Parallel Magnetic Resonance Imaging Reconstruction
Doctoral Thesis

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Thesis Advisor: Dr. Ing. Jan Kybic

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Reconstruction

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Thesis Advisor
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Abstract

The acquisition speed of magnetic resonance imaging (MRI) is an important issue. Increasing the acquisition speed shortens the total patient examination time, it reduces motion artifacts and increases the frame rate of dynamic MRI. Parallel MRI is a way to use multiple receiver coils with distinct spatial sensitivities to increase the MRI acquisition speed. The acquisition is speeded up by undersampling the $k$-space in the phase-encoding direction. The resulting data loss and consequent aliasing is compensated for by the use of additional information obtained from several receiver coils.

In this thesis, we summarize the state-of-the-art in parallel MRI area. We also provide the theoretical background of MRI because full understanding of the principles behind parallel MRI is needed to understand its further extension. The main contribution of this thesis is a novel parallel MRI method. Our method takes advantage of the smoothness of the reconstruction transformation in space. B-spline functions are used to approximate the reconstruction transformation. This reduces the number of the reconstruction parameters and makes the method more robust especially in areas with low signal-to-noise ratio. The B-spline coefficients are estimated by minimizing the total expected reconstruction error.

We compare our new method theoretically and experimentally with two commercially available methods – SENSE and GRAPPA. The experiments were performed on simulated, phantom and in-vivo images. We show that our method outperforms the SENSE and GRAPPA reconstruction methods on a considerable number of input images and reaches the same quality on the rest.
Snímací rychlost je důležitý aspekt zobrazování pomocí magnetické rezonance (MRI). Zvýšením snímací rychlosti dosáhneme zkrácení celkové doby vyšetření, zmírníme pohybové artefakty či zvýšíme vzorkovací frekvence u dynamické MRI. Paralelní MRI je způsob jak využít několika přijímacích cívek s různou prostorovou citlivostí ke zrychlení snímnání. Snímnání je zrychleno podvzorkováním k-prostoru ve směru fázového kódování. Tím způsobená ztráta dat a vzniklé aliasing jsou kompenzovány za použití informací získaných z několika přijímacích cívek.

V této disertační práci popisujeme současný stav vývoje metod pro paralelní MRI. Vysvětlujeme zde základní principy MRI, jejichž znalost je nutná pro plné porozumění paralelní MRI. Hlavním přínosem této disertační práci je představení nové metody pro paralelní MRI. Naše metoda využívá hladkosti rekonstrukční transformace v prostoru a aproximuje rekonstrukční transformaci pomocí B-spline funkci. Tím se sníží počet parametrů rekonstrukce a metoda se stane více robustní zejména v oblastech s nízkým poměrem signálu k šumu. B-spline koeficienty jsou pak stanoveny minimalizováním celkové očekávané chyby.

Naši metodu porovnáváme teoreticky i experimentálně se dvěma komerčně používanými metodami (SENSE a GRAPPA) na simulovaných, umělých a in-vivo datech. Na výsledcích ukazujeme, že naše metoda předčí metody SENSE a GRAPPA na významné části testovaných dat a dosahuje stejné kvality na zbytek.
Acknowledgments

My grateful thanks go to my thesis advisor Dr. Jan Kybic, who led me during my research on the thesis. His advice, ideas and support considerably helped me during my research and writing of this thesis.

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Contents

List of abbreviations xi

1. Introduction 1

2. Theoretical background 3
   2.1. Nuclear Magnetic Resonance .................................................. 3
       2.1.1. Nuclei behavior ......................................................... 3
       2.1.2. Net magnetization ...................................................... 5
       2.1.3. Excitation by a radio-frequency pulse ................................ 7
       2.1.4. Nuclear magnetic resonance signal ................................... 8
       2.2. Magnetic Resonance Imaging .............................................. 10
           2.2.1. Gradient fields ....................................................... 11
           2.2.2. The Bloch equation ................................................... 12
           2.2.3. Slice selection ....................................................... 12
           2.2.4. Fourier imaging ....................................................... 12
           2.2.5. Spin echo imaging sequence ......................................... 14
           2.2.6. Signal equation ....................................................... 16
           2.2.7. Field of view ........................................................ 17
           2.2.8. Image contrast ........................................................ 18
           2.2.9. Coil array .............................................................. 19
           2.2.10. Aliasing ............................................................... 19

3. Problem formulation 23
   3.1. Reconstruction ............................................................... 23
   3.2. Estimation ................................................................. 23

4. State of the art 25
   4.1. Motivation ................................................................. 25
   4.2. History ................................................................. 25
   4.3. Coil sensitivities .......................................................... 26
   4.4. SMASH ................................................................. 27
       4.4.1. Original SMASH ....................................................... 27
       4.4.2. Auto calibration ...................................................... 29
       4.4.3. GRAPPA ............................................................... 30
   4.5. SENSE ................................................................. 33
       4.5.1. Cartesian SENSE ..................................................... 34
       4.5.2. Iterative solution .................................................... 36
       4.5.3. Coil sensitivity extraction .......................................... 37
   4.6. SPACE-RIP ............................................................... 37
   4.7. PILS ................................................................. 38
   4.8. PARS ................................................................. 40
   4.9. Applications .............................................................. 41
4.9.1. Elimination of motion artifacts ........................................ 41
4.9.2. CAIPRINHA ........................................ 41
4.9.3. UNFOLD ........................................... 42
4.9.4. Medical applications ............................................ 43

5. Parallel MRI reconstruction using B-spline Approximation .......... 45
5.1. Notation ........................................................................ 45
5.2. Reconstruction ............................................................... 46
5.2.1. B-spline approximation ................................................ 46
5.3. Simple estimation ............................................................ 48
5.4. Perfect reconstruction conditions ..................................... 50
5.4.1. Justification of the perfect reconstruction conditions .......... 51
5.4.2. Reconstruction error ..................................................... 52
5.5. Acquisition noise ............................................................. 53
5.5.1. Noise in MRI images .................................................... 53
5.5.2. Noise in the estimation .................................................. 55
5.5.3. Noise in the reconstruction ............................................. 57
5.5.4. Error criterion .............................................................. 58
5.5.5. Efficient implementation .............................................. 59
5.6. Choice of reference images ............................................... 61
5.6.1. Variable density scan images ........................................ 62
5.6.2. Reconstruction using variable-density scans ..................... 65
5.7. Continuous error criterion .................................................. 65
5.7.1. Continuous image representation ..................................... 65
5.7.2. Continuous error .......................................................... 66

6. Theoretical comparison ......................................................... 71
6.1. Comparison with SENSE ................................................... 71
6.2. GRAPPA ................................................................. 72
6.2.1. Comparison of basis functions ....................................... 75

7. Experiments ........................................................................ 77
7.1. Data .............................................................................. 77
7.1.1. Phantom images ........................................................... 77
7.1.2. In-vivo images ............................................................. 77
7.1.3. Simulated images .......................................................... 81
7.2. Reconstruction quality ........................................................ 81
7.3. PROBER parameters ......................................................... 82
7.3.1. Estimation grid-size ....................................................... 82
7.3.2. Number of B-splines ...................................................... 83
7.3.3. Choice of reference images .......................................... 86
7.3.4. Using the k-space center ............................................... 86
7.3.5. Parameter λ ................................................................. 86
7.4. PROBER versions .............................................................. 90
7.4.1. Perfect reconstruction conditions ................................... 90
7.4.2. Discrete and continuous error criterion ................................ 93
7.5. Experimental comparison of PROBER, SENSE, and GRAPPA .......... 98
7.5.1. Simulated images .......................................................... 99
7.5.2. Real images ............................................................... 107
7.5.3. Speed .............................................. 112

8. Conclusions ........................................... 115

A. Programs .............................................. 119
   A.1. Directory structure ................................. 119
   A.2. How to run ........................................ 119
      A.2.1. Dataset parameters ........................... 119
      A.2.2. PROBER parameters ............................ 120
   A.3. Input data ......................................... 120
## List of abbreviations

<table>
<thead>
<tr>
<th>Acronym</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>BOLD MRI</td>
<td>blood oxygen-level dependent MRI</td>
</tr>
<tr>
<td>CAIPIRINHA</td>
<td>controlled aliasing in parallel imaging results in higher acceleration</td>
</tr>
<tr>
<td>EPI</td>
<td>echo planar imaging</td>
</tr>
<tr>
<td>FID</td>
<td>free induction decay</td>
</tr>
<tr>
<td>fMRI</td>
<td>functional MRI</td>
</tr>
<tr>
<td>FOV</td>
<td>field of view</td>
</tr>
<tr>
<td>GRAPPA</td>
<td>generalized autocalibrating partially parallel acquisitions</td>
</tr>
<tr>
<td>mod</td>
<td>modulo</td>
</tr>
<tr>
<td>MR</td>
<td>magnetic resonance</td>
</tr>
<tr>
<td>MRI</td>
<td>magnetic resonance imaging</td>
</tr>
<tr>
<td>NMR</td>
<td>nuclear magnetic resonance</td>
</tr>
<tr>
<td>PARS</td>
<td>parallel magnetic resonance imaging with adaptive radius in k-space</td>
</tr>
<tr>
<td>PILS</td>
<td>partially parallel imaging with localized sensitivities</td>
</tr>
<tr>
<td>PROBER</td>
<td>parallel MRI reconstruction using B-spline approximation</td>
</tr>
<tr>
<td>RF</td>
<td>radio frequency</td>
</tr>
<tr>
<td>SENSE</td>
<td>sensitivity encoding (a parallel MRI method)</td>
</tr>
<tr>
<td>SMASH</td>
<td>simultaneous acquisition of spatial harmonics</td>
</tr>
<tr>
<td>SNR</td>
<td>signal-to-noise ratio</td>
</tr>
<tr>
<td>SoS</td>
<td>sum of squares</td>
</tr>
<tr>
<td>SPACE-RIP</td>
<td>sensitivity profiles from an array of coils for encoding and reconstruction in parallel</td>
</tr>
<tr>
<td>SVD</td>
<td>singular value decomposition</td>
</tr>
<tr>
<td>TE</td>
<td>echo time</td>
</tr>
<tr>
<td>TR</td>
<td>repetition time</td>
</tr>
<tr>
<td>UNFOLD</td>
<td>unaliasing by fourier-encoding the overlaps using the temporal dimension (a reconstruction method)</td>
</tr>
</tbody>
</table>
1. Introduction

Magnetic resonance imaging (MRI) is a relatively new field. The fundamental physical principles of nuclear magnetic resonance (NMR) were discovered independently by Felix Bloch and Edward Purcell in 1946 [7, 79]. First MR images were obtained by Paul Lauterbur in 1973 [54]. In 1975, Richard Ernst introduced an improved method of image acquisition [49] that is used until today.

In the last years, MRI became a common method for medical examination. The main advantages of MRI are that it is noninvasive, it does not use any harmful radiation, it produces truly 3D images of high-resolution with a high signal-to-noise ratio (SNR), and it offers contrast mechanisms for imaging many kinds of tissues and tissue properties which is especially useful for soft tissues.

One aspect of MRI that might still be improved is the acquisition time. For example, acquiring a 3D scan of a human head usually takes several minutes, a whole body scan might take tens of minutes. Acquiring a high-quality 2D cross sectional image of a human torso may take up to 30 seconds and must be acquired during breath-hold to avoid motion artifacts. This raises a need for speeding up of the MRI acquisition which would allow to reach a higher image quality, it would increase the number of patients examined per day and reduce the time that patients need to spend in the uncomfortably small space inside the magnet bore. High acquisition speed is also necessary for imaging of dynamic processes.

Nowadays, there are fast techniques that allow to acquire an MRI image of a 2D slice in a single excitation (e.g., echo planar imaging (EPI) [101, 94]). In these single-shot techniques, the magnitude and the switching rate of magnetic gradient fields is increased to encode the signal corresponding to a whole slice during a single excitation. This reduces the acquisition time significantly. However, the magnet strength and rate of change are limited by physical and physiological constraints which does not allow the speed to be increased much further. Moreover, single-shot methods produce images with lower SNR and more pronounced geometric distortions.

Parallel MRI is a technique that exploits the intrinsic spatial encoding of multiple receiver coils with distinct spatial sensitivities to speed up the MRI data acquisition. The increase in the data acquisition speed is achieved by sampling the imaged object more sparsely in the k-space (frequency domain). Due to this subsampling, the images are affected by aliasing. The missing information is synthesized using sensitivity encoding information from the receiver coils. Several different reconstruction algorithms have been proposed which work either in the frequency domain [90, 29, 27, 111] or in the spatial domain [78, 28, 51]. The efficiency of these method to improve the acquisition speed without significantly decreasing the reconstruction quality was proven in a number of medical applications. Nowadays, a parallel MRI reconstruction method is implemented in nearly all scanners newly supplied by the main MRI manufacturers.

\[1\]The physical principle is called NMR because it uses spin properties of the atom nuclei. However, the word nuclear was abandoned due to commercial and psychological reasons because the adjective nuclear invokes the unwanted relation to nuclear armament or nuclear power engineering in lay public. The term magnetic resonance imaging or magnetic resonance is used to point out that NMR does not produce unhealthy radiation of any kind.
1. Introduction

The aim of this thesis is to give a compact insight to the state-of-the-art of the parallel MRI including the necessary introduction to the principles of MRI. Our main contribution is a novel method for parallel MRI [71]. In this method, called PROBER, we take advantage of the linearity and smoothness of the reconstruction transformation and approximate the reconstruction transformation using B-splines. This approach reduces the number of reconstruction coefficients and makes the method more robust in the presence of noise. It also regularizes the reconstruction and makes the reconstruction less sensitive to errors in areas with low signal.

Let us now describe the structure of this thesis. The main principles of MRI as well as the technique to spatially encode the MR signal are given in Chapter 2. We also briefly describe the effect of undersampling during the acquisition and the acquisition using more receiver coils. Since the parallel MRI modifies the acquisition process, it is necessary to know the basics of MRI to fully understand how parallel MRI works. Once the basics have been covered, we formulate the problem of parallel MRI reconstruction in Chapter 3. In Chapter 4 we summarize the state-of-the-art of parallel MRI and describe the most important reconstruction methods. Our reconstruction method (PROBER) is described in Chapter 5. This chapter contains the main contribution of the thesis and we provide here the development progress of our method from the simple idea to the final implementation. We compare PROBER with two commercially available methods: SENSE [78] and GRAPPA [27]. Theoretical differences between all three methods and their possible effect on the reconstruction quality are discussed in Chapter 6. The experimental comparison of PROBER with SENSE and GRAPPA is given in Chapter 7. There, we also experimentally compare the different versions of our algorithm and observe the reconstruction quality of our method for different values of the parameters. The source code of PROBER can be found on CD attached to this thesis. A simple installation and user guide is given in Appendix A. We conclude in Chapter 8.
2. Theoretical background

This chapter describes the basic principles behind magnetic resonance imaging (MRI). Readers familiar with this topic may proceed directly to the following chapter. The basic principles of nuclear magnetic resonance (NMR), namely, spin properties and the way how to use them for NMR signal acquisition, are discussed in Section 2.1. The technique to acquire images using NMR signal is described in Section 2.2. This section also contains details about the imaging sequences and how undersampling can be used to speed up the acquisition.

2.1. Nuclear Magnetic Resonance

The principle of magnetic resonance was discovered independently by Felix Bloch and Edward Purcell in 1946 [7, 79]. Six years later, they were both awarded the Nobel prize for Physics for the discovery. Magnetic resonance uses the fact that every element with nuclear spin (as explained later) placed in an external magnetic field can be excited to a higher energy level by absorbing a photon at a specific frequency. The excited elements return back to the energy equilibrium after some time and release the absorbed energy as photons. From the emitted electromagnetic signal, we can obtain information about physical and chemical properties of the excited elements. Magnetic resonance (MR) principles are used in MR spectroscopy to study the structure of examined objects (Section 2.1.4).

Magnetic resonance can be also used to receive signal from hydrogen atoms which are the main part of a human body. Therefore, it is possible to make images of human tissue that represent the spatial arrangement of the hydrogen atoms. However in NMR, the radiofrequency (RF) excitation pulse is not selective and nor is the receiver coil. Therefore, all hydrogen atoms in the examined tissue are excited at once and the integral of the signal over the whole volume is measured. The important step from NMR to MRI is to add spatial encoding of the signal (Section 2.2). In MRI, it is possible to obtain 2D and 3D images of the imaged tissue.

Magnetic resonance imaging was first introduced in 1973 by Paul Lauterbur [54] who used back-projection for the image reconstruction (see the note in Section 2.2.4). Paul Lauterbur was awarded the Nobel price in Medicine in 2003 together with Peter Mansfield for their discoveries concerning magnetic resonance imaging. In 1975, Richard Ernst [49] introduced MRI Fourier imaging in a similar way as it is used now (see Section 2.2.4) and was awarded the Nobel price in Chemistry in 1991.

2.1.1. Nuclei behavior

Each particle in an atomic nucleus possesses a fundamental property called a spin. Spin refers to presence of angular momentum in each individual particle. Spins can be positive and negative. Spins of opposite signs cancel out. Only nuclei with a non-zero spin (nuclei with an unpaired protons or neutrons) are interesting from the NMR point of view. Such nuclei behave as small magnetic dipoles with a random orientation, see Figure 2.1. The result is
and \( \Delta \) have intensity of the external magnetic field. The anti-parallel (\( \text{in an external magnetic field} \)) state has a higher energy than the parallel state. The energy difference \( \Delta \varepsilon \) between the states is

\[
\Delta \varepsilon = \frac{h\gamma}{2\pi} |B_0| |T|, \tag{2.1}
\]

where \( \gamma \) is a gyromagnetic ratio depending on properties of the atom (for hydrogen \(^1\)H we have \( \gamma/2\pi = 42.58 \text{ MHz/T} \)), \( h \) is a Planck’s constant (\( h = 6.6 \cdot 10^{-34} \text{ Js} \)) and \( |B_0| |T| \) is intensity of the external magnetic field.

Due to this energy difference (2.1), the number of protons in the parallel (\( n_+ \)) and in the anti-parallel (\( n_- \)) state in the equilibrium differs slightly. The difference in the count is approximately 6 protons per million at room temperature. The exact ratio is given by the Boltzmann distribution law

\[
\frac{n_-}{n_+} = e^{-\Delta \varepsilon/k_b T}, \tag{2.2}
\]

where \( k_b \) is the Boltzmann constant (\( k_b = 1.38 \cdot 10^{-23} \text{ J/K} \)), \( T \) is the absolute temperature and \( \Delta \varepsilon \) is the energy difference between the states given by equation (2.1).

**Fig. 2.1.** Spin behavior in an external magnetic field. 
(a) Randomly oriented spins. (b) Spins aligned with the strong external magnetic field \( B_0 \). (c) The net magnetization vector \( M_0 \) in the equilibrium state.

Energy levels

The nuclei behavior is first studied using quantum mechanics. If a group of particles is placed in an external magnetic field \( B_0 \) (oriented in the \( z \)-direction) their spin orientation will tend to align with this magnetic field. Some spins will align parallel and some anti-parallel with respect to the orientation of the magnetic field \( B_0 \). The anti-parallel state has a higher energy than the parallel state. That the magnetization of a high number of nuclei cancels out on the average and the net magnetization is zero.

In the following text, the attention is restricted to hydrogen nuclei \(^1\)H with only one unpaired proton. This is reasonable, since in MRI we primarily focus on the hydrogen atoms. This is because living tissue consists mostly of water and fat which contain many hydrogen atoms and, therefore, approximately 63% of atoms in human body are hydrogen atoms.
Excitation

Spins can switch from the lower energy state to the higher energy state by photon absorption. The energy $E$ of the photon is related to its frequency $f$ as $E = hf$. The photon energy must precisely match the energy difference $\Delta \varepsilon$ between the two states, see equation (2.1). Only a photon with the exact frequency (called Larmor frequency or resonance frequency) causes the transition of a spin to the higher energy state. The resonance frequency $f_0$ of a spin is proportional to the intensity of the external magnetic field $B_0$ and it is derived from its energy (2.1)

$$f_0 = \frac{\gamma}{2\pi} |B_0| \text{ [Hz]}. \quad (2.3)$$

The resonance frequency of $^1\text{H}$ atoms in 1.5 T magnetic field typical for MRI is approximately 63 MHz.

2.1.2. Net magnetization

It is cumbersome to continue with the description of NMR on a microscopic scale. For this reason, we define a spin packet which is a group of spins experiencing the same magnetic field. The net magnetization vector $M_0$ describing the total equilibrium state magnetization of a spin packet is defined as a sum of magnetizations of all spins

$$|M_0| = \frac{\gamma h}{4\pi} (n_+ - n_-) \approx \frac{\gamma^2 h^2 |B_0| N_s}{16\pi^2 kT} \text{ [Am}^{-1}], \quad (2.4)$$

where $N_s$ is the number of spins in the packet [103]. The vector $M_0$ is aligned with the orientation of the main magnetic field $B_0$, see Figure 2.1. From equations (2.1), (2.2) and (2.4) we see that the magnitude of the vector $M_0$ can be increased by lowering the temperature (which is not suitable for medical purposes) or by increasing the intensity of the main magnetic field $|B_0|$ [85, 36].

When not in the equilibrium state, the net magnetization is composed of the longitudinal component $M_z$ which is aligned with the orientation of the main magnetic field $B_0$, and the transversal part $M_T$ that refers to the magnetization in the plane perpendicular to the longitudinal direction.

$T_1$ relaxation

By supplying energy at the resonance frequency (excitation), it is possible to transfer a specific number of spins from the lower energy state to the higher energy state so the longitudinal part of the net magnetization $M_z$ is lower than it was in the equilibrium state $M_z < |M_0|$. The system will gradually return to the equilibrium state with a time constant $T_1$. This effect is called the $T_1$-relaxation or the spin-lattice relaxation. It describes the decay of the $M_z$ magnetization due to the interaction with the surrounding tissue. The longitudinal component $M_z$ returns back to the equilibrium in exponential fashion with a time constant $T_1$ that is on the order of 100 – 1000 ms and is specific for every tissue [85, 36, 101]. The $z$ component $M_z(t)$ of the net magnetization vector $M_0$ at time $t$ after the excitation is

$$M_z(t) = M_z(0) + (|M_0| - M_z(0)) \left(1 - e^{-t/T_1}\right) \text{ [Am}^{-1}]$$

$$= |M_0| - (|M_0| - M_z(0))e^{-t/T_1}, \quad (2.5)$$

where $|M_0|$ is the intensity of the net magnetization vector in the equilibrium state and $T_1$ is the relaxation time in seconds.
2. Theoretical background

The proton magnetic moments are not aligned with the external magnetic field $B$ exactly but at a certain angle. It exerts a torque perpendicular on both the magnetic field $B$ and the proton magnetic moment. This causes a precessing motion of the proton magnetic moments, and subsequently of the net magnetization vectors $M$, around the $z$-axis at frequency $f$ which is equal to the Larmor frequency (2.3), see Figure 2.2.

**Precession**

The proton magnetic moments are not aligned with the external magnetic field $B$ exactly but at a certain angle. It exerts a torque perpendicular on both the magnetic field $B$ and the proton magnetic moment. This causes a precessing motion of the proton magnetic moments, and subsequently of the net magnetization vectors $M$, around the $z$-axis at frequency $f$ which is equal to the Larmor frequency (2.3), see Figure 2.2.

**Rotating frame of reference**

Let us consider a magnetization vector $M$ deflected from the $z$-axis by exciting the magnetization vector $M_0$. Let $B_0$ be an external magnetic field oriented along the $z$-axis. The vector $M$ precesses (see Section 2.1.2) around the $z$-axis at frequency $f_0$ (2.3), see Figure 2.2.

Let $[x', y', z]$ be a new rotating coordinate system called rotating frame of reference. It rotates with the frequency $f_0$ around the $z$-axis of the coordinate system $[x, y, z]$, see Figure 2.3a. In the rotating frame, the precessing vector $M$ seems to be static (see Figure 2.3b) which greatly simplifies further analysis of the vector $M$ behavior.
2.1. Nuclear Magnetic Resonance

2.1.1. Nuclear Magnetic Resonance

The transverse component $M_T$ of the magnetization\(^2\) describes the magnetization in the transverse plane

$$M_T = |\hat{x}M_{x'} + \hat{y}M_{y'}| \quad [\text{Am}^{-1}],$$

where $\hat{x}$ and $\hat{y}$ are unit vectors in the $x$ and $y$-direction. The transverse magnetization decays exponentially with a time constant $T_2$ because of the phase-coherence loss of the precessing nuclei due to spin-spin and molecular interactions. The transverse magnetization decay is characterized by the following equation

$$M_T(t) = M_T(0) e^{-t/T_2} \quad [\text{Am}^{-1}].$$

A typical $T_2$ relaxation time is 40 – 100 ms and it is always shorter than the $T_1$ time.

The second factor influencing the $T_2$ decay is the inhomogeneity of the main magnetic field caused by the susceptibility variations in the tissue. These inhomogeneities cause spins to precess at different frequencies. The time constant of the decay of the transversal magnetization caused by the inhomogeneity is called $T^{inh}_2$. The total decay time constant $T^*_2$ is $T^*_2 = 1/T_2 + 1/T^{inh}_2$ and it is often more than two times faster than the pure $T_2$ decay [101].

2.1.3. Excitation by a radio-frequency pulse

By transmitting a radio-frequency pulse (RF pulse) at the resonance frequency energy is added to the system. A correct amount of energy at the resonance frequency flips the magnetization vector $M_0$ from the longitudinal state in the $z$-direction to the transverse $xy$-plane. This is done by creating a magnetic field $B_1$ rotating around the $z$-axis in the transverse plane. This is equivalent to a magnetic field in the $x'$-direction that seems to be static in the rotating reference frame. The precession of $M_0$ due to the $B_0$ field is not visible in the rotating frame. However, the magnetization vector will start precessing around the $x'$-axis with frequency $f_1$ because of the presence of the magnetic field $B_1$, see Figure 2.4a.

We turn on the rotating magnetic field with the intensity $|B_1|$ for time $t_{90^\circ}$

$$t_{90^\circ} = \frac{1}{4f_1} = \frac{\pi}{2\gamma |B_1|} \quad [s],$$

where $f_1$ is defined as $f_0 = \gamma |B_1|$ and $\gamma$ is the gyromagnetic ratio.

The magnetic field $B_1$ which rotates around the $z$-axis at the resonance frequency $f_0$ is created by a linearly polarized field with the frequency $f_0$ oriented, for example, in the $x$-direction. Such linearly polarized field can be decomposed in two circularly polarized fields

\(^2\)Notation $M_{xy}$ is sometimes used in literature instead of $M_T$.\]
rotating in opposite directions with frequencies $f_0$. The first of the circularly polarized fields rotating at $f_0$ will appear static in the rotating frame of reference producing the desired field $B_1$. The second field will be rotating in the opposite direction with the frequency $2f_0$ in the rotating reference frame and will have a negligible effect on the spins as it is far from the resonance frequency. The linearly polarized field is created by passing an alternating current with the frequency $f_0$ through a static coil placed around the $x$-axis.

2.1.4. Nuclear magnetic resonance signal

In this section, it is shown how the principles described previously are used to measure the NMR signal. It is also shown how NMR is applied in NMR spectroscopy for analysis of chemical and physical properties of molecules.

Free induction decay

After the application of a $90^\circ$ pulse (Section 2.1.3) the magnetization vector $M$ starts precessing in the transversal $xy$-plane creating an electromagnetic field that can be detected by a receiver coil.

We assume repetitive excitation by a $90^\circ$ pulse with an interval $TR$ between the excitations. The value of the $M_z$ component is affected by the length of the $TR$ interval because of the $T_1$ relaxation effect in the previous excitation. For a short repetition time $TR$, the magnetization vector $M$ does not relax back to the equilibrium and, thus, the NMR signal is weaker and also dependent on the $T_1$ time of the imaged tissue (this is described in detail in Section 2.2.8).

The transverse magnetization after the application of the $90^\circ$ pulse is

$$M_T(0) \propto \varrho \left(1 - e^{-TR/T_1}\right) \left[\text{Am}^{-1}\right],$$

where $\varrho$ is the number of protons in the imaged volume.

After the $90^\circ$ pulse, the precessing motion of $M$ generates an alternating current in a receiver coil placed around the $x$-axis and perpendicular to the $y$-axis, see Figure 2.6. The measured signal is called free induction decay (FID). The FID signal is an exponential $T_2$
2.1. Nuclear Magnetic Resonance

Fig. 2.5. The NMR signal. The left graph shows the sinusoidal carrier wave of the NMR signal. In the right graph is the FID – the carrier wave is modulated by the $T_2^*$ decay.

Fig. 2.6. Receiving the NMR signal.

decay (Section 2.1.2) of the signal modulated by the sinusoidal carrier wave with frequency $f_0$ (as in Figure 2.5 on the right). The received signal is

$$s(t) \propto \varrho \left(1 - e^{-TR/T_1}\right) e^{-2\pi if_0 t} e^{-t/T_2^*}.$$

Quadrature detection

The quadrature detection of the NMR signal enables us to obtain the $M_x'$ and $M_y'$ components of the transversal magnetization in the rotating frame of reference from the acquired signal $s(t)$ in the static frame. A product of the received signal with the sinusoidal wave with the resonance frequency gives the $M_x'$ part of the magnetization. The $M_y'$ part is obtained as a product with a sinusoidal wave shifted in phase by $90^\circ$ relatively to the first one. Both components are low-pass filtered and the detected signal $M_T$ is then treated as a complex number with $M_x'$ as the real part and $M_y'$ as the imaginary part

$$M_T = M_x' + iM_y'$$  [Am$^{-1}$].

Spin echo

We give here the description of an often used spin-echo excitation sequence. A spin echo sequence begins with a $90^\circ$ pulse that flips the magnetization vector to the transverse plane, see Figure 2.8a. At time $TE/2$ an $180^\circ$ refocusing pulse is applied. The signal is measured at the echo time $TE$. The excitation is repeated after the repetition time $TR > TE$. The effect of the spin echo sequence is described in more details in the following paragraphs.

Following the $90^\circ$ pulse, small inhomogeneities of the main magnetic field cause the precessing frequency of the spins to vary locally, therefore, the spins begin to dephase, see Figure 2.8b. To compensate for this negative effect an $180^\circ$ refocusing pulse is applied after time $TE/2$. The $180^\circ$ pulse causes the dephasing spin vectors to flip in the transverse plane, effectively changing the sign of the phase lag for each pixel. The precession of the spins
2. Theoretical background

**Fig. 2.7.** The diagram of the spin-echo sequence.
The sequence begins with an excitation by a $90^\circ$ RF-pulse followed by an $180^\circ$ RF-pulse at the time $TE/2$. The signal is strongest at the echo time $TE$.

continues in the same direction and the spins begin to rephase, see Figure 2.8c. After $TE$, the spins are in phase again emitting the maximal signal (echo top), see Figure 2.8d and 2.7.

Spin echo compensates for the $T_{inh}^2$ effect caused by the inhomogeneities in the main magnetic field, see Section 2.1.2. Thus, at the echo time the signal decay is affected only by the pure $T_2$ effect making the magnitude of the signal higher. After the echo top, the transverse magnetization relaxes with the $T_2^*$ time constant again.

This mechanism makes the spin-echo sequence less susceptible to inhomogeneities in the main magnetic field and, thus, improves the quality of the retrieved signal. Even a tomograph with small inhomogeneities in the main magnetic field is then suitable for imaging with the spin-echo sequence. Nowadays, magnets are much more homogeneous then they used to be which makes it possible to use advanced imaging sequences with the emphasis on the speed of the acquisition without having to compensate for tissue inhomogeneities.

