Fat to Muscle Ratio Estimation by Inter-k-Space Motion Based Strategy for Super-Resolution in MRI

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Abstract— Magnetic resonance imaging (MRI) may be used to measure the volumes of muscle and fat from patients. In this paper we develop a method for automatic segmentation of adipose and muscular tissue in human being body. Due to enhanced MR image resolution , our algorithm proves to be more efficient than a regular one. Magnetic Resonance Imaging (MRI) image reconstruction based on a frequency domain Super-Resolution (SR) algorithm, is also presented in the paper. It is shown that the approach improves MRI spatial resolution in cases when Periodically Rotated Overlapping Parallel Lines with Enhanced Reconstruction (PROPELLER) sequences are used. The PROPELLER MRI method collects data in rectangular 'blades' rotated around the origin of the k-space. Inter-blade patient motion is the premise for the use of SR technique. Images obtained from sets of irregularly located frequency domain samples are combined into the high resolution MRI image. Our algorithm covers a cardiac and respiratory movements. The improvements resulted in lower approximation error and higher convergence speed.

Keywords-MRI, MR image automatic segmentation, fat tom muscle ratio estimation

I. INTRODUCTION

Magnetic resonance imaging (MRI) is well known as a non-invasive method routinely used to produce high-quality images of the body's internal tissues. The Motion of a subject during the MRI acquisition generates artifacts and blurring in the resulting image. The PROPELLER technique usually reduces motion artifacts in MRI. Algorithms applied by PROPELLER MRI to estimate and compensate for rigid-body patient motion has been extensively analyzed [19]. MRI technique may be utilized to measure the volumes of fat and muscle from these patients in order to evaluate therapies to reduce fat and increase muscular mass [23]. The high spatial resolution and risk-free feature that offers MRI compared to other technologies based on ionizing radiation are determinant in its daily use. Due to the large amount of data a segmentation method that needs the minor degree of intervention would be useful. The

usage of unsupervisioned analysis tool MR images resolution is one of the key feature here. Super-resolution (SR) is a group of methods aimed at obtaining high resolution images from sets of low-resolution ones. The motion between low-resolution images is the key premise here. In case of MRI if the imaging volume is acquired two or more times with small spatial shifts between acquisitions, a combination of data sets by an iterative SR algorithm gives improved resolution and better edge definition in the slice-select direction than simple low-resolution images averaging. For the first time some SR techniques have been applied to MRI in [18]. R. Peeters proposed MRI SR algorithm to reduce slice thickness in functional MRI [14]. Greenspan et al. [13] proposed MRI reconstruction using SR which improved spatial resolution in cases when spatially-selective RF pulses are used for localization. In this paper frequency domain SR image reconstruction method is used for improving PROPELLER MRI. Low-resolution images are obtained from frequency-domain blades by the conjugate gradient method with non-uniform FFT (NUFFT) at its core [12]. It is shown that, indeed, the new technique enhances the PROPELLER MRI images. The majority of previous SR papers have considered only global, relative displacements between set of low resolution images. In [8] authors proposed a super-resolution method reconstructing tracked objects. However, effective tracking is not always possible. In this paper we are trying to over-come these limitations. We describe a super-resolution method for images containing tissues motion. The motion information is evaluated by a nested motion trajectories scheme. First of all, multiple moving segments are isolated. The motion trajectory models may be characterized by parametric model, such as affine transformations. In other words, such extracted image parts are related by coherent relative, global, locally constant parametric motion vector. Such approach allowed us to think about dynamic scenes as if they were static. Very high accuracy parametric motion estimation and simultaneous segmentation of the motion field is realized by 3D orientation tensors with respect to the affine motion model. The introductory processing part to be presented consists of: estimation of 3D orientation tensors, estimation of motion models parameters, and simultaneous segmentation of the motion field,

respectively. The algorithm is a generalized version of that of Irani and Peleg's one.

II. PROPELLER DATA ACQUIZITION

The data acquisition procedure for Diffusion Tensor Tomography MRI (DTT MR) imaging is based on the PROPELLER method proposed in Cheryauka (2004). Here, the resulting k-space trajectories are called blades, as frequency-domain image is acquired along collections of straight lines forming rectangular patterns ("blades"), see Figure 1. K-space is covered by rotating those blades around the centre of the k-space. The key idea of PROPELLER is that the circular region at the centre of the k-space is covered by many blades. Due to data redundancy, effective information correction can be performed to reduce patient motion artifacts and to improve the SNR. The PROPELLER technique offers an opportunity to choose the diffusion gradient direction while acquiring each k-blade. The conventional procedure is to acquire a full set of PROPELLER data with a fixed direction of the diffusion gradient and to reconstruct the corresponding component of the tensor.
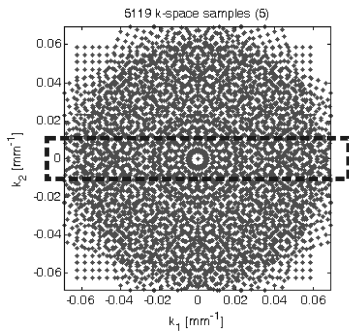

Figure 1.   PROPELLER blades, dash lines show a single data blade (see online version for colours).

