

Accuracy, repeatability, and reproducibility of water-fat magnetic resonance imaging in a phantom and healthy volunteer

Supplementary Material

Supplementary Materials and Methods

Coils

The 16-element phased-array surface coil (dStream Torso coil, Philips Healthcare, The Netherlands) and the posterior body coil embedded in the table (dStream Total Spine coil, Philips Healthcare, The Netherlands) were used in the Philips systems. The posterior body coil embedded in the table (GE Healthcare, USA) was used in the GE systems. These coils were used for both the phantom and volunteer scans.

Delineation of regions-of-interest

Cylindrical regions-of-interest (ROI) with a radius of 8.5 mm and a height of 15 mm were placed in the center of each vial of the phantom PDFF map using a Python script. Each volunteer scan was inspected for artifacts. Box-shaped ROIs were manually placed in 22 vertebrae, from cervical vertebra 5 to sacral vertebra 2. ROIs did not include the bone cortex and, if present, physiological or pathological deviations. Additionally, circle-shaped ROIs were placed in the psoas major muscle and the subcutaneous adipose tissue, both at the level of the fourth lumbar vertebra. The delineations of the volunteer scans were individually performed by two blinded investigators (P.v.G. and A.C.). P.v.G. delineated the vertebral BM on all volunteer scans. A.C. delineated the test scans twice on different days. These measurements by A.C. were used to determine the intra- and interreader variation. A.C. placed the ROIs in the muscle and adipose tissue.

Repeatability coefficient

The repeatability coefficient (RC) per protocol was defined, according to the QIBA consensus guidelines, as:

$$RC = 2.77 * wSD \quad (1)$$

where wSD is the within-subject deviation, which is the square root of the variance of the 22 vertebrae and the 12 vials. The RC represents the least significant difference between two repeated measurements taken under identical conditions and has the same unit as the absolute PDFF [PDFF%].

Lin's concordance correlation coefficient

Reproducibility across all protocols was evaluated using Lin's concordance correlation coefficient (CCC) calculated with the following equation:

$$CCC = \frac{2\rho\sigma_1\sigma_2}{\sigma_1^2 + \sigma_2^2 + (\mu_1 - \mu_2)^2} \quad (2)$$

where μ_1 and μ_2 are the means for the two methods, σ_1^2 and σ_2^2 are the corresponding variances and ρ is the correlation coefficient between the two variables. The epiR package in R was used for this equation.

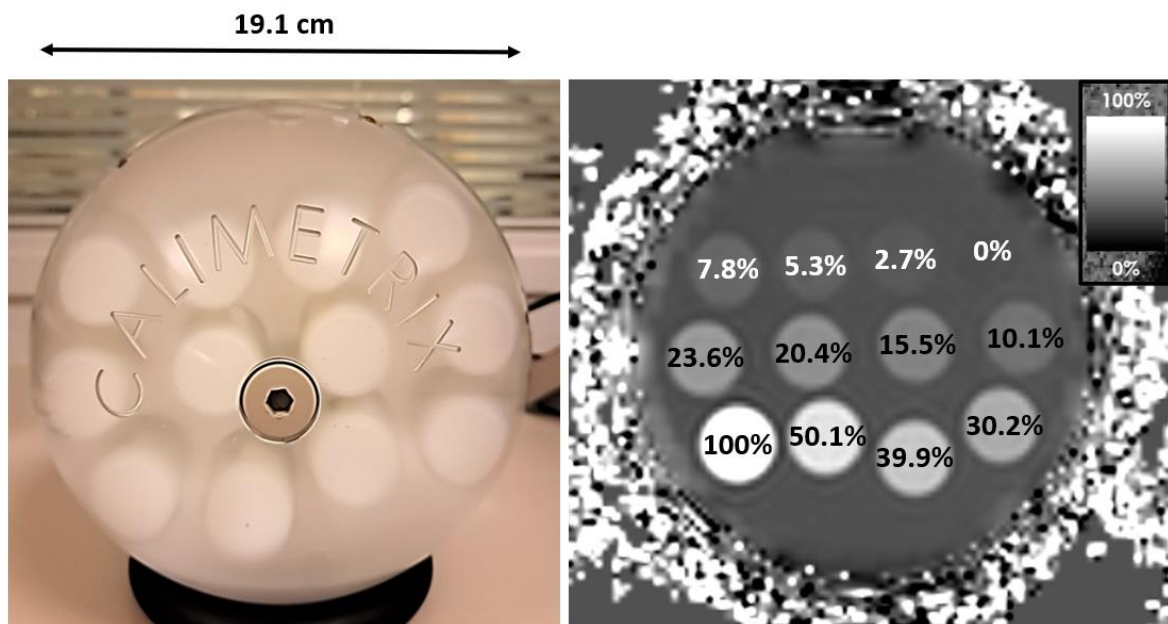


Figure S1: Photograph and PDFF map of the Calimetrix phantom. The PDFF values per vial are indicated in %. *PDFF = proton density fat fraction*

