A general framework for compressed sensing and parallel MRI using annihilating filter based low-rank Hankel matrix

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**Abstract**

**Purpose:** Parallel MRI (pMRI) and compressed sensing MRI (CS-MRI) have been considered as two distinct reconstruction problems. Motivated by recent breakthroughs such as SAKE (simultaneous auto-calibrating and k-space estimation) or LORAKS (Low-rank modelling of local k-space neighborhoods), an annihilating filter based low-rank Hankel matrix approach (ALOHA) is proposed as a general framework which unifies pMRI and CS-MRI as a weighted k-space interpolation problem.

**Theory and Methods:** Our framework exploits an annihilating filter relationship originating from the sparsity in the transform domain as well as from parallel acquisition physics. This results in a rank-deficient Hankel structured matrix, whose missing data can be recovered with a low rank structured matrix completion algorithm after a k-space weighting. In particular, when the underlying image can be sparsified with a wavelet transform, the low rank matrix completion problem can be solved with a multi-scale pyramid resulting in efficient computation.

**Results:** Experimental results with in vivo data for single/multi-coil imaging as well as dynamic imaging confirmed that the proposed method outperforms the state-of-the-art pMRI and CS-MRI.

**Conclusion:** By reformulating the pMRI and CS-MRI as a weighted k-space interpolation problem that can be solved using a low rank Hankel structured matrix completion, the generalized ALOHA framework provides better insight into MRI reconstruction problems.

Keywords: Parallel MRI, Compressed Sensing, Annihilating filter, Structured low rank block Hankel matrix completion, wavelets, Pyramidal representation
Introduction

MRI is an imaging system that sequentially acquires k-space data corresponding to the Fourier transform of an object. This enables us to apply various advanced signal processing techniques. Recently, compressed sensing theory \[1,2\] has been used in accelerated MRI \[3,6\]. Compressed sensing algorithms can restore original signals from much less k-space data by exploiting the sparsity of an unknown image in total variation (TV) or wavelet transform domains, and incoherent sampling schemes such as Gaussian random or Poisson disc are usually required. Accurate MRI reconstruction from less data makes compressed sensing a hot topic in the research community; thus, it has been applied across many different application areas such as in pediatric imaging \[7\], dynamic cardiac MRI \[8,10\], perfusion imaging \[11\], angiography \[12\], and so on.

On the other hand, parallel MRI (pMRI) \[1,3\] exploits the diversity in the coil sensitivity maps that are multiplied by an unknown image. This provides additional spatial information for the unknown image, resulting in accelerated MR data acquisition through k-space sample reduction. Representative parallel imaging algorithms such as SENSE (sensitivity encoding) \[13\] or GRAPPA (generalized autocalibrating partially parallel acquisitions) \[14\] require regularly sampled k-space data for computationally efficient reconstruction. Moreover, additional k-space data, the so-called auto calibration lines (ACS), are often required to estimate the coil sensitive maps or GRAPPA kernels \[14\].

Because the aim of the two approaches is accelerated acquisition by reducing the k-space data, extensive research efforts have been made to synergistically combine the two for further acceleration. One of the most simplest approaches can be a SENSE type approach that explicitly utilizes the estimated coil maps to obtain an augmented compressed sensing problem:

\[
\min_x \|Wx\|_1 \quad \text{subject to } \ g = \begin{bmatrix} g_1 \\ \vdots \\ g_r \end{bmatrix} = \begin{bmatrix} A[S_1] \\ \vdots \\ A[S_r] \end{bmatrix} f
\]

where \(f\) and \(g_i\) denote the unknown image and the k-space measurements from the \(i\)-th coil, respectively; \(A\) is a subsampled Fourier matrix; \(W\) is a sparsifying transform, and \([S_i]\) denotes a diagonal matrix whose diagonal elements come from the \(i\)-th coil sensitivity map. The multichannel version of k-t FOCUSS \[8\] is one of the typical examples of such approaches. On the other hand, \(l_{1}\)-SPIRiT (\(l_{1}\)-iTerative Self-consistent Parallel Imaging Reconstruction) utilizes the GRAPPA type constraint as an additional constraint for a
compressed sensing problem:

\[
\min_{F} \| \Psi F \|_{1,2} \quad (2)
\]

subject to \[ G = AF \quad (3) \]

Vec(F) = M \cdot Vec(F) \quad (4)

where \( F = [f_1 \ f_2 \ \cdots \ f_r] \), \( G = [g_1 \ g_2 \ \cdots \ g_r] \) and \( \Psi \) denote a discrete wavelet transform matrix, and \( M \) is an image domain GRAPPA operator, and \( \text{Vec}(\cdot) \) is the vectorization operator. In both approaches, an accurate estimation of coil sensitivity maps or GRAPPA kernel is important to fully exploit the coil sensitivity diversity.

In order to overcome these difficulties, calibration-less parallel imaging methods have been extensively investigated, among which SAKE (simultaneous autocalibrating and k-space estimation) \[16\] represents one of the first steps. In SAKE, the missing k-space elements are reconstructed by imposing the data consistency and the structural maintenance constraints of the block Hankel structure matrix. However, the origin of the low rankness in the Hankel structured matrix for the case of a single coil measurement was not extensively investigated, and it was not clear whether SAKE could outperform the compressed sensing approach when it is applied to single coil data. Haldar \[17, 18\] ingeniously discovered that a Hankel structured matrix constructed by a single coil k-space measurement is low-ranked when an unknown image has finite support or a slow-varying phase. Based on this observation, he developed the so called LORAKS (Low-rank modeling of local k-space neighborhoods) algorithm \[17\] and its parallel imaging version, P-LORAKS (Low-rank modelling of local k-space neighborhoods with parallel imaging data) \[18\]. However, it is not clear how the existing theory can deal with large classes of image models that are not sparse by themselves but can be sparsified using various transforms such as wavelet transforms or total variations (TV), etc.

Therefore, one of the main goals of this paper is to develop a more general theory that encompasses the existing approaches. Toward that goal, first, we confirmed that SAKE and LORAKS are indeed special cases of a novel algorithm family, what we called ALOHA (Annihilating filter based LOw-rank Hankel matrix Approach). More specifically, we confirmed that the sparsity in the image domain can be directly related to the existence of annihilating filters \[19, 21\] in the k-space. Interestingly, the commutative relation between an annihilating filter and k-space measurements provides a rank-deficient Hankel structured matrix. This observation was first made by Haldar in the LORAKS algorithm \[17, 18\]. Our contribution here is a proof that the rank of the Hankel structured matrix is determined by the sparsity level in the image domain and the number of required MR k-space measurements is given by \( O(k \log^4 n_1) \), where \( k \) is the sparsity and
Another significant contribution of this paper is the generalization beyond the image domain sparsity. More specifically, if an image signal can be sparsified using transforms such as wavelets, TV, etc., we show that there exist annihilating filters and the corresponding low rank Hankel structured matrices in the weighted k-space domain. We verify that the rank of the resulting Hankel structured matrix is determined by the sparsity in the transform domain. This observation led us to seek more efficient sparsifying transforms, among which the dyadic biorthogonal wavelet transform is one of the most popular transforms. Interestingly, when an image can be sparsified with wavelet transforms, we can prove that the low rank structured matrix completion problem can be equivalently represented with a pyramidal decomposition and scale dependent k-space weighting. Accordingly, a low rank matrix structured completion algorithm can be progressively applied for each level of the pyramid to reduce the overall computational burden while maintaining superior image quality. Finally, we investigate multi-channel generalization to unify the parallel MRI with ALOHA. Specifically, we confirm that there exist additional inter-coil annihilating filter relationships that are unique in pMRI and derive a multi-coil extension of the generalized ALOHA scheme. If the uniform weighting scheme is used, then the construction of the stacked Hankel matrix turns out to be equivalent to those of SAKE and P-LORAKS. We further substantiate that the multi-channel stacking of the weighted Hankel structure matrix may fully exploit the coil diversity thanks to the relationship to the algebraic bound of multiple measurement vector (MMV) compressed sensing [22][24].

