

# Reduction of Required Gradient Spoiler Size For AFI B<sub>1</sub> Mapping

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**Introduction:** Actual Flip-Angle Imaging (AFI) [1], a popular technique for B<sub>1</sub> mapping, is subject to large reconstruction errors due to incomplete spoiling of transverse magnetization at the end of each TR. With small spoiling gradients, the reconstructed flip angles will typically be wrong by 2-5° and can err by as much as 10° or 15° for particular combinations of flip angles and tissue types. Accurate flip angle reconstruction requires very large spoiling gradients. The necessary duration of these gradients increases the minimum achievable TR, both increasing scan time and increasing T<sub>1</sub> relaxation errors. Additionally, the large gradient areas demand high power output from the gradient amplifiers and need gradient systems capable of high duty cycle operation. We present a correction scheme that will reduce the need for excessive gradient areas while maintaining B<sub>1</sub> mapping accuracy.

**Theory:** The AFI technique [1] depends on complete spoiling of transverse magnetization at the end of each TR. Incomplete spoiling of the transverse magnetization M<sub>xy</sub> leads to a bias in the flip angle reconstruction (see Fig. 1). This happens particularly at high flip angles where the low signal magnitude in TR<sub>2</sub> is sensitive to incomplete spoiling. This can be avoided with the correct choice of the RF spoiling seed, but the proper seed for the AFI sequence varies across tissues [2]. In the presence of strong gradients, diffusion across the gradient will irreversibly destroy M<sub>xy</sub>, preventing stimulated echoes. To destroy sufficient M<sub>xy</sub> to achieve accurate flip angle reconstruction across all tissues, very large spoiling gradients are necessary.

A large portion of the flip angle error at lower spoiler gradient areas is consistent across tissues. Removing the average simulated reconstruction error for a given reconstructed flip angle will correct a large portion of the error. The correction can be improved by adjusting the expected error to specific tissues found in a given imaging region. For example, the correction for head imaging only needs to account for white and gray matter, lipids, CSF and blood. The correction is designed based on the particular combination of TRs in the sequence and the combinations of relaxation and diffusion expected in the imaging region.

**Methods:** Simulations were performed as originally described by Gudbjartsson and Patz [3] and adapted by Yarnykh [2] for the AFI sequence. The sequence parameters were: TR<sub>1</sub>=15ms, n=6, gradient time based on 3 gradient axes at 4 G/cm, flip angles from 20° to 90°. T<sub>1</sub>, T<sub>2</sub> (in ms), and D (in mm<sup>2</sup>/s x 10<sup>-3</sup>) were chosen to simulate the following tissues (source is [4] unless noted): CSF (4000, 2000, 2.7), gray matter (920, 100, 0.6), white matter (790, 90, 0.7 [2]), liver (490, 40, 1.0 [5]), muscle (870, 50, 1.2 [6]), spleen (780 [7], 62 [7], 0.9 [5]), lipids (260, 80, 0.05), and blood (1200, 50, 2.5).

Separate corrections were developed for the general case and for specific head and body tissues by averaging the simulated reconstruction error over the relevant tissues for each true flip angle. The reconstructed flip angles were corrected using a look-up-table.

The correction was verified experimentally using a GE Signa 1.5T system with a uniform spherical phantom extending past the edge of a transmit/receive head coil to create a variation in flip angle. The phantom has T<sub>1</sub>=370ms, T<sub>2</sub>=300ms, and diffusion of 2.5x10<sup>-3</sup> mm<sup>2</sup>/s. The scan parameters were TR<sub>1</sub>=15ms, n=6, TE=2ms. 64x64x24 matrix, FOV=24cm. An image with a gradient area of 48.5 G·ms/cm in TR<sub>1</sub> served as a fully spoiled reference image. An image with a smaller spoiler (20.8 G·ms/cm) was compared to the reference image before and after correction.

**Results:** The proposed correction decreases the flip angle reconstruction error, particularly at high flip angles. For typical body tissues (Fig. 2 top), small spoiling gradients are sufficient. For head tissues (Fig. 2 bottom), stronger, but still moderate, gradients are necessary for sufficient accuracy. In both cases, B<sub>1</sub> mapping in lipids is more accurate than for the fully spoiled case. The diffusion dephasing is much less effective on lipids than any other tissue due to its low diffusion coefficient, so it is more accurate for lipids to not rely on it. The experimental results (Fig. 3 and Fig 4) show that the correction works in practice, reducing the flip angle error to a reasonable 2° for flip angles up to 80°.

