A Novel Iterative Thresholding Algorithm for Compressed Sensing Reconstruction of Quantitative MRI Parameters from Insufficient Data

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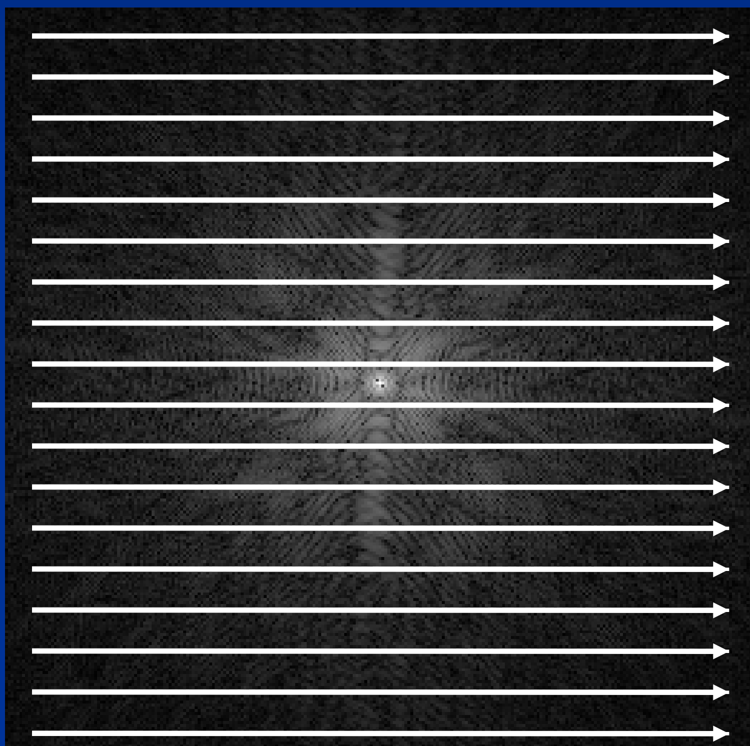
k-Space and Image Space

$2k_{\max}$



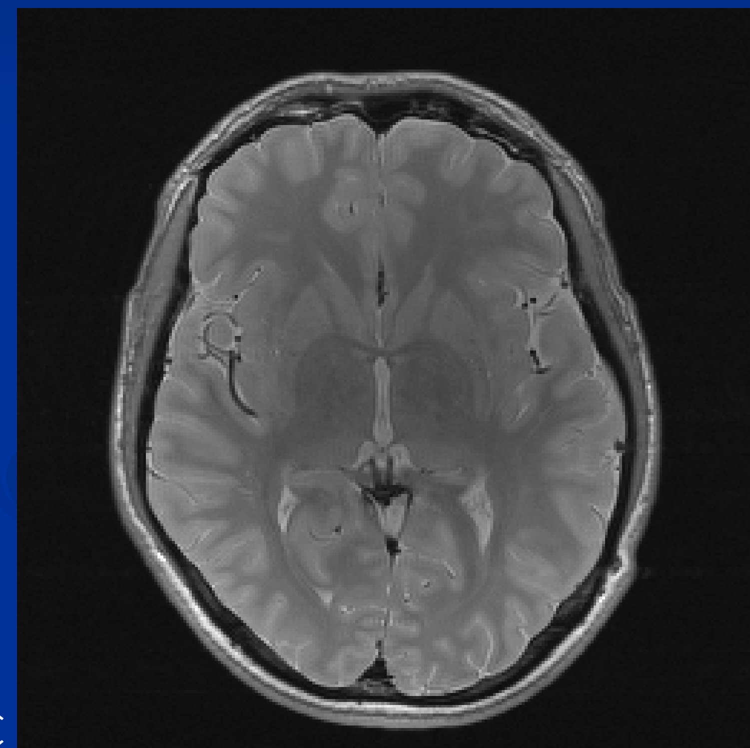
$\updownarrow \Delta k$

Inverse Fourier Transform

$\rightarrow$

FOV

$\Delta x \updownarrow$



$$\Delta k = \frac{1}{FOV}$$

$$\Delta x = \frac{1}{2k_{\max}}$$

Signal Modeling

$$s(\mathbf{k}) = \int_{VOI} \boxed{e^{i\mathbf{k}\cdot\mathbf{r}} c_\gamma(\mathbf{r})} f(\mathbf{r})\, d\mathbf{r}, \quad \gamma = 1, \ldots, N_C$$

$$\mathbf{s} = \mathbf{E}\mathbf{f}$$

Data Vector

The Encoding Matrix

Image Vector

Actual Acquisition:

$$\tilde{\mathbf{s}} = \mathbf{E}\mathbf{f} +$$

i.i.d. Gaussian noise

Quantitative MRI

- Yields maps of physically meaningful parameters underlying MRI contrast mechanisms and often associated with micro-structural tissues features

