Self-similarity of images in the Fourier domain, with applications to MRI

G. S. Mayer and E. R. Vrscay
Department of Applied Mathematics
University of Waterloo, Waterloo, Ontario, Canada

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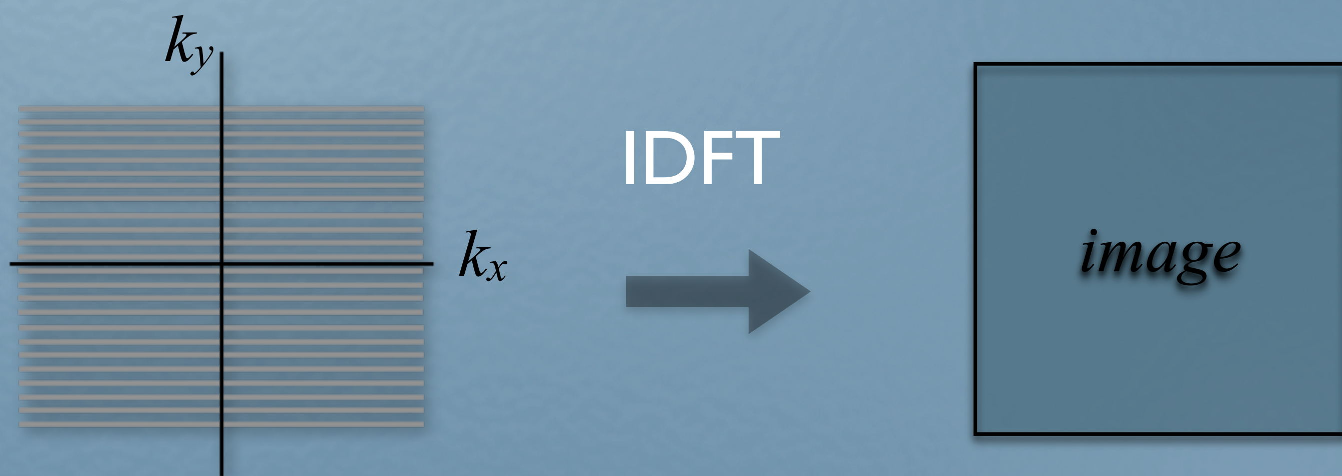
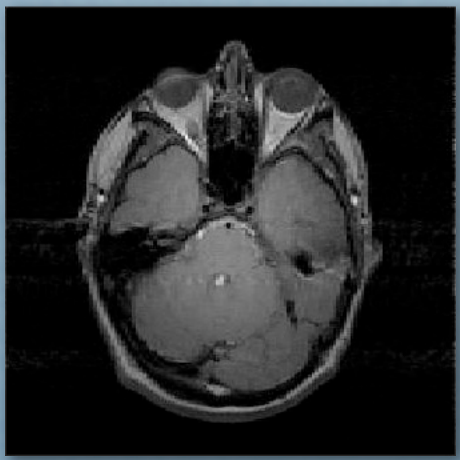
Limitations of MRI

- raw data, U_0, acquired over finite region in Fourier space
- image u_0 obtained via inverse discrete Fourier transform



- discrete image has limited spatial resolution
- artifacts introduced when performing IDFT

Magnetic Resonance Imaging (MRI)



- measures proton density
- non-invasive
- uses radio frequency signals to acquire images
- data acquired in the Fourier domain

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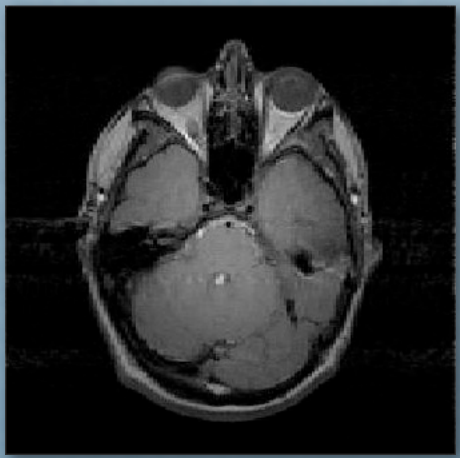

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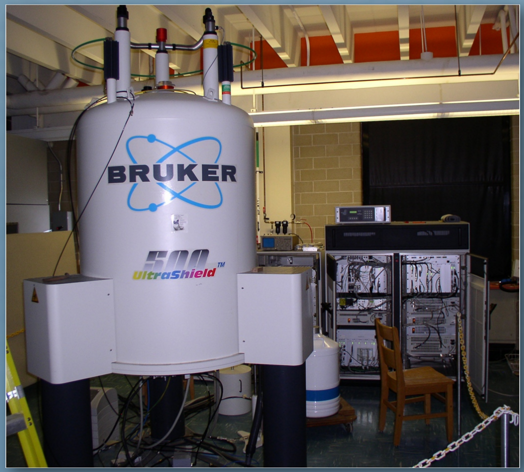

