Flyback Twisted Projection Imaging for Fast Quantitative Sodium Imaging Demonstrated on the Human Brain at 9.4 Tesla

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Purpose: Quantitative 23-sodium (23Na) MR imaging and the derived tissue sodium concentration (TSC) bioscale can inform on tissue viability, cell density, and diseases that disrupt sodium ion homeostasis. Obtaining an accurate TSC map of a human brain requires a series of acquisitions to be performed on the brain under study (to obtain the spatially resolved sodium measurements with B0 and B1 corrections) and on a quantification phantom (to calibrate the signal intensity into biological units). Collecting all the necessary data is time demanding, requiring up to 30 minutes of human imaging (three 23Na scans to collect desired imaging data, B0 correction data, and B1 correction data) followed by another 30 minutes of phantom imaging. We describe a new pulse sequence for rapid quantitative 23Na MR imaging, termed Flyback Twisted Projection Imaging (FB-TPI), that extends the existing flexible TPI (flexTPI) [1]. Fast quantitative sodium imaging using FB-TPI is demonstrated in the human brain at 9.4 T.

Materials and Methods: FB-TPI samples 3D k-space on a non-overlapping double-cone structure as shown in **Figure 1**. The primary difference from flexTPI is the flyback portion of the trajectory, which begins each projection and samples the opposite half of k-space using radial trajectory. Once the flyback fraction (F_{FB}) is reached, the trajectory returns to the center of k-space and continues with the standard flexTPI trajectory that uses a radial projection until reaching the radial fraction (F_R) and then uses a twisting projection [1]. In FB-TPI the center of k-space is sampled twice. This allows two different low-resolution images computed from the data corresponding to the red and blue highlights shown in **Figure 1**. These low-resolution images have different effective echo times, allowing a B0 map to be computed from a single acquisition. This B0 field map can then be used for field correction when reconstructing the complete FB-TPI data.

FB-TPI can alternatively be used to accelerate the acquisition by acquiring only projections that end with $K_Z>0$ (half of the required projections). When FB-TPI is performed in this manner, image data are reconstructed by exploiting the conjugate symmetry of k-space data in the same way as the popular partial-Fourier family of sequences routinely used for rapid proton imaging. Significant time is saved as only half of the projections are needed.

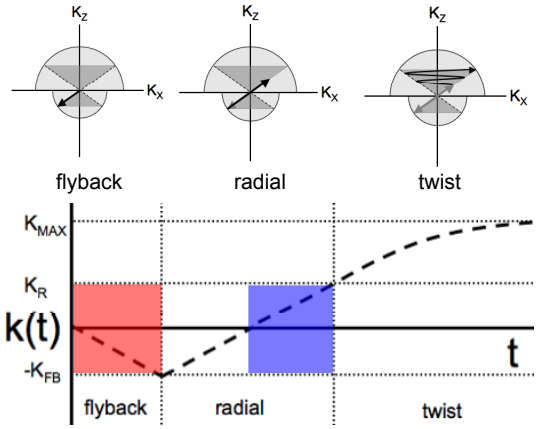
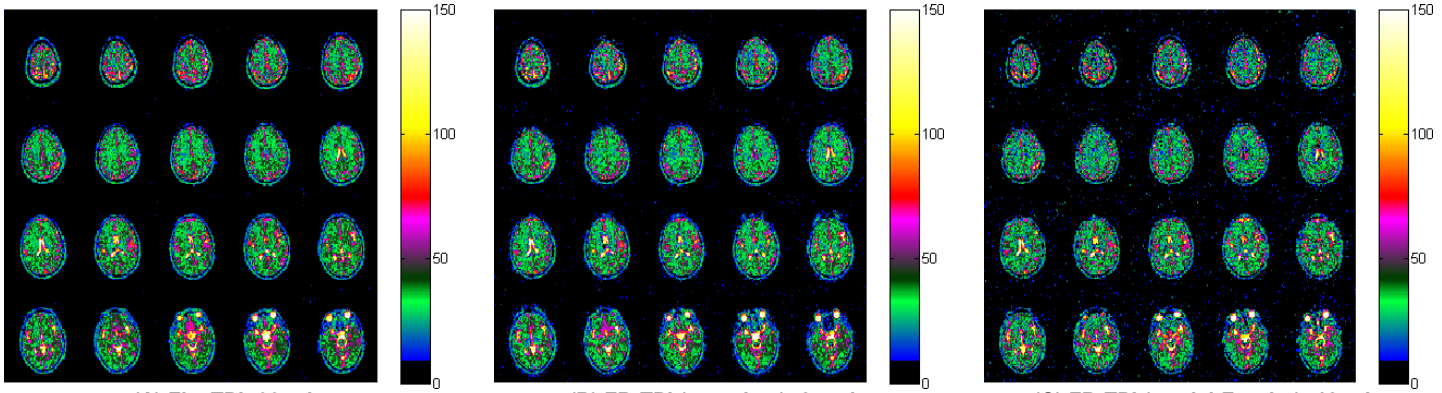


