Respiratory Gated SPAMM Sequence for Magnetic Resonance Cardiac Tagging

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Abstract

SPAMM (Spatial Modulation of Magnetization) sequences for tissue tagging suffer from fading of the tags due to tissue T1 decay. This fading is especially important in cardiac imaging, since it affects the frames acquired in the second half of the cardiac cycle. On the other hand, breath-hold sequences are difficult to hold along a prolonged exploration. We present an alternative SPAMM sequence with respiratory gating that alleviates the mentioned drawbacks. We compare images acquired with the sequence provided by the manufacturer in a Philips Intera 1.5T scanner with images acquired with the proposed sequence. Normal volunteers (n=5) have been scanned with each sequence. The most remarkable result is that tissue-tag contrast almost doubles in the last frames with the proposed sequence as compared to the sequence supplied by the manufacturer.

1. Introduction

There is an increasing demand for non-invasive techniques able to provide quantification of regional myocardial function and strain. In this context, cardiac MR imaging (CMR) plays an important role, it provides high quality images and reasonable exploration times due to the last advances in fast sequences. Myocardial velocity and deformation can be easily measured using multiphase series of frames, that is, images of the same anatomical localization acquired over a whole cardiac cycle.

Nowadays, three techniques are basically used to quantify myocardial function in MR: tagging (1), tissue velocity codification by means of phase contrast sequences (2) and tissue displacement codification with stimulated echoes (DENSE) (3).

Phase contrast images inherently contain velocity information of each voxel, giving a good spatial and temporal resolution in the series of images. However, encoding of the relatively low velocities of the heart walls requires large gradient strengths, fast gradient rise times and long echo times, which results in large phase errors. The strain rate can be directly calculated from the velocity data, and position shift can be obtained by integration. An additional disadvantage is the low blood-tissue contrast, which makes it difficult to segment the myocardium and therefore to quantify on these images (4).

The DENSE pulse sequence directly encodes the tissue shift in position in the phase of the transverse magnetization. The mechanism whereby the magnetization phase angle becomes a function of the displacement is not obvious (5). Furthermore, it is not available on clinical routine scanners.

Spatial tagging relies on manipulation of the magnetization by radiofrequency and gradient pulses to create a regular grid of signal voids superimposed on the heart muscle. This grid moves with the tissue and enables a direct quantification of the myocardial deformation (6). SPAMM sequences for tagging can be implemented on most of the standard clinical MR systems.

Algorithms used to quantify strain and strain rate are heavily dependent on the contrast between the tag lines and the myocardium. However, the grid fades with the T1 decay time of the cardiac muscle (T1 at 1.5T ≈ 880 ms) and almost disappears at the end of the cardiac cycle. CSPAMM (Complementary Spatial Modulation of Magnetization) has been developed to alleviate this fading (7) but, for the moment, its clinical availability is not as widespread as for the SPAMM sequence.

In this work we introduce an enhancement to the free breathing SPAMM sequence provided by the manufacturer for our Philips Intera scanner. The proposed sequence makes use of cartesian k-space filling, turbo gradient echo (GE) pulses and both ECG and respiration gating. It is a good alternative to CSPAMM sequences since the tag marks do not fade out, covering the whole cardiac cycle.

2. Methods

Five healthy volunteers underwent an MR scan following a standard routine protocol established in our

centre. The scans were performed in a Philips Intera 1.5 T (Philips Medical Systems, The Netherlands) with a five elements, two anterior and three posterior, phased-array coil dedicated to cardiac imaging.

2.1. Imaging protocol

The mentioned standard protocol comprises three CINE sequences to which we added two tagging ones. CINE images are acquired in different views: 2 chambers (1 slice, 20 phases), 4 chambers (1 slice, 30 phases) and short axis (15 slices, 30 phases), all of them are breath-hold scans and use Balanced Fast Field Echo (B-FFE) sequences. The two tagging scans (original and proposed sequences), are oriented in the same plane as the medial slice of the short axis CINE scan. The complete study is performed using prospective ECG synchronization, taking the R peak as the triggering signal.

The free breathing tagging sequence provided by the manufacturer is 2D FFE with SPAMM, its main parameters are: matrix = 154*192 (phase*frequency), 2 NSA, rectangular FOV = 70%, acquisition percentage = 80%, TE = 5 ms, TR = 30 ms, flip angle = 13º, slice thickness = 8 mm, orthogonal grid lines spacing = 8 mm, acquisition time = 3'03'', 20 phases for 80 bpm.