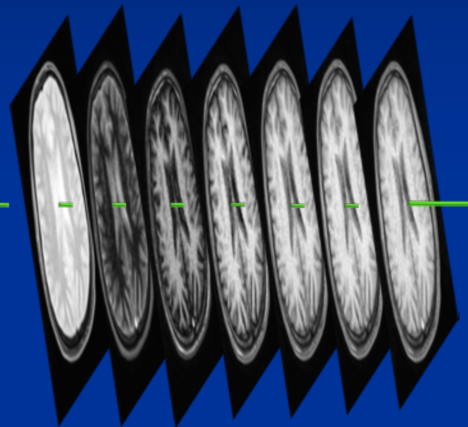
  - T1, T2, diffusion coefficients, magnetization transfer parameters, fat fraction, etc.

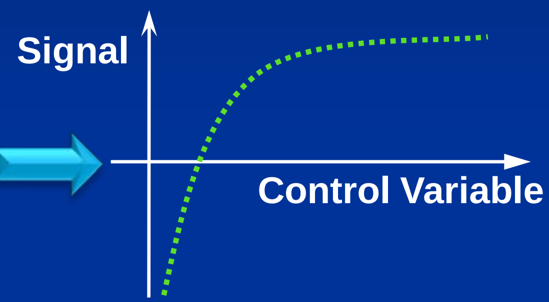
- qMRI is based on analytical models of MRI signal
- Example: T1 relaxometry with inversion recovery

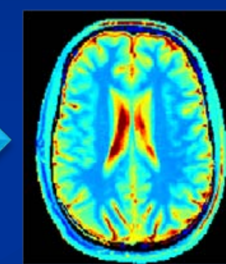
$$F(\underbrace{T_I;}_{\substack{\textbf{Control}\\\textbf{Parameters}\\\textbf{(to be prescribed)}}}\underbrace{M_0, T_1}_{\substack{\textbf{Free}\\\textbf{Parameters}\\\textbf{(to be determined)}}}) = M_0\left(1 - 2e^{-T_I/T_1}\right)$$

Typical qMRI Procedure

Example: Inversion Recovery T1 Mapping







1. Data Acquisition

Several datasets with different values of control variable

$$s_n(\mathbf{k})$$
$$n = 1, .., N$$

2. Image Reconstruction

Inverse FFT, gridding, parallel MRI, iterative methods

$$\mathbf{f}_n = \arg\min_{\mathbf{f}_n} \left\| \mathbf{s}_n - \mathbf{E}\mathbf{f}_n \right\|_2$$

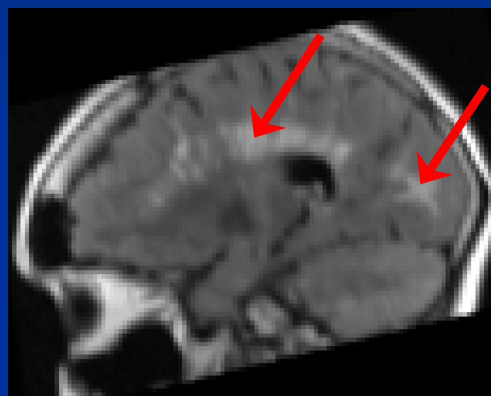
3. Pixelwise fit of the images to the model to yield parametric maps of interest

$$M_0, T_1 = \arg\min_{M_0, T_1} \left\| F\left(T_{I,n}; M_0, T_1\right) - \mathbf{f}_n \right\|_2^2$$

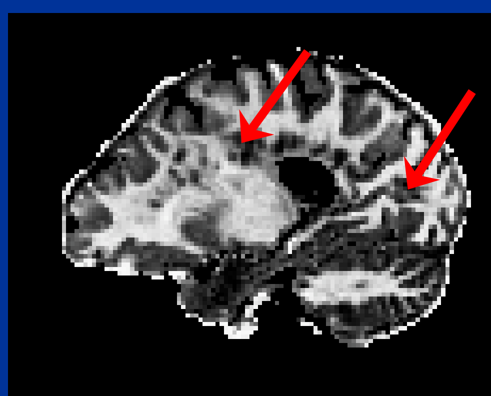
Example qMRI Applications

Imaging Myelin Disruption in Multiple Sclerosis using Multicomponent T2 relaxometry

