A Study of Spatial Encoding and Decoding in MRI

by

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Abstract

Spatial encoding is a key feature (perhaps the key feature) of Magnetic Resonance Imaging (MRI). Since the discovery that magnetic field gradients could be used to localize signal, researchers have sought methods to acquire higher quality images, with greater efficiency. This dissertation investigates three approaches for encoding and decoding the information of MRI to provide useful images for clinical diagnosis.

Partial Parallel Imaging (PPI) introduced a framework that enabled faster data acquisition, allowing reduction in scan time or improved resolution. We present a regionally optimized implementation of the popular PPI technique GeneRalised Au-to-calibrating Partial Parallel Acquisition (GRAPPA). The regional implementation provides images with lower data recovery error and reduced residual aliasing artifact. We assess a number of image quality metrics that would allow automated selection of the optimal reconstructed image.

A number of physical quantities can be mapped via comparison of two images with different sensitivities. When the contrast between these images is smoothly varying, the information may be captured using only a fraction of the k-space data required for full image reconstruction. We present a technique to provide robust recovery of relative information maps between images from minimal k-space data. The effectiveness of the technique is demonstrated through application to phase contrast MRI data.

Many MRI applications are limited by acquisition in 2D multislice mode. In
this regime, the slice direction typically suffers lower resolution than the in-plane directions. We present three strategies to improve through-plane resolution. The relative merits of each technique are investigated, and the performance is quantified with standard measures. The implications of the potential artifacts resulting from each technique are discussed.
Preface

All research presented herein was completed by Thomas A. Depew and Professor Qing-San Xiang. Some supplementary data were provided from prior research:

In Chapter 3 the 4-coil abdominal scan data sets $ABDax_1$ and $ABDax_2$ were acquired on a 1.5T GE scanner at St. Pauls Hospital, Vancouver, BC, Canada, as part of the research work performed by Q-S. Xiang published in [1].

In Chapter 4 the circular water phantom data were obtained on a 4.7T Bruker system at the National Institutes of Health, Bethesda, MD, USA, as part of the research work performed by Q-S. Xiang and F.Q. Ye published in [2].
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List of Abbreviations

AC  Autocorrelation.

DE  Differential Energy.

$E_G$  Gradient Energy.

$H$  Image Entropy.

$H_G$  Gradient Entropy.

RE  Relative Error.

TV  Total Variation.

ACS  Auto-Calibration Signal.

CS  Compressed Sensing.

EPI  Echo-Planar Imaging.

f-MRI  Functional MRI.

FE  Frequency Encoding.

FID  Free Induction Decay.

FOV  Field of View.
FSPGR  Fast SPoiled GRadient.

FT  Fourier Transform.

GRAPPA  GeneRalised Auto-calibrating Partial Parallel Acquisition.

gSMASH  Generalised SMASH.

hpGRAPPA  High Pass GRAPPA.

MR  Magnetic Resonance.

MRA  Magnetic Resonance Angiography.

MRI  Magnetic Resonance Imaging.

NMR  Nuclear Magnetic Resonance.

ORACLE  Off-Resonance Artifact with ConvoLution in k-spacE.

PC  Phase Contrast.

PE  Phase Encoding.

PLACE  Phase Labeling for Additional Coordinate Encoding.

PPI  Partial Parallel Imaging.

RDF  Rotational Differential Field.

RF  radio-frequency.

rGRAPPA  Regional GRAPPA.

rSoS  Root Sum-of-Squares.
**LIST OF ABBREVIATIONS**

**SEER** Simple Edge Enhancing Refinement.

**SENSE** SENSitivity Encoding.

**SLENDER** SLice ENhancement DividER.

**SMASH** SiMultaneous Acquisition of Spatial Harmonics.

**SNR** Signal-to-Noise Ratio.

**SR** Super-Resolution.

**SURESLIDE** SUper-REsolution by SLIce DEconvolution.

**TCP** Truncated Conjugate Product.
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Chapter 1

Outline

Magnetic Resonance Imaging (MRI) provides a non-invasive tool for imaging the human body. Since the techniques for creating images of the human body by exploiting the Nuclear Magnetic Resonance (NMR) phenomenon were first proposed in the 1970s, MRI has experienced widespread use and significant advancement. The nature of MRI data acquisition and the physical interaction of magnetic fields with biological tissue invites a variety of possible techniques to improve image resolution, reduce scan time and provide additional physiological information. In this dissertation, we study methods for producing signal localization (imaging) and techniques to enhance the information retrieved from the images.

Chapter 2 provides an introduction to basic NMR and MRI principles that provide the foundation for the subsequent chapters. Following this background, the dissertation is divided into three main sections:

Chapter 3 concerns the field of Partial Parallel Imaging (PPI), in which spatial information from receiver coil sensitivities aid in signal localization. The concepts of PPI are introduced and the foundational techniques are reviewed. We suggest an optimized version of the data driven PPI technique GeneRalised Auto-calibrating Partial Parallel Acquisition (GRAPPA). The physical underpinnings inspiring the
modification of the standard implementation are discussed, and the optimized method Regional GRAPPA (rGRAPPA) is shown to demonstrate improved reduction of residual aliasing artifact compared to the standard approach. We also introduce a number of image quality metrics that can be used to assess the efficacy of the data recovery in the absence of a fully sampled reference image. The maximum gradient energy, minimum image entropy and minimum autocorrelation sum were found to provide optimal results over a wide range of acquisition parameters. The metrics suited for the GRAPPA framework may be applicable to other data-driven PPI techniques as well.

Chapter 4 presents a novel technique for estimating low frequency contrast information between scans. The mathematical framework behind the convolution fitting technique is described. The ability of the convolution kernel to capture relative k-space information is tested in the context of Phase Contrast (PC) MRI. The kernel fitting procedure was found to robustly estimate relative phase maps between images even when sampling only a fraction of the full k-space and in regions of low Signal-to-Noise Ratio (SNR).

Chapter 5 presents strategies for improving the through-plane resolution of 2D multislice Magnetic Resonance (MR) data. We introduce three unique approaches for achieving through-plane resolution enhancement with either magnitude or complex data. Each technique is applied in simulated and real MRI experiments. The effectiveness of resolution enhancement is measured using an edge width calculation, and the SNR properties of each technique are compared. Artifacts specific to each technique are identified and the strengths and weaknesses of each approach are discussed.

Finally, in Chapter 6 we provide concluding remarks and make recommendations for future work.
Chapter 2

Fundamentals of Magnetic Resonance Imaging

2.1 A Brief History

The development of MRI was dependent on the discovery of the NMR phenomenon; the interaction that occurs when certain atomic nuclei, immersed in a static magnetic field, are subjected to an oscillating magnetic field. NMR was first discovered and described by Isidor Rabi in 1938 [3]. Rabi and his group developed the technique to observe NMR and used it to determine the magnetic moment of sodium nuclei. The discovery that the response of nuclei was dependent on the local magnetic field allowed further characterization of the chemical environment of nuclei. In 1946 Felix Bloch and Edward Mills Purcell refined the technique to investigate the structure of molecules in liquids and solids [4, 5, 6].

The first step towards creating an image using gradients was accomplished by Herman Carr in his 1952 thesis [7], although the images were only 1-dimensional. Finally, in 1974 Paul Lauterbur developed the technique to create true 2D images using magnetic field gradients and created one of the first in vivo demonstrations of
MRI. Around the same time, Sir Peter Mansfield had been using gradients to acquire spatial information in solid state NMR [8] and had developed the mathematical framework that ultimately became the basis for k-space (Mansfield and Lauterbur jointly received the Nobel Prize in Physiology or Medicine in 2003 for their contributions). These advancements culminated in the realization of applying NMR to create clinically relevant images.

2.2 Nuclear Magnetic Resonance

In order to experience the effects of NMR, a nucleus must possess a non-zero nuclear magnetic moment. This occurs when the nucleus is composed of an odd number of protons or neutrons. The nucleons possess an intrinsic quality called spin that is the property by which they interact with magnetic fields. For the purposes of this dissertation, we consider the spin to be a fundamental property of the particle; although we could decompose the nucleons further, the underlying physics is beyond the scope of this thesis.

The combined spin of all particles in the nucleus contribute to the magnetic moment of the nucleus. A nucleus with total spin angular momentum of $\mathbf{I}$ will have a magnetic moment

$$\mathbf{\mu} = \gamma \hbar \mathbf{I}.$$  

(2.1)

Here both $\mathbf{\mu}$ and $\mathbf{I}$ are vectors, the scalar $\gamma$ is the unique ratio of the magnetic moment to the spin angular momentum for a given particle and is known as the gyromagnetic ratio, $\hbar$ is the Planck constant divided by $2\pi$.

2.2.1 The Zeeman Interaction

In the absence of any external magnetic fields the orientation of the magnetic moment $\mathbf{\mu}$ is random. When immersed in a static magnetic field it experiences a torque that
tends to align the moment in the direction of the applied field \((\mathbf{B})\). The energy of this system is

\[
E = -\mu \cdot \mathbf{B}.
\]  

(2.2)

In the NMR system, the static field is conventionally aligned in the \(z\) direction \((B_0 = B_0 \hat{z})\). Substituting Equation 2.1 results in a set of allowed energy levels

\[
E_m = -\gamma \hbar B_0 m_z,
\]  

(2.3)

given the possible values of the spin quantum number \(m_z = I, I - 1, \ldots, -I\). In the context of MRI, we are normally concerned with the H atom (the proton), wherein \(I = 1/2\). Thus there are two allowed energy levels corresponding to the values \(m_- = -1/2\) and \(m_+ = 1/2\). This splitting of the energy levels for the nucleus in a static magnetic field is known as the Zeeman effect. The Zeeman splitting for the \(I = 1/2\) system is shown in Figure 2.1.

\[
B = 0 \quad B = B_0
\]

\[
\begin{align*}
\Delta E &= 0 \\
m_z &= -1/2 \\
m_z &= +1/2
\end{align*}
\]

Figure 2.1: The Zeeman effect; in a magnetic field \(B_0\) the energy levels of the \(I = 1/2\) system are split into two levels separated by \(\Delta E = \gamma \hbar B_0\).

### 2.2.2 Bulk Magnetization & Signal Detection

Although the energy splitting induced by the static field that is the basis of our signal is a quantum phenomenon, the NMR and MRI experiments deal with the net magnetization resulting from large numbers of nuclei (on the order of Avogadro’s number, \(6.022 \times 10^{23}\)). At this point, we transition from quantum mechanics to a
classical picture.

The net magnetization is the sum total of all magnetic moments in a sample

\[ M = \sum_{n}^{N} \frac{\mu_{n}}{V}, \]

(2.4)

where \( V \) is the sample volume.

In the absence of the static field, the nuclei are randomly distributed (Figure 2.2a) and the net magnetization is zero.

![Figure 2.2: The net magnetization is the vector sum of all spin magnetic moments. a) With no field present, the spins are oriented randomly and uniformly. b) When an external field is applied, the spins will tend to align in the direction of the applied field.](image)

With the strong static field applied, one might suppose that the nuclei must align either parallel or anti-parallel to the field (Figure 2.1). However molecular motion will still provide enough local fluctuations to cause the spins to orient in a nearly uniform spherical distribution. There is an overall preference among nuclei to align parallel to the direction of \( B_0 \), as this state \( (m_z = +1/2) \) is energetically preferred. The result is a net magnetization aligned with the static field.

At thermal equilibrium, the ratio of the low and high energy populations of nuclei
will be determined by the ratio of this energy gap to the average thermal energy:

\[
\frac{N_+}{N_-} = e^{-\frac{\gamma \hbar B_0}{k_B T}}. \tag{2.5}
\]

The amplitude of the detectable signal is proportional to the net magnetization, which is dependent on the population difference \((N_+ - N_-)\). Thus it is desirable to have a large net magnetization requiring a larger \(B_0\) field for a given temperature. However, in imaging applications larger static fields present other challenges, such as contrast inhomogeneity.

The torque experienced by the nuclear spins induces precessional motion of the magnetic moments, summarized by the following equation of motion:

\[
\frac{dM}{dt} = \gamma M \times B_0. \tag{2.6}
\]

This motion is analogous to the precession of a spinning top in a gravitational field. Solving Equation 2.6 shows that the magnetization will precess about the field \(B_0\) at an angular frequency

\[
\omega_0 = \gamma B_0. \tag{2.7}
\]

\(\omega_0\) is known as the Larmor frequency. The precessional motion of \(M\) about the field is depicted in Figure 2.3.

Figure 2.3: The net magnetization \(M\) will precess with angular frequency \(\omega_0\) when placed in a magnetic field \(B_0\).
Transitions to the higher energy state are achieved by radio-frequency (RF) irradiation (typically a pulse) at the resonant frequency, $\omega_0$. This matches the energy required for the low to high transition ($\Delta E = \gamma \hbar B_0$). The RF pulse is applied by a current carrying coil surrounding the sample and oriented such that the resulting electromagnetic field will be perpendicular to $B_0$. In the laboratory frame, the applied RF pulse can be described by a complex rotating magnetic field in the $x$-$y$ plane

$$B_1 = B_1 e^{-i\omega_0 t},$$

where the real and imaginary parts are typically assigned to the $x$ and $y$ directions, respectively.

$B_1$ results in a very complicated motion in the lab frame $O(x, y, z)$ and a transformation to the rotating frame $O'(x', y', z)$ is often introduced to simplify the picture. With frame $O'$ rotating at an angular frequency $\omega_{rf}$ about $z$, we introduce a term that will nullify that static field when $\omega_{rf} = \omega_0$. When on resonance, the effective field in the rotating frame is simply $B_1$ (Figure 2.4).

The ultimate effect of the applied RF field is a rotation of the net magnetization $M$ into the $xy$-plane.

After the magnetization has been tipped into the transverse plane the RF pulse
is turned off. The magnetization precesses about the \( z \) axis and will induce an alternating current in a receiver coil surrounding the magnetization and linking the field (Faraday’s Law). The signal that is measured is the transverse magnetization as the system returns to the equilibrium state; this is known as the Free Induction Decay (FID) (Figure 2.5).

\[ V(t) \]

Figure 2.5: The Free Induction Decay (FID); the signal produced by the transverse magnetization and measured by a receiver coil.

The behaviour of the FID depends on the properties of the matter and preparation of the magnetization which will be discussed in the next section.

2.2.3 Bloch Equations and Relaxation

Following excitation of the system with \( B_1 \), Equation 2.6 indicates that the magnetization will precess indefinitely about \( B_0 \). This is not realistic, as energy loss will cause the system to return to the equilibrium state (Equation 2.5). The Bloch Equations:

\[
\begin{align*}
\frac{dM_x(t)}{dt} &= \gamma [M(t) \times B_0(t)]_x - \frac{M_x(t)}{T_2} \\
\frac{dM_y(t)}{dt} &= \gamma [M(t) \times B_0(t)]_y - \frac{M_y(t)}{T_2} \\
\frac{dM_z(t)}{dt} &= \gamma [M(t) \times B_0(t)]_z - \frac{M_z(t) - M_0}{T_1}
\end{align*}
\]  

(2.9)

are a set of phenomenological equations of motion that characterize the time evolution of the magnetization as it “relaxes” back to equilibrium [4]. Bloch introduced the time constants \( T_1 \) and \( T_2 \) based on the observed relaxation of the longitudinal \( (M_z) \)
and transverse ($M_{xy}$) magnetization, respectively. Solving the Equations 2.9:

$$M_x(t) = M_x(0) \cos(\omega_0 t)e^{-t/T_2}$$

$$M_y(t) = M_y(0) \sin(\omega_0 t)e^{-t/T_2}$$

$$M_z(t) = M_0 + [M_z(0) - M_0]e^{-t/T_1}$$

$M_0$ is the total magnitude of the magnetization available at equilibrium (due to the difference $N_+ - N_-$ in the field $B_0$). In general, $T_2 \leq T_1$.

$T_1$ characterizes the time it takes for the longitudinal component of the magnetization ($M_z$) to return to equilibrium. $T_1$ relaxation is the result of nuclei exchanging energy by interacting with their surroundings. For this reason it is also referred to as the spin-lattice relaxation time. On a microscopic level, $T_1$ arises from the redistribution of populations of nuclear spin states due to a variety of interactions (dipolar coupling, chemical shielding, etc.). These interactions are orientationally dependent and influence the local fields experienced by spins. Moreover, thermal motion causes fluctuations in the local fields. The consequence for MRI is that different tissues will have different $T_1$ values; $T_1$s of fluids are generally longer (1500-2000ms), water based tissues are intermediate (400-1200ms) and fat based tissues are shorter (100-150ms). One can determine a theoretical value relating the value of $T_1$ to any number of desired interactions, but that is beyond the scope of this thesis.

$T_2$, characterizes the decay of the transverse component of magnetization ($M_{xy}$) as it rotates about $B_0$. In an actual FID, this decay of $M_{xy}$ is confounded by $B_0$ magnetic field inhomogeneity. Losses due to both the random relaxation processes contributing to $T_2$, as well as dephasing of spins due to $B_0$ field inhomogeneity, are characterized by an effective relaxation time $T_2^*$:

$$\frac{1}{T_2^*} = \frac{1}{T_2} + \gamma \Delta B_0.$$ (2.11)
There are no quantum mechanical exchange interactions, rather the loss of transverse magnetization is due solely to the decoherence of nuclear spins precessing at different rates. The decay of signal due to this decoherence is illustrated in Figure 2.6.

Figure 2.6: $T_2^*$ relaxation caused by spin dephasing: differences in local magnetic fields experienced by spins cause dephasing. Spins experiencing a larger magnetic field will have $\omega > \omega_0$ and rotate faster, leading other spins (green arrow). Spins in a smaller field will have $\omega < \omega_0$ and lag behind (red arrow). Over time there is significant decoherence of the rotating spins causing the transverse magnetization to decay.

The value $T_2$ (the true quantity of interest in terms of characterizing the tissue) represents time-dependent, irreversible effects such as microscopic motion of spins in the sample, and may be isolated from the main field inhomogeneity. Hahn demonstrated that signal lost to field inhomogeneity could be recovered with his classic spin echo experiment [9]. Figure 2.7 shows the essence of the spin echo experiment with spin phase diagrams.
CHAPTER 2. FUNDAMENTALS OF MRI

Figure 2.7: $T_2$ and $T_2^*$. The evolution of magnetization in the rotating frame during a typical Hahn echo pulse sequence. 

a) The magnetization is tipped into the transverse plane with a 90°$x$ pulse. 
b) The magnetization is allowed to precess and dephasing occurs by the $T_2$ relaxation mechanisms. 
c) After time $\tau$, a 180°$x$ pulse is applied, flipping the magnetization about the $y$-axis. While the relative positions of the spins are reversed, their rate of precession remains the same bringing them back in phase with each other. 
d) At time $2\tau$ the signal will be refocused. 