Our proposed tagging sequence is 2D turbo gradient echo (TFE) with SPAMM, its main parameters are: matrix = 192*192 (phase*frequency), 4 NSA, rectangular FOV = 100%, acquisition percentage = 100%, TE = 1.9 ms, TR = shortest (5.5 ms for 80 bpm), flip angle = 13º, turbo factor = 8, slice thickness = 8 mm, orthogonal grid lines spacing = 8 mm, respiratory synchronization = gating, acquisition time = 1'12'', 13 phases for 80 bpm. The actual acquisition time fluctuates, due to its dependence of the patient breathing cadence. Normally it doubles the theoretical one.

2.2. Image analysis

Images were analyzed by means of manually sketched profiles on the first and last images of each tagged series using the ImageJ package (public domain software, National Institutes of Health, USA). These profiles were drawn on the short axis region, close to the septum (Figure 1).

On the sinusoidal profiles obtained from every first and last frame of the series, the features measured are: full width at half maximum (FWHM), separation between maxima and between minima, signal intensity on the maxima (S_t, tissue signal intensity) and on the minima (S_g, grid signal intensity). With these data it is possible to assess the contrast between tag marks and tissue and the persistence of both contrast and shape of the grid.

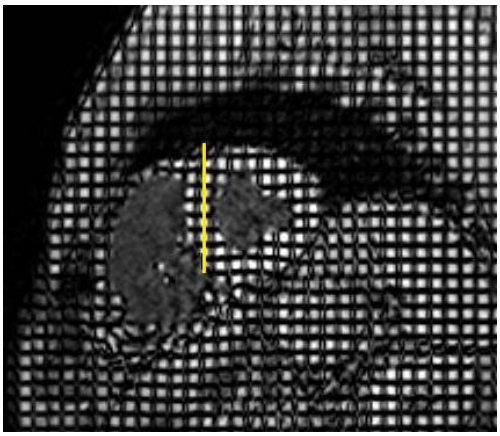

Figure 1. Profile drawn on the myocardium in the first phase of an image obtained with the improved sequence.

The normalized contrast between grid and cardiac muscle is given by,

$$C_n = (S_t - S_g) / S_t$$

where S_t is the tissue signal intensity and S_g is the grid signal intensity.

The signal to noise ratio (SNR) is calculated as

$$SNR = S_t / SD_n$$

where SD_n is the standard deviation of the noise measured in a ROI placed on the background of the image. The contrast to noise ratio (CNR) is calculated as

$$CNR = C_n / SD_n$$

To assess the grid persistence, the loss in C_n and CNR between the first and the last images of each series is measured, as an indicator of signal fading. The FWHM and the separation between peaks are used as indicators of the preservation of the sinusoidal modulation.

3. Results

Tables 1 and 2 show the average and standard deviation for the parameters calculated as described above (Figure 2). The loss on each one is calculated as the average loss from the data of all the profiles, not like the difference between the averages shown in the tables.

ORIGINAL SEQUENCE	first phase	last phase	loss
FWHM (mm)	3.58±0.13	3.79±0.34	-0.22±0.36
C_n	0.91±0.02	0.27±0.10	0.64±0.10
SNR	148±118	81±47	67±78
CNR	0.27±0.14	0.07±0.06	0.20±0.11

Table 1. Results from the profiles obtained with the sequence provided by the manufacturer.

PROPOSED SEQUENCE	first phase	last phase	loss
FWHM (mm)	3.78±0.36	4.04±0.34	-0.15±0.31
C_n	0.94±0.06	0.54±0.15	0.40±0.12
SNR	311±104	123±53	112±120
CNR	0.70±0.28	0.28±0.12	0.42±0.20

Table 2. Results from the profiles obtained with the respiratory gated sequence.

The values for the FWHM and the C_n are very similar for the first phase of both sequences, although they are slightly higher for the proposed sequence. The SNR is 2.1 times greater for the first phase of the improved sequence, and therefore the CNR is also 2.6 times larger.

The differences between the last phases compared are larger than between the first ones. The FWHM is 1.06 wider in the proposed sequence. On the other hand, the C_n is 1.96 times greater, the SNR is 1.52 times larger and the CNR is 4 times higher when using the improved sequence.

