A Self Calibrating Pulse Sequence for Real Time Quantitative Cerebral Perfusion

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Introduction: Cerebral perfusion is a physiologic measurement that reflects the presence and severity of a number of pathologic condition including stroke, cancer, Alzheimers dementia and cerebrovascular occlusive disease. The existence of well known thresholds, below which cell death ensues, have prompted the American Heart Association to recommend in a recent white paper that: "*More research must be conducted to make these technique, especially the MR-based techniques, quantifiable*"[1]. Any pulse sequence that provides quantitative perfusion images will have the greatest impact on the health-care community if it can be easily disseminated to a large number of hospitals. This adds the requirement that image post-processing be eliminated so that highly skilled operators are not needed to produce the images need for rapid diagnosis. We have developed a self-calibrating MR pulse sequence that allows for quantitative MR perfusion images to be automatically calculated without the need for operator input.

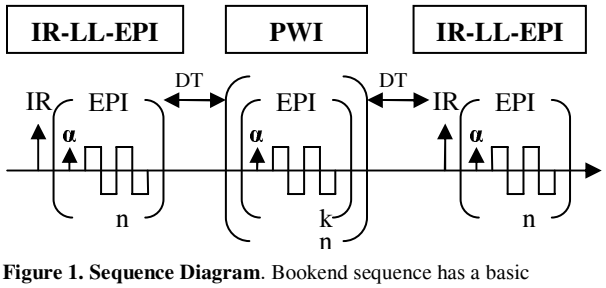

Figure 1. Sequence Diagram. Bookend sequence has a basic structure of GE-EPI. GE-EPI is repeated in ***k*** slices and with ***n*** measurement for the PWI. Before and after PWI, non-selective IR single slice of GE-EPI were repeated with ***n*** measurement. 5 seconds of delay time (DT) was inserted before and after PWI

Methods: There are two components which are required for real-time quantitative perfusion: a self-calibrating pulse sequence and a fully automated reconstruction program. We have developed an MRI pulse sequence based upon a previously reported multi-sequence quantitative perfusion protocol [2,3]. Elimination of user input from the selection of the AIF has been reported by a number of authors. We have extended these ideas [4] to the automation of the Bookend image processing to eliminate all user input need from post processing. This allows the MRI scanner to produce images of CBV, CBF and Mean Transit time, upon scan completion, similar to the calculation of MIP images form angiography.

Pulse sequence: A pulse sequence diagram is shown at the right (Figure 1). It is based on a multi-slices 2D, T2*-weighted single shot EPI pulse sequence as is commonly used for cerebral perfusion imaging. The bookend technique requires knowledge of parenchymal and blood volume T1 changes. Our sequence measures T1 by fixing the slice position and adding an inversion recovery pulse, and reading the magnetization recovery in this single slice. These inversion readout cycles are acquired prior to the multi slice T2*-weighted perfusion weighted EPI scans, and again after the nominal perfusion scans. An adjustable delay time (DT) allows for spins to fully recover to their steady-state. The additional inversion recovery images (including DT) constitute an addition 15 seconds before and 15 seconds after the dynamic susceptibility weight images. In our current implementation, the T1 images are presented to the user for review, however, this step, and the additional images that are generated could be removed as this sequence is developed.

Image Processing: Image processing begins with the nominal filtering and Fourier Transformation. Following image generation relative perfusion images are automatically calculated [4] and calibrated to yield quantitative CBV (in ml/100g) and CBF (ml/100g-min). The IR images are used to calculate T1 images, for both pre-and post contrast image sets, from which the T1 changes white matter and blood pool are automatically segmented out and these used "calibrate" the relative CBV, CBF and MTT images [2,3] to produce quantitative perfusion (See Figure 2).

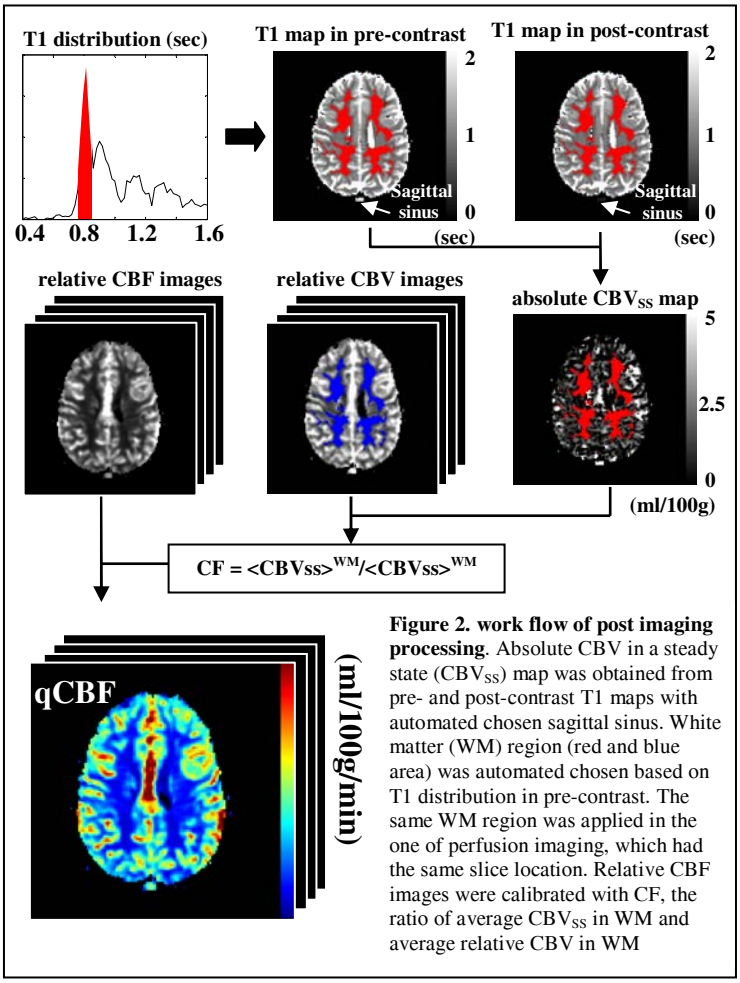

Figure 2. work flow of post imaging processing. Absolute CBV in a steady state (CBV_{SS}) map was obtained from pre- and post-contrast T1 maps with automated chosen sagittal sinus. White matter (WM) region (red and blue area) was automated chosen based on T1 distribution in pre-contrast. The same WM region was applied in the one of perfusion imaging, which had the same slice location. Relative CBF images were calibrated with CF, the ratio of average CBV_{SS} in WM and average relative CBV in WM

Images were acquired on standard 3.0T MRI scanner in a series of 5 volunteers (4 men, 1 woman). The pulse sequence (TR/TE= 1.56 ms/62 ms, total scan time = 2:00) was run in conjuction with a single dose (0.1 mmol/kg of body weight). An additional delay of 15 seconds was inserted between start of scan and injection.

Results: Acquisition and post-processing were successful in all cases. Representative quantitative perfusion images are shown in figure 2. These initial results in humans with normal flow indicated feasibility. Further studies in patient are underway in this ongoing study.

References:

[1] Latchaw et al, *Stroke* 2003 [2] Sakaie et al., *JMRI*, 2005. [3] Shin et al., *MRM*, 2006. [4] Carroll et al., *Radiology*, 2003.