Effect of reduced sampling of MRI k-space on optimal diagnosis of myocarditis with T2 mapping

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Abstract:
The objective of this paper is to evaluate the effect of reduced sampling of MRI k-space on the diagnosis of myocarditis with T2 mapping. A MATLAB model of a digital cardiac phantom was altered from a different source to test which scan acceleration methods in terms of k-space sampling were effective. Results indicated that the reduced matrix sampling method allowed for effective diagnosis, much similar to T2 mapping without the implementation of any reduced k-space sampling methods.

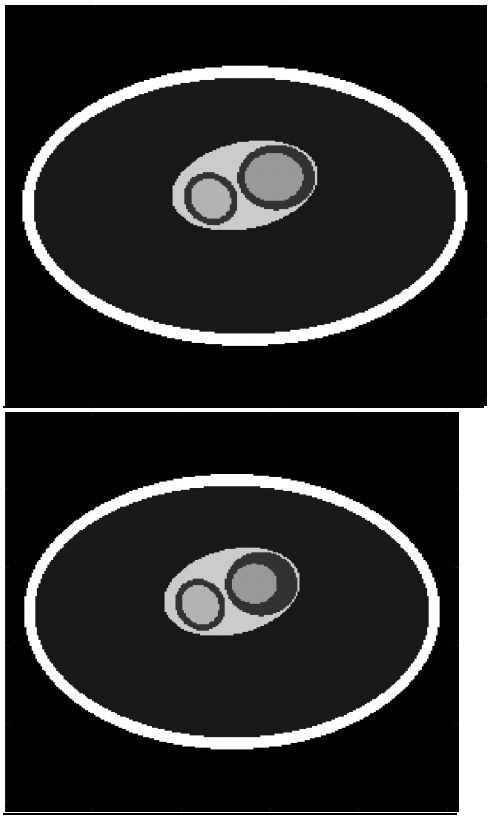
Introduction:
T2 mapping is an MRI technique where T2 (transverse relaxation) times are calculated and mapped in a parametric map to provide quantitative information about scanned tissue. This technique is proven and widely implemented in the detection of myocardial edema in patients with acute myocardial infarction, myocarditis, stress cardiomyopathy, sarcoidosis, and cardiac allograft rejection cartilage.[2] Acute myocarditis results in the inflammation of the myocardium, typically caused by viral infections. The T2 mapping MRI technique allows physicians to easily diagnose acute myocarditis. This paper evaluates a MATLAB model of acute myocarditis, representing an image developed from an MRI scan with reduced k-space sampling, to display how different scan acceleration methods impact diagnostic accuracy.

Methods:
I. Modification of Cardiac Phantom

Initially, the parameters of a digital cardiac phantom, adapted from another source[1], were manipulated to construct a heart with an enlarged left ventricle to represent edema, a characteristic feature of myocarditis. The major and minor ellipse axes for the left ventricle blood pool were reduced from 0.12 to 0.10 and 0.12 to 0.10, respectively. As a result, the left ventricle wall, closest to the leftmost anatomical region, was wider than normal. Another major feature added to this phantom were varying signal intensities as the echo time increased to simulate T2 relaxation. More specifically, the cardiac phantom's signal intensities were manually calculated within a function so that the healthy right ventricle would represent a T2 relaxation time of 50 ms, whereas the diseased left ventricle would represent a T2 relaxation time of 65 ms. These values were found in literature. The equation used to calculate the signal intensities upon specification of a T2 relaxation time and an arbitrary B value is provided below:

$$M_{x,y}(t) = \beta e^{-t/T2}$$

where $M_{x,y}(t)$ is the signal intensity, β is the initial signal intensity, t is the echo time in ms, and *T2* is the relaxation time. In this model, 1000 was selected as the arbitrary β value since the initial signal intensities of the heart after RF pulse excitation were unknown. Figure 1 shows the original and modified cardiac phantoms.



