NEW STRATEGIES FOR IMAGE RECONSTRUCTION FROM ARBITRARY K-SPACE TRAJECTORIES IN MAGNETIC RESONANCE IMAGING

by

Eng. Refaat El-Sayed Abdel Tawab El-Sayed Gabr

Systems and Biomedical Engineering Department Faculty of Engineering, Cairo University

A Thesis Submitted to the Faculty of Engineering, Cairo University In Partial Fulfillment of the Requirements for the Degree of MASTER OF SCIENCE in SYSTEMS AND BIOMEDICAL ENGINEERING

FACULTY OF ENGINEERING, CAIRO UNIVERSITY GIZA, EGYPT July 2003

NEW STRATEGIES FOR IMAGE RECONSTRUCTION FROM ARBITRARY K-SPACE TRAJECTORIES IN MAGNETIC RESONANCE IMAGING

by

Eng. Refaat El-Sayed Abdel Tawab El-Sayed Gabr

Systems and Biomedical Engineering Department Faculty of Engineering, Cairo University

A Thesis Submitted to the Faculty of Engineering, Cairo University In Partial Fulfillment of the Requirements for the Degree of MASTER OF SCIENCE in SYSTEMS AND BIOMEDICAL ENGINEERING

Under the Supervision of

Prof. Dr. Abu-Bakr Mohammed Yousef Dr. Yasser Mostafa Kadah

Systems and Biomedical Engineering Dept. Faculty of Engineering, Cairo University

FACULTY OF ENGINEERING, CAIRO UNIVERSITY GIZA, EGYPT July 2003

NEW STRATEGIES FOR IMAGE RECONSTRUCTION FROM ARBITRARY K-SPACE TRAJECTORIES IN MAGNETIC RESONANCE IMAGING

by

Eng. Refaat El-Sayed Abdel Tawab El-Sayed Gabr

Systems and Biomedical Engineering Department Faculty of Engineering, Cairo University

A Thesis Submitted to the Faculty of Engineering, Cairo University In Partial Fulfillment of the Requirements for the Degree of MASTER OF SCIENCE in SYSTEMS AND BIOMEDICAL ENGINEERING

Approved by the Examining Committee:

Assoc. Prof. Dr. Abu-Bakr M. Yousef, Thesis Main Advisor

Prof. Dr. Mohamed Emad M. Rasmy, Member

Prof. Dr. Safwat Mahroos, Member

FACULTY OF ENGINEERING, CAIRO UNIVERSITY GIZA, EGYPT July 2003

طرق جديدة لبناء الصور من المسارات العامة في البعد الترددي في المعناطيسي

طرق جديدة لبناء الصور من المسارات العامة في البعد الترددي في المعناطيسي

تحت إشراف

د./ یاسر مصطفی إبراهیم قدح

أ.د./ أبو بكر محمد يوسف

أستاذ بقسم الهندسة الحيوية الطبية والمنظومات

مدرس بقسم الهندسة الحيوية الطبية المنظومات

كلية الهندسة – جامعة القاهرة الجيزة-جمهورية مصر العربية يوليو 2003

طرق جديدة لبناء الصور من المسارات العامة في البعد الترددي في الرق جديدة لبناء التصوير بالرنين المغناطيسي

إعداد مهندس/ رفعت السيد عبد التواب السيد جبر قسم الهندسة الحيوية الطبية والمنظومات كلية الهندسة ، جامعة القاهرة

رسالة مقدمة إلى كلية الهندسة ، جامعة القاهرة كجزء من متطلبات الحصول على درجة الماجستير في الهندسة الحيوية الطبية والمنظومات

يعتمد من لجنة الممتحنين :

كلية الهندسة – جامعة القاهرة الجيزة-جمهورية مصر العربية يوليو 2003

TABLE OF CONTENTS

List of Figures	iii
List of Tables	V
Abstract	vi

1. I ı	ntroduction	1
1.1.	A Brief Overview of MRI Physics	1
1.2.	Acquisition of MR Images and the k-Space	3
1.3.	Nonrectilinear Scanning Trajectories	7
1.4.	Motion Artifact	9
1.5.	Clinical Applications of MRI	10
1.6.	Thesis Objectives	.11

2. Current Image Reconstruction Techniques From Non-Rectilinear K-Space

Trajectories	.15
2.1. Problem Formulation	.13
2.2. Brief Review of the Current Gridding Techniques	.15
2.2.1. Interpolation	.15
2.2.2. The Conventional Gridding Algorithm	.15
2.2.2.1. The Convolution Window and Gridding Errors	.19
2.2.2.2. Density Compensation Function (DCF)	.20
2.2.2.2.1. Current Density Compensation Functions	.20
2.2.2.2.2. A New Optimal DCF	.21
2.2.3. Block Uniform Resampling (BURS)	.23
2.2.4. Optimal Gridding Using Structured Matrix Approximation	.24
2.2.5. Gridding Using Least-Squares Spatially Variant Gridding Kernel	.25
2.2.5.1. Original Formulation	.25
2.2.5.2. An Efficient Implementation	.27
2.2.6. Matrix Transformation for Efficient Gridding	.28
2.2.7. Other Gridding Approaches	.29
2.2.7.1. Filtered Back-projection (FBP)	.30

2.2.7.2. A Continuous to Discrete Mapping	2.2.7.2.	A Continuous to Discrete Mapping	31
---	----------	----------------------------------	----

3. It	erative Gridding Using Deconvolution-Interpolation	
3.1.	Introduction	
3.2.	Theory	
3.3.	Methods	
3.4.	Results	
3.5.	Discussion and Conclusion	46

4.1.Introduction494.2.Problem Formulation504.3.Current Techniques514.4.Methods534.4.1.Motion Estimation544.4.2.Motion Correction554.5.Results and Discussions564.6.Conclusion59	4. M	otion Artifact Suppression Using Iterative Gridding	49
4.2.Problem Formulation504.3.Current Techniques514.4.Methods534.4.1.Motion Estimation544.4.2.Motion Correction554.5.Results and Discussions564.6.Conclusion59	4.1.	Introduction	49
4.3.Current Techniques514.4.Methods534.4.1.Motion Estimation544.4.2.Motion Correction554.5.Results and Discussions564.6.Conclusion59	4.2.	Problem Formulation	50
4.4.Methods	4.3.	Current Techniques	51
4.4.1. Motion Estimation544.4.2. Motion Correction554.5. Results and Discussions564.6. Conclusion59	4.4.	Methods	53
4.4.2. Motion Correction	4.4.1.	Motion Estimation	54
4.5. Results and Discussions	4.4.2.	Motion Correction	55
4.6. Conclusion	4.5.	Results and Discussions	56
	4.6.	Conclusion	59

5.	Conclusion	61

References	
Appendix	

LIST OF FIGURES

Figure (1.1): Pulse Sequence Diagram of Fourier Imaging
Figure (1.2): K-Space Traversing of Fourier Imaging7
Figure (1.3): Sequence Diagram for Spiral9
Figure (2.1): Voronoi Diagram for Radial Sampling
Figure (2.2): Projection of an object in computed tomography
Figure (3.1.a): Image reconstructed using the spiral trajectory and IGDI algorithm
Figure (3.1.b): Profile of fig. 3.1.a
Figure (3.2.a): Image reconstructed using the spiral trajectory and Conventional
Gridding (NxN)
Figure (3.2.b): Profile of fig. 3.2.a
Figure (3.3.a): Image reconstructed using the spiral trajectory and Conventional
Gridding (2Nx2N)
Figure (3.3.b): Profile of fig. 3.3.a40
Figure (3.4.a): Image reconstructed using the radial trajectory and IGDI algorithm
Figure (3.4.b): Profile of fig. 3.4.a40
Figure (3.5.a): Image reconstructed using the radial trajectory and Conventional
Gridding (NxN)41
Figure (3.5.b): Profile of fig. 3.5.a
Figure (3.6.a): Image reconstructed using the radial trajectory and Conventional
Gridding (2Nx2N)41
Figure (3.6.b): Profile of fig. 3.6.a
Figure (3.7.a): Image reconstructed using the spiral trajectory and IGDI algorithm for
noisy data42
Figure (3.7.b): Profile of fig. 3.7.a

Figure (3.7.c): Image reconstructed using the spiral trajectory and Conventional
Gridding (NxN) for noisy data42
Figure (3.7.d): Profile of fig. 3.7.c
Figure (3.7.e): Image reconstructed using the spiral trajectory and Conventional
Gridding (2Nx2N) for noisy data
Figure (3.7.f): Profile of fig. 3.7.e
Figure (3.7.g): Image reconstructed using the radial trajectory and IGDI algorithm for
noisy data
Figure (3.7.h): Profile of fig. 3.7.g
Figure (3.7.i): Image reconstructed using the radial trajectory and Conventional
Gridding (NxN) for noisy data43
Figure (3.7.j): Profile of fig. 3.7.i
Figure (3.7.k): Image reconstructed using the radial trajectory and Conventional
Gridding (2Nx2N) for noisy data
Figure (3.7.I): Profile of fig. 3.7.k
Figure (3.8.a): Real MR Image reconstructed using the IGDI Algorithm
Figure (3.8.b): Real MR Image reconstructed using the Conventional Gridding
Algorithm

Figure (4.1): The PROPELLER Sampling Scheme5	53
Figure (4.2): Interpolated Data from Two Successive Strips5	57
Figure (4.3): The PROPELLER Sampling Trajectory in The Presence of Motion	l
5	58
Figure (4.4.a): Image Reconstructed with IGDI In The Absence of Motion5	59
Figure (4.4.b): Profile of fig. 4.4.a5	59
Figure (4.5.a): Image Reconstructed with IGDI In The Presence of Motion5	59
Figure (4.5.b): Profile of fig. 4.5.a	59

LIST OF TABLES

Table (3.1): Optimal Kaiser-Bessel window parameter β for different window	w widths
	36
Table (3.2): RMS error of different sampling/reconstruction schemes with n	oise-free
data	45
Table (3.3): RMS error of different sampling/reconstruction schemes with no	oisy data
	45

ABSTRACT

Magnetic resonance imaging (MRI) is a versatile imaging modality that allows the imaging of both anatomy and function. Using this technique, true 3D imaging and angiography as well as functional and spectroscopic imaging are possible in clinical practice. In order to attain the best spatial and temporal resolutions in MRI data acquisition, several techniques have been proposed to efficiently utilize the imaging hardware. Among those techniques is the use of spiral and radial sampling for image acquisition. In this technique, the k-space (frequency domain) of the image is sampled nonuniformly in order to collect the information required to reconstruct the image. Several methods have been proposed to solve the inverse problem. Even though some of them are currently used in routine studies, the optimality of these methods have not been shown. Moreover, their performance under varying signal-to-noise ratio levels have not been demonstrated or discussed in the literature.

A new method is derived for the image reconstruction problem in MRI from nonuniformly sampled k-space. The new approach tries to compute a super-resolution reconstruction based on the information available from the data. Efficient matrix computation techniques are used to solve this problem numerically to take advantage of the sparsity of the formulation to reduce the computational complexity of the new approach. The proposed method is developed theoretically and verified using both computer simulations as well as real data from a 1.5T MRI system. Results are analyzed both qualitatively and quantitatively and discussed in depth to assess the value of the proposed techniques for clinical use. The new method is also applied to reconstruct images degraded by patient motion which, in general, results in nonuniformity in the acquired k-space. The success of the proposed method shows its potential for practical implementation in clinical settings.

CHAPTER 1

INTRODUCTION

Accurate diagnosis in medical procedures has become widely attainable by the advent of the different medical imaging modalities. Among those, magnetic resonance imaging (MRI) is currently one of the most promising non-invasive diagnostic tools in medicine. In addition to its ability to produce anatomical images of remarkable detail and contrast, it can be used to visualize vascular structures, measure blood flow and perfusion, detect neural activation, and identify the metabolic information of different areas in the acquired images.

Like other medical imaging modalities, MR images reflect the spatial distribution of certain tissue-dependent parameters. When a disease sets in, such parameters deviate from their normal values thereby allowing the detection of its location and spatial extent. Unlike CT, where the X-ray attenuation coefficient is the only physical property being imaged, three primary physical parameters can be manipulated in MRI, namely the proton density and the transverse and longitudinal relaxation times, T1 and T2. From this perspective, MRI is of superior performance for its ability to create images that reflect the effect of one of several parameters or different parameter combinations. That is, one might get T1-weighted, T2-weighted, or proton density images as well as combined parameters-weighted images. When this versatility is added to the volumetric acquisition capabilities of the technique, MRI stands out as a unique diagnostic tool in medicine.

