UNIFIED RECONSTRUCTION AND MOTION ESTIMATION IN CARDIAC PERFUSION MRI

Sajan G Lingala[*]*, Mariappan Nadar*[†]*, Christophe Chefd'hotel*[†]*, Li Zhang*[†] *and Mathews Jacob*[*]

[*]Department of Biomedical Engineering, University of Rochester, NY, USA
[†]Siemens Corporate Research, Princeton, NJ, USA

ABSTRACT

We introduce a novel unifying approach to jointly estimate the motion and the dynamic images in first pass cardiac perfusion MR imaging. We formulate the recovery as an energy minimization scheme using a unified objective function that combines data consistency, spatial smoothness, motion and contrast dynamics penalties. We introduce a variable splitting strategy to simplify the objective function into multiple sub problems, which are solved using simple algorithms. These sub-problems are solved in an iterative manner using efficient continuation strategies. Preliminary validation using a numerical phantom and in-vivo perfusion data demonstrate the utility of the proposed scheme in recovering the perfusion images from considerably under-sampled data.

1. INTRODUCTION

Myocardial first-pass perfusion schemes track the contrast changes resulting from the passage of a contrast agent through the heart. Since it enables the quantitative evaluation of both ischemic and non-ischemic heart disease, perfusion imaging is a key component of most clinical cardiac MRI exams. The standard method is to collect the k-space data of each timeframe during the diastole phase of each heartbeat, where the cardiac motion is minimal. The risk of peripheral nerve stimulation and hardware limitations often restricts the spatio-temporal resolution and spatial coverage, resulting in dark-rim artifacts, underestimation of the transmural extent of defects, inability to visualize all heart regions and inaccurate fitting of the kinetic model.

Conventional $k-t$ space acceleration techniques, which are originally designed for breath-held acquisitions, exploit the sparsity of the signal in the $x-f$ space. Since the data's sparsity in the $x-f$ space is disturbed due to non-periodic respiratory motion and temporal contrast variations, the utility of these schemes are limited in perfusion imaging. To overcome these problems, Pederson et. al proposed to unify the reconstruction of the images and the motion compensation into a single algorithm [1]. They represented the contrast variations using a parametric perfusion model, while motion was modeled as a modulation of a 2-D displacement field, which is estimated from two images acquired at end inspiration and end expiration. The fewer degrees of freedom in this model may be restrictive in practical perfusion imaging applications. Jung et. al, have extended their $k-t$ FOCUSS scheme with motion estimation and compensation for cardiac cine MRI [2]. This scheme approximate the dynamic images as the deformation of fully sampled reference frames, collected before and after the dynamic acquisition. The residuals are then reconstructed from under-sampled k-space data using $k-t$ FOCUSS. Unlike cine MRI, the contrast of the dynamic images are significantly different from the reference images. Hence, the subtraction of the deformed reference image may not generate sparse residuals. Moreover, more complex mutual information similarity measures may be needed for the registration. Fessler recently introduced an elegant energy minimization framework to reconstruct a static image of a moving organ from its measurements [3]. The formulation of the problem as a unified energy minimization scheme enables the appreciation of the tradeoffs in the modeling. However, this scheme is not designed to recover image time series with dynamic contrast variations.

We introduce a novel energy minimization formulation for the joint estimation of the deformation and the images in myocardial perfusion imaging. We model the respiratory motion as an elastic deformation, whose parameters are estimated from the data. We assume the contrast variations due to bolus passage to be smooth in time, once the respiratory motion is removed. This model is considerably less constrained than the parametric scheme used in [1]. Since we do not model the dynamic frames as deformations of pre-contrast reference images, our approach is robust to contrast variations due to bolus passage, in comparison to [2]. Our motion estimation scheme estimates the deformation by registering the dynamic data to a reference dataset that is free of respiratory motion, which is derived from the measurements themselves. We introduce a variable splitting frame work with continuation to minimize the energy function, and thus derive the deformation and the dynamic images. The validation of the proposed scheme using numerical phantom and in-vivo data demonstrate the feasibility in accurately recovering perfusion MRI data from considerably under-sampled data.