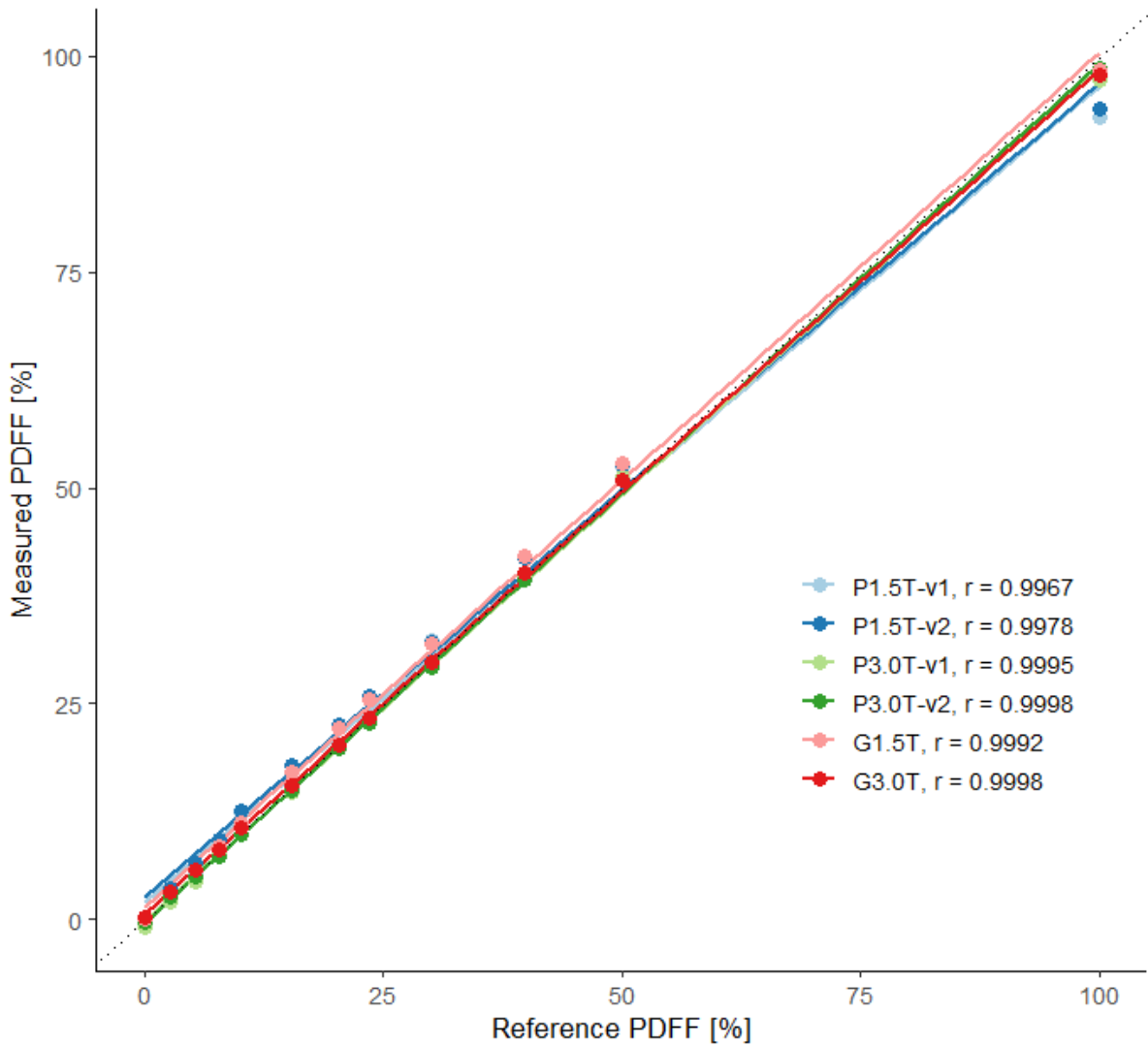


Figure S2: Proton density fat fraction (PDFF) [%] measurements of the phantom per protocol with the corresponding reference PDFF [%], fitted linear regression line, and Pearson correlation coefficient (r). The dotted regression line indicates a perfect correspondence between the measured and reference PDFF. *P1.5T = Philips 1.5 T, P3.0T = Philips 3 T, G1.5T = General Electric 1.5 T, G3.0T = General Electric 3 T, v1 = version 1, v2 = version 2*

