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Tutorial 3:

Continuous domain sparse recovery
of biomedical imaging data using
structured low-rank approaches

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Joint work by several authors

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Overview

Part 1: Theory & Algorithms

Part 2: Applications

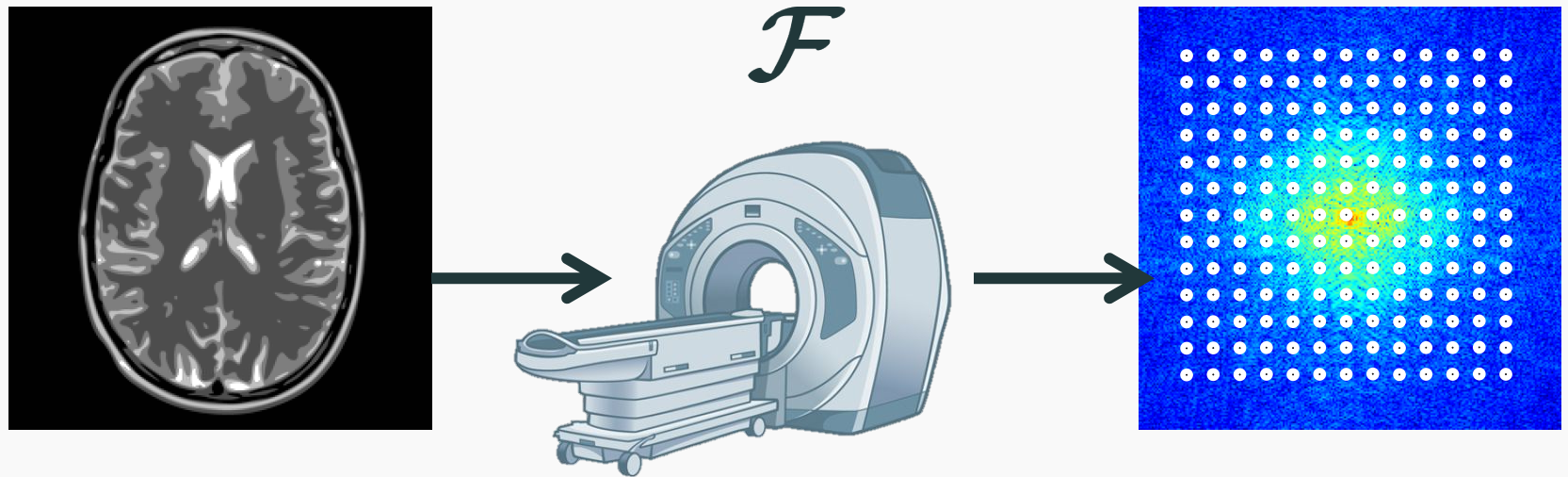
Overview

1. Introduction
2. Review of Compressive Sensing
3. FRI **extrapolation** from uniform samples
4. Structured low-rank **interpolation** for non-uniform samples
5. Fast implementations
6. Biomedical applications

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Motivation: MRI reconstruction

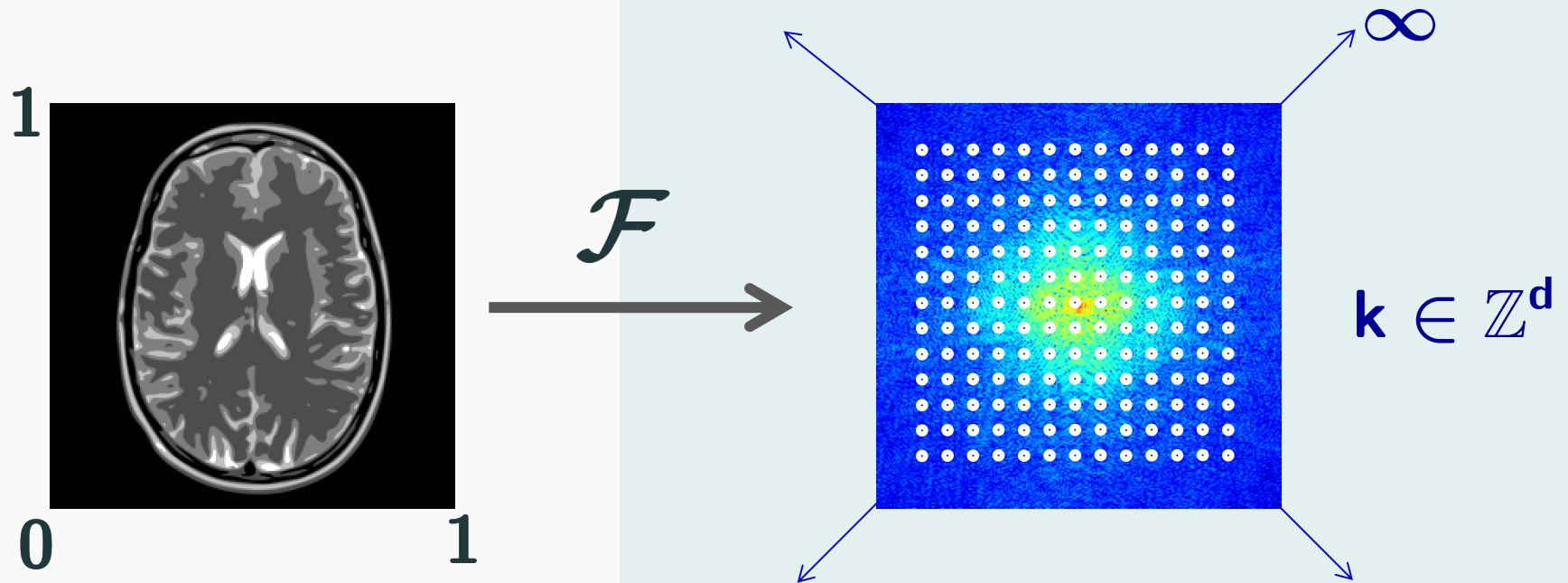


Main Problem:

Reconstruct image from Fourier domain samples

Related: Computed Tomography, Florescence Microscopy

Motivation: MRI Reconstruction



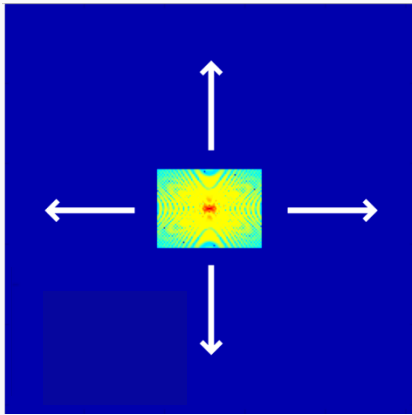
$$f(\mathbf{x}), \quad \mathbf{x} \in [0, 1]^d$$

$$\hat{f}[\mathbf{k}] := \int_{[0,1]^d} f(\mathbf{x}) e^{-j2\pi \mathbf{k} \cdot \mathbf{x}} d\mathbf{x}$$

Uniform Fourier Samples =
Fourier Series Coefficients

Types of “Compressive” Fourier Domain Sampling

low-pass

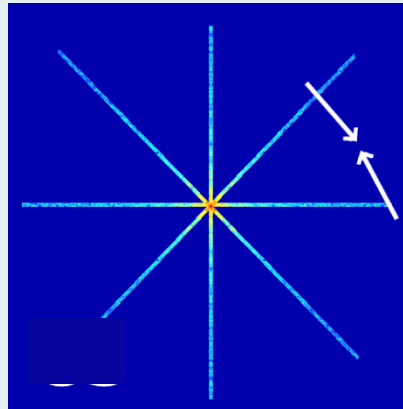


Fourier
Extrapolation



Super-resolution
recovery

radial

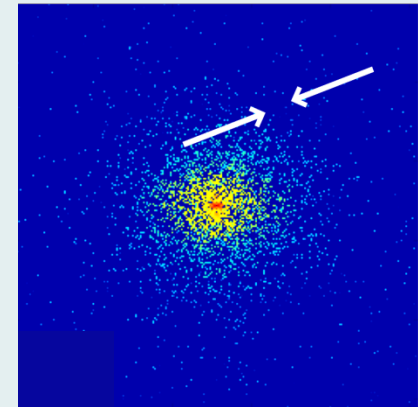


Fourier
Interpolation



“Compressed Sensing”
recovery

random



Extrapolation: super-resolution microscopy

The Nobel Prize in Chemistry 2014



Photo: Matt Staley/HHMI

Eric Betzig

Prize share: 1/3



© Bernd Schuller, Max-Planck-Institut

Stefan W. Hell

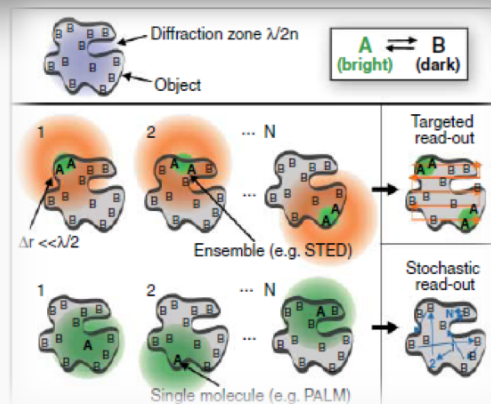
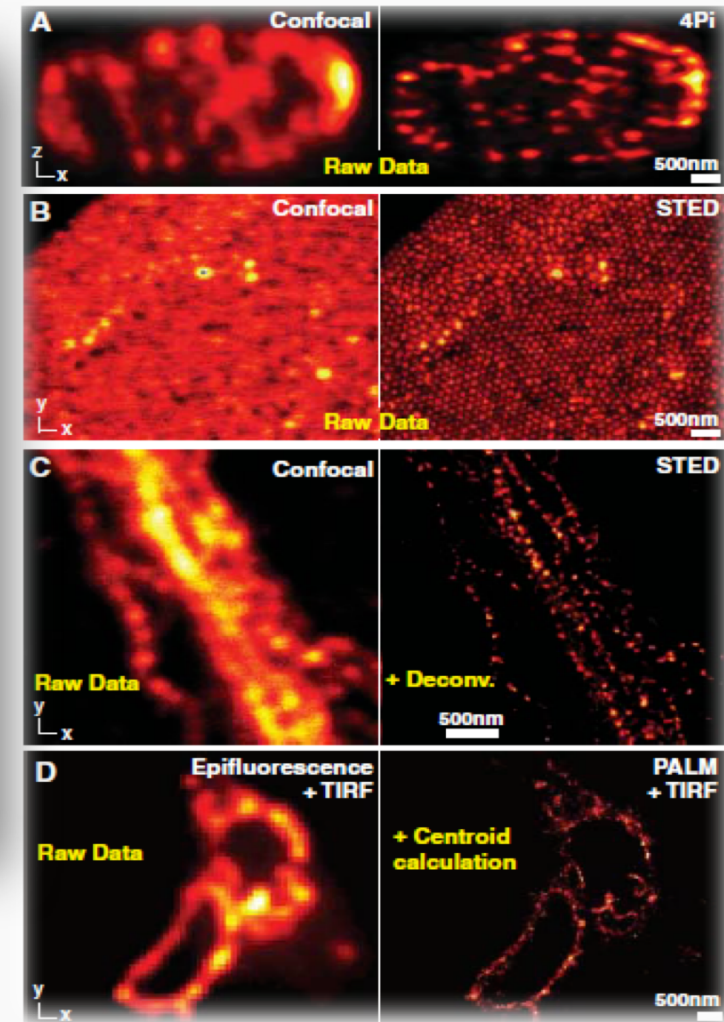
Prize share: 1/3



Photo: K. Lowder via Wikimedia Commons, CC-BY-SA-3.0

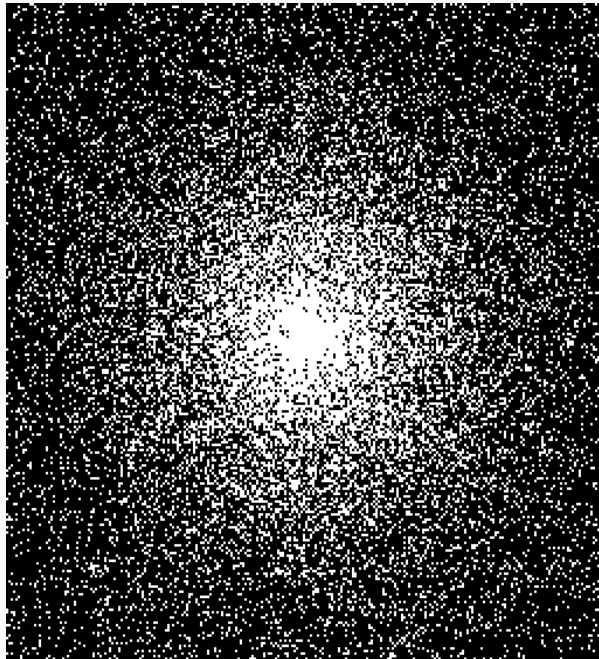
William E. Moerner

Prize share: 1/3



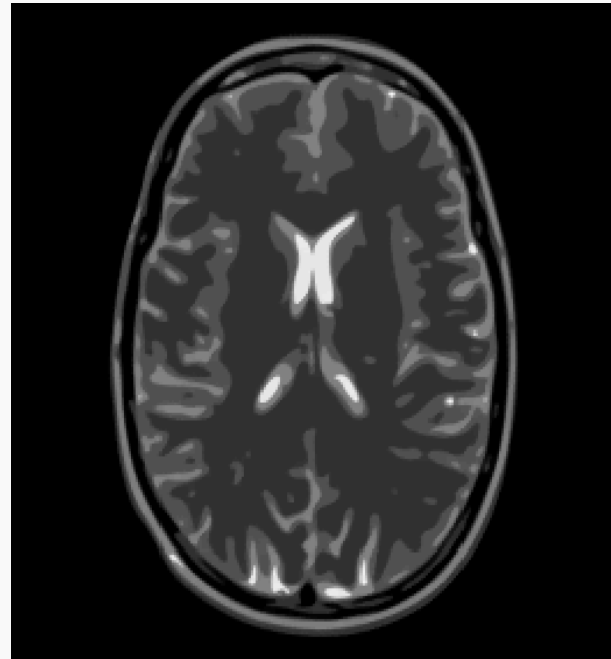
S. Hell et al, Science 2007.

Interpolation: accelerated MRI



25% Random
Fourier samples
(variable density)

TV-min
→



Rel. Error = 5%

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Compressed Sensing (CS)

- Incoherent projection
- Underdetermined system
- **Sparse** unknown vector

$$\begin{array}{c} M \times 1 \\ \text{measurements} \end{array} \quad \mathbf{b} = \mathbf{A} \quad \mathbf{x} \quad \begin{array}{c} N \times 1 \\ \text{sparse signal} \end{array}$$

$M \approx K \log(N) \ll N$

K
non-zeros

The diagram illustrates the Compressed Sensing equation $\mathbf{b} = \mathbf{A} \mathbf{x}$. Matrix \mathbf{A} is a noisy, incoherent projection matrix. Vector \mathbf{b} is the resulting measurements. Vector \mathbf{x} is the sparse signal, represented as a column of boxes with only a few non-zero entries (blue).

Courtesy of Dr. Dror Baron

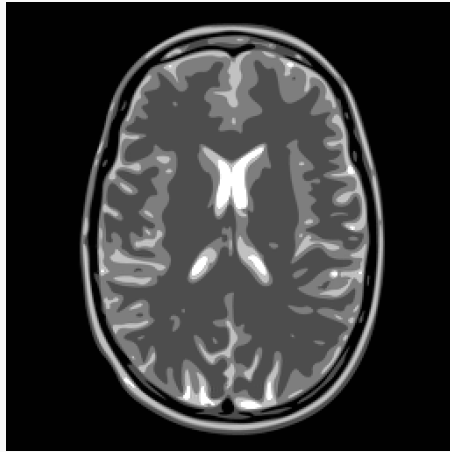
Sparse-Low Rank Recovery in Nutshell

The diagram illustrates the Sparse-Low Rank Recovery equation with the following components and annotations:

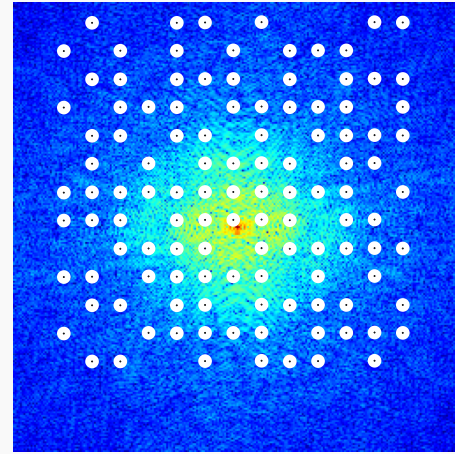
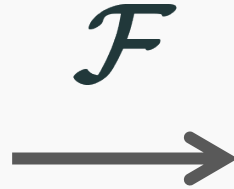
- Reconstructed image:** An arrow points to the variable \hat{x} , which is circled in red.
- Measurement data:** An arrow points to the variable y , which is circled in blue.
- Forward mapping By physics:** An arrow points to the matrix A , which is circled in red.
- Prior Knowledge (smoothness, sparsity, etc):** An arrow points to the regularization term $R(x)$, which is enclosed in a purple circle.

$$\hat{x} = \arg \min_x \|y - Ax\|_2^2 + R(x)$$

Application to biomedical imaging

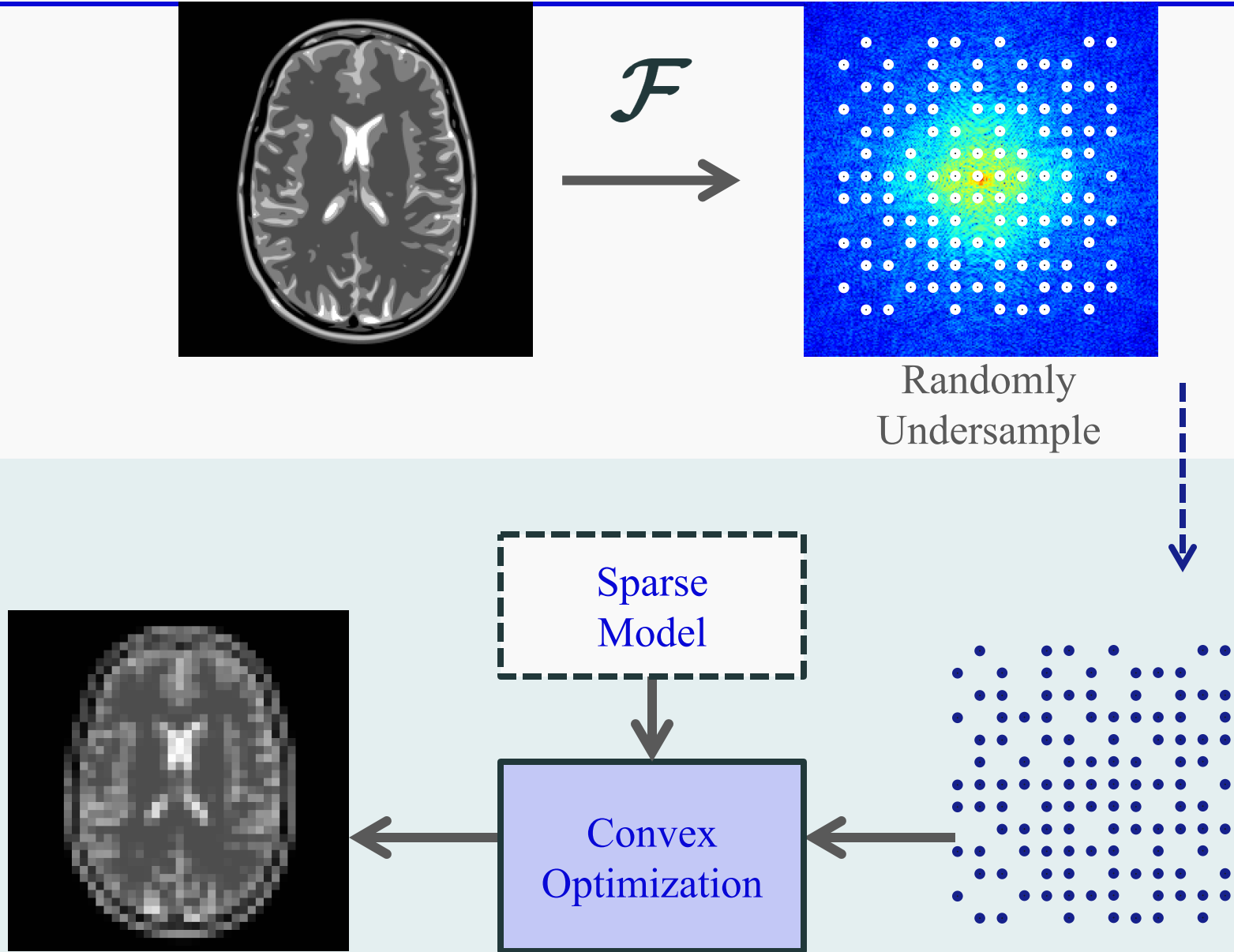


Full sampling is costly!

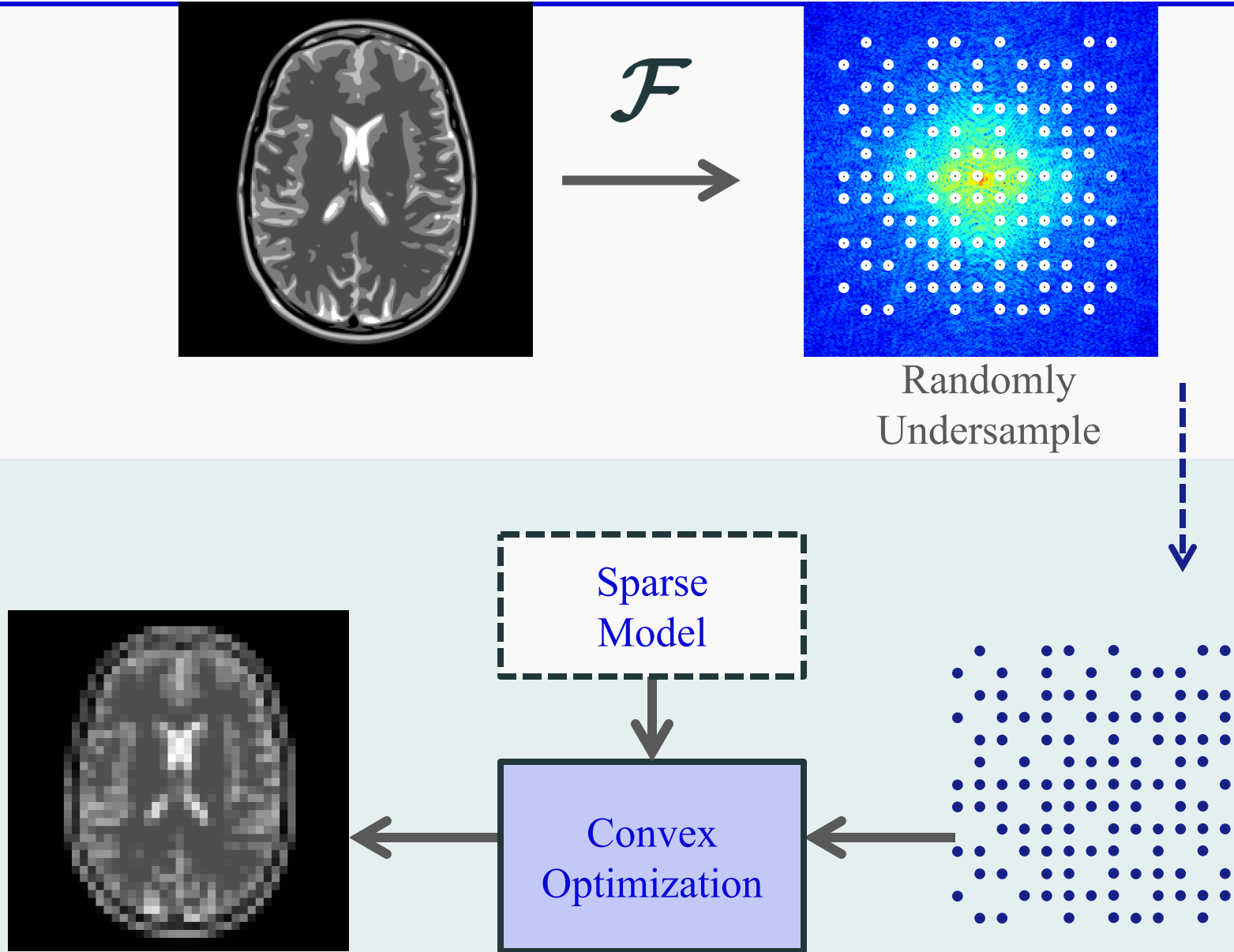


Randomly undersample

Application to biomedical imaging



Analysis formulation of Compressed Sensing

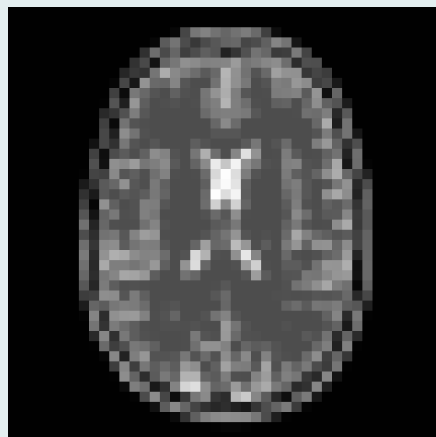
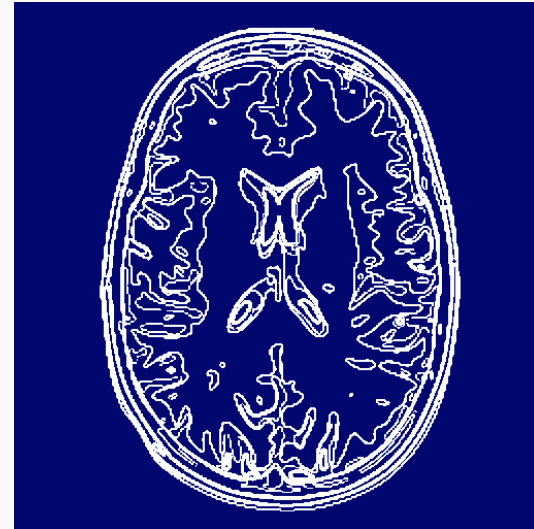


Example:

Assume **discrete gradient**
of image is sparse

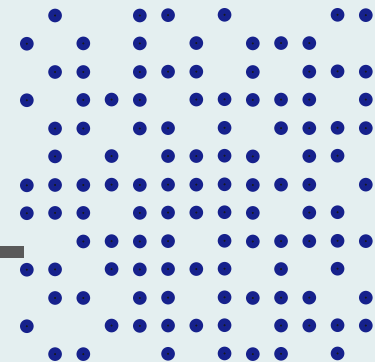


Piecewise constant model



**Sparse
Model**

**Convex
Optimization**



Recovery by Total Variation (TV) minimization

TV semi-norm: $\|\mathbf{g}\|_{\text{TV}} = \sum_{i,j} \sqrt{|\mathbf{g}_{i+1,j} - \mathbf{g}_{i,j}|^2 + |\mathbf{g}_{i,j+1} - \mathbf{g}_{i,j}|^2}$

*i.e., L1-norm of discrete
gradient magnitude*

$$\sum_{i,j}$$



Recovery by Total Variation (TV) minimization

$$\text{TV semi-norm: } \|\mathbf{g}\|_{\text{TV}} = \sum_{i,j} \sqrt{|\mathbf{g}_{i+1,j} - \mathbf{g}_{i,j}|^2 + |\mathbf{g}_{i,j+1} - \mathbf{g}_{i,j}|^2}$$

*i.e., L1-norm of discrete
gradient magnitude*

$$\sum_{i,j}$$



$$\min_{\mathbf{g} \in \mathbb{C}^{N \times N}} \|\mathbf{g}\|_{\text{TV}} \quad \text{subject to} \quad \mathbf{F}_{\Omega} \mathbf{g} = \mathbf{F}_{\Omega} \mathbf{f} \quad (\text{TV-min})$$

Recovery by Total Variation (TV) minimization

$$\text{TV semi-norm: } \|\mathbf{g}\|_{\text{TV}} = \sum_{i,j} \sqrt{|\mathbf{g}_{i+1,j} - \mathbf{g}_{i,j}|^2 + |\mathbf{g}_{i,j+1} - \mathbf{g}_{i,j}|^2}$$

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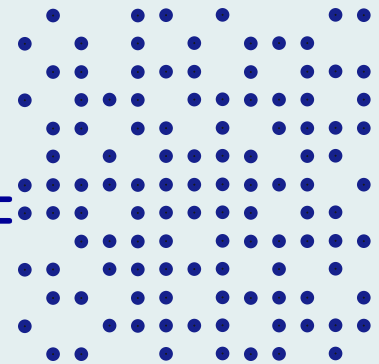
$$\sum_{i,j}$$



$$\min_{\mathbf{g} \in \mathbb{C}^{N \times N}} \|\mathbf{g}\|_{\text{TV}} \quad \text{subject to} \quad \mathbf{F}_{\Omega} \mathbf{g} = \mathbf{F}_{\Omega} \mathbf{f} \quad (\text{TV-min})$$

Restricted DFT

$$\Omega =$$



Sample locations

Recovery by Total Variation (TV) minimization

$$\text{TV semi-norm: } \|\mathbf{g}\|_{\text{TV}} = \sum_{i,j} \sqrt{|\mathbf{g}_{i+1,j} - \mathbf{g}_{i,j}|^2 + |\mathbf{g}_{i,j+1} - \mathbf{g}_{i,j}|^2}$$

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$$\min_{\mathbf{g} \in \mathbb{C}^{N \times N}} \|\mathbf{g}\|_{\text{TV}} \quad \text{subject to} \quad \mathbf{F}_{\Omega} \mathbf{g} = \mathbf{F}_{\Omega} \mathbf{f} \quad (\text{TV-min})$$

Convex optimization problem

Fast iterative algorithms:

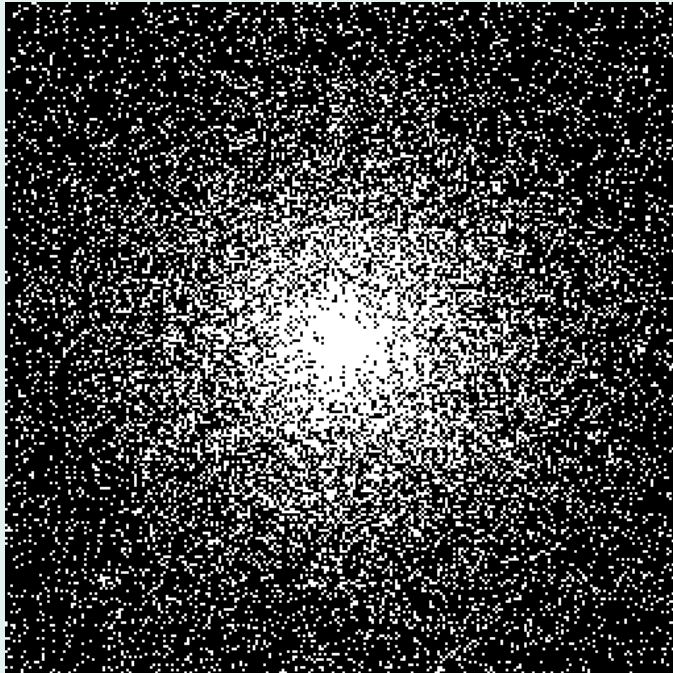
ADMM/Split-Bregman,
FISTA, Primal-Dual, etc.

Restricted DFT

$$\Omega =$$

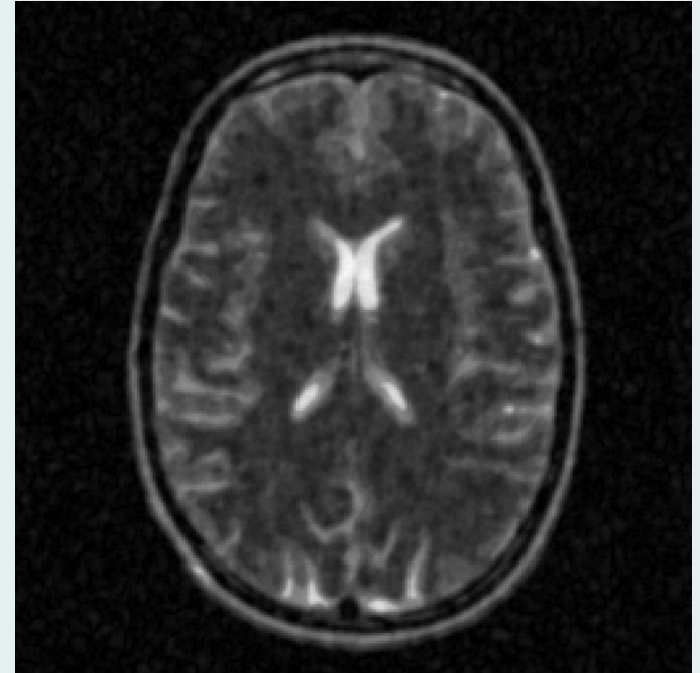
Sample locations

Recovery using zero filled IFFT



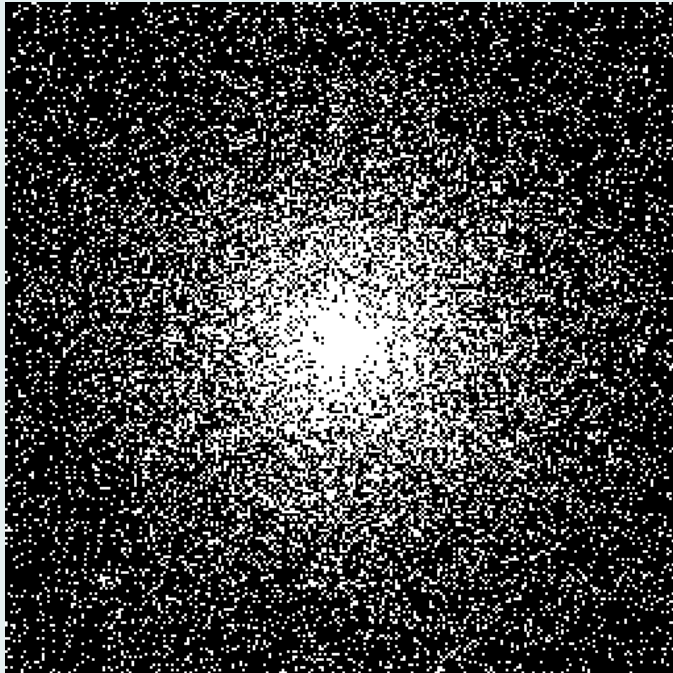
25% Random
Fourier samples
(variable density)

DFT^{-1}
→



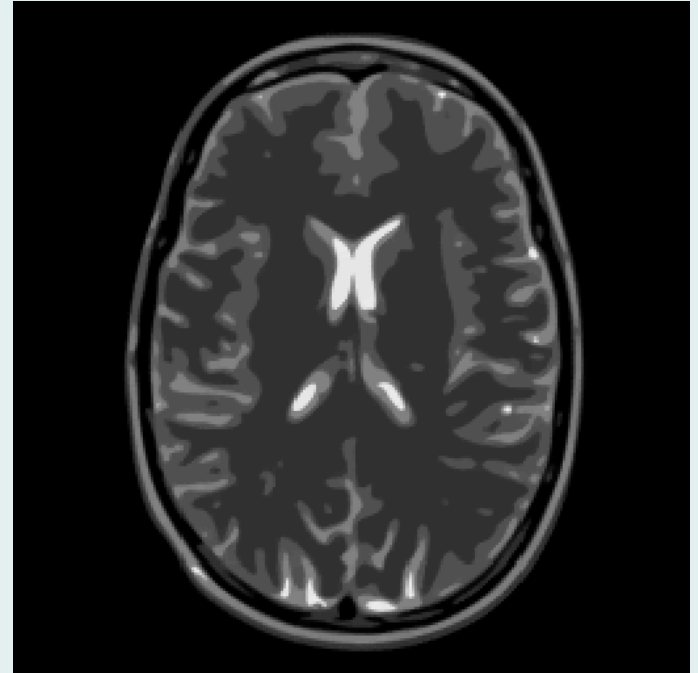
Rel. Error = 30%

Recovery using TV minimization



25% Random
Fourier samples
(variable density)

TV-min
→



Rel. Error = 5%

Limitations of CS

- **Discrete** domain theory
- **Explicit** form of sensing matrix
- **RIP issue** → **no direct interpolation**

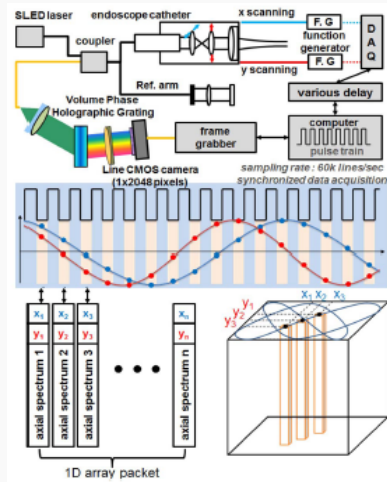
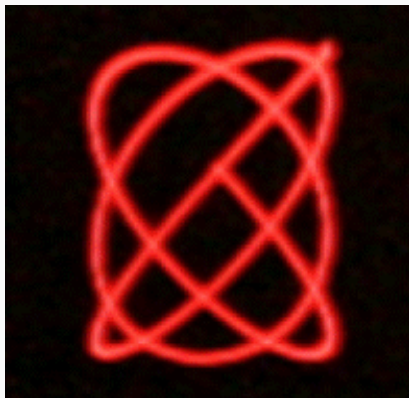
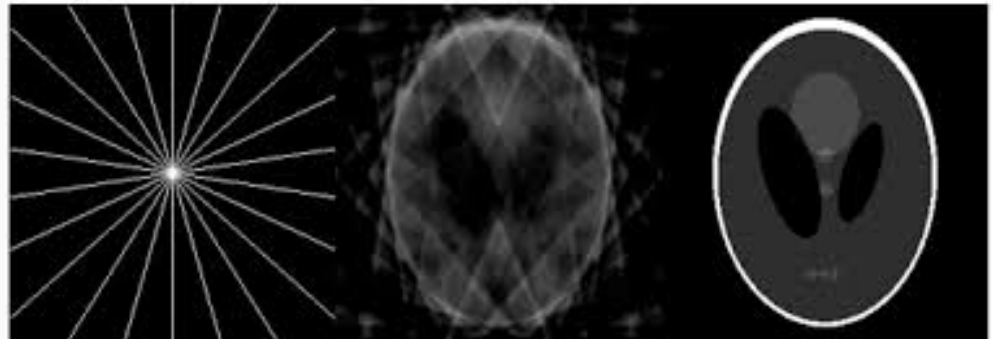


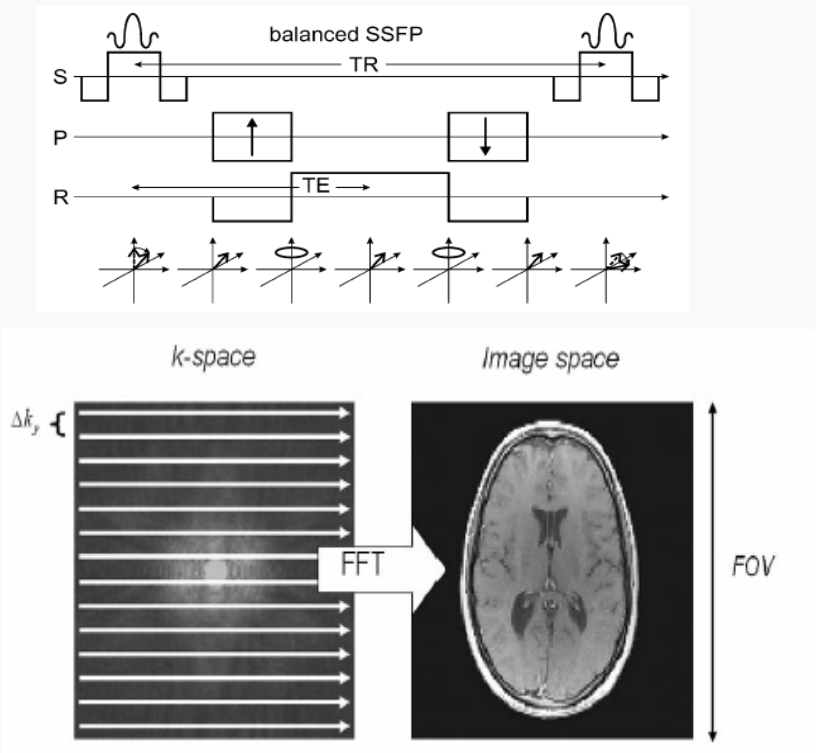
Fig. 2. (Color online) 3D SD-OCT image reconstruction :



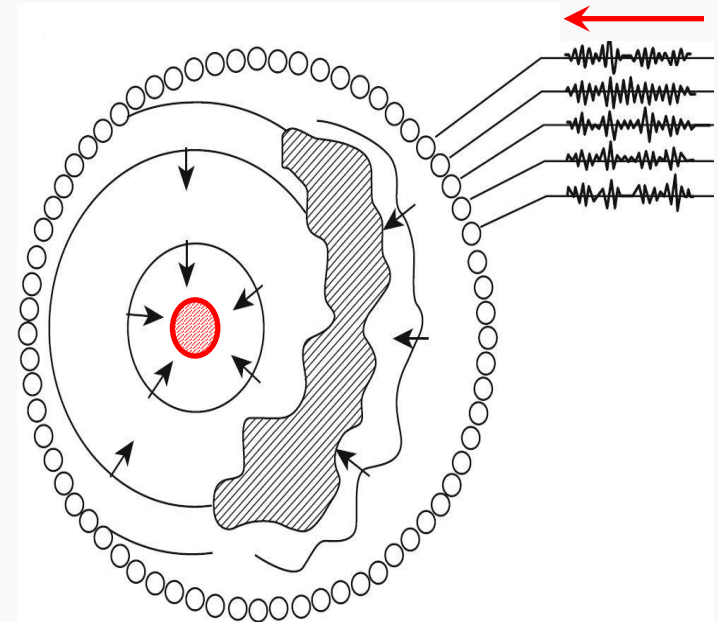
Analytic Reconstruction

*Beautiful analytic reconstruction results from **fully sampled data***

(a) MR Imaging

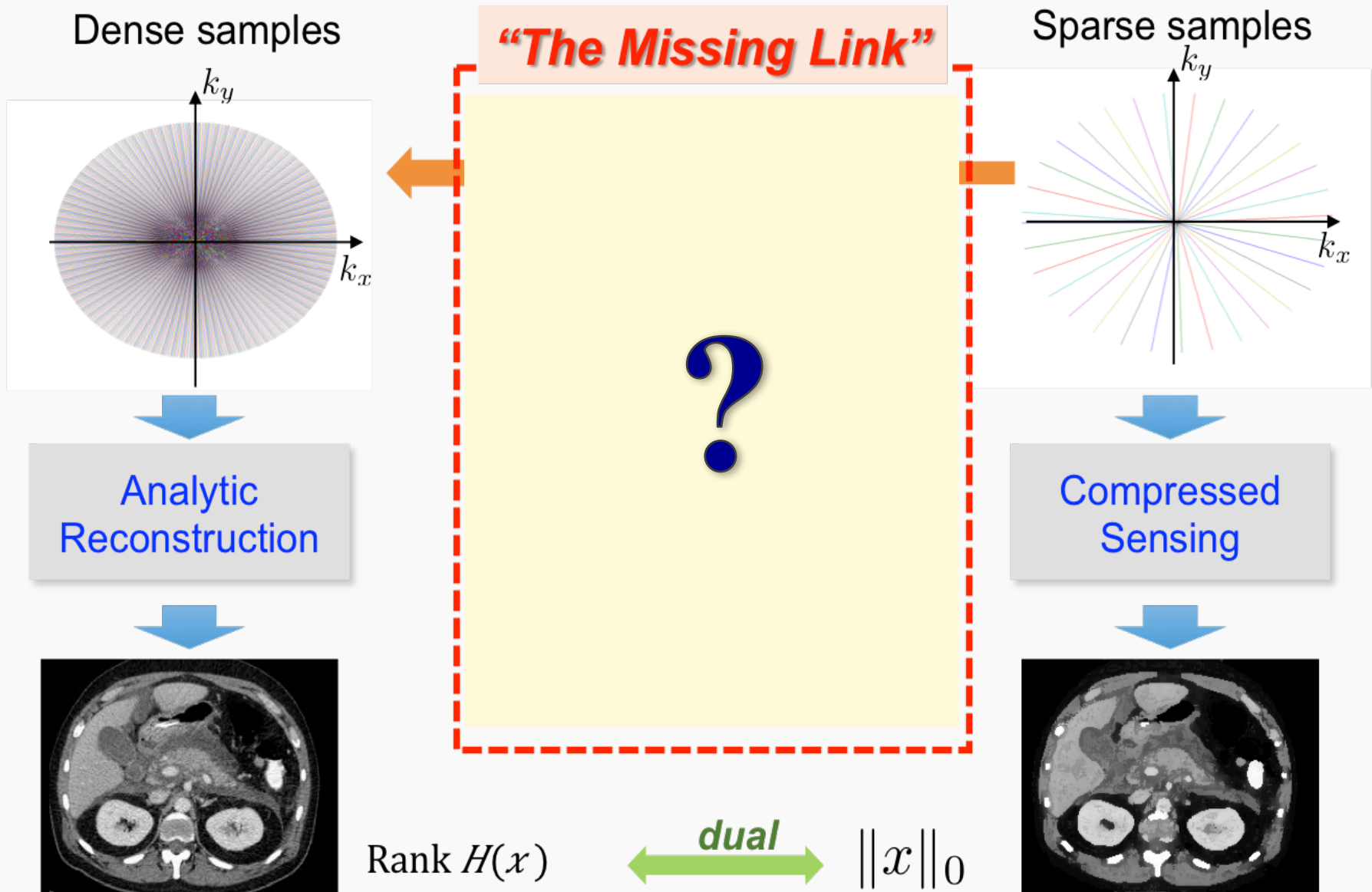


(b) Time-reversal of a scattered wave

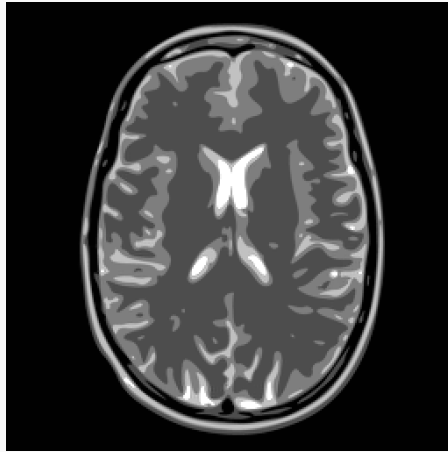


$$\mathcal{I}_1(x) = \int_{\Omega} f(z) \int_0^T \int_{\partial\Omega} \frac{\partial G(x, y, T, t)}{\partial \nu_y} \frac{\partial \Gamma}{\partial t}(z, y, 0, T - t) d\sigma(y) dt dz.$$

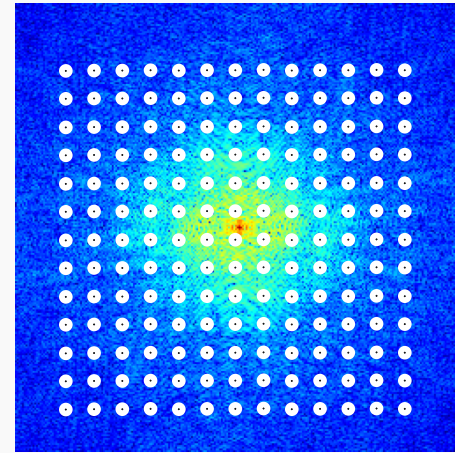
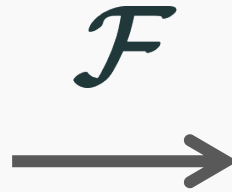
Project Goal: Unification of CS and analytic reconstruction
for biomedical imaging using a **2-layer approach**



“True” measurement model:

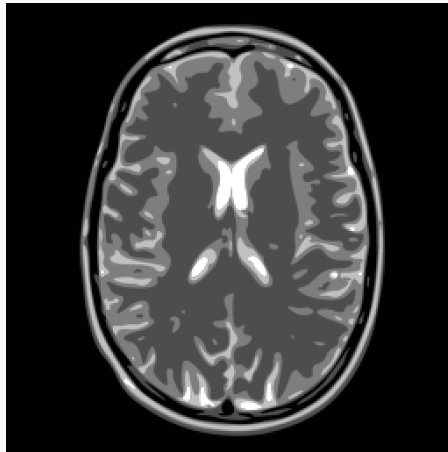


Continuous

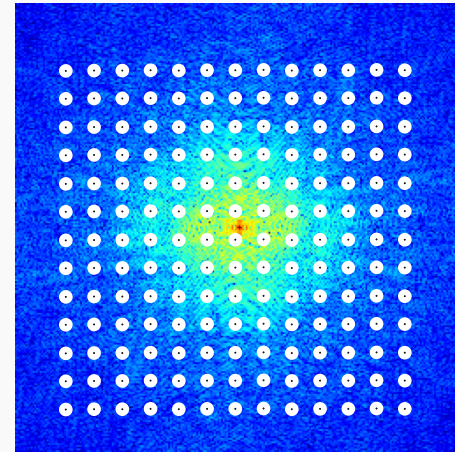
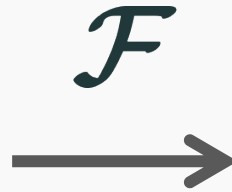


Continuous

“True” measurement model:

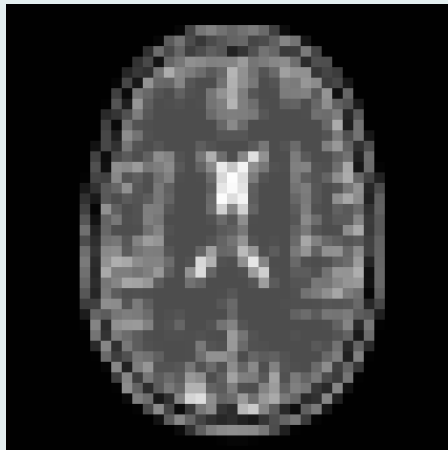


Continuous

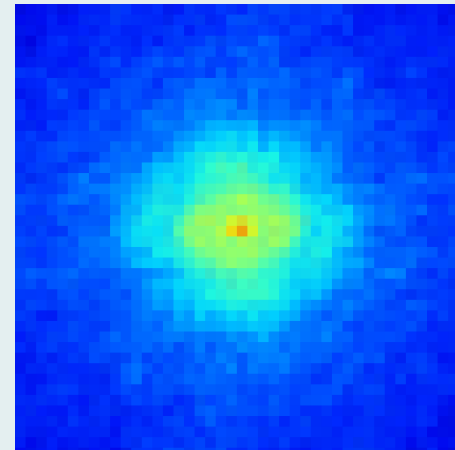


Continuous

Approximated measurement model:

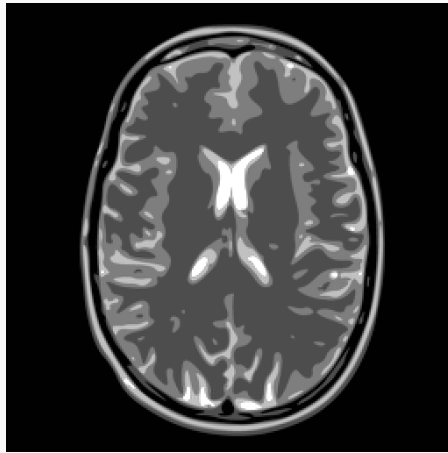


DISCRETE

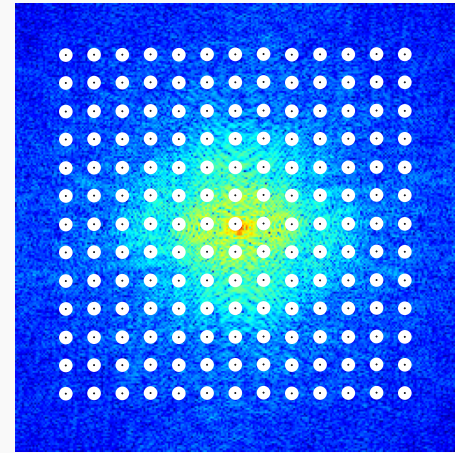
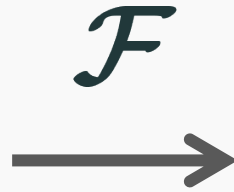


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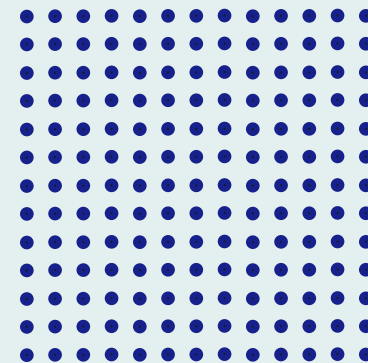
DFT Reconstruction



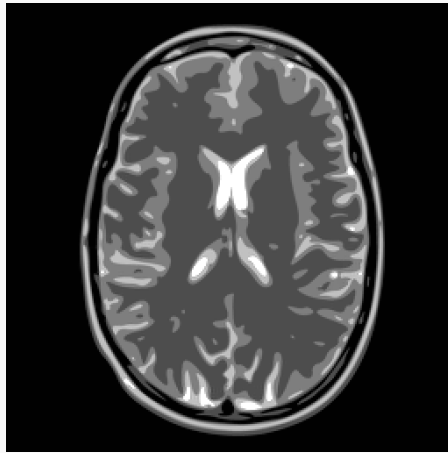
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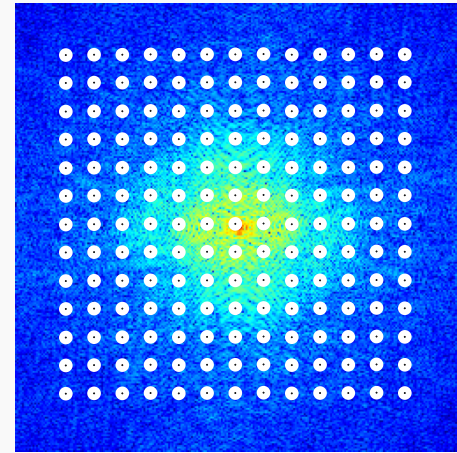
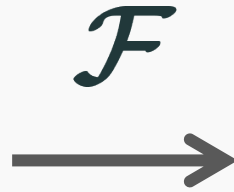
Continuous



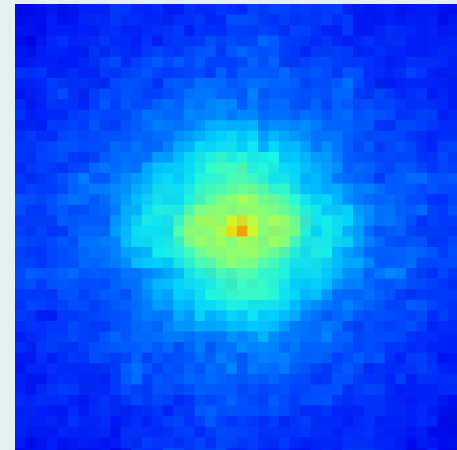
DFT Reconstruction



Continuous

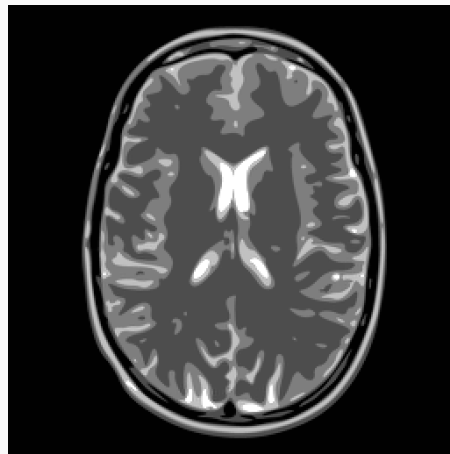


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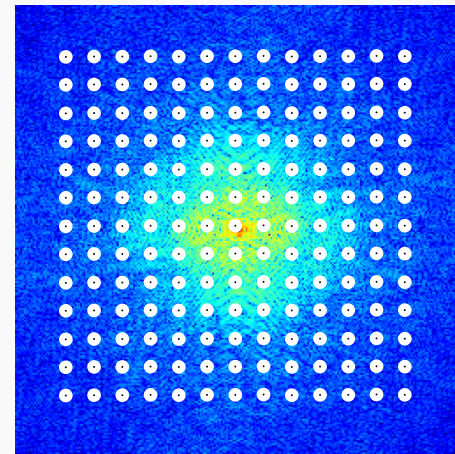
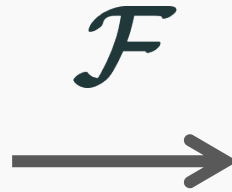


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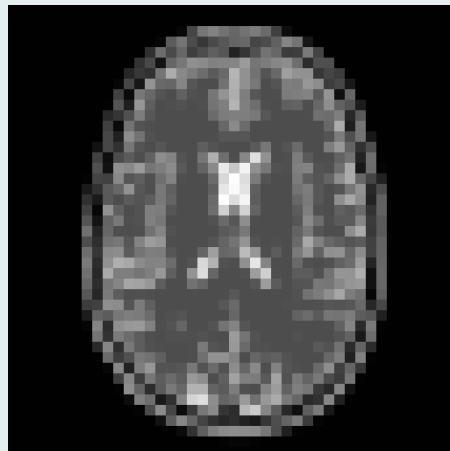
DFT Reconstruction



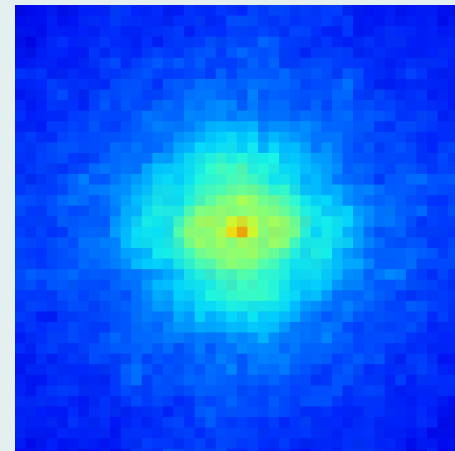
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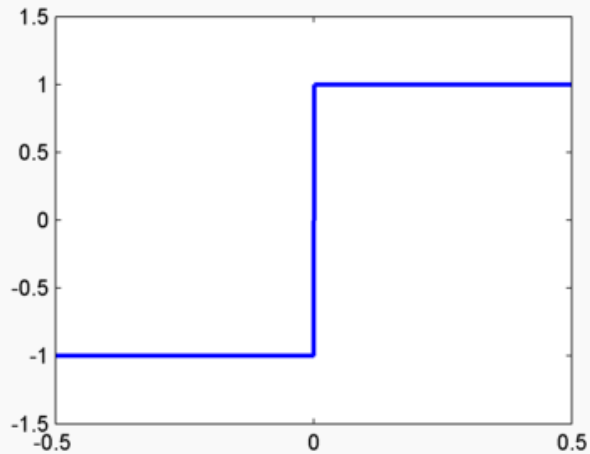
DISCRETE



DISCRETE

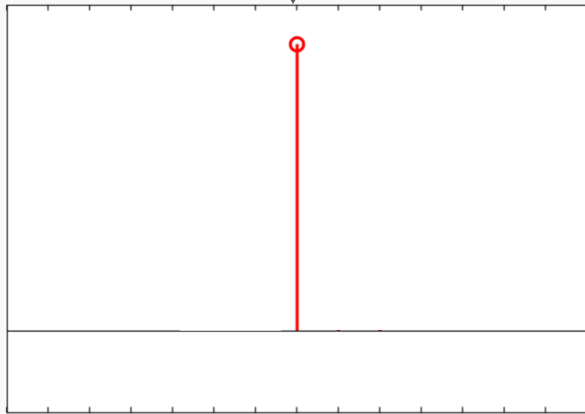
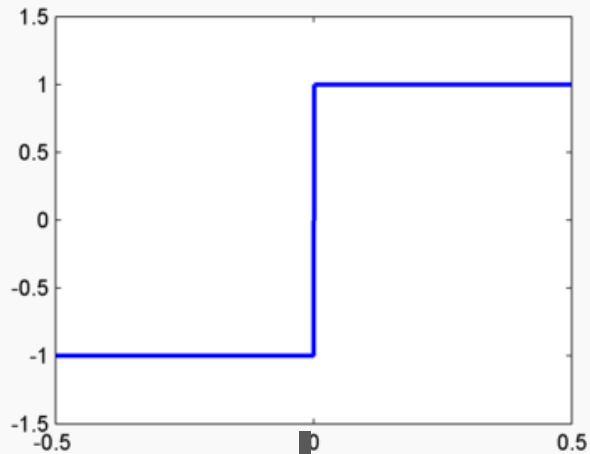
Challenge: Discrete approximation destroys sparsity!

Continuous



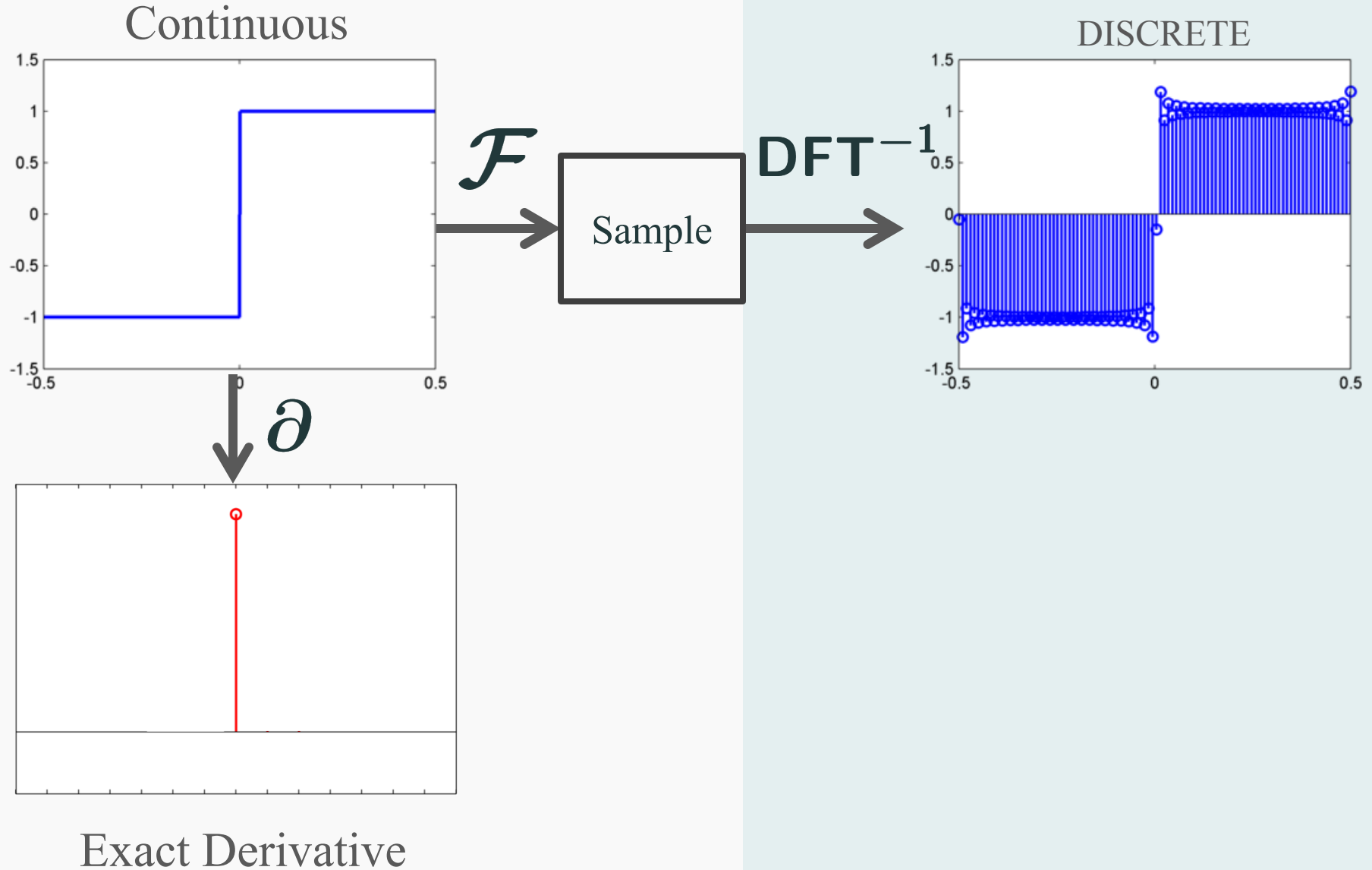
Challenge: Discrete approximation destroys sparsity!

Continuous

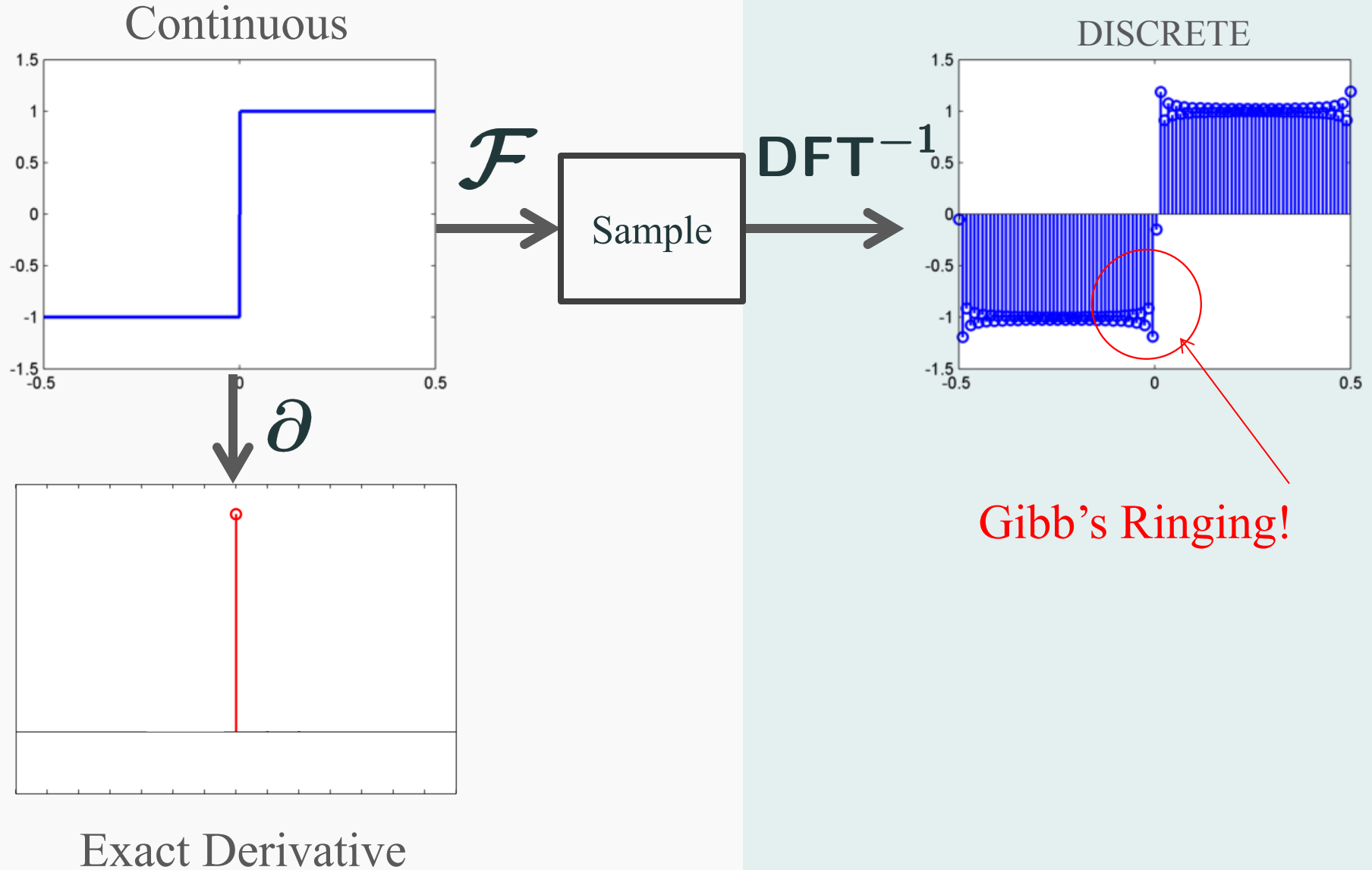


Exact Derivative

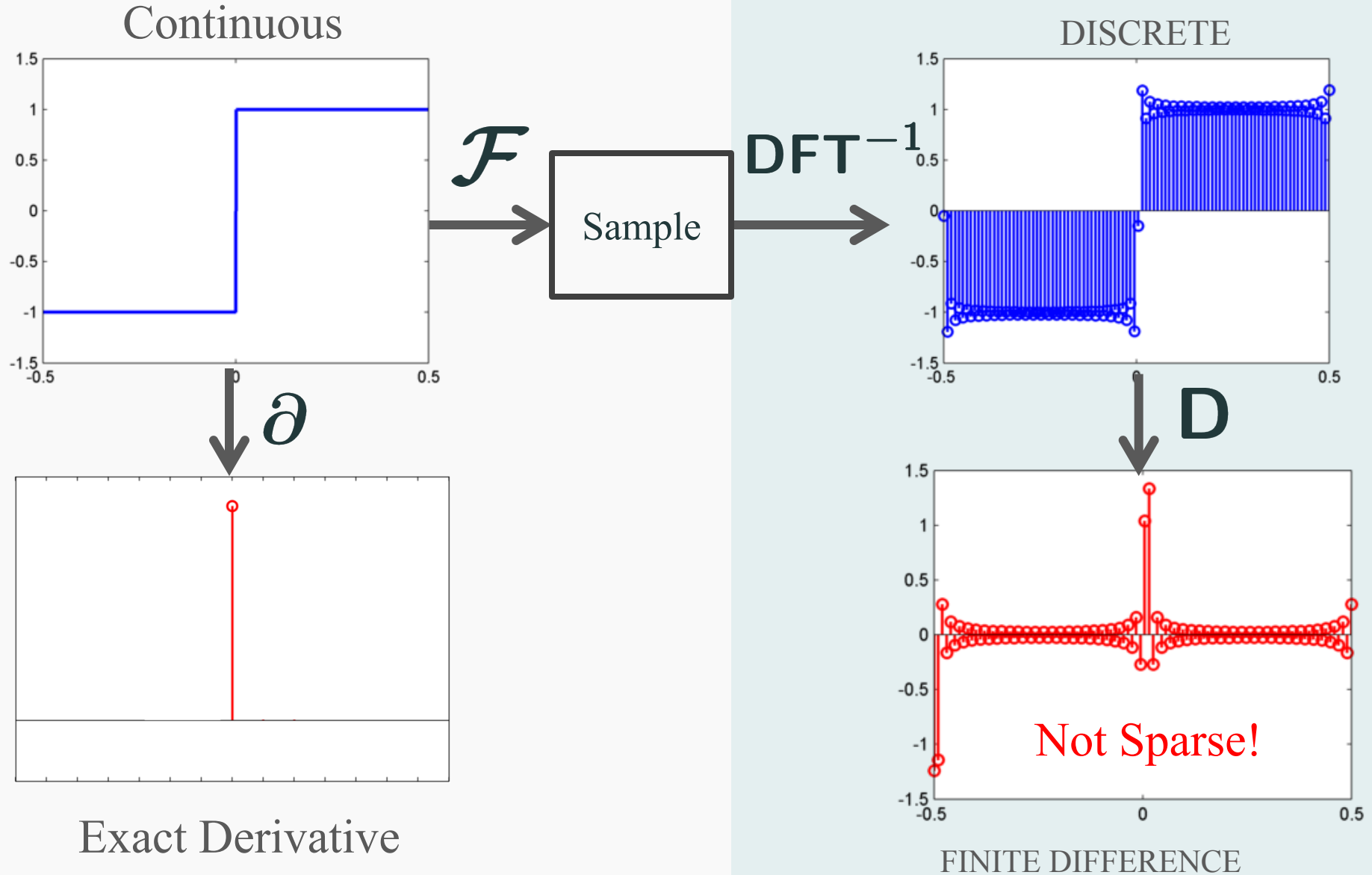
Challenge: Discrete approximation destroys sparsity!



Challenge: Discrete approximation destroys sparsity!

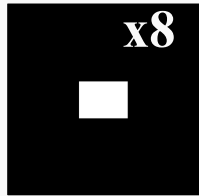


Challenge: Discrete approximation destroys sparsity!

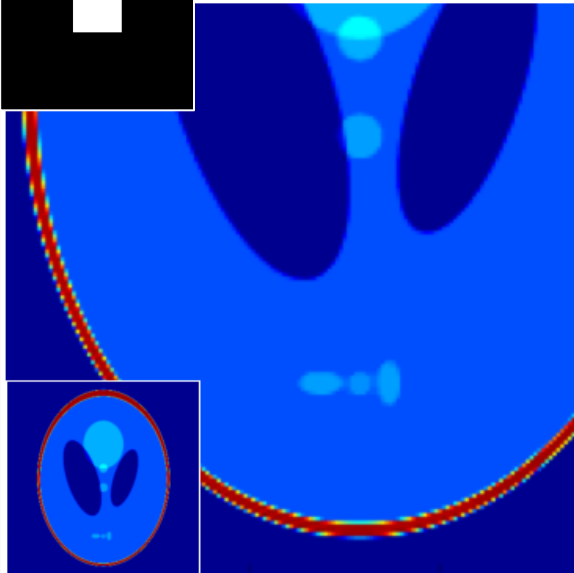


Super-resolution setting: ringing artifacts !!

