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T1 and T2 measurements across multiple 0.55 T MRI systems using open-source vendor-neutral sequences

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ABSTRACT

Purpose

To compare T1 and T2 measurements across commercial and prototype 0.55 T MRI systems in both phantom and healthy participants using the same vendor-neutral pulse sequences, reconstruction, and analysis methods.

Methods

Standard spin echo measurements and abbreviated protocol measurements of T1, B1 and T2 were made on two prototype 0.55 T systems and two commercial 0.55 T systems using an ISMRM/NIST system phantom. Additionally, five healthy participants were imaged at each system using the abbreviated protocol for T1, B1 and T2 measurement. The phantom measurements were compared to NMR-based reference measurements to determine accuracy, and both phantom and in vivo measurements were compared to assess reproducibility and differences between the prototype and commercial systems.

Results

Vendor-neutral sequences were implemented across all four systems, and the code for pulse sequences and reconstruction is freely available. For participants, there was no difference in the mean T1 and T2 relaxation times between the prototype and commercial systems. In the phantom, there were no significant differences between the prototype and commercial systems for T1 and T2 measurements using the abbreviated protocol.

Conclusion

Quantitative T1 and T2 measurements at 0.55 T in phantom and healthy participants are not statistically different across the prototype and commercial systems.

Key words

T1, T2, multi-site repeatability, 0.55 T

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INTRODUCTION

T1 and T2 relaxation times are representative of physical processes. Given that, if the same measurement is made across multiple systems at the same field strength, the measured values should be the same. However, quantitative values vary with measurement method and the experimental acquisitions, reconstructions, and signal modelling must be matched to result in the same measured values. Moreover, these measurements are hardware-dependent, and MRI hardware typically goes through prototype and upgrade cycles as technology advances. As a result, multi-system studies may need to incorporate different hardware and software platforms, even when the systems are from the same manufacturer.

Here, we are specifically investigating measurements across contemporary 0.55T MRI systems, in light of the recent commercialization. It is valuable to characterize these new systems across multiple sites, and to compare with predecessor prototype systems that were “ramped down” from 1.5 T to 0.55 T, for which much of the preliminary quantitative data has been reported[1,2]. The prototype 0.55 T systems have higher-performance gradients, different numbers and layouts of RF coils, and a different bore geometry compared to the commercial 0.55 T design. In theory, measurements of quantitative NMR parameters including T1 and T2 relaxation times made on the prototype 0.55 T systems should be the same as measurements from the commercial 0.55 T systems; however, differences between the design and capabilities of these two systems may lead to variations in measurement values.

Two studies of T1 measurement using closely matched systems (same or similar hardware, software, and pulse sequences) demonstrated high repeatability across the systems.[3,4] To achieve these, it was necessary to compare and harmonize pulse sequence code line-by-line across these systems. Other studies using unmatched sequences have been performed to compare relaxometry measurements across systems and sites, and the results are varied.[5–8] For T1 measurement, the largest differences are typically observed between systems from different vendors, rather than across systems of the same vendor. This has been shown in both phantom[9,10] and in vivo studies.[9,11] The other factors in multi-site T1 measurement differences are the specific sequence implementation[5–7] and software version.[5] Additionally, T1 measurement differences are observed following hardware and software upgrades.[8] T2 measurement is arguably more challenging since it is biased by B1+ and B0 inaccuracies that cannot be easily corrected.[12–14] A survey of myocardial T2 relaxation times reported in healthy adults found the reported values were dependent on vendor and pulse sequence.[15]

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To use T1 and T2 measurements clinically as a diagnostic tool, it is necessary to replicate measurements across systems. Tools have been developed to enable the same experiment across systems and for the implementation of the same post-processing pipelines. Karakuzu et al. used RTHawk and qMRLab to develop a vendor-neutral pulse sequence and analysis workflow.[16] The vendor-neutral workflow significantly reduced inter-vendor T1 measurement differences in phantoms and in vivo. An international T1 mapping challenge demonstrated that open and harmonized acquisition and reconstruction is essential to obtain reproducible quantitative results, even more so when multi-site studies of the same or similar subjects are considered[9]. One tool for this purpose is Pulseq (https://pulseq.github.io/), an open-source vendor-agnostic pulse sequence programming environment, which can be used to develop and execute MRI pulse sequences across different vendor systems and platforms. Pulseq was used to implement the same acquisitions across different systems, including different platforms.[17–20]

In this study, we use Pulseq to implement the same pulse sequences for T1 and T2 measurements across commercial and prototype 0.55 T MRI systems. We compare the measurements using both the ISMRM/NIST system phantom and healthy participants.

METHODS

Measurements were made on two prototype 0.55 T systems and two commercial 0.55 T systems. On each system, prior to the study timeframe, protocols were validated using an ISMRM/NIST system phantom (CaliberMRI, Boulder, CO, USA); this system qualification data is not reported. Following this validation step, healthy participants were imaged, and phantom measurements were completed on each system. The goal was to complete all measurements (phantom and participants) within a two-week study time frame. The phantom measurements were compared to NMR-based reference measurements to determine accuracy, and both phantom and in vivo measurements were compared to assess reproducibility and differences between the prototype and commercial systems.

Phantom measurements

A single ISMRM/NIST system phantom was shipped between the four different systems. The ISMRM/NIST system phantom includes $NiCl_2$ and $MnCl_2$ concentration arrays each containing

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14 vials with a range of T1/T2 relaxation time combinations. The temperature of the phantom before and after imaging along with the ambient room temperature was measured using a thermometer provided with the phantom.

On the prototype systems, the system phantom measurements were acquired using a 12-element head and neck coil. On the commercial 0.55 T systems, the head coil has a smaller diameter and instead the system phantom was placed on the spine coil, and then the large flexible 6-element body coil was wrapped around the phantom (shown in **Figure S1**).