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2. THE OBJECTIVE FUNCTION

The temporal contrast variations of any voxel in perfusion MRI is reasonably smooth if the subject is holding his breath. In this context, a simple approach to recover the dynamic imaging data from under-sampled measurements is to exploit the spatio-temporal smoothness of the signal. However, the temporal smoothness is significantly disturbed in the presence of respiratory motion. Simple temporal smoothing will average out the contrasts from different spatial regions and hence result in artifacts and degraded performance. In this context, we propose to simultaneously recover the motion $\mathcal{D}$ and the dynamic images $f(\mathbf{x},t)$ from under-sampled data $b(\mathbf{k},t)$ using the following energy minimization scheme:

$$\{f,\mathcal{D}\}^* = \arg\min_{f,\mathcal{D}} \underbrace{\|\mathcal{A}(f)-b\|^2}_{\text{data consistency}} + \underbrace{\lambda\,\|(\mathcal{D}f)_t\|^2}_{\text{temporal regln.}} + \underbrace{\mu\,\|\nabla f\|_{\ell_1}}_{\text{spatial regln.}}. \tag{1}$$

Here, $\mathcal{A}$ is the Fourier sampling operator, $\mathcal{D}$ is the deformation model ($\mathcal{D}f$ is the motion compensated version of f), ∇f and $()_t$ denotes the spatial gradient and first order temporal derivative respectively. Note that the temporal regularization term penalizes the roughness of the motion compensated dataset $\mathcal{D}f$, rather than f. This approach ensures that the resulting temporal smoothing does not result in artifacts. The rapid variations in f, induced by respiratory motion will be captured by $\mathcal{D}$, which is also estimated during the joint estimation scheme. This approach is very different from [2], where they estimate the deformation between a reference image and the dynamic images. We model the deformation $\mathcal{D}$ as a diffeomorphism [4, 5], which is considerably more flexible than the constrained model used in [1].

3. THE OPTIMIZATION ALGORITHM

We reformulate the unconstrained problem in (1) to a constrained one in (2) by introducing auxiliary variables g and w:

$$\arg\min_{f,\mathcal{D},g,w} \|\mathcal{A}(f)-b\|^2 + \lambda\,\|(g)_t\|^2 + \mu\,\|\,w\|_{\ell_1}, \quad \text{s.t. } \mathcal{D}f = g \text{ and } \nabla f = w \tag{2}$$

The main motivation for this approach is that the constrained scheme is easier to solve than (1). We then relax the equality constraints and penalize their violations by quadratic functions as:

$$\arg\min_{f,\mathcal{D},g,w} \|\mathcal{A}(f)-b\|^2 + \lambda\,\|(g)_t\|^2 + \frac{\beta_1}{2}\|\mathcal{D}f-g\|^2 + \mu\,\|w\|_{\ell_1} + \frac{\beta_2}{2}\|\nabla f - w\|^2 \tag{3}$$

When the penalty parameters β_1 and β_2 approach ∞, the solution of (3) tends to that of (2) and hence (1). The cost in (3) has to be now minimized with four variables $f, \mathcal{D}, g$ and w. Although, this appears complicated, we solve for each of the variables in an alternating fashion similar to [3], assuming the others to be fixed. Thus, the algorithm involves the following four steps:

Derivation of g: With $f, \mathcal{D}$ and w fixed, the minimization of (3) with respect to g is a quadratic smoothing problem, which is solved exactly in the temporal Fourier domain:

$$\mathcal{F}(g) = \frac{\mathcal{F}(\mathcal{D}f)}{(1+\frac{2\lambda}{\beta_1}\omega^2)} \tag{4}$$

where $\mathcal{F}$ is the temporal Fourier operator and ω the temporal frequency. Thus, g is a low pass filtered version of the deformed object $\mathcal{D}f$. For a fixed λ, low value of β_1 would have a stringent cut off passing only components of extremely low frequency and vice-versa.

Derivation of w: To solve this problem, we adapt the multi-dimensional shrinkage solution derived by [6] to yield,

$$w = \frac{f}{\nabla f}\left(\nabla f - \frac{\mu}{\beta_2}\right)_+ \tag{5}$$

where $(.)_+$ is the shrinkage operator given by,

$$(.)_+ = \begin{cases} . & \text{if} \quad . \geq 0 \\ 0 & \text{else} \end{cases} \tag{6}$$

Derivation of f: We collect the terms in (3) with f and rewrite the minimization problem as

$$\arg\min_f \|\mathcal{A}\,(f)-\mathbf{b}\|^2 + \frac{\beta_1}{2}\|f-\mathcal{D}^{-1}g\|^2 + \frac{\beta_2}{2}\|\nabla f - w\|^2$$

Here, we assume the Jacobian of the transformation $\mathcal{D}$ to be approximately equal to one. Minimizing the above expression, we get