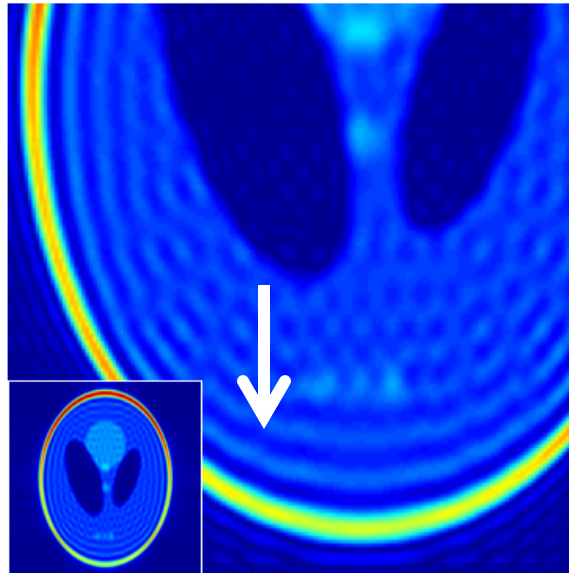
Fourier



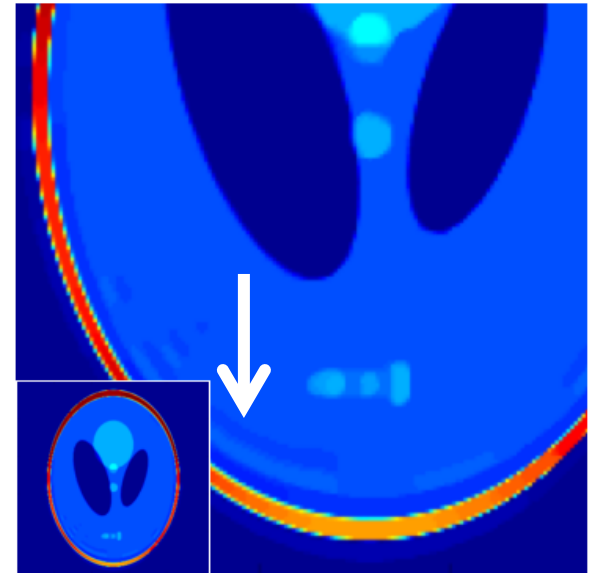
Ringing Artifacts



(a) Fully sampled



(b) IFFT, SNR=10.8dB



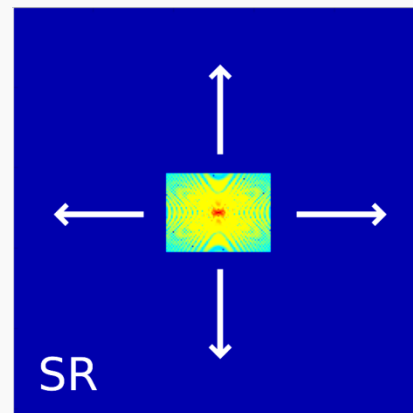
(c) TV, SNR=16.6dB

Overview

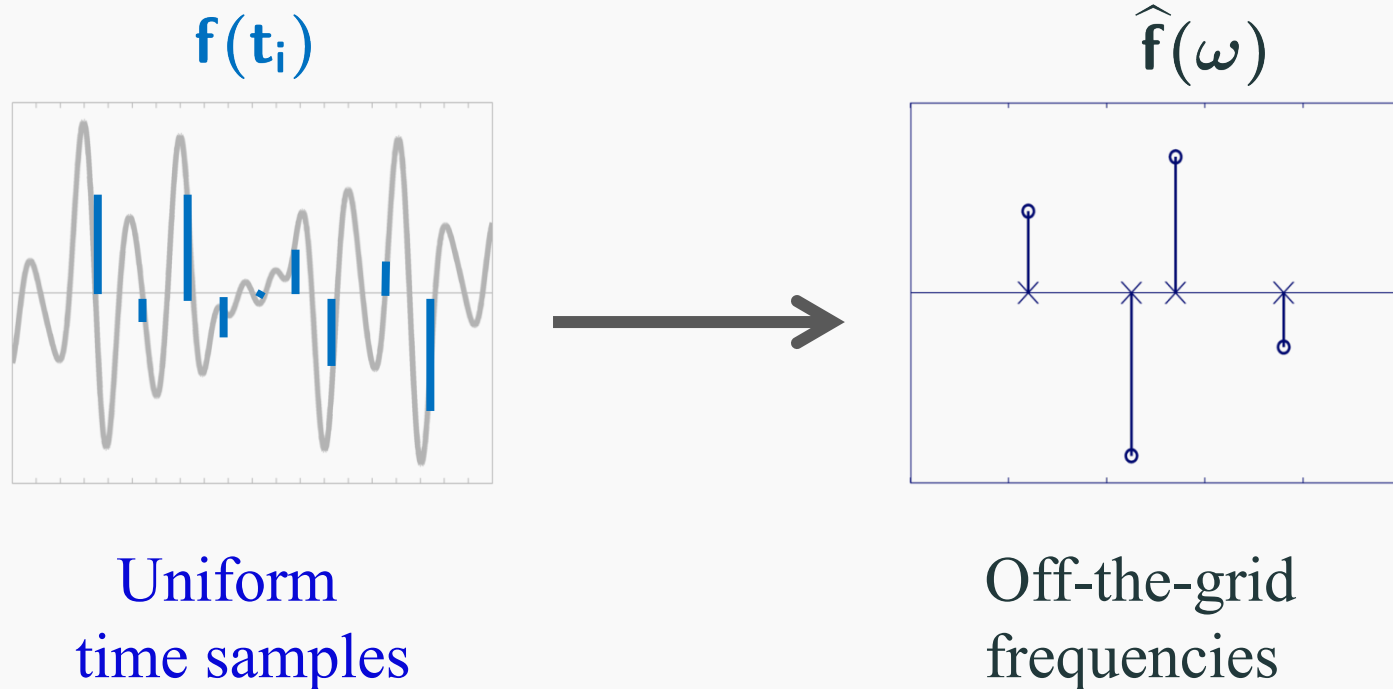
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1-D Theory

4. Structured low-rank **interpolation** for non-uniform samples
5. Fast implementations
6. Biomedical applications



Classical Off-the-Grid Method: Prony (1795)



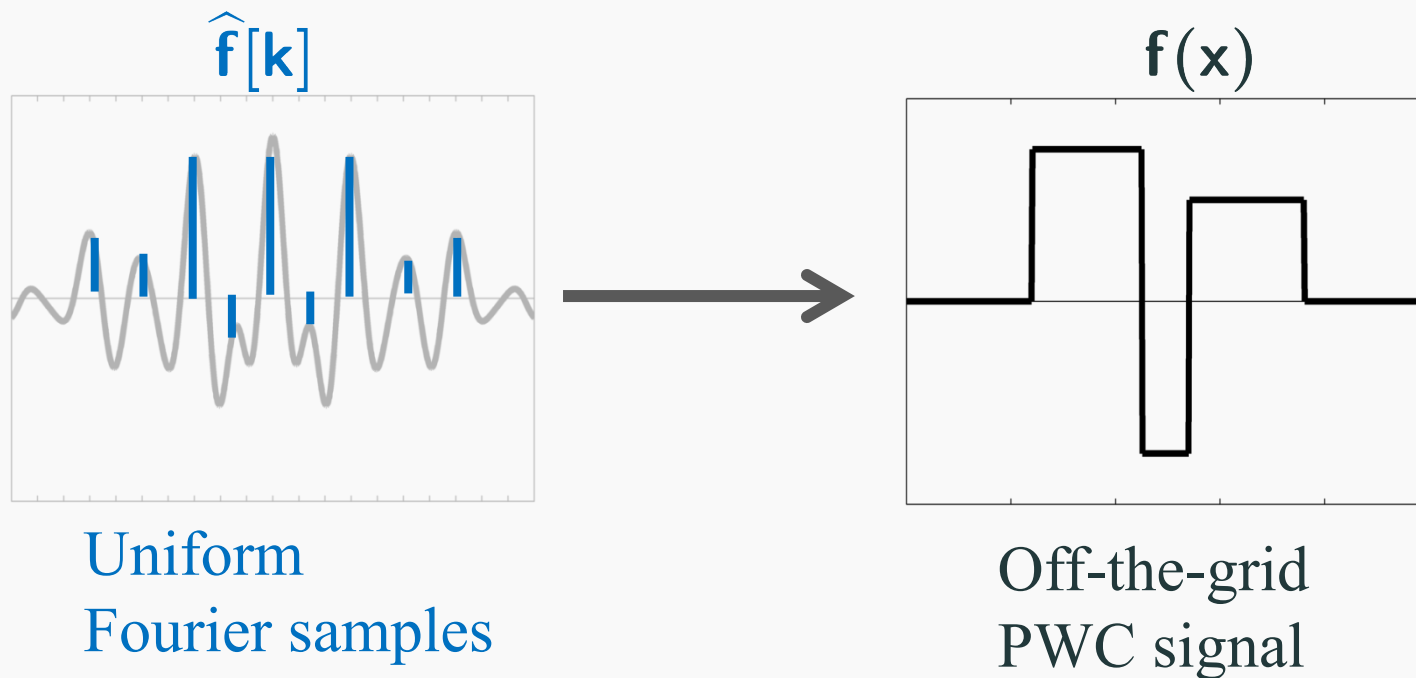
- Robust variants:

Pisarenko (1973), MUSIC (1986), ESPRIT (1989),

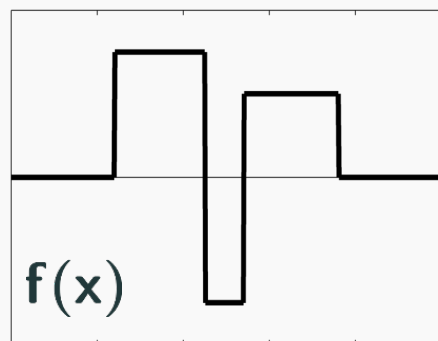
Matrix pencil (1990) . . . Atomic norm (2011)

Main inspiration: Finite-Rate-of-Innovation (FRI)

[Vetterli et al., 2002]

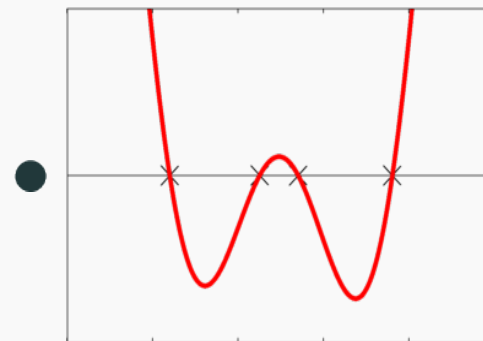
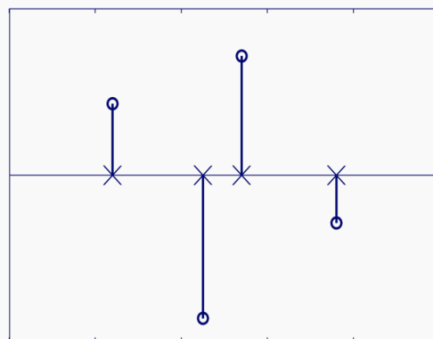


spatial domain



∂

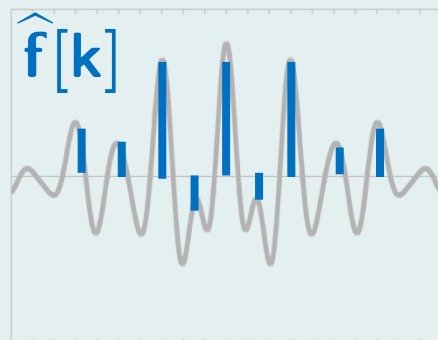
multiplication



$= 0$

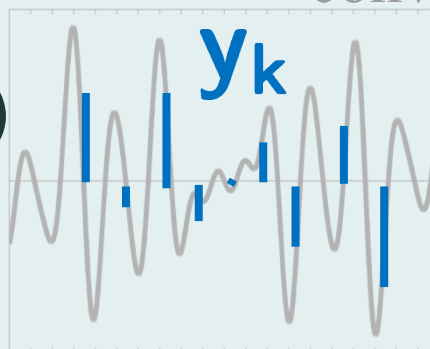
annihilating function

Fourier domain

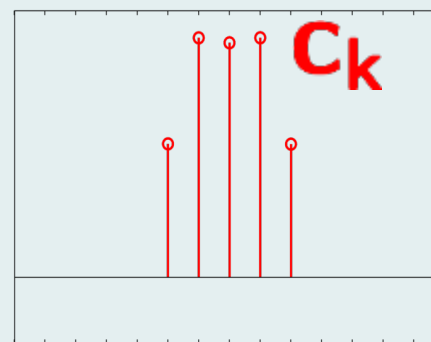


$(j2\pi k)$

convolution



$*$



$= 0$

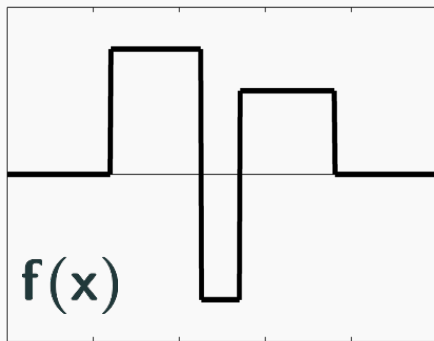
annihilating filter

Annihilation Relation:

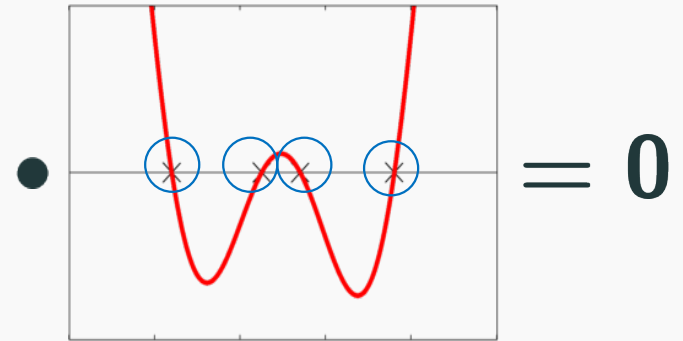
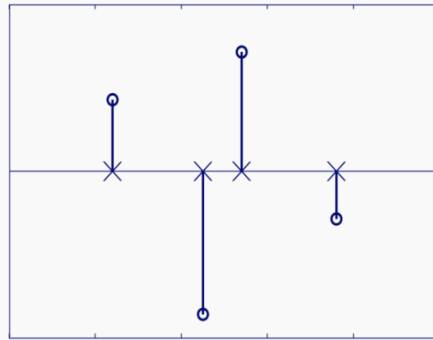
$$\sum_k y_{\ell-k} C_k = 0$$

Stage 2: solve linear system for amplitudes

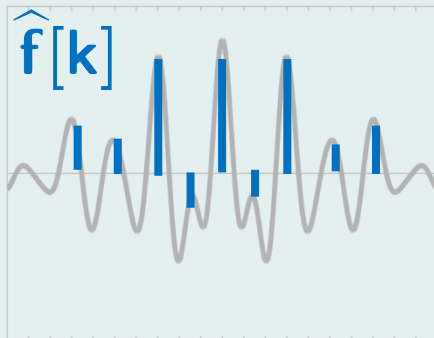
recover signal



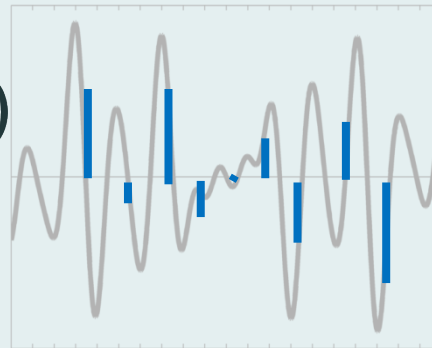
∂



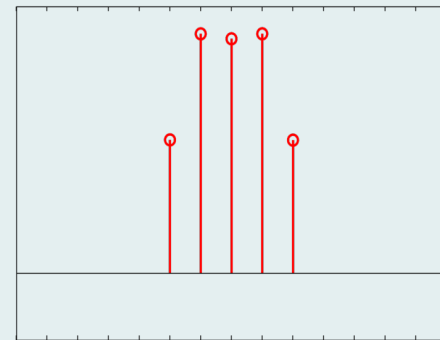
annihilating function



$(j2\pi k)$



*



annihilating filter

Stage 1: solve linear system for filter

Similar 1-D FRI idea by [Liang & Hacke 1989]

IEEE TRANSACTIONS ON ACOUSTICS, SPEECH, AND SIGNAL PROCESSING, VOL. 37, NO. 4, APRIL 1989

Superresolution Reconstruction Through Object Modeling and Parameter Estimation

E. MARK HAACKE, ZHI-PEI LIANG, AND STEVEN H. IZEN

Abstract—Fourier transform reconstruction with limited data is often encountered in tomographic imaging problems. Conventional techniques, such as FFT-based methods, the spatial-support-limited extrapolation method, and the maximum entropy method, have not been optimal in terms of both Gibbs ringing reduction and resolution enhancement. In this correspondence, a new method based on object modeling and parameter estimation is proposed to achieve superresolution reconstruction.

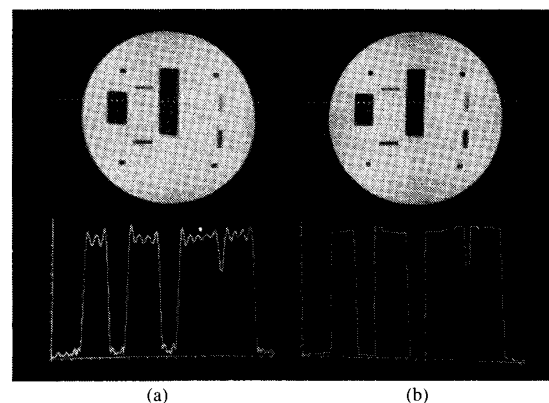
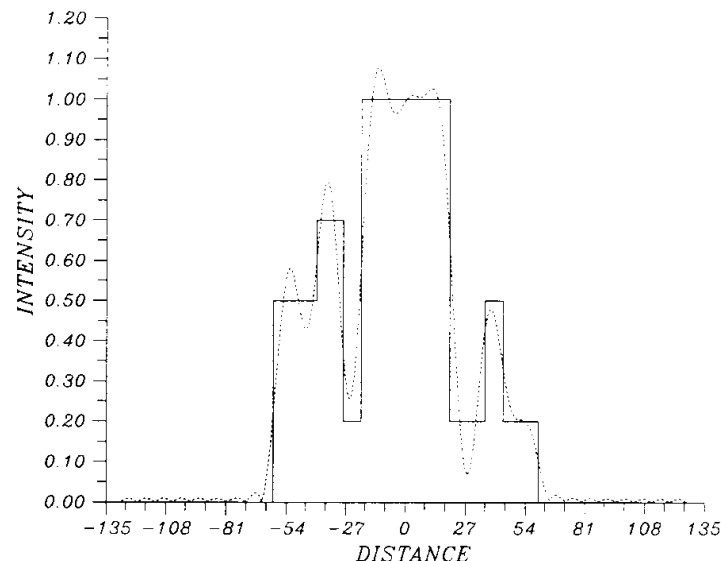
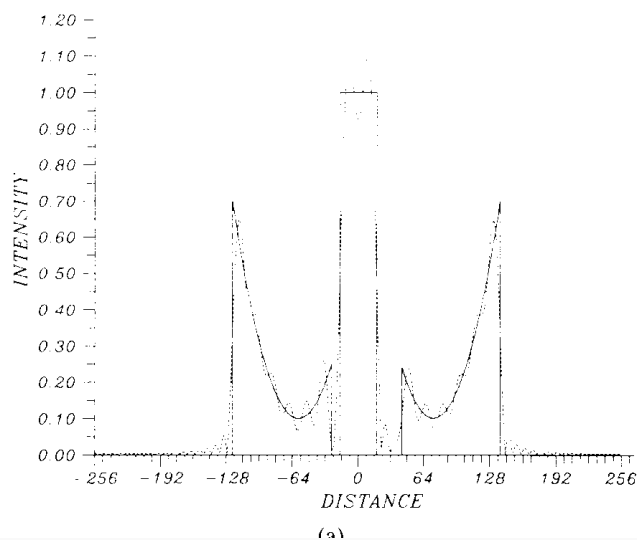
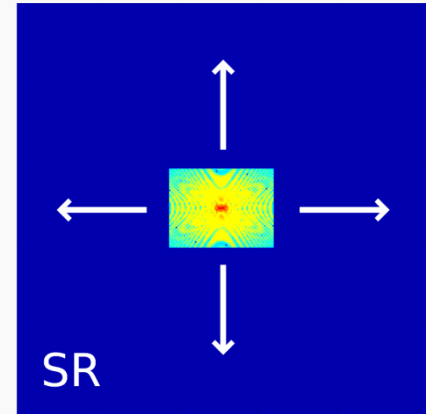


Fig. 2. (a) Fourier reconstruction of a phantom from real magnetic resonance data using 256 data points in the vertical direction and 64 points in the horizontal direction. (b) Same as (a), but vertical direction is reconstructed using the proposed method. An example profile through the phantom shows the improvement in image behavior.

Overview

1. Introduction
2. Review of Compressive Sensing
3. FRI **extrapolation** from uniform samples

2-D Theory

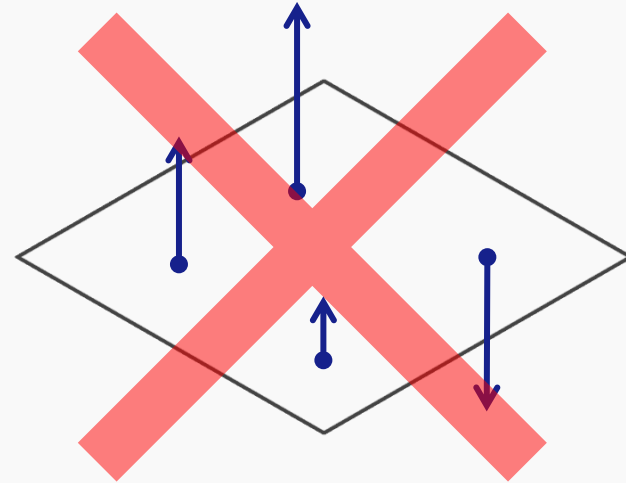
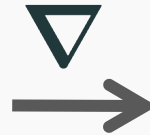
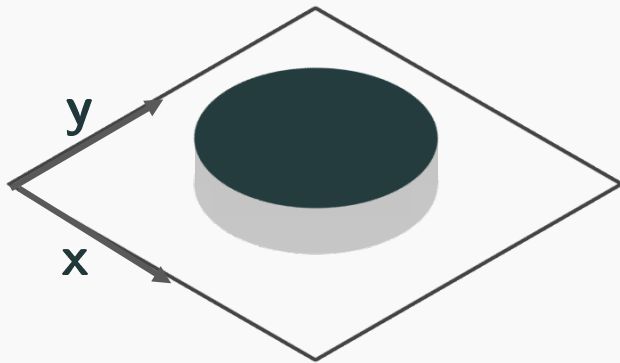


4. Structured low-rank **interpolation** for non-uniform samples
5. Fast implementations
6. Biomedical applications

Extension to higher dims: Singularities not isolated

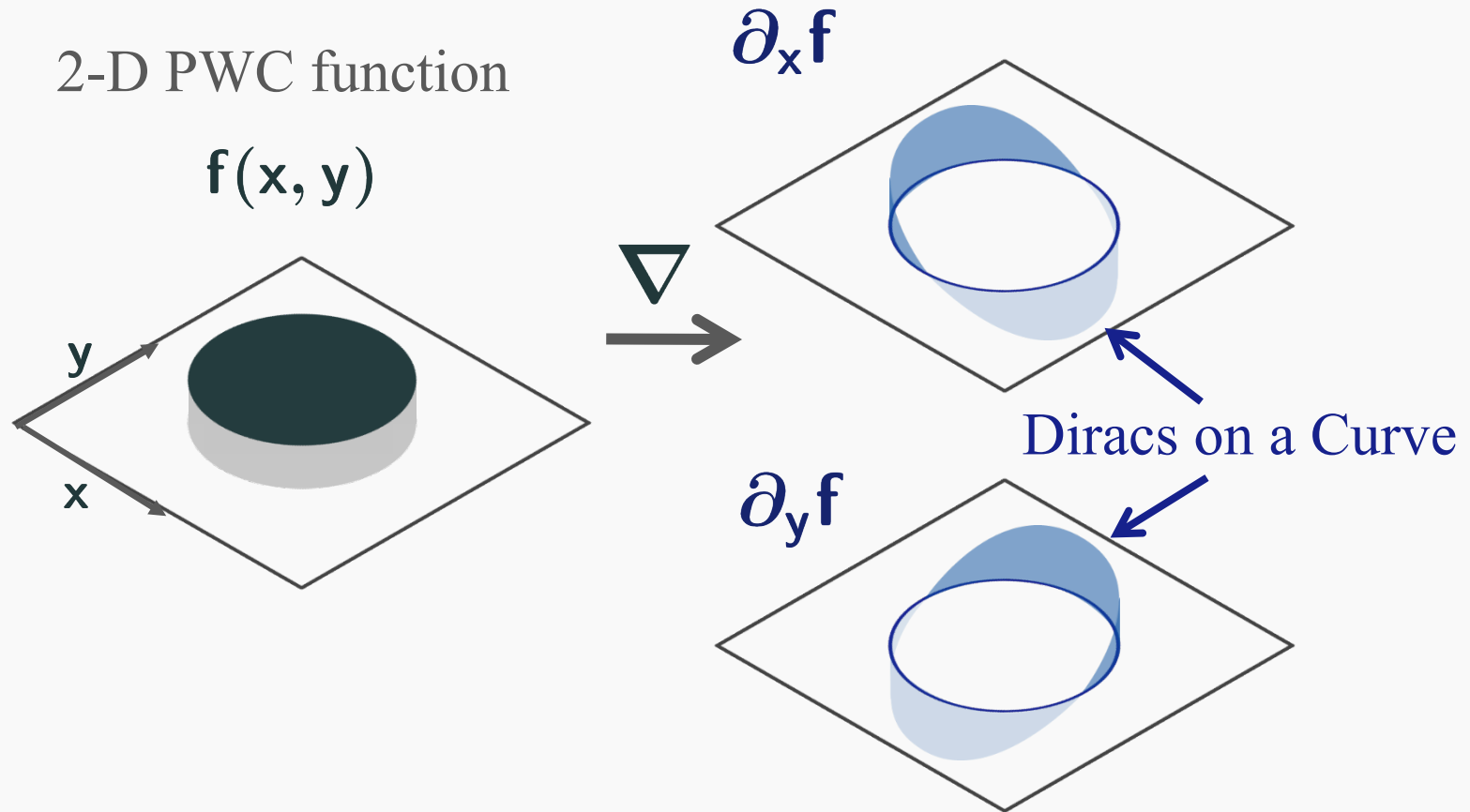
2-D PWC function

$f(x, y)$



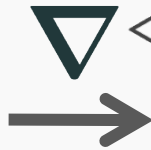
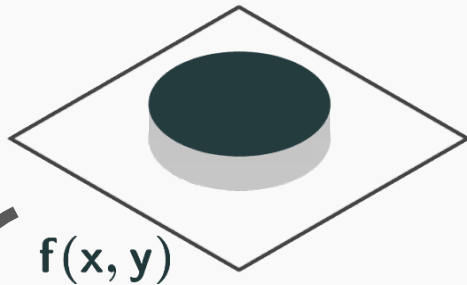
Isolated Diracs

Extension to higher dims: Singularities not isolated

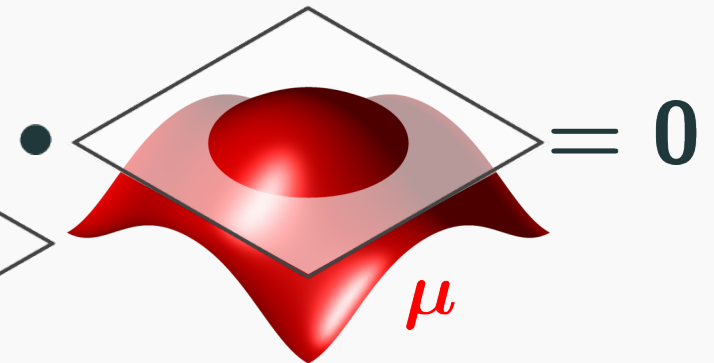


2-D PWC functions satisfy an annihilation relation

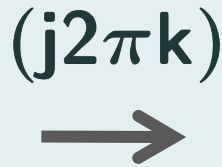
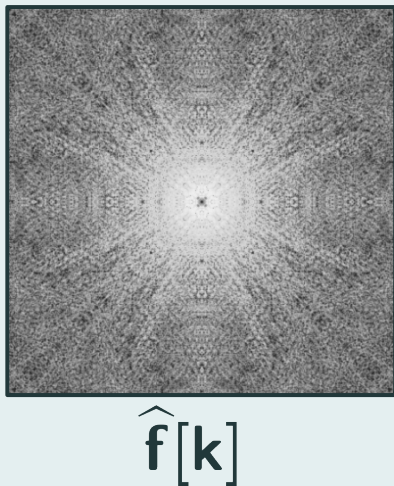
spatial domain



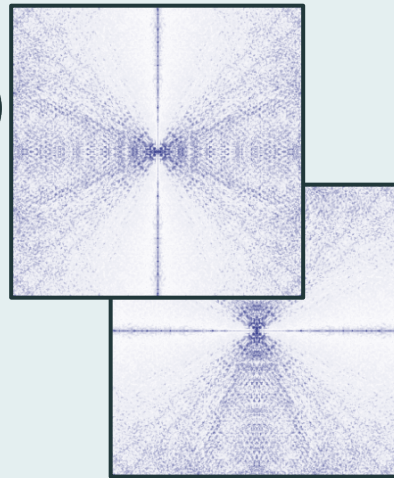
multiplication



Fourier domain



convolution



$= 0$

annihilating filter

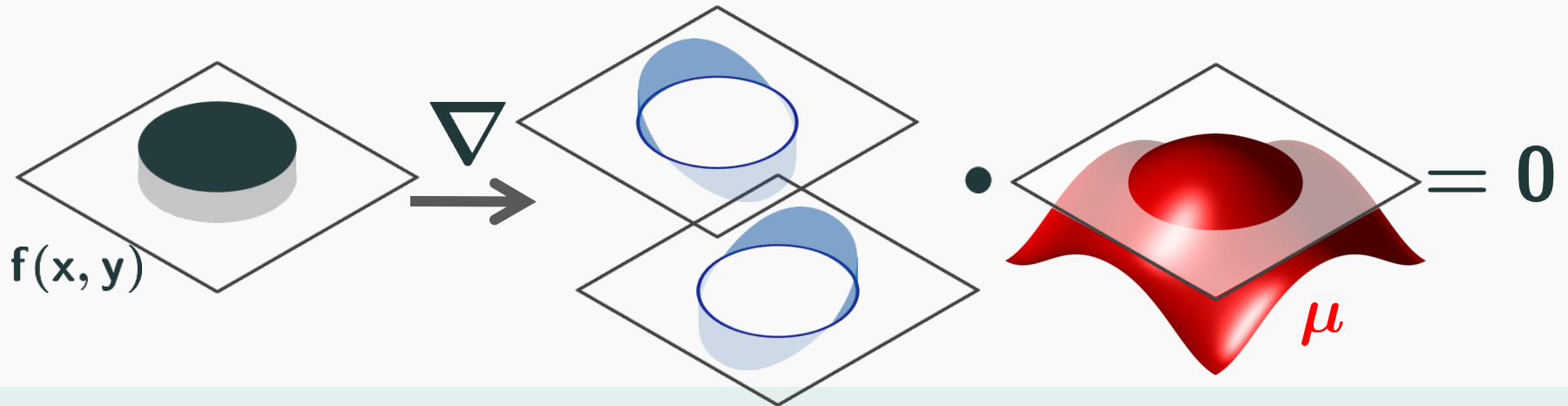
Annihilation relation:

$$\sum_k \nabla^2 \hat{f}[\ell - k] C_k = 0$$

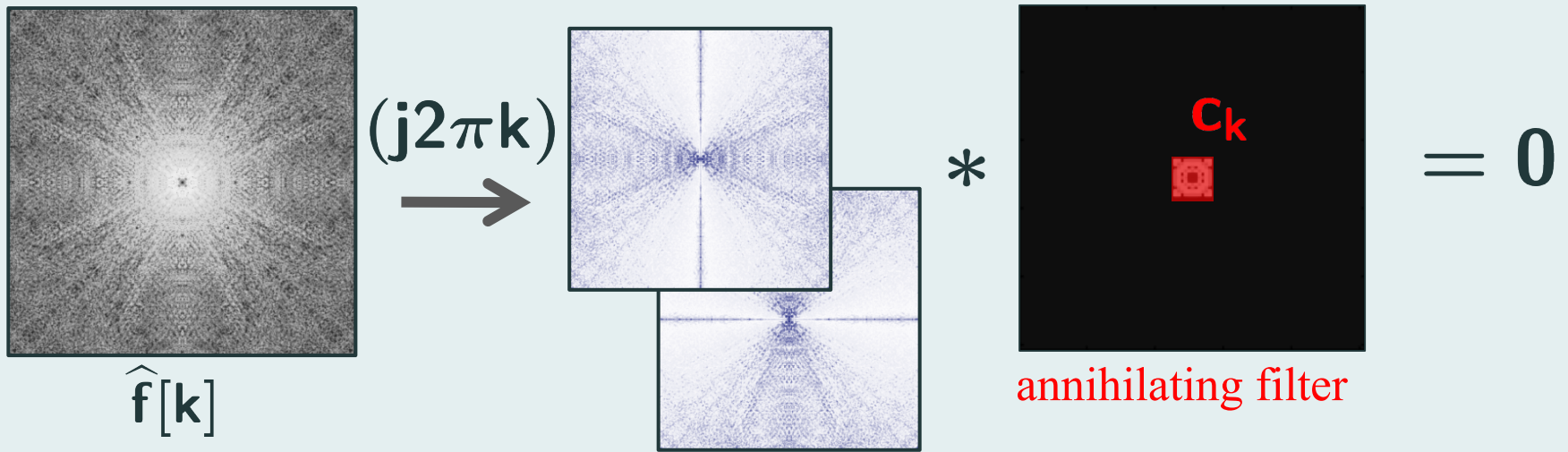
Image recovery



Stage 2: extrapolate given filter

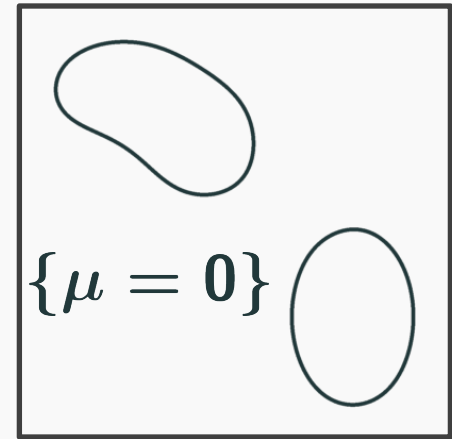
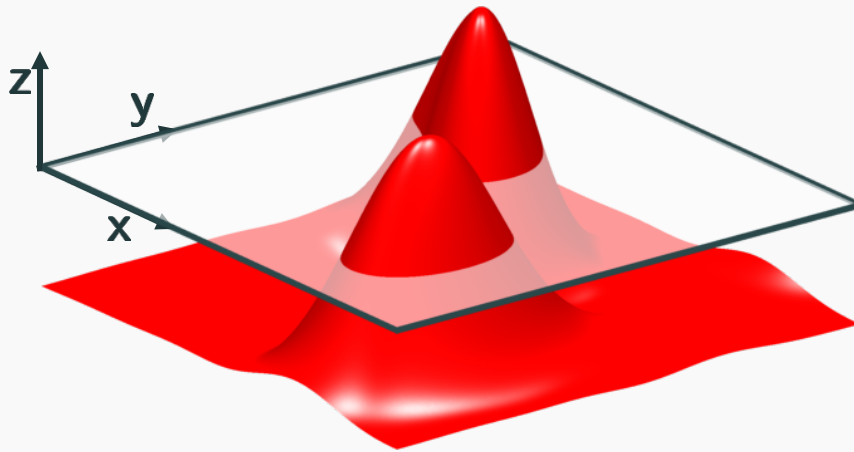


Fourier domain



Stage 1: solve linear system for filter

Bandlimited curves

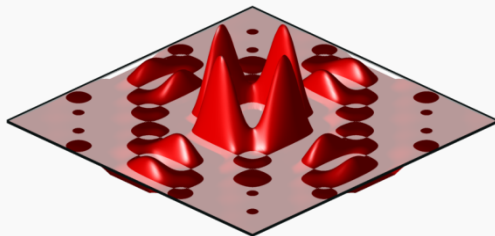
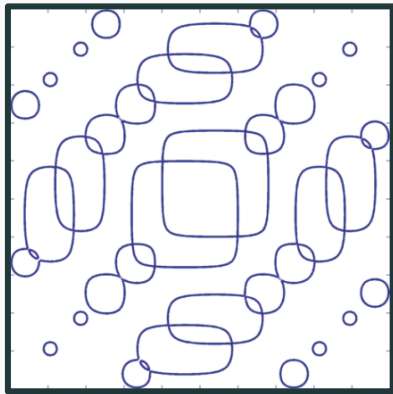


“FRI Curve”



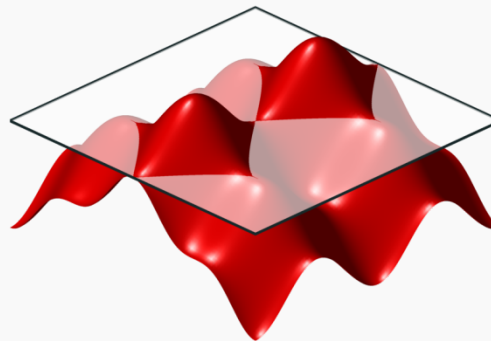
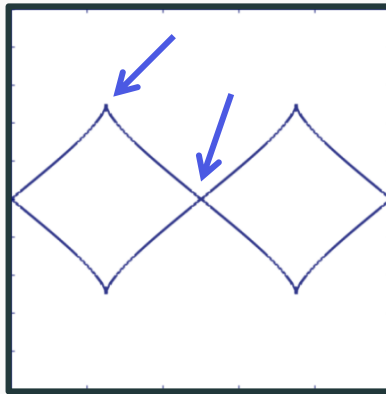
Bandlimited curves can represent complex shapes

Multiple curves
& intersections



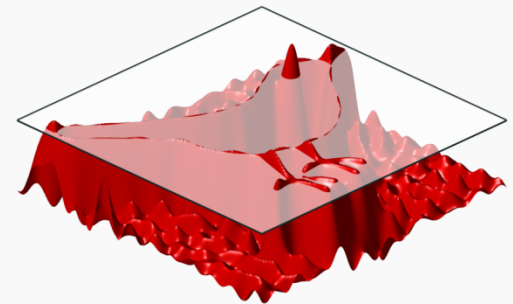
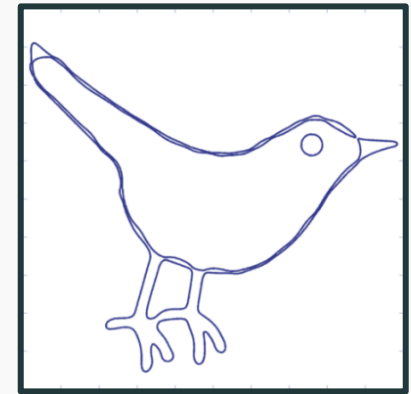
13x13 coefficients

Non-smooth
points



7x9 coefficients

Approximate
arbitrary curves



25x25 coefficients

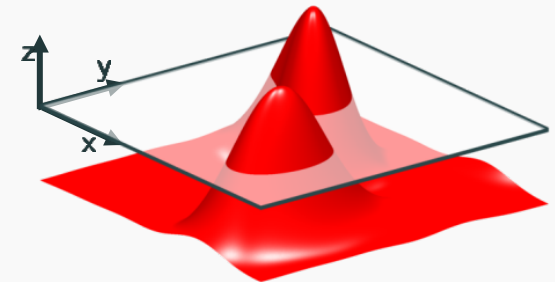
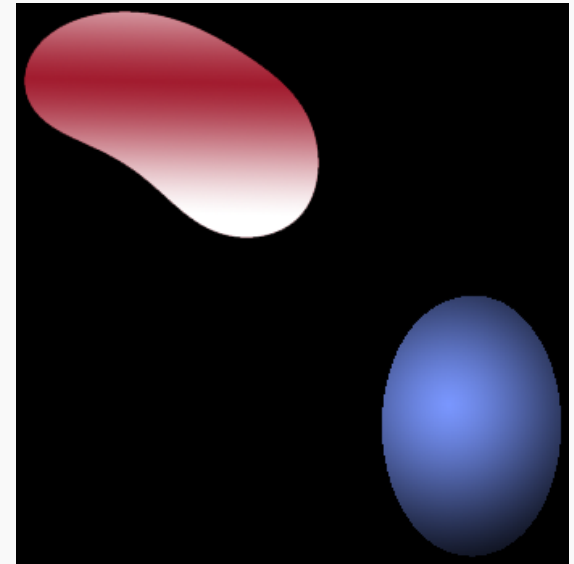
Piecewise analytic model

- Signal model: piecewise analytic signal

$$\mathbf{f}(\mathbf{z}) = \sum_{i=1}^N \mathbf{g}_i(\mathbf{z}) \cdot \mathbf{1}_{\Omega_i}(\mathbf{z})$$

s.t. \mathbf{g}_i analytic in Ω_i

- Not suitable for natural images
- 2-D only
- Recovery is ill-posed: Infinite DoF



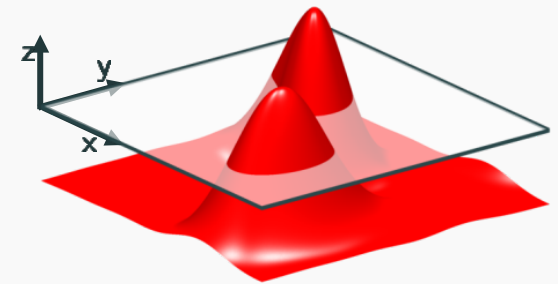
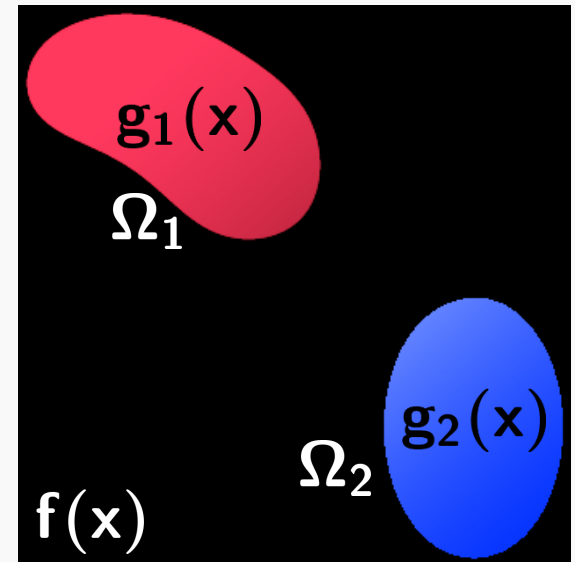
Piecewise smooth model

- New model: **piecewise smooth signals**

$$\mathbf{f}(\mathbf{x}) = \sum_{i=1}^N \mathbf{g}_i(\mathbf{x}) \cdot \mathbf{1}_{\Omega_i}(\mathbf{x})$$

s.t. \mathbf{g}_i smooth in Ω_i

- Extends easily to n-D
- Provable sampling guarantees
- Fewer samples necessary for recovery

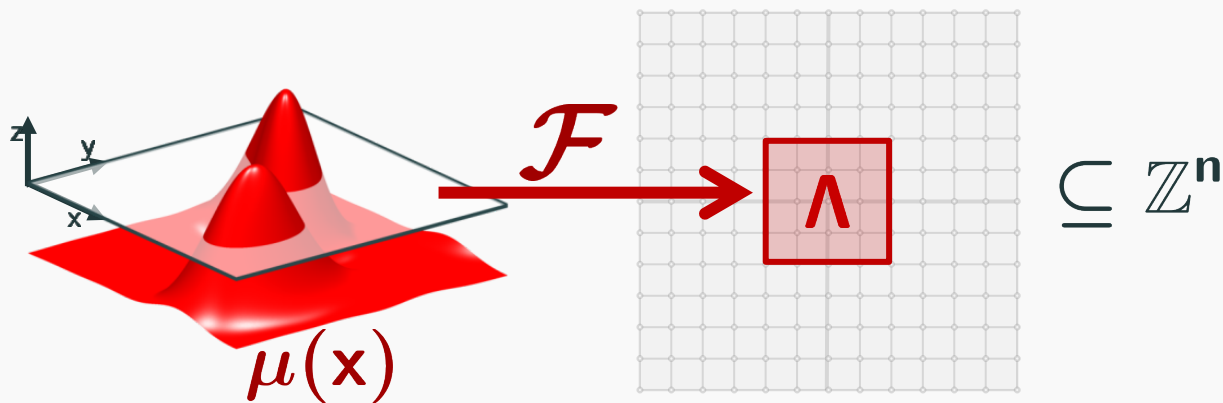
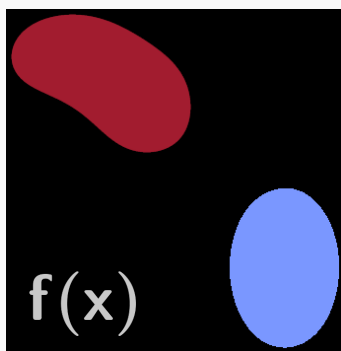


Eg. Piecewise constant functions: annihilation

Prop: If f is PWC with edge set $\mathbf{E} \subseteq \{\mu = 0\}$
for μ bandlimited to Λ then

$$\sum_{\mathbf{k} \in \Lambda} \mathbf{c}[\mathbf{k}] \widehat{\nabla f}[\ell - \mathbf{k}] = \mathbf{0} \text{ for all } \ell$$

any 1st order partial derivative

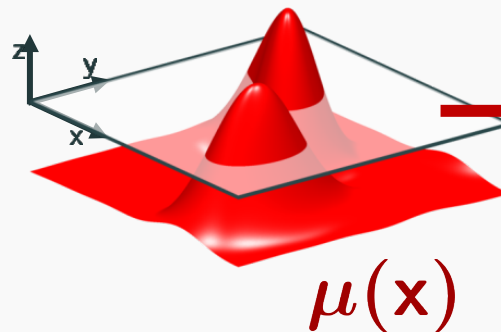
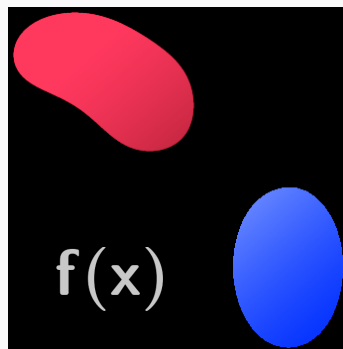


Eg. Piecewise linear functions: annihilation

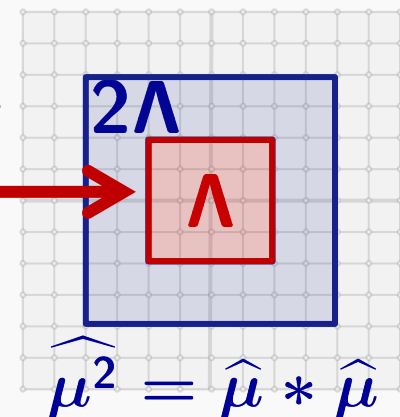
Prop: If \mathbf{f} is PW linear, with edge set $\mathbf{E} \subseteq \{\mu = 0\}$
and μ bandlimited to Λ then

$$\sum_{\mathbf{k} \in 2\Lambda} \widehat{\mu^2}[\mathbf{k}] \widehat{\partial^2 \mathbf{f}}[\ell - \mathbf{k}] = 0, \quad \forall \ell \in \mathbb{Z}^n$$

any 2nd order partial derivative



\mathcal{F}

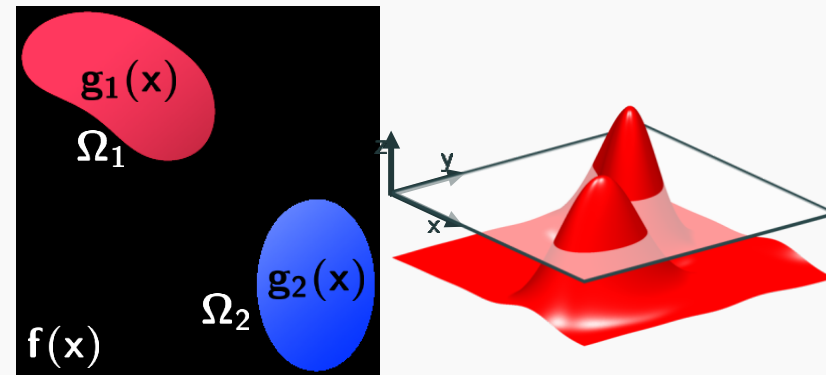


$\subseteq \mathbb{Z}^n$

General signal models

$$\mathbf{f}(\mathbf{x}) = \sum_{i=1}^N \mathbf{g}_i(\mathbf{x}) \cdot \mathbf{1}_{\Omega_i}(\mathbf{x})$$

s.t. $\mathbf{D}\mathbf{g}_i = \mathbf{0}$ in Ω_i



Signal Model:

PW Constant

PW Analytic*

PW Harmonic

PW Linear

PW Polynomial

Choice of Diff. Op.:

$$\mathbf{D} = \nabla$$

$$\mathbf{D} = \partial_x + \mathbf{j}\partial_y$$

$$\mathbf{D} = \Delta$$

$$\mathbf{D} = \{\partial_{xx}, \partial_{xy}, \partial_{yy}\}$$

$$\mathbf{D} = \{\partial^\alpha\}_{|\alpha|=n}$$

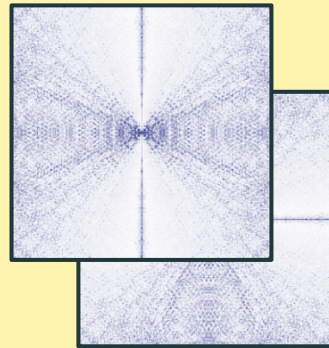
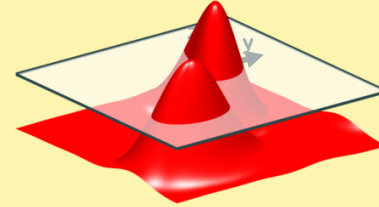
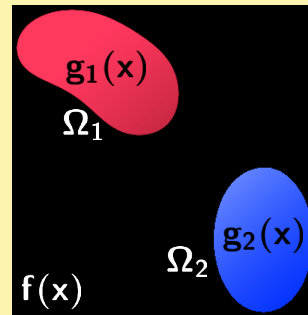
1st order

2nd order

nth order

Can we extrapolate ?

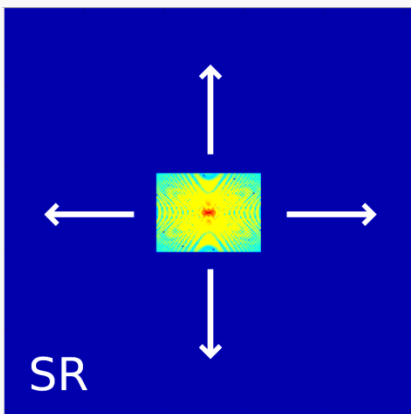
Piecewise smooth
signals satisfy
annihilation
conditions



*



= 0



How much should we sample to
extrapolate?


Recovery guarantees: challenges

1-D FRI Sampling Theorem [Vetterli et al., 2002]:

A continuous-time PWC signal with **K jumps** can be uniquely recovered from **2K+1 uniform Fourier samples**.

Proof (a la Prony's Method):

Form Toeplitz matrix **T** from samples, use uniqueness of Vandermonde decomposition:

$$\mathbf{T} = \mathbf{V}\mathbf{D}\mathbf{V}^H$$


“Caratheodory Parametrization”

Recovery guarantees: challenges

Extends to n -D if singularities isolated [Sidiropoulos, 2001]


$$\xrightarrow{\mathcal{F}} \quad \hat{\mathbf{f}}[\mathbf{k}] = \sum_i \mathbf{a}_i e^{-j2\pi \mathbf{k} \cdot \mathbf{x}_i}$$

Not true when singularities supported on curves:


$$\xrightarrow{\mathcal{F}} \quad \widehat{\nabla \mathbf{f}}[\mathbf{k}] = \oint_{\partial\Omega} e^{-j2\pi \mathbf{k} \cdot \mathbf{x}} \mathbf{n} \, ds$$

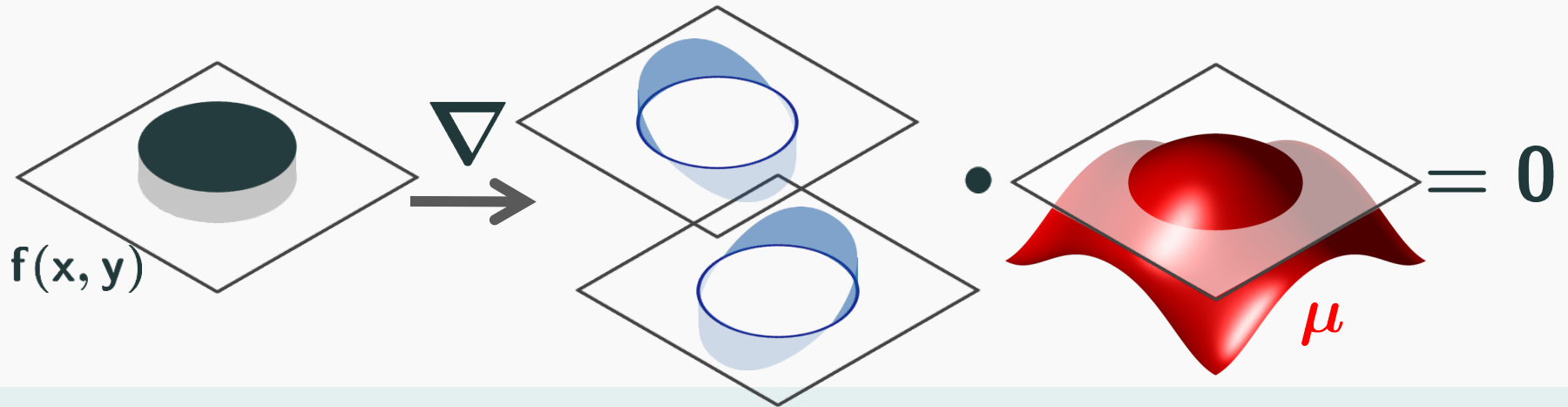
Requires new techniques:

- Spatial domain interpretation of annihilation relation
- Algebraic geometry of trigonometric polynomials

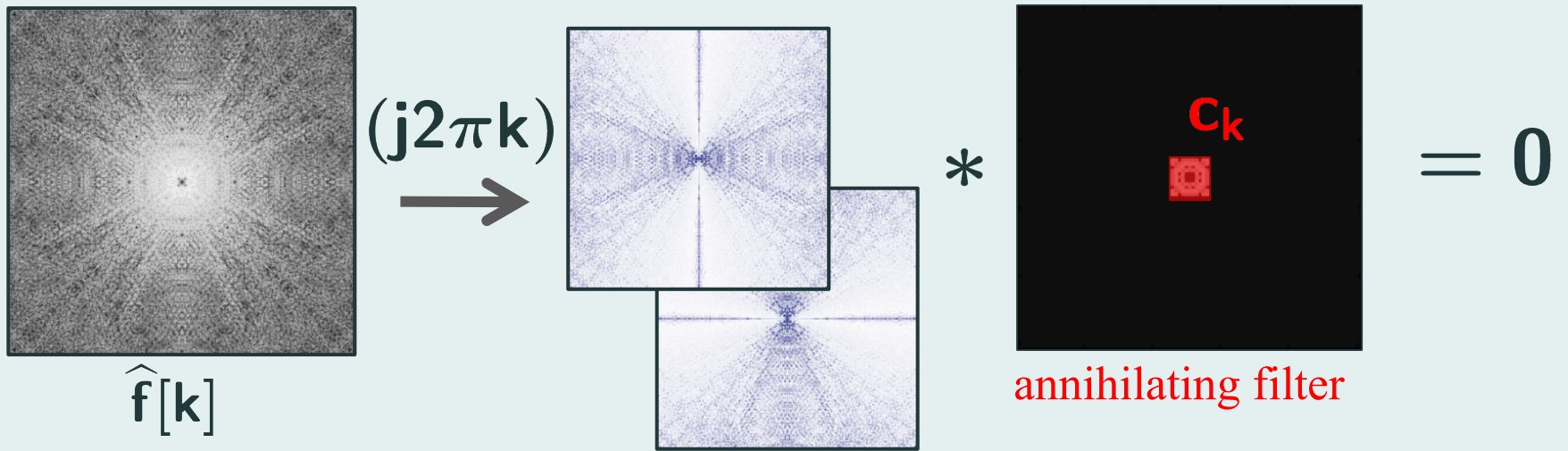
Image recovery



Stage 2: extrapolate given filter



Fourier domain



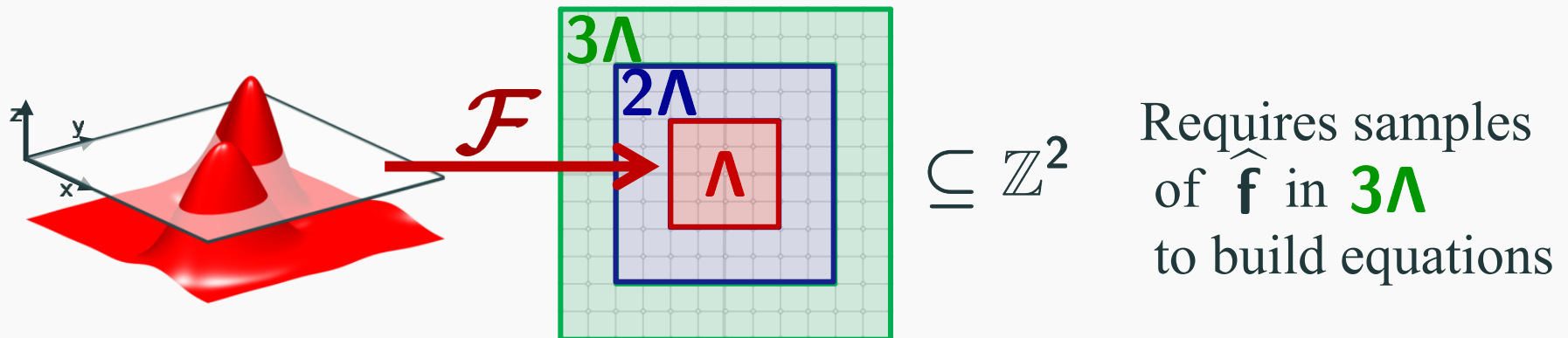
Stage 1: solve linear system for filter

Step 1. When can you recover the **filter** ?

Theorem: If \mathbf{f} is PWC* with edge set $\mathbf{E} = \{\mu = 0\}$ with μ minimal and bandlimited to Λ then $\mathbf{c} = \hat{\mu}$ is the unique solution to

$$\sum_{\mathbf{k} \in \Lambda} \mathbf{c}[\mathbf{k}] \widehat{\nabla} \mathbf{f}[\ell - \mathbf{k}] = 0 \text{ for all } \ell \in 2\Lambda$$

*Some geometric restrictions apply



Step 2. When can you recover the signal **given the filter** ?

Theorem: If \mathbf{f} is PWC* with edge set $\mathbf{E} = \{\mu = \mathbf{0}\}$

with μ minimal and bandlimited to Λ then

$\mathbf{g} = \mathbf{f}$ is the unique solution to

$$\mu \cdot \nabla \mathbf{g} = \mathbf{0} \quad \text{s.t.} \quad \hat{\mathbf{f}}[\mathbf{k}] = \hat{\mathbf{g}}[\mathbf{k}], \mathbf{k} \in \Gamma$$

when the sampling set $\Gamma \supseteq 3\Lambda$

Step 2. When can you extrapolate **given the filter** ?

Theorem: If \mathbf{f} is PWC* with edge set $\mathbf{E} = \{\mu = 0\}$

with μ minimal and bandlimited to Λ then

$\mathbf{g} = \mathbf{f}$ is the unique solution to

$$\mu \cdot \nabla \mathbf{g} = \mathbf{0} \quad \text{s.t.} \quad \hat{\mathbf{f}}[\mathbf{k}] = \hat{\mathbf{g}}[\mathbf{k}], \mathbf{k} \in \Gamma$$

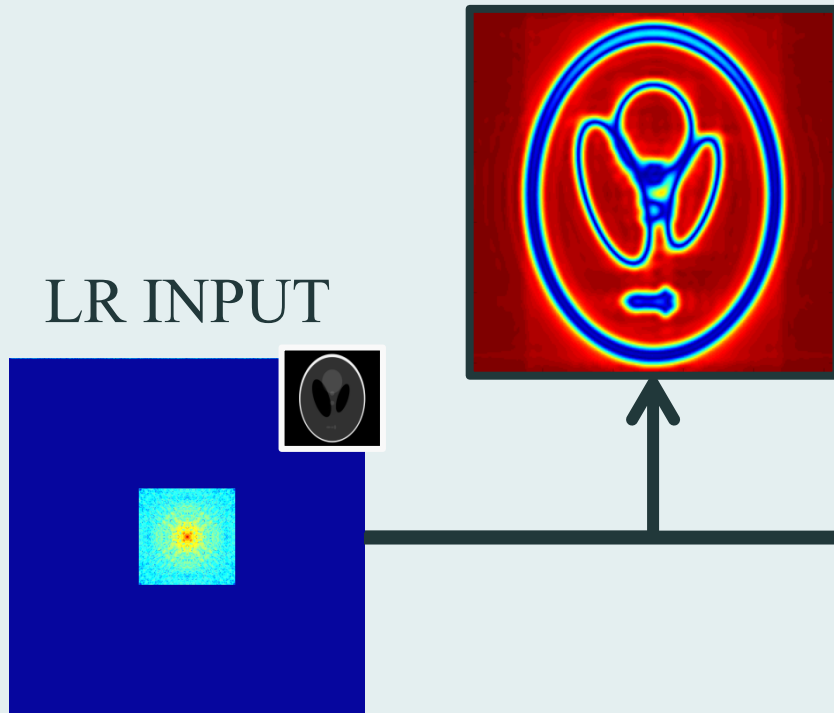
when the sampling set $\Gamma \supseteq 3\Lambda$

Equivalently,

$$\mathbf{f} = \arg \min_{\mathbf{g}} \|\mu \cdot \nabla \mathbf{g}\| \quad \text{s.t.} \quad \hat{\mathbf{f}}[\mathbf{k}] = \hat{\mathbf{g}}[\mathbf{k}], \mathbf{k} \in \Gamma$$

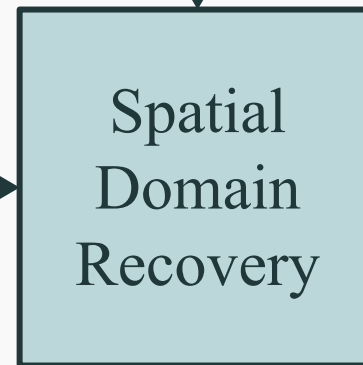
Super-resolution image recovery

1. Recover edge set



2. Recover amplitudes

Discretize

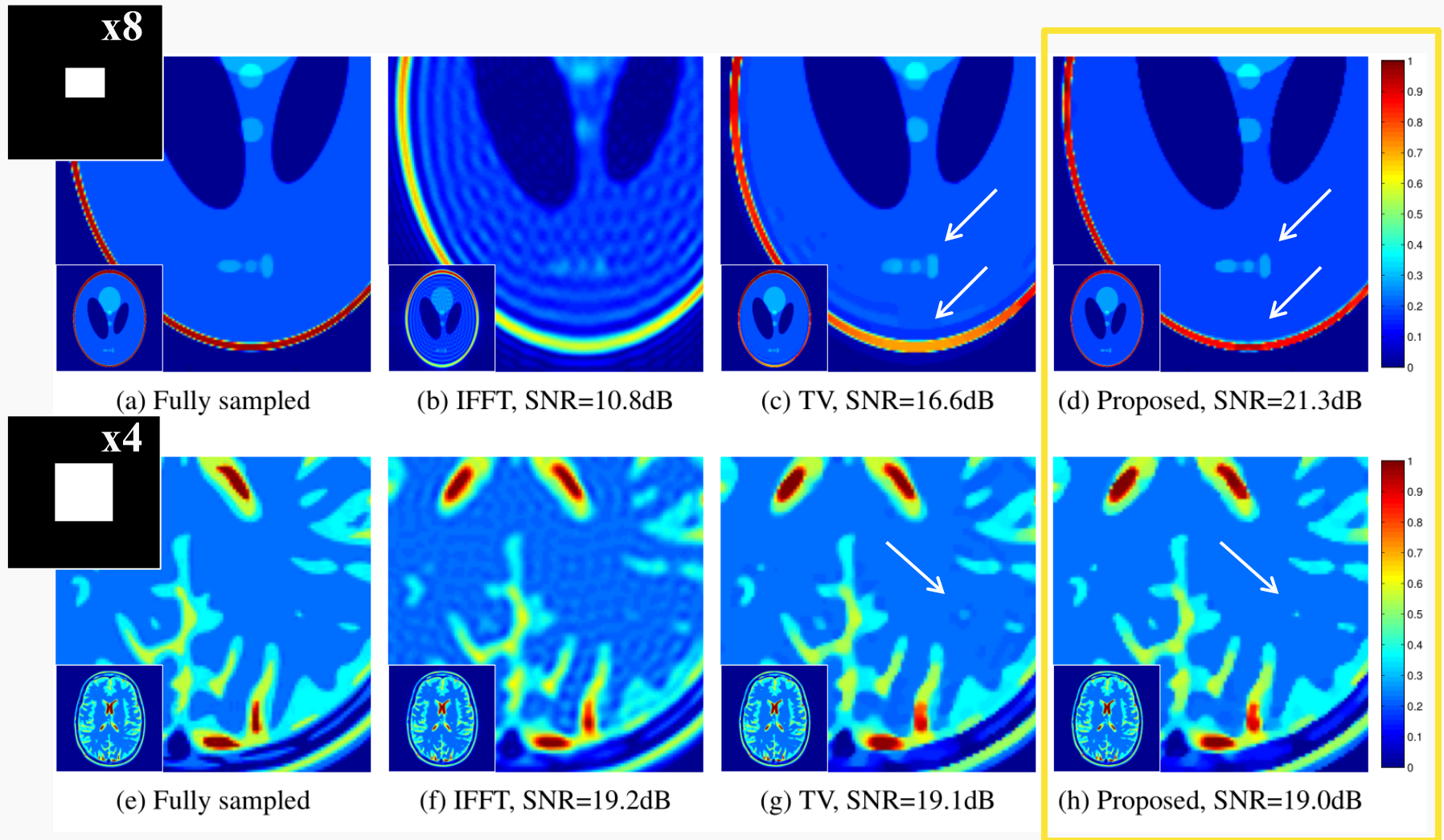


HR OUTPUT

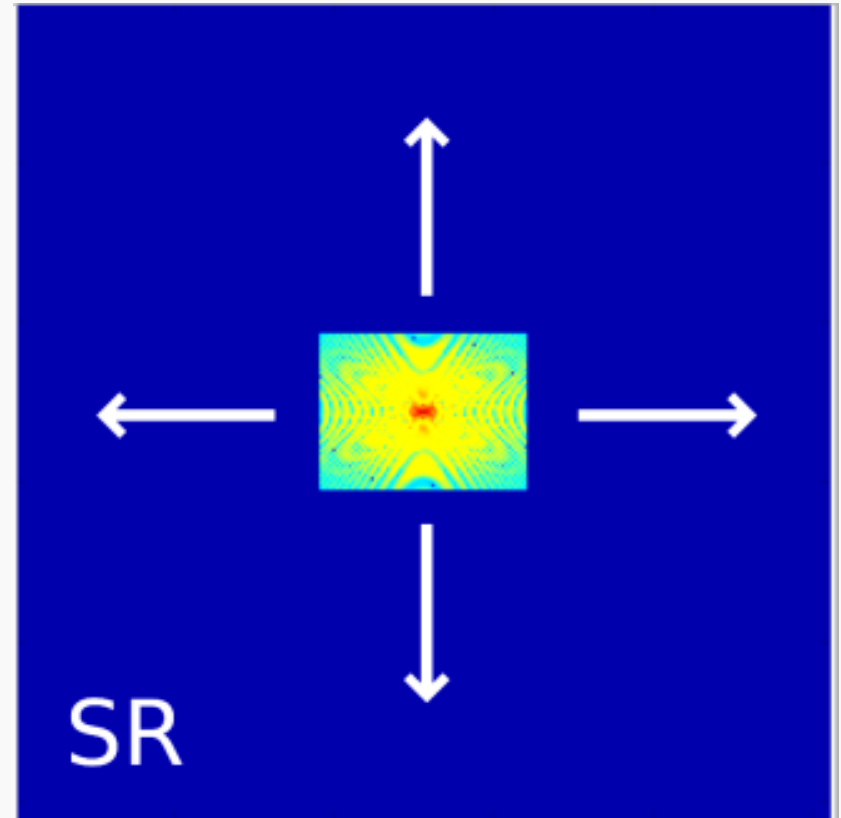
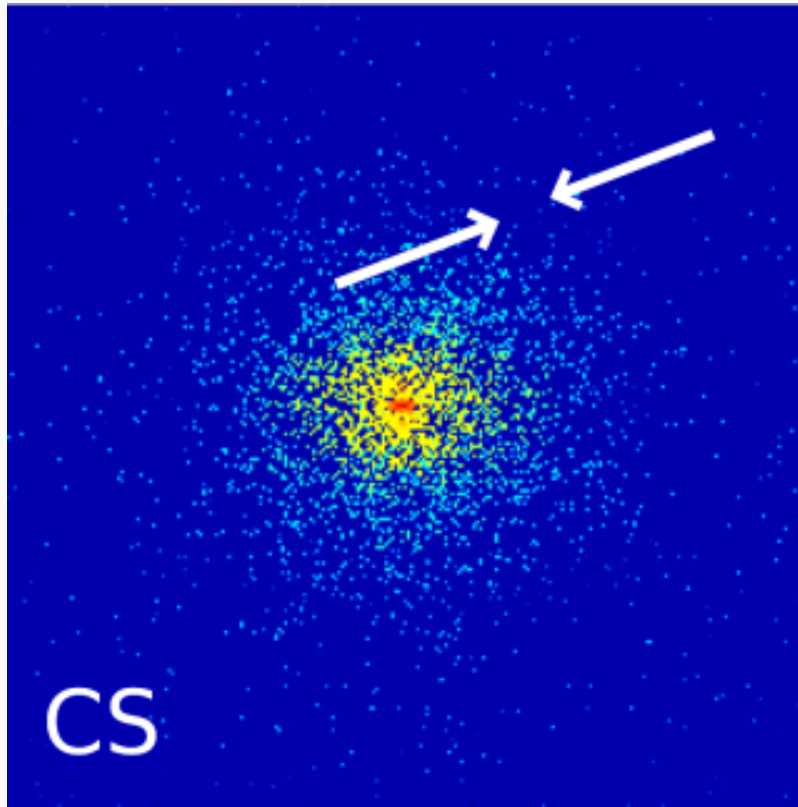


On-the-grid

Super-resolution of MRI Medical Phantoms



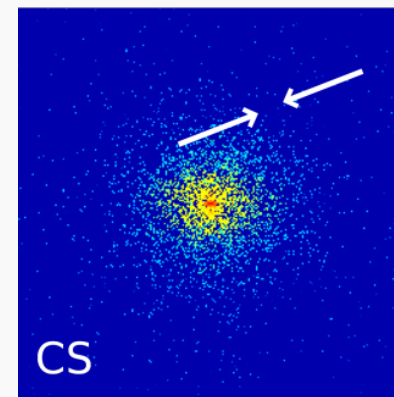
Can we generalize to non-uniform setting ??



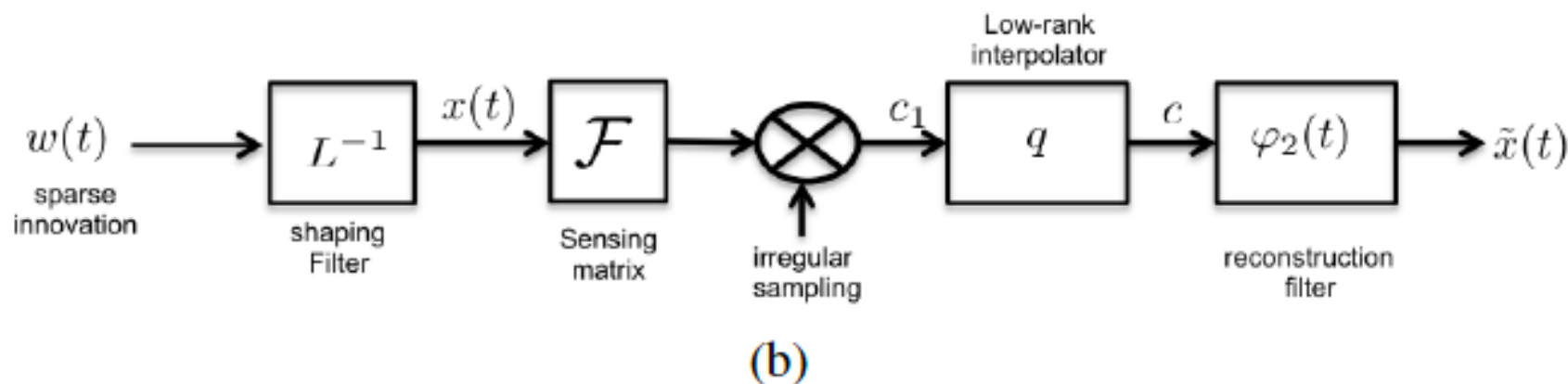
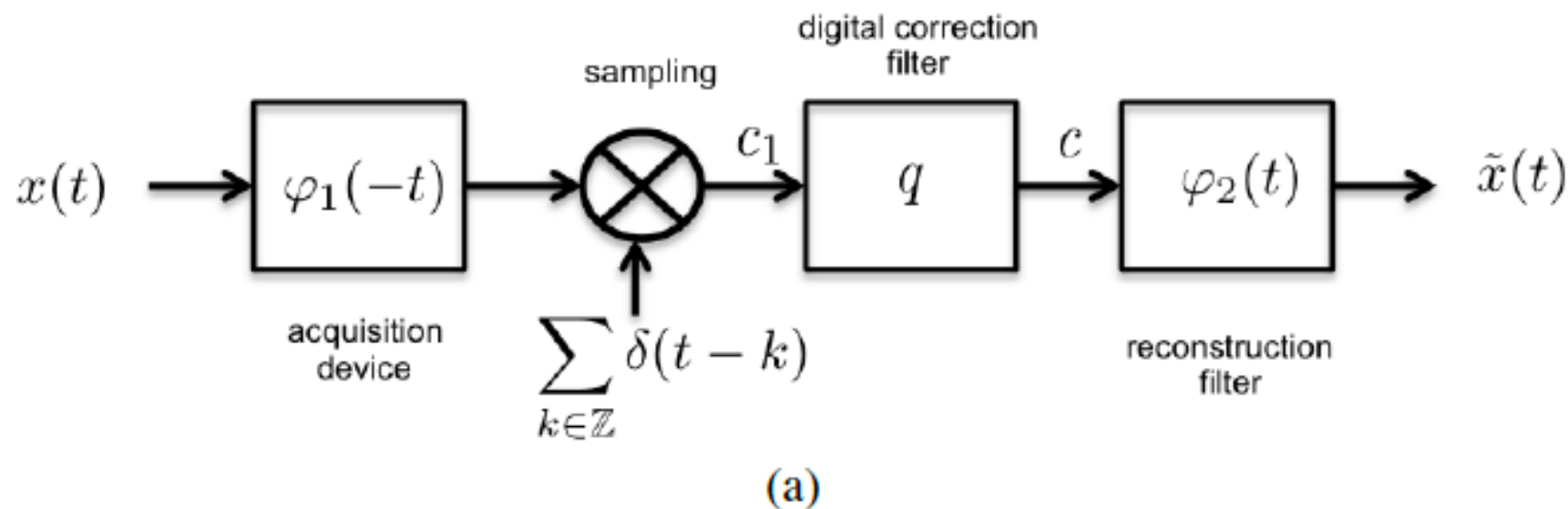
Improve recovery using non-uniform sampling

Overview

1. Introduction
2. Review of Compressive Sensing
3. FRI **extrapolation** from uniform samples
4. Structured low-rank **interpolation** for non-uniform samples
 - 1-D Theory
5. Fast implementations
6. Biomedical applications

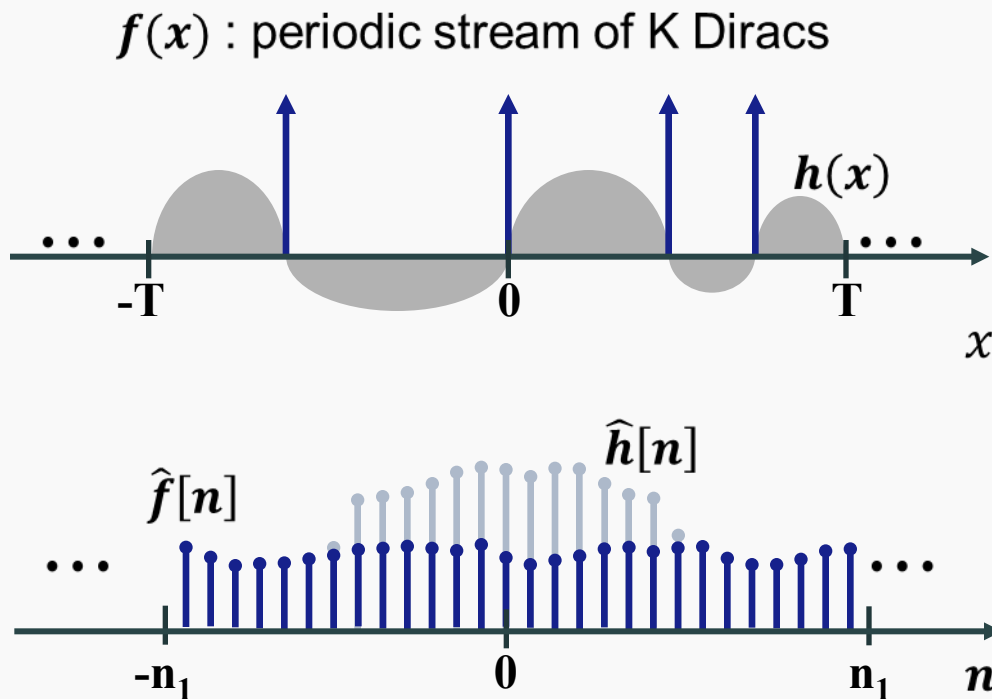


Sampling vs low-rank interpolation



Key idea: annihilating filter

* FRI Sampling theory



$h(x)$: annihilating function

$$f(x) \cdot h(x) = 0$$

$\hat{h}[n]$: annihilating filter

$$\hat{f}[n] * \hat{h}[n] = 0$$

Length of $\hat{h}[n] \geq k+1$

Low rank Hankel matrix

* Jin KH et al. IEEE TCI (to appear)

* Ye JC et al. IEEE TIT, 2016

* Jin KH et al., IEEE TIP, 2015

* ALOHA : Annihilating filter based LOW rank Hankel matrix Approach

Finite length convolution

$$(\hat{h} * \hat{f})[n] = \sum_{I=0}^{\kappa-1} \hat{h}[I] \hat{f}[n-I] = 0$$

κ : # of annihilating filter coef.

