Optimal Image Combination with Minimal Total Deformation (MTD) Constrain To Improve Signal-Noise-Ratio (SNR) For Free-Breathing Cardiac Magnetic Resonance Imaging

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Introduction While cardiac MR has proven its unique value as an important non-invasive modality to evaluate heart disease, the majority of cardiac MR studies still rely on breath-held, segmented k-space, data acquisition. Unfortunately, breath holding is particularly difficult for patients with severe heart disease or for uncooperative pediatric patients. Real-time and single-shot cardiac imaging is therefore of high clinical relevance; however, these techniques, if compared to breath-held ones, must compromise spatial and/or temporal resolution or sacrifice SNR despite the broad use of parallel imaging and rapid imaging sequences [1]. Recent work has shown that SNR can be improved by selectively averaging motion-corrected free-breathing images using the non-rigid image registration. Substantial SNR gains have been reported for high spatial-temporal cardiac cine [1,2], high SNR free-breathing single-shot delayed enhancement imaging [3] and free-breathing single-shot fat-water separated cardiac imaging [4]. All of these studies rely on retrospectively applying image registration to correct the heart motion across multiple heart beats. The corrected images are then combined via the simple uniform averaging to suppress noise. To avoid any significant artifacts introduced by imperfect non-rigid motion correction, all previous studies have applied heuristic criteria to exclude some frames from the final averaging. On the other hand, non-rigid image registration, viewed as an optimization process to find local optima, can lead to variable correction accuracy for both different frames and different regions within a frame. Uniformly averaging multiple motion-corrected frames likely will lead to suboptimal outputs, as all pixels in the corrected frames are weighted equally without considering the registration accuracies. Also, the exclusion of frames lowers the possible SNR gains which can be obtained by including more frames for image combination. A novel image combination algorithm is therefore proposed to compute optimal weights for every pixel after the motion correction. In this formulation, the quality of motion correction will influence outputs by minimizing the total amount of non-rigid deformation brought into the image combination. The optimal weights calculation is formulated as an energy minimization problem and solved efficiently under the variational framework.

Optimal Image Combination As the quality of non-rigid registration is not uniform across different frames or between different regions within a frame, the deformation fields, as the outputs of non-rigid registration process, carry the information of accuracy of motion correction. Often large deformation is more related to visible smearing artifacts introduced by motion correction. Given a group of $\boldsymbol{N}$ *frames* $\boldsymbol{I(x,y,t), t=0,1,2,\dots,N}$ as a free-breathing cardiac MR dataset, the optimal weight is defined as a function $\boldsymbol{w(x,y,t), t=0,1,2,\dots,N}$ to minimize the following energy functional: $\boldsymbol{w(x,y,t)=min_w\, f(w,\overrightarrow{deform})}$ where $\boldsymbol{f(w,\overrightarrow{deform})}$ is defined as:

$$\boldsymbol{f\left(w,\overrightarrow{deform}\right) \stackrel{\text{def}}{=} f\left(w(x,y,t),\overrightarrow{deform(x,y,t)}\right) = \iiint_{\Omega} \left[w^2(x,y,t)\cdot\left|\overrightarrow{deform(x,y,t)}\right| + \mu\cdot|\nabla w(x,y,t)|^2 + \beta\cdot\left(w(x,y,t)-\frac{1}{N}\right)^2\right] dx\,dy\,dt}$$

The first term penalizes the large deformation, which minimizes the total amount of deformation brought into the image combination. The second term is the regularizer. The third term is to keep the weighting to be close to the uniform averaging which is statistically optimal for identically distributed (IID) random additive noise. The above-defined energy function can be minimized by solving the following Euler equation: $\boldsymbol{\mu\cdot\nabla^2 w(x,y,t) - \left(\left|\overrightarrow{deform(x,y,t)}\right| + \beta\right)\cdot w(x,y,t) + \frac{\beta}{N} = 0}$ Here $\boldsymbol{\nabla^2 w(x,y,t)}$ is the Laplace operator derived from the regularization item. Note this Euler equation belongs to the generalized diffusion equation, meaning the convergence of its solver is theoretically guaranteed if the iteration step is sufficient small. This method has been implemented as a self-contained software component and integrated into the reconstruction software of MR scanners. The computational time is typically ~1s. To perform the motion correction, a fast non-rigid registration algorithm [5] is applied here with localized cross correlation as the cost function.

