

Joint Implicit Neural Representation for Fast Scan-Specific Magnetic Resonance Fingerprinting

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IMPLICIT NEURAL REPRESENTATION

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Impact

The method moves toward clinically practical MRF by reducing acquisition and reconstruction time without sacrificing T1/T2 accuracy or precision. By scan specifically learning a shared anatomical prior, it enables fast quantitative mapping and may extend to other quantitative MRI protocols.

Synopsis

Motivation: Magnetic Resonance Fingerprinting (MRF) enables rapid multiparametric mapping, but highly undersampled acquisitions and long time-series make reconstruction slow and ill-posed.

Goals: Achieve fast, scan-specific MRF reconstruction with accurate, precise T1/T2 mapping from shorter acquisitions.

Approach: We propose an implicit neural representation that jointly models MRF subspace images. High-energy components shape a shared anatomical representation that constrains aliased components, acting as an implicit spatial prior. The network is trained in image domain, without external data or iterative k-space data consistency.

Results: On phantom and in vivo brain, the method suppresses aliasing, preserves structure, and produces accurate and low-variance T1/T2 maps with highly undersampled acquisition.

Introduction

MR Fingerprinting (MRF) enables rapid multiparametric mapping^{1,2}. However, the acquisitions are highly undersampled with hundreds of timepoints, making reconstruction ill-posed and slow. Model-based iterative methods³ and network-based priors⁴ can suppress aliasing but have long reconstruction times, limiting clinical applications.

To address these limitations, we propose a scan-specific MRF reconstruction method using a gradient-guided Joint Implicit Neural Representation (INR⁵). A single INR parameterizes all subspace images derived from the MRF time-series, acting as an implicit spatial prior that suppresses subspace-inconsistent aliasing while preserving fine structure. Our proposed method fits INR in the image domain, without training data or iterative k-space data consistency needed for other INR-base methods⁶⁻⁹, reducing reconstruction time. We evaluated our method in quantitative T1 and T2 mapping using the ISMRM/NIST phantom and in vivo brain and compared against maps from low-rank¹⁰ and iterative LLR reconstructions³.

Methods

Let $\mathbf{y} \in \mathbb{C}^{T \times C \times N_s \times N_r}$ be the multi-coil MRF time-series, where T is the number of timepoints, C is the number of coils, and (N_s, N_r) are the number of spiral interleaves and readout samples. We compute a temporal basis $\mathbf{U}_K \in \mathbb{C}^{T \times K}$ by low-rank approximation of an MRF dictionary, and form the initial subspace images $\mathbf{x}^{(0)}$ by applying adjoint encoding operator $\mathbf{A}'$ with density compensation $\mathbf{W}$:

$$\mathbf{x}^{(0)} \triangleq \mathbf{A}'\mathbf{W}(\mathbf{U}_K'\mathbf{y}) \in \mathbb{C}^{K \times N_y \times N_x}.$$

We select K components to preserve 99.99% of MRF signal. A single INR ($f_\theta: \mathbb{R}^d \rightarrow \mathbb{C}^K$) jointly models all K subspace images, mapping each spatial coordinate $\vec{r}$ to the K complex values at that location. This produces a joint feature vector $\phi_\theta(\vec{r})$ at the penultimate layer that encodes anatomy. Each subspace image k is then generated from this shared representation by linear combination at a lightweight output head:

$$\mathbf{x}_{\theta,k}(\vec{r}) = \mathbf{w}_k^T \phi_\theta(\vec{r}) + b_k.$$

This shared architecture ([Figure 1a](#)) enforces a joint implicit prior for all subspace images.

Training is further biased by gradient dominance. The first subspace image has high SNR and minimal aliasing. Early in training, its larger loss gradients force $\phi_\theta(\vec{r})$ to encode a clean anatomical representation. Later, more aliased components cannot introduce new structure; they reuse $\phi_\theta(\vec{r})$ and adjust contrast through their linear heads. This suppresses subspace-inconsistent aliasing while preserving details. [Figure 1b](#) shows $\phi_\theta(\vec{r})$ evolving from noise to an aliasing-free shared representation. Separate encoder and MLP weight regularization⁹ further limits overfitting.

Our method fits INR by iterative optimizing its weights using an image-domain ℓ_2 loss with weight regularization:

$$\hat{\theta} = \arg \min_{\theta} \left\| \mathbf{x}^{(0)} - f_\theta(\vec{r}) \right\|_2^2 + \lambda_{\text{Enc}} \left\| \theta_{\text{Enc}} \right\|_2^2 + \lambda_{\text{MLP}} \left\| \theta_{\text{MLP}} \right\|_2^2, \quad \mathbf{x}_\theta = f_\theta(\vec{r}).$$

The iterative fitting avoids the MRI forward model (e.g., Fourier encoding, gridding), greatly reducing the reconstruction time. Quantitative T1 and T2 maps are obtained by matching the reconstructed subspace images to an MRF dictionary.