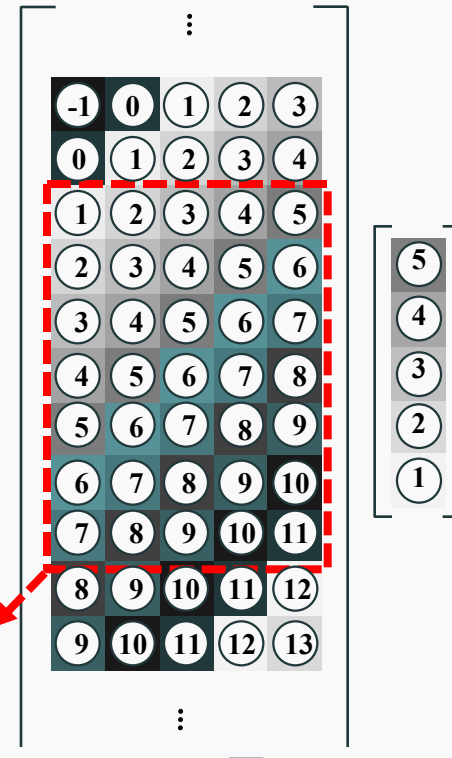
Matrix
Representation

$$\mathcal{C}(\hat{f}) \bar{\hat{h}} = 0$$

$$\mathcal{C}(\hat{f}) \bar{\hat{h}} =$$

($n_1 = 11, \kappa = 5$)

$$\mathcal{H}(\hat{f})$$



Sparsity in spatial domain \Leftrightarrow low rankness in k-space

Low-Rank Hankel matrix minimization

$$\text{Rank} \mathcal{H}(\hat{\mathbf{f}}) = k$$

** Jin KH et al IEEE TCI, 2016*

** Jin KH et al., IEEE TIP, 2015*

** Ye JC et al., IEEE TIT, 2016*

Missing elements can be found by low rank Hankel structured matrix completion

$$\begin{aligned} & \min_{\mathbf{m}} \quad \|\mathcal{H}(\mathbf{m})\|_* \\ & \text{subject to} \quad P_{\Omega}(\mathbf{m}) = P_{\Omega}(\hat{\mathbf{f}}) \end{aligned}$$

$\|\cdot\|_*$

Nuclear norm

P_{Ω}

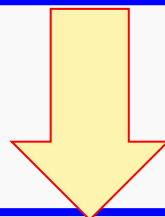
Projection on sampling positions

General TV Signals

$$Lf(x) = \sum_{j=0}^{k-1} a_j \delta(x - x_j), \quad x_j \in [0, \tau].$$

$$L := a_K D^K + a_{K-1} D^{K-1} + \dots + a_1 D + a_0$$

*Piecewise smooth
Splines, polynomials*



Weighted Fourier data

$$\mathcal{F}\{Lf(x)\} = \hat{l}(\omega) \hat{f}(\omega) = \sum_{j=0}^{k-1} a_j e^{-i\omega x_j}$$

$$\hat{l}(\omega) = a_K (i\omega)^K + a_{K-1} (i\omega)^{K-1} + \dots + a_1 (i\omega) + a_0$$

Existence of Annihilating Filter

Annihilating filter for weighted Fourier data

$$\hat{h}(\omega) * \left(\hat{l}(\omega) \hat{f}(\omega) \right) = 0$$

General Low-Rank Hankel Matrix Completion

$$\begin{aligned} (P) \quad & \min_{\mathbf{m} \in \mathbb{C}^n} \quad \text{RANK } \mathcal{H}(\mathbf{m}) \\ & \text{subject to} \quad P_{\Omega}(\mathbf{m}) = P_{\Omega}(\hat{\mathbf{l}} \odot \hat{\mathbf{f}}) , \end{aligned}$$

Extension to general signal models

Stream of Diracs

$$x(t) = \sum_{l \in \mathbb{Z}} \sum_{i=0}^{r-1} c_i \delta(t - t_i - l\tau),$$

$$\hat{h}(z) = \sum_{l=0}^r \hat{h}[l] z^{-l} = \prod_{j=0}^{r-1} (1 - e^{-i2\pi t_j/\tau} z^{-1}) \quad \text{rank} = r$$

Stream of differentiated Diracs

$$x(t) = \sum_{l \in \mathbb{Z}} \sum_{j=0}^{d_j} c_{lj} \delta^{(j)}(t - t_l)$$

$$\hat{h}(z) = \prod_{j=0}^{r-1} (1 - e^{-i2\pi t_j/\tau} z^{-1})^{d_j} \quad \text{rank} = \sum_j d_j$$

**With a proper weighting, the Hankel matrix of the weighted k-space data
→ low ranked.**

Non-uniform spline

$$Lx = \sum_{j=0}^{r-1} c_j \delta(t - t_j)$$

$$L := a_K \partial^K + a_{K-1} \partial^{K-1} + \dots + a_1 \partial + a_0$$

$$\hat{h}(z) = \sum_{l=0}^r \hat{h}[l] z^{-l} = \prod_{j=0}^{r-1} (1 - e^{-i2\pi t_j/\tau} z^{-1}) \quad \text{rank} = r$$

Piecewise smooth polynomial

$$x^{(q+1)}(t) = \sum_{l \in \mathbb{Z}} \sum_{j=0}^q c_{lj} \delta^{(j)}(t - t_l)$$

$$\hat{h}(z) = \prod_{j=0}^{r-1} (1 - u_j z^{-1})^q \quad \text{rank} = rq$$

Performance Guarantees

Exact Recovery

$$\begin{aligned} & \min_{\mathbf{m}} \|\mathcal{H}(\mathbf{m})\|_* \\ & \text{subject to } P_{\Omega}(\mathbf{m}) = P_{\Omega}(\hat{\mathbf{f}}) \\ & m \geq c_1 \mu c_s k \log^{\alpha} n \end{aligned}$$

$$\alpha = \begin{cases} 2, & \text{on grid} \\ 4, & \text{off grid} \end{cases}$$

Stable Recovery

$$\begin{aligned} & \min_{\mathbf{m}} \|\mathcal{H}(\mathbf{m})\|_* \\ & \text{subject to } \|P_{\Omega}(\mathbf{m}) - P_{\Omega}(\hat{\mathbf{f}})\| \leq \delta \\ & \|\mathcal{H}(\mathbf{m}) - \mathcal{H}(\hat{\mathbf{f}})\|_F \leq c_2 n^2 \delta \end{aligned}$$

Mutual Coherence for FRI

$$\mu \leq \max \left\{ \frac{\zeta_{n-d+1}}{\sigma_{\min}(\mathcal{V}_{n-d+1}^* \mathcal{V}_{n-d+1})}, \frac{\zeta_d}{\sigma_{\min}(\mathcal{V}_d^* \mathcal{V}_d)} \right\}$$

Confluent Vandermonde matrix

$$\mathcal{H}(\hat{\mathbf{x}}) = \mathcal{V}_{n-d+1} \mathcal{B} \mathcal{V}_d^T,$$

$$\zeta_N = N \left[\frac{(N-1)!}{(N-l_{\max})!} \right]^2$$

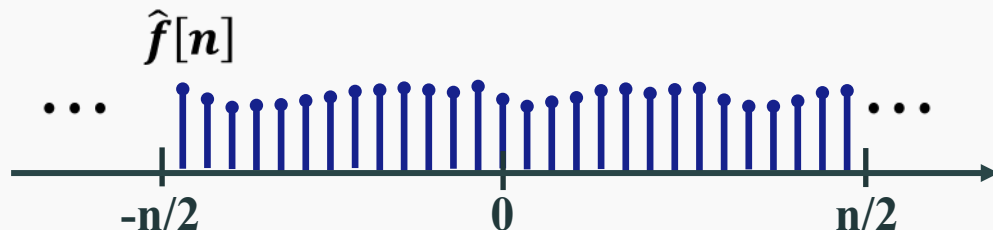
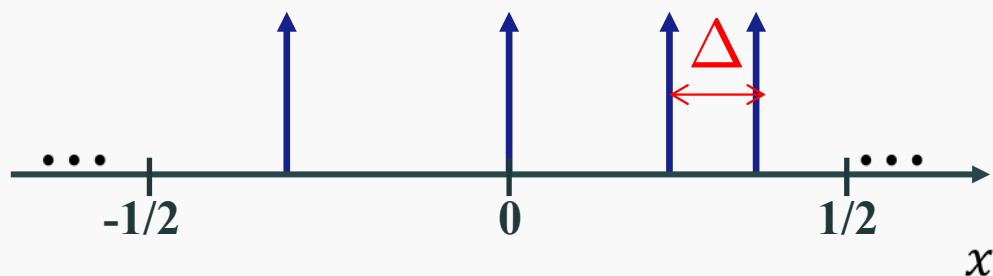
Multiplicity of roots

$$\mu \leq \frac{n/2}{n/2 - 1/\Delta - 1}$$

Using extreme function
for bounding singular value
See Moitra (2015)

Relation to Super-resolution: Minimum separation

$f(x)$: periodic stream of K Diracs



$$\Delta > \frac{2}{n}$$

*Same as
Candes et al (2013)
Tang et al (2015)*

$$\mu \leq \frac{n/2}{n/2 - 1/\Delta - 1}$$

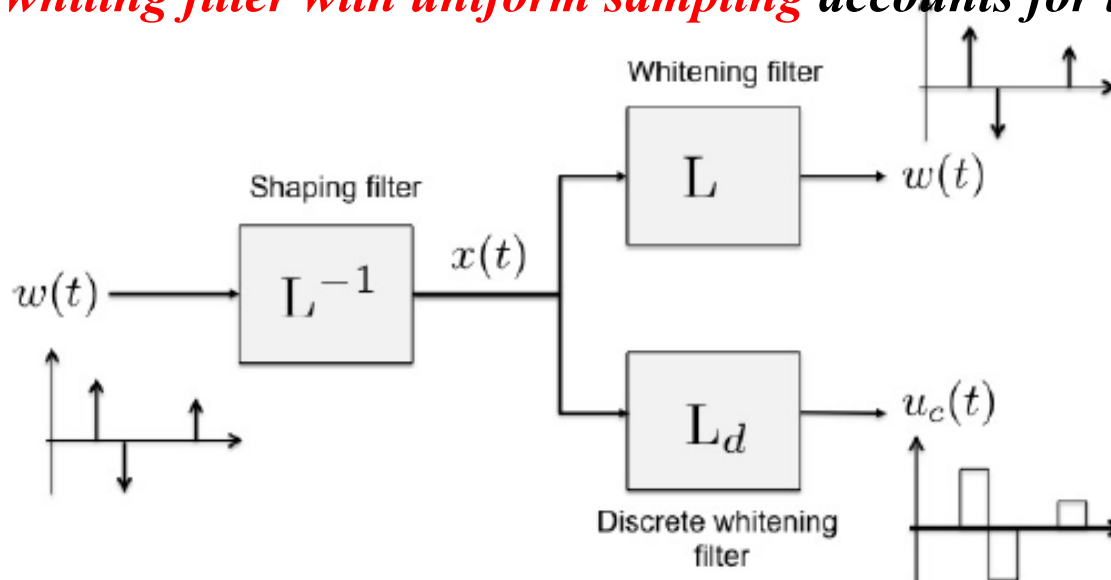
*Using extreme function
for bounding singular value
See Moitra (2015)*

On grid model using cardinal setup

- *Unknown singularities are located on integer grid*

$$\mathbf{L}x(t) = \sum_{l \in \mathbb{Z}} a[l] \delta(t - l)$$

- *Discrete whitening filter with uniform sampling accounts for the sparsity*



Off-Grid vs On-Grid : Hankel

* Ye JC et al., IEEE TIT 2016

Hankel Matrix: off-grid

$$\begin{bmatrix} \hat{y}[0] & \hat{y}[1] & \cdots & \hat{y}[d-1] \\ \hat{y}[1] & \hat{y}[2] & \cdots & \hat{y}[d] \\ \vdots & \vdots & \ddots & \vdots \\ \hat{y}[n-d] & \hat{y}[n-d+1] & \cdots & \hat{y}[n-1] \end{bmatrix}$$

Periodic repetition

$$m \geq c_1 \mu c_s k \log^\alpha n$$

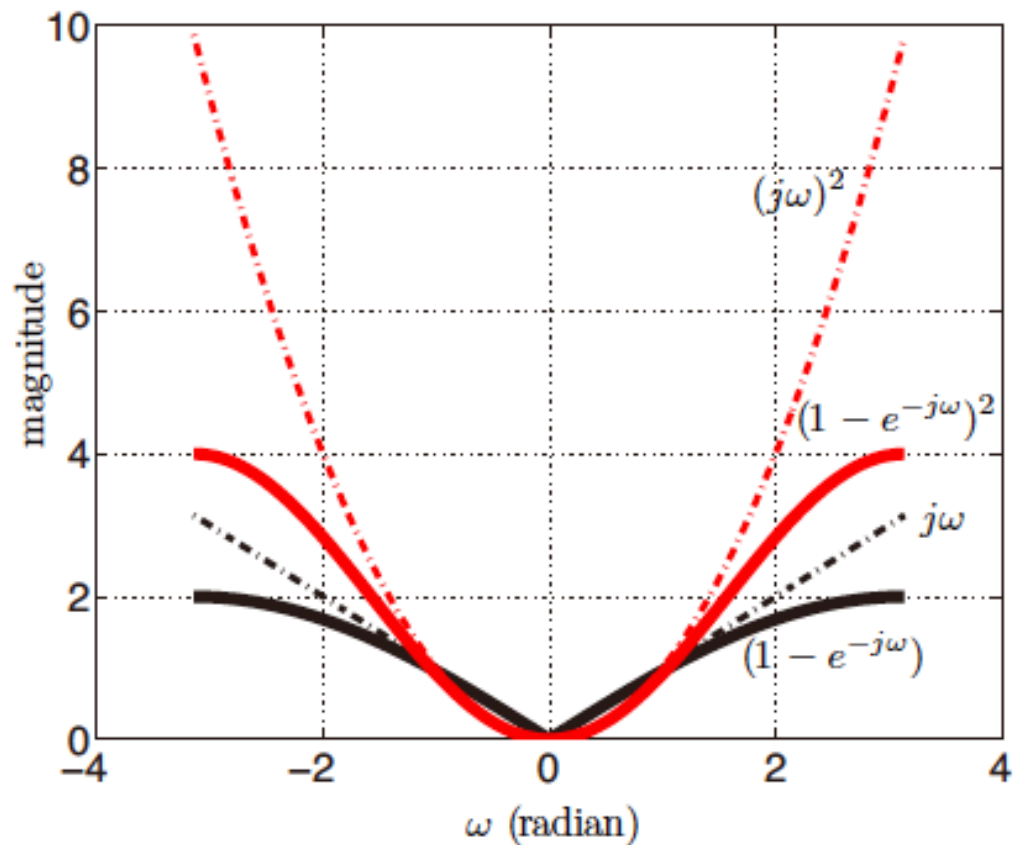
$$\alpha = \begin{cases} 2, & \text{on grid} \\ 4, & \text{off grid} \end{cases}$$

Wrap-around Hankel Matrix: on-grid

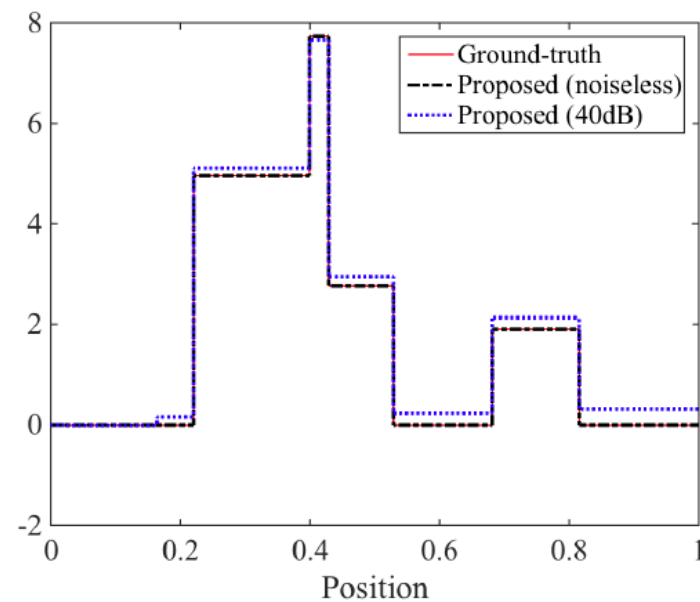
$$\begin{bmatrix} \hat{w}_0[0] & \hat{w}_0[1] & \cdots & \hat{w}_0[d-1] \\ \hat{w}_0[1] & \hat{w}_0[2] & \cdots & \hat{w}_0[d] \\ \vdots & \vdots & \ddots & \vdots \\ \hat{w}_0[n-d] & \hat{w}_0[n-d+1] & \cdots & \hat{w}_0[n-1] \\ \hline \hat{w}_0[n-d+1] & \hat{w}_0[n-d+2] & \cdots & \hat{w}_0[0] \\ \vdots & \vdots & \ddots & \vdots \\ \hat{w}_0[n-1] & \hat{w}_0[0] & \cdots & \hat{w}_0[d-2] \end{bmatrix}$$

Off-grid vs On-grid: weighting

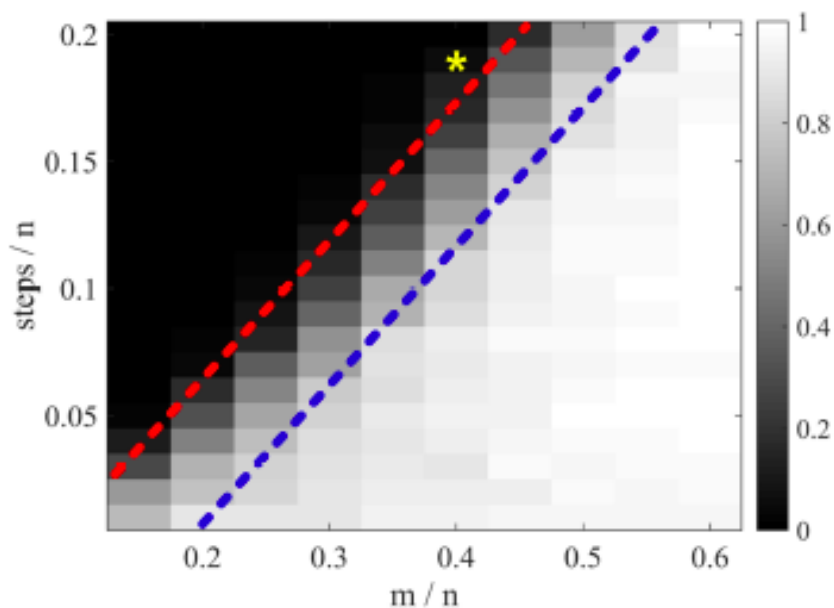
Regularized Weighting → *more stable*



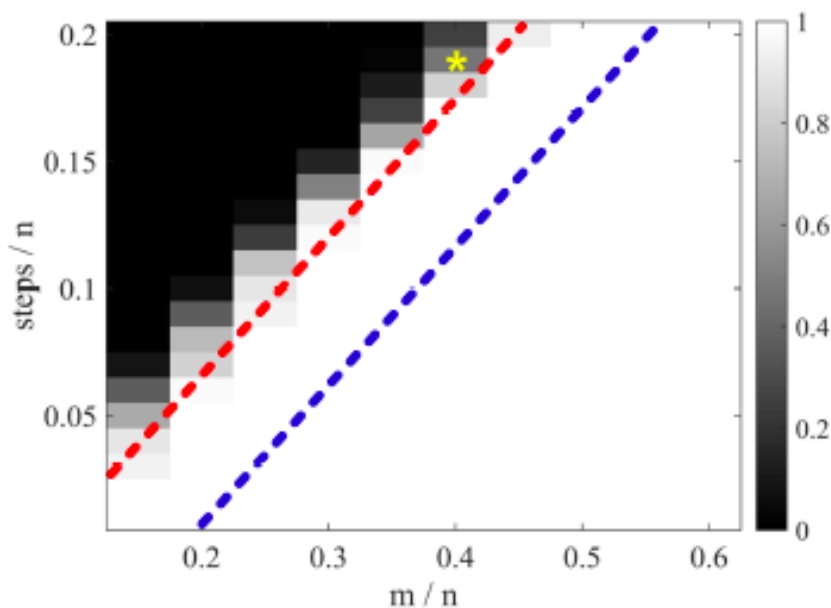
Phase transition: piecewise constant signals



Compressed sensing

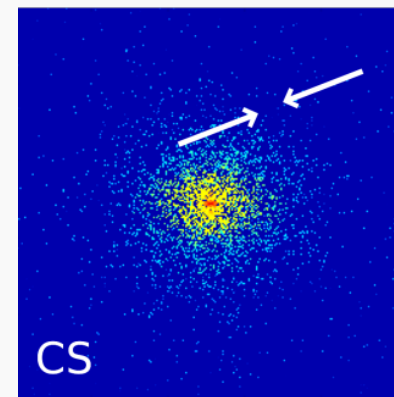


Proposed method



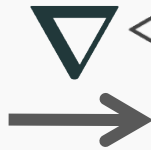
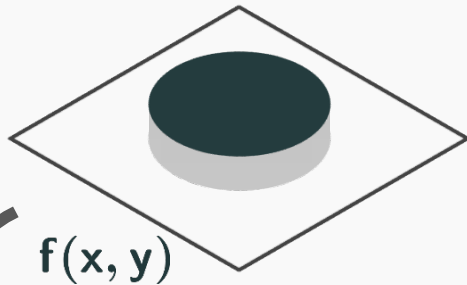
Overview

1. Introduction
2. Review of Compressive Sensing
3. FRI **extrapolation** from uniform samples
4. Structured low-rank **interpolation** for non-uniform samples
 - 2-D Theory
5. Fast implementations
6. Biomedical applications

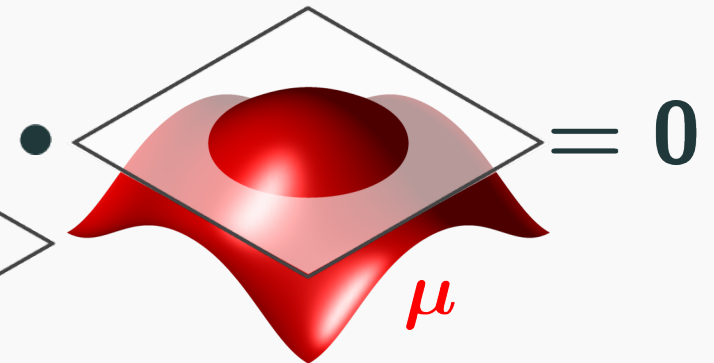


2-D PWC functions satisfy an annihilation relation

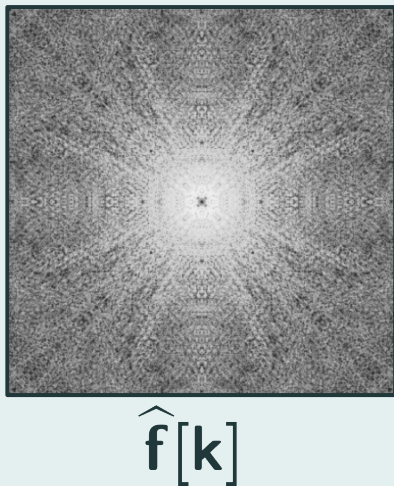
spatial domain



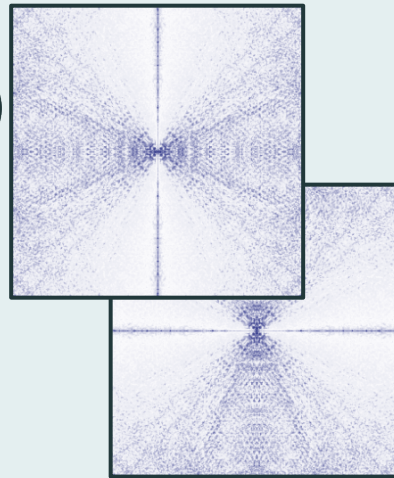
multiplication



Fourier domain

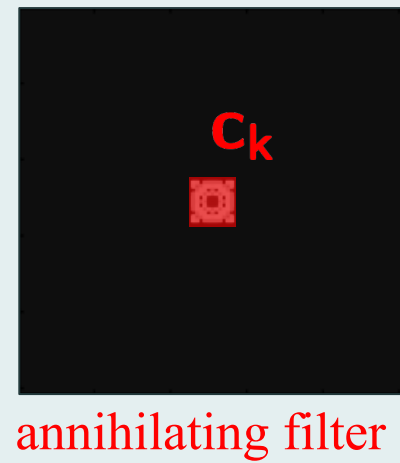


$(j2\pi k)$



convolution

$*$



$= 0$

Annihilation relation:

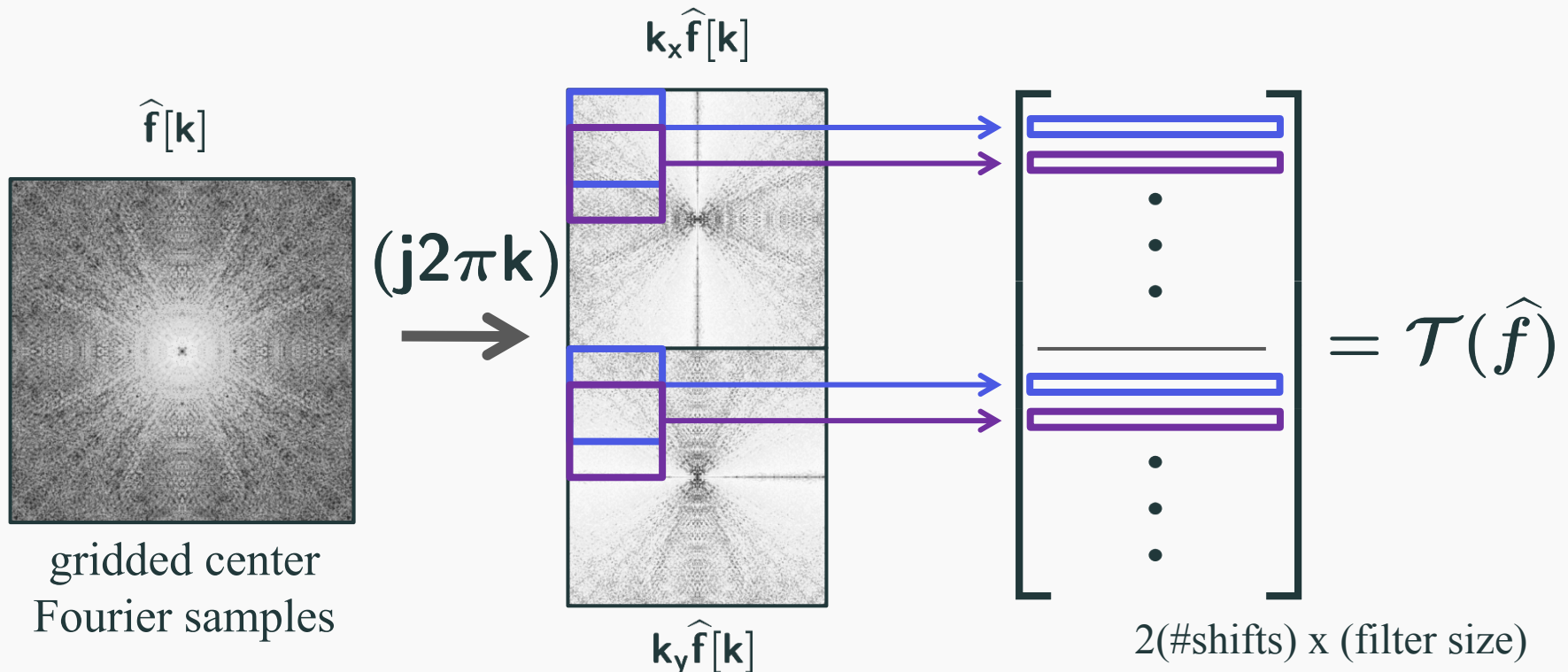
$$\sum_k \nabla^2 \hat{f}[\ell - k] c_k = 0$$

Matrix representation of annihilation

$$\mathcal{T}(\hat{f}) \mathbf{c} = \mathbf{0}$$

2-D convolution matrix
(block Toeplitz)

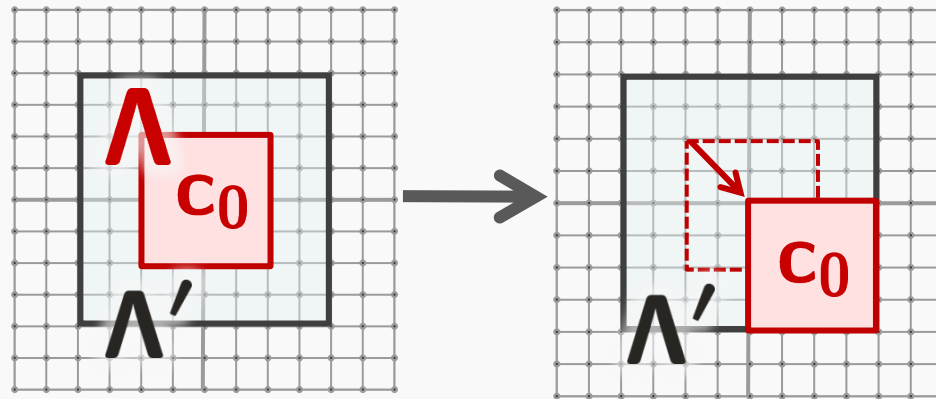
vector of filter coefficients



Basis of algorithms: Annihilation matrix is low-rank

Prop: If the level-set function is bandlimited to Λ
and the assumed filter support $\Lambda' \supset \Lambda$ then
$$\text{rank}[\mathcal{T}(\hat{\mathbf{f}})] \leq |\Lambda'| - (\# \text{shifts } \Lambda \text{ in } \Lambda')$$

Fourier domain



Spatial domain

$$\mu(\mathbf{x}, \mathbf{y}) \longrightarrow e^{j2\pi(\mathbf{k}\mathbf{x} + \mathbf{l}\mathbf{y})} \mu(\mathbf{x}, \mathbf{y})$$

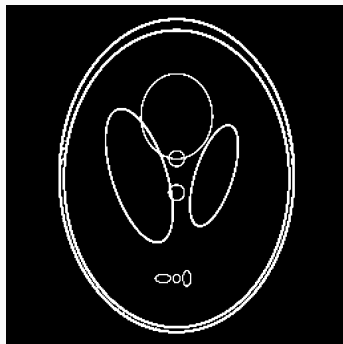
Basis of algorithms: Annihilation matrix is low-rank

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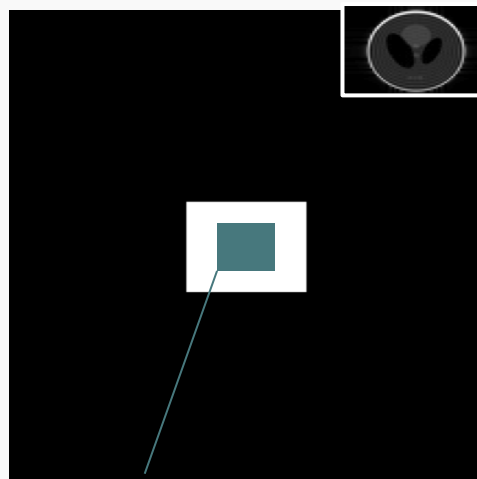
$$\text{rank}[\mathcal{T}(\hat{f})] \leq |\Lambda'| - (\# \text{shifts } \Lambda \text{ in } \Lambda')$$

Example:

Shepp-Logan



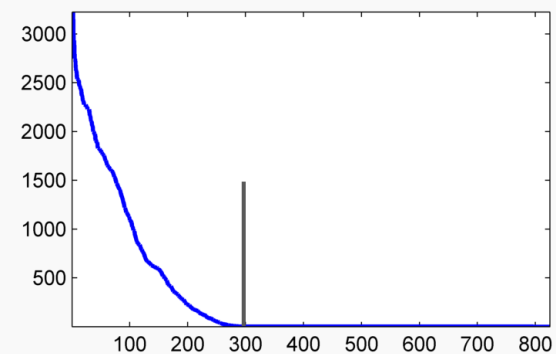
Fourier domain



Assumed filter: 33x25

Samples: 65x49

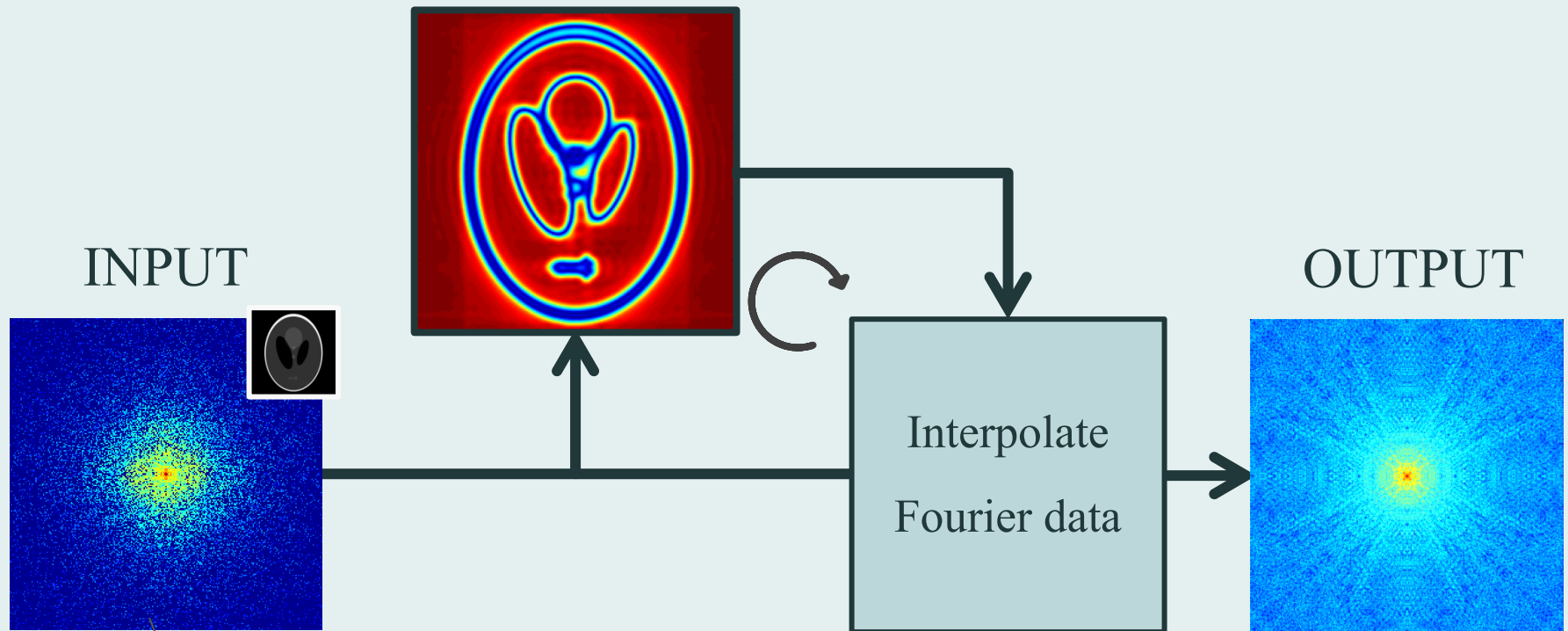
$\sigma(\mathcal{T}(\hat{f}))$



Rank ≈ 300

One Step Algorithm

Jointly estimate edge set and amplitudes



Off-the-grid

Accommodate random samples

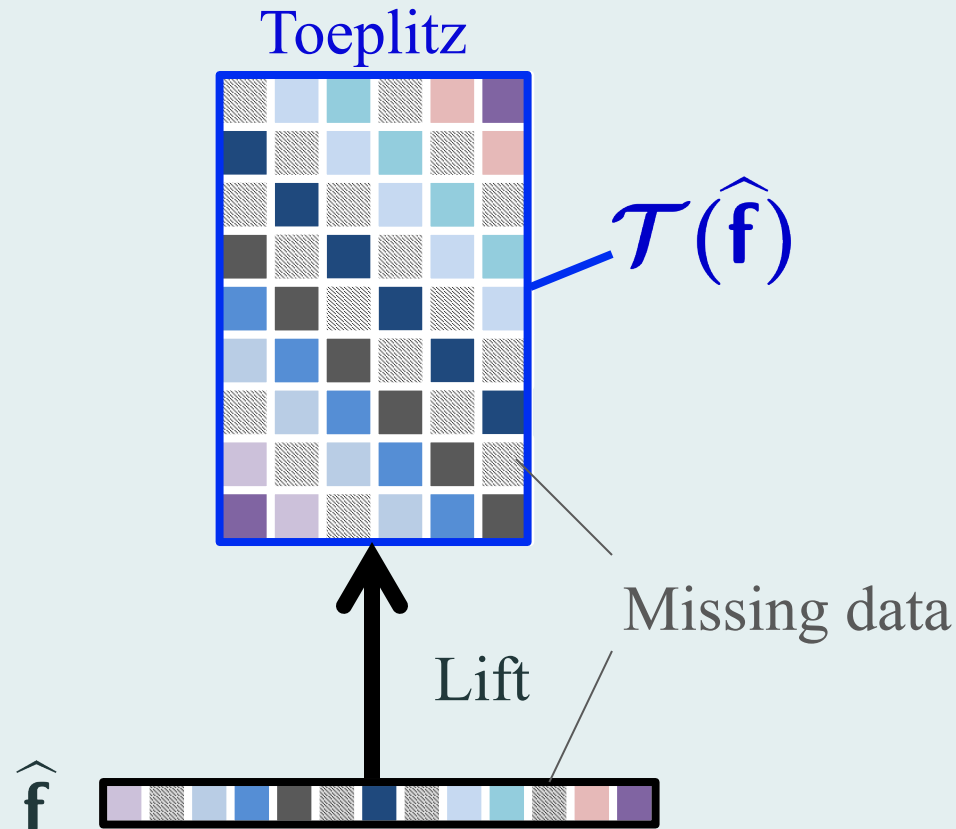
Recovery as a structured low-rank matrix completion

$$\min_{\hat{\mathbf{f}}} \text{rank}[\mathcal{T}(\hat{\mathbf{f}})] \quad \text{s.t.} \quad \hat{\mathbf{f}}[\mathbf{k}] = \hat{\mathbf{b}}[\mathbf{k}], \mathbf{k} \in \Gamma$$

Recovery as a structured low-rank matrix completion

$$\min_{\hat{\mathbf{f}}} \text{rank}[\mathcal{T}(\hat{\mathbf{f}})] \quad \text{s.t.} \quad \hat{\mathbf{f}}[\mathbf{k}] = \hat{\mathbf{b}}[\mathbf{k}], \mathbf{k} \in \Gamma$$

1-D Example:

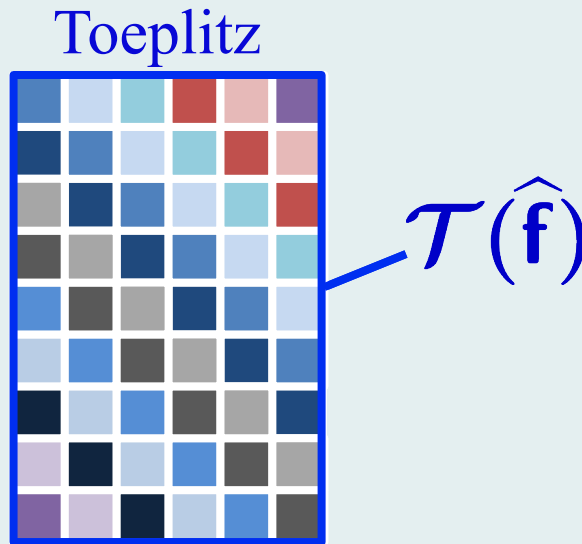


Recovery as a structured low-rank matrix completion

$$\min_{\hat{\mathbf{f}}} \text{rank}[\mathcal{T}(\hat{\mathbf{f}})] \quad \text{s.t.} \quad \hat{\mathbf{f}}[\mathbf{k}] = \hat{\mathbf{b}}[\mathbf{k}], \mathbf{k} \in \Gamma$$

1-D Example:

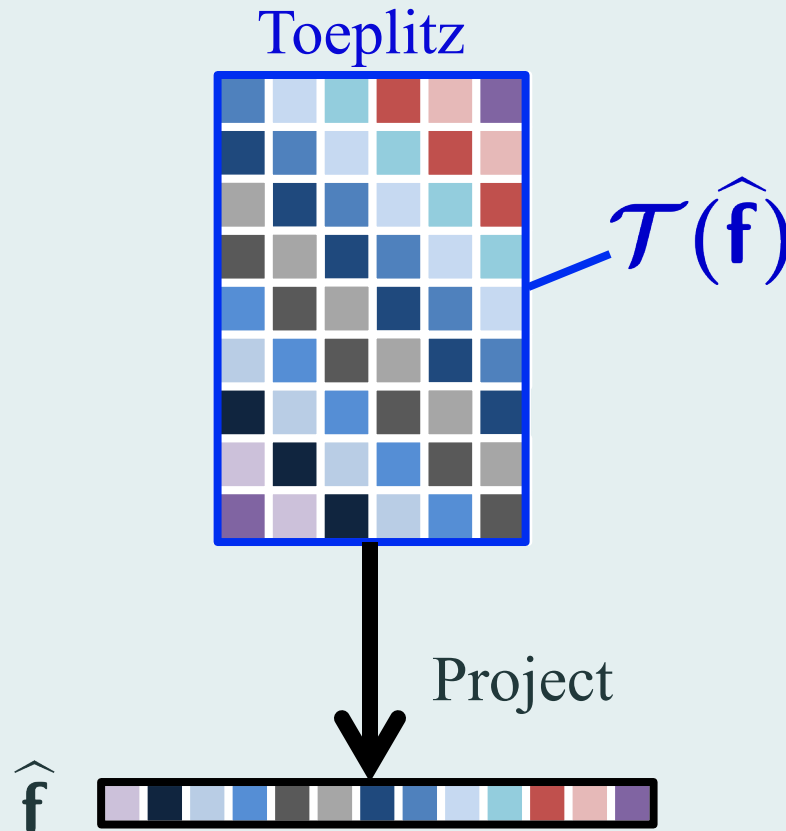
Complete matrix



Recovery as a structured low-rank matrix completion

$$\min_{\hat{\mathbf{f}}} \text{rank}[\mathcal{T}(\hat{\mathbf{f}})] \quad \text{s.t.} \quad \hat{\mathbf{f}}[\mathbf{k}] = \hat{\mathbf{b}}[\mathbf{k}], \mathbf{k} \in \Gamma$$

1-D Example:



Recovery as a structured low-rank matrix completion

$$\min_{\hat{\mathbf{f}}} \text{rank}[\mathcal{T}(\hat{\mathbf{f}})] \quad \text{s.t.} \quad \hat{\mathbf{f}}[\mathbf{k}] = \hat{\mathbf{b}}[\mathbf{k}], \mathbf{k} \in \Gamma$$

NP-Hard!

Recovery as a structured low-rank matrix completion

$$\min_{\hat{\mathbf{f}}} \text{rank}[\mathcal{T}(\hat{\mathbf{f}})] \quad \text{s.t.} \quad \hat{\mathbf{f}}[\mathbf{k}] = \hat{\mathbf{b}}[\mathbf{k}], \mathbf{k} \in \Gamma$$

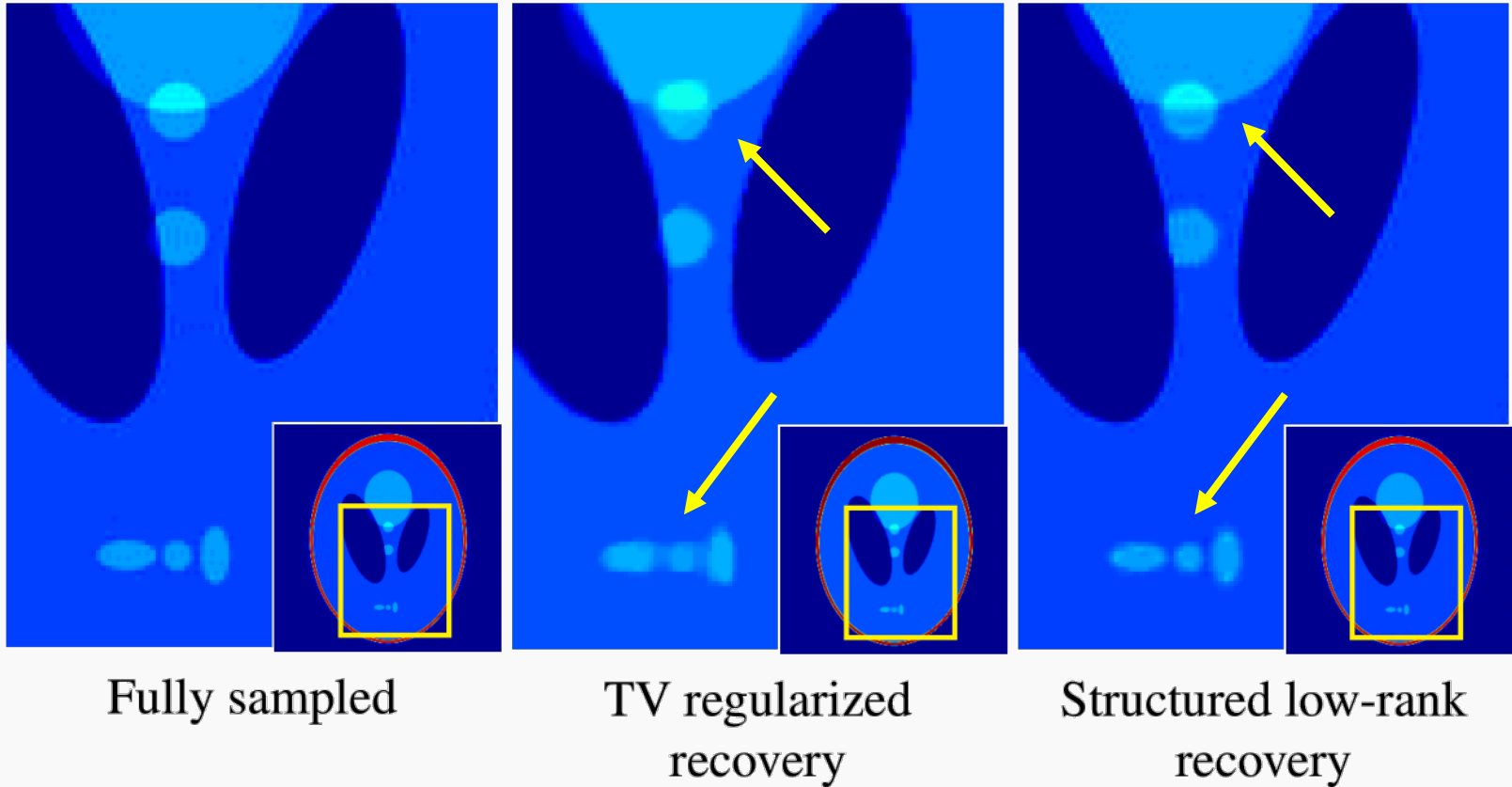


Convex Relaxation

$$\min_{\hat{\mathbf{f}}} \|\mathcal{T}(\hat{\mathbf{f}})\|_* \quad \text{s.t.} \quad \hat{\mathbf{f}}[\mathbf{k}] = \hat{\mathbf{b}}[\mathbf{k}], \mathbf{k} \in \Gamma$$

Nuclear norm – sum of singular values

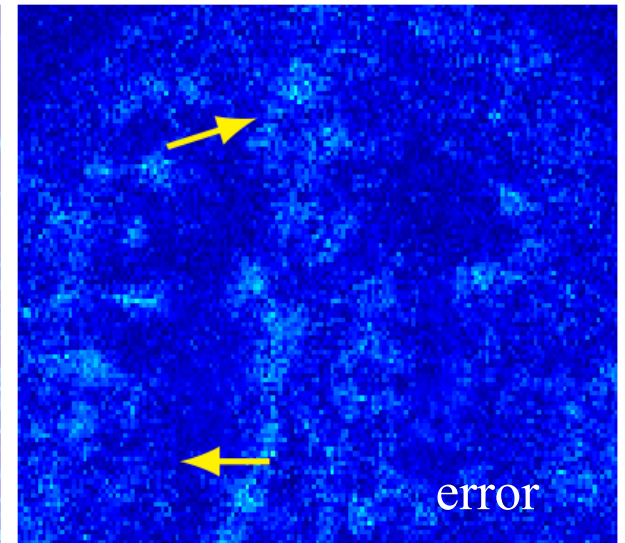
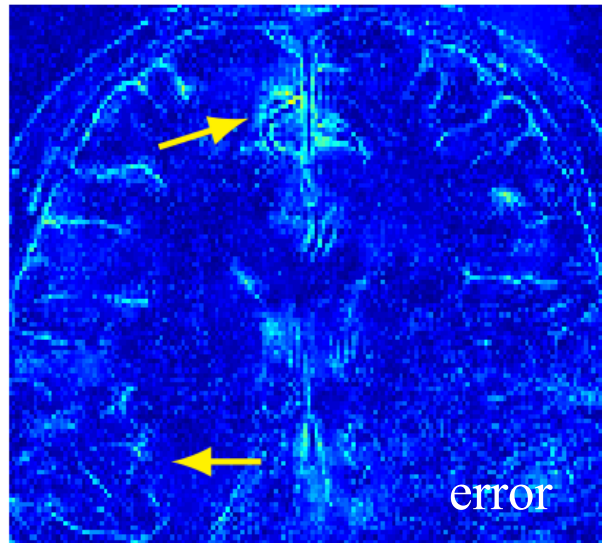
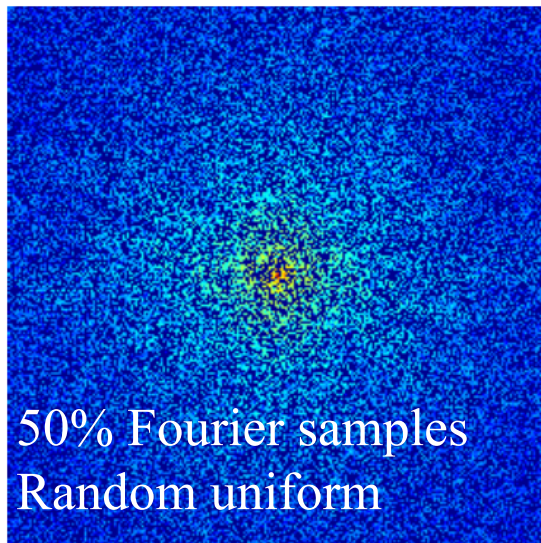
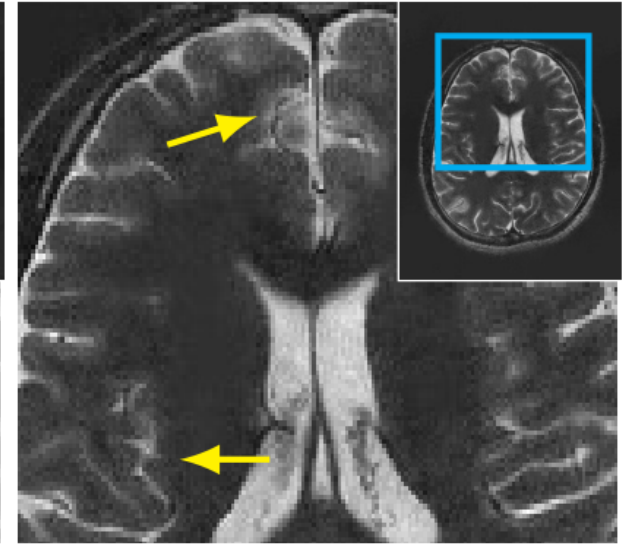
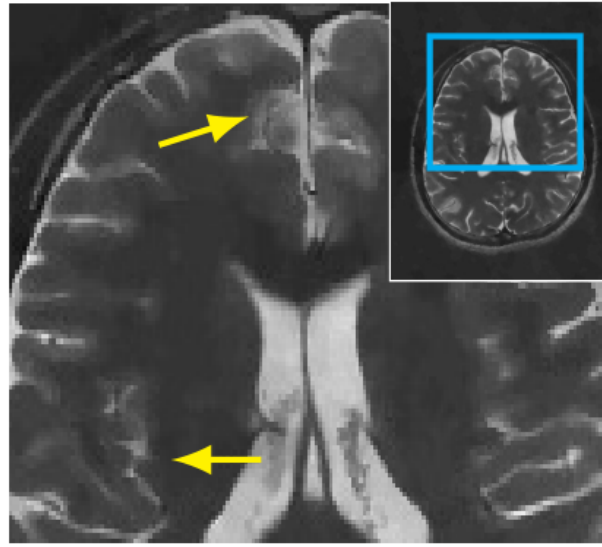
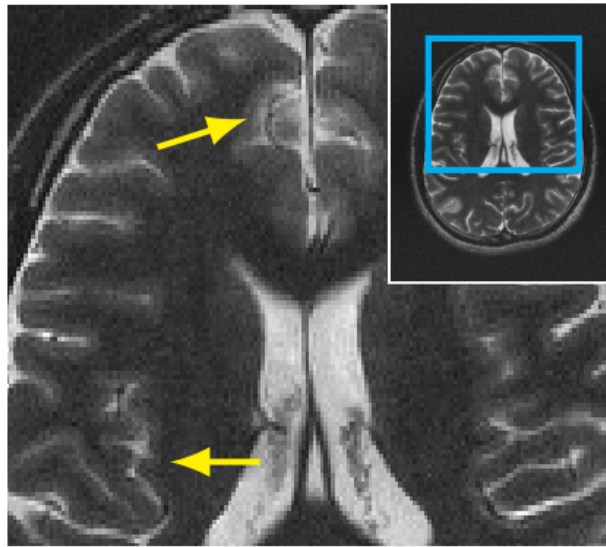
Recovery from 20-fold random undersampled data



Fully sampled

TV (SNR=17.8dB)

GIRAF (SNR=19.0)



Performance guarantee

Let f be a piecewise constant signal with edge set, which is the zero level set of a bandlimited function. Assume that f is sampled uniformly at m locations random on a Fourier domain grid Γ . Then, f can be recovered from the samples using a SLR approach if

$$m > \rho_1 c_s r \log^4 |\Gamma|$$

ρ_1 = incoherence measure of edge-set

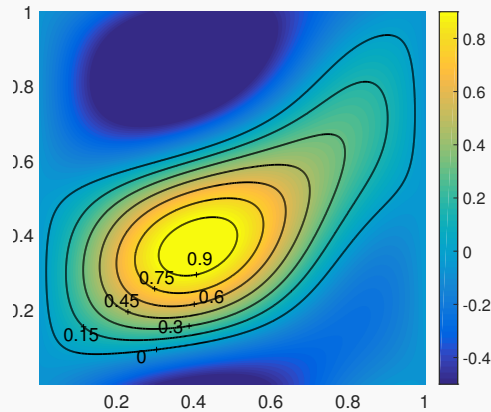
r = rank of $\mathcal{T}(\hat{\mathbf{f}})$

c_s = ratio of grid size to filter size

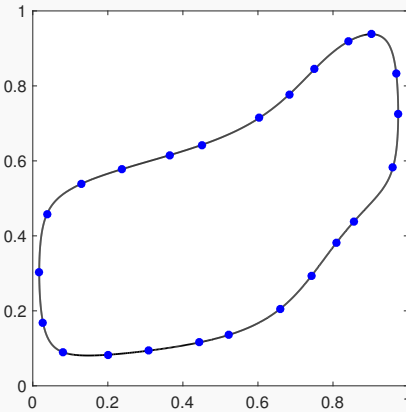
Ongie & Jacob, ICIP16,
<https://arxiv.org/abs/1703.01405>

Incoherency measure ρ_1

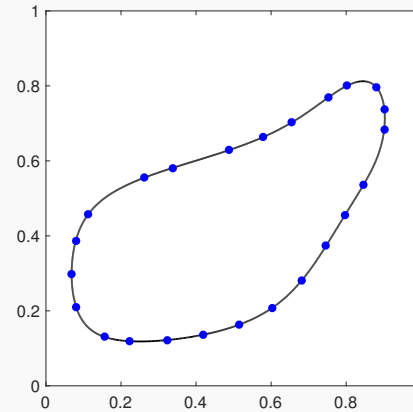
Intuition: minimum separation distance when packing r points on the edge-set curve, where $r = \text{rank } \mathcal{T}(\hat{\mathbf{f}})$



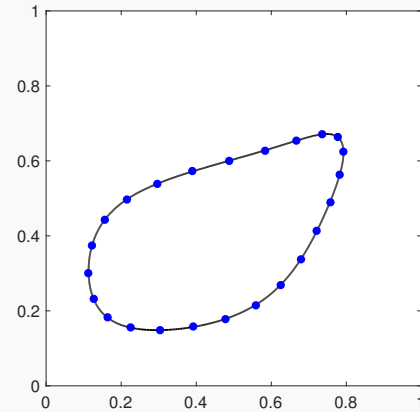
(a) Level-sets of μ_0



(b) $\rho \leq 8.0$



(c) $\rho \leq 264.9$



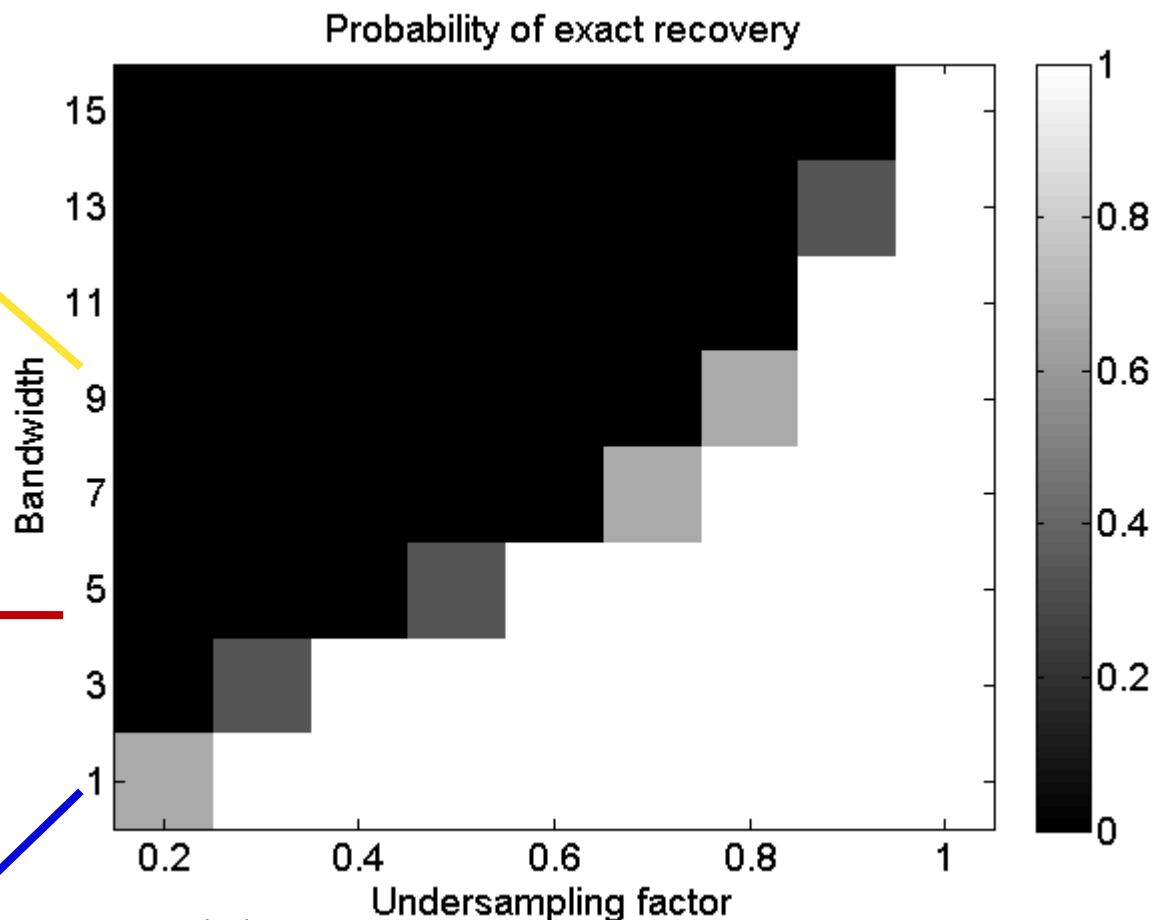
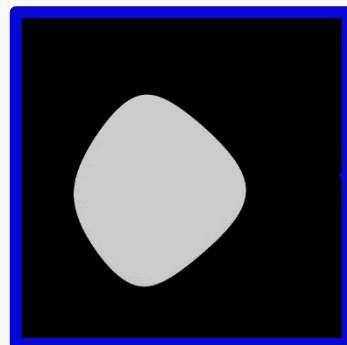
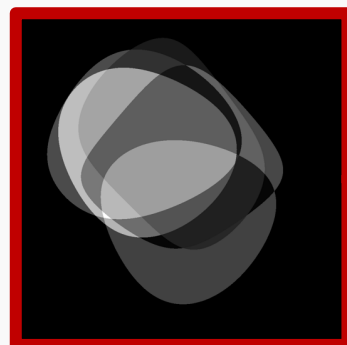
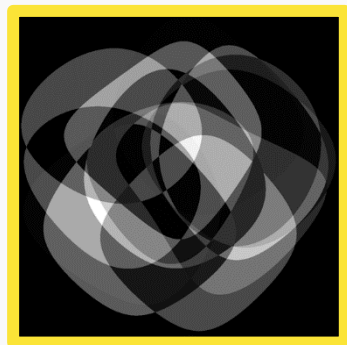
(d) $\rho \leq 5.0 \times 10^4$

Small regions: high incoherence & more measurements

Complex boundaries: high rank/bandwidth

Phase transitions

Randomly generated
synthetic PWC images



- 10 trials
- Uniform random Fourier samples
- 64x64 Fourier sampling window

Ongie & Jacob, ICIP16,
<https://arxiv.org/abs/1703.01405>

SPIRiT: Iterative Self-consistent Parallel Imaging Reconstruction From Arbitrary k -Space

Michael Lustig^{1,2*} and John M. Pauly²

Discrete formulation exploiting multichannel acquisition

Low-Rank Modeling of Local k -Space Neighborhoods (LORAKS) for Constrained MRI

Justin P. Haldar, *Member, IEEE*

Discrete formulation exploiting sparsity, smoothly varying phase, and multichannel acquisition

Overview

1. Introduction
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3. FRI **extrapolation** from uniform samples
4. Structured low-rank **interpolation** for non-uniform samples
5. Fast algorithms
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Nuclear norm minimization

$$\min_{\hat{\mathbf{f}}} \|\mathbf{A}\hat{\mathbf{f}} - \mathbf{b}\|^2 + \lambda \|\mathbf{X}\|_* \quad \text{s.t.} \quad \mathbf{X} = \mathcal{T}(\hat{\mathbf{f}})$$

ADMM = Singular value thresholding (SVT)

1. Singular value thresholding step
 - compute *full SVD* of \mathbf{X} !
2. Solve linear least squares problem
 - analytic solution or CG solve



Alternating projections [“SAKE,” Shin 14], [“LORAKS,” Haldar, 14]

$$\min_{\hat{\mathbf{f}}} \|\mathbf{A}\hat{\mathbf{f}} - \mathbf{b}\|^2 \quad \text{s.t.} \quad \boxed{\mathbf{X} = \mathcal{T}(\hat{\mathbf{f}})}$$
$$\boxed{\text{rank } \mathbf{X} \leq r}$$

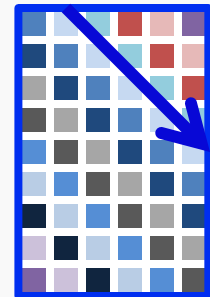
Alternating projection algorithm (Cadzow)

1. Project onto **space of rank r matrices**

-Compute *truncated SVD*: **$\mathbf{X}^* = \mathbf{U}\Sigma_r\mathbf{V}^H$**

2. Project onto **space of structured matrices**

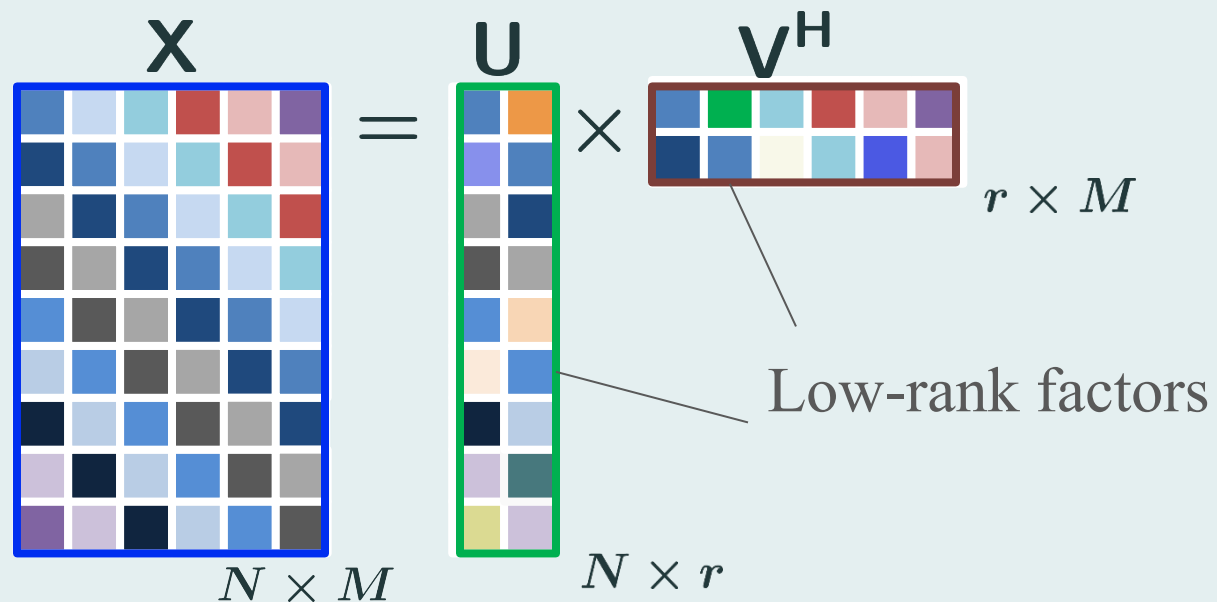
-Average along “diagonals”



$$\min_{\hat{\mathbf{f}}} \|\mathbf{A}\hat{\mathbf{f}} - \mathbf{b}\|^2 + \lambda \|\mathbf{X}\|_* \quad \text{s.t.} \quad \mathbf{X} = \mathcal{T}(\hat{\mathbf{f}})$$

“U, V factorization trick”

$$\|\mathbf{X}\|_* = \min_{\mathbf{X}=\mathbf{U}\mathbf{V}^H} \frac{1}{2} (\|\mathbf{U}\|_F^2 + \|\mathbf{V}\|_F^2)$$



$$\min_{\hat{\mathbf{f}}, \mathbf{U}, \mathbf{V}} \|\mathbf{A}\hat{\mathbf{f}} - \mathbf{b}\|^2 + \frac{\lambda}{2} (\|\mathbf{U}\|_{\mathbf{F}}^2 + \|\mathbf{V}\|_{\mathbf{F}}^2)$$

$$\text{s.t. } \mathbf{U}\mathbf{V}^H = \mathcal{T}(\hat{\mathbf{f}})$$

UV factorization approach

~~1. Singular value thresholding step~~

~~——-compute *full SVD* of X!~~

SVD-free → fast matrix inversion steps

2. Solve linear least squares problem

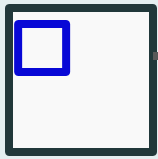
-analytic solution or CG solve



Main challenge : Computational complexity & memory

2-D

$\hat{\mathbf{f}}$



$\mathcal{T}(\hat{\mathbf{f}})$

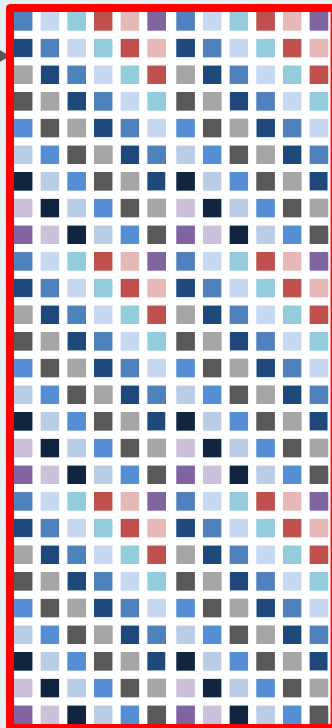


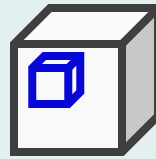
Image: 256x256

Filter: 32x32

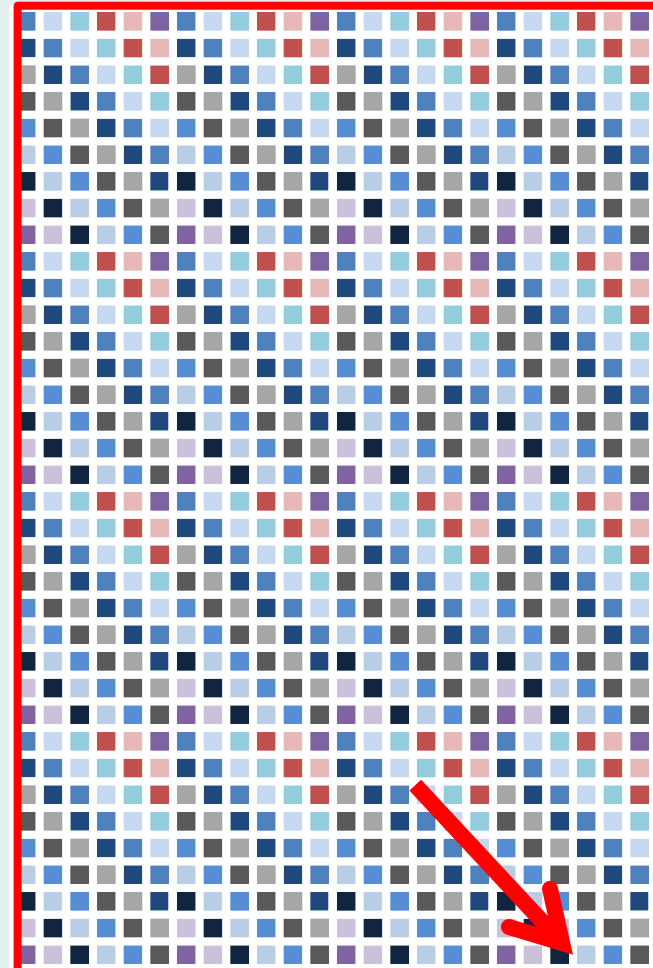
$\sim 10^6 \times 1000$

3-D

$\hat{\mathbf{f}}$



$\mathcal{T}(\hat{\mathbf{f}})$



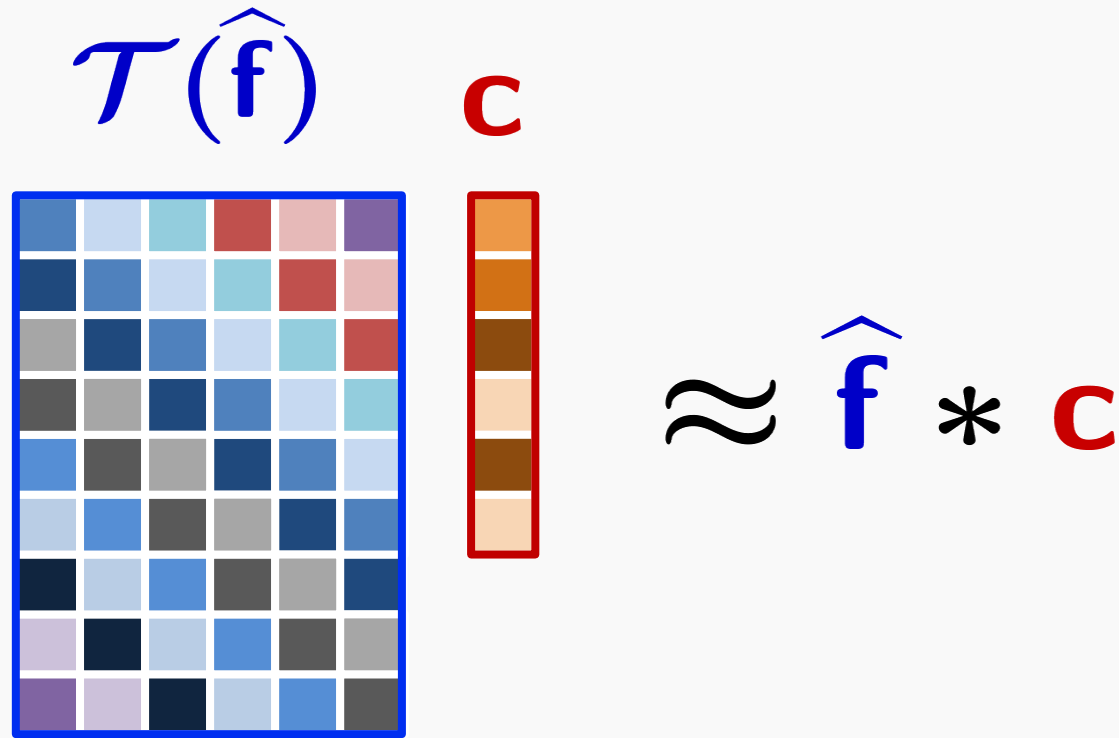
256x256x32

32x32x10

$\sim 10^8 \times 10^5$

Cannot Hold
in Memory!