Anatomical T2-FLAIR



Quantitative Myelin Water Fraction Map



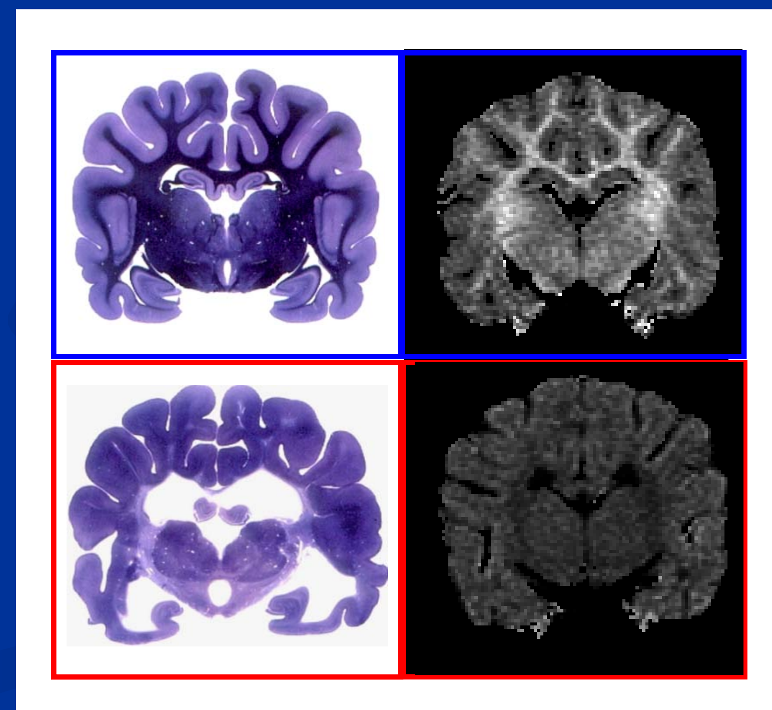
Courtesy of Sean Deoni

Imaging Myelination in Canine Model of Dismyelination Disease using quantitative magnetization transfer

Myelin Stains | Bound Protons

Normal

Myelin Deficient



Samsonov et al, ISMRM 2010

Challenges of qMRI

- Long acquisition times

  - Number of required images should be at least <u>equal to the number of free parameters</u>; in practice, many more are required
  - Patient discomfort, prone to motion

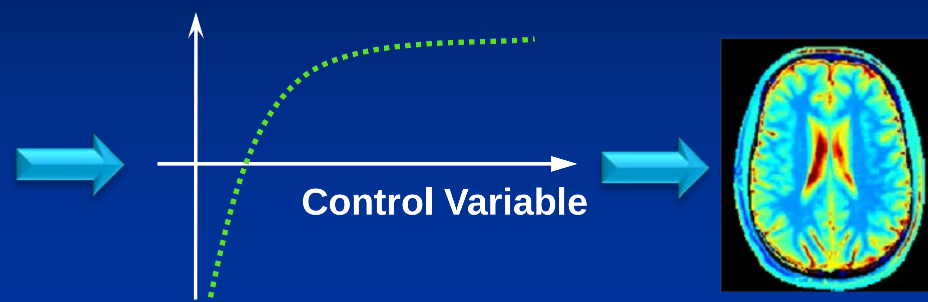
- Accuracy of modeling in the presence of hardware errors/imaging imperfections

The goal is to decrease imaging time while maintaining/increasing SNR efficiency and accuracy of parameter estimation

qMRI Acceleration Approaches

Advanced Modeling	Fast Acquisition	Advanced Recon
Prior Knowledge	Steady-State Sequences	Parallel MRI
Constrained Modeling	Non-Cartesian Trajectories	Parameterized Estimation
		Compressed Sensing