Because sparsity in the wavelet domain or TV is the main property that has been exploited by existing compressed sensing approaches, our generalized ALOHA framework can compete with the existing CS-MRI algorithms, as demonstrated by our in vivo experiments. Another important advantage of the proposed algorithm is that, compared to the existing CS-MRI, the reconstruction errors are usually scattered throughout the entire images rather than exhibiting systematic distortion along edges because the annihilating filter relationships are powerful in estimating the edge signals. Given that many diagnostic errors are caused by the systematic distortion of images, we believe that our generalized ALOHA framework may have great potential in clinical applications.

\[ n_1 \text{ is the dimension of the k-space}. \]

\[ \mathcal{O} \] denotes the “big O” notation.

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1Here, \( \mathcal{O} \) denotes the “big O” notation.
Theory

ALOHA

For better readability, the theory here is outlined by assuming 1-D signals, but the principle is identical for multidimensional signals. Consider a signal \( f(x) \) in the image domain that is composed of a set of \( k \)-Diracs within a support set \([0, \tau]\):

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

Then, the resulting MR signal is given by

\[
\hat{f}(\omega) = \sum_{j=0}^{k-1} c_j e^{-i\omega x_j}.
\]

In highly accelerated MRI, we measure a sparse subset of Fourier samples at \( \{\omega_i\}_{i=1}^m \) from a deterministic grid, whose grid size should be below the Nyquist limit \( \Delta = 2\pi/\tau \) to avoid aliasing artifacts; so the k-space measurement can be represented as

\[
\hat{f}[m] := \hat{f}(m\Delta) = \sum_{j=0}^{k-1} c_j e^{-i2\pi m x_j/\tau}, \quad m \in \Omega.
\]

Here, the index set \( \Omega \) denotes the sparse sampling positions and the k-space dimension \( n_1 \) is determined by the image domain resolution. From these sparse samples, the unknown positions \( \{x_j\}_{j=0}^{k-1} \) and their coefficients \( \{c_j\}_{j=0}^{k-1} \) need to be estimated.

The discrete spectral sampling model in Eq. (7) implies that the unknown signal in the image domain is an infinite periodic streams of Diracs with a period \( \tau \), which is indeed a signal with the finite rate of innovation (FRI) with rate \( \rho = 2k/\tau \) [19–21]. Therefore, theoretical results from the FRI sampling theory can be used [19–21]. In particular, the FRI sampling theory tells us that we can find an annihilating filter \( \hat{h}[n] \) such that

\[
(\hat{h} \ast \hat{f})[n] = \sum_{l=0}^{k} \hat{h}[l] \hat{f}[n-l] = 0, \quad \forall n.
\]

The specific form of the annihilating filter \( \hat{h}[n] \) for the case of (7) is given in Appendix for completeness. By sampling the time domain signal at the rate of innovations, the authors in [19–21] proved that the perfect recovery is guaranteed from noiseless measurement.
However, classical FRI sampling theory is quite limited for highly accelerated MRI, because FRI sampling theory was developed for time domain sampling. To extend the applicability of the theory beyond the time domain, here we propose a generalization to the k-space sampling. Specifically, if $\hat{h}[n]$ is an annihilating filter with $k + 1$ filter taps, then for any $k_1 \geq 1$ tap filter $\hat{a}[n]$, it is easy to see that the following filter with $\kappa = k + k_1$ taps is also an annihilating filter for $\hat{f}[n]$:

$$
\hat{h}_a[n] = (\hat{a} * \hat{h})[n].
$$

(9)

Accordingly, by removing the boundary data from the convolution, we can construct the following matrix equation:

$$
\mathcal{H}(\hat{f})\tilde{\hat{h}}_a = 0,
$$

(10)

where the Hankel structure matrix $\mathcal{H}(\hat{f})$ is constructed as

$$
\mathcal{H}(\hat{f}) = \begin{bmatrix}
\hat{f}[0] & \hat{f}[1] & \cdots & \hat{f}[\kappa - 1] \\
\hat{f}[1] & \hat{f}[2] & \cdots & \hat{f}[\kappa] \\
\vdots & \vdots & \ddots & \vdots \\
\hat{f}[n_1 - \kappa] & \hat{f}[n_1 - \kappa + 1] & \cdots & \hat{f}[n_1 - 1]
\end{bmatrix} \in \mathbb{C}^{(n_1 - \kappa + 1) \times \kappa}.
$$

(11)

and $\mathcal{H}(\hat{f})\tilde{\hat{h}}_a$ denotes a vector that reverses the order of the elements in $\hat{h}_a \in \mathbb{C}^\kappa$:

$$
\hat{h}_a = \begin{bmatrix}
\hat{h}_a[0] \\
\vdots \\
\hat{h}_a[\kappa - 1]
\end{bmatrix}^T = \mathcal{C}(\hat{h})\hat{a}
$$

(12)

$$
\mathcal{C}(\hat{h}) = \begin{bmatrix}
\hat{h}[0] & 0 & \cdots & 0 \\
\hat{h}[1] & \hat{h}[0] & \cdots & 0 \\
\vdots & \vdots & \ddots & \vdots \\
\hat{h}[k - 1] & \hat{h}[k - 2] & \cdots & \hat{h}[k - k_1] \\
\vdots & \vdots & \ddots & \vdots \\
0 & 0 & \cdots & \hat{h}[k - 1]
\end{bmatrix} \in \mathbb{C}^{\kappa \times k_1}
$$

(14)
Since \( \mathcal{C}(\hat{h}) \) is a convolution matrix, it is easy to see that

\[
\dim \mathcal{C}(\hat{h}) = k_1.
\]

Hence, we have

\[
\text{rank} \mathcal{H}(\hat{f}) = \kappa - k_1 = k, \tag{15}
\]

which is equal to the sparsity level. Accordingly, the missing k-space elements can be found by solving the following annihilating filter based low rank Hankel matrix (ALOHA) problem:

\[
(P_{ALOHA}) \quad \min_{m \in \mathbb{C}^{n_1}} \| \mathcal{H}(m) \|_* \tag{16}
\]

subject to

\[
P_{\Omega}(m) = P_{\Omega}(\hat{f}) \tag{17}
\]

where \( \| \cdot \|_* \) denotes the matrix nuclear norm and \( P_{\Omega} \) is the projection operator on the k-space sampling index set \( \Omega \).

Note that the problem \( (P_{ALOHA}) \) is equivalent to the spectral compressed sensing with the enhanced matrix completion (EMaC) \[24\]. In fact, using the powerful dual certificate and golfing scheme originally developed by David Gross \[26\], Chen and Chi \[25\] showed that if the number of spectral sample \( m \) is given by

\[
m > c_1 \mu_1 c_s k \log^4(n_1) \tag{18}
\]

for some constant \( c_1 \), then the perfect recovery of the missing spectral components is possible with a probability exceeding \( 1 - n_1^{-2} \). In \[18\],

\[
c_s = \max\{n_1/\kappa, n_1/(n_1 - \kappa + 1)\} \tag{19}
\]

and the incoherence parameter \( \mu_1 \) grows to one as the annihilating filter size \( \kappa \) increases \[25\]. The annihilating filter size \( \kappa \) corresponds to the “matrix pencil parameter” \[25\] in the spectral compressed sensing approach by Chen and Chi \[25\].

Note that the sampling rate \( m = O(k \log^4 n_1) \) required for ALOHA in \[18\] is nearly optimal since it is proportional to the unknown sparsity level except \( \log^4(\cdot) \) factor. Therefore, to achieve the best reconstruction quality, we need to find a way to reduce the sparsity level of the signal. This is the main motivation of our generalized ALOHA framework, which will be explained later. Note that LORAKS \[17,18\] and the single coil version of SAKE \[16\] basically solve \( P_{ALOHA} \) in \[16\] even though their construction of the Hankel structure
matrix is slightly different (see Methods section). Therefore, we call this class of algorithms as ALOHA family.

