Classification Of Metabolic Parameters by Anatomically Superimposed Scans (COMPASS)

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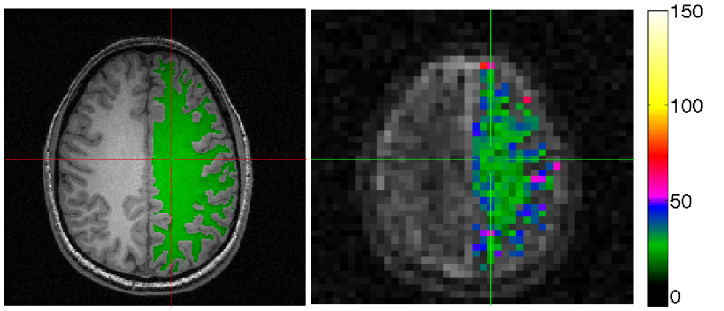
Purpose:
Quantitative sodium MR imaging and its corresponding tissue sodium concentration (TSC) bioscale continue to emerge as metabolic parameters of health and disease, reflecting sodium ion homeostasis and cell packing. Such insight may facilitate earlier disease detection and enable new treatment monitoring strategies for diseases that disrupt normal TSC. The low MR sensitivity of sodium requires that imaging be performed at a nominal resolution of several millimeters in order to obtain a SNR sufficient for computing the TSC bioscale. This low spatial resolution can complicate TSC interpretation, as there can be significant partial volume effects that complicate assignment of tissue types within voxels. We describe a new technique that uses co-registered, high-resolution proton images to classify values in TSC maps based on tissue type automatically determined by FreeSurfer (http://surfer.nmr.mgh.harvard.edu).

Methods:
Co-registered proton and sodium MR imaging was performed on a healthy adult volunteer using a 3T whole-body MR scanner (GE Healthcare) and custom-built proton and sodium RF coils that could be exchanged without moving the subject. IR-SPGR proton data (TR\TE\TI=10790\4.47\300 ms) were acquired at a nominal resolution of 1 x 1 x 1 mm^3 in 9.38 minutes. To correct for image distortion due to B0 inhomogeneity in sodium images, the B_0 field was mapped at a resolution of 2.5 x 2.5 x 5 mm^3 using two SPGR acquisitions with different echo times completed in less than 3 minutes. Co-registered, quantitative sodium data were acquired using flexTPI (TR\TE=160\0.260 ms, radial fraction=0.25,max gradient=4 mT/m) at a nominal resolution of 5 x 5 x 5 mm^3 in approximately 8 minutes [1]. The B_1 field was mapped using a second sodium scan with half the flip angle. All sodium and B_0 acquisitions were repeated on a three-compartment phantom with known concentrations (30 mM, 70 mM, 110 mM). The sodium data were reconstructed with B_0 and B_1 corrections and quantified into TSC as described elsewhere [1]. FreeSurfer was used to automatically segment and classify the tissue types of IR-SPGR voxels. These classifications were transferred to the TSC data by accounting for the resolution difference between the two datasets. The TSC distribution (mean ± standard deviation) for each tissue type was calculated using voxels that were 100% one tissue type, which avoided bias due to partial volume effects due to the limited resolution of the 23Na data.

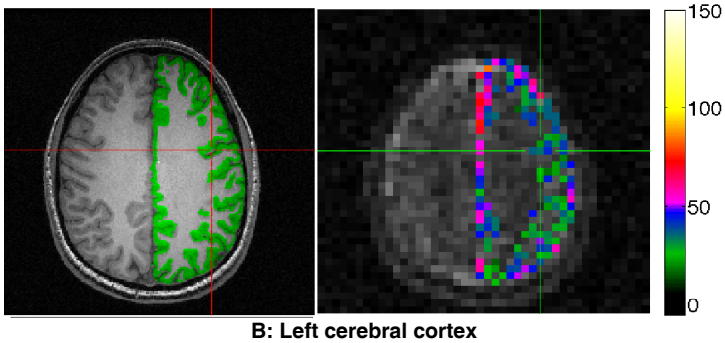
Results:
Figures 1 shows representative proton and TSC data with different tissue types highlighted. Good separation of gray and white matter was automatically achieved by FreeSurfer and could be translated to the TSC values. This allowed the TSC distribution to be calculated based on tissue type.

Conclusion:
Co-registered proton acquisitions can be used to classify metabolic parameters such as TSC based on tissue type, reducing ambiguity due to the inherent low resolution of bioscales.

References: [1] Lu A, Atkinson I, Claiborne T, Thulborn KR. Improved quantitative sodium imaging with a flexible twisted projection design and B0 inhomogeneity correction. Proceedings of ISMRM. #2472. 2009.



A: Left cerebral white matter



B: Left cerebral cortex

Figure 1: Representative proton (left) and TSC (right) voxels classified as left white matter (A) and left cerebral cortex (B. The colorized TSC values have units of millimoles sodium per voxel. All colorized TSC voxels contained at least 50% of the corresponding tissue type. The TSC distributions, which were computed from voxels that contained only of the corresponding tissue types, were A: left white cerebral white matter = 29.81 ± 8.41 millimoles 23Na/voxel, B: left cerebral cortex = 38.29 ± 9.42 millimoles 23Na/voxel.