Application of Reduced-Encoding Imaging with Generalized-Series Reconstruction (RIGR) in Dynamic MR Imaging

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Dynamic MRI has proven to be an important tool in studies of transient physiologic changes in animals and humans. High sensitivity and temporal resolution in such measurements are critical for accurate estimation of dynamic information. Fast imaging, often involving expensive hardware, has evolved for use in such cases. We demonstrate herein the possibility of accelerated data acquisition schemes on conventional machines using standard pulse sequences for dynamic studies. This is achieved by combining reduced-encoded dynamic data (typically 30 to 40 phase encodings) with a priori high-resolution data via a novel constrained image reconstruction algorithm. Such an approach reduces image acquisition time significantly (by a factor of 3 to 4 in the examples described here) without loss in the accuracy of information.

Index terms: Dynamic MR imaging • Fast imaging • Image reconstruction • Reduced encoding imaging

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Abbreviations: BOLD = blood oxygen level dependent, FLASH = fast low-angle shot, FFT = fast Fourier transform, FOV = field of view, FT = Fourier transform, GS = generalized series, LL = Look-Locker, RF = radiofrequency, RIGR = reduced-encoding imaging with generalized-series reconstruction, SEM = standard error of the mean, SNR = signal-to-noise ratio.

IN MAGNETIC RESONANCE (MR) IMAGING, there are tradeoffs between the signal-to-noise ratio (SNR) and both temporal and spatial resolution. This tradeoff leads to compromises in dynamic MR imaging, because measurements have to be made within given time constraints. We have focused our attention on improving the temporal resolution of such measurements by considering the use of advanced signal processing techniques rather than advanced instrumentation. For conventional imaging sequences, it may not always be possible to acquire sufficient data, especially in a dynamic situation, to reconstruct high-resolution dynamic information using direct Fourier reconstruction. Our general approach in such cases is to incorporate additional information into low-spatial-resolution dynamic data sets from a high-spatial-resolution data set acquired at a stationary physiologic state. We report here our preliminary experience with a technique that relies on parametric modeling of the dynamic image function as a generalized series (1). A variant, called "keyhole imaging," also deserves mention in this context (2). Our reconstruction algorithm is called generalized-series (GS) reconstruction and the imaging protocol that uses it has been called reduced-encoding imaging with generalized-series reconstruction (RIGR). Unlike keyhole imaging, this technique modulates the high-frequency data from the basis image to make it consistent with the acquired data, thereby reducing reconstruction artifacts. Use of this reconstruction technique already has been reported in the literature (3) for T2-weighted imaging. To demonstrate the general usefulness of this algorithm, we compare GS reconstruction with direct high-resolution Fourier reconstruction in four independent areas of dynamic MRI: diffusion imaging (4), perfusion imaging (5), blood-oxygen-level-dependent (BOLD) imaging (6), and fast T1 mapping (7). It is demonstrated that a significant reduction in data acquisition time is achievable by using this algorithm, without a concomitant loss of informational accuracy.

• RIGR AND ITS ENCODING SCHEME

In most dynamic imaging problems, the underlying high-resolution anatomic features do not change from one image to the next. Therefore, the stationary anatomic
information may be acquired only once, with a k-space acquisition matrix sufficient to obtain the desired spatial resolution. The subsequent dynamic images may then be acquired with a smaller number of encodings, sufficient to encode the low spatial frequencies of the contrast modulations caused by dynamic variations in T1, T2, perfusion, diffusion, etc. The GS algorithm can combine the anatomic constraints with the low-resolution dynamic information in the reconstruction step to generate high-resolution dynamic images and give a large reduction in data acquisition time.

