A comparison of UTE k-space sampling techniques for the *in vivo* detection of total sodium at 3T

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Background

Higher field strengths, fast readout and sophisticated sparse reconstruction methods have drawn attention to 23Na MR-imaging, making its potential clinical use feasible through improvement of the signal to noise ratio (SNR) and image quality. Total sodium measures can be obtained using MRI scanners with multi-nuclear capabilities, providing that the fast decaying transverse component ($T_{2F} \approx$ 0.5-5ms), which makes up the bulk of the signal, is not lost [1,2,3]. Ultra-short echo time (UTE) sequences with non-Cartesian k-space sampling can detect these fast decaying components *in vivo*, but often suffer from short T_2 blurring. Previous sequence comparisons focussed on phantoms with sodium concentrations and relaxation properties different from brain tissue [4]. For this reason we compared three UTE sequences for the detection of 23Na in the human brain in terms of SNR and assessed the effect of the blurring on resolution using a separate phantom.

Methods

Healthy subjects (n=5, age 30 ±8yrs) were scanned on a Philips 3T Achieva TX system. A proton density weighted (PDw) 6mins ^{1}H-scan was performed using the Q-body coil prior to 23Na MRI for positioning and co-registration to the sodium slices. 23Na-scans were acquired using a single resonant Tx/Rx birdcage coil (Rapid, Rimpar, Germany). Three sequences, namely 3D UTE gradient echo with so-called kooshball (KB), stack of stars (SOS) and spiral (SP) k-space trajectories were tested (Fig.1). The sequence parameters were: TR of 120ms, 4mm resolution, FOV=240mm^2 and BW/pixel=90Hz. Both SOS and KB employ FID sampling and have a TE=0.27ms. The SP scan samples the full echo and was run at a TE=0.8ms. Scans were 18 minutes each, adapting sampling densities to match for time. Bi-lateral regions of interest in the grey (GM) and white matter (WM) were taken for SNR estimation in addition to the ROIs in two 4% agar phantoms with 33 and 66 mM NaCl and a central CSF region, after correcting for Rician noise [5]. Standard deviations were calculated from bi-lateral and multiple slice averages. A paired t-test was performed to assess statistically significant differences ($p>0.05$) between measurements. The same scans were performed on a 4% agar phantom with 80mM NaCl surrounding 4mm holes, varying the bandwidth from 50 to 200 Hz/pixel in four steps to assess resolution and the effect of blurring from short T_2 decay.

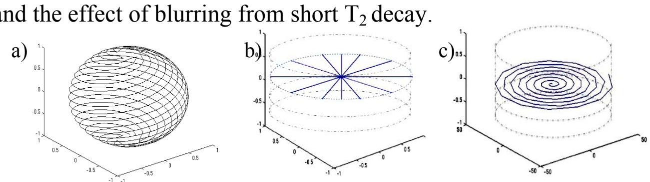
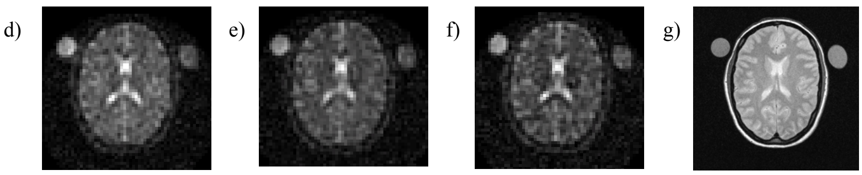


Figure 1: Top row: Illustration of the k-space sampling schemes: a) 3D KB samples discretely from the centre-out along an interleaved trajectory; b) SOS and c) SP have sample points along star- and spiral-like in-plane trajectories respectively, which are cylindrically stacked in 3D. Fewer samples and slices are shown in the SOS and SP for clearer representation.



Bottom row: 23Na KB (d), SOS (e) and SP (f) images, windowed at full-dynamic range. Shown in (g): a proton density image of the same slice. Note the differences in contrast-to-noise in the 23Na images. Cylindrical sodium phantoms (33 & 66mM sodium and 4% agar) were placed in the FOV for further SNR measurement.