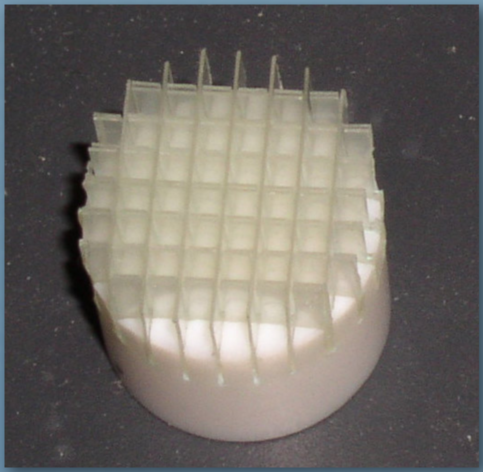

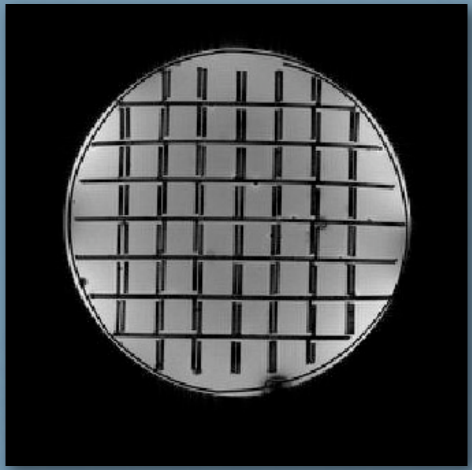

Resolution Enhancement

frequency extrapolation is related to resolution enhancement

$$\Delta x \propto \frac{1}{k_{x,max}}$$

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earlier work on frequency extrapolation include:

Papoulis-Gerchberg algorithm and other Projection methods
ARMA modelling

these techniques use known information about object to extrapolate frequency data

ICIAR 2007

- last year we presented an Iterated Function System based method to perform extrapolation in the frequency domain
- the basic idea:

$$U(k) = \sum_{m=1}^{N_{maps}} \mathrm{e}^{-2\pi i a_m k} \Big[c_m U(s_m k) + F_m(k) \Big]$$

$U(k)$ = given data
$F_m(k)$ = known function
$|s_m| < 1$

- $U(k)$ is determined by $U(s_m k)$
- a mechanism for extrapolation is present

Local Self-Similarity

One Domain Block

$$\mathbf{r} \approx \alpha_m \mathbf{d}_m + \beta_m$$

Linear Combination of Domain Blocks

$$\mathbf{r} \approx \beta + \sum_{m \in \Lambda} \gamma_m \mathbf{d}_m$$

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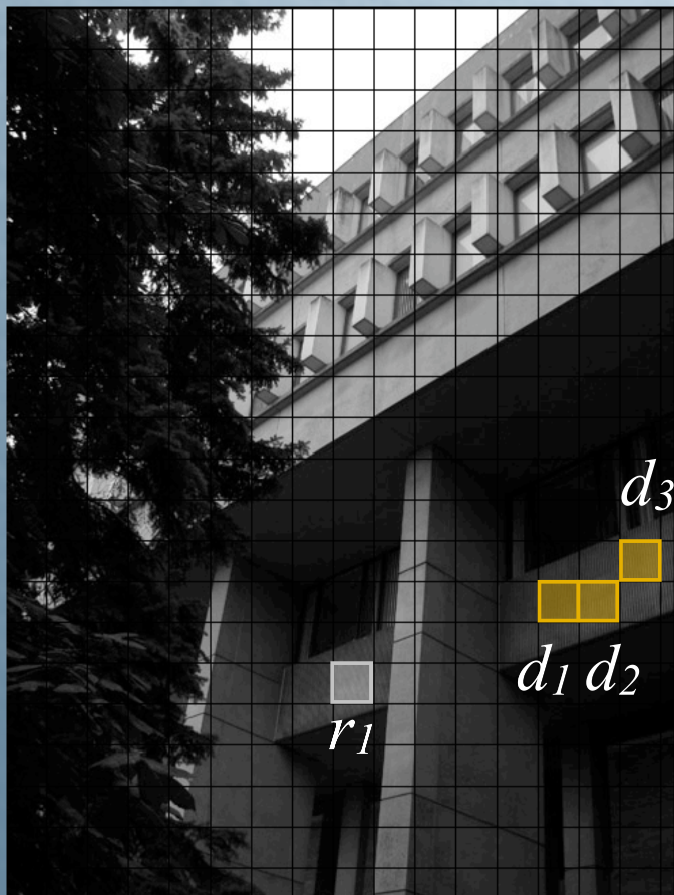

r_1

d_1

d_2

d_3

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Collage Error Probability Histograms (CEPH)

error in approximating range block $\mathbf{r}_{\mathrm{p}}$ by domain block $\mathbf{d}_{\mathrm{q}}$:

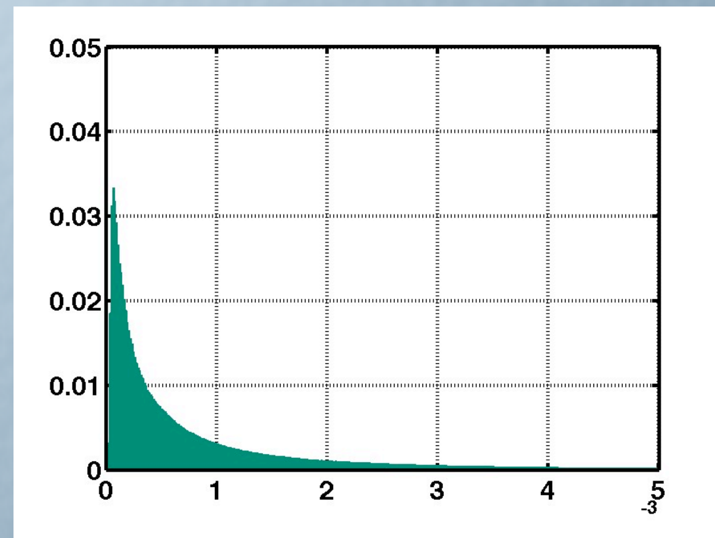
$$\Delta_{p,q} = \sqrt{\frac{1}{N_P^2} \sum_{m,n=1}^{N_P} |\mathbf{r}_p(m,n) - \alpha_q \mathbf{d}_q(m,n) - \beta_q|^2}, \; p,q = 1,2,\ldots,N_{DB}, \; p \neq q$$