**NMR spectroscopy**

NMR spectroscopy is an interesting application of NMR. However, it is not directly relevant for parallel MRI, therefore, we will mention it only briefly. NMR spectroscopy is a method that uses the NMR signal to examine chemical and physical properties of a matter. An excitation pulse with a broad frequency spectrum is used to excite all spins in the examined sample. The frequency spectrum of the retrieved signal is examined. The magnitude and frequency of the measured signal gives information about the quantity and Larmor frequency of the nuclei present in the sample. This allows to precisely and noninvasively analyze the structure of any material containing nuclei with spin properties.

2.2. Magnetic Resonance Imaging

In this section, we describe the technique for spatial encoding of the NMR signal that allows us to produce MR images.
Gradient magnetic fields $\mathbf{G}$ are fields oriented along the $z$-axis and superimposed on the main magnetic field. Intensity of the gradient fields increase linearly in the given direction along the $x$, $y$ or $z$-axis. The total intensity of the magnetic field in the $z$-direction at coordinate $(x, y, z)$ is

$$ |\mathbf{B}(x, y, z)| = |\mathbf{B}_0(x, y, z)| + |\mathbf{G}(x, y, z)| = |\mathbf{B}_0(x, y, z)| + xG_x + yG_y + zG_z \quad [\text{T}] , \quad (2.9) $$

where $G_x$, $G_y$ and $G_z$ are the gradient strengths.

The gradient fields make the total magnetic field intensity position dependent. This consequently makes the resonance frequency also spatially dependent position (2.3, 2.9)

$$ f(x, y, z) = \frac{\gamma}{2\pi} |\mathbf{B}(x, y, z)| \quad [\text{Hz}] . \quad (2.10) $$

The gradient fields have intensity on the order of several $\mu$T and they are rapidly switched on and off during the acquisition in order to encode the spatial position of the NMR signal (see also Section 2.2.5).
2.2.2. The Bloch equation

The behavior of the magnetization vector $\mathbf{M}$ in time is represented by the *Bloch equation* \[101\]

$$\frac{\partial \mathbf{M}}{\partial t} = \gamma (\mathbf{M} \times \mathbf{B}) ,$$

(2.11)

where $\mathbf{B}$ is the total magnetic field consisting of the main magnetic field $\mathbf{B}_0$, the excitation pulse $\mathbf{B}_1$ and the gradient fields $\mathbf{G}$: $\mathbf{B} = \mathbf{B}_0 + \mathbf{B}_1 + \mathbf{G}$. In the following, we shall observe the vector $\mathbf{M}$ in the rotating frame, see Section 2.1.2. Therefore, the precession because of the $\mathbf{B}_0$ is not seen.

The $T_1$ relaxation, see Section 2.1.2, affects the longitudinal component of the magnetization (2.5)

$$\frac{\partial M_z(t)}{\partial t} = - \frac{M_z(t) - |M_0|}{T_1} .$$

The $T_2$ relaxation, see Section 2.1.2, affects the transversal part of the magnetization (2.7)

$$\frac{\partial M_T(t)}{\partial t} = - \frac{M_T(t)}{T_2} ,$$

where $\mathbf{M}_0$ is the magnetization vector in the equilibrium state and $M_T$ is the transversal magnetization as defined in (2.6). The behavior of the magnetization vector $\mathbf{M}$ (2.11) in the rotating reference frame including the effect of $T_1$ and $T_2$ relaxation, the excitation pulse $\mathbf{B}_1$ and the gradient fields $\mathbf{G}$ is described as \[101\]

$$\frac{\partial \mathbf{M}}{\partial t} = \begin{pmatrix} -1/T_2 & \gamma \mathbf{Gr} & -\gamma B_{1y'} \\ -\gamma \mathbf{Gr} & -1/T_2 & \gamma B_{1x'} \\ \gamma B_{1y'} & -\gamma B_{1x'} & -1/T_1 \end{pmatrix} \begin{pmatrix} M_{x'} \\ M_{y'} \\ M_z \end{pmatrix} + \begin{pmatrix} 0 \\ 0 \\ |M_0|/T_1 \end{pmatrix} ,$$

(2.12)

where $\mathbf{r}$ is a vector describing the spatial position of the measured voxels $\mathbf{r} = x\mathbf{x} + y\mathbf{y} + z\mathbf{z}$ ($\mathbf{x}$, $\mathbf{y}$ and $\mathbf{z}$ are unit vectors).

2.2.3. Slice selection

In MRI, only a single slice of the imaged tissue is excited at a time. This is done by imposing a gradient $G_z$ so that the resonance frequency of the spins becomes linearly dependent on the spatial position

$$f(z, t) = \frac{\gamma}{2\pi} (|\mathbf{B}_0| + G_z(t) \cdot z) \ [\text{Hz}] .$$

An RF-pulse with a narrow bandwidth thus excites only a thin slice of the imaged object perpendicular to the $z$-axis, see Figure 2.9. Typical slice thickness is several millimeters.

Spectrum of an ideal RF-pulse is a box function. Such pulse excites a slice with ideal sharp borders. However, a box function in Fourier domain corresponds to the sinc function with infinite duration in the time domain. In practice, an approximate RF-pulse with finite duration is used with typical duration shorter than 5 ms \[101\]. This does not significantly degrade the Fourier profile of the slice.

2.2.4. Fourier imaging

Fourier imaging was introduced in 1975 by Richard Ernst \[49\] and it is used for MR imaging until today. Principles of Fourier imaging MRI are described in the following sections.
2.2. Magnetic Resonance Imaging

The spatial position along the $x$-axis is encoded using the precessing frequency of the spins. For this reason, it is called frequency encoding. The $x$-direction is also called a read-out direction because the frequency encoding gradient is turned on during the signal read-out.

The frequency encoding gradient $G_x$ is applied during the acquisition of the signal. The precessing frequency becomes dependent on $x$

$$f(x) = \frac{\gamma}{2\pi} |B_0| + x \frac{\gamma}{2\pi} G_x \ [\text{Hz}].$$

The frequency encoded signal excluding the relaxation phenomenon is

$$s(t) \propto \int \int_{\text{slice}} \varrho(x,y) e^{-i2\pi f_x t} \ dx\ dy = \int \int_{\text{slice}} \varrho(x,y) e^{-i\gamma G_x x t} \ dx\ dy.$$  

The received signal is a sum of harmonic functions with different frequencies and amplitudes. The amplitude corresponds with the magnetization of the tissue. The frequency of the wave is related to the position on the $x$-axis, see Figure 2.10. Fourier transformation is used to analyze the signal and retrieve the magnitudes and frequencies of all harmonics present in the measured signal, see Section 2.2.6.

Phase encoding

The spatial position along the $y$-axis is phase-encoded. This is done by imposing a gradient field $nG_y$ in the direction of the $y$-axis for a short time $T_y$ before the readout where the integer $n$ changes for each acquisition. This affects the precessing frequency only for the short time when the gradient is turned on. During this time, the spins precess at slightly different frequencies. Their precessing phase is changed depending on the $y$ position by introducing a phase shift $\gamma n G_y y T_y$. The signal after the phase encoding is

$$s(n,T_y) \propto \int \int_{\text{slice}} \varrho(x,y) e^{-i\gamma n G_y y T_y} \ dx\ dy.$$  

A number of phase-encoding steps with different gradient intensity $nG_y$ has to be performed to reach desired image resolution. The details are given in Section 2.2.6.

**Fig. 2.9.** Slice selection.

A magnetic field gradient is applied in the $z$-direction. The resonance frequency becomes dependent on the $z$-coordinate. An excitation pulse with a narrow bandwidth excites only a slice of a selected width.

**Frequency encoding**
2. Theoretical background

2.2.5. Spin echo imaging sequence

In this section, the principles of Fourier MR imaging are demonstrated on the example of the spin echo imaging sequence (Section 2.1.4). The principles of the spin-echo sequence, Section 2.1.4, are extended by the spatial signal encoding using gradient fields.

Let us explain the spin echo imaging sequence according to timing diagram in Figure 2.11. First, the 90° pulse is used to flip the magnetization vector $M$ to the transversal plane. The slice selection gradient $G_z$ is switched on during the excitation in order to excite only a thin slice of the imaged object (Section 2.2.3). The slice selection gradient $G_z$ imposed in the direction of the $z$-axis causes the spins with different position on $z$-axis to precess with different frequencies. After the gradient is switched off, the spins with different $z$-coordinate are not in phase. The dephasing is compensated for by a reverse gradient (called refocusing gradient) with the total energy matching the half of the energy of the slice selection gradient $G_z$. One half of the energy of the slice selection gradient is sufficient because the spins are flipped to the transverse plane after the 90° pulse and, therefore, only the second part of the slice selection gradient causes dephasing. As a results, the slice selection gradient applied during the 90° pulse does not dephase the spins and the following equation holds

$$\int_0^{TE/2-t_p} G_z(t) \, dt = 0 ,$$

where time constant $t_p$ is the duration of the slice-selection pulse.

After the 90° impulse, the signal is phase-encoded by applying gradient in the $y$-direction, see Section 2.2.4. The 180° impulse is emitted at time $TE/2$ after the 90° pulse in order to reach the echo top (maximum signal) at time $TE$, see Figure 2.8.

The 180° pulse flips the magnetization vector in the middle of the duration of the second slice-selection gradient $G_z$ and, therefore, dephasing in the first half and rephasing in the second half of the second slice-selection gradient zeros out on the average

$$\int_{TE/2-t_p}^{TE} G_z(t) \, dt = 0 .$$

Fig. 2.10. Frequency encoding.
A model example of frequency encoding of signal in 7 voxels is shown. Protons belonging to one voxel have approximately the same resonance frequency. (a) Signal emitted by each of the 7 voxels is shown neglecting the carrying frequency. The frequency of the signal emitted by spins in each voxel depends on the spatial position of the voxel. The amplitude corresponds to the total number of spins in the voxel. (b) The acquired signal is a sum of signals from all the voxels. (c) The intensity image is obtained by Fourier transforming the received signal. It reflects the net magnetization in each voxel.
2.2. Magnetic Resonance Imaging

Fig. 2.11. The spin-echo time sequence diagram.
The diagram of the spin-echo sequence describing the usage and timings of the excitation pulses and gradient fields, see Section 2.2.5.

To minimize the dephasing effect of the read-out gradient $G_x$, a gradient with the same intensity as half of the read-out gradient is turned before the $180^\circ$ pulse so that

$$\int_{TE/2}^{TE} G_x(t) \, dt = \int_0^{TE/2} G_x(t) \, dt,$$

$$\int_0^{TE} G_x(t) \, dt = 0.$$  \hspace{1cm} (2.15)

This ensures that the spins are in phase with respect to the frequency encoding gradient at the echo time, see Figure 2.11.

Dephasing caused by the $nG_y$ gradient is intentional. The $nG_y$ gradient is turned on for time $T_y$ and the integer $n$ is changed for each excitation in order to obtain different phase-steps.

The signal is acquired during a time period $T_{acq}$ centered around the echo time $TE$ to ensure the maximum magnitude of the signal. The frequency-encoding gradient that modifies the precessing frequency according to the position on the $x$-axis is turned on during the whole acquisition process, see Section 2.2.4.

**Alternative imaging sequences**

We have selected spin-echo as an example of an imaging sequence. There are several alternative techniques as gradient echo, echo planar imaging (EPI), etc. [101]. We present only a short description of the gradient-echo and the EPI sequences since it is not in the scope of this work to describe all these techniques in details.

The gradient-echo sequence is similar to the spin-echo sequence, however, it lacks the $180^\circ$ refocusing pulse. The method is, thus, more sensitive to inhomogeneities in the main magnetic field. Shorter echo times than in spin-echo are necessary to avoid deterioration of the signal. Gradient-echo lifts the limitation to work with $90^\circ$ excitation pulses only. Smaller values of flip angle are used to reach faster imaging times.

The spin-echo and gradient-echo acquisition times are long because we have to wait for the system to return to equilibrium between the subsequent phase-encoding steps (long repetition...
2. Theoretical background

This issue is addressed by creating more echoes during a single excitation. By effectively controlling the gradients, the whole image can be acquired during a single excitation. EPI is one of such single-shot imaging sequences. EPI acquisition times are many times faster than for spin-echo (on the order of 100 ms). The disadvantage of EPI is its high susceptibility to main magnetic field inhomogeneities and resulting image distortion.

2.2.6. Signal equation

The total transversal magnetization $M_T$ is represented as a complex number using $M_x'$ and $M_y'$ as $M_T = M_x' + iM_y'$, where $i$ is the complex unit. The complex signal $s(t)$ is acquired using quadrature detection, see Section 2.1.4. The signal is obtained by integrating the Bloch equation (2.12)

$$s(t) \propto M_T(0) e^{-i\gamma r \int_0^t G(t') dt'} e^{-t/T_2},$$

(2.16)

where $r$ is the position vector.

Let $m(x, y)$ be magnetization on coordinates $(x, y)$ immediately after the excitation. The total received signal $s(t)$ corresponds to the integral of the magnetization over the whole excited slice [101]. The signal $s(t)$ neglecting the relaxation phenomenon is

$$s(t) = \int \int_{x,y} m(x, y) e^{-i\gamma r \int_0^t G(t') dt'} dx dy$$

$$= \int \int_{x,y} m(x, y) e^{-i\theta(t, r)} dx dy,$$  

(2.17)

where $\theta(t, r) = \gamma r \int_0^t G(t') dt'$ is the spin phase. For simplicity, we assume that the RF-pulses have zero duration and, thus, they have no effect on the precessing phase. The phase at time $t_a = t - TE$ ($t_a$ is relative time after the echo time) is

$$\theta(t_a, r) = \gamma r \int_0^{TE} G(t') dt' + \gamma r \int_{TE}^{TE + t_a} G(t') dt'$$

$$= -\gamma z \int_0^{TE/2} G_z(t') dt' - \gamma y \int_0^{TE/2} G_y(t') dt' - \gamma x \int_0^{TE/2} G_x(t') dt'$$

$$+ \gamma z \int_{TE/2}^{TE} G_z(t') dt' + \gamma x \int_{TE/2}^{TE} G_x(t') dt' + \gamma r \int_{TE}^{TE + t_a} G(t') dt'.$$  

(2.18)

Note that the first three terms describing the gradients have negative sign. This is because of the 180° flip that reverts the phase $\theta$ of precessing, see Figure 2.11. The equation (2.18) can be simplified according to the properties of the spin-echo sequence, see equations (2.13, 2.14, 2.15). The phase $\theta(t_a, r)$ at time $t_a$ then is

$$\theta(t_a, r) = -\gamma y \int_0^{TE/2} G_y(t') dt' + \gamma r \int_{TE}^{TE + t_a} G(t') dt'.$$  

(2.19)

The signal is measured during the time period $T_{acq}$ around the echo top (i.e., the interval $-T_{acq}/2 < t_a < T_{acq}/2$). In this time span, the slice-selection $G_z$ and phase-encoding $G_y$
2.2. Magnetic Resonance Imaging

Gradients are off. Only the frequency encoding gradient $G_x$ is active. The phase $\theta(t_a, r)$ is therefore

$$
\theta(t_a, r) = -\gamma n G_y(t) + \gamma r \int_{TE}^{TE+t_a} G(t') dt'
$$

Assuming rectangular gradient pulses, gives:

$$
\theta(t_a, r) = -\gamma n G_y T_y + \gamma x G_x t_a,
$$

where $T_y$ is the duration of the phase-encoding gradient. From (2.17), the measured signal is [101]

$$
s(t_a, n) = \int \int x, y m(x, y) e^{-i(k_x x + k_y y)} dx dy,
$$

where

$$
k_y = -\gamma n G_y T_y,
$$

$$
k_x = \gamma G_x t_a.
$$

The values of $k_y$ and $k_x$ are functions of the time $t_a$ and of the number of phase-encoding steps $n$. The measured signal $s(t_a, n)$ can, therefore, be written as a function $s(k_x, k_y)$. The domain of $s$ is the $k_x k_y$-plane which is referred to as the $k$-space. The values of magnetization $m(x, y)$ (spatial domain) can be obtained from the measured values $s(k_x, k_y)$ (k-space domain) (2.21) by performing an inverse Fourier transformation

$$
m(x, y) = \frac{1}{2\pi} \int \int k_x, k_y s(k_x, k_y) e^{i(k_x x + k_y y)} dk_x dk_y.
$$

In practice, we obtain k-space values of $s(k_x, k_y)$ at discrete grid by sampling the signal $s(k_x, k_y)$ at appropriate time intervals $t_s$ and for appropriate phase-encoding gradients $n G_y$ with $n = -Y/2, \ldots, Y/2$. The discrete time-domain image $S$ is obtained as a discrete inverse Fourier transform

$$
S(x, y) = \frac{1}{XY} \sum_{k_x = -X/2}^{X/2} \sum_{k_y = -Y/2}^{Y/2} s(k_x, k_y) e^{i(k_x x + k_y y)},
$$

where $X$ is the number of the sampling steps ($T_{acq} = t_s X$).

2.2.7. Field of view

The field of view (FOV) refers to the part of the slice that is imaged. The FOV is influenced by the strengths of the magnetic gradients, their durations and the acquisition time $T_{acq}$.

Values of the real object $m(x, y)$ are represented in a harmonic basis (2.21) with wavelength $\lambda = 2\pi/k_x$. The smallest step in $k$-space $\Delta k_x = \gamma G_x t_s$ determines the largest wavelength and the size of the field-of-view (FOV)

$$
\text{FOV}_x = \frac{2\pi}{\Delta k_x} = \frac{2\pi}{\gamma G_x t_s},
$$

$$
\text{FOV}_y = \frac{2\pi}{\Delta k_y} = \frac{2\pi}{\gamma G_y T_y}.
$$

17
2. Theoretical background

Fig. 2.12. The $k$-space trajectory of the spin echo sequence.
The magnetization vector is flipped from point $0$. The phase-encoding process moves it to the point $A$. The $180^\circ$ flip moves it to the point $B$. The trajectory from $B$ to $C$ represents the read-out process, where $X$ samples are acquired with a sampling time $t_s$.

Fig. 2.13. Fold-over artifact.
An image of a human head. The FOV was set too small for the head to fit inside. The fold-over artifact is visible on the right side of the image – the nose is overlapping over the back side of the head.

It is important to set the FOV to cover the whole imaged object. The encoding function is periodic and, thus, parts of the imaged object outside of the FOV are misinterpreted by aliasing as being inside the FOV. This effect is called the fold-over artifact and it is described in details in Section 2.2.10. See Figure 2.13 for the illustration of the phenomenon.

2.2.8. Image contrast

MRI is a very versatile technique allowing to display various features of the imaged tissue and to tailored to a specific aims of the examination (emphasize contrast agents, tumors, brain structures, etc.). This is called image contrast and imaging sequences allow to acquire images with different properties contributing to the contrast in the acquired image. In Section 2.2.6, we have neglected the effect of relaxation and the retrieved signal was proportional to the net magnetization in each voxel, i.e., to the proton density.

The proton density is not the only one tissue property that can be displayed. Tissues differ also in $T_1$ and $T_2$ times, see Sections 2.1.2 and 2.1.2. By varying the sequence parameters, the echo time $TE$ and the repetition time $TR$, it is possible to emphasize various properties of the imaged tissue.

The main contrast settings are as follows:

- *Proton density* – The RF signal is measured at time $TE$ after the excitation. The
magnitude of the signal is proportional to $e^{-TE/T_2}$ because of $T_2$ relaxation, see Section 2.1.2. For echo time $TE \ll T_2$, the exponential term $e^{-TE/T_2}$ is nearly 1 for all tissues, thus, the $T_2$ differences between tissues is not visible in the image. After the excitation, the $z$ part of the magnetization relaxes back to the equilibrium state with a time constant $T_1$ (2.5). This affects the magnitude of the transverse magnetization $M_T$ in the subsequent excitation as a magnetization vector with smaller magnitude is flipped to the transversal plane. By setting $TE \ll T_2$ and $T_1 \ll TR$ the relaxation phenomenon does not affect the signal intensity and the MRI image displays only the proton density of the tissue.

- **$T_1$ weighting** – If the repetition time $TR$ is short compared to $T_1$ then the $M_z$ magnetization does not relax back to the equilibrium state completely and the signal is weaker in the subsequent excitations. Assuming a series of $90^\circ$ pulses, the intensity of the magnetization shortly after the excitation is

$$M_T = |M_0|(1 - e^{-TR/T_1}).$$

By setting $TR \ll T_1$ the magnitude of the signal becomes dependent on the $T_1$ time and the image becomes $T_1$ weighted.

- **$T_2$ weighting** – The variance in $T_2$ times among tissues is emphasized by setting $TE \gg T_2$. The factor $e^{-TE/T_2}$ and subsequently also the measured signal (2.16) becomes dependent on the $T_2$ time and the images become $T_2$ weighted (i.e., the difference in $T_2$ times in the imaged tissue is emphasized).

The effects of the $T_1$ and $T_2$ weighting can be combined to produce images that are both $T_1$ and $T_2$ weighted.

### 2.2.9. Coil array

In classical MRI, a single receiver coil with an approximately homogeneous spatial sensitivity is used (a body coil). In parallel MRI, the signal is acquired using an array of $L$ receiver coils with distinct spatial sensitivities (coil array) [83]. This brings an additional information about the spatial position of the received signal. For multiple-channel receiver, all coils work in parallel and, thus, the acquisition time remains the same when using array of coils as it is when using a single coil.

Let us neglect sensitivity inhomogeneities in the body coil and noise in the receivers. The image $S_l$ retrieved by the $l$-th receiver from the coil array is related to the body-coil image $S$ as

$$S_l(x, y) = S(x, y)C_l(x, y),$$

(2.26)

where $C_l(x, y)$ is the sensitivity of the $l$-th coil and $S(x, y)$ is the image retrieved by the homogeneous-sensitivity coil, see Figure 2.14.

### 2.2.10. Aliasing

In parallel MRI, the distance between the phase-encoding lines is increased by an acceleration factor $M$. The number of phase-encoding steps $Y$ is reduced but the maximum gradient intensity $YG_y$ remains the same. This reduces the FOV and so causes aliasing in the image. The consequences of skipping every $M$-th line in the phase-encoding direction are shown in Figure 2.15.
2. Theoretical background

a) A body coil image.

b) An array-coil image.

c) Another array-coil image.

**Fig. 2.14.** Different receiver coils.
Images of a vessel phantom acquired by coils with different spatial sensitivities are shown. The coil in the image (a) has almost homogeneous sensitivity. Spatially localized sensitivity is clearly visible in the images (b) and (c). Note that the array-coil images (b) and (c) are less noisy than the body coil image (a). This is because the smaller array coils usually have a higher signal-to-noise ratio (SNR).
This phenomenon is explained as follows. The \( k \)-space image \( s^A \) retrieved with an acceleration factor \( M \) is identical to the complete \( k \)-space image \( s \) except that only every \( M \)-th phase-encoding line is retrieved. The superscript \( A \) in \( s^A \) is to identify that the image \( s \) was acquired by the accelerated acquisition and so contains aliasing. Since the 2D Fourier transformation is separable, the FOV is reduced only in the phase-encoding direction. Thus, we can perform an inverse Fourier transformation in the read-out direction in advance to simplify the equations. The aliased image \( S^A \) retrieved with an acceleration factor \( M \) is an inverse Fourier transformation of \( s^A \) in the \( y \)-direction (2.24) \[91]

\[
S^A(x, y) = \text{DFT}^{-1}_y \{ s^A(x, k_y) \}
\]

\[
= \frac{M}{Y} \sum_{k_y=0,M,2M,...}^{Y-M} s(x, k_y) e^{ik_y y} .
\]

Note that every \( M \)-th line is taken into account. The image \( s \) is transformed back to the image-domain

\[
S^A(x, y) = \frac{M}{Y} \sum_{k_y=0,M,2M,...}^{Y-M} e^{ik_y y} \sum_{y'=0}^{Y-1} S(x, y') e^{-ik_y y'}
\]

\[
= \frac{M}{Y} \sum_{y'=0}^{Y-1} S(x, y') \sum_{k_y=0,M,2M,...}^{Y-M} e^{ik_y y} e^{-ik_y y'}
\]

\[
= \frac{M}{Y} \sum_{y'=0}^{Y-1} S(x, y') \sum_{k_y=0,1,2,...}^{Y/M-1} e^{ik_y y} e^{-ik_y y'} .
\]

(2.27)

The functions \( e^{ik_y y} \) and \( e^{-ik_y y'} \) are orthogonal and the sum over \( k_y \) for \( M = 1 \) produces zero for all \( y \neq y' \). For simplicity, we assume that the fraction \( \frac{Y}{M} \) is integer. For \( M > 1 \) the exponential functions are summed to a sum of \( M \) Kronecker delta functions in an aliasing equation,

\[
S^A(x, y) = \sum_{y'=0}^{Y-1} \sum_{m=0}^{M-1} \delta(y', y \mod \frac{Y}{M} + m \frac{Y}{M}) S(x, y')
\]

\[
= \sum_{m=0}^{M-1} S(x, y \mod \frac{Y}{M} + m \frac{Y}{M}) . \quad (2.27)
\]

Each value in the aliased image \( S^A \) is a superposition of \( M \) values from the complete image.
2. Theoretical background

2.15. Aliasing.
The image (a) has a full FOV. The phase-encoding sampling density is reduced by a factor (b) 2, (c) 3 and (d) 4. This causes aliasing that is visible as a “fold-over” or a “wrap-around” effect in images (b), (c) and (d).
3. Problem formulation

Parallel MRI is a way to use multiple receiver coils with distinct spatial sensitivities to speed up the acquisition process, see Section 2.2.9. The factor determining the MRI acquisition time is the number of phase-encoding steps. This is because each phase-encoding step is applied in a single excitation and the time between subsequent excitations is specified by the repetition time $TR$.

In parallel MRI, the acquisition time is decreased $M$-times by reducing the number of phase-encoding steps $M$-times. Since the total $k$-space coverage is maintained, this causes aliasing in the image domain, see Section 2.2.10. The decrease of the data amount per coil is compensated by the use of multiple receiver coils with distinct spatial sensitivities. This brings additional information about the spatial position of the signal. The task of parallel MRI is to reconstruct an unaliased image from a set of aliased images using the sensitivity information of the used coils.

The whole process is, in principle, divided into two consecutive steps. First, the reconstruction transformation is estimated using sensitivity information extracted from unaliased reference images (unaliased array-coil images and homogeneous-sensitivity image). In the second step, the known reconstruction transformation is applied on the input images (a set of array-coil images with aliasing). The reconstruction process is explained first because it determines the estimation phase.

3.1. Reconstruction

A series of $L$ aliased images $S_l^A$ with given acceleration factor $M$ is retrieved by the coil array as the input for the reconstruction step. The images $S_l^A$ ($l = 1, \ldots, L$) are modulated by the sensitivity function of the array coils (2.26) and they also contain aliasing (2.27)

$$S_l^A(x, y) = \sum_{m=0}^{M-1} S(x, y \text{ mod } \frac{Y}{M} + m \frac{Y}{M})C_l(x, y \text{ mod } \frac{Y}{M} + m \frac{Y}{M}) ,$$  \hspace{1cm} (3.1)

where $S$ stands for an ideal image acquired by a homogeneous sensitivity coil.

In the reconstruction step, the input images $S_l^A$ are used to obtain an unaliased image $\hat{S}$ using the reconstruction transformation $R$

$$R\{S_l^A(x, y)\} = \hat{S}(x, y) .$$  \hspace{1cm} (3.2)

The aim is to find the reconstruction operator $R$ to make the reconstructed image $\hat{S}$ as close to the ideal image $S$ as possible.

3.2. Estimation

A set of $L$ unaliased array-coil images $S_l$ and an unaliased ideal image $S$ are acquired in the estimation step. The ideal image $S$ is acquired using a body-coil that has an approximately homogeneous sensitivity. Alternatively, it is approximated using the unaliased images $S_l$. The
Problem formulation

Reference images $S_l$ and $S$ contain enough information to describe the encoding process, see Equation (2.27). These images are used to calibrate the method and to find the reconstruction transformation $R$. The reconstruction quality criterion for the input images $S_{lA}^A$ (3.2) is the similarity of the reconstructed image $\hat{S}$ to the ideal image $S$ (2.27).

The unaliased images used for the estimation do not necessarily show the same object as the input images with aliasing. However, we assume that the coil configuration (values of the sensitivities $C_l$) does not change between the estimation and the reconstruction step. It is also possible to avoid this restriction by simultaneously acquiring low-resolution unaliased images used for the estimation and high-resolution aliased images used for the reconstruction.

The main task of parallel imaging is to speed up the acquisition process. We have to bear in mind that the parallel imaging reconstruction is computationally more demanding than Fourier transformation used in normal imaging. The proposed algorithm, therefore, should be designed considering also the reconstruction speed. The speed is crucial especially in the case when there is a need to interact on-line with the acquisition process or observe the images shortly after the acquisition.
4. State of the art

This chapter starts with the motivation and the history of the parallel MRI imaging (see Sections 4.1 and 4.2). It continues with a detailed description of the most important and the most used parallel MRI methods (especially methods Simultaneous acquisition of spatial harmonics (SMASH) [90] and Sensitivity encoding (SENSE) [78]). Parallel MRI methods are often modified or used in combination with other methods to further suppress ghosting or motion artifacts. Such modifications of the described methods are mentioned in Section 4.9.

4.1. Motivation

The acquisition time of one slice has decreased from minutes to hundreds of milliseconds during the MRI development. However, there are still several reasons for speeding up the acquisition. Even though the acquisition time of a single slice is short, the acquisition time accumulates rapidly for a 3D scan containing several slices or for images with a high spatial resolution. Faster acquisition time reduces the total examination time and permits to increase the number of patients that are examined per day. It also makes the examination more pleasant to patients by reducing the time they have to lay in a confined space and sometimes even hold their breath.

Another important aspect that accompanies the MRI acquisition is the appearance of motion artifacts caused by an unintentional patient movement during the session. Acceleration of the acquisition helps to reduce the severity of these artifacts.

MR imaging is also used for dynamic imaging of moving objects (e.g., a heart cycle). Parallel MRI decreases the acquisition time of a single slice and, thus, allows to increase the frame rate. This helps to avoid temporal aliasing and to examine the object thoroughly.

4.2. History

The first extreme idea to have a single receiver coil for each pixel was presented in 1988 by Hutchinson and Raff [38] and later in 1991 by Kwiat and Einav [50]. The algorithm employs coils with strongly localized sensitivities each covering only a single pixel. Therefore, it is theoretically possible to acquire the whole image during one excitation without using any spatial encoding at all. However, construction of such an array of receiver coils is almost impossible with current technology.

In 1989, Kelton introduced the idea of speeding up the acquisition by undersampling the $k$-space in the phase-encoding direction and recovering the missing information by using more receiver coils [47]. Kelton used two coils and reduced the sampling step by a factor of $1/2$. In 1991, Ra modified Kelton’s method to work with more receiver coils [80, 81].

Methods that are used nowadays are based on the Kelton’s principle of $k$-space undersampling. The two most widespread methods are SMASH and SENSE. SMASH [90] was introduced in 1997 by Sodickson and it works directly in the $k$-space by reconstructing the missing lines as a weighted combination of the adjacent $k$-space lines. The SMASH method and the methods extending the SMASH approach are presented in Section 4.4. The Sensitivity encoding method (SENSE) [78] was published in 1999 by Pruessmann and it works in
the spatial domain. The unaliased image is reconstructed as a pixelwise combination of the aliased pixels from all coils. Details about SENSE are given in Section 4.5.

