

1 **A quantitative multi-parameter mapping protocol standardized for clinical research in**  
2 **autoimmune neuroinflammatory diseases with white matter abnormalities**

3 **Keywords: quantitative MRI, multi-parameter mapping, neuroimaging, multiple sclerosis,**  
4 **aging, proton density**

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39

## 40 **Abstract**

41 Quantitative magnetic resonance imaging (qMRI) involves mapping microstructure in standardized  
42 units sensitive to histological properties and supplements conventional MRI, which relies on contrast  
43 weighted images where intensities have no biophysical meaning. While measuring tissue properties  
44 such as myelin, iron or water content is desired in a disease context, qMRI changes may typically  
45 reflect mixed influences from aging or pre-clinical degeneration. We used a fast multi-parameter  
46 mapping (MPM) protocol for clinical routine at 3T to reconstruct whole-brain quantitative maps of  
47 magnetization transfer saturation (MT), proton density (PD), longitudinal (R1), and transverse  
48 relaxation rate (R2\*) with 1.6 mm isotropic resolution. We report reference MPM values from a  
49 healthy population with age and gender distributions typical of neuroimmunology studies in whole  
50 brain white matter (WM), T2-weighted WM hyperintensities, cortical grey matter and deep grey  
51 matter regions and present post-processing optimizations including integration of lesions and  
52 normalization of PD maps against cerebrospinal fluid (CSF) for standardized research in multiple  
53 sclerosis (MS) and related disorders. PD maps were affected by WM abnormalities in MS using WM  
54 calibration. The results acknowledge the impact of non-linear age effects on MPM and suggest using

55 CSF calibration for future clinical application in autoimmune neuroinflammatory diseases with WM  
56 abnormalities.

## 57 **1 Introduction**

58 Quantitative magnetic resonance imaging involves mapping microstructure in standardized physical  
59 units containing information about the local tissue environment surrounding the protons, thereby  
60 enhancing comparability in time and space. Quantitative maps supplement conventional MRI, which  
61 relies on contrast weighted images where intensities have no biophysical meaning, in providing  
62 insight into biologically meaningful microstructural properties of the central nervous system at the  
63 mesoscopic scale<sup>1,2</sup>. Research in quantitative relaxometry and magnetization transfer imaging has  
64 shown strong reproducibility and sensitivity, exhibiting a robust correlation with histological  
65 measurements and accepted metrics related to water<sup>3</sup>, myelin<sup>4</sup>, and iron content<sup>5</sup>.

66 Standardized scanning protocols at 3T and tools to reconstruct parametric maps demonstrating multi-  
67 center reproducibility are readily available<sup>6,7</sup> such as the time-efficient multi-parameter mapping  
68 (MPM) protocol<sup>6</sup> consisting of 3D multi-echo fast low angle shot (FLASH) acquisitions. It allows  
69 for estimation of quantitative maps of proton density (PD), magnetization transfer saturation (MT),  
70 longitudinal relaxation rate ( $R1=1/T1$ ), and effective transverse relaxation rate ( $R2^*=1/T2^*$ )  
71 facilitated by the open-source ‘hMRI toolbox’<sup>8</sup>, which includes spatial processing tailored for voxel-  
72 wise statistical analysis of quantitative cerebral MRI data.

73 Several studies have collected quantitative relaxometry, MT and PD maps of healthy brain tissue  
74 using the MPM protocol to obtain normative reference values<sup>7,9</sup>. These studies highlighted the  
75 influence of normal aging on brain microstructure in previous quantitative MRI studies<sup>10,11</sup>.

