Spatial Localization Accomplished by Sensitivity Heterogeneity

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Introduction: Compared to single voxel spectroscopy, phase encoded chemical shift imaging (CSI) has the advantage of obtaining spectra from a rectangular array of voxels in a single study. However, long acquisition times are required to achieve reasonable spatial resolutions due to the time consuming phase encoding steps, which limits clinical applications of CSI. Hu et. al. (1) developed a technique named SLIM (Spectral Localization by Imaging) to reconstruct compartmental spectra based on spectral data collected with a small number of phase encoding steps and compartmental boundary information obtained from anatomical images. Here we show that compartmental spatial localization can be accomplished using the heterogeneity of receiver coil sensitivity. This new technique is referred to as SPLASH (SPatial Localization Accomplished by Sensitivity Heterogeneity). When the number of receiver coils is limited, spatial localization using SPLASH may be further enhanced by adding a small number of phase encoding gradients.

Theory: Based on anatomical images and other *a priori* knowledge, the subject is divided into N compartments such that each compartment can be considered to have a uniform spectrum. The spectrum or FID with P data points detected by each coil m ($m = 1, 2, \ldots, M$) is contributed from the N compartments according to

$$\boldsymbol{D} = \mathbf{S}\boldsymbol{C} \qquad [1]$$

where $\boldsymbol{D}$, $\boldsymbol{C}$, and $\boldsymbol{S}$ are matrices for detected data ($M \times P$), compartmental spectra or FIDs ($N \times P$), and compartmentalized spatial encoding ($M \times N$), respectively. The elements of matrix $\boldsymbol{S}$ are given by

$$S_{mn} = \int_{\text{compartment n}} s_m(\boldsymbol{r})\, d^3\boldsymbol{r} \qquad [2]$$

where $s_m(\boldsymbol{r})$ represents the sensitivity at location $\boldsymbol{r}$ for the mth coil. Eq.[1] can be solved using weighted least square according to

$$\boldsymbol{C} = (\boldsymbol{S}^\dagger \boldsymbol{\Psi}^{-1} \boldsymbol{S})^{-1} \boldsymbol{S}^\dagger \boldsymbol{\Psi}^{-1} \boldsymbol{D} \qquad [3]$$

where $\boldsymbol{\Psi}$ is the noise covariance matrix of the receiver coils (2) and '$\dagger$' denotes conjugate transpose. If K phase encoding gradients are used, the dimension M in Eq. [1] is replaced by $M \times K$, $s_m(\boldsymbol{r})$ in Eq.[2] is multiplied by a phasor denoted by $\exp(-i2\pi \boldsymbol{k}\cdot\boldsymbol{r})$, and $\boldsymbol{\Psi}$ in Eq.[3] is replaced by $\boldsymbol{I} \otimes \boldsymbol{\Psi}$ where $\boldsymbol{I}$ is a $K \times K$ identity matrix and '$\otimes$' denotes tensor product.

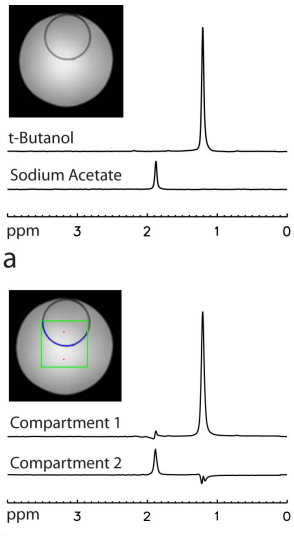

Fig. 1. *Spectra of a two compartment phantom generated by (a) single voxel spectroscopy and (b) SPLASH without phase encoding gradients.*

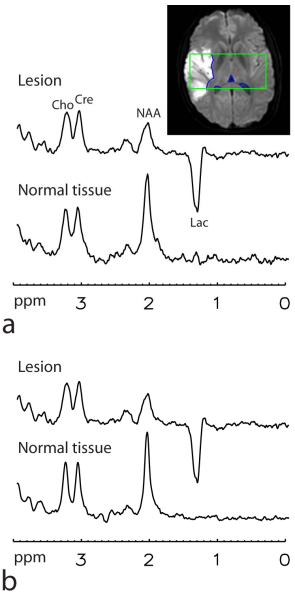

Fig. 2. *Spectra from a stroke patient. (a) SPLASH without phase encoding. Total data acquisition time was 4 s. (b) SPLASH with 11x5 phase encoding steps. Total data acquisition time was 3.7 min.*

