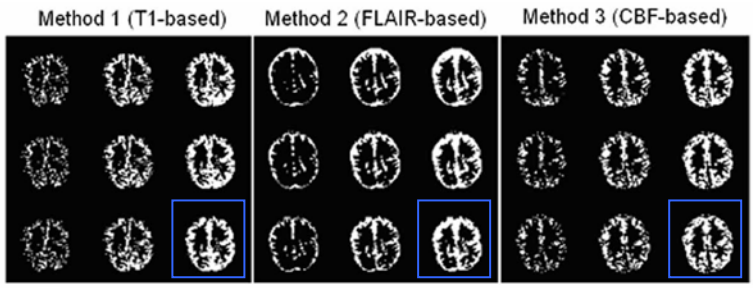

Fig **2.** Gray matter masks generated by different methods. In each method, from top to bottom: offset = {0,4,8}% of the intracranial pixels; from left to right: average window = {20,35,50}% of the intracranial pixels.

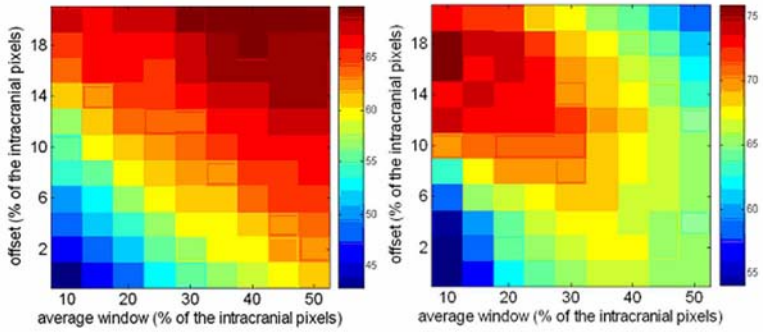

Fig **3.** Mean CBF obtained form masks generated by method 1 (left) and 2 (right), and different offset and average window (expressed in ml/100ml/min). One notices that the color scale is different in two maps.

References

1.Parkes et al. Magn Reson Med 2004;51:736
2.Wong et al., NMR Biomed 1997;10:237
3.Wong et al., Magn Reson Med 1998;39:702
4.Clare et al., Magn Reson Med 2001;630