III. MRI IMAGE RECONSTRUCTION

Recently, sampling of MR signals on a rectangular regularly sampled grid in k-space has been the most popular acquisition method. This regularity was motivated by the use of an easy image reconstruction technique based on the Fast Fourier Transform. Presently, non-uniform sampling patterns of the k-space, such as radial, spiral, or PROPELLER, are gaining importance in various MRI applications. The image reconstruction techniques for arbitrary irregularly sampled grids may be divided into two groups. The first one, called regridding, consists of computationally inexpensive resampling and interpolation of a kernel function into a regularly sampled grid. The next group employs numerical optimization methods that minimize a least-squares cost function. Optimization procedures may consider nonuniform coil sensitivity and off-resonance effects, improve noise suppression, and provide a robust solution within a larger parametric domain [14]. These methods have proved their effectiveness in many clinical applications and imaging methods, while non-uniform acquisition schemes show their capability to suppress noise and to reduce artifacts caused by motion and by eddy currents in functional [15], cardiac [19], arterial [17], and spine [21] imaging as well as others. In the iterative method of reconstructing field-corrected MR images presented in

the paper we use a min–max criterion to derive the temporal interpolator [12]. This interpolator provides fast, accurate, field-corrected image reconstruction even when the field map is not smooth. There are two major steps in most methods for field-corrected MR image reconstruction. Firstly, it is necessary to obtain an estimate of the field map that deals with the spatial distribution of magnetic field inhomogeneities. In this paper, field-corrected MR image reconstruction uses the field map to form the reconstructed image of the transverse magnetization. An accurate, spatially undistorted field map is assumed to be available. When the field map is obtained, one of methods of field-corrected image reconstruction, the conjugate phase method [12] tries to compensate for the phase accrual due to the off-resonance at each time point. Sutton et al. [12] focused on field inhomogeneities, one can also apply iterative image reconstruction methods to compensate for other physical phenomena such as deviations in k-space trajectory and relaxation effects. The degradation model applied in the paper does not require any assumption about its nature, and is therefore applicable to intersecting k-space trajectories such as PROPELLER's blades. The major disadvantage of iterative reconstruction methods has been their computational complexity. Fessler and Sutton [12] developed accurate and fast non-uniform fast Fourier transform (NUFFT), then, the method has been applied to MRI data with spiral k-space trajectories. Namely, the MR image reconstruction problem is closely related to the problem of reconstructing a band-limited signal from nonuniform set of samples in the frequency domain space. Strohmer suggested the use of complex exponentials for finite-dimensional approximations in such problems, and proposed to use an iterative CG reconstruction method with the NUFFT approach at its core [22]. In the algorithm presented below NUFFT-"reverse gridding" and conjugate gradient iterative scheme were combined. It should be noted, that standard NUFFT method by itself does not allow for the compensation of field inhomogeneity effects because the integral signal equation for MR is not a Fourier transform when field inhomogeneities are included. Fessler and Sutton [12] inspired by the time-segmented conjugate-phase reconstruction approach proposed a fast time-segmented forward projector, and its adjoint, that accounts for field effects and uses the NUFFT. We applied this concept in the PROPELLER blade images reconstruction scheme.

IV. PARTIAL MRI IMAGE RECONSTRUCTION FROM A SINGLE BLADE

In MRI, ignoring relaxation effects, the z-th blade signal equation is given by Sutton et al. [12]:

$$s_z(t) = \int \tilde{f}(r)c(r)e^{-i\omega(r)(t+T_E)}e^{-i2\pi(k(t)\cdot r)}dr \tag{1}$$

where $s_z(t)$ is the complex baseband signal at time t the z-th blade readout, T_E is the echo time, $\tilde{f}(r)$ is a continuous function of the object's transverse magnetization at location r immediately following the spin preparation step, $c(r)$ is the sensitivity map of the receiver coil, $\omega(r)$ is the field

inhomogeneity present at r, and $k(t)$ is the k-space trajectory. For simplicity we let