A set amount of time $\tau$ after application of the 90° pulse, a 180° pulse is applied to the sample, and it is allowed to evolve for another period $\tau$. Since the inhomogeneity $\Delta B_0$ is essentially constant, the dephasing that occurs during the first period $\tau$ is reversed by the second after reorientation of the spins. The result is refocusing of the signal dephased due to $\Delta B_0$. Signal lost to true $T_2$ relaxation (i.e. thermal processes), on the other hand, is not recoverable. Figure 2.7e depicts the resulting signal evolution. A measure of $T_2$ can be extracted from fitting an exponential to the signal peaks at times $t = 2n\tau$, where $n$ is a non-negative integer.

2.3 Gradients and Imaging

For many NMR applications, variation in the magnetic field experienced by the spins is an undesired effect that must be mitigated or removed. This very effect is exploited in MRI, achieving spatial localization of signal with the use of gradient magnetic fields. The MRI gradient field is designed to provide a linear change in the local field as a
function of position \( r \). The gradient field \( \mathbf{B}_G \) is always parallel to the static field \( \mathbf{B}_0 \), only its strength varies as a function of \( r \) (Figure 2.8).

![Figure 2.8](image)

Figure 2.8: The \( x \)- and \( y \)-gradient fields provide a field that is in the direction of the static field \( \mathbf{B}_0 \) but has a linearly increasing strength along the respective direction.

The effect of \( \mathbf{B}_G(r) \) is to distribute the Larmor frequency of nuclei as a function of their position \( r \)

\[
\omega(r) = \omega_0 + \gamma r \cdot \mathbf{B}_G. \tag{2.12}
\]

This effect is shown in Figure 2.9 for a gradient along \( x \). A collection of spins distributed along the \( x \)-axis will possess the same frequency if the only field present is \( \mathbf{B}_0 \). The resulting FID will contribute to a single peak at the frequency \( \omega_0 \) (Figure 2.9a). With a gradient field applied \( \mathbf{B}_G(x) = xG_x \) (Figure 2.9b), the spins experience

![Figure 2.9](image)

Figure 2.9: Achieving spatial localization with gradients.
a different field, and therefore will exhibit a distinct frequency depending on their 
$x$-position, $\omega(x) = \gamma (B_0 + xG_x)$. The size of the peak will depend on the number of 
nuclei at a given position $x$. The resulting frequency spectrum can be decomposed 
to determine the location of origin for each nuclei contributing to the signal.

By utilizing gradients in every direction ($G_x, G_y, G_z$) one may encode a unique 
location in 3D space into the signal frequency. A typical MRI experiment follows 3 
encoding steps; slice selection ($z$-location), phase encoding ($y$-location) and frequency 
encoding ($x$-location).

### 2.3.1 Selective Excitation

MRI data is frequently acquired as a set of slices using a technique called selective 
excitation or slice selection. In this case, magnetization in a thin region $\Delta z$ is tipped 
into the $xy$ plane to produce signal. With a $z$-gradient field applied, the spins will 
possess a range of precession frequencies $\omega(z) = \gamma (B_0 + G_z z)$. The magnetization at 
a desired location can be excited by a $B_1$ pulse with the appropriate frequency $\omega_{rf}$ 
(Figure 2.10).

![Selective excitation](image)

**Figure 2.10:** Selective excitation.

The thickness of the slice $\Delta z$ is determined by the bandwidth of the $B_1$ pulse.
Ideally $B_1$ is a sinc pulse that will result in a rectangular response excitation; in this case, all affected spins will rotate by the same angle (90°, for example). In practice however, the excitation is rarely perfect due to the apodization of the pulse and spatial non-uniformity of $B_1$. These effects are of some importance in Chapter 5.

### 2.3.2 Frequency and Phase Encoding

After excitation, the slice selection pulse is turned off and the locations of the excited spins are encoded by applying gradients in the remaining directions ($x, y$). In a general acquisition, location in one direction (normally $x$) is encoded during the acquisition of the FID. This step is known as Frequency Encoding (FE) since the information dictating the location of the signal is encoded in the spins frequency. The $y$ location is encoded in the spins relative phase in a separate step, hence Phase Encoding (PE). Figure 2.11 demonstrates the technique for encoding in the $x$ (FE) and $y$ (PE) directions.

![Diagram](image)

Figure 2.11: Position along the $x$-axis is encoded in frequency, while position along the $y$-axis is encoded in the phase.

The FID will contain frequencies based on the applied $x$-gradient where

$$\omega(x) = \gamma(B_0 + xG_x). \quad (2.13)$$
The main difference between FE and PE is that the FE step occurs during the acquisition of signal, while PE occurs in a preparatory step before the FID is collected. An example of a simple pulse sequence showing the timing of slice select, frequency and phase encoding is shown in Figure 2.12.

![Pulse Sequence Diagram](image)

**Figure 2.12:** A simple 2D pulse sequence; the slice selection ($G_z$) is done during rf excitation. Phase encoding ($G_y$) follows to allow $y$ localization. Frequency encoding ($G_x$) is done during acquisition of the FID.

When considering the standard Cartesian 2D acquisition after slice selection, the gradients applied in the $x$ and $y$ directions encode the position of the local magnetization. During the FID acquisition, the FE gradient $G_x$ imparts a phase of $\gamma x G_x t$ at position $x$ and time $t$. The PE step is normally encoded earlier in the pulse sequence contributing a phase factor depending on the duration $T$ of the $G_y$ gradient; $\gamma y G_y T$.

### 2.3.3 k-Space

The concept of k-space, introduced by Ljunggren and Twieg in 1983 [10, 11], is extremely useful in understanding acquisition of MRI data. The information of MRI is acquired by traversing k-space and subsequently transformed to create the image. The pulse sequence prescribes a specific combination of gradients and RF pulses designed to provide the desired spatial encoding. The magnetization induces a time dependent signal $s(t)$ that is picked up by the detector. $s(t)$ depends on the timing
and duration of pulses and gradients, described by $\int_0^t G(\tau) \cdot r d\tau$ and the spatial distribution of magnetization, $M(\mathbf{r})$. In general,

$$s(t) = \int M(\mathbf{r}) e^{-i \left[ \omega_0 t + \gamma \int_0^t G(\tau) \cdot r d\tau \right]} d^3 \mathbf{r}.$$  \hspace{1cm} (2.14)

To simplify Equation 2.14 we introduce a spatial encoding parameter $k$:

$$k(t) = \gamma \int_0^t G(\tau) d\tau,$$ \hspace{1cm} (2.15)

and we digitize and demodulate the signal by the resonance frequency $\omega_0$ (this is essentially shifting the frequency spectrum by $-\omega_0$). Equation 2.14 can thus be written in terms of the parameter $k$:

$$S(k) = \int M(\mathbf{r}) e^{-i k \cdot \mathbf{r}} d^3 \mathbf{r}.$$ \hspace{1cm} (2.16)

$S(k)$ and $M(\mathbf{r})$ constitute a Fourier Transform (FT) pair; $S$ is referred to as k-space and contains the coefficients of the spatial harmonics that compose the image (Figure 2.13).

Figure 2.13: Image space and k-space; a) magnitude image of a brain and b) the corresponding k-space representation.
k(t) can be considered the trajectory through k-space that results from the prescribed gradient sequence.

Assuming the 2D acquisition from Section 2.3.2, the x and y components are

\[ k_x = \gamma G_x t \]
\[ k_y = \gamma G_y T \]  
(2.17)

and Equation 2.16 becomes

\[ S(k_x, k_y) = \int \int M(x, y)e^{-i(xk_x + yk_y)}dxdy. \]  
(2.18)

The distribution of magnetization (and therefore the image) is recovered via 2D inverse FT of the k-space signal.

Due to the nature of the data acquisition (sampling in the spatial frequency domain), the Field of View (FOV) of the MR image is related to the sampling resolution in k-space. The smallest increment in k-space is the inverse of the FOV in that direction:

\[ FOV_x = \frac{1}{\Delta k_x}, \quad FOV_y = \frac{1}{\Delta k_y}. \]  
(2.19)

Figure 2.14 illustrates the trajectory traced in k-space for a simple gradient sequence.

Figure 2.14: k-space trajectory: Gradients $G_x$ and $G_y$ allow the traversal of k-space. Steps 1-4 show the effect of applying gradients to collect the necessary sampling of k-space. 2D IFT of the acquired data produces the image.
There are a number of different trajectories made possible by manipulating the gradients in different ways during the pulse sequence. Some examples of different k-space trajectories are shown in Figure 2.15. Different trajectories may be useful for particular applications but can also result in unique artifacts that must be considered. To obtain an image without any aliasing effects, one must have complete k-space coverage. This will be a point of interest in Chapter 3, where we seek to reduce the time taken to collect full k-space data using supplemental information.

Figure 2.15: Various k-space trajectories.
Chapter 3

Optimization of Partial Parallel Imaging Techniques

3.1 Introduction to Partial Parallel Imaging

When compared with other medical imaging modalities, a significant limitation for MR scans is the time needed to acquire a clinically relevant image. For standard Cartesian acquisitions, the time cost of spatial encoding in one direction ($x$, the FE direction) is effectively nil. In the other directions ($y$ for a 2D acquisition or $y$ and $z$ for 3D acquisitions), each unique PE position requires a separate excitation, allowing the longitudinal magnetization to recover before subsequent points are acquired. There are a few exceptions, such as Echo-Planar Imaging (EPI) [12] in which the PE direction is fully sampled during a single excitation, but these techniques suffer from other issues, such as geometric distortion, ghosting and limited in-plane resolution [13, 2, 14].

For the high resolution images demanded in some clinical settings, there must be a large number of PE points, resulting in inconvenient or even impractical total scan times. Motion due to breathing, heartbeat and other physiological effects can
introduce ghosting artifacts if the scan time is not much faster than the motion. Applications such as cardiac imaging [15] and Functional MRI (f-MRI) [16] require rapid acquisition to obtain images free of motion artifacts. These demands must be weighed against limitations of the MR system. Gradients are limited by maximum amplitude and slew-rate. In addition, high gradient strength and rapid switching can trigger peripheral nerve stimulation in patients [17].

The introduction of Partial Parallel Imaging (PPI) provides a means for surpassing the limitations of using gradients for spatial encoding. PPI exploits the intrinsic spatial variation of receiver coil sensitivities to supplement the signal localization normally obtained with PE steps, thus reducing the amount of time required to obtain full k-space coverage. This time savings may be useful in mitigating artifacts dependent on acquisition time, or simply increasing MR scanner efficiency to minimize patient discomfort. In real-time applications, such as cine MR or f-MRI, PPI may be used to increase temporal resolution as well.

In a Cartesian acquisition, accelerated scans are achieved by reducing the number of PE steps while maintaining the same outer k-space limits. The degree of sub-sampling is characterized by the reduction factor, $R$; the k-space data is acquired at every $R$th $k_y$ position. When $R > 1$ this results in a violation of the Nyquist sampling theorem and the image is aliased. Figure 3.1 shows the effect of uniform sub-sampling with different $R$ values in a Cartesian acquisition.

PPI techniques exploit the spatial variation in relative sensitivity relationships in an array of receiver coils to recover the missing $k_y$ lines. A pedagogical approach to understanding PPI includes an understanding of the nature of the surface receiver coil and the introduction of the receiver coil array. The pioneering techniques SENSitivity Encoding (SENSE), SiMultaneous Acquisition of Spatial Harmonics (SMASH), and GeneRalised Auto-calibrating Partial Parallel Acquisition (GRAPPA) provide the foundation for most parallel imaging approaches.
Figure 3.1: PPI Cartesian sub-sampling. From left to right, the images are reconstructed using variable fractions \((1/R)\) of k-space data. Fully sampled k-space \((R = 1)\) will have no aliasing, while larger values result in \(R\) aliased images.

### 3.1.1 The Receiver Coil Array

Achieving localization using the receiver coils relies on inherent spatial variation of the coils sensitivity profile. The MRI signal in Equation 2.16 does not account for the receiver sensitivity, which is in general spatially varying [18, 19]. The sensitivity of the coil \(C(x, y)\) will modulate the magnetization and Equation 2.18 becomes:

\[
S(k_x, k_y) = \int \int C(x, y) M(x, y) e^{-i(xk_x + yk_y)} dxdy \tag{3.1}
\]

The sensitivity is a result of the properties of the receiver coil. The reciprocity principle dictates that the sensitivity is related to the magnetic field produced by a coil, this in turn is described by Biot-Savart Law. The magnetic field \(\mathbf{B}\) at a position
\textbf{CHAPTER 3. OPTIMIZATION OF PPI}

$r$ away from a constant current source $Ids$ is

$$
B(r) = \frac{\mu_0}{4\pi} \int_C \frac{Ids \times r}{|r|^3}
$$

Equation 3.2

For a current loop (coil), Equation 3.2 may be integrated around the path of the loop to determine the net field in a given location. Figure 3.2 shows the strength of the magnetic field typical for a surface coil (illustrated by the dotted blue line).

Figure 3.2: The coil sensitivity profile; a surface receiver coil will be more sensitive to signal close to the center of the coil.

Surface coils are tailored to measure signal in a specific location and provide higher SNR in a smaller region when compared with a full volume “body coil”; the body coil is sensitive to a larger volume of noise. Body coils generally have more uniform RF transmission and reception profiles than surface coils [59]. In the following sections we explore how PPI takes advantage of the spatially non-uniform nature of surface coils.
3.1.2 SMASH

SiMultaneous Acquisition of Spatial Harmonics (SMASH) [20], uses the spatially variant nature of surface coils to replace the application of PE gradients in a very literal sense. The coil profiles are combined in such a way as to emulate the effect of small PE steps. This approach requires careful arrangement of coil geometry to facilitate the formation of spatial harmonics across the image FOV.

Consider a coil with a spatial sensitivity mapping $C_1(x, y)$. The coil sensitivity modulates the MR signal generated by spin-density $\rho(x, y)$, resulting in the acquired k-space signal

$$S_1(k_x, k_y) = \int\int \rho(x, y)C_1(x, y)e^{-i(k_xx+k_yy)}dxdy. \quad (3.3)$$

Introducing multiple coils, one may combine the signal from each to create a composite signal

$$S(k_x, k_y) = \int\int \rho(x, y)\sum_j C_j(x, y)e^{-i(k_xx+k_yy)}dxdy. \quad (3.4)$$

where $j$ denotes the coil number.

With the appropriate coil array geometry, one can introduce weighting factors, $w_j$, to the individual coil signals to create sinusoidal modulations in the composite signal. First, the $w_j$’s are chosen such that the sensitivity profiles combine to match a spatial harmonic of the form

$$e^{im\Delta k_y} = \sum_j w_j^m C_j(x, y), \quad (3.5)$$

where $\Delta k_y = 2\pi/FOV$ is the fundamental spatial frequency in the PE direction. The index $m$ is an integer chosen to produce the desired spatial harmonic over the FOV. This step (illustrated in Figure 3.3a for the zeroth and first order spatial harmonics) is done by fitting the coil sensitivity maps to the desired spatial harmonic and therefore requires accurate knowledge of the coil sensitivity profiles.
Figure 3.3: Signal recovery in SMASH imaging. a) Combining properly weighted sensitivity profiles (dotted lines) from an array of coils produce spatial harmonics (solid lines). b) The k-space signals from each coil, modulated by the weights are combined to produce a corresponding shift in the composite k-space.

Once the weights are known, they may be used to create a composite signal

\[ S^m(k_x, k_y) = \int \int \rho(x, y) \sum_j w_j^m C_j(x, y) e^{-i(k_x x + k_y y)} dxdy. \]  

(3.6)

possessing a modulation corresponding to chosen weighting factors. Inserting Equation 3.5 into Equation 3.6

\[ S^m(k_x, k_y) = \int \int \rho(x, y) e^{-im\Delta k_y y} e^{-i(k_x x + k_y y)} dxdy \]

\[ S^m(k_x, k_y) = \int \int \rho(x, y) e^{-i[k_x x + (k_y + m\Delta k_y)]y} dxdy \]

\[ S^m(k_x, k_y) = S(k_x, k_y + \Delta k_y) \]

(3.7)

Equation 3.7 elucidates the fact that the modulation of the acquired k-space lines by the \( m^{th} \) spatial harmonic is equivalent to a shift in k-space by \( m\Delta k_y \).

The recovery of missing lines in SMASH is accomplished by weighted combination of the individual coil signals (Figure 3.3b),

\[ \sum_j w_j^m S_j(k_x, k_y) = S(k_x, k_y + m\Delta k_y). \]

(3.8)
It should be noted that Equation 3.8 represents an approximate relationship, depending on the ability of the coil array to accurately emulate the required spatial harmonics (Equation 3.5). If one can faithfully represent $M$ different spatial harmonics, a reduction factor of $R = M$ is theoretically possible.

The SMASH reconstruction results in a uniform noise distribution [21], but the ability of the coil geometry to emulate order-$m$ spatial harmonics is crucial in the recovery of missing signal offset by $m\Delta k_y$. This can be severely limiting in practical applications as the array typically must be arranged in a linear fashion spanning the PE direction. Furthermore, the selection of weighting factors to match the desired spatial harmonics relies on fitting to known coil profiles. This introduces the need for a calibration scan which requires additional acquisition time and inaccuracies in fitting can lead to errors in the recovered $k_y$ lines.

### 3.1.3 SENSE

The SENSitivity Encoding (SENSE) reconstruction takes place entirely in the image domain. Reduced k-space data is acquired with multiple coils and aliased images are unfolded using the sensitivity maps from each coil. Equation 3.9 allows the pixel-by-pixel reconstruction of an acquisition with a reduction factor $R = 2$. This is shown schematically in Figure 3.4. The solid pixels in the reduced FOV represent a sum of signal from the local pixel as well as aliased signal from a pixel located $\frac{FOV}{2}$ away. That is, at the point $(x_1, y_1)$, there is combined signal from the locations $(x_1, y_1)$ and $(x'_1, y'_1) = (x_1, y_1 + \frac{FOV}{2})$ in the full FOV. The same situation occurs at the location $(x_2, y_2)$. However, the contributions from each location vary in the intermediate images acquired from different coils.

The actual signal, $\rho(x, y)$, can be recovered from the aliased images $I_1(x, y)$ and
Figure 3.4: Aliased pixels in the SENSE reconstruction. The hollow pixels are folded to the locations of the solid pixels at a distance $\frac{\text{FOV}}{2}$ for $R = 2$.

$I_2(x, y)$ provided the coil sensitivities $C_1(x, y)$ and $C_2(x, y)$ are known:

\[
I_1(x, y) = C_1(x, y)\rho(x, y) + C_1\left(x, y + \frac{\text{FOV}}{2}\right)\rho\left(x, y + \frac{\text{FOV}}{2}\right)
\]

\[
I_2(x, y) = C_2(x, y)\rho(x, y) + C_2\left(x, y + \frac{\text{FOV}}{2}\right)\rho\left(x, y + \frac{\text{FOV}}{2}\right)
\]

If the coil sensitivity maps are perfectly accurate, inversion of Equation 3.9 provides an exact reconstruction of the image, $\rho(x, y)$.