Parameterized qMRI Reconstruction



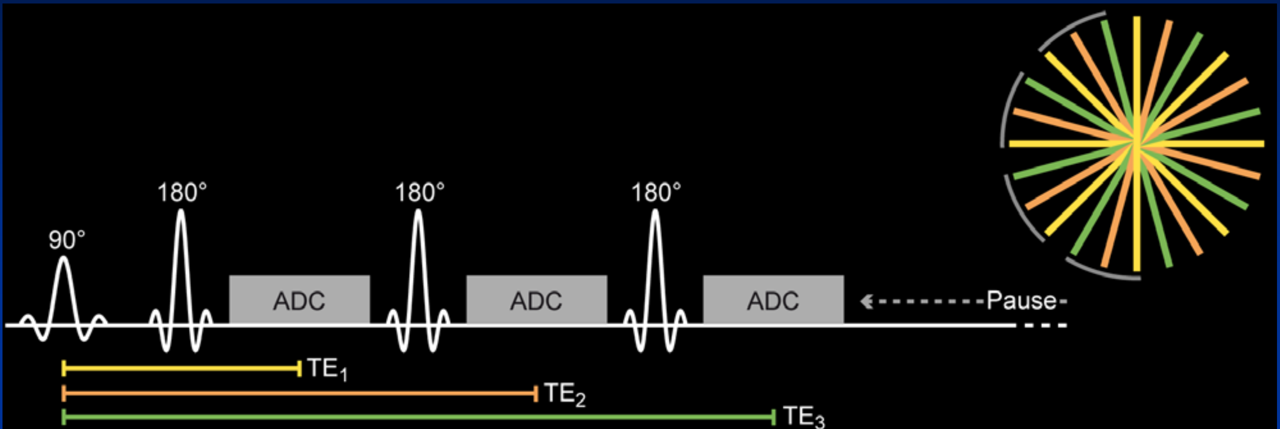
1. Data Acquisition

Several datasets with different values of control parameters

2. Direct estimation of parametric maps fitting to k-space data

- Errors associated with separate image reconstruction step may be reduced
- No need to satisfy Nyquist limit for each image but only for the parametric series as a whole

T2 Mapping From Radial FSE Data

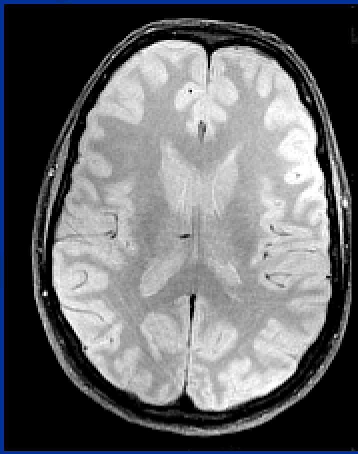


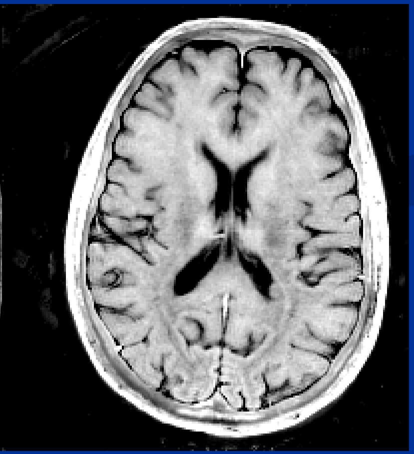
$$F_j(\vec{\rho}, \vec{R}, t, c) = \sum_{\vec{r} \in FOV} \rho(\vec{r}) \cdot e^{-R(\vec{r}) \cdot t} \cdot C_c(\vec{r}) \cdot e^{2\pi i \vec{r} \cdot \vec{k}_j}$$

$$\Phi(\vec{\rho}, \vec{r}) = \sum_t \sum_c \left\| \vec{F}(\vec{\rho}, \vec{r}, t, c) - \vec{y}_{t,c} \right\|_2^2$$

Gridded Echo Image

Proton Density **R2 Relaxivity**





- Parameterized reconstruction allows T2 mapping from significantly reduced radial data

KT Block et al, IEEE TMI 28: 1759-1769, 2009

Problems with Parameterized Recon

- Limited to simple models like single exponential decay; often such models do not describe all image data well enough

  - Example: T2 decay in brain pixels with partial voluming (especially with CSF) may not be single exponential

- Errors from such inadequate modeling may propagate through the rest of the image because estimation is not local anymore
- Very slow convergence of the algorithm and sensitive to the choice of reconstruction parameters