The GS model has been developed (1) to handle “a priori” constraints in a data-consistent manner. In the two-dimensional imaging case, the RIGR encoding scheme is usually applied to the phase-encoding dimension, assumed here to be \( y \). The dynamic image function \( \rho_{\text{GS}}(x,y) \) then is represented as

\[
\rho_{\text{GS}}(x,y) = \rho_{\text{ref}}(x,y) \sum_{m} \exp \left( 2\pi i m \Delta k \right)
\]

where

\[
\rho_{\text{GS}}(x,y) = \text{the generalized series reconstruction of the dynamic image function}
\]

\[
\rho_{\text{ref}}(x,y) = \text{the high-resolution basis image}
\]

\[
\Delta k = \text{is the spatial frequency interval of sampling in k space}
\]

\[
a_m = \text{the ratio Fourier coefficient of the contrast modulation function}
\]

\[
m = \text{an index for the dynamic encoding step}
\]

It is worthwhile to note that the GS-reconstructed image is obtained by direct modulation of the reference or basis image by a Fourier series or a contrast modulation function. The number of terms in the series is dictated by the number of encodings in the dynamic data set, so that the series modifies the basis image at each pixel to match the measured dynamic data. The reconstructed images, therefore, have the same spatial resolution for anatomic boundaries as the basis image. The number of encodings required to register dynamic contrast changes occurring within these anatomic boundaries (whose definition already exists in the constraint used, i.e., the reference image) is usually much lower (\(-30-40\)) than would be required for full high-resolution imaging (\(-128-256\)). Imaging efficiency is therefore increased by using the RIGR imaging method. It is important, however, to remember that the dynamic information is still dependent on the number of dynamic encodings, and very high spatial frequency dynamic changes may not be represented accurately in the GS-reconstructed images (see Discussion section).

Applying the GS model involves three steps:

1. Choosing an appropriate constraint function with optimized parameters to highlight the boundary information that matches the edge information in the dynamic data set.

2. Calculation of the Fourier coefficients \( a_m \); direct Fourier transformation of the model shows that in the signal domain the measured signal \( S(n\Delta k) \) is a convolution of the Fourier coefficients with signals \( S_o(n-m) \Delta k \) from the basis image. Hence

\[
S(n\Delta k) = \sum a_m S_o(n-m) \Delta k
\]

This leads to a set of \( m \) linear equations. Fast algorithms exist to solve such a set of equations and hence estimate each of the Fourier coefficients \( a_m \). If phase constraints are used, the solution is more involved (8). The algorithm is most successful when some caution is exercised regarding the choice of the \( m \) dynamic encodings (see Discussion).

3. Generation of the GS image. After the GS Fourier series coefficients are estimated, the GS image is generated either (a) at each pixel by using the model equations above; (b) by applying a fast Fourier transform (FFT) to the GS coefficients, zero-filled to the size of the data set, and multiplying the result by the reference image; or (c) by reconstructing the missing high spatial frequency k-space data in the dynamic data set and applying an FFT. The three methods are equivalent; however, computationally, (b) is more efficient than (a) and (c). Therefore, (b) was used for the work described in this paper.

In all of our experiments, high-resolution images were generated with the GS algorithm by using information from only a subsection of a high-resolution data set and combining it with a priori information from a basis image. To evaluate the success of this reconstruction scheme, the GS images were then compared with the images generated by Fourier transformation of the full high-resolution data set. In different dynamic cases, the GS-reconstructed images were subtracted from their corresponding Fourier-reconstructed images to reveal the existence of any systematic pixel-to-pixel image intensity discrepancy between the two reconstruction schemes.

### MATERIALS AND METHODS

Diffusion imaging was performed on a 4.7 T/40 cm horizontal bore SISCO (Palo Alto, CA) imaging spectrometer. A 16-cm-diameter radiofrequency (RF) saddle coil was used. Perfusion imaging, BOLD imaging, and fast T1-mapping experiments were performed on a 4.7 T/33 cm SISCO imaging spectrometer. RF pulses were transmitted by an 8.8-cm-diameter saddle coil, and a 3.3-cm-diameter surface coil was used as a receiver.

For the diffusion imaging studies, dogs (\(-17 \text{ kg}\)) were anesthetized with pentothal (20-30 mg/kg) and maintained on 1 to 1.5% isoflurane. Six slices (SE: TR = 1.3 sec; TE = 130 msec; field of view [FOV] = 14 × 14 cm; 256 × 128 encodings) were acquired with the first three b values were discarded to correspond to gradients (slice thickness = 8 mm) with 10 diffusion-sensitized images of each slice.

