

Accelerated Robust Fat/Water Separation at 7T

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Introduction

We are developing MR technologies to assess lipid depots in mice as a function of genes, diet, age, and therapy. Our current work is based on creating a new 3-point Dixon fat/water decomposition method to address the significant field variation on 7T small animal scanners, which challenges the accuracy and robustness capabilities of existing methods such as IDEAL[1]. We used a formulation similar to that reported by Hernando, et al[2] that solves for the fat and water content of each voxel by separating the estimation into a non-linear field map estimation and a linear chemical species estimation. However, the problem of computation time has limited the practical applicability of this method. The purpose of this abstract is to present our work on fat/water separation methods using Markov random field spatial regularization and iterated conditional modes (ICM), which includes several new implementation strategies that greatly reduce computation time while generating decompositions that are negligibly different from those generated by Hernando, et al's algorithm. This reduced computational time removes a major obstacle to the utilization of this robust formulation.

Methods

Three acceleration strategies were used in processing asymmetric spin echo data acquired on a Bruker BioSpec 7T/30cm. First, we employed a stability tracking (ST) strategy during the estimation process, wherein we skipped voxels that were not expected to change between iterations. Second, we masked out the air voxels by performing Otsu's thresholding method[3] on the source magnitude images, followed by morphological hole filling to ensure that all voxels inside the mouse were included. If necessary, this process can be quickly tuned to ensure accuracy of masking. Finally, we used a multiresolution image pyramid (MRIP) to speed convergence (see Figure 1). A single 3-D mouse volume data set was used to compare these acceleration strategies.

Results

The mean time needed for convergence (averaged over the 23 slices in this volume) of each acceleration strategy is shown in Figure 2. For our data, the Hernando algorithm[2] required a mean time of about 7000 seconds per 512x256 slice on our 3.2GHz computer with 8GB of RAM. Combining all three of our acceleration methods allowed us to find the solution within only 117 seconds. This represents a decrease from about 2 days to about 45 minutes of processing time for the 3-D volume data set. Our accelerated method yielded an answer very close to that from the Hernando algorithm[2], with about a 70 fold speed increase. When combined with our extrapolation initialization scheme (presented separately), we were able to quickly, robustly, and correctly separate fat and water where existing methods have failed to do so.

Discussion

We have shown that we can quickly solve the VARPRO-ICM formulation using stability tracking, image masking, and multiresolution image pyramid. Using masking and ST, we are able to skip pixels in each iteration that do not require estimation. Using MRIP, we are able to very rapidly perform the estimation on downsampled versions of the data, allowing us to initialize the estimation at full resolution with a guess that is much closer to the actual solution than other initial guesses, such as zeroes. ST generally yielded the largest speed improvement, because most entries in the field map do not change between the many iterations that the algorithm requires. This is because the data cost remains the same throughout the iteration process, and the smoothness cost only changes if one of the neighboring estimates has changed (see [1] for a description of these terms). However, it is the combination of the three strategies that resulted in almost a 2 order of magnitude decrease in processing time, allowing us to do quantitative calculations on chemical shift volume data within a practically feasible amount of time. The use of VARPRO-ICM formulation is encouraged because it is generally capable of handling the large field variations found at 7T. Acceleration allows this formulation to move towards becoming a practical solution for robustly processing Dixon-type data.

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References

[1] Reeder, S.B, et al. MRM 2005; 54:636-644. [2] Hernando, D., et al. MRM 2008; 59:571-580. [3] Nobuyuki, O. IEEE Trans Systems, Man and Cybernetics 1979; 9:62-66.

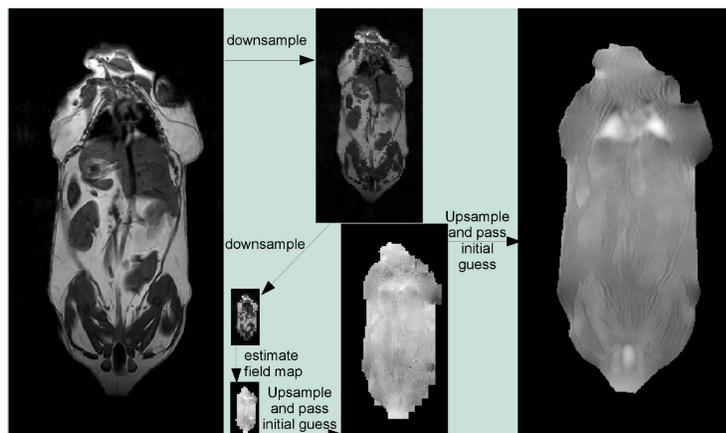


Figure 1: Multi-Resolution Image Pyramid. The image is successively downsampled to create the source images shown. Field map estimation is then performed on the lowest resolution image, and the solution is upsampled to create an initial guess for the intermediate resolution. This process is repeated until a solution is found to the original, full resolution image. In this paper, we use three layers (low, intermediate, and full resolution), where each dimension of each layer was reduced to a 1/4 that of the previous layer.

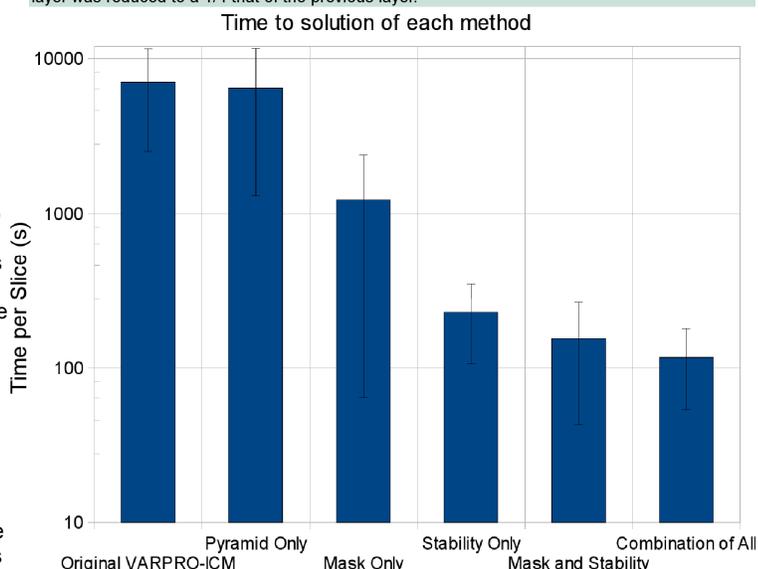


Figure 2: Method Speed Comparison. A single 3-D volume was used to compare the acceleration strategies on a per-slice basis. The original algorithm[2] required a mean of 7048 seconds to terminate, per slice. Using the MRIP strategy decreased this to 6459s. Using the masking strategy, convergence required 1231s, whereas when using stability tracking, convergence took 228s. Combining stability tracking and masking reduced processing time to 155s, and combining all three methods required just 117s. Overall, this represents a decrease from almost 2 days to about 45 minutes for a 3-D whole-mouse data set.