

Magnetic Resonance Fingerprinting Trajectory Optimization

Ouri Cohen¹, Mathieu Sarraoane^{1,2}, Brandon D. Armstrong^{1,2}, Jerome L. Ackerman¹, and Matthew S. Rosen^{1,2}

¹Department of Radiology, MGH/Athinoula A. Martinos Center for Biomedical Imaging, Massachusetts General Hospital, Charlestown, MA, United States, ²Department of Physics, Harvard University, Cambridge, MA, United States

PURPOSE: Magnetic resonance fingerprinting [1] can be used to obtain maps of multiple tissue parameters in a single scan by varying the flip angles (FA) and repetition times (TR) of each acquisition. To uniquely distinguish between the various tissue parameters, current implementations require a large number (>1000) of acquisitions for each phase encoding line. Consequently, the generation of a suitable dictionary, as well as the matching process, requires significant computational resources and processing time. The large number of acquisition entails an increased specific absorption rate and, in order to avoid excessive scan times, a subsampling of k-space that may incur undersampling artifacts. Here we propose an optimization method which addresses these issues, allowing the use of fewer acquisitions ($\times 100$ reduction) without affecting image quality.

METHODS: For simplicity, we describe the method for T_1 mapping only though the extension to other tissue parameters (T_2 , off-resonance etc...) is straightforward. An initial randomly generated seed vector of TRs and FAs of length N is used to simulate the signal for a range P of T_1 values. The resulting $N \times P$ matrix A is then used to calculate a dot product matrix $D = A^T A$. The diagonal elements of D , indicating the closeness of a match between a trajectory resulting from a given T_1 and itself, are equal to 1. Off-diagonal elements, however, are indicative of the quality of matching between every two different elements of the matrix A . Discriminating between T_1 values in the matching process requires that the dot

product of a measured trajectory with the pre-computed trajectory stored in the dictionary be high for the correct T_1 value and, ideally, zero for all others. To find the vector of TRs and FAs which yield this optimum we formulate the optimization problem as:

$$\min_x f(x) \quad s.t. \quad \sum_{i \neq j} D(x)_{ij} - \lambda \sum_{i=j} D(x)_{ij} \quad (1)$$

where $f(x)$ is the function to simulate the

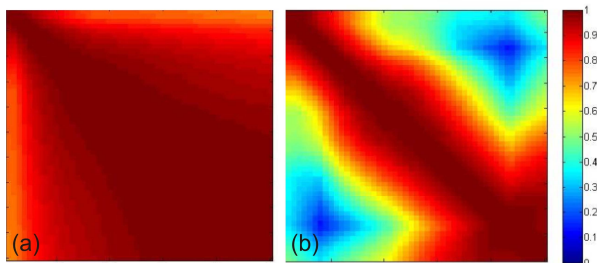


Figure 1: Dot product matrices for the unoptimized (a) and optimized (b) trajectories. Note the superior diagonalization of the optimized matrix.

trajectories and compute the dot product matrix D given a vector x of TRs and FAs. A penalty term λ is applied as well to avoid minimizing the on-diagonal elements. A constrained non-linear solver is then used to solve equation (1).

RESULTS: The optimization over a range $T_1 \in [1, 2000]$ ms was carried out for $N=10$ acquisitions. The resulting un-optimized and optimized dot product matrices are shown in Figure 1. The optimized trajectory was used to image a healthy in-vivo mouse using a surface coil on a 15T Magnex scanner equipped with a Siemens console. The resulting T_1 map is shown in Figure 2.

DISCUSSION & CONCLUSION: The optimized trajectory yields a dot product matrix that is more diagonal, implying better selectivity and consequently better matching. Despite the small number of measurements, the relevant anatomical features are still visible. Artifacts in the image are the result of the severe inhomogeneity of surface coils and can be improved with the use of a volume coil.

REFERENCES: [1] Ma et al, Nature 2013; 495:187-192.

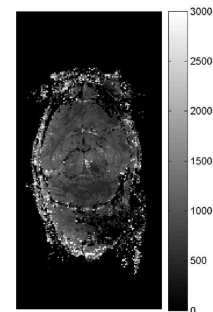


Figure 2: In vivo T_1 map of a mouse brain. The scales are in ms. Note the anatomical features visible despite the small number of measurements,