Simultaneous MPRAGE and Non-Contrast MRA with Prospective Motion Correction using Volumetric Navigators

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PURPOSE The MPRAGE pulse sequence is commonly used for 3D T_1-weighted anatomical imaging. It consists of an inversion recovery (IR) magnetization preparation pulse, then a delay period called the inversion time (TI) to develop suitable T_1-weighted contrast, which is followed by a short-TR 3D segmented spoiled gradient echo readout train (i.e. TurboFLASH). Depending on the application, a recovery period (~500-800ms at 3T) typically follows to allow recovery of the longitudinal magnetization prior to the next IR pulse to improve contrast and SNR.

Previous work [1] demonstrated that the relative signal intensity of blood in MPRAGE is dominated by the effects of the IR pulse, and that by controlling the slab-selectivity of this pulse across multiple measurements one could generate a subtraction MR angiogram (MRA) with excellent static tissue suppression without the need for injection of a contrast agent. In addition, one could generate standard T_1 MPRAGE images from the same data set. However, such a technique is inherently sensitive to motion between the multiple measurements, which limits its applicability. The present work addresses this shortcoming with the addition of recently described [2] volumetric navigators (vNavs) for prospective motion correction, enabling simultaneous MPRAGE and non-contrast MRA even in the presence of subject motion.

METHODS Experiments were performed at 3 Tesla (Trio a Tim System, Siemens) using a 12-channel receive-only head coil. An MPRAGE protocol for T_1-weighted structural imaging with the following parameters was used: axial slab-selective excitation, 144 partitions with 33% slice oversampling, TE/TI/TR 5/1000/2300ms, flip angle 8°, GRAPPA 2, 230x201mm FOV, slice partial Fourier 7/8, $(0.9\text{mm})^3$ resolution, 5:04 scan time per measurement. The vNavs were inserted in the dead time between the IR pulse and the imaging readout train (**Fig. 1**), and consisted of 3D EPI with $(8\text{mm})^3$ resolution and $(256\ \text{mm})^3$ FOV, TE/TR 5/11ms, flip angle 2°, 25 shots, and total acquisition time of 275ms. An additional delay time needed for calculation of motion parameters and updating of imaging gradients made the total duration of the vNav block 355ms, as previously tested and validated [2]. Two complete measurements were performed generating two image sets, one with a slab-selective IR pulse and the other with a non-selective IR pulse optimized to invert spins only in the imaging volume as described in [1]. The vNavs are used for i) prospective motion correction within each measurement, and ii) for prospectively aligning the two measurements, so they compensate for both intra scan and between scan subject motions. **Fig. 1** demonstrates the location of the vNav module and highlights the different RF pulses between the two measurements. The two measurements were then averaged to improve the SNR so that the T_1-weighted images could still be suitable for high quality structural imaging or morphometry. The two measurements were also subtracted to yield an image of only the inflowing blood with the stationary tissues suppressed.

Simulations of the MPRAGE protocol described above were performed to compare the signal levels of gray matter (GM), white matter (WM), CSF, and blood at 3T, both with and without the presence of IR pulses and vNavs. The simulated T_1 values were taken from literature [3].

RESULTS AND DISCUSSION **Fig. 2** shows the numerical simulation of signal levels after achieving steady-state over a single TR for the MPRAGE protocol. The grey box demonstrates the portion which covers the imaging readout. The blood that does not experience an IR pulse has much higher signal for most of the readout. The effect of the vNav module on the blood signal level was less than 3% even in the worst case of static blood (too small to see in Fig. 2), and did not negatively influence the image quality.

Fig. 3 depicts an axial slice of the 3D data set using the slab-selective IR pulse showing bright blood (A) and the non-selective IR pulse showing dark blood (B). Their average (C) exhibits high SNR, while their difference (D) is an inflow angiogram with excellent static tissue suppression. Because the IR pulse covers the complete imaging volume in both measurements, there is no difference for the static tissues. The maximum intensity projections (MIPs) over all slices of the difference images are displayed in axial (E), coronal (F), and sagittal (G) views.