T1 and T2 measurements in both the $NiCl_2$ and $MnCl_2$ arrays were made using two protocols: a standard spin echo protocol (approximately 7 hours) and an abbreviated protocol (approximately 35 minutes) both implemented in Pulseq.[21] All sequence details are provided in **Table 1**. The standard spin echo protocol consisted of inversion-recovery spin-echo (**IRSE**) and single-echo spin-echo (**SESE**) sequences, with one exception. For the commercial system, due to a bug in the sequence development framework at the time of the study, product SESE was used for SESE T2 measurement, instead of Pulseq SESE. For the abbreviated protocol, a 3D Variable Flip Angle Gradient Echo (**VFA-GRE**) sequence was used for T1 mapping, and measurements were made of $MnCl_2$ and $NiCl_2$ arrays simultaneously. The same VFA-GRE sequence with FA 60°, TRs 32 ms and 96 ms was used for actual flip angle imaging (**AFI**).[22,23] The B1 maps were used to calculate actual flip angles for fitting T1 via VFA-GRE. A 2D Multi-Contrast Spin-Echo (**MCSE**) sequence was implemented in Pulseq for T2 mapping. Two slices were acquired to cover both the $MnCl_2$ and $NiCl_2$ arrays. The Pulseq pulse sequences are available at https://github.com/usc-mrel/PulseqT1T2Mapping. The standard spin echo protocol measurements were acquired once, and the abbreviated protocol measurements were acquired three times on each system during the study time frame.

The acquired images were reconstructed using Gadgetron[24,25] and then quantitative MRI maps constructed using qMRLab[16] and StimFit[12] (open-source frameworks available for MATLAB). Raw data from the scanner were converted to the magnetic-resonance raw data (MRD) format.[26] Following the application of an FFT reconstruction in Gadgetron, the background was masked with convex-hull based masking, using MATLAB's `bwconvhull` function, to speed up processing time and make online visualization easier (MATLAB R2021a, Mathworks, Natick, MA, USA). Open-source qMRLab[16] was used on the masked images to calculate T1 and T2 values from the IRSE, SESE, and VFA-GRE data. B1 maps acquired with AFI were used for

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calculating voxel-wise actual flip-angles for fitting T1 VFA-GRE, also using qMRLab. T2 maps based on the MCSE sequence were estimated using the StimFit[12] package, which accounts for stimulated echoes. ROI masks for the vials in the $NiCl_2$ and $MnCl_2$ arrays were applied to the processed T1 and T2 maps.[8] The vial masks were eroded by two pixels to avoid effects of partial volume, and individual voxels were used for the data analysis. For the 3D VFA-GRE acquisition, two slices through the center of the vials were included in the ROI. The reconstruction and mapping code is available at https://github.com/usc-mrel/PulseqGadgetronRecon.

At one prototype 0.55 T system, the SESE acquisition on the $MnCl_2$ array was incomplete; only the first 21 echoes of the 32 prescribed echoes were acquired. The reported results for that measurement use only these 21 echoes instead of the full dataset. No data was excluded from the analysis.

NMR-reference measurements at 0.55 T

Reference measurements were made at 0.55 T using a variable field NMR system (Tecmag Redstone console, TNMR software), and a custom RF probe that allowed sample temperature control at 20°C. Measurements were made on a subset of witness samples from the same batch of $NiCl_2$ and $MnCl_2$ solutions used in the system phantom. In total, eighteen samples were measured: nine from each of the $NiCl_2$ and $MnCl_2$ arrays. A subset of these measurements was previously reported.[27]

NMR-reference T1 was measured using inversion recovery protocols with composite 180-degree pulses; NMR-reference T2 was measured using a Carr-Purcell-Meiboom-Gill (**CPMG**) pulse sequence. T1 was calculated using:

$$S_i = S_0 * (1 - (1 + d) * e^{(-TI/T1)}) \qquad (1)$$

where T1 is the target value to fit, TI the inversion time, d a scaling factor for imperfect inversion, S_0 the nominal signal intensity, and S_i the measured signal intensity. Similarly, T2 was calculated using:

$$S_i = S_0 * e^{(-TE/T2)} \qquad (2)$$

where T2 is the target value to fit, and TE the echo time.

Across both the subset of $NiCl_2$ and $MnCl_2$ arrays, the measured values ranged from 66 ms to approximately 1550 ms for T1 and 41 ms to approximately 915 ms for T2 (**Table S1**).

In vivo measurements

Five healthy participants were imaged at each site under protocols approved by the Institutional Review Board of each institution, after providing written informed consent. Participants were independently recruited at each site. All participants were women between the ages of 22 and 29 years old. Specifically, at Prototype 1 participants were ages 24-29 (mean 26 years old, standard deviation 2.1 years). At Prototype 2 and Commercial 1, participants were 24-28 years old (mean 26.1 years, standard deviation 1.6 years). Finally, at Commercial 2 participants were 22-29 years old (mean 26.2 years, standard deviation 2.6 years).

The abbreviated Pulseq protocols used for in vivo measurements are detailed in **Table 1**. Axial data was acquired over the whole brain for the T1 and B1 measurements, and for T2 measurement a single 2D axial slice was acquired. As described in the section on phantom measurements, the images were reconstructed and quantitative T1 and T2 calculated.

Data analysis

For the phantom MRI measurements and NMR-reference measurements, all comparisons were performed across vials 3-11 of both the $MnCl_2$ and $NiCl_2$ arrays; these vials represent a physiological range of values at 0.55 T. Comparisons were made, via percent bias (%-bias), between 1) the standard spin-echo measurement and 20^{o}C NMR-reference data and 2) the abbreviated protocol and 20^{o}C NMR-reference data. Additionally, the coefficient of variation was calculated for each system's three repetitions of the abbreviated protocol. An ANOVA analysis (SciPy, Python) was completed to compare the abbreviated protocol mean T1 and T2 measurements (vials 3-11) from the prototype and commercial systems. Statistical significance was assessed using $p<0.05$.

For the participant data, T1, B1, and T2 measurements are reported as probability density function histogram of values over the brain volume or single slice, respectively. The T1 histograms are filtered to values between 0 and 3000 ms and the bin width is 25 ms. The B1

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histograms are filtered to values greater than 0.01, and the bin width is 0.02 (relative to a desired flip angle of 1.0). The T2 histograms are filtered to values between 0 and 400 ms, and the bin width is 10 ms. The bin widths show the distribution of relaxation times and are approximately square root of the total counts divided by ten. For the quantitative biomarkers T1 and T2, the location of the histogram peak and the general shape of the histogram can be compared across systems. An ANOVA analysis (MATLAB 2023b, Mathworks) was used to compare the difference in means for the measured T1 and T2 relaxation times between the prototype and commercial systems, and statistical significance was assessed using $p<0.05$.