Currently, parallel MRI methods are used to enhance the speed and quality of the MRI acquisition in a wide range of clinical applications. Methods for parallel imaging are incorporated in all new scanners supplied by the main MRI manufacturers. These commercially used methods are based mostly on the SENSE reconstruction [78] (this is valid for GE, Philips, Siemens and Toshiba). Although a parallel imaging algorithm is implemented in Hitachi MRI machines, it is not explicitly stated if the reconstruction method is based on any of the published methods. The only exceptional manufacturer in terms of parallel MRI is Siemens that offers also the GRAPPA reconstruction [27] as an alternative to the SENSE algorithm.

4.3. Coil sensitivities

Multiple receiver coils with spatially varying sensitivities are used in the parallel MRI process to obtain more information about the spatial position of the signal. Exact knowledge of coil sensitivities is essential for the parallel MRI reconstruction. A basic method to obtain the coil sensitivities is presented in this section.

Full-FOV images without aliasing are used for the sensitivity estimation. Ideally, an object covering the whole FOV without signal-free areas should be used. The estimate \( \hat{C}_l \) of the sensitivity maps \( C_l \) is obtained as a ratio

\[
\hat{C}_l(x, y) = S_l(x, y)/S(x, y),
\]

where \( S_l(x, y) \) is an array-coil image (2.26) and \( S(x, y) \) is an image with a homogeneous coil sensitivity [87]. A body-coil image can be used as \( S \) because of the nearly homogeneous sensitivity of the body coil. The second option is to use spatially homogeneous phantom and set \( S = 1 \).

The equation (4.1) gives a perfect estimate of the sensitivities only for noise-free images. In reality, zero mean Gaussian noise is present in both real and imaginary parts of the signal. This complicates the sensitivity estimation process especially in areas with low signal-to-noise ratio (SNR). These areas have to be discarded during the sensitivity estimation or given less importance to ensure precise estimation of the sensitivity maps [78].

The number of receiver channels in MRI hardware is limited. Thus the body-coil image is usually not acquired together with the array-coil images in practical applications. The body-coil would have to be acquired instead of one of the array-coil images which would result in a lower reconstruction quality since the large body-coil usually has lower SNR than smaller array-coils [66]. The sensitivities are then estimated using the array-coil images only. In this case, the image with homogeneous sensitivity \( S \), equation (4.1), has to be approximated using the array coil images \( S_l \). This can be done by pixelwise summing all of the images. The disadvantage of the summing is that it is susceptible to phase-cancellation artifacts [65, 83]. To avoid this, most of the reconstruction methods use sum-of-squares (SoS) image [92, 113, 78],

\[
S^{SoS}(x, y) = \sqrt{\sum_{l=1}^{L} |S_l(x, y)|^2}.
\]

The SoS combination does not suffer from phase-cancellation artifacts, however, the magnitude of the outcome is biased [65, 12].

The coil array have to fulfill the following conditions to ensure the feasibility of the parallel MRI reconstruction: the number of coils \( L \) must be higher than the acceleration factor \( M \).
(\(L \geq M\)) otherwise the problem becomes singular. At each part of the imaged object, at least one of the coils have to have non-zero sensitivity and the sensitivity maps have to be significantly different from each other lest the problem becomes ill-conditioned.

Noise in the input images also has to be taken into account. The reconstruction process transforms the input values containing noise into the reconstructed image and, thus, noise is propagated to the final image [78]. The noise variance in the reconstructed image is the most important factor of the reconstruction quality apart from removing aliasing.

4.4. SMASH

Simultaneous Acquisition of Spatial Harmonics (SMASH) is the most common parallel MRI reconstruction method that works in the Cartesian sampled \(k\)-space [90]. In SMASH, the missing phase-encoding lines are reconstructed directly in the \(k\)-space using a proper linear combination of the neighboring phase-encoding lines. The disadvantage of SMASH is that the original SMASH method is restricted to coil configurations with sensitivity profiles similar to harmonic functions. The method was later improved to allow reconstruction with arbitrary coil configurations [88, 67]. The auto-calibration technique was introduced in AUTO-SMASH and Variable Density AUTO-SMASH (VD-AUTO-SMASH) [42, 29]. In AUTO-SMASH, fully sampled portions of the \(k\)-space are used to calibrate the method without the need to explicitly extract sensitivity maps (see Section 4.3). A blockwise reconstruction using more auto-calibrating lines was proposed in [14] and later extended as Generalized autocalibrating partially parallel acquisitions (GRAPPA) [27]. Blockwise methods use more \(k\)-space line to reconstruct a single \(k\)-space line and reach a higher reconstruction quality than the non-blockwise methods.

4.4.1. Original SMASH

The SMASH method uses a weighted combination of the array-coil images to generate the harmonic modulation normally produced by the phase-encoding gradients [90, 87]. In other words, the missing lines are produced as a combination of the adjacent \(k\)-space lines.

First, the desired composite sensitivity profile \(C_{comp}^0\) is formed as a linear combination of the sensitivity profiles \(C_l\)

\[
C_{comp}^0(x, y) = \sum_{l=1}^{L} w(l, 0) C_l(x, y).
\]  

The weights \(w(l, 0)\) are usually chosen to produce an image with a uniform sensitivity profile \(C_{comp}^0(x, y) = 1\) if possible.

Then the harmonic spatial modulation on the top of the composite profile \(C_{comp}^0\) is produced using the weights \(w(l, m)\)

\[
C_{comp}^m(x, y) = C_{comp}^0(x, y) e^{im\Delta ky} = \sum_{l=1}^{L} w(l, m) C_l(x, y),
\]  

where \(\Delta ky\) is the size of the phase-encoding step in the \(k\)-space. Fitting of the coil sensitivities to the composite profile is illustrated in Figure 4.1a.

The weights \(w\) are estimated by solving the equations (4.3), (4.4) in the least squares sense for a single chosen \(x_0\) coordinate. This approach is applicable only for coil configurations where the coil sensitivities are approximately separable \(C_l(x, y) \approx C_{lx}(x) C_{ly}(y)\) [88]. This
restricts the use of the method only for certain coil configurations. Better results are reached using multi-line fitting when the weights are estimated and used independently for several \( x \) coordinates. The frequency-encoding direction is segmented into several strips and the weights \( w \) are estimated for a single \( x \)-position from each strip. The weights are then used for a separate reconstruction in each strip [88].

All \( k \)-space lines in the composite image \( s_{\text{comp}} \) are reconstructed from the undersampled coil images using the estimated weights \( w \)

\[
s_{\text{comp}}(k_x, k_y - m\Delta k_y) = \sum_{l=1}^{L} w(l, m) s_l(k_x, k_y),
\]

where \( s_l(k_x, k_y) \), \( s_{\text{comp}}(k_x, k_y) \) is the \( k \)-space representation of \( S_l(x, y) \), \( S_{\text{comp}}(x, y) \), respectively. The composite image \( S_{\text{comp}} \) is equal to the unaliased image \( S \) modulated by the composite sensitivity profile \( C_{\text{comp}} \) \( (S_{\text{comp}} = SC_{\text{comp}}) \). The linear combination of the lines with coordinate \( k_y \) with weights \( w(l, m) \) produces a line shift by \( m\Delta k_y \) in the \( k \)-space (see Figure 4.1b). This is proved by Fourier transforming the combined image and then substituting the equations (2.26), (4.3) and (4.4)

\[
\begin{align*}
\sum_{l=1}^{L} w(l, m) s_l(k_x, k_y) &= \sum_{x, y} \sum_{l=1}^{L} w(l, m) C_l(x, y) S(x, y) e^{-ik_xx - ik_yy} \\
&= \sum_{x, y} \sum_{l=1}^{L} C_{\text{comp}}^l e^{im\Delta k_y} S(x, y) e^{-ik_xx - ik_yy} \\
&= \sum_{x, y} \sum_{l=1}^{L} C_{\text{comp}}^l S(x, y) e^{-ik_xx - i(k_y - m\Delta k_y)y} \\
&= \sum_{x, y} S_{\text{comp}}(x, y) e^{-ik_xx - i(k_y - m\Delta k_y)y} \\
&= s_{\text{comp}}(k_x, k_y - m\Delta k_y).
\end{align*}
\]

The reconstructed image \( S_{\text{comp}} \) is modulated by the composite profile (4.3) and needs to be compensated for

\[
\hat{S}(x, y) = \frac{S_{\text{comp}}(x, y)}{C_{\text{comp}}(x, y)}.
\]

The main disadvantages of the original SMASH method is the need to obtain a precise estimate of sensitivity maps. The method also works only with suitable coil configurations where the harmonic modulations of the composite sensitivity profile \( C_{\text{comp}} \) can be accurately generated using a linear combination of the coil sensitivities (4.4). On top of that, it has been proven that even when the fit described by the equations (4.3) and (4.4) is perfect the SMASH method does not reach the SNR efficiency of the pixel based methods as SENSE [89].

The physical effect of field gradients is most closely emulated by choosing a homogeneous composite profile \( C_{\text{comp}}^0 = 1 \) when estimating the weights \( w \) in the equation (4.4). This is not possible for all coil configurations and it can results in a low quality fit [88] The alternative is to use a composite profile \( C_{\text{comp}} \) created as a sum of the coil sensitivities

\[
C_{\text{comp}}^0(x, y) = \sum_{l=1}^{L} C_l(x, y).
\]

This composite profile allows a better fit that adjusts the harmonic functions to match the asymmetries in coil sensitivities and results in a better reconstruction quality [88]. The weights \( w(l, m) \) are estimated using the equation (4.4) with the composite profile \( C_{\text{comp}}^0 \) (4.7).
4.4. SMASH

![Diagram of SMASH estimation and reconstruction processes.](image)

(a) Estimation. Coil sensitivity profiles are combined to produce a composite profile and harmonic modulation on the top of the profile, equation (4.3). Full and dashed lines represent the real and the imaginary part of the signal and sensitivity, respectively. (b) Estimated weights are used to produce the shift in the \( k \)-space, equation (4.4). The full and dashed lines represent the acquired and the missing lines in the \( k \)-space, respectively. The \( k \)-space lines in images \( S^{comp}(k_y) \) and \( S^{comp}(k_y - \Delta k_y) \) form together an image \( S^{comp} \) with a complete set of \( k \)-space lines and, thus, without aliasing.

4.4.2. Auto calibration

The main weakness of the original SMASH method is that it requires precise estimates of sensitivity maps. For this reason, pre-scan images are obtained. This increases the total scan time. Furthermore, sensitivity maps are not always static in time. They vary because of various reasons (for example due to the motion of coils during the acquisition). At last, the sensitivity extraction as mentioned in Section 4.3 is susceptible to error especially in areas with low SNR.

These problems can be solved by using the raw images \( S_l \) directly for the estimation in the equations (4.3) and (4.4) without estimating the coil sensitivities \( C_l \). The auto-calibration SMASH method was first introduced by Jakob et al as AUTO-SMASH [42, 43]. In AUTO-SMASH, \( M-1 \) auto-calibration lines \( S^{AC}_l \) are acquired besides a fraction \( \frac{1}{M} \) of all \( k \)-space lines (the accelerated acquisition). The auto-calibrating lines can be acquired anywhere in the \( k \)-space, however, they are usually acquired near the \( k \)-space center since this is the \( k \)-space area with the highest SNR. The purpose of the auto-calibration lines is to give an unaliased, though low resolution, image that can be used for the calibration.

Raw images are used for the calibration process in the same way as the coil sensitivities. This is deduced from the equation (2.26) by multiplying both sides with the intensity image \( S \).
and then using the equation (4.3)

\[ C_{0}^{\text{comp}}(x, y) = \sum_{l=1}^{L} w(l, 0) C_l(x, y) \]

\[ C_{0}^{\text{comp}}(x, y) S(x, y) = \sum_{l=1}^{L} w(l, 0) C_l(x, y) S(x, y) \]

\[ S_{0}^{\text{comp}}(x, y) = \sum_{l=1}^{L} w(l, 0) S_l(x, y) . \] (4.8)

Auto-calibration lines \( s_l^{\text{AC}}(k_x, k_y^0 - m\Delta k_y) \) are acquired for a single \( k_y^0 \) coordinate and for shifts \( m = 1, \ldots, M - 1 \). The auto-calibration lines are linearly combined with the weights \( w(l, 0) \) to form the composite image \( s^{\text{comp}}(k_y, k_y^0 - m\Delta k_y) \) for \( m = 0, \ldots, M - 1 \)

\[ \sum_{l} w(l, 0) s_l^{\text{AC}}(k_x, k_y^0 - m\Delta k_y) = s^{\text{comp}}(k_x, k_y^0 - m\Delta k_y) . \]

Then the composite image \( s^{\text{comp}} \) is used to find the weights \( w \) in the least square sense

\[ \sum_{l=1}^{L} w(l, m) s_l(k_x, k_y^0) = s^{\text{comp}}(k_x, k_y^0 - m\Delta k_y) . \] (4.9)

The AUTO-SMASH reconstruction with the known weighting factors \( w \) is performed in the same way as in the original SMASH, equation (4.5).

The main weakness of the AUTO-SMASH method is that each parameter \( w(l, m) \) is estimated using only a single auto-calibrating line \( (k_x, k_y^0 - m\Delta k_y) \), equation (4.9). See Figure 4.2a for illustration. Therefore, the method is not robust to noise and the requirements on the coil configuration stay the same as in the original SMASH (see Section 4.4.1). The AUTO-SMASH principles are improved in Variable Density AUTO-SMASH (VD-AUTO-SMASH) [29, 33]. In VD-AUTO-SMASH, more calibrating lines are acquired (i.e., the center of the k-space is fully sampled). This allows to estimate a single weighting factor using more auto-calibration lines than one, see Figure 4.2b. The weights \( w \) in the equation (4.9) are estimated for a set of k-space lines \( B \) (acquired lines in the fully sampled k-space center)

\[ \forall m = 1, \ldots, M - 1; \forall k_y \in B \quad \sum_{l=1}^{L} w(l, m, k_y) s_l(k_x, k_y) = s^{\text{comp}}(k_x, k_y - m\Delta k_y) . \]

The estimated values for each parameter \( w(l, m, k_y) \) are linearly combined to get the final weight \( w(l, m) \). The weights of the linear combination are proportional to the signal amplitude in the particular position [29].

Usefulness of the SMASH and the auto-calibration SMASH reconstruction methods was demonstrated several times [24, 93, 41, 23]. The SMASH reconstruction has a small number of parameters and, thus, it is very fast to calculate especially compared to the computationally demanding image-based methods (see Sections 4.5, 4.6). However, the reconstruction quality is still not as high as the pixel-based reconstruction methods (like SENSE, Section 4.5).

### 4.4.3. GRAPPA

The GRAPPA method (Generalized Autocalibrating Partially Parallel Acquisitions) [27] uses a blockwise reconstruction. It extends the approach presented in [67, 14] where more than
one acquired lines are linearly combined to reconstruct each missing line (see Figure 4.2c). A block is defined as an acquired line and \( M - 1 \) adjacent missing lines.

The second innovation of GRAPPA over SMASH is the individual reconstruction of the full set of array-coil images. Instead of reconstructing the composite image \( S_{comp} \), as in the equation (4.8), an unaliased version of each array coil image is reconstructed [65]. The final image is reconstructed as a sum-of-squares of the unaliased array-coil images (4.2).

The GRAPPA method uses the following equation to reconstruct the missing \( k \)-space lines of the \( j \)-th coil

\[
s_j(x, k_y - m \Delta_{k_y}) = \sum_{l=1}^{L} \sum_{b \in B} w(j, b, l, m) s_l(x, k_y - bM \Delta_{k_y}),
\]

where \( w(j, b, l, m) \) are the reconstruction weights and the variable \( b \) specifies the reconstruction block. A block is formed of \( M \) \( k \)-space lines. The acquired line \( s_l(x, k_y - bM \Delta_{k_y}) \) from the block \( b \) is used for the reconstruction of the missing line \( s_j(x, k_y - m \Delta_{k_y}) \). The set \( B \) is a set of all reconstruction blocks used for the reconstruction. The number of the blocks in the set \( B \) is a parameter of the reconstruction.

Variable density images are used in GRAPPA to allow both estimation and reconstruction without the need for an additional scan, see VD-AUTO-SMASH in Section 4.4.2. Several auto-calibrating lines \( s_{AC}^{j} \) are acquired in the center of the \( k \)-space. The value of the weights \( w(j, b, l, m) \) is found by solving the following equation separately for each \( k_y \) in the \( k \)-space center in the least squares sense

\[
s_{AC}^{j}(x, k_y - m \Delta_{k_y}) = \sum_{l=1}^{L} \sum_{b \in B} w(j, b, l, m, k_y) s_l(x, k_y - bM \Delta_{k_y}).
\]

The weights \( w(j, b, l, m, k_y) \) found for each \( k_y \) are averaged to form the final weight \( w(j, b, l, m) \). Reconstruction can be done for each \( x \) coordinate separately. However, in practice, the weights \( w \) are estimated for several \( x \) coordinates and the weights for the remaining \( x \)-positions are linearly interpolated. In the reconstruction step, the reconstructed array-coil images are combined using sum-of-squares, equation (4.2) [53, 27].

The authors of GRAPPA suggest so called sliding-block approach [27]. The idea is to use several different sets of blocks \( B_k \) for the reconstruction, equation (4.10). The coefficients \( w_{k}(j, b, l, m) \) are estimated for each set \( B_k \). The coefficients \( w \) used for the reconstruction are computed as a linear combination of the parameters \( w_k \) over all blocks \( B_k \)

\[
w = \frac{\sum_{k} v_k w_k}{\sum_{k} v_k}.
\]

The weights \( v_k \) are set inversely proportional to the approximated reconstruction error for parameters \( w_k \) which is computed as a quality of the fit, equation (4.10).

The number of blocks in \( B \) is a determining parameter of the reconstruction. By reducing the number of blocks to one, GRAPPA becomes equivalent to the original SMASH. When all the acquired blocks are used for the reconstruction then GRAPPA becomes equivalent to the exact SENSE-like (see Section 4.5) reconstruction [27, 86, 91]. However, using the full number of acquired lines for the reconstruction of a single line results in unsteadiness caused by the low SNR of the out-of-center \( k \)-space lines. Using a high number of lines also slows down the whole reconstruction process. In practice, it appears that using from four to eight blocks ensures satisfactory quality of the reconstruction [27]. The blockwise reconstruction utilizes more acquired lines for the reconstruction. This makes the method more robust without limiting its use to specific coil configurations as it is for the original SMASH. The GRAPPA method proved to produce reconstructed images with a higher SNR and a lower level of artifacts than the original SMASH and VD-AUTO-SMASH [27].
4. State of the art

Fig. 4.2. Various SMASH-type reconstructions. The figure shows which lines are used for the estimation and for the reconstruction in four different types of SMASH reconstructions. We show a reconstruction of a line shifted by one line in the \( k \)-space. Solid lines are the acquired lines, dashed lines represent the auto-calibration lines and dotted lines are the missing lines. Solid arrows illustrate which lines are used for the estimation. Dashed arrows represents the reconstruction of the missing lines. (a) AUTO-SMASH uses only a single fit for each line [42]. (b) VD-AUTO-SMASH uses more fits to obtain a parameter describing a single shift in \( k \)-space [29]. The Generalized SMASH (c) uses more acquired lines to fit a single auto-calibrating line [67, 14]. (d) The GRAPPA blockwise method [27].

Fig. 4.3. The time interleaved dynamic acquisition in TGRAPPA. The \( k \)-space is undersampled in each frame with a reduction factor \( M \) (dotted lines are skipped, solid lines are acquired). A different set of lines is acquired in each frame. Thus, \( M \) following frames form a complete set of acquired \( k \)-space lines.

TGRAPPA

Parallel MRI reconstruction methods are often used in dynamic imaging. Temporal GRAPPA (TGRAPPA) is a way to obtain calibration lines for the GRAPPA estimation process (4.10) in dynamic imaging without using variable-density scan and, thus, lowering the acquisition time [9]. In TGRAPPA, the \( k \)-space of each frame is subsampled with a factor \( M \). In \( M \) subsequent frames, the position of the acquired lines is shifted in the \( k \)-space so a different subset of \( k \)-space lines is acquired in each frame, see Figure 4.3. TGRAPPA uses acquired center-lines from \( M \) following frames to generate a fully sampled \( k \)-space center for the GRAPPA calibration.

The reconstruction weights are estimated for each frame separately. Data from the previous frames affect only the calibration process and not the reconstructed image itself. Thus, the reconstructed images are not blurred in the temporal dimension because only data from the current frame are used. Coil sensitivities are static or change only slowly in time. Thus, using data from adjacent time frames does not have significant negative effect on the sensitivity estimation nor on the estimation quality [9].
4.5. SENSE

Fig. 4.4. The dynamic interleaved acquisition of k-t GRAPPA.
The acquisition scheme is the same as in Figure 4.3. Here, the phase-encoding lines are displayed as dots. Full dots represent the acquired lines, empty dots are the missing lines and gray dots are the auto-calibrating lines. Arrows represent the k-t GRAPPA reconstruction, where the adjacent lines in both phase-encoding axis and times axis are used for the reconstruction.

k-t GRAPPA

The k-t GRAPPA method is another application of GRAPPA in dynamic MRI [37]. It works with a similar sampling pattern as TGRAPPA except that auto-calibration lines are acquired in the center of k-space in each time frame. As in GRAPPA, k-t GRAPPA uses the neighboring k-space lines for the reconstruction. On the top of that, k-t GRAPPA uses also k-space lines from the adjacent time frames that have the same phase-encoding coordinates as the reconstructed line, see Figure 4.4. The k-t GRAPPA reconstruction equation is described by the following modification of the equation (4.10)

$$s^t_l(k_y - m\Delta k_y) = \sum_{l=1}^{L} \left( \sum_{b \in B} w_b(j, l, m) s^t_l(k_y - bM\Delta k_y) + \sum_{v=t-m,t+A-m} w^v(j, l, m) s^v_l(k_y - m\Delta k_y) \right), \quad (4.11)$$

where $s^t_l$ and $s^v_l$ corresponds to the k-space image $s_l$ in the $t$-th and $v$-th time frame, respectively. The weights $w_b$ are the weights of the linear combination over the adjacent blocks in the time frame $t$. The weights $w^v$ corresponds to the combination of points with the same k-space coordinates in the adjacent time frames specified by $v$. The first term on the right side of (4.11) is similar to GRAPPA (4.10). The second term represents the contribution from the two adjacent time frames $(t - m)$ and $(t + A - m)$, where $t$ is the index of the current frame. In the set of time frames from $(t - M)$ to $(t + M)$, only in frames $t$, $(t - m)$ and $(t + A - m)$ is the k-space line at coordinate $(k_y - m\Delta k_y)$ acquired. The weights $w_b$ and $w^v$ are estimated by fitting the auto-calibrating lines as in done in GRAPPA, see Figure 4.4. k-t GRAPPA brings higher reconstruction quality when compared with standard GRAPPA by using the time correlation of the signal [37].

4.5. SENSE

Unlike the SMASH and the GRAPPA methods that reconstruct the missing k-space lines directly in the k-space, the SENSE method works in the image domain. The SENSE method
was originally described by Pruessmann et al in 1998 [77, 78]. SENSE uses a linear encoding matrix $E$ to describe the transformation from the ideal image $S$ to the $k$-space values $s_l(k_x, k_y)$ including the coil sensitivity modulation and aliasing

$$s_l(k_x, k_y) = \sum_{k_x, k_y} S(x, y) E_{l, k_x, k_y}(x, y),$$

where the encoding matrix $E$ is

$$E_{l, k_x, k_y} = e^{-i\pi (k_x x + k_y y)} C_l(x, y). \quad (4.12)$$

The reconstruction from the acquired values $s(k_x, k_y)$ is performed using a linear reconstruction matrix $\mathbf{F}$

$$\hat{S}(x, y) = \sum_{l, k_x, k_y} F_{l, k_x, k_y}(x, y) s_l(k_x, k_y). \quad (4.13)$$

The continuous $k$-space is sampled in discrete intervals during the MRI acquisition. The reconstruction $\mathbf{F}$ is estimated under a so-called weak voxel criterion which approximates the shape of the voxel function by a Dirac function [78]. The criterion gives rise to the following condition for the matrix $\mathbf{F}$

$$\mathbf{F} \mathbf{E} = \mathbf{I}, \quad (4.14)$$

where $\mathbf{I}$ is an identity matrix $X \cdot Y \times X \cdot Y$.

This linear system (4.14) is underdetermined leaving degrees of freedom in the solution that are used to minimize the noise propagation by the reconstruction. Noise in the input images is assumed to be Gaussian. It is characterized using the noise correlation matrix $\Psi$ that reflects the variance in each receiver coil as well as correlations between coils. Noise is propagated into the reconstructed image as a product with the reconstruction matrix $\mathbf{F}$. The diagonal entries in the matrix $\mathbf{X} = \mathbf{F}\Psi\mathbf{F}^H$ represents the noise variance in each reconstructed pixel, where $\mathbf{F}^H$ denotes the Hermitian transpose (conjugate transpose) of the matrix $\mathbf{F}$. This variance is minimized for each pixel using the Lagrange multiplicators under the condition (4.14) yielding the SENSE solution (for details see [78]),

$$\mathbf{F} = (\mathbf{E}^H \Psi^{-1} \mathbf{E})^{-1} \mathbf{E}^H \Psi^{-1}. \quad (4.15)$$

The direct solution of the equation (4.15) is numerically challenging. Its time and space complexity is high because of the size $L \cdot X \cdot Y \times X \cdot Y$ of the linear system (4.14), where $X \cdot Y$ is the size of the input images. Two possible solutions that deal with the time complexity of the problem are described in the following sections.

### 4.5.1. Cartesian SENSE

Let us assume the $k$-space is acquired using standard Cartesian sampling and the $k$-space is undersampled regularly with an acceleration factor $M$. Then, the value of each aliased pixel is a linear combination of $M$ pixel values, equation (2.27). Therefore, the encoding matrix $\mathbf{E}$ becomes block diagonal. The consequence is that the inversion of each block corresponding to each pixel can be done independently [78, 102].

The encoding process (4.12) in the regular Cartesian case is simplified to (3.1). This is rewritten in a matrix notation ($\mathbf{S}^A = \mathbf{C} \mathbf{S}$) as

$$\begin{pmatrix}
S_1^A(x, y) \\
S_2^A(x, y) \\
\vdots \\
S_L^A(x, y)
\end{pmatrix}
= \mathbf{C}
\begin{pmatrix}
S(x, y) \\
S(x, y + Y/M) \\
\vdots \\
S(x, y + (M - 1)Y/M)
\end{pmatrix}, \quad (4.16)$$
where the coil sensitivity matrix $C$ is

$$
C = \begin{pmatrix}
C_1(x, y) & \cdots & C_1(x, y + (M - 1)Y/M) \\
C_2(x, y) & \cdots & C_2(x, y + (M - 1)Y/M) \\
\vdots & & \vdots \\
C_L(x, y) & \cdots & C_L(x, y + (M - 1)Y/M)
\end{pmatrix},
$$

(4.17)

where $S_i^A$ is the aliased image (2.27), $M$ is the acceleration factor and $X \cdot Y$ is the FOV size in pixels. For the details of the derivation see equations (2.27) and (2.26) or Appendix in [78]. The equation (4.16) is used for all $x = 1, \ldots, X$ and $y = 1, \ldots, Y/M$.

It is assumed that the reconstruction problem is not ill posed. This requires that the coil sensitivity matrix $C$ is not singular for any $x$ nor $y$ (see also Section 4.3). The reconstruction (4.15) becomes

$$
C^\dagger(x, y) = (C^H \Psi^{-1} C)^{-1} C^H \Psi^{-1} (x, y),
$$

(4.18)

where $C^H$ is the Hermitian transpose of the matrix $C$. The reconstructed image $\hat{S}$ (4.13) is computed from the input aliased images $S_i^A$ as [78]

$$
\begin{pmatrix}
\hat{S}(x, y) \\
\hat{S}(x, y + Y/M) \\
\vdots \\
\hat{S}(x, y + (M - 1)Y/M)
\end{pmatrix} = C^\dagger(x, y) \begin{pmatrix}
S_1^A(x, y) \\
S_2^A(x, y) \\
\vdots \\
S_L^A(x, y)
\end{pmatrix}.
$$

(4.19)

This process is repeated for each pixel in the aliased image to complete the full reconstructed image.

### 2D SENSE

The SENSE method can be adapted to compensate for the aliasing in two dimensions [106]. Clearly, there would be no significant time reduction when undersampling in the frequency encoding direction. The method can be used in 3D Fourier imaging where phase-encoding is applied in two dimensions. The undersampling and subsequent SENSE reconstruction, thus, can be applied in two dimensions. The equation (4.16) has to be modified to reflect the aliasing in both phase-encoding directions and to describe the contribution of each pixel from the unaliased image to pixels in the aliased images. The reconstruction process given by the equation (4.19) is modified in the same sense and solved as in the equation (4.18). The advantage of the 2D SENSE method is that for higher acceleration factors the undersampling can be split in both dimension (e.g. $2 \times 2$ acceleration in 2D SENSE instead of acceleration factor 4 in 1D SENSE). The 2D SENSE method offers better results than 1D SENSE due to the coil-geometry related reduction of noise in the reconstruction [106].

### Regularization

The equation (4.16) can be rewritten in a matrix notation yielding $S_i^A = CS$. The una-liased image $S$ can be obtained using Tikhonov regularization [95]. The solution is given by minimizing (4.16) that is regularized using an apriori information about the solution

$$
\hat{S} = \arg\min_S \left\{ \|CS - S_i^A\| + \lambda\|S - S^0\| \right\},
$$

(4.20)
where $\lambda$ is the regularization parameter, $\| \cdot \|$ is the $L_2$ norm and $S^0$ is the expected solution [55]. The first term in the equation (4.20) is equal to the error from the unconditioned reconstruction. The second term describes the deviation from the apriori information. The regularization parameter $\lambda$ controls the trade-off between the first and the second error term.

The equation (4.20) may be solved using singular value decomposition (SVD) [22] while the ideal value of the parameter $\lambda$ is determined using the L-curve technique [32]. When there is no apriori information about the image (in most cases) the aliased images $S^A_l$ are used as the apriori knowledge of $S^0$ [55].

A different regularization approach is introduced by Kellman in [45]. The solution to the SENSE equation (4.16) is modified by adding a regularization term to the equation (4.18)

$$C^+ (x, y) = A (C^H \Psi^{-1} C + \Lambda)^{-1} C^H \Psi^{-1} (x, y) ,$$

(4.21)

where $A$ is a gain matrix and $\Lambda$ is a positive real diagonal conditioning matrix. The matrix $A$ is calculated to make the diagonal elements of $C^+ C$ equal to 1. The values in the matrix $\Lambda$ regularize the reconstruction by controlling the trade-off between SNR and the artifact suppression in the reconstructed image. The off-diagonal elements of $C^+ C$ specify the artifacts suppression. The matrix $C^+ C$ becomes identity for $\Lambda$ equal zero and the artifacts are fully suppressed at the cost of high noise in the reconstructed image. The values in $\Lambda$ are optimized to meet the desired artifact suppression in the reconstructed image. By changing values in $\Lambda$ the reconstruction SNR may be locally improved while keeping the artifact suppression at a tolerable level [45].