The total scan time (10:10 in the example protocol) is similar to many MPRAGE protocols optimized for morphometry applications, such as the ADNI study [4]. The vNavs allow motion correction in each TR (2.3 sec in this protocol) and alignment between multiple measurements, as well as the reacquisition of motion-corrupted data, which improves robustness to motion for long scan times for both T_1 and MRA images. However, significantly shorter scan times are possible with trade-offs in contrast or resolution for other applications, for example by using higher GRAPPA acceleration and lower $(1\text{mm})^3$ spatial resolution.

Many studies now acquire both ASL perfusion and T_1 MPRAGE data, and could benefit from the additional vascular information that a time-of-flight (TOF) scan could provide, but which is often prohibitive due to the extra scan time. The technique described here has the ability to generate both a motion-insensitive T_1 MPRAGE and a non-contrast MRA 'for free', and may find applications in a wide variety of clinical and research studies.

REFERENCES [1] USPTO 8378680. [2] Tisdall, MRM 68:389-399 (2012). [3] Rooney, MRM 57:308-318 (2007). [4] Jack, JMRI 27:685–691 (2008).

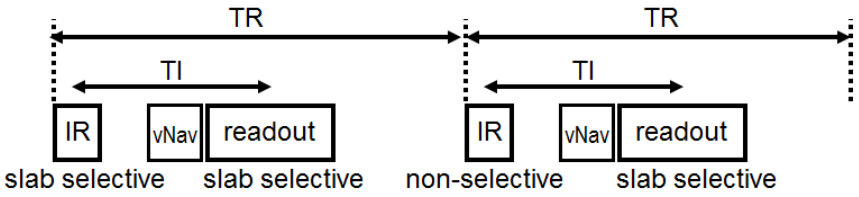

Fig 1. Pulse sequence block diagram.

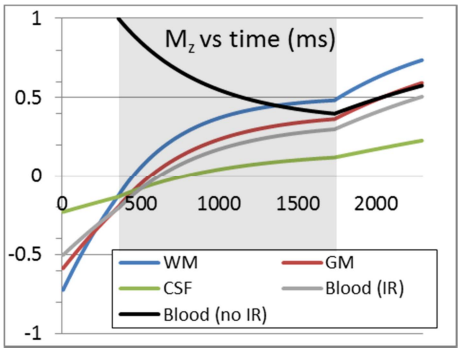

Fig 2. Simulated signal for the described protocol.

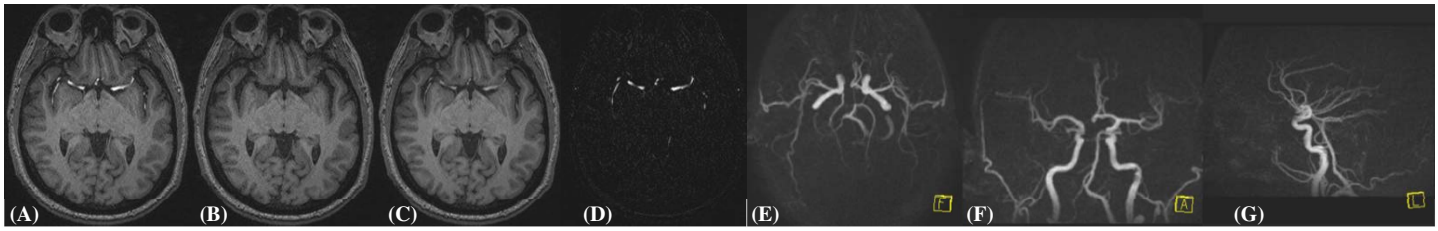

Fig 3. One slice of an axial T_1 3D MPRAGE with slab-selective IR (A) and non-selective IR (B). Their average is shown in (C) and exhibits higher SNR, and their difference is shown in (D) which is an inflow angiogram. The MIP over all slices is shown in axial (E), coronal (F), and sagittal (G) views.