**Generalized ALOHA**

Now, we are interested in extending the ALOHA theory to include general class of signals. This is because some signals may not be sparse in the image domain, but can be sparsified in a transform domain. Our goal is to find a generalized ALOHA framework whose sampling rate can be reduced down to the transform domain sparsity level.

First, signals with a generalized 1-D total variation (TV) in [28] are an important class of signals that cover TV signals as a special case. Specifically, we consider a constant coefficient differential operator

\[
L := a_K D^K + a_{K-1} D^{K-1} + \ldots + a_1 D + a_0
\]

where \( K \geq 1 \), \( D \) denotes the distributional derivative on \( \mathbb{R} \), and each \( a_k \) is a real number. For the operator \( L \) and an interval \( E \subset \mathbb{R} \), the generalized total variation semi-norm can be defined by

\[
\| f \|_{TV(L;E)} := \| Lf \|_{L^1(E)} = \sup_{h \in C_h} \int_E Lf(x) h(x) dx
\]

which is valid when \( Lf \in L^1(E) \) and \( C_h = \{ h \in C_\infty^\ast(E), \| h \|_{L_\infty} \leq 1 \} \). The generalized total variation norm was used in [28] as a generalized regularisation terms for compressed sensing recovery for signals that can be described by

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

By taking the Fourier transform, we have

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

where

\[
\hat{L}(\omega) = a_K(i\omega)^K + a_{K-1}(i\omega)^{K-1} + \ldots + a_1(i\omega) + a_0
\]
Accordingly, the same filter \( \hat{h}[n] \) that annihilates (7) can annihilate the weighted signal \( \hat{l}(\omega)\hat{f}(\omega) \) if it is discretised with the sampling interval \( \Delta 2\pi/\tau \). Therefore, we can estimate the unknown k-space samples by solving the following generalized ALOHA problem and undoing the weighting by \( \hat{l} \):

\[
(P_{gALOHA}) \quad \min_{m \in \mathbb{C}^n} \quad \|M(m)\|_*,
\]

subject to \( P_{\Omega}(m) = P_{\Omega}(\hat{l} \odot \hat{f}) \),

where \( \odot \) denotes the Hadamard product, and \( \hat{l} \) and \( \hat{f} \) denotes the vectors composed of discrete samples of \( \hat{l}(\omega) \) and \( \hat{f}(\omega) \), respectively, which can be represented as follows:

\[
\hat{l} = \begin{bmatrix} \hat{l}[0] & \cdots & \hat{l}[n_1] \end{bmatrix}^T, \quad \hat{f} = \begin{bmatrix} \hat{f}[0] & \cdots & \hat{f}[n_1] \end{bmatrix}^T.
\]

This model includes many class of signals with finite rate of innovations [19–21]. For example, if the underlying signal is piecewise constant, we can set \( L \) as the first differentiation and \( \hat{l}(\omega) = i\omega \). In this case, (21) corresponds to the total variation (TV) norm. Similarly, if an underlying signal is non-uniform splines with degree \( d \), then we can use \( L = D^d \) and \( \hat{l}(\omega) = (i\omega)^d \).

Second, the most important class of signals in our generalized ALOHA framework are the signals that can be sparsely represented using dyadic wavelet transforms. This is because most natural signals can be sparsified using a wavelet transform, so this class of signals have been the main interest in the existing compressed sensing theory. Moreover, the resulting generalized ALOHA framework has very unique pyramidal structure that allows computational efficient and noise robust implementation of a low rank Hankel matrix completion algorithm. Specifically, under some regularity conditions for a mother wavelet \( \psi(x) \), we can represent any function \( f(x) \in L_2 \) in terms of dyadic wavelet expansion:

\[
f(x) = \sum_{s \in \mathbb{Z}} \sum_{l \in \mathbb{Z}} \langle f, \psi_{s,l} \rangle \tilde{\psi}_{s,l}(x)
\]

where

\[
\psi_{s,l} = 2^{-s/2} \psi(x/2^s - l)
\]

and \( \tilde{\psi}_{s,l} \) is the biorthogonal pair of \( \psi_{s,l} \) that satisfies

\[
\langle \tilde{\psi}_{s,l}, \psi_{s',l'} \rangle = \delta_{s,s'}\delta_{l,l'}.
\]
If we define
\[ \tilde{\psi}_s(x) := \tilde{\psi}_{s,0} = 2^{-s/2} \tilde{\psi}(x/2^s), \quad c_{sl} = \langle f, \psi_{s,l} \rangle \]
(31)
then thanks to the bi-orthogonality, we have
\[ (\tilde{\psi}_s f)(x)|_{x=2^s l} = \langle f, \psi_{s,l} \rangle = c_{sl} \]
(32)
where \( \tilde{\psi}(x) = \psi(-x) \) and the samples are obtained at every \( 2^s l \) interval. This implies
\[ \sum_l c_{sl} e^{-i \omega 2^s l} = \frac{1}{2^s} \sum_{n=0}^{2^s-1} \hat{\psi}_s^*(\omega + n \frac{2\pi}{2^s}) \hat{f} \left( \omega + n \frac{2\pi}{2^s} \right) \]
\[ = \frac{1}{\sqrt{2^s}} \sum_{n=0}^{2^s-1} \hat{\psi}^*(2^s \omega + 2\pi n) \hat{f} \left( \omega + n \frac{2\pi}{2^s} \right), \]
(33)
where we use \( \hat{\psi}_s^*(\omega + n \frac{2\pi}{2^s}) = \sqrt{2^s} \hat{\psi}^*(2^s \omega + 2\pi n) \). If the number of nonzero coefficient \( c_{sl} \) is small, then the form of the left hand side of (33) is similar to (7), so annihilating filters and the corresponding low-rank Hankel matrix can be found. In addition, one remarkable observation is that the \( 2\pi/2^s \) repeating spectral structure in (33) implies a pyramidal decomposition of the Hankel structured matrix used in (2b) thanks to the following observation.

More specifically, in MRI the signal \( f(x) \) is reconstructed on discrete grid, and in our definition of dynamic wavelet transform the discrete grid is 1. Furthermore, if the spectral component of \( \hat{f}(\omega) \) is known for \( \omega \in [2\pi/2^s, 2\pi] \), then we can constitute a signal \( f_s(x) \) on a discrete grid by nulling out the frequency content in \( \omega \in [2\pi/2^s, 2\pi] \). Then, for the signal \( f_s(x) \), we have
\[ \sum_l c_{sl} e^{-i \omega 2^s l} = \frac{1}{\sqrt{2^s}} \hat{\psi}(2^s \omega) \hat{f}_s(\omega), \]
(35)
because its high frequency content will no more alias at a frequency inside \([0, 2\pi/2^s]\). Since the signal \( f_s(x) \) is equivalent to consider \( f(x) \) only within k-space region \([0, 2\pi/2^s]\), the k-space data vector \( \hat{f}_s \) from (35) can be constructed by
\[ \hat{f}_s[m] = \hat{f}(\omega)|_{\omega=m2\pi/\tau}, \quad m = 0, \ldots, \frac{n_1}{2^s} - 1. \]
(36)
On the other hand, the weighting vector \( \hat{l} \) in (2b), whose dimension is now \( n_1/2^s \), is composed of following
spectral samples:

\[ \hat{l}^s[m] = \hat{l}^s(\omega) \bigg|_{\omega=m2\pi/\tau} = \frac{1}{\sqrt{2^s}} \hat{\psi}^* (2^s \omega) \bigg|_{\omega=m2\pi/\tau}, \quad m = 0, \ldots, \frac{n_1}{2^s} - 1 \]  

(37)

where the superscript \(^*\) denotes the complex conjugate. Consequently, the resulting algorithm can be decomposed in pyramidal representation as shown in Fig.1(a)(b) (see Methods for more discussion of the figures), where the \(s\)-scale generalized ALOHA problem can be formulated as

\[ (s\text{-scale } P_{gALOHA}) \quad \min_{m \in \mathbb{C}^{n_1/2^s}} \| \mathcal{H}(m) \|_* \quad \text{subject to} \quad P_{\Omega}(\hat{m}) = P_{\Omega}(\hat{\mathbf{f}} \odot \hat{\mathbf{f}}^\dagger) \].

