An Integrated Approach for Perfusion Lesion Segmentation using MR Perfusion for Acute Ischemic Stroke

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Introduction: One of the goals of MR imaging in acute ischemic stroke (AIS) is to identify tissue, which can be salvaged with reperfusion therapies. The salvageable tissue with MRI is approximated as regions of perfusion change without a corresponding diffusion abnormality and termed as the diffusion-perfusion mismatch [1]. Though the ease of its measurement has made mismatch (MM) an attractive candidate for therapeutic decisions in clinical settings, its routine use is hindered by the long time needed to mark the PWI lesion [2]. We have developed a mismatch calculator tool based on fast and reliable segmentation of DWI and PWI lesions. Previous work in this area has focused on using a supervised approach mismatch calculation [3] or automated workflow using a particular type of PWI quantitative map [4]. In this work, we correlate our automated mismatch segmentation across different PWI maps (MTT, Tmax, TTP) with retrospective manual analysis and demonstrate its use in AIS.

Methods and Materials: Patient database: Data for our study was acquired from 2000-2008, from patients treated with standard IV-tPA after a baseline, pretreatment MRI at multiple centers. The appropriate IRBs approved the studies. We segregated our database into two sets, one for which the ground-truth (GT): DWI and PWI lesion markings were available (Set #1, N = 25) and other for which no GT was done (Set #2, N = 59). Imaging: All MRI datasets were acquired on a 1.5 T GE Signa Genesis and GE Signa HDx clinical scanners using an 8-channel head or NV coil. (a) DWI imaging: Axial DWI trace images were acquired using a SE-EPI sequence, TE = 68–100 ms, TR = 4.5–7 s, FA = 90°, NEX = 2, 256x256 matrix, FOV = 240x240 mm², slice thickness = 3.5–7 mm, b = 0 s/mm² and 1000 s/mm². (b) PWI imaging: Axial T2FLAIR (TI = 1000–2000 ms, TE = 1000–2500 ms), 3D images were acquired using a GE-EPI sequence, TE = 29–40 ms, NEX = 2, 256x256 matrix, FOV = 240x240 mm², slice thickness = 3.5–7 mm, FA = 90°. (c) PWI Map generation: PWI data was co-registered to DWI data and facilitated cross talk through the two channels of information. (b) PWI segmentation: Perfusion lesion segmentation is based on contralateral difference analysis of MTT corrected; skull stripped quantitative maps and use feedback from the co-registered DWI and ADC maps. For each region, statistical maps (mean, median, percentiles) was obtained and used to determine the PWI lesion location and an optimal difference threshold for contralateral analysis. Mismatch calculation also took into account the discrete nature of Tmax maps. User input could allow a fixed difference threshold for analysis. To account for differences in symmetry of the brain, a neighborhood kernel was used to decide if the tissue was part of PWI lesion or not. Tissue was part of perfusion lesion if its neighborhood statistics were greater than the optimal threshold or if the tissue quantitative map had indeterminate values. (c) Statistical analysis: Statistical analysis, a clustering algorithm was used to collate the disjoint islands into single lesion and reject the noise islands. The settings of clustering algorithm were varied depending on the morphology and statistics of the islands. Following the clustering, the final PWI lesion was obtained by removing the vertices (using the registered ADC map) from the clustered mask, and generic hole filling. (c) Mismatch: Mismatch between the DWI and PWI lesion was calculated as follows: MM = PWI lesion - PWI lesion × DWI lesion. All the parameters for map generation and image analysis could be easily changed through a flexible xml-based configuration file. The entire pipeline (MSP, map generation, registration, segmentation and mismatch) was implemented using the functionality available in the Insight Toolkit (ITK) [7].

Results & Discussion: We observed a strong correlation (p = 0.69) between GT PWI lesion volume and MTT based automated PWI lesion segmentation volume (Table 1), consistent with those reported previously for using supervised lesion segmentation method [3]. Clustering of segmented islands integrated with feedback from island statistics provides reliable segmentation, which along with ventricle removal, enables to correctly identify the lesion as defined in clinical setting (Fig. 1). Overall, the processing time, from map generation to MM calculation varied from 30 s (25 phases, 64x64 matrix) to 150 s (100 phases, 128x128 matrix). The median Dice value of 0.74 indicated a good overlap between GT PWI lesion and MTT based automated PWI lesion segmentation. For MTT based mismatch calculation, p = 0.88, though lower compared to manually segmented inter-rater correlation (p = 0.96) [8], is consistent with those reported for automated mismatch techniques [4]. For MTT based PWI lesion segmentation and GT include: (a) Inability to mark the entire affected vascular territory accurately, suggesting the need to incorporate clinical knowledge in segmentation and (b) Failure of difference threshold calculation due to improper skull removal. The current algorithm considers each map independently and combining information from different maps can further improve the performance of the algorithm.

Conclusions: A fully automated PWI lesion segmentation and mismatch calculation algorithm is feasible, offering robust segmentation on different quantitative PWI maps and improves on current state-of-the-art algorithms.