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Simultaneous Multi-Slice Magnetic Resonance Fingerprinting (SMS-MRF) with Direct-spiral Slice-GRAPPA (ds-SG) Reconstruction

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Abstract

Purpose—To develop a reconstruction method to improve SMS-MRF, where slice acceleration is used in conjunction with highly undersampled in-plane acceleration to speed up MRF acquisition.

Methods—In this work two methods are employed to efficiently perform the SMS-MRF data acquisition and the Direct-spiral slice-GRAPPA(ds-SG) reconstruction. First, the lengthy training data acquisition is shortened by employing the through-time/through-k-space approach, where similar k-space locations within and across spiral interleaves are grouped and are associated with a single set of kernel. Second, inversion recovery preparation(IR-prepped), and variable flip-angle(FA) and repetition time(TR) are used for the acquisition of the training data, to increase signal variation and improve the conditioning of the kernel fitting.

Results—The grouping of k-space locations enables a large reduction in the number of kernels required and the IR-prepped training data with variable FA and TR provide improved ds-SG kernels and reconstruction performance. With Direct-spiral slice-GRAPPA, tissue parameter maps comparable to that of conventional MRF were obtained at multi-band(MB)=3 acceleration using t-blipped SMS-MRF acquisition with 32-channel head coil at 3T.

Conclusion—The proposed reconstruction scheme allows MB=3 accelerated SMS-MRF imaging with high quality T1, T2, and off resonance maps, and can be used to significantly shorten MRF acquisition and aid in its adoption in neuro-scientific and clinical settings.

Keywords

Direct-spiral slice-GRAPPA; IR-prepped training; t-Blipped SMS-MRF; Magnetic resonance fingerprinting (MRF); Simultaneous multi-slice (SMS)

INTRODUCTION

Magnetic resonance fingerprinting (MRF) (1) is a recently introduced approach to efficiently map multiple tissue parameters. It relies on the generation of temporally and spatially incoherent signal evolutions, or fingerprints, for different tissue types through continuous variation of the acquisition parameters, such as the flip angle (FA), RF phase, TR and k-space sampling pattern. A dictionary matching algorithm is then employed to retrieve the MR parameter maps. In its original setting, MRF uses an IR-trueFISP sequence with highly undersampled spiral trajectory, to enable simultaneous mapping of T_1 , T_2 , off resonance and proton density (M_0). MRF acquisition using the FISP sequence (2) has also been proposed, which can provide accurate T_1 and T_2 maps in the presence of large field inhomogeneity that is detrimental to the original trueFISP MRF acquisition. The concept of MRF has also been extended to enable a ‘plug and play’ parallel transmission which enables mapping of tissue parameters as well as B_1^+ field estimation (3,4). Moreover, the dictionary matching approach of MRF has been adopted in vascular imaging to provide CBV, vessel radius, and blood oxygenation simultaneously (5). MRF, therefore, is an emerging acquisition technology that can efficiently map a number of important tissue and system parameters in vivo.

Nonetheless, MRF requires an acquisition time of 10–20 seconds per imaging slice, which can lead to a slow volumetric imaging time. Over the last decade, various simultaneous multi-slice (SMS) methods (6–12) have been developed to accelerate a number of imaging paradigms within MRI. To accelerate MRF acquisition, we have recently developed the t-Blipped SMS-MRF method (13) which acquires multiple imaging slices simultaneously and utilizes additional G_z gradient blips to create a time varying phase modulation between the simultaneously acquired slices. By utilizing a coil-weighted image reconstruction scheme, which we termed ‘slice-SENSE’, and taking advantage of the t-Blipped signal modulation during the dictionary matching process of MRF reconstruction, we had demonstrated high quality reconstruction at MB-2 acceleration. Nonetheless, high quality tissue parameter mapping results at higher MB factors (e.g. $MB \geq 3$) could not be obtained, due to the incomplete separation of the coupled in-plane and slice aliasing.