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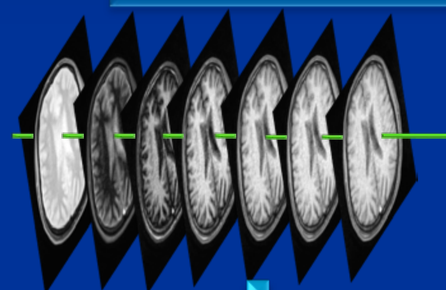
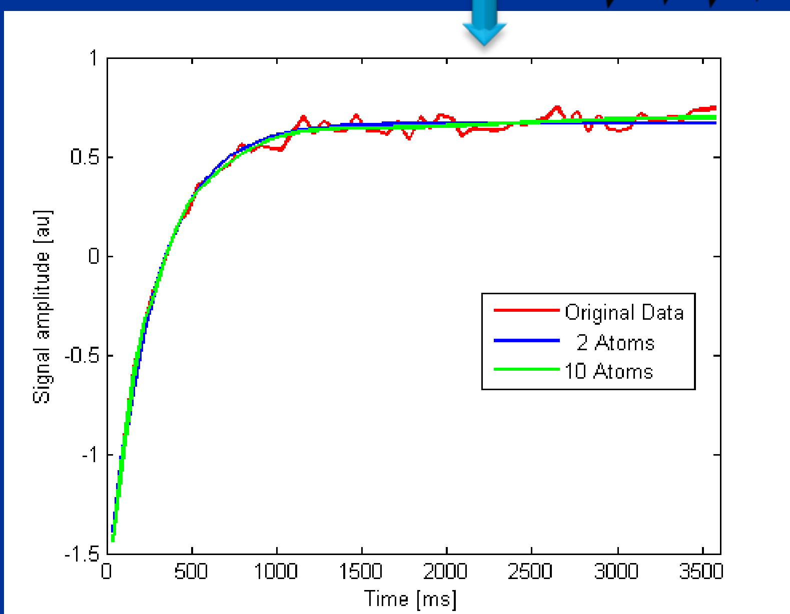
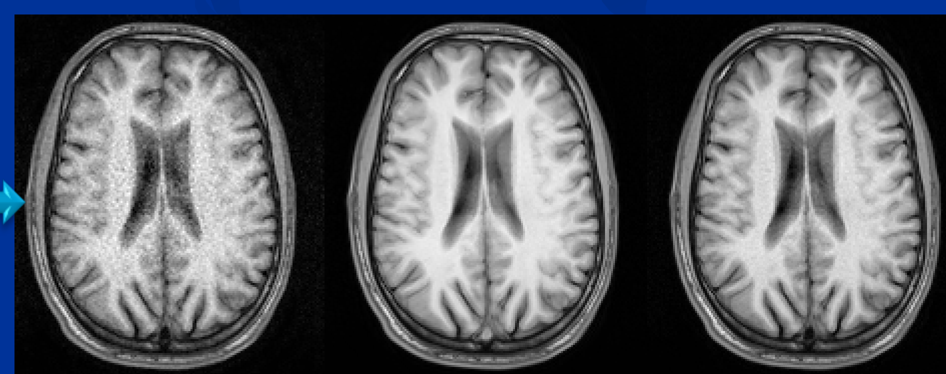
CS with Model-Based Transform

Generate signal prototypes from model → Train dictionary (K-SVD) → Apply dictionary in CS reconstruction (OMP)