Exploit convolutional structure of the matrix

$$\mathcal{T}(\hat{\mathbf{f}}) \quad \mathbf{c} \approx \hat{\mathbf{f}} * \mathbf{c}$$


Fast evaluation using FFT

Direct computation of small Gram matrix: avoid storage

IRLS algorithm along with structure exploitation

- Original IRLS: To recover low-rank matrix \mathbf{X} , iterate

$$\mathbf{W} \leftarrow (\mathbf{X}^H \mathbf{X} + \epsilon \mathbf{I})^{-\frac{1}{2}}$$

$$\mathbf{X} \leftarrow \arg \min_{\mathbf{X}} \|\mathbf{X} \mathbf{W}^{\frac{1}{2}}\|_F^2 + \lambda \|\mathbf{A} \mathbf{X} - \mathbf{B}\|_F^2$$

IRLS

- Original IRLS: To recover low-rank matrix \mathbf{X} , iterate

$$\mathbf{W} \leftarrow (\mathbf{X}^H \mathbf{X} + \epsilon \mathbf{I})^{-\frac{1}{2}}$$

$$\mathbf{X} \leftarrow \arg \min_{\mathbf{X}} \|\mathbf{X} \mathbf{W}^{\frac{1}{2}}\|_{\mathbf{F}}^2 + \lambda \|\mathbf{A} \mathbf{X} - \mathbf{B}\|_{\mathbf{F}}^2$$

- We adapt to structured case: $\mathbf{X} = \mathcal{T}(\hat{\mathbf{f}})$

$$\mathbf{W} \leftarrow (\mathcal{T}(\hat{\mathbf{f}})^H \mathcal{T}(\hat{\mathbf{f}}) + \epsilon \mathbf{I})^{-\frac{1}{2}}$$

$$\hat{\mathbf{f}} \leftarrow \arg \min_{\hat{\mathbf{f}}} \|\mathcal{T}(\hat{\mathbf{f}}) \mathbf{W}^{\frac{1}{2}}\|_{\mathbf{F}}^2 + \lambda \|\mathbf{A} \hat{\mathbf{f}} - \mathbf{b}\|^2$$

IRLS algorithm

- Original IRLS: To recover low-rank matrix \mathbf{X} , iterate

$$\mathbf{W} \leftarrow (\mathbf{X}^H \mathbf{X} + \epsilon \mathbf{I})^{-\frac{1}{2}}$$

$$\mathbf{X} \leftarrow \arg \min_{\mathbf{X}} \|\mathbf{X} \mathbf{W}^{\frac{1}{2}}\|_F^2 + \lambda \|\mathbf{A} \mathbf{X} - \mathbf{B}\|_F^2$$

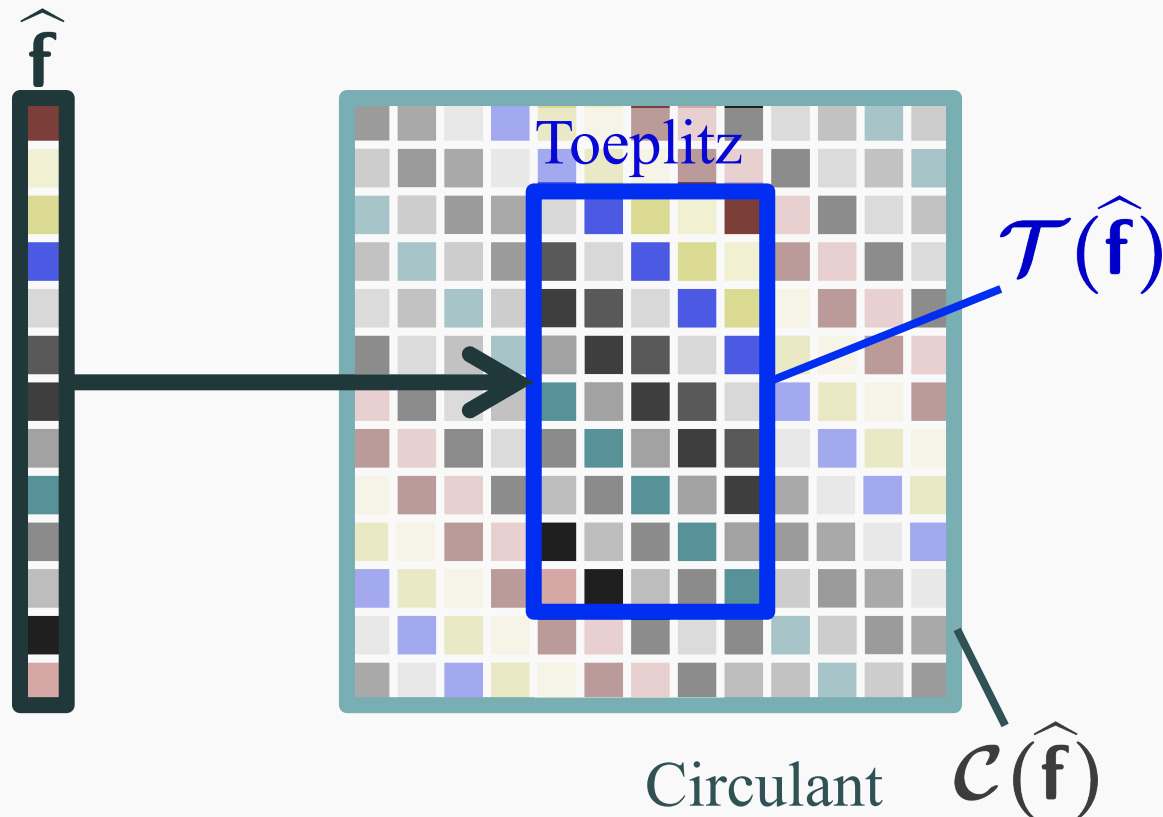
- We adapt to structured case: $\mathbf{X} = \mathcal{T}(\hat{\mathbf{f}})$

$$\mathbf{W} \leftarrow (\mathcal{T}(\hat{\mathbf{f}})^H \mathcal{T}(\hat{\mathbf{f}}) + \epsilon \mathbf{I})^{-\frac{1}{2}}$$

$$\hat{\mathbf{f}} \leftarrow \arg \min_{\hat{\mathbf{f}}} \|\mathcal{T}(\hat{\mathbf{f}}) \mathbf{W}^{\frac{1}{2}}\|_F^2 + \lambda \|\mathbf{A} \hat{\mathbf{f}} - \mathbf{b}\|^2$$

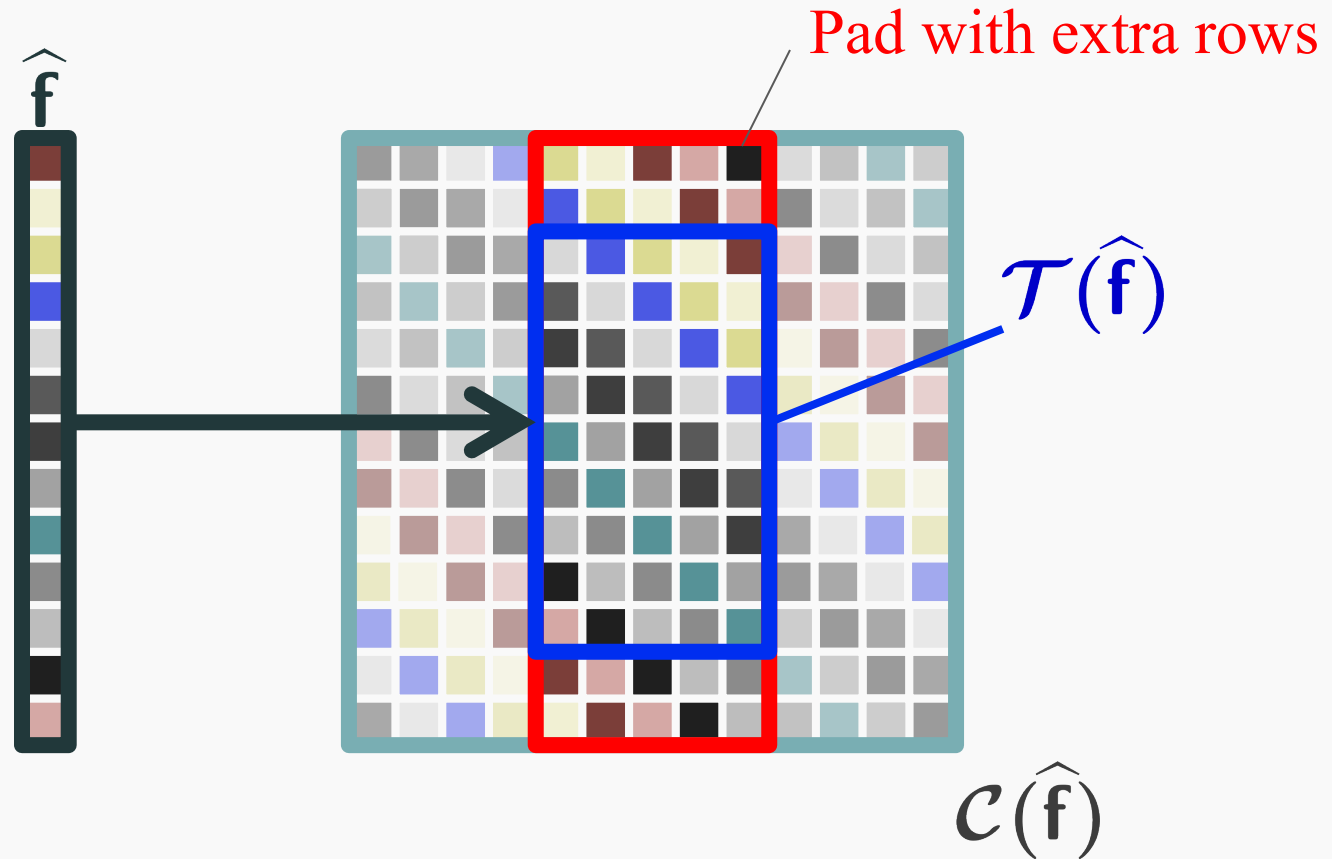
Without modification, this approach is still slow!

Idea 1: Embed Toeplitz lifting in circulant matrix



*Fast matrix-vector products with $\mathcal{T}(\hat{\mathbf{f}})$ by FFTs

Idea 2: Approximate matrix lifting

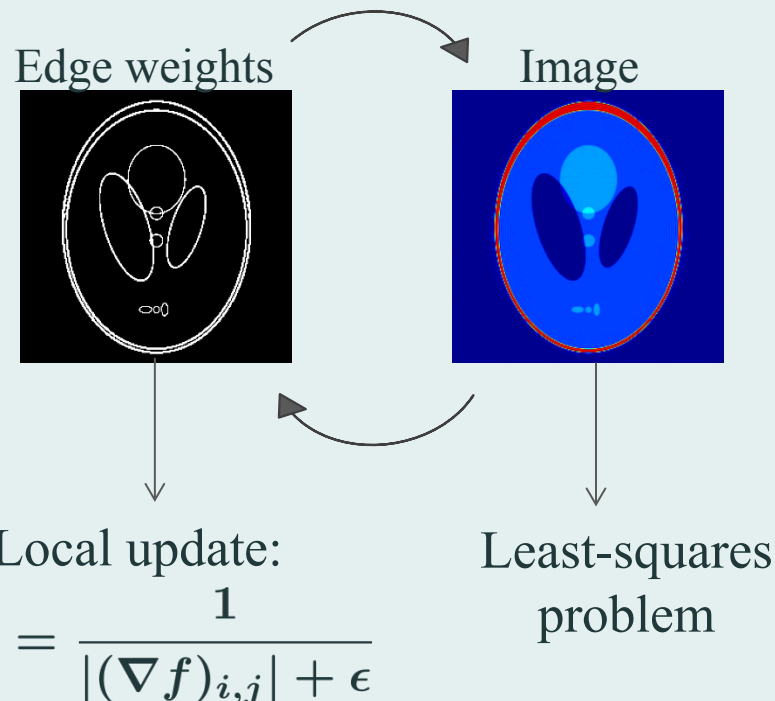


*Fast computation of $\mathcal{T}(\hat{\mathbf{f}})^H \mathcal{T}(\hat{\mathbf{f}})$ by FFTs

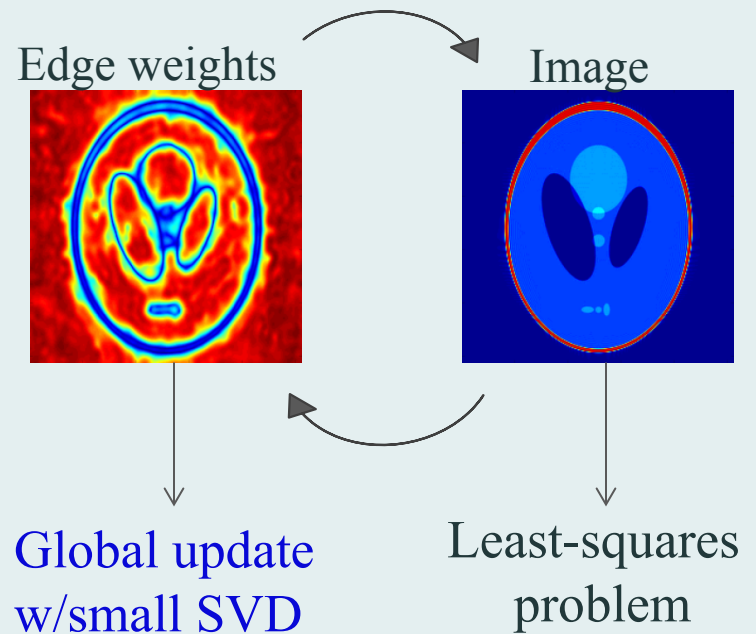
GIRAF: fast [O. & Jacob, 2016 (arXiv)]

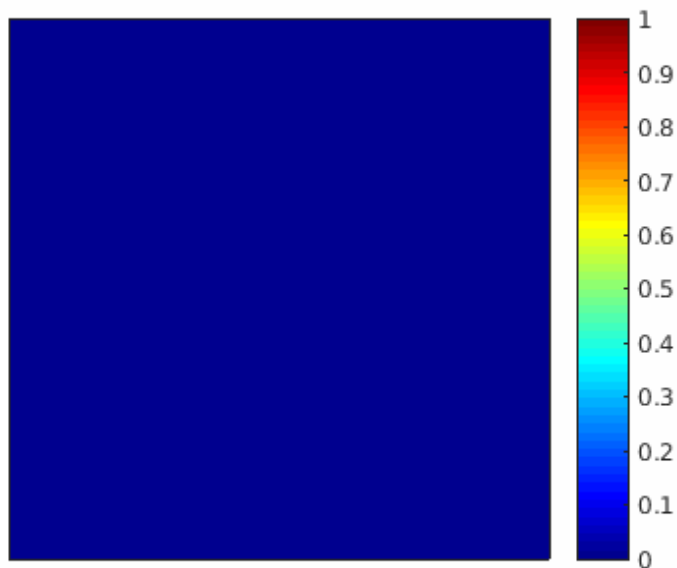
Complexity similar to IRLS for TV minimization

IRLS TV-minimization

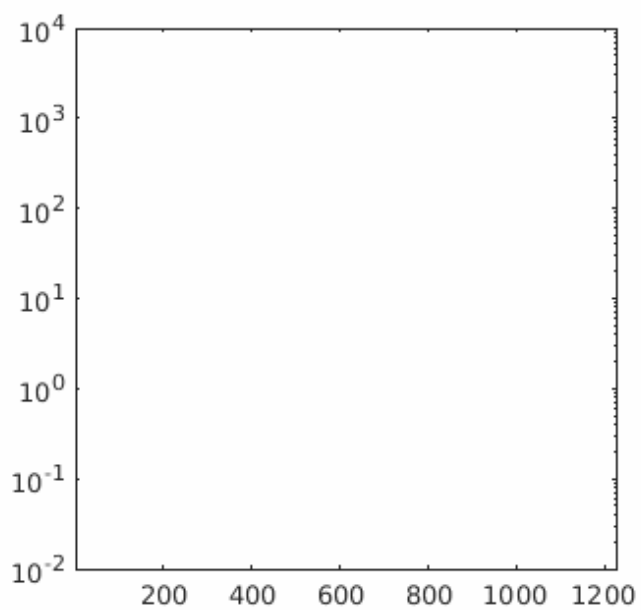
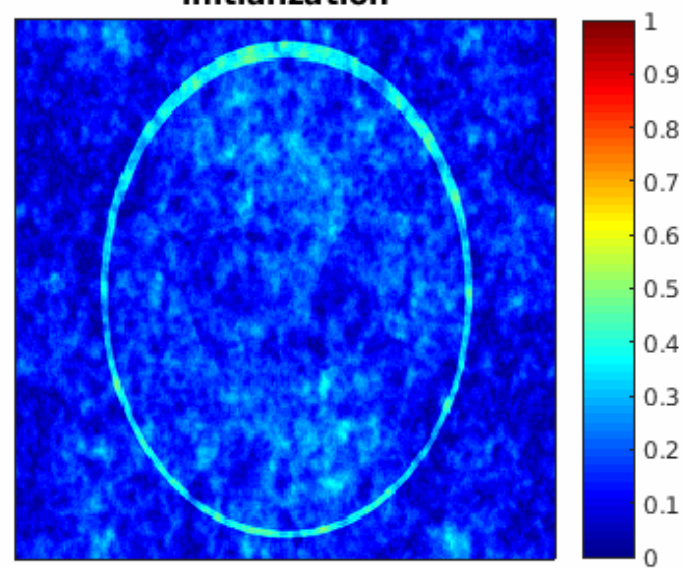


GIRAF algorithm

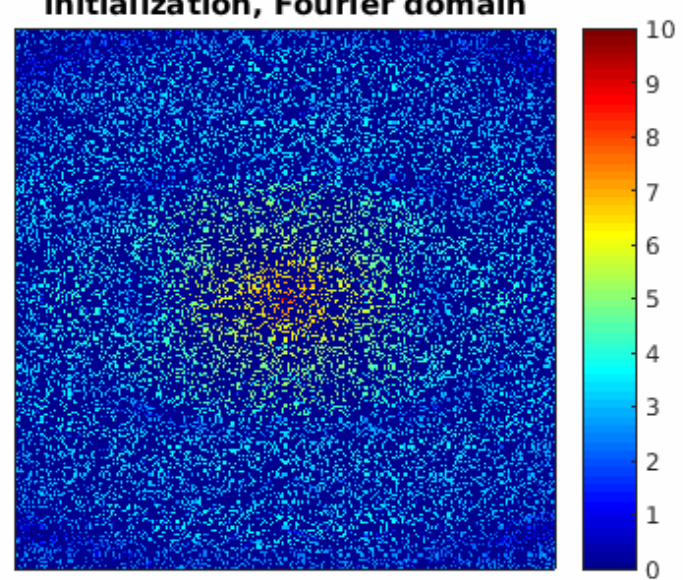




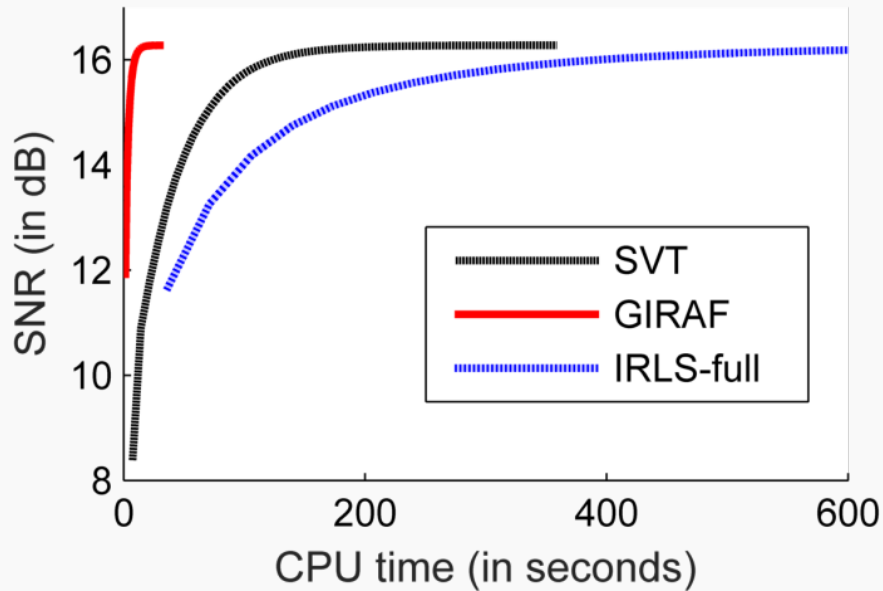
initialization



initialization, Fourier domain



Convergence speed of GIRAF



| Algorithm | 15×15 filter | | 31×31 filter | |
|-----------|--------------|--------|--------------|-------|
| | # iter | total: | # iter | total |
| SVT | 7 | 110s | 11 | 790 s |
| GIRAF | 6 | 20s | 7 | 44 s |

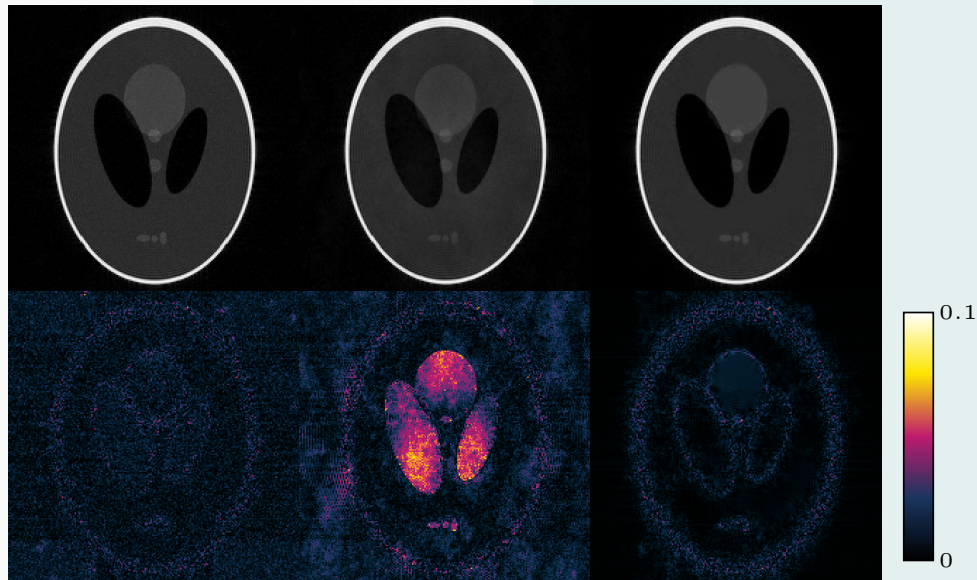
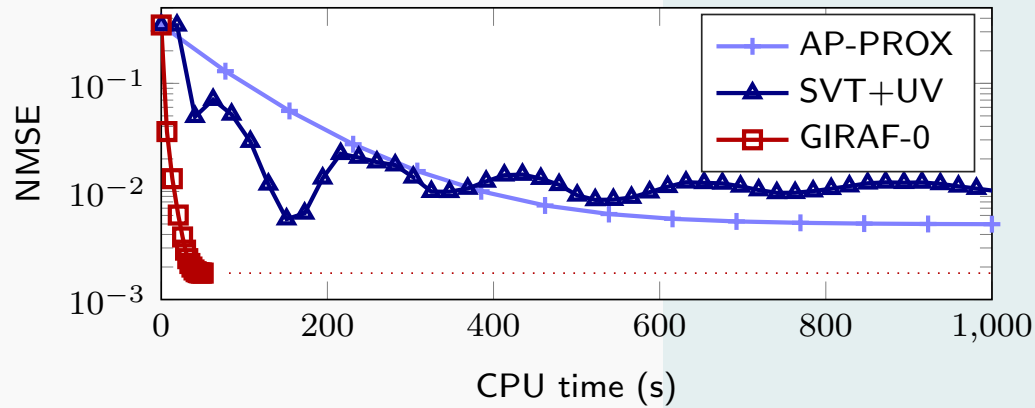
Table: iterations/CPU time to reach convergence tolerance of $\text{NMSE} < 10^{-4}$.

[Ongie & Jacob, ISBI16](#)

<https://arxiv.org/abs/1609.07429>

Software available at <https://research.engineering.uiowa.edu/cbig/software>

Convergence speed of GIRAF



AP-PROX

SVT+UV

GIRAF-0

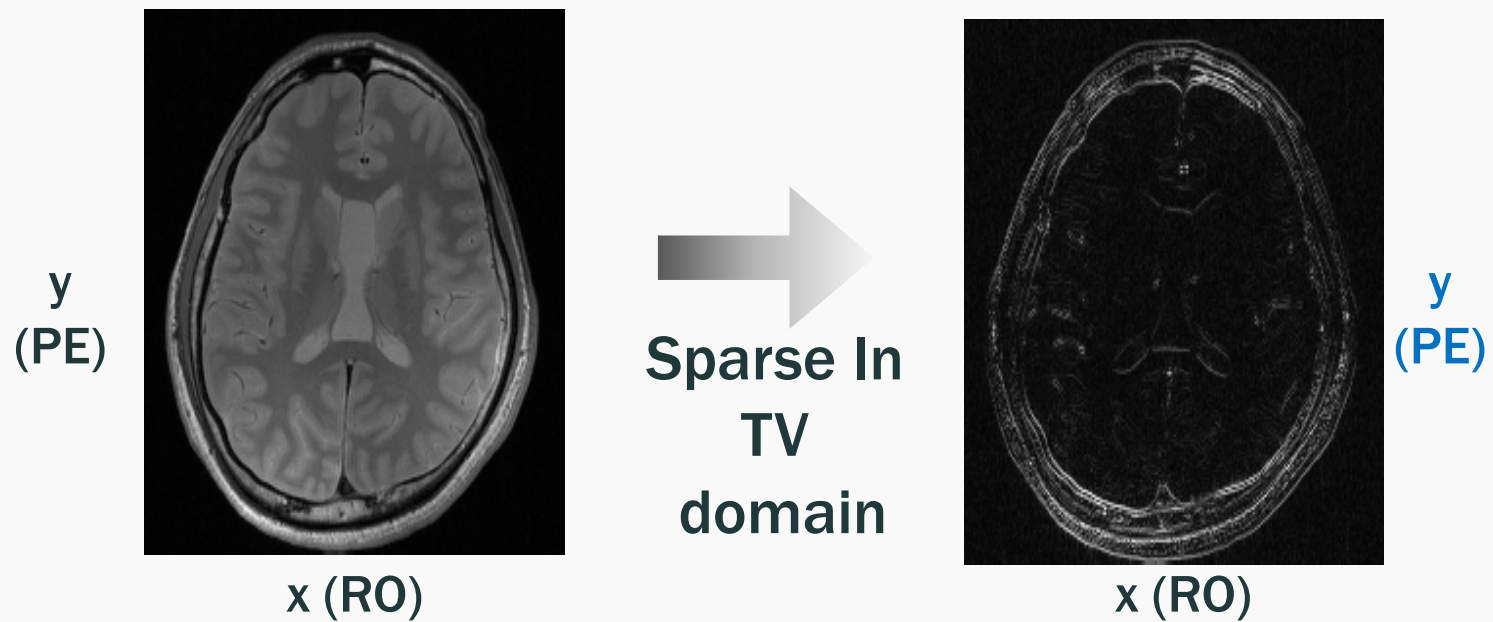
NMSE = $4.9e-3$ NMSE = $11.6e-3$ NMSE = $1.8e-3$

Runtime: 1000 s Runtime: 1090 s Runtime: 49 s

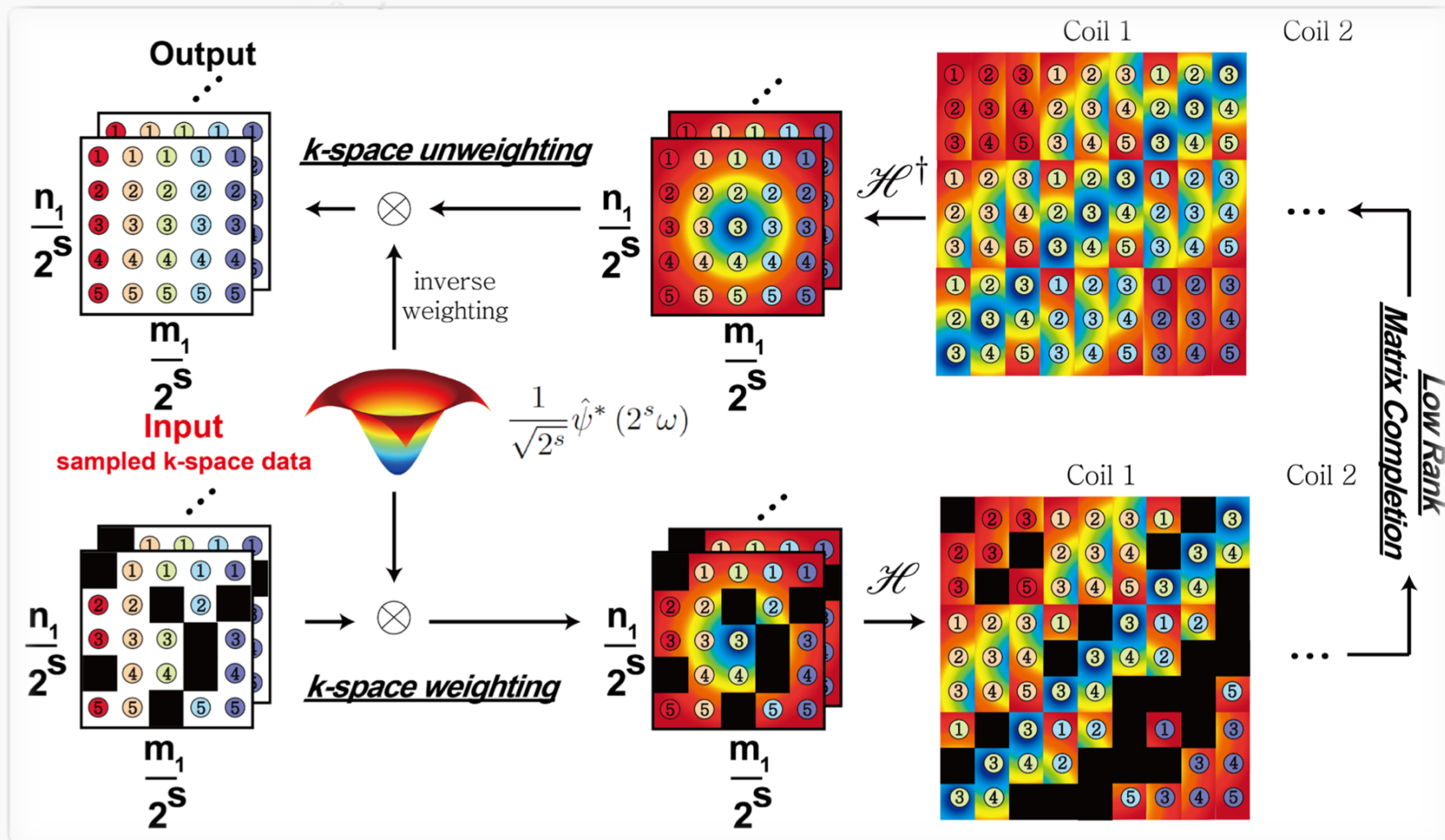
Overview

1. Introduction
2. Review of Compressive Sensing
3. FRI **extrapolation** from uniform samples
4. Structured low-rank **interpolation** for non-uniform samples
5. Fast implementations
6. Biomedical applications
 - a. Applications to MRI
 - b. Other applications

TV-domain sparse signal cases

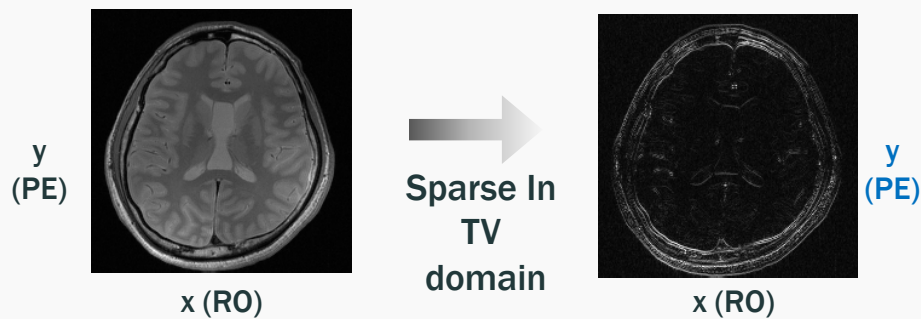


TV-domain sparse signal cases



k-t dynamic sparse signal cases

Sparsity #1

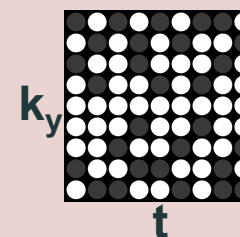


Hankel matrix with wavelet weighing

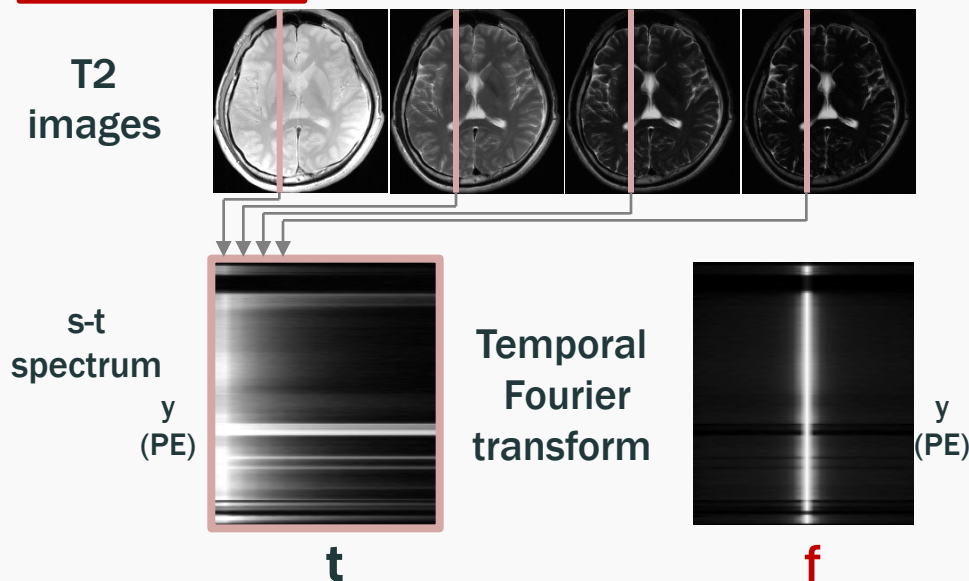
k_y

2D block Hankel matrix on

k_y - t



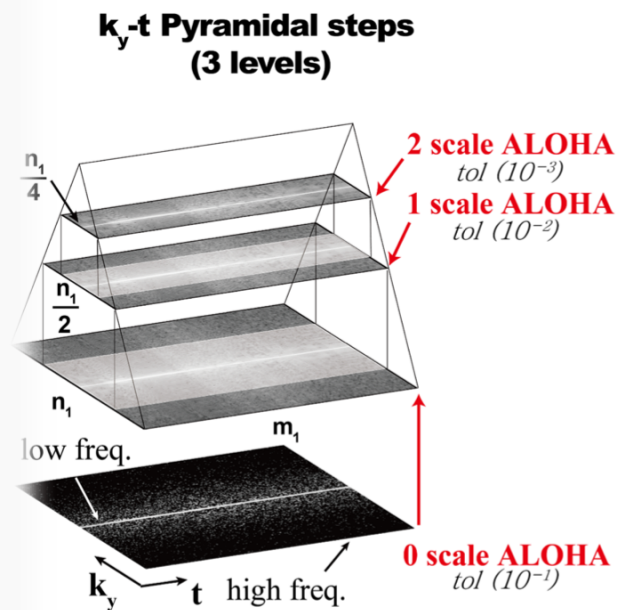
Sparsity #2



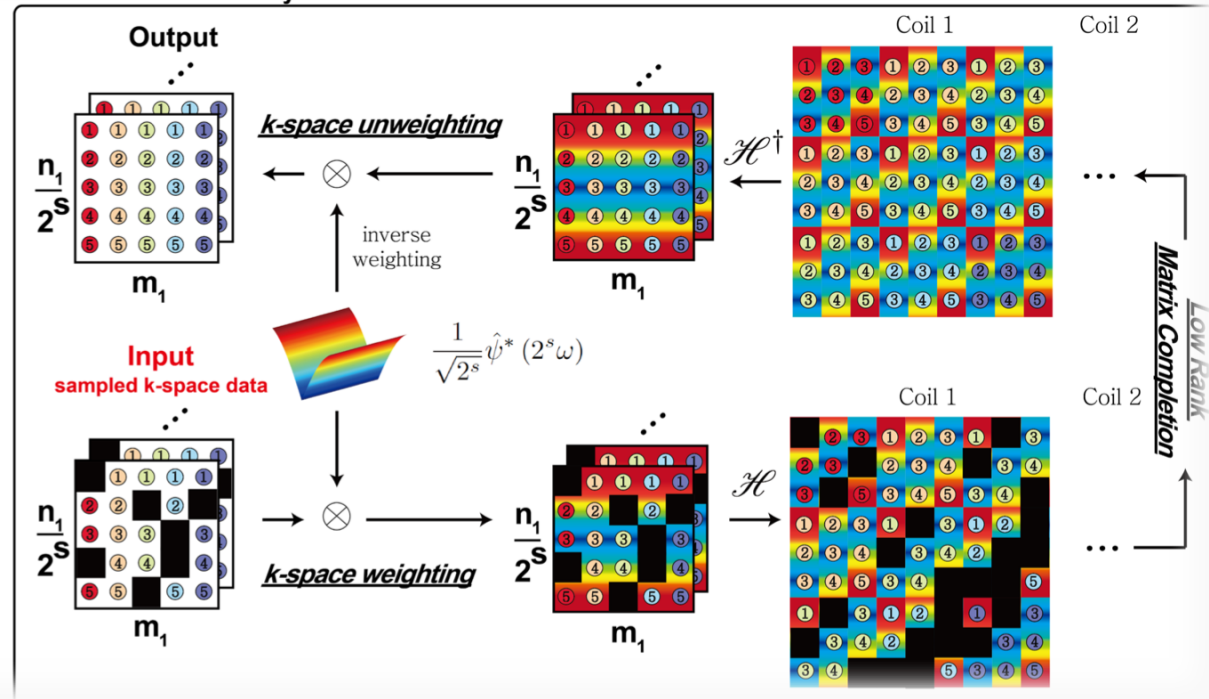
Hankel matrix on

t

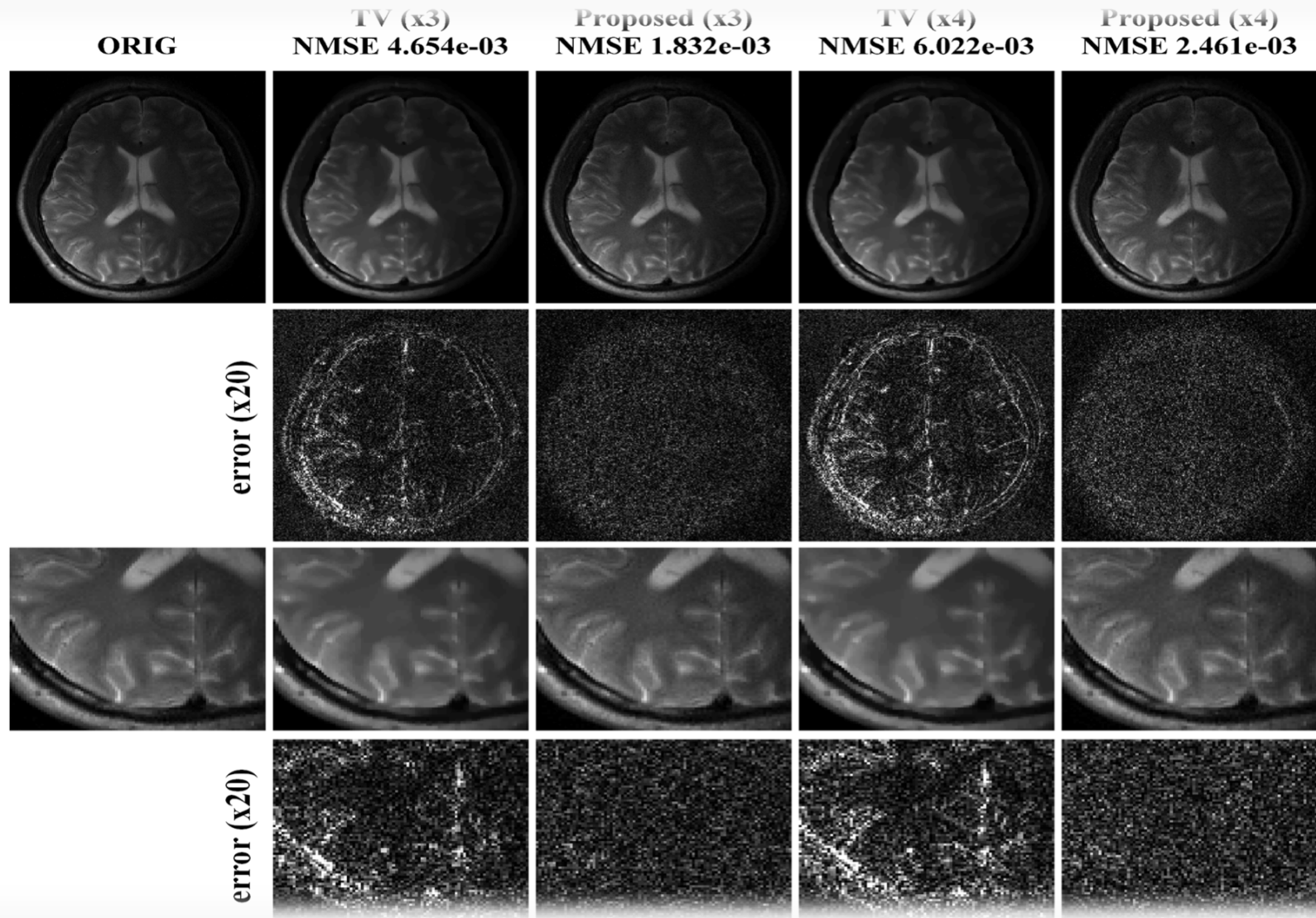
k-t dynamic sparse signal cases



s scale ALOHA (k_y -t)



Single coil static MRI



Rank Bound for Parallel Imaging

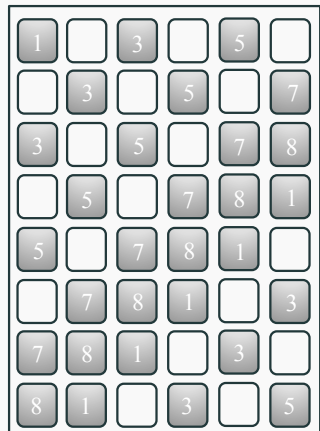
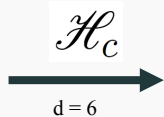
$$\mathcal{Y}_h = \begin{bmatrix} \mathcal{H}_c(\hat{\mathbf{1}} \odot \hat{\mathbf{g}}_1) & \cdots & \mathcal{H}_c(\hat{\mathbf{1}} \odot \hat{\mathbf{g}}_{N_c}) \end{bmatrix}$$

$$\text{RANK} \mathcal{Y}_h \leq \underbrace{\text{RANK} \mathcal{H}_c(\hat{\mathbf{W}})}_{\text{Sparsity of common image}} + \underbrace{\text{RANK} \mathcal{H}_c(\hat{\mathbf{f}}_{tr})}_{\text{Sparsity of sensitivity map}}$$

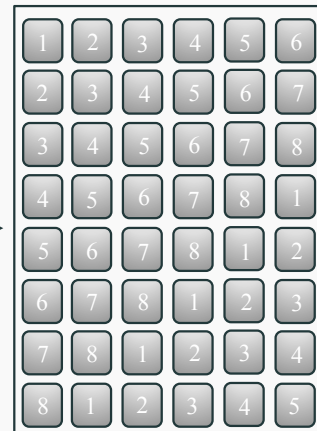
Sparsity of common image
In transform domain

Sparsity of sensitivity map
In Fourier domain

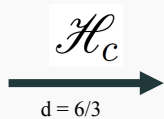
1-channel
signal



Low Rank
Matrix
Completion



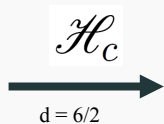
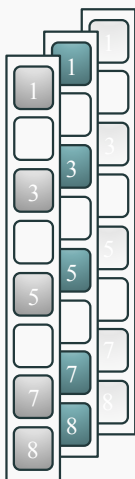
2-channel
signal



Low Rank
Matrix
Completion



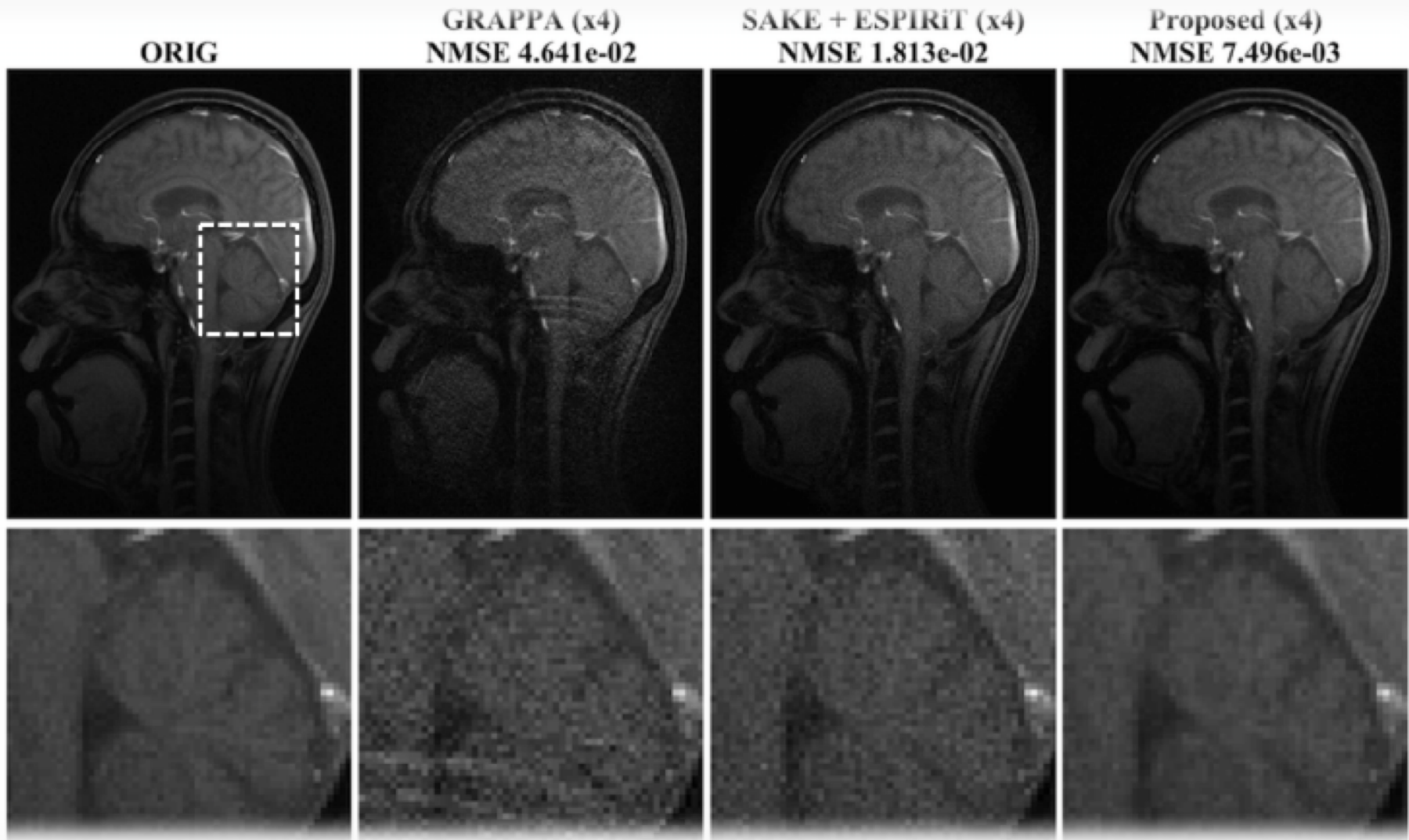
3-channel
signal



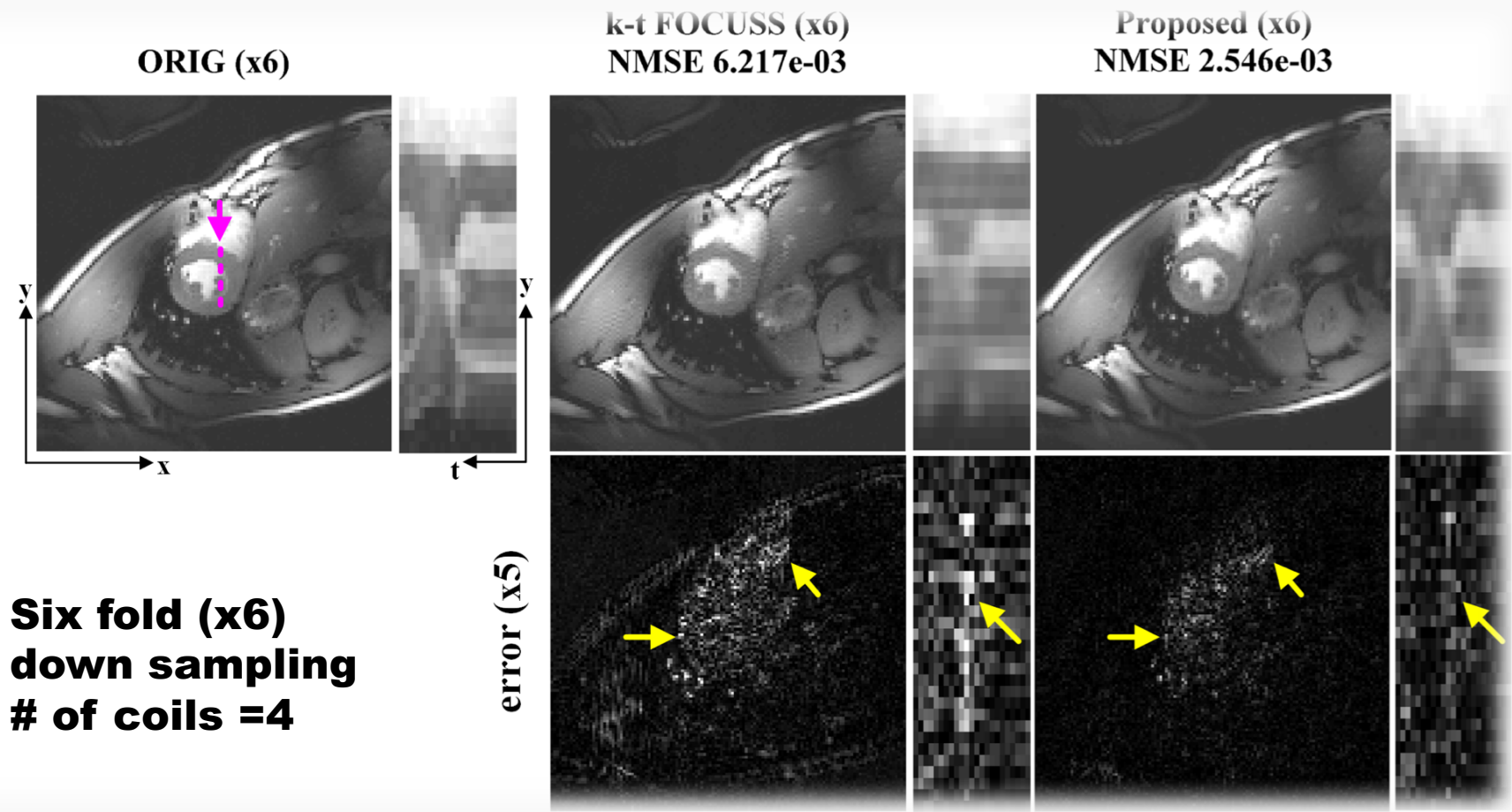
Low Rank
Matrix
Completion



Parallel MRI

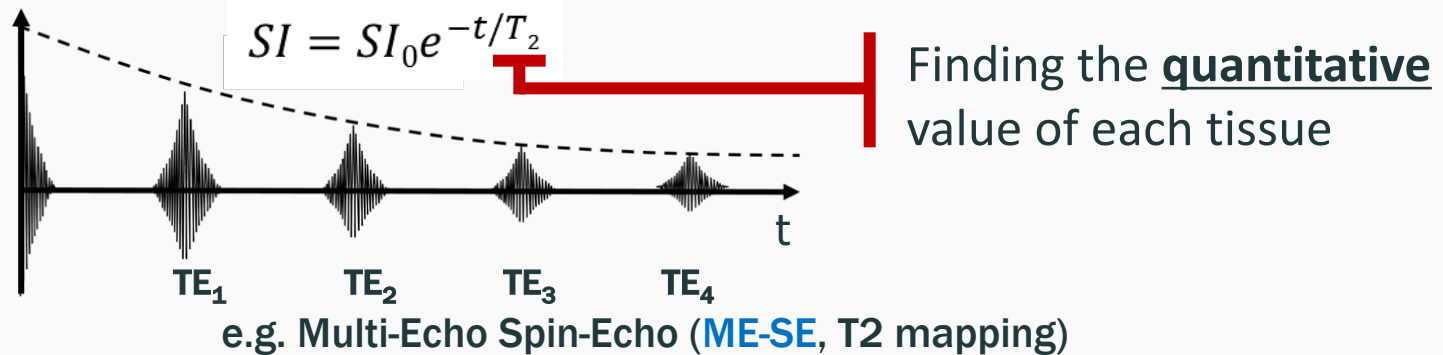


Dynamic MRI – multi coil



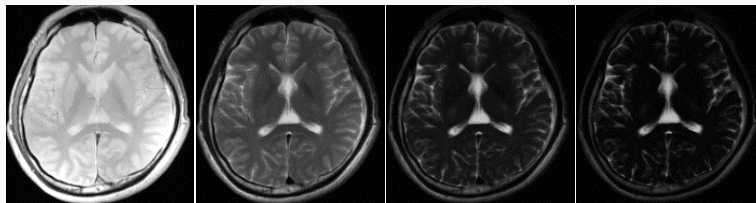
MR Parameter Mapping

What is **MR parameter mapping**?



Pros

Cons



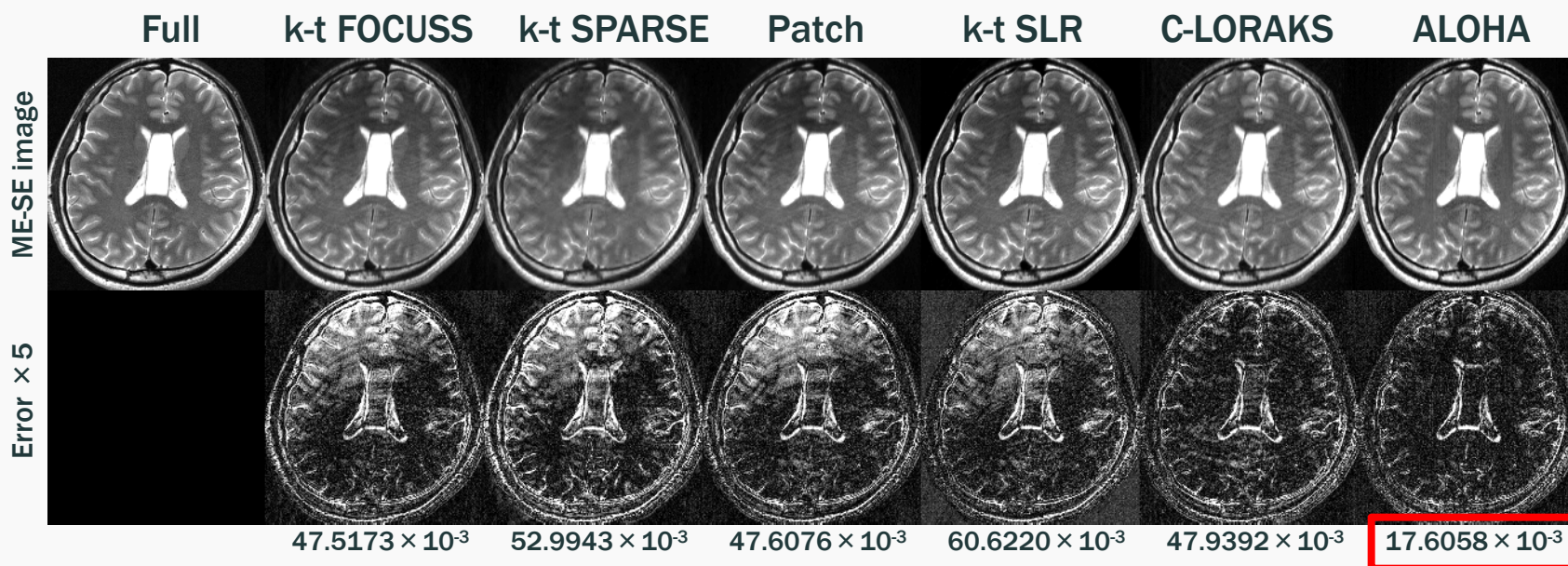
TE_1 TE_2 TE_3 TE_4

e.g. Multi-echo images for T2 mapping

Long scan time

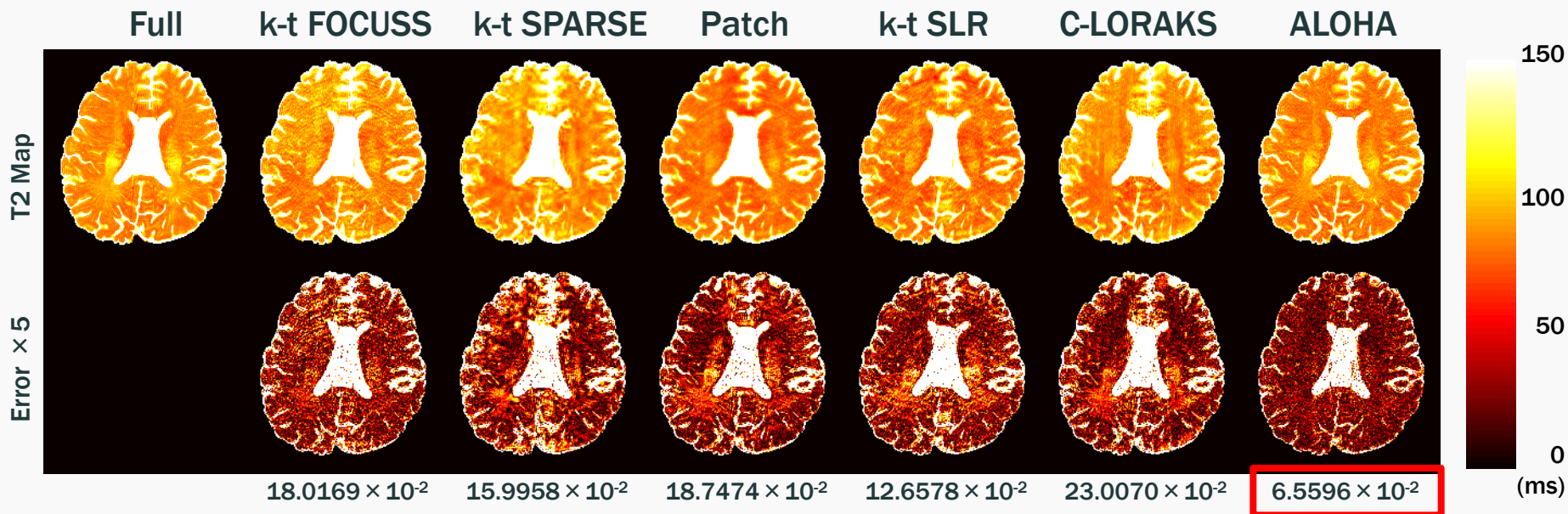
- Needs multiple scans
- Variation of TI, TE, FA, etc.

Result : in vivo acceleration study (ME-SE, T2)



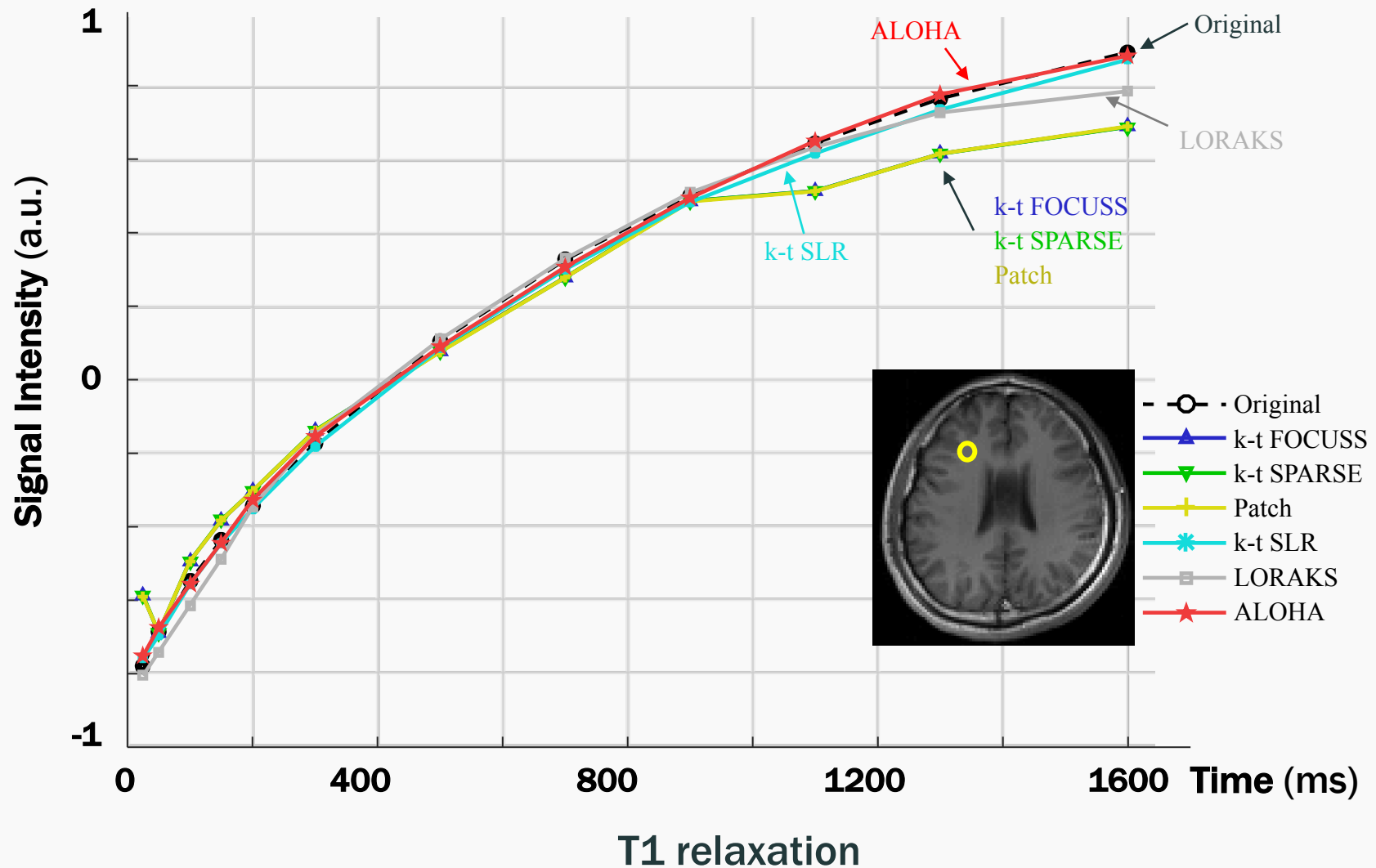
Reconstruction of x12.8 accelerated scan – ME-SE (4th echo)

Result : in vivo acceleration study (ME-SE, T2)



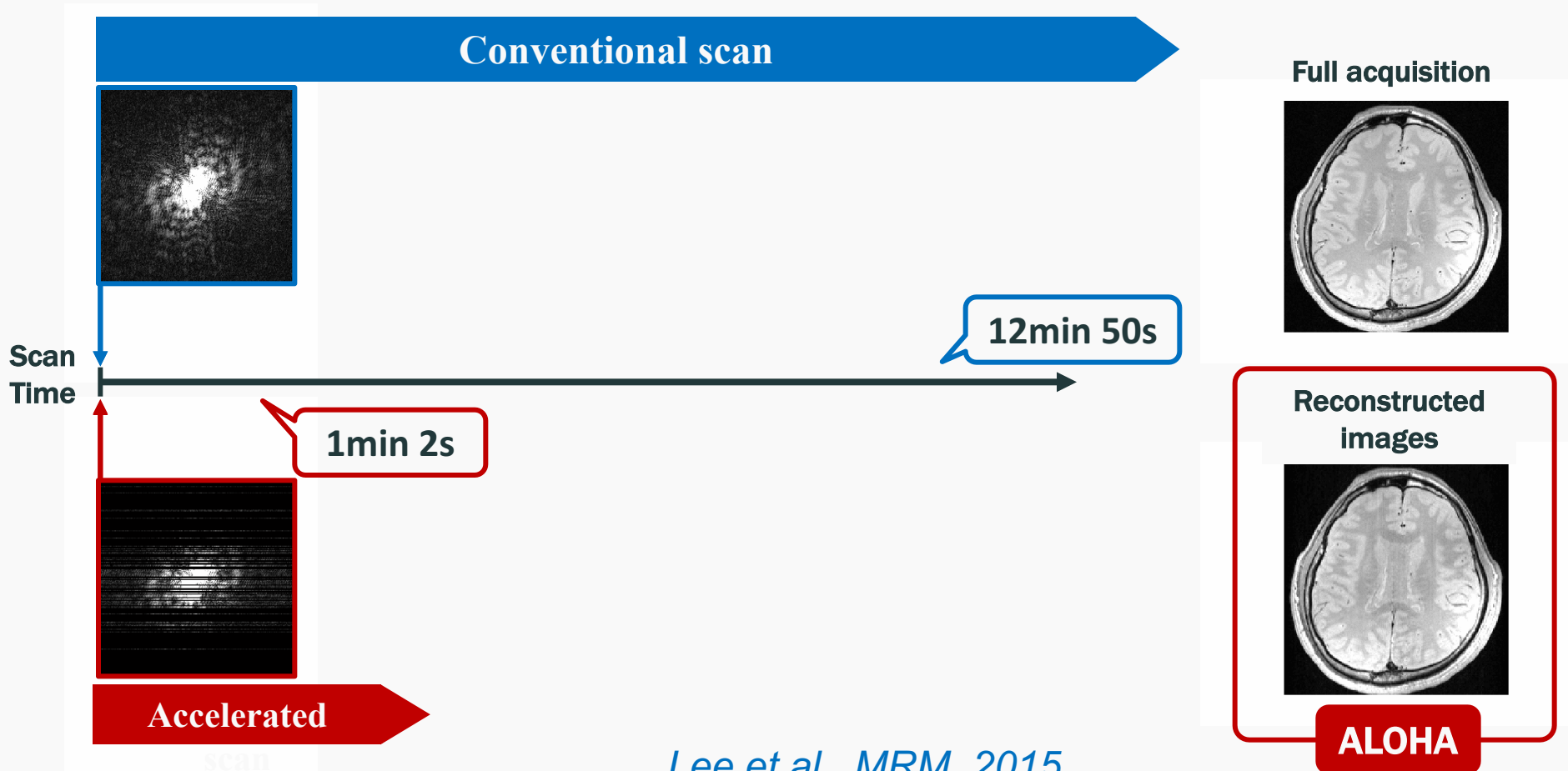
Mapping from the reconstruction of x12.8 accelerated scan – T2 mapping

Result : Signal intensity curves (SE-IR, T1)



Summary of Results

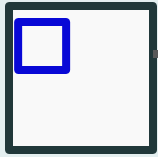
- Goal : **Acceleration of MR Parameter mapping** by undersampling and reconstruction



Extension to 3-D applications using GIRAF

2-D

$\hat{\mathbf{f}}$



$\mathcal{T}(\hat{\mathbf{f}})$

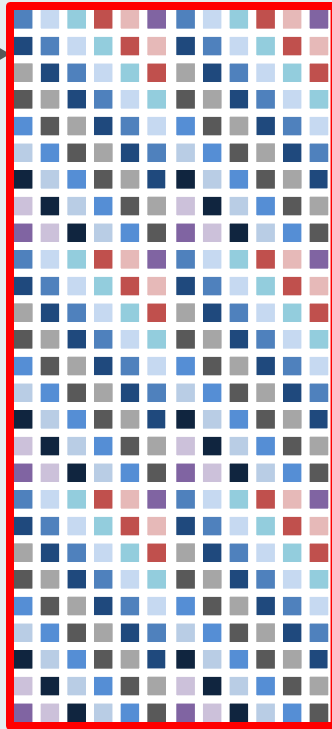


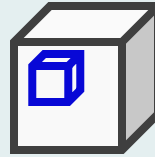
Image: 256x256

Filter: 32x32

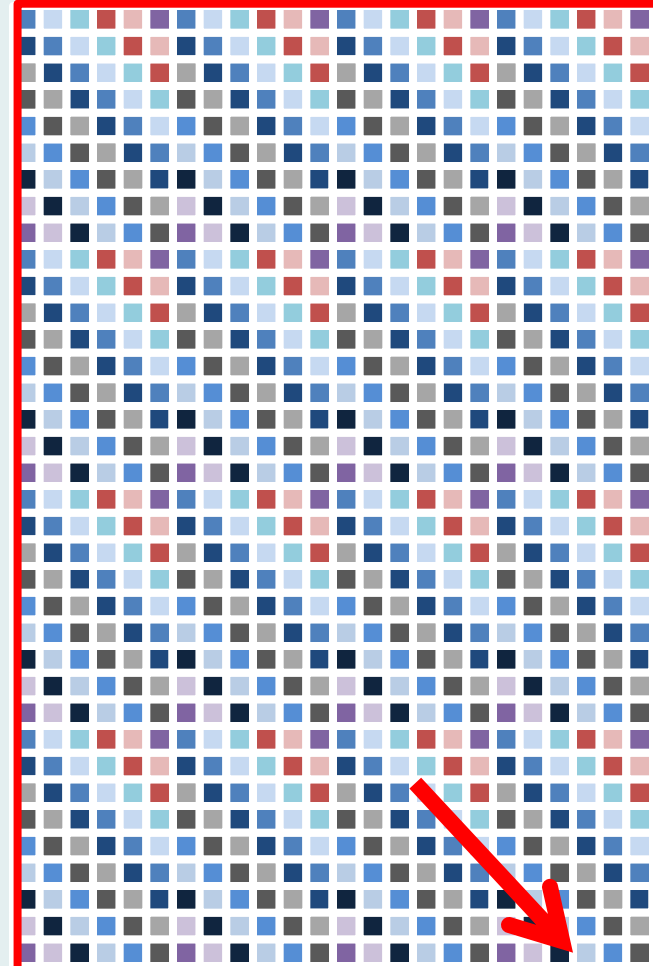
$\sim 10^6 \times 1000$

3-D

$\hat{\mathbf{f}}$



$\mathcal{T}(\hat{\mathbf{f}})$



256x256x32

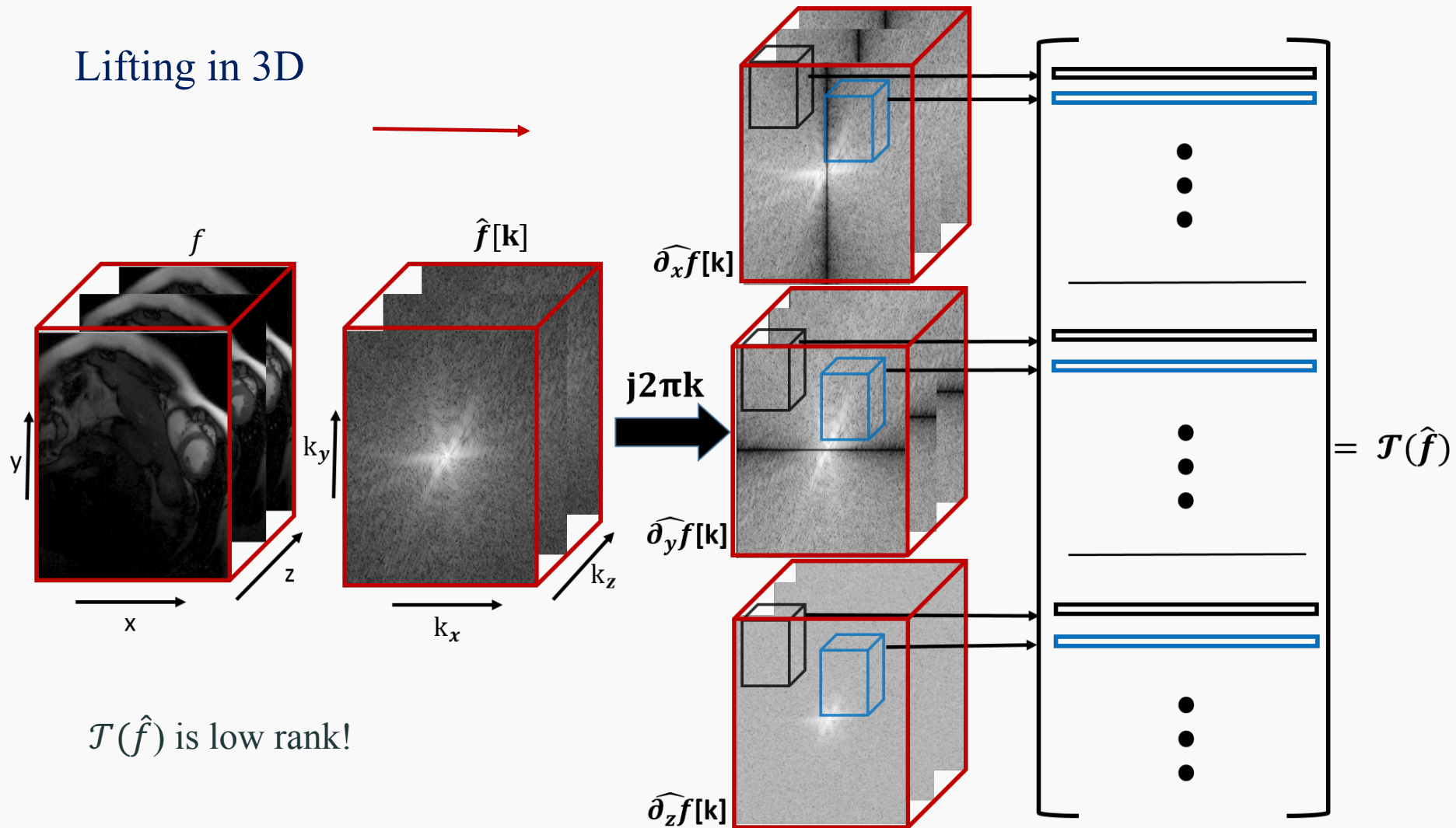
32x32x10

$\sim 10^8 \times 10^5$

Cannot Hold
in Memory!