### 4.5.2. Iterative solution

An iterative solution to the equation (4.15) was proposed by Pruessmann in 2001 [76]. The noise correlation matrix $\Psi$ is assumed to be diagonal to make the calculations simpler. From equations (4.13) and (4.15) we obtain

$$E^H_l E_l s_l = E^H_l s_l ,$$

(4.22)

where the vector $s_l$ is defined as $s_{l,k_x,k_y}$.

The method of conjugate gradients [34] is chosen to find the solution of the equation (4.22). The main computational load, thus, lies in the matrix vector multiplication $E z$ for any given vector $z$

$$(Ez)_{l,k_x,k_y} = \sum_{x,y} e^{-i\pi(x_x + k_y y)} C_l (x, y) z (x, y) .$$

(4.23)

This sum (4.23) may be regarded as an integral of a product of an exponential and a weighted Dirac function [75, 76]. This can be rewritten as an inverse discrete Fourier transformation

$$(Ez)_{l,k_x,k_y} = \int_{x'} \int_{y'} e^{-i\pi(k_x x' + k_y y')} C_l (x, y) z (x, y) \delta (x - x', y - y') dx' dy'$$

$$= FT^{-1} \left[ \sum_{x,y} C_l (x, y) z (x, y) \delta (x - x', y - y') \right] (k_x, k_y) .$$

(4.24)

In the iterative SENSE, the $k$-space is allowed to be sampled using an arbitrary sampling pattern. Therefore, an additional gridding is required to transform the data to a regular Cartesian grid before the discrete Fourier transformation. This can be done using a common gridding reconstruction [39].
4.6. SPACE-RIP

Sensitivity Profiles From an Array of Coils for Encoding and Reconstruction in Parallel (SPACE-RIP) is a parallel MRI reconstruction method that reconstructs the unaliased image in the image domain directly from the acquired k-space values [51]. The encoding process that transforms the ideal image values $S$ to the measured k-space values is represented as inverse Fourier transform in the phase-encoding direction (2.24)

$$s_l(x, k_y) = \sum_y S(x, y) C_l(x, y) e^{-\pi k_y y}.$$  

(4.25)

The Fourier transform in the frequency encoding direction is done prior to the reconstruction, since the frequency encoding direction is fully sampled. This equation is put in a matrix form
expressing the encoding process for all coils and all phase-encoding coordinates in both image domain and $k$-space

$$
\begin{bmatrix}
    s_1(x,k_1^1) \\
    s_1(x,k_y N_k^1) \\
    s_2(x,k_1^2) \\
    \vdots \\
    s_l(x,k_y N_k^l)
\end{bmatrix}
= \begin{bmatrix}
    C_1(x,1) e^{-\pi ik_1^1 y} & \cdots & C_1(x,Y) e^{-\pi ik_1^1 Y} \\
    \vdots & \ddots & \vdots \\
    C_l(x,1) e^{-\pi i k_y N_k^l} & \cdots & C_l(x,Y) e^{-\pi i k_y N_k^l Y}
\end{bmatrix}
\cdot
\begin{bmatrix}
    S(x,1) \\
    \vdots \\
    S(x,Y)
\end{bmatrix},
$$

(4.26)

where $N_k$ is the number of the retrieved $k$-space positions whose $k$-space coordinates are marked $k_1^1, \ldots, k_y N_k^l$. The size of the image is $Y$.

The sensitivities $C_l$ are obtained in the same way as is described in the Section 4.5.3. The equation (4.26) is solved using a pseudo-inversion for each $x$ and it allows the reconstruction of a whole column in the final image. The reconstruction for each $x$ is done separately and, thus, the method can be implemented on a parallel machine to decrease the time complexity significantly.

The main advantage of SPACE-RIP is that it works with an arbitrary set of acquired $k$-space lines and, thus, an efficient way of subsampling can be used [51]. A method for a nearly optimal selection of $k$-space lines is presented by Xu [110] showing that irregular sampling can lower the reconstruction error for a specific image. The disadvantage of the SPACE-RIP method is its high time complexity.

### 4.7. PILS

Partially Parallel Imaging With Localized Sensitivities (PILS) [28] is a simple and fast reconstruction method. PILS utilizes the high spatial localization of sensitivity in smaller coils. Such coils acquire images with a limited FOV (according to the coil sensitivity). Therefore, the acquisition FOV can be reduced to a certain level without causing aliasing in the retrieved images.

The size of the imaged object is defined as $Y$. To acquire an image of such object it is necessary to set the imaging FOV to $Y^I > Y$ to avoid aliasing (see Section 2.2.7). The approximate center of the coil $y_0^l$ is determined by finding a peak in the 1D coil profile. The coil FOV $Y_C^l$ corresponds to the size of the area where the sensitivity is higher than a given threshold. It is assumed that the signal measured by this coil outside of the coil FOV is negligible. The main idea of PILS is that the array-coil image is not affected by aliasing when $Y_C^l < Y^I$ even when the imaging FOV is smaller than the size of the imaged object ($Y^I < Y$), see Figure 4.6. The acceleration factor is set to make the imaging FOV larger than the FOV of the largest coil used ($\forall l \ Y_C^l < Y^I$). The unaliased image is reconstructed by summing together the array coil images. Aliasing is not present in the array-coil images because of the condition given above. Thus, there is no aliasing in the reconstructed image. The image is acquired in a factor $Y^I/Y$ of the original acquisition time.

The PILS method offers reconstruction that is simple to implement, fast and free of significant artifacts up to certain acceleration factor. The main limitation of PILS is that it can be used only with suitable coil geometry since the coils are expected to act as filters in the phase-encoding direction.
4.7. PILS

Fig. 4.6. The PILS method.
Images or a vessel phantom are displayed. (a) The imaging FOV is bigger than the object size, therefore, the image is acquired without aliasing. (b) Halving the FOV size with respect to (a) causes aliasing. (c) The same object as in (a) is retrieved using a coil with a smaller FOV. (d) The FOV of the coil is smaller than the FOV of the reduced acquisition. Thus, there is no visible aliasing in the image obtained by the coil with the localized sensitivity.
4. State of the art

4.8. PARS

Parallel Magnetic Resonance Imaging with Adaptive Radius in $k$-space (PARS) [111] is a $k$-space method for parallel MRI reconstruction introduced by Yeh in 2005. Unlike SMASH [90] and GRAPPA [27] it does not work independently on the $x$ coordinate. PARS uses all neighbors of each pixel to contribute to its reconstruction.

The radius $k_R$ is a parameter of the reconstruction. Each unacquired pixel in $k$-space $s_l(k_x, k_y)$ is reconstructed using pixels that have the Euclidean distance from $(k_x, k_y)$ lower than $k_R$

$$s_l(k_x, k_y) = \sum_{\Delta_x, \Delta_y} L \sum_{l'=1}^L w_{l', \Delta_x, \Delta_y} s_{l'}(k_x - \Delta_x, k_y - \Delta_y) ,$$  \hspace{1cm} (4.27)

where $w$ are the weighting coefficients and the sum is over all $\Delta_x, \Delta_y$ which fulfill the relation $\sqrt{\Delta_x^2 + \Delta_y^2} \leq k_R$. Values from 2 to 10 are used for $k_R$ in practice [111]. The weights are estimated to fulfill the following equation in the least squares sense

$$C_l(x, y) = \sum_{\Delta_x, \Delta_y} L \sum_{l'=1}^L w_{l', \Delta_x, \Delta_y} e^{\pi i (\Delta_x x + \Delta_y y)} C_{l'}(x, y) .$$  \hspace{1cm} (4.28)

We show that the weights $w$ fulfilling the condition (4.28) give the perfect reconstruction as is described by the equation (4.27). Using the knowledge about the MRI signal (2.23) we obtain

$$s_l(k_x, k_y) = \int\int_{x,y} e^{-\pi i (k_x x + k_y y)} C_l(x, y) S(x,y) dx dy ,$$

The equation (4.28) is substituted for the sensitivity $C_l(x, y)$

$$s_l(k_x, k_y) = \int\int_{x,y} e^{-\pi i (k_x x + k_y y)} \sum_{\Delta_x, \Delta_y} L \sum_{l'=1}^L w_{l', \Delta_x, \Delta_y} e^{\pi i (\Delta_x x + \Delta_y y)} C_{l'}(x, y) S(x,y) dx dy$$

$$= \sum_{\Delta_x, \Delta_y} L \sum_{l'=1}^L w_{l', \Delta_x, \Delta_y} \int\int_{x,y} e^{-\pi i (k_x x + k_y y - \Delta_x x - \Delta_y y)} C_{l'}(x, y) S(x,y) dx dy .$$

The integral corresponds to the Fourier transformation of the product $C_{l'}(x, y) S(x, y) = S_{l'}(x, y)$

$$s_l(k_x, k_y) = \sum_{\Delta_x, \Delta_y} L \sum_{l'=1}^L w_{l', \Delta_x, \Delta_y} s_{l'}(k_x - \Delta_x, k_y - \Delta_y) .$$  \hspace{1cm} (4.29)

The PARS technique allows restoration of undersampled $k$-space for any acquisition trajectory. The method becomes similar to general SENSE (see Section 4.5.2) for unlimited radius $k_R$. However, localization of pixels contributing to the solution makes the method more time efficient. Limiting the number of pixels used for the reconstruction also brings a regularization effect reducing the noise propagation by the reconstruction.
4.9. Applications

This section contains description of various methods that use the principles of parallel MRI methods to directly or indirectly improve the quality of MRI images. There is also a large number of practical medical applications of parallel MRI where the described parallel MRI reconstruction methods are used to enhance the imaging of a specific organ or to solve specific issues. We provide a short list of such applications in Section 4.9.4 to show the importance of parallel MRI.

4.9.1. Elimination of motion artifacts

Patient movement during the MRI acquisition is a common source of motion artifacts. To reduce these artifacts, Bydder [13] suggests taking fully sampled k-space images with motion artifacts and dividing the k-space to several sets each containing a distinct subset of the acquired k-space lines (similar as in dynamic imaging, see Figure 4.3). In each set, the missing lines are generated from the rest of the lines in the set using the SENSE reconstruction (see Section 4.5). Images reconstructed for each set should be identical except for the SENSE reconstruction errors. The k-space lines that differ between the images are identified as affected by motion artifacts and these lines are discarded from the fully sampled k-space image. The discarded lines are reconstructed from the neighboring lines using the SMASH reconstruction (see Section 4.4). The SMASH reconstruction is chosen because it is better localized in the frequency domain than SENSE, whereas the SENSE method is chosen to identify the errors because of the better accuracy of SENSE over the basic SMASH. Using this method, the motion artifacts are suppressed in the final image [13].

Better results are achieved using a method called SMASH Navigators [11]. The method processes the k-space lines in the same order as they are acquired. Each newly acquired line is compared with the predicted value approximated from the previous lines using a SMASH reconstruction. An object motion between the subsequent acquisitions is estimated from the difference between the estimated and measured value. The difference is inversely applied to the newly acquired line and to all the following lines to cancel the effect of the movement.

4.9.2. CAIPIRINHA

Controlled Aliasing in Parallel Imaging Results in Higher Acceleration (CAIPIRINHA) for Multi-Slice Imaging [8] is a method for speeding up a multi-slice acquisition using the parallel MRI principles. In a simultaneous multi-slice acquisition, two or more slices are acquired at the same time. It is not possible to separate the pixel values from each slice by means of the standard signal encoding. The simple approach is to use a technique similar to classical parallel MRI working in the slice-selection direction [52]. The disadvantage of this simple method is that the coil sensitivity variation is too small for slices that are close. Thus, the problem becomes ill-conditioned. The solution to this was proposed by Breuer [8]. The phase of each slice is modified by a value \( \Delta_y \). The acquired signal \( S(y) \) for two slices is then

\[
S_1^A(y) = \sum_{k_y} \left( s_1(k_y) C_1^1(k_y) + s_2(k_y) C_2^2(k_y) e^{-i\pi k_y \Delta_y} \right) e^{i\pi k_y \Delta_y}
\]

\[
= S_1(y) C_1^1(y) + S_2(y - \Delta_y) C_2^2(y - \Delta_y),
\]

where \( S_1, S_2 \) are the ideal images and \( C_j^i \) the sensitivities.

The image \( S_2 \) is shifted in the k-space against the image \( S_1 \) by a single k-space line. This corresponds to a period of a half of the FOV in the image space. This produces effect similar
4. State of the art

4.9.3. UNFOLD

Similar to TGRAPPA and $k$-$t$ GRAPPA (see Section 4.4.3), UNFOLD is a method to accelerate a dynamic MRI acquisition. Unlike these methods, UNFOLD (Unaliasing by Fourier-Encoding the Overlaps Using the Temporal Dimension) [58, 60, 59] works using a single receiver coil. UNFOLD uses the fact that the $k$-$t$ space is often not filled densely and the sparsely used parts of the $k$-$t$ space can be used to increase the temporal resolution.

The acquisition is speeded up by undersampling the $k$-space in the phase-encoding direction which causes aliasing (2.27). UNFOLD method works with a single coil so the aliasing cannot be removed from a single image without any prior knowledge. Instead, the temporal information is used to remove the aliasing. A time-dependent phase-shift $f(t)$ is generated in the acquired images by shifting the $k$-space lines in each frame (the sampling scheme is similar to the TGRAPPA acquisition, see Figure 4.3). The phase-shift affecting the superimposed values is spatially dependent. The aliasing modulated by the time-variant shifts yields

$$S^A(x, y, t) = \sum_{m=0}^{M-1} S(x, y \mod \frac{Y}{M} + m\frac{Y}{M}, t) e^{i\pi mf(t)}, \quad (4.31)$$

where $f(t)$ describes the line shift in time $t$.

The phase shift weights the superimposed values and, thus, labels the parts of the aliased pixel. Fourier transform along the $t$ axis is done for each aliased pixel. Let us assume that the signal is static in time. Then the values overlapping in the spatial domain are separated in the temporal frequency domain. In practice, the object is not static and, thus, the variation of magnitude in each pixel is nonzero. The temporal frequency of each pixel becomes a distribution of frequencies instead of a Delta function. Assuming the temporal variation is not high, the values can still be separated by filtering in the temporal frequency domain, see Figure 4.8.
4.9. Applications

- **a)** Moving pixel.
- **b)** Static pixel.
- **c)** Aliased pixel.

Fig. 4.8. The temporal frequency spectrum of two overlapped pixels.

(a) A temporal frequency spectrum of a dynamic pixel. (b) Almost static pixel – the temporal spectrum of this pixel is only sparsely filled. (c) The temporal spectrum of the aliased pixel. Values of both overlapped pixels can be separated using filter $F$.

The technique can be used whenever the temporal variation of the object is low or when the $k$-$t$ space is not homogeneously filled. This is the case when one of the overlapped pixels is subject to fast movement and the second is nearly static, see Figure 4.8. The design of temporal frequency filters is not trivial and has to be adjusted to suit the specific real-time application [46]. It is also possible to use the UNFOLD method to suppress aliasing caused by undersampling in two dimension as is described by Wu [109].

The UNFOLD method can be combined with the SENSE reconstruction. The phase-shift caused by the time-variant shifting of $k$-space lines in UNFOLD does not alter the SENSE formulation and the aliasing artifacts that are not removed by SENSE because of an imperfect sensitivity estimation can be separated and removed by UNFOLD in the temporal frequency spectrum. Therefore, UNFOLD and SENSE are compatible and we can choose which method to apply first. In the combined method, the SENSE reconstruction is usually performed first due to computational advantages [44]. The SENSE method is applied on a series of aliased images. The outcome of SENSE is filtered using a low-pass filter in the temporal frequency spectrum to further suppress the aliasing artifacts [59]. The advantage of the combined use of SENSE and UNFOLD is a higher level of artifact reduction [44, 31, 56].

Estimates of sensitivity maps are necessary for the SENSE reconstruction when combined with UNFOLD. The sensitivity maps are acquired using a standard procedure (see Section 4.5.3) from full-FOV unaliased images. These images can be obtained by applying UNFOLD filtering on the undersampled images [44]. A more efficient approach was introduced by Madore in 2004 [57]. The center of $k$-space is sampled with an acceleration factor 2 and the outer part of the $k$-space is sampled with an arbitrary acceleration factor $M$. The center of the $k$-space is filtered using UNFOLD to obtain low-resolution unaliased images that can be used to obtain approximated sensitivity maps for SENSE.

4.9.4. Medical applications

Parallel MRI has a wide variety of medical applications concerning the enhancement of the spatial and the temporal resolution of the acquisition [10]. It does not require any special equipment except for a coil array and a multichannel receiver which is supplied with the most of modern machines. An implementation of one of the parallel MRI methods is present in most of the scanners and parallel MRI is used in the common practice to enhance the acquisition speed. In this section, we present several selected applications.

One of the applications of parallel MRI is cardiac MRI. Monitoring of heart motion is crucial for the detection of a proper behavior and dysfunction of this organ (for example early detection of stress-related ischemia is enabled by monitoring the cardiac cycle [105]). High frame rate is very important when imaging such a dynamic organ as a heart. Therefore,
4. State of the art

Fast single-shot techniques like EPI [94] are usually used for the acquisition. Parallel MRI is used to further speed up the acquisition. Frame rates up to 40 frames per second can be reached with SENSE for image size $64 \times 64$ pixels [105]. MR cardiac imaging can be efficiently speeded up also by SMASH [41] or PILS [40]. Parallel MRI acceleration on a three Tesla machine is reported in [64]. Unlike standard Fourier MRI, the parallel MRI images exhibit an inhomogeneous noise distribution. It depends on the coil geometry and a special coil design is needed for the cardiac imaging to reach a homogeneous noise distribution over the whole reconstructed images. There are several techniques to ensure high SNR over the whole image for the SENSE reconstruction [104, 105]. Coil configurations for the SMASH reconstruction have an extra requirement that ensures the possibility to generate the spatial harmonics easily as a linear combination of the coil sensitivities [25, 26].

High temporal resolution is important also for a functional imaging of brain. SENSE in combination with fast single shot techniques allows to acquire the whole brain fMRI scan in 1 second [21]. The spiral imaging SENSE reconstruction [76] was also successfully applied for BOLD fMRI imaging [108]. The spatial resolution is enhanced and the artifact level is reduced. However, the SENSE reconstruction of undersampled spiral images takes considerable amount of processing time [76]. The SENSE method can also be combined with diffusion weighted imaging (which is used for example to diagnose stroke patients) [5]. Diffusion-weighted images are usually acquired using the EPI technique. EPI produces many artifacts and distortions due to its high sensitivity to small frequency and phase shifts. SENSE is used to reduce the number of phase-encoding steps and, thus, to increase the velocity in the $k$-space. Shorter duration of the EPI acquisition and higher $k$-space velocity proved to reduce the EPI susceptibility to these artifacts [6]. Thus, the quality of the diffusion-weighted images [5, 4] is enhanced. Design of array coils for brain imaging is as important as for cardiac imaging [114].

MR spectroscopic imaging is an imaging method that allows to obtain the MR spectroscopy independently for each voxel of the imaged object. This can be used to investigate the local metabolite concentrations (for example to study the brain metabolism). The SENSE method was successfully applied to spectroscopic imaging to increase the spatial resolution with only slight reduction in SNR [18, 17].

MR angiography is a technique for imaging blood vessels. The contrast is usually enhanced by injecting a contrast agent. The contrast agent stays active only for a short time ($10−20$ s). Thus, the acquisition time is limited and this limits also the spatial and temporal resolution. One of the options to increase the spatial resolution is to use SENSE [107, 62]. The SENSE method can also be used to shorten the acquisition time. This reduces motion artifacts and makes the examination more comfortable for patients since the angiography is often done in a breathold session.

The SENSE method was applied for detection of hypervascular hepatocellular carcinomas which were detected from arterial phase images. Using SENSE, it is possible to increase the frame rate and, thus, acquire two arterial phase images in one breathold session instead of a single image. This enables more precise detection of carcinomas [112].

Fast switching of MRI scanner gradients during the $k$-space encoding generates a high acoustic noise. This is noticeable especially for single-shot techniques that have a high switching rate. The SENSE method can be used to reduce the number of phase-encoding steps and, thus, reduce the gradients switching rate. This reduces the acoustic noise and makes the examination more comfortable for the patient [113].
5. Parallel MRI reconstruction using B-spline Approximation

In this Chapter, we present a novel method for parallel MRI reconstruction – Parallel MRI Reconstruction using B-spline Approximation (PROBER). PROBER is an image-based reconstruction method that takes advantage of the linearity and smoothness of the reconstruction transformation. The coefficients of the reconstruction transformation are estimated directly by minimizing a reconstruction error that penalizes the presence of aliasing artifacts and the high noise variance in the reconstructed image. Unlike in the other image-based method SENSE [78], the PROBER reconstruction transformation is not estimated independently for each pixel. Instead, the reconstruction transformation is represented using B-spline functions which decreases the number of unknowns in the reconstruction. The smaller number of reconstruction coefficients regularizes the reconstruction and makes the computations more stable and faster.

First, the notation is introduced in Section 5.1. Then, the PROBER method is described in several steps. The PROBER reconstruction step including the B-spline approximation is defined in Section 5.2. There are several ways to estimate the reconstruction coefficients. The simple estimation method using similarity between the aliased and the unaliased images is presented in Section 5.3. This simple estimation is not constrained enough and, therefore, the reconstructed images contain considerable number of aliasing artifacts. This issue is solved by using perfect reconstruction conditions described in Section 5.4. Presence of noise in input images and its influence on the estimation and the reconstruction process is discussed in Section 5.5. A new estimation criterion that further improves the quality of the reconstruction is presented there. In Section 5.6, the problem of obtaining reference images is discussed. The approach using variable-density images as both input and low-resolution reference images is introduced here. Evaluation of the reconstruction error using low-resolution reference images rises the issue of B-spline undersampling during the numerical evaluation of the reconstruction error. The is solved by using continuous instead of discrete error criterion, see Section 5.7.

5.1. Notation

The task of the PROBER method is to reconstruct an ideal image $S(x, y)$ that represents the imaged object as it would be obtained using an ideal homogeneous-sensitivity coil (including relaxation and other phenomena). An array of coils with varying spatial sensitivities $C_l(x, y)$ is used for the acquisition (2.26). These coils should ideally give the images $S_l(x, y) = S(x, y)C_l(x, y)$. Truly observed values $\tilde{S}_l(x, y)$ are the ideal images $S_l(x, y)$ corrupted by noise, see Section 5.5.1. The images $\tilde{S}_l(x, y)$ have full-FOV. We call them reference images and use them to estimate the reconstruction transformation, see Section 5.2. The images $\tilde{S}_l(x, y)$ can be low-resolution and they can display different object than the object to be reconstructed. Conceptually, we should also acquire a reference image $\tilde{S}(x, y)$ using a homogeneous-sensitivity body-coil as a reference. However, in practice, the reference image $\tilde{S}(x, y)$ is estimated using the reference array-coil images $\tilde{S}_l(x, y)$ (see Section 5.6).

The input images $\tilde{S}_A^l(x, y)$ of the object to be reconstructed are obtained using array-coils
in an accelerated acquisition. Therefore, the input images $\tilde{S}_l^A$ contain aliasing (2.27)

$$S_l^A(x, y) = \sum_{m=0}^{M-1} S_l(x, y \mod \frac{Y}{M} + m \frac{Y}{M}).$$

The aliased input images $\tilde{S}_l^A(x, y)$ are used to reconstruct the output image $\hat{S}(x, y)$ which should be as close as possible to the ideal image acquired using the homogeneous-sensitivity coil.

The reference and input images mostly display the same object. However, in few cases it is necessary to distinguish which object is displayed in the images. We use a notation $S(x, y)\[v]$ to refer to the image of the object $v$. In sections where all the images display the same object, the notation $S(x, y)\[v]$ is simplified to $S(x, y)$. In this chapter, we are using a simplified notation. A symbol $S_l$ is used for $S_l(x, y)$ and symbol $S_{l,m}$ is used for $S_l(x, y \mod \frac{Y}{M} + m \frac{Y}{M})$.

### 5.2. Reconstruction

The task of the parallel MRI reconstruction is to reconstruct an unaliased image $\hat{S}$ from a set of input images $\tilde{S}_l^A$ (see Section 3.1). Noise-free images $S_l^A$ are formed from the ideal image $S$ by a composite transformation of the aliasing transformation (2.27) and the modulation by the coil sensitivity (2.26). Both transformations are linear in $S$. Thus the composite transformation from the ideal image $S$ to the array-coil image with aliasing $S_l^A$ is also linear.

We assume invertibility of this composite transformation which is an implicit assumption of all reconstruction methods and it is generally the case for any reasonable coil configuration. The inverse transformation is also linear and, neglecting the noise, we can write it as a linear combination of $L$ input images $\tilde{S}_l^A$ in the reconstruction transformation equation,

$$\hat{S}(x, y) = \sum_{l=1}^{L} \alpha_l(x, y) \tilde{S}_l^A(x, y),$$

(5.1)

where $\alpha_l(x, y)$ are complex weighting coefficients for the $l$-th coil at points $y = 1, \ldots, Y$; $x = 1, \ldots, X$ (see Figure 5.1). Since the noiseless images $S_l^A$ are not available for the reconstruction, the input images with noise $\tilde{S}_l^A$ are used. Propagation of noise to the reconstructed image is discussed in Section 5.5. The reconstruction weights $\alpha_l$ are estimated in a way to make the reconstructed image $\hat{S}$ similar to the reference images $\tilde{S}$. We present several methods to estimate the coefficients $\alpha_l$ in the following sections.

#### 5.2.1. B-spline approximation

We assume that the coil sensitivities change slowly and smoothly in space due to physical properties of the receiver coils. Consequently, the same is valid for the reconstruction transformation $\alpha_l$. Therefore, the reconstruction weights $\alpha_l$ in equation (5.1) need not to be calculated in each point independently. Instead, we approximate the weights $\alpha_l$ by smooth functions such as B-splines [2]. The solution to the parallel MRI reconstruction problem is then found in a restricted space of smooth functions represented in a B-spline basis. This has a regularization effect and it is advantageous from the computational point of view as well. The number of reconstruction parameters is reduced significantly as a low number of B-splines is sufficient to represent the reconstruction transformation (as low as 5 splines in one dimension proved to be enough to approximate the reconstruction transformation). Consequently, it is possible to estimate all the reconstruction parameters at once in a realistic time.
5.2. Reconstruction

\[ \tilde{S}_1^A \]
\[ \alpha_1 \]
\[ \tilde{S}_1^A \alpha_1 \]

\[ \tilde{S}_L^A \]
\[ \alpha_L \]
\[ \tilde{S}_L^A \alpha_L \]

\[ \hat{S} = \sum_l \tilde{S}_l^A \alpha_l \]

Fig. 5.1. The PROBER reconstruction.
The PROBER reconstruction of an unaliased image \( \hat{S} \) from a set of aliased array-coil images \( \tilde{S}_l^A \) (5.1).
The images \( \tilde{S}_l^A \) are linearly combined using complex weights \( \alpha_l \) in order to form the unaliased image \( \hat{S} \).

(Unlike in the Cartesian SENSE method [78] which does the reconstruction independently for each pixel).

B-splines

B-splines \( \beta^p \) of degree \( p \) are piecewise polynomial functions with a compact support. They are widely used for their good approximation properties [98]. We have chosen B-splines for our purpose because they approximate well smooth and slowly changing functions as are the reconstruction weights \( \alpha_l \). The approximation properties of B-splines and harmonic functions are compared in Section 6.2.1 to show the advantage of using a B-spline approximation over the approximation using harmonic functions used in the SMASH-like methods.

The zero degree B-spline \( \beta^0 \) is a box function (i.e., piecewise constant)

\[ \beta^0(x) = \begin{cases} 
1, & |x| < \frac{1}{2} \\
\frac{1}{2}, & |x| = \frac{1}{2} \\
0, & |x| > \frac{1}{2} 
\end{cases} \quad (5.2) \]

A B-spline function of degree \( p \) is obtained by \( p \) convolutions of the zero-order B-spline with itself (see Figure 5.2). Cubic B-splines have been chosen as basis functions in this work for their good cost-performance ratio [99]. Cubic B-splines are defined as

\[ \beta^3(x) = \begin{cases} 
\frac{2}{3} - |x|^2 + \frac{|x|^3}{2}, & 0 \leq |x| < 1 \\
\frac{(2-|x|)^3}{6}, & 1 \leq |x| < 2 \\
0, & 2 \leq |x| 
\end{cases} \quad (5.3) \]

47
5. Parallel MRI reconstruction using B-spline Approximation

Fig. 5.2. B-spline functions of order 0 to 3.

Approximation using B-splines

B-spline functions as presented in the previous section are one dimensional. A tensor product of shifted and scaled B-splines (see Figure 5.3) is used to represent the two-dimensional reconstruction transformation $\alpha_l$

$$\alpha_l(x, y) = \sum_{i=1}^{I} \sum_{j=1}^{J} g_{ijl} \varphi_i(y) \varphi_j(x), \quad (5.4)$$

where $J$ and $I$ is the number of B-splines used in the readout and the phase encoding direction $x$, $y$, respectively. The B-spline coefficients $g_{ijl}$ are used to represent $\alpha_l$ for the $l$-th coil. The one-dimensional B-splines $\varphi_i$ and $\varphi_j$ are evenly spaced over the image in the phase and in the frequency encoding direction, respectively,

$$\varphi_i(y) = \beta^3 \left( \frac{y - 1}{H_y} - i + 2 \right), \quad \forall i = 1, \ldots, I; \forall y = 1, \ldots, Y,$$

$$\varphi_j(x) = \beta^3 \left( \frac{x - 1}{H_x} - j + 2 \right), \quad \forall j = 1, \ldots, J; \forall x = 1, \ldots, X, \quad (5.5)$$

where $Y$, $X$ is the image size in the phase, the frequency encoding direction, respectively, and $H_y$, $H_x$ are spline function widths (i.e., the scale)

$$H_y = \frac{Y}{I-3},$$

$$H_x = \frac{X}{J-3}. \quad (5.6)$$

Note that the shift ($+2$) in the equation (5.5) is chosen so that at least three basis functions are non-zero at each pixel position to ensure full representability of any spline with given knots [98].

The values of $I$ and $J$ are determined according to the desired quality of the reconstruction. Higher number of B-splines allows to approximate the reconstruction transformation more precisely but it increases the computational complexity of the algorithm. Usually 4 to 15 splines are used in each dimension. This topic is discussed more thoroughly in Section 7.3.2.

5.3. Simple estimation

In this Section, we derive a simple method for estimation of the reconstruction weights $\alpha_l$ in the equation (5.1). The reconstruction quality criterion is the square difference error

$$e = \| \hat{S} - \tilde{S} \|^2_{x,y}, \quad (5.7)$$
where $\| \cdot \|^2_{x,y}$ is a squared $l_2$ norm over all $x = 1, \ldots, X - 1$ and $y = 1, \ldots, Y$.