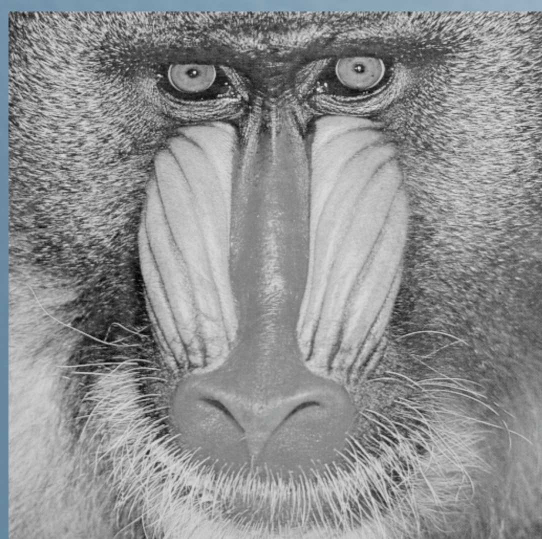
N_P^2 = number of points in each block

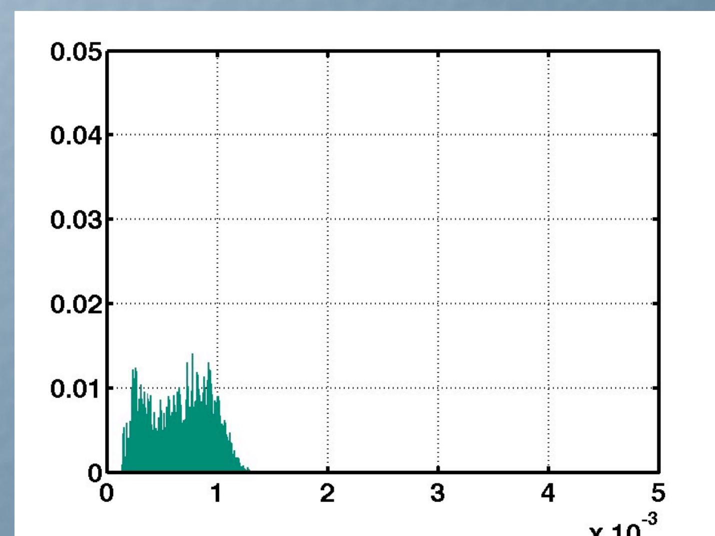
N_{DB} = number of domain blocks

$\Delta_{p,q}$ = "collage error" between $\mathbf{r}_p$ and $\mathbf{d}_q$

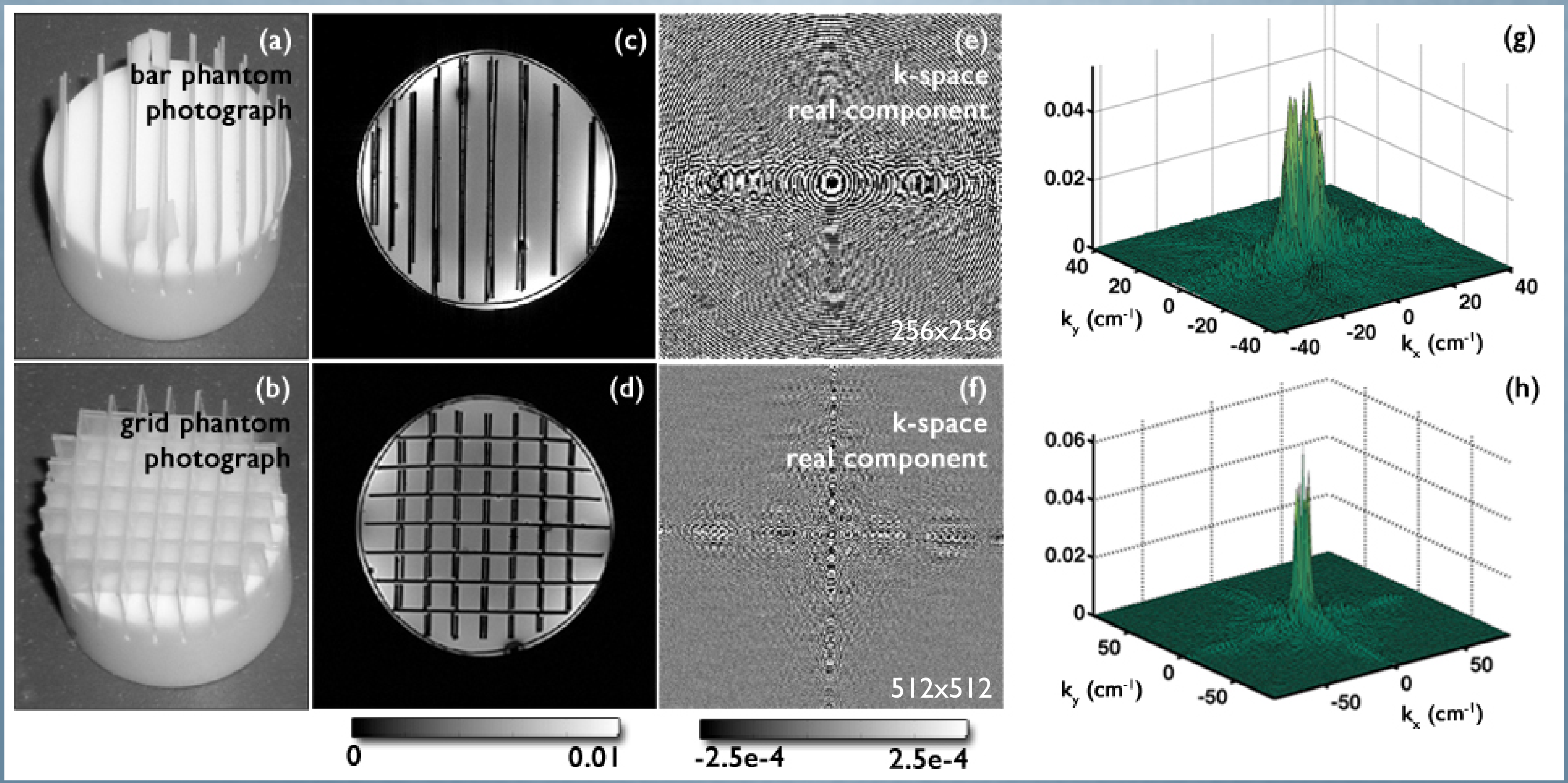
CEPH: Examples





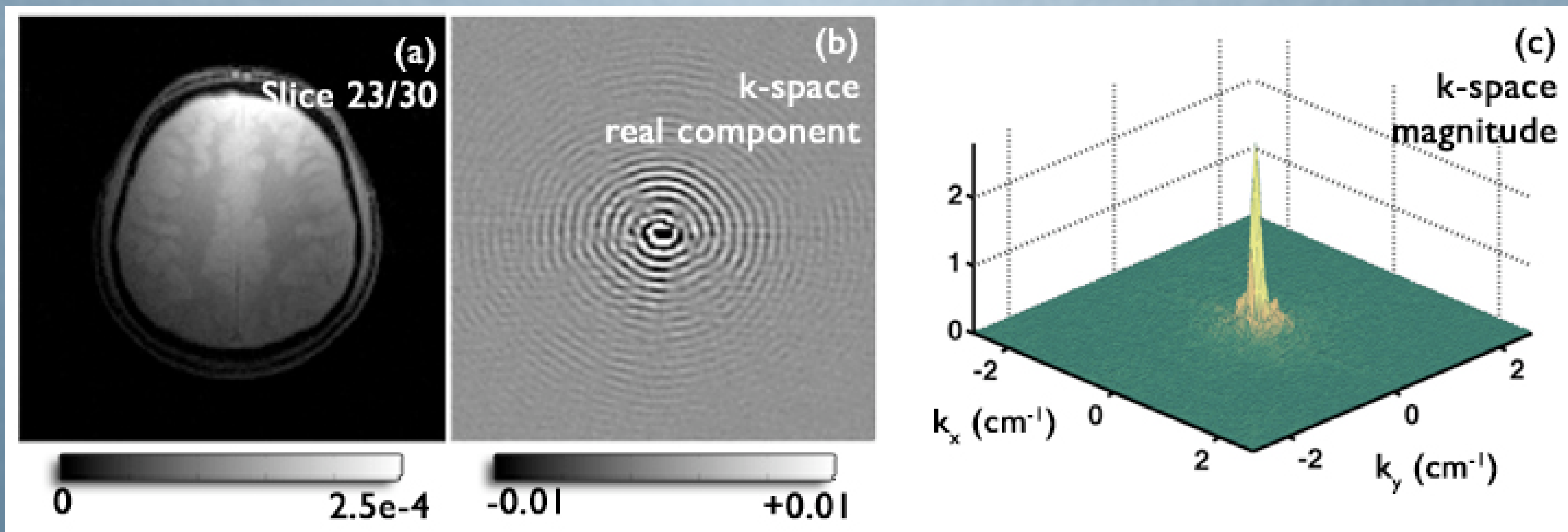


Phantom MRI Data



11.7 T MRI system (Bruker), using a gradient echo sequence, TR/TE 800/5 ms, FOV 3 cm

Human Brain MRI Data

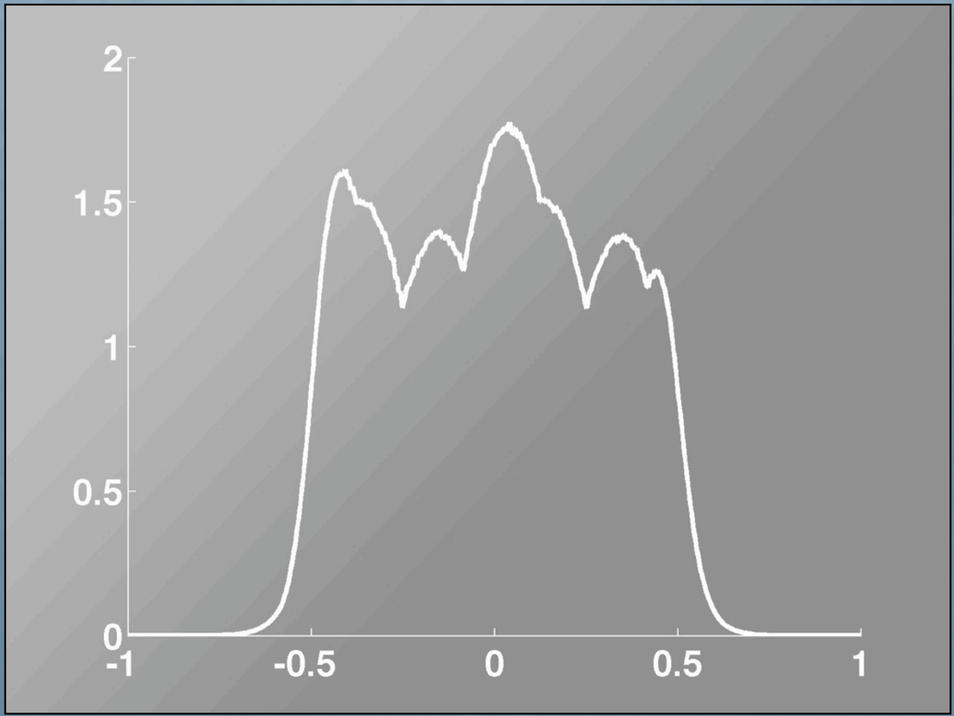


