Spoiling properties of the VAFI method for fast simultaneous T1 and B1 mapping from actual flip-angle imaging (AFI) and variable flip-angle (VFA) data.

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ntroduction: Accurate measurements of both T_1 and flip angle (FA) are important to many quantitative imaging applications. The use of steady-state sequences offers a fast way to acquire 3D volumetric maps of these parameters, and the recently proposed combined fitting of variable flip angle (VFA) [1] and actual flip-angle imaging (AFI) [2] data (VAFI) has been shown to be highly accurate and efficient even in the presence of long TR or short T_1 times [3]. In spite of its insensitivity to T_1-related errors in B_1 estimation, this method still requires data to be fit to an ideally spoiled signal model, and recent work has shown that significant errors may be introduced due to improper spoiling [4]. Although the case for each individual sequence has been considered, VAFI presents a unique combination of the two sequences with its own unique spoiling requirements. Therefore, the purpose of this work is to investigate the spoiling behavior of VAFI and determine an optimal spoiling scheme.

Simulation Methods: Simulated SPGR and AFI signals were generated for prototypical white matter tissue at 3T (T_1 = 1000 ms, T_2 = 70 ms, and diffusion coefficient D = 0.70 mm^2/s) using a combined isochromat summation and diffusion propagator model [4]. SPGR signals were generated for TR = 10 ms, FA = [3 18]° for two different spoiler gradient areas corresponding to the weak (A_G=38 mT*ms/m) and strong (A_G=110 mT*ms/m) spoiling regimes. AFI signals were generated for FA=55°, ratio of TR2/TR1=5, ratio of $A_{G,TR2}/A_{G,TR1}$=5, and four different spoiler gradient areas representing weak (TR1=10 ms, $A_{G,TR1}$=38 mT*ms/m), intermediate (TR1=10 ms, $A_{G,TR1}$=110 mT*ms/m), strong (TR1=15, $A_{G,TR1}$=280 mT*ms/m), and nearly complete (TR1=30ms, $A_{G,TR1}$=450 mT*ms/m) spoiling. Signals were generated over a range of RF phase increments φ_0 from 0˚ to 180˚.

Data were fit using a conventional AFI FA estimate [2] which is subsequently applied to a linearized VFA fit using both SPGR flip angles [1]. The data were also processed using the newer VAFI method by simultaneously estimating PD, T_1, and FA via direct nonlinear least-squares fitting of the signal equations:

$$[PD, T1, FA] = \arg\min \left\| \begin{matrix} S_{AFI,1} - PD\sin(FA\cdot\alpha_{AFI})(1-E_2+(1-E_1)E_2\cos(FA\cdot\alpha_{AFI}))/C \\ S_{AFI,2} - PD\sin(FA\cdot\alpha_{AFI})(1-E_1+(1-E_2)E_1\cos(FA\cdot\alpha_{AFI}))/C \\ S_{SPGR} - PD\sin(FA\cdot\alpha_{SPGR})(1-E_{SPGR})/(1-E_{SPGR}\cos(FA\cdot\alpha_{SPGR})) \end{matrix} \right\|_2^2, \quad \begin{matrix} E_{1,2} = \exp(-TR_{AFI1,2}/T_1) \\ E_{SPGR} = \exp(-TR_{SPGR}/T_1) \\ C = 1 - E_1E_2\cos^2(FA\cdot\alpha_{AFI}) \end{matrix}$$

Within the VAFI method, two processing options were considered based on using either one SPGR FA (1FA, 3°) or both SPGR FAs (2FA, 3° & 18°) with the same AFI dataset. Spoiling-related errors were analyzed assuming either ideal AFI spoiling and non-ideal SPGR spoiling, or ideal SPGR spoiling and non-ideal AFI spoiling.

***In-vivo* Methods:** SPGR and AFI brain images were acquired on a 3T scanner (GE MR750; Waukesha, WI) from a healthy human subject in compliance with local institutional ethics policies. Two SPGR scans were acquired with TR=10 ms, FA=[3 18]°. To test the effects of AFI spoiling, two AFI datasets were acquired, one with weak spoiling (TR1/TR2=10/50 ms, $A_{G,TR1}/A_{G,TR2}$=38/190 mT*ms/m) and one with nearly complete spoiling (TR1/TR2=30/150 ms. $A_{G,TR1}/A_{G,TR2}$=450/2250 mT*ms/m). All scans were acquired with a 128x96x50 matrix and an isotropic resolution of 2x2x2 mm placed near the center of the brain. To reduce noise, all *in-vivo* FA maps were smoothed using a local polynomial fit [5] and re-input into a second iteration of the VAFI algorithm.

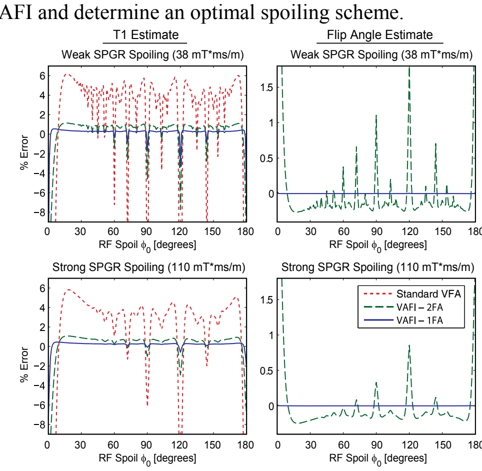

Fig. 1: T_1 and FA estimates as a function of SPGR phase increment, assuming ideal AFI spoiling, for 2 gradient spoiler areas.