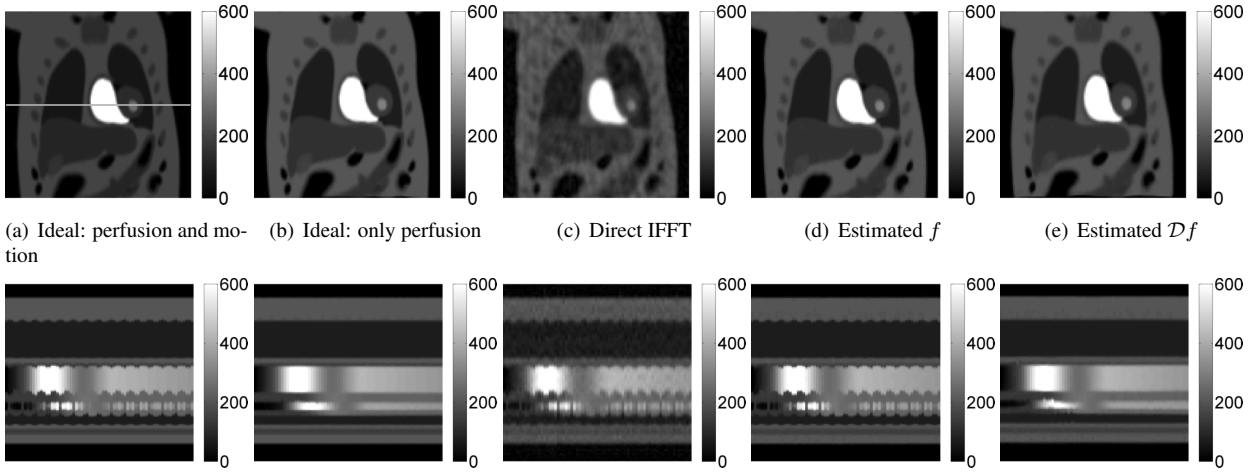
$$\mathcal{A}^*\mathcal{A}(f) + \frac{\beta_1}{2}f + \frac{\beta_2}{2}\nabla^2 f = \mathcal{A}^T b + \frac{\beta_1}{2}\mathcal{D}^{-1}g + \frac{\beta_2}{2}\nabla^T w \tag{7}$$

As shown by the authors in [7], the above problem can be efficiently solved in the spatial Fourier domain if the operator $\mathcal{A}$ obtains the samples on a Cartesian grid.

Derivation of the deformation $\mathcal{D}$: Assuming all the variables in (3) to be known, we solve for the deformation as

$$\mathcal{D}^* = \arg\min_{\mathcal{D}} \|\mathcal{D}f - g\|^2 \tag{8}$$

This is a registration problem, where the dynamic scene $f(\mathbf{x},t)$ is registered frame by frame with a reference scene $g(\mathbf{x},t)$. Note that the reference series is derived from the measurements itself as shown in (4); we do not require additional high resolution reference frames. The temporal profiles of the reference dataset g is significantly more smooth compared to f. This approach enables us to decouple the effects



(a) Ideal: perfusion and motion (b) Ideal: only perfusion (c) Direct IFFT (d) Estimated f (e) Estimated $\mathcal{D}f$

Fig. 1. Performance demonstration of the proposed unifying frame work on PINCAT data: (top row): A spatial frame, (bottom row): image time series profile through the line in (a). The reconstructions in f (d) is devoid of artifacts (which are present in the zero filled direct IFFT reconstruction (c)) and is close to the ideal data (a). The motion is corrected in $\mathcal{D}f$ as is evident in the image time series plot

of smooth perfusion induced contrast changes and the more rapid changes resulting from respiratory motion.

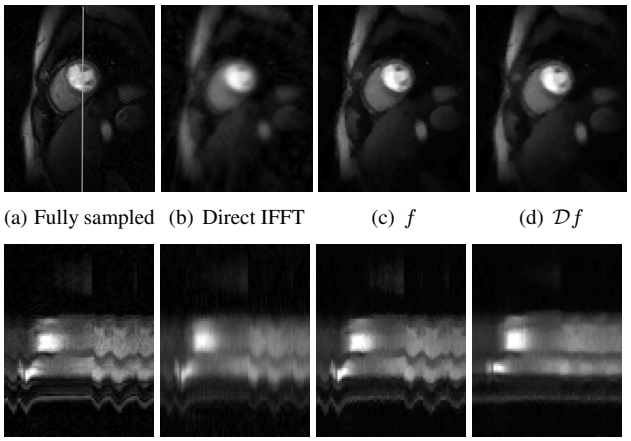
We use a fast flexible deformation algorithm by [4, 5] in our experiments. It uses a Gaussian based regularizer which penalizes irregular deformations. The degree of flexibility of the deformation could be controlled by tuning the width of the regularizer. Specifically, it estimates the deformation such that the vector field that gives for each pixel on the reference its corresponding location on the target image is smooth. It uses a template propagation method to estimate large deformations by the composition of small displacements. A multi-scale approach is used to reduce the non convex problem to multiple simpler problems that can be solved efficiently. The implementation of the algorithm was highly optimized for speed and practical usage.

