IDENTIFYING PERFUSION DEFICITS WITH SIMULTANEOUS MULTI SLICE ACCELERATION EPI TECHNIQUE: A NON-INVASIVE METHOD

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Target audience: Radiologists, neurologists, scientists and MRI researchers interested in brain perfusion imaging.

Introduction: Simultaneous Multi slice acceleration (SMS) EPI technique provides a new tool for measuring the DSC-MR and BOLD signal with higher spatial and/or temporal resolution[1]. Its advantages in DSC-MR could be found in patients with small perfusion deficits[2]. On the other hand, many researchers focus on harvesting the extra information provided by SMS EPI from BOLD signal. The estimation of neuronal activity based on BOLD signal changes has been widely used for neuroscience research, while other signal components have usually been removed during the pre-processing steps of fMRI data analysis. Based on previous evidence, the low-frequency fluctuation (0.1~0.01Hz) of BOLD signal, which is treated as the "background" signal, shows a similar temporal pattern across brain areas[3]. In this study, we applied an iterative algorithm to extract the global pattern by averaging the time series of each voxel after re-alignment based on its time-shift. In addition, by using SMS EPI sequence for rs-fMRI data acquisition, higher temporal resolution (TR = 1000 ms) and higher spatial resolution can be achieved to provide more accurate results.

Materials and methods: 8 patients with brain perfusion deficits participated in this study. Besides a general protocol for brain vascular disease patients, the MR exam includes one high-resolution resting-state fMRI (SMS rs-fMRI) session and one high-resolution DSC-MR (SMS DSC) session, both based on prototype SMS EPI-based sequences. All data were collected on a MAGNETOM Trio 3T MR scanner (Siemens AG, Erlangen, Germany). The parameters are as follows, SMS rs-fMRI: TR=1000 ms, TE=40 ms, flip angle=60°, 40 slices, slice thickness=3 mm, distance factor=0%, FOV=230×230 mm^2, matrix= 144×144, slice acceleration factor=4, measurements=360. The SMS DSC protocol has the same parameters as SMS rs-fMRI except for measurements=95. The data of SMS DSC-MR were analyzed using the Perfusion Evaluation tools on a syngo.via workstation (Siemens AG, Erlangen, Germany). The fMRI data were pre-processed with standard pipeline for resting-state data analysis (without regressing out the global signal). After pre-processing, a time-shift map could be obtained using the following steps: 1) Averaging the time series of the whole brain to create the first time series template. 2) For each voxel, the time course was shifted from -10TR to +10TR and was correlated with the template at each TR. Each voxel was then labeled as the number of TR that has the highest correlation coefficient value. 3) Realigning the time series of all voxels based on their time-shift value determined by step 2. 4) Averaging the re-aligned time series of the whole brain to create a new global template. 5) Repeating step 2 to 4 until the number of voxel, who had changed their time-shift value between two iterations, is less than 100. 6) Calculating a t-test map based on the general linear model using the global template. In order compare with low resolution, the SMS rs-fMRI data were down sampled to the same as standard EPI protocol (voxel size=3x3x3.5mm^3, gap=20%, TR=2000ms) and then obtained the time-shift map (TSM). The areas that show abnormal TTP in SMS DSC and long time delay in TSM were used for computing the degree of overlap among all subjects.

Results: Fig.1 and Fig.2 show the results of SMS DSC-MR of a patient with bilateral middle cerebral artery stenosis that translates into a long TTP in the whole left hemisphere and right frontal lobe; while the relCBF map shows low CBF in the left frontal and parietal lobe. In the time-shift map in Fig.1, we can observe that the left hemisphere and right frontal lobe have large time-shift that represents a late arrival of the blood flow in these areas. The group-averaged degree of overlap is 0.74 with the SMS protocol and 0.59 with the standard EPI sequence. The signal weight of the global template at each voxel present in Fig.2 demonstrates low signal weight in left frontal and parietal lobe. Another area with malacia in the right parietal lobe also shows low signal weight and matched with relCBF well.

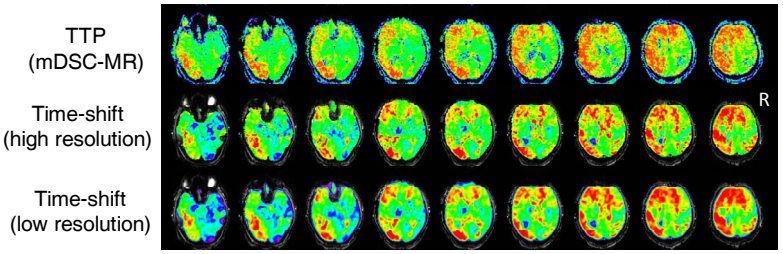

Figure 1. Results of TTP (obtained from DSC-MR) and time-shift-map (obtained from resting-state fMRI) with high resolution (TR=1000ms, voxel size=1.6 mm x 1.6 mm x 3 mm, gap=0 mm) and low resolution (TR=2000ms, voxel size=3mm x 3mm x 3.5 mm, gap=0.7 mm) dataset.

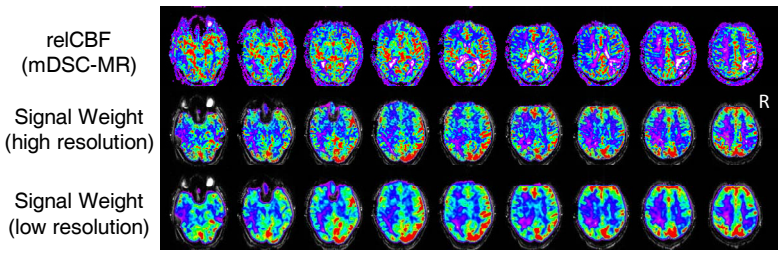

Figure 2. Results of relCBF (obtained from DSC-MR) and signal weight of the global template (t-statistic value, obtained from resting-state fMRI) with high resolution (TR=1000ms, voxel size=1.6 mm x 1.6 mm x 3 mm, gap=0) and low resolution (TR=2000ms, voxel size=3mm x 3mm x 3.5 mm, gap=0.7 mm) dataset.

Conclusions: The timing information of blood flow could be measured by exploiting the low-frequency fluctuation component in rs-fMRI data without the use of contrast agent. The results of TSM and signal weight are largely consistent with DSC-MR. With further optimization of the SMS technique, the performance of TSM could be improved in both spatial and/or temporal resolutions.

References: 1. Xu J, et al., Neuroimage. 2013. 2. Wang et al., ISMRM 2013. 3. Lv Y, et al., Annuals of Neurology 2013.