Method and Results: Experiments were performed on a Philips 3T scanner equipped with an eight-channel phased array head coil. A two compartment phantom consisting of 25 mM t-Butanol in the inner sphere and 25 mM sodium acetate in the outer bottle was made in our lab. A gradient echo sequence (TR = 800 ms, TE = 10 ms, FOV = 240 x 240 mm^2, slice thickness = 4 mm, number of slices = 35) was used to acquire axial images of the phantom (Fig. 1a). A point resolved spectroscopy (PRESS) sequence with TR = 2 s, TE = 60 ms, volumes of interest (VOI) = 2 x 2 x 2 mm^3 was used to acquire two spectra (Fig1. 1a), one localized in the inner sphere and the other localized in the outer bottle. Next, the same phantom was scanned using a single-voxel PRESS sequence without any phase encoding gradients for SPLASH reconstruction (TR = 2s, TE = 60 ms, VOI = 72 x 72 x 12 mm^3, number of signal averages (NSA) = 72). Software was developed using IDL and C++ programming languages to allow the user to manually draw curves to define compartment boundaries on top of an anatomical image. After the gradient echo image and the acquired PRESS data were loaded into the software, the PRESS VOI was displayed as a green box (Fig. 1b). A blue curve was drawn by the user to divide the VOI into two compartments. The user also drew two red dots which were used by the software as seeds for region growing to automatically generate the two compartments defined by the blue curves and the green box in the three image slices covered by the VOI. Subsequently, the spectra for the two compartments were reconstructed using Eqs. [2] and [3]. The results are shown in Fig. 1b. The spectra for the two compartments are correctly reconstructed. Cross contamination between the two spectra is low as compared to spectral leakage in conventional Fourier transform CSI spectra. An in vivo experiment was also performed on a stroke patient with right middle cerebral artery stroke three days after symptom onset. The patient was consented in accordance with procedures approved by our institutional review board. Diffusion weighted imaging (DWI) images with slice thickness of 3.5 mm were used to prescribe the PRESS VOI and thereafter to define two compartments for SPLASH reconstruction (see Fig. 2a). The first compartment contains the lesion area and the second compartment contains normal brain tissue. The ventricles are surrounded by manually drawn blue curves and thus prevented from being grown into either of the two compartments because cerebrospinal fluid does not contribute to the metabolite signals. The PRESS sequence used TR = 2 s, TE = 144 ms, NSA = 2, VOI = 110 x 50 x 14 mm^3 which covered four DWI slices. The boundaries were drawn in all four covered DWI slices. The spectra shown in Fig. 2a were computed using only the data with $\mathbf{k} = 0$, for which the total data acquisition time was 4 s. The spectra shown in Fig. 2b were reconstructed using data collected with $\mathbf{k} = 11$ x 5 phase encoding steps, which had a data acquisition time of 3.7 min. We can see that the spectra in Figs. 2a and 2b agrees very well except differences in signal-to-noise ratio (SNR). The inverted J-coupled lactate peak (TE = 1/J) is clearly present in lesion but absent in the normal tissue in both Figs. 2a and 2b.

Discussion and Conclusions: This work demonstrates the feasibility of multi-compartmental spectroscopy using SPLASH with or without phase encoding. Unlike parallel imaging methods that use coil sensitivity profiles to unwrap overlapped images, SPLASH is based on the integrated difference in sensitivity between different areas of interest. Because phased array coils are routinely used in clinical scans, it would be more convenient and time efficient to perform spectroscopy on a patient using the same phased array coil as for other imaging sequences. SPLASH offers an alternative to Fourier transform based SENSE-CSI for performing spectroscopy using phased array coils. SPLASH allows the user to manually prescribe compartments following natural anatomical or physiological boundaries to reduce partial volume artifacts associated with conventional CSI and SENSE-CSI. For spectroscopic applications that have sufficient SNR and reasonably large VOI compared to the coil size, SPLASH can generate multi-compartmental spectra in a single shot. With the advent of phased array coils with a large number of small coil elements, SPLASH has the potential to be useful in many spectroscopic applications.

References: 1. Hu X, *et. al.*, MRM 8:3146-322 (1988) 2. Pruessmann K, *et. al.*, MRM 42: 952-62 (1999)