1.1. A Brief Overview of MRI Physics

MRI is based on the effect of magnetic field on certain nuclei in the human tissues, particularly those containing an odd number of protons and neutrons which

gives a net charge. The main idea is that molecules are affected to different extents when they are placed in a magnetic field. Among many substances in the body, the hydrogen nuclei (protons) are the most useful from the imaging point of view. This is primarily due to the fact that the organic compounds constituting the human tissues are rich of hydrogen atoms which consequently yield high signal-to-noise ratios. Moreover, their presence in different amounts and distributions allows a clear distinction between the tissues if proton-based images are acquired [1].

In nature, protons have what is called *nuclear spin*. That is, they are spinning around their axes the same way Earth turns around its own axis. Since a spinning charged particle generates an electromagnetic field, spinning nuclei will have magnetic dipole moments. In other words, each nucleus can be thought of as a tiny bar magnet that is oriented in a random direction in the absence of outside influences. In this state, the statistical vector sum of all dipole moments is zero. However, in the presence of a strong magnetic field, such tiny bar magnets tend to align along the direction of that field. In such case, the vector sum of all magnetic dipole moments per unit volume tends to have a non-zero value, which is usually referred to as the *magnetization vector*. It is noteworthy that the magnetization is a bulk property of the sample rather than a property of the individual spins [1,2].

An important property of the magnetic dipole moments is that they precess. This means that each of these vectors has a fixed tail while its head is revolving, resulting in a wobbling motion. The frequency of precession w is related to the strength of the applied magnetic field, H, by the Larmor equation [1,2] given by,

$$\mathbf{w} = \boldsymbol{\gamma}.\mathbf{H} \tag{1.1}$$

where γ is the gyromagnetic ratio, which is constant for a given nucleus and equals 42.577 MHz/Tesla for the hydrogen nucleus. Different elements, even the different isotopes of the same element, exhibit significantly different gyromagnetic ratios.

As a result of the precession of magnetic dipoles, a radio-frequency (RF) signal is emitted from the precessing nuclei. This signal can be detected by a coil that is placed around the precessing nuclei. The strength of this radio-frequency signal is a direct function of the number of magnetic dipoles or equivalently to the number of nuclei in the uniform field.

The number of spins that align with the magnetic field and generate the magnetization vector is a very small fraction of the total number of spins even under high magnetic fields. Specifically, this fraction is given by the Boltzmann ratio, which is a function of the magnetic field strength, absolute temperature, and quantum number. The magnetic field applied to align the spins is called the *static field*, and is usually chosen in the Tesla range (0.5-9 T) to allow for a reasonable value (range of parts per millions) of the Boltzmann ratio [1,2].

1.2. Acquisition of MR Images and the k-Space

In order to reconstruct an image in MRI, the imaged object has to be excited by an amount of energy via a radio frequency pulse. This causes the magnetization vector to tip from the z-axis, the initial position, toward the transverse plane. The tipping angle depends on the duration and strength of the RF magnetic field and the gyromagnetic ratio of the sample. When the spins relax, they re-emit the acquired energy in a form of radio frequency signal whose frequency and phase depend on the applied magnetic field. To correctly reconstruct the image, a unique correspondence between the signal emitted from a particular location within the object and its spatial location must be established. To achieve this, a gradient system must be used to generate a spatially-varying and time-varying magnetic field within the sample.

Two complementary procedures are commonly followed to apply the magnetic gradients. In the first one, a static gradient is applied along a given direction while the signal is being read. This is referred to as the *readout gradient*. In this case, the frequency of the magnetization is dependent upon the spatial position along the

gradient direction, which is called the *frequency-encoding* direction. In the second method, the gradient is applied as a sequence of pulses and is thereby called the *gradient pulse*. This means that the spins are phase shifted according to their locations and the strength of the gradient pulse.

In the conventional Fourier imaging technique [1], a classical MRI imaging technique, an RF pulse is first applied thus the magnetization tips towards the *x-y* plane with a certain angle, usually $\pi/2$. Next, a gradient pulse is applied in the *y*-direction, followed by a readout pulse in the *x*-direction and the measured signal, which represents a line of the data, is stored. The pulse sequence diagram of this operation is illustrated in figure 1.1. Then, after a recovery period, the cycle is repeated until the entire image samples are acquired. Stepping the gradient pulse slightly in each cycle is required to assign a different phase (code) for each line in the *y*-direction, which is thus referred to as the *phase-encoding* direction. The recovery period is required for the spins to return completely to their equilibrium status, which allows measuring a significant signal when the spins are re-excited with the next RF pulse. This recovery period takes a few seconds in conventional MRI techniques. It is noteworthy that after each of the $\pi/2$ RF pulses the spins attempt to dephase in the transverse plane thus reducing the measured signal. Therefore, in order to refocus the spins, a π RF pulse is applied midway between each measurement and the $\pi/2$ RF.

Starting from the Bloch equation [1,3,4], which is a basic theory in MR and the one that approximately governs the dynamics of the spins, the measured MR signal was found [3,4] to be given by:

$$s(t) = \int_V m(\vec{r}) e^{-2\pi i f(\vec{r}) t} d\vec{r}$$
(1.2)

where t is the time at which the signal is sampled, $m(\vec{r})$ is the magnetic momentum amplitude of the spins, at spatial location \vec{r} , $f(\vec{r})$ is the precession frequency at that location and V is the imaged volume. The precession frequency at a certain location



Fig.1-1 Pulse Sequence Diagram of the conventional Fourier imaging. 'G' is abbreviation of Gradient and $G_y(l)$ is the strength of the phase-encoding gradient during the acquisition of line 'l' in the k-space.

depends on both the applied static magnetic field B_0 as well as the magnetic gradient \vec{G} as follows,

$$f(\vec{r}) = \frac{\gamma}{2\pi} \vec{B}(\vec{r}) = \frac{\gamma}{2\pi} \left(B_0 + \vec{G} \cdot \vec{r} \right)$$
(1.3)

If the gradient is time varying, the measured signal is given by,

$$s(t) = \int_V m(\vec{r}) e^{\gamma B_0 t} e^{\int \gamma \left(\vec{G}(t) \cdot \vec{r}\right) dt} d\vec{r}$$
(1.4)

$$s(t) = e^{\gamma B_0 t} \int_V m(\vec{r}) e^{\int \gamma(\vec{G} \cdot \vec{r}) dt} d\vec{r}$$
(1.5)

Dropping constant (position-independent) terms,

$$s(t) = \int_{V} m(\vec{r}) \ e^{\int \gamma \left(\vec{G} \cdot \vec{r}\right) dt} d\vec{r}$$
(1.6)

Now define,

$$\vec{k}(t) = \frac{\gamma}{2\pi} \int_{0}^{t} \vec{G}(\tau) d\tau$$
(1.7)

We get,

$$s(\vec{k},t) = \int_{V} m(\vec{r}) \ e^{2\pi i \vec{k} \cdot \vec{r}} d\vec{r}$$
(1.8)
Or,

$$s(t) = \mathcal{F}\{m(\vec{r})\}|_{\vec{k}=\vec{k}(t)}$$
 (1.9)

where $\vec{k}(t)$ is the spatial frequency variable at time *t*. The above equation demonstrates that the measured signal is just the Fourier Transform of the spin distributions. Therefore, the acquired samples are points from the spatial frequency domain, which is commonly referred to as the *k-space*. The *k*-space variable $\vec{k}(t)$ is a function in the time and the applied gradient. For the special case of fixed gradient vector, \underline{G} , the variable \underline{K} equals $\gamma \underline{G}.t/2\pi$ where *t* is the period of applying the gradient. Therefore, traversing the *k*-space is made possible by either the gradient magnitude or the interval in which the gradient is on. However, the direction of the traverse is determined only by the gradient direction. Traversing the *k*-space using the conventional pulse sequence (figure 1.1) is shown in figure 1.2.



Fig.1-2. Traversing of the k-space using conventional pulse sequence. The arrows indicate the progress in the time.

1.3. Nonrectilinear Scanning Trajectories

Form equation (1.7) it can been shown that the sampling trajectory in the k-space depends on the time variation of the applied magnetic gradient. In the simplest case, the gradient are time pulses and the samples are collected on a rectilinear grid. The fast Fourier transform (FFT) can then be used to efficiently reconstruct the image. If

other non-rectilinear sampling scheme is used, use of the FFT is not possible unless the samples are first interpolated onto a rectilinear grid. This is called the gridding problem. Developing efficient algorithms for calculating the Fourier transform from nonuniform samples has attracted the research for a long period.

Although rectilinear trajectories have the advantage of efficient reconstruction, several advantages can be obtained by using other non-rectilinear trajectories. One of the most important advantage of non-rectilinear trajectories is their inherent fast acquisition. It is possible to acquire the entire k-space in a single shot in trajectories like the echo-planar [7], spiral [5] or Lissajous [8] trajectories. Nonrectilinear trajectories requires less slew time and gradient power and the waveform of the gradient is smoother.

Another advantage is artifact-immunity of some of these trajectories. Some studies [5] showed the immunity of the spiral trajectory to flow artifacts. Center-out imaging methods such as projection-reconstruction and spiral MRI [5] have been shown to reduce motion artifacts. This is attributable in part to over-sampling of central *k*-space, which reduces artifact in a manner similar to multiple averaging in conventional imaging.

One of the most widely used nonrectilinear sampling schemes is the spiral trajectory. Spiral scanning is accomplished by combining two increasing, oscillating gradients. Figure 1.3 depicts a round spiral coverage of k space and a gradient-echo version of a related imaging sequence using sinusoidal gradient waveforms. Practical implementations on conventional scanners frequently take advantage of interleaved techniques (i.e. segmented scanning) rather than emphasizing single-shot capabilities as interleaving improves the SNR and reduce the gradient power.



Fig.1-3. Rapid spiral imaging. (A), Pathway through k space for a round spiral sequence. (B), Gradient-echo implementation of a corresponding imaging sequence

1.4. Motion Artifact

Image artifacts are structures appearing in the image without any correspondence to actual structures in the imaged object. Their major cause is that the RF signal from a particular tissue voxel is misdirected and displayed in a wrong pixel location.

Artifacts due to object motion are almost always encountered in MRI images. The longer the acquisition time the higher the possibility of the patient movements, either voluntary or otherwise, to distort the acquired images. Therefore, motion artifacts are most prominent in Fourier imaging where it takes several minutes to acquire the entire image [1]. One of the symptoms of motion artifacts is the blur, which makes it difficult to resolve small structures. Repetitive motion generates ghost-like replicas of the moving structures. These ghosts either add to or subtract from the image intensity of the underlying structures, thereby degrading the image contrast and reducing the detectability of lesions. Until recently, motion artifacts have limited the clinical usefulness of MRI in many clinical studies such as those of abdomen.

1.5. Clinical Applications of MRI

MRI has become a major diagnostic imaging modality with applications spanning virtually every part of the human body [3,6]. This is because it allows the acquisition of high spatial resolution images at any arbitrary orientation and the possibility of obtaining high resolution three-dimensional data sets within a reasonable amount of time. Furthermore, MRI has superior soft tissue discrimination as compared to the conventional X-ray modalities. MRI has proven successful in applications such as imaging of the musculoskeletal system, including the knee, shoulder, wrist, foot and ankle. The superb clarity of the images is due to the static nature of these structures, thereby eliminating the motion artifacts so common elsewhere in the body. Moreover, the small size of these structures makes them readily amenable to surface coils, which provide high SNR and spatial resolution. Perhaps more importantly, the normal absence of signal from bones, tendons or ligaments (because of the lack of free protons) provides sharp contrast for the presence of any signal within their structures due to abnormalities.

The use of contrast agents has made abdominal and pelvic imaging important applications of MRI. Examples include spleen, pancreatic, and hepatic imaging for the evaluation of the neoplasia. For vascular hepatic disease, the role of MR is to identify occlusive disorders of the hepatic and portal veins where this is suspected but not detectable on alternate imaging. For example, not all instances of portal vein thrombosis are evident on conventional ultra-sound (US), which is a reflection of the threshold sensitivity of US to slow flow. However, when thrombosis is suspected, it is readily identified using MRI GRE imaging due to its high sensitivity to the magnetic susceptibility phenomenon of the deoxy-haemoglobin (highly concentrated in thrombus). Furthermore, MR plays a role in the diagnosis of metabolic hepatic disease because of its ability to detect the deposition of iron, and to a lesser extent, fat within the liver.

Another strongly emerging application is the so-called functional MRI in which the brain response to a certain stimulus is to be registered. The result is a map or even an evaluation of the brain functions.