The pulse sequence was made sensitive to diffusion along the slice-selective direction (gradients = .0, .094, .189, .285, .379, .473, .668, .852, 1.014, 1.136 G/cm; b factors corresponding to gradients = .0, 5.81, 23.27, 52.36, 93.09, 145.45, 285.07, 471.23, 703.94, 841.46 sec/mm²). Only the fourth slice was chosen to demonstrate the validity of the GS reconstruction algorithm. The data were zero-filled to 256 × 256 and Fourier reconstruction was used to generate the high-resolution images. Images acquired with the first three b values were discarded to minimize artifacts from microrotation (9).

Subsequently, GS reconstruction was used to reconstruct high-resolution diffusion-weighted images from only 32 phase encodings (an asymmetric set composed of the -8th to ±23rd phase encodings) taken from the corresponding k-space data and using the first image as the basis image.

For the perfusion and BOLD imaging studies, Sprague-Dawley rats (\(-500 \text{ g}\)) were anesthetized with 1:1 \( \text{O}_2/\text{N}_2\) mixture and 1.5 to 2.0% halothane and were subsequently maintained at 1.25 to 1.5% halothane. For perfusion imaging with arterial spin inversion (5), magnetization inversion at the neck was achieved by adiabatic fast passage. The RF field used for the inversion was 60 mG with a gradient of 1 G/cm. The use of RIGR imaging
in the arterial spin-inversion technique was demonstrated via a two-stage strategy. First, the accuracy of generating a T1 map was tested and then the accuracy of the subtraction image (5) was demonstrated. To measure T1 accuracy, a specific slice in the rat brain with cerebrospinal fluid (CSF)-filled ventricles was chosen to ensure varying contrast with varying T1 weighting (SE; 256 × 128 encodings; FOV = 4 × 5 cm; TR/TE = 12,000/35 msec; time after saturation = .6, 1.3, 4.6, 5.8, 7.9 seconds). Accurate reconstruction of images with such changing features along the saturation curve served as a good challenge for the GS algorithm. To test the GS al-

Figure 1. (a) The FT-reconstructed diffusion-weighted images generated from full k space used for the diffusion calculations (upper row). The GS-reconstructed images from 32 phase encodings (middle row). The difference images (upper row − middle row) demonstrating no significant artifacts are introduced by GS reconstruction (lower row). (b) A representative profile along the images shows the signal variation in the FT, GS, and the difference images.
The diffusion map generated by fitting a decaying monoexponential through the FT images (left) and GS images (right). A representative profile along the images shows that for most pixels the ADC obtained using the GS reconstruction is a good estimate of that obtained with FT of the high resolution data set.

Algorithm, the last image on the saturation recovery curve was used as the basis image. Thirty-two phase encodings (−8 to ±23), from each k-space representation of the other four T1-weighted images, were then used as the reduced phase-encoded data and the images were reconstructed using the GS reconstruction algorithm. In a separate experiment, the accuracy of the GS algorithm in the reconstruction of the difference image was tested. High-resolution control and tagged (implying images obtained with spin inversion at the carotids) images (SE: TR/TE = 2,000/28 msec; FOV, 4 x 5 cm; 256 x 128 encodings) were first acquired (SE: TR/TE = 2,000/28; 256 x 256 encoding). Subsequently, control and tagged images were acquired (256 x 64 encodings; four signal averages). A saturation recovery data set was collected with parameters identical to those used for the T1 experiment except for only 64 encodings being collected. Control, tagged, and T1-weighted images were then generated using only 32 asymmetric encodings (−8 to 23) of its k-space representation and using the control image as the basis image. The subtraction of these images generated the GS-reconstructed difference image (image B). Image B was then subtracted from image A to evaluate the success of the GS algorithm.
Figure 3. (a) Upper row: T1-weighted images (SE; TR/TE = 12,000/35; FOV = 4 × 5 cm; 256 × 128 encodings scaled down to 128 × 128; slice thickness = 2.0 mm; delay times after saturation = .6, 1.3, 4.6, 5.8, 7.9 seconds) generated by Fourier reconstruction of the full-encoded data set. Middle row: T1-weighted images reconstructed using the GS algorithm and using only the 32 phase encodings. The last image, with full encoding, is used as the basis image. Lower row: the difference images at each point of the saturation recovery curve. (b) A representative intensity profile along the vertical bar confirms the absence of image artifacts in the difference image.
Figure 4. Upper row (from left to right): the high resolution control image, the tagged images, and difference image A (SE: TR/TE = 2,000/28; FOV = 4 × 5 cm; slice thickness = 2.0 mm; 256 × 128 encodings interpolated to 256 × 256) generated from Fourier reconstruction of the full data set. Lower row: the control image, tagged image, and difference image B generated with the GS algorithm, using the control image as the basis image.