RESULTS

Phantom and in vivo measurements were completed on the two prototype and two commercial systems using the open-source vendor-neutral Pulseq protocols and reconstruction pipeline (**Figure S2**). On Prototype 1, the phantom and in vivo measurements were completed in 12 days. On Commercial 2, the phantom and in vivo measurements were completed in 15 days. On Prototype 2 and Commercial 1, the in vivo measurements were completed in 6 days; however, the total study time frame for in vivo and phantom measurements was 30 days.

Phantom measurements

Across all systems, the standard spin echo protocol resulted in T1 measurements in all vials in the $NiCl_2$ array which were within +/-10 % of the NMR-reference measurement (**Figure 1 A**). In general, the standard spin-echo T1 measurement of the $MnCl_2$ array was overestimated compared to the NMR-reference measurement (**Figure 1 B**). Additionally, for $MnCl_2$ vials with long T1 times, the %-bias was up to 15 %. The standard spin echo T2 measurement of $NiCl_2$ generally overestimated compared to the NMR-reference measurement and the %-bias was up to 20 % (**Figure 1 C**). Finally, for T2, the standard spin echo measurement of the $MnCl_2$ array was within +/-10 % of the NMR-reference measurement except for two vials (**Figure 1 D**).

Using the abbreviated protocol, the T1 measurement for both the $NiCl_2$ and $MnCl_2$ arrays were within approximately +/-30 %-bias from the NMR-reference measurement (**Figure 2 AB**) except for two $NiCl_2$ measurements on one commercial system (**Figure S3**). The abbreviated protocol included B1 measurement for the calculation of T1. For three systems, the mean measured B1 (relative to a desired flip angle of 1.0) for the $MnCl_2$ array varied from 0.87-1.02, while for the

$NiCl_2$ array it was lower, varying from 0.67-0.84 (**Table S2**). For the Prototype 1 system, there was less difference in measured B1 between the $NiCl_2$ and $MnCl_2$ arrays. Also on Prototype 1, one B1 measurement was much greater than the other two repetitions, resulting in mean value across the $NiCl_2$ and $MnCl_2$ arrays of 1.22+/-0.26 and 1.24+/-0.21, respectively. For comparison, the next highest mean B1, across all systems and repetitions, was 1.02+/-0.17. The T2 results for both the $NiCl_2$ and $MnCl_2$ arrays were largely within +/-10 %-bias from the NMR-reference measurement (**Figure 2 CD**).

The abbreviated protocol T1 measurement repetitions had a wide range of coefficients of variations (**Figure 3 AB**). For the $NiCl_2$ array, in particular, the shorter T1 vials, the coefficient of variation was greater than 5 % and as large as 35 % (**Figure 3 A**). Prototype 1 had a high coefficient of variation, approximately 25 % across all measurements. Excluding Prototype 1, the coefficients of variation for T1 measurement of the $MnCl_2$ array was <5 % (**Figure 3 B**). The abbreviated protocol was repeatable for T2, with coefficients of variation of <5% across all $NiCl_2$ and $MnCl_2$ measurements in vials 3-11 (**Figure 3 CD**).

Finally, the temperature measurements of the phantom are reported in **Table 2**. The temperature is reported as the average and standard deviation of the pre- and post- scan session temperatures. Both measurements were not always recorded. For some systems and sessions, only the pre-session temperature was recorded. For one commercial system, the average temperature recorded by a temperature logger was reported, and the standard deviation is not available. For one measurement on a prototype system, the phantom temperature increased by approximately 4^{o}C from the pre- to post-measurement. For the remaining sessions, across all systems, the temperature change was approximately 1^{o}C or less during the measurement session.

In vivo measurements

Histograms of the measured T1, B1 and T2 values across all participants and systems are shown in **Figure 4**. The T1, B1 and T2 histograms include all brain tissues; these are not segmented for white or gray matter. The histograms from a single system and across all systems have similar shapes and overlapping ranges of values. Across the T1 histograms, the peak location is 496 ms +/- 34 ms. For all T2 histograms, the histogram peak is typically located at 95 ms (n=14), with some peaks at 85 ms (n=2) or 105 ms (n=4). Representative T1, B1, and T2 map slices of a representative participant from each system are shown in **Figure 5**. The

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mean B1 (relative to a desired flip angle of 1.0) measured in participants across all systems and participants was 0.96 +/- 0.10 (**Table S3**).

Comparison of prototype and commercial systems

There was no difference in the mean brain T1 and T2 relaxation times between the prototype and commercial systems (ANOVA, T1 p=0.254 and T2 p=0.533). There were no significant differences between the prototype and commercial systems across all phantom measurements using the abbreviated protocol (**Table 3**).

DISCUSSION

The purpose of this study was to assess the accuracy and reproducibility of T1 and T2 measurements on different 0.55 T MRI scanners. Vendor-neutral Pulseq protocols were implemented and deployed across two commercial and two prototype 0.55 T systems; these protocols and reconstruction code are freely available. There were no statistically significant differences between abbreviated phantom T1 and T2 measurements on the commercial and prototype 0.55 T MRI systems. Additionally, the participant T1 and T2 measurements were not statistically different between the two types of systems. While there are differences in hardware and software between the commercial and prototype systems, it was possible to implement the same protocols and conduct quantitative measurements across the systems.

In this study, the phantom measurements served two purposes. First, the phantom was used to confirm correct implementation of the study protocol. The phantom was then used to characterize the performance of each system at the time of the participant measurements. The phantom measurements provided confidence in the T2 measurements and alerted the team to possible errors with the B1 measurement. Overall, there were no substantial differences in the phantom measurements across the systems, and thus no concerns about the system performance for participant measurements.

