TIME SAMPLES SELECTION IN SPIRAL ACQUISITION FOR SPARSE MAGNETIC RESONANCE SPECTROSCOPIC IMAGING

Jabrane Karkouri[1,2] *- Fabien Millioz*[1] *- Magalie Viallon*[1] *- Rémy Prost*[1] *- Hélène Ratiney*[1]

[1]Université de Lyon, INSA Lyon, Université Claude Bernard Lyon 1, UJM-Saint Etienne
CNRS, Inserm, CREATIS UMR 5220, U1206, F69621 LYON, France
[2] Siemens Healthineers, 93210 Saint-Denis, France

ABSTRACT

Magnetic resonance spectroscopic imaging (MRSI) has multiple interests in clinical practice, and especially for brain disease diagnosis. However, it faces quite long acquisition time in practice which limits their use in a clinical environment. Fast MRI acquisitions can help to reduce this acquisition time and intensify their clinical use. In this work, a new fast Magnetic Resonance Spectroscopic image acquisition method is introduced and evaluated based on a k-t space spiral sampling. The time-domain subsampling, below the Shannon-Nyquist rate, is allowed on the hypothesis of a sparse spectrum with an a priori known support. Then the nonzero components of the spectrum of each voxel are recovered using an overdetermined least square problem. When data are noise-free the recovered spectrum is exact. In the real-world noisy scenario the error in the recovered spectrum highly depends on the acquired samples. We reduce this error to an acceptable level by selecting irregularly the samples using the Sequential Backward Selection algorithm. A realistic simulated irregular spiral acquisition proves the feasibility of the proposed approach.

Index Terms— Magnetic resonance spectroscopic imaging, spiral spectroscopic imaging, k-space, compressed sensing, under-sampling

1. INTRODUCTION

Nuclear Magnetic Resonance Spectroscopy is an *in vivo* technique that can provide information about metabolite concentration in the human body. Magnetic Resonance Spectroscopic Imaging (MRSI) [1] is a non-invasive imaging technique that gives spatial distribution of metabolite signals in a specific region, these metabolites signals themselves being characterized by their resonance frequencies. MRSI has indeed various clinical applications in different organs such as the brain, the liver, breast and muscles. Its drawbacks are due to its long acquisition time, low spatial resolution, difficulty to reach an acceptable Signal to Noise Ratio (SNR) and due to its sensitivity to spatial magnetic field inhomogeneity. Nowadays, fast MRSI techniques based on simultaneous spatial (k-space) and spectral (t-space) encoding already exist [1]. These particular sampling techniques can reduce the total acquisition time compared to the conventional phase-phase encoding. Compressed sensing (CS) is another way to reduce the number of samples acquired below the Shannon-Nyquist criterion. The sparsity of the signal is mandatory for the signal reconstruction using CS. In the case of Magnetic Resonance Imaging (MRI), applying CS can then significantly reduce the acquisition time. Some work has been done in order to apply CS in MRI[2] and MRSI[3].

In [4] a fast multidimensional MRS is proposed for sparse spectra. It relies on prior knowledge of the spectrum support to recover a multidimensionnal spectrum using undersampled NMR acquisition. We propose to extend this method to magnetic resonance spectroscopic imaging. Due to the separability of the 3D discrete Fourier transform- two dimension in the k-domain (kx, ky, i.e the spatial frequency domain), one dimension in the time domain, which is called the Free Induction Decay (FID) signal, the problem is reduced to independent one dimensional problems for each (kx, ky). In this work, we chose a spiral encoding scheme because it uses oscillating, continuous gradient which is an efficient way to encode the k-t space.