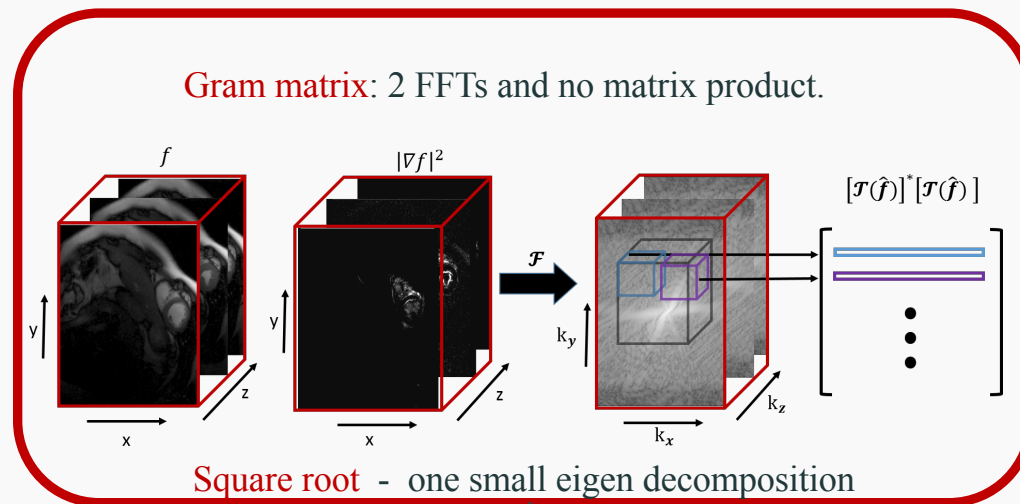
3D applications: dynamic MRI

Lifting in 3D

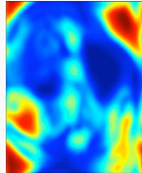


Fast 3-D implementation using GIRAF

Weight Update:



Fourier data update:



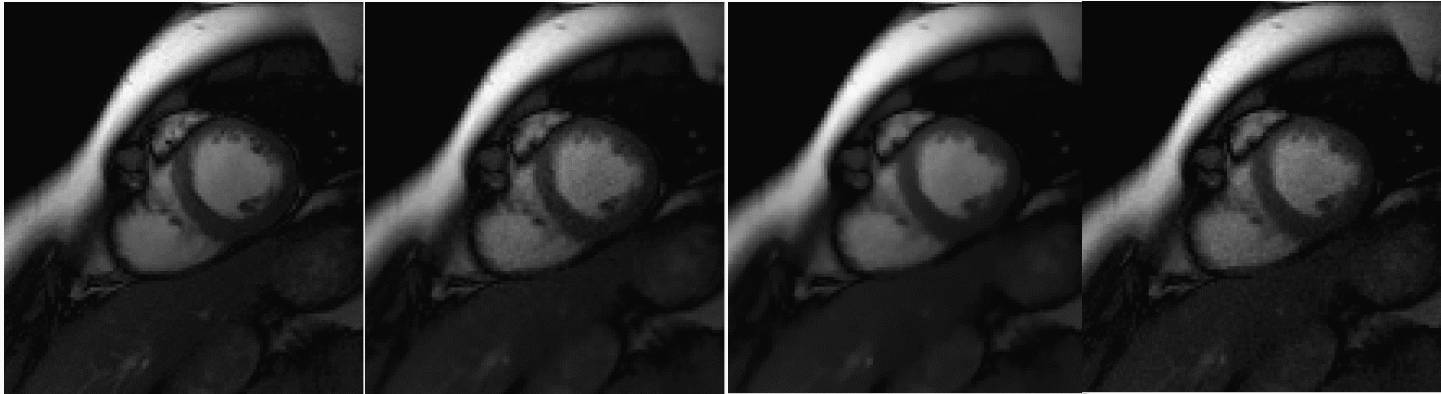
1 frame of μ_{sos}

$$\|\mathcal{T}(\mathcal{Q}\mathcal{F}_t\hat{\mathbf{f}})\mathbf{W}^{\frac{1}{2}}\|_F^2 \rightarrow \text{simplifies to } \|\mathcal{Q}(\mathcal{F}_t\hat{\mathbf{f}}) \star \hat{\mu}_{\text{sos}}\|_F^2$$

Where, $\mu_{\text{sos}} = \sqrt{\sum_{i=1}^N |\mathcal{F}^{-1}(\mathbf{w}_i)|^2}$

Need few iterations of CG to solve.

Cardiac CINE MRI

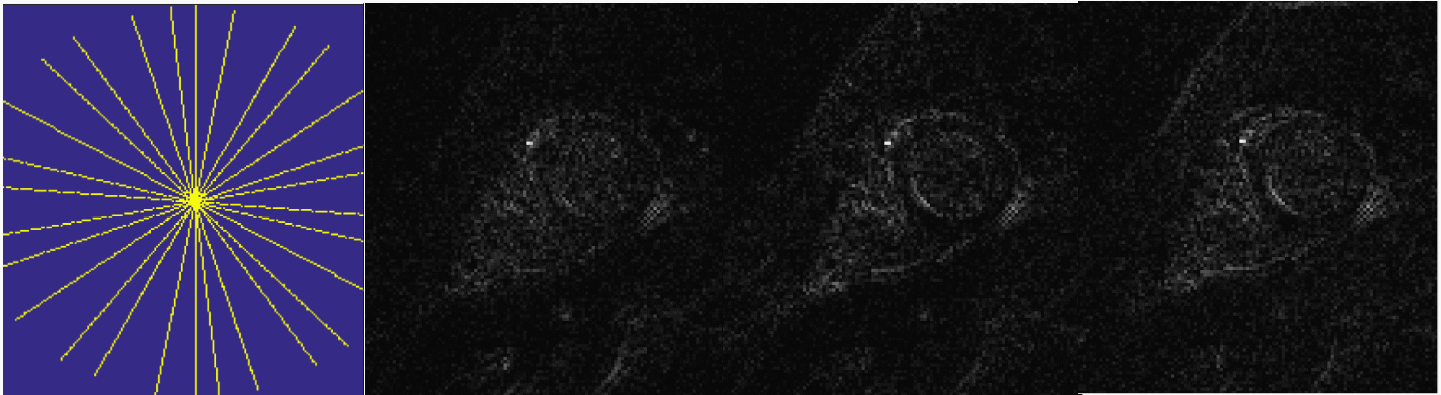


Truth
Golden angle (14lines)

Proposed
SNR – 23.32
HFEN– 0.109

TV
SNR – 23.27
HFEN– 0.121

Fourier Sparsity
SNR – 21.52
HFEN– 0.15

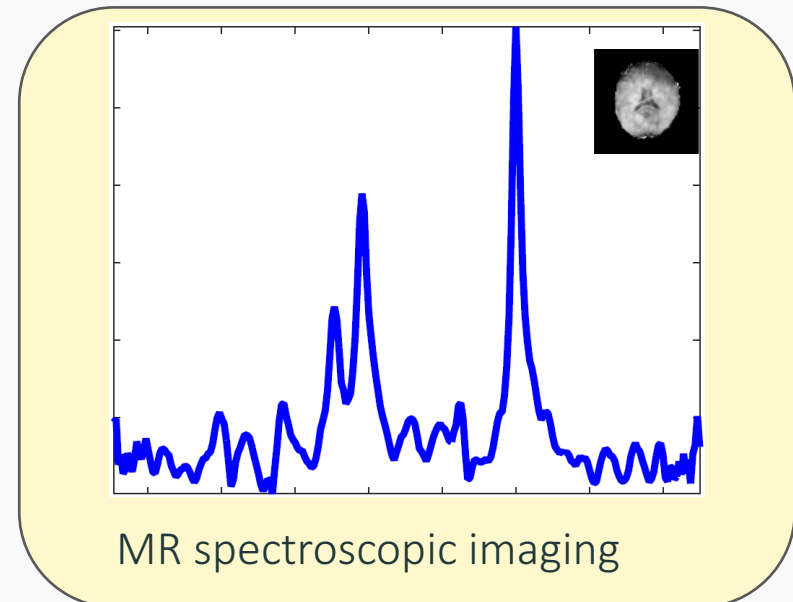
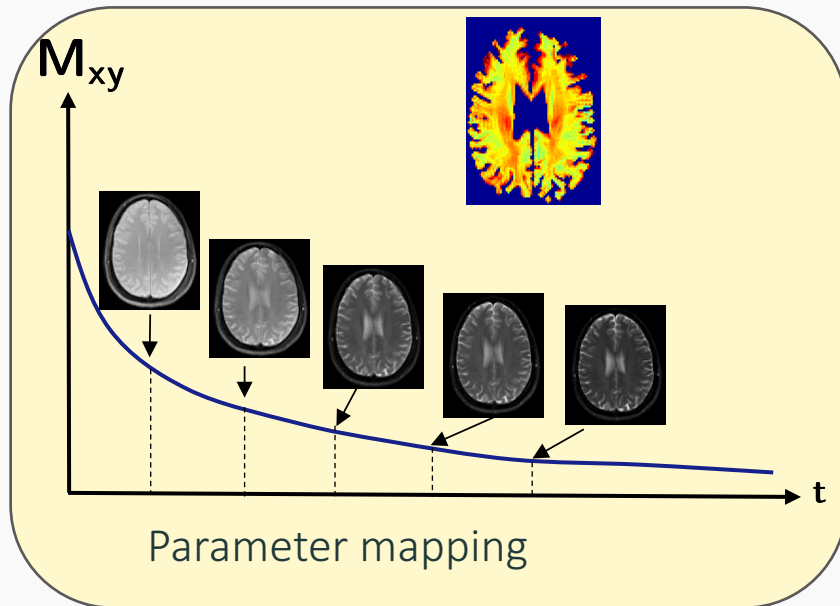


Balachandrasekaran & Jacob, ICIP 16

Exponential signal model

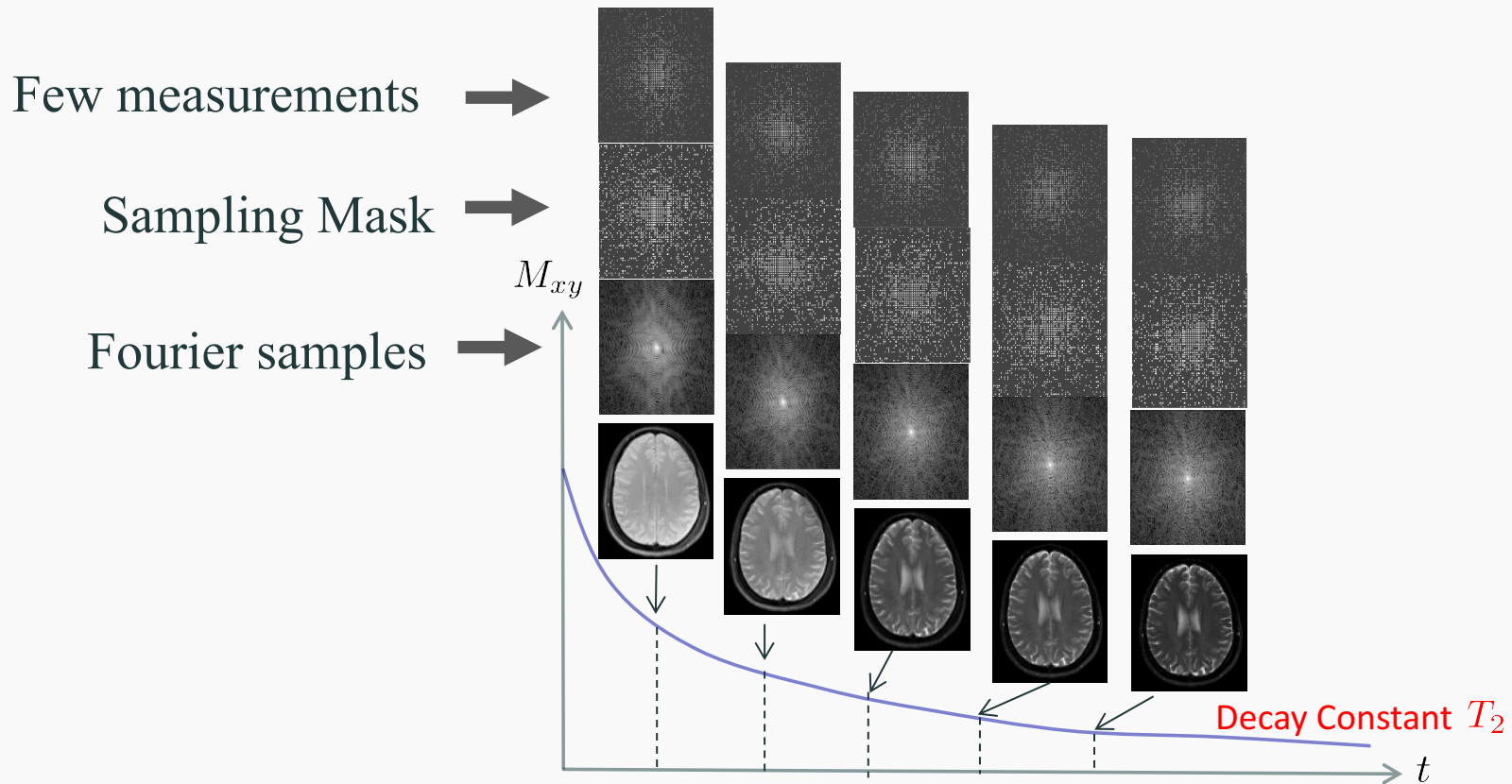
Linear combination of exponentials

$$\rho[\mathbf{r}, \mathbf{n}] = \sum_{i=1}^L \alpha_i(\mathbf{r}) \beta_i(\mathbf{r})^n$$



Acceleration the acquisition of exponentials

$$\rho[\mathbf{r}, \mathbf{n}] = \sum_{i=1}^L \alpha_i(\mathbf{r}) \beta_i(\mathbf{r})^n$$



MR parameter mapping

State of the art

Exploit correlations between voxel profiles

Low rank methods [Doneva et al,..]

Dictionary learning methods [BCS;Bhave et al]

Exploit correlations within an exponential voxel profile

Pixel by pixel structured low-rank [MORASSA: Peng et al,2016]

Structured low-rank with wavelet models

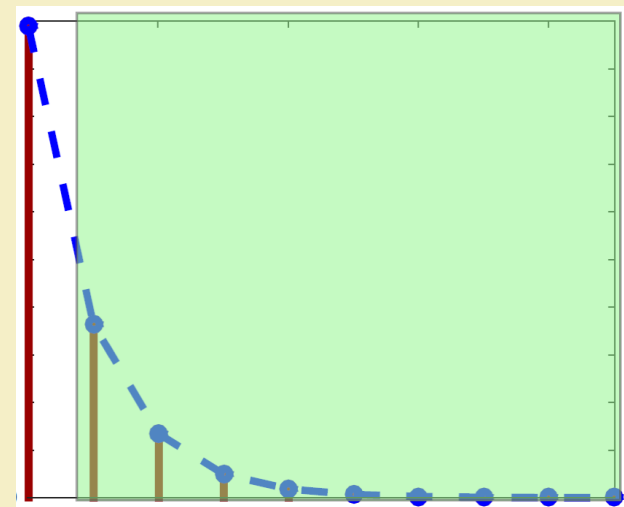
Exploit sparsity of $kx-t$ planes in wavelet domain [ALOHA]

Unify above strategies !!

1-D signal satisfies an annihilation relation

$$y[n] = \sum_{m=0}^L \rho[n-m]h[m] = 0$$

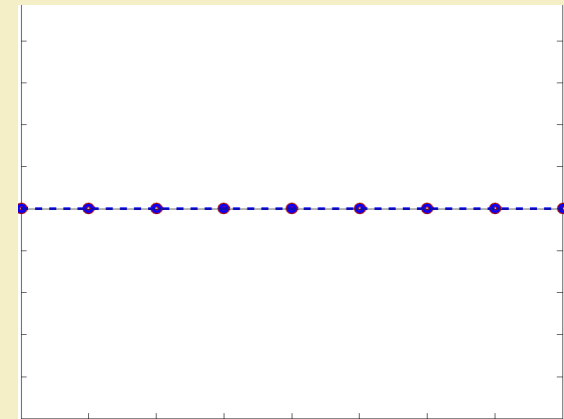
$$\rho[n] = \alpha^n$$



Possible shifts of filter

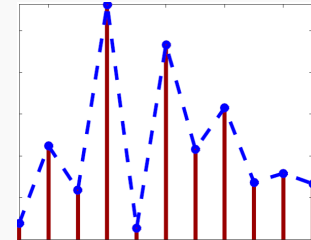
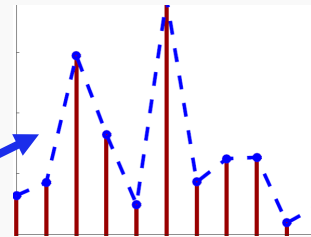
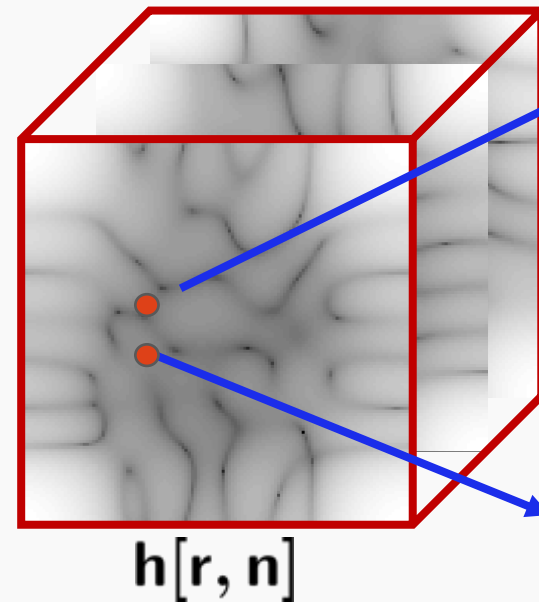
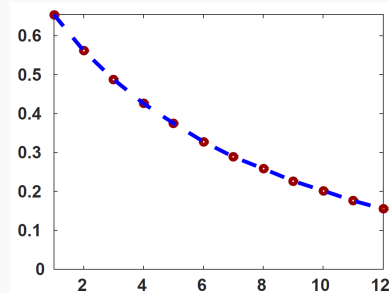
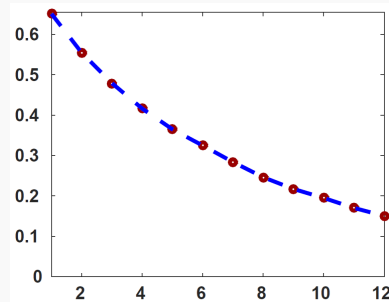
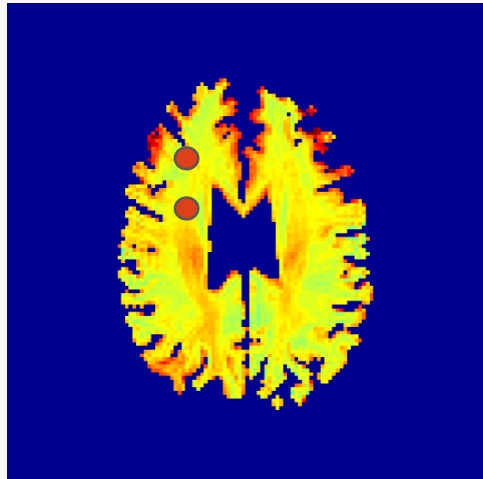
$$* h[n] = [1, -\alpha^{-1}] =$$

$$y[n] = 0$$

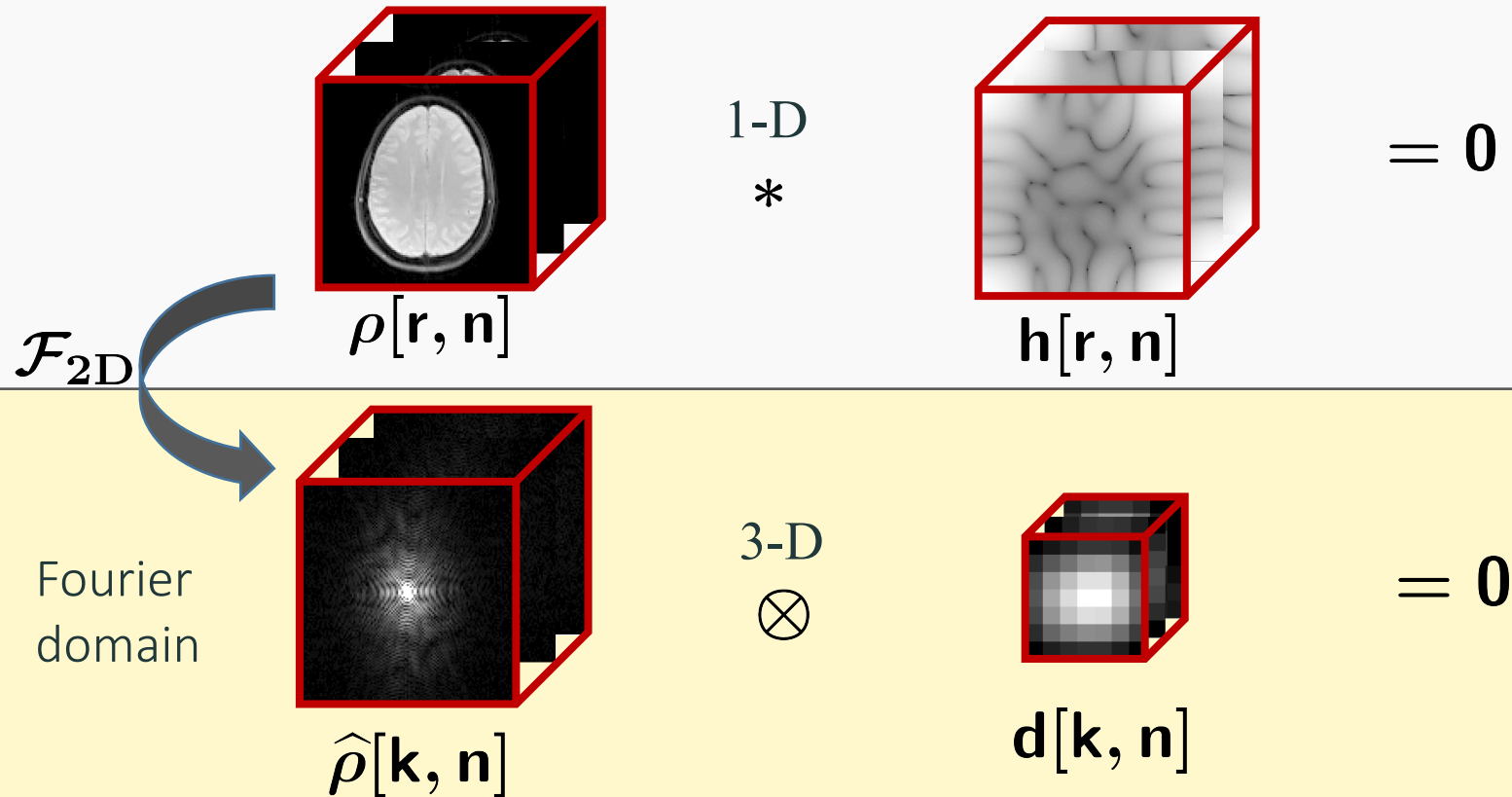


Exponential parameters are spatially smooth

Filter coefficients are spatially smooth

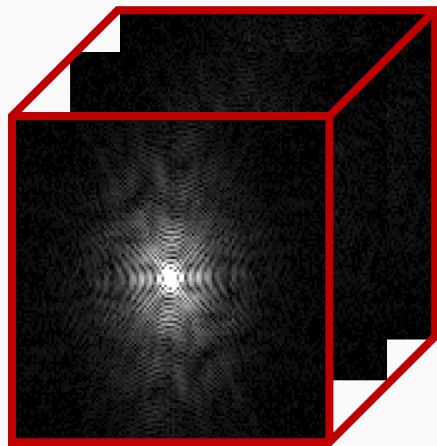


Spatially smooth filters: FIR in Fourier domain



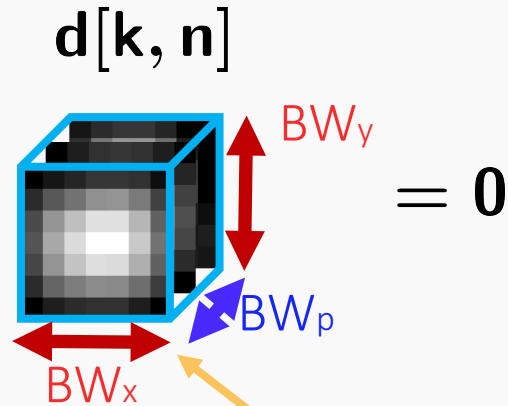
Annihilation relation: $\hat{\rho}[k, n] \otimes d[k, n] = 0$

Bandwidth of filter & spatial smoothness



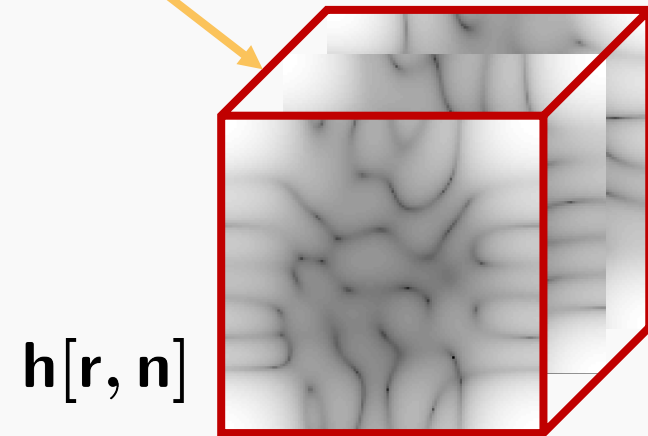
$\rho[\mathbf{k}, \mathbf{n}]$

\otimes
3-D



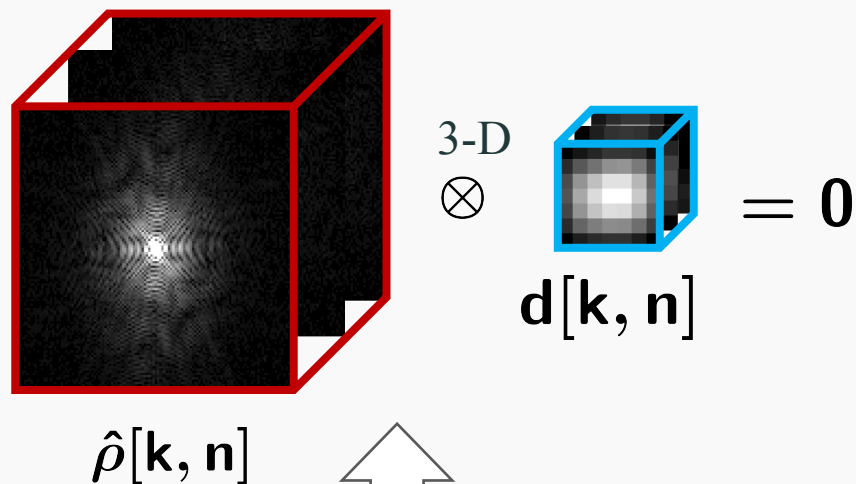
BW_x & BW_y : spatial smoothness of parameters.

BW_p : number of exponentials.



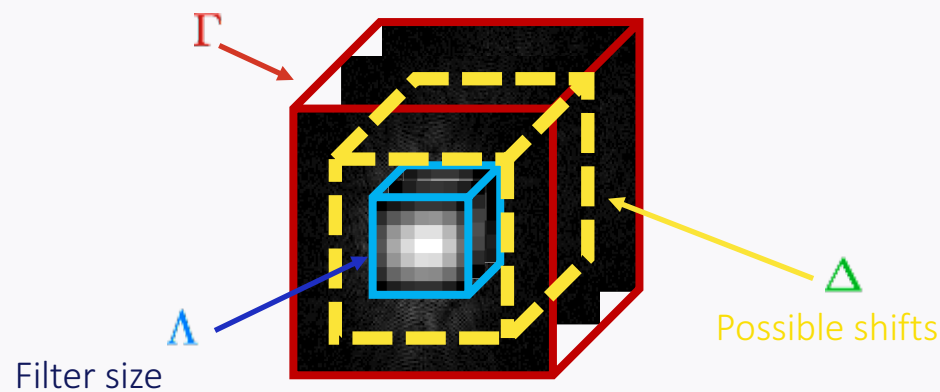
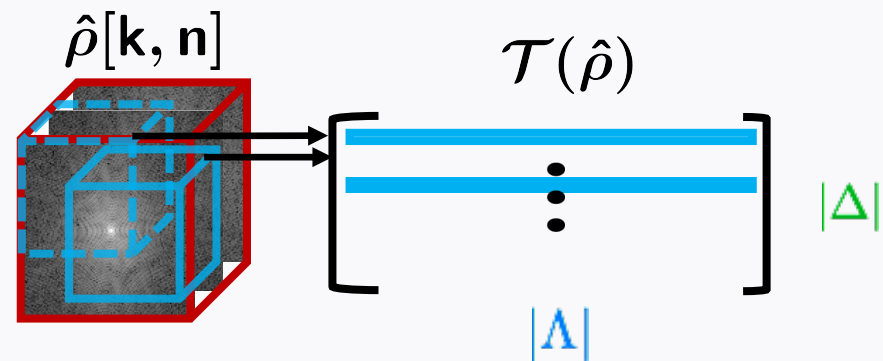
$h[\mathbf{r}, \mathbf{n}]$

Annihilation as a matrix-vector product



$$\hat{\rho}[k, n] \otimes d[k, n] = 0$$

$$\mathcal{T}(\hat{\rho}) \mathbf{d} = 0$$

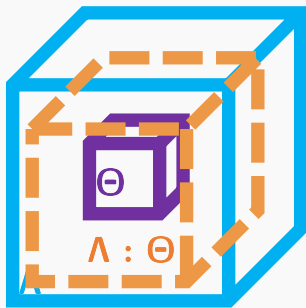


Minimal filter & assumed filter size

Minimal filter: exact size is unknown

Assumed filter: larger than **minimal filter**

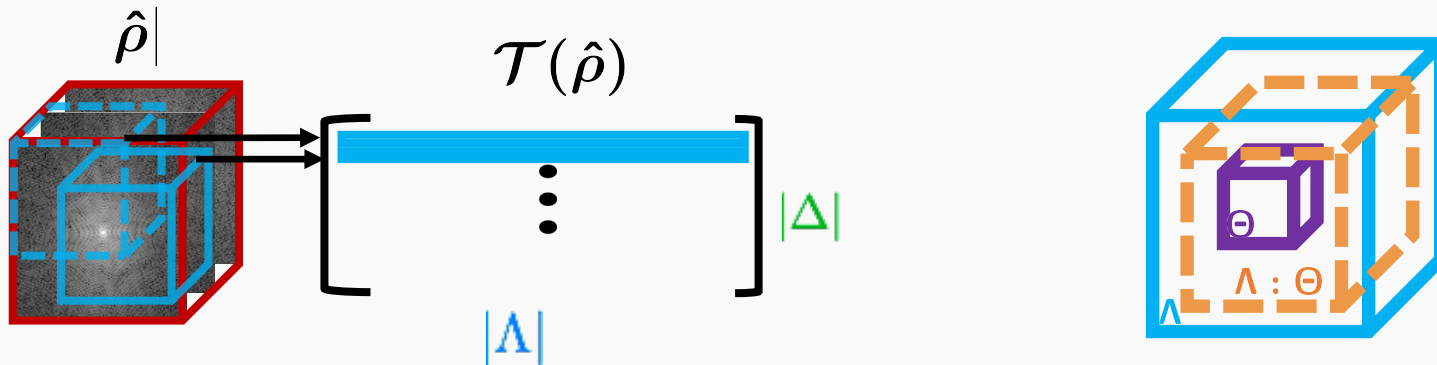
➡ Several possible annihilating filters



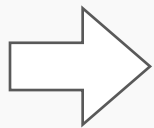
$$\underbrace{d[k, n]}_{\text{Assumed filter}} = \underbrace{c[k, n]}_{\text{Minimal filter}} \otimes \underbrace{e[k, n]}_{\text{FIR filter}}$$

$$\text{Dimension of annihilating subspace} \geq |\Lambda : \Theta|$$

Rank of the matrix



Dimension of annihilating subspace $\geq |\Lambda : \Theta|$

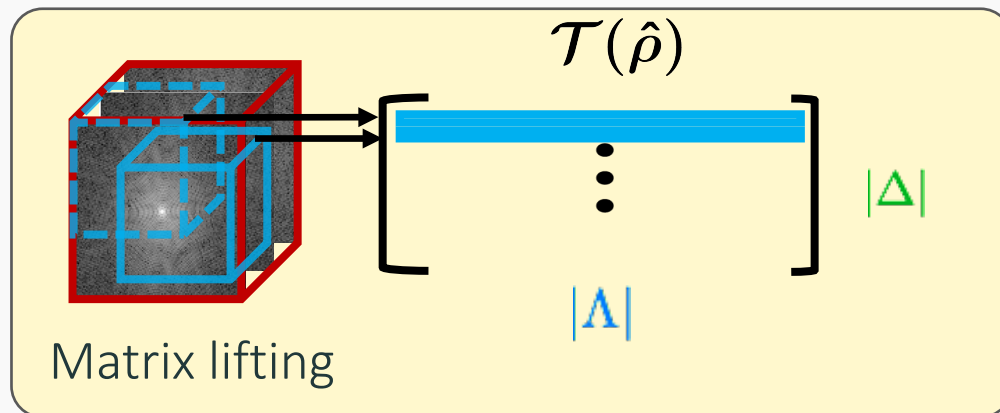


$$\text{Rank}(\mathcal{T}(\hat{\rho})) \leq |\Lambda| - |\Lambda : \Theta|$$

Structured low-rank optimization problem

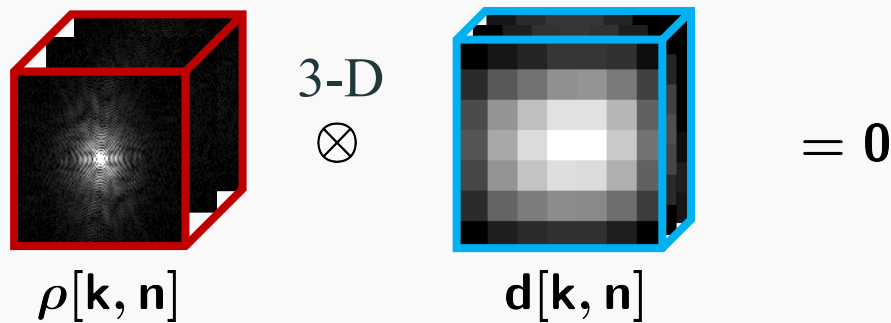
Find the signal that satisfies data consistency & minimizes rank

$$\hat{\rho}^* = \arg \min_{\hat{\rho}} \|\mathcal{T}(\hat{\rho})\|_{\text{p}} + \frac{\mu}{2} \|\mathcal{A}(\hat{\rho}) - \mathbf{b}\|_2^2$$



Special case: no spatial smoothness

Spatial dimension of **filter** is the same as Γ

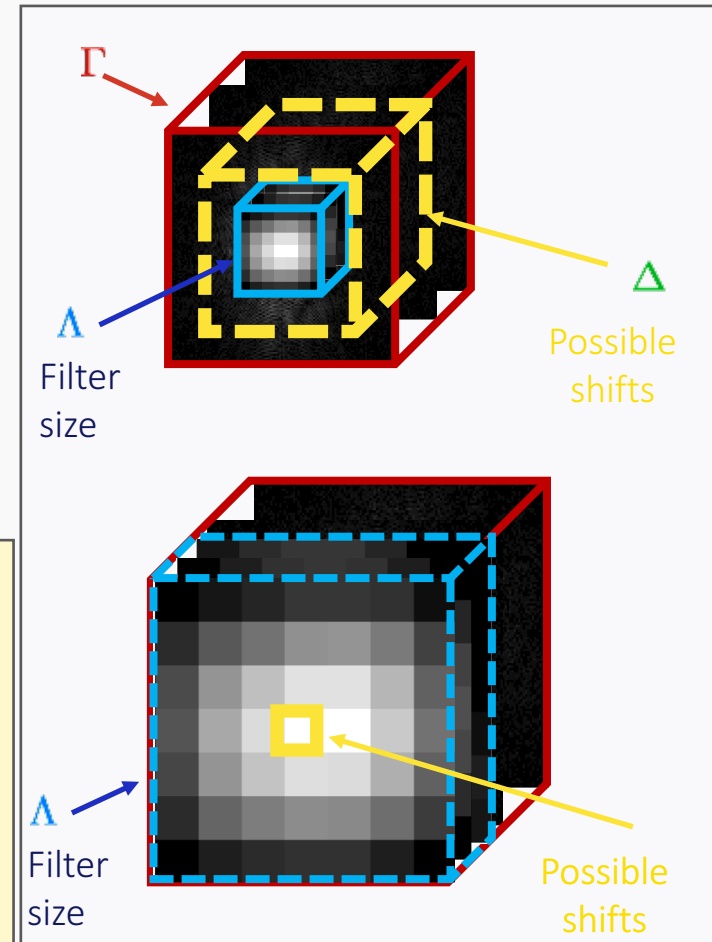


The diagram illustrates a 3-D convolution operation. On the left is a 3D volume $\rho[\mathbf{k}, \mathbf{n}]$ with a red border. In the middle is a 3D volume $\mathbf{d}[\mathbf{k}, \mathbf{n}]$ with a blue border. A red arrow labeled Γ points to the top face of ρ . A blue arrow labeled Δ points to the top face of \mathbf{d} . The operation is represented by \otimes and the result is $= 0$.

$$\rho[\mathbf{k}, \mathbf{n}] \otimes \mathbf{d}[\mathbf{k}, \mathbf{n}] = 0$$

Lifting: concatenation of pixel-by-pixel Toeplitz matrices

$$\mathcal{T}(\rho) = [\mathcal{T}(\rho_1) | \dots | \mathcal{T}(\rho_N)]$$



Relation to other structured low-rank priors

Pixel independent structured low-rank prior [MORASSA, Peng et al., 2016]

$$\{\rho_m\} = \arg \min_{\{\rho_m\}} \sum_m \|\mathcal{T}(\rho_m)\|_* + \|\mathcal{A}(\boldsymbol{\rho}) - \mathbf{b}\|^2$$

Does not exploit spatial correlations

Proposed special case: nuclear norm of concatenated matrices

$$\mathcal{T}(\rho) = [\mathcal{T}(\rho_1) | \dots | \mathcal{T}(\rho_N)]$$

Combination of low-rank & exponential priors: exploit spatial correlations

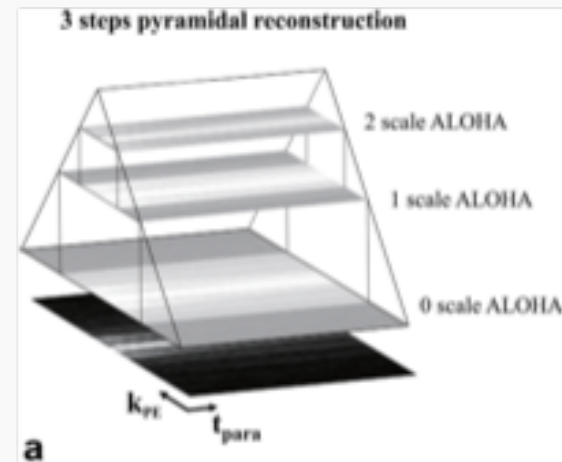
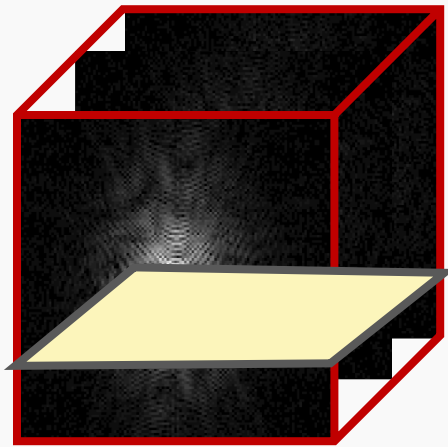
Only one small EVD per iteration: considerably faster

ALOHA based solution discussed earlier ..

2-D prior: fills in kx - t planes using structured low-rank interpolation

Signal sparse in wavelet domain

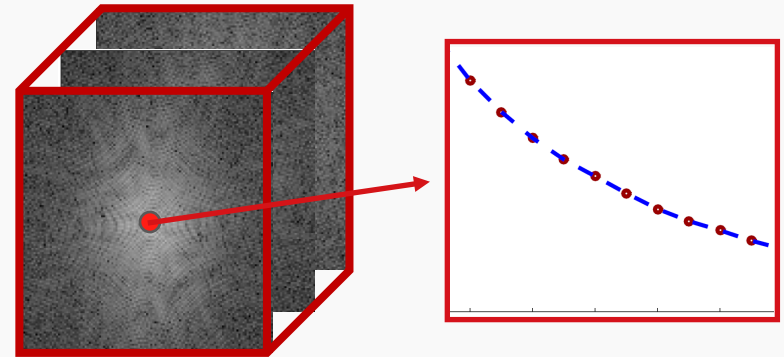
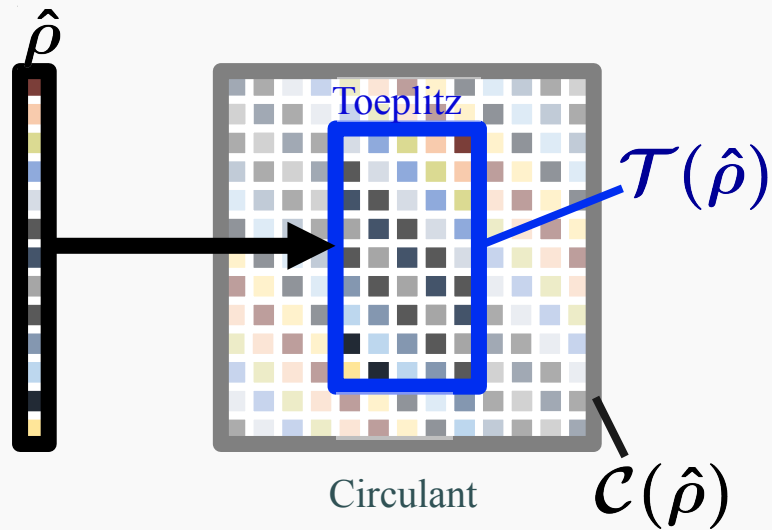
Does not exploit exponential decay of signal



Use signal weighting: ALOHA-like prior

GIRAF: Circulant approximation is not accurate

Approximation is good if signal amplitude is negligible at boundaries



High signal amplitude: poor approximation

Solution: hybrid approach

Circular convolution in space

Linear convolution along parameter dimension

$$\mathbf{w}[\mathbf{k}, \mathbf{n}] \otimes \hat{\rho}[\mathbf{k}, \mathbf{n}] = \sum_{\mathbf{m}} \underbrace{\sum_p \hat{\rho}[\mathbf{k} - \mathbf{p}, n - m] h[\mathbf{p}, m]}_{\approx \mathbf{g}_{n-m, m} = \hat{\rho}_{n-m} * \mathbf{h}_m}$$

Sum of spatial circular convolutions: computed using FFT

Weight evaluation

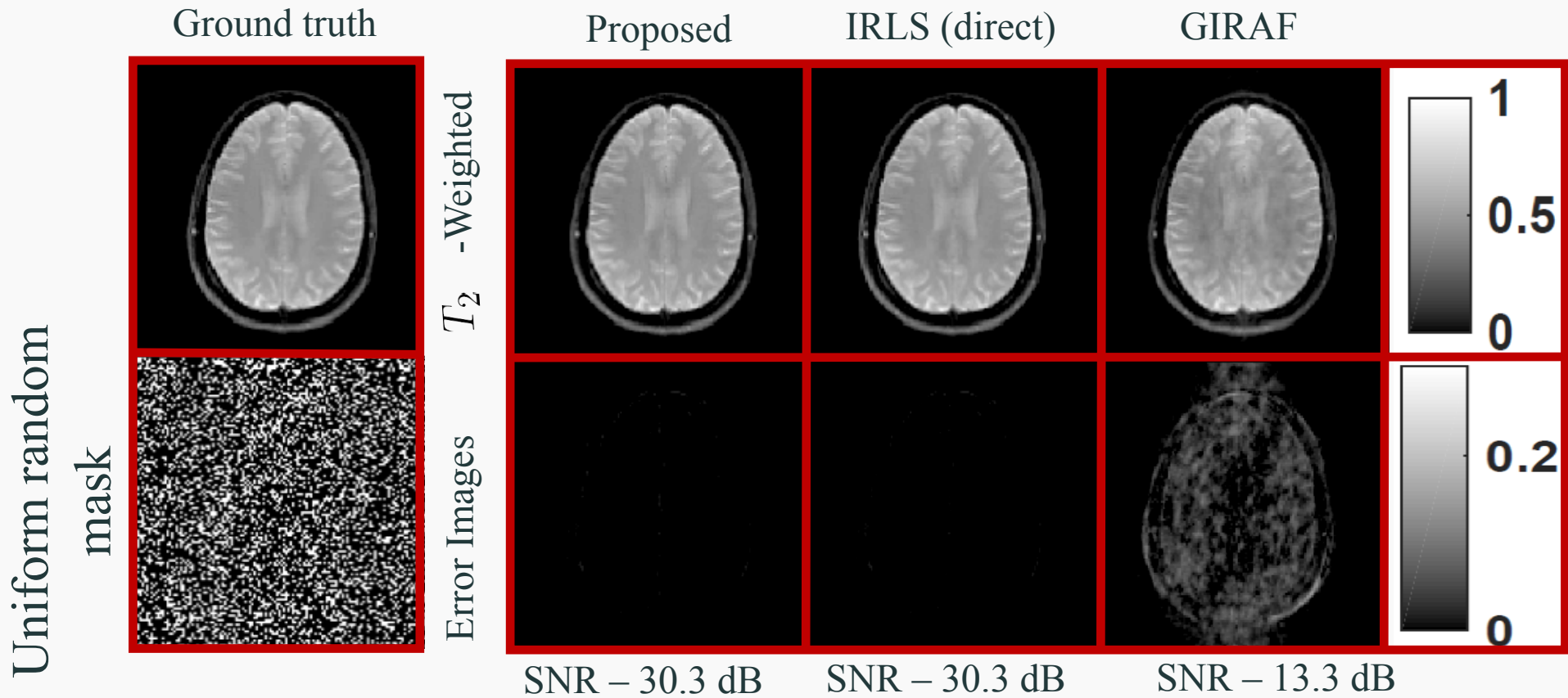
$$\mathbf{W} \leftarrow \underbrace{(\mathcal{T}(\hat{\rho})\mathcal{T}(\hat{\rho})^H)}_{\mathbf{R}} + \epsilon \mathbf{I} \Big)^{\frac{p}{2} - 1}$$

$$\mathbf{R} = \begin{pmatrix} \mathbf{R}_{1,1} & \mathbf{R}_{1,2} & \cdots & \mathbf{R}_{1,M} \\ \mathbf{R}_{2,1} & \mathbf{R}_{2,2} & \cdots & \mathbf{R}_{2,M} \\ \vdots & \vdots & \cdots & \vdots \\ \vdots & \vdots & \cdots & \vdots \\ \mathbf{R}_{M,1} & \mathbf{R}_{M,2} & \cdots & \mathbf{R}_{M,M} \end{pmatrix}$$

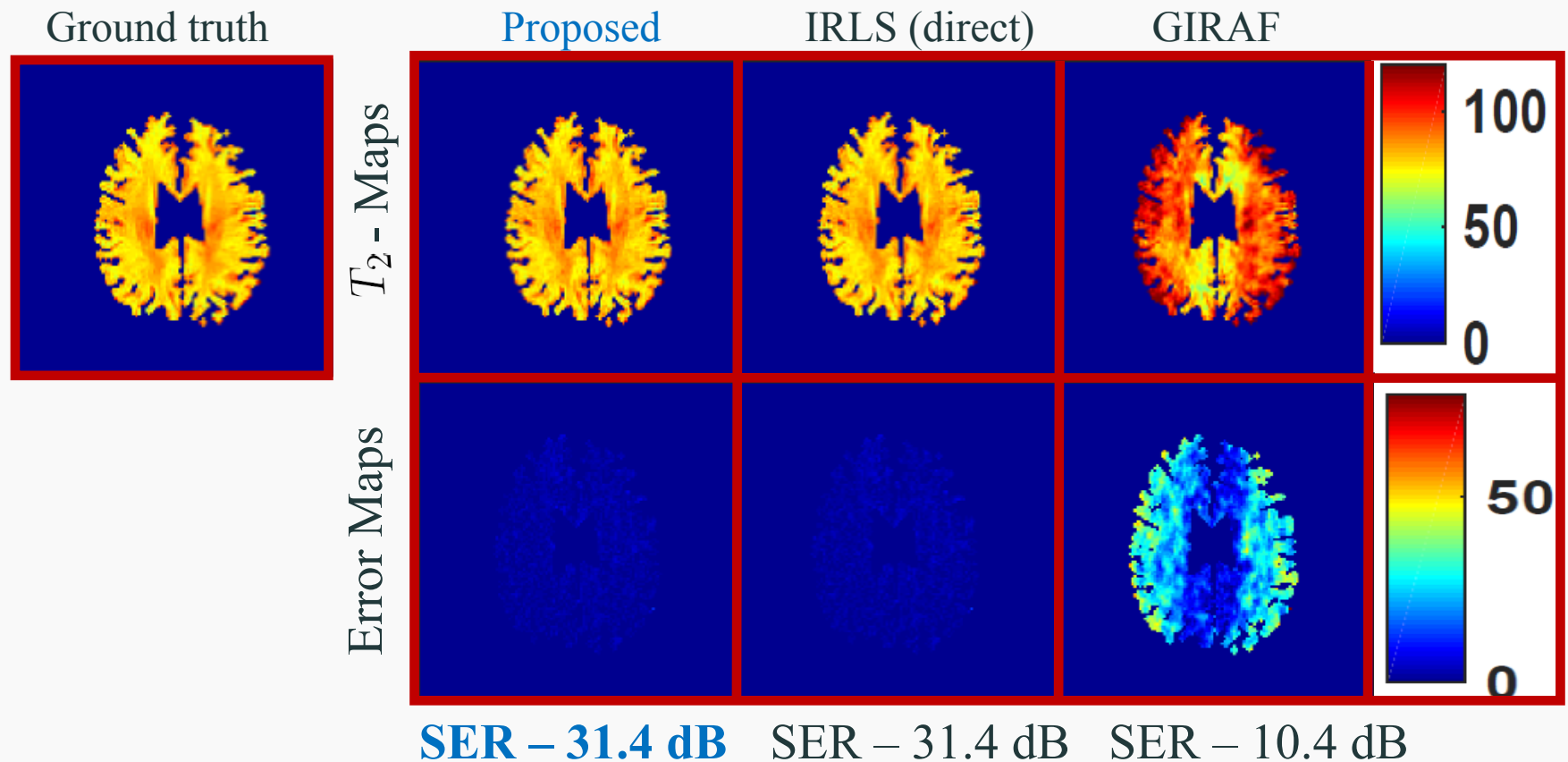
Sum of spatial circular convolutions: computed using FFT

$$\mathbf{R}_{p,q} = \sum_{i=1}^k \underbrace{\mathbf{T}(\hat{\rho}_{p+i-1})\mathbf{T}(\hat{\rho}_{q+i-1})^*}_{}$$

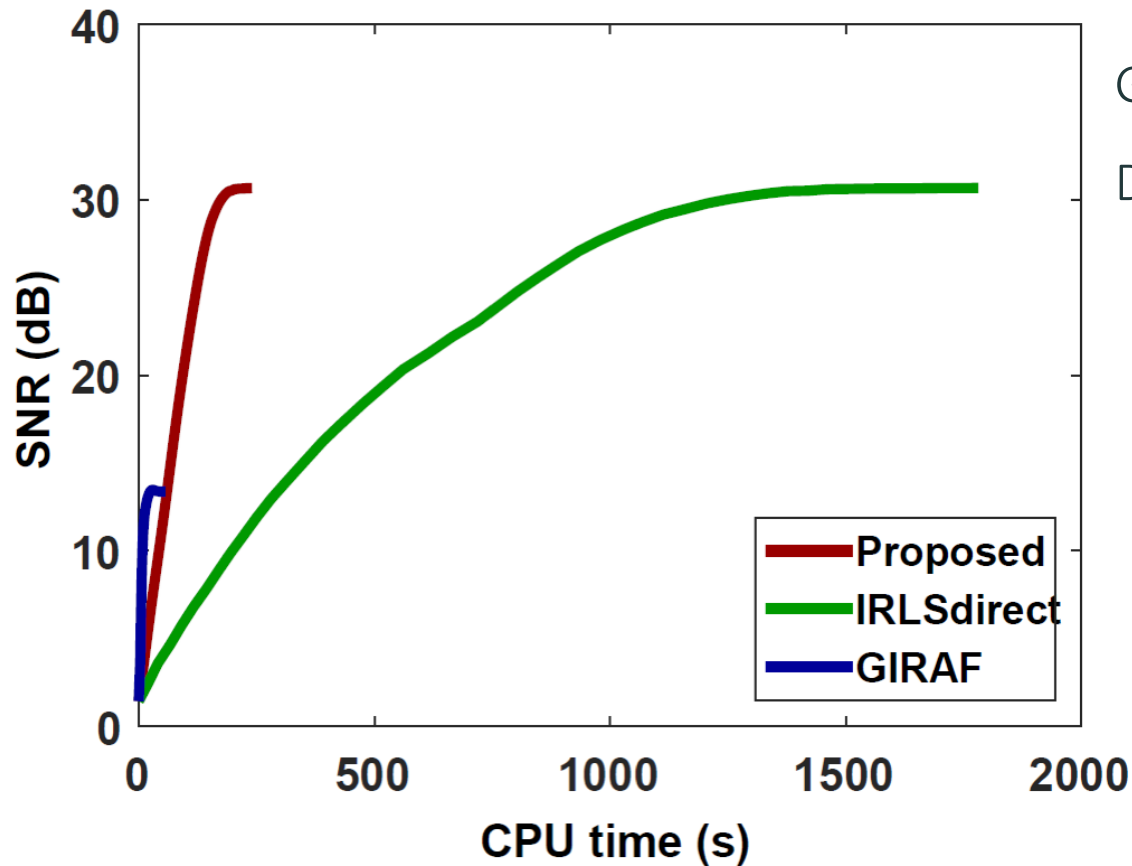
Validation using single channel data (sim)



Validation using single channel data (simulation)



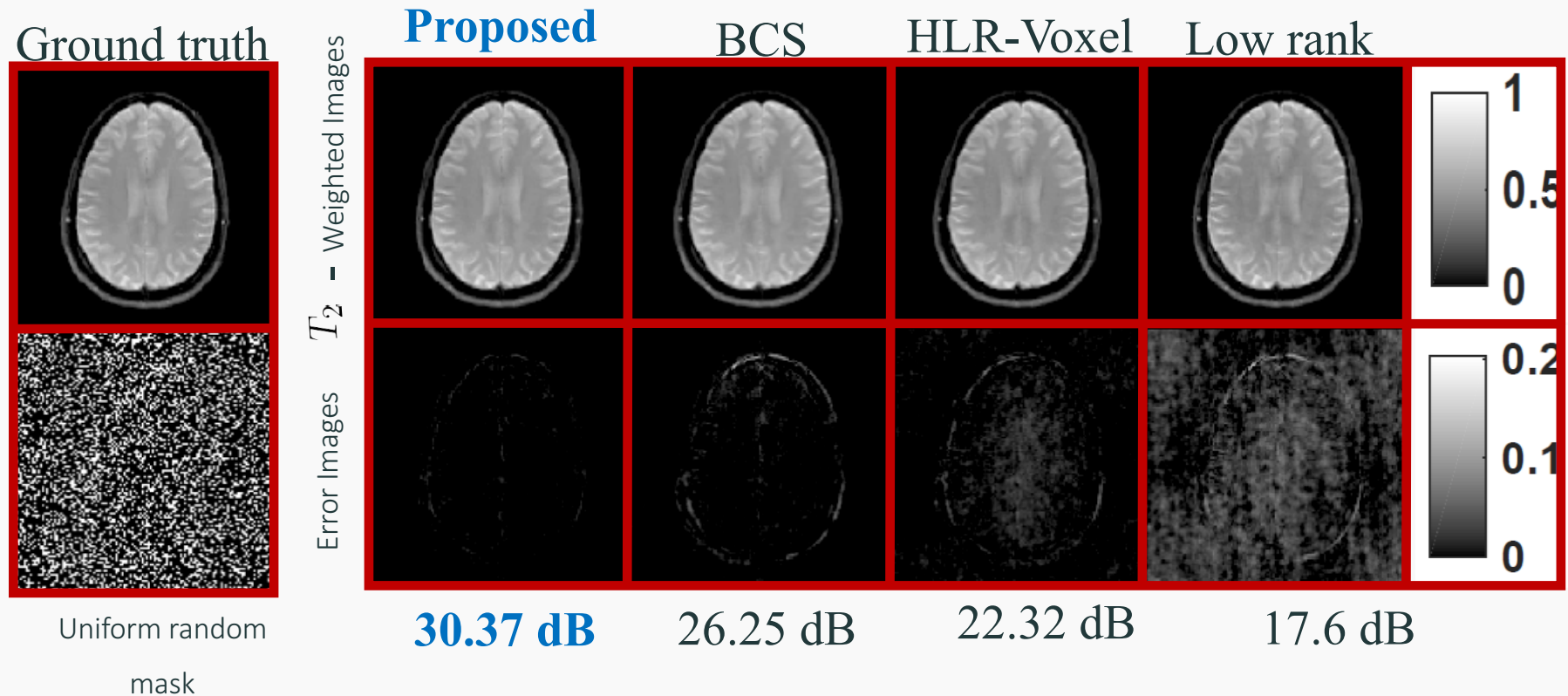
Fast convergence



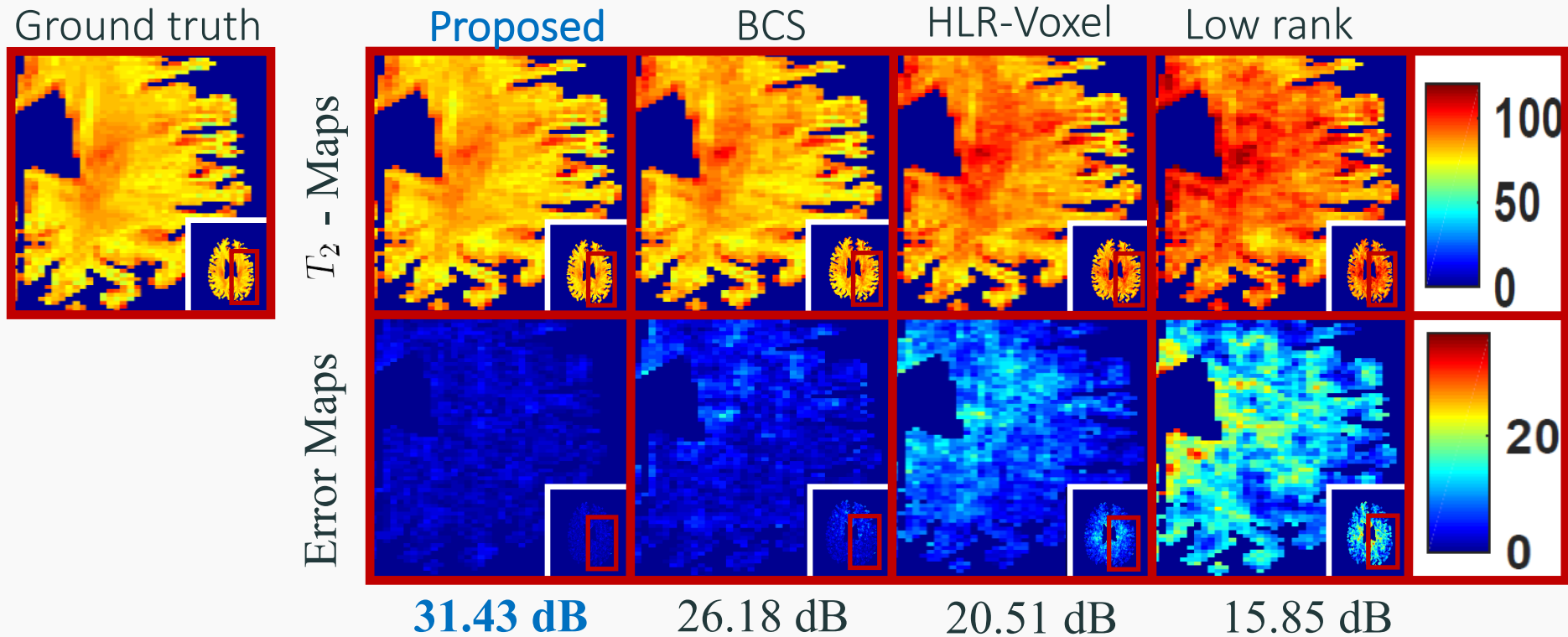
GIRAF: poor approximation

Direct IRLS: slow

Comparison with state of the art



Comparison with state of the art



Multichannel acquisitions

- TR=2500 ms,
- slice thickness = 5mm
- FOV = 22x22 cm²
- Matrix size : 128x128,
- No of coils = 12,
- TE = 10 to 120 ms

Smaller filters provide better results

| filter size | SNR |
|-------------------|--------------|
| 128x128x10 | 28.05 |
| 122x122x10 | 30.30 |
| 114x114x10 | 31.00 |
| 108x108x10 | 31.12 |
| 102x102x10 | 31.21 |
| 100x100x10 | 31.20 |

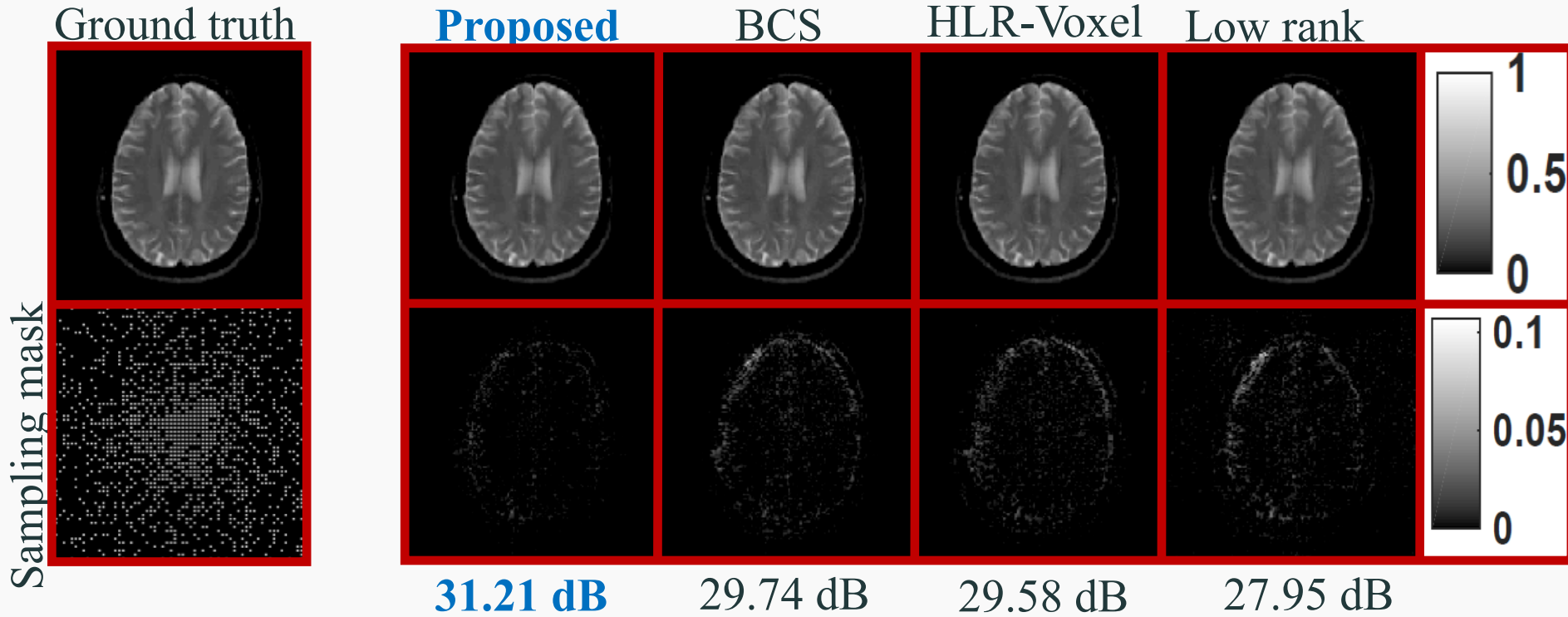
(a) Varying spatial dimension

| filter size | SNR (dB) |
|-------------------|--------------|
| 102x102x11 | 30.80 |
| 102x102x10 | 31.21 |
| 102x102x7 | 31.13 |
| 102x102x4 | 30.96 |
| 102x102x2 | 30.78 |
| 102x102x1 | 29.88 |

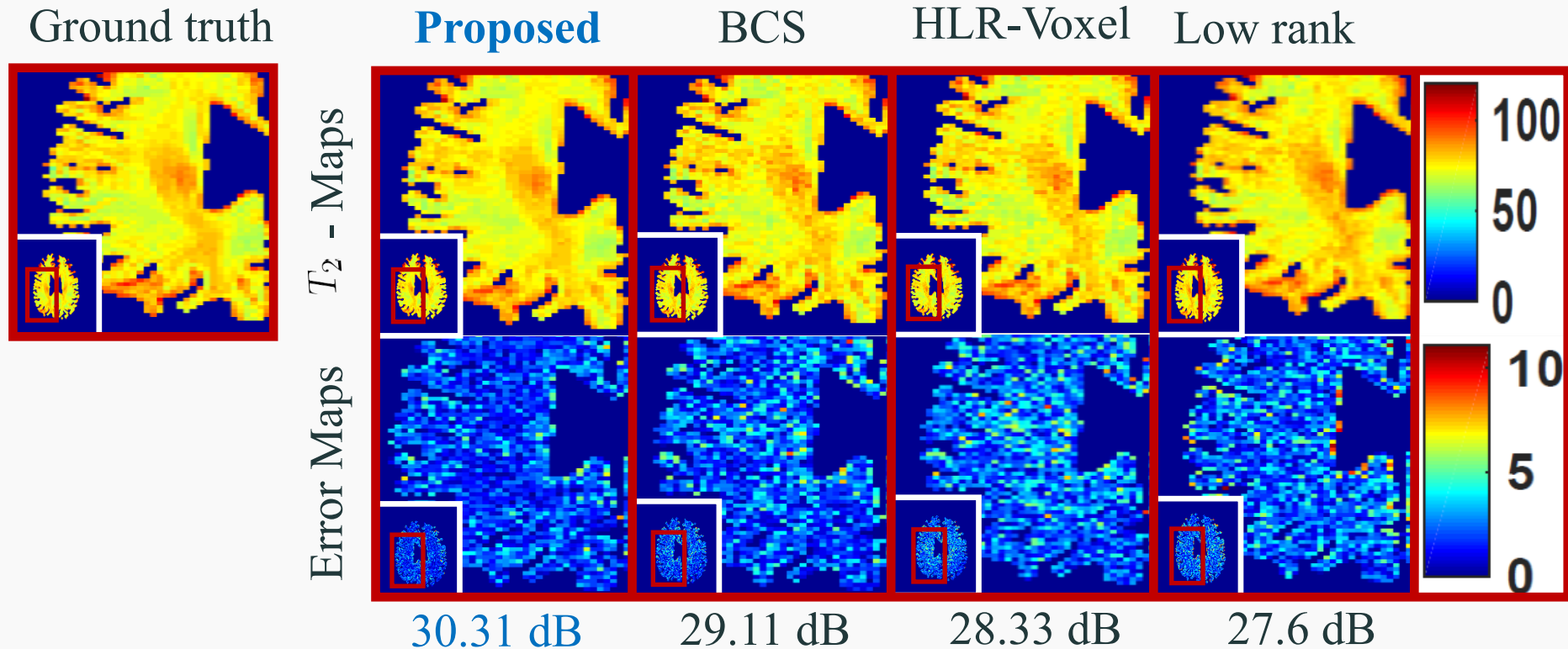
(b) Varying temporal dimensions

Smaller filters: spatial regularization

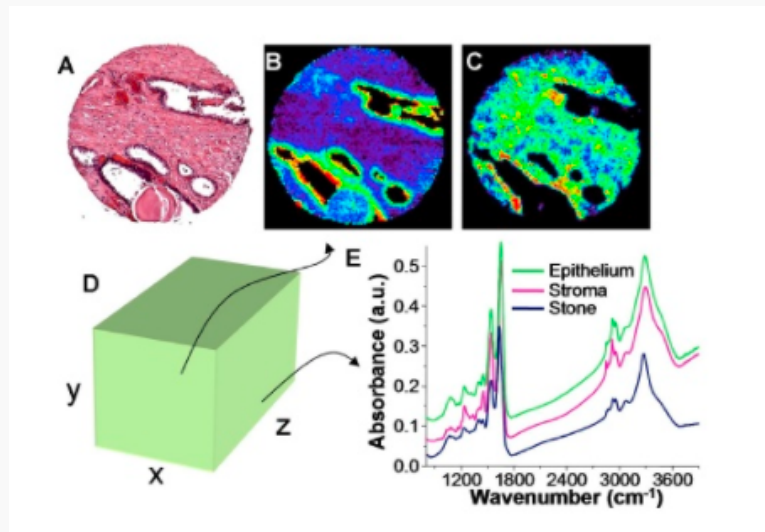
Multichannel acq: T2 weighted images



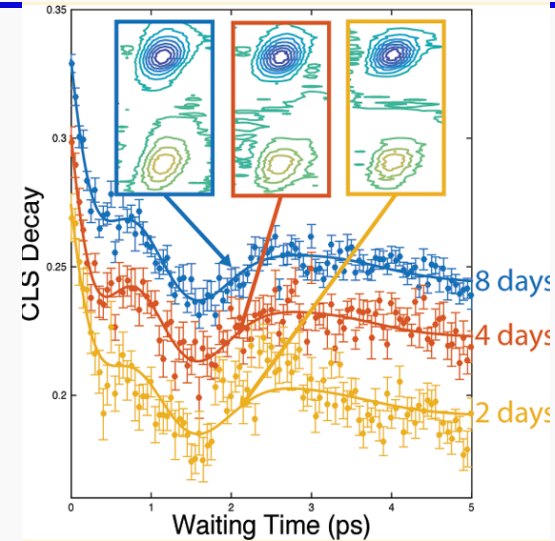
Multichannel acquisition: parameter maps



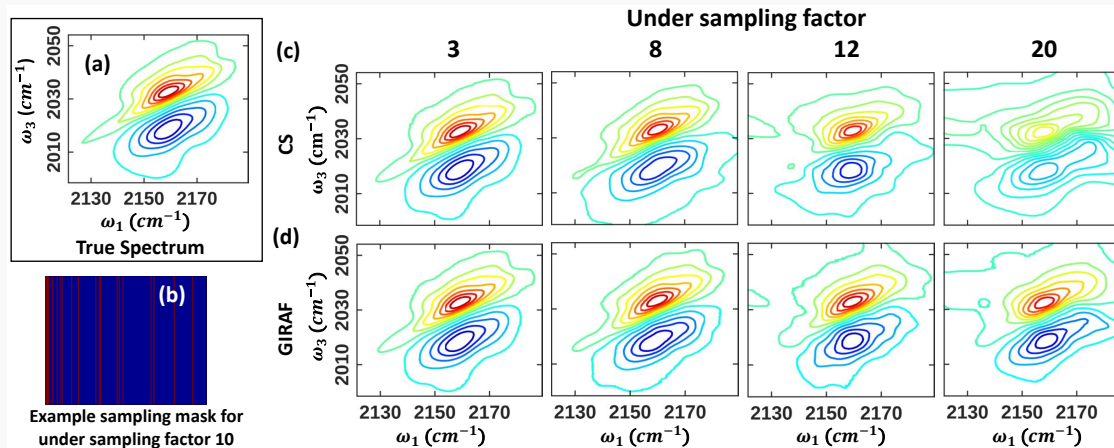
Infrared spectroscopy



1D IR spectroscopy



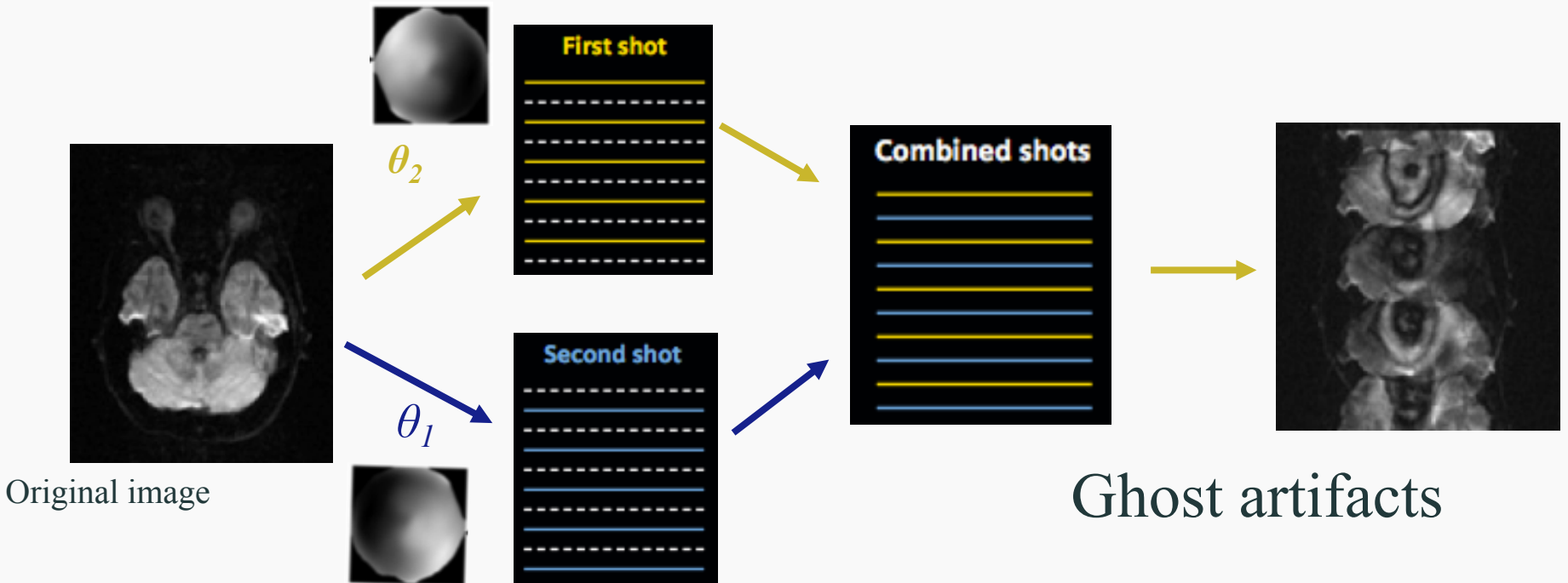
2D IR spectroscopy



Accelerated imaging using GIRAF

Correction of Nyquist ghosts in multishot MRI [MUSSELS]