Temperature was measured for the phantom measurements on all systems; however, one limitation of this study is that the same temperature measurement protocol was not followed. Errors due to temperature variation are typically systematic across all measurements for that session, and this type of systematic error was not observed. The majority of reported

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temperature variations within a measurement session and across systems are sufficiently small that they are unlikely to impact the results.[28]

The multi-echo spin echo T2 measurement was highly repeatable on each system (across all vials and systems, the coefficient of variation ranged from 0.09% to 4.93% for measurements on the $NiCl_2$ array and from 0.08 % to 5.16 % for the $MnCl_2$ array). This is most likely due to the T2 analysis using StimFit,[12] which accounts for the stimulated echoes that can introduce error in the T2 measurement.

The abbreviated protocol T1 measurement used the VFA method, which requires a B1 correction using a B1 map. In the selection of our protocol, we considered several B1 mapping methods: double angle, saturated double angle, Bloch-Siegert, and AFI. Saturated double angle did not provide accurate results due to insufficient saturation. Double angle and AFI provided consistent results; however, double angle was an order of magnitude slower than AFI and not feasible for whole-brain imaging. Finally, we chose AFI over Bloch-Siegert since AFI is easy to implement and provides fast and accurate B1 maps.

The abbreviated protocol had no statistical difference between the T1 measurements on prototype and commercial systems. However, the measurement of B1 on the Prototype 1 system was approximately 20% high for one measurement session. We do not know the cause of the B1 measurement error; possible causes include an increase in scanner temperature during that scan session or a miscalibration of the RF transmit. As a result of the B1 measurement on Prototype 1, while the majority of T1 measurements across all systems ranged from -10% to 30% bias from the NMR-reference, there is a large coefficient of variation of T1 on this system (approximately 25%), and this measurement is an outlier with a -30% bias from the NMR-reference. Excluding the results from Prototype 1, the coefficient of variation results from the $MnCl_2$ array, 0.86 % to 4.10 %, are comparable to previous work.[3,4] The $NiCl_2$ array had greater variation, even when excluding the results from Prototype 1 and two outliers from Commercial 1 vial 11: the coefficient of variation ranged from 0.94 % to 12.64 %. This measured variability is comparable to other multi-site studies of T1 measurement via VFA.[10]

The variation in the $NiCl_2$ array is most likely due to the B1 variability at the location of the $NiCl_2$ array. When the phantom center is at isocenter of the system, the $NiCl_2$ array is located well above isocenter. For Prototype 2, Commercial 1 and Commercial 2, the phantom center was at

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isocenter, and the average B1 measured on the $NiCl_2$ array was 8 % to 34 % lower than average B1 measured on the $MnCl_2$ array. However, on the Prototype 1 system, the phantom was positioned with isocenter between the $NiCl_2$ and $MnCl_2$ arrays, and there was only a -1 % to -5 % difference between the average B1 measured on the $NiCl_2$ array compared to the $MnCl_2$ array across the three repeated measurements. The discrepancy in phantom position is a limitation of the study, and future studies should specify the position of the phantom center relative to isocenter.

The 35-minute abbreviated protocol was feasible for healthy participant imaging. One limitation of our in vivo study is the lack of tissue differentiation or regional analysis. For the purposes of this study, we chose to compare histograms across the entire brain, and found good similarity in mean value and distribution between systems. While the phantom measurements had substantial B1 variation, this was not the case with the participant measurements. B1 was measured for each participant at the time of the T1 VFA measurements, and mean B1 measured in participants across all systems and participants was 0.94-0.98, which is consistent with the tolerance of the system's specified transmit calibration. Other quantitative T1 measurement methods, such as Magnetic Resonance Fingerprinting,[29] are more robust to measurement errors and could be used in the future.[30,31]

We note two limitations specifically with the phantom measurements. First, the phantom did not fit in the head coil on the commercial systems. As a result, we could not use the same coil for the phantom and in vivo measurements. Second, we are unable to explain the B1 measurement error on Prototype 1. If we had recorded the pre-scan parameters, we may have observed a miscalibration on the RF transmit that would allow us to explain the measurement error.

CONCLUSION

Quantitative T1 and T2 measurements at 0.55 T in phantom (ISMRM/NIST phantom) and in vivo (healthy young adults) are not statistically different across systems when using the same vendor neutral pulse sequences, reconstruction, and analysis methods.

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DATA AVAILABILITY STATEMENT

The phantom data is available along with a representative in vivo data set: https://dx.doi.org/10.6084/m9.figshare.25892944. The Pulseq pulse sequences are available at https://github.com/usc-mrel/PulseqT1T2Mapping. The reconstruction and mapping code is available at https://github.com/usc-mrel/PulseqGadgetronRecon.

DISCLOSURES

NHLBI authors are investigators on a US Government Cooperative Research and Development Agreement (CRADA) with Siemens Healthcare. Siemens participated in the modification of the MRI systems from 1.5 T to 0.55 T.

Certain commercial equipment, instruments, software or materials are identified in this paper in order to specify the experimental procedure adequately. Such identification is not intended to imply recommendation or endorsement by NIST, nor is it intended to imply that the materials or equipment identified are necessarily the best available for the purpose.

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TABLES:

Table 1 Pulse sequence details

Table 1	Abbreviated			Standard spin echo		NMR-reference	
	T1-mapping	**B1-mapping**	**T2-mapping**	**T1-mapping**	**T2-mapping**	**T1-NMR**	**T2-NMR**
Sequence	3D VFA-GRE	3D AFI-GRE	MCSE	IRSE	SESE	Inversion Recovery	CPMG
FoV [mm^3]	256x256x80	256x256x80	256x256x1	256x256x8	256x256x8	-	-
Resolution [mm^3]	2x2x2	8x8x8	2x2x6	2x2x6	2x2x6	-	-
Flip Angles [^{o}]	5.4772, 9.6549, 17.019, 30.0	60	90, 180	180, 90, 180	90, 180	180,90	90, 180
TE/ES [ms]	4	4	32 steps, ranging from 15 - 480	15	32 steps, ranging from 15 - 480	-	20 steps ranging from 1-5000
TI [ms]	-	-	-	50, 100, 200, 400, 800, 1600, 4500	-	20 steps ranging from 6-6000	-
TR [ms]	23	32, 96	5000	5000	5000	10000	10000
Scan Time [h:m:s]	00:19:38	00:04:02	00:10:40	01:14:40	05:41:20	01:59:43	01:31:22
Tread [ms]	6.4	6.4	6.4	6.4	6.4	-	-

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Table 2 Phantom temperature at the time of MRI measurements

Temperature in °C reported at each system at the time of phantom measurements. Temperatures were measured of the phantom and/or of the ambient temperature in the scan room. The temperature is reported as the average and standard deviation of the pre- and post-scan session temperatures. Both measurements were not always recorded.