3.0 T MRI system (General Electric Medical Systems; Waukesha, WI), using a multislice spoiled gradient-recalled echo sequence, FOV 24 cm, slick thickness 4 mm, TR/TE 200/3.1 ms, flip angle 18 degrees

One Dimensional MRI Model

piecewise constant “boxcar” model for spatial data

$$u_{N_C}(x) = \sum_{m=1}^{N_C} c_m W_m(x), \quad W_m(x) = \begin{cases} 1, & \left|\frac{x-p_m}{\Delta x}\right| \leq \frac{1}{2} \\ 0, & \left|\frac{x-p_m}{\Delta x}\right| > \frac{1}{2} \end{cases}$$



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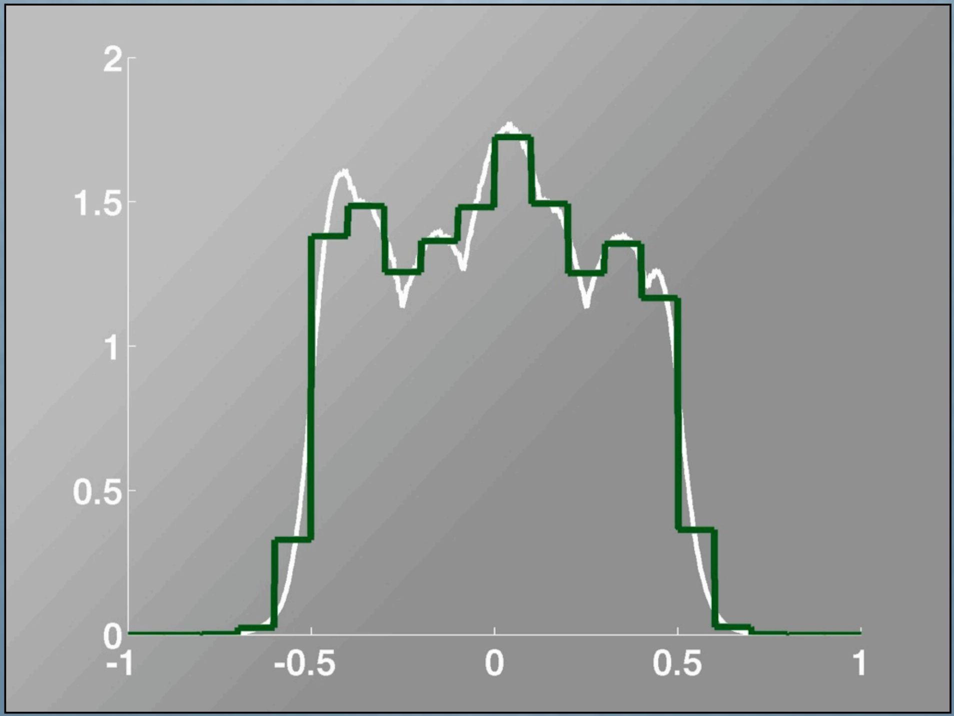