In the simple method, noise in the observed images is neglected. The reconstructed image $\hat{S}$ is expressed from the reconstruction equation (5.1) yielding

$$
e = \left\| \sum_{l=1}^{L} \alpha_l \tilde{S}_l^A - \hat{S} \right\|^2_{x,y}
= \sum_{x=1}^{X} \sum_{y=1}^{Y} \left( \sum_{l=1}^{L} \alpha_l (x, y) \tilde{S}_l^A (x, y) - \hat{S} (x, y) \right)^2.
$$

The reconstruction weights $\alpha_l$ are not estimated directly. Instead, the B-spline approximation is used (5.4). The error criterion is then rewritten as

$$
e = \sum_{x,y=1}^{X,Y} \left( \sum_{l'=1}^{L} \sum_{i,j=1}^{I,J} g_{ijl'} \varphi_i (y) \varphi_j (x) \tilde{S}_l^A (x, y) - \hat{S} (x, y) \right)^2.
$$

We also use the identity $|z|^2 = zz^*$, where $^*$ stands for the complex conjugated value.

$$
e = \sum_{x,y=1}^{X,Y} \left( \sum_{l'=1}^{L} \sum_{i,j=1}^{I,J} g_{ijl'} \varphi_i \varphi_j \tilde{S}_l^A \hat{S} - \tilde{S}^* \right) \left( \sum_{l=1}^{L} \sum_{i,j=1}^{I,J} g^*_{ijl} \varphi_i \varphi_j \tilde{S}_l^A^* \hat{S}^* - \hat{S}^* \right).
$$

(5.8)

The task is to find the B-spline coefficients $\hat{g}_{ijl}$ that minimize the reconstruction error given by the equation (5.7)

$$
\hat{g}_{ijl} = \text{argmin}_{g_{ijl}} e.
$$

Partial derivatives of the error criterion (5.8) are computed for each $i, j$ and $l$. They have to be zero at the minimum. The function $e(g_{ijl}, g^*_{ijl})$ is considered to be a function of $g_{ijl}$ and $g^*_{ijl}$ and the partial derivatives with respect to $g^*_{ijl}$ are computed. The derivatives $\partial e/\partial g^*_{ijl}$ are set to zero in order to find the minimum of the reconstruction error (5.7)

$$
\frac{\partial e}{\partial g^*_{ijl}} = 0
$$

$$
= \sum_{x,y=1}^{X,Y} \sum_{l'=1}^{L} \sum_{i,j=1}^{I,J} g_{ijl'} \varphi_i \varphi_j \varphi_{i'} \varphi_{j'} \tilde{S}_l^A \tilde{S}_l^A^* - \varphi_i \varphi_j \tilde{S}_l^A \hat{S}
= \sum_{x,y=1}^{X,Y} \sum_{l'=1}^{L} \sum_{i,j=1}^{I,J} g_{ijl'} \varphi_i \varphi_j \tilde{S}_l^A \tilde{S}_l^A^* - \hat{S},
$$

(5.9)
5. Parallel MRI reconstruction using B-spline Approximation

Fig. 5.4. Simple PROBER.
In the simple PROBER estimation, reference images with aliasing are used for the estimation. The correlation between these aliased images and the ideal image is used to determine the reconstruction coefficients. The same transformation is, thus, used in the estimation and the reconstruction.

The equation (5.9) is evaluated for \( \forall i, j, l \) yielding \( I \cdot J \cdot L \) linear equations with the same number of variables. There are several ways how to solve this linear system of equations such as the Gauss-Newton elimination method or the Singular value decomposition (SVD) [20]. The solution of the system is a vector of the reconstruction coefficients \( g_{ijl} \) that is used to compute the reconstruction weights \( \alpha_l \) (5.4) which are in turn used for the reconstruction (5.1).

The simple solution has several disadvantages. The sensitivity information from the reference images \( \tilde{S}_l[v] \) is not used during the estimation step (5.8). Instead, the aliased version of the reference images \( \tilde{S}^A_l[v] \) is used. Thus only the correlation between the homogeneous-coil reference image \( \tilde{S}_l[v] \) and the unaliased images \( \tilde{S}_l[v] \) is used to determine the reconstruction coefficients, see Figure 5.4. The effect of this is that the reconstruction method is working well only if the reference \( \tilde{S}_l[v] \) and input images \( \tilde{S}_l^A[w] \) images display the same object \( (v = w) \). The reconstruction quality is degraded when low resolution reference images are used. Aliasing artifacts appear when a different object appears in the reference and input images \( (v \neq w) \) [70]. See Section 7.4.1 for example of the problems in the simple reconstruction.

5.4. Perfect reconstruction conditions

The simple estimation is not constrained enough. The information in the reference images \( S_l \) can be used to improve the estimation of the reconstruction coefficients. This is done by stating the orthogonality reconstruction conditions [68, 72].

Substituting the aliasing equation (2.27) in the reconstruction transformation equation (5.1) yields

\[
\tilde{S}(x, y) = \sum_{l=1}^{L} \alpha_l(x, y) \sum_{m=0}^{M-1} S_l(x, y \mod \frac{Y}{M} + m \frac{Y}{M}) = \sum_{l=1}^{L} \sum_{m=0}^{M-1} \alpha_l(x, y) S_l(x, y \mod \frac{Y}{M} + m \frac{Y}{M}).
\]  

As can be seen from the equation (5.10), each pixel is reconstructed as a linear combination of values on several spatial positions. Due to generality of the imaged objects, the intensity
5.4. Perfect reconstruction conditions

The perfect reconstruction conditions (5.11) are illustrated in the figures (a), (b) for the acceleration factor \( M = 2 \). In the figure (a), we show the conditions for the upper half of the image – the sum \( \sum_{l=1}^{L} \alpha_l(x, y) S_l(x, y) = S(x, y) \) for \( y = 1, \ldots, Y/2 \) whereas the contribution of the aliased component is zero \( \sum_{l=1}^{L} \alpha_l(x, y + Y/2) S_l(x, y + Y/2) = 0 \). The reconstruction is showed in (c). The input images \( S^A \) contain aliasing. The lower and the upper part of the images are summed. They correspond to the sum of the images from (a), (b). By applying the reconstruction transformation \( \alpha \) estimated under the perfect reconstruction conditions, we obtain an image \( \hat{S} \) without aliasing (c).

Values of \( S(x, y) \), \( S_l(x, y) \) are independent of values of \( S(x', y') \), \( S_l(x', y') \), respectively, on any other spatial position \( (x \neq x', y \neq y') \). Hence, the value of \( \hat{S}(x, y) \) must be independent on \( S_l(x, y \mod \frac{Y}{M} + m \frac{Y}{M}) \) for \( m \neq 0 \). This observation gives rise to the perfect reconstruction conditions that further constrain the reconstruction transformation \( \alpha \). The condition is (in the full and then in the shortened notation)

\[
\sum_{l=1}^{L} \alpha_l(x, y \mod \frac{Y}{M} + m \frac{Y}{M}) S_l(x, y \mod \frac{Y}{M} + m' \frac{Y}{M}) = \delta_{m,m'} S(x, y \mod \frac{Y}{M} + m \frac{Y}{M}),
\]

\[
\sum_{l=1}^{L} \alpha_l m S_l = \delta_{m,m'} S_m,
\]

for all \( m, m' = 0, \ldots, M - 1 \) and \( y = 1, \ldots, \frac{Y}{M} \), where \( \delta_{m,m'} \) is Kronecker delta that is equal to 1 for \( m = m' \) and zero elsewhere. The reconstruction conditions for the acceleration factor \( M = 2 \) are illustrated on an example in Figure 5.5.

5.4.1. Justification of the perfect reconstruction conditions

The estimation step is done using the reference images \( S_l[v] \) displaying the object \( v \). Under the assumption that the value of \( S \) is non-zero everywhere, it can be divided out from the
equation (5.11) using (2.27) as follows

\[ \sum_{l=1}^{L} \alpha_{l,m} S_{l,m'}[v] = \delta_{m,m'} S_{m}[v] \]

\[ \sum_{l=1}^{L} \alpha_{l,m} S_{m'}[v] C_{l,m'} = \delta_{m,m'} S_{m}[v] \]

\[ \sum_{l=1}^{L} \alpha_{l,m} C_{l,m'} = \delta_{m,m'} , \quad (5.12) \]

This constrains the transformation \( \alpha_{l} \). The transformation \( \alpha_{l} \) is then used to reconstruct the unaliased image from the set of images \( S_{l}^{A}[w] \) of a different object \( w \). Images \( S_{l}^{A}[w] \) are acquired using the same coil configuration as the images \( S_{l}[v] \).

\[ \sum_{l=1}^{L} \alpha_{l,m} S_{l}^{A}[w] = \sum_{l=1}^{L} \alpha_{l,m} \sum_{m'=0}^{M-1} S_{l,m'}[w] C_{l,m'} \]

\[ = \sum_{m'=0}^{M-1} S_{m'}[w] \sum_{l=1}^{L} \alpha_{l,m} C_{l,m'} = \sum_{m'=0}^{M-1} S_{m'}[w] \delta_{m,m'} \]

\[ = S_{m}[w] . \]

This shows that an unaliased image corresponding to the input images is perfectly reconstructed even when the reconstruction transformation is estimated using different object but the same coil configuration. This validates the perfect reconstruction conditions (5.11).

### 5.4.2. Reconstruction error

Ideally, the reconstruction conditions (5.11) should be fulfilled. However, neither the noise-free reference images \( S_{l} \) nor the sensitivity maps \( C_{l} \) are directly available. We can only access images \( \tilde{S}_{l} \) which are corrupted by noise. Therefore, we shall use the noisy reference images \( \tilde{S} \) and \( \tilde{S}_{l} \) instead and solve the system of equations analogous to (5.11) in the least square sense by minimizing the error

\[ e = \sum_{m,m'=0}^{M-1} \left( \sum_{l=1}^{L} \alpha_{l,m} \tilde{S}_{l,m'} - \delta_{m,m'} \tilde{S}_{m} \right)^{2} . \quad (5.13) \]

The reference images \( \tilde{S}_{l} \) are complex and the error (5.13) can be rewritten as

\[ e = \sum_{x,y=1}^{X,Y} \sum_{m,m'=0}^{M-1} \left( \sum_{l=1}^{L} \alpha_{l,m} \tilde{S}_{l,m'} - \delta_{m,m'} \tilde{S}_{m} \right)^{2} . \]

\[ = \sum_{l=1}^{L} \sum_{m,m'=0}^{M-1} \left( \sum_{l=1}^{L} \alpha_{l,m} \tilde{S}_{l,m'} - \delta_{m,m'} \tilde{S}_{m} \right)^{2} \]

We substitute the B-spline approximation of the reconstruction weights \( \alpha \) (5.4). The partial derivatives with respect to \( g_{ij}^{*} \) are computed and set to zero in order to find the minimal
5.5. Acquisition noise

From the equation (5.14) we derive the solution which is a system of \( I \cdot J \cdot L \) linear equations with the same number of variables

\[
\sum_{x,y=1}^{X,Y} \varphi_i \varphi_j \tilde{S}_l^* = \sum_{m,m'=0}^{M-1} \sum_{x,y=1}^{X,Y} \sum_{i',j',l'=1}^{I,J,L} g_{i'i'} \varphi_{i,m} \varphi_{j,m'} \tilde{S}_{i',m'}^* \tilde{S}_{l,m'}^* .
\]  (5.15)

The system is solved using the standard means as in the simple case, see Section 5.3.

The estimation using the perfect reconstruction conditions (5.11) gives better estimates of the reconstruction weights \( \alpha_l \). The difference in the reconstruction quality between the images reconstructed using simple reconstruction conditions and the perfect reconstruction conditions is shown in Section 7.4.1. The estimation now depends less on the characteristics of the reference images. Thus, the reference and the input objects can be different without any significant negative effects on the reconstruction quality.

5.5. Acquisition noise

Presence of noise in the reference images is still not taken into account explicitly in the reconstruction method that uses the perfect reconstruction conditions described in Section 5.4. However, the effect of noise needs to be studied to ensure high-quality reconstruction with noisy images. This section describes how to deal with the image noise issues. The newly proposed approach is compared with the method from the previous section in Section 7.4.2.

In MRI, the acquired data is corrupted by noise. Thus, the observed values \( \tilde{S}_l \) are not identical with the ideal values \( S_l \) – there is an additive noise present in the images (see also Section 5.5.1). This complicates the parallel MRI reconstruction in two ways. First, noise in reference images deteriorates the estimation process especially in the areas with low signal (see Section 5.5.2). Second, noise in the input images is amplified by the reconstruction transformation, it is propagated to the final image and it degrades its quality (see Section 5.5.3).

Here, we present a way how to suppress the negative effect of noise and improve the quality of the reconstruction. A new stochastic term is added to the reconstruction error and a more efficient solution is derived (see Section 5.5.4). At the end of the section we show how to implement the estimation process more efficiently (see Section 5.5.5).

5.5.1. Noise in MRI images

It is assumed that MRI images contain zero mean Gaussian noise in the both real and imaginary parts of the image. The real and the imaginary parts of the noise are uncorrelated and characterized by the same variance. We also assume that the images are prewhitened to
5. Parallel MRI reconstruction using B-spline Approximation

Fig. 5.6. Rician distribution.
Probability density functions of the Rician distribution for $S = 0, 0.5, 1, 2, 4$ and standard deviation (a) $\sigma = 1$, (b) $\sigma = 0.25$. The image (c) shows the modified Bessel functions of the first kind $I_0$.

remove the noise correlation between receiver channels. This can be done by multiplying the data with the inverse of the Hermitian square root of the noise covariance matrix [53].

The observed values containing the additive noise are defined as

$$\tilde{S}_l(x, y) = S_l(x, y) + v_l(x, y),$$
$$\tilde{S}(x, y) = S(x, y) + v(x, y),$$

(5.16)

where $v$ and $v_l$ are random variables corresponding to the noise in the acquired images. Probability distribution of the random variables is zero-mean Gaussian

$$p(v_l(x, y)) \sim N(0, \sigma_l),$$
$$p(v_i(x, y)) \sim N(0, \sigma_l),$$

(5.17)

where the random variables $v_r$ and $v_i$ describes the noise properties of the real and the imaginary part, respectively, of the signal in the $l$-th receiver coil.

**Rician distribution**

A squared reconstruction error and magnitude reference images $|\tilde{S}_l|$ are used in the following sections in the estimation of the reconstruction coefficients. The noise probability distribution in these images is described by the Rician distribution.

Absolute value $|\tilde{S}|$ of $\tilde{S}$ as described in (5.16) and (5.17) has Rician distribution [82],

$$p(|\tilde{S}| \mid |S|) = \frac{|\tilde{S}|}{\sigma^2} e^{-\left(|\tilde{S}|^2 + |S|^2\right)/2\sigma^2} I_0 \left(\frac{|\tilde{S}| |S|}{\sigma^2}\right),$$

(5.18)

where $I_0$ is the modified zeroth order Bessel function of the first kind (see Figure 5.6) and $\sigma^2$ is the variance of the real and the imaginary part of the Gaussian noise in the image.

Shape of the probability density function of Rician noise differs with the image SNR $=$ $|S|/\sigma$, see Figure 5.6. For large SNR, the Rician probability density function (5.18) becomes approximately Gaussian

$$p(|\tilde{S}| \mid |S|) \approx \frac{1}{\sqrt{2\pi}\sigma^2} e^{-\left(|\tilde{S}| - \sqrt{|S|^2 + \sigma^2}\right)^2 / 2\sigma^2}.$$

The variance of the Rician distribution in the magnitude image with high SNR is $\sigma^2$ and mean is $\sqrt{|S|^2 + \sigma^2}$ [30].
5.5. Acquisition noise

In the regions with noise only (i.e., $|S| = 0$), Rician distribution becomes Rayleigh distribution [1]. The probability density function of a random variable $v$ with Rayleigh distribution is (5.17)

$$p(|v|) = \frac{|v|}{\sigma^2} e^{-|v|^2 / 2\sigma^2}.$$  \hfill (5.19)

Shape of the density function is shown in Figure 5.7. The mean value is

$$E(|v|) = \sigma \sqrt{\pi/2}$$

and the variance is

$$\text{var}(|v|) = (2 - \pi/2) \sigma^2.$$  \hfill (5.20)

Properties of Gaussian distribution

In the following computations, several basic properties of Gaussian distribution are used. Let $X \sim N(0, \sigma_X^2)$ and $Y \sim N(0, \sigma_Y^2)$ be independent zero-mean random variables with Gaussian distribution and variances $\sigma_X^2$ and $\sigma_Y^2$.

A linear combination $aX + bY$ with arbitrary constants $a$, $b$ has zero mean and variance $a^2\sigma_X^2 + b^2\sigma_Y^2$. The product distribution $XY$ has also zero mean.

The mean of $X^2$ is computed as

$$E(X^2) = \text{var}(X) = \sigma^2.$$  

Let $Z$ be a complex random variable that is composed of two independent real normal distributions $X, Y$ as $Z = X + iY$. The mean of $|Z|^2 = ZZ^*$ is

$$E(ZZ^*) = E(X^2 + Y^2) = E(X^2) + E(Y^2) = 2\sigma^2.$$  \hfill (5.20)

5.5.2. Noise in the estimation

The reconstruction transformation $\alpha_l$ is estimated using noisy reference images $\tilde{S}_l$. Noise in the reference images makes the estimation less stable especially in regions with low SNR. In the previous section, the reconstruction coefficients are estimated by minimizing the error in the perfect reconstruction conditions, equation (5.13). In this section, we show how to minimize the expectation of the true error $e = ||\tilde{S} - S||$ that is the squared difference of the reconstructed image compared with the ideal noise-free image. Let us analyze the error (5.13)
computed using noisy images (5.16)

\[
\tilde{e} = \sum_{m,m'=0}^{M-1} \left( \sum_{l=1}^{L} \alpha_{l,m} \tilde{S}_{l,m'} - \delta_{m,m'} \tilde{S}_m \right)^2
\]

\[
\tilde{e}_{x,y}^{m,m'} = \sum_{l=1}^{L} \alpha_{l,m} (S_{l,m'} + v_{l,m'}) - \delta_{m,m'} (S_m + v_m)
\]

\[
\tilde{e}_{x,y}^{m,m'} = \sum_{l=1}^{L} \alpha_{l,m} (S_{l,m'} + \delta_{m,m'} S_m)
\]

\[
+ 2 \text{Re} \left( \left( \sum_{l} \alpha_{l,m} S_{l,m'} - \delta_{m,m'} S_m \right) \left( \sum_{l} \alpha_{l,m} \delta_{m,m'} v_m \right) \right)
\]

\[
- 2 \text{Re} \left( \sum_{l} \alpha_{l,m} \delta_{m,m'} v_m \right) + \left| \sum_{l} \alpha_{l,m} v_{l,m'} \right|^2 + \left| \delta_{m,m'} v_m \right|^2.
\]  

The mean of \( E[\tilde{e}] \) is

\[
E[\tilde{e}_{x,y}^{m,m'}] = E \left[ \sum_{l} \alpha_{l,m} S_{l,m'} - \delta_{m,m'} S_m \right]^2
\]  

\[
+ E \left[ 2 \text{Re} \left( \left( \sum_{l} \alpha_{l,m} S_{l,m'} - \delta_{m,m'} S_m \right) \sum_{l} \alpha_{l,m} \delta_{m,m'} v_m \right) \right]
\]  

\[
- E \left[ 2 \text{Re} \left( \left( \sum_{l} \alpha_{l,m} S_{l,m'} - \delta_{m,m'} S_m \right) \delta_{m,m'} v_m \right) \right]
\]  

\[
+ E \left[ \sum_{l} \alpha_{l,m} v_{l,m'} \right]^2 + \left| \delta_{m,m'} v_m \right|^2.
\]  

Probability distribution of the random variable \( v(x, y) \) describing noise in the ideal reference image \( \tilde{S} \) depends on the way how the image \( \tilde{S} \) is obtained. Construction of the image \( \tilde{S} \) is discussed in Section 5.6. We have restricted our attention to the case when the array-coil image \( \tilde{S}_l \) is chosen as the ideal reference image \( \tilde{S} = \tilde{S}_l \) (see Section 5.6). The variable \( v(x, y) \) becomes equal to \( v_l(x, y) \) for \( l' \) determining the reconstructed array-coil image.

The term (5.22) is a deterministic value and its mean value is equal to the true error \( \tilde{e}_{x,y}^{m,m'} \) (5.21). Terms (5.23) and (5.24) contain linear combinations of random variables with zero-mean Gaussian distribution and their mean value is, thus, zero. The term (5.25) can be rewritten as

\[
E \left[ 2 \text{Re} \left( \sum_{l} \alpha_{l,m} \delta_{m,m'} v_m \right) \right] = \delta_{m,m'} E \left[ 2 \text{Re} \left( \sum_{l \neq l'} \alpha_{l,m} \delta_{l,m} v_{l',m} + \alpha_{l',m} \delta_{l',m} v_{l,m} \right) \right].
\]
The first term is a product of two independent zero-mean Gaussian random variables and has a zero mean. The second term has a mean equal to \( 4 \langle \delta_{m,m'} \rangle \text{Re}(\alpha_{l',m}) \sigma^2_{\alpha_l} \).

The first term in (5.26) is a square of a linear combination of Gaussian random variables (5.20). Its mean value is \( 2 \sum_l |\alpha_{l,m}|^2 \sigma^2_{\alpha_l} \). The mean value of the second term is \( 2 \delta_{m,m'} \sigma^2_{\alpha_l} \). The mean value of the observed error \( \tilde{e} \) calculated using noisy reference images is therefore

\[
\mathbb{E}[e^{m,m'}_{x,y}] = \left| \sum_l \alpha_{l,m} S_{l,m'} - \delta_{m,m'} S_m \right|^2 - 4 \delta_{m,m'} \text{Re}(\alpha_{l,m}) \sigma^2_{\alpha_l} + 2 \sum_l |\alpha_{l,m}|^2 \sigma^2_{\alpha_l} + 2 \delta_{m,m'} \sigma^2_{\alpha_l} \\
= e^{m,m'}_{x,y} - 4 \delta_{m,m'} \text{Re}(\alpha_{l',m}) \sigma^2_{\alpha_l} + 2 \sum_l |\alpha_{l,m}|^2 \sigma^2_{\alpha_l} + 2 \delta_{m,m'} \sigma^2_{\alpha_l} . \tag{5.27}
\]

The last term \( (2 \delta_{m,m'} \sigma^2_{\alpha_l}) \) depends only on the noise variance in the reference images. It is independent of the reconstruction transformation values and we can neglect it.

The error (5.27) was deduced as a mean value of the squared error (5.13). Thus, the mean error should be equal to or greater than zero. We show this in the following text:

\[
e^{m,m'}_{x,y} - 4 \delta_{m,m'} \text{Re}(\alpha_{l',m}) \sigma^2_{\alpha_l} + 2 \sum_l |\alpha_{l,m}|^2 \sigma^2_{\alpha_l} + 2 \delta_{m,m'} \sigma^2_{\alpha_l} \geq 0 .
\]

The deterministic part of the error \( e^{m,m'}_{x,y} \) is always positive, thus, it can be removed from the inequality

\[
2 \sum_l |\alpha_{l,m}|^2 \sigma^2_{\alpha_l} - 4 \delta_{m,m'} \text{Re}(\alpha_{l',m}) \sigma^2_{\alpha_l} + 2 \delta_{m,m'} \sigma^2_{\alpha_l} \geq 0 .
\]

Terms in the first sum are positive, thus, we remove them for \( l \neq l' \). The inequality is then divided by 2

\[
\left( \text{Re}^2(\alpha_{l',m}) + \text{Im}^2(\alpha_{l',m}) \right) \sigma^2_{\alpha_l} - 2 \delta_{m,m'} \text{Re}(\alpha_{l',m}) \sigma^2_{\alpha_l} + \delta_{m,m'} \sigma^2_{\alpha_l} \geq 0
\]

The imaginary part of the first term is positive and, thus, it is removed without changing the validity of the inequality

\[
2 \text{Re}^2(\alpha_{l',m}) \sigma^2_{\alpha_l} - 2 \delta_{m,m'} \text{Re}(\alpha_{l',m}) \sigma^2_{\alpha_l} + \delta_{m,m'} \sigma^2_{\alpha_l} \geq 0
\]

The inequality is divided by a positive term \( \sigma^2_{\alpha_l} \) and we use the fact that for Kronecker delta it is valid that \( \delta_{m,m'} = \delta^2_{m,m'} \)

\[
\text{Re}^2(\alpha_{l',m}) - 2 \delta_{m,m'} \text{Re}(\alpha_{l',m}) + \delta^2_{m,m'} \geq 0
\]

\[
\left( \text{Re}(\alpha_{l',m}) - \delta_{m,m'} \right)^2 \geq 0 ,
\]

which proves the positiveness of the mean error as computed in the equation (5.27).

5.5.3. Noise in the reconstruction

An important source of errors in the reconstructed image is the noise in the input images \( S_l^A \). The input images \( S_l^A \) are linearly combined using the reconstruction transformation \( \alpha_l \). Thus, the input noise is also combined and propagated into the reconstructed image \( \hat{S} \). Our aim is to minimize this effect and, thus, reduce the noise variation in the reconstruction.
5. Parallel MRI reconstruction using B-spline Approximation

Propagation of noise by the reconstruction (5.1) is described in the following equation (assuming a perfect reconstruction with no aliasing artifacts)

\[ \hat{S}(x, y) = \sum_{l=1}^{L} \alpha_l(x, y) \tilde{S}_l^A(x, y) = \sum_{l=1}^{L} \left( \alpha_l(x, y) \tilde{S}_l^A(x, y) \right) + \sum_{l=1}^{L} \left( \alpha_l(x, y) v_l(x, y) \right). \quad (5.28) \]

Noise \( v_l \) in the input images \( \tilde{S}_l \) has zero-mean and it has Gaussian distribution. Thus, the noise in the reconstructed image \( \hat{S} \) is also zero-mean Gaussian. We shall minimize the total noise variance in the equation (5.28) in order to achieve a high quality [71].

Noise variance in the real part of the reconstructed image \( \hat{S} \) is

\[ \sigma_R^2 = \text{var} \left( \text{Re} \left( \sum_{l=1}^{L} \alpha_l v_l \right) \right) = \text{var} \left[ \sum_{l=1}^{L} \left( \alpha_l^R v_l^R - \alpha_l^I v_l^I \right) \right] \]

\[ \sigma_R^2 = \sum_{l=1}^{L} \text{var} \left[ \alpha_l^R v_l^R \right] - \text{var} \left[ \alpha_l^I v_l^I \right] = \sum_{l=1}^{L} (\alpha_l^R)^2 \sigma_l^2 + (\alpha_l^I)^2 \sigma_l^2 \]

\[ \sigma_R^2 = \sum_{l=1}^{L} |\alpha_l|^2 \right \} \sigma_l^2. \quad (5.29) \]

Noise variance in the imaginary part is computed in a similar way and the result is equivalent to the variance in the real part (5.29). Magnitude of the reconstructed image then has Rayleigh distribution (5.19) and its total noise variance is

\[ \text{var} \left( |\hat{S}| \right) = (2 - \pi/2) \sum_l |\alpha_l|^2 \sigma_l^2. \quad (5.30) \]

The values of the reconstruction transformation \( \alpha_l \) should be estimated in a way to minimize the total noise variance in the reconstruction (5.30) to further improve the quality of the reconstruction. This is done by minimizing the squared sum of the reconstruction transformation amplitude \( \alpha_l \) in each point weighted by the coil noise variance as is described in the following section.

5.5.4. Error criterion

The knowledge about noise derived in the previous two sections is used to improve the error equation and consequently to improve the quality of the PROBER estimation. The expected value of the error is minimized (5.27). A term minimizing the output noise is added (5.30). The error, as stated here, is computed for the case coil image \( \tilde{S}_k \) taken as the reference image \( \hat{S} \)

\[ e = \sum_{m,m'=0}^{M-1} \left\| \sum_{l=1}^{L} \alpha_{l,m} \tilde{S}_{l,m'} - \delta_{m,m'} \tilde{S}_m \right\|_{x,y}^2 + \lambda \sum_l |\alpha_l|^2 (4 - \pi/2)|\alpha_l|^2 x,y) - 4 \lambda \text{Re}(\alpha_k)\sigma_k^2, \quad (5.31) \]

where the parameter \( \lambda \) controls the tradeoff between the deterministic and the stochastic part of the error. The parameter \( \lambda \) can be ideally set to 1 to produce the lowest error. However in practice, removing of aliasing can be more important than the level of noise in the reconstructed image. Thus, the parameter \( \lambda \) can be decreased to reduce noise suppressing in the reconstruction in favor of the aliasing removal. The quality of the results is then increased although the reconstruction error is decreased. This is shown in Section 7.3.5 where the optimal value of \( \lambda \) is discussed.
The error is minimized in the same way as in the previous section, cf. (5.14). Thus, it is necessary to compute only the partial derivatives of the new term
\[ e^{\text{noise}} = \lambda \sum_i \sigma_i^2 \left( (4 - \pi/2)|\alpha_i|^2_{x,y} - 2 \lambda(\alpha_k + \alpha_k')\sigma_k^2 \right) \]

\[
\frac{\partial e^{\text{noise}}}{\partial g_{ijl}} = \lambda \sum_{x,y} \varphi_i \varphi_j \left( 2\sigma_k^2 + \left( \sum_{i',j'} (4 - \pi/2) \sigma_i'^2 g_{i'j'} \varphi_i' \varphi_j' \right) \right). \tag{5.32}
\]

The term (5.32) is added to the linear system (5.15). This gives rise to a system of linear equations
\[
AG = B, \tag{5.33}
\]
where \( G \) is a vector of the unknown B-spline coefficients \( g_{ijl} \) and the matrices \( A \) and \( B \) are defined as follows
\[
A_{ijkl} = \sum_{m,m'=0}^{M-1} \sum_{x,y=1}^{X,Y} \varphi_{i,m} \varphi_{i',m'} \varphi_j \varphi_{j'} \left( \tilde{S}_{i',m'} \tilde{S}_{l,m'} + \frac{4 - \pi/2}{M} \delta_{i,l'} \lambda \sigma_k^2 \right),
\]
\[
B_{ij} = \sum_{x,y=1}^{X,Y} \varphi_i \varphi_j \left( \tilde{S}_i \tilde{S} + 2\lambda \sigma_k^2 \right). \tag{5.34}
\]

### 5.5.5. Efficient implementation

An efficient implementation of the PROBER estimation using the error criterion taking into account noise (5.31) is described in this section.

It is computationally very demanding to build the matrix \( A \) prescribed by the equation (5.34). It can be seen that \( O(X^2 I^4 L^4 M) \) multiplications are needed (assuming \( X = Y \) and \( I = J \)). This process can be speeded up by using the symmetry in the matrix. The matrix is symmetric in \( i/i', j/j' \) and Hermitian in \( l/l' \) – therefore it is sufficient to compute just 1/8 of the elements of the matrix \( A \) and the rest is given by symmetry.

B-splines are separable in \( x/y \). This fact can be used for evaluating values of the matrices \( A \) and \( B \). The summations can be regrouped and computed separately which reduces the time complexity significantly to \( O(X/MI^2 L^2 (X + I^2)) \)

\[
A_{ijkl} = \sum_{y=1}^{Y} \left( \sum_{m=0}^{M-1} \varphi_{i,m} \varphi_{i',m} \right) \left( \sum_{x=1}^{X} \varphi_j \varphi_{j'} \left( \tilde{S}_{i',m} \tilde{S}_{l,m} + \frac{4 - \pi/2}{M} \delta_{i,l'} \lambda \sigma_k^2 \right) \right),
\]
\[
B_{ij} = \sum_{x=1}^{X} \varphi_i \sum_{x=1}^{X} \varphi_j \left( \tilde{S}_i \tilde{S} + 2\lambda \sigma_k^2 \right),
\]

where the vectorization of the 2D matrix \( A \) is defined as
\[
A_{ijkl} = A(i + jI, i' + j'I, l + l'I)
\]
and likewise for the vectors \( g \) and \( B \).