(38)

Note that sampling interval for \(\hat{\psi}^*(\omega)\) widens by factor of 2 for each successive scale to construct the k-space weighting vector \(\hat{\mathbf{f}}\), although it is not the case for the k-space data vector \(\hat{\mathbf{f}}\) and lower frequency k-space data are used more often. For this reason, the generalized ALOHA (38) is solved from the lowest scale, i.e. \(s = 0\), up to the highest scale. Because sparsity can be imposed only on the wavelet coefficients, the low frequency k-space data that correspond to the scaling function coefficients should be acquired additionally during MR data acquisition. This information as well as the annihilating filter size then determines the the depth of the pyramidal decomposition. We will discuss this in detail later.

We are aware that a two-level decomposition was used for low-rank MRI [29]. However, in [29], the relationship to wavelet transform and the optimal decomposition level were not clearly identified.

Multi-channel generalized ALOHA

Beside the annihilation property originating from sparsity in the transform domain, there exists an additional annihilation relationship that is unique in parallel MRI. The relationship we described here is indeed what has been explored in SAKE and P-LORAKS using a uniform k-space weighting, and our contribution is a theoretical interpretation for general k-space weighting schemes. A theory for multi-channel Hankel matrix formation is described here using a signal model belonging to the generalized TV, and the same Hankel matrix construction will be used for general class signals. The theory behind the general class signals is, however, more involved, so it is not covered in this section.

Specifically, in pMRI, the unknown image \(g_i(x)\) from the \(i\)-th coil can be represented as

\[ g_i(x) = s_i(x)f(x), \quad i = 1, \ldots, r, \]
where $s_i(x)$ denotes the $i$-th coil sensitivity map and $f(x)$ is an unknown image. Then, by applying the differential operator \((20)\) to $g_i(x)$, we have

\[
Lg_i(x) = s_i(x)Lf(x) + f(x)Ls_i(x) .
\]

(39)

If we further assume that the coil sensitivity map $s_i(x)$ varies more slowly such that it belongs to the null space of $L$ operator, then we have

\[
Lg_i(x) = s_i(x)Lf(x), \quad i = 1, \cdots, r.
\]

Accordingly, it is easy to see the following inter-coil relation:

\[
s_j(x)Lg_i(x) = s_i(x)Lg_j(x), \quad i, j = 1, \cdots, r, \text{ and } i \neq j,
\]

(40)

which can be equivalently represented in Fourier domain as

\[
\hat{s}_j(\omega) * \left( \hat{l}(\omega) \hat{g}_i(\omega) \right) - \hat{s}_i(\omega) * \left( \hat{l}(\omega) \hat{g}_j(\omega) \right) = 0, \quad i \neq j, \quad \forall \omega.
\]

(41)

Consequently, Hankel matrix from each channel can be stacked side by side to form a matrix $\mathcal{Y}$:

\[
\mathcal{Y} = \left[ \mathcal{H}(\hat{l} \odot \hat{g}_1) \cdots \mathcal{H}(\hat{l} \odot \hat{g}_r) \right] \in \mathbb{C}^{(n_1 - \kappa + 1) \times Kr},
\]

(42)

and the multichannel version of the generalized ALOHA becomes

\[
(P_{MALOHA}) \quad \min_{\{m_i\}_{i=1}^r} \quad \left\| \left[ \mathcal{H}(m_1) \cdots \mathcal{H}(m_r) \right] \right\|_*
\]

subject to \( P_{\mathcal{H}}(m_i) = P_{\mathcal{H}}(\hat{l} \odot \hat{g}_i), \quad i = 1, \cdots, r \).

(43)

Here, the augmented matrix $\mathcal{Y}$ in \(\text{(42)}\) has an important geometric interpretation. Since Eq. \(\text{(41)}\) holds for every pair among $r$-channels, it is easy to show that

\[
\mathcal{Y} S_1 = 0.
\]
where $\mathcal{S}_1$ is defined recursively as follows:

$$
\mathcal{S}_{r-1} \triangleq \begin{bmatrix}
\hat{s}_r \\
-\hat{s}_{r-1}
\end{bmatrix}
$$

and

$$
\mathcal{S}_t \triangleq \begin{bmatrix}
\hat{s}_{t+1} & \hat{s}_{t+2} & \cdots & \hat{s}_C & 0 \\
-\hat{s}_t \\
\ddots \\
-\hat{s}_t
\end{bmatrix}
$$

Moreover, $\text{rank}(\mathcal{S}_1) = \binom{r}{2} = r(r-1)/2$. Therefore, we have

$$
\text{rank } \mathcal{Y} \leq kr - \frac{r(r-1)}{2} = \frac{r(2k-r+1)}{2}.
$$

This bound is of great importance. Because the rank of $\mathcal{Y}$ is $r(2k-r+1)/2$ and there exist additional degrees of freedom that belong to the amplitudes of Diracs in the transform domain, the total degrees of the freedom for the FRI signal are $r(2k-r+1)$ [19–21]. In parallel MRI, if $m$ denotes the number of k-space sampling locations, then k-space data are sampled simultaneously from $r$-coils and the total number of k-space samples becomes $mr$. Since the number of the samples should be larger than the degree of the freedom, we have

$$
mr \geq r(2k-r+1) \iff k \leq \frac{m+r-1}{2}
$$

which is equal to the algebraic bound for the multiple measurement vector problem (MMV) that exploits the joint sparsity [22–24]. Therefore, the formulation (43) may fully exploit the multi-channel diversity from parallel acquisition.
Methods

2D Hankel Structured Matrix Construction

In multi-slice or dynamic acquisition of MR data, the readout direction is usually fully sampled and the other two encoding directions are under sampled. Therefore, this section presents an explicit way of constructing a 2D Hankel structured matrix. If $\hat{h}[n,m]$ is a $p_1 \times q_1$ size 2D annihilating filter, then the corresponding annihilating filter relation is given by

$$(\hat{h} \ast \hat{f})[n,m] = \sum_{i=0}^{p_1-1} \sum_{j=0}^{q_1-1} \hat{h}[i,j]\hat{f}[n - i, m - j] = 0, \quad \forall n, m \in \Omega.$$  \hfill (49)

Let $n_1 \times m_1$ k-space data matrix be defined by

$$\hat{F} := \begin{bmatrix} \hat{f}[0,0] & \cdots & \hat{f}[0,m_1-1] \\ \vdots & \ddots & \vdots \\ \hat{f}[n_1-1,0] & \cdots & \hat{f}[n_1-1,m_1-1] \end{bmatrix} = \begin{bmatrix} \hat{f}_0 & \cdots & \hat{f}_{m_1-1} \end{bmatrix}$$ \hfill (50)