1.6. Thesis Objectives

It has been shown that the use of non-rectilinear sampling trajectories, like in spiral and radial sampling, has many advantages, however, image reconstruction in this case becomes a serious one as we have to solve the inverse problem. Even though there exist many techniques that solve this problem and some of them are currently used in routine studies, the optimality of these methods has not been shown. In this thesis, a new solution is derived for the image reconstruction problem in MRI from arbitrary sampled k-space. The new approach tries to compute and achieve an accurate reconstruction based on the information available from the data. Efficient matrix computation techniques are used to solve this problem numerically to take advantage of the sparsity of the formulation to reduce the computational complexity of the new approach. In chapter 2, we review current solutions to the gridding problem and compare their performance from the viewpoint of the reconstruction accuracy as well as the reconstruction speed. In chapter 3, we propose an iterative gridding solution. The proposed solution is developed theoretically and verified using computer simulations as well as real data from a 1.5T MRI system. Results are analyzed both qualitatively and quantitatively and discussed in depth to assess the value of the proposed techniques for clinical use. Chapter 4 is devoted to an application of the new gridding method to the reconstruction of images degraded by patient motion which, in general, results in nonuniformity in the acquired k-space.

CHAPTER 2

CURRENT IMAGE RECONSTRUCTION TECHNIQUES FROM NON-RECTILINEAR K-SPACE TRAJECTORIES

Reconstruction of an image from the nonuniform samples of its frequency domain is a common problem that arises in many fields ranging from radio astronomy to medical imaging (including CT and MRI), 2D-FIR filter design, image processing, geophysics and many other fields. An efficient solutions to this problem is to find the frequency domain values at a uniform grid so that the FFT can be used to reconstruct the image. This solution is referred to as "Gridding". The gridding problem is basically an interpolation problem and getting the optimal interpolation kernel lies at the heart of this problem. In this chapter we review many of the techniques used in solving this problem. We consider the problem of image reconstruction in MRI and use its terminology, however, the manipulation is general and applicable to other areas sharing the same problem.

2.1. Problem Formulation

Let M be the continuous Fourier transform of the object m to be imaged and S be the nonuniform sampling function consisting of a series of impulses at the required sampling locations, that is,

$$S(\mathbf{k}) = \sum_{j=1}^{L} \delta (\mathbf{k} - \mathbf{k}_{j})$$
(2.1)

where \mathbf{k} is the position vector in the k-space and *L* is the total number of data points. The sampled data is then given by:

$$M_s = M.S \tag{2.2}$$

The gridding problem is concerned with getting a "good" estimate of the Fourier transform of the object at a rectilinear grid so that the image can be reconstructed efficiently using FFT operations.

Given the finite object extent in the image domain, the Nyquist sampling theorem states that the measured nonuniform samples are related to the data onto the grid via an infinite sinc interpolation. This is,

$$M(\mathbf{k}_j) = \sum_{n=1}^{N} M(\mathbf{k}_n) \operatorname{sinc}(\left|\mathbf{k}_j - \mathbf{k}_n\right|) , \quad j = 1:L$$
(2.3)

where N is the required number of grid points, $|\cdot|$ is some distance measure, $[\mathbf{k}_j]$ is the set of k-space coordinates at which the samples are collected, and $[\mathbf{k}_n]$ is the set of rectilinear grid points at which the k-space is interpolated. We can rewrite this equation in a matrix form as,

$$\mu_s = A \,\mu_r \tag{2.4}$$

This is basically a linear system problem with a dense system matrix of sinc factors. Solving this system of linear equations is feasible if the number of points is small so that the inversion of A is practical. This solution is known as the Least Squares Reconstruction (LSR) [9]. In cases where the number of points is large, as in the case of MRI, or 2-D imaging in general, the inversion is not practical.

2.2. Brief Review of the Current Gridding Techniques

In the following sections, an overview of the current gridding algorithms is presented. We can divide the techniques in literature to two broad categories. The fist one use a convolution-interpolation to estimate the k-space on a uniform grid. These techniques are robust and efficient. However, they suffers from many artifacts. The second categories tries to achieve a higher accuracy through approximating the LSR with sub-optimal, but practical, solutions.

2.2.1. Interpolation

The most basic interpolation method used was the fast nearest-neighbor which represent a zero-order interpolation. A weighted average of the neighbors of each grid point like in bilinear, Gaussian, or truncated sinc function interpolation represent a slower but a more accurate solution, although still far beyond the optimal one.

2.2.2. The Conventional Gridding Algorithm

Based on the sampling theorem O'Sullivan [10] presented the conventional gridding algorithm that is a convolution-interpolation procedure. In this algorithm nonuniform data samples are convolved with an interpolation kernel, and the result of this convolution is sampled onto a Cartesian grid, that is

$$M(\mathbf{k}_n) = \sum_j M(\mathbf{k}_j) C(\left|\mathbf{k}_j - \mathbf{k}_n\right|), n = 1, 2, 3, \dots, N$$
(2.5)

where C(.) is the convolution window used. The image is then obtained by applying a two-dimensional inverse Fourier transform (2D-IFFT) to the gridded data and a post-compensation for the convolution roll-off effect is then performed by dividing the image by the inverse Fourier transform of the interpolation kernel c(r).

O'Sullivan [10] showed that the optimal interpolation method of a band-limited function is a convolution with an infinite-width sinc function. This solution is not practical and the sinc function has to be truncated, however, the performance degrades much when this truncation is carried out. O'Sullivan proposed a criterion for selecting another convolution function that is to be of finite width, this criterion is the maximization of the main lobe of the Fourier domain of the convolution function relative to the side lobes equation (2.13). The optimal function from this viewpoint is a zero-order prolate spheroidal wave function (PSWF). He suggested the Kaiser-Bessel function as a relatively easy-to-calculate function that approaches the optimality of PSWF which is harder o calculate. Kaiser-Bessel function is based on a zero-order modified Bessel function of the first kind,

$$C(u) = \frac{1}{W} I_0(\beta \sqrt{1 - (2u/W)^2})$$
(2.6)

and its inverse is given by,

$$c(x) = \frac{\sin(\sqrt{\pi^2 W^2 x^2 - \beta^2})}{\sqrt{\pi^2 W^2 x^2 - \beta^2}}$$
(2.7)

This process was termed "Gridding" and consists of the following steps:

- 1. Convolution of the nonuniform samples with a Kaiser-Bessel window calculating the result on a rectilinear grid
- 2. Performing inverse 2D-IFFT
- 3. Dividing by the inverse Fourier transform of the Kaiser-Bessel window to compensate for the roll-off resulting form the convolution step.

Due to the nonuniformity in the sampling process, the discrete convolution in step (1) is erroneous. The samples should first be compensated for this nonuniformity in the sampling density. O'Sullivan suggested that compensation be performed, however he has not provided any means to perform it.

Later on, Jackson et al. [11] investigated many other convolution functions. For each of the discussed windows they obtained the optimal window parameters using a modified version of the criterion of O'Sullivan equation (2.14) with the conclusion that encourage using the Kaiser-Bessel window. They also introduced the important concept of compensating each data point for the variable sampling density, known as Density Compensation Function (DCF). They defined a formula for getting this compensation factors that is referred to as Area Compensation Factors (ACF) and is defined as,

$$\rho(u) = S(u) \otimes C(u) \tag{2.8}$$

The gridding algorithm of Jackson was then known as the conventional gridding algorithm that consists of the following steps:

- Compensating each data point for the nonuniformity in the sampling density by multiplying by its ADF
- 2. Convolution of the compensated nonuniform samples with a Kaiser-Bessel window calculating the result on a rectilinear grid
- 3. Performing inverse 2D-IFFT
- 4. Dividing by the inverse Fourier transform of the Kaiser-Bessel window to compensate for the roll-off resulting form the convolution step.

This algorithm can be described by the following equation,

$$M(\mathbf{k}_n) = \sum_j \frac{1}{\rho(\mathbf{k}_j)} M(\mathbf{k}_j) \quad C(\left|\mathbf{k}_j - \mathbf{k}_n\right|) \quad , \qquad n = 1, 2, ..., N$$
(2.9)

where *j* runs over a small neighborhood of the interpolated grid point \mathbf{k}_n . We can write this convolution-interpolation as,

$$M_{SWCS} = \left(\frac{M.S}{\rho} \otimes C\right). III$$
(2.10)

where M_{SWCS} represent the nonuniform samples, weighted, convolved, and uniformly sampled onto a rectilinear grid, \otimes stands for convolution, and *III* is the grid sampling function, the shah function, consisting of a uniformly spaced set of impulses. In the image domain, this is equivalent to:

$$m_{SWCS} = (((m \otimes s) \otimes^{-1} \rho). c) \otimes III$$
(2.11)

where small letter variables stands for the inverse Fourier transform of capital letter variables. The roll-off due to the convolution step is compensated to get the final image,

$$m_{SWCS} = [(((m \otimes s) \otimes^{-1} \rho). c) \otimes III]. \frac{\Pi(FOV)}{c}$$
(2.12)

where $\Pi(FOV)$ is a gate function defined over the field of view.

Note that the object is repeated (aliased) by the convolution with the shah function in equation (2.11). This is because the convolution function C is of finite width and is therefore not band-limited in the image domain. The side lobes of c is aliased back by the shah function causing ghost repetitions of the imaged object that is amplified by the division by c to correct the convolution roll-off. The amplified amplitudes at the periphery of the image is a known artifact of the conventional gridding algorithm known as "wings" [12]. The repetition period of the ghosts is inversely proportional to the grid spacing in the frequency domain. The repetition period can by increased (less aliasing artifact) by sampling onto a finer grid in the frequency domain. This increases the computational load as an over-sampling by a factor of two in each direction for example increases the computational load four times.

Due to the smoothing effect of convolution step, the SNR is improved. The convolution in equation (2.10) is efficient since every rectilinear samples is estimated from only a small number of its nonuniform neighbors. The gridding algorithm is so

robust and efficient, hence widely used. However it suffers from two problem; first, the acquired samples must be compensated for the varying sampling density which is not easily fulfilled as the proper DCF may be not available analytically, based on only intuitive approaches with no optimality criterion, or not practical to compute. Second, the correction for the roll-off resulting form the convolution step results in "wings" as a result of the aliasing side lobes of the finite-width convolution kernel. It can be seen that the discretized convolution implemented in the gridding algorithm is not an accurate convolution [13].

The conventional gridding algorithm of Jackson *et al.* then became the most widely used method for image reconstruction from nonuniform samples. Many authors later tried to optimize the Kaiser-Bessel window parameters and measure the gridding accuracy. Another direction in research was to find the best DCF that minimize the error in the convolution process.

2.2.2.1. The Convolution Window and Gridding Errors

It has been shown that the side lobes of the Fourier transform of the convolution window results in aliasing of the imaged object, that is, ghost repetitions of the object wrap into the field of view. A window with a large main lobe and minimum side lobes energy is preferred. O'Sullivan introduced a measure for selecting a convolution window that maximize,

$$R = \frac{\int_{V} |c(\mathbf{r})|^{2} w(\mathbf{r}) d\mathbf{r}}{\int_{-\infty}^{\infty} |c(\mathbf{r})|^{2} w(\mathbf{r}) d\mathbf{r}}$$
(2.13)

where c is the inverse Fourier transform of the convolution window and w is some weighting function. Jackson et al. modified this criterion to include the convolution correction step. The functional to be minimized is,

$$J = \frac{\int_{\mathbf{r} \notin V} \left| c(\mathbf{r}) \cdot \left[\frac{\Pi(\mathbf{r})}{c(\mathbf{r})} \otimes III(\mathbf{r}) \right] \right|^2 d\mathbf{r}}{\int_{-\infty}^{\infty} \left| c(\mathbf{r}) \cdot \left[\frac{\Pi(\mathbf{r})}{c(\mathbf{r})} \otimes III(\mathbf{r}) \right] \right|^2 d\mathbf{r}}$$
(2.14)

The optimal window from this view point is the zero-order prolate spheroidal wave function PSWF. The PSWF is hard to compute accurately. An approximation that is easier to compute is the Kaiser-Bessel window. Jackson *et al.* [11] tested many other convolution windows with the Kaiser-Bessel giving best results. Wajer *et al.* [18] provided a simple equation to calculate the window parameter taking into account the required oversampling required to reduce the aliasing effect. They also analyzed the gridding errors in [19,20].

2.2.2.2. Density Compensation Function (DCF)

Proper sampling density compensation is necessary for accurate calculation of the discrete convolution in equation (2.9). Finding the optimal DCF attracted research for a long period. In this section we review the currently used Density Compensation Functions DCFs and introduce a new DCF that is optimal in the sense that it minimizes the reconstruction ghosts within the field of view (FOV).