The matrix \( A \) is Hermitian and positive definite (proof follows) [71]. Therefore, it is possible to use Cholesky decomposition (that always exists for a Hermitian and positive definite matrix [22]) to solve the linear system (5.33). Cholesky decomposition is about twice as fast as the Gauss-Newton elimination method and it is also more stable [73]. Cholesky decomposition is used to obtain the decomposition \( A = Q^TQ \), where \( Q \) is an upper triangular matrix. Finding the solution of (5.33) with the decomposed matrix \( A \) is handled by simple back substitution.
Matrix $A$ properties

Let us prove that the matrix $A$ (5.33) is Hermitian and positive definite. It is clear from (5.33) that the matrix $A$ is symmetric for $i/i'$ and also for $j/j'$ (note that the functions $\varphi_j$ and $\varphi_i$ are real). From

$$ S_{ij} S_{i'}^* = (S_{i'}^* S_{ij})^* $$

it is obvious that $A_{[ijl; i'j'l']} = A_{[i'j'l'; ij]}^*$ which is the definition of the Hermitian matrix property.

The matrix $A$ is also positive definite. The definition of positive definiteness is that for all nonzero vectors $\forall g \in \mathbb{C}^I$, $g \neq 0$

$$ 0 < g^H A g, $$

$$ 0 < \sum_{m,m'=0}^{M-1} \sum_{x,y=1}^{X_Y} \sum_{i,j,l} \sum_{i',j',l'} g_{ijl} g_{i'j'l'} \varphi_{i,m} \varphi_{i',m} \varphi_j \varphi_{j'} \left( \tilde{S}_{i',m'} \tilde{S}_{i,m'}^* + \frac{4 - \pi/2}{M} \delta_{i',i} \lambda \sigma_i^2 \right) $$

$$ 0 < \sum_{m,m'=0}^{M-1} \sum_{x,y=1}^{X_Y} \sum_{i,j,l} \sum_{i',j',l'} g_{ijl} g_{i'j'l'} \varphi_{i,m} \varphi_{i',m} \varphi_j \varphi_{j'} \left( \tilde{S}_{i',m'} \tilde{S}_{i,m'}^* \right) $$

$$ + \sum_{i,j,l} \sum_{i',j',l'} g_{ijl} g_{i'j'l'} \frac{4 - \pi/2}{M} \delta_{i',i} \lambda \sigma_i^2. $$

The last term is always greater than or equal to zero. So it suffices to prove that

$$ 0 < \sum_{m,m'=0}^{M-1} \sum_{x,y=1}^{X_Y} \sum_{i,j,l} \sum_{i',j',l'} g_{ijl} g_{i'j'l'} \varphi_{i,m} \varphi_{i',m} \varphi_j \varphi_{j'} \left( \tilde{S}_{i',m'} \tilde{S}_{i,m'}^* \right) $$

(5.35)

where $g^H = (g^*)^T$ is a complex conjugate of the transposed vector $g$. For any sequence $r_l \in \mathbb{C}^L$ is valid that

$$ \sum_{l,l'} r_l^* r_{l'} = \left( \sum_{l} r_l^* \right) \left( \sum_{l} r_l \right) = \left( \sum_{l} r_l \right)^* \left( \sum_{l} r_l \right) \geq 0, $$

(5.36)

thus, for $\forall x, y, m, m'$ it holds that

$$ \left( \sum_{i,j} g_{ijl} \varphi_{i,m} \varphi_j \tilde{S}_{i,m'}^* \right) \left( \sum_{i',j'} \varphi_{i',m} \varphi_j \tilde{S}_{i',m'} \right) \geq 0 $$

(5.37)

and

$$ \frac{\lambda}{M} \sum_l \sum \sigma_i^2 \left( \sum_{i,j} g_{ijl} \varphi_i \varphi_j \right) \left( \sum_{i',j'} \varphi_{i',m} \varphi_j \tilde{S}_{i',m'}^* \right) \geq 0. $$

(5.38)

The equality arises only when $\sum_l r_l = 0$ in (5.36). The functions $\varphi_i \varphi_j(x, y)$ form a linearly independent basis. Thus, the sum $\sum_{i,j} g_{ijl} \varphi_i \varphi_j$ is equal to zero only for $g = 0$ and the inequality (5.38) is sharp. We obtain the proof of (5.35) by summing the inequalities (5.37) and (5.38) over all $x, y, m, m'$. 

60
5.6. Choice of reference images

So far, the reconstruction algorithms have been described without specifying how to obtain the reference images $\tilde{S}$ and $\tilde{S}_l$. The homogeneous unaliased image $\tilde{S}$ is often not available because the body-coil image is not acquired. This is because the number of receiver channels is limited and the body-coil acquisition would have to be done instead of acquiring one of the array-coil images that usually have higher SNR. The homogeneous reference image $\tilde{S}$ has to be constructed from the unaliased array coil images $\tilde{S}_l$.

We use three ways to estimate the reference image $\tilde{S}$ that differ in the reconstruction quality and speed.

**Linear combination**

The first option is to construct the image $\tilde{S}$ as a linear combination of the reference array-coil images \[ \tilde{S}(x, y) = \sum_{l=1}^{L} w_l(x, y) \tilde{S}_l(x, y) , \]

where $w_l(x, y)$ are the weights of the linear combination that should be ideally set using knowledge about the coil configuration. In practice, the array-coil sensitivities are not known. However, array-coil design allows to use $w_l(x, y) = 1; \forall l, x, y$.

Linear combination of the images preserves the phase in the reference image $\tilde{S}$ and, thus, the phase information is also available in the reconstructed image. A disadvantage of this method is its susceptibility to the phase cancellation effect (when the phase of the complex array-coil images is not exactly aligned) \[12\], see Figure 5.8.

**Sum-of-squares**

In terms of SNR, the ideal estimation of $\tilde{S}$ without the exact knowledge of coil sensitivities is the sum-of-squares (SoS) \[53\]

\[ \tilde{S}(x, y) = \sqrt{\sum_{l=1}^{L} |\tilde{S}_l(x, y)|^2} . \] (5.39)

This approach eliminates the problems with the phase-cancellation effects. It is used in most of the practical SENSE implementations. The disadvantage is that SoS images lack the phase information that is important for certain applications. The sum-of-squares images are modulated by a SoS of the true coil sensitivities which brings a position dependent intensity bias to the reconstructed image \[12\]. We reached better results with linear combination than with sum-of-squares, see Section 7.3.3.

**Reconstruction of all array-coil images**

The third possibility is to consider each array-coil image $\tilde{S}_l$ in turn to be the reference image $\tilde{S}$. Each coil image $\tilde{S}_l$ can be regarded as reference image determining for all other array-coil images $\tilde{S}_l$ the modified sensitivities $C_{ll} = C_l C_l^{-1}$

\[ S_l(x, y) = C_l(x, y) S(x, y) = C_l(x, y) C_l^{-1}(x, y) S_l(x, y) = C_{ll}(x, y) S_l(x, y) . \]
5. Parallel MRI reconstruction using B-spline Approximation

The reconstruction transformation $\alpha_{l,l'}$ is estimated separately for each array-coil reference image by taking $\tilde{S}_p$ as the ideal reference image $\tilde{S}$ by in (5.31). The solution $g_{ijl,l'}$ is found for each $\tilde{S}_p$ by solving the linear system $B = Ag$, where the matrix $B$ is defined as

$$B_{ijl,l'} = \sum_{x,y=1}^{X,Y} \varphi_i \varphi_j (\tilde{S}_l^* \tilde{S}_l + 2\sigma_l^2).$$

The matrix $A$ (5.34) is independent of $\tilde{S}$. Thus, the matrix $A$ for each array-coil image is equivalent with the single reference image case (5.34) and needs to be built and inverted only once.

The coefficients $g_{ijl,l'}$ are used to reconstruct separately each array-coil image

$$\hat{S}_p(x, y) = \sum_{l=1}^{L} \sum_{i=1}^{I} \sum_{j=1}^{J} g_{ijl,l'} \varphi_i(y) \varphi_j(x) \tilde{S}_l^A(x, y).$$

The final image $\hat{S}$ is computed as sum-of-squares (5.39) of the reconstructed array-coil images $\hat{S}_p$.

The phase information is present in all reconstructed images $\hat{S}_p$. However, the phase is not preserved by the SoS that is used to combine the reconstructed array-coil images. To obtain the phase information in the composite image $\hat{S}$, it is necessary to use other method than SoS, for example linear combination. If linear combination is used, the phase of the images needs to be corrected to avoid phase-cancellation artifacts. We refer the reader to the literature for phase-correcting algorithms [3, 16, 15].

Out of the three mentioned methods: linear combination, sum-of-squares, reconstruction of each array-coil image separately; we have reached the highest reconstruction quality using the latest method (Section 7.3.3). The disadvantage of reconstructing a separate image for each array-coil is that the estimation and reconstruction time is increased.

5.6.1. Variable density scan images

So far, we have considered estimation of reconstruction coefficients $g_{ijl}$ using full resolution reference images $\tilde{S}_l$ and $\tilde{S}$. As the sensitivity information is changing slowly and smoothly in space, it is sufficient to use low-resolution images for the estimation step [66]. Similar to the existing auto-calibration techniques as VD-AUTO-SMASH [29] or GRAPPA [27], low-resolution images without aliasing can be acquired at the same time as the downsampled $k$-space data using variable-density sampling of the $k$-space. In the variable density images, the $k$-space center is fully sampled and the rest of the $k$-space is undersampled with an acceleration factor $M$. The size of the fully-sampled center is usually relatively small (typically 24 lines) compared to the number of all phase-encoding lines (image size is usually from $128 \times 128$ to $512 \times 512$ pixels). Therefore, acquiring a fully sampled $k$-space center causes only a small prolongation of the total acquisition time.

The advantage of a variable-density scan is that the estimation process uses images that are acquired with exactly the same coil configuration as the input images. The sampling pattern of variable-density images is shown in Figure 5.9. An example of a variable density image scan is in Figure 5.10.

Our estimation and reconstruction algorithm has to be adapted as the resolution of the images $\tilde{S}_l$ used for the estimation differs from the resolution of the images $\tilde{S}_l^A$ used for the reconstruction. Thus, the size of the transformation $\alpha_l$ also differs in the estimation and the reconstruction step. The transformation $\alpha_l$ is represented using B-splines which are
5.6. Choice of reference images

**Fig. 5.8.** Ideal image construction.
A distortion phantom is shown. Magnitude of a single array-coil image is in (a). The phase of the image (a) is in (b). The array-coil images are combined to produce a single image. Negative effect of phase-cancellation is visible on image (d) which is a linear combination of the array-coil images. This is solved by using SoS to combine the images (e).

**Fig. 5.9.** Different $k$-space sampling patterns.
Black lines represent the acquired lines and blank spaces represent the skipped lines. A standard image without aliasing is shown in (a). The unaliased low resolution image (b) and the high-resolution image with aliasing (c) are acquired simultaneously as a variable-density image (d).
5. Parallel MRI reconstruction using B-spline Approximation

Fig. 5.10. Different $k$-space sampling patterns.
The variable density image (c) is a sum of a high resolution image with aliasing (a) and a low resolution image without aliasing (b). Note that the size of the low-resolution image is several times smaller than the size of the high-resolution image. The low resolution image is showed upsampled to allow comparison.

Continuous. Inconsistency in the size of $\alpha_l$ is solved by sampling the B-spline basis with different resolution in both steps (estimation and reconstruction). This is done by changing the scale of the B-splines by setting $Y$, respectively, $X$ to the size of the reference, respectively, input images in (5.6). B-splines as defined in the equation (5.5) are shifted so the B-splines $\varphi_i(y), \varphi_j(x)$ with indices $i,j = 1, i = I$ and $j = J$ are centered on the center of the border pixels. The relative shift with respect to the image border is, therefore, changing with the image resolution. The equation (5.5) is modified to ensure that the relative shift of the B-spline basis is the same in the low and high-resolution images. The border B-splines are shifted so their center lies exactly on the image border

$$\varphi_i(y) = \beta^3\left(\frac{y-1}{H_y} - i - \frac{1}{2H_y} + 2\right), \quad \forall i = 1,\ldots,I; \forall y = 1,\ldots,Y,$$

$$\varphi_j(x) = \beta^3\left(\frac{x-1}{H_x} - j - \frac{1}{2H_x} + 2\right), \quad \forall j = 1,\ldots,J; \forall x = 1,\ldots,X.$$
5.7. Continuous error criterion

Avoiding the interpolation artifacts is to use a continuous representation of the error. In this case, B-splines are not sampled in a discrete grid but a continuous scalar product is used in equation (5.34) and the problem does not arise at all. The continuous error criterion is discussed in Section 5.7.

5.6.2. Reconstruction using variable-density scans

The k-space center (low frequencies) usually carries the most information about the image. The extra lines acquired in the k-space center can be used to improve the reconstruction quality. The easiest method is to take the additional lines and replace their counterparts in the reconstructed image k-space. This can be performed when an unaliased image is reconstructed for each coil. The quality of the reconstructed image is improved using the center lines (see Section 7.3.4). However, the reconstructed image needs to be Fourier transformed so the lines can be replaced in the k-space and the reconstruction time is, thus, increased.

5.7. Continuous error criterion

Imaged objects are in essence continuous. The PROBER reconstruction transformation $\alpha_l$ (5.4) is represented in a continuous B-spline basis and it is, therefore, also continuous. So far, we have been evaluating the reconstruction error criterion using the low-resolution reference images $\tilde{S}_l$ in a discrete space. This is a possible source of errors as the reconstruction map $\alpha_l$ is in fact estimated in low-resolution and it is upscaled using B-spline interpolation (see Section 5.6.1). We propose to use a continuous representation of the reference images and a continuous error criterion [69].

5.7.1. Continuous image representation

During the MRI acquisition, the k-space is sampled at discrete intervals. In order to evaluate the continuous reconstruction error, it is necessary to transform the reference images to a continuous representation. We have decided to represent the reference images $\tilde{S}_l$ in a continuous B-spline representation. The reason is a higher computational efficiency of the B-spline representation over the representation in a harmonic basis. B-spline functions are real-valued and spatially localized. These properties are used to speed up the estimation process as will be described later. The additional time necessary to convert the images to the B-spline representation is negligible when compared with the total estimation time.

Reference images in the continuous form $\tilde{S}_l$ are represented in the B-spline basis $\psi_p(y)$, $\psi_q(x)$ by coefficients $h_{pql}$

$$\tilde{S}_l(x, y) = \sum_{p,q=1}^{P,Q} h_{pql} \psi_p(y) \psi_q(x),$$

where $P$, respectively, $Q$ is the number of B-spline functions used to represent the image in the phase, respectively, the frequency encoding direction. The B-splines are equally spaced over the image (5.3),

$$\psi_p(y) = b_{vp}(y - p) = \beta^3(y/v_p - p),$$
$$\psi_q(x) = b_{vq}(x - q) = \beta^3(x/v_q - q).$$

(5.41)

The scaling $v_p$ and $v_q$ is defined as $v_p = Y/P$, $v_q = X/Q$, where $Y \times X$ is the size of the reference image. The spline spacing of 1 pixel is normally used to ensure accurate representation (although the number of splines can be decreased to increase the speed of the estimation.
process). We test the reconstruction quality according to the number of B-splines \( P, Q \) used for the approximation and the results are given in Section 7.3.2.

The B-spline coefficients can be obtained using recursive filtering with an inverse filter \((b^3_d)^{-1}\). Z-transform of the forward filter \(B^3_v(z)\) and the inverse filter \((B^3_v)^{-1}\) is [96]

\[
B^3_v(z) = \frac{z^{2(v-1)}}{v^3} \left( \frac{1 - z^{-v}}{1 - z^{-1}} \right)^4 \sum_{k=-2}^{2} \beta^3(k/v)z^{-k}.
\]  

(5.42)

For the case \( v = 1 \), the Z-transform is simplified to

\[
B^3_1(z) = (z + 4 + z^{-1})/6,
\]

\[(B^3_1)^{-1}(z) = \frac{6}{z + 4 + z^{-1}}.\]  

(5.43)

See [97, 100] for the details of the inverse filter implementation.

In parallel imaging, the images at the input are given in the \( k \)-space (Fourier domain). Therefore, the inverse B-spline filter can be applied directly in the Fourier domain without the need for an extra Fourier transform. The Fourier transform \((D^3_v)^{-1}(f)\) of the inverse filter \((b^3_d)^{-1}\) is computed by replacing \( z \) by \( e^{i2\pi f} \) in its Z-transform representation (5.43) [96]

\[
(D^3_v)^{-1}(f) = (B^3_v)^{-1}(e^{i2\pi f})
\]

\[
(D^3_v)^{-1}(f) = \nu^3 \left( \frac{\sin(\pi f)}{\sin(\pi \nu f)} \right) \left( b^1_l(0) + \sum_{k=1}^{2} 2b^3_l(k) \cos(2\pi f k) \right)^{-1}.
\]

Both B-spline filtering and Fourier transform are separable. The B-spline coefficients \( h_{pq}\) are obtained by multiplication with \((D^3_v)^{-1}(f)\) in the Fourier domain

\[
h_{pq} = \text{DFT}_x \left\{ \text{DFT}_y \left\{ \mathcal{S}(k_x, k_y) (D^3_v)^{-1}(k_y) \right\} (D^3_v)^{-1}(k_x) \right\}.
\]  

(5.44)

### 5.7.2. Continuous error

The continuous error criterion is derived from the perfect reconstruction conditions, see Section 5.4. The \( l^2 \) norm in (5.13) is replaced with the \( L^2 \) norm. The discrete representation of the reference images \( \bar{S}_l \) is replaced by the continuous representation of the images (5.40). The continuous error then yields [69]

\[
e = \sum_{m,m'=0}^{M-1} \left\| \sum_{l=1}^{L} \left( \alpha_{l,m} \mathcal{S}_{l,m'} - \delta_{m,m'} \bar{S}_m \right) \right\|^2_{x,y}
= \sum_{m,m'=0}^{M-1} \int_{x,y} \left\| \sum_{l=1}^{L} \left( \alpha_{l,m} \sum_{p,q=1}^{P,Q} h_{pq} \psi_{p,m} \psi_{q} \right) - \delta_{m,m'} \sum_{p,q=1}^{P,Q} h_{pq} \psi_{p,m} \psi_{q} \right\|^2 \, dx \, dy
= \sum_{m,m'=0}^{M-1} \int_{x,y} \left\| \sum_{l=1}^{L} \left( \sum_{i,j=1}^{I,J} g_{ijl} \varphi_{i,m} \varphi_{j,m'} \sum_{p,q=1}^{P,Q} h_{pq} \psi_{p,m} \psi_{q} \right) - \delta_{m,m'} \sum_{p,q=1}^{P,Q} h_{pq} \psi_{p,m} \psi_{q} \right\|^2 \, dx \, dy,
\]

(5.45)

where \( \psi_p, \psi_q \) are the B-spline basis used for the reference image representation, the equation (5.41).
The error is minimized by computing the partial derivatives $\partial e / \partial g_{ijl}$ and setting them to zero

$$\frac{\partial e}{\partial g_{ijl}} = \sum_{m,m'=0}^{M-1} \int_{x,y} \left\{ \sum_{p'q'} \sum_{p'q'} \right. \left. h_{p'q'lv} \psi_{p',m'} \psi_{q'} g_{v',j'lv} \varphi_{v',m} \varphi_{j'} \sum_{pq} h^*_p q_m \psi_{p,m'} \psi_{q,i,m} \varphi_{j} \right\} dx dy$$

$$= \sum_{i'j'l'} g_{i'j'l'} \left\{ \sum_{pp'} \int_{x,y} \sum_{m,m'=0}^{M-1} \psi_{p',m'} \varphi_{i',m} \psi_{p,m'} \varphi_{i,m} \sum_{qq'} h_{p'q'lv} h^*_pq_m \psi_{q,i,m} \varphi_{j} \right\}$$

$$= \sum_{i'j'l'} g_{i'j'l'} \left\{ \sum_{pp'} \left( \int_{x,y} \psi_{p',m'} \psi_{p,m'} \varphi_{i,m} \sum_{qq'} h_{p'q'lv} h^*_pq_m \int_{x,y} \psi_{q,i,m} \varphi_{j} \right) \right\}$$

$$= \sum_{i'j'l'} \left\{ \Phi^y(p,p',i) \sum_{qq'} h_{p'q'lv} h^*_pq_m \Phi^x(q,q',j) \right\}, \quad (5.47)$$

where the B-spline kernels $\Psi^x, \Psi^y, \Phi^x$ and $\Phi^y$ are defined as

$$\Psi^y(p,p',i,i') = \int_{y} \sum_{m,m'=0}^{M-1} \psi_{p',m'} \varphi_{i,m} \psi_{p,m'} \varphi_{i,m} \ dy$$

$$\Psi^x(q,q',j,j') = \int_{x} \psi_{q,i} \psi_{q,j} \varphi_{j} \ dx$$

$$\Phi^y(p,p',i) = \sum_{m=0}^{M-1} \int_{y} \psi_{p',m} \psi_{p,m} \varphi_{i,m} \ dy$$

$$\Phi^x(q,q',j) = \int_{x} \psi_{q,i} \psi_{q,j} \ dx. \quad (5.48)$$

The B-spline kernels (5.48) are integrals of a product of several piecewise polynomial functions. The solution to the integral equations can be sought analytically [35]. However, this would be very laborious and out of scope of this work. Instead, we evaluate the integrals (5.48) numerically using the extended trapezoidal rule [73]. The integration step was chosen experimentally by to achieve error lower than 0.1%. The error $e_n$ in the evaluation of $\Psi^y$ for the step size $1/n$ of the integration domain is approximated as a ratio

$$e_n = \frac{\sum_{p,p',i,i'} \Psi^y_n(p,p',i,i')}{\sum_{p,p',i,i'} \Psi^y_2(p,p',i,i')},$$

where $\Psi^y_n(p,p',i,i')$ is the kernel that is numerically evaluated for the step size $1/n$ of the integration domain. A fraction 1/256 of the span of the function domain showed to be sufficient to accurately evaluate the kernels (5.48).

The B-spline kernels are independent on the reference images. Therefore, they can be precomputed to speed-up the reconstruction process. The size of the reference images and consequently also the numbers $P,Q$ are usually between 16 and 64 pixels. The number of B-splines $I,J$ used to estimate the reconstruction weights ranges from 5 to 15. The sizes of
the kernels $\Phi, \Psi$ are relatively small and it is possible to precompute the kernels for all likely combinations of the parameters $P, Q, I, J$.

Setting the partial derivatives to zero in the equation (5.47) leads again to a system of $I \cdot J \cdot L$ linear equations with the same number of variables $B = AG$, where the matrices $A$ and $B$ are

\[
A_{ijkl} = \sum_{pp'} \sum_{qq'} \Phi(p, p', i, i') \sum_{h} h_{p'q'q''} h_{pq}^* \Psi(q, q', j, j') \\
B_{ijkl} = \sum_{pp'} \Phi(p, p', i) \sum_{qq'} h_{p'q'} h_{pq}^* \Psi(q, q', j).
\]

(5.49)

It is computationally demanding to evaluate the matrix $A$ in the equation (5.49). In our implementation, we explore properties of the B-spline kernels to speed-up the computations. The B-spline kernels (5.48) are symmetric in $p/p', q/q', i/i'$ and $j, j'$, as well as in the discrete version (5.34), the matrix $A$ is hermitian and symmetric in $i, i'$ and $j, j'$ as a direct consequence of the B-spline kernels symmetry (5.50)

\[
A_{ijkl} = A_{ijkl}^* = A_{i'j'l'i'},
\]

(5.51)

thus, only a fraction $1/8$ of all the matrix $A$ elements needs to be evaluated and the rest can be obtained by symmetries.

Symmetry of the B-spline kernel $\Psi(x, q', j, j') = \Psi(x, q, j, j')$ (5.48) can be used to further reduce the number of multiplications to one half as is showed in the following equation

\[
\sum_{q,q'} h_{p'q'q''} h_{pq}^* \Psi(x, q, q', j, j') = \sum_{q,q' \leq q} h_{p'q'q''} h_{pq}^* \Psi(x, q, q', j, j') + \sum_{q,q' > q} h_{p'q'q''} h_{pq}^* \Psi(x, q, q', j, j') \\
= \sum_{q,q' \leq q} h_{p'q'q''} h_{pq}^* \Psi(x, q, q', j, j') + \sum_{q', q' > q} h_{p'q'q''} h_{pq}^* \Psi(x, q, q', j, j') \\
= \sum_{q,q' \leq q} (h_{p'q'q''} h_{pq}^* + (1 - \delta_{q, q'}) h_{p'q'q''} h_{pq}^*) \Psi(x, q, q', j, j'),
\]

(5.52)

where $\delta$ is Kronecker delta.

The same is valid also for the other kernels $\Phi^y, \Phi^x$ and $\Phi^y$. Applying equation (5.52) when evaluating the values in matrices $A$ and $B$ also reduces the total computation time by one
coefficients linear system (5.49) can be solved using Cholesky decomposition as before. The resulting is also positive definite (the proof is similar to the proof in the discrete case (5.5.5)). The

\[ A_{ijkl} = \sum_{p',q'} \Phi^y(p, p', i, j') \left( \sum_{q',q \leq q'} (h_{p'q'} h_{pq}^* + (1 - \delta_{q,q'}) h_{p'q'q}^*) \right) + (1 - \delta_{p,p'}) h_{p'q}^* h_{p'q'q}^* \]

(5.53)

Although the matrix \( A \) evaluation in the equation (5.49) is speeded up several times using the matrix \( A \) properties in the equation (5.51) and the B-spline kernels in the equation (5.52), its complexity is \( O(X^4 I^2 L^2 + X^2 I^4 L^2) \) (assuming \( I = J \) and \( P = Q = X = Y \) in the low-resolution reference images). Only \( O(X^2 I^2 L^2 + X I^4 L^2) \) operations are necessary for the matrix \( A \) evaluation in the discrete case (5.15). Fortunately, we can now use the fact that the B-splines used to represent the reference images \( \psi \) are highly spatially localized. This means that they are zero on most of its domain of definition. Thus, the integral \( \int_x \psi_p(x) \psi_{p'}(x) \, dx \) is zero for most of \( p' \neq p \). Because of this, the B-spline kernels (5.48) are sparse. Only the product with a non-zero kernel needs to be evaluated in (5.53). This reduces the complexity of the matrix evaluation in the continuous case to \( O(X^2 I^2 L^2 + X I^4 L^2) \) and the complexity can be further reduced by using less functions \( \psi_p, \psi_q \) to represent the reference images.

The continuous error criterion can be combined with the approach derived in Section 5.5.3 to suppress the noise propagation from the input images to the reconstruction. This is done by adding a term \( A_{noise} \) to the matrix \( A \) (5.49), where the matrix \( A_{noise} \) is a continuous version of the term in (5.31, 5.32)

\[ A_{noise} = \lambda \sigma_l^2 \int_{x,y} \varphi_i \varphi_{i'} \varphi_j \varphi_{j'} \, dx \, dy \]

(5.54)

The matrix \( A \) computed using the continuous criterion (5.49) is Hermitian (5.51) and it is also positive definite (the proof is similar to the proof in the discrete case (5.5.5)). The linear system (5.49) can be solved using Cholesky decomposition as before. The resulting coefficients \( g_{ij} \) are used to obtain the reconstruction weights \( \alpha_l \) in the same way as it is done in the discrete case (5.4). The reconstruction process itself is identical to the discrete case (5.1).

The PROBER estimation using the continuous criterion (5.45) avoids the problems caused by discrete sampling of the B-spline basis \( \varphi_i, \varphi_j \) during the estimation when using low-resolution reference images. It also allows more precise evaluation of the reconstruction error which improves the overall quality of the reconstruction. The speed of the estimation using the continuous criterion is comparable with the estimation speed using the discrete criterion. The estimation speed depends on several parameters and the speed of the discrete and the continuous version of PROBER should be compared regarding also the reconstruction quality. This is explained in Section 7.4.2.
5. Parallel MRI reconstruction using B-spline Approximation
6. Theoretical comparison

In this Chapter we discuss the theoretical difference between our PROBER method explained in Chapter 5 and two other parallel MRI reconstruction methods – SENSE (see Section 4.5.1) and GRAPPA (see Section 4.4.3). We compare the reconstruction equations and discuss the differences to point out the possible advantages of each of the methods. Experimental comparison is provided in Chapter 7.

6.1. Comparison with SENSE

In both the Cartesian SENSE (Section 4.5.1) and the PROBER (Chapter 5) reconstructions, the unfolded image is calculated as a weighted pixelwise linear combination of the aliased images (4.16), (5.1)

\[ \hat{S}(x, y) = \sum_{l=1}^{L} \alpha_l(x, y) \tilde{S}^A_l(x, y). \]

The methods differ in estimating the reconstruction transform \( \alpha_l(x, y) \). In SENSE, the sensitivity maps \( C_l \) are spatially smoothed but the reconstruction coefficients \( \alpha_l(x, y) \) are considered independent for each \((x, y)\). The direct solution by matrix inversion is numerically prohibitive since it involves large matrix inversion (4.15). Instead, the weights \( \alpha_l(x, y) \) are found independently for each pixel in the equation (4.18) by a small matrix inversion for each aliased pixel.

The SENSE reconstruction weights are calculated using estimated sensitivity maps that have to be smoothed to overcome local imperfections in the estimation mainly caused by calculating a ratio of the intensity images in regions with a low SNR (see Section 4.5.3). Although smoothing removes small imperfections and singularities, it also distorts the estimation. The spatial dependency of the sensitivity estimate quality is not taken into account for the estimation of the reconstruction coefficients (4.18), which makes the estimation suboptimal.

Intensity values from a single pixel in the \( L \) aliased images \( \tilde{S}^A_l(x, y) \) are used to reconstruct pixels on \( M \) positions in the reconstructed image \( \hat{S}(x, y \mod M + m \frac{Y}{M}) \). Regions of low SNR around one of the aliased positions \((x, y \mod M + m \frac{Y}{M})\) causes poor sensitivity estimation at that point and the error propagates to the whole inverse matrix \( C^+(x, y) \) (4.16, 4.18). This results in reconstruction errors in all respective position in the reconstructed image \( \hat{S}(x, y \mod M + m \frac{Y}{M}) \). This effect can be seen in Figure 6.1 where strong aliasing artifacts are present in the left part of the image that contains low SNR regions.

The PROBER method uses a B-spline approximation of the reconstruction weights \( \alpha_l \) given by the equation (5.4). This effectively reduces the number of the reconstruction parameters. In PROBER, the B-spline reconstruction coefficients are found globally by minimizing the expected reconstruction error. This involves solving a small linear system (5.34) which can be done in a reasonable time and the most time consuming (more than 80% of the estimation time) is assembling the matrices \( A \) and \( B \) (5.34).

The aliasing artifacts due to incorrect sensitivity estimation are reduced in the PROBER reconstruction thanks to the implicit regularization of the B-spline approximation. The in-
6. Theoretical comparison

(a) Body-coil image.  
(b) SENSE reconstruction.  
(c) PROBER reconstruction.

Fig. 6.1. Comparison of SENSE and PROBER.

The SENSE (b) and the PROBER (c) reconstructions of the image (a) with an acceleration factor 2 are shown. The left part of the original image (a) contains regions with low SNR. This spoils the sensitivity estimation and it has a negative effect on the SENSE reconstruction that exhibits strong aliasing artifacts in the left part of the image (shown by a white frame) (b); the right part of the SENSE reconstruction is acceptable. The PROBER reconstruction (c) is free of significant aliasing artifacts in the whole image.

formation from regions with high signal together with the regularization compensates for the parts without signal. The autocalibrating images are used directly to evaluate and minimize the expected reconstruction error, unlike in SENSE. This makes the estimation more stable and the reconstruction is estimated correctly even in flat areas if they are not too far from regions with high signal. An example is shown in Figure 6.1 where the PROBER reconstruction is free of aliasing artifacts that occur in the SENSE reconstruction.