The SENSE reconstruction is spatially localized and provides a robust reconstruction with minimal constraints on the physical coil geometry. This makes SENSE the ultimate localized parallel reconstruction technique. However, the nature of the reconstruction results in a different SNR at each pixel location; the numerical condition of the unfolding equation determines the local noise properties. Like SMASH, SENSE requires a calibration scan to provide accurate coil sensitivity maps for the unfolding step. These coil maps are difficult to estimate with a high degree of accuracy in practice.
3.1.4 GRAPPA

To address the shortcomings of the original SMASH and SENSE algorithms, many variations have been formulated. To alleviate the problems of coil geometry dependency, modifications such as Tailored SMASH [22] and Generalised SMASH (gSMASH) [23] were proposed. In Tailored SMASH, the fitting was reformulated to consider additional degrees of freedom, allowing a fit to a spatial harmonic with $C(x, y) \neq 1$. This relaxed some of the rigid requirements on the coil profiles, and improved reconstructions in non-ideal practical settings. gSMASH went a step further to remove the highly restrictive geometric constraints on the coil array. In this approach, the coil sensitivities $C(x, y)$ were represented by the sum of their Fourier space coefficients. By using the Fourier space representation of the coil profiles, the intermediate step of fitting to spatial harmonics specific to the image FOV was avoided and the requirement of a matching coil geometry was relaxed.

The remaining inconvenience of requiring a calibration scan was addressed by AUTO-SMASH [24]. In this approach, information about the coil sensitivity is extracted from relationships between acquired signal and extra Auto-Calibration Signal (ACS) lines. This information is then used to create a composite k-space signal at the desired $k_y$ location, synthesizing the missing PE line. In the AUTO-SMASH approach, the weighting factors for $m$ spatial harmonics are computed with $m$ ACS lines. To improve the calibration and the resulting artifact removal, VD-AUTO-SMASH [25] included a larger ACS region in the fitting procedure.

These advancements ultimately paved the way for GeneRalised Auto-calibrating Partial Parallel Acquisition (GRAPPA). GRAPPA is essentially a more general extension of VD-AUTO-SMASH in which the missing k-space data are generated in a coil-by-coil reconstruction, using a larger subset of ACS lines. This has the benefit of mitigating phase cancellation effects and allowing the final coil images to be combined in some optimal way. Moreover, the ACS lines may be included in the individual coil
In the GRAPPA algorithm, missing PE lines for a single coil are estimated using a linear superposition of the surrounding acquired lines from all coils. The recovery of the missing information can be broken down into two main steps: the calibration step, in which the linear weights relating target and source data are calculated using the extra acquired ACS lines and the synthesis step, in which the missing data is recovered using the fitted weights. Figure 3.5a shows the typical GRAPPA acquisition coverage and the respective locations for the calibration and synthesis steps.

The linear summation to reconstruct the missing target signal \( S_i \) at location \( k_y \) in the \( i \)th coil dataset is

\[
S_i(k_y) = \sum_{j=1}^{N_c} \sum_{m=1}^{N_m} w_{ij}^m S_j \{ k_y + [(m - N_m/2) R - 1] \Delta k_y \},
\]

where, \( j \) is the source signal coil, \( N_m \) is the number of shifted PE lines used in the combination, \( R \) is the reduction factor. There is a unique weighting factor \( w_{ij}^m \) relating lines for each coil pairing and relative offset \( (m \Delta k_y) \). The number and position of the source lines relative to the target line is known as the GRAPPA kernel. Figure 3.5b shows the GRAPPA kernel for a 3 coil acquisition with \( R = 2 \) and \( N_m = 4 \) \( (m = -3, -1, 1, 3) \). The magenta lines represent the weighting factors linking the target and source data.

Equation 3.10 is commonly written in the more compact matrix form:

\[
S_{tgt} = GS_{src}.
\]

\( S_{tgt} \) and \( S_{src} \) represent concatenations of the missing (target) and acquired (source) signal data, respectively. The matrix \( G \) contains the weighting factors to be used in the signal combination. While Equation 3.10 represents the computation required to reconstruct a single data point at location \( k_y \) in the \( i \)th coil data set, the matrix
formulation conveniently expresses the relationship between all target and source data.

For the calibration step, the acquired ACS lines are inserted as the target signal matrix, $S_{tgt}$. $G$ may then be determined by solving the system

$$G \rightarrow \text{argmin} \left( \left\| S_{src}G - S_{ACS} \right\|_2 \right), \quad (3.12)$$

where, $\left\| \cdot \right\|_2$ represents the $L_2$ norm. Equation 3.12 represents an over-determined system that may be solved by invoking the Moore-Penrose pseudoinverse ($\dagger$, see Appendix A for more) of the source data matrix, $S_{src}$:

$$G = S_{src}^\dagger S_{ACS} \quad (3.13)$$

The conditioning of Equation 3.13 is further improved by inclusion of multiple ACS lines from central k-space in the fitting.

Following calibration, the shift invariant kernel is used to synthesize missing lines.
in the undersampled regions of k-space for that coil (green dots in Figure 3.5a). This process is repeated until missing data in each coil k-space is fully recovered. The final image is created by combining the individual, complex coil images $I_j(x, y)$ in a Root Sum-of-Squares (rSoS)

$$rSoS = \sqrt{\sum_j I_j(x, y)I_j^*(x, y)}$$  (3.14)

where, * denotes the complex conjugate. The rSoS is typically used as it provides a robust method for component coil image combination [26].

### 3.2 rGRAPPA

A number of improvements to the GRAPPA algorithm have been proposed, attempting to minimize reconstruction errors, reducing noise and residual aliasing artifact. Such approaches include regularization techniques [27, 28, 29], iterative reconstruction techniques [30] and filtering [31]. We focus our attention on improving the GRAPPA reconstruction by careful consideration of the calibration and synthesis of missing data in terms of the underlying physical system.

#### 3.2.1 Theory

In standard GRAPPA algorithms, the weighting factors are calculated using information spanning the entire FE range of the image domain. If we consider a weighting factor $w_{ij}$ that links PE lines in the $i$th and $j$th coil, the weight depends on the local relative relationship between the sensitivities of the two coils. Since typical surface coils have spatially varying sensitivities, a single weight will not be accurate for every location $x$ of the image domain. Figure 3.6 illustrates this fact. In the standard GRAPPA approach, the resulting weighting factors represent an *average* weight that provides the lowest least square error between target and source lines across the entire FOV. It has been shown that allowing the weighting factors to vary as a function of
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Figure 3.6: Sensitivity profile variation in a 2-coil MR experiment.

$x$ increases the accuracy of the resulting recovered lines.

A number of approaches have accounted for this variation in a few different ways. Including extra $k_x$ points in the kernel provides some sensitivity to FE variation of relative coil profiles [32]. This increases the computation time when inverting Equation 3.11 and, if only a few extra $k_x$ lines are used, only low frequency coil profile variation can be represented. Other approaches used a set of smoothly varying basis functions to represent the weighting factors as a function of $x$ [33, 34]. These implementations also result in higher computation times and added complexity to the weight calculation.

We have found, given the picture in Figure 3.6, that the best approach is to simply target the GRAPPA fitting in a limited region along the $x$ direction. To facilitate this the GRAPPA calibration and synthesis steps are considered in hybrid $(x, k_y)$ space. In the standard GRAPPA implementation the entire $k_y$ line is considered in the fitting of a single set of weights (Figure 3.7a). The resulting weights are an average across the FOV and fitting in either k-space or hybrid space will give the same values. The subsequent synthesis step applies the average weighting values ($w_{ij}(m)$) to all points along $x$. This is shown schematically in Figure 3.7c.

The rGRAPPA calibration is restricted to data in a smaller region, $d$ (Figure 3.7b), recovering unique weighting factors to be applied to the data in that region. The
location specific weights $w_{ij}^m(x, k_y)$, are more appropriate for the local coil sensitivity relationships. The resulting synthesis employs the regionally targeted weights to recover missing data with greater accuracy.

![Figure 3.7: a) Standard GRAPPA and b) rGRAPPA calibrations. c) An average weighting value results from the standard GRAPPA calibration fit and is applied to recover all data in the line, $k_y$. d) rGRAPPA implementation in which the weight values are allowed to vary along $x$ providing a unique weight for each synthesized region.](image)

The localized fitting produces more accurate weights using fewer source data and does not require selection of a basis set to model the weight variation (as in [34]). Instead, the optimal weight is found for a given region and used to synthesize the local data, accounting for coil profile variation across the FOV. This is the key to the improved function of rGRAPPA. The reconstruction employs a sliding window approach; weights are computed in the sliding window region and overlapping synthesized signal is averaged. This has a combined effect of allowing a more localized...
representation of weighting factors and additional noise averaging.

The computation of local weighting factors $w^m_{ij}(x, k_y)$ is facilitated by working with the image in hybrid space $(x, k_y)$. Truncated $k_y$ lines representing a limited range in the $x$-direction result in a set of $N_x$ weights. Equation 3.10 becomes:

$$S_i(x, k_y) = \sum_{j=1}^{N_x} \sum_{m=1}^{N_m} w^m_{ij}(x) S_j\{x, k_y + [(m - N_b/2)R - 1] \Delta k_y\},$$  (3.15)

where we have introduced the label $x$ to identify the location. Since the data contain noise, a fit targeting a single point $x$ and the corresponding source data can be significantly corrupted. Increasing the region width ($d$) of the fitting data results in better conditioning in Equation 3.12. Selecting the optimal width $d$ balances a trade off between noise and accuracy of the local weighting factors. This optimal size depends on the relative coil geometry and noise characteristics of the acquisition setup.

### 3.2.2 Method

Simulated rGRAPPA acquisitions were created by selecting every $R$th $k_y$ line from fully acquired, in vivo, multi-coil datasets. $N_{ACS}$ lines in central k-space were kept for the calibration. The accuracy of the data recovery for a given $d$ can be quantified by the Relative Error ($RE$) between the recovered image $I(x, y)$ and the fully sampled reference image $I_0(x, y)$:

$$RE = \sqrt{\frac{\sum_{x,y} [I(x, y) - I_0(x, y)]^2}{\sum_{x,y} I_0(x, y)^2}}.$$  (3.16)

In the rGRAPPA reconstruction, $I$ and $I_0$ are rSoS images. The $RE$ was calculated for recovered images over the reconstruction parameter space ($d$) to identify the optimal region width.
Datasets $ABDax1$ and $ABDax2$ are 2 slices from an axial abdominal scan, 4 coil acquisition on a 1.5T General Electric (GE) scanner, $256 \times 256$ matrix, $TR/TE = 120/2.12$ms, 5mm slice thickness.

Simulated datasets were also created using images of a Shepp-Logan phantom ($Shepp$) and a brain ($Brain$), shown in Figure 3.8. Coil images were sampled from the static pictures using Gaussian sensitivity profiles with random, low frequency phase modulation. Complex Gaussian white noise was added to each coil image and the resulting k-space datasets were used to generate the desired undersampled acquisitions for rGRAPPA reconstruction.

**Figure 3.8:** Simulation Datasets a) $Shepp$ image and b) $Brain$ image.

*Computational Complexity*

The calibration and synthesis steps of the GRAPPA algorithm represent operations using large data matrices and present the bulk of the computational processing. For an implementation with $N_c$ coils, a reduction factor $R$, a full k-space of $N_x \times N_y$ matrix size, $N_m$ kernel positions and $N_{ACS}$ ACS lines we may summarize the order of operations required for each step.

In the calibration step, the $S_{tgt}$ matrix is organized into $N_c$ rows, one for each coil, containing $N_{ACS}$ ACS lines. Each line has length $d$, the size of the region used for reconstruction (for standard GRAPPA $d = N_x$, the number of FE points in the
acquisition). The $S_{ACS}$ matrix has size $N_c \times (N_{ACS}d)$. The corresponding source data in the signal surrounding the ACS lines make up the matrix $S_{src}$. Each ACS line is fit to $N_m$ surrounding lines from all $N_c$ coils, resulting in a matrix size $(N_c N_m) \times (N_{ACS}d)$.

To determine $G$, we calculate the pseudoinverse of the matrix $S_{src}$ and multiply by $S_{ACS}$. The source data provides a heavily over-determined system; there are $N_c N_m$ unknowns (the weights), determined by fitting $N_{ACS}d N_c N_m$ data points. The number of floating point operations ($flops$) in the calibration step (Equation 3.13) is

$$flops_{cal} = N_c^2 N_m N_{ACS}d + 2N_c^2 N_m^2 N_{ACS}d + N_c^3 N_m^3,$$

in terms of complex multiplications.

For the synthesis, there are $N_s = \text{floor}\{N_y (1 - 1/R)\} - N_{ACS}$ lines to be recovered ($\text{floor}\{\cdot\}$ rounding down to the nearest integer). In this case, the size of $S_{tgt}$ is $N_c \times (N_s d)$. The corresponding source data matrix $S_{src}$ will be size $(N_c N_m) \times (N_s d)$, and the number of $flops$ required for synthesis (Equation 3.11) is

$$flops_{syn} = N_c^2 N_m N_s d.$$  

For the standard GRAPPA implementation, $d = N_x$, the total number of acquired points in the $k_x$ direction. In the rGRAPPA calibration, the optimal region width is typically much smaller than the full FOV ($d << N_x$). However, there are $N_x - (d - 1)$ unique calibration steps in rGRAPPA, resulting in an increase in the number of computations. When $d = 1$, there is no overlap, and the number of operations is practically equal to the standard GRAPPA case ($d = 256$).

To contrast these computational complexities, the number of operations for a standard MRI reconstruction is limited to a single 2D Fast Fourier Transform (FFT). The popular Cooley-Tukey FFT algorithm results in $N \log N$ operations for a length $N$ 1D FFT [35]. Extending to 2D requires $N_x N_y \log (N_x N_y)$ $flops$. For an image of
size $256 \times 256$ this translates to $7.3 \times 10^5$ computations. A GRAPPA reconstruction (with parameters $N_m = 4$, $N_c = 4$ and $N_{ACS} = 24$) registers $5.2 \times 10^6$ computations, and with an optimized $d = 8$ rGRAPPA implementation $4.2 \times 10^7$.

### 3.2.3 Results

The four component coil images for the first dataset ($ABDax1$) are shown in Figure 3.9. The corresponding fully acquired rSoS image is shown in Figure 3.10a. Figure 3.10b shows the aliasing effect after removal of k-space lines to emulate an accelerated acquisition with $R = 2$ and $N_{ACS} = 16$.

![Figure 3.9: ABDax1 coil images.](image)

![Figure 3.10: Effect of undersampling on abdominal scan ABDax1 a) fully sampled rSoS image, b) aliased rSoS image due to missing PE lines.](image)
First we examine the benefits of spatially varying weighting factors in the rGRAPPA reconstruction over the initial GRAPPA method. The missing k-space lines were synthesized using region widths, \( d = 1 \rightarrow 256 \) and the resulting rSoS images were compared to the gold-standard image using full k-space data.

For the \( ABDax1 \) dataset, a plot of the \( RE \) is shown in Figure 3.11a. The results indicate that rGRAPPA provides a better reconstruction than standard GRAPPA.
for virtually all region widths, $d$. The optimal $d$ value (providing the lowest $RE$) is much smaller than the GRAPPA equivalent region width, $d = 256$. In this case, a small region with $d = 7$ is optimal for computing accurate weights, suggesting that the local variation of weighting factors is indeed significant. At the lower end of $d$ values, the $RE$ is seen to increase rapidly (near $d = 1, 2$ pixels). This is due to noise in the k-space data corrupting the fitting between source and calibration data.

Figure 3.11b shows an example of the variation of the weighting factors. The real part of one of the complex weighting factors, $w$, is plotted as a function of the $x$ position. The GRAPPA reconstruction computes a single weight across the FE direction (orange line). When only a single column of data ($d = 1$) is used, the weighting values fluctuate rapidly due to noise (blue line). The optimal result ($d = 7$) is a compromise between the two extremes (red line).

The optimal rGRAPPA reconstruction provides better aliasing artifact suppression than the standard GRAPPA reconstruction. The resulting rSoS images for $ABDax1$ are displayed in Figure 3.12. The reduction of aliasing artifact is particularly evident in the difference maps (Figures 3.12b and 3.12d). The difference map for each reconstruction setup is displayed with the same scale for comparison.

Similar behaviour is seen in the simulated data sets. The four component coil images from the simulated dataset $Brain$ are shown in Figure 3.13. The resulting $RE$ curve for the $Brain$ dataset is shown in Figure 3.14. In this case, the optimal region width is lower, at $d = 5$ pixels. This effect is due in part to the fact that the simulated images have less severe noise. It is possible that the idealized, simulated coil sensitivity profiles also contribute. Compared with the $ABDax1$ real data case (Figure 3.11a) the $Brain$ image reconstruction at small $d$ values experiences a less dramatic increase in $RE$.

The $Brain$ image rSoS reconstructions are shown in Figure 3.15. Once again, visible reduction of aliasing artifact is seen in the rGRAPPA rSoS image and difference
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Figure 3.12: Abdominal scan $ABDax1$ reconstruction, $R = 2$, $N_{ACS} = 16$ a) GRAPPA reconstruction and b) difference map. c) Optimal ($d = 7$) rGRAPPA reconstruction and d) difference map.

Figure 3.13: Brain coil images.
map (Figures 3.15c and 3.15d, respectively), compared with those of the standard GRAPPA implementation (Figures 3.15a and 3.15b, respectively).

With \( d = 1 \), the region is too small and noise begins to corrupt the reconstruction. While this does not have terribly adverse effects at low accelerations (\( R = 2 \) Figure 3.16), the reconstruction suffers more as we move to higher \( R \) values.

The ability of rGRAPPA to reduce aliasing artifact is also shown for higher \( R \) factors. Figures 3.17 and 3.18 show results for the real dataset \( ABDax1 \) with \( R = 3 \) and \( R = 4 \), respectively. In general, the optimal \( d \) for reconstruction did not vary significantly for different \( R \), changing only by a few points.
Figure 3.15: Brain image simulation reconstruction, $R = 2, N_{ACS} = 16$ a) GRAPPA reconstruction and b) difference map. c) Optimal ($d = 5$) rGRAPPA reconstruction and d) difference map.
Figure 3.16: $d = 1$ Abdominal scan $ABDax1$ reconstruction, $R = 2$, $N_{ACS} = 16$ a) rGRAPPA reconstruction and d) difference map.
Figure 3.17: Abdominal scan $ABDax1$ reconstruction, $R = 3$, $N_{ACS} = 24$ a) GRAPPA reconstruction and b) difference map. c) Optimal ($d = 10$) rGRAPPA reconstruction and d) difference map.
Figure 3.18: Abdominal scan $ABDax1$ reconstruction, $R = 4$, $N_{ACS} = 24$ a) GRAPPA reconstruction and b) difference map. c) Optimal ($d = 9$) rGRAPPA reconstruction and d) difference map.
3.2.4 Discussion

For this study, the RE was chosen as the gold-standard metric for the reconstruction, since the goal of rGRAPPA is to provide a final image that most accurately matches the fully sampled reconstruction. The optimal region width $d$ is thus determined by the rGRAPPA reconstruction that results in the minimum $RE$ value. In general, the optimal $d$ value was much smaller than the full FOV range (i.e. the standard GRAPPA reconstruction), validating the rGRAPPA framework. The optimal $d$ value seems to increase slightly for higher acceleration factor (Figure 3.17).

