Optimized partial parallel imaging of trabecular bone microstructure in the distal tibia

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Introduction

Micro-MRI of trabecular bone (TB) is capable of measuring microstructural changes related to metabolic bone disease **[1]**. Quantification of the 3D TB structure requires high resolutions leading to long scan times. Through partial-parallel imaging (PPI), the signal-to-noise (SNR) gained at higher fields can be traded for reduced scan times. The use of PPI in μMRI has been studied in the calcaneus, knee, and hip using a steady state free precession (SSFP) sequence with an auto-calibrated approach **[2]**. In general **[3],** an auto-calibration region (ACR = product of number of calibration samples in k_y and k_x) is acquired and used in the fitting of a weighting kernel that represents the contributions of the nearest neighboring k_y and k_x points in every channel's k-space to a missing datum in a single channel's k-space, thus allowing recovery of the skipped phase encoding (PE) lines. Since TB imaging requires resolutions on the order of the structural thickness (~150μm), changes in SNR due to reduced scan time and noise inflation and reconstruction artifacts can adversely affect the derived structural parameters. Here, a generalized partial-parallel acquisition (GRAPPA) with multi-column multi-line interpolation (MCMLI) has been employed using the fast large angle spin echo (FLASE) pulse sequence **[4]**. The method has been optimized for TB imaging in the distal tibia at 3T for an approximate two-fold acceleration and the residual root mean squared (RRMS) relative to the fully sampled data was evaluated. The reconstruction was then used to empirically map the SNR of the accelerated image for comparison with the fully sampled image. Finally, TB topological parameters were computed using digital topological analysis (DTA) **[5]** to estimate the effect of the parallel acquisition on structural parameters.

Methods

An in-vivo (15min22s) FLASE (TE/TR=10.5/80 ms) scan of the distal tibia was acquired on a Siemens TIM Trio using a four-channel, overlapping phased-array with preamplifier decoupling (INSL, Worcester, MA). The fully sampled dataset (137x137x410 μm^3 resolution) was reconstructed and used as reference (**Fig 1a**) for the optimization. The k-space acquisitions of the four channels were down-sampled along the k_y direction to simulate an accelerated acquisition. The auto-calibration region is located symmetrically around k_y center and its size denoted by the number of auto-calibration lines (#ACL), which was varied from 5-200 representing scan times of 8min10s (R=1.88) to 15min(R=1.03). For each #ACL, the GRAPPA-MCMLI was performed with rectangular weighting kernels of varying sizes along k_y and k_x directions, denoted LxC, where L is the number of neighboring PE lines (k_y) and C is the number of neighboring k_x points. The RRMS was computed to quantify the reconstruction artifact with respect to #ACL and kernel size.

To evaluate the SNR of the optimally reconstructed accelerated data, SNR maps were estimated from the reconstructed fully sampled and accelerated images. The noise component $N_{full,j}$ from the fully sampled data was approximated by complex Guassian-distributed noise with standard deviations matching those measured in the pure noise regions of each j channel's complex image. The accelerated complex noise images $N_{PPI,j}$ were found by reconstructing the down-sampled Fourier transform of each $N_{full,j}$ using the GRAPPA-MCMLI. The signal components $S_{full,j}$ and $S_{PPI,j}$ were estimated by low-pass filtering the individual channel images. After low-pass filtering all $N_{full,j}$ and $N_{PPI,j}$, the SNR maps were obtained by summing the squared ratio of the signal and noise components for each channel over all channels, i.e. $SNR_{full(PPI)} = \sum_{j=1}^{4} \left[S_{full(PPI),j} / N_{full(PPI),j} \right]^2$.

The fully sampled scan and a repeat accelerated scan were processed using the virtual bone biopsy system to assess the effect of the reduced scan time and reconstruction artifact on the topological parameters. Scans were automasked **[6]**, bone volume fraction mapped **[7]**, sinc interpolated to 3x the resolution in each direction, skeletonized **[8]**, and processed using DTA to compare bone volume fraction (BVF) and surface to curve ration (S/C).