(-8 to ±23 encodings) from the respective k spaces. These images were then used to generate the ratio image, the T1 map, and the perfusion map. The perfusion values obtained for each specific region ideally should be compared with those obtained from an actual high-resolution (256 × 128) perfusion data set to test their accuracy. However, it was not possible to keep the animal in a physiologically stable condition for the time needed to collect all of the necessary data for the calculation of a high-resolution perfusion map. The perfusion values obtained in our RIGR experiment were therefore compared with the corresponding values obtained when all the encodings of the 256 × 64 data set (after zero-filling to 256 × 256) are used.

For BOLD contrast variation in the rat brain, the oxygen content of the inhaled gas was varied in a cyclic fashion from 50 to 10%, then to 50%, 25%, 10%, and again back to 50%. High-resolution (128 × 128) imaging was performed at each step of the cycle to encode all transient high spatial resolution features. Using a spoiled fast low-angle shot (FLASH) [10] pulse sequence, a high-resolution data set (TR/TE = 1,000/13 msec; 128 × 128 encodings, zero-filled to 256 × 256; FOV = 5 × 5 cm; slice thickness = 2 mm; flip angle = 60°) was first collected, with one image at every step of the oxygen variation cycle. The first image, with 50% oxygen level in the breathing gas, was then used as the basis image. Using the basis image and the GS reconstruction algorithm, the other five images were subsequently reconstructed with only 40 phase encodings (the -7th to the ±32nd phase encoding) from each of their k-space representations. The choice of the first image as the basis image is deliberate. This image has the least high-spatial frequency features arising from BOLD contrast and therefore poses a bigger challenge for the RIGR algorithm, because high-spatial frequency features have to be reconstructed from the reduced encoded data set without adequate constraints from the basis image. In such a case, in which a very high spatial resolution image feature that is not constrained by the basis image is to be reconstructed using GS reconstruction, a larger number of encodings would be necessary for accurate boundary and intensity estimations. As such, we decided to use 40 encodings instead of 32 as used elsewhere. The image with 10% oxygen was farthest from the basis image in contrast and, hence, it was used for testing the reconstruction accuracy.

For the fast T1-mapping experiment, an Alderman-Grant coil was used for both transmission and reception.
A three-compartment phantom (an outer 2.3-cm-diameter tube filled with 1% agar gel and two inner tubes (.5 cm in diameter) containing different concentrations of copper-sulfate-doped water) served as a test phantom for the study. A Look-Locker (LL) imaging sequence (7,11) was then implemented with a saturation pulse. A recovery time of 400 msec was allowed between each acquisition. A tip angle of 10°, an echo time of 8 msec, and a total TR of 12 seconds were used. The total imaging time was only 25 minutes. To validate the LL imaging results, a slow saturation recovery experiment with long TR was performed (TR/TE = 16,000/25 msec; FOV = 8 x 8 cm; number of encodings: 256 x 128). Twelve images with variable delay (t,) between the saturation pulse and the imaging 90° pulse were collected (t, = 0.2, 0.4, 0.8, 1.0, 1.4, 1.8, 2.3, 3.2, 4.0, 5.5, 7.8, 9.7 seconds). The total image acquisition time was approximately 6.8 hours. To test the validity of the GS reconstruction in the LL experiment, the last image of the T1-weighted high-resolution data set was taken as the basis image, and all of the other images were reconstructed from only 32 encodings (an asymmetric set consisting of the -8th to -23rd phase encodings) of their respective k-space representations. The imaging time would have been only 6 minutes if such a reduced encoded data set had actually been collected. This reduced encoded data set will be referred to as the LL-RIGR data set. The LL-RIGR data set was then subtracted pixel by pixel from the high-resolution LL data set.