For some data and $R$ factors, the $RE$ minimum was found at a relatively large $d$ value, and the general rule $d << N_x$ was not upheld. In such cases, there was also a local minimum at a small region width (Figure 3.19). Figures 3.20a & 3.20b display the local minimum, small region ($d_s$) reconstruction & difference map, respectively. Figures 3.20c & 3.20d display those of the global minimum, large region ($d_L$) reconstruction.

For $d_s$ the primary contribution to the $RE$ is noise amplification. Conversely, the $RE$ is owed primarily to residual aliasing artifact in the $d_L$ reconstruction. In general, noise-like error distributed over the entire FOV is preferable to local residual artifact since it is less likely to resemble anatomical structure or pathology. In cases
where there are two such competing $RE$ minima, the smaller $d$ value is most likely optimal. However, in certain cases the noise may be so great as to render the image diagnostically useless. It is not well understood why the two minima occur in such a way, and may be an interesting point for future study.

The fact that the optimal $d$ value was normally much smaller than the full FOV suggests that the weight variation occurs on a relatively small scale. As such, the hybrid space approaches such as rGRAPPA and others [33, 34] are well suited to
take advantage of this type of spatial variation. A k-space based kernel (as in [32]) would require extensive support to be sensitive to the same scale of variation. In other words, to account for spatial variation on the order of a few points along $x$, the kernel would require inclusion of a very large number of $k_x$ points. This results in extremely large computational costs to provide essentially the same information as the hybrid space calibration techniques.

This tendency to a small optimal $d$ does not seem to depend on the acceleration factor, $R$. If the number of ACS lines $N_{ACS}$ is kept constant, the data used for calibration are virtually identical for any reasonable $R$, although the kernel fitting relationships in terms of relative $(x, k_y)$ positions can vary. Decreasing $N_{ACS}$ can compromise the conditioning of the pseudoinverse problem (Equation 3.12). In conditions with poor SNR, this is likely to be more detrimental to rGRAPPA than the standard implementation, but with our tests the conditioning was typically sufficient to get an accurate result, even with smaller $d$.

The coil geometry and SNR conditions seem to be more important to the determination of optimal region width than the imaged object. In simulation the impact of the underlying object to the weighting factors could be tested; using identical coil setups, the Brain and Shepp-Logan reconstructions were optimal with the same $d$, although the actual $RE$ values were different. It is also worth noting that the rGRAPPA weighting factors are dependent on not only the coil sensitivity relationships, but the underlying subjects contrast information. This is shown in Figure 3.21 and could be reflected in the $RE$ curve variation. In the end, the variation of optimal $d$ found between different $R$ factors for a given subject, as well as between different subjects was quite low.

In addition to the variation of weighting factors across the FOV one might very well suppose that the optimal $d$ should also depend on $x$. Probing this possibility we found that there was indeed some variation of $d$ across the FOV but the variability of
the $d$ values was small in regions with reasonable SNR. Significant changes occurred in regions with very little available signal, where a larger $d$ could allow a dramatic improvement in the conditioning of Equation 3.12. However, since these regions are largely composed of noise, there is little impact on the overall quality of the reconstruction. The additional computational cost required to account for a variable optimal $d$ provided little benefit in terms of the total $RE$.

The number of flops required for an optimal rGRAPPA reconstruction of $d = 8$ was found to be roughly one order of magnitude larger than the standard GRAPPA...
implementation ($d = 256$). This corresponds to a minimal impact on a modern computing system; on the research system (GNU Octave v3.4.3, Intel i5 2.30 GHz CPU, 3.8GB RAM) the difference between these computation times was $\sim 0.5$ seconds. As such the rGRAPPA implementation allows reasonable reconstruction times for clinical settings.

A nice feature of the segmented approach of rGRAPPA is that it can be implemented in parallel with other strategies. The High Pass GRAPPA (hpGRAPPA) technique, for example [31], improves the calibration of weighting factors by computing them in a sparse domain (after high-pass filtering). This technique could be combined with rGRAPPA, implementing the high-pass calibration on each window region, taking advantage of sparsity to improve the calibration and synthesis of data therein. It remains to be seen if the gains provided by rGRAPPA and hpGRAPPA would combine synergistically, or result in diminishing returns.

### 3.3 Optimization Metrics

Since the $RE$ requires a fully sampled reference scan, it is not a viable metric for a practical PPI application. There are a number of alternatives that have been proposed that allow quantification of various MRI artifacts and do not require a reference image for comparison. Implementations in auto-correction of motion artifacts [36, 37] have applied a variety of such *a posteriori* quantification metrics. Artifacts due to motion, such as blur and ghosting are similar in nature to PPI artifact [15]. Using *in vivo* and simulated data, we compare the $RE$ metric to a number of widely used image quality metrics in selecting the optimal region width, $d$.

The final reconstruction is a rSoS image composed of bright and dark regions with no remaining phase information. The typical PPI artifact due to Nyquist violation is aliasing or $N/R$ ghosting (see for example Figure 3.1), where $N$ is the number of
pixels in the PE FOV and \( R \) is the reduction factor. If synthesis of missing lines is not perfect, there will be residual aliasing artifact. Furthermore, noise can be amplified in signal synthesis when the fitting matrix is not well conditioned.

Table 3.1 lists the image fidelity metrics considered for the determining optimal region width in a practical setting (without knowledge of the full k-space data). The performance of each metric is rated by comparing the optimal \( d \) value identified by the metric versus the optimal \( d \) value provided by the \( RE \). While this study specifically treats the GRAPPA style PPI reconstruction, the metrics should provide similar behaviour for other Cartesian k-space recovery methods.

The image gradient \( G(x, y) \) is used frequently, due to the nature of PPI reconstruction artifact; Cartesian sub-sampling and errors in the regeneration of missing \( k_y \) lines result in regular ghosting, increasing the amount of “edges” in the image. An example image and corresponding gradient map is shown in Figure 3.22.

![Figure 3.22: a) A rSoS image \( I(x, y) \) and b) corresponding gradient map \( G(x, y) \).](image)

A number of the metrics found in Table 3.1 can be computed in slightly different ways; for example, those involving gradients can be computed with only the \( y \)-gradient applied (since the reduction of lines is along the PE direction). The metric may also be computed from normalized image, or gradient maps. The normalized versions of
### Table 3.1: Image Quality Metrics

<table>
<thead>
<tr>
<th>Metric</th>
<th>Symbol</th>
<th>Formula</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Gradient Energy</strong></td>
<td>$E_G$</td>
<td>$\sum_{xy} G(x, y)^2 \sum_{xy} \left( \frac{G(x, y)}{\sum_{xy} G(x, y)} \right)^2$</td>
<td>[37]</td>
</tr>
<tr>
<td>$E_{Gy}$</td>
<td>$\sum_{xy} G_y(x, y)^2 \sum_{xy} \left( \frac{G_y(x, y)}{\sum_{xy} G_y(x, y)} \right)^2$</td>
<td>[36, 37]</td>
<td></td>
</tr>
<tr>
<td><strong>Total Variation</strong></td>
<td>$TV$</td>
<td>$\sum_{xy}</td>
<td>G(x, y)</td>
</tr>
<tr>
<td>$TV_y$</td>
<td>$\sum_{xy}</td>
<td>G_y(x, y)</td>
<td>$</td>
</tr>
<tr>
<td><strong>Entropy</strong></td>
<td>$H$</td>
<td>$\sum_{xy} \frac{I(x, y)}{\sum_{xy} I(x, y)} \log \frac{I(x, y)}{\sum_{xy} I(x, y)}$</td>
<td>[36]</td>
</tr>
<tr>
<td><strong>Gradient Entropy</strong></td>
<td>$HG$</td>
<td>$\sum_{xy} \frac{G(x, y)}{\sum_{xy}</td>
<td>G(x, y)</td>
</tr>
<tr>
<td>$HG_y$</td>
<td>$\sum_{xy} \frac{G_y(x, y)}{\sum_{xy}</td>
<td>G_y(x, y)</td>
<td>} \log \frac{G_y(x, y)}{\sum_{xy}</td>
</tr>
<tr>
<td><strong>Auto-correlation</strong></td>
<td>$AC_{2D}$</td>
<td>$\sum_{ab} P(a, b)$</td>
<td>[36]</td>
</tr>
<tr>
<td>$AC_y$</td>
<td>$\sum_b P(0, b)$</td>
<td>[36]</td>
<td></td>
</tr>
<tr>
<td>$AC_{pk}$</td>
<td>$\sum_b P(0, b), \quad b = [\pm N_y/R]$</td>
<td>[36]</td>
<td></td>
</tr>
<tr>
<td><strong>Differential Energy</strong></td>
<td>$DE$</td>
<td>$\sum_n [S(n) - S_0(n)][S(n) - S_0(n)]^*$</td>
<td>[40, 41, 42]</td>
</tr>
</tbody>
</table>

where, $G(x, y) = \sqrt{G_x(x, y)^2 + G_y(x, y)^2}$

$G_x(x, y) = I(x + 1, y) - I(x - 1, y)$, $G_y(x, y) = I(x, y + 1) - I(x, y - 1)$

$P(a, b) = \sum_{xy} I(x, y)I(x - a, y - b)$
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a metric appear to the right of the standard version in Table 3.1, where applicable.

3.3.1 Differential Energy

Most of the image metrics are applied to the final rSoS image. The Differential Energy ($DE$) (Table 3.1) metric provides a slightly different measure and warrants extra discussion. This measure was inspired by a study of the GRAPPA algorithm that reinterpreted the application of the matrix $G$ (Equation 3.13) as an operator [43]. The so-called GRAPPA operator, $G$, exploits the translation invariance of the kernel, shifting data in k-space with repeated applications, much like the ladder operators of quantum mechanics, to produce $k_y$ lines shifted by a desired amount.

Consider the $R = 2$ case shown in Figure 3.23. After one application of $G$ we reconstruct the missing lines. Applying the $G$ operator on the newly synthesized lines creates an estimate of $k_y$ lines shifted once more, which just happens to land back in the original positions. Thus, after 2 applications of the $G$ operator, we have recovered estimates of lines in the position of the originally acquired lines. Comparison of the synthesized lines $S$ to the originals $S_0$ will provide a measure of the accuracy of the reconstruction. For the $R = 2$ case for example, we may compare $S \leftrightarrow G^2 S_0$.

The set of possible comparisons used to calculate $DE$ are shown in Figure 3.24. The case shown is for $R = 2$, but these comparison classes may be extended to higher
$R$ factors.

Figure 3.24: Possible k-space coverage patterns for $DE$ data consistency matching. In a practical acquisition, only the acquired lines $(S(k))$ are known. The $RE$ compares final images created by using the recovered data as well as lines from the fully sampled k-space. Comparison A matches lines after application of $G_{ACS}$, but only in the ACS region. Comparison B matches lines after application of $G^2$. C is the sum of A and B, using all available data for comparison.

In simulation, when the “missing” lines that we synthesize are known, we may compute the $DE$ between the lines synthesized by the algorithm with their true values. This $DE$ uses the same source data for comparison as the $RE$ ($RE$ Equivalent). In a practical setting, we may not make this comparison, but may complete a comparison on a small subset of this data, which is known in the ACS region. This is comparison A ($G_{ACS}$ in Figure 3.24), computing the $DE$ between lines synthesized with a single application of $G$ and the known ACS lines at the corresponding position.
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Comparison B ($G^2$ in Figure 3.24) applies the $G$ twice to predict the signal at the position of the original acquired lines. While providing a comparison over the full region of k-space (rather than limited to the ACS region) there may be additional errors imparted by compounding effects from the multiple applications of $G$. Comparison C provides is the sum of comparisons A and B, comparing all available synthesized data points without using any reference data.

3.3.2 Results

A representative plot for each metric class is shown in Figure 3.25. For the plots in Figure 3.25, the imaging subject was $ABDax2$, with $R = 2$ and $N_{ACS} = 24$.

The image quality metrics were tested on multiple datasets using reconstructions of $R = 2, 3, 4$. The average disparity between the optimal region width predicted by the $RE$ and the optimal region width predicted by the metric $M$ were compared, that is

$$\delta_d = |d_M - d_{RE}|$$

(3.19)

The results across $ABDax1$ and $ABDax2$ are shown in Figure 3.26a. Simulated datasets (a brain image and Shepp-Logan phantom) with identical simulated coil setups were also tested. The results of these two datasets for $R = 2, 3, 4$ are shown in Figure 3.26b. The metrics are ordered from best predictor of optimal $d$ value in terms of the mean distribution of $\delta_d$ for the real data. The $RE$ and $DE_{RE}$ measures are shown for comparison, but are not viable metrics since they use data from the fully sampled reference.

Amongst the real data assessments, the best performing metric was the (normalized) $E_{Gy}$ in terms of predicting the same optimal $d$ as the $RE$. However, when $R > 2$, it was found that the global maximum was located at $d = 256$ (the standard GRAPPA result). In this case, the local maximum was selected for inclusion in the
Figure 3.25: Image Metrics vs $RE$.

final average (refer to Section 3.2.4). This result could be ensured by limiting the reconstruction parameter space to a fraction of the overall FOV (i.e. $d < N_x/3$). The results were similar for the total (normalized) $E_G$. Care must be taken when considering the $E_G$ maximum as a metric choice.

The Autocorrelation ($AC$) metrics also performed well, with the $AC_{2D}$ in second
place. The sum in $AC_y$ restricted the correlation lags to be $y$-directional and was a reasonable predictor as well. The peak region autocorrelation, $AC_{pk}$, specifically targeted $FOV/R$ ghosting lags, by summing the autocorrelation entries in a small region surrounding the expected peak locations.

The Image Entropy ($H$) was a good performer across all $R$ values, returning a lower standard deviation amongst all acquisition setups than the $AC_{2D}$, although slightly higher $\delta_d$. The Gradient Entropy ($H_G$) and $y$-specific Gradient Entropy ($H_{Gy}$) also performed reasonably well.

In terms of the $DE$ measures, the most accurate (after $RE$ equivalent) was the $DE_B (= DE_{C2})$. However, this had some large deviations for certain reconstructions. This is likely due to the relative flatness of the curve over a large range of $d$ values (Figure 3.27c). When the $DE_{C2}$ sum was restricted to signal outside of the ACS region (making a better analog to the $RE$ equivalent), the result was even poorer performance.

The Total Variation ($TV$) measures showed some ability to predict optimal $d$ at $R = 2$, however they completely failed to identify a minimum at higher $R$. The minimum values were at $d = 256$ for both $TV$ and $TV_y$. For this reason, the $TV$
measures were omitted from the comparisons in Figure 3.26.

The results for $DE$ measures were more varied; Figure 3.27 shows the various possibilities for the $R = 2$ case. The $RE$ and $DE_{RE}$ curves are very similar, which is expected since the source data for comparison are identical. The $DE_A (= DE_{G1acs})$ results in an expected optimal $d = 1$. This is an interesting feature, that suggests the optimal reconstruction has a unique weighting factor for each $x$. However, this is likely due to the fact that it is limited to the ACS region, where the SNR is relatively high.

The $DE_B (= DE_{G2})$ predicts a larger optimal region width. In this measurement, the synthesized lines are reconstructed from a second application of the $G$ operator. This does not act on acquired lines, but rather the lines recovered after the first data

Figure 3.27: $RE$ and $DE$ metrics as a function of $d$ for reconstructed images. a) The $RE$ equivalent comparison. b) Comparison A, recovered lines in ACS region. c) Comparison B, recovered lines after 2 applications of $G$. d) Comparison C, combining A and B.
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application of $\mathbf{G}$. Any errors in the first data synthesis may be propagated in the second operation.

The $DE_C(= DE_{G_1G_2})$ is simply $DE_A + DE_B$. This provides a comparison between recovered lines and all possible acquired lines. The smaller optimal $d$ values predicted by this metric may be due to the fact that the comparisons in the ACS region contribute the majority of the sum. It should also be noted that the comparison in the ACS region provides comparisons that are not consistent with the $RE$, since the acquired ACS lines are inserted prior to final reconstruction.

3.3.3 Discussion

Initially it was assumed that the Gradient Energy ($E_G$) would provide an ideal optimization metric, having previously found success in deghosting applications [37]. The gradient of an image is generally smaller when there are more uniform signal regions and fewer edges. For the rGRAPPA implementation, errors in missing line regeneration result in increased aliasing, thereby increasing the number of edges in the reconstructed image. Higher noise will also contribute to higher Gradient Energy ($E_G$) values, thus we expect that the ideal final image will have minimum $E_G$.

It was found that there was poor correlation between $RE$ and the raw $E_G$. This may be due to overall image intensity variation; as the size of the edge increases, the contribution to $E_G$ increases. The image intensity variation (Figure 3.28a), can potentially influence the $E_G$ calculation (Figure 3.28b).

The intensity variation for different reconstruction parameters is inherent to the GRAPPA algorithm, since the synthesis of missing k-space lines does not conserve energy. This can increase or decrease the value of $E_G$ without necessarily adding more edges (stronger aliasing artifact). This factor may be addressed by using the normalized $E_G$.

Division by the total amount of signal in the gradient maps accounts for the effects
of the overall contrast variation, allowing us to compare $E_G$ from various different reconstructions on equal footing. However, the normalized $E_G$ (i.e. Figure 3.25a) displayed an inverse correlation with the $RE$ curve; the optimal reconstruction has the maximum gradient energy!

It is possible that this is due to the quadratic nature of the $E_G$ measure; larger edges in $G(x, y)$ contribute with a much greater impact than smaller ones. An image with a few large edges will have higher energy than one with many smaller ones. Further investigation suggested that the maximum normalized $E_G$ may be a reasonable metric for selecting optimal width in a rGRAPPA reconstruction. Ultimately, the maximum normalized $E_{Gy}$ gradient provided one of the best reconstructions in terms of $RE$. The $E_G$ metrics may encounter problems in images with low SNR; as noise levels comparable to signal levels may heavily influence the overall $E_G$, even when normalized.

$TV$ has found significant success in MR reconstruction optimization. This metric has been used extensively in Compressed Sensing (CS) MRI implementations [39, 44] to promote sparsity in certain domains of the image information. It has also been used in conjunction with some PPI and undersampled reconstructions (e.g. [45]). In this study we used the gradient operator as the sparsifying transform; finding the $TV$
of the image gradient $G(x, y)$. We expect the gradient to be sparse, since it selects only the edges and should have small (effectively zero) signal in other regions.

The $TV$ measures are similar to the $EG$, but are a linear summation of $G(x, y)$ (whereas the $EG$ is quadratic). The TV metric relaxes the preference for large edges compared to the $EG$ measure. For the $R = 2$ case, the TV measures predicted the optimal $d$ with good accuracy. However, for a majority of reconstructions, both the $TV$ and $y$-specific ($TV_y$) minima were local. In some reconstructions the lower ($d_s$) minimum did not occur at all. For this reason it is not recommended as a good quantifier for rGRAPPA optimization. The motion autocorrection study [36] reported average performance of the $TV$.

