Sodium boost SPRITE imaging of the human brain

S. Romanzetti[1], E. D. Pracht[1], and N. J. Shah[1,2]
[1]Institute of Neuroscience and Medicine 4, Medical Imaging Physics, Forschungszentrum Juelich, Juelich, Germany, [2]Faculty of Medicine, Department of Neurology, RWTH Aachen, Aachen, Germany

Introduction

MRI imaging of nuclei such as ^{23}Na, ^{31}P, and ^{17}O is becoming increasingly popular for their fundamental significance in the physiology of the cell. Unfortunately, the concentration of these nuclei in tissues is very low and their relaxation times are very short. Dedicated sequences and a high degree of optimisation are therefore fundamental. Among various strategies, the SPRITE sequence has recently shown its ability to acquire in vivo images of the sodium in the human brain at ultrashort encoding times (1). In this work, a novel way to improve the sensitivity of the standard multiple FID point SPRITE sequence by a factor 2 is presented. This is of particular importance for all applications where there is SNR starvation.

Theory

In a SPRITE measurement with acquisition of multiple FID points, each individual point can be used to obtain images of decreasing FOV(2). If relaxation during readout of multiple point can be neglected, the SNR of an early image, r, is related to the SNR of the last one, f, as:

$$SNR_r \propto \cdot \Delta x_r \Delta y_r \Delta z_r \sqrt{NEX} = \left(\frac{tp_f}{tp_r}\right)^3 \Delta x_f \Delta y_f \Delta z_f \sqrt{NEX} = \Delta x_f \Delta y_f \Delta z_f \sqrt{\left(\frac{tp_f}{tp_r}\right)^6 NEX} = SNR_f \sqrt{NEX} \sqrt{pNEX}$$

Images can be resampled to a common FOV using the chirp-z transform(3). This operation result is a series of images of increasing resolution and SNR proportional to the pseudo-number of averages pNEX. A large number of multiple FID points can therefore be used to increase the sensitivity. However, the simple average of these images would result in a total loss of resolution. With a carefully selection of a normalization function a given target resolution can be achieved.

Methods

A sectorial SPRITE sequence was programmed on a Siemens 4T whole-body scanner (Erlangen, Germany). The RF probe was a dual birdcage coil (Rapid Biospin, Würzburg, Germany) tuned at the resonant frequencies of ^{1}H and ^{23}Na. Figure 1 shows the timing diagram of the sequence. The predefined Cartesian trajectory started at the origin of k-space and moved out covering a small sector (4). The trajectory was then repeated with 864 different orientations to sample a spherical k-space volume. A delay of 10 ms between trajectories was allowed to obtain a density weighted contrast. To boost signal intensity, at each k-space location N =100 FID points were acquired with a receiver bandwidth of 100kHz (δ=10 us) starting at tp=100us. A dynamic reduction of repetition time was used to shorten the total acquisition time (5). The TR in the k-space centre was 10 ms and 1.4 ms at the k-space edges. Other parameters were: FOV=200×200×200mm, matrix size = 48×48×48, flip=6º. Fig. 2 shows the normalisation function and cutoff point used to achieve a final target resolution of ~5.94 mm^3 isotropic. Fig. 3 shows the point spread function obtained using the normalisation function in Fig.2. Fig.3 shows the distribution of FWHM for the whole range of cutoff points and the respective integral of the PSF function. A resolution phantom containing mineral oil was used to test the method. To simulate a low SNR measurement, 0.6% white noise was added to the raw data. Sodium *in vivo* imaging was performed on an informed healthy volunteer. The acquisition was repeated 10 times. Total acquisition time was 30 minutes.

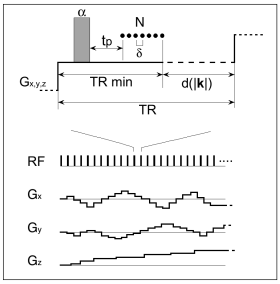

Figure 1. Sectoral SPRITE time diagram

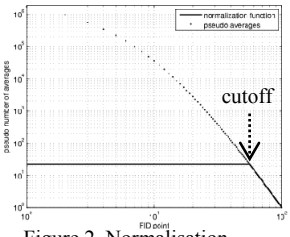

Figure 2. Normalisation function for a target resolution of ~ 5.97mm^3

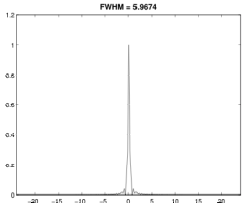

Figure 3. PSF function

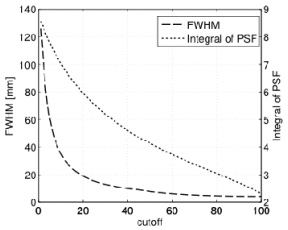

Figure 4. FWHM and PSF integral distributions

Results

Figure 5 shows the results of the measurements performed on the resolution phantom filled with mineral oil. Image (A) was obtained using a single point, image (SNR = 2), (B) with the full range of multiple FID points summed without normalisation, (C) with a multiple FID SPRITE method (SNR = 27, and (D) with the novel boost SPRITE method (SNR = 51). An increase of a factor ~25 in SNR is visible between images A) and D). A factor 2 increase in SNR is shown between images C) and D). Profiles along the dotted line (only shown in A) reveal a major resolution increase between B) and D) and an improvement between C) and D). Fig. 6 shows the results of *in vivo* measurements: A) single point image (which is basically only noise), B) sum of the full range of images without normalisation, C) standard multiple FID SPRITE method, D) boost SPRITE image with a a target resolution of ~6mm^3.

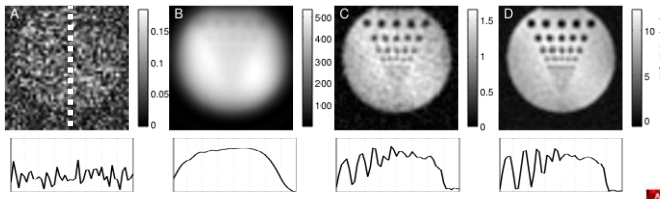

Figure 5. Resolution phantom filled with mineral oil.A) SPI image, B) Full range sum, C) standard SPRITE, D) boost SPRITE.

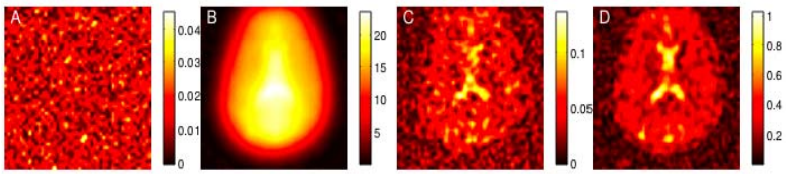

Figure 6.*In vivo* measurements. A) SPI image, B) Full range sum, C) standard SPRITE with multiple FID point, D) Boost SPRITE method. In D) an increase sensitivity and in resolution are achieved.

Discussion and Conclusion

This method increases the sensitivity by a factor of 2 as compared to a standard SPRITE sequence with multiple FID point acquisition and a factor 25 compared to a standard Single Point Imaging method by trading off a limited amount of resolution. The application of this method could prove to be very important for imaging of nuclei with very low concentration and with very short relaxation times.

References

(1) Romanzetti et al. Proc. ISMRM (2005); (2) Halse et al. JMR 169 (2004),102 ; (3)Kaffanke et al. JMR 178 (2006),121; (4) Khrapitchev et al. JMR 178(2006),288; Shah et al., JMR199 (2009),136.