All images were processed with VIEWIT (NCSA, Urbana, IL) and figures were generated with the software package ANALYZE (CNSoftware, UK).

**RESULTS**

Figure 1 displays the Fourier diffusion-weighted images (upper row) and the GS diffusion-weighted images (middle row) used for diffusion coefficient mapping. The difference images, displayed in Figure 1 (last row), have negligible intensities (close to the noise level). A representative profile through the fourth image of each of the three sets of images (Fourier transform [FT], GS, and difference images) confirmed the absence of any significant artifact from GS reconstruction. Diffusion maps were then obtained by fitting a single decaying exponential through the Fourier-reconstructed images and the GS-reconstructed images. Figure 2 shows the diffusion maps obtained by using the Fourier images (left) and the GS images (right). The D values obtained from the GS reconstruction images agreed closely with those obtained from the high-resolu-
tion Fourier data set. To compare one specific example, the
$D$ value obtained from the Fourier-reconstructed images
in the deep brain regions (as outlined by the box in Fig. 2)
was \(0.543 \pm 0.026 \times 10^{-5} \text{ cm}^2/\text{sec}\) and the corresponding
value obtained from the GS images was \(0.540 \pm 0.020 \times 10^{-5} \text{ cm}^2/\text{sec}\) (mean ± standard error of the mean [SEM];
\(n = 25\) pixels in both cases). A profile through the respec-
tive diffusion maps demonstrated that, for most pixels, the
local diffusion coefficients obtained from the GS-recon-
structed images were good estimates of the corresponding
coefficients obtained from the high-resolution images.

Figure 3 shows the set of five high-resolution \((256 \times 128)\)
T1-weighted saturation recovery images (SE: TR/TE = 12,000/35 msec) generated by Fourier reconstruction
using full encoding (upper row). The middle row shows
the images obtained with the GS algorithm. The GS re-
constructed images were then subtracted from the Four-
rier-reconstructed images (generated from all encodings).
The lower row displays the difference images, which had
near-noise level intensities. A representative profile
through the third image on the saturation recovery curve
for all three rows is also shown. The mean intensity value
over a 1,200-pixel region in this image, for both the Fou-
rier reconstruction and the GS reconstruction, was com-
pared for a more quantitative estimate of the reconstruc-
tion accuracy. The value in the Fourier reconstructed
image was \(4,440 \pm 13\) (mean ± SEM) and the corre-
sponding value for the GS-reconstructed image was
\(4,442 \pm 13\). This confirmed that no significant system-
atic error had been introduced by the reconstruction al-
gorithm for generating the saturation recovery images.

Figure 4 (upper row) shows the high-resolution control
and tagged images, obtained with direct Fourier recon-
struction of the high-resolution data set and the subtrac-
tion image (image A). The corresponding GS-reconstructed
images are also shown (lower row). Figure 5 compares the
two subtraction images (image A and image B). Repre-
sentative profiles through image A, image B, and the
image A-B are also shown (lower section). The SNR in the
difference images, such as image A and image B, was ex-
tremely small \((-6:1)\), as expected. Therefore, for a quan-
titative analysis of the accuracy of the reconstruction of
such difference images, it should be borne in mind that
at certain isolated pixels the intensity values in image A-
B might be on the order of the signals in image A or image
B. Therefore, only the mean value over a chosen testing

Figure 6. Upper row: the high-resolution image of the slice of interest (SE: TR/TE = 2,000/28; FOV = 4 \times 5 \text{ cm}; 256 \times 256 encodings;
slice thickness = 2.0 mm). Lower row: the control and the tagged image obtained from reduced encoded data sets by using the GS
reconstruction algorithm along with the high-resolution image. The reduced encoded data sets used were generated from 256 \times 32
encodings; four signals were averaged.
kernel was compared. The mean intensity value over a 2,000-pixel region in the brain taken from image A was 1,578 ± 24. The corresponding value in image B was 1,549 ± 21. The close agreement of the mean intensity values confirms that no significant systematic error is introduced by using the GS reconstruction algorithm for generating the difference images.