The application of parallel imaging reconstruction to SMS-MRF should enable improved parameter mapping at higher MB accelerations. However, parallel imaging in SMS-MRF is made difficult by the ultra-high acceleration factor, at more than 100 fold in each imaging frame (e.g. $R_{\text{inplane}} \times MB = 48 \times 3$), making e.g. a full SENSE based reconstruction (14) for each frame extremely ill-conditioned. With the MRF sequence, each imaging frame is also acquired with a markedly different imaging contrast, which also prevents us from grouping different k-space data points from neighboring imaging frames into one combined k-space to improve parallel imaging reconstruction (as in steady state signal acquisition/dynamic

imaging (15)). As such, in our previous work (13), we utilized slice-direction SENSE reconstruction, one imaging frame at a time, to provide ‘partial’ unaliasing in the slice direction, prior to the MRF dictionary matching reconstruction (which takes care of in-plane aliasing and creates the desired tissue parameter maps). The slice-SENSE procedure was shown to be beneficial, however such method is ill formed and does not provide clean slice-unaliasing. This is because, in the SENSE parallel imaging approach, the slice and in-plane unaliasing are coupled in the reconstruction process. On the other hand, unlike SENSE, k-space parallel imaging approaches have been shown to be able to cleanly unalias accelerated data in one spatial direction at a time (16). As such, the application of a k-space based algorithm such as slice-GRAPPA (11,16) to unalias SMS-MRF data in the slice direction only (at a comparatively low acceleration factor of e.g. $MB = 3$), should be well conditioned and allow clean slice separation prior to MRF dictionary matching for each imaging slice.

The application of slice-GRAPPA to variable density spiral in SMS-MRF is not straightforward since it requires a large number of position-specific kernel sets. With a large number of kernel sets, a lengthy training data acquisition is needed, hampering the acquisition time reduction achieved by SMS acquisition. Approximation methods (17,18), based on dividing spiral k-space data into pie-shape sections, each sharing a single kernel set has been shown to dramatically reduce the number of kernel sets required for undersampled uniform density spiral. However, the application of such approach to highly undersampled variable density spiral is made difficult due to the highly non-uniformity in the radial direction. For variable density spiral and radial acquisitions where much large number of kernel sets are needed, it has been modified and expanded upon to reduce the required training data length (19,20). Specifically, a through-time/through-k-space approach was developed where similar k-space locations within and across spiral/radial interleaves of the training data are grouped and are associated with a single set of kernel.

In this work, we propose to complement our t-Blipped SMS-MRF acquisition with ‘direct-spiral’ slice-GRAPPA (ds-SG) reconstruction, which applies slice-GRAPPA kernels directly to the highly undersampled spiral data to achieve slice-unaliasing. To avoid the need for a large training dataset, the through-time/through-k-space fitting approach, which was previously used in the in-plane direction, is adopted for the slice direction. Additionally, we modified the time-series training data acquisition with an inversion recovery preparation (IR-prep) and employed variable FA and TR trains to increase the time series’ signal variation. This was demonstrated to improve the conditioning of the kernel fitting and result in improved reconstruction. The performance of ds-SG reconstruction with improved training is demonstrated *in vivo*, through an $MB=3$ t-blipped SMS-MRF scan at 3T using a 32-channel head coil. Here, the short training data and the $MB=3$ acceleration result in a total imaging time of just 3.83s/slice, with comparable reconstruction performance to the standard MRF acquisition at 10s/slice. Such improvements in MRF acquisition and reconstruction should help enable multi-slice MRF imaging to be more readily adopted in neuro-scientific and clinical settings.

METHODS

Direct-spiral Slice-GRAPPA: kernel fitting and reconstruction

With direct-spiral slice-GRAPPA (ds-SG), k-space position dependent slice-GRAPPA kernels are applied directly to the undersampled SMS-MRF spiral data to perform slice-unaliasing. As in inplane accelerated spiral reconstruction, a large number of kernels are needed for the reconstruct of different k-space locations that are not uniformly spaced. To provide enough data observations to train such a large number of kernel sets, a time-series of single-band, in-plane under-sampled spiral data are acquired as training data in a sequential manner for each slice position of interest. These data are summed across the slice dimension to generate a slice-collapsed SMS like dataset; on which the kernels are trained to unalias into slice-separated datasets. To shorten the training data acquisition time, the through-time/through-k-space approach (19,20) is adopted for ds-SG, which is depicted schematically in Fig. 1. Here a cross-like 5 point GRAPPA kernel pattern is used at each k-space location as indicated by the red diamond markers, labeled 1 to 5 in fig. 1a (where the marker with index 1 is at the data location of interest). For the training data, similar k-space patterns from within and across spiral interleaves at different time points are grouped together to increase the number of data observations available for each kernel pattern fitting (fig. 1b). To illustrate this, in each k-space interleave of fig. 1b, three different observations with a similar kernel pattern as the objective one are shown and denoted with markers in different colors and shapes. With three observations from each k-space interleave and with a total of 96 time points in this example, a total of $3 \times 96 = 288$ observations could be used for the kernel fitting of each k-space pattern. The slice-GRAPPA kernel fitting is performed for each k-space pattern separately in a sequential manner, and looping over all the kernel patterns and all the slices, a large number of kernels can be obtained and can be applied to any spiral k-space location from the SMS-MRF acquisition to obtain the slice-separated MRF data.