76 This study aimed to optimize the post-processing of a previously described MPM protocol based on  
77 standard manufacturer sequences with 1.6 mm isotropic voxel resolution<sup>12</sup> for disease-related  
78 research, i.e. autoimmune neuroinflammatory diseases with white matter lesions such as multiple  
79 sclerosis (MS) or neuromyelitis optica spectrum disorder (NMOSD). MS and NMOSD are immune-  
80 mediated inflammatory diseases of the central nervous system with overlapping clinical  
81 characteristics shown to predominantly affect women, given a markedly high female to male ratio in  
82 MS<sup>13</sup> and NMOSD<sup>14</sup>. In a large healthy cohort with a gender distribution typical of  
83 neuroimmunology studies, we established reference values of MT, R1, PD and R2\* in white matter  
84 (WM), T2-weighted (T2w) WM hyperintensities, cortical grey matter (CGM) and deep gray matter  
85 (DGM) regions. We compared WM and T2w WM hyperintensities values across MS patients and  
86 healthy controls. We standardized PD maps using reference values for water in cerebrospinal fluid  
87 (CSF) of the lateral ventricles<sup>15</sup> and compared them to maps scaled to 69% in WM to highlight the  
88 impact of focal and diffuse white matter damage between MS patients and healthy controls. We  
89 further evaluated MPM-derived parameters and their associations with age and sex to inform future  
90 studies that may require strategies to correct for confounding effects of these factors when using  
91 MPM in clinical research.

92

## 93 **2 Materials and Methods**

### 94 **2.1 Subjects**

#### 95 **2.1.1 Informed Consent**

96 The analysis was performed as part of the BERLimmun<sup>16</sup> (EA1/362/20, DRKS00026761), ViMS<sup>17</sup>  
97 (EA1/182/10) and CAMINO<sup>18</sup> (EA2/007/21) neuroimmunology studies, approved by the  
98 institutional ethics committee of our institution and conducted in accordance with the Declaration of  
99 Helsinki in its applicable version for the conduction of the study. All participants gave written  
100 informed consent.

#### 101 **2.1.2 Study Population**

102 Demographics are summarized in Table 1. From April 2015 to September 2022, we pooled healthy  
103 participants recruited from the 3 previous separate registries. For the control group, participants  
104 without history of neurological or psychiatric disorders (and without previous COVID-19 infection  
105 for the CAMINO cohort) were recruited in Germany. Additional inclusion criteria were the  
106 following: self-declared healthy, older than 18 years of age, an active health insurance, competent to  
107 give written informed consent. Exclusion criteria consisted of contraindication to MRI investigation  
108 at inclusion, pregnancy, disease hindering the conduct of the study or inability to cooperate. Initially,  
109 we collected scans from 78 healthy participants. We excluded one participant from analyses because

110 scans were of poor image quality. In total 77 healthy controls, 60 (77.9%) women and 17 (22.1%)  
111 men, with age ranging from 20 to 75 years, with a mean [ $\pm$ standard deviation (SD)] of  $42.1 \pm 14.1$   
112 years, were included (14 from BERLimmun, 14 from ViMS, 49 from CAMINO). Additionally, 27  
113 patients diagnosed with MS (18 women (67%), mean age  $50 \pm 9.9$  years) were included from the  
114 ViMS study according to the revised McDonald diagnosis criteria <sup>19</sup>.

## 115 **2.2 MRI**

### 116 **2.2.1 Acquisition**

117 MRI scans were acquired on a single 3T MR scanner (Magnetom Prisma, Siemens Healthineers,  
118 Erlangen, Germany) using a 64-channel receive radiofrequency (RF) head-neck coil covering brain  
119 and cervical spinal cord. To maintain reproducibility across participants and time points, the  
120 acquisition protocol, and participant positioning remained identical to that detailed in a prior study,  
121 aside from updating the head coil <sup>12</sup>. Briefly, the MPM sequence is 7 minutes in length, 1.6 mm  
122 isotropic resolution with three distinct 3D multi-echo fast low-angle shot (FLASH) gradient-echo  
123 acquisitions. For post-acquisition bias-field correction, a radiofrequency (RF) transmit (B1+) map  
124 was acquired during each session with an isotropic resolution of 4 mm from spin-echo/stimulated  
125 echo acquisitions utilizing a standard vendor sequence <sup>7</sup>. MT-weighting was achieved by applying an  
126 off-resonance Gaussian pulse (500°, 10 ms, 1,200 Hz off-resonance, 192 Hz bandwidth) prior to non-  
127 selective excitation. In addition, the BERLimmun scan protocol included a structural T1-weighted

128 (T1w) scan (3D MPRAGE, TR=1,900 ms, TE=2.55 ms, TI=900 ms, 0.8 mm isotropic resolution) and  
129 T2w fluid-attenuated inversion recovery (3D FLAIR, TR=6,000 ms, TE=388 ms, TI=2,100 ms, 0.8  
130 mm isotropic resolution). The CAMINO scan protocol included a 3D-MPRAGE (1 mm isotropic  
131 resolution, TR=1900 ms, TE=2.22 ms, TI=2100 ms).

