

Motion Correction of a new T1-w Propeller Sequence (SE-prop)

Stefan Skare¹

¹Dept of Clinical Neuroscience, Karolinska Institutet, Stockholm, Sweden

Introduction: The Cartesian *Spin Echo* sequence (SE) is often the sequence of choice for clinical T_1 -w brain imaging. Acquiring one phase encoding (p.e.) line per TR makes however the sequence very sensitive to both head motion and flow. Motion-robust propeller-type T_1 -w pulse sequences have been proposed recently (1, 2), where the T_1 -w contrast is due to a leading *inversion pulse*. As such inversion pulse may sometimes be undesired for post-Gd scans, we have implemented a new T_1 -w propeller-based Spin-Echo sequence (SE-prop) with the same tissue contrast characteristics at the classical T_1 -w SE sequence, while attempting to overcome the mentioned motion artifacts. Previous propeller sequences for T_2 -w (3-4), T_1 -w FLAIR (2) or diffusion-weighted contrast (5) have in common that a whole blade is read out after each excitation. In T_1 -w SE-prop, only one p.e. line within a blade is acquired per TR (Fig. 1). Thereby, motion may also occur *within* a blade (intra-blade motion), alongside with the blade-to-blade (inter-blade) motion, and needs to be addressed differently in the image reconstruction.

Materials and Methods: *Acquisition:* The following sequence parameters were used on a healthy volunteer; $FOV = 24$ cm, sl. thk. = 4 mm, 21 slices, flow compensation in freq. & slice, $RBW = \pm 62.5$ kHz, 24 blades of size 288×32 (gridded resolution = 288×288), $TE/TR = 14/500$ ms, 8-channel head coil, GE 3T DVMR 750 scanner. The temporal order of the phase encoding steps within each blade were sorted in a double-interleaved manner to prepare for optional parallel imaging operations in the reconstruction, while acquiring all p.e. blade lines during the acquisition (Fig. 3). The acquisition time for one blade became $TR \times 32 = 16$ s in this study, hence 6:24 min for the scan using 24 blades. The volunteer was instructed to move as much as possible within the constraints of the head coil for about 8-10 s during five random periods of the acquisition and also to change the head orientation in between. Hence, a subset of the blades were subject to very large intra-blade motion in addition to an overall inter-blade motion. A motion-free case was also acquired with identical parameters.

Image reconstruction: For the motion scan, GRAPPA weight estimation was performed on each (fully sampled) blade, with "acceleration" $R = 2$. In this GRAPPA least squares fitting process, the associated fit error was used to identify blades that were *inconsistent* with the GRAPPA model (presumably due to intra-blade motion). Blades with an average fit error (across slices) 4 times higher than the blade with the lowest GRAPPA fit error were *partly* sorted out from the reconstruction. Partly, because instead of rejecting a whole blade, parallel imaging (GRAPPA) (for the moment using "good" pre-calculated GRAPPA weights from the non-motion scan), with $R = 4$ was used to synthesize four - temporally separated - blades. After Fourier transformation, an entropy metric was applied to the synthesized blade images, and the one(s) with the highest image entropy were removed. This way, the smallest "temporal footprint" per blade was reduced from 16 to 4 seconds. Following this data rejection phase, a 3D rigid body motion correction was performed between the remaining blade volumes (i.e. stack of 2D slices) with the blade volume having the lowest GRAPPA fit error as reference. The motion corrected data was Fourier transformed back to k -space for final gridding.

Results: Fig. 2 shows the GRAPPA fit error (averaged over slices) vs. blade number for both the non-motion scan (blue) and the motion scan (red). Blade images for an arbitrary slice (#14) for three of the blade images (#4, #8, #19) are shown above the graph to illustrate how well the GRAPPA fit error reflects the presented image ghosting coming from inconsistencies in the k -space data. The dashed lines correspond to four times the lowest GRAPPA fit error encountered among the blades, and was found to be a reasonable choice to separate good blades from bad ones. In Fig. 3, blade #4 is shown without and with motion, reconstructed with $R = 1$, $R = 2$ (resulting in two images) and $R = 4$ (four images), only some of which are corrupted by motion. Finally, Fig. 4 shows gridded data without and with inter-blade motion correction and rejection.

Discussion: Sequences based on propeller trajectories are well-known to be robust to motion, with 2D or 3D motion correction applied between blades. In this study, we have developed a Spin-Echo propeller sequence (SE-prop) with identical T_1 -w tissue contrast as the established Cartesian Spin-Echo. We have here suggested additional measures to handle potential intra-blade motion. Parallel imaging (GRAPPA) was used only as a way to "repair" damaged blades by effectively reducing the temporal footprint of a blade from 16 to 4 s, rather than to accelerate the scan itself. Next, we will implement our previously published angularly continuous GRAPPA kernel (6), and use only those blades that are free from motion for the GRAPPA calibration. Thereby, no pre-calculated GRAPPA weights from earlier scans will be necessary.

Acknowledgements

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References

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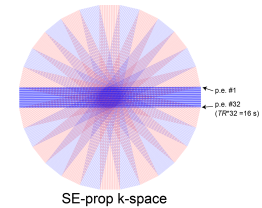


Figure 1. SE-prop k-space trajectory. Different from other propeller sequences is that only one line is acquired each TR

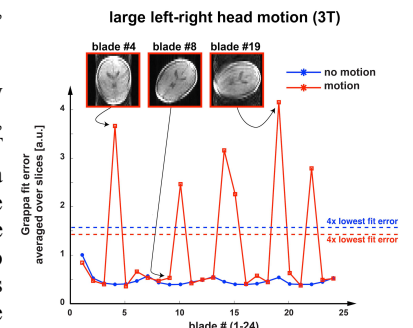


Figure 2. 3T data on a healthy volunteer instructed to move as much as possible during five intervals. The average GRAPPA fit error vs. blade index is shown. During motion, the fit error increases up to about ten-fold, making the bad blade identification fairly easy.

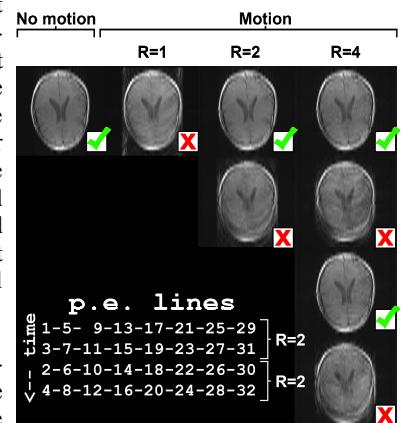


Figure 3. Slice 14 from blade #4 in Fig. 1. While normal FFT lead to image ghosting ($R=1$), applying GRAPPA on two or four interleaves, the motion-free portions of the blade can be saved.

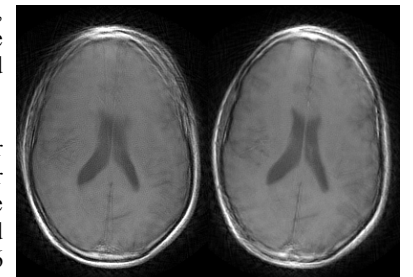


Figure 4. Gridded SE-prop data on volunteer. Left panel: No correction. Right panel: Motion correction