In addition, the acquisition of the training data is modified with an IR-prep and variable FA and TR trains similar to the ones used in the actual MRF acquisition. We show that this increases the signal variations within the time series, and causes the observations in the kernel-fitting matrix to be less correlated. This will in turn improve the kernel fitting to allow for use of a smaller training dataset. An additional benefit of acquiring the training data with an MRF-like acquisition is that such data can also be included as part of the data used in the MRF parameter mapping process, which should improve the accuracy of the parameter mapping.

Once the ds-SG kernels are estimated from the training data, they can be directly applied to the SMS-MRF data to generate a slice-unaliased time-series. This time-series is then concatenated together with the single-band MRF training data and processed using conventional MRF reconstruction pipeline (1), where gridding is performed on the data, followed by coil combination and dictionary matching. Here, the dictionary is built to account for the concatenation of the SMS-MRF and training data, and for the case of t-Blipped SMS-MRF acquisition, accounts for the additional slice specific phase modulation.

Acquisition

To test the performance of ds-SG, data were acquired *in vivo* from a healthy volunteer with institutionally approved protocol consent, using a 3T Siemens Skyra scanner and a standard Siemens 32-channel head array coil. The following datasets were acquired: i) three slices of conventional MRF data at a distance of 35 mm apart and ii) t-Blipped SMS-MRF data at MB=3 acceleration for the same imaging slices. Additionally, two sets of ds-SG training data were acquired, one with and one without IR-prep.

For MRF acquisition, an IR-trueFISP sequence with varying FA and TR as described in (1) was used. Specifically, a Perlin noise shaped TR time series (8.2ms to 10.56ms) and a FA train of noise-added sinusoidal shape (0° to 60°) were used. Non-selective adiabatic inversion pulse was used, and the excitation RF in each TR has a slice thickness of 5mm. At each TR, one of the 48 variable density spiral interleaves (48X) was used to read out the signal, with a designed square FOV of 300mm and square matrix size of 128. The 48 spiral interleaves are acquired in a sequential manner repeatedly until a total of 1000 TRs are generated per inversion pulse.

For t-Blipped SMS-MRF (13) acquisition, the excitation RF in each TR is multiband and VERSEd(21). Moreover, additional G_z pre-wind and re-winding lobes of size ' A_{blip} ' were added before and after each spiral readout (sequence diagram shown in supporting figure 1 (fig. s1A). The size of the G_z blips was varied from one TR to the next to generate a time-varying inter-slice phase difference between the SMS slices as shown in Fig. s1B. A total of 850 time points (TRs) were acquired with the same spiral trajectory as in conventional MRF, resulting in a scan time of ~8.5s. For the single-band training data acquisition, the standard single-band MRF data with spiral trajectory was acquired slice-by-slice. A total of 96 time points were acquired for each slice, resulting in a training data acquisition time of 1s/slice and 3s/slice-group for our MB3 case. Due to the short acquisition time of each imaging slice's training data (1s), the non-selective IR pulse of the standard single-band MRF sequence was replaced with a slice-selective IR pulse to avoid saturating the signal of the next imaging slice and having to wait for its recovery prior to its acquisition. With these imaging parameters, the combined training data and SMS-MRF acquisition time is 11.5s/slice-group for MB3 or 3.83s/slice (consists of 2.83s/slice SMS-MRF data acquisition and 1s/slice training data acquisition). The slice ordering of the SMS-MRF data and the training data acquisition are illustrated in supporting material fig. s2.

Reconstructions parameters and evaluation

For ds-SG reconstruction which is shown in fig. 1, all 96 time-points of the training data were used in determining the weights for each GRAPPA kernel pattern. For each pattern, 400 different locations were grouped from within and across the spiral interleaves (48×2) according to the similarity in the 5-point distribution. As such, for each kernel pattern, a total of 400 training elements were used for the calculation of 160 unknown weights ($5\text{-point} \times 32\text{-channel}$). For the outer k-space locations where the radial under-sampling is very high, a 3-point kernel along the tangential direction is used instead of the 5-point kernel (by omitting the 4th and 5th kernel positions of the 5-point kernel shown in Fig 1a). This is done because in such case the radial kernel points which are of large distances away will be

unlikely to provide useful information for the reconstruction. To minimize the inter-slice signal leakage, the leak-block slice-GRAPPA formulation from (22) was used to calculate the kernels.