## 132 **2.2.2 Quantitative map reconstruction**

133 We generated quantitative PD, MT, R1, and R2\* maps utilizing MATLAB (MathWorks) with the  
134 hMRI toolbox<sup>8</sup> implemented within SPM12 (<http://www.fil.ion.ucl.ac.uk/spm/software/spm12/>).  
135 These maps were reconstructed given the PD-weighted (PDw), MT-weighted (MTw), and T1w  
136 echoes acquired through FLASH acquisitions and corrected for transmit and receive field  
137 inhomogeneities<sup>20</sup>. Correction of Gibbs ringing artifacts<sup>21</sup> was performed prior to reconstruction of  
138 the quantitative maps, consisting in the removal of oscillatory patterns situated around tissue borders  
139 from all six echoes of the raw images (PDw, MTw, T1w). Motion degradation index for each of the  
140 raw averaged echo images (PDw, MTw, T1w) were obtained from the toolbox to identify scans with  
141 motion artifacts<sup>22</sup>. Correlation of motion degradation index with age was assessed to evaluate the  
142 impact of motion on R2\* variability with age (Sup. Fig. S1). Finally, given the use of an off-  
143 saturation MT pulse with a flip angle of 500°, we linearly rescaled MT maps to harmonize values for  
144 comparison to literature values obtained with a 220° flip angle, as recent evidence showed that a  
145 linear rescaling to harmonize MT maps across manufacturers effectively reduced the inter-site bias<sup>7</sup>.



### 146 **2.2.3 Post-processing**

147 T1-MPRAGE and T2-FLAIR images underwent bias-field correction using non-parametric non-  
148 uniform intensity normalization<sup>23</sup> and were subsequently reoriented to the Montreal Neurological  
149 Institute (MNI) standard reference space for further lesion delineation using FSL FLIRT  
150 (<http://www.fmrib.ox.ac.uk/fsl>).

### 151 **2.2.4 Segmentation**

152 Two expert MRI technicians (15-17 years of experience) performed manual segmentation using ITK-  
153 SNAP (available at [www.itksnap.org](http://www.itksnap.org)) of T2w hyperintense brain lesions on FLAIR images linearly  
154 co-registered to MPRAGE images<sup>24</sup>. We subsequently refer to our segmentations as WM lesions  
155 (WML), rather than the general T2w-hyperintensities. We only included lesion masks with a WML  
156 mean volume above a pragmatic cutoff of 0.20 mL, corresponding to a Fazekas visual rating score of  
157 1<sup>25,26</sup>. Generation of a brain mask and tissue segmentation of T1-MPRAGE images to obtain WM,  
158 CGM and DGM masks were achieved via FastSurfer<sup>27</sup>. Lesion-filled WM masks were obtained by  
159 subtracting lesions from WM masks. Additionally, for each mask, voxels with T1 values higher than  
160 4s within the tissue masks were removed for further correction of partial volume effect<sup>28</sup>. All masks  
161 and structural images were then linearly co-registered via FSL FLIRT to native space using the T1w  
162 image as reference. Median parameter values were extracted from WM, CGM and several atlas-  
163 defined deep grey matter structures (thalamus, caudate nucleus, putamen, globus pallidus,

164 hippocampus, amygdala, and nucleus accumbens) for each participant with both hemispheres  
165 summed.

### 166 **2.2.5 PD calibration**

167 The PD map output from the hMRI toolbox was corrected for  $R2^*$  by extrapolating the signal at  
168  $TE=0ms$  and was originally calibrated as 69% water content in the WM<sup>8</sup>. To demonstrate bias  
169 resulting from WM abnormalities in MS patients, PD maps calibrated using a whole WM mask and a  
170 lesion-filled WM mask were compared respectively in the whole WM region (including WML) and  
171 the normal appearing WM region free of WML (NAWM).