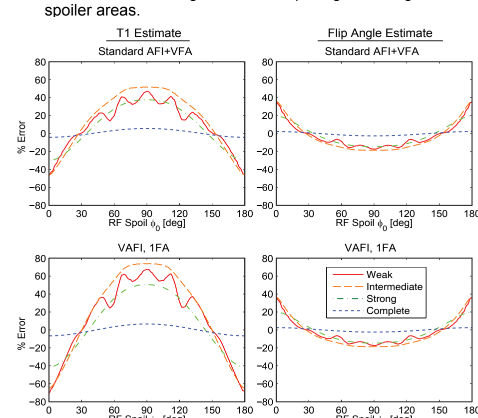

Fig. 2: T_1 and FA estimate as a function of AFI phase increment, assuming ideal SPGR spoiling, for 4 different spoiler gradient areas (see text).

Results & Discussion: Fig. 1 presents simulation results for the effect of SPGR spoiling on VFA and VAFI measurements, assuming ideally spoiled AFI. Compared to the standard VFA, the spoiling-dependent errors of T_1 estimates are greatly reduced using the VAFI technique. The relative errors of FA estimates in VAFI have a minor spoiling dependence (< 2% range). The use of a single SPGR FA in VAFI corresponding to a PD-weighted image reduces spoiling-related errors, as compared to the variant with 2 FAs. Specifically for the case of weak SPGR spoiling, assuming one chooses a phase increment that does not fall near one of the sharp peaks, VAFI with 2FA will achieve an error < 0.26% in FA and < 1.15% in T_1, while for 1FA errors are < 7.3×10^{-4}% in FA and < 0.55% in T_1. The strong spoiling regime produces similar results, with less sharp peaks. Unlike traditional VFA, VAFI measurements become highly insensitive to the choice of RF increment. Fig. 2 presents simulation results for the effect of AFI spoiling on estimation of T_1 and FA, assuming ideal SPGR spoiling. General behavior of spoiling-related errors is similar for combined VFA and AFI, VAFI-1FA, and VAFI-2FA (data not shown) techniques. The accuracy of VAFI results strongly depends on proper choice of the AFI φ_0. For the case of estimating T_1, this choice is 30°, 30°, 36°, and 44°, for weak, intermediate, strong, and complete spoiling. For the case of FA, these values are slightly different: 29°, 27°, 35°, and 43°, respectively. Fig. 3 presents *in-vivo* T_1 maps obtained by VFA and VAFI methods with weakly and strongly spoiled AFI data. Based on ROI measurements in frontal white matter, with weakly spoiled AFI, T_1 estimates were 1.120 ± 0.0634 for VFA reconstruction and 1.169 ± 0.0625 for VAFI reconstruction. With strongly spoiled AFI, T_1 was 1.009 ± 0.0564 for VFA and 0.986 ± 0.0489 for VAFI. Weak and strong spoiling in AFI resulted in FA estimates of 54° and 56°, respectively. As predicted in simulations, improper AFI spoiling results in underestimation of FA and overestimation of T_1 in both AFI and VAFI sequences. Strong AFI spoiling removes the majority of these errors, and the VAFI method further reduces the T_1 estimate, most likely due to the mitigation of spoiling errors caused by a short SPGR TR.

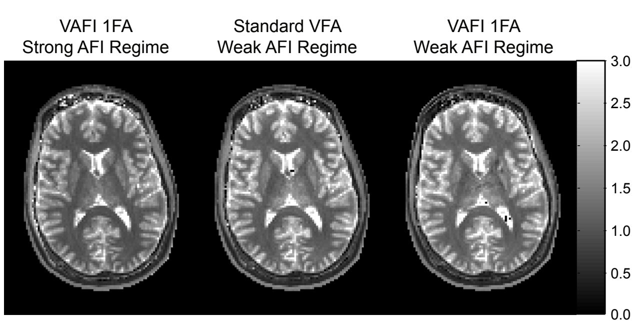

Fig 3: *In-vivo* results of T_1 mapping. VAFI with 1FA provides the most accurate results, while in the weak regime VFA over-estimates T_1 and VAFI presents artifacts near the center of the image (corpus callosum) due to inconsistent signals.

Conclusions: VAFI is a method which is highly insensitive to T_1-related errors in FA; however it still requires proper spoiling due to the steady-state nature of the sequence. Spoiling-related errors in VAFI arise primarily from the T_1-weighted AFI dataset, and the phase increment of AFI should be chosen with careful consideration to the strength of spoiler gradients used and the spoiling regime of the sequence in a particular tissue. The optimal spoiling increment for T_1 accuracy is slightly different from that for FA accuracy, though the distinctions are minor and result in negligible errors (<2%) in the strong spoiling regime. Importantly, the use of VAFI, especially with a single proton-density weighted flip angle, mitigates the need for robust SPGR spoiling. If a single SPGR FA is utilized, one may acquire data with small spoiler gradients and a short TR and still achieve accurate results. Overall, the VAFI method offers a shorter scan time and higher accuracy than separate VFA and AFI measurements due to a reduced number of SPGR datasets and relaxed SPGR spoiling requirements.

Acknowledgements: This work was supported by the NIH, NINDS R01NS065034.

References: [1] Deoni S.C.L. et al. MRM, 2003;49:515 [2] Yarnykh V.L. MRM, 2007;57:192 [3] Hurley S.A. et al. Proc. ISMRM 2009;3080 [4] Yarnykh V.L. MRM, 2010;63:1610 [5] Pruessmann K. et al MRM 1999;42:952