To examine the benefit of IR-prep for training data acquisition, ds-SG kernel-fitting matrices were formed using both of the acquired training datasets, one with and one without IR-prep. The condition number of these matrices were calculated and compared, whereby a lower condition number represents an improved conditioning in the kernel fitting process. Moreover, to examine the signal variation differences between the two training data's time-series, the signal for gray-matter (GM), white-matter (WM) and cerebrospinal fluid (CSF) were simulated using the Bloch equation. Additionally, images at different TR positions along the time-series of these training data were simulated using the Bloch equation and the gold-standard tissue parameters estimated from the 10s/slice MRF acquisition. Lastly, the resulting SMS-MRF tissue parameter maps resulting from these different training datasets were compared.

To examine the performance of MB=3 SMS-MRF acquisition with ds-SG reconstruction (at 3.83s/slice imaging time), tissue parameter maps from this acquisition/reconstruction combination were compared with ones obtained from standard MRF at 10s/slice and 3.83s/slice (which represents a shorten time-matched acquisition). Furthermore, these results were also compared with ones from the same MB=3 SMS-MRF data reconstructed using our previously proposed slice-SENSE reconstruction (at 3.83s/slice imaging time— here 11.5s of SMS-MRF data was used with no training data needed for this reconstruction). The error maps and correlation plots of the tissue parameter estimates of the various cases were calculated/plotted by treating the tissue parameter estimates from the 10s/slice MRF as gold-standard.

RESULTS

Fig. 2 shows the signal variation in the training data time-series acquired without and with IR preparation. The top row shows the simulation of the signal for GM, WM and CSF as a function of TR, where significantly larger variations are observed in the IR-prepped acquisition. These larger variations are reflected in the simulation of the images at different TR indexes across the training data shown at the bottom of Fig. 2. Note that these images are simulated with no undersampling thus they do not resemble the highly aliased images reconstructed from training data/conventional MRF data. Here, image contrast is much more different across time-points for the IR-prepped acquisition. The condition number of the ds-SG training matrices (averaged across the different kernel pattern cases) are 1076 and 425 for the training data without and with IR preparation respectively. The larger than 2-fold reduction in the condition number of the IR-prepped training data matrices is a result of the reduction in the correlation of the data observations at different TRs used in forming these matrices.

Fig. 3 shows T_1 , T_2 , off-resonance and M_0 maps of the three imaging slices from 10s/slice conventional MRF and 3.83s/slice SMS-MRF with IR-prepped training and ds-SG reconstruction. Overall, the results from these acquisitions are of comparably high quality,

thereby demonstrating the ability for SMS-MRF to markedly accelerate MRF acquisition. Note that a ring shaped T_2 null artifact is observed in the most inferior slice of both reconstructions, which is likely resulted from the banding artifacts in the trueFISP based MRF acquisition that causes low signal intensity in regions with a specific B_0 value.

Fig. 4 provides comparison of tissue parameter maps from MRF and SMS-MRF acquisitions with various reconstruction methods. Specifically, the results from the center slice which suffer the most error are shown. The top two rows show T_1 and T_2 maps from i) conventional MRF at 10s/slice, ii) conventional MRF at 3.83s/slice, iii) MB=3 t-Blipped SMS-MRF at 3.83s/slice with slice-SENSE reconstruction iv) MB=3 t-Blipped SMS-MRF with ds-SG reconstruction using *non-IR* preparation training data, with a total acquisition time of 3.83s/slice (2.83s/slice of SMS-MRF plus 1s/slice of training data), and v) MB=3 t-Blipped SMS-MRF with ds-SG reconstruction using IR-prepped training data, again with a total acquisition time of 3.83s/slice. The results from the center slice group of the MB=3 acquisition, where the larger reconstruction error/artifact occurs (due to this slice having the lowest SNR and least coil sensitivity variations) were displayed to represent the worst-case result. Using the results from conventional MRF at 10s/slice as gold standard, the normalized root mean square error (NRMSE) for the other four acquisition/reconstruction cases are 11.75%, 14.41%, 8.73% and 4.4% for T_1 and 54.51%, 234.00%, 8.11% and 8.09% for T_2 respectively. With the conventional MRF at a shorten acquisition time of 3.83s/slice, the tissue parameter estimates deteriorated significantly, in particular for T_2 where the NRMSE is 54.5%. MB=3 SMS-MRF acquisition with slice-SENSE reconstruction also provides unacceptable result with large residual slice aliasing that corrupts the parameter fitting process, particularly in the middle region of the brain. With ds-SG reconstruction, the parameter estimate improves significantly, resulting in low estimation error. With the use of IR-prepped training data, the tissue parameter estimates from ds-SG reconstruction are further improved, with a ~2x reduction in NRMSE for T_1 estimates. The relative error maps for the cases with and without IR-prepped training data at green-rectangle region are shown blue-rectangle at Fig. 4 at 10X scaling. Fig. 5 provides the correlation plots of the case iv and v against case i to better show the parameter accuracy at different parameter range.