Motion-induced inter-shot phase errors



Self calibration methods: Image domain

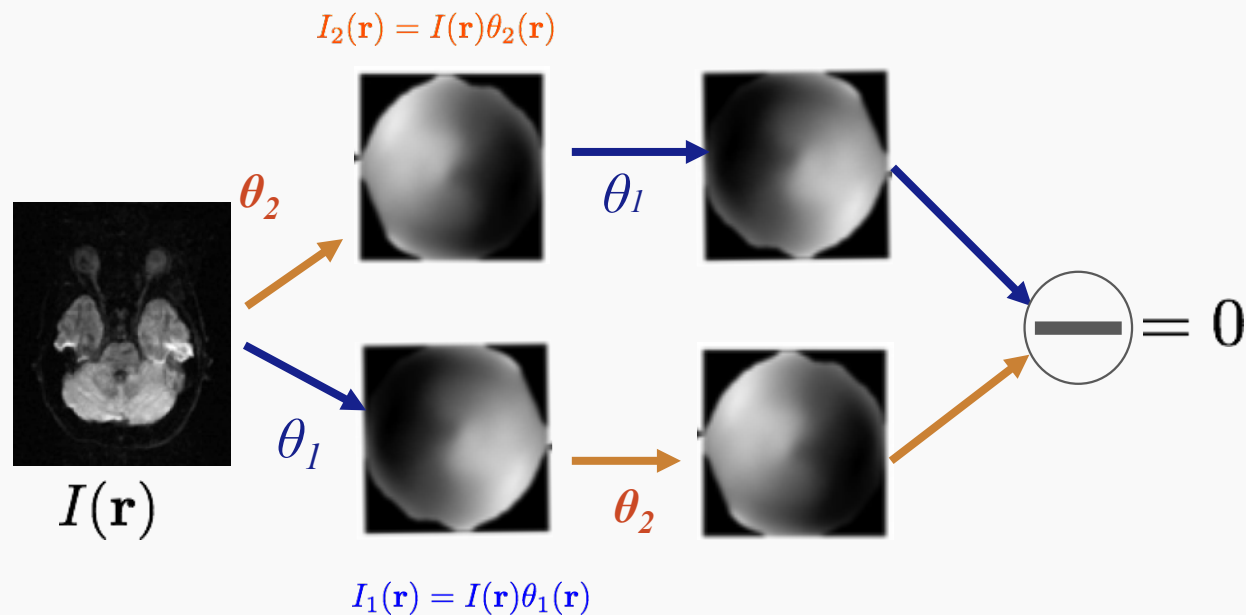


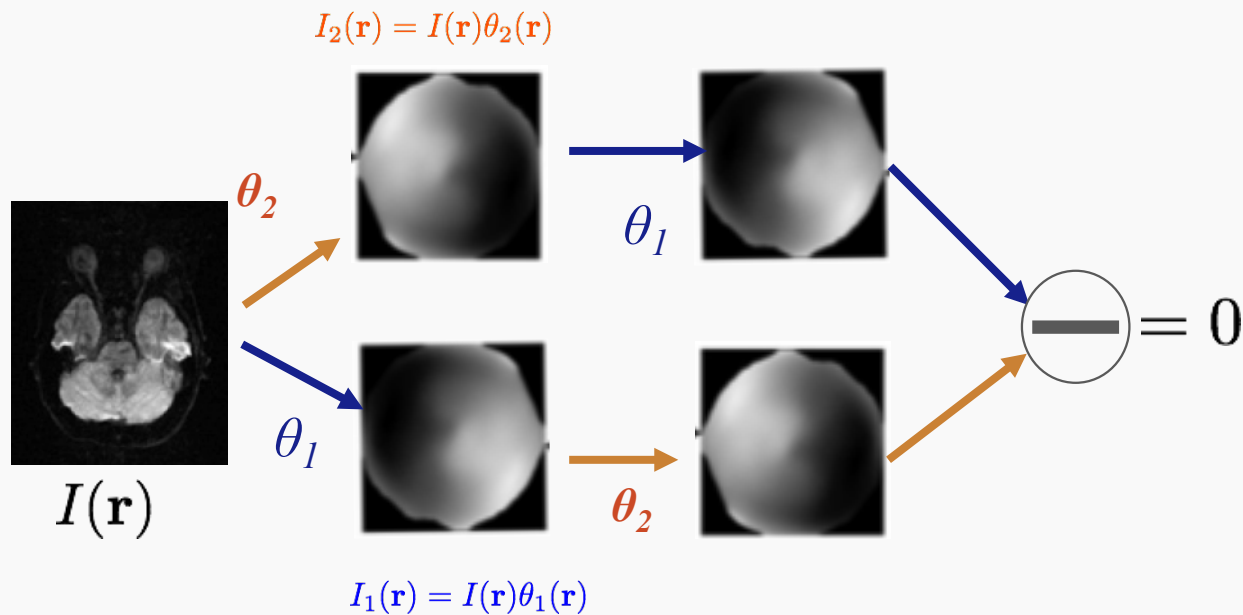
Image domain annihilation relation [Morrisson, Do & Jacob 2007]

$$I_2(\mathbf{r}) \cdot \theta_1(\mathbf{r}) - \hat{I}_1(\mathbf{r}) \cdot \hat{\theta}_2(\mathbf{r}) = 0$$

Model sensitivities as polynomials: EVD

Better than SOS estimates

Self calibration methods: Fourier domain



Fourier domain relation [Lustig 2012, Halдар 2014]

$$\hat{I}_2[\mathbf{k}] * \hat{\theta}_1[\mathbf{k}] - \hat{I}_1[\mathbf{k}] * \hat{\theta}_2[\mathbf{k}] = 0$$

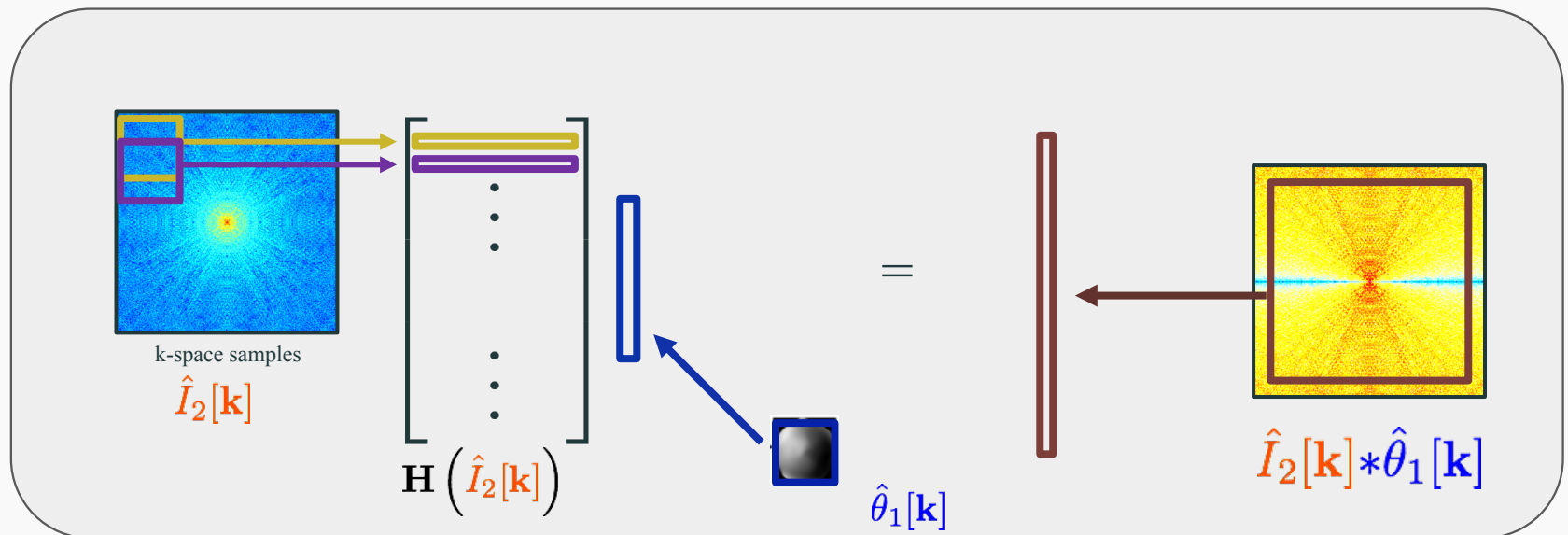
Phase: linear combination of exponentials \rightarrow FIR filter

Self calibration methods: matrix form

Fourier domain relation

$$\hat{I}_2[\mathbf{k}] * \hat{\theta}_1[\mathbf{k}] - \hat{I}_1[\mathbf{k}] * \hat{\theta}_2[\mathbf{k}] = 0$$

Convolution: matrix multiplication



Self calibration methods: Fourier domain

Fourier domain relation

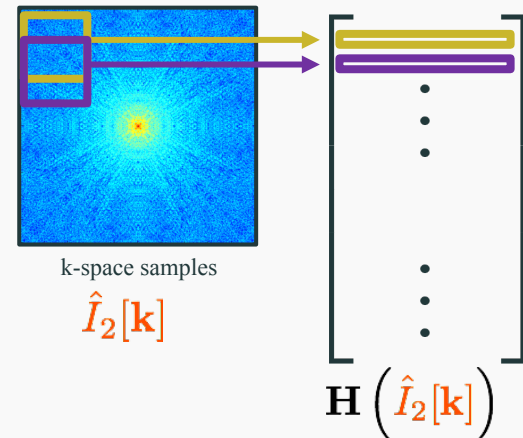
$$\hat{I}_2[\mathbf{k}] * \hat{\theta}_1[\mathbf{k}] - \hat{I}_1[\mathbf{k}] * \hat{\theta}_2[\mathbf{k}] = 0$$

Compact matrix representation

$$\underbrace{\left[\mathbf{H} \left(\hat{I}_2[\mathbf{k}] \right), \mathbf{H} \left(\hat{I}_1[\mathbf{k}] \right) \right]}_{\mathbf{Q}(I_1, I_2)} \begin{bmatrix} \hat{\theta}_1[\mathbf{k}] \\ -\hat{\theta}_2[\mathbf{k}] \end{bmatrix} = 0$$

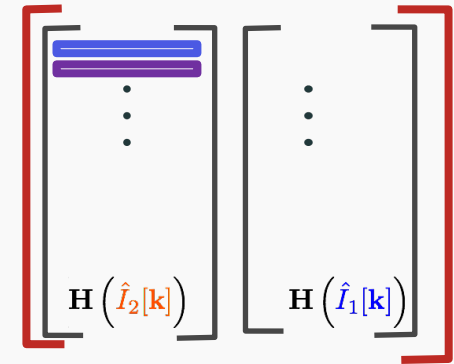
N shots: $\binom{N}{2}$ null space vectors

Q is low-rank & structured

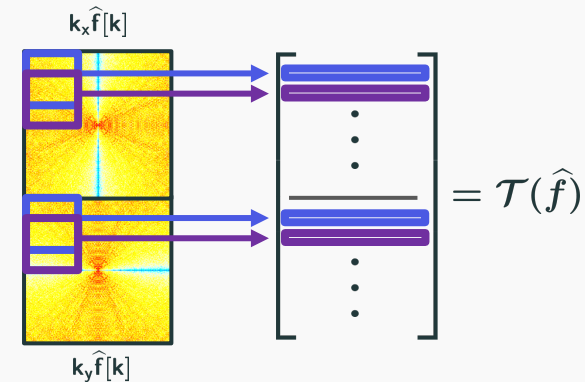


Smoothness regularized multishot MRI

Multi-shot recovery



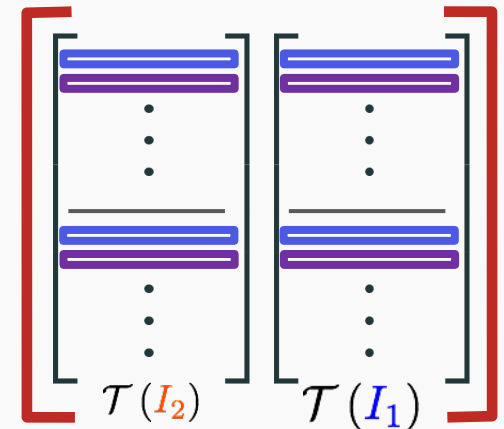
Smoothness regularization



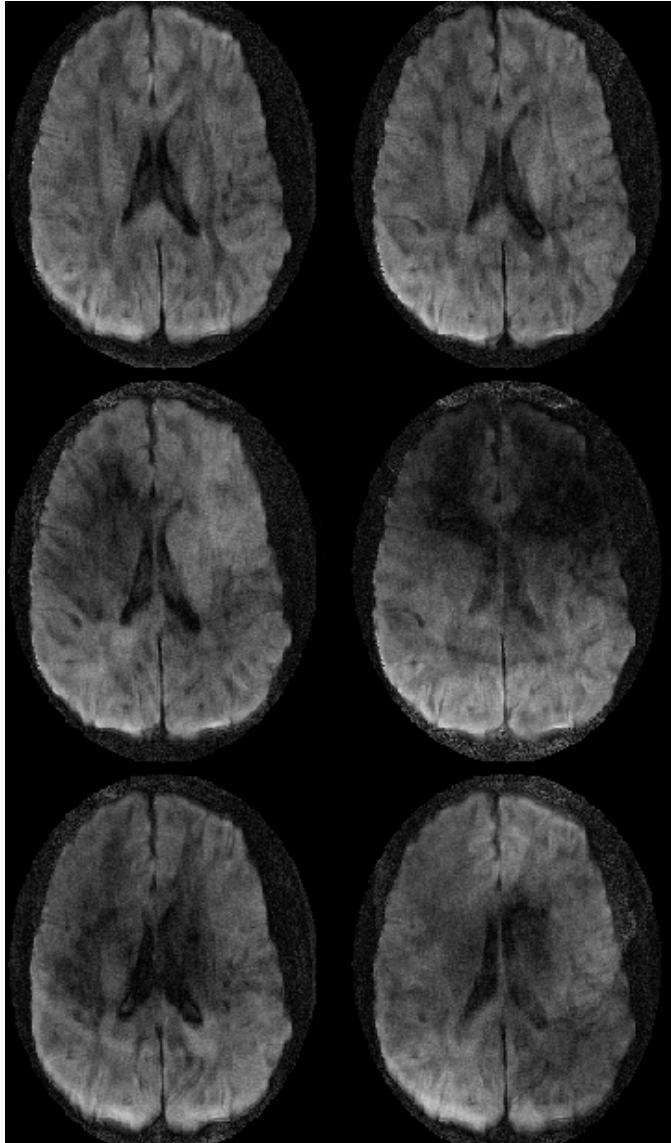
Combine the matrix liftings

Structured low-rank recovery

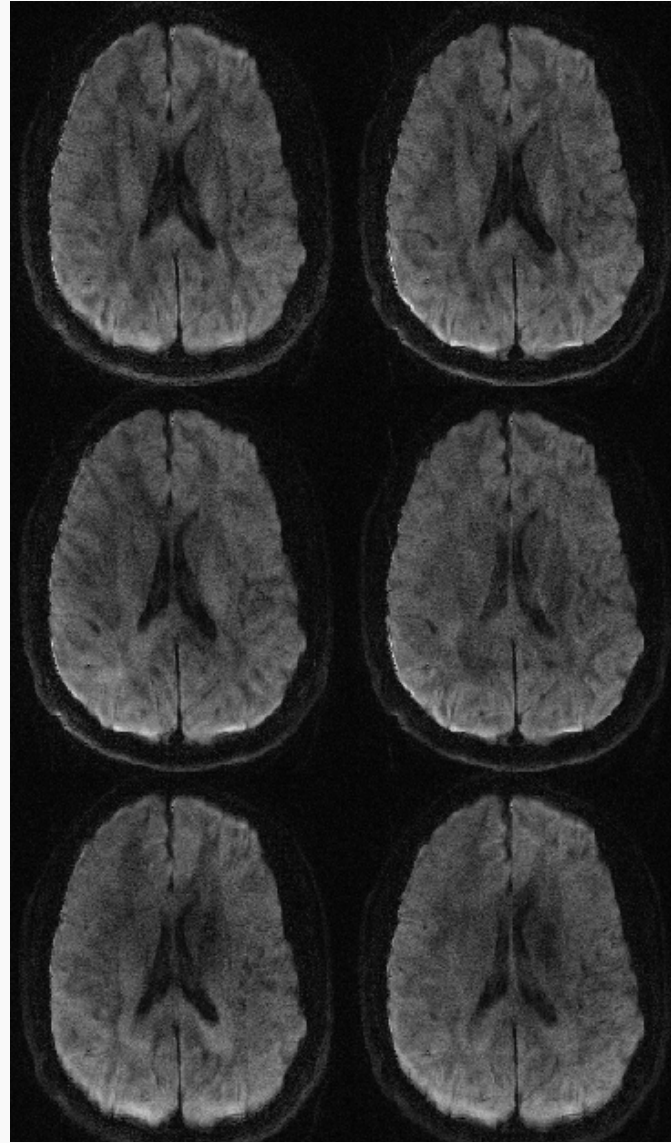
$$\|\mathcal{A}(\mathbf{I}_1, \mathbf{I}_2) - \mathbf{b}\|^2 + \lambda \|\mathcal{G}(\mathbf{I}_1, \mathbf{I}_2)\|_*$$



Structured low-rank recovery: MUSSELS



MUSE



MUSSELS

Comparison with MUSE (state of the art)

Average #1

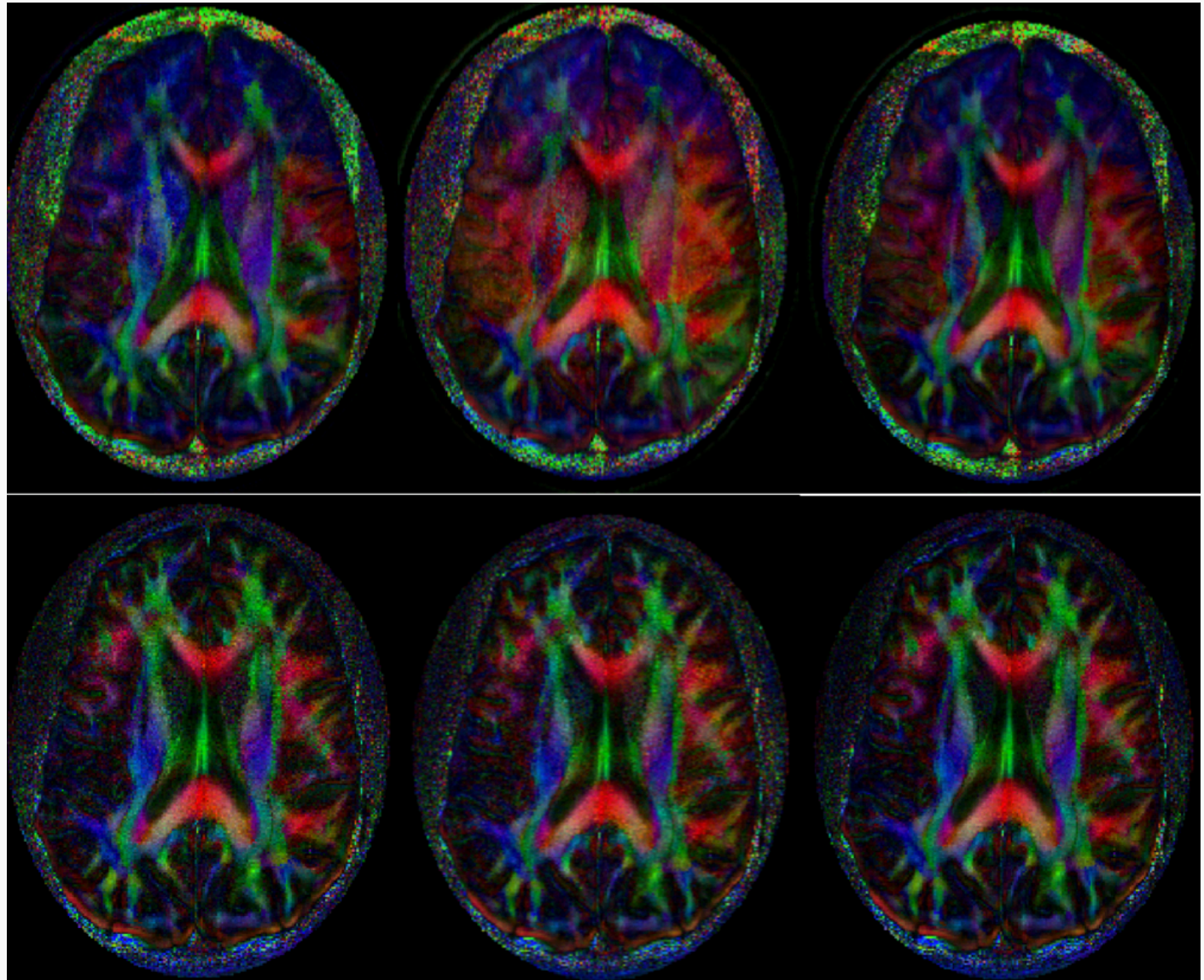
Average #2

Combined

MUSE

VS

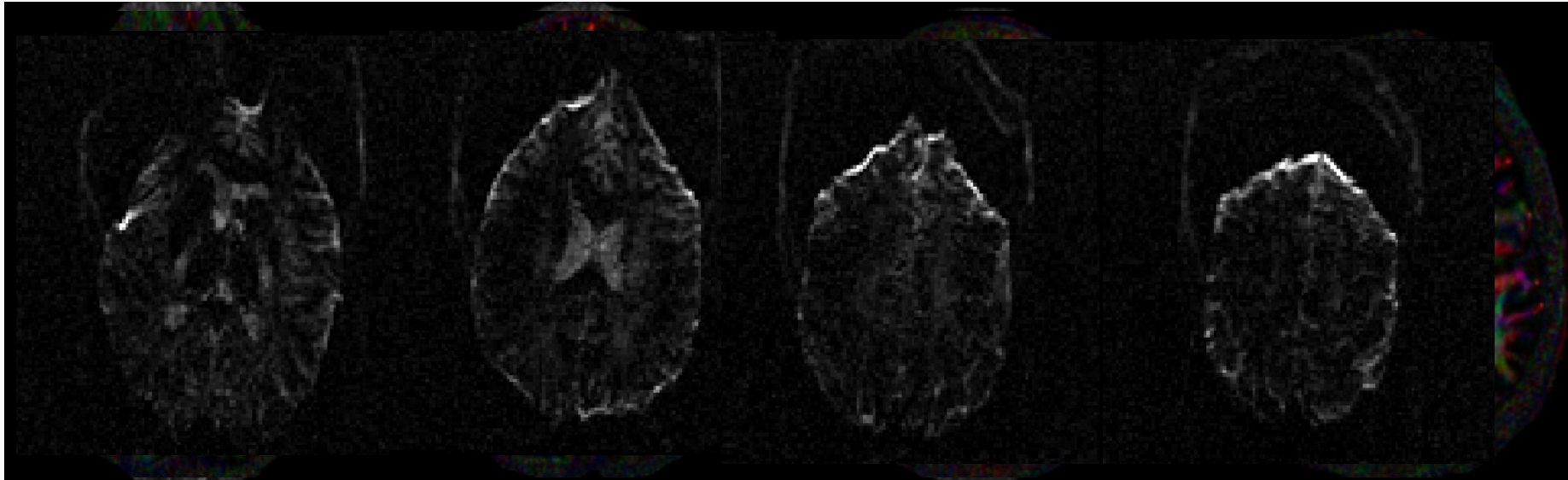
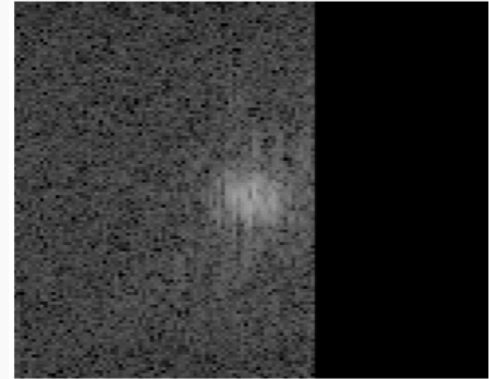
MUSSELS



Odd even shifts & partial Fourier in EPI

Multishot & partial Fourier

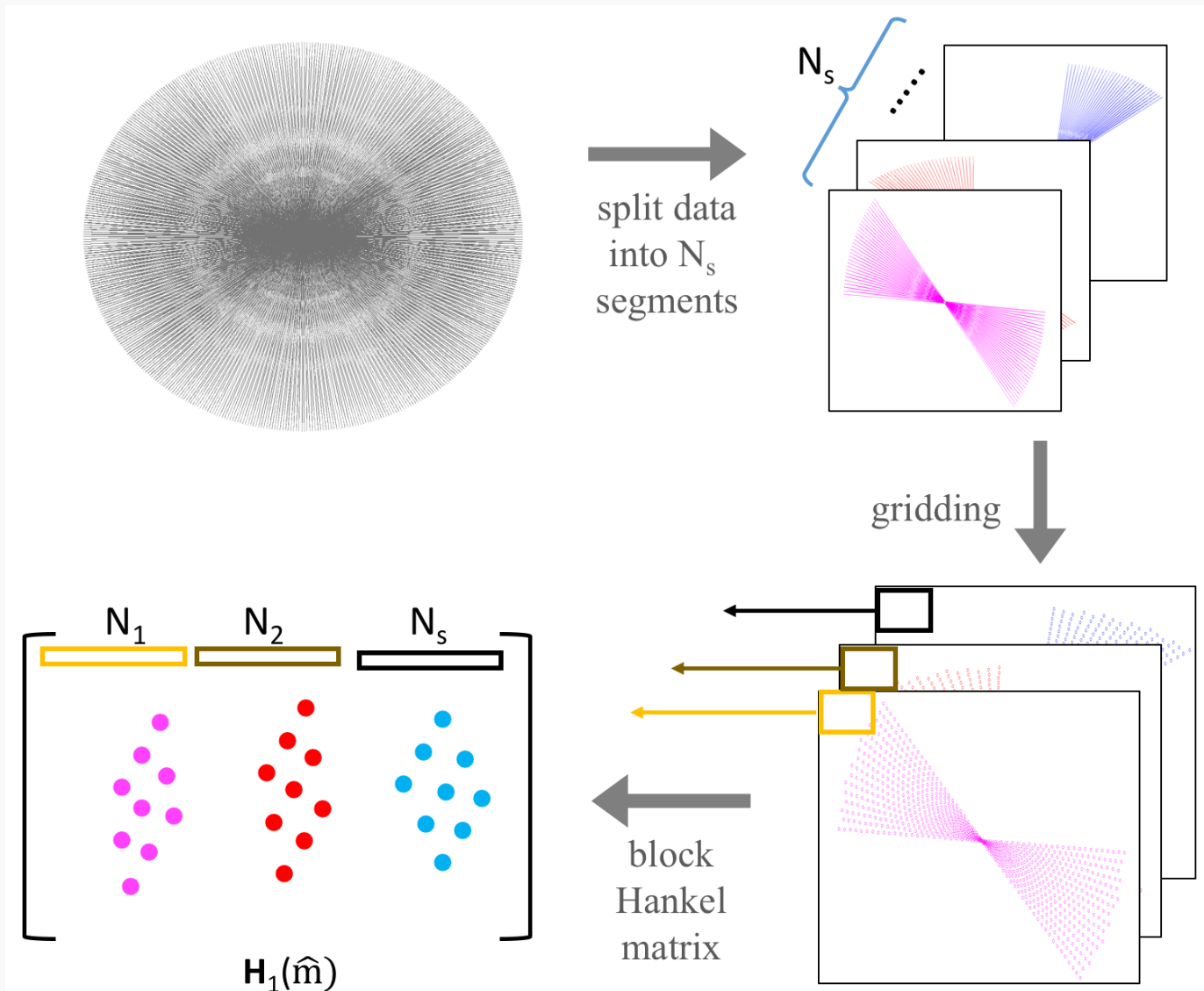
Improved SNR & reduced distortion



0.8 x 0.8 x 2mm; 3 avgs; 25 directions; b=700

Mani & Jacob, Magnetic Resonance Medicine, in press, EMBC 2016

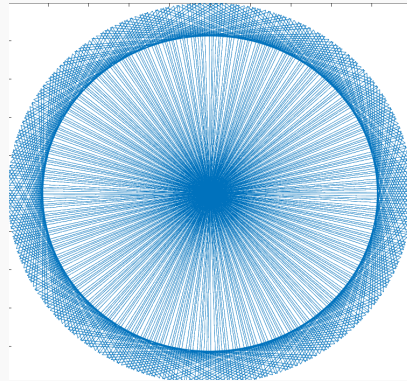
Radial trajectory correction



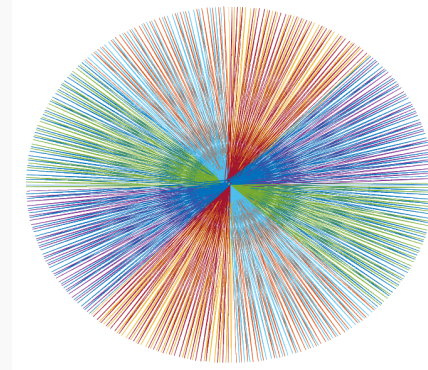
Results: MUSSELS based radial traj. correction

➤ Radial data:

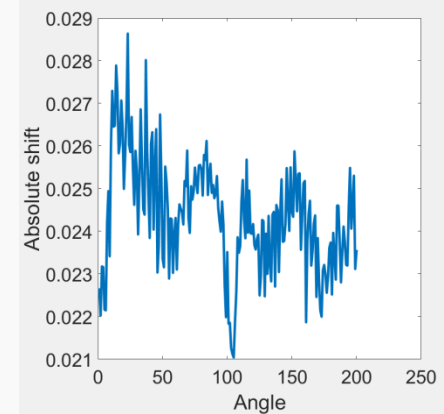
- 3T GE scanner
- 256 spokes
- 154 points per spoke
- partial Fourier acq.
- 32 channels



Ideal Radial trajectory



The 8 segments

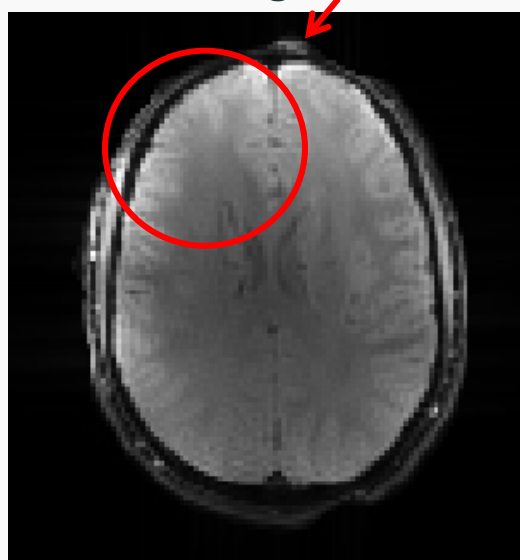


Plot of trajectory shift vs angle

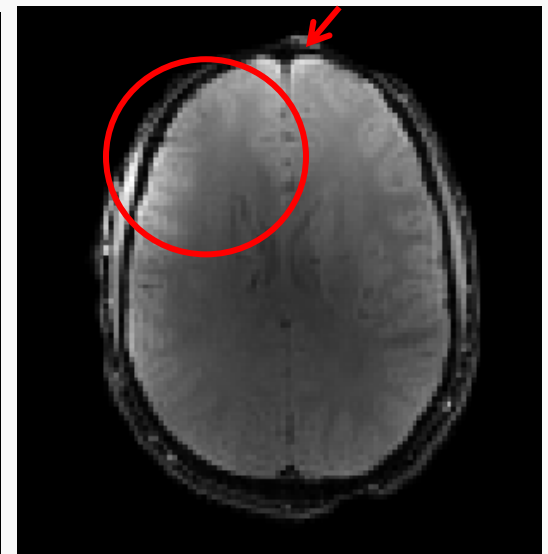
Recon using NUFFT



Recon using MUSSELS



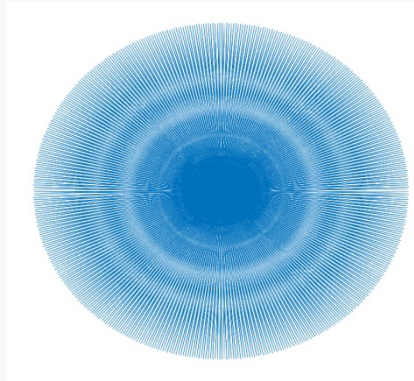
Recon using TrACR



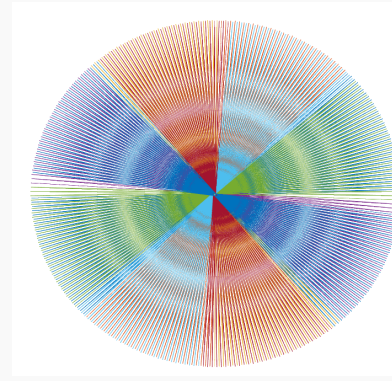
Results: MUSSELS based radial traj. correction

➤ Radial data:

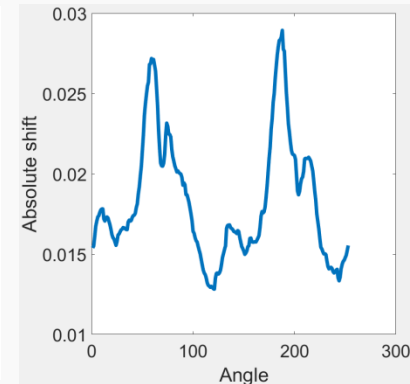
- 3T Siemens scanner
- 512 spokes
- 512 points per spoke
- 5 channels



Ideal Radial trajectory



The 8 segments



Plot of trajectory shift vs angle

Recon using NUFFT



Recon using MUSSELS



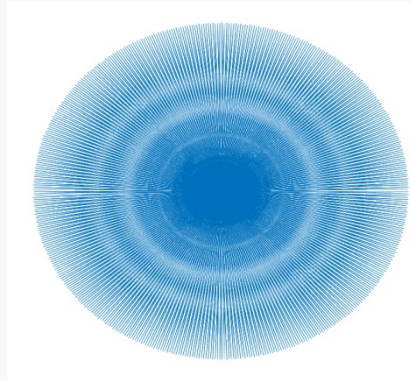
Recon using TrACR



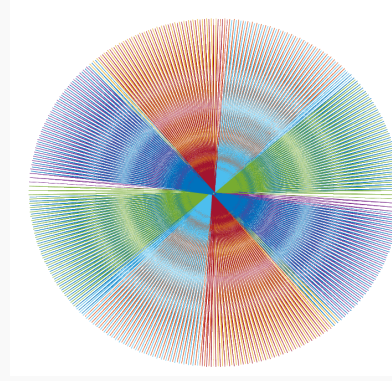
Results: MUSSELS based radial traj. correction

➤ Radial data:

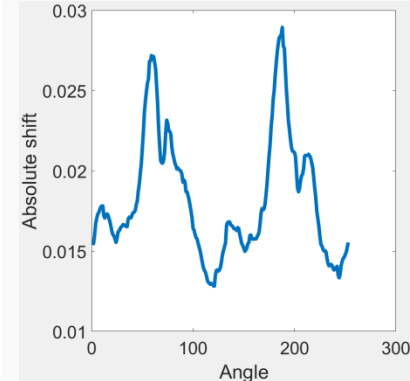
- 3T Siemens scanner
- 512 spokes
- 512 points per spoke
- 5 channels



Ideal Radial trajectory



The 8 segments



Plot of trajectory shift vs angle

Recon using NUFFT



Recon using MUSSELS



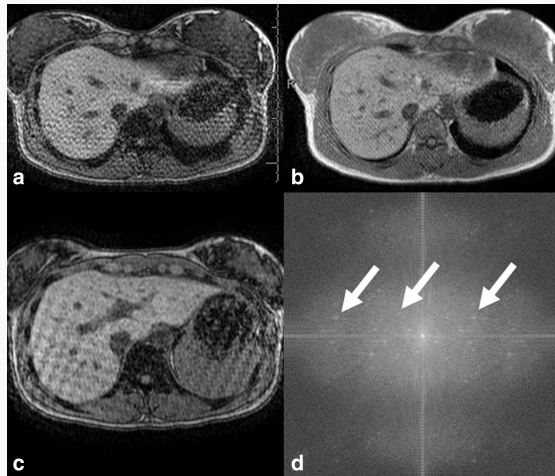
Recon using TrACR



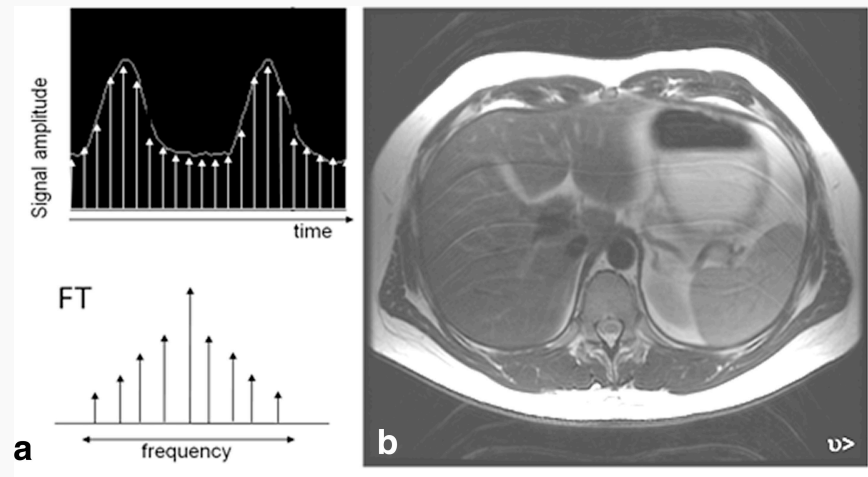
MR artifacts

- What is MR artifacts?

During acquisition, external interruptions (ex. fluctuation power supply of gradient, motion of object, etc.) distort signals.

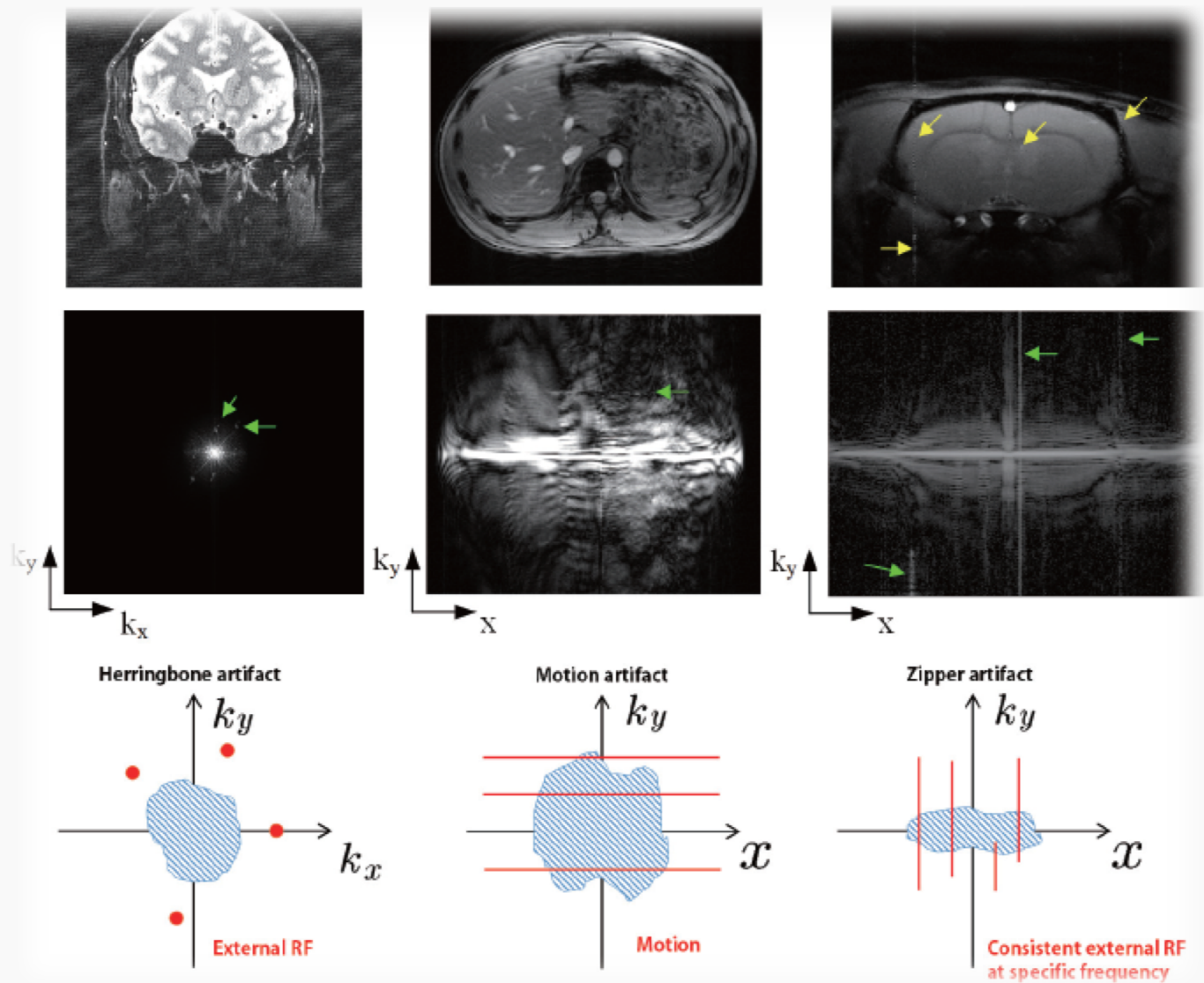


Spike noise



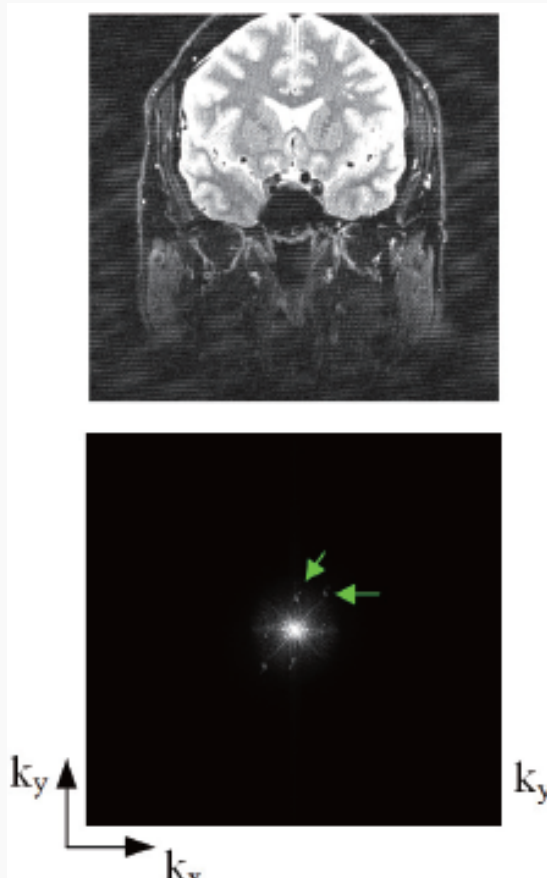
Respiratory motion

Motivation

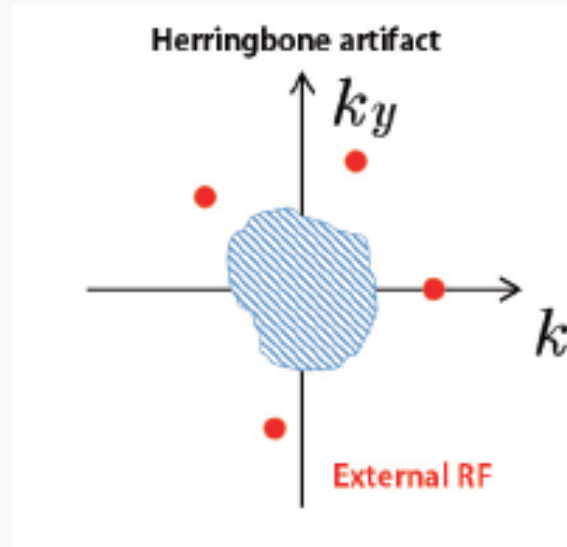


Motivations: MR artifacts as sparse outliers

- ✓ Herringbone (spikes 2-D k-space)



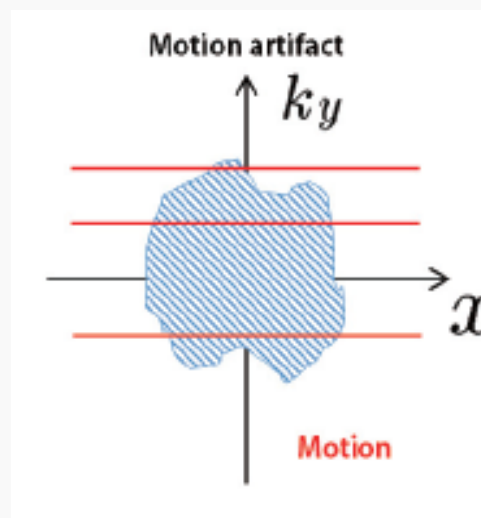
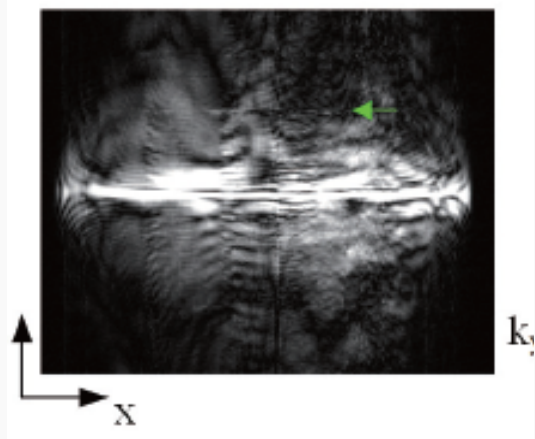
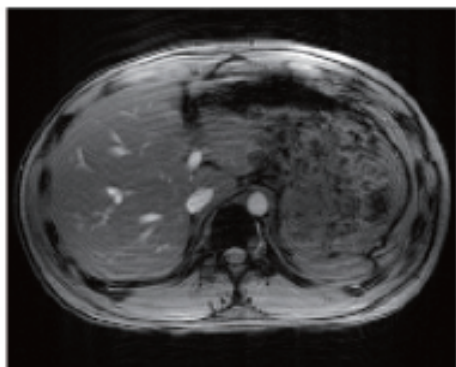
$$\widetilde{M}(k_x, k_y) = \widehat{M}(k_x, k_y) + \underbrace{\sum_{j=1}^S \epsilon_j \delta[k_x - k_{x_j}, k_y - k_{y_j}]}_{\text{sparse outliers}},$$



Motivations: MR artifacts as sparse outliers

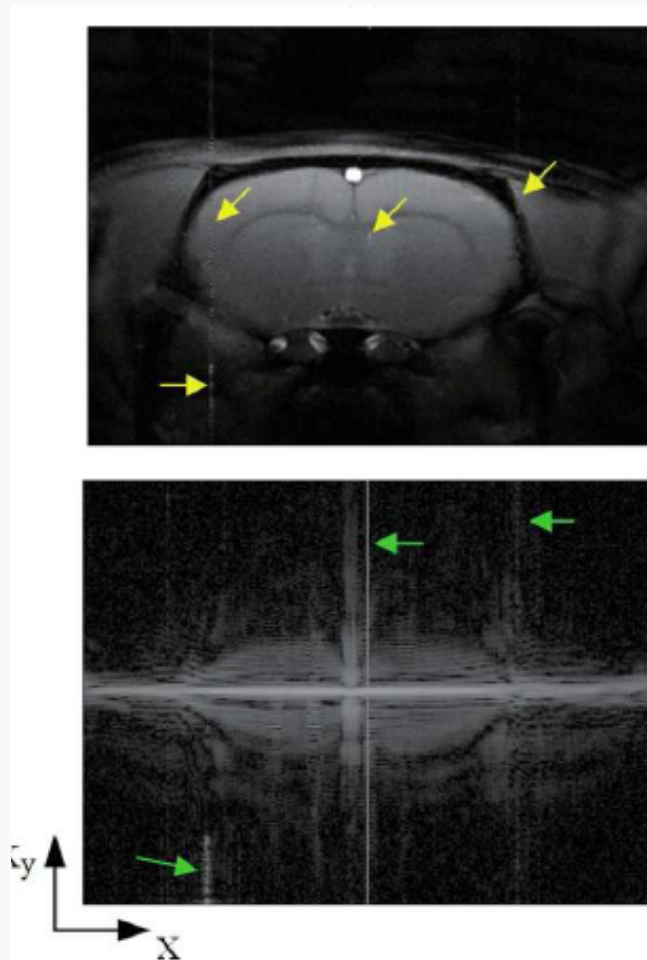
- ✓ Motion artifact (spikes 1-D k-space parallel to readout)

$$\begin{aligned}\widetilde{M}(x, k_y) &= \begin{cases} \widehat{M}(x, k_y) \exp(j2\pi k_y d(k_y)), & \text{when } k_y \in \{k_{y1}, \dots, k_{yS}\} \\ \widehat{M}(x, k_y), & \text{otherwise} \end{cases} \\ &= \underbrace{\widehat{M}(x, k_y) + \sum_{j=1}^S \widehat{M}(x, k_y) (\exp(j2\pi k_y d(k_y)) - 1) \delta[k_y - k_{y_j}]}_{\text{sparse outliers}}\end{aligned}$$

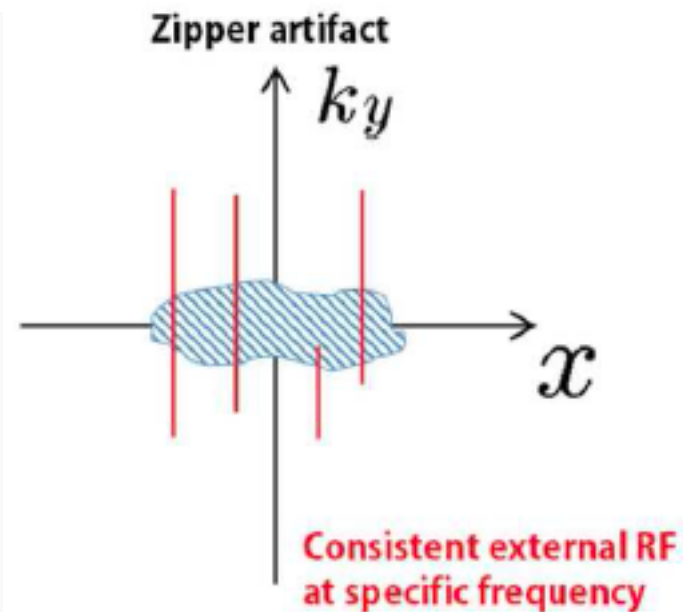


Motivations: MR artifacts as **sparse** outliers

Zipper artifact (spikes 1-D k-space perpendicular to readout)

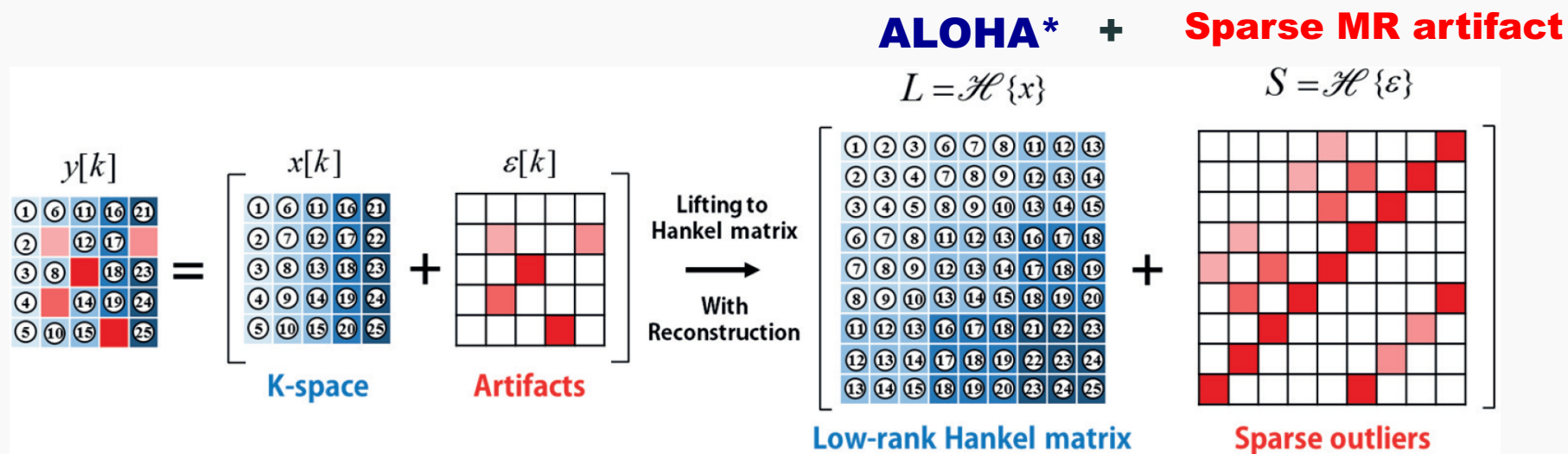


$$\widetilde{M}(x, k_y) = \widehat{M}(x, k_y) + \underbrace{\sum_{j=1}^S \epsilon_j \delta[x - x_j]}_{\text{sparse outliers}},$$



Key Observation : Sparse outliers

* Sparse outlier is still sparse in weighted Hankel matrix



- **ALOHA: Annihilating filter based Low rank Hankel matrix Approach**

[†] E. Candes, et. al, JACM (2011), R. Otazo, et. al, MRM (2015)

^{*} K.H. Jin, et. al, IEEE TIP (2015), K.H. Jin, et. al, arXiv (2015), J. C. Ye, et. al, arXiv (2015), J. Lee, et. al, MRM (2016), D. Lee, et. al, MRM (2016)

RPCA for weighted Hankel matrix

$$\begin{aligned} & \min_{\mathbf{M}, \mathbf{E}} \quad \underbrace{\|\mathcal{H}\{\mathbf{M}\}\|_*}_{\text{signal}} + \underbrace{\tau \|\mathbf{E}\|_1}_{\text{Sparse outlier}} \\ & \text{subject to} \quad \mathbf{P}_{\Omega} \left(\underbrace{\widehat{\mathbf{W}}}_{\text{K-space weighting}} \odot \widehat{\mathbf{L}} \right) = \mathbf{P}_{\Omega} (\mathbf{M} + \mathbf{E}), \end{aligned}$$

- ✓ *Extension of ALOHA for decomposition of sparse outliers (E) out of mixed signal**
- ✓ *Can be addressed ADMM[†]*
- ✓ *K-space weighting*

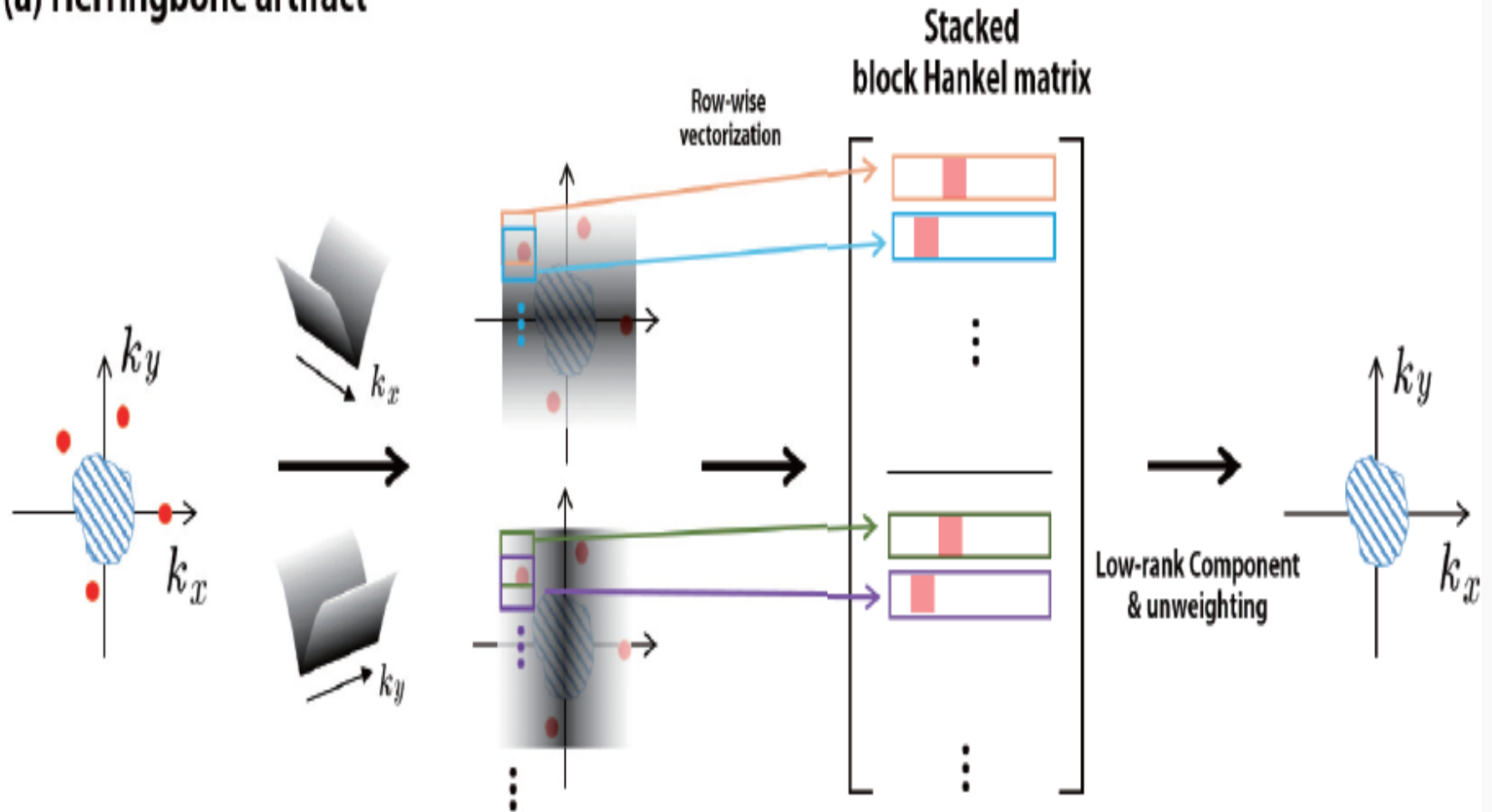
* E. Candes, et. al, JACM (2011), R. Otazo, et. al, MRM (2015)

[†] S. Boyd, et. al., Foundations and Trends in Machine Learning (2011)

[‡] Z. Wan, et. al., Mathematical Programming Computation (2012)

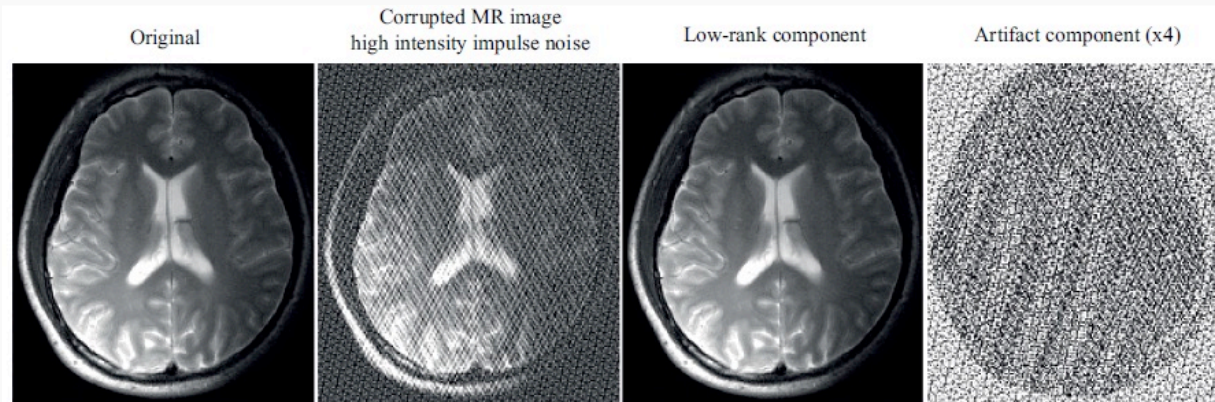
Algorithm Flowchart

(a) Herringbone artifact

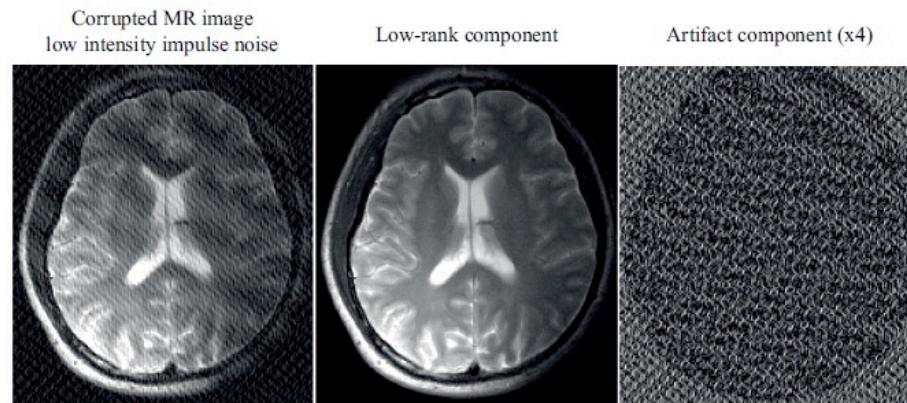


Retrospective results

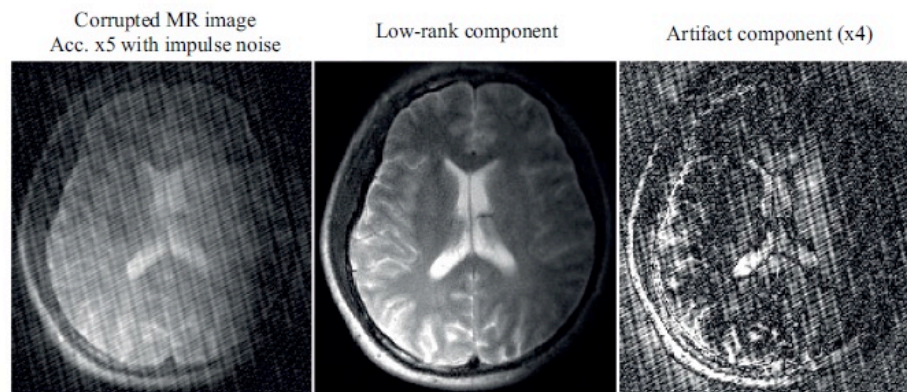
High intensity
Spike noise



Low intensity
Spike noise
(low frequency region)

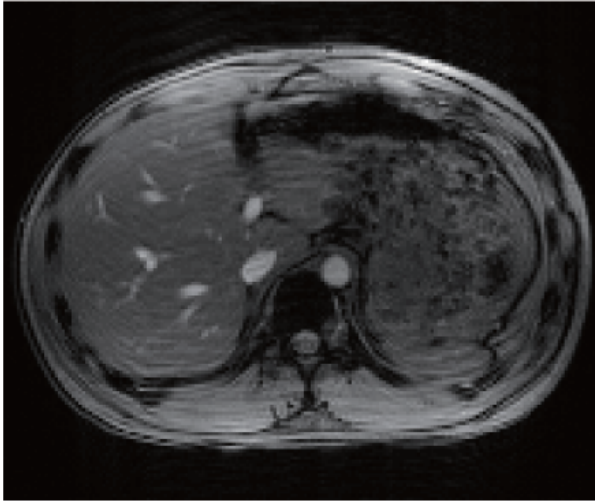


Spike noise
with down sampling (x5)

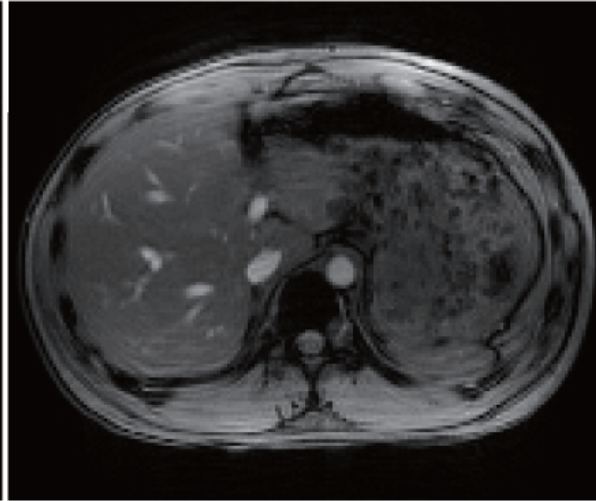


In Vivo Motion artifact

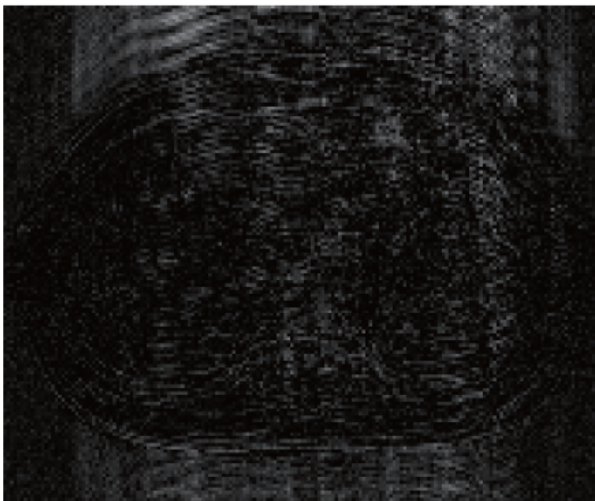
Corrupted image
motion artifact



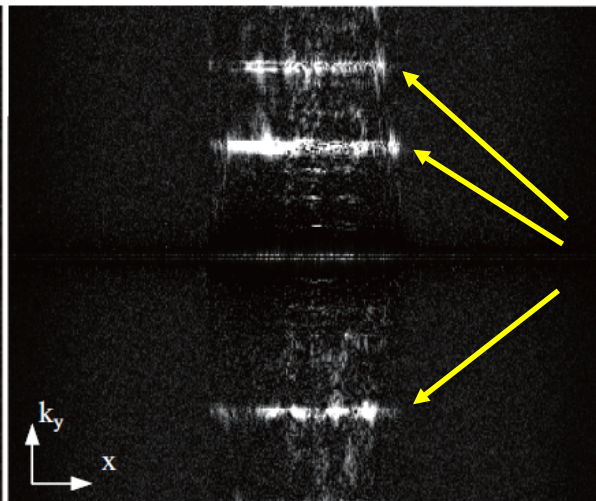
Low-rank component



Artifact component



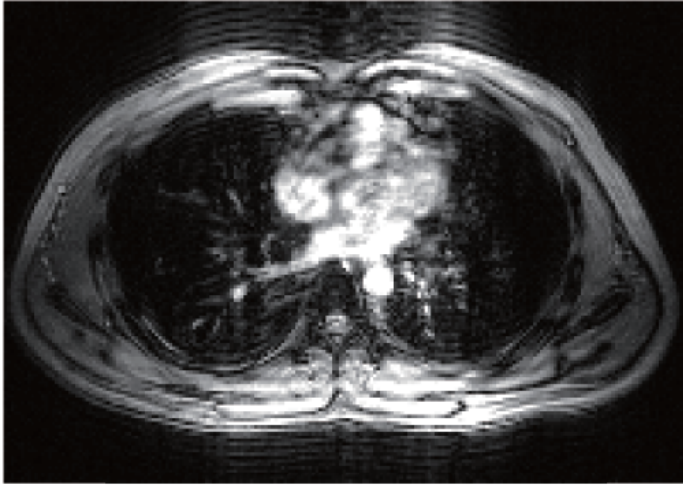
Spectrum of artifact



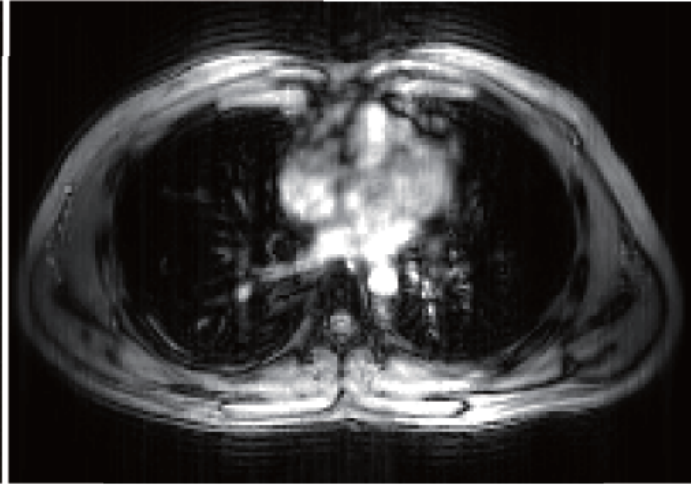
sudden motion
(3 times)

Cardiac Motion artifact

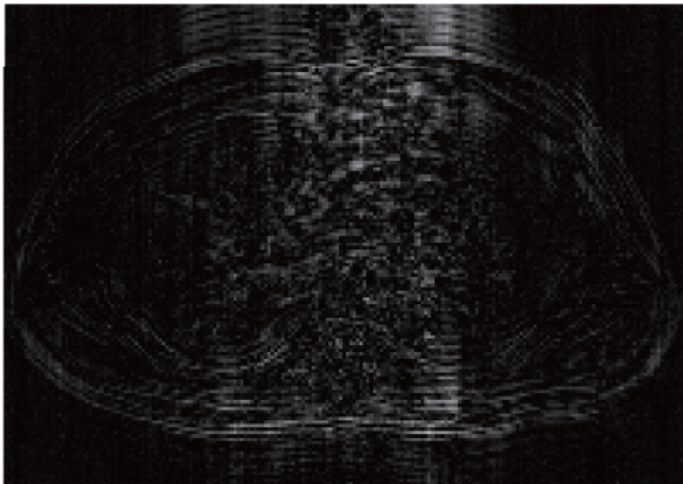
Corrupted image
motion artifact



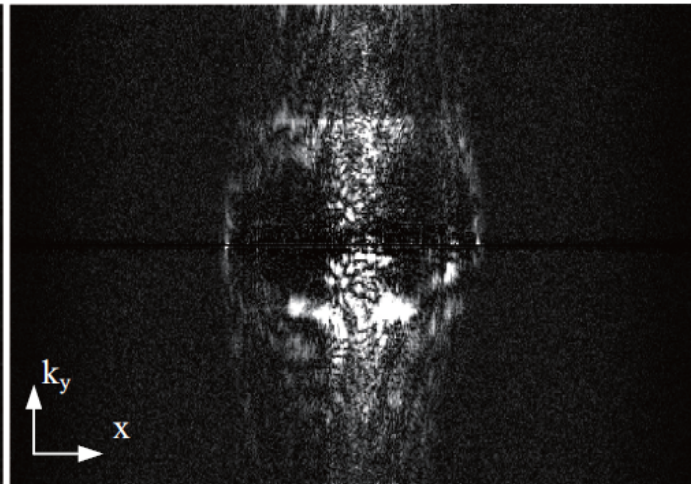
Low-rank component



Artifact component

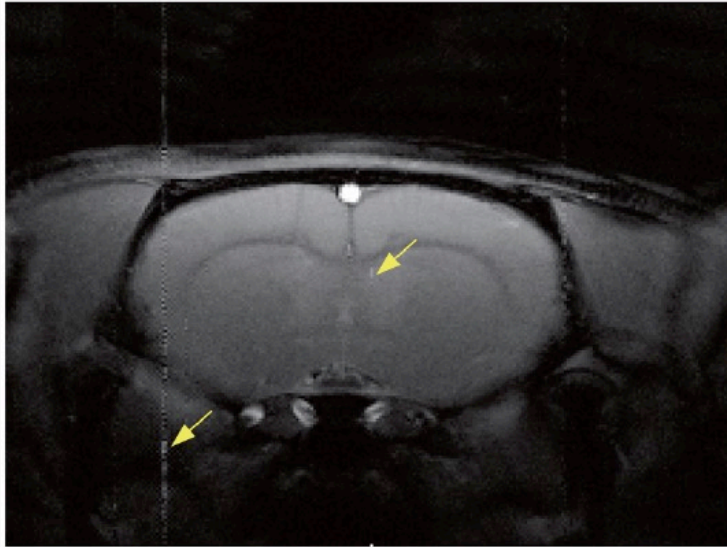


Spectrum of artifact

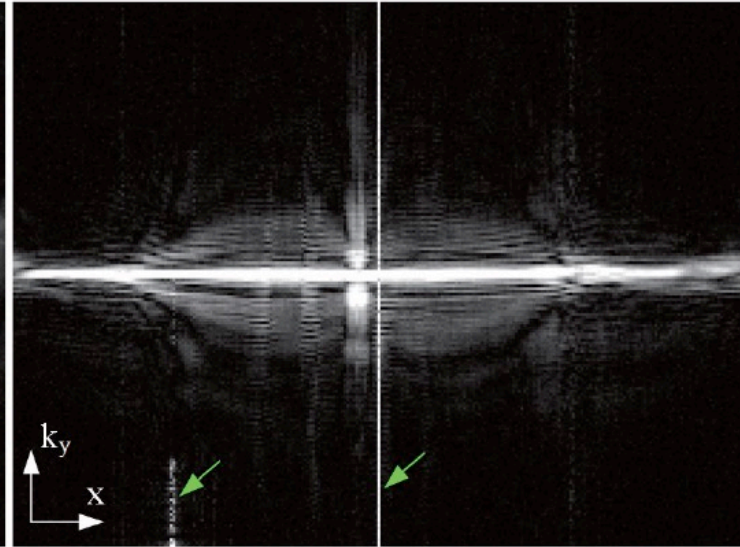


Zipper artifact

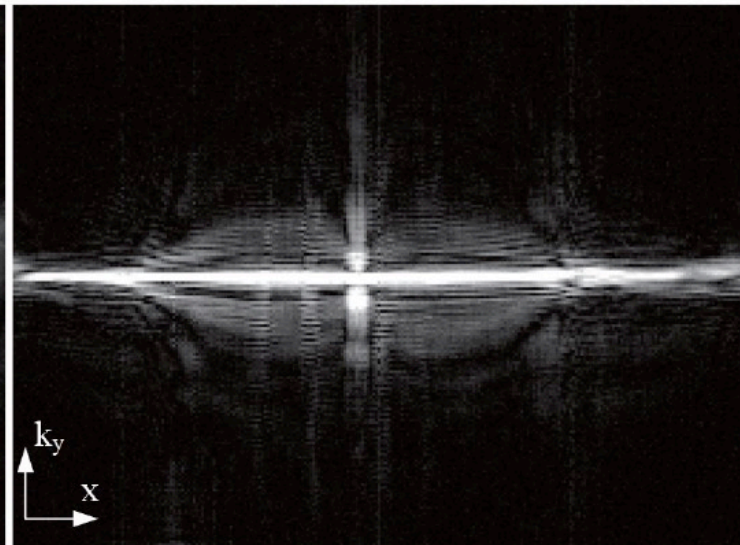
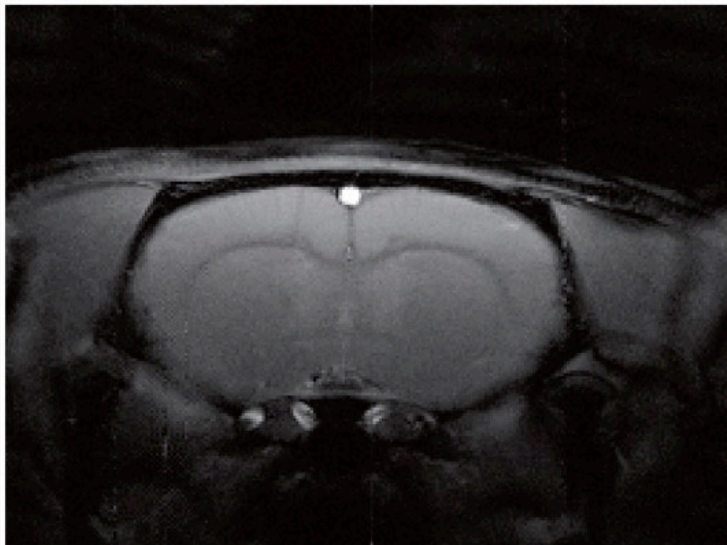
Corrupted image
zipper artifact



k_y - x

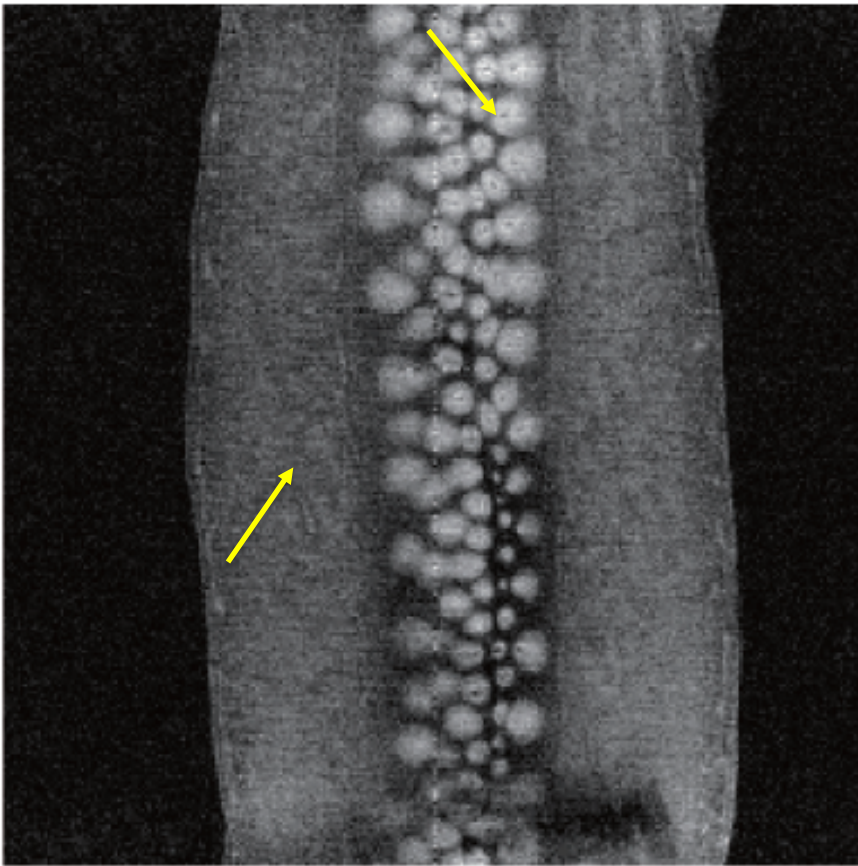


Low-rank component

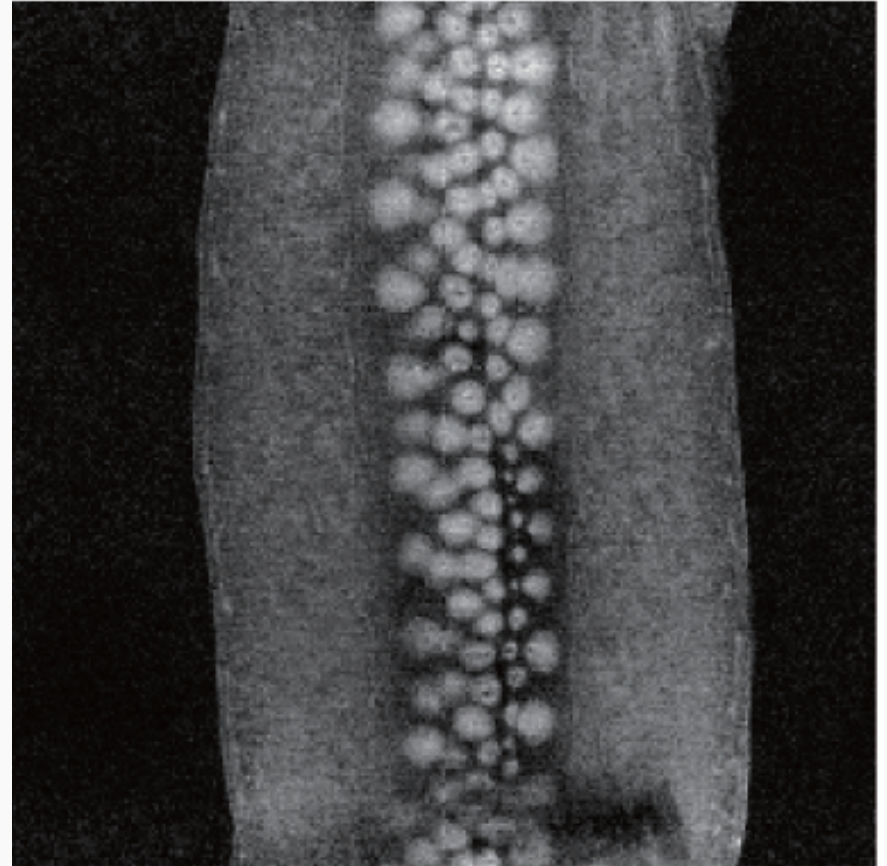


2-D herringbone (in-vivo)

before

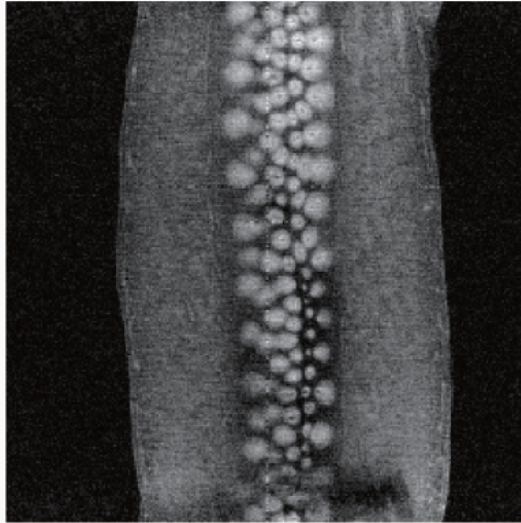


after

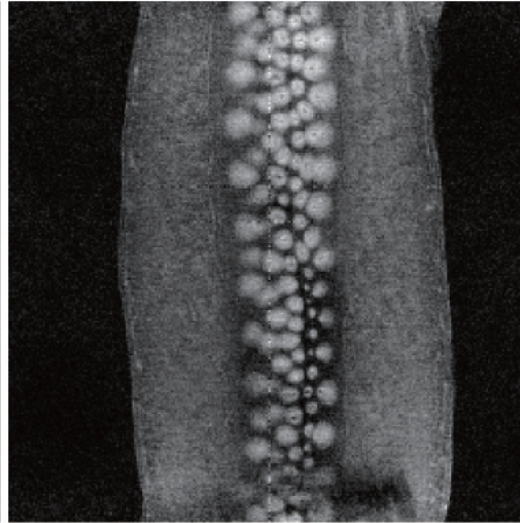


2-D herringbone (in-vivo)