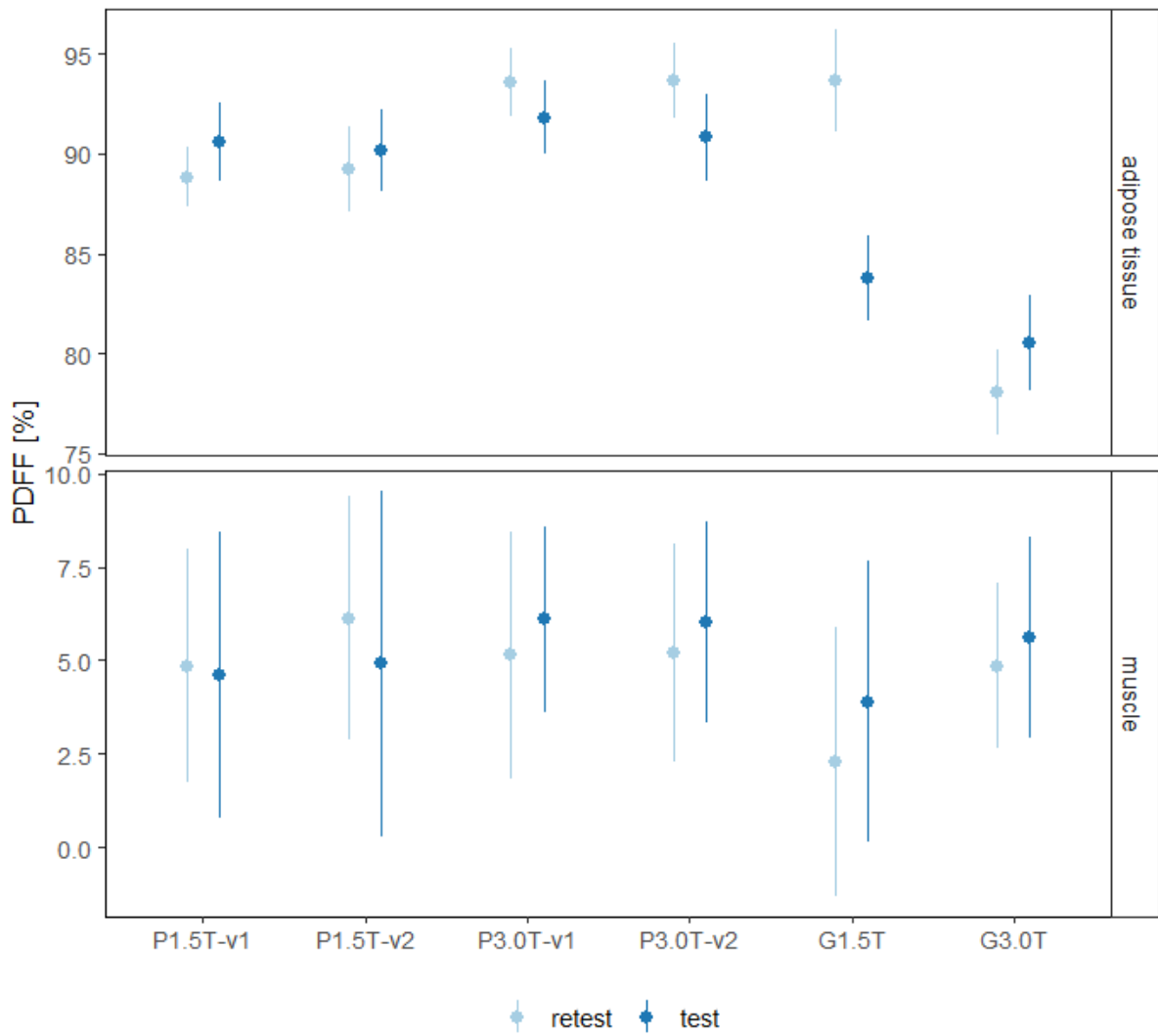


Figure S3: Proton density fat fraction (PDFF) [%] measurements of the subcutaneous adipose tissue and psoas major muscle in the volunteer per protocol. The mean PDFF and corresponding standard deviation per region-of-interest are visualized for the repeated measurements. *P1.5T = Philips 1.5 T*, *P3.0T = Philips 3 T*, *G1.5T = General Electric 1.5 T*, *G3.0T = General Electric 3 T*, *v1 = version 1*, *v2 = version 2*

Table S1: Water-fat sequence parameter settings for each water-fat MR imaging protocol