Similarly, we define $p_1 \times q_1$ annihilating filter matrix $\hat{H}$. Then, by removing the boundary effect from the 2D convolution as shown in Fig. 2(a), the 2D annihilation property should hold only inside of the domain and (49) can be equivalently represented as

$$\mathcal{H}(\hat{F})\hat{h} = 0,$$ \hfill (51)

where a 2-D Hankel structured matrix $\mathcal{H}(\hat{F})$ is constructed as

$$\mathcal{H}(\hat{F}) = \begin{bmatrix} \mathcal{H}(\hat{f}_0) & \mathcal{H}(\hat{f}_1) & \cdots & \mathcal{H}(\hat{f}_{q_1-1}) \\ \mathcal{H}(\hat{f}_1) & \mathcal{H}(\hat{f}_2) & \cdots & \mathcal{H}(\hat{f}_{q_1}) \\ \vdots & \vdots & \ddots & \vdots \\ \mathcal{H}(\hat{f}_{m_1-q_1}) & \mathcal{H}(\hat{f}_{m_1-q_1+1}) & \cdots & \mathcal{H}(\hat{f}_{m_1-1}) \end{bmatrix}$$ \hfill (52)
with

\[ \mathcal{H}(\hat{f}_j) = \begin{bmatrix}
\hat{f}[0,j] & \hat{f}[1,j] & \cdots & \hat{f}[p_1-1,j] \\
\hat{f}[1,j] & \hat{f}[2,j] & \cdots & \hat{f}[p_1,j] \\
\vdots & \vdots & \ddots & \vdots \\
\hat{f}[n_1-p_1,j] & \hat{f}[n_1-p_1+1,j] & \cdots & \hat{f}[n_1-1,j]
\end{bmatrix} \in \mathbb{C}^{(n_1-p_1+1) \times p_1}, \quad (53) \]

and the annihilating filter vector is given by

\[ \hat{h} = \overline{\text{Vec}(\hat{H})}, \quad (54) \]

where the overline denotes an operator that reserves the order of a vector. Using this, we can construct an augmented matrix \( \mathcal{Y} \) in (42) from \( r \)-channels.

The augmented matrix structure \( \mathcal{H}(\hat{F}) \) illustrated in Fig. 2(b) is similar to those of SAKE and LORAKS/P-LORAKS in Fig. 2(c) and (d), respectively, with the following differences. Compared to SAKE, ALOHA stacks the multi-coil Hankel matrices side by side. Unlike the SAKE and ALOHA, LORAKS uses 4-neighbors. Nonetheless, the main novelty of the proposed method is the k-space weighting before the Hankel structured matrix construction.

**Hankel structured matrix completion algorithm**

In order to solve Eqs. (16), (25), (25), and (43), we employ an SVD-free structured rank minimization algorithm [30] with an initialization using the low-rank factorization model (LMaFit) algorithm [31]. This algorithm does not use the singular value decomposition (SVD), so the computational complexity can be significantly reduced. Similar approaches have been studied in previous researches [32, 33]. Specifically, the algorithm is based on the following observation [34]:

\[ \|A\|_* = \min_{U,V:A=UV^H} \|U\|_F^2 + \|V\|_F^2. \quad (55) \]

Hence, (16) can be reformulated as the nuclear norm minimization problem under the matrix factorization constraint:

\[
\min_{U,V: \mathcal{H}(\mathbf{m})=UV^H} \|U\|_F^2 + \|V\|_F^2, \\
\text{subject to } P_\Omega(\mathbf{m}) = P_\Omega(\hat{f}), \quad (56)
\]
By combining the two constraints, we have the following cost function for an alternating direction method of multiplier (ADMM) step \[35\]:

\[
L(U, V, m, \Lambda) := \iota(m) + \frac{\mu}{2} \|U\|_F^2 + \frac{\mu}{2} \|V\|_F^2 + \frac{\mu}{2} \|\mathcal{H}(m) - UV^H + \Lambda\|_F^2,
\]

where \(\iota(m)\) denotes an indicator function:

\[
\iota(m) = \begin{cases} 
0, & \text{if } P_{\Omega}(m) = P_{\Omega}(\hat{f}) \\
\infty, & \text{otherwise}
\end{cases}
\]

One of the advantages of the ADMM formulation is that each subproblem is simply obtained from \[57\]. More specifically, we have

\[
m^{(k+1)} = \arg \min_m \iota(m) + \frac{\mu}{2} \|U\|_F^2 + \frac{\mu}{2} \|\mathcal{H}(m) - UV^H + \Lambda^{(k)}\|_F^2
\]

\[
U^{(k+1)} = \arg \min_U \frac{1}{2} \|U\|_F^2 + \frac{\mu}{2} \|\mathcal{H}(m^{(k+1)}) - UV^{(k)} + \Lambda^{(k)}\|_F^2
\]

\[
V^{(k+1)} = \arg \min_V \frac{1}{2} \|V\|_F^2 + \frac{\mu}{2} \|\mathcal{H}(m^{(k+1)}) - U^{(k+1)}V^H + \Lambda^{(k)}\|_F^2
\]

\[
\Lambda^{(k+1)} = \gamma^{(k+1)} - U^{(k+1)}V^{(k+1)}H + \Lambda^{(k)}
\]

It is easy to show that the first step can be reduced to

\[
m^{(k+1)} = P_{\Omega^c} \mathcal{H}^\dagger \left\{ U^{(k)}V^{(k)H} - \Lambda^{(k)} \right\} + P_{\Omega}(\hat{f}),
\]

where \(P_{\Omega^c}\) is a projection mapping on the set \(\Omega^c\) and \(\mathcal{H}^\dagger\) corresponds to the Penrose-Moore pseudo-inverse mapping from our block Hankel structure to a vector. Hence, the role of the pseudo-inverse is taking the average value and putting it back to the original coordinate. Next, the subproblem for \(U\) and \(V\) can be easily calculated by taking the derivative with respect to each matrix, and we have

\[
U^{(k+1)} = \mu \left( \gamma^{(k+1)} + \Lambda^{(k)} \right) V^{(k)} \left( I + \mu V^{(k)H}V^{(k)} \right)^{-1}
\]

\[
V^{(k+1)} = \mu \left( \gamma^{(k+1)} + \Lambda^{(k)} \right)^H U^{(k+1)} \left( I + \mu U^{(k+1)H}U^{(k+1)} \right)^{-1}.
\]

Now, for faster convergence, the remaining issue is how to initialize \(U\) and \(V\). For this, we employ an algorithm called the low-rank factorization model (LMaFit) \[31\]. More specifically, for a low-rank matrix \(Z\), LMaFit solves the following optimization problem:

\[
\min_{U, V, Z} \frac{1}{2} \|UV^H - Z\|_F^2 \text{ subject to } P_1(Z) = P_1(\mathcal{H}(\hat{f}))
\]
and $Z$ is initialized with $\mathcal{H}(\hat{f})$ and the index set $I$ denotes the positions where the elements of $\mathcal{H}(\hat{f})$ are known. LMaFit solves a linear equation with respect to $U$ and $V$ to find their updates and relaxes the updates by taking the average between the previous iteration and the current iteration. Moreover, the rank update can be done automatically. LMaFit uses QR factorization instead of SVD, so it is also computationally efficient. A similar matrix factorisation algorithm was proposed in [32, 33]. Even though the problem (65) is non-convex due to the multiplication of $U$ and $V$, the convergence of LMaFit to a stationary point was analyzed in detail [31]. However, the LMaFit alone cannot recover the block Hankel structure, which is the reason we use an ADMM step afterward to impose the structure.

We are aware that SAKE, LORAKS and P-LORAKS use non-convex formulation for low rank completion since they work better than a convex formulation using the nuclear norm. However, the convex formulation (56) is necessary to arrive at the explicit sampling rate $m = O(k \log n_1)$ by Chen and Chi [25], since they employed the dual certificate and golfing scheme by David Gross [26] for nuclear norm minimization. Therefore, our approach also utilizes the nuclear norm minimization.

**Reconstruction Flow**

As shown in Fig. 1, the generalized ALOHA framework is comprised with several major steps: pyramidal decomposition, k-space weighting, Hankel matrix formation, rank estimation, SVD-free low rank matrix completion, and k-space unweighting.