The perfusion images obtained with the RIGR acquisition strategy are shown in Figures 6, 7, and 8. Figure 6 shows the high-resolution image that was used for the basis image (upper row) and the control and the tagged images (Mb” and Mb, respectively) generated from the reduced encoded data set (lower row). Figure 7 shows the T1-weighted images obtained by using GS reconstruction and the reduced encoded data set. A T1 map was generated by fitting a single exponential through each pixel of the T1-weighted images. Figure 8 shows the subtraction image (top left) and the T1 map (top right) used for the calculation of the perfusion image. The ratio image (5 × [Mb” – Mb]/Mb”) and the representative perfusion sensitive image (obtained from the ratio image and the T1 map) are also shown in Figure 8 (bottom right and bottom left, respectively). The average perfusion value in the reduced-encoding experiment, obtained over a 24-pixel region in the periphery of the brain was 204 ± 8 ml/100 g/min (mean ± SEM), over a 48-pixel region in the hippocampal fissure was 81 ± 4 ml/100 g/min, and over a 36-pixel region in the base of the brain was 248 ± 6 ml/100 g/min; the values from the corresponding regions of the perfusion map generated with zero-filling were 190 ± 8 ml/100 g/min, 81 ± 4 ml/100 g/min, and 241 ± 8 ml/100 g/min, respectively. The pixels were chosen from the areas outlined on the perfusion image in Figure 8. The overall average taken over a 2,200-pixel region over the entire brain was 154 ± 1 ml/100 g/min with RIGR and 155 ± 1 ml/100 g/min in the zero-filled case. The overall average perfusion value reported by Williams et al (5) of 139 ± 19 ml/100 g/min agrees well with our results. Regional perfusion values for their experiment were not reported.
The high-resolution data set collected along the oxygen curve for BOLD contrast is shown in Figure 9 (upper row). As the oxygen content of the inhaled gas mixture is brought down, contrast from small blood vessels starts to show up. This effect is completely reversible. Figure 9 (middle row) shows the GS-reconstructed images using the first image as the basis image. Pixel-by-pixel subtraction of the corresponding images gave near-noise-level intensities as shown in Figure 9 (lower row). The average intensity value over a 360-pixel region in that image, reconstructed with Fourier transform and all 128 encodings, was the same (within about 1%) as the corresponding value in the GS image, reconstructed with only 40 encodings. The image details from dynamic BOLD changes remained sharply defined in the GS-reconstructed images. A profile is drawn through the sharpest high-resolution image feature in the 10% image to illustrate the intensity variation along the high-resolution FT-reconstructed image and the RIGR image. With only 40 encodings, as used here, the high spatial frequency features are still represented in the dynamic images without significant blurring, but some fluctuations in the intensity exist. Figure 10 shows two difference images obtained by the subtraction of the second image (10% oxygen) from the first image (50% oxygen) for both the FT reconstructed (left) and the GS reconstructed image set (right). The image on the left highlights the high spatial resolution information (obtained by a high-resolution data set) that exists in the second image but not in the first. The image on the right demonstrates how well such high spatial resolution features are represented in the GS-reconstructed image. A profile through both of the images shows some intensity fluctuations but no significant systematic errors. The largest error occurs, as explained above, in estimating the intensity over a small central "spot" (a few pixels wide and in turn, therefore, consisting of very high spatial frequency components) in which a huge change in intensity (~30%) occurs because of change in the oxygen content of the breathing gas. This error occurs in this case because the basis image did not provide adequate constraints for such large changes to occur within this small area. In such cases in which a big change in intensity is expected to occur over a very small area, as in functional MRI, either the basis image should have the relevant boundary information for the area of change or a second reference image (see below) may be required. In the absence of either, as above, a larger (>40) number of dynamic encodings would be required for more accurate results.