The challenge is that all (kx, ky) points should be acquired at the same time t. Reaching both the desirable spatial and temporal resolution within one excitation is usually impractical. As the result, multiple excitations are usually invoked which increases the acquisition time. In our method, the nonzero components of the spectrum will be recovered using an overdetermined least square problem. The result is exact when data are noise-free. In the noisy scenario the error in the recovered spectrum highly depends on the acquired samples. We both reduce this error to an acceptable level and approach the simultaneous time acquisition of the (kx,ky) FID by selecting irregularly the samples using the Sequential Backward Selection (SBS)algorithm [5] in spiral-based k-space trajectories acquisitions [6]. We will show that, by this way, the total number of excitations can be reduced and thus total scan time. Note that our proposal differs from [7] in the sense that, here, it is the a priori known spectral support which is used

to reduce the scan time and not the spatial support. Spatial and spectral information are acquired simultaneously in spiral acquisition while in [7] conventional phase-phase k-space encoding was used.
The paper is organized as follows: section 2 presents the proposed approach. Section 3 shows some results and a discussion follows. Finally a conclusion is given.

2. METHOD

2.1. Estimation of the spectrum support

In the particular case of *in vivo* MR spectroscopy, the spectrum support S is known. The chemical shifts (i.e resonating frequencies) of the different chemical compounds and metabolites are a priori known.In addition, measured B0 field inhomogeneity map to account for the peak linewidth (i.e the damping factor in the time domain) could be used to complete the support estimation. Note that the linewidth reduces the spectrum sparsity. An experimental approch could be also used to estimate the spectrum support. The support could be deduced from the spectrum acquired on the full volume of interest.

2.2. Spectrum reconstruction by Least-Square

Problem statement:

- given the sampled time domain FID signal y related to a kx-ky point in the discrete k space
- find its non-zero spectrum samples in its a priori known support S.

The FID signal y is a vector of size n related to its spectrum, also of size n, by:

$$y = Fx \tag{1}$$

Where F is the unitary discrete Fourier matrix of size $n \times n$. We denote x_s the restriction of x to its m non-zeros values (its support S). Then, we can restrict the Fourier matrix F to F_s of size $n \times m$, then (1) can be rewritten:

$$y = F_s x_s \tag{2}$$

The columns of F_s correspond to the non-zero samples of the spectrum. Acquiring $p > m$ with $p < n$ FID samples results in an over-determined equation system:

$$y_p = Ax_s \tag{3}$$

Where A is a $p \times m$ matrix obtain by selecting from F_s the rows which correspond to the p-acquired elements from y. Then we solve this system by Least-Square (LS):

$$x_s = (A^*A)^{-1}A^*y_p \tag{4}$$

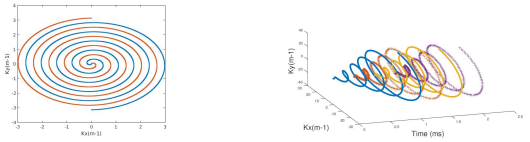
Where * denotes conjugate and transpose. The matrix is full-rank [[8], from Lemma 1.3 (proof for n prime)] and the recovery of x_s is exact. It has been recognized in [[9]-Theorem 1] that *"in the absence of any other information, one could easily argue that no method would exhibit a fundamentally better performance"*. When data are noisy (hypothesis of a zero mean noise identically distributed with variance σ^2) it results an error with mean square error given by [4]:

$$E||x - x_s||^2 = \sigma^2 tr[(A^*A)^{-1}] \tag{5}$$

Clearly as F is unitary the lower error is obtained for $p = n = m$, subsampling the FID signal results in noise magnification. The trace in (5) increases monotically as rows are removed.[5] proposes to minimize this trace by selecting the sample in y (the FID signal) by an algorithm known as *Sequential Backward Selection* (SBS), it results an irregular sampling. The SBS algorithm sequentially eliminates one row at a time from the m candidates until p rows remain. At each step the resulting inverse matrix is computed at a low cost from the Sherman-Morrison formula. Note that the indexes of the samples to be retained are computed once and for all before the acquisition. Finally, using the SBS algorithm, we under-sample the time dimension and reconstruct the spectrum.

2.3. k-t space spiral sampling

After the radio-frequency pulse excitation, possibly localizing the Volume of Interest (VOI), the spiral encoding sequence for MRSI uses successive time varying gradients during the acquisition time period. These gradient waveforms trace successive spirals in the kx-ky space starting usually from its center. One time sample is acquired at each spiral (kx-ky space). A trade-off needs to be found between the duration of the spiral, the spatial resolution and the resulting spectral bandwidth.