2.2.2.2.1. Current Density Compensation Functions

The first DCF introduced was that of Jackson *et al.* [11] and is defined as in equation (2.8). This DCF represent a normalization factors for the interpolation process such that energy is uniformly distributed over all grid points. Another approach [9] calculates the DCF in a way that minimizes the squared error between the gridding reconstruction and the LSR solutions. Another [14] iteratively calculates the DCF such that the inverse Fourier transform of the DCF-weighted Sampling trajectory, namely $\mathcal{F}^{-1}\left\{S(\vec{k})DCF(\vec{k})\right\}$, approaches a delta function. Another [15]

partitions the k-space into unit cells such that the area around each nonuniform sample is closer to that sample than to any other sample. The unit cell area represent an estimation of the inverse of the sampling density. This type of space portioning is commonly known as Voronoi diagram. Figure (2.1) shows the Voronoi diagram for radial sapling.



Fig.2-1. Voronoi diagram for radial sampling

In cases where the trajectory has a well defined and differentiable form, the determinant of the Jacobian of transformation from the trajectory coordinates to a uniform grid is taken to be the compensation factor [16]. In certain cases the density compensation is derived from the analytical expression of the sampling trajectory [17].

2.2.2.2.2. A New Optimal DCF

In this part we propose a new DCF based on the analysis proposed by Wajer *et al.* [20]. Let $m(\bar{r})$ be the image vector of length N resulting by stacking the image columns on top of each other and $S(\bar{k})$ be the k-space vector of length L corresponding to L data points which is related to the image by the well-known Fourier transform,

$$S(\vec{k}) = \int m(\vec{r}) e^{-2\pi i \vec{k} \cdot \vec{r}} d\vec{r}$$
(2.15)

$$m(\vec{r}) = \int S(\vec{k}) e^{2\pi i \vec{k} \cdot \vec{r}} d\vec{k}$$
(2.16)

discretizing the convolution,

$$\hat{m}(\vec{r}) \approx \sum_{n} S(\vec{k}) e^{2\pi i \vec{k}_{n} \cdot \vec{r}} \Delta k_{n}$$
(2.17)

$$\hat{m}(\vec{r}) \approx \sum_{n} \left[\int m(\vec{r}') e^{-2\pi i \vec{k} \cdot \vec{r}'} d\vec{r}' \right] e^{2\pi i \vec{k}_n \cdot \vec{r}'} \Delta k_n$$
(2.18)

and Δk_n represent a patch of k-space around k_n

$$\hat{m}(\vec{r}) \approx \int \left[\sum_{n} \Delta k_n \, e^{2\pi i \, \vec{k} \cdot (\vec{r} - \vec{r}')} \right] \, m(\vec{r}') \, d\vec{r}' \tag{2.19}$$

$$\hat{m}(\vec{r}) \approx PSF(\vec{r}) \otimes m(\vec{r}) \tag{2.20}$$

where \otimes stands for convolution and $PSF(\vec{r})$ is the point spread function is defined as :

$$PSF(\vec{r}) = \sum_{n} \Delta k_n e^{2\pi i \vec{k} \cdot \vec{r}}$$
(2.21)

By tuning the factors Δk_n we can obtain a PSF that approximate a Kronecker-delta function. Let us develop a solution to this problem. Writing the above equation in a matrix form:

$$PSF = E d \tag{2.22}$$

where $E_{nn} = e^{2\pi i \vec{r}_m \cdot \vec{k}_n}$ and $d_n = \Delta k_n$ and *PSF* is a delta function that has a value of one at the origin and zero elsewhere. The least squares minimum norm solution to the above equation is given by:

$$d = (E^{H}E)^{-1}E^{H}PSF$$
(2.23)

where ^{*H*} denotes Hermitian (conjugate transpose). Looking carefully at the *nl* entry of the matrix $E^{H}E$

$$(E^{H}E)_{nl} = \sum_{m} e^{-2\pi i \vec{r}_{m} \cdot \vec{k}_{n}} e^{2\pi i \vec{r}_{m} \cdot k_{l}}$$

$$= \sum_{m} e^{2\pi i (\vec{k}_{l} - \vec{k}_{n}) \cdot \vec{r}_{m}} = D(\vec{k}_{l} - \vec{k}_{n})$$
(2.24)

where $D(\vec{k_l} - \vec{k_n})$ is a Dirichlet-like function defined as

$$D(t) = e^{-\pi i t/N} \frac{\sin(\pi t)}{\sin(\pi t/N)}$$
(2.25)

The resulting matrix $E^{H}E$ is easily calculated from the analytical expression in equations (2.24) and (2.25) and can be transformed to a sparse format by simply truncating "tiny" elements. The term $E^{H}PSF$ turns out to be a constant unit magnitude vector [1 1 1]. What remains is to solve the system $(E^{H}E) d = E^{H}PSF$ using the conjugate gradient method. The solution is obtained very fast due to the sparse nature of $E^{H}E$ and usually a small number of iteration is sufficient to yield a good accuracy.

2.2.3. Block Uniform Resampling (BURS)

In the Uniform Re-Sample algorithm (URS), μ_r is directly obtained from μ_s by inverting the matrix A in equation (2.4). While such matrix inversion is readily

obtained for 1-D signals, the URS algorithm becomes impractical in the 2-D signals due to the tremendous size of the matrix *A* in this case.

The Block Uniform Re-Sampling algorithm (BURS) [12] was introduced as an approximation to the URS method in order to reduce the computational effort. The BURS algorithm is in essence a numerical method for obtaining the inverse of a large matrix. It is based on isolating a small block, A^b , of the matrix A centered at entries $(i_j j)$, where j represents an unknown point in μ_r , which is to be estimated from a few measured non-rectilinear samples centered around the entry i in μ_s . The block is assumed to reasonably approximate the entire mapping for the unknown point j. Next, the inverse of the matrix A^b is obtained, namely $(A^{b)-1}$, of which one row corresponding to the sample j is kept. This row is used later, during image reconstruction, to estimate the rectilinear sample j from the selected few measured samples. This process is repeated for the entire points in μ_r .

The amount of calculation done to construct the gridding matrix is huge, however, it has to be made only once for a given trajectory. Regularization is an important issue that must be carefully studied while inverting each block A^b . Unreasonable estimate of the rectilinear points was obtained when Lissajous trajectories are used to acquire the k-space as pointed out by Hisamoto, *et al* [8]. The BURS solution was found to be very sensitive to noise. This is due to the higher sampling density at the periphery of the k-space in this trajectory. Later on, Hisamoto, *et al.* [21] and Rosenfeld [22] independently investigated this problem from the viewpoint of regularization theory and estimation theory and suggestions of regularized inversions was made to improve the reconstruction accuracy and avoid estimation errors.

2.2.4. Optimal Gridding Using Structured Matrix Approximation

Sedarat *et al.* carried out a deep investigation of DCF used in the gridding algorithm and showed that the gridding method is an approximation to the least square reconstruction (LSR) in equation (2.4) and found the "optimal" compensation factors
in the sense that it minimizes the difference between the gridding solution and the LSR solution. They proposed a matrix approximation technique for structured matrices (such as diagonal or banded matrices) to obtain the optimal DCF. They also proposed a framework for finding both the interpolation kernel and the deapodization (convolution compensation) factors that is optimal in that sense. However the matrix approximation step is not computationally efficient even for the standard MRI image sizes as 128x128 or 256x256.

2.2.5. Gridding Using Least-Squares Spatially Variant Gridding Kernel

Fahmy *et al.* [23] followed another approach to get the optimal spatially-varying interpolation kernel. Based on a model for the object as a series of a basic functions (impulse or boxcar) in the spatial domain, they obtained an optimal shift-varying interpolation matrix by solving a linear system for each grid point to get the least square solution. Each sample on the rectilinear grid is estimated from its neighboring sampling on the non-rectilinear grid so that every grid point system has a high number of equation representing the object model (a series of impulses or a series of boxcar function, ...etc.) and a small number of unknowns that represent the interpolation coefficients. The following sub-section presents the mathematical formulation of the proposed method and an improved implementation suggested to make the gridding matrix construction feasible.

2.2.5.1. Original Formulation

From the sampling theory, one sample f_i^r on the rectilinear grid can be perfectly reconstructed by the deconvolution of an infinite *sinc* function and the non-rectilinear samples. This can be represented as follows:

$$f_i^r = R_i \{ f^{nr} \}$$
(2.26)

where R_i . For the representation of the deconvolution with an infinite sinc function, sampling the result at point *i* of the rectilinear grid. Using the finite extent property of the MR image, one can select a suitable set of orthogonal basis vectors, $(\Phi_1, \Phi_2, \Phi_3, \dots, \Phi_m)$ to define the space of the images, that is

$$f^{nr} = \sum_{j=1}^{m} c_j \Phi_j$$
(2.27)

This basis can be a set of impulses or boxcar functions uniformly distributed in the image plane. Using the linearity of the deconvolution operator R_i (.), then

$$f_i^r = \sum_j c_j R_i \{ \Phi_j \}$$
(2.28)

The rectilinear sample f_i^r is to be calculated from a limited number of the measured signal to reduce the computations required by the gridding process. This can be represented as,

$$f_i^r \approx \langle a^i, Tf^{nr} \rangle \tag{2.29}$$

where a^i is a mapping vector, <.,.> is the inner product operator, and T is a truncation matrix that sets the entries of the vector f^{nr} to zero except for a small number of samples neighboring the sample f_i^r . Substituting from (2.16) into (2.15), we get

$$f_i^r \approx \sum_j c_j < a^i, T \Phi_j >$$
(2.30)

Considering only the non-zero entries of the above equation. And taking a to be a vector containing these entries of a^i that correspond to non-zero entries of $T\Phi_j$, and Φ_j is the non-zero entries of $T\Phi_j$, we get

$$f_i^r = \sum_j c_j R_i \{ \Phi_j \} \approx \sum_j c_j < a^i, T \Phi_j >$$
(2.31)

Due to the orthogonality of Φ_j , the following set of linear equations can be obtained

$$R_i \{ \Phi_j \} \approx \langle a^i, T \Phi_j \rangle \qquad j = 1:m \tag{2.32}$$

Or,

 $\mathbf{r} = \mathbf{\Phi} \mathbf{a}$

where $r = [R_i \{\Phi_1\}, R_i \{\Phi_2\}, ..., R_i \{\Phi_m\}]^{tr}, \Phi = [\Phi'_1, \Phi'_2, ..., \Phi'_m]^{tr}$, and tr is the matrix transpose operator. Note that calculation of $R\{\Phi_i\}$ is not a problem if the analytical expression of Φ_i is available. For example, a set of impulses distributed within the object region can be used as the desired basis set, whereby the elements of Φ_i , and $R\{\Phi_i\}$ are samples of a complex exponential function taken from a non-rectilinear and a rectilinear grid, respectively. Since the number of the basis vectors, *m*, is always greater than the number of unknowns, i.e. the entries of *a*, equation (2.20) represents a system of over-determined equations, which can be solved using the least squares criterion.

2.2.5.2. An Efficient Implementation

In this section we propose an efficient method for calculating the spatiallyvarying interpolation kernel. Consider the least-square solution to (2.20) which is given by the pseudo-inverse of the matrix Φ and can be expressed as

$$\mathbf{a} = (\mathbf{\Phi}^{\mathrm{H}} \mathbf{\Phi})^{-1} \mathbf{\Phi}^{\mathrm{H}} \mathbf{r} \tag{2.34}$$

 $\Phi^{H}\Phi$ is a J x J matrix where J is the number of nonuniform neighboring samples for the rectilinear grid point (k_{xi}, k_{yi}) and $\Phi^{H}r$ is a J x 1 vector. It can be shown that:

$$[\mathbf{\Phi}^{\mathbf{H}}\mathbf{\Phi}]_{kl} = \sum_{n} e^{-j\pi \left(\omega_{xk} x_{n}^{+} + \omega_{yk} y_{n}^{-}\right)} e^{j\pi \left(\omega_{xl} x_{n}^{+} + \omega_{yl} y_{n}^{-}\right)}$$
$$= D\{\left(\omega_{xk} - \omega_{xl}\right)/2\} \cdot D\{\left(\omega_{yk} - \omega_{yl}\right)/2\}$$
(2.35)

where D(.) denote a Dirichlet-like function defined as as in equation (2.5). Similarly, we get:

$$[\mathbf{\Phi}^{\mathbf{H}}\mathbf{r}]_{j} = D((\mathbf{w}_{xj} - \mathbf{k}_{xi})/2) \cdot D((\mathbf{w}_{yj} - \mathbf{k}_{yi})/2)$$
(2.36)

The problem now reduces to performing the following 2 steps for each rectilinear grid point:

- 1. Construct $\Phi^{H}\Phi$ and $\Phi^{H}r$ using the analytical expression above.
- 2. Solve the small-size linear system $(\Phi^{H}\Phi) a = \Phi^{H}r$ using SVD.