$$f(r) = \tilde{f}(r)c(r)e^{-\omega(r)T_E}. \qquad (2)$$

After discretization z-th blade signal equation is as follows:

$$s_z(t) \approx \Phi(k(t)) \sum_{n=0}^{N-1} f_n e^{-i\omega_n t} e^{-i2\pi(k(t)\cdot r_n)}. \qquad (3)$$

where $\Phi(k(t))$ denotes Fourier transform of $\phi(r)$, the voxel indicator function [12]. In PROPELLER MRI blade measurements are noisy samples of the signal (1):

$$y_i = s(t_i) + \varepsilon_i, i = 1,...,M, \qquad (4)$$

where ε_i denotes noise. Assuming that the dominant noise is the white Gaussian, we estimate y_i by minimizing the following penalized least-squares cost function

$$\psi(f) = \frac{1}{2}\|y - Af\|^2 + \beta R(f), \text{ so that,}$$
$$\hat{f} = \arg\min_f \psi(f).$$

Computation of Af corresponds to evaluation of (3). The $R(f)$ is a regularization function, that penalizes the roughness of the estimated image. This regularization can decrease the condition number of the image reconstruction problem and, therefore, speed up the convergence. Minimization of cost function is realized iteratively by the conjugate gradient algorithm [12]. As PROPELLER trajectories in k-space are not Cartesian grids, multiplication by the matrix A is the most computationally demanding operation of the conjugate gradient algorithm. Nevertheless, a NUFFT can be used for this purpose to rapidly and accurately evaluate the discrete signal (3). However, the NUFFT method is not directly applicable when the field inhomogeneity is included because (1) is then not a Fourier transform integral.

V. MR BLADE BASED SEQUNCE PARTITIONING

Being accurate and powerful, the iterative backprojection SR algorithm [1] have some drawbacks, e.g. only globally static scenes may be processed. Then, if we want to apply the IBP scheme directly, images or video frames should be segmented into areas with uniform motion. We have devised such segmentation scheme for coherent tissues motion areas [4], see Figure 2.

Simultaneous segmentation and velocity estimation

For best results, estimation of affine motion field should be done over a region with coherent motion. In [4] authors proposed a different approach, weighted neighbourhoods around each pixel have been interpreted

as regions. In this section an efficient algorithm for simultaneous segmentation and velocity estimation, given an orientation tensor field for only one frame, is presented. The task for the segmentation is to partition the image into a set of disjoint regions, so that each region is characterized by a uniform motion described by affine model. In this section a region R is defined to be a nonempty, connected set of pixels. The segmentation algorithm has been based on a competitive region growing approach [11].
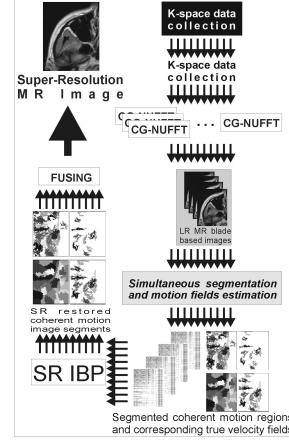

Figure 2. The proposed SR MRI image reconstruction scheme.

A cost function $C_R(x)$ is associated with each region defined for all pixels in the image. Regions are growing by adding one pixel at a time. To preserve connectivity the new pixel must be closest to the region, and to preserve disjointedness it must not be already assigned to some other region. The new pixel should be as "inexpensive" as it is possible. The details are as follows. Let the border ΔR of region R be the set of unassigned pixels in the image which are adjacent to some pixel in R. For each region R, the possible candidate, $N(R)$, to be added to the region is the least expensive pixel bordering to R, i.e.

$$N(R) = \arg\min_{x \in \Delta R} C_R(x) \qquad (5)$$

The corresponding minimum cost for adding the candidate to the region is denoted $C_{\min}(R)$. In the case of an empty border, N(R) is undefined and $C_{\min}(R)$ is infinite. Assuming that a number of regions $\{R_n\}$ have been obtained in some way, the rest of the image is partitioned as follows.

1. Find the region R_i for which the cost to add a new pixel is the least, i.e. let $i = \arg\min_n C_{\min}(R_n)$.
2. Add the least expensive pixel $N(R_i)$ to R_i.
3. Repeat first 2 steps until no unassigned pixels remain.