The idea of entropy has been applied to many imaging fields to restore noisy and incomplete data. The Maximum Entropy Method [46] is used successfully in many fields (radio and X-ray astronomy, crystallography and geophysics), but is not generally applicable to MRI [47]. However, minimizing entropy has proven useful in some imaging applications [48]; in MR specifically, it has been successfully employed in motion autocorrection [36] and alignment of scan data in SENSE imaging [49].

The entropy measure ($H$, Table 3.1) is smaller when more of the overall image energy is in fewer pixels. Minimizing the image entropy favours a reconstruction in which there are more dark (low signal) pixels. Increased aliasing artifacts and noise would generally result in higher image entropy as more image energy is distributed to a greater number of pixels.

We also found that the entropy of the gradient of the image was useful, a similar argument holds for $HG$ and $HG_y$. The entropy measures possess an implicit normalization to the total energy of the image, the need for which is reflected in the case of the $EG$. This appears to be crucial in such reconstructions in which missing k-space lines are synthesized, since there is no constraint that energy be conserved in the reconstruction. The entropy measures are implicitly less sensitive to the sizes of the
edges, favouring images with overall uniformity.

The autocorrelation summations specifically target the aliased ghosts in the sub-optimal reconstructions. The most effective autocorrelation metric incorporated the sum of all lags in both $x$ and $y$ directions, outperforming the other measures targeted specifically in the undersampled direction ($AC_y$) or at the known location of $FOV/R$ sub-sampled ghosts ($AC_{pk}$).

Unlike the $RE$, the $DE$ is calculated separately for each coil, directly from the complex data. The $DE$ provides a unique way to identify the optimal region width ($d$), unlike other metrics computed using the rSoS image. A similar measurement was used to help identify optimal reconstruction kernels in a standard GRAPPA implementation [42]. However, in this computation, only the ACS region was used to enforce data consistency resulting in an assessment of the reconstruction parameters on a limited part of k-space. Further amendments [40, 41] utilized the translation invariance of the reconstruction kernel to extend the comparison to the limits of k-space, similar to the comparisons used in the present study.

The $DE$ can provide a comparison between the complex signal at any image or k-space location. The $DE$ defined in Table 3.1 is invariant under Fourier transformation (a consequence of Parseval’s Theorem). As such, it may be used to compare signal in k-space, image space or hybrid space. A particularly attractive feature is that this comparison may be done before final reconstruction, potentially saving some post-processing time by doing “on-the-fly” optimization. The author notes that the $E_G$ metrics should, in theory have similar characteristics.

One of the limitations of the rGRAPPA approach is the lack of predictive power of the metrics studied. Although some of these metrics have been shown to locate the optimal region width $d$, it is impractical to require a complete set of reconstructions for all possible $d$ values. A potential goal for future work would be to characterize the $RE$ (or other metric) curves in relation to the imaging setup, coil number and
geometry, and SNR characteristics to provide a way to predict \textit{a priori} the optimal region width for reconstruction.
Chapter 4

Extracting Low Spatial Frequency Information from Partial k-space

4.1 Introduction

Many MRI applications seek to exploit the behaviour of spins to encode relative information between two scans. This can be achieved by preparing the spin system such that it will be sensitive to some quantity of interest. The information may be extracted by examining the difference between a pair of scans that are prepared in a slightly different manner. A few examples include intensity non-uniformity correction, wherein the sensitivity variation of surface coils may be corrected by comparison with a reference scan, and Phase Contrast (PC) MRI, where information about various physical properties is encoded in the phase of the MR signal.

Uniform intensity is important in quantitative MRI analysis and can be compromised by $B_1$ inhomogeneity. $B_1$ inhomogeneity arises from interactions of the excitation field with dielectric tissue as well as RF attenuation, causing non-uniform intensity in images [56, 57], especially at higher field. Quantitative measures are performed on pixels that are assumed to have similar intensities when representing
the same tissue. If the intensity is not uniform, it will corrupt the subsequent measurements [58]. Intensity non-uniformity correction methods compare the intensity between surface coils and a body coil reference image [59], which normally has a much more uniform spatial intensity profile. The surface coil reception sensitivity ($B_1^-$) can also be estimated using a reference scan in which a phantom with well known, uniform spatial distribution of signal is measured prior to the real imaging object [60].

In PC MRI, the estimation of relative phase maps is crucial to extracting accurate representations of the desired information. Numerous physical properties such as chemical shift effects [50], flow or motion [51], temperature [52], and even tissue elasticity [53] can be encoded in the phase of MRI signal. $B_0$ inhomogeneity can also be encoded in signal phase [13]. $B_0$ inhomogeneity is a common problem in many MR applications, causing blurring, distortion and loss of contrast [54, 55]. EPI acquisitions are particularly affected [13, 14].

The contrast difference maps in such applications are typically obtained by direct comparison of two fully sampled complex images acquired with different sensitivities for some physical quantity of interest. A direct image space comparison provides poor results in regions of low SNR. The additional scans require undesired extra acquisition time, and if full k-space data is not used, the images will be degraded by truncation artifact. However, when the spatial variation is smooth, as is often the case in such situations [61, 2, 13, 62], it may be represented by a smaller region of k-space.

In this chapter, we present a convolution fitting technique that can provide accurate representation of the relative information maps using only a fraction of k-space. This approach is unlikely to work in certain applications where the contrast information is not slowly varying, such as cardiac or Magnetic Resonance Angiography (MRA) phase contrast imaging. However, when the low frequency assumption is valid, the relative contrast may be represented with a compact Fourier expansion, allowing the information about the quantity of interest to be encoded with minimal
extra time. We test the efficacy of the convolution fit information map within a
framework of PC MRI wherein the contrast information is smoothly varying.

4.2 Theory

The relative information between two images is often retrieved by an image space
product operation. In general, we may have two images $I_1$ and $I_2$, that contain
a representation of an identical image, but there is a modulation representing the
desired quantity of interest,

$$I_1(x, y) = C(x, y)I_2(x, y).$$  \hspace{1cm} (4.1)

$C(x, y)$ represents the complex image space contrast modulation and should not be
confused with the coil sensitivity of Chapter 3. In k-space, Equation 4.1 may be
represented by a convolution:

$$S_1(k_x, k_y) = h(k_x, k_y) \otimes S_2(k_x, k_y)$$  \hspace{1cm} (4.2)

In our PC MRI example, images $I_1$ and $I_2$ possess a relative phase difference map
defined on $r = x\hat{x} + y\hat{y}$, that may be obtained by conjugate product:

$$I_1(r) = e^{i\Delta\theta(r)}I_2(r)$$  \hspace{1cm} (4.3)

We are interested in determining $\Delta\theta(r)$, which contains quantitative information
needed for analysis or correction, such as $B_0$ field inhomogeneity. The FT convolution
theorem states that Equation 4.3 is equivalent to

$$S_1(k) = h(k) \otimes S_2(k)$$  \hspace{1cm} (4.4)
When the information contained in $\Delta \theta(r)$ is slowly varying, it may be captured in a convolution kernel $h$ of a relatively small size. The kernel is found using a fitting procedure similar to that of GRAPPA [63] and Off-Resonance Artifact with ConvoLution in k-spacE (ORACLE) [61]. $h$ then represents the FT of the image space phase modulation between $I_1$ and $I_2$, namely $\Delta \theta(r)$.

4.2.1 Mathematical Approach

We digress at this point to discuss the mathematical methods to determine the kernel, $h$ that captures the relative relationship between two k-space datasets, $f$ and $g$. We begin with the convolution:

$$f = h \otimes g,$$  \hspace{1cm} (4.5)

where $f$ and $g$ contain k-space data from the two acquisitions, and $h$ is the unknown convolution kernel. We seek to represent Equation 4.5 as a matrix equation to obtain $h$ using a least squares approach. We now examine the practical application of the convolution operation as a matrix multiplication for 1D and 2D cases in detail.

1D Convolution

In the 1D convolution case, our target and source data ($f$ and $g$) are represented by length $N$ vectors $f$ and $g$, respectively.

$$f = \begin{bmatrix} f_1 & f_2 & f_3 & \ldots & f_N \end{bmatrix}$$

$$g = \begin{bmatrix} g_1 & g_2 & g_3 & \ldots & g_N \end{bmatrix}$$  \hspace{1cm} (4.6)

We desire to know $h$, the vector representing the convolution kernel that relates $f$ and $g$. The convolution operation can be expressed using the Toeplitz matrix (see for example [64]); since we seek the kernel $h$, we construct the convolution matrix from
the known source data vector \( \mathbf{g} \):

\[
\mathbf{G}_{1D} = \begin{bmatrix}
g_1 & g_2 & \cdots & g_N & 0 & 0 & \cdots \\
0 & g_1 & g_2 & \cdots & g_N & 0 & \cdots \\
0 & 0 & g_1 & g_2 & \cdots & g_N & \cdots \\
0 & 0 & 0 & g_1 & g_2 & \cdots & \cdots \\
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots
\end{bmatrix}.
\] (4.7)

Then we may write Equation 4.5 as

\[
\mathbf{f} = \mathbf{hG}_{1D}
\]

\[
\begin{bmatrix}
0 \\
\mathbf{f}_1 \\
\mathbf{f}_2 \\
\mathbf{f}_3 \\
\vdots \\
\mathbf{f}_N \\
0
\end{bmatrix}^T
= \begin{bmatrix}
\mathbf{h}_1 \\
\mathbf{h}_2 \\
\mathbf{h}_3 \\
\vdots \\
\mathbf{h}_k
\end{bmatrix}^T \begin{bmatrix}
g_1 & g_2 & \cdots & g_N & 0 & 0 & \cdots \\
0 & g_1 & g_2 & \cdots & g_N & 0 & \cdots \\
0 & 0 & g_1 & g_2 & \cdots & g_N & \cdots \\
0 & 0 & 0 & g_1 & g_2 & \cdots & \cdots \\
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots
\end{bmatrix}.
\] (4.8)

The number of rows of \( \mathbf{G}_{1D} \) must match the number of elements in the kernel, \( \mathbf{h} \). The size of \( \mathbf{G}_{1D} \) is \( K \times (N + K - 1) \) and the zero padding in \( \mathbf{f} \) positions the target vector to the valid region of the convolution.

2D Convolution

The 2D convolution is slightly more involved; \( \mathbf{f} \) and \( \mathbf{g} \) are both \( M \times N \) matrices, in general, with respective entries \( f_{mn} \) and \( g_{mn} \) (\( m = 1, \ldots, M; n = 1, \ldots, N \)). In a Cartesian partial k-space framework, \( M \) represents the number of PE lines of the acquired data and \( M < N \). The kernel \( \mathbf{h} \) is a \( K \times K \) matrix, where \( K \leq M \).
Again, we set up the convolution using the entries of the source data \( g_{mn} \). The first step is to determine the row specific Toeplitz matrix representing a 1D convolution along the \( m \)th row.

\[
G_m = \begin{bmatrix}
g_{m1} & g_{m2} & g_{m3} & \cdots & g_{mN} & 0 & 0 & \cdots \\
0 & g_{m1} & g_{m2} & g_{m3} & \cdots & g_{mN} & 0 & \cdots \\
0 & 0 & g_{m1} & g_{m2} & g_{m3} & \cdots & g_{mN} & \cdots \\
0 & 0 & 0 & g_{m1} & g_{m2} & g_{m3} & \cdots & \cdots \\
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots
\end{bmatrix} \quad (4.9)
\]

The 2D convolution matrix can then be constructed as a block Toeplitz matrix using the \( G_m \):

\[
G_{2D} = \begin{bmatrix}
G_1 & G_2 & G_3 & \cdots & G_M & 0 & 0 & \cdots \\
0 & G_1 & G_2 & G_3 & \cdots & G_M & 0 & \cdots \\
0 & 0 & G_1 & G_2 & G_3 & \cdots & G_M & \cdots \\
0 & 0 & 0 & G_1 & G_2 & G_3 & \cdots & \cdots \\
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots
\end{bmatrix} \quad (4.10)
\]

The rows of the kernel matrix \( h \) are concatenated into a single row:

\[
h = \begin{bmatrix}
h_{11} & h_{12} & \cdots & h_{1K} & h_{21} & h_{22} & \cdots & h_{KK}
\end{bmatrix} \quad (4.11)
\]

Target data \( f \) is zero-padded to align the valid convolution region, and organized into a single vector of length \((M + K - 1)(N + K - 1)\). The convolution is then realized by Equation 4.12:

\[
f = hG_{2D} \quad (4.12)
\]

Multiplying the target signal vector \( f \) by the pseudoinverse of the Toeplitz matrix \( G^\dagger \).
(either the 1D or 2D) allows computation of the kernel:

\[ h = f G^\dagger \] (4.13)

Once the kernel \( h \) is known, inverse FT provides a representation of the low spatial frequency contrast difference between the two images. This system is solved in a manner similar to GRAPPA, seen in Chapter 3; weighting factors are acquired that correspond to relative k-space relationships in a local neighbourhood.

### 4.2.2 Application to Phase Contrast MRI

We now apply the convolution fitting framework to find \( \Delta \theta(r) \) as alluded to in Equation 4.3. With two fully sampled datasets, the phase difference map \( \Delta \theta(r) \) can be obtained from the argument of a pixel-by-pixel conjugate product, and is represented by the phasor \( P_0 \):

\[ P_0 = e^{i \Delta \theta(r)}, \quad \Delta \theta(r) = \arg [I_1(r)I_2^*(r)] \] (4.14)

This is shown in Figure 4.1, the phases of the two sample images are shown on either side and the relative difference (in this case a bilinear ramp) phase map in the center.

![Figure 4.1: Example of phase contrast between two acquisitions.](image)

With only a small sub-sampling of \( k \)-space (Figure 4.2a), this “gold-standard”
computation of the phase is not available, but reasonable approximations can be made if the phase difference between $I_1$ and $I_2$ is smooth. An example of a fitted kernel is shown in Figure 4.2b; the smoothly varying spatial information is captured in a small region of k-space.

Figure 4.2: Kernel found using truncated k-space. a) $f'(k)$ is a possible subset of the full k-space $f(k)$ from which to take sample data. b) The magnitude of the fitted kernel $h$, representing low spatial frequency information between two datasets.

The undersampled data can simply be zero padded and Fourier transformed, computing the conjugate product phasor from truncated k-space, $P_t(r)$. The estimated phase map from truncated data is $\Delta \theta_t(r)$

$$P_t(r) = e^{i\Delta \theta_t(r)}, \quad \Delta \theta_t(r) = \arg \left[ \left( \mathcal{F}^{-1} \{ f'_1(k) \} \right) \left( \mathcal{F}^{-1} \{ f'_2(k) \} \right)^\ast \right]. \quad (4.15)$$

Alternatively, we may use the convolution fitting technique to determine $h$ and obtain a representation of the phase, $\Delta \theta_h(r)$. The estimated phase map from kernel fitting is

$$P_h(r) = e^{i\Delta \theta_h(r)} = \mathcal{F}^{-1} \{ h(k) \}, \quad (4.16)$$

where the kernel $h$ has been zero-padded to the full k-space size.

Since the truncated source data k-spaces $f'$ and $g'$ will have sharp discontinuities between acquired and zero padded regions, $P_t$ will suffer from truncation artifact
(Figure 4.3a). On the other hand, since the relative kernel information decays quickly to zero for low spatial frequency contrast, the subsequent zero padding does not result in a discontinuity and the resulting phasor $P_h$ is much smoother (Figure 4.3b).

![Figure 4.3](image)

Figure 4.3: Phase mapping from small fraction of k-space. a) Truncation and zero filling, b) estimation from convolution kernel.

For Cartesian style acquisitions, limiting the span of k-space data in the FE direction has little impact on scan time. In theory, the approach will work for any number of truncated directions. For practical considerations, we consider that the truncation only takes place in the number of $k_y$ lines. With this type of data, we may consider doing the convolution fitting only in the $k_y$ direction after a 1D IFT. The impact of relative $x$ variation on the k-space data does not modulate signal in the $y$ direction of hybrid $(x, k_y)$ space. In this case a 1D kernel may be fit for each position $x_i$ and subjected to IFT to recover the phase difference $\Delta \theta(x_i, y)$.

### 4.3 Method

We compare the phasors $P_t$ and $P_h$ representing the estimated phase difference maps to the “gold-standard” phasor $P_0$ created from fully sampled k-space. Simulated and real MR data are used to evaluate the effectiveness of 1D and 2D convolution fittings versus the truncated conjugate product.
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The simulation consists of a set of k-space data simulated from a $256 \times 256$ Shepp-Logan image and subjected to a known relative phase map. The image was modulated by a random low-frequency phase map $P_{bgnd}(x, y)$ to emulate background phase and two images were created:

$$I_1(x, y) = I_0(x, y)P_{bgnd}(x, y)$$
$$I_2(x, y) = I_0(x, y)P_{bgnd}(x, y)P_{d}(x, y)$$

(4.17)

where, $P_d$ is the simulated phase difference map between $I_1$ and $I_2$. 1% Gaussian noise was added. The truncated data was selected from the resulting k-space signals $S_1(k_x, k_y)$ and $S_2(k_x, k_y)$ after FT. Both linear and parabolic phase maps $P_d$ were tested.

The real data is from a set of EPI acquisitions obtained for the geometric distortion correction technique Phase Labeling for Additional Coordinate Encoding (PLACE) [2]. The PLACE technique utilizes a pre-phase PE “blip” on one of two similarly acquired EPI images to capture information about the distortion. The PE blip results in a relative linear phase ramp along the image $y$-direction. The EPI sequences acquired complex images of a circular water phantom in a 4.7T vertical bore Bruker scanner, 2mm slice thickness, $T_R/T_E = 2000/30$ms and $128 \times 128$ matrix size. The imparted linear phase difference between the PLACE acquisitions corresponds to low frequency phase information, making it a good candidate for estimation from limited k-space data.

A variety of k-space trajectories, sampled from the available target and source data, were tested to determine the accuracy of the estimated phase maps given the size of input data, location in k-space and convolution kernel size. Both 1D ($K \times 1$) kernels fit in hybrid $(x, k_y)$ space, and 2D ($K \times K$) kernels fit in pure $(k_x, k_y)$ space were tested for kernel sizes $K = 2 \rightarrow 32$. For the 1D case, a unique kernel is found for each $x$ position, zero-padded and fed into the appropriate position in $P_{h1D}$. 

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The agreement between the estimated phasors and the gold-standard \( P_0 \) is described by a refocusing ratio:

\[
RR = \frac{\left| \sum_{x,y} C_0(x,y)P_{h/t}^*(x,y) \right|}{\sum_{x,y} \left| C_0(x,y)P_{h/t}^*(x,y) \right|}. \tag{4.18}
\]

where \( C_0(x,y) = T(x,y)P_0(x,y) \). To isolate the phase difference information, a threshold mask \( T(x,y) \) is used to eliminate contributions to the summation from noise only regions, where the phase of \( P_0 \) is totally random. The threshold mask is defined:

\[
T(x,y) = \begin{cases} 
1, & \text{if } |I_1(x,y)| < \delta, \\
0, & \text{otherwise,}
\end{cases} \tag{4.19}
\]

where \( \delta \) is chosen to be just above the noise level. A similar measure was used to qualify a nonlinear phase correction algorithm [65].