	Prototype 1		Prototype 2		Commercial 1		Commercial 2	
	Phantom	Ambient	Phantom	Ambient	Phantom	Ambient	Phantom	Ambient
1	22.25 (2.99)	23.84 (0.06)	19.44 (0.15)	19.35 (pre)	19.70 (pre)	18.28 (pre)		19.66 (NA)
2	24.37 (0.41)	24.05 (0.01)	18.67 (0.19)	18.17 (pre)	18.80 (0.11)	18.42 (0.10)		19.98 (NA)
3	20.13 (0.32)	21.79 (0.65)			19.13 (0.28)			20.68 (NA)

Table 3 ANOVA results (p-values) for comparing the T1 and T2 measured using the abbreviated protocols on the prototype and commercial systems

Vial	T1		T2	
	$NiCl_2$	$MnCl_2$	$NiCl_2$	$MnCl_2$
3	0.623	0.308	0.309	0.800
4	0.613	0.296	0.289	0.957
5	0.690	0.306	0.304	0.910
6	0.770	0.407	0.431	0.696
7	0.898	0.515	0.651	0.786
8	0.771	0.598	0.254	0.568
9	0.603	0.538	0.757	0.376
10	0.915	0.601	0.300	0.926
11	0.669	0.759	0.680	0.348

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FIGURE CAPTIONS:

Figure 1: Plots of the %-bias from the NMR-reference measurement for the T1 and T2 measurements via the 7-hour standard spin echo protocols (IRSE and SESE) in the $NiCl_2$ and $MnCl_2$ arrays of the ISMRM/NIST system phantom. The black solid line is 0 %-bias, and the dashed lines indicate +/- 10 %-bias. The majority of the measurements using the spin echo protocols are within +/- 10 %-bias from the NMR-reference measurement.

Figure 2: Plots of the %-bias from the NMR-reference measurement for the T1 and T2 measurements via the 35-minute abbreviated protocols (VFA and MCSE) in the $NiCl_2$ and $MnCl_2$ arrays of the ISMRM/NIST system phantom. These measurements were repeated three times on each system. The black solid line is 0 %-bias, and the dashed lines indicate +/- 10 %-bias. Two measurements from Commercial system 1, vial 11 are not shown here (they are shown in Figure S3); these measurements were greater than 100 %-bias. The abbreviated T1 measurement in the phantom has a large variability, while the abbreviated T2 measurements are mostly within +/- 10 %-bias.

Figure 3: Coefficient of variation for the repeated measurements of the abbreviated protocol of the T1 and T2 measurements of the $NiCl_2$ and $MnCl_2$ arrays at each of the four systems. The Prototype 1 system has a high coefficient of variation due to a high B1 map measurement on one of the three measurements, which affected the T1 measurement. The coefficient of variation for all T2 measurements across all systems is approximately 5 % or less.

Figure 4: Histograms of the in vivo measured T1 and T2 values across all twenty participants at all four systems (different participants are plotted in different colors for each system). The location of the histogram peak for each participant is given in the legend. For each measurement, the histograms across all systems have similar shapes and overlapping ranges of values. Please note, the T2 map was acquired on a single slice, whereas the T1 map was acquired over the entire volume. As a result, the T2 histogram is coarser than the T1 histogram.

Figure 5: Representative maps of T1 (left), B1 (center), and T2 (right) measured in vivo from a representative participant on each system. The resulting maps are comparable across the four systems.

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SUPPORTING INFORMATION CAPTIONS:

Figure S1:

Photos of the ISMRM/NIST system phantom prepared for imaging on a commercial 0.55 T system.

Figure S2:

Illustration of the T1 and T2 acquisition and reconstruction pipeline.

Figure S3:

Plot of the %-bias from the NMR-reference measurement for the T1 and T2 measurements via the 35-minute abbreviated protocols (VFA and MCSE) in the $NiCl_2$ and $MnCl_2$ arrays of the ISMRM/NIST system phantom. This plot shows the two outlier data points from Commercial system 1 on vial 11, which have greater than 100% deviation from the NMR value. These measurements were repeated three times on each system. The black solid line is 0 %-bias, and the dashed lines indicate +/- 10 %-bias.

Table S1 System phantom values at 0.55 T

NMR measured values for the T1 and T2 in ms of the $NiCl_2$ and $MnCl_2$ arrays of the ISMRM/NIST system phantom at 0.55 T. The reported value is the mean and standard deviation (in parentheses) at 20^{o}C.

Table S2 Phantom measured B1

Measured B1 (relative to a desired flip angle of 1.0) of the $NiCl_2$ and $MnCl_2$ arrays of the ISMRM/NIST system phantom at 0.55 T. The mean B1 value and standard deviation are reported over the phantom slices used for the VFA-GRE measurement. Measurements are reported for the three repeated measures of the abbreviated protocol.

Table S3 In vivo measured B1

Mean and standard deviation of the measured B1 value (relative to a desired flip angle of 1.0) in participants reported for each system. The participants are not the same across all systems.