(a) (b)

Figure 1: *(a) Original cardiac phantom. (b) Modified cardiac phantom with enlarged left ventricle to represent inflammation and edema caused by myocarditis (right).*

II. T2 Mapping Algorithm

The objective of the code was to identify the β and *T2* values for each element in the image matrix by using lsqcurvefit, and then inputting the calculated *T2* values into the T2 map matrix. The first step in the code sets the image matrix to a variable called image. The image variable was made so that the different image matrices for the scan acceleration methods can easily be input into the code without changing more than one line. Then, the size of the image was computed, and set to sx, sy, and sz. A nested for loop was created in which the first loop ranged from 1 to sx and the second loop ranged from 1 to sy. This allows for the algorithm to parse through each of the elements in the code. Within the second loop, another for loop was made so that an empty array called xarray could be filled in a vertical manner with the signal intensity values for all the echo times at that element of the image. Outside of this previous for loop but still within the second for loop, the function for 2 parameter fit equation was constructed. In the next step, the lsqcurvefit function called for the two-parameter fit equation, initial estimated values of 800 and 65 for β and *T2*, the echo time array, and the transposed x array. Finally, the computed *T2* value was input into an empty T2 map with sx and sy dimensions into the correct elemental index. The experiments conducted in this methodology selected echo times ranging from 0 to 49 ms with a step size of 1 ms. The T2 map was displayed with a modified colormap and color bar with values ranging from 0 to 90 ms.

III. T2 Mapping with Implementation of Scan Acceleration Methods

Because k-space data and image space data are related by the Fourier Transform, we can obtain our desired image by taking the inverse Fourier transform of the k-space data. Scan Acceleration methods are often used in MRI image acquisition and processing to obtain the image at a faster rate. Individual points in the MRI k-space domain do not represent respective points or pixels in the image domain. Data is rather dispersed based on spatial frequency in the k-space with high spatial frequency around the edges and low spatial frequency close to the center of the k-space image. With that, k-space images can be carefully manipulated to obtain faster acquisition times. Types of reduced k-space sampling used in scan acceleration methods, shown in Figure 2, include: the half Fourier - the method where the top half of the k-space domain data is zeroed out and the bottom half is scanned; the partial echo - the method where the left half of the k-space domain is zeroed and the right half is scanned; and the

reduced matrix - the method where a selected size of the top and bottom of the k-space is zeroed and the remaining part is scanned. These reduced sampling methods come at the detriment of the Signal-to-Noise ratio (SNR) with an approximated 30% loss because we are not acquiring the total k-space.

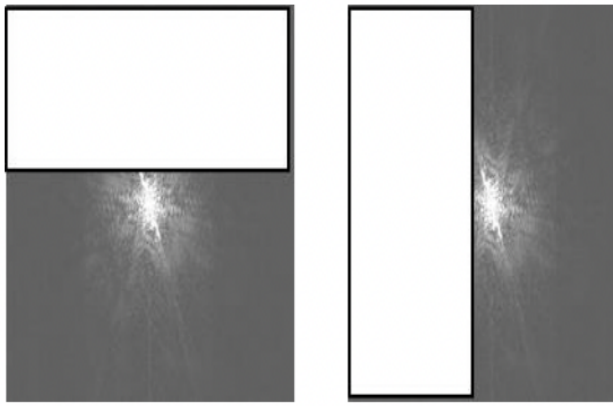


Figure 2: *Samples of half fourier, partial echo, and reduced matrix scan acceleration methods (L-R), reprinted with permission from Dr. Keigo Kawaji.*

Using MATLAB, the scan acceleration methods were implemented by first taking the Fourier transform of the cardiac phantom and setting it to the image variable. The regions not needed depending on the type of scan acceleration method being implemented were zeroed out after the Fourier transform of the phantom image was taken. Finally, the inverse Fourier transform was taken to obtain the image needed. This method was repeated for the half Fourier, partial echo, and the reduced matrix methods.

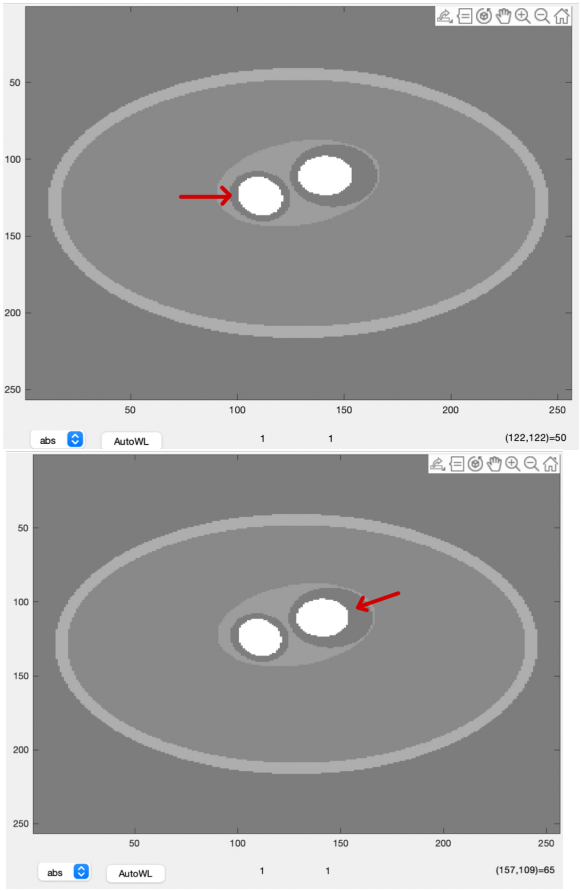
Results and Analysis:

I. Overview

The cardiac phantom was manipulated so that the ventricle would appear inflamed simulating an enlarged ventricular structure on an MRI scan to represent myocarditis. Increasing the amount of sampling can increase the image quality. However, decreasing the number of samples reduces the time necessary to run the MRI scan. Between these two parameters, there is an optimal number of samples that can be acquired to efficiently use time and formulate an accurate and precise image. Running the T2 mapping code constructs a T2 map consisting of the T2 relaxation times for the different points in the map. The T2 value is proportional to the amount of water molecules present in the structure. The higher the value, the more water molecules are present. A greater number of water molecules is a sign of edema in the heart walls, a symptom of myocarditis. When comparing the T2 map values of a patient to one who does not have myocarditis, the one with myocarditis will have higher T2 values in the diseased region.

II. Verification of T2 Map accuracy using Vis

After formulating the T2 map of the altered digital cardiac phantom model with myocarditis features without any scan acceleration methods implemented, the T2 value of the ventricles was checked by placing the cursor over the region of interest. When the cursor was hovered over the ventricular walls, the T2 value was shown. As seen in Figure 3, the T2 relaxation time of the left ventricular wall was 65 ms, and the right ventricular wall was 50 ms. These values demonstrate that the altered digital cardiac phantom model was functional and was accurately representing myocarditis as per our specifications.



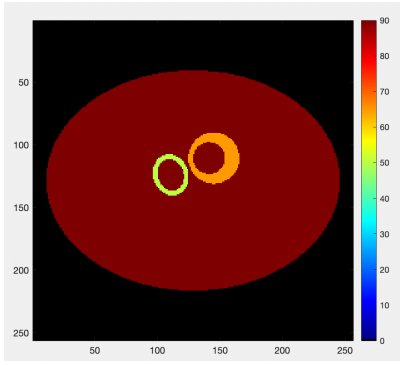
(a) *(b)*

Figure 3: *T2 value on the (a) right ventricular wall = 50 ms and (b) left ventricular wall = 65 ms.*

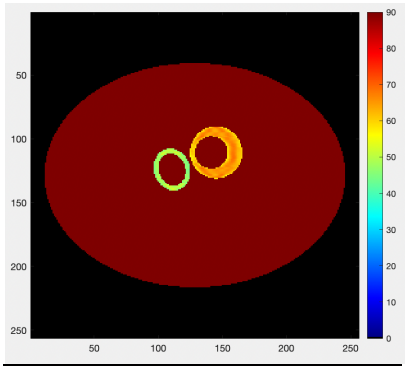
III. T2 Maps with Scan Acceleration Methods Implemented

The color map was used to indicate regions of different T2 relaxation values. Regions of the T2 map with burgundy color as shown in Figure 4 suggests that the T2 relaxation value was well above the 90, which was set as the max value for this colormap. This occurred because the modified cardiac phantom was not modeled to appropriately represent real tissue for the regions of the heart outside the ventricle in addition to the blood pools. The same case applied to the area outside the heart but within the large ellipse, which is representative of the tissue in the remaining portions of the body. The signal intensities were not modified for simplicity purposes since the focus of the simulations and experiments were only on the ventricles. The largest ellipse represents the human body. The black regions signifying zero intensity are correct because there is no tissue present for any T2 relaxation values to be calculated.