172 Subsequently, reconstructed PD maps from the hMRI toolbox were recalibrated as pure water (100 %  
173 reference) based on the median CSF signal in the lateral ventricles<sup>28</sup>, using a mask from the Harvard  
174 Oxford template distributed with FSL (Functional MRI of the Brain Software Library,  
175 <http://www.fmrib.ox.ac.uk/fsl/>) warped into subject native space. To reduce partial volume effects,  
176 lateral ventricles masks were eroded by 1 voxel then corrected by multiplying them with a CSF tissue  
177 mask obtained from the respective tissue probability map (threshold of 0.9). Finally, we excluded  
178 voxels with T1 values lower than 4s to obtain only voxels with pure water in CSF, based on the  
179 quantitative R1 map output from the reconstruction toolbox. To account for a potential bias  
180 introduced by CSF volume or T1 variability in CSF, we compared our method to a calibration  
181 selecting only the 100 voxels with the shortest T1 times above the 4s cutoff, therefore obtaining a

182 mask with the same volume across participants over voxels with a small range of T1 above 4s. We  
183 calculated coefficients of variation (CoV) of the scaling factor, which is the multiplication factor  
184 obtained to scale each individual PD map by dividing 100 % by its respective median in CSF.

## 185 **2.3 Statistical Analyses**

### 186 **2.3.1.1 Descriptive statistics**

187 Histogram analysis of brain tissues was first done to assess distribution of the entire dataset in WM,  
188 WML, CGM and DGM (Sup. Fig. S2). To get a better representation of a healthy population cross-  
189 sectional data for each brain region of interest (ROI), all subsequent analyses were performed on data  
190 free from respective outliers outside the ROI-specific 2<sup>nd</sup>-98<sup>th</sup> percentile. Statistical analysis was  
191 conducted in R (R Core Team, <https://www.r-project.org>). Normality of data distribution was tested  
192 using a Shapiro-Wilk test. Median MPM metrics in each brain ROI were used for statistical analysis.  
193 Structural volume of the considered ROI was normalized by intracranial volume to obtain an adjusted  
194 volume and account for intracranial volume differences between men and women. Differences  
195 between WM and WML across MS patients and healthy controls were assessed using ANOVA and  
196 linear regression models adjusted for age and sex followed by post-hoc Tukey tests.

### 197 **2.3.1.2 Sex differences**

198 Interaction between sex and age was tested before excluding the former variable as a possible  
199 covariate for MPM-derived parameters. Analysis of sex on median MPM parameter showed no

200 difference between men and women, including normalized structure volume as an additional  
201 covariate in the linear regression model. Therefore, all regression models were fitted non-stratified,  
202 i.e. by combining data from both men and women.

### 203 **2.3.1.3 MPM age effects**

204 For the assessment of the relationship between MPM-derived parameters and age, MS subjects were  
205 excluded. Linear and non-linear relationships between each MPM parameter and age were tested for  
206 every structure. A polynomial regression model was built for each tissue parameter with age, adding  
207 normalized volume and sex as covariables. Orthogonal polynomials were used to reduce  
208 multicollinearity effects of age predictors (e.g. covariance of age, age<sup>2</sup>, age<sup>3</sup>). This was implemented  
209 in R using the “poly()” function from the “stats” package. Non-linear volume dependency with age  
210 was further assessed by exploring the significance of the quadratic term.

211 Additionally, visual inspection of MPM-by-age scatterplots with LOESS-fitted trend lines indicated  
212 that a 1-knot linear spline model could best fit the age-related distribution. We selected a cutoff of 55  
213 years ( $\geq 55$ ) for the spline, which represented a split at approximately the 80<sup>th</sup> quantile. This is  
214 consistent with the upper age limit of most clinical drug trials in multiple sclerosis, as the  
215 confounding effect of vascular lesions and other comorbidities increases beyond this cut-off.  
216 Furthermore, diffusion tensor imaging studies revealed that age-related decline is more apparent in  
217 the fifth decade of life <sup>29</sup>.