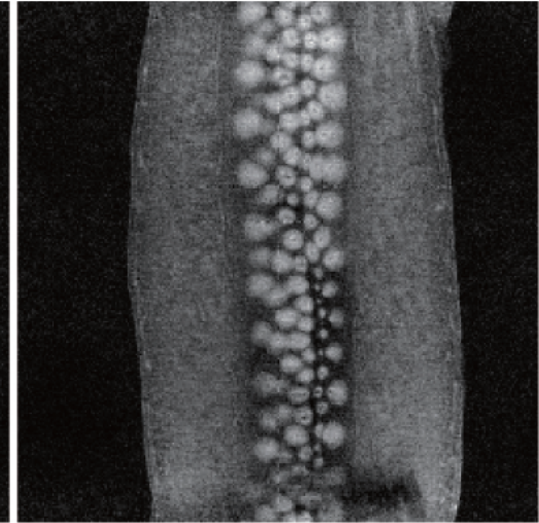
Corrupted MR image



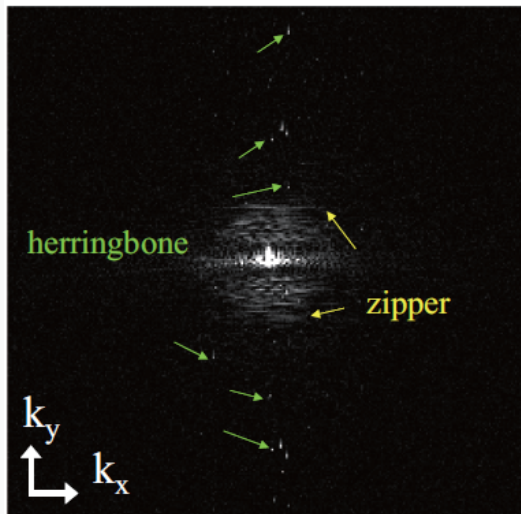
Intermediate recon. after
herringbone artifact removal



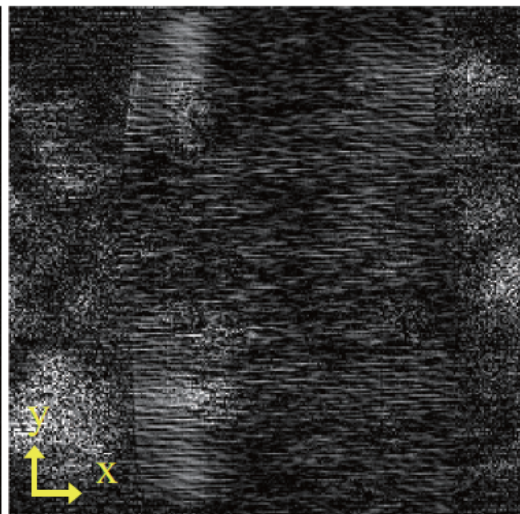
Final recon. after
Herringbone + zipper artifacts removal



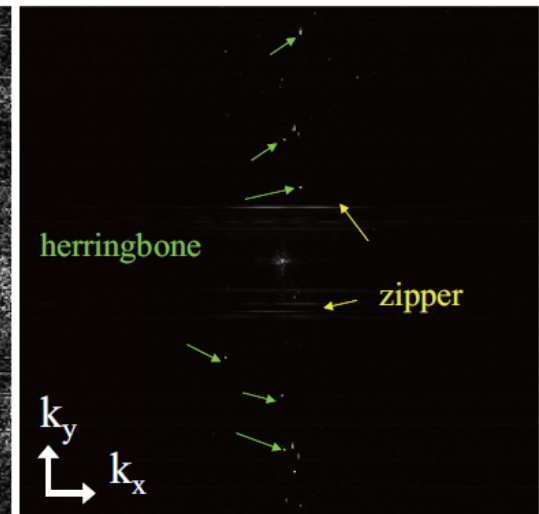
Spectrum of corrupted image



Herringbone image (x25)

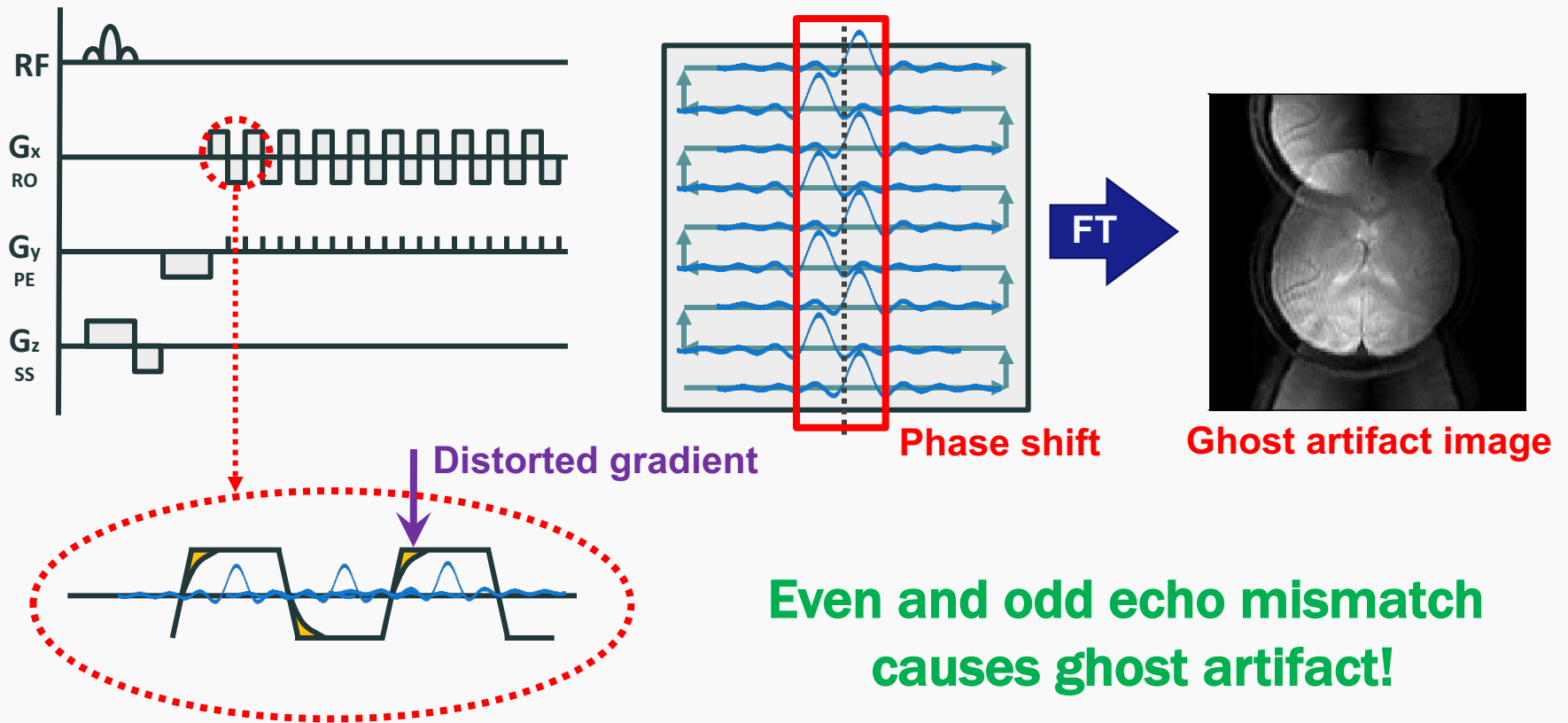


Spectrum of residual image



EPI Ghost artifact

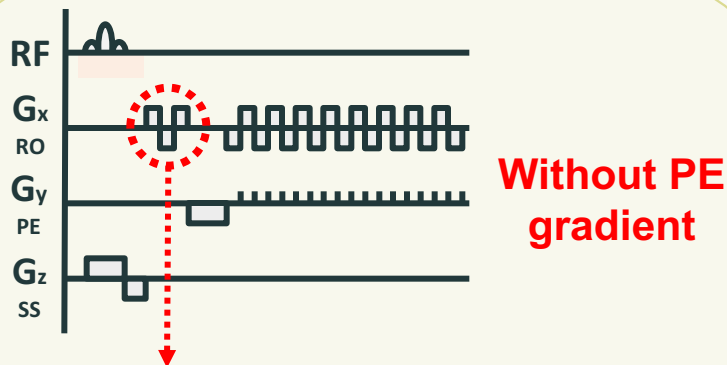
In EPI, Gradient is distorted by eddy currents and this causes phase shift



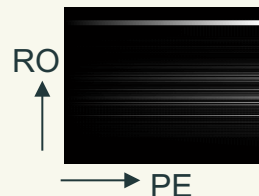
Conventional correction

- Navigator : pre-scan or reference scan

Navigator-based



Calculate **difference** of phase
between 1st -2nd line, 2nd -3rd line

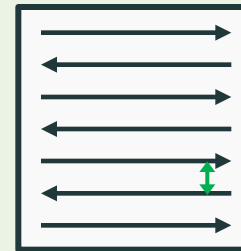


**Make phase
difference map**

only possible to *linear phase correction*

Navigator-free

- Pulse sequence compensation¹⁾
- Without any modification²⁾
 - Using Parallel Imaging Information
 - others



Calculate
Phase disparity
from EPI data itself

lower performance compared to
the reference-based approaches

1) Xiang QS et al., MRM, 2007
Poser BA et al., MRM, 2013

2) Zhang et al., MRM, 2004
Kim YC et al., JMIR, 2007

EPI model

EPI data can be expressed as

N : Total # of echoes
n : Index of each line
x : Read-out
y : Phase-encoding

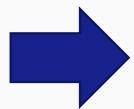
Echo time

$$S_n(k_x, k_y) = \int \int m(x, y) e^{j2\pi [\Delta f(x, y) ((TE + (n - N/2) ESP) + (-1)^n (\frac{k_x}{\gamma G_x})) + k_x x + k_y y]} dx dy$$

Image intensity

Frequency offset

Echo spacing (time between each echo)



$$S_{n,+}(k_x, k_y) = \int \int m(x, y) e^{j2\pi [\Delta f(x, y) ((TE + (n - N/2) ESP) + (\frac{k_x}{\gamma G_x})) + k_x x + k_y y]} dx dy$$

Virtual k-space
(even signals)

$$= \int \int A e^{j2\pi \Delta f(x, y) \frac{k_x}{\gamma G_x}} \cdot e^{j2\pi (k_x x + k_y y)} dx dy$$

$$S_{n,-}(k_x, k_y) = \int \int m(x, y) e^{j2\pi [\Delta f(x, y) ((TE + (n - N/2) ESP) - (\frac{k_x}{\gamma G_x})) + k_x x + k_y y]} dx dy$$

Virtual k-space
(odd signals)

$$= \int \int A e^{-j2\pi \Delta f(x, y) \frac{k_x}{\gamma G_x}} \cdot e^{j2\pi (k_x x + k_y y)} dx dy$$

Different!

where $A = m(x, y) \exp(j2\pi [\Delta f(x, y) ((TE + (n - N/2) ESP))])$

Sparsity of difference

The ghost generating phase term can be changed into a sine term

$$\begin{aligned} S_{n,\Delta}(k_x, k_y) &= S_{n,+}(k_x, k_y) - S_{n,-}(k_x, k_y) \\ &= \int \int A(x, y) \left(e^{j2\pi\Delta f(x,y)\frac{k_x}{\gamma G_x}} - e^{-j2\pi\Delta f(x,y)\frac{k_x}{\gamma G_x}} \right) e^{j2\pi(k_x x + k_y y)} dx dy \\ &= \int \int A(x, y) 2j \sin \left(2\pi\Delta f(x, y) \frac{k_x}{\gamma G_x} \right) e^{j2\pi(k_x x + k_y y)} dx dy \end{aligned}$$



$$\sin \left(2\pi\Delta f(x, y) \frac{k_x}{\gamma G_x} \right) \simeq 2\pi\Delta f(x, y) \frac{k_x}{\gamma G_x}$$

$$\begin{aligned} S_{n,\Delta}(k_x, k_y) &\simeq j2\pi k_x \int \int \frac{2}{\gamma G_x} A(x, y) \Delta f(x, y) e^{j2\pi(k_x x + k_y y)} dx dy \\ &= \frac{2}{\gamma G_x} \mathcal{F} \left[\frac{\partial A(x, y) \Delta f(x, y)}{\partial x} \right] \text{ Sparse} \end{aligned}$$



How can we use this sparsity?

Sparsity of difference (Cont.)

$$S_{n,\Delta}(k_x, k_y) = \mathcal{F}(\textit{Sparse signal})$$

➡ **Hankel structure matrix constructed by $S_{n,\Delta}(k_x, k_y)$ is low-ranked**

$$\mathcal{H}(S_{n,\Delta})\mathbf{h} = (\mathcal{H}(S_{n,+}) - \mathcal{H}(S_{n,-}))\mathbf{h} = \mathbf{0}$$



$$\begin{bmatrix} \mathcal{H}(S_{n,+}) & \mathcal{H}(S_{n,-}) \end{bmatrix} \begin{bmatrix} \mathbf{h} \\ -\mathbf{h} \end{bmatrix} = \mathbf{0}$$

**Low rank structured matrix
completion algorithm**

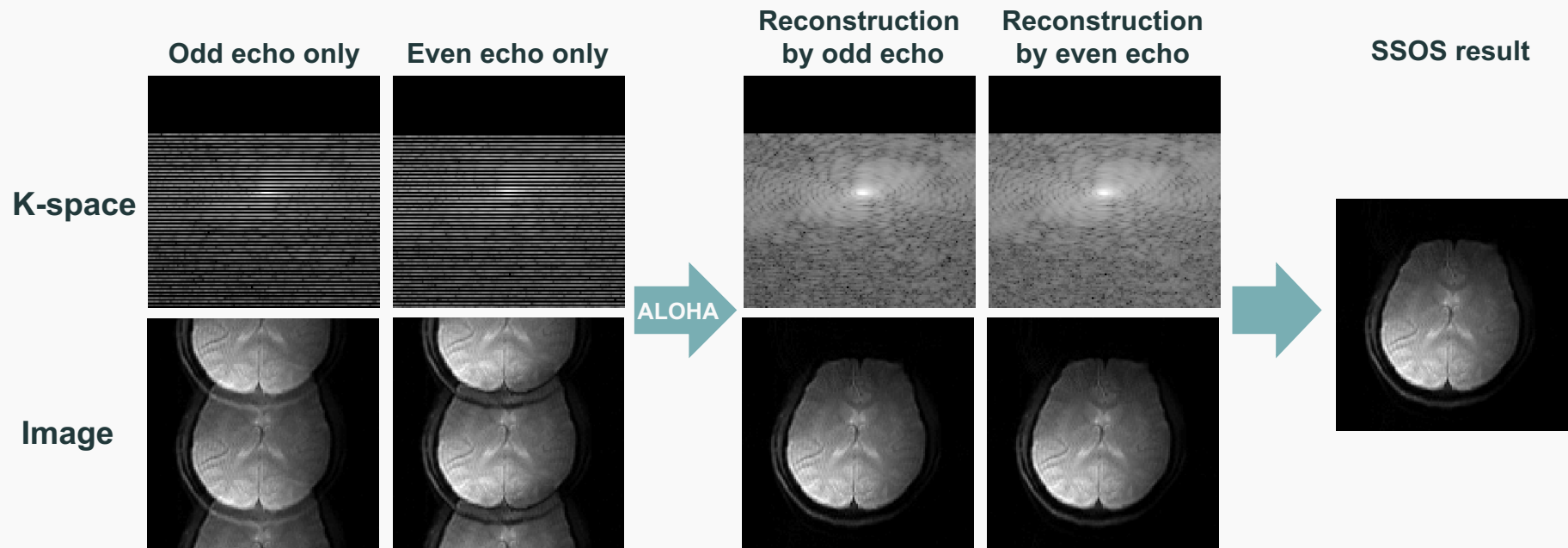
**EPI ghost correction
Problem**



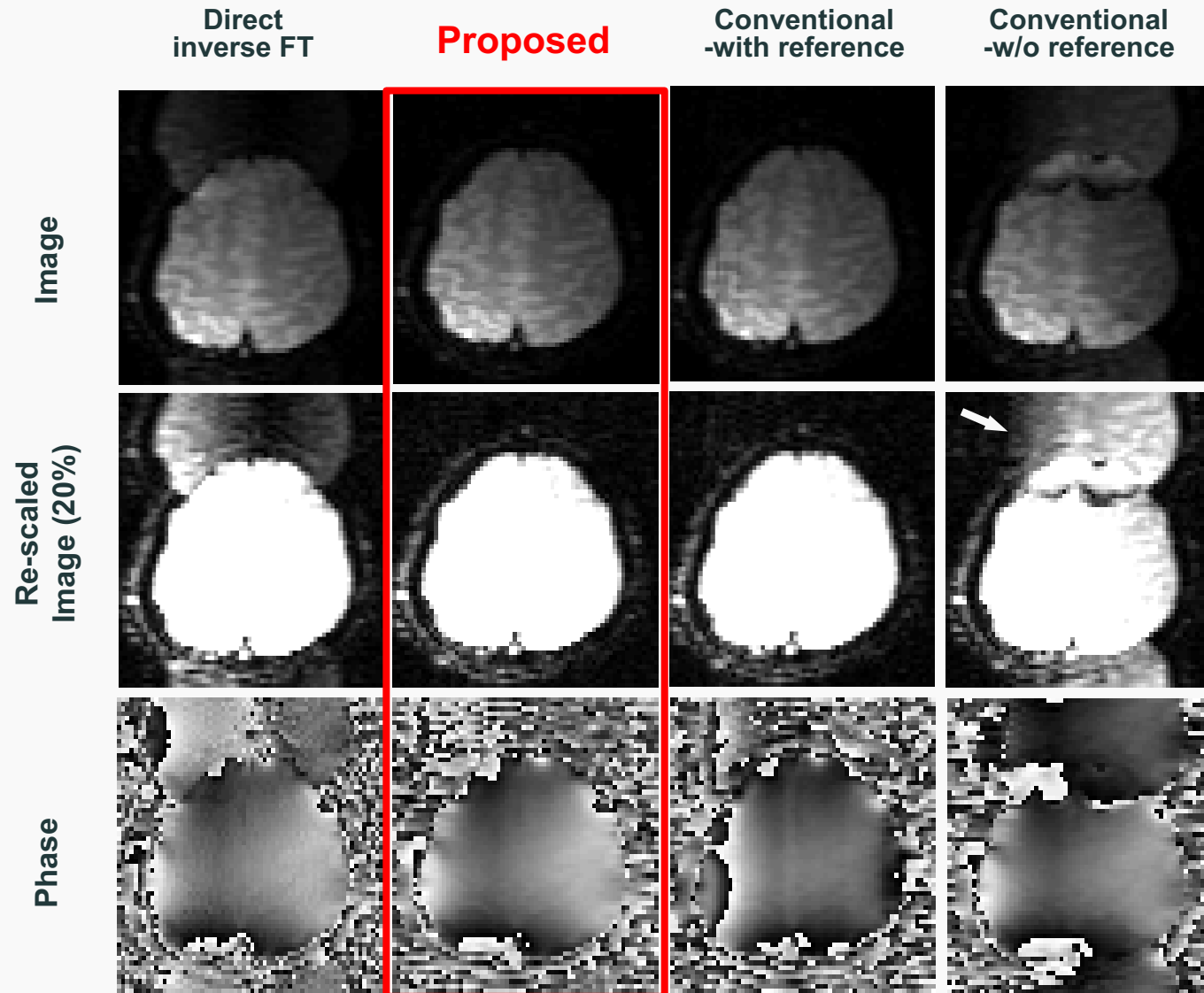
**k-space interpolation Problem
using low rank structure**

Reconstruction flow

- SE-EPI in-vivo data, 128x128 matrix size, 6/8 partial Fourier



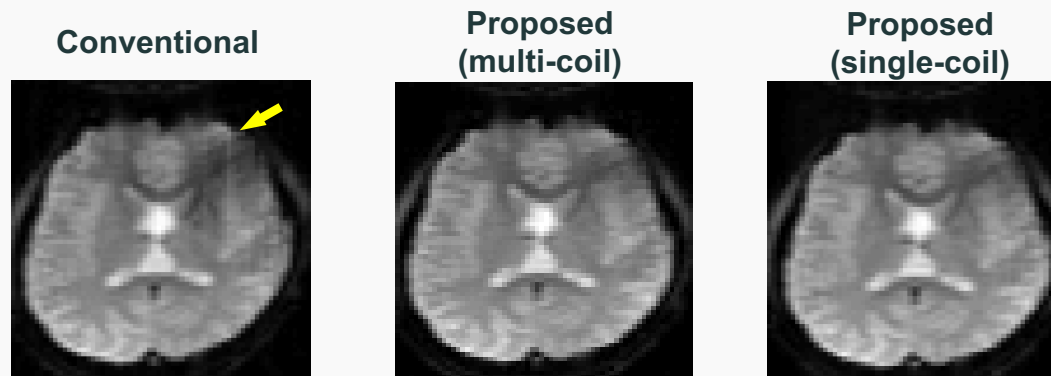
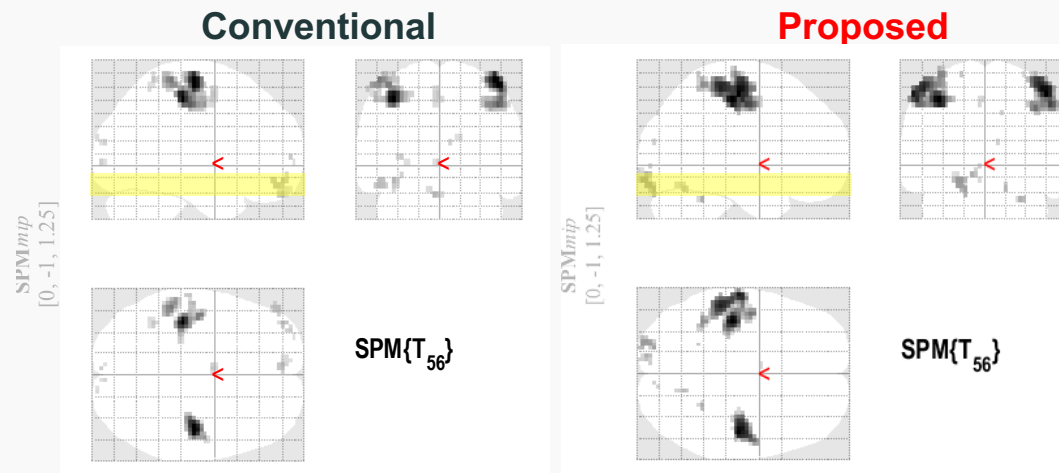
Result : GRE-EPI in-vivo



Result : fMRI analysis

fMRI analysis of GRE-EPI using **SPM**

- Pair hand squeezing stimulation
⇒ Motor cortex activation
- Familywise error, $p \leq 0.05$



Applications to Image Processing

Inpainting & Impulse noise removal

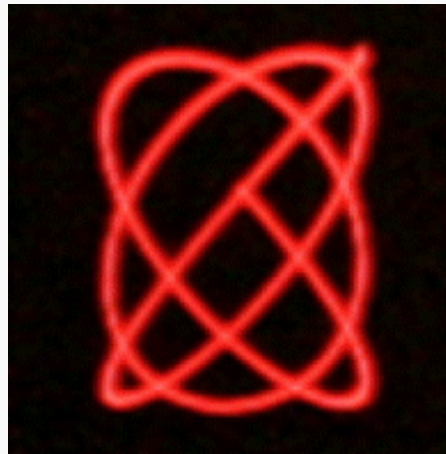
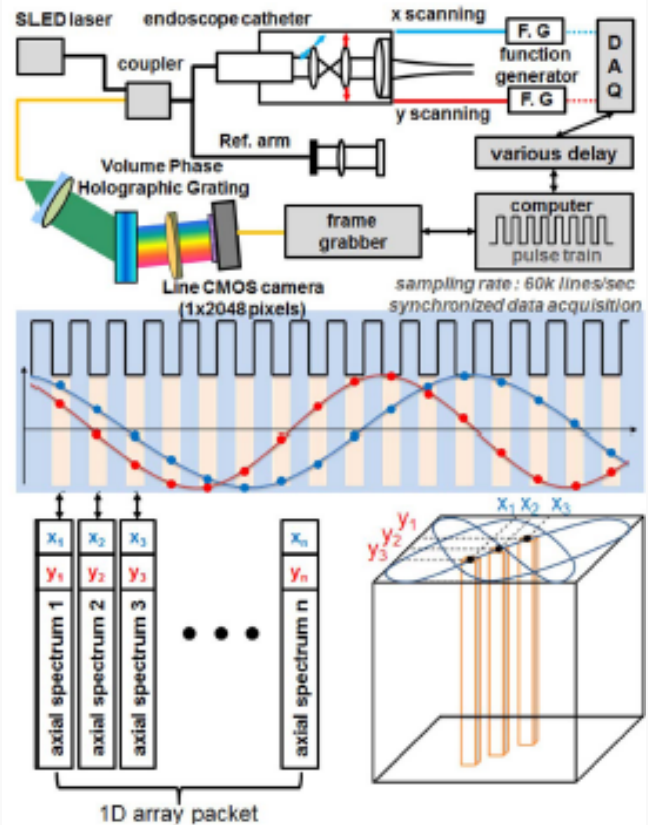
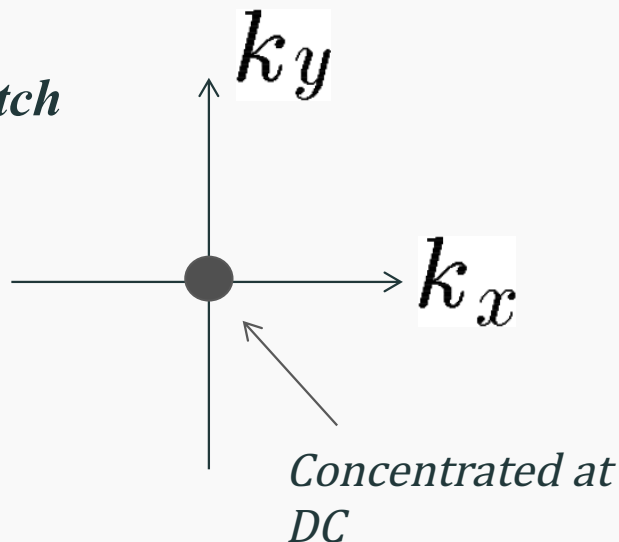


Fig. 2. (Color online) 3D SD-OCT image reconstruction :

Spectral Domain Sparsity

Smooth patch

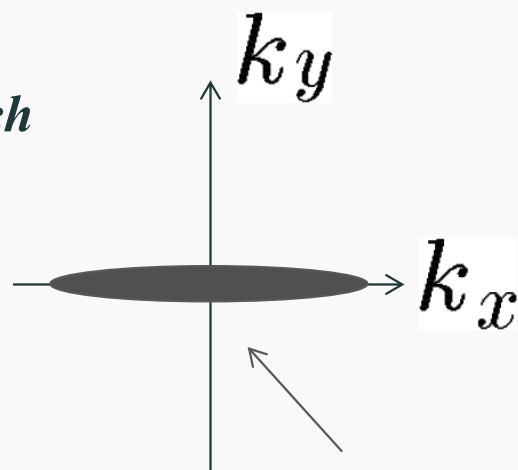
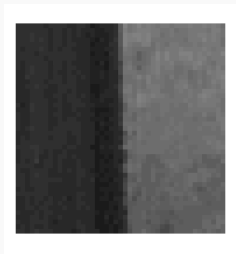


Smoothness, texture, pattern

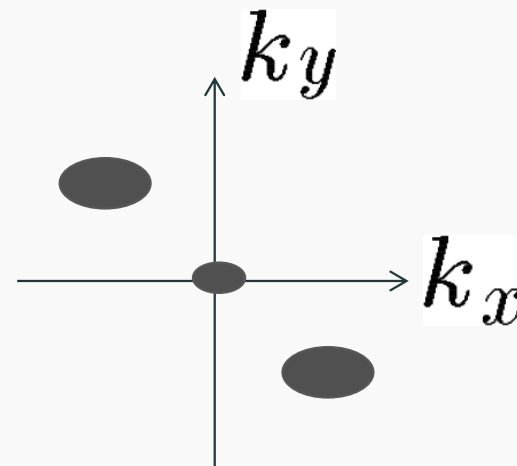
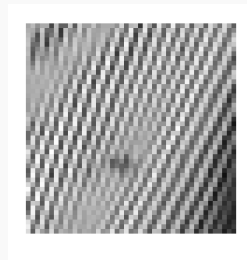


Sparse spectrum

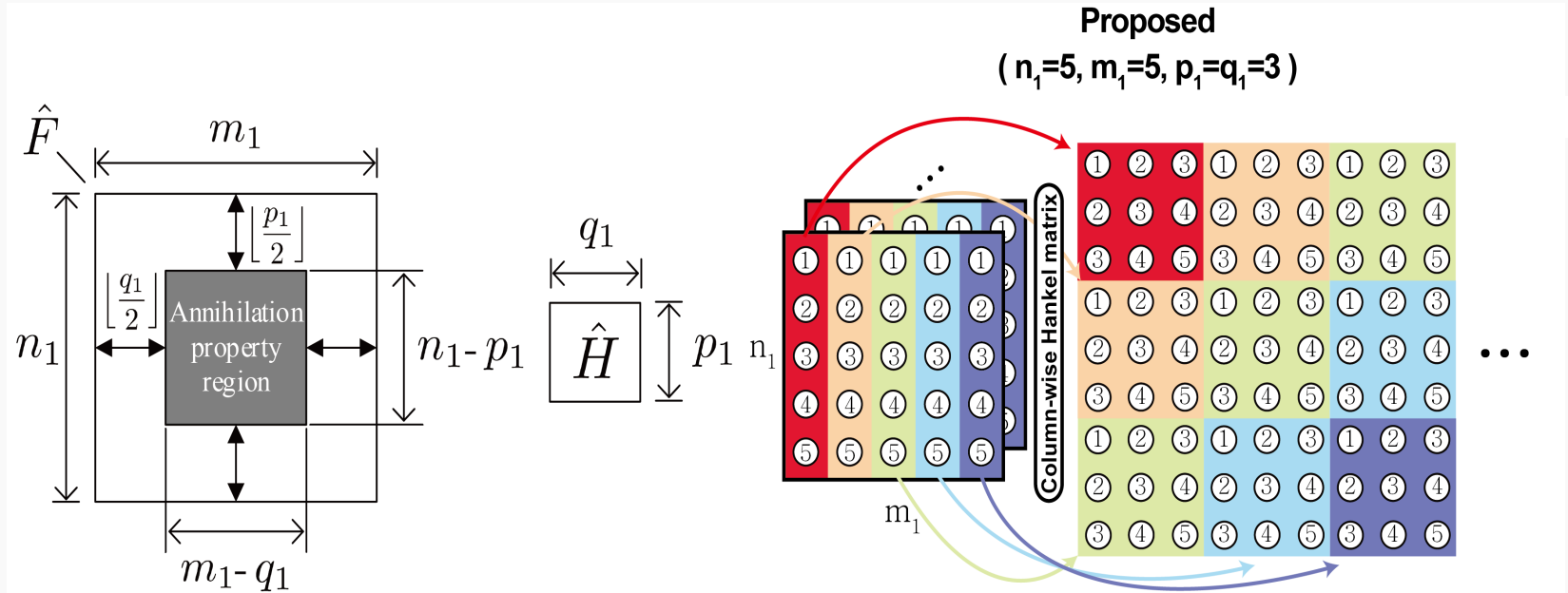
Edge patch



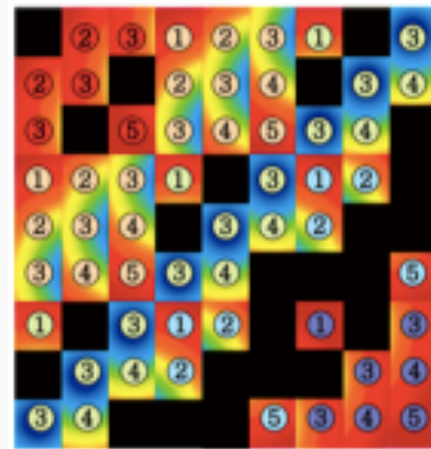
Texture patch



2-D Hankel matrix

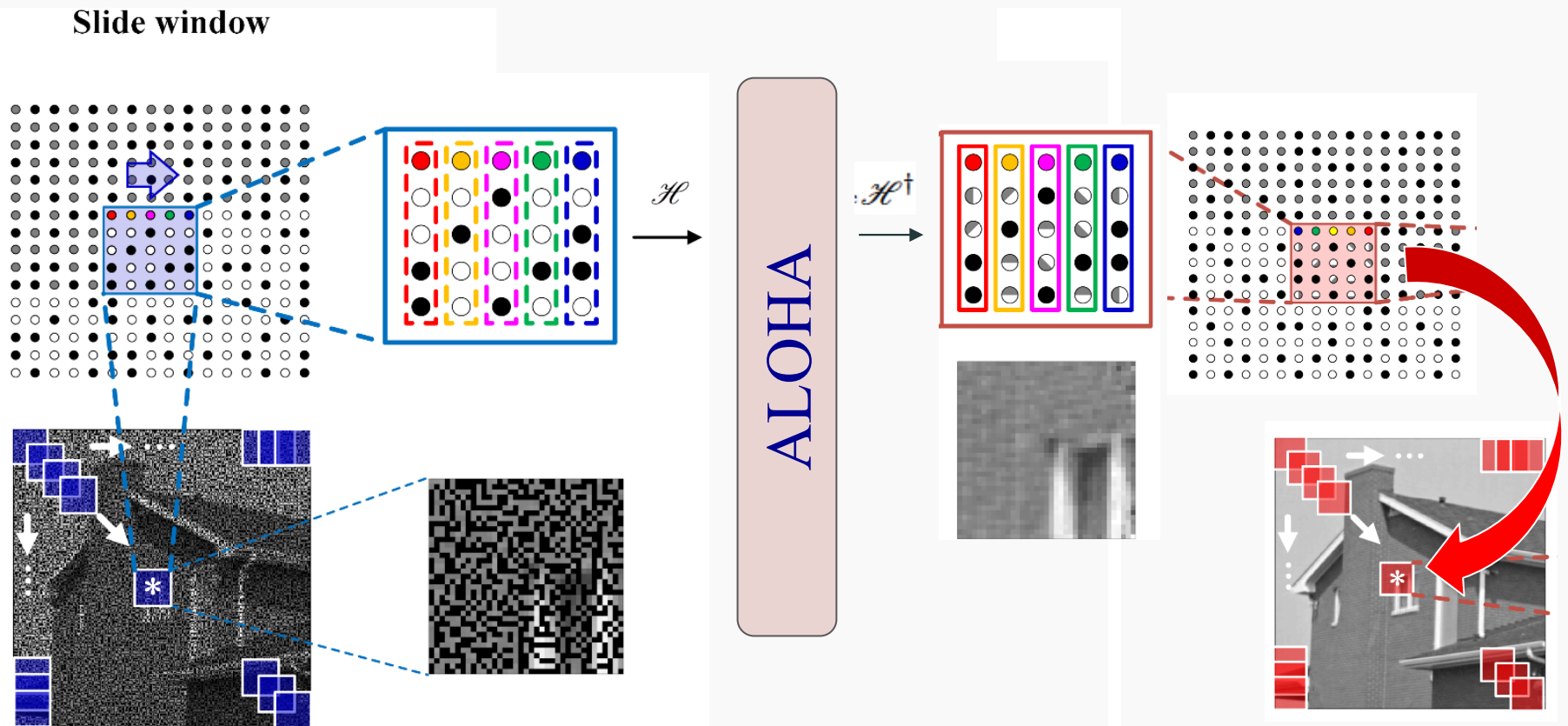


**Hankel
Matrix
construction**

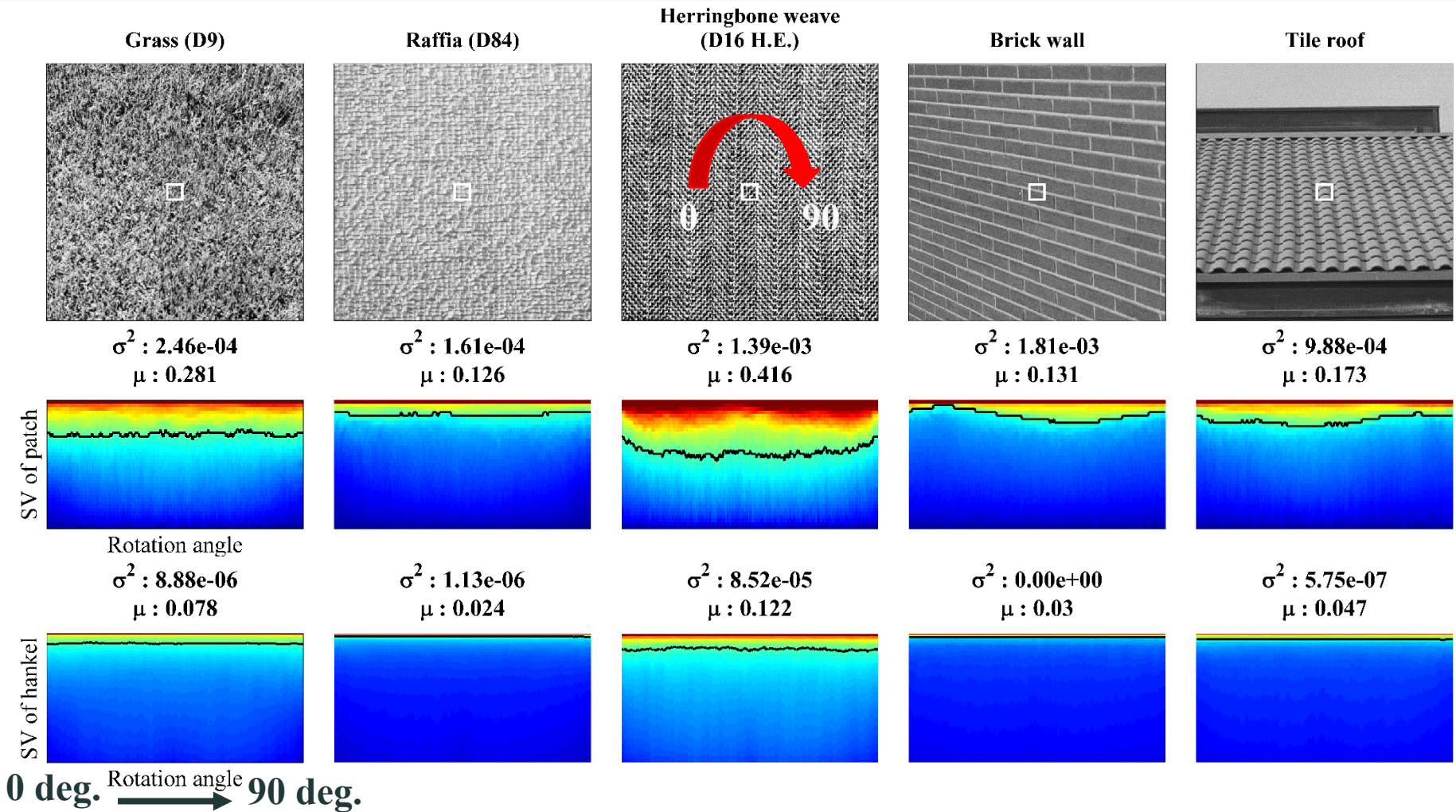


Why patch processing ?

- *Spectrum changes for each patch*
- *Need to adapt the local Image statistics*



Rotation invariant sparsity



Hankel structured matrix is intrinsic low rank !!

Experimental results (x5)

Barbara

Missing (80%)
PSNR 6.54
SSIM 0.06374

Mesh
PSNR 23.09
SSIM 0.8042

Kernel
PSNR 22.91
SSIM 0.7551



Kernel (Steering)
PSNR 23.08
SSIM 0.7491

K-SVD
PSNR 24.27
SSIM 0.8075

C-SALSA
PSNR 23.38
SSIM 0.7918

Proposed
PSNR 31.34
SSIM 0.9547



Experimental results (x5)

Barbara

Missing (80%)

Mesh

Kernel



Kernel (Steering)

K-SVD

C-SALSA

Proposed



Text inlayed image reconstruction

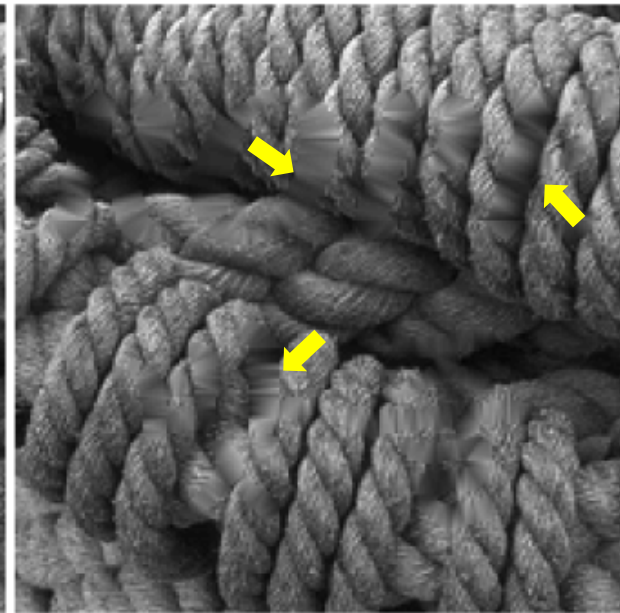
ORIG



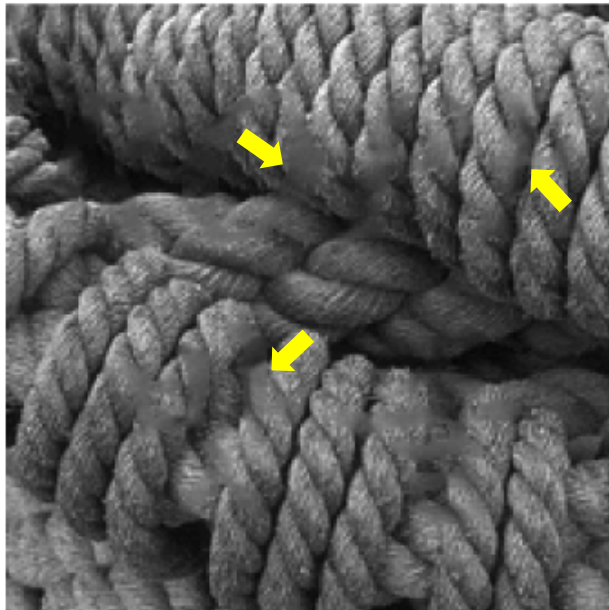
Missing(15.3%)



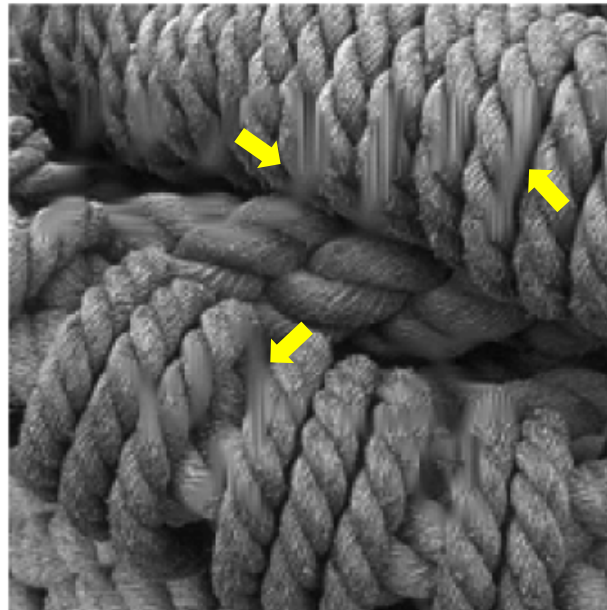
Mesh



PatchMatch



IPPO



Proposed



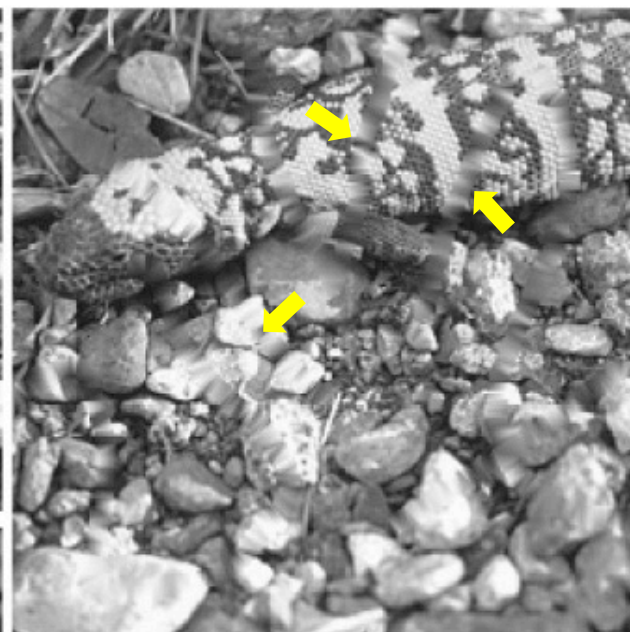
Line scratches
ORIG



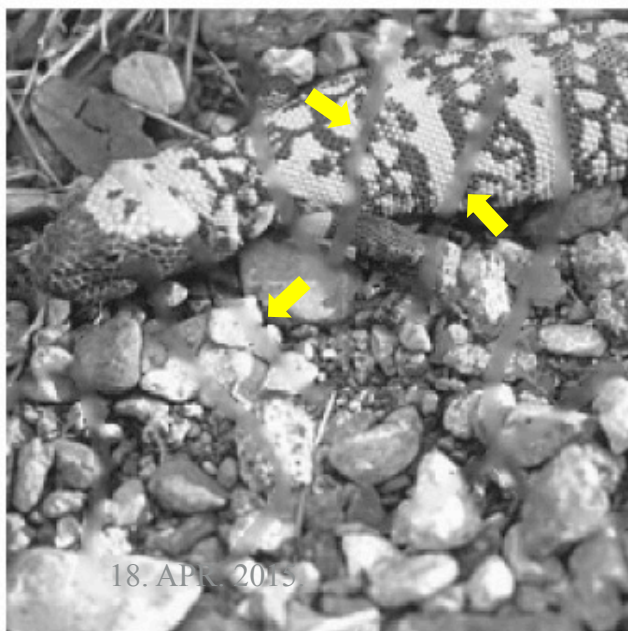
Missing(12.7%)



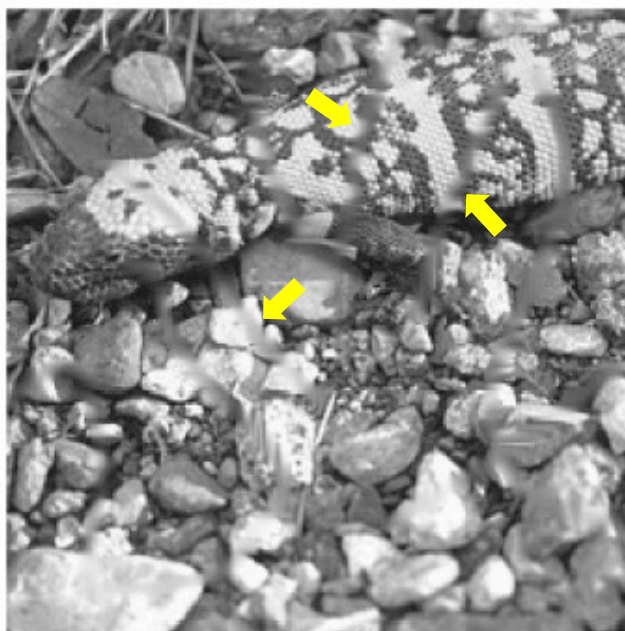
Mesh



PatchMatch



IPPO



Proposed



Object removal

ORIG

Missing(7.99%)

Mesh



PatchMatch

IPPO

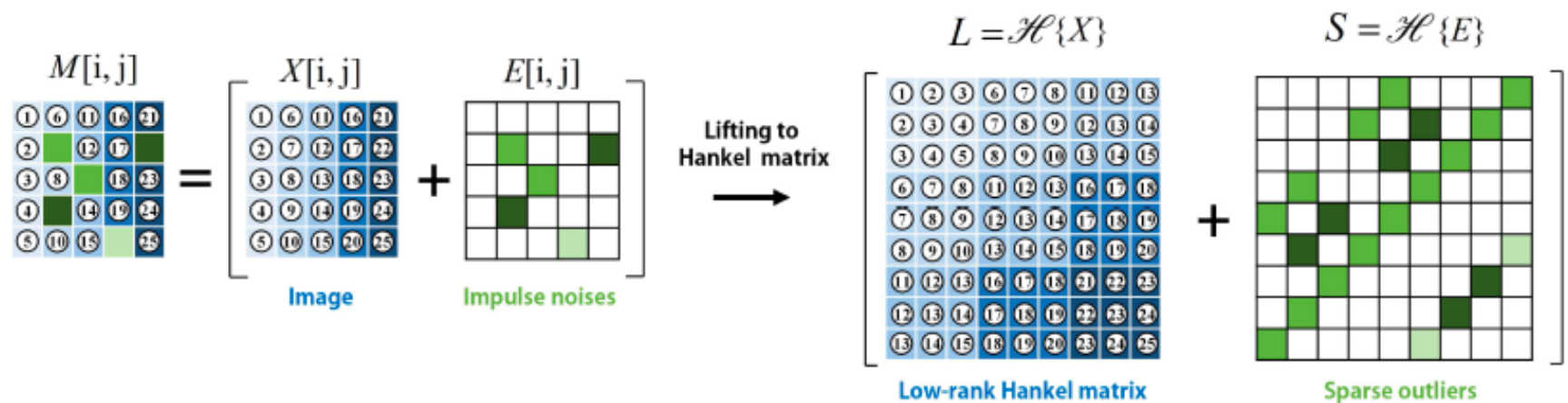
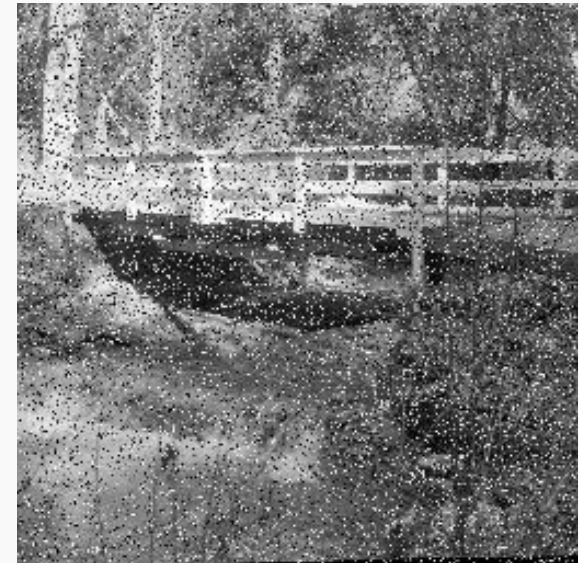
Proposed





*K.H. Jin, et. al, IEEE TIP (2015)

Impulse Noise Removal



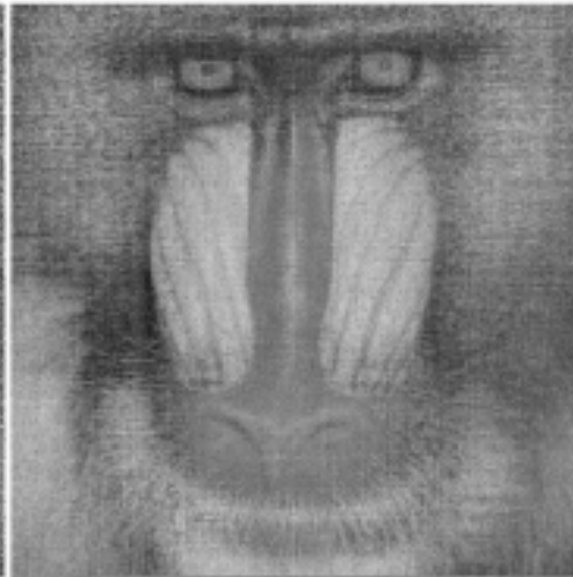
Impulse Noise (40%)

PSNR : 13.52



RPCA

PSNR : 19.76



RPCA (patch)

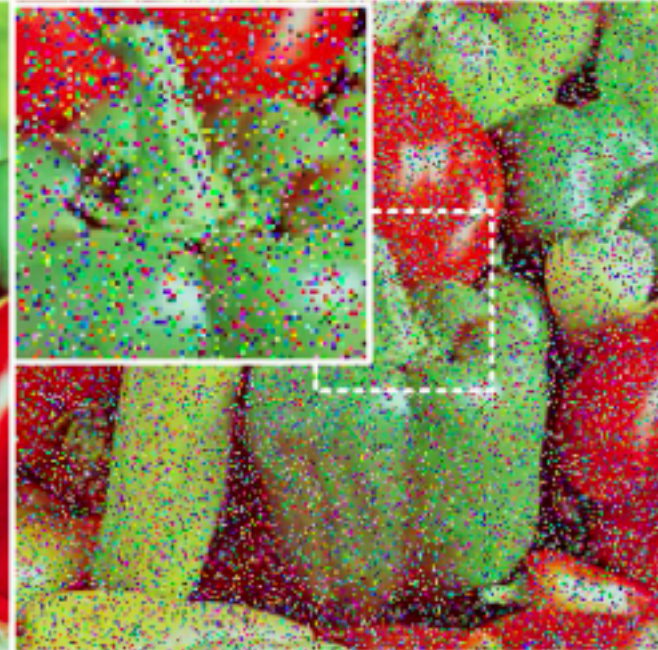
PSNR : 17.26



Robust ALOHA

PSNR:22.46



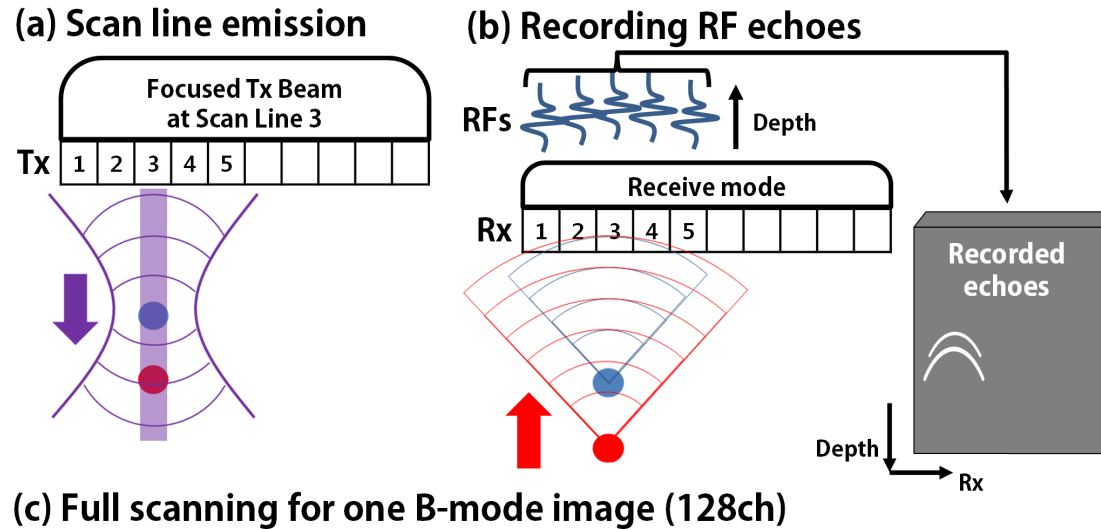


TVL1
PSNR : 28.68

Robust ALOHA
PSNR : 29.68



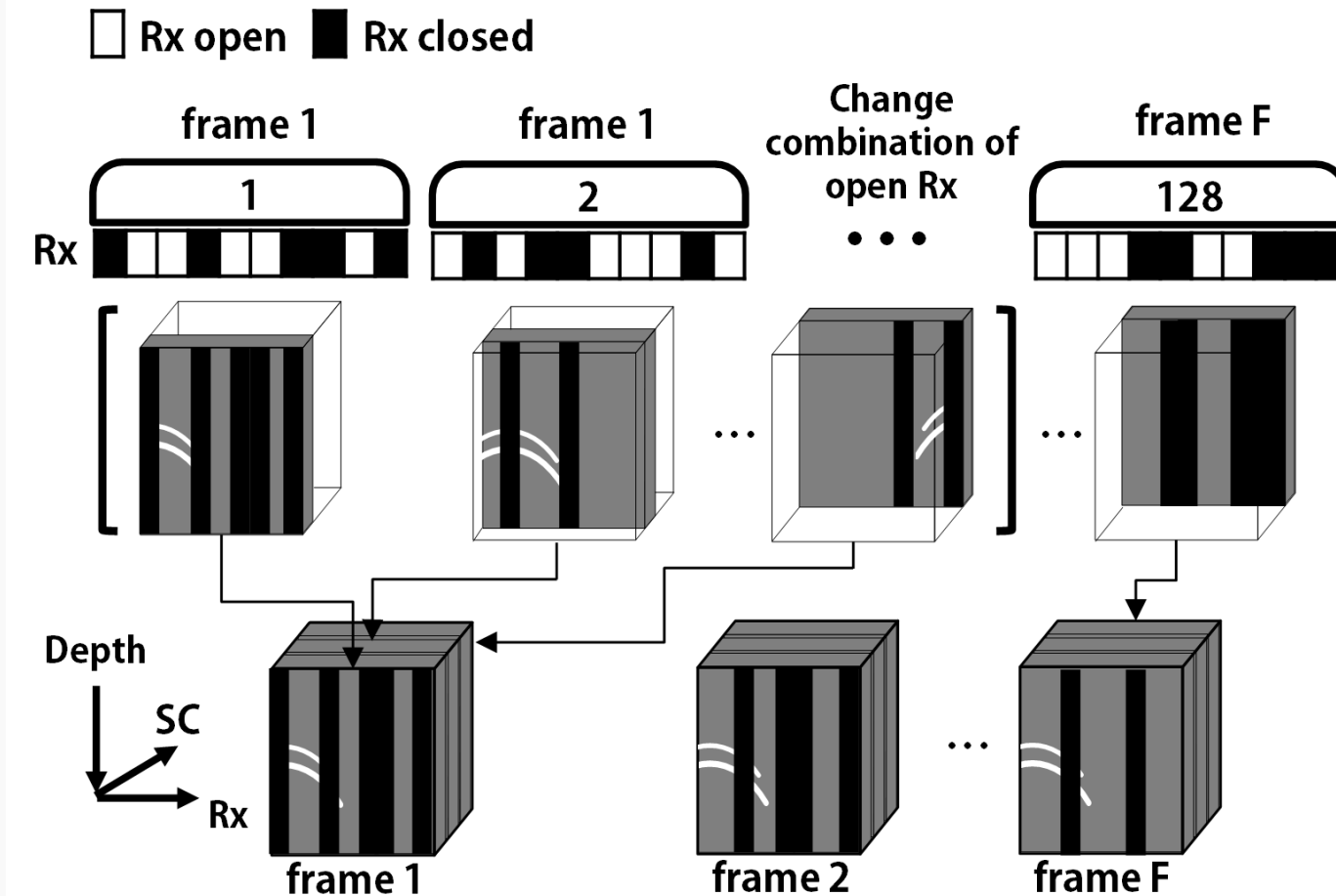
Application to B-mode US Imaging



All Rx should be used
→ high power consumption,
High data rate

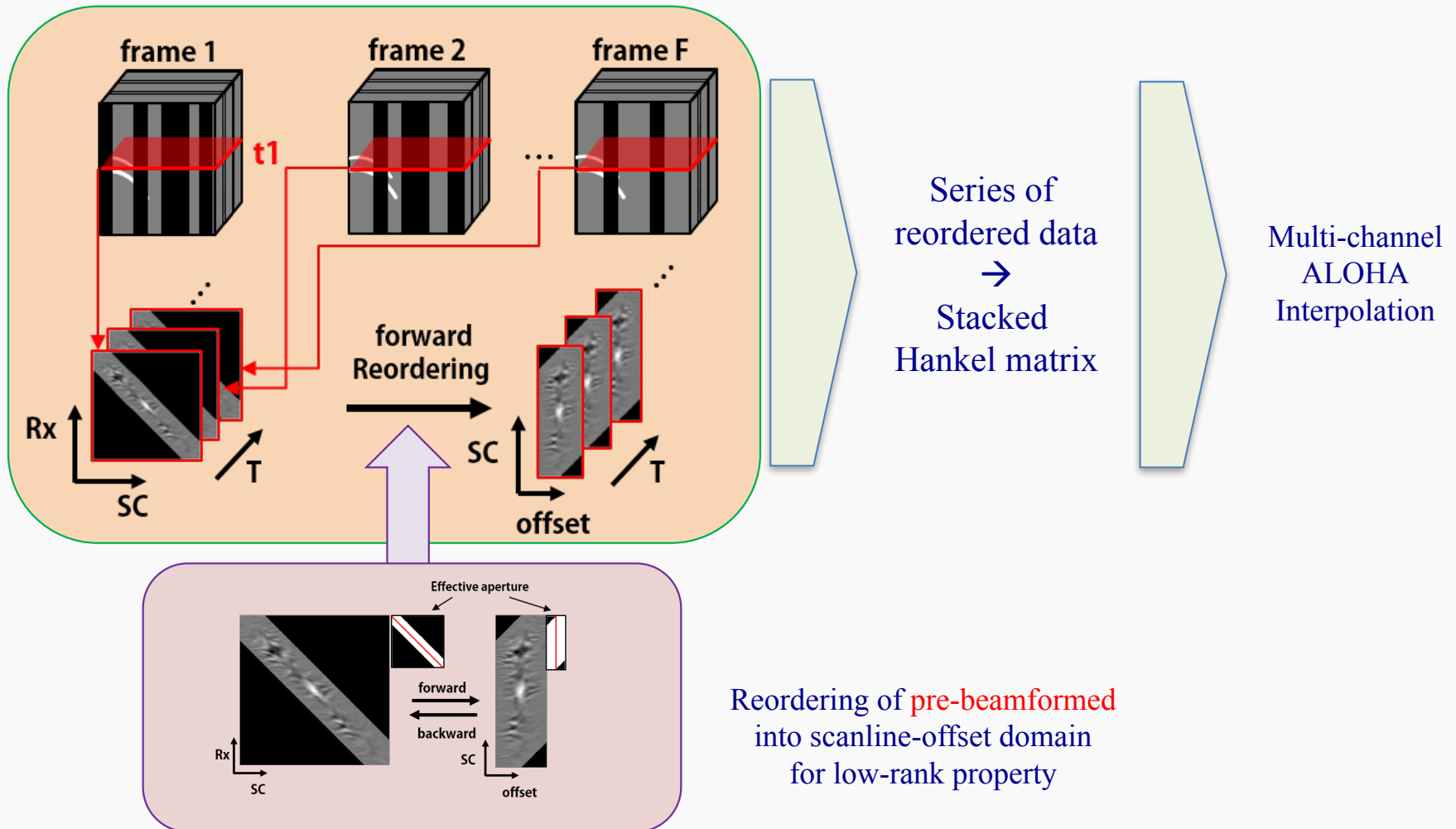
1. Probes deliver beamformed B-mode image, only.
2. After DAS, raw measurements discarded.