Phantom and In vivo experiments: The ISMRM/NIST phantom and three volunteers were scanned using a FISP-based MRF² (Variable flip angle, TE=2 ms, TR=9 ms and 1000 timepoints) at 3T (Vida, Siemens). Each timepoint was highly undersampled using a single interleaf (readout duration=2.21 ms) of a variable-density spiral trajectory, which requires 96 interleaves to fully sample the k-space.

We compared the proposed method against the low-rank reconstruction¹⁰ and an iterative reconstruction with LLR regularization³. All methods were implemented in PyTorch on the NVIDIA A40 GPU.

Results

Figure 2 shows all subspace images during INR fitting. Early iterations collapse to a shared image resembling the first subspace, and later iterations gradually disentangle contrast across subspaces.

Figure 3a shows correlation plots comparing T1/T2 from the proposed method with 500 timepoints and the values from 1000-timepoint low-rank reconstruction. The proposed method ($R^2=0.9980$) outperforms the 500-timepoint low-rank reconstruction ($R^2=0.9089$), especially for long T2 (>300 ms). It also has the lowest coefficient of variations (**Figure 3b**): 4.3% T1 and 9.4% T2 vs 4.9% and 19.3% of the 1000 timepoints reference.

Figure 4 compares subspace images and maps from low-rank reconstruction, LLR, and the proposed method, showing improved image and map quality from the proposed method.

Figure 5 presents representative slices of brain maps. The proposed method suppresses aliasing and avoids the blurring, compared to low-rank reconstruction and LLR. It also produces the lowest T2 standard deviation in white matter. The reconstruction time of the proposed method was 12.6 s, compared to 158 s of LLR and ~5.6 s of non-iterative low-rank reconstruction.

Discussion and Conclusion

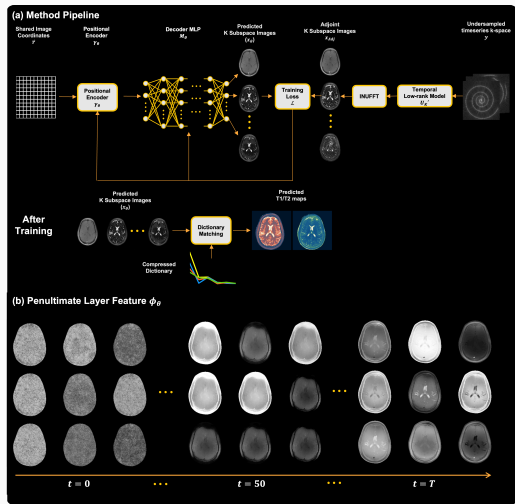
The proposed method learns a shared, scan-specific spatial representation and uses it as an implicit prior to suppress aliasing in highly undersampled MRF. This yields sharp, low-variance T1/T2 maps from as few as 500 timepoints. The approach is fully image-domain, needs no external training data, and avoids iterative k-space data consistency, enabling faster reconstruction while improving map quality. These results suggest that reduced acquisition time and near-real-time reconstruction is feasible for MRF without sacrificing quantitative accuracy or precision.

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Scan for high-resolution version

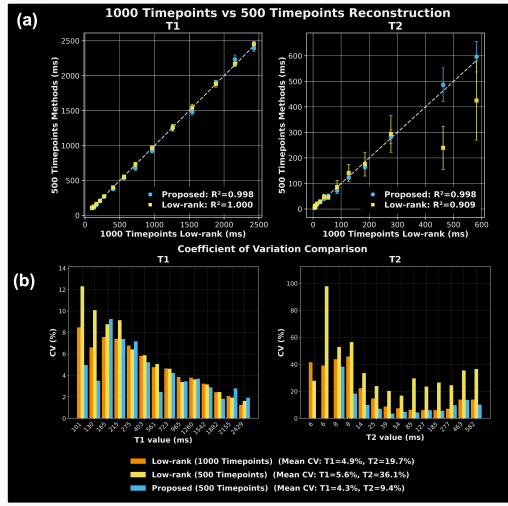
Figure 1: (a). Proposed reconstruction pipeline. (b). Evolution of the shared penultimate-layer feature representation ϕ_θ (first nine channels). Early iterations learn a common anatomical structure from the high-energy subspace with dominant loss gradient, which is then reused by all subspaces. This shared representation suppresses aliasing in later, more corrupted subspace images.