The pyramidal decomposition is performed as follows. In multi-slice MR data acquisition illustrated in Fig. 1(a), the $k_x - k_y$ data matrix at the current scale only contains one-fourth of data around zero frequency from that of the previous scale. On the other hand, in the case of dynamic imaging shown in Fig. 1(b), the $k - t$ data in the current scale contains a half of the data from that of the previous scale. In both cases, the estimated k-space data at the lower scale are used to initialize the low rank matrix completion algorithm at the current scale. This accelerates the convergence speed. Moreover, due to the additional chance of refining the estimates, more important k-space samples at the low frequency regions are refined furthermore compared to the high frequency k-space samples. Consequently, the overall computational burden of the low rank matrix competition algorithm is significantly reduced while the overall quality is still maintained.

The k-space weighting is performed using wavelets. Specifically, we use a biorthogonal wavelet expansion using the second order spline dyadic wavelets [36] whose spectrum is given by

$$\hat{\psi}(\omega) = \frac{i\omega}{4} \left( \frac{\sin \omega/4}{\omega/4} \right)^4 \exp \left( \frac{i\omega}{2} \right).$$  \hspace{1cm} (66)
The corresponding k-space weighting at the $s$-scale is given by

$$\hat{l}_s(\omega) = \frac{1}{\sqrt{2^s}} \frac{-i2^s\omega}{4} \left( \frac{\sin 2^s\omega/4}{2^s\omega/4} \right)^4 e^{-i2^s\omega}. $$

Care needs to be taken when applying the weighting to 2D Fourier domain because there are two frequency variables ($\omega_x, \omega_y$). One could use a separable weighting $\hat{l}(\omega_x, \omega_y) = \hat{l}(\omega_x)\hat{l}(\omega_y)$; however, the resulting problem is that the missing k-space components along the frequency axis $\omega_x = 0$ or $\omega_y = 0$ cannot be recovered. Consequently, we applied the weighting sequentially along each axis, i.e. we solve (25) by applying $\hat{l}(\omega_x)$ first, which is followed by solving (25) with $\hat{l}(\omega_y)$.

Because generalized ALOHA can be used for various signal classes by changing the k-space weighting in (25), we also compared various type of signal models and the corresponding k-space weighting schemes to answer why wavelet transform has many advantages. Specifically, the following signal models and the corresponding k-space weighting schemes were evaluated:

1. Sparse signals: $\hat{l}(\omega) = 1$.
2. 1st order TV signals: $\hat{l}(\omega) = i\omega$.
3. 2nd order TV signals: $\hat{l}(\omega) = (i\omega)^2 = -\omega^2$
4. $s$-scale dyadic spline wavelet represenation: $\hat{l}_s(\omega) = \frac{1}{\sqrt{2^s}} \frac{-i2^s\omega}{4} \left( \frac{\sin 2^s\omega/4}{2^s\omega/4} \right)^4 e^{-i2^s\omega}$

For the case of the 2nd order TV, rather than using the sequential weighting for $\omega_x$ and $\omega_y$ directions, we found that the radial weighting

$$\hat{l}(\omega_x, \omega_y) = -\omega_x^2 - \omega_y^2$$

was sufficiently accurate and provided faster reconstruction. This is because (67) implies that the Laplacian of an image is sufficiently smooth except the image edges, which is an often used assumption in the partial differential equation (PDE) based image processing.

We use TITAN GTX graphic card for graphic processor unit (GPU) and i7-4770k CPU and the codes were written in MATLAB (Mathwork, Natick). To accelerate the algorithm, most part of the MATLAB codes were implemented using Compute Unified Device Architecture (CUDA) for GPU.
MR Acquisition and Reconstruction Parameters

To assess the performance of ALOHA for single coil compressed sensing imaging, k-space raw data from an MR headscan was obtained with Siemens Verio 3T scanner using 2D SE sequence. The acquisition parameters were as follows: TR/TE = 4000/100ms, 256 × 256 acquisition matrix, and six z-slices with 5mm slice thickness. The field-of-view (FOV) was 240 × 240mm², and the number of coils was four. To perform single coil reconstruction, we chose MR raw data from one coil out of the four coils.

A retrospective down-sampling mask was generated according to a two dimensional Gaussian distribution and the data at the central 7 × 7 region around zero frequency were obtained additionally. This is equivalent to assume a 3D imaging scenario where the readout direction is fully sampled and the downsampling is done in the remaining 2-D phase encoding direction. Downsampling factors of 3 and 4 were used to generate sampling masks. The k-space weighting in (66) was used. The generalized ALOHA reconstruction was conducted using the following parameters: three levels of pyramidal decomposition, and decreasing LMaFit tolerance values (10⁻¹, 10⁻², 10⁻³) at each level of the pyramid. In addition, an initial rank estimate for LMaFit started with one and was refined in an increasing sequence, the annihilating filter size was 15×15, and the ADMM parameter was $\mu = 10^3$. For the compressed sensing approach, we used the split Bregman method for the total variation [37] with the same data and the same sampling masks. The parameters for the TV approach were optimized to have the best performance in terms of the normalised mean square error (NMSE), which is defined by $\text{NMSE}(x) = \|x - y\|_2^2 / \|y\|_2^2$, where $x$ and $y$ denote the reconstructed and the ground-truth images, respectively.

To evaluate the performance of ALOHA in static parallel imaging, the same brain data was used. Retrospectively undersampled 2-D k-space data at the acceleration factor of five were obtained according to a two dimensional Gaussian distraction in addition to the 7 × 7 central region around zero frequency. The data from 4 receiver coils were used. For comparison, we used the identical data and sampling masks for SAKE [16], SAKE with ESPIRiT [38], and GRAPPA [14]. Note that GRAPPA requires ACS lines, so with the additional 10 samples along ACS, the effective downsampling ratio was 4.61. SAKE and SAKE with ESPIRiT are both low rank matrix completion algorithms for Hankel structured matrix collected from the whole k-space data. However, SAKE with ESPIRiT reduces the computational burden of the original SAKE by performing low rank matrix completion only for the 65 × 65 central region with 5 × 5 filter, after which coil sensitivities are estimated using the reconstruction data. The estimated coil sensitivities are used to estimate the remaining k-space missing data through ESPIRiT [38]. The parameters for SAKE and SAKE with ESPIRiT were chosen such that they provided the best reconstruction results. The parameters for the generalized ALOHA are as follows: four levels of pyramidal decomposition with decreasing LMaFit toler-
ances ($10^{-1}, 10^{-2}, 10^{-3}, 10^{-4}$), and $5\times5$ annihilating filter. The same LMaFit rank estimation strategy and ADMM parameter used for single coil experiments were employed. We generated the square root of sum of squares (SSoS) image from multi-coil reconstructions.

We also validated the performance of ALOHA for accelerated dynamic cardiac data in the k-t domain. A cardiac cine data set was acquired using a 3T whole-body MRI scanner (Siemens; Tim Trio) equipped with a 32-element cardiac coil array. The acquisition sequence was bSSFP and prospective cardiac gating was used. The imaging parameters were as follows: FOV = $300 \times 300\text{mm}^2$, acquisition matrix size = $128 \times 128$, TE/TR = $1.37/2.7\text{ms}$, receiver bandwidth = $1184\text{Hz/pixel}$, and flip angle = $40^\circ$. The number of cardiac phases was 23 and the temporal resolution was $43.2\text{ms}$. The k-t space samples including four lines around zero frequency were retrospectively obtained at the reduction factor of six according to a Gaussian distribution. For comparison, k-t FOCUSS [8] was used. The regularisation parameter in k-t FOCUSS was selected to give the best NMSE values. For the generalized ALOHA, the following parameters were used: three level of pyramidal decomposition only along the phase encoding direction, decreasing LMaFit tolerances ($10^{-1}, 10^{-2}, 10^{-3}$) at each scale, and $17\times5$ annihilating filter. The same LMaFIT rank estimation strategy and ADMM parameter used before were employed. The k-space weighting in Eq. (66) was applied only along the phase encoding direction.