(a) (b)

Fig. 1. a) spatial interleaving ($N_{spat} = 2$), and b) temporal interleaving ($N_{time} = 4$)

In order to reduce the duration time of a spiral, a method consists in sampling the k-space with multiple acquisitions and interleaved spirals instead of one (Figure 1a). If one spiral duration is larger than the required temporal resolution to reconstruct the spectroscopic bandwidth, temporal interleaves are necessary to acquire each time sample. This technique consists in applying at each pulse Repetition Time (TR) (each excitation) successive spirals for the acquisition with a delay proportional to the temporal resolution (Figure 1b)

The following additional notation will be used:

- N_{spat} the number of spatial interleavings
- Δt_{cs} the time sample interval required for the wanted temporal resolution according to Nyquist sampling.

- T_s the duration of a spiral
- T_{sig} is the acquisition window length time
- N_{time} the number of temporal interleaving
- N_{ex} is the number of excitations needed in order to sample all the temporal and spatial points in the k-space. $N_{ex} = N_{spat} \times N_{time}$
- $n = T_{sig}/\Delta t_{cs}$ is the total number of time samples in the conventional spiral acquisition approach (see (1)).
- p, the number of time samples, irregularly spaced and defined by the SBS algorithm (see (3))

In conventional spiral MRSI acquisition, the total acquisition time is $T = N_{ex} \times TR$. We aim to demonstrate the possibility to reduce the total acquisition time, in the spiral MRSI case, by using the irregular sampling scheme given by SBS and a subsequent LS reconstruction.

2.4. Implementation Method

Two sampling strategies were implemented and compared: A) the so-called *Conventional spiral sampling Approach* B) the SBS-based irregular sampling for spiral trajectories. For both approaches, successive conventional Archimedean spirals were used. Once the k-t space was obtained, a gridding algorithm was used to resample the data onto a cartesian grid before computing the discrete Fourier transform [10].

A) Conventional spiral MRSI: time domain uniformly sampled

In the conventional sampling the full k-space is uniformly sampled at each time sample with a number N_{spat} spirals. With a number N_{time} of temporal interleaving, all the desired temporal points are sampled. The number of temporel necessary interleaving is $N_{time} = T_s/\Delta t_{cs}$. Then the total acquisition time is: $T = N_{ex} \times TR = N_{spat} \times N_{time} \times TR$

B) SBS based time domain irregular sampling for spiral trajectories

Preliminary

The FID signal is both complex and causal. Following [11] we construct a symmetrized signal by time reversal and complex conjugate of the FID that improves the sparsity of the resulting signal because its Fourier transform is real.

Problem Statement:

- given a subsampling factor p/n , a spiral duration T_s and the spirals gradient constrained by the technology (3T MR system in our simulations)
- find the minimum number $N_{exsbs} < N_{ex}$ of excitations.

Proposed solution: With SBS the number of spatial interleaving N_{spat} does not change from the conventional method. The number of temporal interleaving is reduced, and the number of excitation is reduced to a number N_{exsbs} depending on the length of a spiral T_s, see the pseudo-code below for finding N_{exsbs}. The gain $G = N_{ex}/N_{exsbs}$, which is directly related to the reduction of the acquisition time, can be deduced.

Pseudo code for finding N_{exsbs}

Input and variables: p previouly calculated SBS irregular positions are stored in the vector P, recall that $p < n$, and the acquired sample number p_t at the current discrete time index t are stored in the vector P_t. The index t_{prev} is used to select two time samples ensuring a spacing greater than the spiral length.