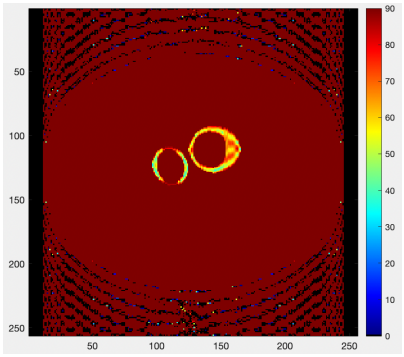
Figure 4 shows the T2 maps with different scan acceleration methods implemented. The (a) T2 map is the original T2 map that shows a 50 ms T2 value for the normal right ventricle and 65 ms T2 value for the diseased left ventricle. The (b) T2 map shows that the T2 values within the right ventricle range between 45 and 50 ms, and the values within the left ventricle range between 60 and 65 ms. This shows that the half fourier scan acceleration method introduces some error within the T2 map, which may impact how physicians may diagnose myocarditis. However, from the general ranges, it is reasonable for physicians to assume that this patient has some signs of myocarditis in the left ventricle.



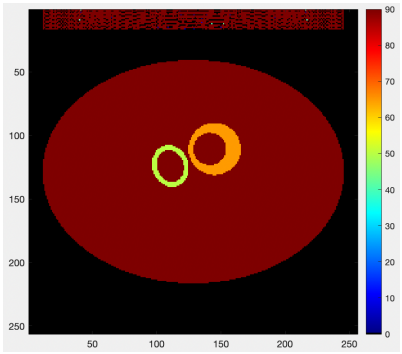
(a)



(b)



(c)



(d)

Figure 4. T2 Maps of Modified Cardiac Phantom with (a) no scan acceleration method, (b) half Fourier scan acceleration method, (c) partial echo scan acceleration method, and (d) reduced matrix scan acceleration method

The (c) T2 map is constructed upon implementation of the partial echo scan acceleration method. As evident from the image, there is a lot of noise in the map in the regions outside the human body, which should be zero. Furthermore, the noise within the map of both ventricles is too high for physicians to be able to truly differentiate between the normal and diseased ventricle. This suggests that the partial echo scan acceleration method may not be the best for evaluation whether patients have myocarditis or not. The partial echo scan acceleration method may be revised to sample less columns of the MRI k-space in different areas to improve the T2 map quality. The (d) T2 map implements the reduced matrix scan acceleration method on the cardiac phantom. The bar at the top of the image is evident of noise produced by the reduced matrix. The image shows evidence that reducing the matrix size can produce an image of clear quality for the region of interest for a physician. From these results, it is clear that the reduced matrix scan acceleration method produces the optimum results for T2 mapping out of the other methods for evaluating the presence of myocarditis.

Discussion:

The half Fourier and the partial echo scan methods (images b, c) show diagnostic inconsistency due to the SNR deficit caused by the selective frequency sampling in the k-space domain. The reduced matrix method proved to have the best result out of the three scan acceleration techniques. These errors could be attributed to the fact that the modified cardiac phantom was not modeled to properly represent real tissue in the entire image. Another factor that could have affected the results was that the k-space values were zeroed out rather than filling in the missing data using Hermitian symmetry. Taking the inverse Fourier transform of the regions with zero as the value in the k-space may have poorly affected results.

Conclusion:

The T2 mapping technique is a powerful tool used in MRI for tissue characterization and disease detection in functional organs. However, it is necessary to identify which MRI pulse sequences and reduced k-space sampling methods can be implemented to ensure a good trade-off between SNR and image acquisition and processing time, without affecting the accuracy of the diagnosis.

References:

1. Kawaji, K., Patel, M. B., Cantrell, C. G., Tanaka, A., Marino, M., Tamura, S., Wang, H., Wang, Y., Carroll, T. J.,

Ota, T., & Patel, A. R. A fast, noniterative approach for accelerated high-temporal resolution cine-CMR using dynamically interleaved streak removal in the power-spectral encoded domain with low-pass filtering (DISPEL) and modulo-prime spokes (MoPS). Medical physics, 44, 3450-3463, (2017)

2. Liu, L., Yin, B., Shek, K., Geng, D., Lu, Y., Wen, J., Kuai, X., & Peng, W. Role of quantitative analysis of T2 relaxation time in differentiating benign from malignant breast lesions. The Journal of international medical research, 46, 1928-1935, (2018)