#### 218 **2.3.1.4 Model selection**

219 We compared the performance of linear, linear spline, quadratic, cubic and exponential models to  
220 choose the simplest best fitting model according to a likelihood ratio test in addition to Akaike  
221 information criterion (AIC) comparison. The simplest model was generally chosen when the  
222 likelihood ratio-test did not return a significant difference.

223

### 224 **3 Results**

#### 225 **3.1 PD calibration**

226 We chose to standardize PD based on ventricular CSF (see Fig.1 for an illustration of the pipeline),  
227 since calibration methods using lesion-filled WM masks and whole WM masks in 27 MS patients  
228 resulted in different PD values in NAWM and WM (Fig.2a). In contrast, no difference was found  
229 between NAWM and WM in effective PD (without calibration) or when using CSF as reference  
230 (Fig.2b and 2c).

231 Lateral ventricles masks had a median volume of 5685(7934) [median(IQR)] voxels or 23.3(32.5)  
232 mL. Exclusion of voxels with a T1 below 4s resulted in a median mask volume of 2683(4596) voxels  
233 or 10.99(18.82) mL. The average percentage of voxels remaining above this T1 threshold was  
234 44.31% (mask voxel number ranging from 262 to 31396) with a range of T1 times from 4 to 13.4s.  
235 Median T1 across participants was 5.4s in this CSF mask. CoV of the scaling factor using CSF were

236 1.51%, 0.74% and 2.38% for respective T1 thresholds at 3s, 4s and 5s, compared to 37.79% for the  
237 calibration using WM. Using only the first 100 voxels with T1>4s in the mask resulted in a CoV of  
238 the scaling factor of 2.20%. Normalized lateral ventricles volume was correlated with age and scaling  
239 factor for the calibration using CSF, as well as scaling factor with age. However, there was no  
240 association between PD in the lateral ventricles and age (Sup. Fig. S3). After normalization with the  
241 CSF signal, mean intra-subject CoV of PD was  $5.2 \pm 0.33\%$  in WM,  $8.26 \pm 0.58\%$  in CGM and  $4.84$   
242  $\pm 0.48\%$  in DGM. Intra-subject variability remained identical to the WM-based calibration due to the  
243 linear rescaling of effective PD. SD of PD across subjects were higher in WM (1.27 vs 0.17), CGM  
244 (1.10 vs 0.68) and DGM (1.19 vs 0.69) with the normalization to CSF compared to calibration of PD  
245 against WM resulting in higher inter-subject CoV in WM (1.82% vs 0.24%), in CGM (1.40% vs  
246 0.86%) and in DGM (1.54% vs 0.88%).

### 247 **3.2 Healthy cohort reference values**

248 Table 2 presents descriptive statistics of MPM measurements in WM, WML, CGM, DGM, thalamus,  
249 hippocampus and CSF. Data for caudate nucleus, putamen, globus pallidus, amygdala, nucleus  
250 accumbens are presented in Sup. Tables S1-2. Reported mean or median values across ROIs are in  
251 line with those reported in previous studies (Sup. Table S2).  
252 Histograms (Fig.3) show clearly distinct peaks and normal distributions of MPM median values for  
253 WM, WML, CGM and DGM. Detailed distribution density of median parameter values in DGM

254 structures is shown in Figure 4a. The pallidum stands out among the deep grey matter structures with  
255 higher MT, R1 and R2\* and lower PD (Fig.4a). This is further illustrated in Figure 4b displaying a  
256 brain slice sampled from each population averaged parameter map.

### 257 3.3 White matter lesions

258 Fifty-two out of 77 healthy participants (67.5%) had at least one T2w WMH segmented as lesion  
259 (single lesion volume > 0.01 mL) and 20 (26%) participants (mean age 50.5±14y, 6 (30% male)) had  
260 a mean WML volume above the pre-defined cutoff of 0.2 mL. Mean (SD) number of lesions was  
261 41.9 (46.6) and mean WML volume was 1.39 (1.63) mL (Table 1 and 2). MPM metrics and lesion  
262 volume scatterplots against age are shown in Sup. Fig. S4.