Table 1 shows a discrepancy of less than 5% between the T1 values obtained with the LL sequence and with the long SR experiment. The values shown here are averaged over all the pixels in each of the specific regions. Thus, the T1 values obtained from the LL experiment will be considered for testing the accuracy of the GS reconstruction. Figure 11 shows representative images from the LL data set (upper row) and the LL-RIGR data set (middle row). The pixel-by-pixel subtraction image shown in Figure 11 (lower row) demonstrates a near-noise-level intensity without any significant artifacts.
Figure 9. (a) Upper row: the high-resolution images obtained by direct Fourier reconstruction of the high-resolution oxygen-sensitive data set. Middle row: the corresponding GS-reconstructed images. Lower row: the subtraction of the GS-reconstructed images from the Fourier reconstructed images. The second image (taken when the rat was breathing 10% oxygen) was chosen because it was farthest from the basis image in BOLD contrast-induced features.

300-pixel region from the third image in the LL-RIGR data set had a value of 6,019 ± 30 as against a value of 6,013 ± 37 for the high-resolution LL data set. Table 1 shows further the accuracy of estimation of T1 using the LL-RIGR data set.

- DISCUSSION

The above results demonstrate that for most commonly used contrast mechanisms and pulse sequences in dynamic MR imaging, the RIGR imaging method can represent, with reasonable accuracy, a high-resolution data acquisition followed by direct Fourier reconstruction. This, in turn, implies that a significant decrease in imaging time, which could be used either to increase temporal resolution or to do more signal averaging for low SNR dynamic imaging, is achievable. The SNR characteristics of the GS-reconstructed images depend primarily on the SNR of the basis image (acquired with encoded) if the number of encodings (N_e) in the dynamic image is small. This property of the reconstruction algorithm is desirable because it facilitates high SNR dynamic imaging by acquiring a high SNR stationary reference image. In many of the examples provided above, the RIGR images have an apparent reduction in noise when compared to the full reconstruction (eg, in Figs. 1 and 2) because the basis images used have high SNR (eg, in Figure 1 the b = 0 image is used as the basis image). If a sufficiently large number of encodings is used for the dynamic
Figure 10. (a) Difference image obtained by subtracting the second image (10% O₂) from the first image (50% O₂) for the FT-reconstructed image set (left) and the GS-reconstructed image set (right). (b) A representative profile through the images shows the intensity variations along the two images, demonstrating the accuracy of estimation of such high spatial frequency edge information using only 40 encodings and the GS reconstruction algorithm.

data set, then the SNR of the GS-reconstructed images depends on the SNR of the dynamic data set and is similar to a conventional Fourier reconstruction of a low-resolution \( (N_e, \text{encodings}) \) data set zero-filled to high resolution \( (N_t, \text{encodings}) \). The SNR advantage obtained would, therefore, be equal to the square root of \( N_t/N_e \). A detailed analysis of SNR in RIGR is described elsewhere.

The choice of the basis image is critical for RIGR imaging. In our demonstration of the success of the reconstruction algorithm, we deliberately chose the basis images that were the least similar in spatial features to the test images. In practice, however, if some knowledge exists about the nature of the boundary information that would be important in the dynamic data sets, then the contrast of the basis image should be adjusted with suitable changes in imaging parameters to highlight the corresponding boundary information in high resolution. The reconstruction is expected to be more accurate if that is done, because the basis image would provide the most