It is worth noting that this efficient method was developed by Fessler *et al.*[24] in their solution to the gridding problem. The solution they developed tries to minimize the maximum error between the nonuniformly interpolated samples from their uniform counterparts. It is not surprising that they got the same interpolation kernel as proposed by Fahmy *et al.* [23] who minimize the least-squares error between the uniformly interpolated samples from their nonuniform counterparts. This is because the various error norms are basically equivalent.

2.2.6. Matrix Transformation for Efficient Gridding

In another model-based approach [25], the image is assumed to be piecewise constant to take into account the practical display method using pixels.

$$f(x, y) = \sum_{n=0}^{N-1} \sum_{m=0}^{M-1} \alpha_{n,m} \cdot \Pi(x - x_n, y - y_m)$$
(2.37)

Using the continuous Fourier transform, the mapping of these unknown pixel values to the available frequency domain values is derived as ,

$$F(kx, ky) = \int_{-\infty-\infty}^{\infty} \int_{m=0}^{\infty-\infty} \sum_{m=0}^{M-1} \alpha_{n,m} \cdot \Pi(x - x_n, y - y_m) \cdot e^{-j2\pi(k_x x + k_y y)} dxdy,$$
(2.38)

$$F(kx, ky) = \int_{-\infty-\infty}^{\infty} \int_{n=0}^{\infty-1} \sum_{m=0}^{M-1} \alpha_{n,m} \cdot \Pi(x - x_n, y - y_m) \cdot e^{-j2\pi(k_x x + k_y y)} e^{j2\pi\Delta v(x_n, y_m)t(k_x, k_y)} dxdy$$
(2.39)

$$F(k_x, k_y) = Sinc(ak_x) \cdot Sinc(bk_y) \sum_{n=0}^{N-1} \sum_{m=0}^{M-1} \alpha_{n,m} \cdot e^{-j2\pi(k_x x_n + k_y y_m)} e^{j2\pi\Delta v(x_n, y_m)t(k_x, k_y)}$$
(2.40)

Or in matrix form, Av=b. The resultant model consists of a linear system with a system matrix of *L* rows by *N* columns, where *L* is the number of available frequency domain samples and *N* is the number of required pixels in the spatial domain. Even though the system matrix of this problem is shown to be dense and too large to solve for practical purposes, applying a simple Fourier transformation to the rows of this matrix converts the matrix into a sparse format. This is analogous to the DCT compressive property used for image compression in standard JPEG.

$$\vec{b} = \mathbf{A}\vec{v} = \mathbf{A} \cdot \mathbf{H}^{H} \cdot \mathbf{H} \cdot \vec{v} = (\mathbf{H} \cdot \mathbf{A}^{H})^{H} \cdot \vec{V} = \mathbf{M} \cdot \vec{V}, \qquad (2.41)$$

The problem now becomes the one of solving a large linear system with a sparse matrix to obtain the 1-D DFT of the vector containing the spatial domain pixel values in the image. This system is subsequently solved using the iterative conjugate gradient method. Each iteration has a computational complexity of O(L) with only a few steps needed to achieve a reasonable accuracy.

2.2.7. Other Gridding Approaches

In this section we briefly review other image reconstruction technique that involves the nonuniformity of the sampling pattern. Among those the filtered backprojection (FBP) is well-known as it is the standard image reconstruction technique in computed tomography (CT).

2.2.7.1. Filtered Back-projection (FBP)

The Filtered Back-projection (FBP) is a well-known algorithm for the reconstruction of images from projections. This algorithm is the most widely and preferred reconstruction technique used in computed tomography (CT). A close link between the reconstruction from projections and the gridding algorithm is derived from the Fourier slice theorem. It can be shown that the Fourier transform of the projection array of an object at a given angle is just a radial line in the k-space of this object (figure 2.2). Thus the whole set of projection sat all angles is just the well-known radial (or polar) sampling trajectory. The FBP algorithm consists of the following steps that is performed iteratively: for all projection profiles until a suitable solution is achieved:

- 1. Get The Fourier transform of the projection array
- 2. Filter the transformed projects with a suitable filter that is usually a smoothed version of a ramp filter(This is equivalent to a ramp DCF)
- 3. Inverse Fourier transform the filtered data
- 4. Back-Project each filtered projection along its path through the object

The Fourier slice theorem provide a means for solving the image reconstruction problem in CT using the fast gridding method rather than the slower back-projection technique currently employed. It has been shown that FBP is also applicable to a class of spiral trajectories.



Fig.2-2. Projection of an object in computed tomography.

2.2.7.2. A Continuous to Discrete Mapping

This solution [27] formulate the nonuniform sampling process as a continuous to discrete mapping that maps the continuous object space into a finite set of samples. They managed to inverse this operator using SVD to get a discrete to continuous mapping that has the advantage of arbitrary sampling in the image domain. The huge amount of calculation, due to the huge matrix to be inverted, makes this solution impractical.

CHAPTER 3

ITERATIVE GRIDDING USING DECONVOLUTION-INTERPOLATION

3.1. Introduction

In this chapter we present a new iterative gridding algorithm that overcomes the limitations of the conventional gridding algorithms discussed in the previous chapter. One of the most important problems by-passed in the new formulation is the calculation of the density compensation function (DCF). The proposed method tries to achieves a higher reconstruction accuracy at a reasonable computational cost. The basic idea is to interpolate the data using a deconvolution-interpolation approach that is more accurate than the convolution-interpolation technique used in the conventional gridding algorithm. The problem then reduces to the solution of a linear system with a sparse matrix. The conjugate gradient method (Appendix A) is used for solving this system iteratively. Finally, the deconvolution effect is compensated in the image domain.

3.2. Theory

Starting from the sampling theorem, we found in chapter 2 that the least-squares reconstruction (LSR) is obtained by solving the linear system, $\mu_s = A \mu_r$, where $\mu_s = [M(\mathbf{k}_j)]$ is the sampled k-space data vector and $\mu_r = [M(\mathbf{k}_n)]$ is a vector of uniformly spaced samples and A is a matrix of sinc factors. The LSR is not practical to carry out as the size of the matrix A is prohibitively large. Let us instead solve the system,

$$\mu_s = C \,\hat{\mu}_r \tag{3.1}$$

where $\hat{\mu}_r$ is an estimate of the data on the grid and *C* is an interpolation matrix of small width convolution kernel. This linear system can be solved efficiently using the conjugate gradient CG method [28] because *C* is sparse. Few number of iterations is usually sufficient to give good accuracy. Solving (3.1) obtains \hat{M}_r as the deconvolution of the measured data with a small window $C(\mathbf{k})$ and sampling the result of the deconvolution onto a rectilinear grid, that is,

$$\hat{M}_{r}(\mathbf{k}) = (M_{s}(\mathbf{k}) \otimes^{-1} C(\mathbf{k})) \cdot \mathbf{\Pi}(\mathbf{k})$$
(3.2)

where \otimes^{-1} stands for deconvolution and $\mathbf{III}(\mathbf{k})$ is the shah function, consisting of a uniformly spaced set of impulses,

$$\mathbf{III}(\mathbf{k}) = \sum_{n=1}^{N} \delta (\mathbf{k} - \mathbf{k}_{n})$$
(3.3)

Using Fourier analysis of this process, the effect of this step in the image domain reveals that,

$$\hat{m}_{r}(\mathbf{r}) = \frac{m(\mathbf{r}) \otimes s(\mathbf{r})}{c(\mathbf{r})} \otimes III(\mathbf{r})$$
(3.4)

where small letter variables stands for the inverse Fourier transform of capital letter variables. It is worth noting that solving (3.1) is an accurate deconvolution in contrary to the discretized convolution in the conventional gridding algorithm. Note that convolution with the shah function $III(\mathbf{r})$ results in aliasing of the object in the image domain with a repetition period that is the inverse of the grid spacing.

After solving (3.1) for $\hat{\mu}_r$ a 2D-IFFT is performed to get the image. The deconvolution step is corrected for in the central region of the image by multiplying

by $c(\mathbf{r})$, the inverse Fourier transform of the convolution window. The final image estimate $\hat{m}(\mathbf{r})$ is obtained as,

$$\hat{m}(\mathbf{r}) = \left[\frac{m(\mathbf{r}) \otimes s(\mathbf{r})}{c(\mathbf{r})} \otimes III(\mathbf{r})\right] \cdot c(\mathbf{r}) \cdot \Pi(\frac{\mathbf{r}}{FOV})$$
(3.5)

where $\Pi(\frac{\mathbf{r}}{FOV})$ is a gate function defined over the FOV.

A Kaiser-Bessel interpolating window of width four in each direction is used in all experiments of this study. The Kaiser-Bessel window is chosen because of its good side-loop behavior [11]. The optimal window parameter is obtained using the same criterion used in the conventional gridding algorithm, equation (2.14), except for interchanging the role of $c(\mathbf{r})$ and $1/c(\mathbf{r})$, where $c(\mathbf{r})$ is the inverse Fourier transform of the Kaiser-Bessel window, that is,

$$J = \frac{\int_{\mathbf{r} \notin V} \left| \frac{1}{c(\mathbf{r})} \cdot [(\Pi(\mathbf{r}) c(\mathbf{r})) \otimes III(\mathbf{r})] \right|^2 d\mathbf{r}}{\int_{-\infty}^{\infty} \left| \frac{1}{c(\mathbf{r})} \cdot [(\Pi(\mathbf{r}) c(\mathbf{r})) \otimes III(\mathbf{r})] \right|^2 d\mathbf{r}}$$
(3.6)

where *V* is the volume of interest. The optimality criterion employed herein is that of minimizing the aliased energy into the region of interest after correcting for the deconvolution. Table (3.1) presents the optimal free window parameter β for various kernel widths. This algorithm iteratively performs the griodding using the deconvolution process, hence it is termed Iterative Gridding using Deconvolution Interpolation (IGDI).

Window width	β
2	8.5
2.5	8.2
3	8.5
3.5	11.7
4	14.1
4.5	17.5
5	21

Table 3.1. Optimal Kaiser-Bessel window parameter β for different window widths

3.3. Methods

The most widely used technique for comparing reconstruction algorithms has been to compare the reconstructions when applied to data from human subjects. Another technique is to use what physicians call "phantom," which means taking data from a physical object of known structure instead of a human subject. The later approach is useful because we know what the true object is. Errors in the reconstruction, however, may be due to errors in the data or to errors in the algorithm. Shepp and Logan [26] introduced a "mathematical phantom" that simulate a head section. The "phantom" consists of multiple piece-wise constant functions , circles and ellipses, that is of known dimensions and intensity. This phantom is widely known in the image reconstruction community as the Shepp-Logan phantom. In a mathematical phantom, there is no measurement error, so any errors in the reconstruction are due to the algorithm. Furthermore, any measurement errors can be simulated to study its effect.

Sampling of the continuous frequency domain of the Shepp-Logan phantom using the analytical expression in [27] is simulated. A 128^2 data points were sampled and the reconstructed image resolution was 128x128. Usually, the number of samples is greater to achieve better reconstruction and higher SNR, however, we choose to work on the same number of point to emphasize the effect of the reconstruction algorithm in cases in which undersampling can occur in some regions of the k-space. Two sampling trajectories are used in this study; spiral and radial (polar). In spiral sampling, the trajectory traverse a constant angular velocity single-shot spiral. In radial sampling, the outer region of the k-space is sampled below the Nyquist limit in the azimuthal direction, while the center region is oversampled. The IGDI algorithm is implemented and the number of iterations is fifteen. For purpose of comparison the image is also reconstructed by the conventional gridding algorithm with two different subsampling ratios (NxN) and (2Nx2N) [11]. The simulated data is corrupted with random noise with different levels of SNR to test the performance of the new gridding algorithm against that of other algorithms. Gaussian-distributed white noise was added to the both real and imaginary parts of the original simulated data. The mean of the noise was 0 and the ratio of the standard deviation of the noise to the average magnitude of the original data was 3:11. this is a typical on MR machines [8]. The reconstruction errors is measured using the root mean squared error (E_{rms}) between each reconstructed image and the standard phantom after normalizing images so that the maximum gray level is equal to one. In all experiments a Kaiser-Bessel window is used with optimal parameter satisfying equation 3.6 for the IGDI algorithm and equations 2.14 for conventional gridding respectively.