Parameter	P1.5T-v1	P1.5T-v2	P3.0T-v1	P3.0T -v2	G1.5T	G3.0T
System	Philips Ingenia	Philips Ingenia	Philips Ingenia	Philips Ingenia	GE Optima MR450w	GE Signa Premier
Field strength [T]	1.5	1.5	3.0	3.0	1.5	3.0
Scanner software version	5.6.1.3	5.6.1.3	5.6.1.3	5.6.1.3	DV26.0_R 03	RX29.1_R 02
Imaging technique	mDixon Quant	mDixon Quant	mDixon Quant	mDixon Quant	IDEAL IQ	IDEAL IQ
Pulse sequence	3D GRE	3D GRE	3D GRE	3D GRE	3D GRE	3D GRE
Breath-hold	Yes	No	Yes	No	No	No
Acceleration	SENSE (2.0 x 1.0)	None	SENSE (2.0 x 1.0)	None	ARC (1.0 x 2.0)	ARC (1.0 x 2.0)
Number of echoes	6	6	6	6	6	6
TR [ms]	5.3	6.1	5.7	6.3	9.0	6.3
First TE [ms]	0.9	1.0	1.0	1.1	1.1	0.8
Δ TE [ms]	0.7	0.7	0.7	0.8	1.2	0.8
Flip angle [degrees]	5	5	3	3	6	3
Phase encoding direction	AP	LR	AP	LR	LR	LR
Frequency encoding direction	LR	AP	LR	AP	AP	AP
Acquisition matrix [M x P]	132 x 118	132 x 117	160 x 140	160 x 140	120 x 80	120 x 80
Number of slices per stack	85	170	77	154	120	120
Acquisition resolution [§] [mm]	3.0 x 3.0 x 6.0	2.5 x 2.5 x 3.0	2.5 x 2.5 x 6.0	2.5 x 2.5 x 3.0	2.0 x 3.0 x 2.0	2.0 x 3.0 x 2.0

Reconstruction resolution [§] [mm]	2.1 x 2.1 x 3.0	2.1 x 2.1 x 1.5	2.1 x 2.1 x 3.0	2.1 x 2.1 x 1.5	0.9 x 0.9 x 2.0	0.9 x 0.9 x 2.0
Scan duration per stack [min:sec]	0:31	01:00	00:16	01:08	2:10	1:15
Number of stacks	3	3	3	3	4	4

[§] = frequency x phase x slice. *PLF* = Philips Low Field protocol, *PHF* = Philips High Field protocol, *GLF* = GE Low Field protocol, *GHF* = GE High Field protocol, *v1* = version 1, *v2* = version 2, *3D* = three-dimensional, *GRE* = gradient recalled echo, *SENSE* = sensitivity encoding, *TE* = echo time, *AP* = anterior-posterior, *LR* = left-right, *CC* = cranial-caudal

Table S2: Paired t-tests comparing the PDFF for the test and retest volunteer scans per vertebra or reference region for the six scan protocols.

ROI	Degrees of freedom	Mean difference [PDFF%]	95% confidence interval of the difference [PDFF%]		p-value
			Lower limit	Upper limit	
C5	5	-1.10	-3.34	1.14	0.26
C6	5	1.07	-1.46	3.59	0.33
C7	5	0.55	-2.84	3.93	0.70
T1	5	0.94	-2.46	4.35	0.51
T2	5	0.77	-1.73	3.26	0.47
T3	5	0.56	-1.35	2.47	0.49
T4	5	-1.65	-3.62	0.32	0.08
T5	5	-0.62	-2.22	0.97	0.36
T6	5	-2.67	-5.74	0.40	0.08
T7	5	-1.13	-2.52	0.25	0.09
T8	5	-0.99	-3.92	1.95	0.43
T9	5	-1.12	-3.76	1.53	0.33
T10	5	-0.96	-2.22	0.31	0.11
T11	5	1.92	-0.12	3.95	0.06
T12	5	1.05	-5.05	7.14	0.68
L1	5	-2.07	-7.47	3.33	0.37
L2	5	-0.11	-2.50	2.28	0.91
L3	5	1.51	-1.89	4.92	0.31
L4	5	1.36	-0.66	3.39	0.14
L5	5	0.52	-2.29	3.34	0.65
S1	5	2.49	0.45	4.53	0.03*
S2	5	-1.04	-5.00	2.91	0.53
adipose tissue	5	1.55	-3.28	6.38	0.45
muscle	5	-0.45	-1.50	0.61	0.33

* = $p < 0.05$. ROI = region-of-interest, PDFF = proton density fat fraction