The distribution of phase error in the resulting estimated phasor is shown in a phase difference map

\[
\Delta P(x,y) = \sqrt{\left| C_0(x,y)P_{h/t}^*(x,y) \right|^2}. \tag{4.20}
\]

**Computational Complexity**

The bulk of the computational costs in this technique lie in the kernel fitting step (Equation 4.13). The size of the target data matrix \( G \) depends on the size of the kernel \( K \) and the length of the input data vectors \( f \) and \( g \). For the truncated Cartesian acquisitions, \( f \) and \( g \) represent rectangular, \( M \times N \) portions of k-space (\( M \) representing the truncated direction, \( M < N \)).

For a 1D kernel, the Toeplitz matrix \( G_{1D} \) will have a matrix size \( K \times (M+K-1) \).
and the number of flops to compute the kernel is

\[ \text{flops}_{1D} = 3K^3 + (2M - 1)K^2 + (M - 1)K. \]  \hspace{1cm} (4.21)

This 1D kernel fitting must be done at each \( x \) location in \((x, k_y)\) hybrid space, for example, requiring \( N \) times the amount of fittings indicated by Equation 4.21.

For the 2D case, the Toeplitz matrix \( G_{2D} \) is much larger, with a size \( K^2 \times (M + K - 1)(N + K - 1) \). The resulting number of flops for the 2D kernel computation is

\[ \text{flops}_{2D} = K^6 + K^2(2K^2 + 1)(M + K - 1)(N + K - 1). \]  \hspace{1cm} (4.22)

For typical values \((K = 8, N = 256\) and \(M = 32)\) we have \( \text{flops}_{1D} = 1.49 \times 10^6 \) and \( \text{flops}_{2D} = 8.49 \times 10^7 \). For larger \( K \), the 2D case increases quickly, owing to the terms of high degree in \( K \).

### 4.4 Results

Figure 4.4 shows results for the simulated Shepp-Logan phantom with parabolic phase difference between successive images. The phasor \( P_0 \) representing the gold-standard phase map obtained from direct comparison of the images obtained from full k-space is shown in Figure 4.4a. The parabolic phase difference is visible in regions with appreciable signal (the region highlighted by threshold mask \( T(x, y) \), Figure 4.4e) with noisy phase data everywhere else. The truncated conjugate product approach results in a phasor \( P_t \) with heavy truncation artifact (Figure 4.4b). The 1D and 2D kernel fitted phasors (Figure 4.4c and d, respectively) exhibit no truncation artifact and smoothly transition into regions of low SNR.

The phase difference maps for \( P_t, P_{h1D} \) and \( P_{h2D} \) are shown in Figures 4.4f-h, respectively. The difference maps show the spatial distribution of phase error of the
Figure 4.4: Shepp-Logan phantom with simulated (parabolic) phase difference map. a) Phase of gold-standard phasor $P_0$, b) phase of truncated conjugate product phasor $P_t$ (32 $k_y$-lines), c) phase of $P_{h1D}$ ($K = 8$ kernel, 32 $k_y$-lines), d) phase of $P_{h2D}$ ($K = 8$ kernel, 32 $k_y$-lines) e) the threshold mask $T(x, y)$ displaying signal region, f)-h) difference maps ($\Delta P$) between $P_0$ and the estimated phasors shown in b)-d), respectively. Note: the difference maps are restricted to the threshold region $T(x, y)$.

estimated phasor relative to $P_0$, but only in the regions where the signal is above threshold (i.e. the signal regions in Figure 4.4e). The RR calculations and phase difference maps $\Delta P(x, y)$ are computed after thresholding to remove the effect of pure noise regions (seen in the periphery of Figure 4.4a).

The results for the 1D and 2D kernel fittings show similarities in the $y$ direction, and the distribution of error shown in the difference maps (Figure 4.4g and h) is roughly the same. The 1D fitting appears to be more sensitive to the underlying structure of the imaging object, whereas the 2D fitting is much smoother over the central voids (eyes) of the Shepp-Logan phantom.

Figure 4.5 shows the RR results for the Shepp-Logan phantom simulation. Figure 4.5a displays $RR$ as a function of the kernel size $K$. The kernels were fit with a sample of 32 central $k_y$ lines from the source k-space data. For the parabolic phase map, a kernel size of $K = 8$ was essentially optimal; larger kernels provided diminishing
returns at higher computation costs. At kernel sizes above $K = 12$, the $RR$ value began to decrease.

Figure 4.5b shows the effect of source k-space data on the $RR$. The source data was centered around $k_y = 0$ and used to fit a kernel with size $K = 8$. As the sample data size increases, the fitted phase map has a higher $RR$. Figure 4.5c shows the $RR$ resulting from sampling k-space data from regions offset from $k_y = 0$. These results indicate that the best results are obtained when the sample is taken from central k-space. The kernel fit (both 1D and 2D) maps produce better results, especially for smaller input sample sizes. There does not appear to be a clear advantage of using the 2D kernel over the 1D kernel in terms of $RR$.

Figure 4.6 shows the phase estimation results for the circular water phantom.
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Figure 4.6: Water phantom PLACE data with linear phase difference map. a) Phase of gold-standard phasor $P_0$, b) phase of truncated conjugate product phasor $P_t$ ($24 \ k_y$-lines), c) phase of $P_{h1D}$ ($K = 4$ kernel, $24 \ k_y$-lines), d) phase of $P_{h2D}$ ($K = 4$ kernel, $24 \ k_y$-lines) e) the threshold mask $T(x, y)$ displaying signal region, f)-h) difference maps ($\Delta P$) between $P_t$ and the estimated phasors shown in b)-d), respectively. Note: the difference maps are restricted to the threshold region $T(x, y)$.

PLACE acquisition. Figure 4.6e shows the threshold region $T(x, y)$. The geometric distortion of the circle is evident, however, here we are only concerned with predicting the relative phase map (shown in Figure 4.6a).

Once again, the truncated conjugate product $P_t$ results in strong ringing artifact (Figure 4.6b). The kernel fittings, both 1D (Figure 4.6c) and 2D (Figure 4.6d), provide smoother phase map estimates, although there is some streaking noticeable in the 1D case. The relative phase contrast in this case is captured effectively by a smaller kernel ($K = 4$), due to lower spatial frequency content (Figure 4.7a). There is only a mild improvement in $RR$ of the $P_h$ over $P_t$ in this case, possibly due to the simple nature of the phase map and underlying object. The relative smoothness seen in the $P_h$ difference maps (Figure 4.6g and h) is potentially a more desirable effect.

As in the simulation example, central k-space is the best candidate for source data (Figure 4.7c).
Figure 4.7: Refocusing Ratio (RR) of estimated phase maps (Water Phantom) versus; a) kernel size (sample size 24 $k_y$-lines), b) sample size (kernel size $K = 4$) and c) offset from central k-space. Truncations of sample data to central $k_y$-space.

### 4.5 Discussion

In both simulation and real data, the convolution fittings provided better performance than the Truncated Conjugate Product (TCP) in terms of RR and smoothness of the resulting phase map. The convergence to high RR was faster for the kernel fittings as the sample size was increased. The RR should go to exactly 1.0 when the sample size is the full k-space ($P_0$). The kernel fittings also outperformed TCP when utilizing peripheral k-space source data, although in general, it is best to use central k-space data due to the SNR advantage.

The interesting features of the variable kernel size study, is that when $K$ reaches a certain point, the RR actually decreases (Figures 4.7a and 4.5a). This is also evident
when looking at the resulting phase maps and difference maps for higher $K$ values. For the water phantom, the optimal $K$ size was only 4! Comparing the results for $K = 4$ and $K = 8$ it is apparent that larger kernels not only result in lower $RR$ but greater visible error in the estimated phase map and difference map (Figure 4.8). A

![Figure 4.8: Oversized kernel effects. $K = 4$ size was optimal for a) 1D and c) 2D kernels, difference maps e) and g). $K = 8$ size resulted in a poorer fit for both b) 1D and d) 2D kernels, difference maps f) and h). Results shown for water phantom data with 24 central $k_y$-lines sample size.](image)

possible explanation for this is that the relative contrast map has been affected by the underlying image structure. If we extend the kernel size to the full FOV, the convolution operation becomes equivalent to the image space multiplication. It is possible that a large enough kernel will become sensitive to the truncation effects of the reduced k-space limits, but this is not well understood at this point.

For larger kernel and source data sizes, the 1D fitting technique is computationally much faster. For our PC MRI results, this comes at some cost to continuity along the orthogonal direction $x$, where the 2D fitting appears to generate smoother maps in both directions. The suitability of 1D or 2D fittings may vary for different applications; if the contrast variation is less smooth, a larger kernel is required and the 1D approach may be preferable to the more computationally intensive 2D approach.
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Depending on the nature of the phase distortion, the convolution kernel can effectively determine an accurate phase difference map with a limited amount of k-space data. For certain applications, it could provide acquisition time savings for the extra scans, as full k-space data need not be acquired. This is the acquisition strategy used in “keyhole” imaging [66, 67], where only central k-space is updated and peripheral k-space is sourced from a single reference scan. The initial keyhole techniques were applied in contrast enhanced MR angiography to improve temporal resolution.

The convolution fitting provides a distinct advantage over pixel-by-pixel image space computations in regions of low signal, allowing one to extrapolate the contrast relationship to regions of low signal without being corrupted by noise. This could be particularly useful for coil sensitivity and inhomogeneity estimation, as well as in quantitative mapping applications where divide-by-zero operations can have catastrophic results.
Chapter 5

Techniques for Through-Plane Resolution Enhancement in 2D Multislice MRI

5.1 Introduction

In many MR applications, high-resolution 3D images are desirable to facilitate effective diagnoses. True 3D MR images using FE (along $x$) and PE (along $y$ and $z$) to localize signal in a full volume excitation may be obtained with isotropic, sub-millimeter resolution. However, in many cases this type of 3D acquisition can be difficult. $T_2$- and diffusion-weighted imaging typically require long $TR$ and $TE$ times, which, along with the additional PE dimension, greatly increase the total scan time. In EPI acquisitions, the longitudinal magnetization may decay completely before traversing the entire 3D k-space. Other constraints, such as patient motion may inhibit the allowable acquisition time, putting the desired sampling density out of reach. When significant 3D volume coverage is required, the data may be acquired as a set of 2D slices. This 2D multislice data usually suffers lower resolution in the through-plane
The through-plane resolution depends on the slice thickness, usually on the order of a few mm [54]. Although obtaining thinner slices is possible, acquiring them in practice presents a number of complicating factors. First, there is increased demand on the excitation bandwidth; the RF pulse needs a longer duration to achieve the narrower bandwidth capable of producing a thinner slice. Furthermore, with a smaller slice volume there is less overall signal and a subsequent decrease in SNR.

An additional consideration for the slice thickness is the impact on the in-plane resolution due to the partial volume effect. A thick slice will be sensitive to signal over a larger distance along $z$, and unable to distinguish detail variation on a scale smaller than the slice thickness $\Delta z$ (Figure 5.1a). As in-plane resolution demands increase, the slice thickness may present a bottleneck in resolving fine detail. The subsequent demand for thinner slices could result in decreased SNR, requiring averaging of multiple acquisitions to produce an image acceptable for clinical use.

In this chapter, we present three different approaches to improving the through-plane resolution of 2D multislice MRI data. The techniques are applicable to virtually
any 2D multislice sequence. Two require no sequence modification, but provide scalable through-plane resolution gains at the cost of additional acquisitions. These techniques consider magnitude only data, although in principle, they may be applied to complex data as well; the phase simply provides no utility in achieving the resolution enhancement. The third approach is a novel technique that uses phase information to provide signal localization. The technique employs an additional slice encoding gradient requiring only a slight modification to the sequence.

We begin by describing the theory and methods for each technique. The techniques are tested using simulated and real MR data and the resulting enhanced images are evaluated using measures applied to similar resolution enhancement studies. The strengths and weaknesses of each technique are assessed and discussed.

### 5.2 Magnitude Based Enhancement

The two magnitude based techniques are inspired by the principle of geometric Super-Resolution (SR), in which multiple lower resolution views of an object are combined to provide an image with higher resolution. SR techniques have been adapted from the field of image processing and applied to radar, astronomical and other types of data.

The basic idea behind SR is to use multiple lower resolution images taken from unique viewpoints and combine them into an image with increased spatial resolution. The SR algorithm gains additional spatial information from the differences between viewpoints. In the context of the present problem, we wish to improve the resolution of 2D multislice MRI data in the through-plane direction, which is limited by the slice thickness.

The application of multiple-frame SR to stacked 2D multislice MRI data is visualized in Figure 5.2. A number of 2D multislice datasets (henceforth referred to as
“slabs”), are acquired at positions staggered by a fraction of the slice thickness, $\Delta z$ (Figure 5.2). Information from the low resolution slabs, $S_1$ and $S_2$ is combined by the resolving algorithm to produce a final image with enhanced resolution ($I_E$). One of the first techniques to improve through-plane resolution in MRI used this acquisition approach [69], employing an iterative back-projection [68] as the resolving algorithm.

The problem has also been approached using orthogonal scans, in which each direction is provided with optimal in-plane resolution [70, 71], but this approach can result in errors if the orthogonal views are not accurately registered. To further complicate registration, geometric distortion due to chemical shift occurs primarily in the FE direction, resulting in inconsistent datasets from orthogonal views. Rotational viewpoints have also been attempted [72, 73] with promising results, but are prone to similar types of confounding issues. Both the orthogonal and rotational approaches require more than 2 scans at minimum to achieve the proper resolution enhancement. For further reading on the application of SR to the field of MRI, we direct the reader to [74].

We thus focus our approach to obtaining similar slab acquisitions and applying the enhancement to the through-plane direction of the slab. This approach provides multiple intrinsic benefits. Registration is not an issue, since the FE and PE direc-

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Figure 5.2: Acquisition of staggered low resolution images for resolution enhancement. For a 2-fold increase in resolution, 2 slabs are acquired with a shift of $\frac{\Delta z}{2}$. 
tions are the same for all data sets. The staggered slab acquisition strategy is scalable, allowing one to acquire more slabs to reach desired resolution. Finally, it requires no sequence modification and may be adapted easily for any 2D multislice MRI data. We now introduce the magnitude based resolution enhancement algorithms based on the staggered slab approach. Both techniques begin with identical acquisitions; multiple shifted slabs interleaved into a blurred image, $I_B$. The first technique, SUper-REsolution by SLIce DEconvolution (SURESLIDE), uses a conditioned deconvolution operator to enhance $I_B$. The second, Simple Edge Enhancing Refinement (SEER), invokes a simple filtering process to refine the details of $I_B$.

### 5.2.1 SURESLIDE

The strategy for SURESLIDE is shown in Figure 5.3. We have limited the consideration of data to 1D (the $z$ direction) for simplicity. Multiple slab acquisitions $S_1, S_2, \ldots, S_N$, shifted by $\Delta z/N$ (an $N = 3$ staggered slab acquisition is illustrated) are interleaved to form a composite image $I_B$. The image $I_B$ is a blurred representa-

![Figure 5.3: SURESLIDE approach. The slab voxels represent a summation of the underlying voxels of the higher resolution image $I_E$. Interleaving multiple staggered slabs provides a blurry image that may be interpreted as $h \otimes I_E$, where $h$ represents a blurring kernel.](image)

$S_1, S_2, \ldots, S_N$, shifted by $\Delta z/N$ (an $N = 3$ staggered slab acquisition is illustrated) are interleaved to form a composite image $I_B$. The image $I_B$ is a blurred representa-
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tion of the underlying structure that we wish to extract ($I_E$).

We can mathematically describe the situation in Figure 5.3; the blurred image $I_B$, is found by convolving the underlying image $I_E$, with a blur operator $h$ [75]

$$I_B(z) = h(z) \otimes I_E(z)$$  \hspace{1cm} (5.1)

where we restrict ourselves to a 1D convolution along the slice direction. For the $N = 3$ case illustrated, $h = \frac{1}{3} \begin{bmatrix} 1 & 1 & 1 \end{bmatrix}$.

Equation 5.1 can be reformulated as a matrix equation

$$I_B = H I_E$$  \hspace{1cm} (5.2)

where the convolution with $h$ is represented by constructing the appropriate Toeplitz matrix. For a general kernel, $h = \begin{bmatrix} h_1 & h_2 & h_3 \end{bmatrix}$;

$$H = \frac{1}{|h|} \begin{bmatrix} h_1 & h_2 & h_3 & 0 & 0 & 0 & \ldots \\ 0 & h_1 & h_2 & h_3 & 0 & 0 & \ldots \\ 0 & 0 & h_1 & h_2 & h_3 & 0 & \ldots \\ 0 & 0 & 0 & h_1 & h_2 & h_3 & \ldots \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots \end{bmatrix}.$$  \hspace{1cm} (5.3)

If $I_B$ is an $N \times N$ image, then $H$ will be $N \times (N + K - 1)$, where $K$ is the length of the kernel, $h$. The higher resolution image $I_E$ may then be determined by inverting $H$

$$I_E = H^{\dagger} I_B,$$  \hspace{1cm} (5.4)

where $\dagger$ represents the pseudoinverse. This is a similar approach to that used in Chapter 4, but in this case the kernel is known and is used to construct the Toeplitz matrix representing convolution.
The banded Toeplitz matrix $\mathbf{H}$ in this case is ill-conditioned and the result $\mathbf{H}^\dagger$ is very sensitive to noise [76, 77]. In the SURESLIDE technique, this is addressed by using a row specific Gaussian smoothing on the deblurring matrix $\mathbf{H}^\dagger$. The form of the smoothing function is

$$f_s(z, c) = e^{-\frac{(c-z)^2}{2\sigma_s^2}}, \quad (5.5)$$

where, $\sigma_s$ is the width. $c$ and $z$ represent the column and row numbers of the entry of $\mathbf{H}^\dagger$, respectively. The result is a Gaussian function centered at the desired $z$ location of the output image $I_E$. These details are discussed at greater length in Section 5.6.3.

### 5.2.2 SEER

The required acquisition for SEER is identical to that of SURESLIDE. The SEER algorithm is outlined in Figure 5.4.

![Figure 5.4: SEER approach. The blurred image is considered in terms of low and high spatial frequency components $I_B = I_L + I_H$. 1) A representation of $I_L$ is found by low-pass filtering. 2) $I_H$ is found as the difference $I_L - I_B$. 3) An enhanced resolution image $I_E$ is found by increasing the amount of $I_H$ component in $I_B$.](image)

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Following collection and arrangement of the slabs, we may consider the blurred image $I_B$ to be composed of two parts; the high resolution ($I_H$) and low resolution ($I_L$) content, that is

$$I_B = I_L + I_H \quad (5.6)$$

We may now make an estimate of the lower resolution image component by smoothing $I_B$. This is accomplished with a blurring operator, $h$:

$$I_L = I_B \otimes h \quad (5.7)$$

where, $h$ is a square kernel, for example. This is analogous to using a low-pass filter. Now we may compute the remaining component

$$I_H = I_B - I_L, \quad (5.8)$$

and finally create a new image, $I_E$, that has enhanced resolution. This is accomplished by increasing the contribution from $I_H$ by a factor, $w$:

$$I_E = I_B + wI_H = I_B + w(I_B - I_L). \quad (5.9)$$

The filter type ($h$) and tuning factor $w$ may be determined by optimization or visual inspection.

