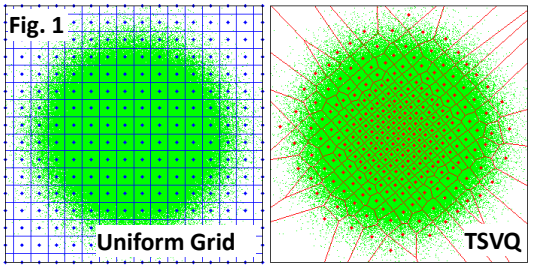
Efficient Dictionary Design for MR Fingerprinting using Tree-Structured Vector Quantization

Zhitao Li[1], Benjamin Paul Berman[2], Diego R Martin[3], Maria I Altbach[3], and Ali Bilgin[1,4]

[1]*Electrical and Computer Engineering, University of Arizona, Tucson, Arizona, United States,* [2]*Applied Mathematics, University of Arizona, Tucson, Arizona, United States,* [3]*Department of Medical Imaging, University of Arizona, Tucson, Arizona, United States,* [4]*Biomedical Engineering, University of Arizona, Tucson, Arizona, United States*

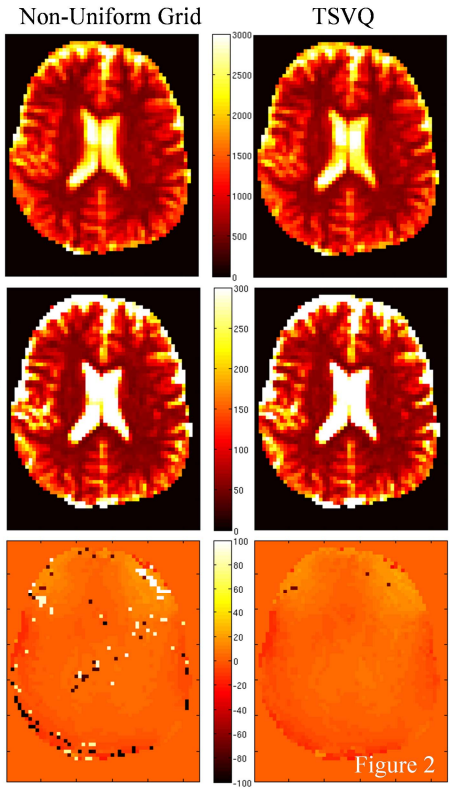
Introduction: MR fingerprinting (MRF) is a recent method for estimation of multiple tissue parameters from rapidly acquired data[1]. In MRF, a time series of signal evolution is acquired rapidly while acquisition parameters (such as TR and flip angle) are changed in a pseudorandom manner at each time point. The signal evolution of each pixel over time is referred to as a "fingerprint". Each acquired fingerprint is used to search a dictionary of precomputed fingerprints obtained using Bloch simulations for a range of tissue parameters. Once the closest match in the dictionary is determined, the tissue parameters corresponding to this atom in the dictionary are assigned to the current pixel. While the data necessary to generate multiple tissue parameter maps can be acquired rapidly in MRF, reconstruction of the parameter maps can be very computationally demanding when tissue parameters are estimated at clinically acceptable resolutions. Accurate parameter estimation requires large dictionaries with many atoms, each with thousands of time points. However, storage of such dictionaries require large memory and the matching process becomes increasingly demanding with increasing dictionary size. Therefore, efficient design of dictionaries used in MRF remains an open problem. In this work, we propose the use of Vector Quantization (VQ) to design efficient dictionaries for MRF. Our proposed method produces compact dictionaries, with corresponding reductions in memory and computational requirements, while providing accurate parameter maps.

Methods: The conventional dictionary design procedure in MRF can be summarized as follows: First, the typical physiological limits of each tissue parameter are determined. This range is divided into uniform intervals for each tissue parameter and Bloch simulations are performed to generate dictionary atoms that correspond to the resulting high-dimensional grid of tissue parameters. In [1], this design method was improved by dividing the full parameter range into two and using different increments in different regions (e.g. T1 values were taken to be between 100 and 5,000 ms, with increments of 20 ms below a T1 of 2,000 ms and increments of 300 ms above 2,000 ms). The motivation behind this non-uniform grid is to use finer sampling in regions of expected tissue parameters and coarser sampling in regions of unlikely tissue parameters. In this work, we illustrate that the MRF dictionary design problem can be formally stated as quantization of a high-dimensional vector of tissue parameters. Hence, determining the finite number of centroids to represent the parameter grid corresponds to VQ [2]. Given the probability density function (PDF) of vectors of interest, VQ design procedure creates a mapping of each parameter vector to a centroid under minimum distance rule. Specifically, we propose to use a Tree-Structured Vector Quantizer (TSVQ) for MRF dictionary design which can be summarized as follows: K-means clustering is applied to the training set of vectors (of tissue parameters) to divide the data into two clusters. The k-means algorithm is then repeated to divide each of these two clusters into two additional clusters. This procedure is repeated until a tree of desired depth is achieved. The centroids of the clusters at the leaves of the tree are the final centroids. Bloch simulations are then performed to create the fingerprints corresponding to these centroids. Since TSVQ recursively divides the vector space into two pieces using hyperplanes at each iteration, an efficient clustering of the vector space can be achieved quickly. Fig. 1 illustrates a comparison of clusters achieved using the uniform grid and the proposed TSVQ procedure. The green points in the figure denote the training data. It is easy to see that the average quantization error obtained using TSVQ is significantly smaller. To quantify the benefits of the proposed approach in MRF, three MRF dictionaries were simulated each with roughly 5000 centroids. Simulated training and test data sets were generated using the range of T1 and T2 values reported in literature for white matter (μ_{T1}=560ms, σ_{T1}=25ms, μ_{T2}=60ms, σ_{T2}=5ms), gray matter (μ_{T1}=1150ms, σ_{T1}=51ms, μ_{T2}=100ms, σ_{T2}=3ms) and CSF (μ_{T1}=2500ms, σ_{T1}=217ms, μ_{T2}=320ms, σ_{T2}=60ms) at 3T. *in vivo* data was also acquired using an inversion recovery TrueFISP MRF sequence on a 3T scanner (16-channel head coil, slice thickness=5mm, image matrix=128x128, FOV=340mm, single-shot VD spiral trajectory). TR and flip angles were varied as described in [1] to acquire 1000 time points. The acquired data was reconstructed using a non-uniform grid dictionary with 962880 atoms, as well as a TSVQ dictionary with 57174 atoms. In our *in vivo* experiment, T1, T2 and off-resonance effects were all considered.



	Average Error
Uniform Grid	23.9101
Non-Uniform Grid	12.933
TSVQ	6.5588

Results and Discussion: The average quantization error obtained using different clustering methods on simulated data are shown in the table. As shown in the table, The TSVQ method reduced the average error by roughly 3.7 times compared to the uniform grid. It was determined that the number of clusters in TSVQ can be lowered to 200 to achieve the same average quantization error as the uniform grid with 5000 clusters, a 25X reduction in dictionary dimension. The *in vivo* results are shown in Fig. 2. It can be seen that, although the TSVQ dictionary has a size of only 1/17 of the non-uniform grid dictionary, it can still generate parameter maps as accurate as the non-uniform grid dictionary.



Conclusions: We proposed a TSVQ-based clustering approach for MRF dictionary design. The proposed approach allows significant reduction in dictionary dimensions and can enable clinically relevant reconstruction accuracy and time which is a major bottleneck for clinical usefulness of MRF.

References: [1]D. Ma et al., Nature, 2013. [2]Gersho and Gray, Vector Quantization and Signal Compression, Springer, 1991.