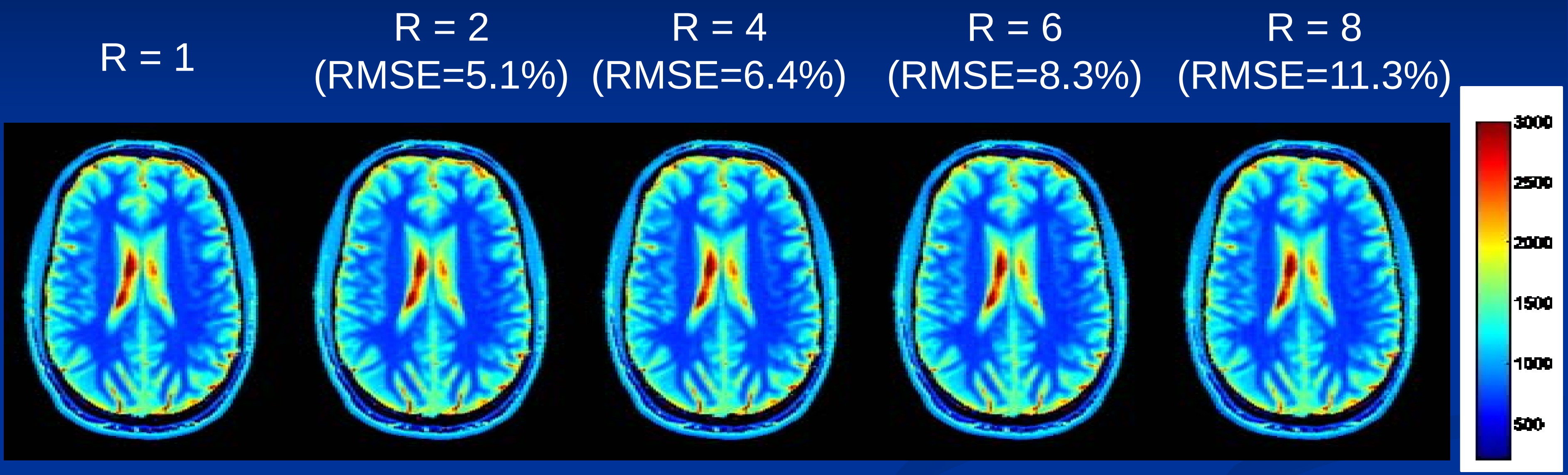




Original image 2 Atoms 10 Atoms

Courtesy of M. Doneva

T1 Mapping

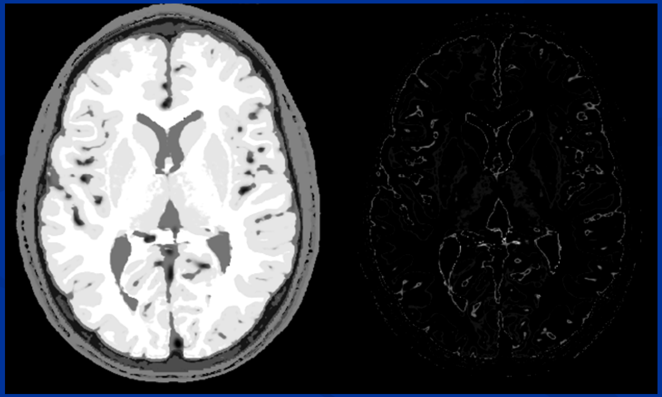


- CS with model based transform allows efficient acceleration of T1 mapping
- Adequate representation requires many atoms (up to 8), which limits acceleration and may in principle be excessive for most tissues

Courtesy of M. Doneva

Rationale for Proposed Method

- Perfect knowledge of underlying analytical in parametric series is a rare situation
  - imaging imperfections
  - partial voluming (multiple tissue types within one voxel)
  - inaccurate modeling
- <u>Example:</u> Determination of longitudinal relaxation time T1 using variable flip angle SPGR
  - DESPOT1, Deoni et al. MRM 2004
  - Norm of residual reveals pixels with poor fit but used analytical model



- **<u>Approach:</u>** Use analytical model to "glue" images for reconstruction from incomplete data

Use CS to gain robustness against pixels which are poorly described by the analytical model

Algorithm

$$\overline{\mathbf{f}}^{(k+1)} = H_\sigma\left(\overline{\mathbf{f}}^{(k)} + \overline{\mathbf{E}}^H\left(\overline{\mathbf{s}} - \overline{\mathbf{E}}\overline{\mathbf{f}}^{(k)}\right)\right)$$

$$\overline{\mathbf{f}} = \left[\mathbf{f}_1,\dots,\mathbf{f}_N\right]^T; \overline{\mathbf{s}} = \left[\mathbf{s}_1,\dots,\mathbf{s}_N\right]^T$$

$$\overline{\mathbf{E}} = diag\left(\left[\mathbf{E}_1,\dots,\mathbf{E}_N\right]\right)$$

$$H_\sigma\left(\overline{\mathbf{f}}_i\right) = \begin{cases} \overline{\mathbf{f}}_i, & \left\|\mathbf{r}_i\right\| \geq \sigma \\ F\left(\overline{\mathbf{p}}_i\right), & \left\|\mathbf{r}_i\right\| < \sigma \end{cases};$$

$$\overline{\mathbf{p}}_i^* = \arg\min_{\overline{\mathbf{p}}_i} \left\|F\left(\overline{\mathbf{p}}_i\right) - \overline{\mathbf{f}}_i\right\|_2^2; \mathbf{r}_i = F\left(\overline{\mathbf{p}}_i^*\right) - \overline{\mathbf{f}}_i;$$

$$F - analytical\ model; \overline{\mathbf{p}} - MR\ \ parameters$$

Step 1: Steepest descent update of the solution vectors

Step 2: Fit MR parametric maps and find the residual

Step 3: Threshold the norm of residual and update the solution pixels with analytically recalculated signal if the thresholded value is 0 (CS enhancement)
Go to **Step 1**.

Non-CS version: all pixels are updated in Step 3

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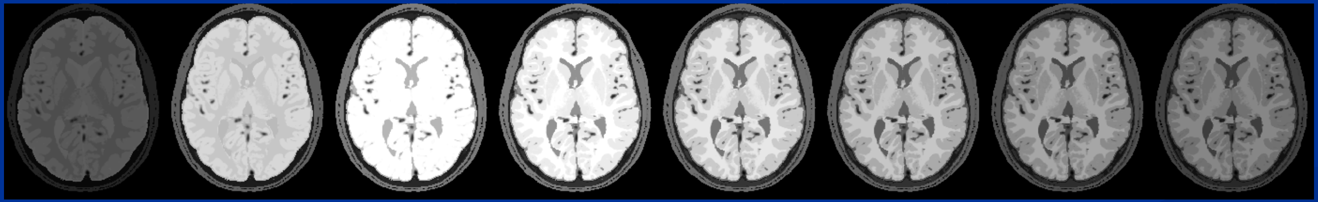
Results