For a fixed β_1 and β_2, we solve the above four individual sub problems in an alternating manner until convergence is met. Note that one requires a high value of β_1 and β_2 for the constraints in (2) to hold; however at high values of β_1 and β_2, the problem becomes ill conditioned and would result in poor convergence properties. On the other hand, choosing a low value for β_1 and β_2, would ensure fast convergence but with the accuracy compromised. We incorporate a continuation strategy that has been used in related works [7] that uses the variable splitting frame work. Specifically, we start with low values of β_1 and β_2, to solve the modified cost in (3). Once the stopping criterion is met, we then increment β_1 and β_2 and again solve (3). This is repeated until the constraints in (2) are satisfied. This continuation strategy improves the overall convergence rate significantly while maintaining the desired accuracy levels.

4. RESULTS AND DISCUSSIONS

We perform our experiments on the Physiologically Improved Non uniform CArdiac Torso (PINCAT) phantom [8] and in-vivo perfusion data. We focus on a single slice of the phantom $(128\text{x}128)$, which has the cross section of the heart and consider free breathing dynamic contrast enhanced images with a temporal resolution of one heart-beat ($\approx$1 sec) with 70 frames. The fully sampled in-vivo data was acquired with a FLASH-saturation recovery (TR/TE=2.5/1 ms, saturation recovery time=100 ms) sequence on a Siemens 3T scanner at the University of Utah in accordance with the institute's review board. A single short axis slice of size phase/frequency encodes/time frame:$(90\text{x}190\text{x}70)$ of the in-vivo data was considered. The subject was unable to hold his breath during the entire imaging duration and hence the data had residual breathing motion. In our experiments, we using an equiangular pseudo-radial trajectory in the $k-t$ space. The trajectory is rotated by a certain angle in each temporal frame. We consider an under-sampling factor of approximately 5 which corresponds to 25 radial spokes/frame for the PINCAT data and 20 in the in-vivo data set.

In figure 1, we show the validations on the PINCAT data. It is seen that the reconstructed dataset f closely matches the fully-sampled data. This is in sharp contrast to the standard zero filled IFFT reconstruction. The performance of the motion correction task can be evaluated by comparing the image time profiles of f and $\mathcal{D}f$. During the iterations, we used a strategy to initially correct for simpler deformations and as the algorithm converge, we correct for more complex deformations. This is very similar to the coarse to fine correction strategies popularly used in many registration algorithms. Specifically, in the initial iterations, as the floating dynamic scene, f is noisy due to the streak artifacts, we use a highly rigid model, which is robust to noise but less accurate to ob-



(a) Fully sampled (b) Direct IFFT (c) f (d) $\mathcal{D}f$

Fig. 2. Performance demonstration on in-vivo data: (top row): A spatial frame, (bottom row): Image time profile through the cross section marked by the line in (a). The estimated quality of f is close to that of the fully sampled data, resolving the artifacts in the zero filled direct IFFT reconstruction. The motion (ripples in the first three columns) has been corrected in $\mathcal{D}f$ (last column)

tain a decent first guess estimate of the deformations. Note that these artifacts are filtered out in the reference scene, g (4). As the iterations proceed, the floating data gets more cleaner, hence we incorporate a more flexible deformation algorithm thats more accurate to update the estimate of $\mathcal{D}$.

Figure 2 shows the verification of the algorithm on in-vivo data. Similar to the PINCAT results, we observe good correlation of f with the fully sampled data, in contrast to the direct IFFT reconstructions. To estimate the motion, we followed the same strategy of adaptively tuning the flexibility of the deformation algorithm through the iterates.

This work presented the formulation of the unifying reconstruction and motion estimation frame work and preliminary results at moderate under-sampling factors. A more comprehensive analysis of the utility of the proposed frame work at higher under-sampling factors in comparison with reconstruction schemes without motion compensation is a study which we plan to investigate in the future.

5. CONCLUSION

We introduced a novel framework to unify reconstruction and motion estimation steps in first pass cardiac perfusion MRI. The unifying framework had a global objective function with penalties on the spatial smoothness, motion and the contrast dynamics. The global objective was solved by a variable splitting strategy with continuation, where we decompose the complex cost to simpler sub problems. We had sub problems that took well defined forms: low pass filtering of the deformed object, TV shrinkage, analytical Fourier replacement and a l_2 minimizing problem that could be dealt by a standard registration tool. Adaptive tuning strategies to update the estimates of the deformations at different points of iterations were used. Experiments and initial findings on the PINCAT phantom data and in-vivo data demonstrated the usefulness of the proposed scheme.

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7. REFERENCES

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