Animated Figure 2

This figure contains animation/video content. To view the animation, scan the QR code with your mobile device or visit the online version of this abstract.

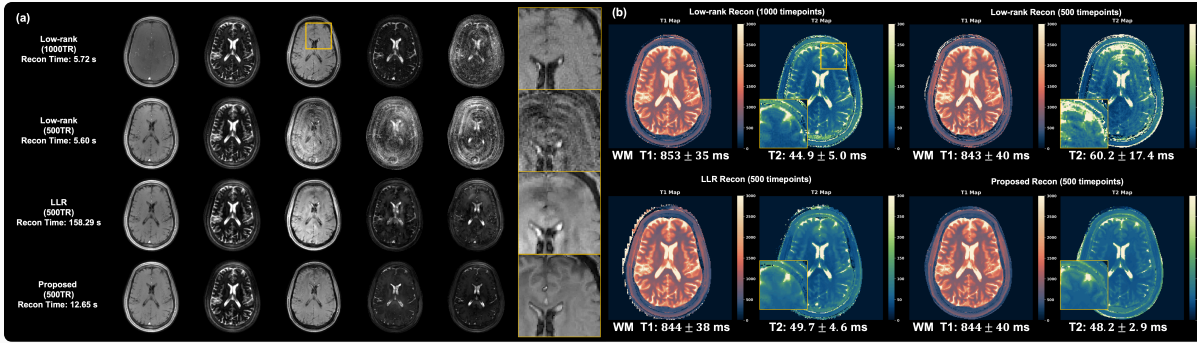


Figure 2: Method Illustration (2D Brain MRF reconstruction). The animated evolution of subspace images and T1/T2 maps is shown. Early high-energy subspace defines a shared anatomical prior; later components gain contrast while preserving anatomy structure and suppressing aliasing artifacts.



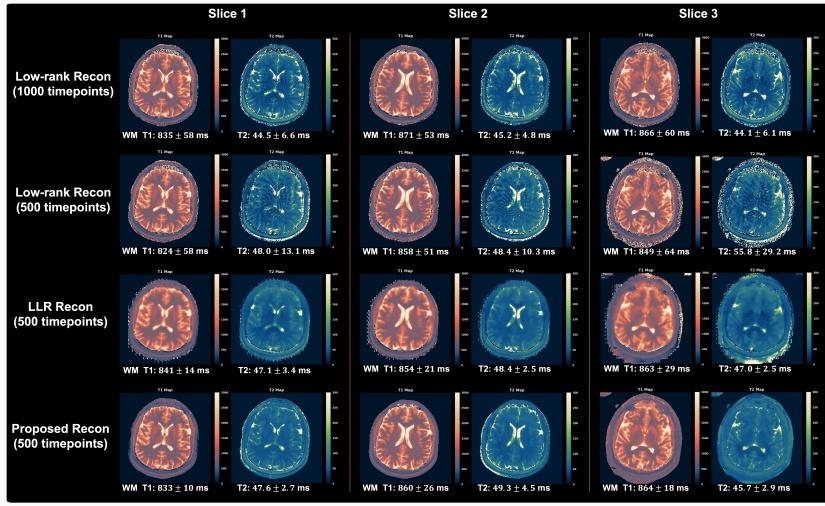
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Figure 3: ISMRM/NIST phantom results (variable-density spiral, 2.21 ms readout, 48–96 $\times$ undersampled). (a) Correlation of T1/T2 between the proposed/low-rank reconstruction (500 timepoints) and 1000 timepoints low-rank reconstruction reference, (b) coefficient of variation comparison. The proposed methods has the lowest mean coefficient of variation (T1: 4.3%, T2 9.4%), even lower than 1000 timepoints reference (T1: 4.9%, T2 19.3%).



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Figure 4: Single-slice 2D brain MRF reconstruction comparing low-rank adjoint (500/1000 timepoints), LLR (500 timepoints), and the proposed method (500 timepoints). (a) Subspace coefficient images with per-method runtime. (b) T1/T2 maps with white-matter mean $\pm$ std. The proposed suppresses subspace-inconsistent aliasing, preserves anatomy, and yields the lowest white-matter T2 standard deviation. Regularization strength of iterative LLR reconstruction is tuned by grid search.



Scan for high-resolution version

Figure 5: Multi-slice 2D brain MRF (three representative slices, 2.21 ms readout). The proposed method suppresses aliasing and blur versus low-rank and LLR, preserves sharper anatomical structure, and yields the lowest white-matter T2 standard deviation. Runtimes: proposed 12.6 s; LLR 158 s; low-rank adjoint (non-iterative) ~5.6 s. Regularization strength of iterative LLR reconstruction is tuned by grid search.