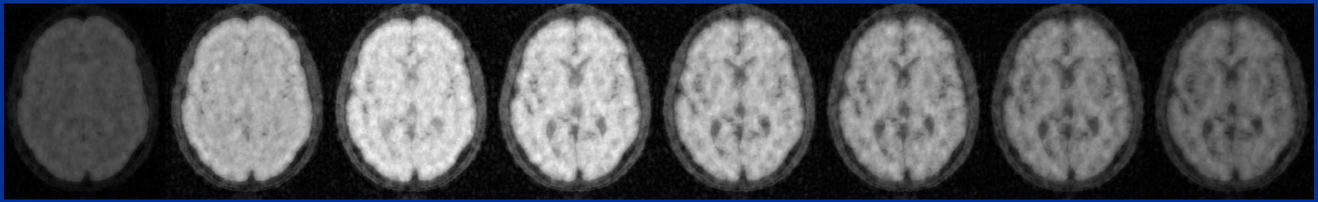
- BrainWeb digital brain phantom; DESPOT1 T1 mapping
  - TR=5 ms, α=[1 3 5 8 11 14 18 23]°, randomized undersampling by 3.5 times

$$F(\alpha, T_R; M_0, T_1) = M_0 \sin\alpha \frac{1 - e^{-T_R/T_1}}{1 - e^{-T_R/T_1}\cos\alpha}$$

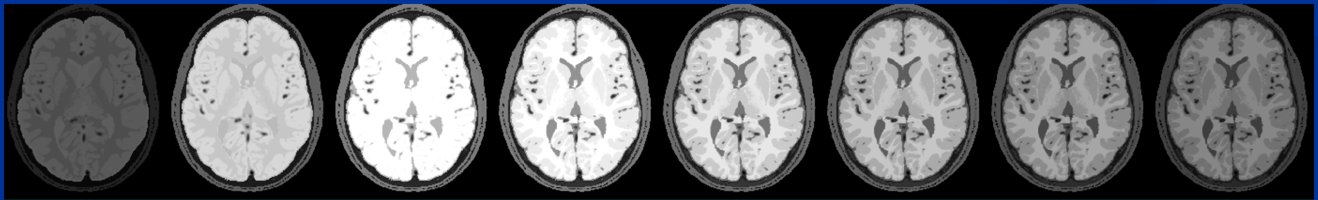
Fully Sampled Images



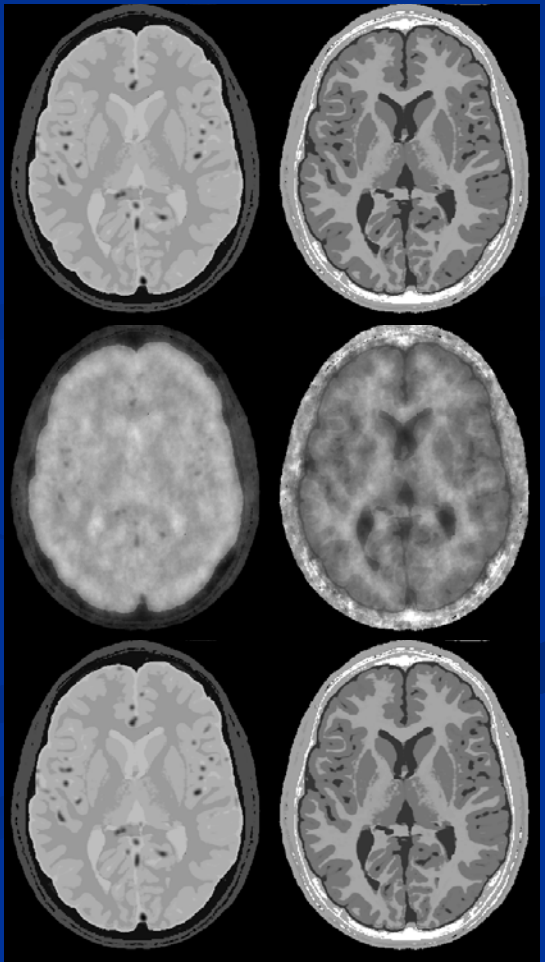
Regular Recon (zero-filling, iFFT)