<table>
<thead>
<tr>
<th>Method/Area</th>
<th>Average T1 in Area 1</th>
<th>Average T1 in Area 2</th>
<th>Average T1 in Area 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Saturation recovery</td>
<td>2.36 ± .03</td>
<td>2.70 ± .02</td>
<td>1.73 ± .01</td>
</tr>
<tr>
<td>Look-Locker</td>
<td>2.26 ± .02</td>
<td>2.58 ± .02</td>
<td>1.72 ± .03</td>
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<td>Look-Locker RIGR</td>
<td>2.38 ± .02</td>
<td>2.69 ± .01</td>
<td>1.72 ± .01</td>
</tr>
</tbody>
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Figure 11. (a) Upper row: a set of four representative images taken from the high-resolution LL data set. Middle row: the corresponding four images taken from the LL-RIGR data set. Lower row: the set of difference images obtained by subtracting the images of the middle row from the upper row. (b) A representative profile along one image of each of the three data sets shows that no significant image artifacts are introduced via GS reconstruction.
relevant constraint information. If the basis image fails to provide effective constraints for some of the high spatial frequencies occurring in the dynamic changes, these changes would be sampled in low resolution (because of reduced encodings), and the images would not be free from the associated truncation artifacts unless a sufficient number of dynamic encodings were used. In our examples, although each of the RIGR anatomical images (e.g., the control and tagged images in Fig. 5; the T1-weighted images in Fig. 11 or Fig. 7) reconstructed from only 32 encodings are relatively free from truncation artifacts, the dynamic maps (e.g., the perfusion map in Fig. 8 or the diffusion maps in Fig. 2) do have some low-resolution blurring. This is because some of the very high spatial frequency dynamic changes either did not get sampled adequately by the reduced encoded data set or were not constrained by the boundary information obtained from the reference images.

There is no fixed rule of thumb for choosing the number of dynamic encodings that would be necessary to obtain an accurate reconstruction. The number of encodings to be used for a reduced encoded data set depends on the anticipated spatial frequencies of the signal changes and the efficacy of the basis image to provide valid constraints. Moreover, the reduced encodings may be applied either symmetrically or asymmetrically in $k$-space. The latter, of course, encodes more high spatial frequency information for the dynamic data but reduces effective SNR by including more noise from the high frequency dynamic $k$-space data. Hence, if high spatial frequency changes are expected to occur in the dynamic data sets, then use of asymmetric subsampling, together with appropriate phase constraints for GS reconstruction, would be preferred (8). On the other hand, if the basis image provides most necessary boundary constraints and the dynamic changes are expected to occur only within these boundaries, then use of central symmetric encodings would yield higher SNR in the RIGR images. In general, the choice of symmetry in the dynamic subsampling dictates the tradeoff between SNR and reconstruction accuracy of new high spatial frequency dynamic boundary information.

A very recent algorithm describes the use of two reference images (12) to generate a better constraint function for dynamic signal variations. In this algorithm, the basis image used for RIGR is a difference image (obtained from two high-resolution images acquired under different dynamic states) that provides the high spatial frequency components of the dynamic changes leading to a more accurate reconstruction. The artifacts arising from the lack of high spatial frequency components of the dynamic changes, prominent in keyhole imaging (13,14) are avoided in this approach.

It is important to note that although all data presented here demonstrate the applicability of the RIGR scheme in two-dimensional imaging, this method can be extended
easily to three-dimensional or even four-dimensional imaging. The gain in data acquisition time in these cases would be correspondingly larger. A secondary advantage of using fewer encodings comes from the fact that, in fast three-dimensional imaging, RF power deposition per unit time would be lower because of fewer RF pulses. Moreover, because RIGR uses rigorous anatomic constraints to build high-resolution images, these images are expected to be more free from artifacts than images generated from direct zero-filling of low-resolution data sets. The dynamic information map (usually derived from respective dynamic images using simple image algebra) obtained by RIGR and by direct zero-filling of the low-resolution k space in each of the above cases are compared in Figure 12. Although the advantage of RIGR is apparent, it should be noted that in these cases, the recently proposed two-reference RIGR algorithm (12) has the potential to perform better by incorporating high-resolution constraints based on a second high-resolution dynamic data.

The computational time required for RIGR is on the order of that required for three Fourier transformations. When phase information from the basis image is also used as a constraint, solving for the Fourier coefficients becomes a linear least squares problem and computation times are higher (8).

In conclusion, it is demonstrated that in several dynamic imaging methods, it is feasible to acquire low-resolution fast data sets and reconstruct high-resolution dynamic images from them by incorporating a priori information from a stationary image. This can result in a very significant increase in imaging efficiency by decreasing the data acquisition time.

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