Both IGDI and the conventional gridding algorithm (NxN) is applied to the reconstruction of a real MR image obtained from a 1.5T MRI system. A sixteen-interleaved spiral trajectory is used with each interleaf containing 1024 point, so the total number of data points is also 128^2 .

3.4. Results

The reconstructed image for the spiral trajectory using IGDI and its profiles (64th row and 64th column) are shown in figure 3.1. Note the high image quality, and the similarity between the reconstructed and actual lines of the image profiles. The reconstructed image obtained using the spiral trajectory with conventional gridding (original sized matrix gridding) and its profiles are shown in figure 3.2. As can be seen, profile distortions are exhibited in the peripheral regions. The reconstructed image and its profiles when subsampling the k-space data onto a double-sized matrix are shown in figure 3.3. Although the image quality is greatly improved when compared to figure 3.2, there are still small deviations from the ideal profiles due to suboptimal weighting. Figure 3.4 shows the reconstructed image and its profiles for radial trajectory using the IGDI reconstruction scheme. Note the effect of undersampling in the azimuthal direction. Figures 3.5 and 3.6 show the reconstructed images and their profiles using the conventional gridding algorithm (original-sized and double-sized matrices gridding, respectively) with the radial trajectories. Note the large "wings" which appear in the peripheral regions of the reconstructed image, which have been reported in earlier studies as well [8, 12]. The "wings" artifacts are almost eliminated in figure 3.6. However, a ringing artifact, which is an intrinsic problem of spiral sampling because of its coverage of a subregion of the targeted kspace area, is still visible. The RMS errors between the numerical phantom and the reconstructed image using the noise-free data for each trajectory/ gridding scheme are summarized in Table 3.2. Note that the quality of the reconstructed images using the IGDI is better than those using the conventional gridding algorithm (NxN and 2Nx2N subsampling). The reconstructed images with noise-corrupted data (1/11 noise level to the average of the original data) and their profiles (64th row and 64th column) using spiral/IGDI, spiral/conventional gridding (NxN and 2Nx2N), radial/IGDI, and radial/conventional gridding (NxN and 2Nx2N) reconstruction schemes are shown in figure (3.7). The RMS error each reconstructed image is summarized in table 3.3. The RMS error of IGDI scheme is better than those of conventional gridding methods.

Finally, IGDI and the conventional gridding algorithm (NxN) is applied to the reconstruction of a sixteen-interleaved spiral real MR image. Figure 3.8 represents the image reconstructed from each algorithm. Note the loss of resolution and ghost artifacts in the image reconstructed using conventional gridding and the absence of these artifacts in IGDI-reconstructed image.



Fig.3-1 Image reconstructed using the spiral trajectory and IGDI algorithm (a) and its profiles (b)



Fig.3-2. Image reconstructed using the spiral trajectory and the conventional gridding algorithm (sampling on NxN grid) (a) and the corresponding profiles (b,c)



Fig.3-3. Image reconstructed using the spiral trajectory and the conventional gridding algorithm (sampling on 2Nx2N grid) (a) and the corresponding profiles (b,c)



Fig.3-4. Image reconstructed using the radial trajectory and the IGDI algorithm (a) and the corresponding profiles (b,c)



Fig.3-5. Image reconstructed using the radial trajectory and the conventional gridding algorithm (sampling on NxN grid) (a) and the corresponding profiles (b,c)



Fig.3-6. Image reconstructed using the radial trajectory and the conventional gridding algorithm (sampling on 2Nx2N grid) (a) and the corresponding profiles (b,c)



a



















g



h







Fig.3-7. The reconstructed images using the data containing noise. The mean of the noise is 0 and the ratio of the standard deviation of the noise to the average magnitude of the original data was 1:11. (a) Image reconstructed using spiral/IGDI scheme. (b) Profiles at the 64^{th} row and 64^{th} column of (a). (c) Image reconstructed using a spiral/conventional gridding scheme (NxN gridding). (d) Profiles at the 64^{th} row and 64^{th} column of (c). (e) Image reconstructed using a spiral/conventional gridding). (f) Profiles at the 64^{th} row and 64^{th} column of (e). (g) Image reconstructed using radial/IGDI scheme. (h) Profiles at the 64^{th} row and 64^{th} column of (g). (i) Image reconstructed using a radial/conventional gridding scheme (NxN gridding). (j) Profiles at the 64^{th} row and 64^{th} column of (i). (k) Image reconstructed using a radial/conventional gridding scheme (NxN gridding). (j) Profiles at the 64^{th} row and 64^{th} column of (i). (k) Image reconstructed using a radial/conventional gridding scheme (NxN gridding). (j) Profiles at the 64^{th} row and 64^{th} column of (i). (k) Image reconstructed using a radial/conventional gridding scheme (NxN gridding). (j) Profiles at the 64^{th} row and 64^{th} column of (i). (k) Image reconstructed using a radial/conventional gridding scheme (NxN gridding). (j) Profiles at the 64^{th} row and 64^{th} column of (i). (k) Image reconstructed using a radial/conventional gridding scheme (NxN gridding). (l)



Fig.3-8. Real MR image reconstructed using the IGDI (a) and the conventional gridding algorithm (sampling on NxN grid) (b) Note the loss of resolution and ghost artifact in (b)

Algorithm		Trajectory	
		Spiral	Radial
IGDI		13.2833	9.1816
Conventional	Gridding	19.0673	18.1835
(NxN)			
Conventional	Gridding	14.3560	10.3484
(2Nx2N)			

 Table 3.2. RMS error of different sampling/reconstruction schemes with noise-free data

Algorithm		Trajectoty	
		Spiral	Radial
IGDI		13.9758	9.4320
Conventional	Gridding	19.4112	18.3457
(NxN)			
Conventional	Gridding	15.0286	10.6565
(2Nx2N)			

 Table 3.3. RMS error of different sampling/reconstruction schemes with noisy data.

3.5. Discussion and Conclusion

As seen in tables 3.2 and 3.3, the reconstructed image with a radial/IGDI scheme has a lower RMS error and high visual similarity with the numerical phantom when compared with other schemes. The RMS error of the spiral/IGDI and radial/IGDI reconstructed image is better than those of spiral/radial using the conventional gridding (NxN and 2Nx2N griddings, respectively). These results arise because the IGDI provides accurate deconvolution of the data rather than the approximated discretized convolution implemented in conventional gridding algorithm. In the conventional gridding algorithm, the "wings" artifact results from the amplification of the spatial aliasing caused by the suboptimal weighting. The IGDI algorithm is applicable to many kinds of trajectories and its reconstructed image is generally of high quality. The ringing artifact noted in the reconstruction appears due to lack of sampling near the corners of the targeted area of k-space with the spiral trajectory. Most of the k-space trajectories generated by the time-varying gradients, such as the spiral, circular, and rosette trajectories, cover only a subregion of the targeted k-space area. So the reconstructed image is affected, no matter how slightly, by the ringing artifacts associated with the trajectory's further truncation of the sampled region of kspace.

The conventional gridding algorithm, in which convolution is performed in gridding, is less sensitive to noise because convolution using Kaiser-Bessel window function more or less averages the data within the window. As a consequence, the reconstructed image is not as affected by noise as that using the IGDI algorithm. This is demonstrated in Table 3.3, in which the RMS errors of the IGDI algorithm are raised by an amount higher than those of the conventional gridding (NxN and 2Nx2N gridding).

The proposed method is superior to the conventional gridding algorithm from the view point of accuracy. It bypass the problem of calculating the density compensation. The computational requirement is larger than the conventional gridding algorithm as a cost of the increased accuracy. The dominating step in solving

a linear system with a sparse matrix using CG method is a sparse matrix-vector multiplication involving the system matrix C. A small number of iterations is usually sufficient to achieve a reasonable accuracy and the whole algorithm is still O(rL), where r is the number of iterations.

A nice property of the proposed algorithm is that the mapping matrix C can be computed efficiently for trajectories that are not known *a prioi*, This property is absent in many current gridding algorithms [12,23,24,25,27], where the mapping matrix construction involves a huge amount of computations and hence must be performed off-line and any change of the sampling trajectory requires re-construction of the mapping matrix. The simplicity of the construction of the mapping matrix in the proposed technique extends its application to areas where the location of the samples change often, like in 2-D FIR filter design and motion artifact correction [29].

CHAPTER 4

MOTION ARTIFACT SUPPRESSION USING ITERATIVE GRIDDING

4.1. Introduction

One of the major problems in the present MRI technology is its susceptibility to substantial artifacts when motion occurs during the image acquisition time. Even though fast acquisition methods such as EPI and spiral imaging provide a solution to this problem for some applications, these techniques are extremely sensitive to magnetic field inhomogeneity effects as compared to regular scanning methods and have a generally low signal-to-noise ratio. This makes it difficult to accurately correlate the generated images with the physical anatomy because of geometric distortion in addition to more profound signal loss within the areas of large susceptibility mismatches. Moreover, when these imaging sequences are used in such applications as functional magnetic resonance imaging (fMRI), where a set of slices are acquired repeatedly, patient motion persists in the form of low delectability of activation sites as a result of misregistration of images along the sequences.

Due to practical constraints from the MRI machine hardware, signal-to-noise ratio, and image contrast of MRI, the imaging time commonly extends to several minutes. As a result, different parts of the collected k-space are acquired at different time instants. In the ideal scenario, the imaged object does not change during the period of the experiment, and the image calculated by inverse Fourier transformation is undistorted. However, in clinical MRI setups, this scenario is not usually guaranteed because of physiological and occasional voluntary patient motion and can be even impossible to realize for moving organs such as the heart and abdominal structures. Consequently, the constructed images suffer varying degrees of distortion

depending on the characteristics of the imaging sequence and the severity of motion during the scan duration.

4.2. Problem Formulation

It is well known that patient motion during the image acquisition causes artifacts in the reconstructed image, which for two-dimensional Fourier Transform (2DFT) imaging techniques appears as blurring and ghost repetitions of the moving structure [29]. Patient motion can be classified according to its nature as rigid motion in which all the object points undergo the same motion and non-rigid motion such as physiological movements (respiratory, cardiac). Here we consider the case of rigid motion, which is commonly encountered in MR images of head, brain and limbs. First, consider the relation between the MR signal and the density distribution of the target in the imaging plane. This is given by,

$$F(k_x, k_y) = \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} f(x, y) \exp[-j2\pi(k_x x + k_y y)] dxdy$$
(4.1)

where $F(k_x,k_y)$ is the MR signal, k_x and k_y are the spatial frequency coordinates in the readout and phase-encoding directions, respectively, f(x,y) is the density distribution of the nonmoving imaging target, and x, y are horizontal and vertical coordinates in the imaging plane. In (4.1) it is seen that the MRI signal is the 2-D Fourier transform of f(x,y). Considering the case when the k-space is acquired as consecutive bands, as in the case of PROPELLER or segmented EPI, one can neglect the inter-band motion. This is true because the entire band is acquired during a single read-out period. Thus, planar rigid motion parameters during the acquisition can be regarded as a function of the band number. A planar rigid motion is the combination of translational and rotational motions. It is well known that the rotation of an object about the center of the image domain results in the same rotation of its k-space, while translational shift results in a linear phase term multiplied in the k-space [29]. Thus the effect of the motion can be written as,

$$F_d(k_x, k_y) = \exp[-j2\pi(\delta_x k_x + \delta_y k_y)] \cdot F_\theta(k_x, k_y)$$
(4.2)

Here $F_d(k_x,k_y)$ is the motion-distorted MRI signal and δ_x , δ_y , and θ are the translation in the x-direction, the translation in the y-direction and the rotation angle, respectively, and $F_{\rho}(k_x,k_y)$ is defined as,

$$F_{\theta}(k_x, k_y) = F(k_x \cos \theta + k_y \sin \theta, -k_x \sin \theta + k_y \cos \theta)$$
(4.3)

To correct for the distortion resulting from motion, one first should estimate the unknown motion parameters δ_x , δ_y , and θ and use these parameters to reconstruct an artifact-free image from the motion-distorted data.

