Effect of ISODATA Dimensionality on Spatiotemporal Evolution of Ischemic Brain Injury in Acute Ischemic Stroke

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Introduction

Perfusion/diffusion MRI mismatch has offered enormous insights into heterogeneous ischemic tissue damage, and remains promising to guide acute stroke treatment [1]. In addition, iterative self-organizing data analysis technique algorithm (ISODATA), an unsupervised segmentation algorithm based on cluster analysis, has been increasingly used to classify distinguished tissue types for stroke assessment with multi-parametric data [2-4]. Our study aims to compare the performance of ISODATA in segmenting perfusion/diffusion mismatch using two different dimensionalities (1D vs. 2D) of signature vector in ISODATA parameter space.

Materials and Methods

Animal Stroke Model: Permanent middle cerebral artery occlusion (MCAO) was induced in adult male Wistar rats (240-320 g; *N* = 5) with STZ-induced type-1 diabetes, 8 weeks after hyperglycemia onset.

Multi-parametric MRI: MRI experiments were performed on a 4.7T Bruker scanner. Animals were anesthetized, with heart rate and blood pO_2 monitored online. In addition, body temperature was maintained within the normal physiological range. Multislice MRI (5 slices, slice thickness/gap = 1.8/0.2 mm, field of view = 25x25 mm^2, acquisition matrix = 64x64) was obtained with single-shot echo-planar imaging (EPI) (receiver bandwidth = 200 kHz). Specifically, isotropic diffusion-weighted imaging (DWI) was measured with two b-values of 250 and 1000 s/mm^2 (TR/TE = 3250/54 ms, NA = 16) at approximately 30, 40, 50, 60, 70, 80, 90, 120 and 150 min after MCAO, while perfusion imaging was acquired with a continuous arterial spin labeling (CASL) technique (TR/TE = 6500/14.8 ms, NA = 32, time of saturation = 3250 ms) at approximately 90, 120 and 150 min after MCAO. In addition, T_1 images were acquired using an inversion recovery sequence, with seven inversion delays from 250 ms to 3000 ms (TR/TE = 6500/14.8 ms, NA = 4).

ISODATA Analysis: ADC and T_1 maps were obtained by mono-exponential fitting of the signal intensities against b-value and inversion time, respectively. Cerebral blood flow (CBF) maps were obtained with $CBF = \lambda \cdot (I_{control} - I_{label})/(2 \cdot T_1)$ in which λ is brain/blood partition coefficient for water, 0.9 ml/g. Due to relatively low SNR of CASL signal, we averaged three CBF maps to characterize perfusion, assuming unchanged CBF after permanent MCAO. Pixels with ADC > 0.85 mm^2/s were attributed to cerebral spinal fluid (CSF) and excluded from analysis. ISODATA segmentation using Mahalanobis metric with spatial contiguity [4] was performed individually at each time point over the whole brain in five slices. Perfusion and diffusion lesion volumes were estimated using CBF and ADC as 1D signature vector in ISODATA parameter space, respectively. Perfusion/diffusion mismatch volume was then computed as the difference between CBF and ADC lesion volumes. For comparison, diffusion lesion and perfusion/diffusion mismatch volumes were estimated using CBF and ADC together as 2D signature vector in parameter space.

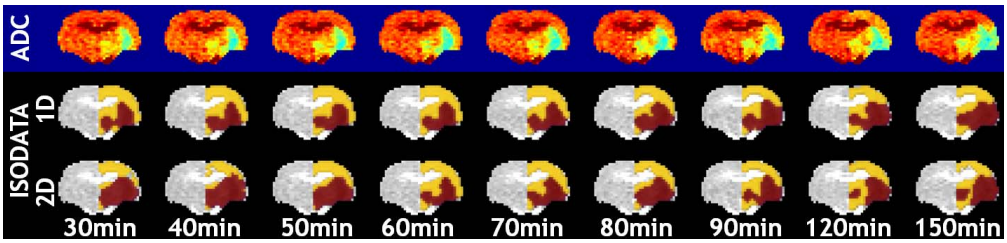

Fig. 1. ADC maps (top row), segmented ADC lesion (red) and CBF/ADC mismatch (yellow) using 1D (middle row) and 2D signature vector (bottom row) in ISODATA parameter space from 30 to 150 min after onset of stroke.

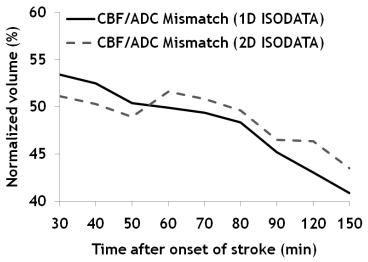

Fig. 2. Temporal evolution of CBF/ADC mismatch volumes (*N* = 5).

Results

Fig. 1 shows the ADC maps and ISODATA theme maps overlaid on the ADC maps of a representative animal during acute stroke. ISODATA segmentation using 1D signature vector in parameter space consistently yielded stable and superior delineation of ADC lesion than that using 2D signature vector. Fig. 2 shows the averaged CBF/ADC mismatch volume as a percentage of the total CBF lesion volume of the five animals. The temporal evolution of CBF/ADC mismatch was shown to be smooth and steady using 1D ISODATA signature vector. In contrast, the evolution of segmented clusters using 2D signature vector fluctuated over time, which was not consistent with the serial ADC images, which showed persistent evolution.

Discussions and Conclusion

In this study, we showed that ISODATA analysis using 1D signature vector in parameter space outperform that using 2D signature vector on segmenting diffusion lesion and perfusion/diffusion mismatch on multi-parametric MRI data (CBF and ADC). The superior performance of ISODATA segmentation using 1D signature vector is likely due to the absence of confounding effects from a number of noisy CBF pixels on the classification of ADC lesion pixels because CBF maps estimated using ASL technique are generally of lower SNR. It is worthwhile to note that the CBF and ADC values of different tissue clusters can be readily obtained based on the ISODATA theme maps, complementing subjective and tedious manual region-of-interest (ROI) analysis of the spatiotemporal evolution of ischemic brain injury. In conclusion, accurate delineation of CBF/ADC mismatch using ISODATA analysis with 1D signature vector could offer a useful means to identify ischemic penumbra (potentially salvageable tissue) which is of most interest for therapeutic intervention [5].

References [1] Wu O et al. Stroke 2001;32:933-942. [2] Jacobs MA et al. JMRI 2000;11:425-437. [3] Jacobs MA et al. Stroke 2001;32:943-949. [4] Shen Q et al. JCBFM 2004;24:887-897. [5] Alberts GW et al. Stroke 1999;30:2230-2237.