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Under-sampled spiral 31P-MRSI for dynamic exercise applications at 3T

Jabrane Karkouri^{1,2,3}, Magalie Viallon¹, Arthur Coste¹, Josef Pfeuffer⁴, Thomas Troalen², Sylvain Grange¹, Remy Prost¹, Fabien Millioz¹, Pierre Croisille¹, and Helene Ratiney¹

¹Université de Lyon, INSA-Lyon, Université Claude Bernard Lyon 1, UJM-Saint Etienne, CNRS, Inserm, CREATIS UMR 5220, U1206, Lyon, France, Lyon, France, ²Siemens Healthcare SAS, Saint-Denis, France, ³Wolfson Brain Imaging Center, University of Cambridge, Cambridge, United Kingdom, ⁴Siemens Healthcare SAS, Erlangen, Germany

Synopsis

In this abstract, a novel approach based on spiral MRSI and under-sampling of the temporal dimension is applied in the case of dynamic phosphorus at 3T. The goal was to assess mitochondrial capacity of different individual muscles within the calf at once.

Introduction

Quantifying energetic muscular metabolism and mitochondrial capacity is of crucial interest to reveal muscular disorders, metabolic diseases or cardiovascular diseases. 31P spectroscopy is a well-known non-invasive way to monitor energetic metabolism and dynamic concentrations of phosphorylated metabolites during exercise or after, during recovery, and provides pieces of information on mitochondrial and oxidative capacity. In clinical practice, mostly non-localized 31P spectroscopy is done, preventing metabolic information from different individual muscles to be measured, and averaged information results from the whole muscle as collected at once by the surface coil used for the experiment. In this work, the recently proposed MRSI approach detailed in [5] coupling spiral k-space sampling and temporal under-sampling was applied on dynamic phosphorus experiment, to evaluate its performance to spatially resolve 31P signal within individual muscles of the calf at rest but also dynamically during controlled exercise at 3T.

Methods

The sequence has been developed on a Siemens MR machine (figure 1). The prototype sequence has been tested on a Prisma 3T scanner (max slew rate SR= 200T/m/sec and Max Gradient amplitude Gmax=80mT/m). The total acquisition time Tacq depends on the number of spatial interleaves Nspat, the number of temporal interleaves Ntemp (repetition of the spiral train with a delay equal to the spectroscopic temporal resolution) and the repetition time TR:

$$T_{acq} = TR \times N_{spat} \times N_{temp}$$

The method in [6] has been implemented (figure 2) as well. The SBS algorithm enabling to define the irregular sampling has been implemented on the scanner and outputs the temporal samples to acquire given the frequency support, the vector size and the reduction factor for the under-sampling that the user defines in a Special Card (on siemens MR machine windows interface).

31P experiments at rest were made using a 31P-CSI double phase encoding sequence with a TR of 4s, a bandwidth of 2000Hz and a 8x8 matrices size. A 31P-CSI spiral sequence with the same acquisition parameters has been done at rest. A reduction factor of 3 has been used for the under-sampled spiral CSI, with a frequency support chosen such that it contains PCr, Pi and gamma-ATP resonances. The resulting acquisition times were 2min56s for the fully temporal spiral CSI sequence and 1min36s in the under-sampled case, which results in a gain in the terms of acquisition time of 1.8. The two methods fully and under-sampled are compared in terms of signal to reconstruction error ratio (SRER) which is computed according to the fully and regularly sampled signal.

Dynamic 31P experiments were done with an isometric flexion movement. The TR used for dynamic experiments was of 2s for the fully sampled spiral CSI and under-sampled for the under-sampled spiral CSI. The bandwidth for proper 31P spectra reconstruction has been set to 2000Hz. The number of temporal interleaves was of 4 for the fully sampled spiral CSI and 2 for the under-sampled spiral CSI, which lead to a resolution between full reconstructed spectra of 8s in the fully sampled case and 4s in the under-sampled case. The data processing pipeline is given on figure 3.

Results

Figure 4 shows PCr and Pi maps acquired at rest with the two methods fully spiral CSI and under-sampled spiral CSI. Reconstructed spectra are shown as well for a voxel of the image. The SRER in the highlighted voxel is of 19, 01 dB, which corresponds to an energy of the reconstruction error 9 times smaller than the energy of the signal. The SRER has also been averaged within all the voxels containing soleus and gastrocnemius muscle and its value is 17, 31 dB. Concerning dynamic 31P experiments, PCr depletion was of 47 % in the soleus muscle and 34 % in the gastrocnemius muscle for the fully temporal spiral CSI case and 38 % in the soleus muscle and 31 % in the gastrocnemius muscle for the under-sampled spiral CSI case. Normalized PCr by PCr + Pi evolution over time is shown in figure 5 for both methods in the soleus and the gastrocnemius muscles. The sum of PCr and Pi is also given. PCr recovery constant times were of 45,4s in the soleus and 34,7s in the gastrocnemius for the fully sampled case and 44,2s in the soleus and 39,3s in the gastrocnemius for the undersampled case.