Initialisation:

$P_t = [],\ p_t = 0,\ Nexsbs = 0$

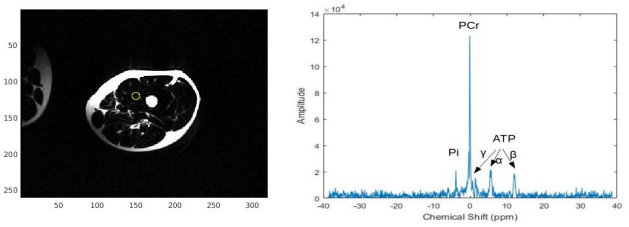
Procedure:

while $p_t < p$ **do**
  $N_{exsbs} = N_{exsbs} + 1$
  $t_{prev} = -T_s/\Delta t_{cs}$
  for $t = 0$ to $T_{sig}/\Delta t_{cs}$ **do**
    if $t \in P$ & $(t - t_{prev}) > T_s/\Delta t_{cs}$ **then**
      $t_{prev} = t, p_t = p_t + 1, \{P_t\}_{p_t} = t$
    end if
  end for
end while

2.5. MR Spectroscopy signal simulations

Both approaches were tested on ^{31}P MRSI data, showing sparse spectral feature and derived from real in vivo data as shown Fig. 2. A three compartment phantom (Fig. 3) was used with different metabolite ratio in each compartment. The FOV was of 25 cm, the image matrix size was 64×64. For the conventional approach A, a spiral length time of 1ms, 256 spirals per excitation, a number N_{time} of temporal interleaving of 4 so that there is a total of 1024 temporal points with a temporal resolution of 0.25 ms were used. For the approach B using SBS, we chose a reduction factor of 4, which means that we will sample 4 times less temporal points than Shannon-Nyquist. Here, we retain $p = 256$ points from $n = 1024$. The two approaches will be compared using the Signal Reconstruction to Error Ratio (SRER):

$$SRER = 20log\frac{||originalspectrum||_{L_2}}{||originalspectrum - reconstructedspectrum||_{L_2}}$$



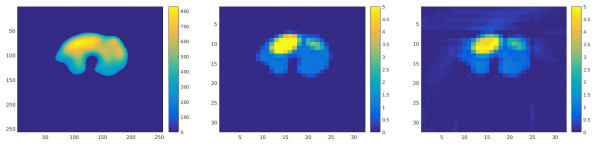
(a) (c)

Fig. 2. *In vivo* anatomic and ^{31}P spectrum (from the highlighted voxel) acquired on the quadriceps of a man at 3T. The three metabolites Phosphocreatine (PCr), Adenosine Triphosphate (ATP) and Phosphate Inorganic (PI) are indicated and show to constitute a sparse spectrum

3. RESULTS

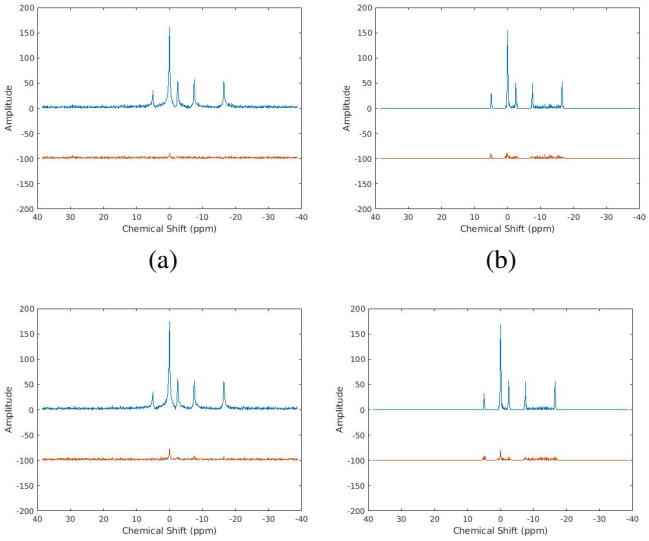
Spiral length in Ts/Δtcs	64	32	16	8	4
Gain G	3.6	3.2	2.7	2.7	2

Table 1. Excitation gain vs the spiral length for $n/p = 4$



(a) (b) (c)

Fig. 3. For t=0, a) Acquired *in vivo* ^{31}P image at 3T b) Phantom (based on *in vivo* image) ; c) Reconstructed image with a gridding algorithm



(a) (b)

(c) (d)

Fig. 4. Magnitude of the reconstructed spectrum (σ noise 10% PCr) of a voxel in the left ellipse of the image (fig.3) (a) for the method A , (b) for the proposed approach B. A voxel in the right ellipse (c) for A, (d) for B. The reconstruction error magnitude (shifted by -100) is given on the bottom.)