Figure 1: Example trajectory segments along the surface of the double-cone (top) and k-space magnitude of flyback TPI (bottom).

FB-TPI was implemented on a custom-built 9.4T MR scanner optimized for human brain imaging. Data were collected from a healthy volunteer after informed consent was obtained using both the existing flexTPI (FOV=20 cm, 4 mm isotropic resolution, TR/TE=175/0.260 ms, F_R=0.43) acquisition sequence and the new FB-TPI (FOV=20 cm, 4 mm isotropic resolution TR/TE=175/0.260 ms, F_R=0.55, F_{FB}=0.25) sequence. FB-TPI was performed with complete sampling (integrated B0 mapping) and with partial-Fourier sampling (scan acceleration). The readout time of the all acquisitions were matched at 5.82 ms in order to approximately match the T2-blurring incurred during readout. Three 10-minute flexTPI acquisitions were necessary collect the base data and to map the B0 (acquisition with TE=1.260 ms) and B1 (acquisition with ½ the flip angle of the base acquisition) inhomogeneities. FB-TPI with complete sampling required only two 12-minute acquisitions (base data and acquisition with ½ the flip angle of the base acquisition) since the B0 map could be computed from a single FB-TPI scan. FB-TPI with partial sampling required three scans for B0 and B1 mapping, but each scan was only 6 minutes long. All acquisitions were repeated on a three-compartment phantom with known concentrations (30 mM, 70 mM, 110 mM) and electrical loading equivalent to a human head. The sodium data were reconstructed with B_0 and B_1 corrections and quantified into TSC as described elsewhere [1]. The flexTPI and FB-TPI with complete sampling used a gridding-based reconstruction. FB-TPI with partial-Fourier sampling used a gridding + projection onto convex sets (POCS) reconstruction.

Results and Conclusion: Figure 2 shows the TSC maps computed from the flexTPI, FB-TPI with complete sampling, and FB-TPI with partial-Fourier sampling, respectively. A 20% reduction in acquisition time was achieved using FB-TPI with complete sampling. FB-TPI with partial-Fourier sampling produced a 40% time reduction, albeit with the normal reduction in SNR associated with partial-Fourier imaging techniques. FB-TPI offers reduced acquisition time for sodium MR imaging without sacrificing the accuracy of the TSC bioscale.

References: [1] Lu A, Atkinson I, Claiborne T, Thulborn KR. Improved quantitative sodium imaging with a flexible twisted projection design and B0 inhomogeneity correction. Proceedings of ISMRM. #2472. 2009.



(A) FlexTPI: 30-min **(B) FB-TPI (complete): 24-min** **(C) FB-TPI (partial-Fourier): 18-min**

Figure 2: Comparison of **TSC maps computed from the three different acquisition and processing schemes with different total human data acquisition time. Phantom data of equivalent duration were also acquired in order to quantify the sodium MR signal into the TSC bioscale. All the TSC maps have units of millmoles 23Na/voxel.**