6.2. GRAPPA

The GRAPPA method works in the $k$-space. It reconstructs missing (not acquired) $k$-space lines as a linear combination of several adjacent acquired lines as expressed in equation (4.10). We will show that PROBER can be viewed as an image-domain version of GRAPPA that differs in the choice of the basis functions. This can be seen from Fourier transform of the GRAPPA reconstruction equations.

The GRAPPA method estimates the reconstruction for several fixed $x$ coordinates and the reconstruction transform for the rest of the coordinates is obtained using interpolation (Section 4.4.3). Thus for simplicity, we write the equation only for the 1D case omitting the
6.2. GRAPPA

$x$ coordinate. GRAPPA reconstructs an unaliased image $\hat{S}_j$ for each array coil $j$ (4.10) as a combination of the acquired lines

$$\hat{s}_j(k-m) = \sum_l \sum_{b=0}^{B-1} w(j, b, l, m) \tilde{s}_l(k-bM),$$

$$k = 0, M, 2M, \ldots, N_k - M; m = 0, 1, \ldots, M - 1,$$  \hspace{1cm} (6.1)

where the coordinate $k$ defines the acquired lines. The parameter $m$ goes from 1 to $M - 1$ where $M$ is the acceleration factor. The coordinate $(k-m)$ then correspond to the $k$-space coordinate of the missing lines.

The acquired lines $\tilde{s}_l(k)$ need not to be reconstructed. Thus, we can extend the equation (6.1) for $m = 0$

$$\hat{s}_j(k) = \tilde{s}_j(k)$$

$$\hat{s}_j(k) = \sum_l \sum_{b=0}^{B-1} w(j, b, l, 0) \tilde{s}_l(k-bM).$$

To satisfy this, we shall require

$$\forall j, b, l; b \neq 0 \lor l \neq j,$$

$$w(j, 0, j, 0) = 1,$$

$$w(j, b, l, 0) = 0.$$

We rewrite the GRAPPA equation (6.1) in terms of $k_y = k - m$ for all $k_y = 0, \ldots, N - 1$

$$\hat{s}_j(k_y) = \sum_l \sum_{b=0}^{B-1} w(j, b, l, -k_y \mod M) \tilde{s}_l(k_y + (-k_y \mod M) - bM),$$

$$k_y = k - (-k_y \mod M).$$  \hspace{1cm} (6.2)

Note that the parameter $b$ of $w$ from the equation (6.2) takes values $b = 0, \ldots, (B-1)$, $bM$ takes values $0, M, \ldots, (B-1)M$, and the parameter $m$ takes values $0, 1, \ldots, M - 1$. Hence, without loss of generality the term $w(j, b, l, m)$ can be replaced with $\bar{w}(j, bM - m, l)$

$$\hat{s}_j(k_y) = \sum_l \sum_{b=0}^{B-1} \bar{w}(j, bM - (-k_y \mod M), l) \tilde{s}_l(k_y + (-k_y \mod M) - bM).$$  \hspace{1cm} (6.3)

We introduce a new variable $k'_y = k_y + (-k_y \mod M) - bM$ which, substituted to (6.3), gives

$$bM = k_y + (-k_y \mod M) - k'_y,$$

$$\hat{s}_j(k_y) = \sum_{k'_y = k_y - BM}^{k_y + (M-1)} \bar{w}(j, k_y + (-k_y \mod M) - k'_y - (-k_y \mod M), l) \tilde{s}_l(k'_y) \delta(0, k'_y \mod M)$$

$$\hat{s}_j(k_y) = \sum_{k'_y = k_y - BM}^{k_y + (M-1)} \bar{w}(j, k_y - k'_y, l) \tilde{s}_l(k'_y) \delta(0, k'_y \mod M).$$  \hspace{1cm} (6.4)
Let us express the terms from (6.4) as Fourier transforms of their image domain representations

\[ \hat{s}_j(k_y) = \frac{1}{N} \sum_{y=0}^{N-1} e^{-2\pi i k_y y} \hat{S}_j(y), \]

\[ \hat{s}_l(k_y') \delta(0, k_y' \mod M) = \frac{1}{N} \sum_{y=0}^{N-1} e^{-2\pi i k_y y} \hat{S}_l(y), \]

\[ \bar{w}(j, k_y - k_y', l) = \frac{1}{N} \sum_{y'=0}^{N-1} \mathbf{W}_{j,l}(y') e^{-2\pi i y'(k_y - k_y')} . \]  

(6.5)

We rewrite the equation (6.4) using the image domain expressions from (6.5)

\[ \sum_{y=0}^{N-1} e^{-2\pi i k_y y} \hat{S}_j(y) = \sum_{l} \sum_{k_y' = k_y - BM}^{k_y + (M-1)} \sum_{y=0}^{N-1} e^{-2\pi i k_y y} \hat{S}_l(y) \frac{1}{N} \sum_{y'=0}^{N-1} \mathbf{W}_{j,l}(y') e^{-2\pi i y'(k_y - k_y')} , \]

we rearrange the sums and regroup the exponents of \( e \)

\[ \sum_{y=0}^{N-1} e^{-2\pi i k_y y} \hat{S}_j(y) = \sum_{l} \sum_{y=0}^{N-1} \hat{S}_l(y) \frac{1}{N} \sum_{y'=0}^{N-1} e^{-2\pi i y' y} \mathbf{W}_{j,l}(y') \sum_{k_y' = k_y - BM}^{k_y + (M-1)} e^{-2\pi i (y-y') k_y'} . \]

We subtract the term \( k_y \) from the sum over \( k_y' \) and add it to the exponent of \( e \) and rearrange the sums

\[ \sum_{y=0}^{N-1} e^{-2\pi i k_y y} \hat{S}_j(y) = \sum_{l} \sum_{y=0}^{N-1} \hat{S}_l(y) e^{-2\pi i y k_y} \mathbf{W}_{j,l}(y') \sum_{k_y' = -BM}^{k_y' + M-1} e^{-2\pi i k_y' y} \frac{1}{N} \sum_{y'=0}^{N-1} \mathbf{W}_{j,l}(y') e^{2\pi i y y} . \]  

(6.6)

The last term of (6.6) is a Fourier transform of \( \bar{w} \)

\[ \frac{1}{N} \sum_{y=0}^{N-1} e^{-2\pi i k_y y} \hat{S}_j(y) = \sum_{l} \frac{1}{N} \sum_{y=0}^{N-1} \hat{S}_l(y) e^{-2\pi i k_y y} \sum_{k_y' = -BM}^{k_y' + M-1} e^{-2\pi i k_y' y} \bar{w}_{j,l}(k_y') \]

\[ \frac{1}{N} \sum_{y=0}^{N-1} e^{-2\pi i k_y y} \hat{S}_j(y) = \sum_{l} \frac{1}{N} \sum_{y=0}^{N-1} \left[ \hat{S}_l(y) \sum_{k_y' = -BM}^{k_y' + M-1} \bar{w}_{j,l}(k_y') e^{-2\pi i y k_y'} \right] e^{-2\pi i k_y y} . \]  

(6.7)

Next, we take an inverse FFT of both sides yielding the image-domain representation of the GRAPPA reconstruction

\[ \hat{S}_j(y) = \sum_{l} \hat{S}_l^A(y) \sum_{k_y' = -BM}^{M-1} \bar{w}_{j,l}(k_y') e^{-2\pi i y k_y'} . \]

This can be rewritten by replacing \( \psi_{k_y'}(y) = e^{2\pi i y k_y'} \)

\[ \hat{S}_j(y) = \sum_{l} \hat{S}_l^A(y) \sum_{k_y' = -BM}^{M-1} \bar{w}_{j,l,k_y'} \psi_{k_y'}(y) . \]  

(6.8)
If in the sum $k_y'$ goes over all $k$-space lines in the GRAPPA reconstruction (6.8), we obtain an exact SENSE like reconstruction for each pixel.

The GRAPPA reconstruction (6.8) is similar to the PROBER reconstruction (5.1)

$$\hat{S}_j(y) = \sum_l \hat{S}^A_l(y) \sum_i g_{j,l,i} \varphi_i(y).$$

The difference is that in GRAPPA, harmonic functions $e^{-i2\pi y k_y'}$ are used while B-splines (or any arbitrary basis functions) are used in PROBER (5.4).

Harmonic functions are localized in frequency. This is advantageous during the GRAPPA $k$-space reconstruction as the each missing line is obtained by a linear combination of only $B$ acquired lines (4.10). On the other hand, B-spline functions are more suitable than harmonic functions for the PROBER image-domain reconstruction. B-splines are localized in the image-domain and they are real valued. This is advantageous for the speed of the PROBER estimation process as is described in Section 5.5.5. Another advantage of B-spline functions is that they are more appropriate for representing the reconstruction weights than harmonic functions as is discussed in the following section.

6.2.1. Comparison of basis functions

B-spline functions have good properties for approximation of smooth functions such as sensitivity maps and their inverse [98, 99]. Using B-splines for approximation of the reconstruction coefficients should therefore allow us to reach the same precision as with harmonic functions by using a lower number of the basis functions.

To validate this hypothesis we used SENSE reconstruction maps estimated from noise-free simulated images as described in Section 7.1.3. The SENSE reconstruction maps were then projected to the harmonic and B-spline basis and back to the image domain. The approximation error was computed as the $l^2$ difference between the SENSE map and its representation in the given basis, see Figure 6.2.

The results proved that a lower number of B-splines than harmonic functions is needed to reach the same quality of approximation and, therefore, that B-splines are more suitable for approximation of the reconstruction weights $\alpha$ provided that SENSE reconstruction maps are close to the ideal reconstruction maps. The GRAPPA and PROBER reconstructions are compared experimentally in Chapter 7.
6. Theoretical comparison

Fig. 6.2. Reconstruction maps approximation error using harmonic and B-spline functions.
The images show the error of the B-spline approximation (blue line) and the approximation error using harmonic functions (red line) of the SENSE reconstruction maps. Simulated images were used for this purpose (Section 7.1.3). The horizontal axis refers to the number of basis functions used. The vertical axis displays the ratio of error to magnitude of the original image. We can see that the B-spline approximation is more precise for most of the images. The B-spline error is also converging to zero faster than error of the harmonic approximation where a full set of functions is necessary to reach a perfect representation.
7. Experiments

This chapter describes experiments performed to evaluate the reconstruction quality of the newly suggested method PROBER (Section 5) and to compare PROBER to other reconstruction methods. First, we describe datasets used in the experiments, Section 7.1, and the means to quantify the reconstruction quality, Section 7.2. The tests comparing the PROBER results with different input parameters can be found in Section 7.3. We compare the reconstruction quality of the different PROBER versions from Chapter 5 in Section 7.4. The most important part of this chapter is Section 7.5 where we compare the PROBER method with the main competing methods SENSE and GRAPPA in terms of the reconstruction quality and reconstruction speed.

7.1. Data

We have acquired 30 sets of phantom and in-vivo images. We use the information retrieved from the phantom and the in-vivo images to generate simulated images. We thank Dr. Michael Bock and Dr. Sven Müller from German Cancer Research Center in Heidelberg for cooperation and for providing us with the data.

7.1.1. Phantom images

We have acquired 18 sets of phantom images on a clinical 1.5T MR system (Magnetom Symphony, Siemens Medical Solutions, Erlangen, Germany) using a spoiled gradient echo pulse sequence [101]. The imaging parameters are listed in Table 7.1. Variable-density scans (Section 5.6.1) were acquired with 24 fully sampled lines in the $k$-space center whereas the outer part of the $k$-space was undersampled with the acceleration factor 2 or 4.

The first eleven datasets (1-11) were acquired with an 8-channel head coil and a plexiglass phantom filled with a 1:100 Gd-DTPA:water solution that was designed to measure image distortions, see Figure 7.2a. Photographs of head coils and a distortion phantom are in Figure 7.1. Datasets 9, 10 and 11 were acquired using a different distortion phantom, see Figure 7.2b. For datasets 12 to 18, a vessel phantom was visualized using a 6-channel spine array coil, see Figure 7.2c, d.

7.1.2. In-vivo images

To assess the methods performances on real images, we have acquired 12 sets of in-vivo head and body images of a 25 year old healthy volunteer. A 1.5T MR system with 32 receiver channels (Magnetom Avanto, Siemens Medical Solutions, Erlangen, Germany) was used for this purpose. The imaging parameters are listed in Table 7.2. We have acquired two sets of transversal (datasets 20 and 21) and three sets of sagittal head images at the mid-line (sets 24-26). Datasets 19, 23 and 27-30 contain coronal images of torso and the set 22 displays a transversal image of torso, see Figure 7.3.
### 7. Experiments

#### Dataset

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<th>TR [ms]</th>
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**Table 7.1.** Imaging sequence parameters of the phantom image acquisitions.

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**Fig. 7.1.** An example of head array-coils and a distortion phantom.

- a) Head coils.
- b) Distortion phantom.
### 7.1. Data

- **Dataset 2** – a distortion phantom.
- **Dataset 10** – a different distortion phantom.
- **Dataset 13** – a vessel phantom.
- **Dataset 14** – a vessel phantom, a different slice.

**Fig. 7.2.** Sum-of-square images of the phantom datasets 2 (a), 10 (b), 13 (c) and 14 (d).

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**Table 7.2.** Imaging sequence parameters of the in-vivo image acquisitions.
7. Experiments

Fig. 7.3. In-vivo datasets.
Sum-of-squares images of the in-vivo datasets 21, transversal image of head (a); 23, coronal image of torso (b); 24, sagittal image of head (c); 25, sagittal image of head (d); 28, coronal image of torso (e) and 30, coronal image of torso (f).
7.2. Reconstruction quality

7.1.3. Simulated images

We have taken 11 datasets (both phantom and in-vivo images) to create the simulated images. The advantage of the simulated images is that it is possible to control the noise variance in the images. Also, the ground truth is known. Thus, the reconstruction quality can be evaluated more precisely.

Acquired datasets 8, 13, 21, 18, 19, 23, 24, 10, 11, 25 and 27 were used to create the simulated datasets 1 to 11, respectively. The homogeneous-sensitivity image $S$ was obtained as sum-of-squares of the array-coil images. The intensity bias caused by the sum-of-squares combination was corrected using a non-parametric intensity correction method [84] and the image intensities were normalized to the mean 0.5. Sensitivity maps $C_l$ were extracted by dividing array-coil images by the homogeneous image $S$. The sensitivity maps were filtered to remove noise [78].

Simulated images with size $256 \times 256$ pixels were generated by multiplying the homogeneous images $S$ with the sensitivity maps $C_l$, see equation (2.26). White additive Gaussian noise was added to both real and imaginary components of reference and input images.

7.2. Reconstruction quality

We observe two types of errors in the reconstructed images – aliasing artifacts and noise. To quantify the aliasing artifacts we take the mean $\bar{S}$ of 20 reconstructions $\hat{S}_k$. The mean $\bar{S}$ is obtained as $\bar{S} = \sum_{k=1}^{20} \hat{S}_k / 20$. We calculate the artifact power (AP) [67] as

$$AP = \sqrt{\frac{\|S - \bar{S}\|_{x,y}^2}{\|S\|_{x,y}^2}},$$

(7.1)

where $S$ is the true image.

Noise in the reconstruction is quantified using the signal-to-noise ratio (SNR)

$$SNR = 20 \log_{10} \sqrt{\frac{\sum_{k=1}^{20} \|S\|_{x,y}^2}{\sum_{k=1}^{20} \|\hat{S}_k - \bar{S}\|_{x,y}^2}}.$$

(7.2)

The AP and the SNR are evaluated only for the simulated datasets for which it is possible to obtain 20 sets of input images that differ only in noise. Unfortunately, we cannot obtain the mean image $\bar{S}$ for the phantom and in-vivo measurements due to the subject movement between the acquisitions. Thus for these datasets, we evaluate only the following $SNR_{\text{real}}$

$$SNR_{\text{real}} = 20 \log_{10} \sqrt{\frac{\|S\|_{x,y}^2}{\|\hat{S} - S\|_{x,y}^2}}.$$

(7.3)

Moreover, the ground truth image $S$ is obtained as the sum-of-squares of only a single set of fully sampled images. Therefore, it contains noise which makes the quantification using $SNR_{\text{real}}$ less meaningful and less reliable. Another disadvantage is that $SNR_{\text{real}}$ is affected both by aliasing artifacts and by noise in the reconstruction.

The signal-free background regions are excluded from evaluation of AP, SNR and $SNR_{\text{real}}$. These regions are identified by thresholding with the threshold value set to 2% of the maximal intensity value. There are several reasons for excluding the background regions. The SENSE
and SMASH methods behave differently at the edges of the FOV. Some of the methods threshold the reconstructed images and the sensitivity maps and set the regions below the threshold to zero. The regions containing only noise are also not interesting from the medical point of view [61].

The artifact power (AP) and the signal-to-noise ratio (SNR) often vary significantly for different datasets. If we want to display a comparison of different methods on several datasets in one Figure, the results have to be scaled for each dataset to make sure all the results will be clearly visible. This can be done since the relative values are more important for the comparison than the absolute values. Because of this, we often normalize the results by scaling the maximal AP or SNR value to 1 for each dataset. Sometimes we display SNR and AP as a mean over all simulated datasets. In this case, the values have to be normalized for each dataset to make the mean over all datasets unbiased.

### 7.3. PROBER parameters

The PROBER algorithm has several parameters defining, e.g., the basis functions. In this section, we observe dependency of the reconstruction quality on values of input parameters and discuss the optimal parameter settings. We discuss how to find the ideal estimation grid-size (see Section 5.6.1) of the discrete PROBER method in Section 7.3.1. The continuous PROBER method (Section 5.7) is considered for the rest of the tests to find the optimal parameters – the number of B-splines $I, J$ used to represent the reconstruction transformation (Section 7.3.2), the number of B-splines $P, Q$ used to represent reference images (Section 7.3.2), the choice of the ideal reference images (Section 7.3.3) and the value of the parameter $\lambda$ (Section 7.3.5).

#### 7.3.1. Estimation grid-size

A discrete dot product of the B-spline basis $\phi_i(y), \phi_j(x)$ with the image function $\tilde{S}_l(x, y)$ is evaluated during the estimation step in the discrete PROBER method, see the equation (5.34). Prior to this, the B-spline basis needs to be resampled with the same resolution as the images $\tilde{S}_l(x, y)$. The reference image $\tilde{S}_l$ is usually small ($24 \times 24$ pixels in our experiments) and representing B-splines with the same resolution is often not satisfactory. The solution is to sample the B-spline functions with a higher resolution and to interpolate the intermediate image values $\tilde{S}_l(x, y)$ accordingly. We upsample the image $\tilde{S}_l(x, y)$ by Fourier transforming a larger part of the $k$-space where the part outside of the $k$-space center is padded with zeros.

We have tested the reconstruction quality depending on the estimation grid-size from 24 to 192 pixels. We have performed the reconstruction of all simulated images with the size $256 \times 256$ pixels ($X = Y = 256$), the acceleration factor 2 ($M = 2$) and the receiver noise variance $\sigma_l^2 = 10^{-3}$ and $10^{-4}$. Discrete PROBER with $9 \times 9$ B-splines ($I = J = 9, \lambda = 1$) was used and the artifact power, equation (7.1), and the noise level in the reconstruction, equation (7.2), was evaluated.

The AP and the SNR were normalized by scaling the maximal value to 1 for each dataset and the normalized AP and SNR was averaged over all datasets.

The aliasing artifact power is monotonically decreasing with the increasing estimation grid-size up to 192 pixels, see Figure 7.4. For the estimation grid-size 76 pixels and more, no aliasing artifacts are visible in the reconstruction. The ideal grid-size for estimation in terms of AP is 192 pixels. However, the difference in AP for 128 pixels and 192 pixels is minimal, Figure 7.4. The example of reconstructions of the simulated dataset 1 with
7.3. PROBER parameters

![Graph](image)

**Fig. 7.4.** The reconstruction AP depending on the estimation-grid size. The normalized AP averaged over all simulated datasets is shown for the PROBER reconstructions using estimation grid-sizes from 24 to 192 pixels. Noise variance in the reference and input images is $\sigma_l^2 = 10^{-4}$ (a) and $\sigma_l^2 = 10^{-3}$ (b).

Different sizes of the B-spline basis is shown in Figure 7.5. The estimation grid-size does not have significant influence on the reconstruction SNR. Although the SNR is slightly increasing with the increasing estimation grid-size, the total difference is less than 1%.

### 7.3.2. Number of B-splines

The number of B-splines $I, J$ used to represent the reconstruction transformation is an important aspect for the reconstruction speed and quality. We have performed tests on all simulated datasets ($X = Y = 256, M = 2, \sigma_l^2 = 10^{-4}, 10^{-3}$) using from $4 \times 4$ to $14 \times 14$ B-splines to represent the reconstruction transformation ($I = J = 4, \ldots, 14$). The continuous PROBER method with $16 \times 16$ splines representing the reference images ($P = Q = 16, \lambda = 1$) was used to reconstruct the unaliased images for each coil separately. The final image was obtained as sum-of-squares of the unaliased array-coil images and the AP and SNR were evaluated.

The AP and SNR were normalized and averaged over all datasets, see Figure 7.6. The SNR increases with the increasing number of B-splines. The differences between the SNR for $4 \times 4$ and $14 \times 14$ B-splines is within 6%, while the difference between $8 \times 8$ and $14 \times 14$ B-splines is less than 2% for both tested noise variances. The AP is decreasing for the B-splines number from $4 \times 4$ to approximately $9 \times 9$ B-splines and then it starts to increase slightly. The exact optimum location depends weakly on the noise level. Based on the quantitative results, $5 \times 5$ B-splines are used for the fast reconstruction and $9 \times 9$ B-splines are used for the high quality reconstruction. Higher number of B-splines increases the precision of the reconstruction transformation approximation and, thus, improves the image quality. However, when the number of B-splines is too high, the estimation becomes more susceptible to noise and the transformation is less constrained. Therefore, the quality starts to degrade.

In continuous PROBER, B-splines are used to represent also the reference images. We have tested the reconstruction quality on all simulated images ($M = 2, X = Y = 256, \sigma_l^2 = 10^{-4}, 10^{-3}$) for $6 \times 6$ to $24 \times 24$ B-splines used to represent the reference images ($P = Q = 6, \ldots, 24$). Unaliased images were reconstructed for each coil separately and combined using sum-of-squares ($I = J = 8, \lambda = 1$). The AP and SNR were normalized and averaged over all datasets, see Figure 7.7.

The AP for less than $12 \times 12$ B-splines is 30% higher than the minimal value and the reconstructions exhibit strong aliasing artifacts, see Figure 7.7c. For $16 \times 16$ B-splines, there are no visible aliasing artifacts in the reconstruction and the decrease of AP for more than 20 B-splines is insignificant. The same holds also for SNR, however, the difference is small. For the rest of the experiments we have chosen to use $16 \times 16$ B-splines for fast reconstruction and $20 \times 20$ and also $24 \times 24$ B-splines for the high quality reconstruction.
7. Experiments

Fig. 7.5. The reconstruction quality depending on the estimation-grid size for the simulated dataset 1 with noise variance $\sigma_l^2 = 10^{-4}$. Reconstructions using estimation grid-sizes 24 (a), 48 (b) and 192 pixels (c) are shown. The graph in (d) shows the normalized AP. There are aliasing artifacts visible in (a) and (b).

Fig. 7.6. Number of B-splines for the reconstruction transformation approximation. PROBER was tested with $4 \times 4$ to $14 \times 14$ B-splines used to approximate the reconstruction transformation. The normalized AP (a) and SNR (b) is averaged over all simulated datasets with noise variances $\sigma_l^2 = 10^{-4}$ and $\sigma_l^2 = 10^{-3}$. 

84
7.3. PROBER parameters

Continuous PROBER was tested for 4 × 4 to 24 × 24 B-splines used to represent the reference images. The normalized AP (a) and SNR (b) averaged over all simulated datasets is shown. The reconstruction of dataset 1 is shown for 6 × 6 (c) and 16 × 16 (d) B-splines. There are noticeable aliasing artifacts in the images (c).
7. Experiments

7.3.3. Choice of reference images

In Section 5.6, we describe three methods to obtain the homogeneous-sensitivity reference image: using a linear combination of array-coil images, using sum-of-squares or reconstructing unaliased image for each array-coil separately. We have compared the reconstruction quality of the mentioned methods on all simulated datasets \((M=2, X=Y=256, \sigma_l^2 = 10^{-4}, 10^{-3})\). The unaliased images were reconstructed using continuous PROBER \((I = J = 8, \lambda = 1, P = Q = 20)\). The AP and SNR were evaluated and normalized for each dataset, see Figure 7.8.

The reconstruction of each array-coil separately is free of visible aliasing artifacts on all simulated images, see Figure 7.9a, d, g. Except the datasets 5 and 8, images reconstructed using a linear combination are also free of visible artifacts or contain only minor aliasing artifacts (the datasets 10 and 11), see Figure 7.9b, e. The artifacts in the datasets 5 and 8 are caused by phase-cancellation artifacts in the homogeneous image, see Figure 7.9h. The phase-cancellation artifacts can be avoided by using sum-of-squares which gives satisfactory results for the datasets 5 and 8 and also for the datasets 3 and 9.

In Figure 7.8 we can see that the reconstruction of each array-coil separately offers the best AP and SNR for all tested images. The linear combination produces reasonable results that are in most cases comparable to the independent coil reconstruction as long as the phase-cancellation artifacts are avoided. The method using sum-of-squares showed the worst quality.

7.3.4. Using the \(k\)-space center

The fully-sampled \(k\)-space center from the variable-density scans is used for the estimation process, see Section 5.6.1. However, the \(k\)-space center can also be used to improve the reconstruction quality by replacing the reconstructed lines in the \(k\)-space center by their acquired counterparts, see Section 7.3.4.

We have compared the quality of the reconstruction with and without replacing of the \(k\)-space center lines by the acquired values. Tests were performed on the simulated datasets \((M=2, X=Y=256, \sigma_l^2 = 10^{-4}, 10^{-3})\). Unaliased images were reconstructed using continuous PROBER \((I = J = 8, P = Q = 20, \lambda = 1)\) and the AP and SNR was evaluated, see Figure 7.10.

The reconstructed images with the replaced \(k\)-space center has a higher AP than the other methods for all simulated images with noise variance \(\sigma_l^2 = 10^{-4}\). The reconstruction with the added \(k\)-space center is clearly better because the acquired \(k\)-space data are close to optimal. For noise variance \(\sigma_l^2 = 10^{-3}\), the method without replacing center lines has better AP on more than a half of the images. This is caused by the fact, that the acquired \(k\)-space lines themselves contain a lot of noise and, therefore, are suboptimal. The lines that are reconstructed as a linear combination over several coils can have even a better quality than the acquired lines. Hence, replacing the \(k\)-space center can paradoxically increase AP. In terms of SNR, the method that replaces the center lines is better on all tested images. The difference between the methods is shown in Figure 7.11 where the replacement of the center \(k\)-space lines leads to reduction of the aliasing artifacts.

7.3.5. Parameter \(\lambda\)

The parameter \(\lambda\) controls the tradeoff between the stochastic and the deterministic part of the error criterion and, thus, determines the level of artifact and noise suppression in the reconstructed image, see Section 5.5.2.
7.3. PROBER parameters

Fig. 7.8. The reconstruction quality depending on the different construction of the ideal reference image. Different types of ideal image construction were tested on the simulated datasets with the noise variance $\sigma^2_l = 10^{-4}$ (a, b) and $\sigma^2_l = 10^{-3}$ (c, d). Normalized AP (a, c) and SNR (b, d) of PROBER is shown for reconstructions where the homogeneous-sensitivity reference image is obtained as a linear combination or sum-of-squares or where the unaliased image is reconstructed for each array-coil separately (FEC).
7. Experiments

Fig. 7.9. Different types of the PROBER ideal image construction.
Comparison of the PROBER reconstructions that use linear combination or sum-of-squares to obtain the homogeneous-sensitivity reference image or that reconstructs each array-coil image separately. The methods are compared on simulated datasets 1 (a-c), 2 (d-f) and 8 (g-i). In (a-c), all three methods produce good results. The reconstruction using the sum-of-squares suffers from aliasing artifacts on the second set of images (f). The reconstruction using linear combination exhibits phase-cancellation artifacts whereas the reconstruction using the sum-of-squares gives satisfactory results on the third set (h, i).
7.3. PROBER parameters

Fig. 7.10. The reconstruction quality depending on the replacing of the $k$-space center lines. Reconstructions with and without replacing of the $k$-space center lines are tested on the simulated datasets with noise variance $\sigma^2_l = 10^{-4}$ (a-b) and $\sigma^2_l = 10^{-3}$ (c-d). The graphs shows the normalized AP (a, c) and the SNR (b, d).

Fig. 7.11. Replacing the $k$-space lines in the reconstruction. The difference between reconstructions with and without replaced $k$-space center lines is shown. The original image (a) is reconstructed using the standard method (b) and with the $k$-space center lines replaced (c).
7. Experiments

Let us define a parameter $\bar{\lambda}$

$$\bar{\lambda} = \lambda \sigma_l^2,$$

that embodies both parameter $\lambda$ and the noise variance $\sigma_l^2$ in the input images, see the equation (5.34). This way, the parameter $\bar{\lambda}$ can be set without the exact knowledge of $\sigma_l^2$ which proved to be advantageous for the real images.

We have tested the PROBER method on all simulated images ($M = 2$, $X = Y = 256$, $\sigma_l^2 = 10^{-4}, 5 \cdot 10^{-4}, 10^{-3}, 5 \cdot 10^{-3}$) with the parameter $\bar{\lambda}$ varying from $10^{-1}$ to $10^{-7}$. The PROBER method was used to reconstruct each array-coil image separately ($I = J = 8$, $P = Q = 16$) and the images were combined using sum-of-squares. The SNR and AP were measured as well as the overall SNR, see Figure 7.12. The overall SNR corresponds to the SNR$_{real}$ (7.3) which contains both deterministic and stochastic parts of the error. Results for noise variance $\sigma_l^2 = 5 \cdot 10^{-3}$ can be regarded with less importance since they correspond to very noisy images.

The highest SNR$_{real}$ is reached for $\bar{\lambda} \approx \sigma_l^2$ that is $\lambda \approx 1$. However, the highest SNR$_{real}$ does not necessarily mean the highest reconstruction quality. This is shown on the reconstruction AP and SNR for simulated images, see Figure 7.12. The SNR is increasing monotonously with the increasing value of $\lambda$ whereas the AP reaches the minimum for the value of $\bar{\lambda}$ depending on the noise variance $\sigma_l^2$.

Setting $\bar{\lambda} = 10^{-4}$ appears to be close to optimal for any noise level. With this value, we reach reasonable level of the artifact suppression even when the exact noise variance is not known, see Figures 7.13 and 7.14. However, the highest possible SNR is not reached. The value of the parameter $\bar{\lambda}$ can be, thus, slightly changed to improve the reconstruction SNR without significantly increasing the level of aliasing in the reconstruction. In the experiments, we have seen that reconstructions with $\bar{\lambda} = 5 \cdot 10^{-4}$ still reach good level of aliasing suppression, while the reconstruction images for $\bar{\lambda} = 10^{-4}$ are completely free of visible aliasing artifacts as is shown in Figures 7.13, 7.14.