Sub-sampled Dynamic Aperture B-mode Imaging

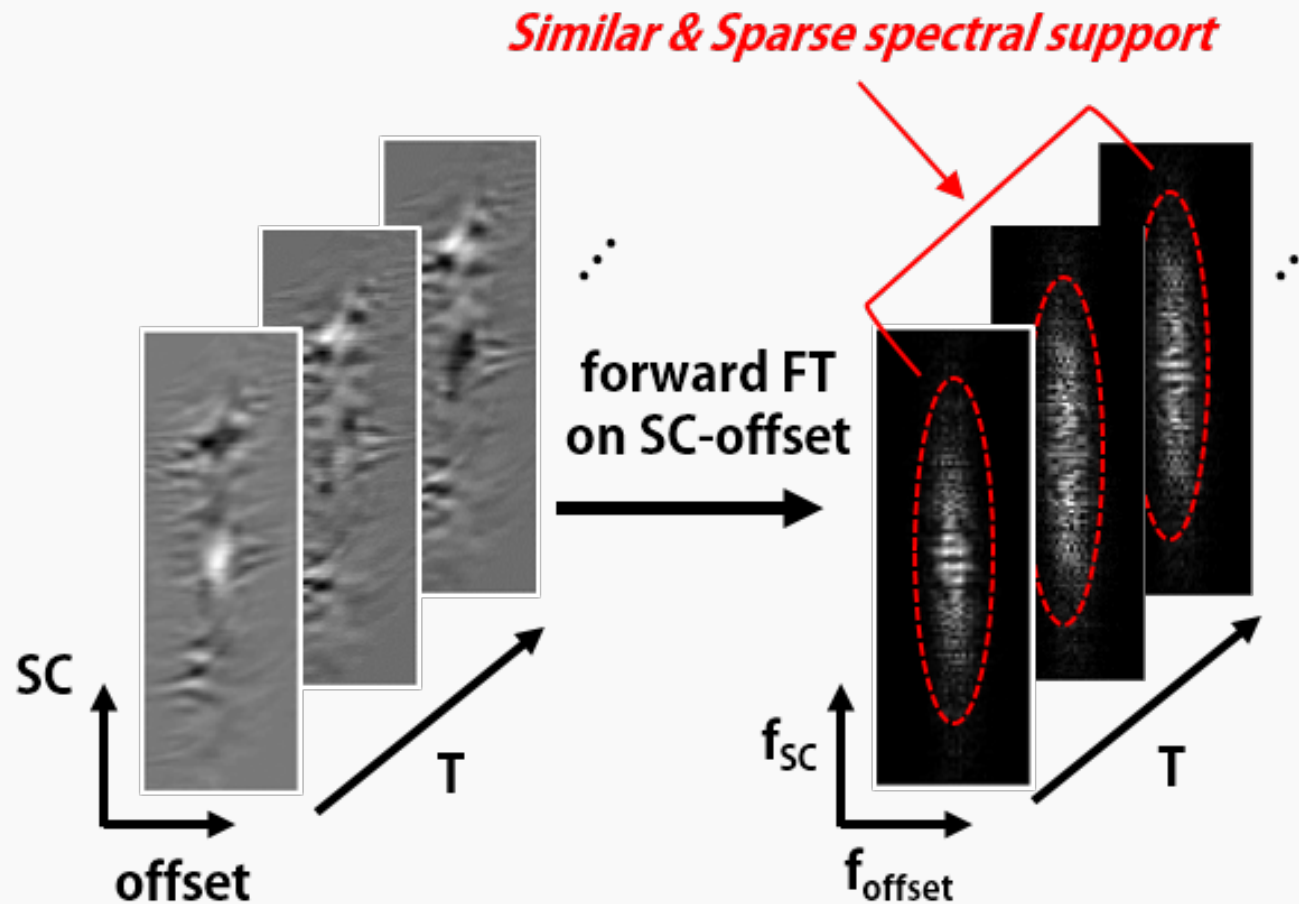


Low-Rankness of B-mode US Data

Temporal slices of
Pre-beamformed RF data



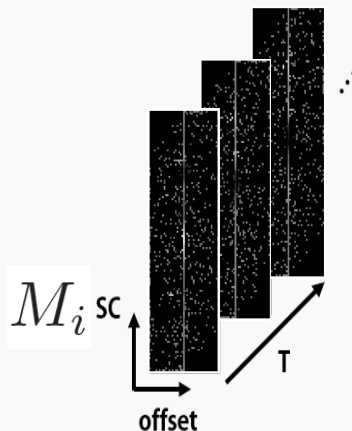
Sparsity of the Spectrum



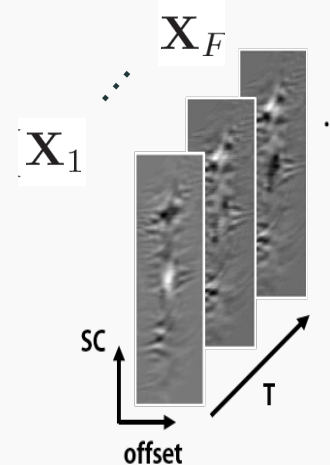
Exploiting Temporal Redundancy

→ inter-temporal annihilating filter

$$\begin{aligned} & \min_{\mathcal{X}} \quad \|\mathcal{Z}\{\mathcal{X}\}\|_* \\ & \text{subject to} \quad \mathcal{Z}\{\mathcal{X}\} = [\mathcal{H}\{\mathbf{X}_1\} \cdots \mathcal{H}\{\mathbf{X}_F\}] . \\ & \quad \quad \quad X_i(j, k) = M_i(j, k), \end{aligned}$$

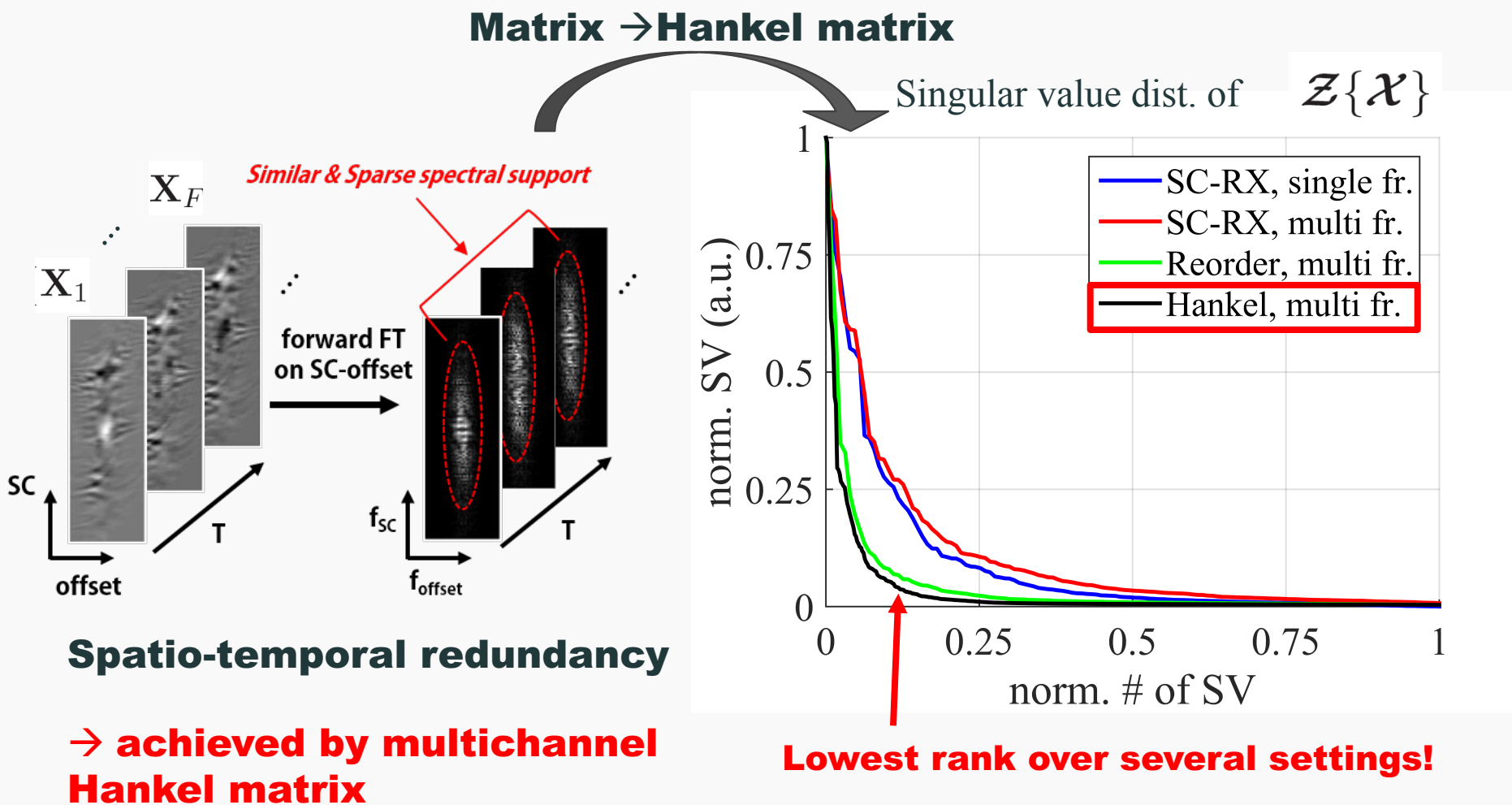


Reordered subsampled pre-beamformed data

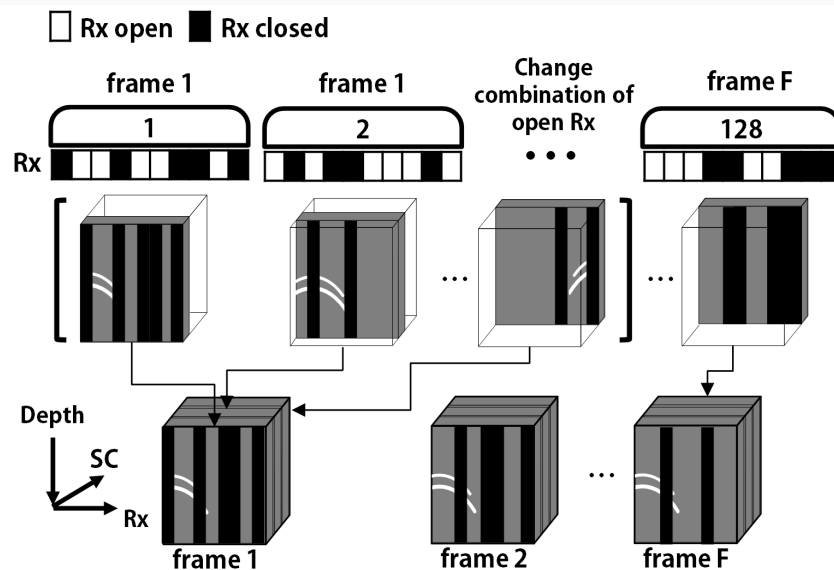


Reconstructed slices

Low-Rankness of B-mode US Data

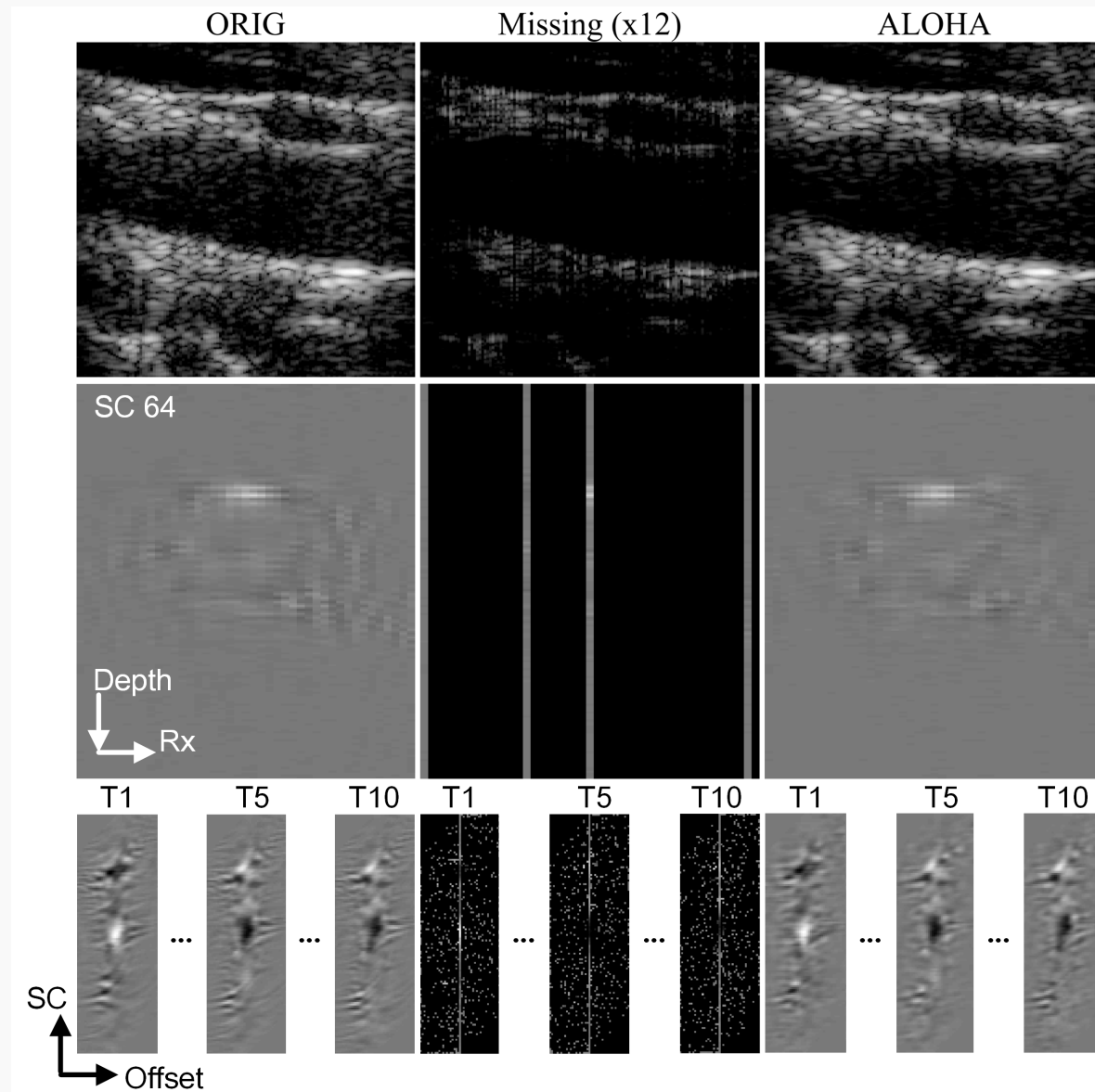


In-vivo Acquisition



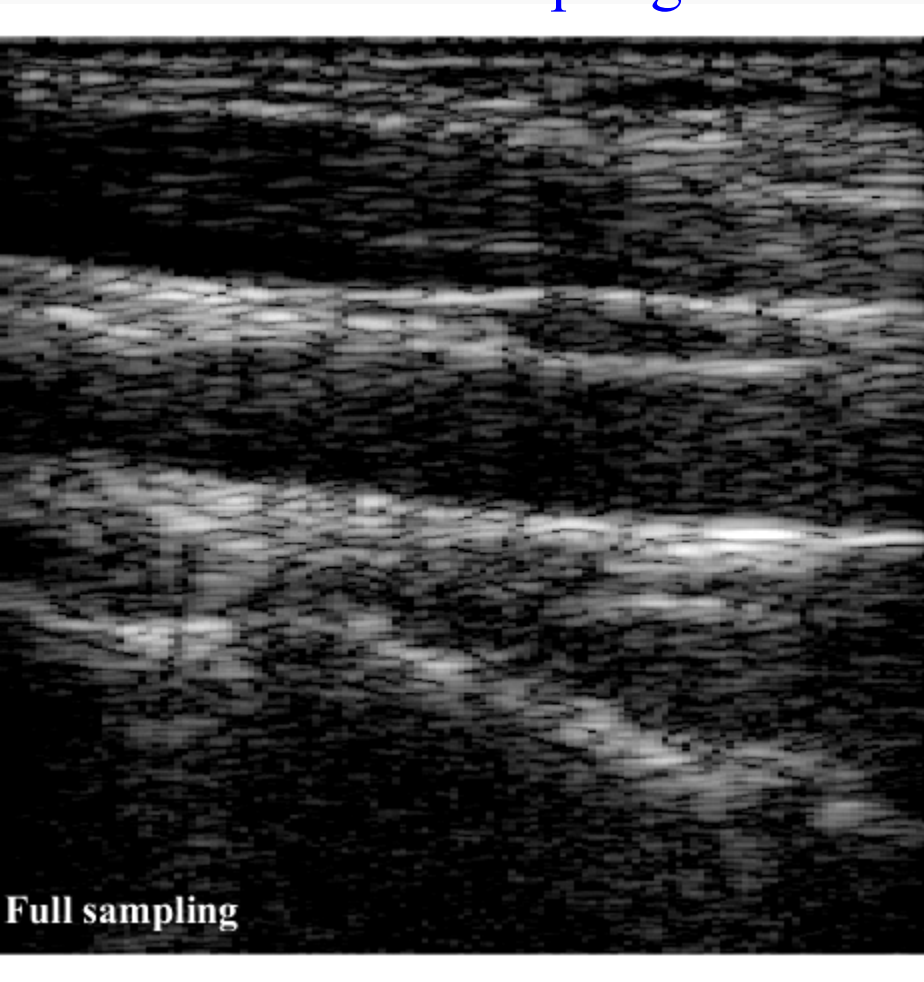
- Verasonics system with a Linear type probe (L7-4)
- Center freq: 5 MHz
- Sampling: 20 MHz.
- 128 scanlines (SC) x 128 RX channels
- RX element
 - Width: 133 μm
 - space between RX elements : 158 μm

Snapshot image from dynamic scan

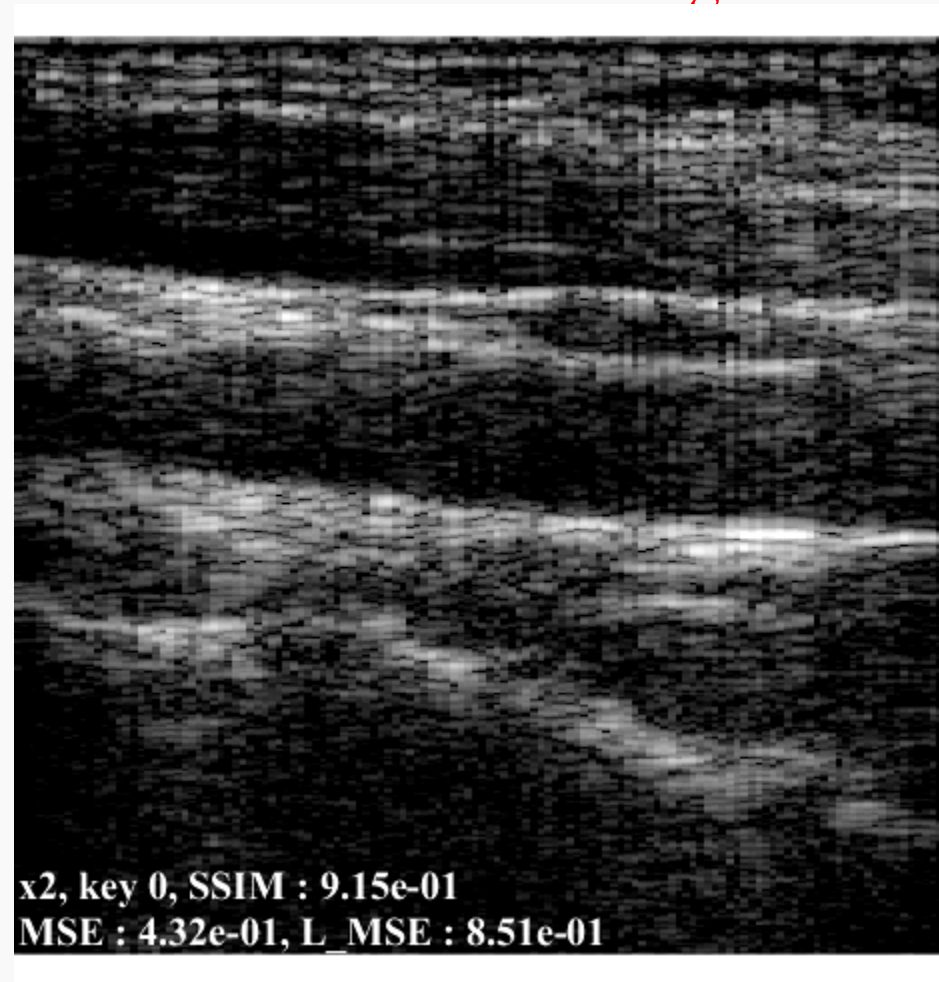


Dynamic reconstruction (x2)

Full Sampling

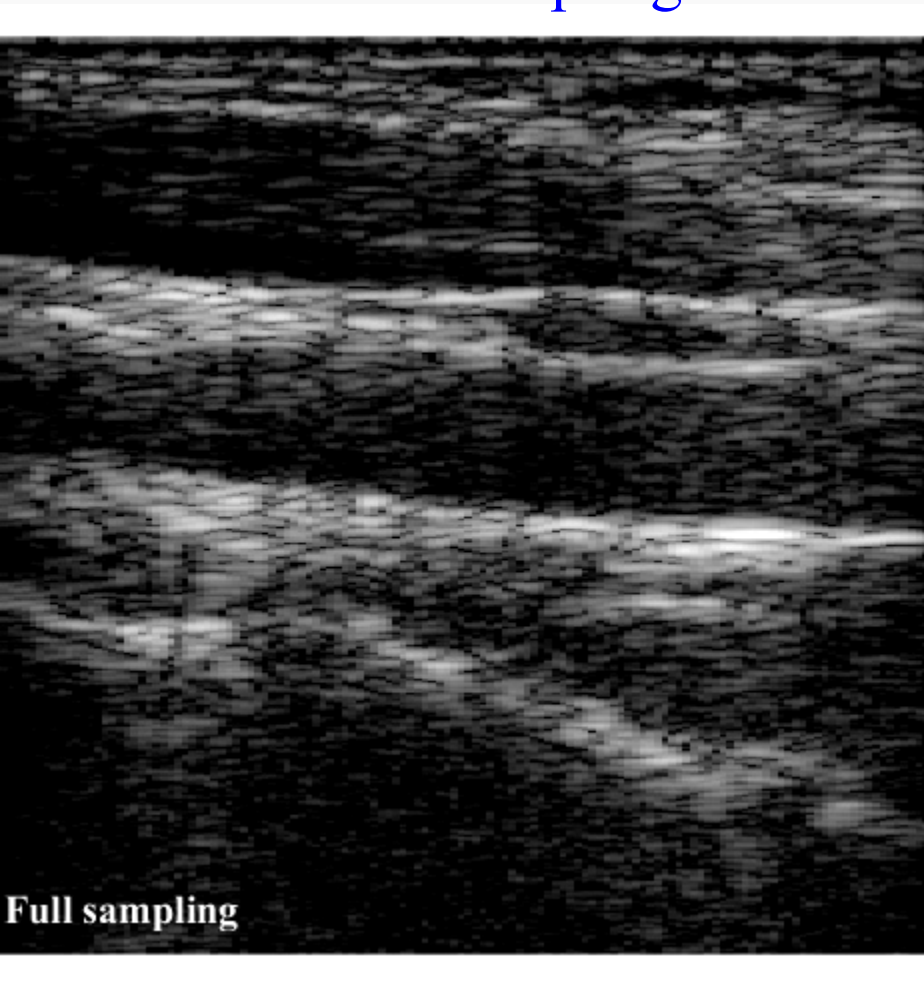


Beam forming

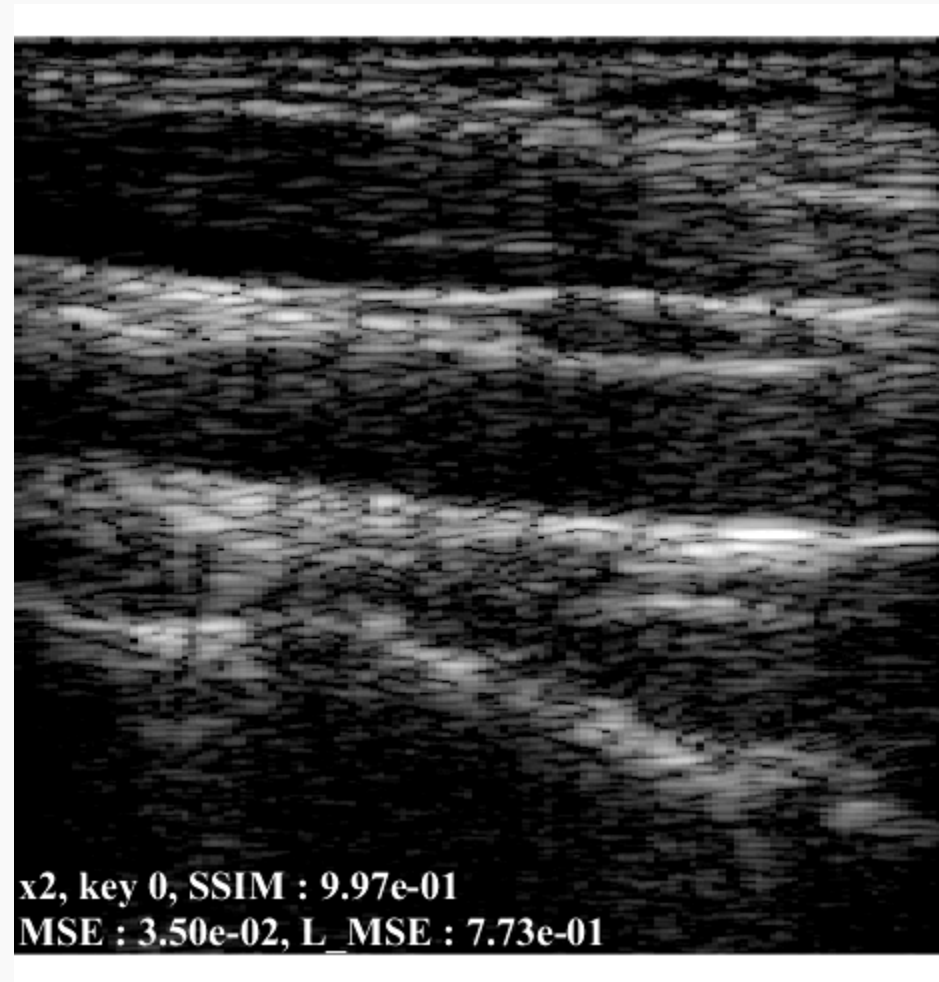


Dynamic reconstruction (x2)

Full Sampling

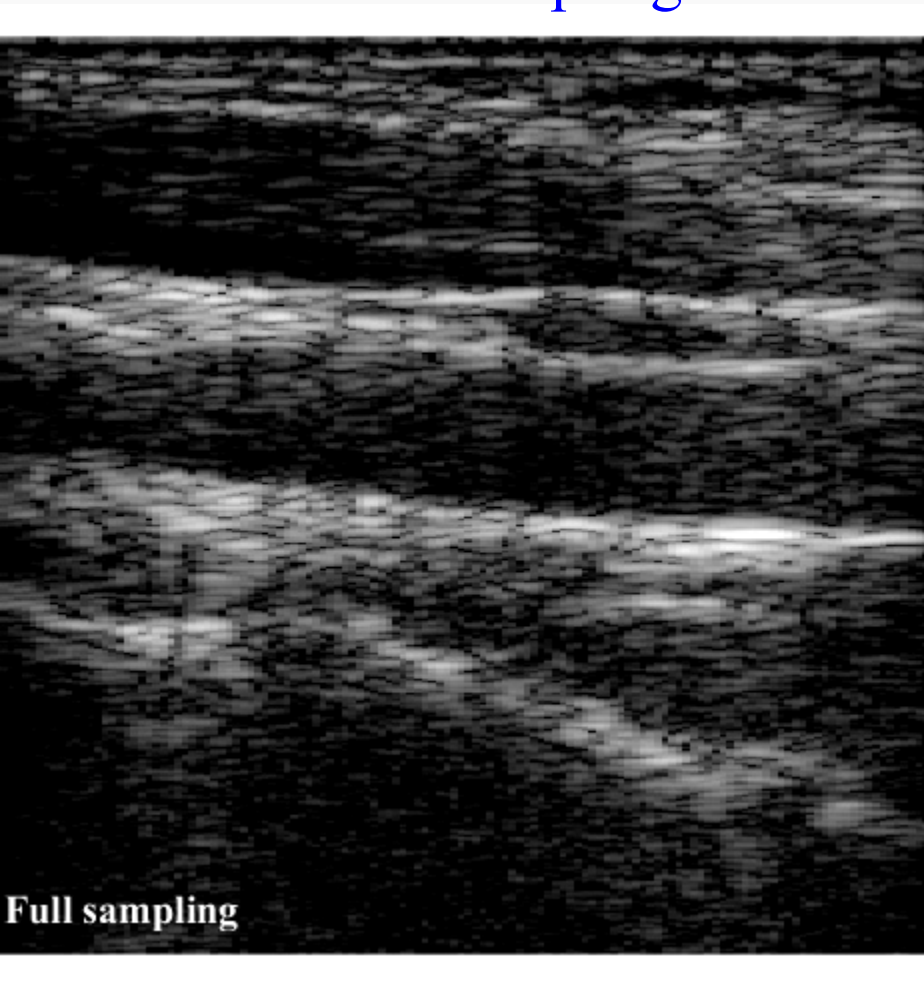


ALOHA

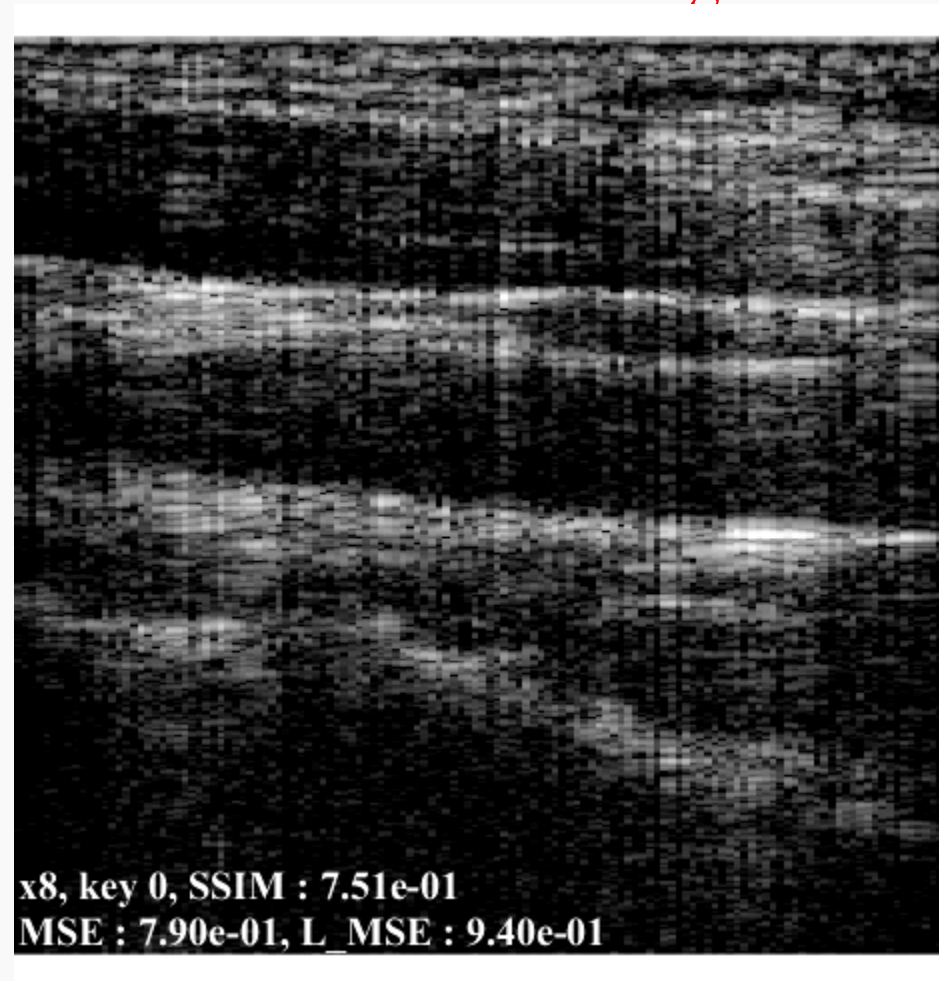


Dynamic reconstruction (x8)

Full Sampling

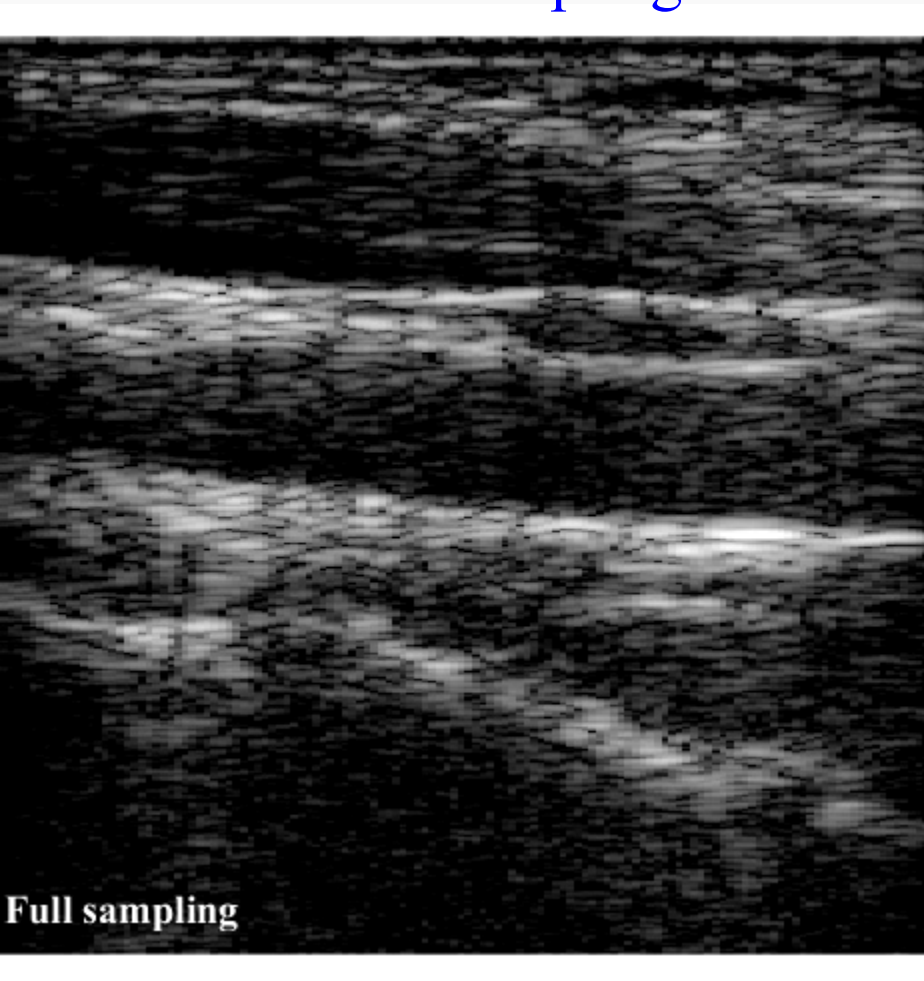


Beam forming

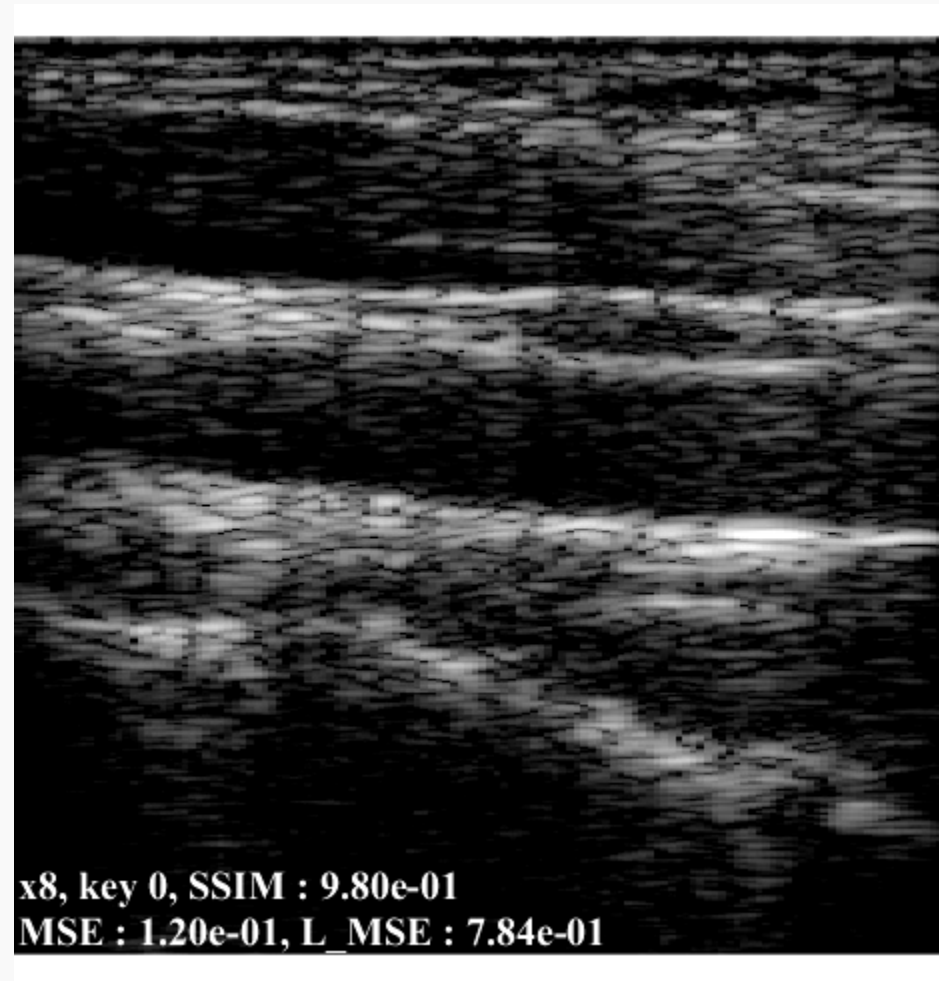


Dynamic reconstruction (x8)

Full Sampling

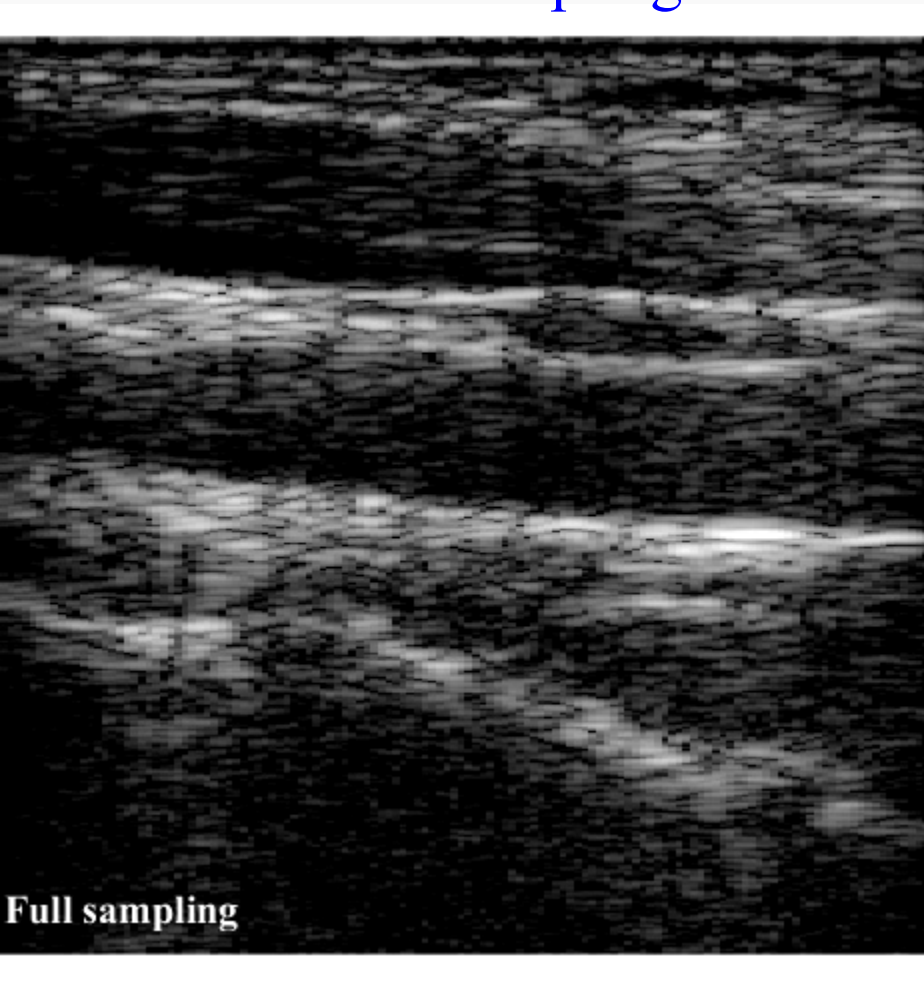


ALOHA

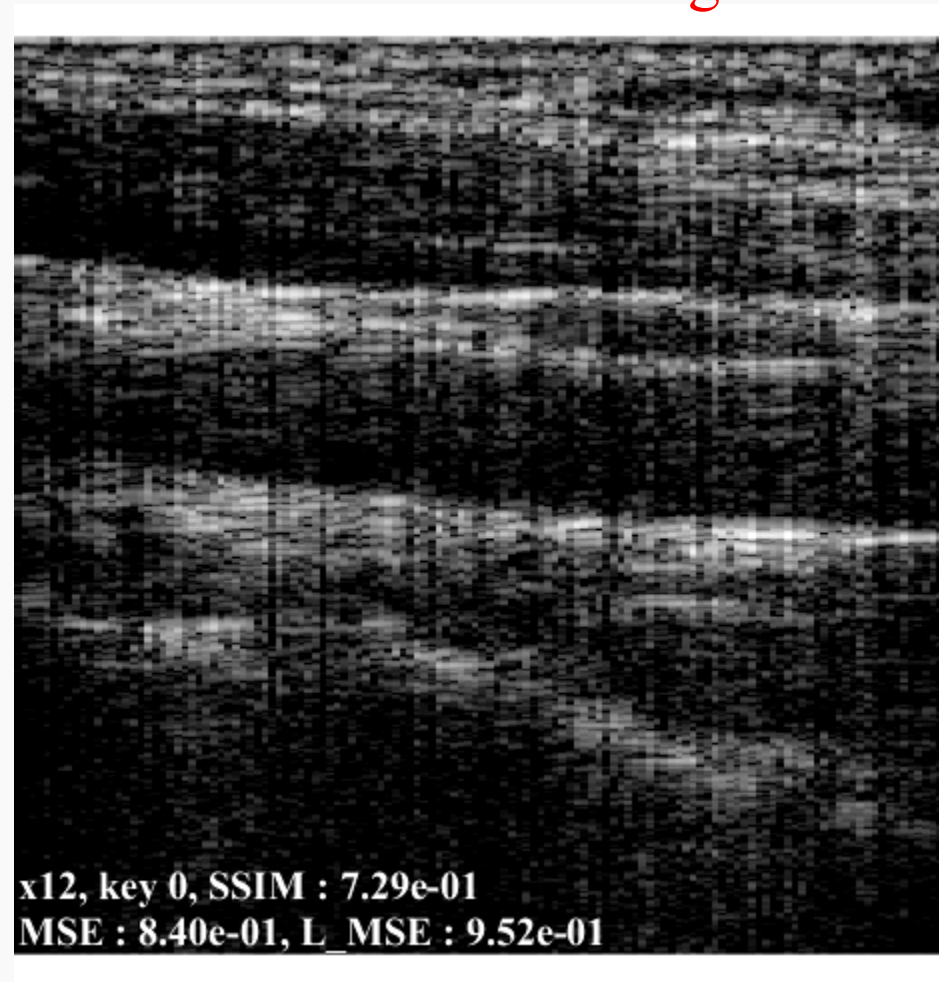


Dynamic reconstruction (x12)

Full Sampling

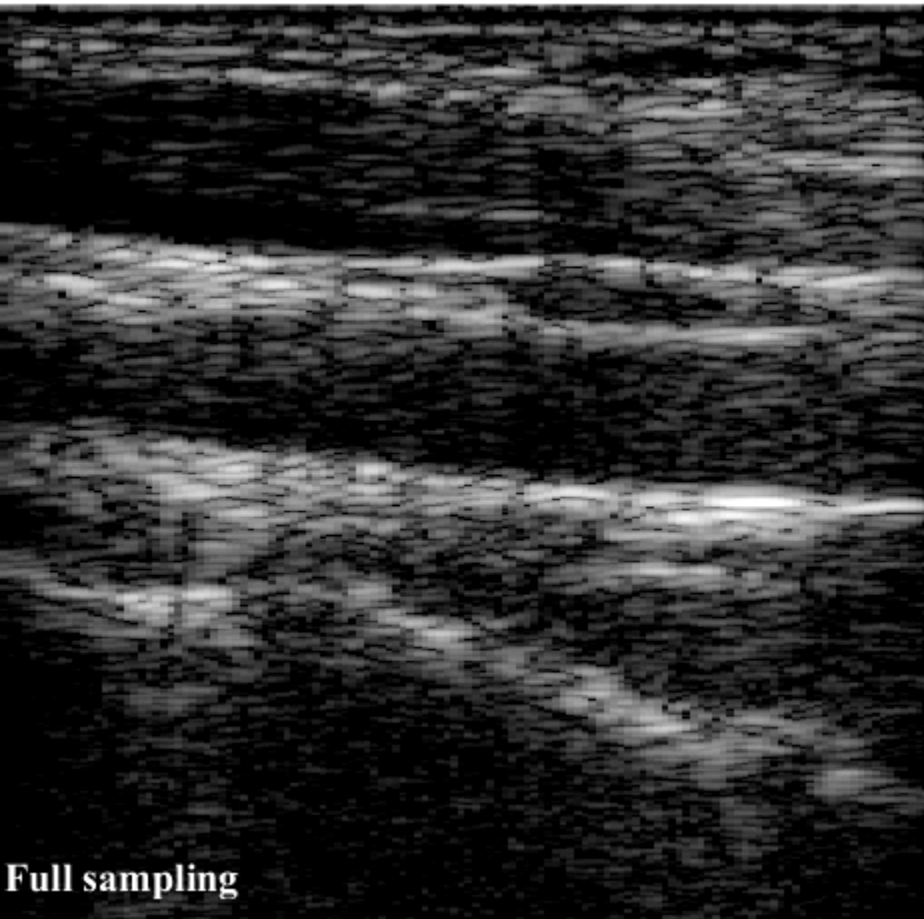


Beam forming

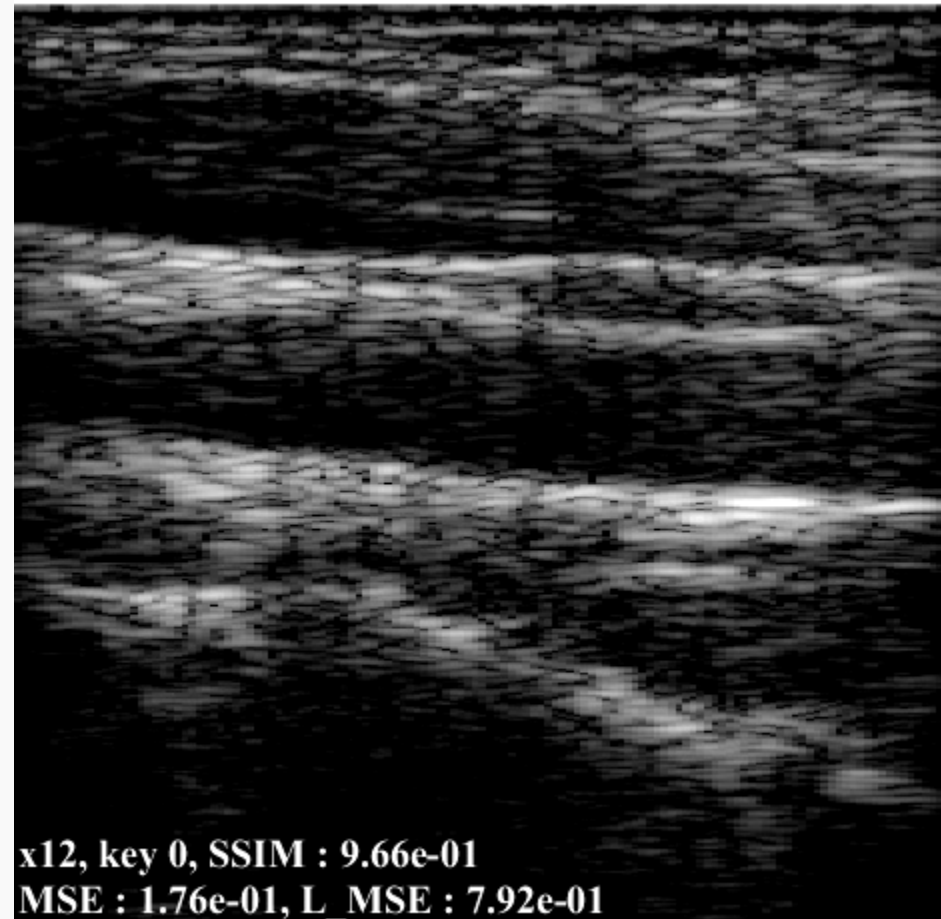


Dynamic reconstruction (x12)

Full Sampling



ALOHA

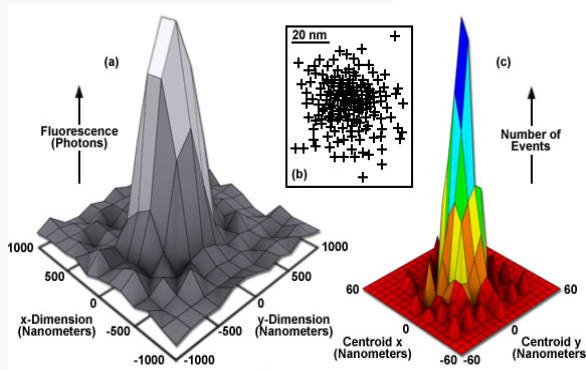


Localization microscopy

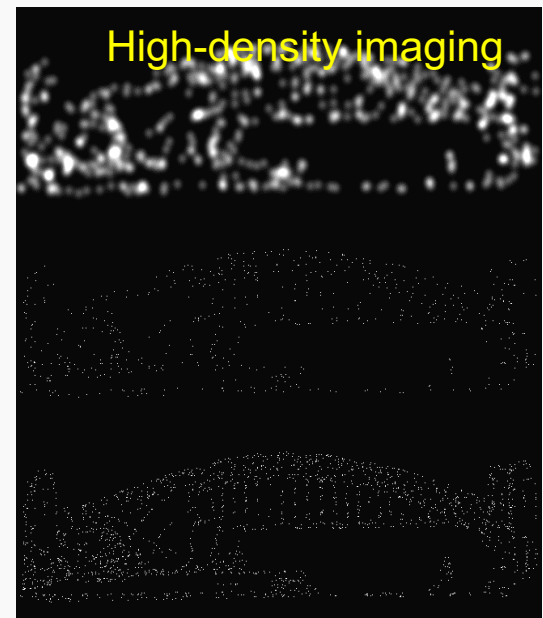
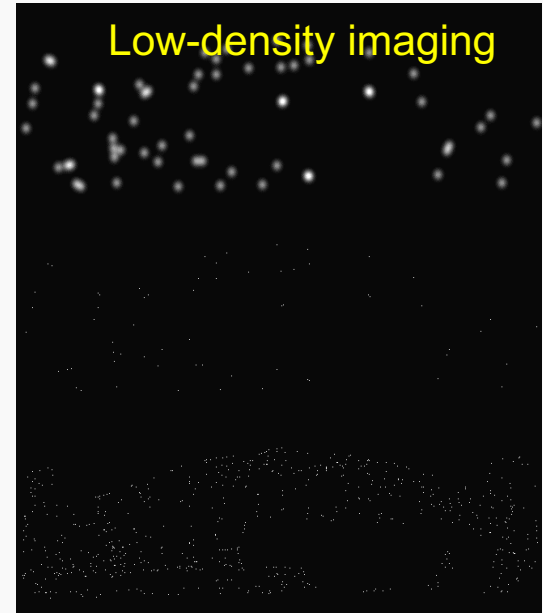
- Nanoscopy based on localization
 - Localization precision is not diffraction limited
 - Sparsely activated probes + localization => super-resolution image

$$\sigma_{\mu_i} = \sqrt{\left(\frac{s_i^2}{N} + \frac{a^2/12}{N} + \frac{8\pi s_i^4 b^2}{a^2 N^2} \right)}$$

Thompson et al. BPJ 2002



- However, sparse activation scheme has too slow temporal resolution for live imaging
 - Tens of seconds or several minutes
- High-density imaging for fast live imaging
 - Require a robust localization algorithm and system



Existing high density algorithm

Greedy approach

DAOSTORM: an algorithm for high-density super-resolution microscopy

In the Editor: Astronomy and biology have more in common than you might expect. Here we show that methods originally used to study crowded stellar fields can improve the performance of localization-based super-resolution microscopy (stochastic optical reconstruction microscopy (STORM)¹, photoactivated localization microscopy² and others), which currently have slow imaging rates (typically < 0.01 image s⁻¹), limiting their utility in studies of live-cell dynamics.

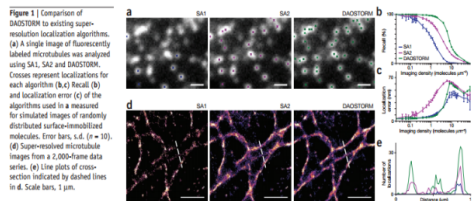
These techniques, which use stochastic photoswitching to resolve closely spaced fluorophores and then reconstruct super-resolved images, require that the specimen has a low density of active fluorophores (hereafter called 'molecules') < 1 molecule μm⁻², limiting imaging speed and spatial resolution (Supplementary Discussion). A major cause of this issue is that current super-resolution localization algorithms work by fitting images of fluorescent molecules using only a single model point spread function (PSF; the diffraction-limited image of a fluorophore). We observed that astronomy software, DAOPHOT II (refs. 3,4), can simultaneously fit overlapping molecular PSFs (hereafter called 'molecules') with multiple model PSFs instead of just one, facilitating analysis of high imaging density (up to 10 molecules μm⁻²). We developed DAOSTORM (Supplementary Software and Supplementary Note), which adapts DAOPHOT II for super-resolution imaging by increasing its automation and robustness (Supplementary Fig. 1 and Supplementary Methods).

We compared DAOSTORM to two common localization algorithms. 'Sparse algorithm 1' (SA1) fits candidate molecules with a single Gaussian PSF of variable size and ellipticity. Localizations arising from overlapping molecules are rejected if the fitted PSF appears too elliptical (shape-based filtering), too large or too small (size-based filtering). 'Sparse algorithm 2' (SA2) fits candidate molecules with a single Gaussian PSF of fixed shape and size, without shape- or size-based filtering.

We first investigated the qualitative performance of each algorithm for images of Alexa Fluor 647-immobilized microtubules in fixed COS-7 cells. We recorded data at high imaging density using total internal reflection fluorescence microscopy and direct (dSTORM) photoswitching conditions⁵ (100 ms integration time, ~4,000 photons fluorophore⁻¹ frame⁻¹). We plotted localizations on raw images, illustrating the characteristic performance of each algorithm (Fig. 1a). SA1 only localized isolated molecules, which were fitted with small localization error. SA2 localized a larger fraction of the molecules but yielded large localization errors for overlapping molecules. DAOSTORM outperformed both in terms of live-cell dynamics, identifying almost all molecules with small localization error.

We quantified the performance of each algorithm by analyzing simulations of randomly distributed surface-immobilized fluorophores⁶. We compared observed localizations to simulated positions, calculating the recall⁷ and localization error at different imaging densities. Recall is the percentage of simulated fluorophores detected. Localization error is the root-mean-square distance between a localization and the simulated position. We also measured the precision⁸ and redundancy (Supplementary Methods), which did not vary substantially.

DAOSTORM substantially outperformed the sparse algorithms in simulations at high signal-to-noise ratio typical of STORM data (bright organic fluorophores, 5,000 photons molecule⁻¹ frame⁻¹; Fig. 1b–d). SA1 showed poor recall at high density, with imaging density at half-maximum recall, $\rho_{1/2} = 1.2$ molecule μm⁻². However, SA1 yielded small localization errors even at high imaging density because most overlapping molecules were rejected. SA2 had better recall performance ($\rho_{1/2} = 3.4$ molecule μm⁻²) but gave large localization errors even at low imaging density (> 0.1 molecule μm⁻²). In contrast, DAOSTORM gave small localization errors similar to the other 'precise' algorithm, SA1, together with a sixfold improvement in recall performance ($\rho_{1/2} = 7.5$ molecule μm⁻²). For simulations at low signal-to-noise ratio typical of photoactivated localization microscopy data (fluorescent proteins, 200 photons molecule⁻¹ frame⁻¹;



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Holden, S. et al, Nat Methods, 2011

CORRESPONDENCE

Sparsity based approach

Faster STORM using compressed sensing

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In super-resolution microscopy methods based on single-molecule activation, the rate of accumulating single-molecule activation events often limits the time resolution. Here we developed a sparse-signal recovery technique using compressed sensing to analyze images with highly overlapping fluorescent spots. This method allows an activated fluorophore density an order of magnitude higher than what conventional single-molecule fitting methods can handle. Using this method, we demonstrated imaging microtubule dynamics in living cells with a time resolution of 1 s.

Despite many achievements in the field of super-resolution microscopy in the past few years^{1–3}, live cell imaging remains a challenge because of the need for high temporal resolution. Using the same optical system and detector as in conventional light microscopy, super-resolution microscopy naturally requires longer acquisition time to obtain more spatial information, leading to a trade-off between its spatial and temporal resolution. In super-resolution microscopy methods based on single-molecule stochastic switching, also known as stochastic optical reconstruction microscopy (STORM) or (fluorescence) photoactivated localization microscopy (FPALM)^{4–6}, each camera image samples a random subset of probe molecules in the sample. The temporal resolution is mostly determined by the time required to accumulate enough single-molecule switching events so that adjacent localization points can be closer than one-half of the desired spatial resolution (Nyquist criterion)⁷. Achieving a 50- to 70-nm spatial resolution usually requires several thousand frames, or tens of seconds. Increasing the switching rates using stronger excitation can improve the time resolution⁸, but such high excitation intensity can increase photobleaching. Moreover, in the case of fluorescent proteins, which are often the best labels for live samples, attempting a fast switching rate can cause signal degradation⁹.

An alternative approach is to increase the density of activated fluorophores so that each camera frame samples more molecules. However, this high density of fluorescent spots causes them to overlap, invalidating the widely used single-molecule localization method. Recently, a number of methods have been reported that can efficiently retrieve single-molecule positions even when

the single fluorophore signals overlap. These methods are based on fitting clusters of overlapped spots with a variable number of point-spread functions (PSFs) with either maximum likelihood estimation¹⁰ (for example, using the DAOSTORM algorithm¹¹) or Bayesian statistics¹². The Bayesian method has also been applied to the whole image set^{13,14}. Here we present another approach based on global optimization using compressed sensing, which does not involve estimating or assuming the number of molecules in the image. We show that compressed sensing can work with much higher molecule densities compared to DAOSTORM and demonstrate live-cell imaging of fluorescent protein-labeled microtubules with 1-s temporal resolution.

Compressed sensing has shown great success in many different fields of signal processing^{15,16}. If the original signal is sparse (that is, mostly zero) or can be made sparse after a given transformation, compressed sensing can precisely recover signal from highly noisy or corrupted measurements. Compressed sensing classically deals with a linear measurement b of the original signal x

$$b = Ax \quad (1)$$

where the matrix A is a known measurement function. If x is sparse, it can be exactly recovered by minimizing its L_1 norm (the sum of the absolute value of each element)

$$\text{minimize } \|x\|_1 \text{ subject to } b = Ax \quad (2)$$

even when b has far fewer elements than x has.

In STORM, the camera image has a linear and shift-invariant relationship with the true molecule distribution to be recovered. To model this relationship as in equation (1), we introduce a discrete grid to describe the molecule positions instead of using a list of molecule coordinates as is typically done to represent super-resolution images. The grid spacing is kept much smaller than the camera pixel size (for example, one-eighth the pixel size) to ensure sufficient accuracy. In this representation, both the molecule distribution in each camera frame, x , and the final super-resolution image summed from all frames are gridded images (Supplementary Fig. 1). In each camera frame, every grid point in x represents the brightness of a molecule located at this point. Grid points with no molecules fluorescing will have a value of 0. We then model the camera image as the correlation of the fluorescence distribution, x , with the PSF, in a matrix form, as shown in equation (3). In this case, b corresponds to the camera image, and A corresponds to the PSF. The stochastic switching events sparse fluorophore distribution in each frame that is, most of

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FALCON: fast and unbiased reconstruction of high-density super-resolution microscopy data

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Super resolution microscopy such as STORM and FPALM is now a well known method for biological studies at the nanometer scale. However, conventional imaging schemes based on sparse activation of photo-switchable fluorescent probes have inherently slow temporal resolution which is a serious limitation when investigating live-cell dynamics. Here, we present an algorithm for high-density super-resolution microscopy which combines a sparsity-promoting formulation with a Taylor series approximation of the PSF. Our algorithm is designed to provide unbiased localization on continuous space and high recall rates for high-density imaging, and to have orders-of-magnitude shorter run times compared to previous high-density algorithms. We validated our algorithm on both simulated and experimental data, and demonstrated live-cell imaging with temporal resolution of 2.5 seconds by recovering fast ER dynamics.

Supplementary Information is available for this article. Supplementary Information is available for this article. Supplementary Information is available for this article.

Min, J. et al, Sci. Rep., 2014

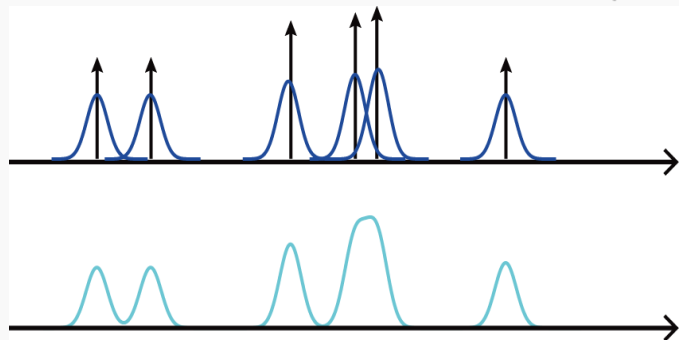
Better Localization Performance

ALPHA for localization microscopy

ALPHA principle

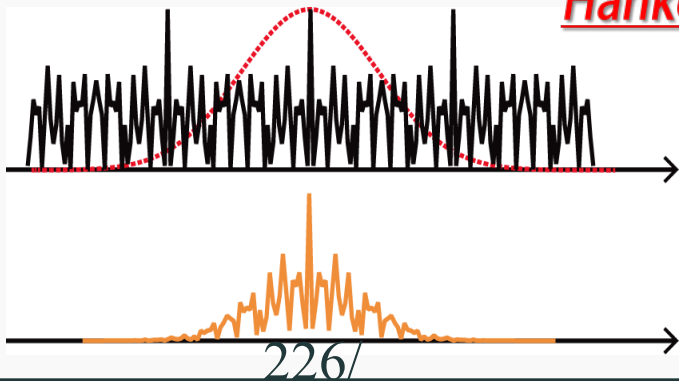
Image: $g = h * f$

f : Sparse



Fourier: $\hat{g} = \hat{h} \odot \hat{f}$

\hat{f} : Low-rank
Hankel matrix



✓ *PSF estimation*

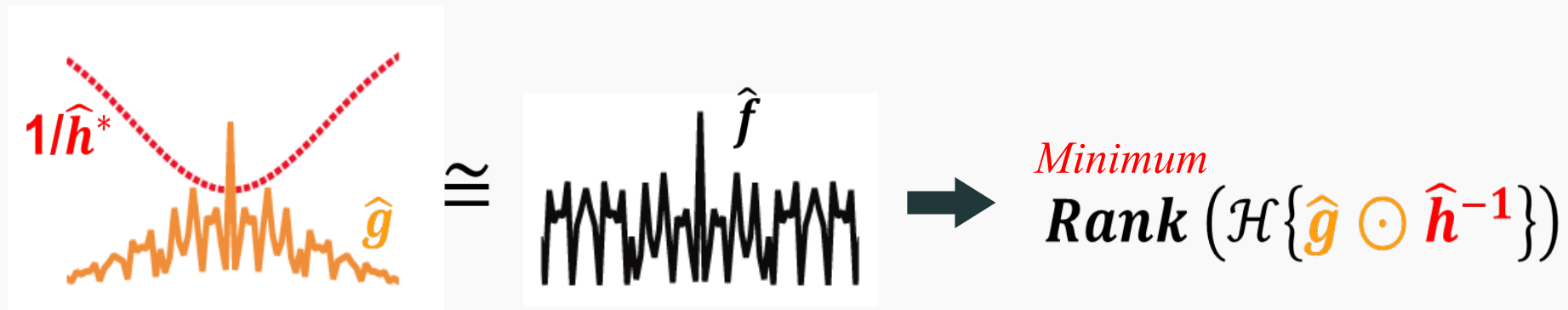
✓ *Deconvolution*

✓ *Grid-free localization*

PSF estimation

- HD localization algorithms usually assume that PSF is known and fixed
 - Requiring additional training low-density data set
 - In live experiment, PSF is varying in time and space both.

Key idea: Optimal PSF h^* \Rightarrow minimum rank of Hankel matrix



- Under symmetric Gaussian PSF model, its width (σ) is estimated by minimizing Schatten norm

$$\sigma^* = \min_{\sigma} \left\| \left(\mathcal{H} \{ \hat{g} \odot \hat{h}_{\sigma}^{-1} \} \right) \right\|_P \quad (p < 1)$$

Grid-free localization

- Now, we have entire Fourier spectrum \hat{f}
- Localization is nothing but spectral estimation problem!

$$\hat{f}(m, n) = \sum_i c_i e^{-j2\pi(\frac{mx_i}{M} + \frac{ny_i}{N})} = \sum_i c_i p_i^m q_i^n$$

- We used ACMP (algebraically coupled matrix pencils) algorithm (Vanpoucke et al, 1994)
- Data matrix $Z^{M \times N}$ of rank k , having no shared harmonics of p_i, q_i

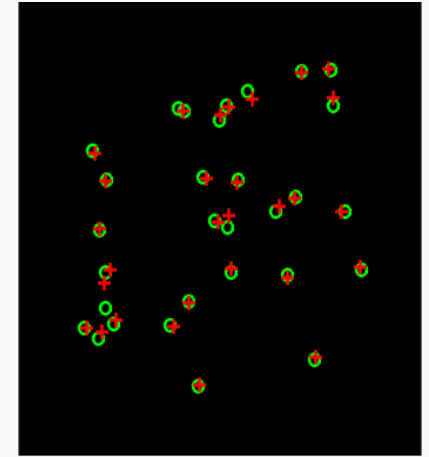
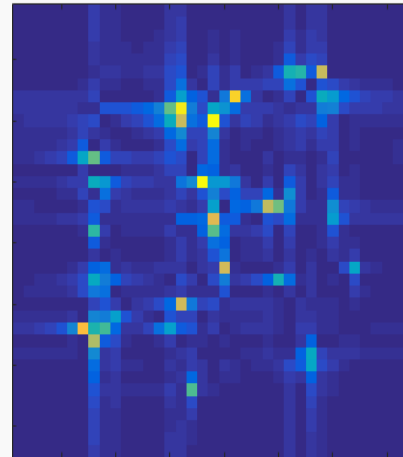
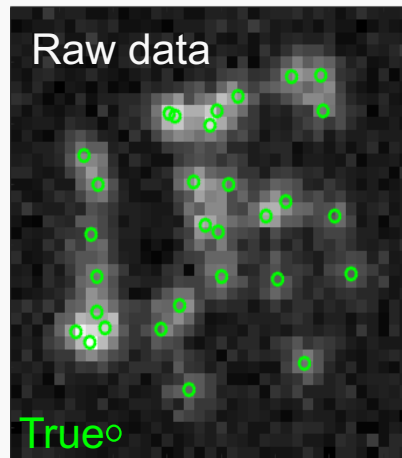
$$Z^{M \times N} = P^{M \times k} C^{k \times k} Q'^{N \times k}$$

- In Matrix form: $Z^{M \times N} = P^{M \times k} C^{k \times k} Q'^{N \times k}$

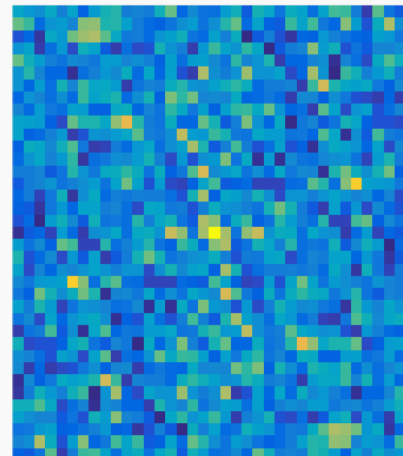
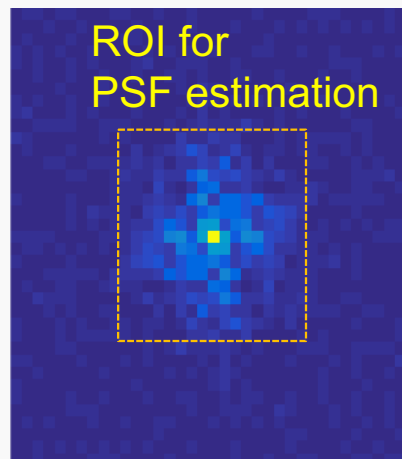
- P, Q are Vandermonde matrix, C is diagonal

Algorithm procedure

Image



Fourier

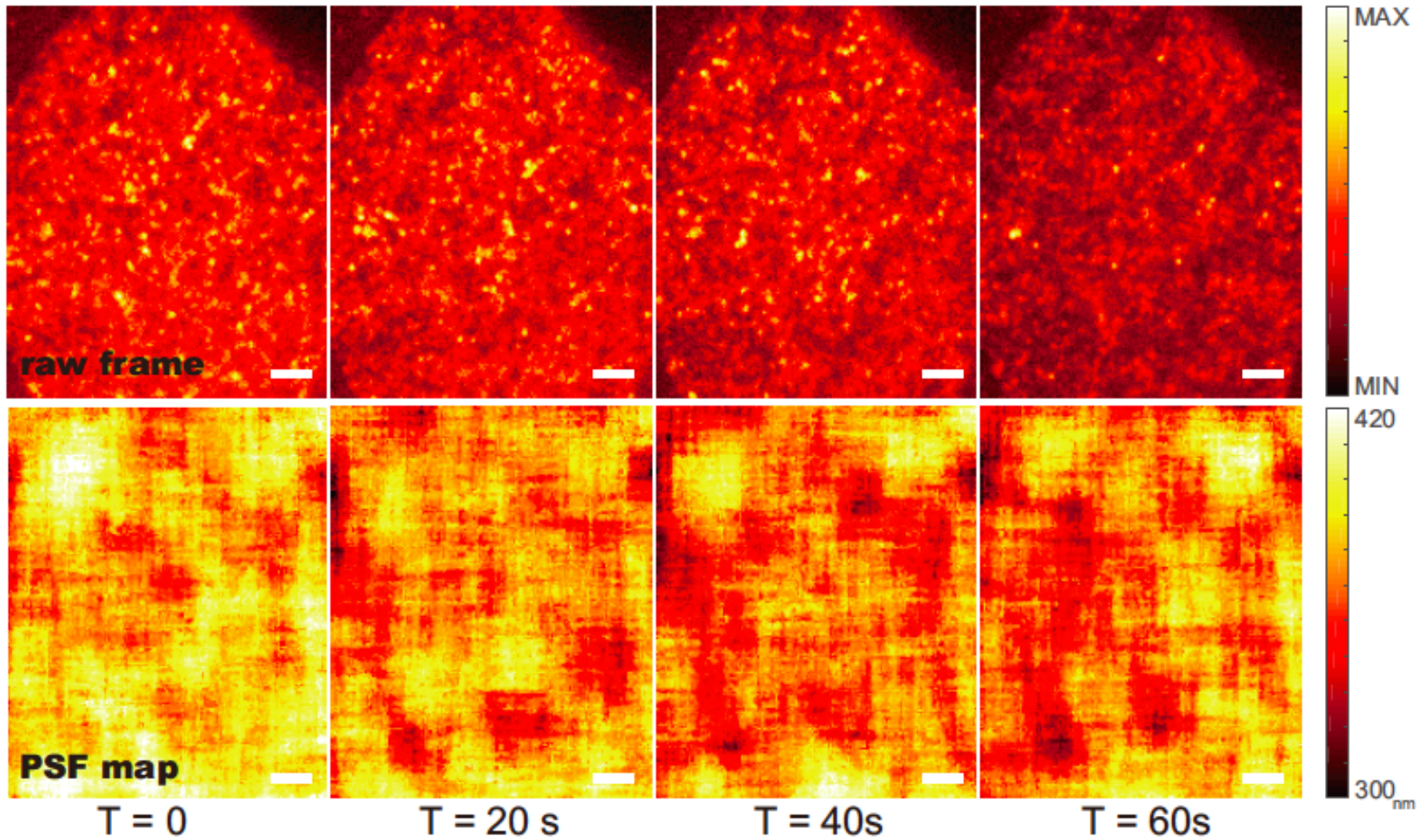


**3. Grid-free
Localization**

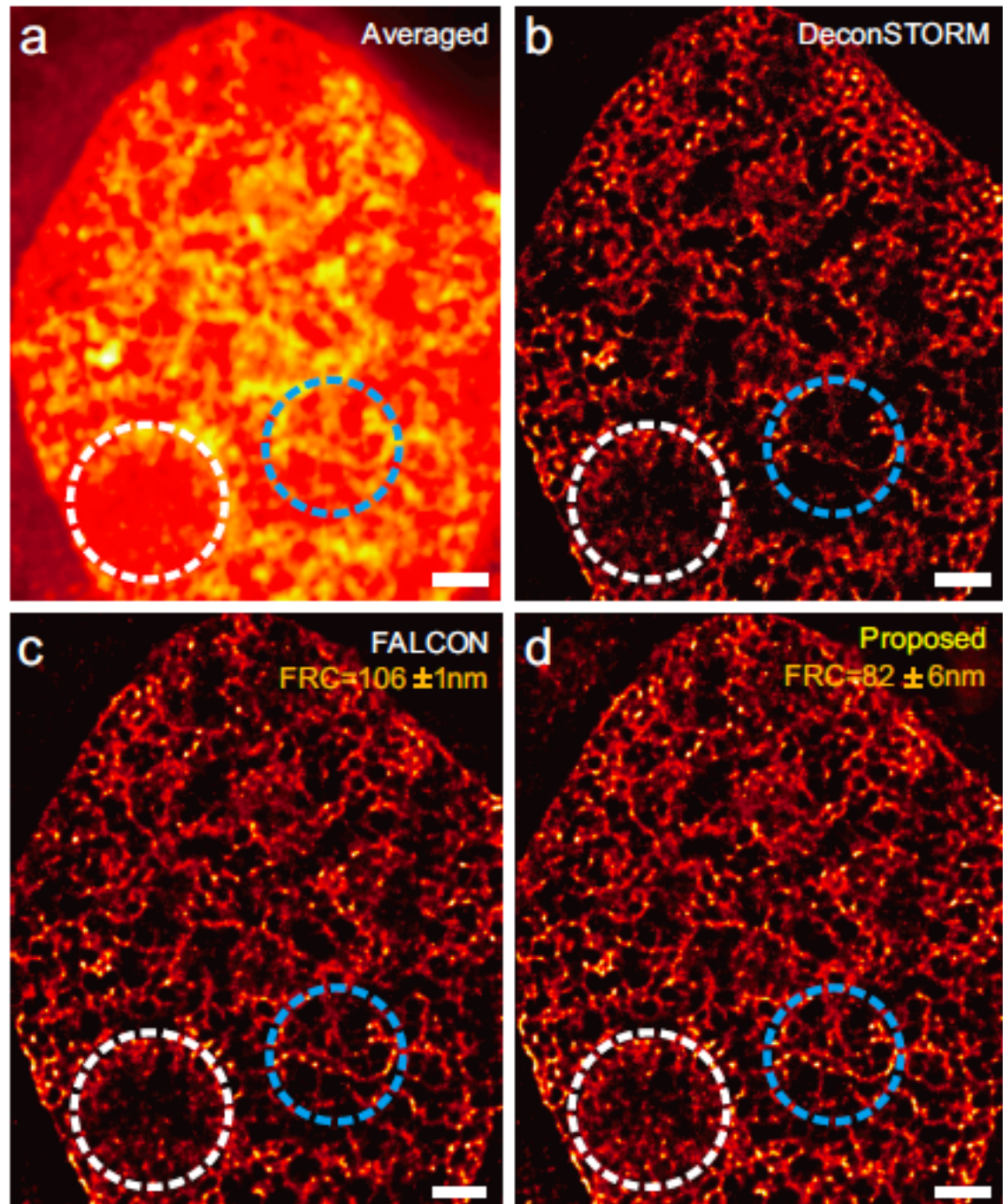
1. PSF estimation

2. Deconvolution

PSF variation along time

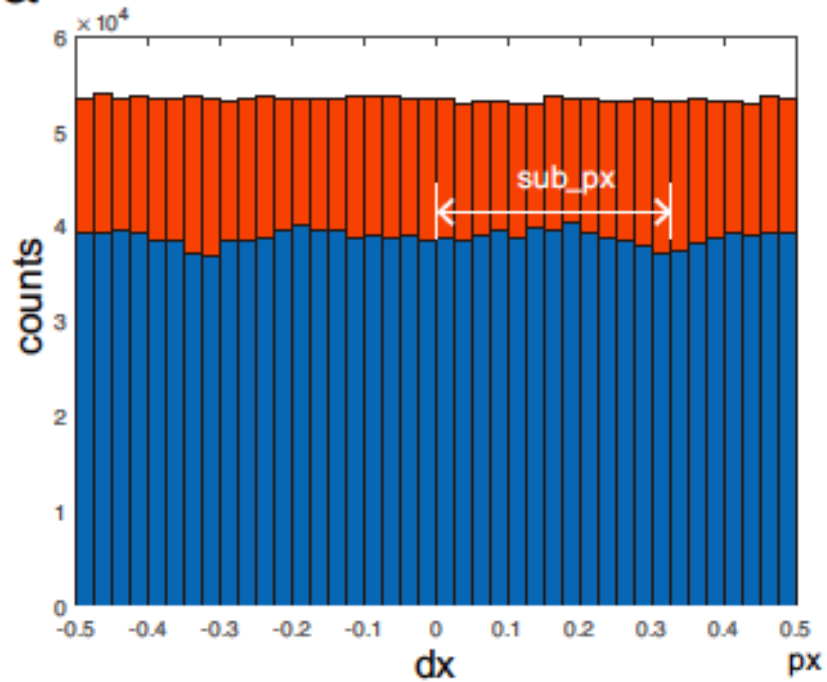


Reconstruction

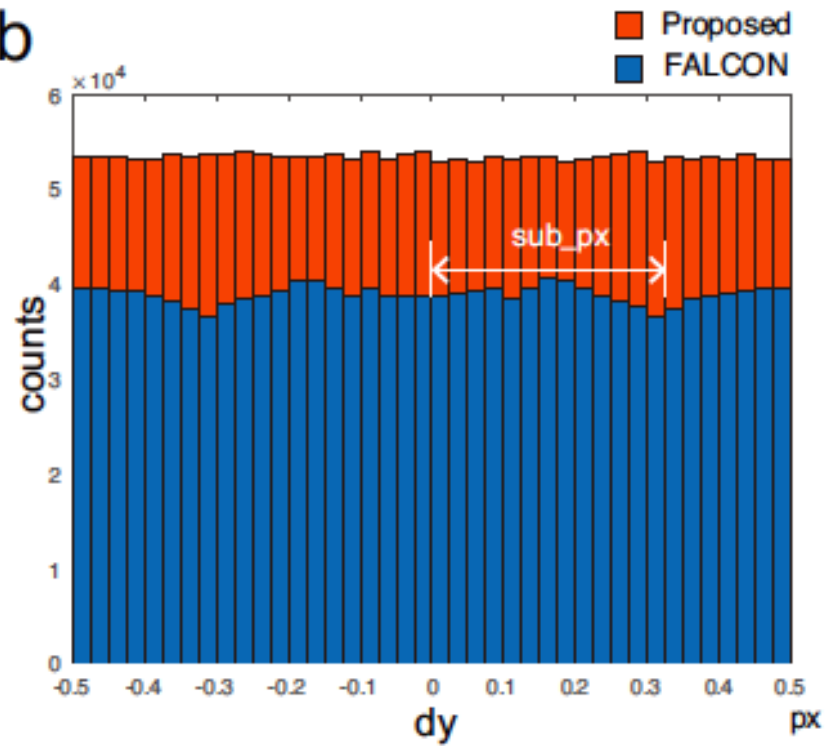


Localization bias

a



b



Free MATLAB software available

<https://research.engineering.uiowa.edu/cbig/software>

<http://bispl.weebly.com/aloha-for-mri.html>

Conclusions

- Off-the-grid = Continuous domain representation
- *Compressive off-the-grid imaging:*
Exploit continuous domain modeling to improve image recovery from few measurements
- Two realizations: extrapolation, interpolation
 - Extrapolation: FRI theory
 - Interpolation: Structured low-rank matrix completion
- Performance guarantee for structured low-rank approach
 - 1D, 2D theory \rightarrow near optimal performance guarantee

Conclusions (cont.)

- Extensive applications
 - MRI
 - Compressed sensing MRI, parallel MRI
 - Super-resolution MRI
 - MR artifact removal
 - Image processing: inpainting, impulse noise denoising
 - Other imaging applications
 - US imaging
 - Optics
- A missing link between analytic recon and CS ?

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