Appendix:

```
%Original Image
image=4000*CardiacPhantomModified_Shivam([0:1:49],[50,65]);

%SAM1 = Scan Acceleration Method 1
FTSAM1 = fft2d(4000*CardiacPhantomModified_Shivam([0:1:49],[50,65]));
[x,y,z]=size(FTSAM1);
FTSAM1(:,1:1:0.4*sy) = 0;
CPhalffourier = ifft2d(FTSAM1);
%vis(CPhalffourier)
imageSAM1=CPhalffourier;

%SAM2 = Scan Acceleration Method 2
FTSAM2 = fft2d(4000*CardiacPhantomModified_Shivam([0:1:49],[50,65]));
[x,y,z]=size(FTSAM2);
FTSAM2(1:1:0.40*sx,:) = 0;
CPpartialecho = ifft2d(FTSAM2);
%vis(CPpartialecho)
imageSAM2=CPpartialecho;

%SAM3 = Scan Acceleration Method 3
FTSAM3 = fft2d(4000*CardiacPhantomModified_Shivam([0:1:49],[50,65]));
[x,y,z]=size(FTSAM2);
FTSAM3(1:1:0.15*sx,:) = 0;
FTSAM3(0.85*sx:1:end,:) = 0;
CPreducedmatrix = ifft2d(FTSAM3);
%vis(CPreducedmatrix)
imageSAM3=CPreducedmatrix;
```

Figure 5: *MATLAB code for scan acceleration methods*

```
%for Scan acceleration methods, run 4 times
%save the t2Map into seperate variables: t2Map,t2MapSAM1,t2MapSAM2,t2MapSAM3
%save each as .mat files before running the second section of this code to
%display all the t2 maps
image=imagemaskB;
[sx,sy,sz]=size(image);
parfor j=1:sx
    t=1:1:49;
    xarray=zeros(1,numel(t));
    for k=1:sy
        for l=1:numel(xarray)
            xarray(1,l)=image(j,k,l);
        end
        fcn = @(x,xd) x(1) .* exp(-xd(:) /x(2));
        [x_normal]=lsqcurvefit(@(x,xd) fcn(x,xd),[800 65],t,xarray');
        t2val=x_normal(2);
        t2Map(j,k)=t2val;
    end
end
BackgroundColor = [0 0 0];
MAX_PALLETE_SIZE = 256;
mycolormap = jet(MAX_PALLETE_SIZE);
mycolormap(1,1:3) = BackgroundColor;
imagesc(abs(t2Map),[0 90]);
axis image;
colormap(mycolormap);
colorbar
title('Myocardial T2 Map')
```

Figure 6: *MATLAB code for T2 mapping algorithm*

```
function [heart, out] = CardiacPhantomModified_Shivam(TE,model_T2)
if nargin == 1
    %any model_T2 values cannot be input at this time because the.
    %signal intensities would need to be manipulated
    TE = [0:1:49]; %echo times in ms
    model_T2 = [52,65]; %preset T2 values for right and left ventr
    B = 1000; % arbitrary max signal intensity
    M =[];
    for k = 1:n
        M(:,k) = B.*exp(-TE./model_T2(k));
    end
end
%modified phantom
%column 1: signal intensity
%column 2: ellipse major axis length
%column 3: ellipse minor axis length
%column 4: x-axis translation
%column 5: y-axis translation
%column 6: rotation angle
E_ph= [ 1.0000    0.9200 0.6900        0         0         0;... %
    -0.9000        0.8740 0.6300         0         0         0;...
    0.7000        0.3100 0.2100        0    0.1000   18.0000;... %
    -0.8000         0.1600 0.1600   0.1300    0.1400         0;...
    0.5000        0.1000 0.1000   0.1000    0.1400         0;... %
    -0.8000         0.1300 0.1100  -0.1400    0.0350  108.0000;...
    0.5000        0.1000 0.0800  -0.1400    0.0350  108.0000;... %
    ];
% Visualization of the phantom
P = phantom(E_ph,256);
% Create T2 varying model
out = [];
for j = 1:length(TE)
    E_new = E_T2(E_ph,TE(j),[model_T2(1),model_T2(2)]);
    out(:,:,j) = E_new; heart(:,:,j) = phantom(E_new,256);
    figure(1); imagesc(phantom(E_new,256)); colormap('gray'); paus
end
end

function E_out = E_T2(E_ph, t, T2)
B = 0.25;
M = B.*exp(-t./T2);
E_out = E_ph;
E_out(4,1) = E_ph(4,1) + M(2);
E_out(6,1) = E_ph(6,1) + M(1);
end
```

Figure 7: *MATLAB code for modified cardiac phantom*