The SEER algorithm can be seen as an extrapolation process, first moving backwards to determine the difference between lower and higher resolution stages, then applying the difference forward to provide an image with resolution enhanced beyond the initial stage $I_B$. 

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5.3 Phase Based Enhancement

Whilst the preceding techniques embody the spirit of SR with staggered low resolution slab acquisitions, the final approach is fundamentally different. The technique offers a compromise between full 3D spatial encoding and 2D multislice MRI. SLice ENhancement DividER (SLENDER) is a new framework that employs additional phase encoding to localize signal in the slice direction.

5.3.1 SLENDER

SLENDER uses additional phase encoding to achieve sub-voxel signal localization rather than seeking to deblur or refine lower resolution images. The acquisition still requires $N$ slabs, but they are not spatially staggered. Instead, the acquired data is composed of a normal in-phase slab, $S_1$ and a phase encoded slab, $S_2$ that has a gradient applied along the slice ($z$) direction (Figure 5.5).

![Figure 5.5: The SLENDER approach; the oblong voxel is split into sub-voxels A and B using an in-phase and slice-phase encoded acquisition.](image)

The $z$-gradient can be easily applied by altering pre-phase gradient lobes or adding the gradient area separately. This is akin to the PLACE acquisition [2], although in this case, the applied gradient is generally larger, causing significant intra-voxel dephasing.

The voxels in the slab acquisitions $S_1$ and $S_2$ at a given location $(x, y, z)$ are
defined as:

\[ S_1(x, y, z) = [A(x, y, z) + B(x, y, z)] P_0(x, y, z) \]
\[ S_2(x, y, z) = [A(x, y, z) + B(x, y, z)e^{i\alpha}] P_0(x, y, z) P_1(z) \] (5.10)

where, \( P_0(x, y, z) \) represents the background phase error, \( P_1(z) \) is the local phase accrual due to \( z \)-gradient encoding and \( \alpha \) represents the phase angle between the resolved sub-pixel components \( A \) and \( B \). \( P_1(z) \), by definition, is a phase ramp with a slope \( b \)

\[ P_1(z) = e^{i(bz + a)}, \] (5.11)

an additional phase correction, \( a \), is allowed to compensate for zeroth order phase error (such as \( z \)-gradient isocenter offset). A factor of \( e^{-i\alpha/2} \) is absorbed into the zeroth order term \( a \) to simplify the expression for \( S_2 \) in Equation 5.10.

Before we can determine \( A \) and \( B \), \( \alpha \) must be known and \( P_0 \) and \( P_1 \) must be considered. \( P_0 \) is explicitly known from the argument of \( S_1 \) and should be constant for subsequent scans. The local phase accrual due to \( P_1 \) is related to the strength of the encoding gradient and the position of the voxel relative to the \( z \)-gradient isocenter.

Once \( P_1 \) is known, we may directly solve for \( A \) and \( B \):

\[ A = \frac{J_2 - J_1 e^{i\alpha}}{1 - e^{i\alpha}} \]
\[ B = \frac{J_1 - J_2}{1 - e^{i\alpha}} \] (5.12)

where, \( J_1 = S_1P_0^* \) and \( J_2 = S_2P_1^*P_0^* \) (Note: we could also solve this system using \( J_1 = S_1 \) and \( J_2 = S_2P_1^* \) as the effects of \( P_0 \) are common to both). The final image \( I_E \) is created by interleaving \( A \) and \( B \).
Rotational Differential Field

To determine $P_1$ we employ a Rotational Differential Field (RDF) measurement [65]. The phase difference between one slice and the next in the phase encoded image $S_2$ represents a complex rotation of the underlying signal. This information can be extracted by looking at the RDF $\Delta_1 = S_2(z)^*S_2(z+1)$. $\Delta_1$ is the 1st order RDF (denoted by the subscript 1). Substituting Equation 5.10 into the RDF, we have

$$\Delta_1 = [A(z) + B(z)e^{-i\alpha}][A(z+1) + B(z+1)e^{i\alpha}]P_1^*(z)P_1(z+1)$$

$$\Delta_1 = [A(z)A(z+1) + B(z)A(z+1)e^{-i\alpha}$$

$$+ A(z)B(z+1)e^{i\alpha} + B(z)B(z+1)]P_1^*(z)P_1(z+1). \quad (5.13)$$

While the phase of the term in square brackets depends on the angle $\alpha$ and the relative sizes of $A$ and $B$ at the positions $z$ and $z+1$, when summing over all voxels the total phase contribution averages to zero. Taking the statistical sum $\langle S_2(z)^*S_2(z+1) \rangle$, we are left with the important complex factor

$$\Delta_1 = \sum_z P_1^*(z)P_1(z+1)$$

$$= \sum_z e^{-i(bz+a)} e^{i[b(z+1)+a]}$$

$$= e^{ib}. \quad (5.14)$$

Once $b$ is known, it may be used to compute the zeroth order correction, $a$; since, $P_1(z) = e^{i(bz+a)}$ we have

$$\sum P_1(z)e^{-ibz} = e^{ia} \quad (5.15)$$

The phase of the RDF sum and the subsequent zeroth order correction are related to the slope and the offset of the phase ramp (Equation 5.11) across the slices.

One must be careful when interpreting the argument of the RDF phasor as the
slope. The RDF provides a statistical average of the phase difference between adjacent voxels with $-\pi < b < \pi$. Since there is a definite possibility of phase wrap, there is ambiguity in the argument $b$ modulo $2\pi$. When the applied gradient is small enough, $0 < b < \pi$ and represents (approximately) the slope of the phase ramp along $z$. When $b < 0$ it indicates that the slope is negative, contrary to the setup of the experiment. The true slope is then likely $b + 2\pi$. It is prudent to introduce a new variable $\beta$ to represent the true underlying phase ramp (or phase rotation) behind the phasor argument $b$.

The accuracy of the phase difference determined by the $\Delta_1$ RDF can be improved by using larger shifts $n > 1$ [65]. In this case, the solution of the $n$-pixel shift RDF will result in a higher order phasor:

$$\Delta_n = \sum P_1^*(z)P_1(z+n)$$
$$\Delta_n = e^{inb}$$

We desire to find $b$ from $\Delta_n$, but there are $n$ complex roots that represent a phase rotation, each of which provide the correct phase difference from $z$ to $z+n$ when applied $n$ times. However, only one of these roots represents the true phase rotation and underlying phase ramp. To determine which is correct, we find another RDF for a shift $m \neq n$. If $m$ and $n$ are relative prime they will only share one root that represents the correct phase rotation from $z$ to $z+1$. Figure 5.6 shows the complex roots for the $\Delta_1$, $\Delta_4$ and $\Delta_7$ RDF phasors.
Figure 5.6: RDF roots. The roots for \( n = 4 \) (blue) and \( n = 7 \) (magenta). The common root provides the correct value of \( b \). The \( n = 1 \) root (black) is less accurate.

The relative prime solutions will share one common root from which we may extract the correct value of \( b \). Taking the \( n = 7 \) root as the RDF \( b \) value provides a more accurate representation of \( P_1 \).

5.4 Qualification of Enhanced Images

The effectiveness of the enhancement strategy is assessed by examining the ability to improve resolution, and the accuracy of the reconstruction in terms of noise propagation. The SNR efficiency is a measure used to determine how much signal is gained versus the additional time required for the extra slab acquisitions.

Edge Width

The resolution gain may be characterized by examining the sharpness of the edges. Past SR studies have used an edge width measurement [69, 74] to quantify the degree
of resolution gain. The edge width is determined by fitting a sigmoid function to the magnitude image along the direction of the resolution enhancement. The edge width function

\[ f(z) = \frac{1}{1 + e^{-a(z-z_0)}} \]  

(5.17)

where, \( z_0 \) is the relative edge location and \( a \) represents the steepness of the edge. The “width” of the edge \( (w_e) \), then is related to the parameter \( a \) and may be considered as the amount of run required to see a rise from 10-90% of the peak:

\[ w_e = \frac{4.4}{aR_S}, \]  

(5.18)

\( R_S \) is a resolution scale factor to account for the relative size of pixels between images at different resolutions.

**SNR**

When utilizing additional acquisitions SNR efficiency, \( \eta_{SNR} \), is an important consideration. SNR efficiency is defined as the ratio between the resulting image SNR and the square root of the data acquisition time, \( \tau \):

\[ \eta_{SNR} = \frac{SNR}{\sqrt{\tau}} \]  

(5.19)

SNR is commonly defined as the mean of pixel values in a region of relatively uniform (and strong) signal, divided by the standard deviation of pixel values in a region of signal void (pure noise). For the purposes of this study this definition will suffice.

A previous study demonstrated that the SNR efficiencies for 3D and 2D multislice acquisitions are roughly equivalent [78]. We compute the SNR of the magnitude enhanced images solely to provide an additional measure for the relative performance of the proposed SNR techniques.
5.5 Method

Simulation

Figure 5.7: Full resolution reference images. a) Brain image for simulation (256 × 256). b) Box image for simulation (256×256). c) Sphere image with lesion for simulation (256×256).

2D multislice staggered (spatial and PE) slab acquisitions were simulated from a 256 × 256 magnitude only brain image (Figure 5.7a). The simulation is intended to show a proof of concept and the efficacy of each technique. The slice direction is along the vertical and the slice thickness was chosen to be Δz = 8 pixels. Simulated acquisitions for 2- and 4-fold (N = 2 and N = 4, respectively) resolution enhancements were created.

A simple square phantom (Figure 5.7b) was employed to study the resolution enhancement and edge width effects for each technique. The edge width measurement requires a transition from signal void to high SNR with spatial uniformity on either side of the edge. The properties of the square phantom facilitate an isolated study of the edge width.

A spherical phantom (Figure 5.7c) was also constructed to provide a more realistic structure (such as the top of the head) and a signal void region was placed in the sphere to simulate the effect of a lesion. The lesion was sized to be approximately half of the slice thickness (4 × 4 × 4 voxels, 8-fold rebinning to slice). The ability of
each technique to resolve the lesion was investigated.

For SEER and SURESLIDE acquisitions, $N$ slabs staggered by $\delta = 8/N$ pixels were simulated. A downsampled image $I_{DS}$ was obtained by rebinning signal from $I_0$ into $8/N$ pixel bins to provide a comparison for the resulting enhanced image $I_E$. For the SLENDER simulations only the $N = 2$ case was treated. The additional slab was not spatially staggered but acquired with an additional linear phase encoding in the slice direction. A low-frequency random phase map was applied to an upsampled initial image prior to slab creation to simulate realistic $P_0$ and $P_1$ effects.

**Real Data**

![Figure 5.8: Full resolution reference image; GE Resolution phantom (96 × 256).](image)

A General Electric (GE) geometric daily quality assurance phantom (sagittal cross section; Figure 5.8a) was imaged to determine resolution enhancement with real MR data. The GE phantom also lends itself to the edge width analysis since it possesses well defined edges surrounded by relative signal uniformity. Staggered slab acquisitions were obtained on a 3T GE scanner using a 2D axial multislice Fast SPOiled GRadient (FSPGR) sequence; $T_R/T_E = 8.2/3.4$ms, $256 \times 256$ matrix size, $1\text{mm}^2$ in-plane resolution, $4\text{mm}$ slice thickness. 24 slices were acquired at one position and a second set of 24, shifted by $\Delta_\zeta/2 = 2\text{mm}$ for a total of $N = 2$ slab acquisitions.
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A full 3D FSPGR acquisition with similar imaging parameters was obtained as a gold-standard for comparison. The 3D acquisition has $256 \times 256 \times 96$ matrix size with $1\text{mm}^3$ isotropic resolution. For each approach, the optimal enhanced image was selected by visual inspection, as well as consideration of resulting edge width and SNR measurements. The regions used to calculate SNR and $w_e$ are highlighted over the full resolution images in Figure 5.9.

Figure 5.9: Positions of SNR and Edge Width measurements; SNR a) Simulated Box and b) GE phantom; Edge width c) Simulated Box and d) GE phantom.
Computational Complexity

For the three techniques, we begin with a set of $N$ slabs, consisting of $N_x \times N_y \times N_z$ voxels, where $N_x$ and $N_y$ represent the in-plane matrix size and $N_z$ the number of slices.

SURESLIDE relies on solution of a linear least squares system via matrix pseudo-inverse, much like the convolution fitting in Chapter 4. The main difference is the kernel operator is used to form the Toeplitz matrix. The convolution kernel will be of length $N$, resulting in matrix $H$ of size $N_z \times (N_z + N - 1)$. The computation of $H^\dagger$ requires $N_z^3 + 2N_z^2(N_z + N - 1)$ operations and occurs only once. The de-blurring matrix is subsequently applied to the blurred image volume $I_B$ resulting in $N_xN_yN_z(N_z + N - 1)$ operations. The total operational cost is

$$flops_{SURE} = N_z^3 + 2N_z^2(N_z + N - 1) + N_xN_yN_z(N_z + N - 1). \quad (5.20)$$

The smoothing to generate $H_S^\dagger$ incurs additional operations, in general $N_z^2$, although this can be significantly less if a small smoothing width is used; entries outside the smoothing window may be simply set to 0.

In SEER the convolution has $N_xN_yN_z(N_z + N - 1)$ operations, and subsequent matrix subtraction and scaled addition, each have $N_xN_yN_z$ operations. This results in

$$flops_{SEER} = N_xN_yN_z(N_z + N - 1) + 2N_zN_yN_z. \quad (5.21)$$

SLENDER involves a number of steps to determine the final sub-voxel component matrices $A$ and $B$. To determine the correct value of $\alpha$ (and the global phase slope $b$ for $P_1$ removal) we employ the RDF. Prior to this, the background phase must be removed from each slab acquisition, requiring $2N_xN_yN_z$ operations. The RDF calculation incurs a number of shifts and complex matrix subtractions. If we compute 2 shifts to find the relative prime root factor that provides $\alpha$ we require an-
other $2N_x N_y N_z$ operations. Following this there is the removal of $P_1$ from the phase encoded slab $S_2$, resulting in $N_x N_y N_z$ complex multiplications. Finally, the solution to Equation 5.12 may be found, resulting in another $2N_x N_y N_z$ operations. The total operations for the SLENDER algorithm is

$$flops_{\text{SLENDER}} = 7N_x N_y N_z.$$  

(5.22)

For comparison in this case we consider a 3D FFT algorithm with

$$flops_{\text{3DFFT}} = N_x N_y N N_z \log(N_x N_y N N_z)$$  

(5.23)

computations (we have assumed the number of points in the $z$ direction is $NN_z$ to correspond with the number of points in the interleaved slabs). If $N_z < N_x, N_y$, which is typical for 2D multislice acquisitions, the most demanding of the three reconstructions in terms of operations is SLENDER. Taking $N_x = N_y = 256$, $N_z = 64$ and $N = 2$ the SLENDER result requires $2.9 \times 10^7$ flops, an order of magnitude lower than the amount for the 3D FFT with equivalent size ($1.3 \times 10^8$).

5.6 Results

5.6.1 Simulation

Figure 5.10 shows results for the simulated brain image for $N = 2$. 

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Figure 5.10: Brain image simulation $N = 2$ enhancement results. a) Full resolution $I_0$; (256 × 256). b) Downsampled $I_{DS}$; c) blurred interleaved image $I_B$; d) SEER $I_E$; e) SURESLIDE $I_E$ and f) SLENDER $I_E$. b)-f) are 64 × 256.

To provide a comparison for the $N = 2$ enhancement, the full resolution image $I_0$ (Figure 5.10a) was rebinned into a downsamlepd image $I_{DS}$ with $z$ resolution on the same scale as the enhanced images. In the case of the $N = 2$ brain image simulation this is a downsample factor of 4 between $I_0$ and $I_{DS}$.

The 2-fold enhancement provides limited improvement. The zoomed plots shown in Figure 5.11 show some variation in the enhancement technique results.
Visual inspection of the images indicate that each method is capable of providing modest resolution gains. The white arrows highlight a small amount of contrast recovery in $I_E$s (Figure 5.11d-f), compared with $I_B$ (Figure 5.11c). The edge fitting in the $N = 2$ case was difficult for the brain phantom, as suitable edge interfaces were not present. The top and bottom edges where uniform signal is found do not extend for an adequate number of pixels to obtain accurate fittings.

Figure 5.12 shows resolution enhancement on the brain images for the $N = 4$ case (excluding SLENDER results).
Here the difference between SEER and SURESLIDE enhancements is more apparent. The SEER image suffers from less noise, while the SURESLIDE image appears to do better at returning original high resolution information.

The arrows in the zoomed plot (Figure 5.13) show the recovery of features that are present in $I_{DS}$ in the SURESLIDE image. These features were not recovered in the final SEER image.
Figure 5.13: Brain image simulation $N = 4$ enhancement results (zoomed). a) Downsampled $I_{DS}$; b) blurred interleaved $I_B$; c) SEER and d) SURESLIDE $I_E$. All images $128 \times 256$.

Results for the box phantom are shown in Figure 5.14 for $N = 2$. The resolution enhancement effects between $I_B$ (Figure 5.14c) and the resulting enhanced images $I_E$ (Figures 5.14d-f) are once again difficult to see. However, the edge width calculations were well suited to the geometry of the phantom and allow a more quantitative investigation of the resolution gains.
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Figure 5.14: Simulated box image N = 2 enhancement results. a) Full resolution $I_0$; (256 × 256). b) Downsampled $I_{DS}$; c) blurred interleaved image $I_B$; d) SEER $I_E$; e) SURESLIDE $I_E$ and f) SLENDER $I_E$. b)-f) are 64 × 256.

The resulting edge widths and SNR measures for the enhanced images are summarized in Table 5.1.

<table>
<thead>
<tr>
<th></th>
<th>$I_0$</th>
<th>$I_{DS}$</th>
<th>$I_B$</th>
<th>$I_E$</th>
<th>SEER</th>
<th>SURESLIDE</th>
<th>SLENDER</th>
</tr>
</thead>
<tbody>
<tr>
<td>Edge Width [pix]</td>
<td>0.36</td>
<td>1.15</td>
<td>7.82</td>
<td>6.03</td>
<td>1.25</td>
<td>3.43</td>
<td></td>
</tr>
<tr>
<td>Improvement [%]</td>
<td>95.4</td>
<td>85.3</td>
<td>0.0</td>
<td>22.9</td>
<td>84.0</td>
<td>56.1</td>
<td></td>
</tr>
<tr>
<td>SNR</td>
<td>–</td>
<td>–</td>
<td>44.1</td>
<td>37.4</td>
<td>27.9</td>
<td>46.3</td>
<td></td>
</tr>
</tbody>
</table>

Table 5.1: Summary of results for box image N = 2. The edge width measurements are given in terms of pixels in the high resolution image $I_0$. 

