Validation of Tissue Characterization in Mixed Voxels Using MR Fingerprinting

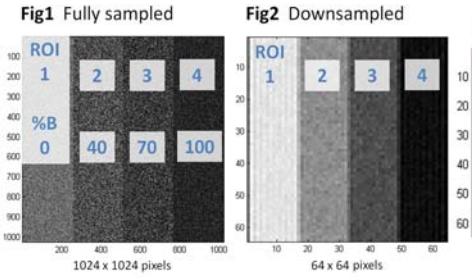
Anagha Vishwas Deshmane[1], Dan Ma[1], Yun Jiang[1], Elizabeth Fisher[2], Nicole Seiberlich[1], Vikas Gulani[1,3], and Mark Griswold[1,3]

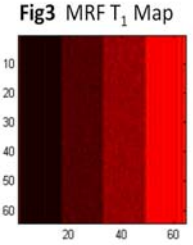
[1]*Biomedical Engineering, Case Western Reserve University, Cleveland, OH, United States,* [2]*Biomedical Engineering, Cleveland Clinic Lerner Research Institute, Cleveland, Ohio, United States,* [3]*Radiology, University Hospitals of Cleveland, Cleveland, OH, United States*

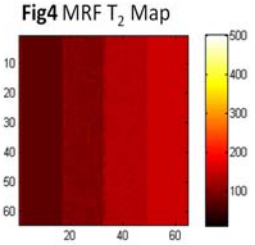
AUDIENCE: Scientists interested in quantitative imaging, parameter mapping, and estimating/resolving partial volume effects.

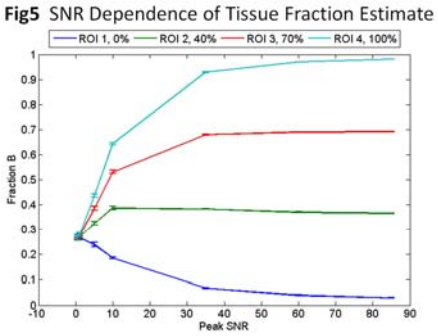
PURPOSE: A common problem in all types of imaging is the so-called partial volume effect that results from voxels with mixed content. Several investigators have previously used multi-exponential fitting to derive separate components of a voxel [1-3]. However, these methods are unstable and extremely sensitive to noise. A major cause of this problem is that the signal evolutions for the different components of the voxel are similar (i.e. exponential decays) and thus difficult to separate. A recently proposed framework, Magnetic Resonance Fingerprinting (MRF) [4,5], has the potential to open up numerous new possibilities for MR. Unlike the vast majority of MR acquisitions in which a fixed pulse sequence is repeated multiple times to encode spectral, spatial or decay information (or some combination of these quantities), MRF uses a pseudorandomized sequence which is simultaneously sensitive to multiple parameters during a single acquisition. This provides a rich signal that is no longer described by a simple exponential decay. Thus in MRF, signal evolutions can look very different and are more easily separable. *We seek to demonstrate that MRF can resolve multiple material components from single voxels made up of several tissue types, validate the derived tissue fractions in a realistic simulation model and demonstrate its use in vivo.*

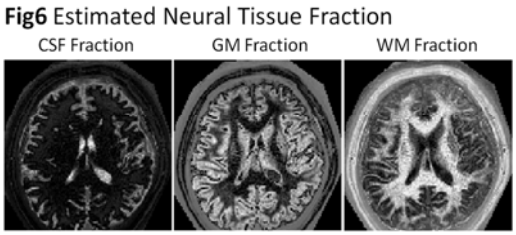
MATERIALS & METHODS: The fingerprint of each mixed voxel is modeled as a weighted sum of components of interest, D, whose signal evolutions are known *a priori* from the Bloch equations: $S_{voxel}=Dw$. The relative fraction attributed to the tissue type in each voxel is determined by solving for the weights using conventional pseudoinverse methods, namely $(D^HD)^{-1}D^HS_{voxel}=w$. To this end, we investigate simulated MRF signals in heterogeneous mixed tissue. Two tissue types are considered: Tissue A, with T_1=180ms and T_2=75ms, and Tissue B with T_1=1850ms and T_2=150ms. A QUEST MRF sequence [5] was modeled to collect signal evolutions at 225 time points. A 225 image series (resolution 1024x1024) was generated with a uniform random distribution of pixels assigned to carry the fingerprint of either tissue A or tissue B within four regions of interest (ROIs) such that the fraction of tissue B in each ROI was 0, 0.4, 0.7, and 1 (Fig 1). The randomized image was downsampled to a lower resolution by factor 16, simulating the acquisition of an image containing voxels with four possible mixtures of tissue A and tissue B (Fig 2). Simulations were repeated 10 times each with varying levels of added Gaussian random noise. The added noise was calculated based on desired peak SNR, which was defined as the maximum magnitude k-space signal value divided by the noise variance and downsampling factor. MRF was used to estimate the mean T_1 and T_2 values in each ROI. The fraction of signal B in each voxel was estimated using the weight equations described above. *In vivo* brain imaging was performed using a 3T Skyra system (Siemens Medical Solutions, Erlangen, Germany) on healthy volunteers after informed written consent, with a 16-shot MRF-QUEST sequence [5] (5mm slice thickness, 300mm field-of-view). Fraction maps, displaying each component tissue fraction on a scale from 0 to 1, were generated from the reconstructed images with three selected tissues of interest: cerebrospinal fluid (CSF, T_1=2300ms, T_2=200ms), grey matter (GM, T_1=1250ms, T_2=100ms), and white matter (WM, T_1=760, T_2=80ms).











RESULTS As expected, even with single-component MRF, the estimates of T_1 and T_2 in heterogeneous regions reflect the estimated properties of a mixed tissue rather than the pure components (Figs 3&4), and these estimates vary as a function of SNR. However, when using the two component estimates, the tissue fraction estimates are robust even at very low SNR levels (Fig 5). *In vivo* application of multicomponent analysis by MRF yields good separation of CSF, grey matter and white matter, including visualization of mixed tissues in the cortex and basal ganglia (Fig 6).

DISCUSSION We have presented and validated a method for both visualizing and quantifying the contributions of multiple tissue types towards MR signals from heterogeneous voxels. Although the method relies on a priori knowledge of the T_1 and T_2 of the tissue species of interest, literature values suffice to draw initial estimates, and can be refined through further iterations. This technique provides a framework with which to study relative changes in tissue composition over time.

ACKNOWLEDGEMENTS Support from NIH grant 1R01EB017219 and Siemens Healthcare.

REFERENCES [1] Deoni, et al. MRM 60, 1372–87 (2008). [2] Gareau, et al. JMRI 11, 586–95 (2000). [3] Qian, et al. MRM 64, 1426–31 (2010). [4]Ma D, et al. Nature 495, 187-92 (2013). [5] Jiang Y, et al. , Proc. ISMRM 21, 19 (2013).