Results and Discussion

Mean SNR for all subjects are shown in the bottom row of table 1. In individual mean ROIs, SOS performed best in three out of five cases, but taking the standard deviations into account, is comparable to the KB results for this population and sample size. Spiral performs worse but provides the best resolved features in the phantom (not shown), possibly due to less blurring but reduced signal at the longer TE. The results between the three protocols do however show no significant statistical differences ($p>0.05$). Resolution was visually indistinguishable for KB and SOS, despite an estimated 16% larger FWHM-linewidth of the point-spread function (PSF) for SOS [6]. SNR for corresponding ROIs vary from subject to subject, possibly due to differences in susceptibility and resultant shim (table 1). Expected blurring due to the long read-out window was minimal and did not hinder resolving the features of the resolution phantom for all but in the 50 Hz/pixel bandwidth scan.

Table 1: SNR values observed in identical ROI's for each sequence for all subjects. Bottom row gives the averaged results for all subjects. SD given for bi-lateral and averaged measures.

SNR	Kooshball (KB)					Stack-of-stars (SOS)					Spiral (SP)				
	GM	WM	CSF	40	80	GM	WM	CSF	40	80	GM	WM	CSF	40	80
Subject 1	10.59 ±0.48	6.82 ±0.01	16.61 ±1	7.24	13.08	8.97 ± 0.4	8.74 ±0.07	18.44 ±2.1	9.97	16.67	9.94 +0.91	4.62 ±0.59	11.95 ±1.78	6.78	11.25
Subject 2	8.75 ±0.01	6.02 ±0.02	11.8 ± 1.67	5.47	11.15	11.58 ±0.28	5.92 ±0.03	13.42 ±1.42	5.93	12.06	6.55 ±0.14	5.82 ±0.25	9.35 ±1.43	7.55	15.48
Subject 3	6.59 ±0.15	6.37 ±0.12	11.48 ±1.27	5.98	10.87	7.57 ±0.51	5.15 ±0.22	14.73 ±0.69	5.73	10.62	3.28 ± 0.2	4.35 ±0.18	10.74 ±1.1	5.15	8.83
Subject 4	6.59 ±0.44	7.78 ±0.21	18.56 ±2.15	10.53	16.69	9.26 ±0.33	7.77 ±0.19	17.73 ±1.5	6.39	11.51	5.92 ±0.1	4.23 ±0.06	11.53 ±1.3	6.74	12.66
Subject 5	6.63 ±0.56	5.81 ±0.71	12.71 ±1.38	5.01	10.03	7.23 ±0.08	4.83 ±0.08	12.53 ±0.9	5.9	10.18	5.55 ±0.1	4.56 ±0.18	12.66 ±1.3	5.45	10.15
Mean (SD)	7.83 ±1.72	6.56 ±0.78	14.23 ±3.17	6.85 ±2.22	12.36 ±2.66	8.88 ±1.73	6.48 ±1.61	15.37 ±2.61	7.64 ±2.24	11.35 ±3.84	6.25 ±2.29	4.72 ±0.64	11.25 ±1.26	6.33 ±1	11.67 ±2.55

Conclusions

KB and SOS SNRs did not significantly differ in this pilot study. Stronger signal amplitude at the cost of more blurring in the case of SOS compared to KB, as expected from theory [6], was not visible at this resolution, although SOS showed a slightly higher SNR. SP performed worse than SOS and KB, albeit also with statistically insignificant differences. The relatively long read-out window of 5.6ms did not impair resolving the features in the resolution phantom, which has slightly longer T_2s than the in vivo tissue. Further development on our system is under way to implement a conical 3D spiral acquisition (3D-cones [7]), which promises an improvement in both SNR and resolution by using a high sample-point density adapted trajectory, which makes efficient use of gradient slew rate and amplitude restrictions and does not require numerical smoothing as in twisted projection (TPI) sequences [7].

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