Phase correction in two-point Dixon water and fat imaging using a three-dimensional region-growing algorithm

J. Ma[1]

[1]Imaging Physics, University of Texas M. D. Anderson Cancer Center, Houston, TX, United States

Introduction

Region-growing techniques for phase correction in MRI allow for spatial phase propagation without assuming a parametric model for the phase distribution [1-3]. Other approaches (such as by fitting functions) often impose an a priori model on the uncorrected phase, and therefore are generally not as applicable. A disadvantage of many previous region growing approaches, however, is the need for an empirically-determined threshold value for phase coherence between two neighboring pixels. As a trade-off, certain regions of an image may become excluded from the region growing process.

In this research, we present an extension of a two-dimensional (2D) region-growing algorithm [4] that was recently developed for two-point Dixon water and fat imaging to three-dimensional (3D). As in 2D, the new algorithm does not require an empirical threshold for phase coherence. An added advantage for 3D is the ability to propagate phase information through other slices into regions that are seemingly isolated in a 2D image.

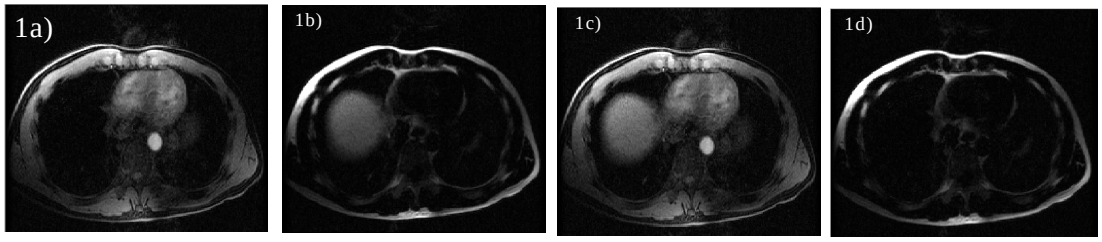
Methods

In two-point Dixon water and imaging, the out-of-phase image after removing the time-independent phase contained in the in-phase image can be written as: $S_1'(x,y) = (W - F)e^{-i\phi}$, where W and F represent respectively the water and fat signals in a given pixel, (x,y) represent the pixel location, and ϕ is the phase error that is due to field inhomogeneity. The main task of phase correction is to determine the phase factor $e^{-i\phi}$, which could be parallel to either $S_1'(x,y)$ or $-S_1'(x,y)$, depending on whether W is larger or smaller than F for a given pixel.

In the 3D algorithm, we construct prior to the region growing a 3D image $S_1'(x,y,z)$ by stacking up all $S_1'(x,y)$ in a given acquisition according to their spatial location along the slice direction. As a first step in phase correction, we calculate G, the directional difference of $S_1'(x,y,z)$ between every two nearest neighbor pixels in all three spatial directions. Region growing is then initiated by selecting a seed pixel, either randomly or with some other criteria. By default, the $S_1'(x,y,z)$ value for the initial seed pixel is assumed to be parallel to its phase factor $e^{-i\phi}$. As the next step, each of the six nearest neighbors of the seed pixel is visited by the region growing. Upon visit, each of the pixels is placed onto a series of empty but ordered pixel stacks according to the G values. When the directional difference falls into a range that is small, the corresponding pixel is placed onto a pixel stack that has a low order. Conversely, a pixel will be placed onto a pixel stack that has a higher order if the directional difference falls into a larger range. In the subsequent rounds of region growing, the pixel in the lowest and non-empty pixel stack is selected as the new seed pixel. As for the initial seed, each of the six nearest neighbor pixels of the new seed, except those that have been visited previously, will now be visited and placed onto the pixel stacks. In order to determine the phase factor $e^{-i\phi}$ for the new seed pixel, an amplitude-weighted average of the phase factors for the pixels whose phase factors have been previously determined and that lie within a boxcar neighborhood (for example, 7x7x5) centered at the seed pixel is calculated. The direction of the averaged phase factor is then used to help select either $S_1'(x,y,z)$ or $-S_1'(x,y,z)$ as representing the phase factor for the new seed pixel. The entire region growing continues until all pixels in the 3D image has been visited, or equivalently, until all the pixel stacks become empty.

Experiments and Results

The above algorithm was implemented in Matlab (MathWorks, Natick, MA) and evaluated using in vivo data. With a commercially available fast gradient echo dual echo sequence running on a 1.5T clinical scanner (GE Medical Systems, Milwaukee, WI), both in-phase (TE ≈ 4.6ms) and out-of-phase (TE ≈ 2.3ms) images of an entire abdomen can be collected in a single breath-hold. For signal reception, a 4-channel torso-phased array coil was used.



For a specific slice processed by the 2D algorithm, the dome of the liver, which appears disconnected from the other tissues, is absent from the water-only image (Fig. 1a) and incorrectly assigned to fat-only image (fig 1b). With the 3D algorithm, correct phase propagation is achieved via adjacent slices. As a result, no misidentification of the tissue type is seen on the water-only (Fig. 1c) and fat-only (Fig 1d) image.

Conclusions

By extending region growing from 2D to 3D, we demonstrated that correct phase correction of seemingly isolated tissues in a given slice can be achieved with growing through adjacent slices. Since the region-growing is designed to follow a path with maximum directional smoothness, performing region growing in 3D could be more reliable than in 2D.

References

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