

Standardization of rCBV values improves tumor contrast.

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Introduction

Interpatient rCBV measurements provide inconsistent values for the same tissue types, such as white matter (WM) within the brain. This results in difficulties scaling for proper contrast and comparing across studies. Though rCBV is generally normalized to contralateral brain or normal-appearing WM, the choice of these reference region of interests can be quite subjective thereby adding variability to the results. Therefore, the objective of this study was to apply an automated standardization routine originally developed for morphological MRI to rCBV maps in order to provide consistent values for normal tissue types such as gray matter (GM) and WM and enable better comparison of tumor rCBV across patients.

Methods

A retrospective analysis was performed using brain tumor patients ($N=12$). T_1 (pre- and post-contrast), T_2 FLAIR, and DSC perfusion-weighted imaging [1] were acquired on a 1.5-T MR scanner. The rCBV values were calculated as described in [1]. The rCBV maps from all 12 patients were used to train a standardization scheme as detailed in [2], for both SE and GE rCBV values. This scheme performs a piecewise-linear transformation to transpose values within selected percentile ranges to the standardized range generated from the training data. The middle slice was selected for 4 of the 12 patients to test the standardization method. Using the coregistered morphological images as inputs, fuzzy c -means (FCM) was used for segmentation, followed by manual classification of clusters to one of seven tissue types (background, GM, WM, CSF, necrosis, edema, or tumor). Standardized SE and GE rCBV maps were generated from the original SE and GE rCBV maps, respectively. To account for differences in the range of pre-standardization rCBV values between patients, the pre- and post-standardization rCBV for each patient was normalized by its maximum value which varied for the original maps but was the same for all standardized maps. Mean and standard deviations were then calculated for the normalized rCBV values within WM and GM for each patient, and a one-sided Students t -test was used to test for differences between WM and GM mean rCBV values, under the alternative hypothesis that rCBV of WM is less than that of GM.

Results

Figures 1 and 2 show the pre- and post-standardization maps for rCBV_{GE} and rCBV_{SE}, respectively. The box plots in Figures 3 through 6 show the overlap in mean rCBV values for tissues prior to standardization and separation post-standardization, though the differences were not found to be significant. Ratios between GM and WM rCBV remained nearly the same post-standardization.

Discussion

While the results for the small sample size did not provide significant differences, they did show an increase in contrast with a tendency towards reduction in the overlap of mean rCBV values for WM, GM, and GBM. This shows the potential to allow better discrimination of tissue types. Standardization should make rCBV values insensitive to slight protocol changes, which will be investigated in future work.

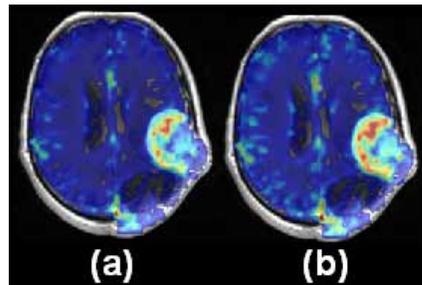


FIGURE 1. Sample rCBV_{GE} map (a) pre- and (b) post-standardization for a meningioma.

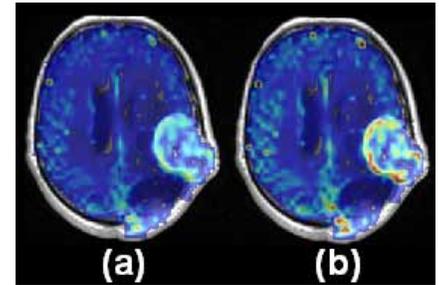


FIGURE 2. Sample rCBV_{SE} map (a) pre- and (b) post-standardization for a meningioma.

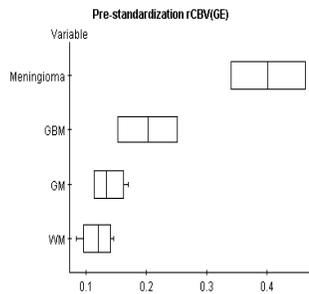


FIGURE 3. Mean rCBV_{GE} prior to standardization.

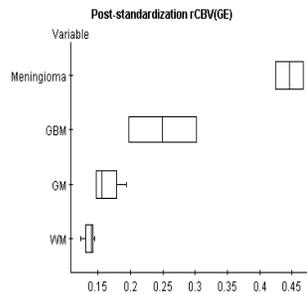


FIGURE 4. Mean rCBV_{GE} post standardization.

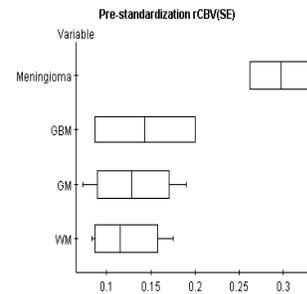


FIGURE 5. Mean rCBV_{SE} prior to standardization.

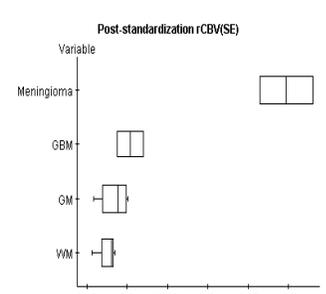


FIGURE 6. Mean rCBV_{SE} post standardization.

Acknowledgements

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References

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- [2] Nyul, L.G., *et al.*, New variants of a method of MRI scale standardization, *IEEE Tran Med Imaging*, 2005;19(2):143-150.