### 7.4. PROBER versions

We describe several versions of the PROBER method in Chapter 5. In this section, we compare them experimentally.

#### 7.4.1. Perfect reconstruction conditions

In this section, we compare the 1D and 2D trivial reconstruction (Section 5.3) with the reconstruction constrained by using the perfect reconstruction conditions (Section 5.4). The 1D
7.4. PROBER versions

- a) Original.
- b) \( \lambda = 3 \times 10^{-3} \), AP = 6.5 \( \cdot \) 10^{-4}, SNR = 48 dB.
- c) \( \lambda = 10^{-4} \), AP = 3.6 \( \cdot \) 10^{-5}, SNR = 47 dB.
- d) \( \lambda = 10^{-6} \), AP = 3.1 \( \cdot \) 10^{-5}, SNR = 41 dB.

**Fig. 7.13.** Reconstructions of the simulated dataset 1 with different \( \lambda \).
Reconstructions of the simulated dataset 1 with different values of the parameter \( \lambda \). The original image is in (a). The reconstructions for \( \lambda = 3 \times 10^{-3} \) (b), \( \lambda = 10^{-4} \) (c) and \( \lambda = 10^{-6} \) (d) are shown. The image (b) contains aliasing artifacts and the image (d) has a higher level of noise than the other images. The reconstruction in image (c) is a good trade-off in terms of both the AP and SNR.
7. Experiments

Fig. 7.14. Reconstructions of the in-vivo dataset 22 with different values of $\bar{\lambda}$.
Reconstructed images of the in-vivo dataset 22 with a varying value of the parameter $\bar{\lambda}$ used for the reconstruction. The original image is in (a). The reconstructions for $\bar{\lambda} = 3 \cdot 10^{-3}$ (b), $\bar{\lambda} = 10^{-4}$ (c) and $\bar{\lambda} = 10^{-6}$ (d) are shown. The image (b) contains aliasing artifacts and the image (d) has a higher level of noise than the other image. The reconstruction in image (c) is good in terms of both the AP and SNR.
7.4. PROBER versions

trivial method is similar to the 2D method, except that the B-spline approximation, the equation (5.4) is applied only in the phase-encoding direction. The reconstruction transformation in the 1D method is estimated, the equation (5.9), for each $x$-coordinate separately.

We tested the methods on all simulated datasets with an acceleration factor 2, image size $256 \times 256$ pixels and noise variance $10^{-4}$ and $10^{-3}$ ($M = 2$, $X = Y = 256$, $\sigma_l^2 = 10^{-4}$, $10^{-3}$). Variable-density scans were used with the $k$-space center size 24 lines and also 128 lines. This was done to show the inefficiency of the trivial method when using low-resolution reference images.

Unaliased images were reconstructed for each array-coil separately using $8 \times 8$ B-splines to estimate the reconstruction transformation. The AP and SNR was evaluated, see Figure 7.15.

The constrained PROBER method (using the perfect reconstruction conditions) is clearly better than the trivial method for variable-density scans with 24 reference lines. The AP of the constrained method is 70% to 90% lower than the AP of the trivial method. The SNR of the trivial reconstruction is lower than the SNR of the constrained method for the input noise variance $\sigma_l^2 = 10^{-4}$. SNRs are comparable for the noise variance $\sigma_l^2 = 10^{-3}$. This can be seen in Figures 7.16 and 7.17 where the images reconstructed using the trivial methods contain significant aliasing artifacts.

The reconstruction quality of the trivial methods improves significantly for larger reference images ($128 \times 128$ pixels). The reason is that the reference image becomes similar to the input images which is advantageous for the less constrained methods. The 2D trivial method has the same or better AP than the 2D constrained method for half of the datasets. The SNR of the 2D trivial method is comparable to the SNR of the constrained method, see Figure 7.15. The 1D trivial method still has the lowest quality of the three tested versions of PROBER. In practice, high resolution reference images are not available for the estimation. This makes the results for the reference image size $128 \times 128$ pixels irrelevant for practical purposes. Consequently, the use of the perfect reconstruction conditions is necessary.

The trivial methods are also less precise in the case when the reference object is different from the reconstructed object. This is shown in Figure 7.18. The trivial method reaches worse results than the constrained PROBER method even when high-resolution reference images are used. There are visible aliasing artifacts in the trivial reconstruction especially in the 1D case. The constrained method produces images with no visible aliasing.

7.4.2. Discrete and continuous error criterion

In this section, we compare the discrete PROBER methods that uses the perfect reconstruction conditions (Section 5.4), the discrete PROBER with the additional constraints to prevent noise amplification (Section 5.5.4), and the continuous PROBER method (Section 5.7).

We have performed tests on all simulated images ($M = 2$, $X = Y = 256$, $\sigma_l^2 = 10^{-4}$, $10^{-3}$). The general PROBER parameters were $I = J = 8$. The estimation-grid size of the discrete methods was set to 192 pixels. The continuous method used $24 \times 24$ B-splines to approximate the reference images. The parameter $\lambda$ was set to $10^{-4}$. The unaliased images were reconstructed for each array-coil separately and then combined using sum-of-squares.

All three tested methods produce images without visible aliasing artifacts. The discrete PROBER method without noise constraints reaches the lowest SNR on all datasets, see Figure 7.19. The AP of the unconstrained PROBER is also the worst for all images with noise variation $\sigma_l^2 = 10^{-3}$. For low noise variation $\sigma_l^2 = 10^{-4}$, the unconstrained PROBER method reaches lower AP than the constrained PROBER method on half of the simulated datasets. However, this was done at the expense of significantly lower SNR. The reason for this is that the unconstrained PROBER assumes noise-free input images which results in lower stability of
7. Experiments

Fig. 7.15. Reconstruction quality of trivial and constrained PROBER.
The normalized AP (a, c, e, g) and SNR (b, d, f, h) of the 1D and the 2D trivial PROBER method and the 2D constrained PROBER method (using perfect reconstruction conditions) is shown for all simulated datasets. The noise variance in the input images is \( \sigma_l^2 = 10^{-4} \) (a, b, e, f) and \( \sigma_l^2 = 10^{-3} \) (c, d, g, h). Variable-density scans with the fully-sampled k-space center consisting of 24 reference lines (a-d) and 128 reference lines (e-h) are used.
Fig. 7.16. Reconstructed images of trivial and constrained PROBER.
Reconstructions of the simulated dataset 1 with 24 reference lines. The original image (a), the 1D trivial method (b), the 2D trivial method (c), the 2D method using perfect reconstruction conditions (d). There are significant aliasing artifacts visible in images (b) and (c).
7. Experiments

Fig. 7.17. Reconstructed images of trivial and constrained PROBER.
Reconstructed images of the simulated dataset 10 with 24 reference lines. The original image (a), the 1D trivial method (b), the 2D trivial method (c), (d) the 2D constrained method using perfect reconstruction conditions (d). There are noticeable aliasing artifacts in the reconstructed images (b) and (c).
7.4. PROBER versions

Fig. 7.18. Reconstructions of images with different reference and input objects.
The reconstruction transformation was estimated on the simulated dataset 3 with the reference image size $128 \times 128$ pixels. The reconstruction was performed on the simulated dataset 1 (which has the same coil configuration). The 1D trivial reconstruction (a) contains a high number of aliasing artifacts. The 2D trivial reconstruction (b) contains minor aliasing artifacts. The constrained reconstruction (c) is aliasing free.
The method—this shows especially on the SNR. The continuous PROBER method has better SNR than the discrete PROBER method with noise constraints in all cases and better AP in 8 out of the 11 cases for both input noise variances. The constrained continuous PROBER method is better than the discrete PROBER method because the continuous representation of the error criterion enables more precise evaluation of the error and, thus, more precise estimation.

7.5. Experimental comparison of PROBER, SENSE, and GRAPPA

The reconstruction quality and the reconstruction speed of continuous and discrete PROBER methods were compared to those of SENSE [78] and GRAPPA [27]. Tests were performed on all simulated, phantom and in-vivo datasets for acceleration factors 2 and 4. Reconstructed images were compared in the terms of SNR (7.2) and AP (7.1). Based on the experiments described in the preceding sections, we have chosen 6 settings of the PROBER algorithm which differ in the reconstruction quality and speed, see Table 7.3. Standard Siemens implementations of GRAPPA and SENSE were used for the experiments (as implemented in the Magnetom Avanto machine).
7.5. Experimental comparison of PROBER, SENSE, and GRAPPA

<table>
<thead>
<tr>
<th>Method</th>
<th>Discrete/continuous</th>
<th>Reconstruct</th>
<th>$I \times J$</th>
<th>Estimation grid-size [pix]</th>
<th>$P \times Q$</th>
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</thead>
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<td>76</td>
<td>-</td>
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<tr>
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<td>$5 \times 5$</td>
<td>128</td>
<td>-</td>
</tr>
<tr>
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<td>$5 \times 5$</td>
<td>-</td>
<td>$16 \times 16$</td>
</tr>
<tr>
<td>PROBER 4</td>
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<td>$9 \times 9$</td>
<td>128</td>
<td>-</td>
</tr>
<tr>
<td>PROBER 5</td>
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<td>$9 \times 9$</td>
<td>-</td>
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</tr>
<tr>
<td>PROBER 6</td>
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<td>$9 \times 9$</td>
<td>-</td>
<td>$24 \times 24$</td>
</tr>
</tbody>
</table>

Table 7.3. PROBER settings.

The PROBER method was tested with six different settings. The methods PROBER 1-3 were optimized to achieve a high reconstruction speed whereas the methods PROBER 4-5 were expected to reach a high reconstruction quality. The settings indicate if the continuous or discrete PROBER was used; if the unaliased image was reconstructed for each coil separately; the number of B-splines $I \times J$ used to represent the reconstruction transformation; the estimation grid-size; and the number of B-splines $P \times Q$ used to represent the reference images.

7.5.1. Simulated images

We have performed tests on all simulated datasets with the acceleration factor 2 and the noise variance $10^{-4}$ and $10^{-3}$ ($M = 2$, $\sigma_l^2 = 10^{-4}, 10^{-3}$). The parameter $\lambda$ was set to $10^{-4}$ for images with the noise variance $\sigma_l^2 = 10^{-4}$ and $\lambda$ was set to $5 \cdot 10^{-4}$ for the variance $\sigma_l^2 = 10^{-3}$. AP, the equation (7.1), and SNR, the equation (7.2), were evaluated. The AP was normalized by scaling the maximal value to 1 for each dataset.

The results for the fast PROBER methods 1-3 are showed in Figure 7.20. PROBER 1-3 has unsatisfactory results on datasets 5 and 8 due to phase-cancellation artifacts. On the datasets 2, 4, 6 and 7, the PROBER methods 1-3 have a lower level of aliasing artifacts than SENSE. On the datasets 1, 3 and 9 PROBER reaches the lowest AP of all the tested methods. The PROBER SNR is the same or slightly lower than the SNR of SENSE and GRAPPA. On the dataset 9, the fast PROBER 1-3 has the highest SNR and the lowest AP of all three methods, see Figure 7.22.

The results for PROBER 4-6 are shown in Figure 7.21. PROBER reaches the lowest AP on all simulated images with the noise variance $\sigma_l^2 = 10^{-3}$. PROBER also has the lowest AP for $\sigma_l^2 = 10^{-3}$ on all simulated datasets except the datasets 1 and 8 where the SENSE method has the lowest AP. The SNR of PROBER 4-6 is the same or higher than the SNR of SENSE and GRAPPA. This makes PROBER 4-6 clearly the most efficient methods for the simulated images. For example of the reconstruction see Figure 7.23.

We have performed tests on all simulated datasets also with the acceleration factor 4 with the noise variance $\sigma_l^2 = 5 \cdot 10^{-4}$, see Figure 7.24. The PROBER parameter $\lambda$ was set to $5 \cdot 10^{-4}$ for these tests. The reconstruction for the acceleration factor 4 is often ill-conditioned due to an unfavorable coil configuration. Therefore, the quantitative results need to be interpreted with care. PROBER 1-3 has lower AP and higher SNR than SENSE and GRAPPA for the simulated datasets 1 and 3. On the rest of the datasets, PROBER 1-3 reaches the same or worse quality than SENSE and GRAPPA. PROBER 4-6 has the lowest AP for all simulated datasets. PROBER 4-6 has higher SNR than GRAPPA on the datasets 6, 7, 9 and 11 and it also has higher SNR than SENSE on all datasets except the datasets 4 and 11.
7. Experiments

Fig. 7.20. Quality comparison of PROBER 1-3 with SENSE and GRAPPA.
Comparison of the PROBER 1-3, SENSE and GRAPPA reconstruction quality on all simulated datasets with the input noise variance $\sigma^2_l = 10^{-4}$ (a-b) and $\sigma^2_l = 10^{-3}$ (c-d) for the acceleration factor 2 is shown. The figures display reconstruction AP (a, c) and SNR (b, d).
7.5. Experimental comparison of PROBER, SENSE, and GRAPPA

We show the reconstruction quality of PROBER 4-6, SENSE and GRAPPA as tested on all simulated datasets with the input noise variance \( \sigma_l^2 = 10^{-4} \) (a-b) and \( \sigma_l^2 = 10^{-3} \) (c-d) for the acceleration factor 2. The reconstruction AP (a, c) and SNR (b, d) is shown.

Fig. 7.21. Quality comparison of PROBER 4-6 with SENSE and GRAPPA.
Fig. 7.22. The SENSE, GRAPPA and PROBER reconstructions of the simulated dataset 9. Reconstructed images from the simulated dataset 9 with the acceleration factor 2 and the noise variance $\sigma^2 = 10^{-4}$ are shown. The original (a), PROBER 3 (b), SENSE (c) and GRAPPA (d) images are shown. There are minor aliasing artifacts in the SENSE reconstruction. The GRAPPA and PROBER 3 reconstructions are aliasing free. All PROBER 1-6 methods have lower AP and higher SNR than GRAPPA, see Figure 7.20.
7.5. Experimental comparison of PROBER, SENSE, and GRAPPA

Fig. 7.23. The SENSE, GRAPPA and PROBER reconstructions of the simulated dataset 10. Reconstructions of the simulated dataset 10 with the acceleration factor 2 and the noise variance $\sigma_l^2 = 10^{-3}$. The original image (a). PROBER 4 (b), SENSE (c) and GRAPPA (d) reconstructions. There are several aliasing artifacts in the GRAPPA and SENSE reconstructed images. The artifacts are visible especially in the flat region of the oral cavity.
7. Experiments

The reconstruction quality of PROBER 1-6, SENSE and GRAPPA was tested on all simulated datasets with the input noise variance $\sigma^2_l = 5 \cdot 10^{-4}$ and with the acceleration factor 4. The reconstruction AP (a, c) and SNR (b, d) is shown for PROBER 1-3 (a-b) and for PROBER 4-6 (c-d).

Fig. 7.24. Quality comparison of PROBER 1-6, SENSE and GRAPPA for acceleration factor 4.
7.5. Experimental comparison of PROBER, SENSE, and GRAPPA

Fig. 7.25. Quality comparison of PROBER, SENSE and GRAPPA on the simulated dataset 6. Reconstructions of the simulated dataset 6 with the acceleration factor 4 and the noise variance \( \sigma^2_l = 5 \cdot 10^{-4} \). The original image (a), PROBER 1 (b), PROBER 4 (c), PROBER 5 (d), SENSE (e) and GRAPPA (f) reconstructions. There are several artifacts visible in the PROBER 1 reconstruction (b). There are only minor artifacts in the PROBER 4 (c) and PROBER 5 (d) reconstructions. Aliasing artifacts are clearly visible in the GRAPPA reconstruction (f). The SENSE reconstruction (e) is impaired by strong aliasing artifacts.
Fig. 7.26. Quality comparison of PROBER, SENSE and GRAPPA on the simulated dataset 9. Reconstructions of the simulated dataset 9 with the acceleration factor 4 and the noise variance $\sigma^2 = 5 \cdot 10^{-4}$. The original image (a), PROBER 6 (b), SENSE (c) and GRAPPA (d) reconstructions. The PROBER 6 reconstruction (b) is free of visible artifacts and there is moderate noise in the image. The SENSE reconstruction (c) contains significant aliasing artifacts. The GRAPPA reconstruction (d) contains strong aliasing artifacts as well as a considerable amount of noise in the image.
7.5. Experimental comparison of PROBER, SENSE, and GRAPPA

![Graph showing SNR for Phantom and In-vivo images.]

**Fig. 7.27.** Quality comparison of PROBER 1-3, SENSE and GRAPPA on real images. The reconstruction SNR as measured on the phantom (a) and the in-vivo (b) datasets. The PROBER 1-3, SENSE and GRAPPA SNR\textsubscript{real} is displayed.

### 7.5.2. Real images

The results reached on the simulated datasets were confirmed on real data. Noise-free ground-truth images are not available for the real measurements and we used only the SNR to quantify the reconstruction quality, see the equation (7.3). Therefore, the results on real images should be regarded as indication only. For the same reason, we have only performed tests with an acceleration factor 2. The PROBER parameter $\bar{\lambda}$ was set to $10^{-4}$ for all datasets.

The fast PROBER methods 1-3 have the quality comparable to the GRAPPA and SENSE in half of the cases. However, in 15 cases, the SNR of PROBER 1-3 is lower than the SNR of both SENSE and GRAPPA, see Figure 7.27. The PROBER 4-6 have higher SNR than both SENSE and GRAPPA on 15 phantom datasets and the same SNR on the rest of the phantom datasets. PROBER 4-6 have the same SNR as GRAPPA on all in-vivo datasets and better SNR than SENSE on most of the in-vivo datasets. Examples of the reconstructions are shown in Figures 7.29, 7.30 and 7.31.
7. Experiments

Fig. 7.28. Quality comparison of PROBER 4-6, SENSE and GRAPPA on real images. The reconstruction SNR as measured on the phantom (a) and the in-vivo (b) datasets. The PROBER 4-6, SENSE and GRAPPA SNR is displayed.
Fig. 7.29. Quality comparison of PROBER, GRAPPA and SENSE on the phantom dataset 3, acceleration factor 2.

The original image is shown in (a). Images reconstructed using (b) PROBER 2 ($\text{SNR}_{\text{real}} = 36.5\, \text{dB}$), (c) PROBER 3 ($\text{SNR}_{\text{real}} = 36.2\, \text{dB}$), (d) PROBER 6 ($\text{SNR}_{\text{real}} = 39.9\, \text{dB}$), (e) SENSE ($\text{SNR}_{\text{real}} = 36.9\, \text{dB}$) and (f) GRAPPA ($\text{SNR}_{\text{real}} = 33.6\, \text{dB}$) are shown. There are minor aliasing artifacts in the (b) PROBER 2, (c) PROBER 3, (e) SENSE and (f) GRAPPA reconstructions. The noise level in the GRAPPA reconstruction (f) is slightly higher than in the other reconstructed images.
7. Experiments

Fig. 7.30. Quality comparison of PROBER, GRAPPA and SENSE on the phantom dataset 15, acceleration factor 2.

The original image is shown in (a). Images reconstructed using (b) PROBER 1 (SNR$_{\text{real}} = 28.3dB$), (c) PROBER 4 (SNR$_{\text{real}} = 35.7dB$), (d) PROBER 5 (SNR$_{\text{real}} = 34.5dB$), (e) SENSE (SNR$_{\text{real}} = 26.7dB$) and (f) GRAPPA (SNR$_{\text{real}} = 34.6dB$) are shown. There are minor aliasing artifacts in the (b) PROBER 1 and (e) SENSE reconstructions.
7.5. Experimental comparison of PROBER, SENSE, and GRAPPA

Fig. 7.31. Quality comparison of PROBER, GRAPPA and SENSE on the in-vivo dataset 23, acceleration factor 2.
The original image is shown in (a). Images reconstructed using (b) PROBER 4 (SNR\textsubscript{real} = 23.4dB), (c) SENSE (SNR\textsubscript{real} = 13.6dB) and (d) GRAPPA (SNR\textsubscript{real} = 23.0dB) are shown. The PROBER 4 (b) and GRAPPA (d) reconstructions are free of visible aliasing artifacts whereas there are strong artifacts in the SENSE (c) reconstruction near the heart.
7. Experiments

**Fig. 7.32.** The PROBER 1-3 reconstruction speed.
The reconstruction speed of PROBER 1-3 was compared with the speed of SENSE and GRAPPA methods for image sizes from $128 \times 128$ to $768 \times 768$ pixels. The speed was tested using 4 (a), 8 (b, d) and 12 (c) coils for the acceleration factor 2 (a-c) and 4 (d).

### 7.5.3. Speed

The speed of the PROBER method was compared with the reconstruction speed of the commercial implementations of the GRAPPA and SENSE algorithms implemented in the Siemens Magnetom Avanto scanner. All methods were implemented in C++ and identical routines were used for the non method-specific calculations such as the Fourier transform and matrix inversion. All algorithms were run on an AMD K8 4.4 GHz processor with 4GB RAM. The total time of the estimation and the reconstruction processes was measured 30 times for each method and the minimum value was considered. The simulated dataset 10 was used for the experiments; 4, 8 or 12 coils were considered. The reconstruction speed was measured for image sizes from $128 \times 128$ to $768 \times 768$ pixels.

The results for PROBER 1-3 and PROBER 4-6 are shown in Figures 7.32 and 7.33, respectively. For 4 receiver coils, the PROBER 1 method is faster than both SENSE and GRAPPA reconstruction for images larger than $180 \times 180$ pixels. The PROBER 2 and 3 are faster than SENSE for all image sizes and they are also faster than GRAPPA for images larger than $512 \times 512$ pixels. The speed advantage of PROBER 1-3 becomes more significant for a higher number of receiver coils. For 8 and more coils, the PROBER 1 method is faster than SENSE and GRAPPA for all tested image sizes. As is shown in Figure 7.33, the PROBER 4-6 is the slowest of all the tested methods. However, the PROBER 4-6 reconstruction times are still comparable to the SENSE and GRAPPA reconstruction times.
7.5. Experimental comparison of PROBER, SENSE, and GRAPPA

Fig. 7.33. The PROBER 4-6 reconstruction speed.

The reconstruction speed of PROBER 4-6 was compared with the speed of SENSE and GRAPPA methods for image sizes between 128 × 128 and 768 × 768 pixels. The speed was tested using 4 (a, c) and 8 (b, d) coils with the acceleration factor 2 (a-b) and 4 (c-d).
7. Experiments
8. Conclusions

MRI is one of the most important medical imaging modalities. The main advantages of MRI are high image quality, various tissue-contrast mechanisms, and the fact that MRI is noninvasive and does not produce any harmful radiation. Parallel MRI is a technique that increases the acquisition speed. This is advantageous for dynamical imaging and it also increases the number of patients examined per day and, thus, makes the MRI examination more available. In this thesis, we have addressed the topic of parallel MRI reconstruction methods.

We have formulated the problem of parallel MRI reconstruction from the undersampled $k$-space data and provided the necessary theoretical background that is essential for a thorough understanding of the problematics. The state-of-the-art of parallel MRI was written to summarize the main reconstruction algorithms with references to literature.

We have proposed and implemented a new reconstruction technique called PROBER. The PROBER method uses a B-spline approximation of the reconstruction transformation. This regularizes the transformation and lowers the number of unknown parameters. Hence, the reconstruction process becomes faster and more robust. We have implemented our method in C++ and Matlab so that it could be easily tested offline as well as incorporated into an MRI scanner software. PROBER was tested along with two commercially used methods SENSE and GRAPPA. The results showed that PROBER produced images with a higher reconstruction quality than SENSE and GRAPPA on most of the tested images.

The disadvantage of the PROBER method is an up to four fold increase of reconstruction time when high-quality settings are used. This can be compensated for by lowering the approximation precision which leads to more than two times faster reconstruction times than SENSE and GRAPPA but it also slightly decreases the reconstruction quality. A further optimization of the PROBER method should achieve both high reconstruction speed and quality.

There are several other possibilities for future improvements of our method. The method can be extended to work with a time sequence of images or in 3D. The variations of coil sensitivity and consequently of reconstruction coefficients between successive slices in time or space is low and this fact can be used to improve the estimation quality. Second, the method can use a statistical model of the MRI image intensity distribution. The reconstruction coefficients can be sought in order to maximize the likelihood of the reconstructed image and, thus, further constrain the reconstruction transformation.

To conclude, we have developed a parallel MRI reconstruction method that improves the state-of-the-art reconstruction methods. It offers a reasonable alternative to commercially used methods in terms of both speed and quality of the reconstruction. It has been explained theoretically and validated on a series of experiments. Our method can be directly used in practice but it can also serve as a basis for a future improvements of the parallel MRI reconstruction methods.
Appendices
A. Programs

We have implemented the PROBER methods described in Chapter 5 in Matlab (The MathWorks, Inc.; version 7.2.0.294 [63]) and in C++ (compiler GNU C++ 4.1.1 or Microsoft Visual C/C++ 7.1) programming languages. The source code is located on the attached CD in the directory PROBER. In this Chapter, we give a short guide on how to compile and run the programs. Simulated datasets (see Section 7.1.3) are included on the CD in the directory PROBER/simulateData and they can be used to test the algorithms. The code can be used freely for non-commercial purposes on condition that this thesis will be cited. The code can be distributed in unmodified form. The C++ implementation of GRAPPA and SENSE built-in the MRI scanner (Magnetom Avanto, Siemens Medical Solutions) was used, however, the source code is not included for legal reasons.

A.1. Directory structure

The subdirectory mathTools contains implementation of the necessary mathematical tools (Fourier transformation, Cholesky decomposition and various matrix operations) [73]. The compiled code and executable files are stored in the directory bin. The Windows library for Fourier transformation is in the directory fftw (FFTW package by Matteo Frigo and Steven G. Johnson [19]). The directories proberCont, proberDisc and proberTrivial contain the source code of the continuous, discrete and trivial PROBER methods, respectively. The Matlab datafiles used to generate the simulated datasets and the corresponding Matlab scripts are located in the directories simulatedData and simulatedImages, respectively. The directory tools contains additional Matlab scripts.

A.2. How to run

Let us provide short instructions how to compile and run the programs. First, the whole directory PROBER needs to be copied to a writable media. The Matlab script init.m performs the path initialization. The source code is compiled using the Matlab scripts makeWindows.m or makeLinux.m (depending on the platform). The reconstruction process itself is performed by running the script testProber.m. There are several parameters at the beginning of the file that set properties of the generated dataset and the PROBER method.

A.2.1. Dataset parameters

The directories simulatedData and simulatedImages contain Matlab scripts and data that are used to generate the simulated datasets, see Section 7.1.3. The dataset parameters are set at the beginning of the script testProber.m. The dataset to create is determined by the parameter simSet. Variable density scans are generated with FOV size siz×siz pixels, an acceleration factor AF and the number of reference lines in the k-space center is refLines, see Section 5.6.1. Gaussian noise with variance noiseVar is added to both real and imaginary components of the k-space data, see Section 7.1.3. The number of datasets used to statistically evaluate the reconstruction quality is set by the parameter attmps, see Section 7.2. If the
number of datasets is set to 1 then only the reconstruction SNR is evaluated. Otherwise,
both AP and SNR are evaluated.

A.2.2. PROBER parameters

PROBER parameters can be changed at the beginning of the Matlab script `testProber.m`,
after the dataset parameters. The version of the PROBER method is chosen by changing the
parameter `methodType` where values 1, 2, 3 and 4 correspond to continuous PROBER (see
Section 5.7), discrete PROBER (Section 5.4) and 1D and 2D trivial PROBER (Section 5.3),
respectively. The first two methods are implemented in C++ whereas the other two methods
are implemented in Matlab. For this reason, the reconstruction time of trivial PROBER is
several times longer than the reconstruction times of the discrete and continuous PROBER.

There are three parameters to set for all the PROBER versions: the number of B-splines $I$, $J$
used to represent the reconstruction transformation (see Section 5.2.1), and the parameter
FEC that defines if the unaliased images are reconstructed for each coil separately. The discrete
and continuous PROBER methods also have the parameter $\lambda$ which defines the value
of $\bar{\lambda}$ (Section 7.3.5) and the parameter `reconType` determining if the acquired $k$-space center
lines are added to the reconstruction (Section 5.6). The discrete PROBER method has a
parameter `sizBspln` referring to the estimation-grid size, see Section 5.6.1. The continuous
PROBER method is parameterized by the number of B-splines $P$, $Q$ used to represent the reference images (see Section 5.7.1) and by the parameter `itgN` defining the number of steps
of the numerical integration, see Section 5.7.2.

The Matlab scripts serve only as an input/output interface. The discrete and continuous
PROBER methods can be easily transferred completely to C++. This can be done by editing
the main functions `mexFunction` in files `proberC.cpp` and `proberD.cpp` and by providing all
the input data directly. Thus, after a slight modification, the PROBER method can be used
in any MRI machine that uses C++ programming language to implement the parallel MRI
reconstruction methods. For a more detailed description of the provided Matlab scripts and
C++ code, we refer the reader to the comments in the source code.

A.3. Input data

The PROBER methods can also be tested with an alternative input apart from the supplied simulated images. This can be done by changing the variable `imVD` referring to the variable-density images. The data are supplied in a hybrid $k$-space form as a 3D matrix. The first dimension of the `imVD` matrix represents the phase-encoding direction. The data are given in the $k$-space with the zeroth frequency shifted into the center. The second dimension of the `imVD` matrix refers to the frequency encoding direction and the data are supplied in the image space. Indices in the third dimension of the `imVD` matrix specify the different receiver coils.

As a result of the accelerated acquisition, only rows 1, $M + 1, 2M + 1, \ldots$ are non-zero
and the remaining lines are filled with zeros. The $k$-space center with the size specified by
the number `refLines` is fully sampled – the $k$-space center corresponds to the rows from
$((Y - \text{refLines})/2 + 1)$ to $(Y + \text{refLines}/2)$ of the `imVD` matrix, where $Y$ is the image size in
the phase-encoding direction.
Index

acceleration factor, 19, 23
aliasing, 19, 23
AP, see artifact power
array coils, see coil array
artifact power, 81
AUTO-SMASH, 29

B-spline, 47
Bloch equation, 12
body coil, 19

CAIPIRINHA, 41
coil array, 19, 23
coil sensitivity, 19, 23, 26
continuous PROBER, 65
discrete PROBER, 50
echo time, 9
echo top, 10
EPI, 15
excitation, 5

FID, see free induction decay
field of view, 17
Fourier imaging, 12
FOV, see field of view
free induction decay, 8
frequency encoding, 13

gradient fields, 11
GRAPPA, 30, 72
gyromagnetic ratio, 4

input image, 23, 45
k-space, 17

Larmor frequency, see resonance frequency
longitudinal, 5

magnetic gradients, see gradient fields
magnetic resonance imaging, 10
net magnetization, 5

nuclear magnetic resonance, 3
parallel MRI, 23
PARS, 40
perfect reconstruction conditions, 50
phase encoding, 13
PILS, 38
precession, 6
PROBER, 45, 71

quadrature detection, 9

radio frequency pulse, 7
reference image, 24, 45
relaxation
   $T_1$ relaxation, 5, 12
   $T_2$ relaxation, 7, 12
resonance frequency, 5, 11
RF pulse, see radio frequency pulse
Rician distribution, 54
rotating frame of reference, 6

SENSE, 33, 71
sensitivity, see coil sensitivity
signal to noise ratio, 81
slice selection, 12
SMASH, 27
SNR, see signal to noise ratio
SPACE-RIP, 37

spatial encoding, see Fourier imaging
spin, 3
spin echo, 9, 14

transversal, 5

UNFOLD, 42

variable density scan images, 62
Bibliography


Bibliography