DISCUSSION and CONCLUSION

In this work, we developed the Direct-spiral slice-GRAPPA (ds-SG) reconstruction method for SMS-MRF acquisition and demonstrated its capability in providing high quality reconstruction for MB=3 slice-accelerated t-Blipped acquisition. While ds-SG requires additional training data to estimate the GRAPPA kernels, we have been able to limit the imaging time of this training acquisition to 1s/slice by employing IR-preparation and variable TR and FA trains, similar to the ones used in the actual MRF acquisition. The inversion preparation was shown to markedly increase the contrast variation in the training data, which improved the conditioning of the kernel training matrices by more than 2-fold. The additional benefit of this training data is that it could be grouped together with the slice-unaliased SMS-MRF data and used for the tissue parameter mapping estimation.

In the current implementation, the variable TR and FA schemes used for the training data are the same as ones at the beginning part of the SMS-MRF acquisition. The use of a different

TR and FA schemes for the training data could potentially provide a more useful dataset for the parameter mapping process. Moreover, the TR and FA schemes could also be optimized to increase the signal variation in the training data to allow for further improvement in the ds-SG kernel fitting process. Through the use of IR-prep, the condition numbers of the kernel training matrices have already been reduced by more than two fold to provide improved robustness in the kernel fitting and high quality parameter mapping results. However, the condition numbers are still relatively high at around 400, when compare to a typical MB-3 SMS-EPI acquisition case, where we have observed the condition number of around 100. Therefore, further reduction in the condition number should still lead to further improvement in the kernel fitting. Future work will explore the optimization of the TR and FA schemes to come up with a training dataset that provides improved robustness to the ds-SG kernel fitting, while also providing more useful information for the tissue parameter mapping. Furthermore, we note that our concept of purposefully creating signal variation in the training data should also be valuable in shortening the training data for other reconstruction cases such as in-plane reconstruction of undersampled spiral and undersampled radial.

The training data acquisition for ds-SG utilizes the same spiral trajectories as that of the SMS-MRF acquisition. As such, k-space trajectory errors and B_0 inhomogeneity related phase evolution/spatial blurring should be the same for the training data and the SMS-MRF acquisition; a desirable property that should improve the quality of ds-SG kernels. Prior to our work on ds-SG, we have also investigated an alternative approach for slice-unaliasing in SMS-MRF, using a combination of GROG and slice-GRAPPA (23). With this approach, the GROG algorithm is used to grid the spiral data onto in-plane Cartesian locations after which slice-GRAPPA is applied for slice unaliasing. The advantage of this combined approach is that only a small number of kernel patterns are needed for GROG and slice-GRAPPA. However, such approach utilizes Cartesian training data, which does not contain the same trajectory error and B_0 inhomogeneity related phase issue as the SMS-MRF spiral data. This mismatch combines with the two-step parallel imaging reconstruction, which increases noise amplification and results in an inferior reconstruction performance compared to ds-SG. Moreover, unlike the ds-SG training data, the Cartesian training data do not provide additional useful information for the tissue parameter mapping process.

In this work, we have demonstrated good reconstruction performance at MB=3 acceleration, but at higher MB factors the reconstruction performance of SMS-MRF data degrades significantly due to larger noise amplification and increased residual signal leakage between slices. Future direction includes the use of blipped-spiral trajectory acquisition (24) which imposes controlled aliasing between the SMS slices to reduce noise amplification and signal leakage. Moreover, the use of different flip-angle train for each of the SMS slices as recently proposed in (25) can also be incorporated to increase signal differences between the SMS slices. The combination of these techniques should provide more room for further MB acceleration in SMS-MRF to enable MRF imaging in a rapid fashion. In addition, the minor banding artifacts observed in MRF acquisitions shown in fig. 5 are likely due to the use of trueFISP based acquisition and the associated low signal intensity in regions with specific B_0 value, which causes poor dictionary matching and parameter mapping. To improve upon this, future work involves the development of less B_0 sensitive MRF sequences (e.g. FISP

MRF (2)) for SMS-MRF acquisition, and improved MRF reconstruction to replace gridding and dictionary matching reconstruction (e.g. maximum likelihood reconstruction (26)).

