A Self Automated Normalization Algorithm of CBV Maps for Glioma Grading

R. T. Seethamraju[1], H. You[2,3], J. Qu[4,5], E. A. Macklin[6], and G. S. Young[7]

[1]MR R and D, Siemens Medical Solutions, USA Inc., Charlestown, MA, United States, [2]Radiology, Peking Union Medical College Hospital, Beijing, China, People's Republic of, [3]Neuro Radiology, Brigham and Women's Hospital, Boston, MA, United States, [4]Radiology, Tiantan Hospital, Beijing, China, People's Republic of, [5]Radiology, Henan Tumor Hospital, Zhengzhou, China, People's Republic of, [6]Biostatistics Center, Massachusetts General Hospital, Boston, MA, United States, [7]Radiology, Brigham and Women's Hospital, Boston, MA, United States

Introduction: The value of dynamic susceptibility contrast perfusion weighted MRI (DSC PWI) for grading gliomas is widely accepted. The hot spot method is the most widely used technique for analysis of DSC PWI maps [1-5]. In this technique, regions of interest (ROI) are selected on the relative cerebral blood volume (relCBV) maps in the portion of tumor that appears to have the highest relCBV. The measured relCBVmax is divided by the relCBV of ROI selected in the contralateral normal appearing white matter (NAWM) to yield a dimensionless ratio called the normalized CBV (nCBV). The measured nCBV may vary with size and placement of ROI both in the tumor and in the NAWM, leading to substantial operator dependence. We present a method for automating the determination of NAWM relCBV in order to reduce the operator dependence of the hot spot and other DSC PWI analytic methods. A method based on histogram analysis of a single brain section has been reported [6]. In this method a brain section was selected containing no visible tumor on either the conventional image or DSC PWI relCBV maps. It was reported that after elimination of the tails of the histogram, the modal relCBV of the remaining histogram approximated the mean relCBV in ROI selected within NAWM. While this method reduced operator dependence in estimation of NAWM relCBV, it did not totally eliminate it, because selection of a tumor free section may still vary between operators. We report a revised method that eliminates operator dependence and present initial validation data to support its use.

Method: An IRB approved retrospective analysis was performed of DSC PWI data acquired on12 patients after resection of pathologically confirmed high grade glioma (HGG). DSC PWI data had been collected for each subject before and after whole brain radiation therapy (RT). relCBV histograms for each slice were generated. The histogram for each slice in the brain (Fig. 1a) were aggregated and detrended to reduce variation among the individual histograms (Fig 1.b). The detrended histograms were then averaged to yield a single histogram (Fig. 1c) which was smoothed by polynomial fitting. The relCBV value at the peak of this smoothed whole brain histogram was then considered to represent the relCBV of NAWM for calculation of nCBV from the relCBV measure in the tumor ROI (Fig. 1d). The whole brain histogram-based estimates of NAWM relCBV were compared to the average of NAWM relCBV measurements performed in multiple ROI in NAWM of each scan by an expert reader. At least 5 NAWM ROI were selected in each scan. Pearson correlation was used to compare histogram and manual expert operator derived estimates of NAWM relCBV. In addition, reproducibility of the histogram estimates was estimated by the intra-class correlation between histogram derived values from the pre and post-RT time points.

Results and Discussion: In most slices a unique major NAWM peak was observed in the range 400 to 3800 for rCBV values ranging from 0 to 4096. The relCBV value of this peak differed somewhat among slices and in some slices no peak was observed, but in all exams at both time points, a strong cluster of histograms was observed, generating a single whole brain average peak. For this cohort of patients, the intra-class correlation of relCBV values from the major peaks of whole brain histograms from pre and post-RT scans was (r=0.7327, P=0.0193). In 10 of 12 subjects the shape of the histogram was qualitatively identical between the two time points (Fig 2a). In 6 of 12 subjects, the shape of the major peak varied in amplitude (Fig 2b). Representative relCBV and nCBV maps from one subject are shown in Fig 3. The Pearson correlation coefficient between the average NAWM value measured by the expert readers and the automated histogram derived estimate was 0.72 for pre RT and 0.83 for post RT (P<0.001) as can be seen from the scatter plots in Fig. 4.

Conclusion: Estimates of NAWM relCBV derived from the novel whole brain histogram analysis of relCBV maps reported above are highly correlated with measurements performed manually be expert readers and reproducible between time points before and after brain RT. Since this method eliminates operator dependence in estimation of NAWM, it is expected to improve the reproducibility of nCBV estimation for use in grading and follow up of HGG.

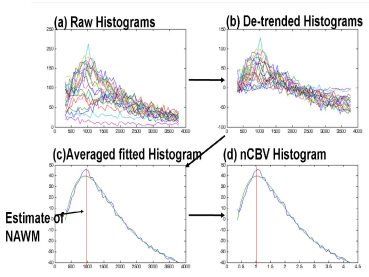

Fig 1. Workflow of the processing steps

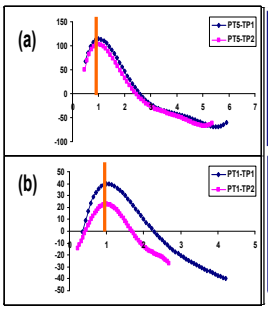

Fig 2. Representative nCBV histograms

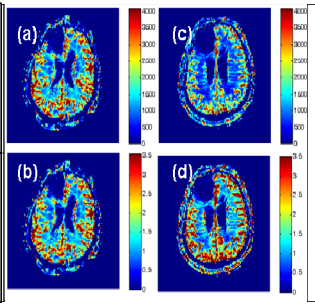

Fig 3. Left panel Pre RT, right panel Post RT. Top Panel relCBV and bottom panel corresponding nCBV map samples.

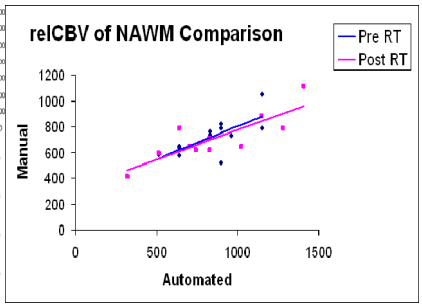

Fig 4. Scatter plots comparing automated to manual picking of NAWM reCBV values

References: [1] Hakyemez B et al. Clin Radiol 2005;60(4):493–502. [2]Shin JH et al. AJR 2002;179(3):783–9. [3] Knopp EA et al. Radiology 1999;211:791–8. [4] Sugahara et al. AJR 1998;171:1479–86. [5] Aronen HJ et al. Radiology 1994;191(1):41–51. [6] Seethamraju et. al. WMIC, 2009.