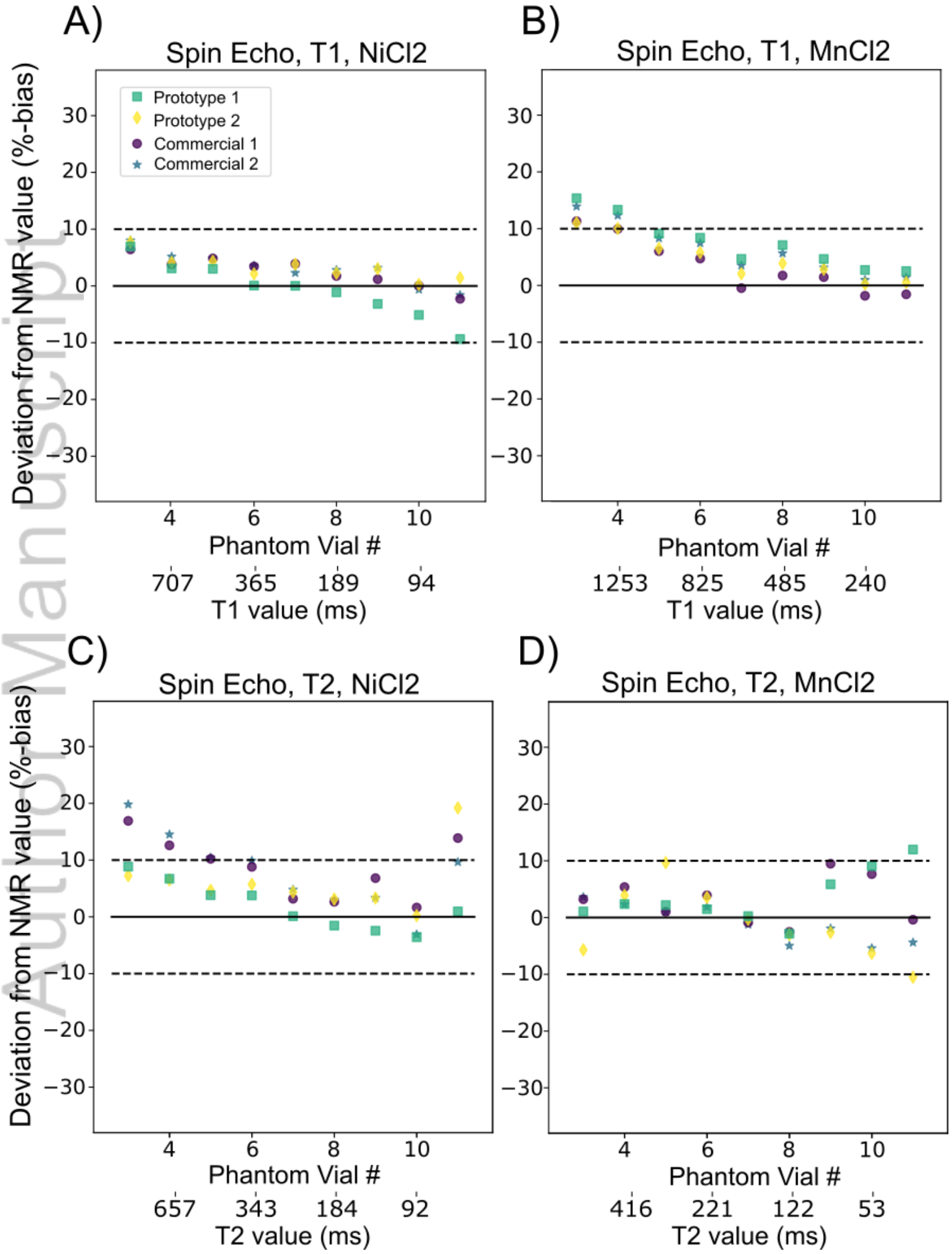


Figure1.png

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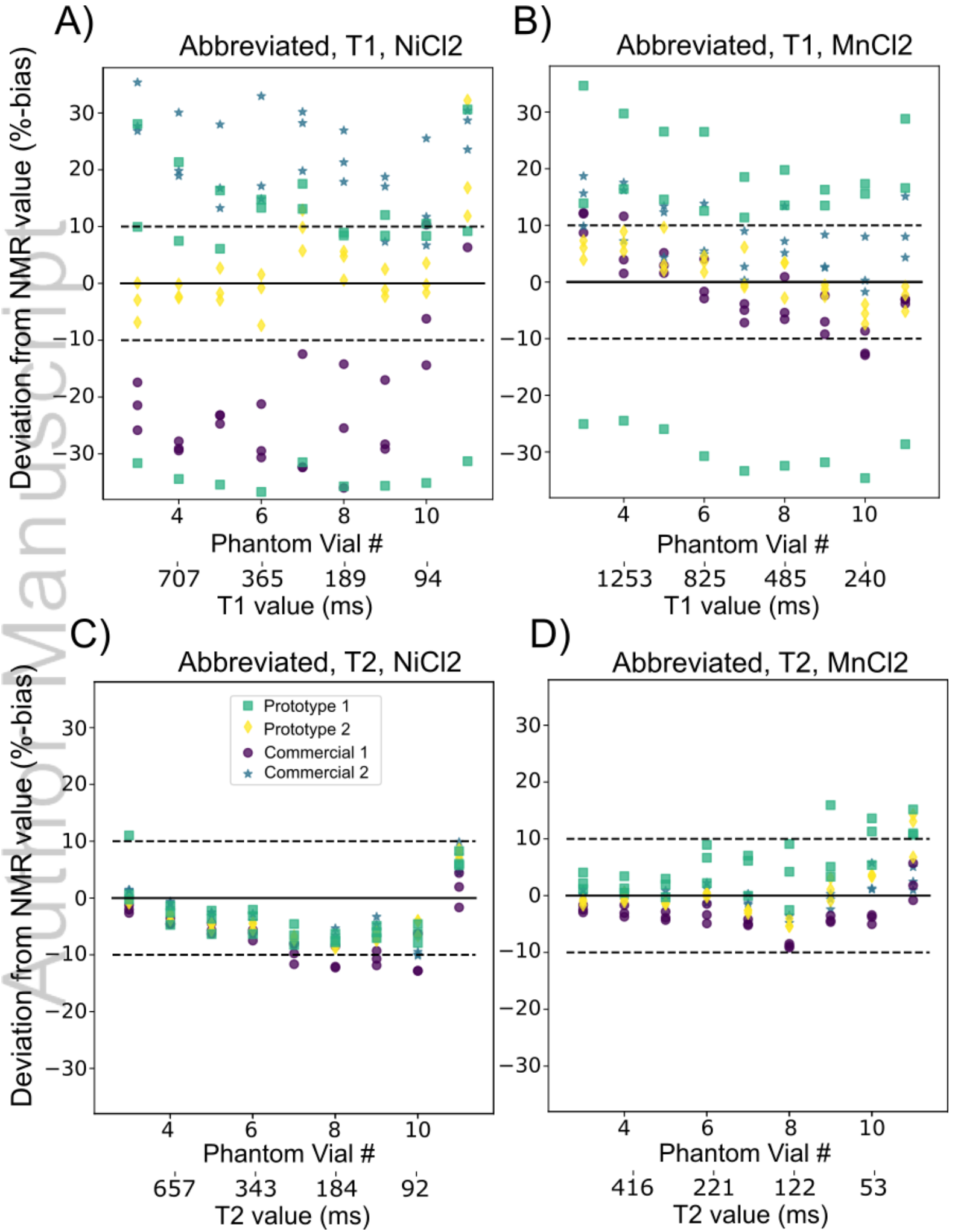


