

Appendix

Table 1. Summary of imaging parameters used across protocols.

<i>Image Acquisition Parameters</i>	Whole-Body		Abdomen-Pelvis	
Acquisition Type	Echo-planar imaging		Echo-planar imaging	
Columns	134 (Interpolated to 268)		160 (Interpolated to 320)	
Rows	108 (Interpolated to 216)		108 (Interpolated to 216)	
Pixel Spacing (mm²)	3.2x 3.2 (1.6 x 1.6)		1.375x 2.375 (1.188 x 1.188)	
Slice Thickness (mm)	5		5	
Slices per Station	40		34	
Pixel Bandwidth (Hz/px)	1964		1954	
Echo Time/Repetition Time(ms)	73/6270		73/6400	
Inversion Times (ms)	180		-	
Parallel Imaging	GRAPPA (R = 2)		GRAPPA (R = 2)	
(Reference scan mode)	GRE/separate		EPI/separate (32 ref. lines)	
Fat Suppression	STIR		SPAIR	
Diffusion Scheme	Bipolar / MDDW		Bipolar / MDDW	
b-values (s/mm²)	50(N=2),600(N=2),900(N=3)		100 (N = 1), 600 (N = 1), 1050 (N = 1)	
b-value directions	0.0, -0.7, 0.7	0.7, -0.7, 0.0	0.4, -0.4, 0.9	0.4, 0.4, 0.9
			0.4, -0.9, 0.4	0.9, 0.4, -0.4
	0.7, 0.0, -0.7	0.0, -0.7, - 0.7	0.4, 0.4, -0.9	0.4, -0.9, - 0.4
			0.4, 0.9, 0.4	0.9, 0.4, 0.4
	-0.7, 0.0, -0.7	-0.7, -0.7, 0.0	0.4, -0.4, - 0.9	0.4, 0.9, -0.4
			0.9, -0.4, 0.4	0.9, -0.4, - 0.4

Table 2. Details of differences between training parameters for *DNIF*, *whole-body* and *abdomen-pelvis* versions of the *Enhanced-quickDWI* models.

<u>Training Parameters</u>	<i>DNIF</i> (Whole-Body + Abdomen-Pelvis)	<i>Enhanced-quick-DWI</i> (Whole-Body)	<i>Enhanced-quick-DWI</i> (Abdomen-Pelvis)
Input Channels	1 (1 slice, 1 b-value)	9 (3 slices, 3 b-values)	9 (3 slices, 3 b-values)
Output Channels	1 (1 slice, 1 b-value)	3 (1 slice, 3 b-values)	3 (1 slice, 3 b-values)
Data pre-processing	Image standardisation	Log-transform + image standardisation	Log-transform + image standardisation
Input image shape	320 columns/224 rows	272 columns/224 rows	320 columns/224 rows
Number of training patients	42 (Whole-Body)	42	42
	42 (Abdomen-Pelvis)		
Number of training slices	25066 (low b-value)	16480	5469
	25066 (mid b-value)		
	25066 (high b-value)		
Number of validation patients	8 (Whole-Body)	8	8
	8 (Abdomen-Pelvis)		
Number of validation slices	2356 (low b-value)	2960	1122
	2356 (mid b-value)		
	2356 (high b-value)		
Learning rate	10^{-4}	10^{-4}	10^{-4}
Optimizer	Adam	Adam	Adam
Batch size	20	30	30
Epochs	40	200	30 (weights initialised using trained whole-body model)