4.3. Current Techniques

Several attempts to solve the problem of motion artifact in MRI have been reported in the literature. In general, the available techniques can be classified into four main categories. The first category attempts to suppress relative patient motion among different k-space lines within a given image through either through breath holding and chest strapping or by using cardiac and respiratory gating [30]. This minimizes the physiological component of motion between these lines at the expense of increased discomfort to the patient and/or significantly longer acquisition times. The second category uses averaging of different acquisitions to suppress the motion artifacts as well as to improve the signal-to-noise ratio of the final image. This can be done by taking the average of the corresponding k-space lines in a number of consecutive image acquisitions, or more generally by composing a weighted average of the two based on optimizing a certain objective function under given constraints [30,31]. The third category applies extra magnetic gradient lobes in the imaging sequence to eliminate the effects of motion through signal refocusing assuming a simple polynomial model for this motion [32,33]. This technique is used to minimize

signal loss from moving blood and CSF within a given voxel[34]. Finally, the fourth category assumes simple forms of rigid body motion including translational and rotational components and corrects for them in a post-processing step. The motion in this category is estimated using external monitoring [35], navigator echo (only for translational motion) [36,37], symmetry constraints [38], motion periodicity constraint [39,40], or through automated techniques [29,41-46]. The effect of translational motion can be suppressed by post-processing through modifying the phase of the k-space lines according to the *a priori* knowledge about the motion [29,47,48].

In spite of the success these methods have met in some applications, they represent solutions to only a restricted class of artifacts and cannot generally be applied to more complex types of motion such as deformable body motions. Moreover, the convergence properties of automatic techniques are not generally guaranteed and therefore a general lack of robustness of these methods hindered their clinical use outside research facilities. As a result, if the patient moves significantly during the experiment, the motion artifact in the resultant images cannot be corrected. As a result, the scan has to be repeated at the expense of inefficient use of MRI machines and added discomfort to the patient. Moreover, this might not even be possible to tolerate in emergency cases. This also complicates the procedure of imaging moving organs such as the heart by adding the cardiac/respiratory gating, which again contributes to a significant prolongation of the examination time. Therefore, a technique for motion artifact suppression that does not impose any constraints on the current procedures while robustly constructing images that are free of motion artifact will have a rather profound impact on the current MRI technology and many of its clinical applications.

One of the new motion artifact suppression techniques is the PROPELLER MRI proposed by Pipe [49]. In this technique data is collected in concentric rectangular strips rotated about the k-space origin. The central region of k-space is sampled for every strip, and used to estimate relative motion between strips during the scan (figure 4.1). This technique is termed (Periodically Rotated Overlapping ParallEL Lines with Enhanced Reconstruction (PROPELLER MRI).



Fig.4-1. The PROPELLER sampling scheme. Note the superimposed hypothetical circle in the overlapping area

4.4. Methods

In the PROPELLER technique, A method dedicated for motion artifact correction, data is collected in concentric rectangular strips rotated about the k-space origin [49]. The central region of k-space is used to estimate motion between strips. The translation motion is directly corrected by multiplying by a linear phase term corresponding to the estimated translation. At the end of a slice scan, the data is gridded using the conventional gridding algorithm with a modified density compensation function [14,49]. We propose a method for accurate and efficient estimation of the motion parameters using the inherent "orbital navigator" information in the data. We also propose a method for accurate and efficient gridding of the measured data using a look-up table-based version of the proposed gridding algorithm.

4.4.1. Motion Estimation

Motion of an object during an MRI scan causes two types of errors; bulk rotation of the object causes identical rotation of its k-space, while shifts produce linear phase shifts in the k-space. In the original ROPELLER method, the central circle common to all strips is used to estimate the inter-strip motion of the object as follows :

- 1. Define a set of Cartesian coordinates that spans the central circle as R.
- 2. The data magnitude of each strip is gridded onto R after being rotated with a series of angles spanning a range that covers the expected range of motion. The gridded data is then correlated with an averaged data set used as a reference. The correlation is measured as a function of rotation angle and fitted to a second-order polynomial. The peak of the fit polynomial is estimated to be the angle of rotation for this strip. The strip coordinates are then rotated to match the estimated rotation.
- 3. To estimate translational motion, complex data is gridded onto R and an average complex data set is used as a reference. Translation in the x and y directions is estimated by detecting linear phase shifts between the gridded strip and the reference. This is done by simply finding the peak of the magnitude of the Fourier transform of this phase shift.

The problem with such method is that gridding onto R with all possible rotation angle is obviously inefficient and large unexpected rotation may lead to incorrect results. Furthermore, the reference data set obtained by averaging is not the optimal way to handle data redundancy and may lead to estimation errors. We propose a simple, accurate and more efficient method for the estimation of rotational and translational motion. First a predefined set of points spanning a circle C in the k-space is defined with a specified angular spacing (figure 4.1). The circle C should be smaller than the central circle common to all strips. The data measured for each strip is interpolated on C using a small Kaiser-Bessel window to form the vector D_n where n is the strip number. Relative rotational motion between strips causes identical rotation of the circle C and thus identical circular shifts in the vector D_n . The maxcorrelation between the magnitude of every two successive vectors D_n and D_{n+1} is then used to estimate the rotation angle. The correlation is performed efficiently by evaluating it using the fast Fourier transform (FFT),

$$\theta = \arg \max | \mathbf{\pounds}^{-1} \{ \mathbf{\pounds} \{ \mathbf{D}_n \} \, . \, \mathbf{\pounds} \{ \mathbf{D}_{n+1} \}^* \}$$
(4.4)

where \pounds is the Fourier transform operator and * represent complex conjugate. This may restrict us to choose the number of points on C to be FFT-friendly. It is worth noting that estimation the k-space on C is an alternative to measuring it as in the orbital navigator echo (ONAV) method used in a prospective way to correct for patient motion [50.]. The points on C is then rotated by the rotation angle estimated and the phase shift between the two point sets is fitted to a first-order polynomial in each direction to estimate the translation motion in both x and y directions. Finally, correction for the translational motion is done by removing the corresponding linear phase in that strip. Rotational motion is corrected by a gridding procedure of the data with its coordinates adjusted by the estimated motion parameters.

4.4.2. Motion Correction

Once a slice acquisition is finished, a gridding phase is carried out. The data is interpolated onto a rectilinear grid using the conventional gridding algorithm. A modified density compensation function (DCF) is used that is iteratively evaluated using the estimated data locations [14]. To make it practical, an initial estimate of this DCF is pre-calculated and few iterations are carried out during image reconstruction. However, the gridding algorithm in this case is not so efficient since the gridding coefficients cannot be pre-calculated. Nevertheless, the conventional gridding algorithm has been thoroughly investigated and shown to lack optimality [4]. In chapter 3, we presented an iterative gridding algorithm that is shown to perform much more better than conventional gridding. Given the measured data samples μ_s , the

following relation between μ_s and $\hat{\mu}_r$ (the gridded data stacked into a vector form) was derived: $\mu_s = C \hat{\mu}_r$. This equation is solved iteratively using the conjugate gradient (CG) method and few iterations are usually sufficient to yield good accuracy.

Considering the rigid body assumption, rotation of an object in the image space produces identical rotation of its *k*-space, while translational motion produce linear phase shifts in the *k*-space data. An accurate and efficient implementation of the PROPELLER method can be carried out using the proposed gridding algorithm by first noting that rotation of any strip about the k-space origin is identical for all strips. All possible locations of all strips are just the rotated versions of any strip with all possible rotation angles. The matrix *C* is partitioned into sparse sub-matrices each corresponding to an acquired strip data set. All possible sub-matrices can be precalculated for all possible rotation angles of a strip for a given angular resolution (say 0.5°) and the calculated sub-matrices are stored and loaded during image reconstruction according to the estimated rotation angle of each strip. The reconstruction algorithm can be summarized as follows:

- 1. Initialize the mapping matrix *C* to empty.
- 2. Loop on all measured strips and perform 3, 4, and 5.
- 3. Estimate the rotational and translational motion of the acquired strip.
- 4. Correct for the translational motion by multiplying the strip data by a linear phase corresponding to the estimated translation.
- 5. Plug the proper sparse sub-matrix in the proper location in the mapping matrix *C* according to the estimated rotation angle.
- 6. Solve equation (3.1) using CG method for $\hat{\mu}_r$.
- 7. Finally, the image is obtained by a 2-D IFFT operation on $\hat{\mu}_r$ followed by the deconvolution compensation discussed in chapter 3.

4.5. Results and Discussions

Simulation of the proposed algorithm was carried out using the analytical expression for the k-space of the Shepp-Logan phantom. Six strips were acquired with seventeen lines per strip. The reconstructed image dimensions was 64x64. Figure 4.1 shows the PROPELLER sampling scheme. Note the hypothetical circle C used in the estimation phase.

Figure 4.2 shows a plot of the D_n vector (the interpolated data on circle C) for two successive strips. The second strips was sampled with a simulated rotation error of five degrees. The similarity between the two curves are obvious. The detection accuracy was less than 0.1 degree for noise-free data.



Fig.4-2. The interpolated data onto circle C (see text) from two successive strips. Note the similarity between the two curves.

The inherent navigator information are easily calculated since the interpolation coefficients are the same for all strips. so they can be pre-calculated and stored efficiently. The method proposed can be easily generalized for any acquisition pattern that include such redundancy in the measured k-space data

Inter-strip rotational motion was simulated such that the sampling pattern is as shown in figure 4.3. Provided that the motion estimation phase of PROPELLER is perfectly correct, the reconstructed image after fifteen iterations in figure 4.5 shows good quality compared to the motion-free image in figure 4.4. The RMS error of the motion-free and motion-corrupted data was 6.1718 and 6.2882 respectively Note that rotations of the acquired strips result in large void areas in the k-space, however, the reconstructed image is still of good quality justifying the accuracy of the proposed gridding algorithm.



Fig.4-3. The PROPELLER sampling trajectory in the presence of simulated inter-strip motion



Fig.4-4. Image reconstructed using IGDI in the absence of motion (a) , and the corresponding profiles (b)



Fig.4-5. Image reconstructed using IGDI in the presence of motion indicated in fig. 4.3 (a) , and the corresponding profiles (b)

4.6. Conclusion

We proposed two new techniques for motion detection and correction in PROPELLER MRI. The new estimation techniques is especially efficient since the data has to be interpolated only on the circle points and not on all the overlapping area as in the original PROPELLER. The gridding algorithm presented was discussed in the previous chapter and its performance was shown to be better than the conventional gridding implemented in PROPELLER. The proposed algorithm uses pre-calculated gridding matrices that is calculated for all possible orientations of the sampling strips.
CHAPTER 5

CONCLUSIONS

A new image reconstruction technique from non-uniformly sampled MR data has been proposed in this thesis. This technique replace the current convolutioninterpolation gridding with a deconvolution-interpolation one so that the image reconstruction becomes a problem of solving a linear system. The system matrix has a sparse structure, so the system can be solved efficiently using the conjugate gradient method. This technique has the advantage of increasing the reconstruction accuracy and reducing artifacts in current gridding algorithms. The solution accuracy can be increased by increasing the number of iterations performed in the conjugate gradient method, however, as the number of iterations increase, the reconstruction time increases and the SNR decrease. The number of iterations then becomes a control variable the trade-offs various reconstruction parameters. The price paid for the increased accuracy is the increased amount of computations.

An advantage of the proposed technique is that the system matrix can by constructed efficiently, hence, the application of the proposed gridding technique is extended to situations in which the k-space trajectory is not know in advance. The non-uniformity in k-space sampling due to patient motion during the scan is an example of this case. PROPELLER MRI (REF) is a new technique used to collect the k-space data in a manner the facilitate the detection and correction of patient motion. We proposed a technique to implement the PROPOLLER method with improved performance.

Based on the results of this thesis, further research can be proposed in the following points:

• Constrained reconstruction

- Artifact-free reconstruction of EPI data based on k-space measurements
- Reconstruction for dynamic imaging data
- Further applications to motion artifact suppression
- Partial k-space data imaging
- Further investigation of the relation between the gridding algorithm and filtered back projection (FBP)

REFERENCES

- 1. Ray H. Hashemi, and William G. Bradley, "MRI: the basics," Williams & Wilkins, 1997.
- E. Mark Haacke, Robert W. Brown, Michael R. Thompson, and Ramesh Venkatesan, "Magnetic Resonance Imaging, Physical Principles and Sequence Design," chapter 4, John Wiley, New York, 1999.
- Micheal J. Bronskill, Perry Sprawls, "The Physics of MRI," pp. 135-150, AAPM Summer School Proceedings (1992).
- Z. H. Cho, H. S. Kim, H. B. Song, and James Cumming, "Fourier Transform Nuclear Magnetic Resonance Tomographic Imaging," Proceedings of IEEE, vol. 70, no. 10, Oct. 1982.
- Meyer CH, Hu BS, Nishimura DG, Macovski A. Fast spiral coronary artery imaging. Magn Reson Med 1992;28:202–213.
- Micheal J. Bronskill, Perry Sprawls, "The Physics of MRI," pp. 206-233, AAPM Summer School Proceedings (1992).
- H. Bruder, H. Fischer, H. E. Eeinfelder, and F. Schmitt "Image Reconstruction for Echo Planar Imaging with Nonequidistant k-Space Sampling". Magn Reson Med 1992;23:311–323.
- H. Moriguchi, M. Wendt, and J. L. Deurk "Applying the Uniform Resampling (URS) Algorithm to a Lissajous Trajectory: Fast Image Reconstruction With Optimal Gridding". Magn Reson Med 2000;44:766–781.