Figure2.png

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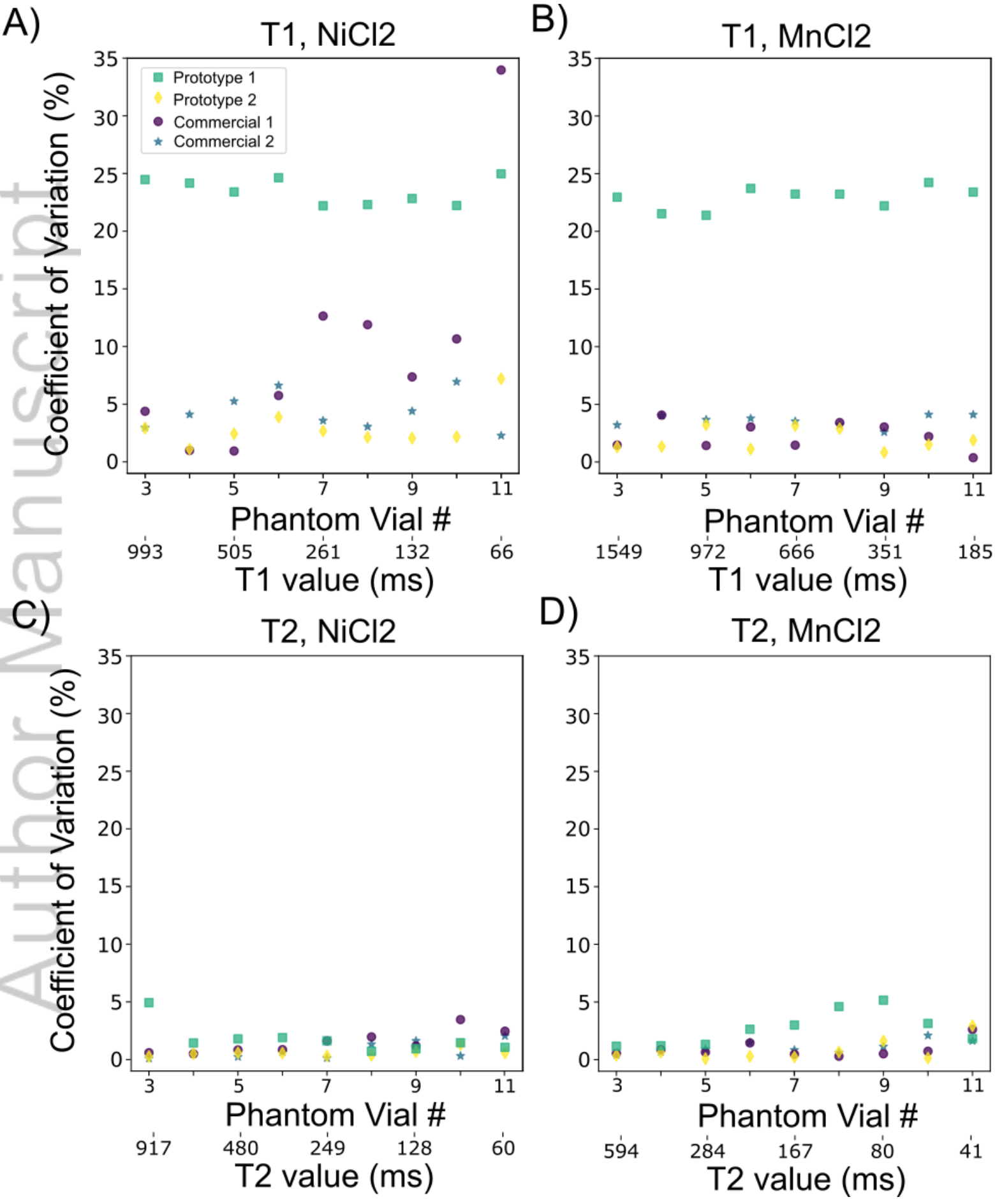