263 In healthy participants, compared to normal appearing WM, MPM values in WML were significantly  
264 reduced for MT ( $t=-7.53$ , 95% CI=[-0.43, -0.24],  $p < 0.001$ ), R1 ( $t=-5.83$ , 95% CI=[-0.14, -0.07],  $p$   
265  $< 0.001$ ) and R2\* ( $t=-8.05$ , 95% CI=[-3.56, -2.09],  $p < 0.001$ ) and significantly increased for PD  
266 ( $t=5.51$ , 95% CI=[2.31, 5.12],  $p < 0.001$ ). In addition, WML showed a substantially wider range of  
267 MPM values across all parameters, compared to healthy WM (Fig.3).

268 MS patients had a mean T2w WMH volume of 21.5 (12.2) mL ranging from 10.3 mL to 58.2 mL  
269 across patients and a mean number of lesions of 86.8 (53.7). MS-WML had increased PD and  
270 reduced MT, R1 and R2\* compared to MS-NAWM, HC-WM and HC-WML (Fig.3b).

### 271 3.4 MPM age related changes

272 As part of our objective to explore the impact of brain aging on the quantitative maps, Table 3  
273 compiles effect sizes from the regression models, including 95% confidence intervals. Only models  
274 revealing a significant association between parameter and age in WM, CGM, DGM, thalamus and  
275 hippocampus are presented in Table 3 and outcomes of model selection are summarized in Sup. Fig.  
276 S5. For data visualization, scatterplots with the trajectory of the curve fitting in the various ROIs are  
277 attached in Fig.5 and Sup. Fig. S6.

278 Regression of MT, R1 and R2\* showed a non-linear association with age in the quadratic term in both  
279 WM and CGM. In the thalamus, fitting MT and R1 with a quadratic function against age showed  
280 significant association, both described by a slow increase from 20 to 40y followed by a decline after  
281 50y. In the hippocampus only R1 presented a quadratic evolution with age indicating a slow increase  
282 from 20 to 50y followed by a decline after 60y.

283 In WM, a linear spline performed better than a quadratic fit in explaining changes in MT and R2\*  
284 with age. Summarizing the results of the model selection in WM (Table 3), MT showed an average  
285 decrease of -0.154%/year ( $p < 0.001$ ) after 55y, R2\* a decrease of  $-0.648s^{-1}/\text{year}$  ( $p < 0.001$ ) after 55y  
286 and PD increased linearly by 0.033%/year ( $p=0.002$ ). R1 revealed a quadratic association with age  
287 ( $p=0.005$ ) with a slow increase over 20-40y followed by a decline after 50y. Remarkably, there was  
288 no age association in both MT and R2\* in WM between 20y and 55y.



289 In CGM, selected models were quadratic for MT, R1 and R2\* and linear for PD. In the thalamus, a  
290 quadratic fit was selected for MT and R1 and in the hippocampus R1 also showed a quadratic  
291 trajectory with age.

292 Finally, there was no non-linear volume dependency with age across ROIs when testing the quadratic  
293 term, although correlation was present (Sup. Table S3).

## 294 **4 Discussion**

295 In this study we present an acquisition and post-processing protocol for a fast quantitative multi-  
296 parameter mapping of the brain with inclusion of T2w white matter hyperintensities and calibration  
297 of proton density using CSF. We standardize the reconstructed quantitative maps for future clinical  
298 application in demyelinating diseases and recommend calibrating PD maps as pure water in CSF to  
299 avoid bias introduced by pathology. We report reference MPM brain data for 77 healthy subjects of  
300 Caucasian ethnicity aged between 20 and 75 years and discuss age-dependence of the MPM  
301 parameters.

### 302 **4.1 PD calibration**

303 PD maps using the standard approach from the hMRI toolbox reconstruction are calibrated to 69% in  
304 WM which may lead to an underestimation of its reported variability<sup>7</sup>. In addition, pathologic  
305 changes of PD in WM may not be reflected, especially when considering its possible use in diseases

306 with WM abnormalities, e.g. multiple sclerosis. Using CSF-based calibration avoids these problems,  
307 as CSF does not contain relevant amounts of macromolecules or paramagnetic ions and the magnetic  
308 properties of CSF are largely unaffected by most neurological disorders<sup>30</sup>.