Discussion

The novel fast spiral MRSI acquisition strategy has been presented and tested in-vivo on phosphorus experiments. The very first in vivo experiments at rest to compare the two methods resulted in satisfactory SRER. For dynamic phosphorus applications, we are particularly interested in PCr and Pi evolutions over time. The spectrum support has been considered as sparse allowing to apply the acceleration method. Results showed that we were able to extract the recovery constant of PCr even in the under-sampled case. In the case of an undersampling, the temporal resolution of the dynamic experiment (time between each full 31P spectra) is lower than in the fully sampled case, here with a contained amplification of the noise.

Acknowledgements

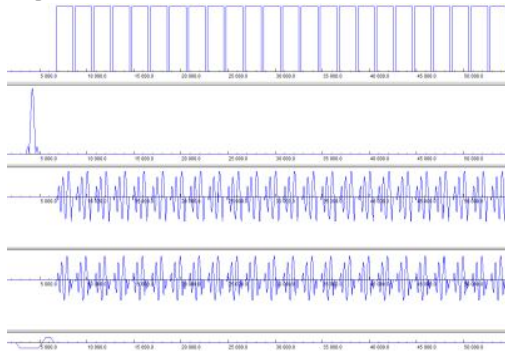
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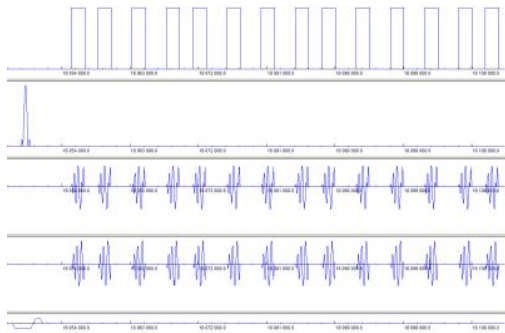
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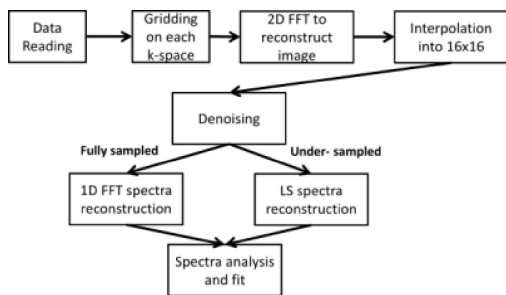
Figures



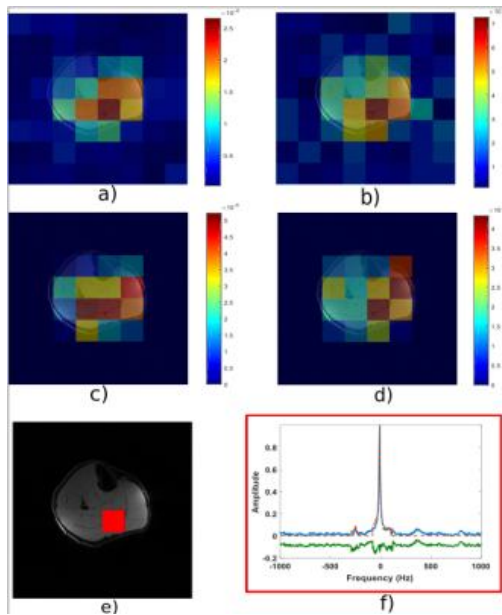
Sequence diagram of the spiral MRSI sequence taken from Siemens' IDEAsimulator environment. The first line is for the ADC, second line is for the pulse excitation, third line for the readout gradient, fourth for the phase gradient and fifth for the slice selective gradient.



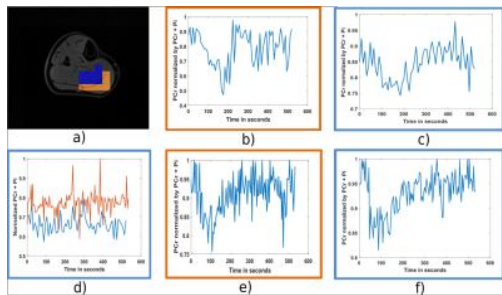
Sequence diagram of the spiral under-sampled MRSI sequence taken from Siemens' IDEA simulator environment. The first line is for the ADC, second line is for the pulse excitation, third line for the readout gradient, fourth for the phase gradient and fifth for the slice selective gradient. Some dead times are present due to the under-sampling of the temporal dimension.



Reconstruction steps for 31 P data analysis



Reconstructed PCr and Pi maps for the fully spiral CSI acquisition (a, c) and for the under-sampled spiral CSI acquisition (b, d)). The anatomic image is given in e), overlaid with the voxel localization where the spectra in f) were reconstructed. In blue, the reconstructed spectra for the fully case and in dotted red for the under-sampled case, normalized by the amplitude of PCr. The shifted error spectrum is given in the bottom in green.



Normalized PCr time evolution in the soleus and gastrocnemius muscles for both acquisition methods (b, c, e, f)). Sum of PCr and Pi is given in d) for the soleus muscle, in blue for the fully case and in red for the under-sampled case.