Figure3.png

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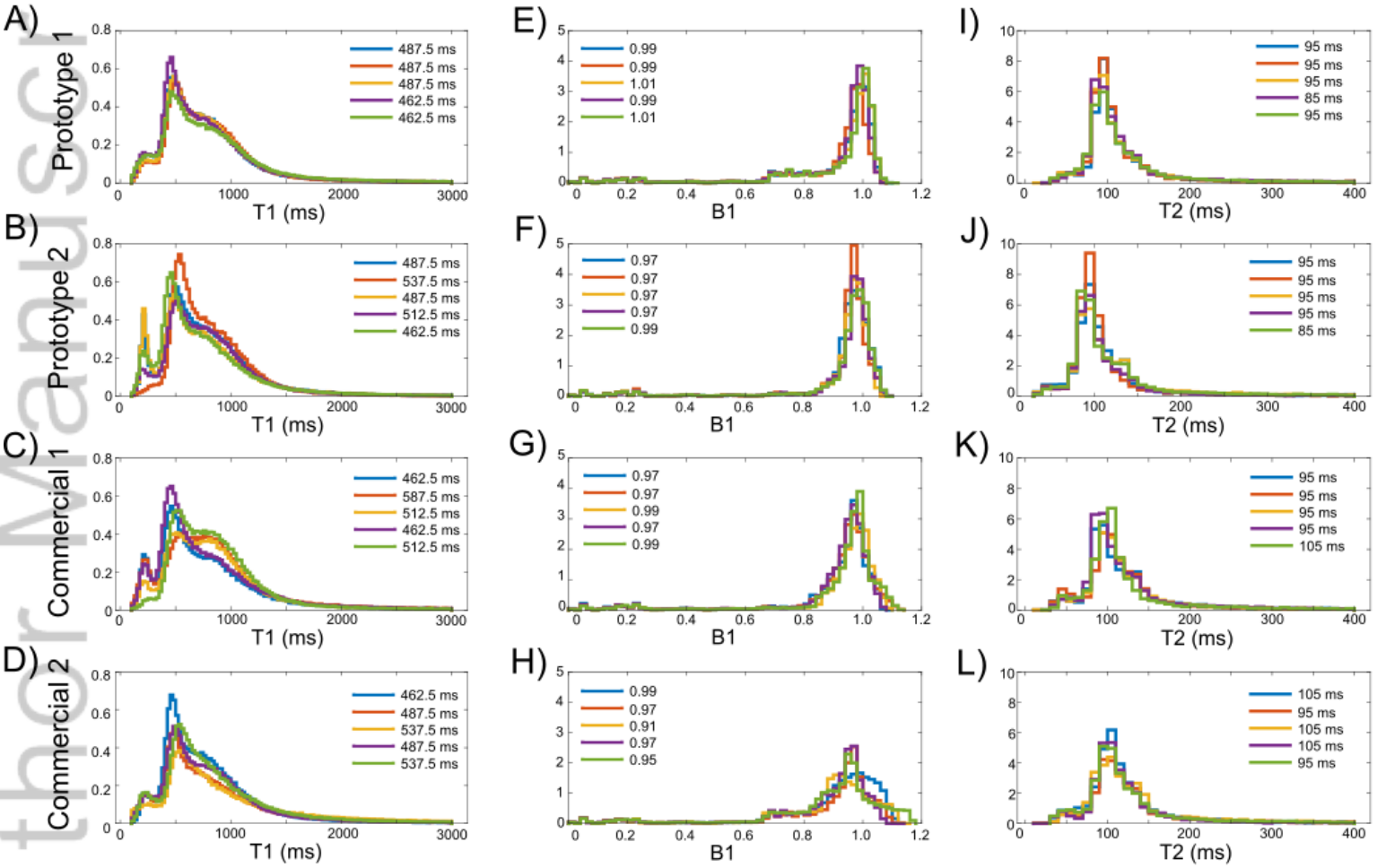


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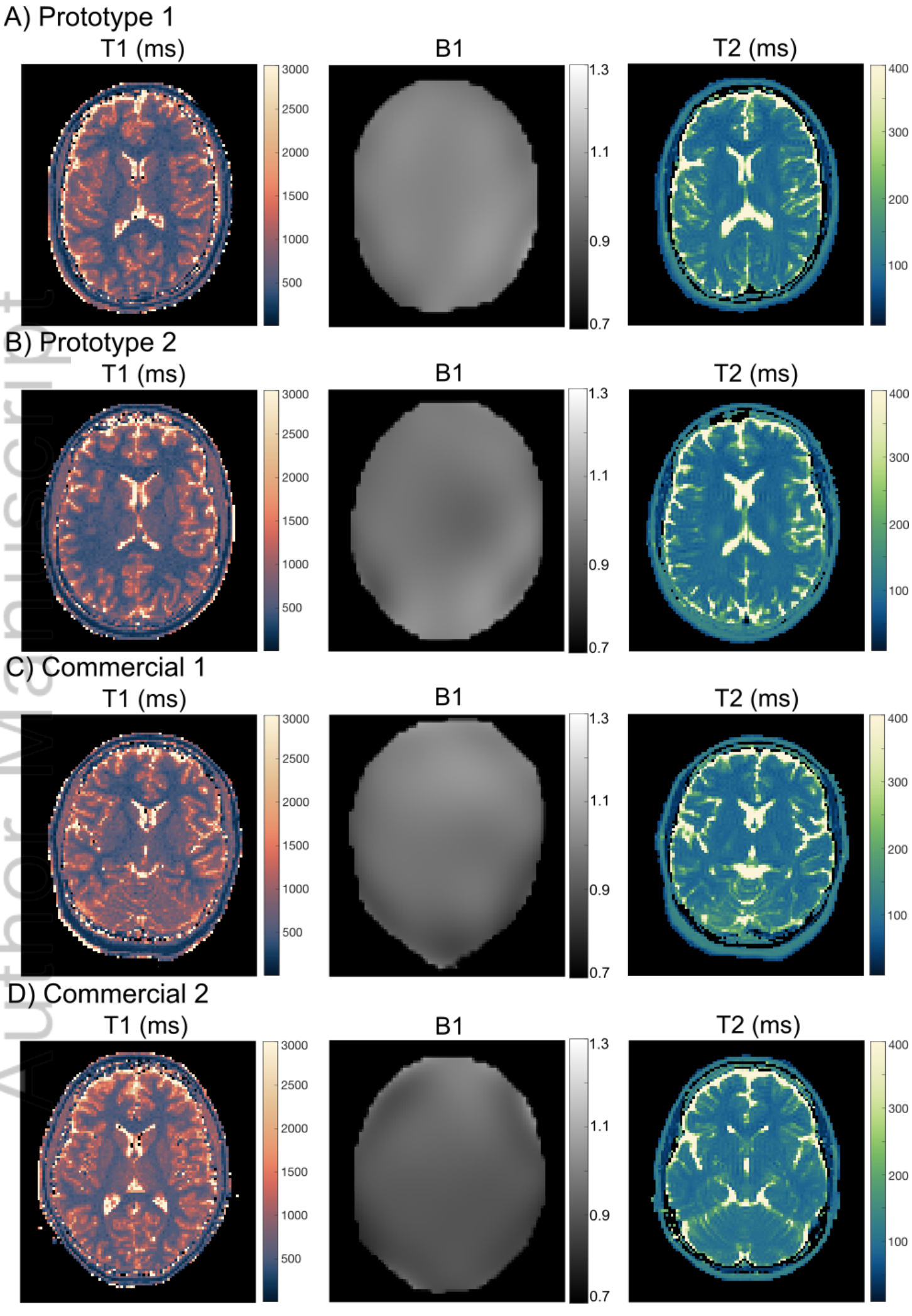


Figure5.png

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