Partial volume correction of ^{1}H brain CSI by grid shifting (PANGS)

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Target audience: Scientists or clinicians engaged in research or clinical MRS and chemical shift imaging (CSI).

Purpose: Due to scan-time and signal-to-noise ratio considerations, the resolution of CSI[1] in ^{1}H human brain studies is typically limited to about 1 cm^3. The low resolution renders CSI susceptible to partial volume errors (PVE) especially in peripheral voxels where intense signals from the scalp can bleed into adjacent brain voxels, obscuring important metabolic information. To compensate, a spatial apodization filter (e.g., a cosine filter) is often applied to the *k*-space data prior to Fourier transformation (FT). However, spatial cosine filtering reduces the nominal spatial resolution by ~40%[2]. Here, a new method—PArtial volume correctioN by Grid Shifting (PANGS)—is proposed to minimize PVE and signal bleed, by changing the image spatial reconstruction coordinates in a specific region, without altering the *k*-space data or affecting spatial resolution. PANGS is applied to brain CSI to reduce lipid contamination of major metabolites (*N*-acetylaspartate, NAA; total Creatine, CR; and Choline, Cho) and metabolite maps.

Methods: In CSI, spatial voxels are resolved by discrete FT (DFT) of the *k*-space data. FT involves two reciprocal variables relating to the sampling grid in *k*-space, and the reconstruction grid in image space. Generally, both the *k*-space and image space grids are uniformly distributed resulting in a uniform DFT for reconstruction. In the uniform DFT, the reconstruction coordinate is placed in the geometric center of each voxel, with the implicit assumption that the point source in the geometric center can represent the whole voxel. For voxels filled with homogeneous tissue, this assumption holds and little PVE is expected. However, when voxels are only partially filled–such as in voxels in the scalp–their centers of mass differ significantly from their geometric centers, causing significant PVE. PANGS reduces PVE by shifting the reconstruction coordinates to match the mass centers instead of the geometric centers, by means of non-uniform FT reconstruction. The centers of mass are estimated in an iterative optimization process.

The method was implemented on consenting volunteers using a single-slice spin-echo ^{1}H CSI sequence in a 3T Philips MRI system (repetition time =2 s; echo-time =144 ms; resolution =1x1cm; and field of view = 20x18 cm, with outer volume suppression and "VAPOR[3]" water suppression pre-pulses). CSI was first co-registered with scout MRI to identify the scalp region. For conventional CSI, the reconstruction coordinates are at the geometric centers, as illustrated in Fig. 1. Inspection reveals that the tissue mass centers of most of the voxels in the scalp region do not coincide with their geometric centers. PANGS iteratively shifts the reconstruction coordinates for each scalp voxel and chooses the coordinates that minimize the lipid signal in non-scalp regions.

Results: After minimizing the lipid signals, the reconstruction coordinates of the scalp voxels no longer reside at the geometric centers while the non-scalp voxels are unmoved. Fig. 2 shows that PANGS spectra have significantly reduced baseline contamination and artifact (red arrows) compared to CSI, with or without cosine filtering. PANGS metabolite maps (Fig. 3b) are free from hyper-intense bleed artefacts (red arrows) seen in CSI (Figs. 3a,c). The rim artifact (Fig. 3c) is due to the reduced spatial resolution from cosine filtering, which is unaltered by the PANGS algorithm.

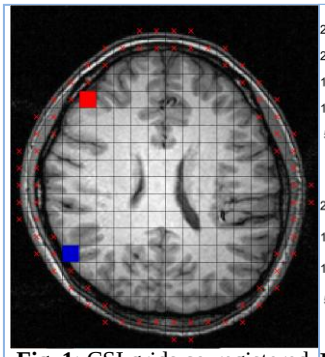

Fig. 1: CSI grids co-registered with scout MRI (x =geometric centers of scalp voxels.

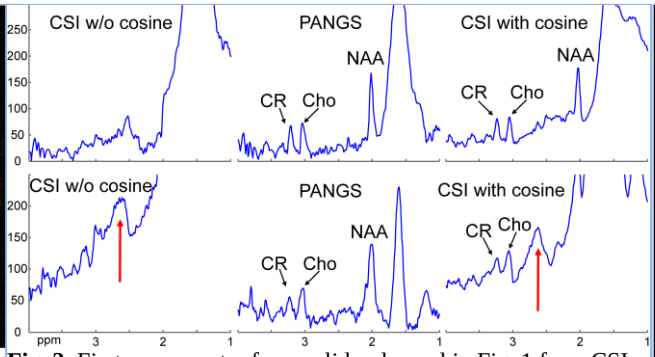

Fig. 2: First row: spectra from solid red voxel in Fig. 1 from CSI without cosine filter, PANGS and CSI with cosine filter (left to right). Second row: spectra from the blue box in Fig. 1.

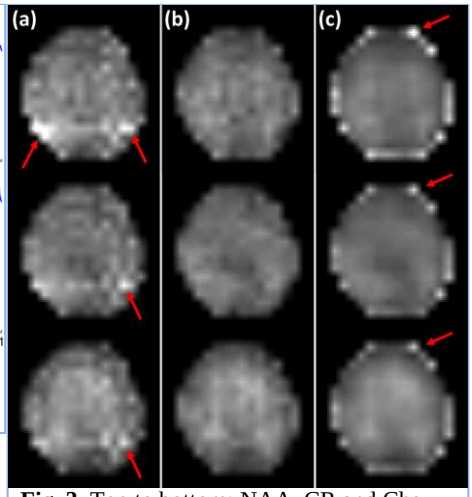

Fig. 3. Top to bottom: NAA, CR and Cho metabolite maps (a) CSI without cosine filter; (b) PANGS; and (c) CSI with cosine filter.

Conclusion: PANGS can significantly reduce partial volume bleed in CSI without compromising spatial resolution. The method can considerably improve the detection, quantification and display of metabolites, especially in cortical regions.

References: [1] Brown TR, et al. PNAS 1982. [2] De Graaf RA. Wiley 2007. [3] Tkac I, et al. MRM 1999.

Grant support: NIH R01 EB007829, R01 EB009731, R01 CA166171.