Next, we investigated the synergetic improvement of dynamic imaging from multi-channel acquisition. Four representative coils out of 32 were used. After the reconstructions of k-space samples, the inverse Fourier transform was applied, and the SSoS images were obtained by combining the reconstructed images. In the generalised ALOHA, the annihilating filter size was $5\times5$. The same LMaFIT rank estimation strategy and ADMM parameter used before were employed.

Results

Static MR experiments

Reconstructed results from a single coil brain data are shown in Fig. 3 with the NMSE values. From the NMSE values, we observed that the performance ALOHA was quantitatively superior to the performance of TV based compressed sensing approach. The reconstruction results by ALOHA has less perceivable distortion compared to TV. This can be easily observed from the difference images in the second and the fourth rows of Fig. 3. In the case of TV, structural distortion around the image edges was easily recognizable. In the last row of Fig. 3 the edges were reconstructed accurately by ALOHA. On the other hand, contrast
between grey matters and white matters in TV reconstruction was significantly distorted compared with that of ALOHA.

Next we compared our parallel imaging results with those of the existing approaches for the same brain data set. The NMSE results in Fig. 4 showed that ALOHA was most accurate. From the difference images at the second row of Fig. 4 we observed that proposed method provided reconstruction results more accurately than other algorithms. In SAKE, the structures were distorted around the inner skull and the boundaries of tissues. In SAKE with ESPIRiT, overall reconstruction errors were quantitatively higher than those from SAKE and ALOHA. The reconstruction time was 14sec with our preliminary GPU implementation of ALOHA, which attained a speed-up factor of 2.5 compared to CPU implementation. On the other hand, the computational time for MATLAB version of GRAPPA, SAKE, and SAKE+ESPIRiT were 10.9s, 85.3s, and 17.5s, respectively.

**Dynamic MR experiments**

Using the sub-sampled k-space data at the acceleration factor of six, the average NMSE values of k-t FOCUSS and ALOHA were $6.217 \times 10^{-3}$ and $2.546 \times 10^{-3}$, respectively. The sub-sampled data was collected according to a Gaussian distribution and included the four center lines around zero frequency. The average NMSE values were calculated using all temporal frames. These results confirmed that the proposed method outperformed k-t FOCUSS. As shown in Fig. 5(b), the temporal profile (indicated as a broken purple line) of the proposed reconstruction provided more accurate structures that were comparable to the true one, whereas the temporal variation in the k-t FOCUSS reconstruction became smoother and more blurry along the temporal dimension.

The NMSE values of the parallel dynamic imaging results from k-t FOCUSS and the proposed method using four coil k-space data were $1.35 \times 10^{-2}$ and $8.981 \times 10^{-3}$, respectively, which quantitatively showed that the proposed method outperformed k-t FOCUSS. Reduced residual artefacts were perceivable in the ALOHA difference images in Fig. 5(a). Moreover, the temporal profiles of the proposed reconstruction showed more accurate structures which were comparable to the true one, whereas the dynamic slice profile from k-t FOCUSS showed smoother and more blurry transition. The proposed algorithm resulted in more accurate reconstructions of dynamic signal changes at the heart wall as shown in Fig. 5(a).
Effects of k-space weighting

Figure 6 illustrates the magnitudes of the various k-space weighting schemes in the 1D Fourier domain. Note that $\hat{l}(\omega) = 1$ corresponds to that of SAKE and LORAKS/P-LORAKS, and the others usually give more weight to higher frequency data. Fig. 6 shows the corresponding image when a k-space weighting $\hat{l}(\omega_y)$ is applied in the $\omega_y$ direction, except for the 2nd order TV model that gives the radial weighting. Unlike the uniform weight in SAKE and LORAKS/P-LORAKS, the other k-space weighting schemes enhanced the image edges. In addition, when we applied a generalized TV weight to real MR data, the resulting images became very noisy. This is because the 1st order TV (resp. 2nd order TV) gives linearly (quadratically) increasing weight to higher frequency k-space data, which also boosts noises. On the other hands, the k-space weight by spline dyadic wavelet works better in avoiding such noise amplification by reducing the weight to the high frequency k-space data.

In order to identify the best k-space weighting scheme that promotes sparsity, at the rightmost column of Fig. 6 we plotted the normalized singular value distribution of Hankel matrices from the $1/4 \times 1/4$ central k-space region. The reason we chose the central region is to avoid the noise amplification effect at higher frequency regions that can deteriorate our analysis. As shown in Fig. 6, the singular value spectrum of the Hankel structured matrix with non-uniform weights decayed much faster than the uniform weight. Among various weighting schemes, the spline dyadic wavelets and the first order TV provided the the best singular value spectrum distributions and two spectrums were nearly identical and overlapped each other in Fig. 6.

Table summarises the NMSE values of reconstructed images with the generalized ALOHA using various k-space weighting schemes. Here, we used the pyramidal decomposition for the case of spline dyadic wavelets, but for the other weighting schemes, single scale reconstruction was performed because their signal models are defined in the single resolution. The results showed that even though the 1st and 2nd order TV have better spectral distribution for the low frequency regions, the reconstruction performance were not consistent compared to the uniform weighting. This was due to the noise amplification from the corresponding spectral weights. In the case of high SNR k-space data (ones from Shepp-Logan or brain data), the 1st order TV weighting scheme consistently outperformed the uniform weighting scheme at the cost of increased complexity. Here, the computational time implies the run time of an algorithm until convergence. However, for low SNR data such as cardiac scan, the uniform weighting showed better reconstruction than the 1st order TV weights. However, the spline dyadic wavelet transforms resulted in the smallest NMSE values even with less computational complexity thanks to the synergistic combination of non-uniform weights and the pyramidal decomposition.
Table 1: Reconstruction NMSEs and computational time from various weighting schemes.

| Data                  | weighting         | Uniform | 1st TV | Laplacian | Spline wavelet |
|-----------------------|-------------------|---------|--------|-----------|----------------|
| single coil           |                   | NMSE    |        |           |                |
| Brain (x4) (Fig. 3)   |                   | NMSE    |        |           |                |
|                       |                   | Time(s) | 53.9   | 102.5     | 54.7           |
| Brain (x4) (Fig. 3)   |                   | NMSE    | 3.49×10⁻³ | 3.47×10⁻³ | 2.46×10⁻³     |
|                       |                   | Time(s) | 72.6   | 149.8     | 76.7           |
| Cardio (Fig. 5(a))    |                   | NMSE    | 1.04×10⁻² | 1.83×10⁻² | 8.98×10⁻³     |
|                       |                   | Time(s) | 423    | 457       | 446            |
| multi coils           |                   | NMSE    |        |           |                |
| Brain (Fig. 4)        |                   | NMSE    | 1.63×10⁻³ | 1.64×10⁻³ | 1.23×10⁻³     |
|                       |                   | Time(s) | 24.3   | 49.9      | 24.2           |
| Cardio (Fig. 5(b))    |                   | NMSE    | 3.42×10⁻³ | 8.7×10⁻³  | 2.55×10⁻³     |
|                       |                   | Time(s) | 258    | 245       | 236            |

Discussion

In order to show the importance of the pyramidal decomposition, Fig. 7(a) plots the computational time versus NMSE values of parallel brain data by changing the number of decomposition levels. As discussed before, the maximum decomposition level is determined by the acquired low frequency components and the annihilating filter size. In this data set, k-space dimension was 256 × 256 and the annihilating filter size was 5 × 5, and 7 × 7 k-space data around zero frequency were acquired. By considering the Hankel matrix dimension in (52), we should impose constraints

$$\frac{256}{2^s} - 5 + 1 \geq \max\{5,7\},$$

where $s$ is the scale. This provides $s \leq 4$, and the maximum scale becomes 4. Fig. 7(a) shows that the performance gain increases as a pyramidal level increases; however, at the last decomposition level, the performance improvement was negligible. Similar behaviour was observed in other data sets. Therefore, the decomposition level was determined as the maximum minus one.