Figure 3. Illustration of the competitive algorithm [4]

Regrowing is performed for one candidate region at a time, which means that there is no competition between regions but rather between pixels. At the beginning the candidate region contains only one point, its starting point, which is also the centre point of the initial rectangle surrounding it. The cost function used is $(\hat{v}T\hat{v})/trT$ where v is the velocity of the candidate region's current motion model. The competitive algorithm is then running until the candidate region has grown to a specified size. This size is called the candidate region size, m_0 and is a design parameter of the segmentation algorithm. The result of the regrowing scheme is that the candidate region consists of m_0 connected pixels, that are most consistent with the candidate region's motion model. When the candidate region has been regrown, new optimal parameters are computed. Each candidate region is regrown twice [11], a number which seems to be sufficient to obtain reasonably coherent regions.

VI. MODIFIED IBP SR

Starting with an initial guess f_0 [1] for the high resolution image, the imaging process is simulated to obtain a set of low resolution images $\left\{g_k^{(0)}\right\}$ corresponding to the observed input images $\left\{g_k\right\}$ If f_0 were the correct high resolution image (1), then the simulated images $\left\{g_k\right\}$ should be identical to the observed images. The difference images $\left(g_k - g_k^n\right)$ are used to improve the initial guess by "back projecting" each value in difference images onto its coresponding field in f_0, yielding an improved high resolution image f_1. This process is repeated iteratively to minimize the remaining error. This iterative update scheme can be expressed by:

$$f^{(n+1)} = f^{(n)} + \frac{1}{K}\sum_{k=1}^{K}T_k^{-1}(((g_k - g_k^{(n)})\uparrow s)*p)$$

where K is the number of low resolution images $\uparrow$ arrow an upsampling operator by a factor s and p is a back projection kernel determined by h and Tk. Taking the average of all discrepancies has the effect of reducing noise.

VII. SEGMENTATION [23]

Adipose tissue typically presents higher intensity level than muscle tissue in thigh MRIs, while background is supposed to be darker. Therefore, intensity thresholding seems the most reasonable approach to perform this segmentation. However, the intensity source in resonance images is not homogenic and its pixels corresponding to the same tissue suffer significant variations of intensity. The main technique employed in utilized approach is adapted thresholding [23], where the image is splited into a group of smaller subimages and then the thresholding is applied independently to each subimage. As a final point the results of the different segmentations have to be joined in an overall segmentation. Bones tissues also present in MRI scans have usually lighter intensity levels than muscle tissue, and comparable to that of fat. Thus, an appropriate procedure should be included to isolate the image region corresponding to the bone. The overall scheme is implemented in four stages, explained thereafter:
a) Image division and segmentation of subimages, b) Creation of templates c) Bone extraction, d) Final segmentation. This algorithm has been successfully applied [23] giving average results were above 90 % of success in most of the regular resolution images.

VIII. EXPERIMENT

In this experiment twenty MRI GE 1.5 T scanner's blade based partial frequency images have been taken. Coherent tissues motion has been included. At the beginning the motion parameters in the frequency domain space have been calculated. The next step involved MRI image reconstruction procedure from single blades.

Twenty shifted images were acquired in order to reconstruct an SR image with doubled resolution. It is clearly visible that there are many more details in the high-resolution image obtained in this way, see Figure 4.

These SR resolution images have been segmented. The segmentation algorithm is fully automatic in the sense that specialist intervention is not required. Due to improved input resolution higher accuracy of the segmentation has been achieved.
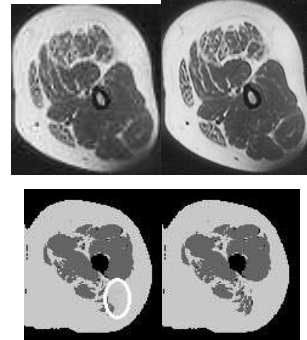

Figure 4. From left to right: (upper row) patient suffering from obesity image obtained by "typical" PROPELLER-MRI procedure, the super reconstructed MRI-PROPELLER image, (lower row) regular resolution segmented image (small adipose tissue areas not detected), SR segmented image (improved segmentation)

IX. CONCLUSION

The new PROPELLER MRI super resolution algorithm, based on tissues movements analysis, has been presented. In general, when applying SR to MRI we can break down limits on inherent resolution of existing MR imaging hardware. The same can be told about the proposed algorithm, which in addition does not add significant time to data reconstruction, if compared to the typical PROPELLER procedure. When using the new algorithm the overall spatial accuracy and stability in the field of view of MRI machines are increased. It has been proved that higher image definition makes the segmentation part easier and more accurate. Thus, the

proposed technique may find applications in all PROPELLER MRI machines. Moreover, the proposed scheme takes into account tissues movements. The new SR technique and more robust segmentation may find applications in unsupervised measurement systems of fat and muscle tissues.

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