Table 1 gives the gain G with the length of the spiral. Fig. 3 illustrates the MRSI phantom data used in this study and Fig. 4 the reconstructed spectra in 2 different regions. The SRER are respectively 25.8 dB and 24.9 dB without noise for method A and B, for the pixel in the center and 23.6 dB and 19.8dB for method A and B with noise (averaged with 20 noise realisations, σ = 10% PCr). These results show that, additionnaly to being able to reconstruct the original image, we are able with our method to reconstruct the spectroscopic signal without significantly decreasing the SRER.

4. CONCLUSION

We have proposed a novel way to reduce the scan time by a technique based on LS reconstruction and the SBS algorithm acting for undersampling the temporal direction in MRSI spiral-based acquisition. We have evaluated the relevance of such approach by implementing this acquisition strategy on an MR scanner where the spiral acquision is simulated. The results prove the feasability of the proposed approach.

5. ACKNOWLEDGEMENTS

This work was partly supported by the LABEX PRIMES (ANR-11-LABX-0063), program "Investissements d'Avenir" (ANR-11-IDEX-0007) and Siemens Healthineers.

6. REFERENCES

[1] S. Posse, R. Otazo, S.R. Dager, and J. Alger, "MR spectroscopic imaging: principles and recent advances.," *Journal of magnetic resonance imaging : JMRI*, vol. 37, no. 6, pp. 1301–25, 2013.

[2] M. Lustig and D.L. Donoho, "Compressed sensing MRI," *IEEE Signal Processing Magazine*, vol. 25, no. 2, pp. 72–82, 2008.

[3] S. Hu, M. Lustig, A. Balakrishnan, P.E. Larson, R. Bok, J. Kurhanewicz, S.J. Nelson, A. Goga, J.M. Pauly, and D.B. Vigneron, "3D compressed sensing for highly accelerated hyperpolarized 13C MRSI with *in vivo* applications to transgenic mouse models of cancer," *Magn. Reson. Med.*, vol. 63, no. 2, pp. 312–21, 2010.

[4] D. Merhej, H. Ratiney, C. Diab, M. Khalil, M. Sdika, and R. Prost, "Fast multidimensional NMR spectroscopy for sparse spectra," *NMR Biomed*, vol. 27, no. 6, pp. 640–55, 2014.

[5] S.J. Reeves and L.P. Heck, "Selection of observations in signal reconstruction," *IEEE Trans. Signal Proc.*, vol. 43, pp. 788–791, 1995.

[6] E. Adalsteinsson, P. Irarrazabal, S. Topp, C. Meyer, A. Macovski, and D.M. Spielman, "Volumetric spectroscopic imaging with spiral-based k-space trajectories.," *Magn. Reson. Med.*, vol. 39, no. 6, pp. 889–898, 1998.

[7] Y. Gao and S. Reeves, "Optimal k-space sampling in MRSI for images with a limited region of support," *IEEE Trans. Med. Imaging*, vol. 19, pp. 1168–1178, 2000.

[8] T. Tao, "An uncertainty principle for cyclic groups of prime order," *Mathematical Research Letters*, vol. 12, no. 1, pp. 121–127, 2005.

[9] E.J. Candès, J.K Romberg, and T. Tao, "Stable signal recovery from incomplete and inaccurate measurements," *Communications on Pure and Applied Mathematics*, vol. 59, no. 8, pp. 1207–1223, 2006.

[10] J. Fessler, "Image reconstruction toolbox," *https://web.eecs.umich.edu/ fessler/code*.

[11] M. Mayzel, K. Kazimierczuk, Orekhov, and V. Yu., "The causality principle in the reconstruction of sparse NMR spectra," *Chem. Commun.*, vol. 50, pp. 8947–8950, 2014.