Motion-corrected 350 µm isotropic MPRAGE at 3 T using volumetric navigators (vNavs)

M. Dylan Tisdall[1,2], Jonathan R. Polimeni[1,2], and André J. W. van der Kouwe[1,2]

[1]*A. A. Martinos Center for Biomedical Imaging, Massachusetts General Hospital, Charlestown, MA, United States,* [2]*Radiology, Harvard Medical School, Boston, MA, United States*

Target Audience Researchers interested in high-resolution neuroanatomical imaging and motion correction without additional hardware.

Purpose High-resolution MRI inherently requires long measurement times to achieve an acceptable signal-to-noise ratio (SNR). Even motivated subjects may not be able to remain still for these durations. Previous work has demonstrated success using fiducial markers and cameras to track and correct for subject motion prospectively [1]. This abstract presents initial results using the EPI-based volume navigator (vNav) prospective motion and frequency drift correction system [2,3] to acquire a 350 µm isotropic T1-weighted whole-head volume using a 3D-encoded MPRAGE sequence employing partition-loop (i.e., inner-loop) GRAPPA to retain TI and TR values giving good contrast between grey matter, white matter, and CSF [4]. We propose this system for achieving high-contrast, high-resolution scans at 3 T without additional hardware, calibration, or restraints on subject motion.

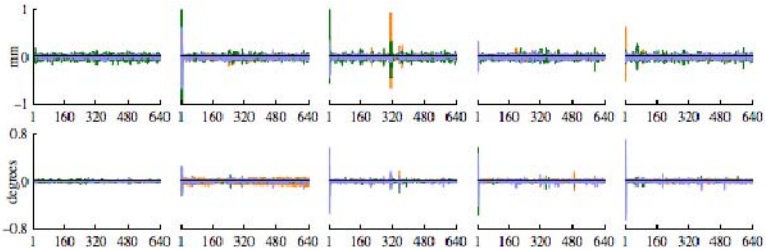

Fig. 1 Estimated subject motion over all six scans (change from previous TR; total movement would be the integral of this plot). Top row is translations and bottom row is rotations around the X (orange), Y (green), and Z (blue) axes. Note, in particular, the significant movement during scan 3 that would have invalidated the complete scan.

Methods One volunteer (having given informed consent) was scanned in a 3 T TIM Trio (Siemens Healthcare, Erlangen, Germany) using the Siemens 32-channel head coil. The subject was supported with standard cushions, and no additional restraint was applied. T1-weighted imaging was performed with MPRAGE scan having FOV 224×179.2×224 mm with 640×512×640 voxels giving 350 µm isotropic resolution. 4× acceleration was applied in the partition loop to allow time for the 275 ms vNav, 103 ms for navigator registration and feedback, and measurement of a complete phase-loop step of the scan with TI 1180 ms and TR 2573 ms. Bandwidth of 200 Hz/px gave a TE of 4.42 ms and a total scan time of 27:37, repeated five times for a total session time of 138:05. Each scan produced 32.4 GB of data; too large to be reconstructed on the scanner. The data was streamed in real-time to an offline reconstruction system and image volumes were produced with a custom implementation of the GRAPPA algorithm.

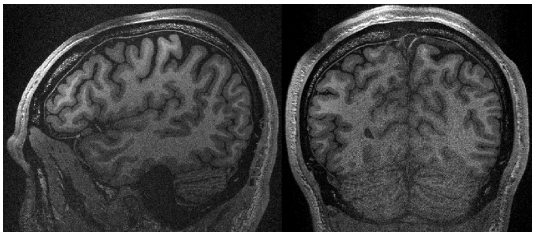

Fig. 2 Example sagittal and coronal slices, demonstrating grey/white/CSF contrast similar to that achieved with 1mm isotropic MPRAGE. Note that SNR is maximized at the cortex relative to the center of the brain due to the receive sensitivity profiles of the custom coil array.

In addition to using the vNavs to correct subject motion (see Fig. 1), their phase-correction lines were used to prospectively correct frequency drift after each navigator; this is significant as gradient heating during this long scan session resulted in frequency drift large enough to induce an artificial shift in the EPI-based navigators. Without correction, this "false-motion" would corrupt our motion tracking and render the system insufficiently accurate for high-resolution imaging.. The five final magnitude image volumes were registered using FLIRT [5] and RMS averaged to produce a single final magnitude volume.

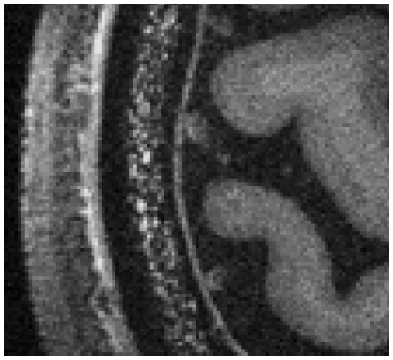

Fig. 3 Zoomed section of an axial slice, showing anatomical details that were successfully acquired at 350 µm despite subject motion.

Results Fig. 2 shows two slices illustrating the CNR and SNR attained. Fig 3. shows a zoomed region of an axial slice with clearly defined grey and white matter, vessels, dura, and bone marrow.

Discussion Fig. 1 illustrates that even a highly motivated subject has difficulty remaining sufficiently still for high-resolution MRI to be feasible without some form of motion compensation. While methods that use external hardware have many advantages (e.g., no loss of time or contrast to navigator sub-sequences), we have demonstrated a viable system for enabling high-resolution on any 3 T scanner without modification. The use of inner-loop GRAPPA is critical to this method's success, as it allows time for the navigator and a sufficiently long FLASH pulse-train to be acquired each TR without compromising the preferred TI and TR values. Fig. 2 shows that we have indeed preserved the desirable contrast properties of MPRAGE at this high resolution. Fig. 3 illustrates the scale of anatomy that can be visualized with 350 µm imaging at 3 T using our modified pulse sequence; the sharpness reinforces the success of both the prospective frequency- and motion-correction updates applied over the duration of the study.

Acknowledgements The authors would like to thank Himanshu Bhat and Keith Heberlein, Siemens Medical Solutions USA, for their assistance. This work was supported by: NIH R21MH096559, R01HD071664, R21EB008547, R33DA026104, K01EB011498, P41RR014075, and the Ellison Medical Foundation.

References [1] Andrews-Shingaki et al. "Prospective motion correction for magnetic resonance spectroscopy using single camera retro-grate reflector optical tracking" (2011) JMRI 33(2):498-504 [2] Tisdall et al. "MPRAGE Using EPI Navigators for Prospective Motion Correction" ISMRM 2009, 4656 [3] Tisdall et al. "Volumetric Navigators (vNavs) for Prospective Motion Correction and Selective Reacquisition in Neuroanatomical MRI" (2012) MRM 68(2):389-399 [4] van der Kouwe et al. Brain morphometry with multiecho MPRAGE, Neuroimage 2008, 40(2):559-569 [5] Jenkinson et al. "A global optimisation method for robust affine registration of brain images" (2001) Medical Image Analysis, 5(2):143-156