

# T1/T2 Ratio Maps for the Production of fcMRI Seed Region Based on Gray Matter Myeloarchitecture

Daniel L Shefchik<sup>1</sup>, Andrew S Nencka<sup>1</sup>, Andrzej Jesmanowicz<sup>1</sup>, Edgar A DeYoe<sup>1</sup>, and James S Hyde<sup>1</sup>  
<sup>1</sup>Biophysics, Medical College of Wisconsin, Milwaukee, WI, United States

## **Introduction:**

It has been found that  $T_1$  and  $T_2$  weighted images have correlations to myelin concentrations in gray matter and that this concentration varies throughout different regions of the brain (1,2,3). These correlations have been found by comparing MR images to myelin stained sections of the same tissue. Bock has shown that histological measurements of myelin concentration can accurately segment several cortical areas (4).  $T_1$  values show a direct correlation to the concentration of myelin in a given voxel, whereas  $T_2$  values provide an inverse correlation to the myelin concentrations. Glasser used this to show that a ratio of  $T_1$  to  $T_2$  provides a myelin weighed map that enables the separation of functional areas (5). Such separation of functional regions is of use in functional connectivity MRI (fcMRI) for the determination of regions interest in correlation analysis.

In this work, we produce maps of  $T_1$  and  $T_2$  with an echo planar imaging (EPI) pulse sequence that includes the same readout used in an fcMRI acquisition (6). Thus, a ratio map is generated with identical distortions and partial volume fractions as are found in the fcMRI data. The ratio map is used for the determination of a region of interest which is in turn used as a seed in fcMRI analysis. Thus, magnetic resonance imaging based cytoarchitecture (mCytoarchitecture) analysis, rather than functional scout scans or independent component analysis, can be used to classify regions of interest for fcMRI.

## **Method:**

A healthy human subject was imaged after informed consent was obtained. An 8-channel head receiver was utilized on a 3.0 T General Electric Signa LX scanner. The GREASE pulse sequence (6) scanning parameters were TR = 2 s, ETE<sub>Echo1</sub> = 31 ms, ETE<sub>Echo2</sub> = 32 ms, ETE<sub>Echo3</sub> = 32 ms, ETE<sub>Echo4</sub> = 0 ms, ETE<sub>Echo5</sub> = 64 ms, SE<sub>1</sub> = 130 ms, SE<sub>2</sub> = 260 ms, flip angle 90 degrees, acquisition matrix 96 x 96, field of view 19.2 cm, slice thickness 2 mm, and 5 repetitions. Acceleration was achieved using GRAPPA with an acceleration factor of 2 and 4 ACS lines. Resting state data were acquired with the same EPI readout with a single echo pulse sequence with TE 31 ms and 135 repetitions.

Voxel-wise  $T_1$ ,  $T_2$  and  $T_2^*$  relaxivity maps were calculated via a non-linear least squares algorithm in MATLAB. A mask of gray matter was created by thresholding the  $T_1$  map. A ratio map of  $T_1$  to  $T_2$  was computed and masked to gray matter. A region of interest in the right motor cortex was defined using the ratio map. Resting state data was smoothed with a 4mm FWHM Gaussian filter, temporally filtered with a band-pass filter from 0.01 to 0.10 Hz, and correlated with the average filtered time series from the region of interest.

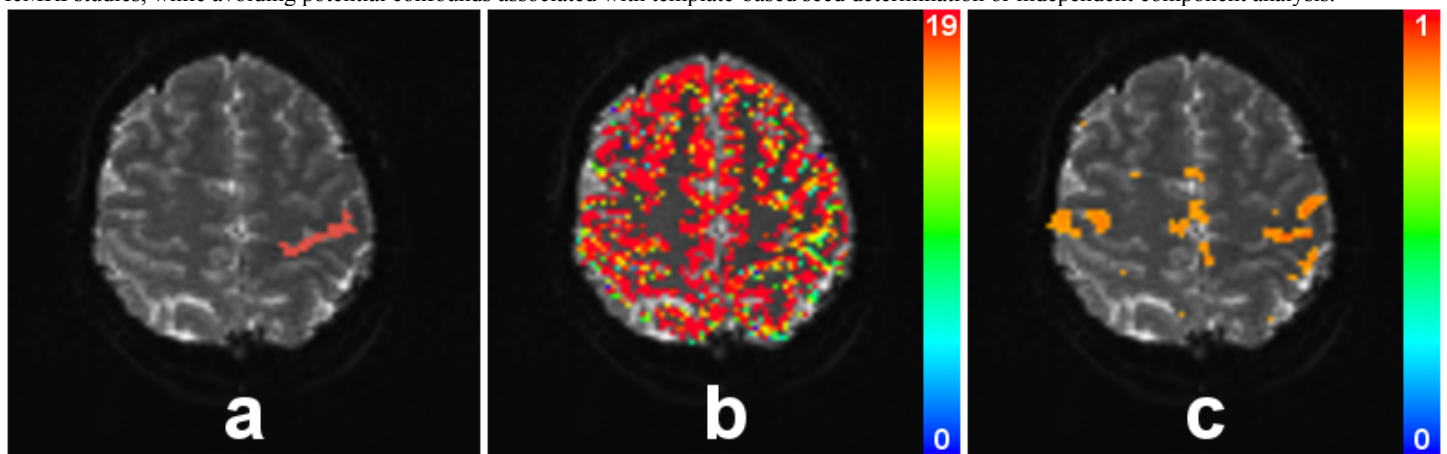
## **Results:**

Figure a illustrates the region of interest, extracted from the  $T_1$  to  $T_2$  ratio map which is shown in Fig. b. Figure c shows the resting state correlation with the average signal from the defined region of interest. The contralateral motor cortex, along with the supplementary motor area are found to be correlated.

## **Discussion:**

As fcMRI continues to grow in use, it is important to consider means of determining seed regions for seed-based analysis. Functional localizer scans in which a subject performs a known task are robust means of determining such regions, but detract from the fcMRI advantage of not requiring a task. Independent component analysis methods can robustly identify cortical networks, but matching disease states to known, healthy networks can be a challenge. Similarly, as disease may alter the morphology of the brain, seeds based upon a standard template space can yield imperfect results. To further emphasize the problem, analysis based upon imperfect region of interest definition will yield inaccurate results (7). The selection of regions of interest based upon mCytoarchitecture thus holds great promise as such regions of interest can be determined independently of resting state data in the matched patient space of fcMRI data without the need for task performance while still enabling hypothesis-driven analysis.

**Conclusion:** Preliminary data show that a  $T_1$  to  $T_2$  ratio map can be used to generate a seed region for fcMRI analysis. The acquisition of  $T_1$  and  $T_2$  maps in the same EPI space as fcMRI data allows a direct, one-to-one relationship between the ratio map and the functional data for a precise definition of the regions of interest. fcMRI analysis based upon seeds from mCytoarchitecture removes the need for functional scout scans from fcMRI studies, while avoiding potential confounds associated with template-based seed determination or independent component analysis.



**References:** 1. Fischl et al., 2004 Neuroimage 23:S69–S84. 2. Salat et al. 2009. Neuroimage 48:21–28. 3. Yoshiura et al. 2000 Radiology 214:217–221. 4. Bock et al. 2009. J Neurosci Methods 185:15–22. 5. Glasser, et al. J Neurosci, 2011. 31(32): p. 11597-616. 6. Shefchik et. al. Proc. ISMRM. 2011. 19:4510. 6. Cole, et al. Front Sys Neurosci, 2010. 7(8) doi 10.3389/fnsys.2010.00008