- Hossein Sedarat, and Dwight G. Nishimura, "On the optimality of the gridding reconstruction algorithm," IEEE Trans. on. Medical Imaging, vol. 19, no.4, April 2000.
- J. D. O'Sullivan, "A Fast sinc Function Gridding Algorithm for Fourier Inversion In Computer Tomography", IEEE Trans. Med. Imag., Vol. 4, 200-207, 1985.
- J. I. Jackson, C. H. Meyer, D. G. Nishimura, and A. Macovski "Selection of a Convolution Function for Fourier Inversion Using Gridding", IEEE Trans. Med. Imag., Vol. 10, 473-478, 1991.
- D. Rosenfeld, "An optimal and efficient new gridding algorithm using singular value decomposition," vol. 40, pp 14-23 (1998).
- H. Schomberg, and J. Timmer, "The Gridding Method for Iamge Reconstruction by Fourier Transformation," IEEE Trans. On Medical Imaging, vol. 14, no. 3, September 1995.
- J. G. Pipe, and P. Menon, "sampling density Compensation in MRI: Rationale and an Iterative Numerical Solution," Magn Reson Med 1999;41:179–186.
- 15. V. Rasche, R. Proska, R. Sinkus, P. Bornert, and H. Eggers, "Resampling of data betweenarbitrary grids using convolution interpolation," IEEE Trans. On Medical Imaging, vol. 18, no. 5, May 1999.
- R. Hoge, R. Kwan, and G. B. Pike, "Density Compensation Functions for Spiral MRI" Magn Reson Med 1997;38:117–128.

17. M. Soumekh, "Reconstruction and sampling constraints for spiral data," IEEE Trans. Acoustics, Speech, Signal Processing, vol. 37, pp. 882–891, 1989.

- F. T. A. W. Wajer, E. Woudenberg, R. de Beer, M. Fuderer, A. F. Mehlkopf, and D. van Ormondt, "Simple Equation for optimal window parameters" ISMRM International Conference, 1999.
- 19. F. T. A. W. Wajer, R. Lethmate, J. A. C. van Osch, D. Graveron-DDemilly, M. Fuderer, and D. van Ormondt, "Simple Formula for The Accuracy of Gridding " ISMRM International Conference, 2001.
- 20. F. T. A. W. Wajer, R. Lethmate, J. A. C. van Osch, D. Graveron-DDemilly, M. Fuderer, and D. van Ormondt, "Interpolation from Arbitrary to Cartesian Sample Positions: Gridding " Proc. Of the ProRISC/IEEE workshop, 2000.
- 21. H. Moriguchi, and J. L. Deurk "Modified Block Uniform Resampling (BURS) Algorithm Using Truncated Singular Value Decomposition: Fast Accurate Gridding With Noise and Artifact Reduction". Magn Reson Med 2001;46:1189–1201.
- 22. D. Rosenfeld, "New Approach to Gridding Using Regularization and Estimation Theory". Magn Reson Med 2002;48:48–193.
- 23. A. S. Fahmy, B. S. Tawfik, and Y. M. Kadah, "Gridding Using Spatially Variant Gridding Kernel" ISMRM International Conference, 2002.
- 24. J. A. Fessler, and B. p. Sutton, "A Min-Max Appraoch to The Multidimensional Nonuniform FFT: Application to Tomographic Image Reconstruction" IEEE T-SP submitted 2001-12-19
- 25. Y. M. Kadah, S. Sarkar, and X. Hu "A New Model-Based Algebraic Solution to the Gridding Problem" ISMRM International Conference, 2002.

- 26. L. A. Shepp, and B. F. Logan "The Fourier reconstruction of a head section" IEEE Trans Nucl. Sci. 1974;NS-21:21-43
- 27. R. V. de Walle, H. H. Barrett, K. J. MyersM. I. Altbach, B. Sesplanques, A. F. Gmitro, J. Cornelis, and I. Lemahieu, "Reconstruction of MR Images from Data Acquired on a General Nonregular Grid by Pseudoinverse Calculation," IEEE Trans. On Medical Imaging, vol. 19, no. 12, Dec. 2000.
- 28. G. H. Golub, and C. F. Van Loan, "Matrix Computations," The Johns Hopkins University Press 2nd edition.
- R.A. Zoroofi, Y. Sato, S. Tamura, and H. Naito, "MRI artifact cancellation due to rigid motion in the imaging plane," *IEEE Trans. Med. Imag.* 15, no. 6, pp. 768-784, 1996.
- M.L. Wood and R.M. Henkelman, "Suppression of respiratory motion artifacts in magnetic resonance imaging," *Med. Phys.* 13, no. 6, pp. 794-805, 1986.
- B. Madore and R.M. Henkelman, "A new way of averaging with applications to MRI," *Med. Phys.* 23, no. 1, pp. 109-113, 1996.
- 32. P.M. Pattany, J.J. Phillips, L.C. Chiu, J.D. Lipcamon, J.L. Duerk, J.M. McNally, and Surya N. Mohapatra, "Motion artifact suppression technique (MAST) for MR imaging," *J. Comput. Assist. Tomogr.* **11**, no. 3, pp. 369-377, 1987.
- 33. E.M. Haacke and G.W. Lenz, "Improving MR image quality in the presence of motion by using rephasing gradients," *AJR* **148**, pp. 1251-1258, 1987.

- 34. J.L. Durek and P.M. Pattany, "Analysis of imaging axes significance in motion artifact suppression technique (MAST): MRI of turbulent flow and motion," *Magn. Reson. Med.* 7, pp. 251-263, 1989.
- X. Hu, T.H. Le, T. Parrish, and P. Erhard, "Retrospective estimation and correction of physiological fluctuation in functional MRI," *Magn. Reson. Med.* 34, pp. 201-212, 1995.
- 36. Y.M. Kadah, K. Heberlein, and X. Hu, "Floating navigator echo for in-plane translational motion estimation," *ISMRM 10 th Scientific Meeting*, Honolulu, p. 2309, May 2002.
- 37. R.L. Ehman and J.P. Felmlee, "Adaptive technique for high-definition MR imaging of moving structures," *Radiology* **173**, vol. 173, pp. 255-263, 1989.
- 38. L. Tang, M. Ohya, Y. Sato, S. Tamura, H. Naito, K. Harada, and T. Kozuka, "Artifact cancellation in MRI due to phase encoding axis motion," *Systems and Computers in Japan* 26, no. 1, pp. 88-97, 1995.
- 39. T. Mitsa, K.J. Parker, W.S. Smith, A.M. Tekalp, and J. Szumowski, "Correction of periodic motion artifacts along the slice selection axis in MRI," *IEEE Trans. Med. Imag.* 9, no. 3, pp. 310-317, 1991.
- M. Hedley and H. Yan, "Suppression of slice selection axis motion artifacts in MRI," *IEEE Trans. Med. Imag.* 11, no. 2, pp. 233-237, 1992.
- M. Hedley, H. Yan, and D. Rosenfeld, "An improved algorithm for 2-D translational motion artifact correction," *IEEE Trans. Med. Imag.* 10, no. 4, pp. 548-553, 1991.
- 42. R. Steagall, S. Amartur, and E.M. Haacke, "Correcting motion artifacts via a fast, iterative, POCS procedure," *Proc. SMR Eighth Annual Meeting*, 1990.

- 43. M. Hedley, H. Yan, and D. Rosenfeld, "A modified Gerchberg-Saxton algorithm for one-dimensional motion artifact cancellation in MRI," *IEEE Trans. Sig. Proc.* 39, no. 6, pp. 1428-1433, 1991.
- 44. M. Hedley, H. Yan, and D. Rosenfeld, "Motion artifact correction in MRI using generalized projections," *IEEE Trans. Med. Imag.* 10, no. 1, pp. 40-46, 1991
- 45. J.P. Felmlee, R.L. Ehman, S.J. Riederer, and H.W. Korin, "Adaptive motion compensation in MR imaging without use of navigator echoes," *Radiology* 179, pp. 139-142, 1991.
- 46. T.S. Sachs, C.H. Meyer, P. Irarrazabal, B.S. Hu, D.G. Nishimura, and A. Macovski, "The diminishing variance algorithm for real-time reduction of motion artifacts in MRI," *Magn. Reson. Med.* 34, pp. 412-422, 1995.
- H.W. Korin, F. Farzaneh, R.C. Wright, and S.J. Riederer, "Compensation for effects of linear motion in MR imaging," *Magn. Reson. Med.* 12, pp. 99-113, 1989.
- 48. R.A. Zoroofi, Y. Sato, S. Tamura, H. Naito, and L. Tang, "An improved method for MRI artifact correction due to translational motion in the imaging plane," *IEEE Trans. Med. Imag.* 14, no. 3, pp. 471-479, 1995.
- J. G. Pipe, "Motion Correction With PROPELLER MRI: Application to Head Motion and Free-Breathing Cardiac Imaging," Mag Reson Med 1999;42:963– 969.
- 50. C. C. Lee, R. C. Grimm, A. Manduca, J. P. Felmlee, R. L. Ehman, S. J. Riederer, and C. R. Jack "A Prospective Approach to Correct for Inter-Image Head Rotation in FMRI," Mag Reson Med 1998;39:234–243.

APPENDIX

CONJUGATE GRADIENT METHOD

There are many techniques for solving systems of linear equations, i.e., solving for x in Ax = b. It is often the case that the system is sparse. The Conjugate Gradient (CG) method is suitable for solving any linear system where the coefficient matrix A is both symmetric and positive definite. A matrix 'A' is positive definite if $\langle x, Ax \rangle$ is greater than zero for all nonzero vectors x. This condition is equivalent to all the eigenvalues of A being positive. The Conjugate Gradient method is often used for sparse systems, because each iteration requires only a single matrix-vector multiplication operation. In fact, a "matrix free" formulation does not even require that you actually have A, but only that you have a function for computing the product of A and a vector, say v.

Roughly speaking, CG is an iterative minimization procedure for the equation

$$\Phi(\mathbf{x}) = \frac{1}{2}\mathbf{x}^{\mathrm{T}}\mathbf{A}\mathbf{x} - \mathbf{x}^{\mathrm{T}}\mathbf{b}$$
(A.1)

The minimization is performed a long of A-conjugate directions. A sketch of the CG algorithm:

- 1. x = initial guess for solution of Ax=b
- 2. r = b Ax = residual, to be made small
- 3. p = r = initial "search direction"
- 4. do while (new_r , new_r) not small

- v = Ap ... matrix-vector multiply
- a = (r, r) / (p, v) ... dot product
- $x = x + a^*p$... updated approximate solution
- r_new = r a*v ... update the residual
- $g = (r_new, r_new) / (r, r)$
- $p = r_new + g^*p$... update search direction
- $r = r_new$

end do

CG maintains 3 vectors at each step, the approximate solution x, its residual r=Ax-b, and a search direction p, which is also called a conjugate gradient. At each step x is improved by searching for a better solution in the direction p, yielding an improved solution x+a*p. This direction p is called a gradient because we are in fact doing gradient descent on a certain measure of the error (namely sqrt(r, A^{-1} r)). The directions p_i and p_j from steps i and j of the algorithm are called conjugate, or more precisely A-conjugate, because they satisfy (p_i , A p_j) = 0 if $i \neq j$. One can also show that after i iterations x_i is the "optimal" solution among all possible linear combinations of the form:

$$a_0 x + a_1 (Ax) + a_2 (A^2 x) + a_3 (A^3 x) + \dots + a_i (A^i x)$$
 (A.2)

For most matrices, the majority of work is in the sparse matrix-vector multiplication v=Ap in the first step. Operations in CG are also easy to parallelize. The rate of convergence of CG depends on the condition number of A. The condition number is ratio of the largest to the smallest eigenvalue of A. A roughly equivalent quantity is $||A||^* ||A^{-1}||$ where the norm of a matrix is the magnitude of the largest entry. The larger the condition number, the slower the convergence. One can show that the number of CG iterations required to reduce the error by a constant g<1 is proportional to the square root of the condition number. One can speed up convergence by "preconditioning" at an intermediate stage of the calculatin, solving a related system Mz=q, where M is an approximate inverse of A and easy to invert. Choosing a good preconditioner is something of an art.