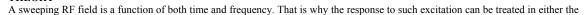
Continuous SWIFT

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INTRODUCTION

The SWIFT method (SWeep Imaging with Fourier Transform) [1] has significant benefits for studying objects with ultra fast spin-spin relaxation rates and has already found unique applications ([2,3]). The regular (gapped) SWIFT sequence uses swept radiofrequency (RF) excitation and virtually simultaneous signal acquisition in a time-shared mode. Due to the finite time required to switch between transmit/receive modes (T/R), very high excitation bandwidths can be difficult to achieve with gapped SWIFT. To overcome this, here we describe a first attempt to implement SWIFT in a continuous mode (cSWIFT) for imaging and spectroscopy. **THEORY**



time or frequency domain, which in the case of a constant amplitude of RF, can be represented by a chirp function: $c^- = exp(-i\pi bt^2) = exp(-j\omega^2/4\pi b)$, where *b*- is sweep rate in sec⁻² and subscript "-" denotes the sign of sweep direction. In continuous mode the acquired raw signal (*S*) contains the convolution (linear approximation) of a free induction decay (FID) (h(t)) with the chirp, which is mixed with "leakage" from the transmitted signal: $S = (h(t) \oplus c^+)c^- + Ae^{i\phi}$, where multiplication

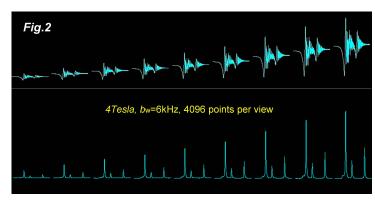
by c^- describes a phase sensitive detection with the receiver frequency changing synchronously relative to the excitation frequency (the frequency-modulated (FM) frame [4]), and where A and φ are the amplitude and phase of the "leakage". In the FM frame, the transmitter signal is a smooth function (for an ideal transmitter), which can be subtracted by using a regular baseline correction method. Afterwards, the spectrum of the spins $(H(\omega))$ can be extracted by existing schemes of de-convolution: (a) considering a signal in the time domain as in the SWIFT method: $H(\omega) = F\{h(t) \oplus c^+\} * F\{c^+\}$, or (b) as a frequency domain signal, used in Rapid Scan method

[5,6]:
$$H(\omega) = F\{F^-\{(h(t) \oplus c^+)c^-\}c^-\}$$
, where the symbol $F\{\ \}$ represents

Fourier transformation. In practice however, the baseline correction is incapable of fully removing the transmitter leakage signal. One can show that the residual transmitter signal will be transformed differently in these two specific deconvolution procedures, which could be used as a test of the quality of baseline correction and a combination of the results might be used as additional tool to clean up the resulting spectrum.

To reduce the dynamic range of the acquired signal and to decrease the contribution from the transmitter's systematic and thermal noise in the resulting spectra, the amplitude A must be minimized. There are many different schemes to reach acceptable T/R insulation using mostly a combination of hybrids and circulators. Additionally, the transmitter signal measured with an independent receiver channel can be used for digital compensation of transmitter instability.

The amplitude of the RF field, B_1 , with chirp excitation, in the case when acquisition bandwidth is equal to excitation bandwidth (b_{ω}) needs to satisfy the



relation: $B_1 \propto \theta b_m / \gamma Q \sqrt{N}$, where γ is the gyromagnetic ratio, θ is the flip angle, Q is the coil's quality factor, and N is the number of samples [7].

METHOD

Spectroscopic and imaging data were acquired using 9.4T (animal-bore) and 4T (clinical-bore) MRI scanners equipped with Varian (Agilent) DirectDrive consoles. The spectra and images were acquired with the basic connection scheme presented in Fig.1, which uses a hybrid and quadrature coil. Transmitter coupling through the hybrid as observed by the console was minimized through adjustment of individual coil tune and match conditions.

RESULTS and CONCLUSIONS

Fig.2 presents the array of raw data (top) and de-convolved spectra (bottom) of an ethanol-water mixture (in 15 cm diameter glass sphere) with increasing flip angles (from left to right) in continuous mode. As expected the baseline of raw data increases with increasing flip angle and is approximately equal to amplitudes of the FIDs.

With appropriate tune/matching the connection shown in Fig.1 gives about 20db T/R insulation. The first cSWIFT image of human total knee arthroplasty sample is presented in Fig.3 (left) and compared with a gapped SWIFT image (right) with approximately similar flip angles. It is worth noting that the relative intensity of cartilage is higher in continuous mode. The different contrast in these images might relate to additional saturation of broad collagen signal [8] from the sidebands created in the gapped mode, but a definite conclusion requires more detailed study.

Even though the signal-to-noise ratio of the presented spectra and images in continuous mode are notably lower than in gapped mode, these results can be considered as a successful "proof of principle" of the continuous SWIFT technique. Improvement of this technique is expected with stabilization/filtering of the transmitter output and development of dedicated schemes for additional T/R isolation.

Fig.3

cSWIFT

SWIFT

9.4Tesla, bw=71kHz, 128000 views, 256 points per view, total acquisition time =7.7 minutes

There are two main factors which distinguish SWIFT from pulsed NMR techniques and therefore allow using SWIFT in continuous mode. The first is that SWIFT with chirp excitation pulse uses the lowest possible amplitude of RF field for given flip angle and bandwidth, because the power is evenly distributed in time. Second, because the spin signal (convolved with the excitation pulse) is also distributed in time, this allows the lowest possible dynamic range, which allows a regular ADC to resolve the spin signal on top of the relatively high "leakage" transmitter signal. In conclusion, due to the absence of a "dead time" cSWIFT extends the application of MR imaging and spectroscopy to studying ultra fast relaxing spins or spin systems with ultra broad chemical shift distribution beyond that of gapped SWIFT or UTE type sequences.

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REFERENCES

[1] Idiyatullin (JMR2006); [2] Zhou (MRM2010); [3] Idiyatullin (JOE2010*in press*); [4] Garwood (JMR 2001); [5] Dadok (JMR1974); [6] Gupta (JMR1974); [7] Idiyatullin (JMR2008); [8] Ling (NMRBiomed2008).