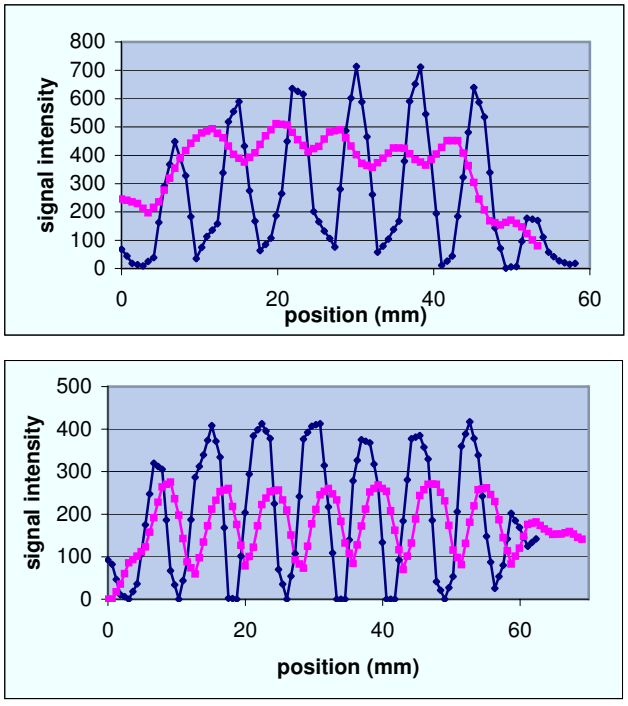

Figure 2. Comparison between the profiles on the first (dark line) and the last (light line) phases from the same sequence. The upper panel corresponds to the original sequence and the lower to the improved one.

The number of phases in the original sequence series is 24.0 ± 3.0 and in the proposed sequence is 12.4 ± 1.9.

4. Discussion and conclusions

Nowadays, objective assessment of regional strain and strain rate plays an important role in the diagnosis of many cardiac diseases. CMR sets non-invasive marks on the myocardium that can be tracked over the whole cardiac cycle, providing a direct measurement of the displacement and velocity of every pixel.

From the different techniques for setting marks in CMR the more widespread presently is the saturation grid or tagging. Algorithms used to calculate displacements and velocities need to reliably follow the marks, therefore any fading of the grid makes these algorithms to fail at the end of the cardiac cycle. In the SPAMM sequences, the grid is generated before acquiring the images, spatially modulating the transversal magnetization of the tissue. This grid fades because the magnetization naturally relaxes and disappears according to the T1 of the tissue. For the cardiac muscle, T1 at 1,5 T is almost equal to the length of the cardiac cycle. It is then important to find methods to enhance and maintain the contrast between the marks and the tissue until the last image of the dynamic series.

The sequence proposed in this work achieves visible contrast of the marks in the last frame (Figure 3). The C_n, is almost double than the one obtained with the original manufacturer sequence and the CNR is four times higher, making it suitable for the quantification algorithms. The respiratory synchronization plays a double role: it minimizes the movement artefacts inherent to a free breathing scan and the patient has not to suffer another breath-hold scan, which is important for patients that need to undergo a cardiac exploration. Nowadays, most of the sequences in a cardiac protocol require the patients to perform many breath-holdings and by the end of the study it becomes difficult to keep the thorax position, which may lead to quantification errors.

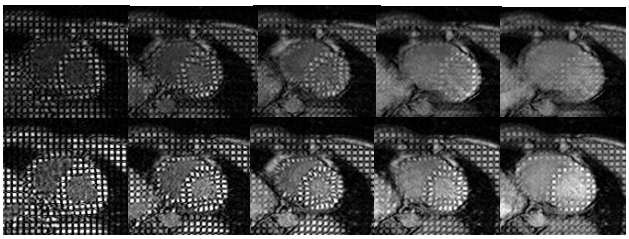

Figure 3. The upper row shows images acquired with the original sequence and in the lower they were acquired with the enhance one. Every vertical pair of images corresponds to the same cardiac phase.

In our centre, we attempted to speed up the breath-hold SPAMM sequence by using parallel imaging (SENSE) and partial Fourier acquisitions. However, the image

quality obtained was insufficient for both HARP and non-rigid registration algorithms (8) to track the grid until the end of the cardiac cycle. Therefore, our alternative was to implement the best non breath-holding sequence possible.

The main drawback of our sequence is that the number of phases acquired is roughly half of the number reached with the original one. One way to alleviate this disadvantage is to launch the sequence two times: the second one with a time shift between the triggering signal and the acquisition of the first frame equal to half the time between consecutive frames. Then, by interleaving both series we obtain a single set of images with double temporal resolution. Of course, also the acquisition time doubles, but the patient remains calmed because do not suffer any apnea and high-quality temporal and spatial resolution images are obtained.

Other approaches to obtain images suitable for the quantification algorithms are to use CSPAMM sequences, navigator echoes or non-cartesian k-space fillings, in order to speed up the acquisition, but they are not available yet in standard clinical scanners. Therefore, the sequence presented here can be easily implemented in any scanner able to use SPAMM sequences.

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