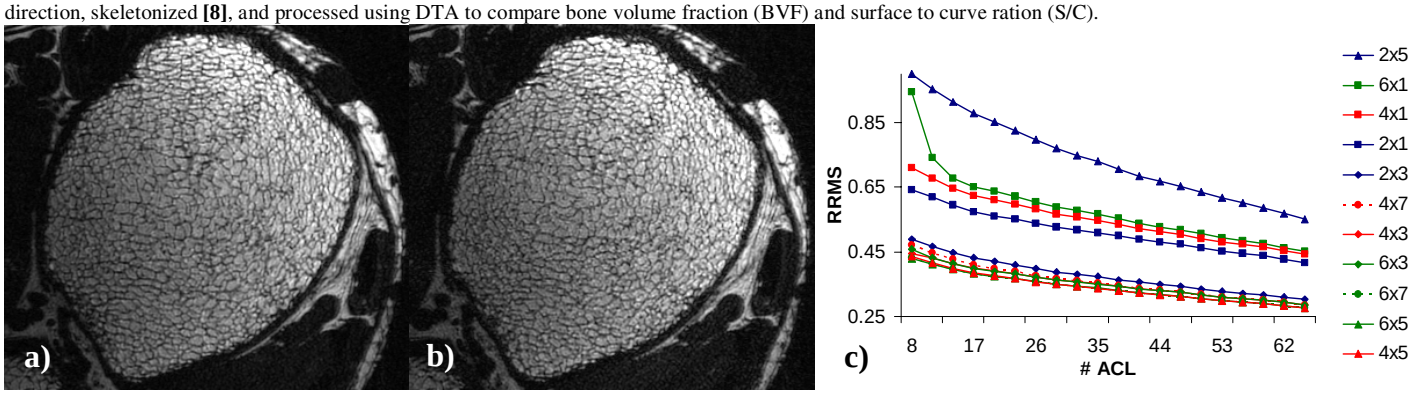

Figure 1. a) 3T FLASE (15min22s); b) R=2 (8min 54s), #ACL=28, LxC=4x5; c) Normalized RRMS versus #ACL for various kernel sizes denoted LxC.

Results and Discussion

The normalized RRMS data is plotted with respect to #ACL for 11 rectangular kernels in **Fig. 1c**. As expected, independent of kernel size, the normalized RRMS approaches 0 as the #ACL approaches half the total number of PE lines. Standard GRAPPA, corresponding to a 2x1 kernel, performs better than the other linear kernels, 4x1 and 6x1 which use more neighboring phase encodings in the interpolation. GRAPPA with MCMLI is superior to standard GRAPPA for most kernel sizes. By contrast, the 2x5 kernel has the highest RRMS over the range of #ACL. As seen in **Fig 1.c**, there are several kernel sizes that produce low reconstruction errors for lower #ACL. To further analyze the performance within this group, the first derivative of the RRMS was taken over the range of ACR sizes from 11 to 76. For #ACL=28, the 4x5 kernel produced the lowest RRMS value and its derivative was closest to zero. Using #ACL=28 and the 4x5 kernel, an accelerated FLASE scan was acquired and reconstructed for the same subject (**Fig. 1b)**. The SNR map indicated an average SNR in the TB region of the accelerated acquisition equal to 80% of the SNR from the fully sampled acquisition. BVF and S/C for the fully sampled (accelerated) images were 0.102(0.106) and 8.75(8.22), respectively. The higher BVF and lower S/C in the accelerated scan reflect erroneous identification of new bone voxels, most of which are identified as curves due to the reduced SNR.

Conclusions

As demonstrated by Wang et al. **[9]**, MCMLI performs better than the standard GRAPPA reconstruction. For the present application, a 4x5 kernel with a total scan time of 8min 54s (#ACL=28) was found to minimize reconstruction artifacts while approximately halving the scan time. The empirical approach presented for PPI performance evaluation obviates the need for multiple scans or field simulations. Lastly, the data suggest that the SNR penalty and reconstruction artifacts have only a minor, expected effect on the derived structural parameters.

References: **[1]** Wehrli et al. *NMR Biomed*. 19, 2006. **[2]** Banerjee et al. *MRM* 56, 2006. **[3]** Griswold et al. *MRM* 47, 2002. **[4]** Ma et al. *MRM* 35, 1996. **[5]** Gomberg et al. *Med Phys*. 30, 2003. **[6]** Magland et al. *ISMRM* 2006. **[7]** Vasiclic et al. *ISMRM* 2005. **[8]** Manzanera et al. *Lec. Comp. Sci.* 1568, 1999. **[9]** Wang et al. *MRM* 56, 2006.

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