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The SNR is calculated as described in Section 5.4 and reported for the initial blurry image, $I_B$, and the final enhanced images, $I_E$. The edge widths are computed via Equations 5.18 and 5.17. The edge width displayed in the table represents an average of 8 different edge width fittings from suitable interfaces in the image (see for example Figure 5.9c). Figure 5.15 shows a comparison of such fittings for the high resolution image, blurred image and a SEER enhanced image.

![Figure 5.15: Fittings to determine edge widths. Data from the box phantom image; high resolution image $I_0$, $N = 2$ blurred image $I_B$ and SEER enhanced image $I_E$.](image)

While all methods improve on the resolution of the interleaved image $I_B$, they fall short of matching the resolution of the comparable reference image ($I_{DS}$). SURESLIDE provides the best resolution gain in this case, but suffers greatly from noise contamination. On the other hand, SEER results in better SNR but does not offer greatly improved resolution. The SLENDER technique provides a more balanced result offering a 2-fold increase of resolution over the initial interleave image, and the highest SNR efficiency of the enhancement techniques. Each of the techniques results in a slightly different artifact to be discussed in detail in Section 5.6.3.

The spherical phantom with added lesion results are shown in Figure 5.16 (zoomed in for better visualization). The lesion can be seen clearly in the full resolution $I_0$ (Figure 5.16a) and downsampled $I_{DS}$ (Figure 5.16b) images. In Figure 5.16c, the effect of a lesion with a size on the order of half a slice thickness is shown in the
blurred interleave image $I_B$. The signal void affects all slices that overlap its position, and each slice will have some signal picked up from the surrounding area. As a result, the “lesion” appears with less sharpness and contrast. While the SEER and SURESLIDE enhancements (Figures 5.16d and e, respectively) provide some recovery of contrast, the clear winner in the lesion test is SLENDER. The signal void has been recovered to match the original size shown in $I_{DS}$. There is only a slight difference in contrast due to the loss of SNR compared with the original image.
CHAPTER 5. THROUGH-PLANE RESOLUTION ENHANCEMENT

5.6.2 Real Data

Figure 5.17 displays the results of the application of each technique to the GE resolution phantom data.

![Images of GE phantom N = 2 enhancement results.](image)

(a) | (b) | (c) | (d) | (e) | (f)
---|---|---|---|---|---
- $I_0$ | $I_{DS}$ | $I_B$ | $I_{SEER}$ | $I_{SURESLIDE}$ | $I_{SLENDER}$

Figure 5.17: GE phantom $N = 2$ enhancement results. a) Full resolution $I_0$; (96 × 256). b) Downsampled $I_{DS}$; c) blurred interleaved image $I_B$; d) SEER $I_{SEER}$; e) SURESLIDE $I_{SURESLIDE}$ and f) SLENDER $I_{SLENDER}$. b)-f) are 48 × 256.

In this case, the downsampled image $I_{DS}$ represents a 2-fold rebinning of the high resolution image $I_0$. The SLENDER result was subjected to an additional tuning of the relative phase angle $\alpha$ to improve signal localization and reduce noise (see Section 5.6.3). The zoomed plots are shown in Figure 5.18. Once again the SURESLIDE and SLENDER enhancements provide slightly better resolution than SEER.
This is particularly noticeable in the restoration of the sharp edges at the top and bottom of the signal void (arrows, Figure 5.18c compared with Figures 5.18e and f). The SEER enhancement results in a slight blurring artifact (arrow, Figure 5.18d).

Similar to the simulation results, there is improvement over the initial image $I_B$ (Figure 5.17c), but the enhanced images are not as sharp as the downsampled comparison image $I_{DS}$ (Figure 5.17b). The resulting edge widths and reconstructed image SNR are compiled in Table 5.2.
### Table 5.2: Summary of results for GE resolution phantom $N = 2$. The edge width measurements are given in terms of pixels in the high resolution image $I_0$.

<table>
<thead>
<tr>
<th></th>
<th>$I_0$</th>
<th>$I_{DS}$</th>
<th>$I_B$</th>
<th>$I_E$</th>
<th>SEER</th>
<th>SURESLIDE</th>
<th>SLENDER</th>
</tr>
</thead>
<tbody>
<tr>
<td>Edge Width [pix]</td>
<td>1.17</td>
<td>2.11</td>
<td>5.23</td>
<td>3.68</td>
<td>3.85</td>
<td>2.07</td>
<td></td>
</tr>
<tr>
<td>Improvement [%]</td>
<td>77.8</td>
<td>59.9</td>
<td>0.0</td>
<td>29.9</td>
<td>26.8</td>
<td>60.7</td>
<td></td>
</tr>
<tr>
<td>IP Width [pix]</td>
<td>1.72</td>
<td>1.76</td>
<td>2.18</td>
<td>1.92</td>
<td>1.89</td>
<td>1.95</td>
<td></td>
</tr>
<tr>
<td>SNR</td>
<td>–</td>
<td>–</td>
<td>62.9</td>
<td>46.8</td>
<td>41.7</td>
<td>43.5</td>
<td></td>
</tr>
</tbody>
</table>

With real MR data, the SEER and SURESLIDE techniques are on equal footing, providing roughly the same resolution enhancement and SNR characteristics. The SLENDER technique provided better resolution gains and considerably higher SNR. The results listed in Tables 5.1 and 5.2 represent the optimal results for each enhancement technique.

Resolution gain was also characterized by inspecting in-plane enhancements. With through-plane resolution improvements, we reduce the partial volume effect, which may cause apparent resolution loss in-plane due to the thickness of objects. For the GE resolution phantom, the central ramp thickness was measured by fitting a Gaussian function along the $y$ direction (see Figure 5.19). The in-plane width results are tabulated in the Table 5.2 after the normal edge width calculations. The in-plane images are shown in Figure 5.20.
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Figure 5.19: In-plane ramp width. a) In-plane view showing location of central ramp fittings. b) Example fit of central ramp for $I_0$ and $I_B$.

Figure 5.20: GE phantom $N = 2$ enhancement in-plane; a) Full resolution $I_0$; b) downsampled $I_{DS}$; c) blurred interleaved image $I_B$; d) SEER $I_E$; e) SURESLIDE $I_E$ and f) SLENDER $I_E$. Showing central $150 \times 150$ region, $1\text{mm}^2$. 
The enhanced images (Figure 5.20d-f) display visible reduction of the central ramp width compared with the initial interleaved image (Figure 5.20c). The in-plane width (Table 5.2) corroborates this and further indicates a resolution gain provided by the enhancement techniques.

5.6.3 Artifacts from Enhancement Techniques

SEER

Since each resolution enhancement technique approached the problem in a different way, the resulting final images each display a unique type of artifact. For the SEER technique we can see an “over-correction” effect if the enhancement factor $w$ is too large. Excessive contribution from $I_H$ causes the signal to overshoot and dip on either side of the edge. This creates peaks and troughs around large edges in the final image (Figure 5.21), and can have significant impact on the edge width measurement (Figure 5.21b).

The over-correction effects were more likely to occur when using the boxcar filter to generate $I_L$, rather than a Gaussian. Larger kernels would cause these effects to extend further from the edge. The choice of kernel type, size and enhancement factor $w$ must be carefully made to provide the greatest amount of resolution gain without incurring degrading levels of artifact. In general it was found that the Gaussian kernel provided better results in terms of managing artifact, although the boxcar kernel was able to achieve marginally higher resolution gains.

SURESLIDE

With the SURESLIDE technique, the excessive noise is controlled with targeted Gaussian damping in the deblurring matrix $H^\dagger$. It is possible that this is related to the fact that the assumed kernel $h = \begin{bmatrix} 1 & 1 \end{bmatrix}$ used in deconvolution is a naive idealization. In
Figure 5.21: SEER enhancement artifact with $h = \text{BOX}_7$ a) $w = 0.2$, a reasonable enhancement factor. b) $w = 0.6$ over-correction causing signal dip/overshoot on either side of edge. c) and d) Corresponding real and e) and f) simulated images.
reality, $h$ should be somehow related to the slice selection profile, often approximated as Gaussian in shape [68, 69, 74].

The excessive noise can be attributed to signal pile up from non-local regions in the image. Careful inspection of the deblurring matrix, $H^\dagger$ (Figure 5.22) makes the signal pile up apparent. Referring to Figure 5.23, for a pixel in the enhanced image $I_E$ there is contribution from the entire column in the source image. Because the support

![Figure 5.22: The entries of the matrix $H^\dagger$.](image)

![Figure 5.23: Improving $H^\dagger$ conditioning with smoothing. a) Blurry interleaved image $I_B$. The solid boxes indicate pixel locations that, in the final enhanced image, are reconstructed from source data spanning the entire column (dashed lines). b) Corresponding rows of $H^\dagger$ that contribute to the pixels of the final reconstructed image. c) Targeted Gaussian damping in $H_s^\dagger$ suppresses the contribution from non-local signal.](image)
of the $H^\dagger$ row covers a good deal of the source image, noise effects are compounded at the final image pixel location. Limiting the support of the rows in the $H^\dagger$ matrix to a small neighbourhood around the target point in the deblurred image $I_E$. After localized Gaussian smoothing of the rows in $H^\dagger$, we are left with a smooth deblurring operator, $H_S^\dagger$, resulting in greatly reduced noise and streaking artifact. Figure 5.24 shows the effects of $H^\dagger$ versus $H_S^\dagger$.

Figure 5.24: Improved SURESLIDE reconstruction with $H_S^\dagger$. a) Blurred interleave image $I_B$; b) Noisy deblurred image $H^\dagger I_B$. c) Smooth deblurred image $H_S^\dagger I_B$.

However, the width of the applied Gaussian $\sigma_s$ must be chosen carefully. If the width of this damping $\sigma_s$ is too large, noise will not be reduced. If the width becomes too short, a ringing artifact can appear near edges. This is likely an effect of truncating the reconstruction terms in $H^\dagger$. The key to an optimal reconstruction is to balance the poor conditioning of the deblurring matrix without introducing the truncation artifact.
Figure 5.25: Choosing the optimal smoothing width for SURESLIDE enhancement. a) $\sigma_s = 0.2$, over-smoothing resulting in truncation of $H_S^\dagger$ rows and ringing artifact. b) $\sigma_s = 4.6$, residual noise and signal pile up due to insufficient smoothing.

With the magnitude approaches, the edge width measure should be utilized with care. The ringing and overshoot artifacts can impact the edge width calculation significantly, causing the apparent edge width to decrease but not necessarily representing a resolution gain.

**SLENDER**

The SLENDER artifact is different and relates primarily to inaccuracies in the estimation of $P_0$ and $P_1$. Intra-voxel $P_0$ effects could cause variation in the expected angle $\alpha$ between $A$ and $B$, but generally these effects are very small.

There is reason to believe that the phase difference between adjacent slice centers does not correspond exactly with the phase difference between the resolved sub-voxels $A$ and $B$. This is evidenced by the fact that the phasor used to remove $P_1$ does not provide the optimal resolved image (Figures 5.26a and 5.26b), prompting additional tuning of the angle $\alpha$ used for separation of $A$ and $B$ (Equation 5.12).
Figure 5.26: SLENDER $\alpha$ tuning; the additional tuning of $\alpha$ enables a slight improvement in edge width and noise properties. a) Image constructed assuming $\alpha = \beta/2$. b) Improved image constructed with $\alpha > \beta/2$. c) & d) Corresponding edge width fittings.

While the tuned $\alpha$ can improve apparent edge width and SNR, it may also alter the effective spatial encoding, resulting in improper signal localization. This effect is seen in Figure 5.27.
CHAPTER 5. THROUGH-PLANE RESOLUTION ENHANCEMENT

Figure 5.27: “Over-tuning” of $\alpha$ causes improper signal localization. a) Properly tuned. b) Improperly tuned.

Another candidate is the effect of slice profile. Figure 5.28 demonstrates a model of how the slice profile can cause $\alpha \neq \beta/2$.

Figure 5.28: The slice profile can cause a disparity between $2\alpha$ and $\beta$. If we consider a region of uniform signal, the applied gradient will impart a phase ramp across the signal. a) If there is no magnitude modulation in the slice, the resulting angle will be $\alpha_0 = \beta/2$. b) When the signal magnitude is reduced further from the slice center (a typical slice profile), the resulting $\alpha$ will be smaller. c) Since $\beta$ is defined by two slice midpoints, the effects of the slice profile will cancel on either side of the midpoint, and $b$ is not affected by a nonuniform slice profile.
When this effect was tested in simulation, it was found that the optimal angle was indeed less than the nominal value $\alpha_0$ acquired from the RDF calculation. However, in real data the opposite was seen; $\alpha_{\text{opt}} > \beta/2$. This indicates that either the slice profile model is incorrect, or there are additional factors at play. This is an interesting point for future study.

5.7 Discussion

The acquisition times between SLENDER and the two magnitude based techniques are virtually identical for the same number of acquired slabs, $N$. Some additional time may be involved in the preparation of the phase encoded slab for SLENDER, but the impact on total scan time will be minimal. The reconstruction times of all three techniques are reasonable when compared to a 3D FFT required for reconstruction of full 3D MRI.

In terms of performance in the $N = 2$ case, SLENDER is a strong candidate for the best choice. The slightly more involved reconstruction process is rewarded by improved resolution gain compared with SEER and better SNR characteristics than SURESLIDE. Although SURESLIDE is a clear winner in terms of minimizing the edge width, the noise corruption presents a serious problem for practical use. An additional weakness of SURESLIDE is the inability to resolve smaller details when $N$ is small. This is evidenced most clearly in the lesion test, but is also noticeable to a lesser extent in the other $N = 2$ tests.

Both the SEER and SURESLIDE reconstructions assume spatially invariant blur in the slice direction. This is likely a reasonable assumption, but allowing for spatially variant blur operators may provide improvement in the enhanced image. The SLENDER reconstruction could be modified to allow a more realistic representation of the slice profile.
SEER and SURESLIDE are attractive in terms of their simplicity of implementation. Both can be applied to magnitude only data and require no modification of the pulse sequence. While SEER offers only a modest improvement in resolution, it is easily understood and possesses intrinsic noise mitigation effects that are desirable. Although the SLENDER technique is limited to the $N = 2$ case, when considering the limitations on through-plane resolution in 2D multislice MRI, even a twofold improvement can provide added benefit. The slice thickness is cut in half without compromising the SNR and without the added complications of acquiring thinner slices. There is a need to modify the pulse sequence by adding the additional $z$ gradient area to the phase encoded slab, but this modification is minimal.
Chapter 6

Conclusion

The purpose of this study was to investigate various methods for encoding and decoding signal in MRI. The technique rGRAPPA introduced an improvement on the standard implementation inspired by the spatial variation of the receiver coil sensitivities. rGRAPPA reconstructions resulted in lower Relative Error (RE) and suppressed residual aliasing artifact in comparison with standard GRAPPA. The rGRAPPA implementation provides a calibration sensitive to the localized nature of the weighting factors without the need for excessive kernel sizes or additional assumptions about the nature of the weights. The improved reconstruction accuracy of rGRAPPA allows for faster scan times or increased spatial resolution. The notion of combining the gains of rGRAPPA with a technique such as hpGRAPPA [31] to obtain even higher reconstruction quality is an interesting possibility.

A number of viable optimization metrics were discovered, capable of predicting the optimal rGRAPPA reconstruction region width $d$ and corresponding image without need of a reference scan. However, future studies should address the shortcomings of the optimal region prediction to further accelerate the offline reconstruction time. It is also possible that a weighted combination of metric measures (not considered in our analysis) could provide a better result.
The convolution fitting technique proved effective in predicting phase difference maps in real and simulated MR data. Limiting trajectories for minimum required source data were explored and it was found that central k-space data produced the best results. However, there is still much work to be done in this area. The methods developed here could prove useful in other applications, such as characterizing coil inhomogeneity, or predicting relative coil profile relationships that could be helpful in PPI. There is a potential for an impact in quantitative mapping applications and k-space extrapolation techniques such as keyhole imaging. In addition to testing the convolution fitting technique on other MRI applications, future studies should conduct a thorough investigation of the dependence of the kernel on the underlying spatial information, allowing corruption free estimation of the relative contrast information.

We have presented three possible techniques to achieve through-plane resolution enhancement in 2D multislice MRI data. Each approach has its own relative strengths and weaknesses. SEER is a simple enhancement that can be performed on any blurry data to provide edge enhancement. The applied blurring kernel can be selected to achieve the desired results, however, the ultimate resolution enhancement seems to be modest in comparison to the other techniques. SURESLIDE presents a deblurring operation that provides good recovery of fine detail, but suffers from noise amplification in the reconstruction. SLENDER, while still in its infancy, represents a bridge between 2D multislice and true 3D acquisitions. Though only applied in the most trivial case (a 2-fold enhancement), this technique provides a robust improvement of through-plane resolution and could have significant potential.

As the demand for higher in-plane resolution increases, there will be a correlated demand for through-plane resolution to overcome partial volume effects. Future work should study the optimal phase encoding required for SLENDER and investigate the possibility of extending the resolution gain to higher factors, such as splitting the slice into 3 or more sub-voxels. The techniques presented have shown evidence of
providing resolution enhancement, but there is yet much room for optimization.
Bibliography


Appendix A

The Moore-Penrose Pseudoinverse

The Moore-Penrose pseudoinverse [79, 80] provides a least squares solution to a system of linear equations. For the system

\[ \mathbf{Ax} = \mathbf{b}, \]  

(A.1)

the vector \( \mathbf{x} \) which solves the system may not exist, or if it does, may not be unique. The pseudoinverse \( \mathbf{A}^\dagger \) provides the minimum least squares solution:

\[ \mathbf{x} \rightarrow \arg\min (\|\mathbf{Ax} - \mathbf{b}\|_2), \]  

(A.2)

If the rows of \( m \times n \) matrix \( \mathbf{A} \) are linearly independent, it is said to have full row rank. Generally, \( m < n \) and \( \mathbf{A} \) represents a system with more equations than unknowns. In this case, the Moore-Penrose pseudoinverse is defined

\[ \mathbf{A}^\dagger = \mathbf{A}^H (\mathbf{AA}^H)^{-1}, \]  

(A.3)

where, \( \mathbf{A}^H \) represents the Hermitian (conjugate) transpose and \( \mathbf{A}^{-1} \) represents the inverse of \( \mathbf{A} \).
APPENDIX A. THE MOORE-PENROSE PSEUDOINVERSE

Computational Complexity

Straightforward computation of $A^\dagger$ requires a number of floating point operations ($flops$) outlined in the sequence below. Beginning with the $m \times n$ matrix $A$ and the $n \times m$ matrix $A^H$, we track the resulting matrix size and the number of $flops$ for each step;

\[
\begin{array}{c|c|c}
\text{Step} & (m \times m) & nm^2 \\
\hline
AA^H & (m \times m) & m^3 \\
(AA^H)^{-1} & (n \times m) & nm^2 \\
A^H(AA^H)^{-1} & (n \times m) & nm^2 \\
\end{array}
\]

In general, the number of floating point operations in terms of complex multiplications for the computation of the pseudoinverse of $m \times n$ matrix $A$ is

\[flops = m^3 + 2nm^2\]