309 We found that both diffuse and focal WM abnormalities affected the WM-based calibration. On one  
310 hand, focal lesions led to a slight underestimation of PD values. On the other hand, diffuse WM  
311 damage might also impact the calibration resulting in slight PD differences (~0.1-0.2 p.u) between  
312 NAWM and WM while there was no difference in effective PD or when using CSF as reference. In  
313 such a ROI analysis, the impact from WM lesions may be occluded by the relative volume difference  
314 to whole white matter across patients. However, at the single subject level, their effect may be  
315 amplified. Therefore, we recalibrated PD as 100% in CSF, so that inter-subject variability in CSF  
316 would be negligible<sup>28</sup>. To ensure that calibration is only based on voxels containing CSF and to  
317 avoid partial volume effects, we excluded voxels with T1 lower than 4s from the ventricle masks,  
318 which is an appropriate threshold given that the model estimated T1 of free water in brain tissue is  
319 3.7s<sup>31</sup>. Although T1 of CSF is known to be independent of field strength<sup>32</sup>, reported values in  
320 literature show some variability ranging from 4s to 5s. The CoV of the scaling factor did not vary  
321 substantially between the usage of different T1 cut-offs from 3s to 5s. It was dramatically lower  
322 using CSF (0.74% vs 37.79%). We effectively scale all voxels based on the assumption that CSF has  
323 the highest water fraction. One could either assume that the highest water fractions might be capped

324 by the maximum intensity measured by the scanner or that biological variability in CSF is of lower  
325 order of magnitude.

326 Inter-subject variability is higher than in a previous study which used the conventional WM-based  
327 calibration, while intra-subject CoV is in the same order of magnitude<sup>12</sup>. However, our current  
328 sample has a wider age range ( $42.1 \pm 14.1$  vs  $35 \pm 7$ y) than the study by Cooper and colleagues. Given  
329 the variability of ventricles sizes, the resulting inter-subject CoV is higher compared to normalization  
330 to a larger homogeneous WM region. Nonetheless, taking into consideration the variation in  
331 ventricular volume in the linear models, both linear association of PD with age and CoV remained  
332 similar whether we used the ventricles mask or a fixed set of 100 voxels within it. Although  
333 correlation exists between ventricular volume and age, as well as between ventricular volume and  
334 scaling factor, the scaling factor was not correlated to age. This means that although age variability in  
335 ventricular volume introduces variability in the PD scaling factor, the resulting inter-subject  
336 variability remains low compared to inter-subject variability from WM. An alternative approach  
337 would be to obtain a scaling factor with the use of an external reference such as a phantom to benefit  
338 from a stable and homogeneous volume<sup>33</sup>. However, due to a lack of practicality, it is hardly  
339 considered for use in a clinical setting.

340 Finally, PD quantification methods may differ on the determination of the receiver sensitivity profile  
341 and values reported here are standardized for the method of quantitative B1 mapping<sup>34</sup>. Volz et al.

342 pointed out that physiological bias might be smoothed out and recommended to proceed carefully in  
343 the presence of pathology which may cause segmentation algorithms to fail or wherein the  
344 relationship between T1 and effective PD may be locally distorted <sup>15</sup>.

## 345 **4.2 Age-related effects**

346 We observed a non-linear age dependency of MT, R1 and R2\* across various ROIs. Age effects  
347 could be best modelled linearly for PD and we found arguably a reduced impact of non-linear effects  
348 between 20y and 55y for both MT and R2\* in WM. Our findings corroborate MPM studies on brain  
349 aging which reported negative correlation between age and MT across the cortex along positive  
350 correlations between age and R2\* in the basal ganglia <sup>9-11,35</sup>.

351 A quadratic model provided the most accurate representation of the non-linear relationship between  
352 MT and age, illustrating the U-shaped pattern in myelination over lifespan, consistent with myelin-  
353 driven changes in volume and MRI contrast across the cortex <sup>36</sup>. Quantitative R1 has also shown a  
354 quadratic trajectory against age indicative of region-specific myelin maturation stabilizing into  
355 middle age followed by degeneration <sup>37</sup>. Our results indicate that age-related MT and R1 changes  
356 were generally coincident, both sensitive to tissue myelin <sup>35</sup>. However, R1 is less sensitive to myelin  
357 and reflects several physiological processes which can occur simultaneously, as modelled by its  
358 linear dependency on free water, myelin, macromolecules or iron assuming a mono-exponential  
359 decay <sup>31</sup>.