Another alternative approach to conventional 2D-MRF is 3D-MRF, which has recently been employed in the context of MUSIC-MRF(27) – an MRF method that enables pleasant sound to be played out during the MRI scan. 3D-MRF has the advantage of being more SNR efficient than its 2D and SMS counterparts, due to better signal averaging. Nonetheless, with 3D-MRF, a large amount of volumetric k-space encoding is required at each temporal point in the MRF time-series, which necessitates the use of multi-shot/segments acquisition. As such, each imaging volume in the time-series has to be generated by combining data from multiple acquisitions that are spread throughout the imaging period of several minutes. This can cause 3D-MRF to be much more sensitive to motion than its 2D counterparts. With SMS-MRF, the motion sensitivity is similar to that of its 2D counterpart since data for a given slice are acquired within the time frame of a single SMS slice-group's acquisition. We note that large motion between the training data and the SMS-MRF acquisition could still affect the SMS-MRF reconstruction performance. Nevertheless, this issue can be minimized by acquiring the training data and the SMS-MRF data in an interleave fashion. For example, in an MB=3 acquisition, the training data for the first MB slice group should be acquired after the SMS-MRF acquisition of the second slice group and the training data for the second MB slice group should be acquired after the SMS-MRF acquisition of the third slice group and so forth. This interleaved scheme reduces the temporal gap between the SMS-MRF and the training data acquisitions of each slice-group, while allowing enough time for the signal of a particular slice group to recover prior to the training dataset collection. In addition to its motion insensitivity, another advantage of SMS-MRF over 3D-MRF is the unique new opportunities of performing additional signal encoding in the slice-direction through techniques such as the t-Blipped method (13) and the use of different FA train for the SMS slices (25), which help enable extra acceleration in the MRF acquisition.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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Fig. 1. Illustration of the proposed Direct-spiral slice-GRAPPA reconstruction and kernel fitting. Fig1a: for a particular k-space location (index 1) in the SMS-MRF data, which is summation of the SMS slices (s_1 , s_2 and s_3), a five-point-kernel pattern (index 1 to 5) is determined. Fig1b: similar patterns in the training k-space data to this particular kernel pattern (within and across spiral interleaves (int) as denoted by the square, circle and triangle markers in various colors) are then identified and grouped together for use in calculating the slice-GRAPPA kernel weight for this kernel. The calculated kernel is then applied to the SMS-MRF data to obtain the slice-separated MRF data.

Fig. 2.

Comparison between non IR-prepped and IR-prepped training signal from simulated three different tissues (White matter (WM), Gray matter (GM), Cerebral fluid (CSF)) and selected simulated time frame images illustrated the increased contrast variation in the training data with IR-preparation. P.s. the images shown are simulated from synthetic brain phantom and without the any undersampling thus do not reflect the actual images from the training data acquisition.

Fig. 3.

In vivo T1, T2, off-resonance and M0 maps from 10s/slice conventional MRF and 3.83s/slice MB-3 t- Blipped SMS-MRF, reconstructed with Direct-spiral slice-GRAPPA and IR prepped training data.

Fig. 4.

In vivo T1 and T2 maps from i) 10s/slice conventional MRF (gold standard), ii) 3.83s/slice conventional MRF, iii) 3.83s/slice t-blipped SMS-MRF with slice-SENSE reconstruction, iv) 3.83s/slice t-blipped SMS-MRF with non-IR-prepared training data and ds-SG reconstruction, v) 3.83s/slice t-blipped SMS-MRF with IR-prepared training data and ds-SG reconstruction. Results from the center slice group of the MB-3 acquisition, which contains the largest reconstruction error, are displayed to represent the worst case performance. Normalized RMSE values (lower right corner of the corresponding maps) are displayed. The relative error maps in the green rectangle region are displayed at 10x scaling in the blue rectangle region.

Fig. 5.

T1 and T2 correlation plots between the t-Blipped SMS-MRF case result and gold standard case result. Left column shows the w/o IR-prepped training result, and right column shows the with IR-prepped training result. Plots at small T1 range of 0–2000ms and small T2 range of 0–300ms are circled and enlarged to better show the details.