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algebraic manipulation (Fourier transform, multiply by -2π*ik*, sampling) yields a <u>complex trigonometric polynomial</u>

$$\hat{s}_{N_C}(n) = \sum_{m=1}^{2N_C} d_m e^{-2\pi i n r_m}, \; n = 0, 1, 2, \ldots, N_S - 1$$

this is our model of 1D MRI data

Linear Prediction Equation

$$\hat{s}_{N_C}(n) = \sum_{m=1}^{2N_C} d_m e^{-2\pi i n r_m},\ n = 0, 1, 2, \ldots, N_S - 1$$

complex polynomials are linearly predictable:

$$\hat{s}_{N_C}(n) = -\sum_{m=1}^{2N_C} a_m \hat{s}(n-m), \quad n = 2N_C, 2N_C + 1, \ldots, N_S - 1$$

- consequence of Prony's method
- provides a mechanism for extrapolation
- suggests self-similarity

Fractal Coding of 1D MRI Data

consider a complex discrete signal

$$s(n) \in l^2(\mathcal{C}), \quad n = 0, 1, 2, \ldots N_S - 1$$

$s(0)$	$s(1)$	$s(2)$											$s(N_S\text{-}2)$	$s(N_S\text{-}1)$

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construct a range block **r** from the last N_P points:

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r

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$\mathbf{d}_1$

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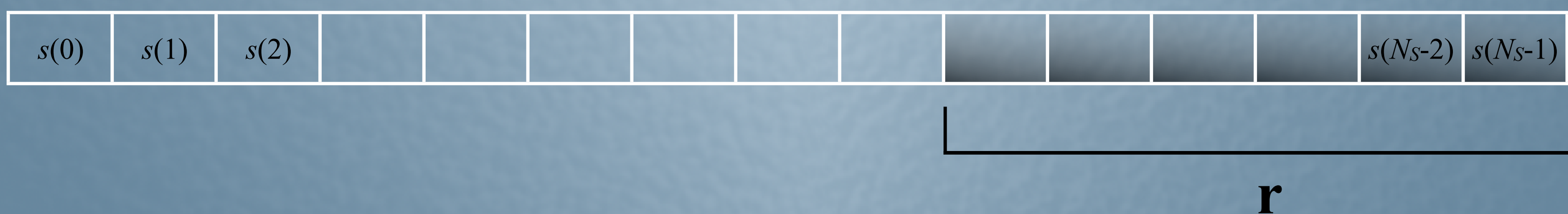

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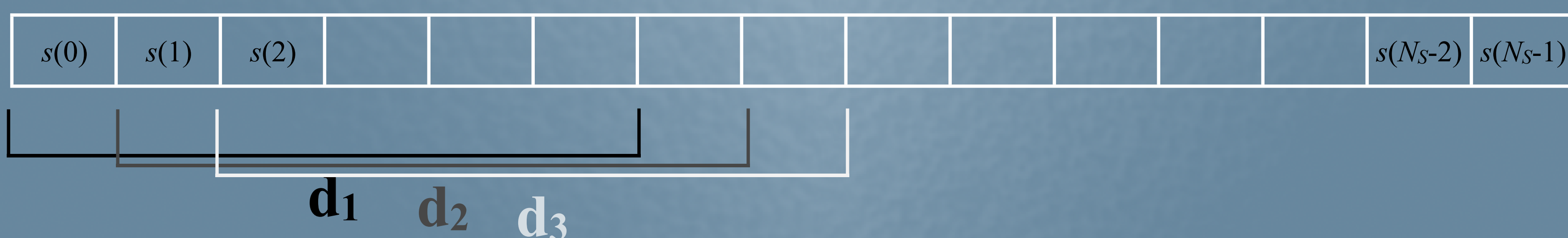


Results of 1D Analysis

1. range block represented <u>exactly</u> by a sum of domain blocks (consequence of Prony's method)

$$\mathbf{r} = -\sum_{m=1}^{2N_C} a_m \mathbf{d}_m$$

2. establishes relation between physical and fractal parameters:

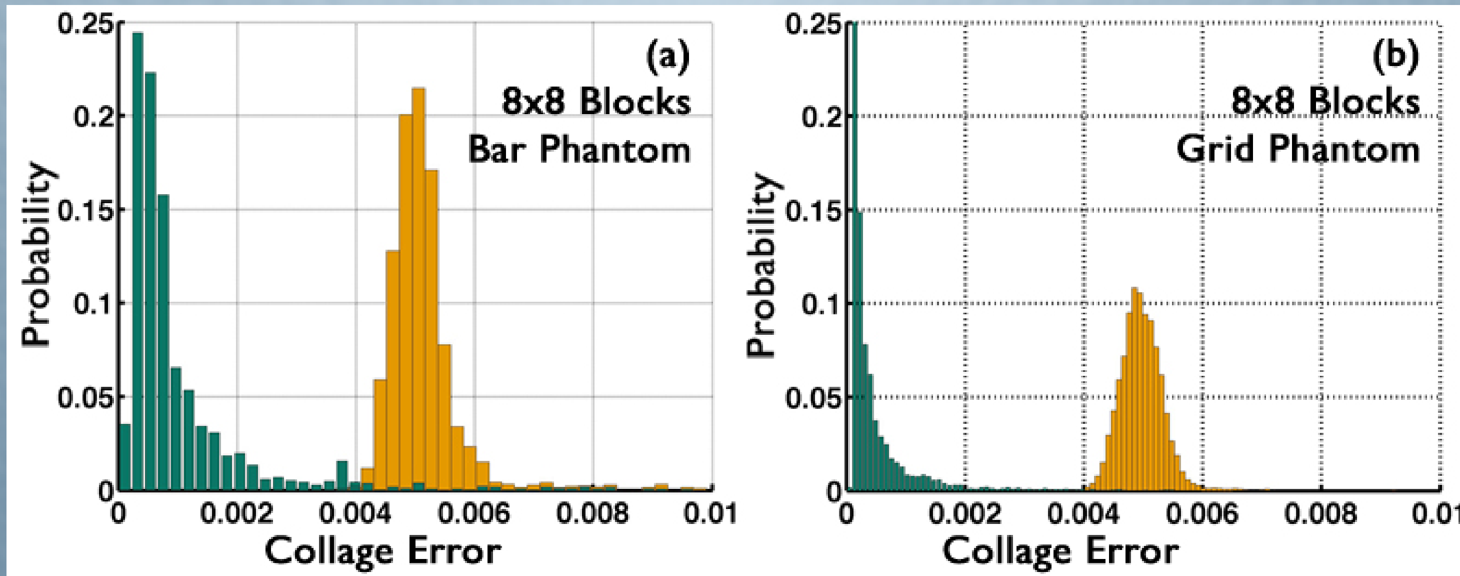
$$\alpha_m = -a_m, \quad m = 1, 2, 3, \ldots, 2N_C$$

3. this shows that 1D MRI data, with piecewise constant model, is self similar

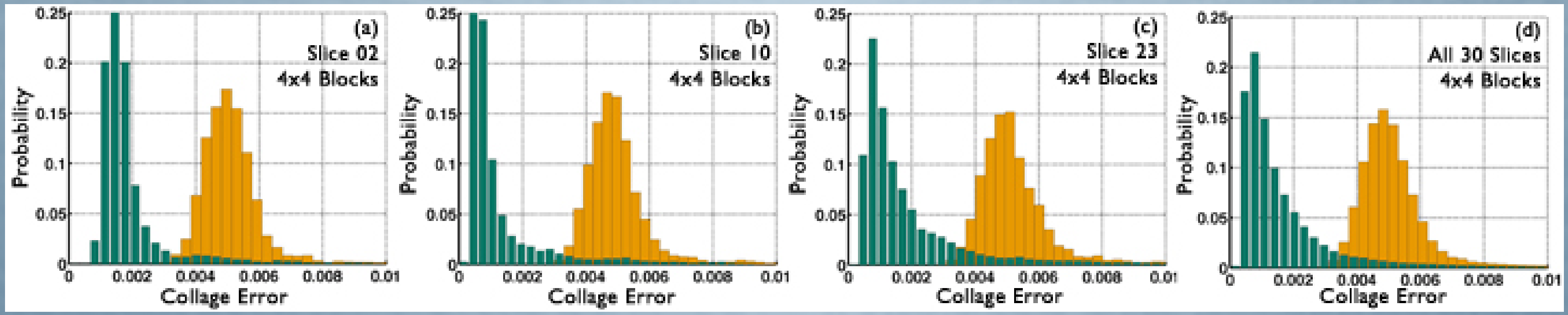
2D Empirical Analysis

- constructed collage error probability histograms (CEPH)
- partitioned *k*-space data sets into non-overlapping blocks
- domain and range block sets were exactly the same
- for each range block, $\mathbf{r}_p$, all possible domain blocks, $\mathbf{d}_q$, were compared using this norm:

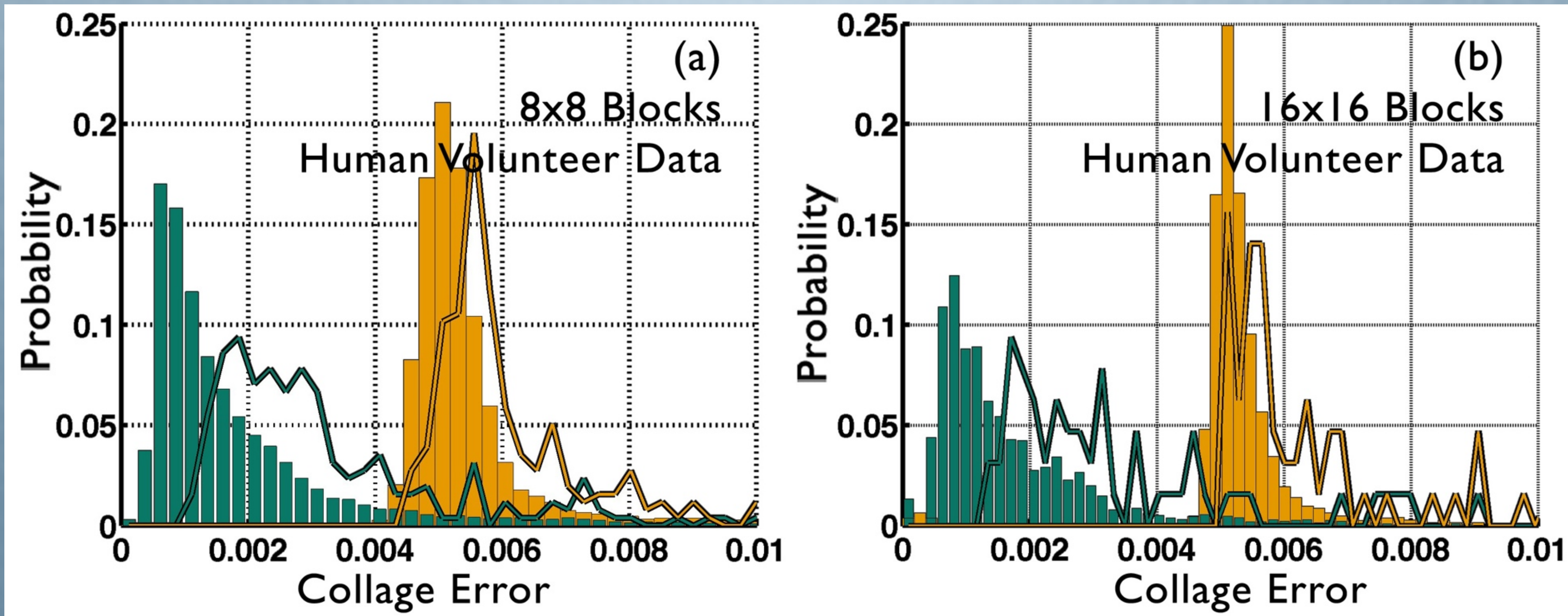
$$\Delta_{p,q} = \sqrt{\frac{1}{N_P^2} \sum_{m,n=1}^{N_P} |\mathbf{r}_p(m,n) - \alpha_q \mathbf{d}_q(m,n) - \beta_q|^2}, \; p,q = 1,2,\ldots,N_{DB}, \; p \neq q$$



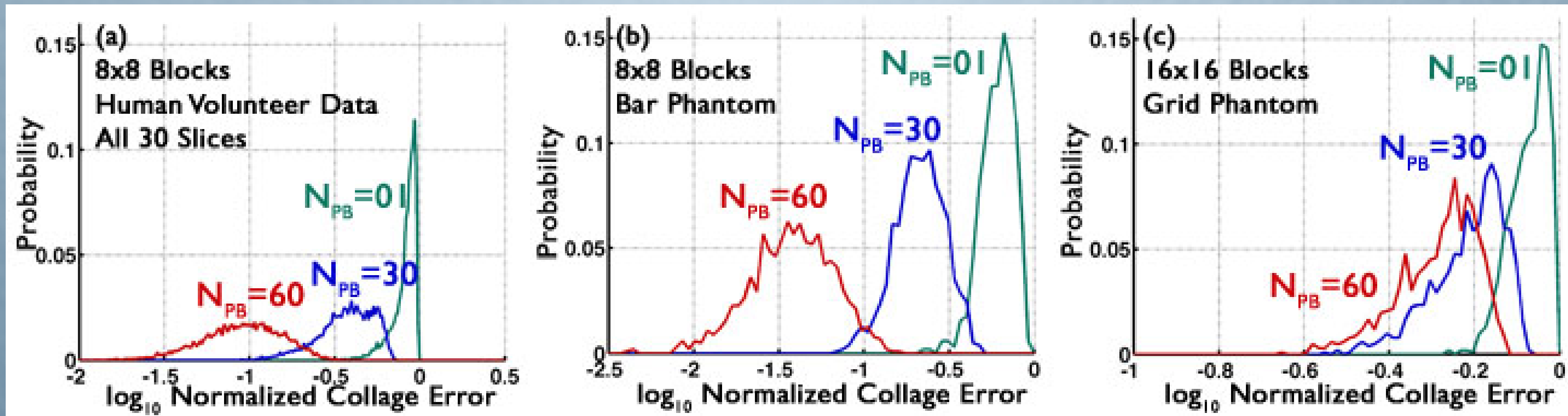
- CEPHs from phantom data using 8 x 8 blocks (green)
- corresponding histograms with added complex zero mean noise with SD 0.005 (orange)



- (a) to (c) human volunteer CEPHs (green) using 4x4 blocks
- corresponding CEPHs after noise was added (orange)
- CEPHs in (d) were calculated from all 30 slices.



- (a) and (b) human volunteer CEPHs (green) from all 30 slices using different block sizes, and the corresponding CEPHs after noise was added (orange).
- Green and orange lines correspond to range block SD histograms.



- normalized multi-parent CEPHs using N_{PB}=1, 30, and 60
- from various data sets
- errors plotted on $\log_{10}$ scale
- collage errors normalized by the SD of range block
- N_{PB} blocks for each range block with the lowest collage errors used to calculate least squares projection onto N_{PB} blocks

Conclusions

1D Analysis

- extended IFS methods to frequency data
- found self-similar model for 1D MRI data
- discovered physical interpretation of fractal parameters

2D Analysis

- explored self-similarity of 2D complex Fourier MRI data
- both phantom and human brain data exhibit self-similarity

Future Work

- use self-similarity as a constraint for frequency domain extrapolation of MRI data