Experiment and Results The performance of proposed method was tested on free-breathing fat-water imaging. In this experiment, a free-breathing, single shot fat-water separated imaging protocol was developed using parallel imaging acceleration. The details of imaging sequence and fat-water separation method can be found in [3]. A total of 7 volunteers were scanned using this sequence and each scan included 8 repetitions of two echoes, which led to 8 water and 8 fat images after fat-water separation. For every dataset, a key/reference frame is first selected by searching for the minimal mean square error to all other frames on the water+fat images. The motion correction is then applied to both water and fat images. Every frame except the reference is registered to the key frame and the resulting deformation fields serve as inputs to estimate the optimal weighting functions. Fig. 1 illustrates the superior performance of MTD combination. First, if compared to the result of 50% combination with 4 frames excluded from averaging, the MTD output shows better noise suppression. Second, although the 100% combination image shows the similar SNR to the MTD image, the latter leads to less smearing artifacts introduced by motion correction. When the performance of registration is less satisfied, the smearing artifacts can even be visible in the 50% combination image, while the MTD strategy effectively suppressed these artifacts (Fig. 2). To quantify the effects of noise suppression, a retrospective noise variance estimation algorithm based on Karhunen-Loeve transform and Marcenko-Pastur distribution [6] is applied to the original images and 50%/100%/MTD combined images. For the comparison purpose, all noise variances are normalized against the corresponding key-frame. Table 1 summarizes the results. The noise suppression of MTD is comparable to 100% averaging and better than 50% combination and its gain is further supported by less visible motion-correction artifacts.

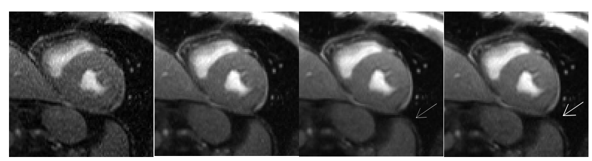

Fig. 1. An illustration of MTD combination. From left to right, the single shot water image; 50% combination, 100% combination and MTD output.

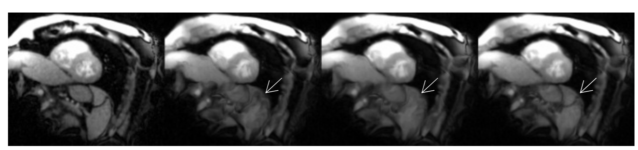

Fig. 2. An illustration of smearing artifacts introduced by imperfect motion correction. From left to right, the single-shot water image; 50% combination, 100% combination and MTD image.

Table 1. Estimated normalized noise variances for water/fat imaging.

	Original	*50%*	*100%*	*MTD*
water	1.0	0.206±0.081	0.159±0.058	0.180±0.066
fat	1.0	0.334±0.135	0.221±0.073	0.232±0.044

Conclusion A novel image combination algorithm is proposed to perform retrospective noise suppression for the free-breathing cardiac MR imaging via the estimation of optimal weights with the minimal total deformation constraint. Compared to the simple uniform averaging used in previous studies, this approach achieves good noise suppression and provides better tolerance to artifacts possibly introduced by imperfect motion correction. This method is fully automated and computationally efficient mainly attributing to its variational formulations. While its performance was demonstrated here on free-breathing fat-water imaging, potential applications of this technique can be easily extended to other free-breathing cardiac imaging applications, because the estimation of MTD weighting function does not rely on any particular imaging contrast or specific sequence features.

References [1] Kellman P et al., MRM 62:1557-1564 (2009) [2] Kellman P et al., MRM 59:771-778 (2008) [3] Kellman P et al., MRM 53:194-200 (2005) [4] Hernando D et al., MRM 63:79-90 (2010) [5] Chefd'hotel C et al., ISBI 753-756 (2002) [6] Ding Yu et al., MRM 63 782-789 (2010)