Water/fat decomposition using globally optimal non-iterative graph surface estimation

Chen Cui[1], Xiaodong Wu[2], Milan Sonka[2], and Mathews Jacob[2]

[1]*Electrical and Computer Engineering, The University of Iowa, Iowa city, IA, United States,* [2]*Electrical and Computer Engineering, The University of Iowa, Iowa city, Iowa, United States*

Introduction

The separation of water and fat signals is a classical problem in MRI with great clinical importance. Recently, Dixon-like methods that estimate the concentrations from a sequence of images acquired with different echo-times, assuming the model [1]:

$$s(x,y,t_n) = \rho_{\text{water}}(x,y)e^{i2\pi f(\mathbf{x})t_n} + \rho_{\text{fat}}(x,y)e^{i2\pi(f(\mathbf{x})+\Delta)t_n}, n = 1,..,N \qquad (1)$$

has received considerable attention. The classical approach is to solve for the unknowns (concentrations $\rho_{\text{water}}(\mathbf{x})$ & $\rho_{\text{fat}}(\mathbf{x})$) as well as the magnetic field inhomogeneity $f(\mathbf{x})$) at each pixel independently either analytically or using a non-linear optimization scheme. However, these approaches often fail due to the non-linearity of equation (1), presence of multiple feasible solutions, presence of noisy pixels, and the large range of field map. Recently several authors have proposed to exploit the smooth variation of the field inhomogeneity map by using region growing/region merging/iterative graph cut approaches to constrain the problem and thus obtain better solutions. While these methods have been shown to provide good solutions in many applications, they cannot guarantee globally optimal solutions. This may result in in-accurate estimates in challenging applications.

Methods

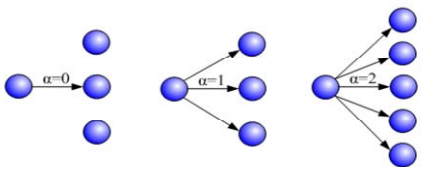
We introduce a novel fat-water decomposition based on non-iterative graph surface estimation, which is guaranteed to converge to a globally optimal solution. We approximate the field map values to lie on a discrete grid ($f = r\delta$), where δ is the grid spacing. We formulate the recovery of the field map at each pixel as the constrained global optimization scheme:

$$\hat{f}(x,y) = \arg\min_f \sum_{p=1}^{P} C\left(f(x_p,y_p)\right) \quad \text{such that} \quad \begin{aligned} &f(x_p+1,y_p) - f(x_p,y_p) \in \{-\alpha\delta,..,0,..\alpha\delta\} \\ &f(x_p,y_p+1) - f(x_p,y_p) \in \{-\alpha\delta,..,0,..\alpha\delta\}, \forall (x_p,y_p) \end{aligned} \qquad (2)$$

The criterion $C(f(x,y))$ is likelihood measure for the field-map and can be derived either using the VARPRO formulation in [3] or the approximate harmonic retrieval based measure in [1]. The range of the field-map is chosen to account for phase wraps. Note that we do not add a smoothness penalty for the field-map as in [3] to make the problem well posed. We instead rely on the constraints, which ensure that the differences in the field map values between adjacent pixels are constrained to lie in a small range (See Fig. 1); these constraints ensure that the problem is well-posed, even when the likelihood measure may have multiple minima at several pixels. In addition, the constraints considerably reduce the computational complexity of the algorithm. We solve (2) using the global graph search algorithm, introduced in [2]. The algorithm is theoretically guaranteed to provide the global minimum of (2). Once the optimal field map is obtained, the fat and water concentrations at each pixel can be determined as $\rho = (\mathbf{A}_{\text{f}}^T\mathbf{A}_f)^{-1}\mathbf{A}_f^T\mathbf{s}$, where $\mathbf{s}$ is the vector of measurements and the matrix $\mathbf{A}_f$ models the equation (1).

Results and Discussion

We validated the proposed algorithm using the datasets provided as part of the ISMRM fat-water decomposition challenge [http://www.ismrm.org/challenge/] . Graph search was conducted in a field-map range of [-1/Δt, 1/Δt] with grid spacing $\delta =$ 10Hz and smoothness constraint factor $k = 1$. 1/Δt is the period of uniformly spaced TEs. The proposed method provided good decomposition on all the datasets. We compare the proposed scheme with the Iterative Graph Cut Algorithm(IGCA) in [3], whose implementation was made available by the authors. The decomposition provided by both algorithms on two datasets are shown in Fig. 2. We observe that the iterative graph cut scheme resulted in a swap, which was resolved correctly by the proposed scheme. The processing time for dataset 2 (size: 250 x 175) was around 30 seconds on an Intel Xeon processor, while the iterative approach [3] took around 60 seconds. The proposed scheme can be readily extended to account for multi-peak lipid models, which will improve the fat estimates. Our current implementation uses a restricted search range, resulting in ambiguities in some datasets. We plan to address these issues in the future.



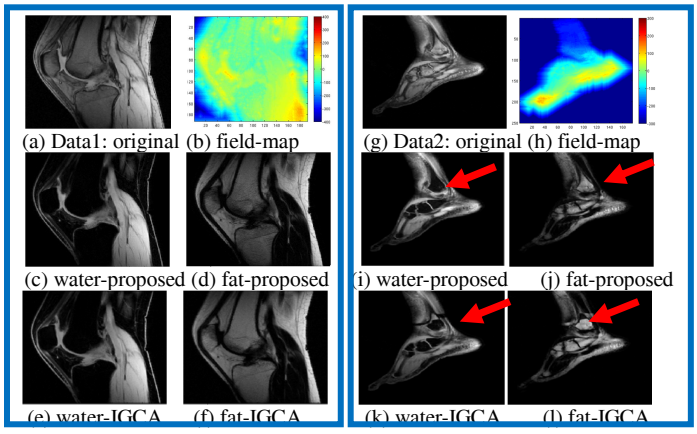


Fig.2

Figure 1(Upper).Illustrating the smoothness constraint with its values of 0, 1, and 2. Figure 2(Right): Separation results comparison between the proposed method and IGCA . Dataset 1:(a)-(f)for foot sagittal; dataset 2:(f)-(j) for knee sagittal . **Reference**:[1] M. Jacob and B.P. Sutton. Medical Imaging, IEEE Trans,2009.[2] X. Wu and D. Chen Automata, Languages and Programming,2002.

[3] D. Hernando, P.Kellman, J.P.Haldar, and Z.P.Liang. Magnetic Resonance in Medicine, 2008.