The other important reconstruction parameters include the size of the annihilating filter, the number of iterations, and tolerances used in LMaFit algorithm. Recall that the annihilating filter size corresponds to the matrix pencil size in sensor array signal processing [27], and it should be set larger than the sparsity level of the transform coefficients. In fact, by considering the expression of $c_s$ in [19], the optimal annihilating...
filter size for 2D data is \( n_1/2 \times m_2/2 \), where \( n_1 \times m_1 \) denotes the full k-space data size. However, such large annihilating filter size introduces significant computational burden, so we tried to reduce the filter size as long as the image quality is not degraded. As a rule of thumb, we found that in single coil image, the filter size should be sufficiently large as the annihilating filter size is solely determined by the sparsity level. In parallel imaging, there exist additional annihilating filters from the intercoil relationship, so the annihilating filter size can be set smaller than that of a single coil imaging.

The number of iterations for ADMM steps were determined scale by scale. Specifically, for high frequency k-space data reconstruction, many iterations are not required because the measurements are noisy, so the constraints in (10) do not need to be met tightly. On the other hand, because reconstruction accuracy of low frequency k-space data is important, more iteration is required at high scales. Fig. 7(b) shows the NMSE value versus execution time for two different strategies: one with the same number of iterations for all scale, and the other with the increasing number of iterations for higher scales. The results clearly showed that the increasing number of iteration with the scale was most effective.

Finally, the tolerance level for LMaFit, which corresponds to the fitting accuracy, plays key role in determining the initial rank estimate. The initial rank estimate need not be close to the exact rank, but it was used to define the dimension of \( U \) and \( V \) in ADMM. As a rule of thumb, the tolerance level was determined by considering different noise contributions in k-space data. Specifically, higher frequency components are usually contaminated by higher level of noises compared to the low frequency k-space data, so the LMaFit fitting accuracy need not be enforced strictly. This was the case when LMaFit was applied at a lower scale, since high frequency k-space data are more weighted and noises were boosted. On the other hand, more accurate fitting is required for higher scale data where the lower frequency k-space data are more weighted. Consequently, we chose decreasing values of tolerances per scale for in-vivo experiments.

**Conclusion**

In this paper, we proposed a general framework for annihilating filter based low-rank Hankel matrix approach (ALOHA) for static and dynamic MRI inspired by recent calibration-free k-space methods such as SAKE and LORAKS/P-LORAKS. We confirmed the existing observation that the low rankness of the Hankel structured matrix in SAKE and LORAKS/P-LORAKS are derived from inter-coil correlation and image domain sparsity, and revealed that the required number of k-space data is given by \( \mathcal{O}(k \log^2 n_1) \), where \( k \) denotes the sparsity level. Because natural images can be much more effectively sparsified in the transform domains such as generalized TV or wavelets, we generalized the idea to include signals that can be sparsified
in the transform domains. Our analysis showed that the transform domain sparsity can be equivalently represented as low-rank Hankel structured matrix in the weighted k-space domain, whose weighting function is determined solely by the transform, not by the data. One of the most significant discoveries was that when signals are effectively sparsified in dyadic wavelet transform, the corresponding low rank Hankel matrix completion problem can be equivalently represented with a pyramidal decomposition, which significantly reduces the overall computational complexity. Moreover, unlike other weighting schemes applied at single scale, the pyramidal decomposition using spline wavelets provided best reconstruction quality that was less sensitive to noise. For parallel imaging data, we verified that by stacking Hankel matrix from each coil side by side, we may fully exploit the coil sensitivity diversity thanks to its relationship to MMV compressed sensing.

Reconstruction results from single coil static MR imaging confirmed that the proposed method outperformed the existing compressed sensing framework with TV regularization. We further demonstrated superior performance of the proposed method in static parallel MR imaging even without calibration data. Furthermore, the algorithm was successfully extended to dynamic accelerated MRI along k-t domain with both single coil and multi coil dynamic MR data. Therefore, we concluded that the proposed algorithm was very effective in unifying the compressed sensing and parallel MRI.

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Appendix

Spectral domain uniform sampling at the distance of $\frac{2\pi}{\tau}$ generates the periodic stream of Diracs:

$$f(x) = \sum_{j=0}^{k-1} c_j \sum_{n \in \mathbb{Z}} \delta(x - x_j - n\tau)$$
which can be represented as
\[
f(x) = \sum_{j=0}^{k-1} c_j \frac{1}{\tau} \sum_{n \in \mathbb{Z}} e^{i(2\pi n(x-x_j)/\tau)}
\]
\[
= \sum_{n \in \mathbb{Z}} \hat{f}[n] e^{i2\pi nt/\tau}
\]
where the Fourier series coefficient \(\hat{f}[n]\) is given by
\[
\hat{f}[n] = \frac{1}{\tau} \sum_{j=0}^{k-1} c_j e^{-i2\pi x_j n/\tau}.
\]

If we construct a filter
\[
h(z) = \sum_{n=0}^{k} \hat{h}[n] z^{-n} = \prod_{j=0}^{k-1} (1 - e^{-i2\pi x_j/\tau} z^{-1}),
\]
then we can show that it annihilates the signal \(\hat{f}[n]\) because
\[
(\hat{h} * \hat{f})[n] = \sum_{l=0}^{k} \hat{h}[l] \hat{f}[n-l]
\]
\[
= \sum_{l=0}^{k} \sum_{j=0}^{k-1} c_j \hat{h}[l] u_j^{n-l}
\]
\[
= \sum_{j=0}^{k-1} c_k \left( \sum_{l=0}^{k} \hat{h}[l] u_j^{n-l} \right) u_j^n = 0
\]
where \(u_j = e^{-i2\pi x_j/\tau}\).

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Figure 1: Generalized ALOHA with dyadic wavelet transform from (a) $k_x-k_y$ and (b) $k-t$ domain subsampled data, respectively.
Figure 2: (a) A boundary removed region where annihilation property holds. Various ways of constructing block Hankel matrices: (b) ALOHA, (c) SAKE, and (d) LORAKS. In (d), $N_R$ denotes the number of neighborhood pixels.
Figure 3: Comparison with TV compressed sensing and the proposed method at various acceleration factors. The data was acquired from a single channel coil. The first row shows reconstructed images, and the second row shows difference images between the ground-truth and the reconstructions, and the third row shows the magnified views of distorted regions in the reconstructed images. The last row shows the difference images in the magnified views.

| ORIG | TV (x3) | Proposed (x3) | TV (x4) | Proposed (x4) |
|------|---------|---------------|---------|---------------|
|      | NMSE 4.654e-03 | NMSE 1.832e-03 | NMSE 6.022e-03 | NMSE 2.461e-03 |
Figure 4: Parallel imaging results using GRAPPA, SAKE, SAKE with ESPIRiT and the proposed method at five fold acceleration. The second row shows the difference images. Areas with systematic artefacts are indicated by yellow arrows.
Figure 5: Reconstruction results from 6 fold accelerated k-space data using (a) single coil and (b) four coils data set. Purple lines denote the regions corresponding to y-t cross sections that are magnified along temporal axis. The second rows in both (a) and (b) show the difference images between the ground-truth and the reconstructions.
Figure 6: Various k-space weighting schemes (uniform, 1st order TV, the second order TV (Laplacian) and spline wavelet of order 2) and the corresponding image domain representation of the weighted spectrums. The right most column shows singular value distribution of weighted Hankel matrices from the $1/4 \times 1/4$ central k-space region.
Figure 7: NMSE plots from four channel static parallel imaging reconstruction results for the brain data in Fig. 4. (a) NMSE values with respect to different decomposition levels. (b) NMSE values with respect to different iteration strategy. The number on each line segment refers to the iteration number.