Proposed CS Recon

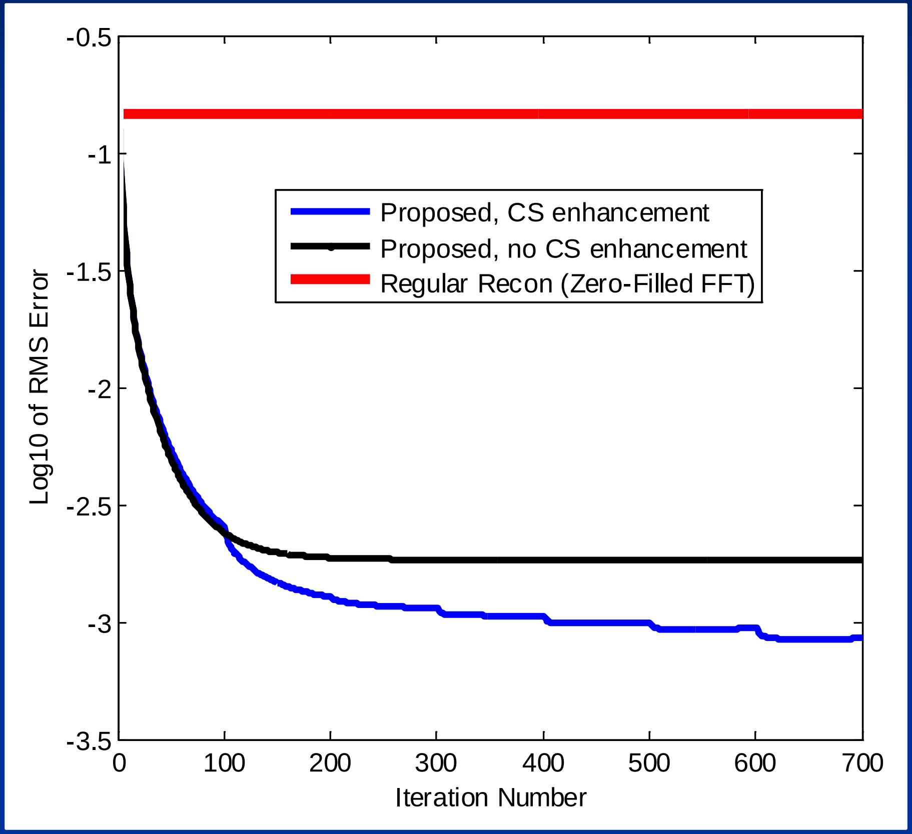


M0 R1=1/T1



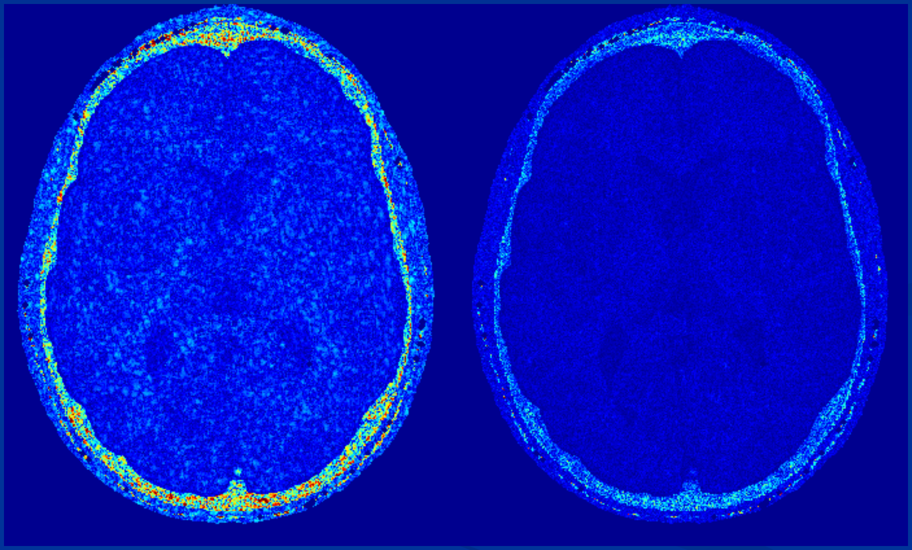
Errors

Image RMS Error vs. Iteration Number



R1 Map Error

No CS (σ=Inf) CS



CS version of the proposed algorithm reduces reconstruction error (due to robustness to partial volume pixels)

Discussion

- The proposed algorithm utilizes the knowledge of analytical dependence of images in parametric series to allow reconstruction of images themselves and parametric maps from undersampled data
- CS-enhanced version of the proposed algorithms provides robustness in situations when analytical model does not describe all image pixels, which improves reconstruction accuracy
- <u>Future work:</u> validation on real data, applicability to other quantitative MR applications

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THANK YOU!!!