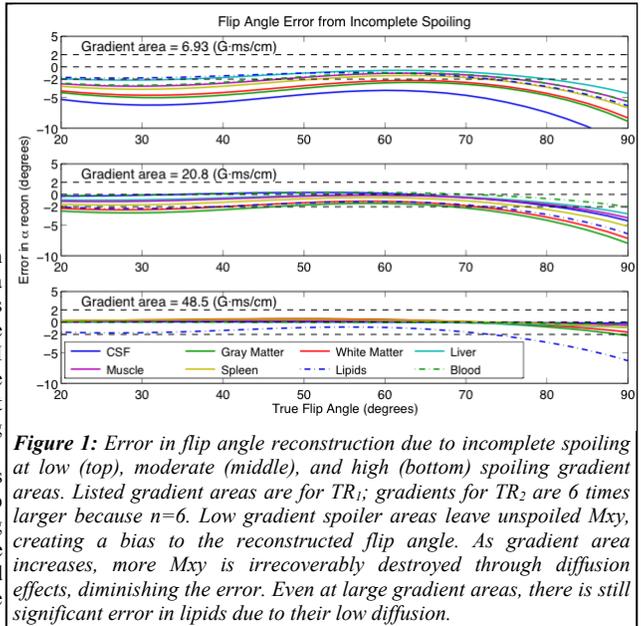
**Discussion:** AFI is a powerful B<sub>1</sub> mapping technique but is hampered by requiring very large spoiling gradients. Even with very strong spoiling gradients, the flip angle in lipids is biased due to their low diffusion. By correcting for the reconstruction bias that occurs in all tissues, the error can be reduced to a comparable level to the fully spoiled case while using much smaller spoiling gradients and also producing more accurate results in lipids.

**References:** [1] Yarnykh, MRM 57:292, 2007; [2] Yarnykh, MRM 63:1610, 2010; [3] Gudbjartsson and Patz, MRM 34: 567, 1995; [4] Bernstein et al, *Handbook of MRI Pulse Sequences*, 2004; [5] Kim et al, AJR 173:393, 1999; [6] Damon et al, MRM 48:27, 2002; [7] Butts Pauly and Gold, RAD220 Course Notes, Stanford University, 2007.

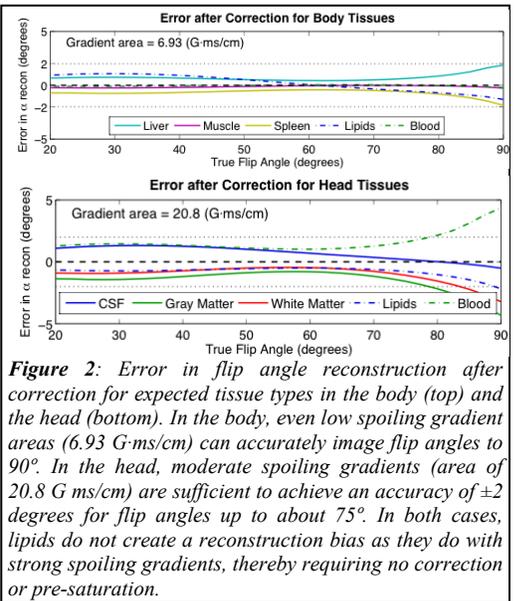


**Figure 3:** Flip angle map (in degrees) for fully spoiled acquisition (left), and error maps from moderately spoiled acquisition without (center) and with correction (right). The underestimation of the flip angle from the smaller spoiling gradient is reduced with the correction.

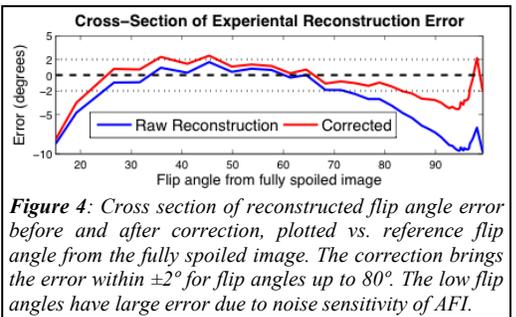
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**Figure 1:** Error in flip angle reconstruction due to incomplete spoiling at low (top), moderate (middle), and high (bottom) spoiling gradient areas. Listed gradient areas are for TR<sub>1</sub>; gradients for TR<sub>2</sub> are 6 times larger because n=6. Low gradient spoiler areas leave unspoiled M<sub>xy</sub>, creating a bias to the reconstructed flip angle. As gradient area increases, more M<sub>xy</sub> is irrecoverably destroyed through diffusion effects, diminishing the error. Even at large gradient areas, there is still significant error in lipids due to their low diffusion.



**Figure 2:** Error in flip angle reconstruction after correction for expected tissue types in the body (top) and the head (bottom). In the body, even low spoiling gradient areas (6.93 G·ms/cm) can accurately image flip angles to 90°. In the head, moderate spoiling gradients (area of 20.8 G·ms/cm) are sufficient to achieve an accuracy of ±2 degrees for flip angles up to about 75°. In both cases, lipids do not create a reconstruction bias as they do with strong spoiling gradients, thereby requiring no correction or pre-saturation.



**Figure 4:** Cross section of reconstructed flip angle error before and after correction, plotted vs. reference flip angle from the fully spoiled image. The correction brings the error within ±2° for flip angles up to 80°. The low flip angles have large error due to noise sensitivity of AFI.