360 Except for its linear increase in WM, we did not find any age-related association to PD in the  
361 investigated ROIs. Across the cortex, this is consistent with Seiler et al. who reported that global  
362 cortical PD did not show a significant correlation with age<sup>38</sup>. Looking at interregional differences  
363 they detected in the temporal and occipital lobes a positive association with age. Filo et al. did not  
364 find differences in macromolecular tissue volume (MTV=1-PD, non-water tissue fraction) corrected  
365 for  $R2^*$  in the frontal cortex, hippocampus, amygdala and frontal cortex between young adults and  
366 older adults<sup>39</sup>. Overall, PD as a surrogate for water may be less sensitive to age-related changes of  
367 tissues, although values extracted from a single ROI do not allow generalization of the results to the  
368 whole cortex because of regional heterogeneity.

369 Linear and polynomial fits of  $R2^*$  versus age performed significantly better on our data across ROIs  
370 than exponential saturation functions as the latter could not keep up with the increase in  $R2^*$  and its  
371 variability in older participants. Yet early exponential growth in the putamen and caudate nucleus  
372 was noticed (Sup. Fig. S7) following the putative steep iron increase from early childhood to  
373 adulthood, in line with global cubic fits for the caudate, putamen, and globus pallidus reported in  
374 another study<sup>40</sup>. Pallidal calcification was often seen in our older healthy participants, which we  
375 considered as a normal aging phenomenon contributing to the  $R2^*$  inter-subject variability in the  
376 basal ganglia as hyperintensities may originate from the presence of minerals such as calcium and  
377 zinc especially around the globus pallidus<sup>41</sup>. Although age-related increase in  $R2^*$  has also been  
378 reported for the hippocampus<sup>42</sup> we did not observe a dependency of  $R2^*$  with age in the

379 hippocampus and thalamus, what may be a result of structural differences in rates of myelination or  
380 iron accumulation<sup>41</sup>, or due to volume shrinkage impacting iron concentration.

381 Interestingly, we noticed a concurrence between  $R1$ ,  $MT$  and  $R2^*$  in WM and CGM owing to their  
382 sensitivity to macromolecular, myelin, iron and water content<sup>43</sup>. Tissue areas rich in iron often co-  
383 localize with regions of elevated myelin content<sup>44</sup>, owing to the role of iron in myelin synthesis and  
384 homeostasis, or the high iron concentration within glial cells<sup>45</sup>, adding to the dependence of  $R2^*$  on  
385 the orientation of WM fibers with respect to the magnetic field<sup>46</sup>.

386 Finally, increased variability with age in  $R2^*$  may partly be explained by noisier measurements given  
387 the sensitivity to motion inherent to the multi-echo FLASH acquisition. As shown by the correlation  
388 between age and motion degradation index, motion may also be a predictor as the ability to remain  
389 still in the scanner may worsen with age. Specifically, head motion extends to the noise level of  
390 relaxometry estimates derived from the raw echoes quantified by the variability of  $R2^*$  in WM<sup>47</sup>.

### 391 **4.3 Implications for future research and clinical practice**

392 Strengths of this study include using manufacturer sequences, which allow ready implementation on  
393 standard scanners. Absolute deviations in mean or median between our MPM values across ROIs and  
394 those reported in literature were in the same range as differences between previous studies  
395 highlighting the reproducibility of quantitative MPM<sup>6,7</sup>. The prevalence and severity of WML tend  
396 to rise with age with a majority of non-demented people aged above 60 exhibiting cerebral lesions<sup>48</sup>.

397 In consideration of future research implicating WM lesions and abnormalities in multiple sclerosis  
398 and related disorders, we aimed to include them in the general pipeline for lesion-filling and to  
399 improve PD quantification, as i) the presence of lesions or enlarged ventricles may cause  
400 segmentation to fail and ii) global effects observed in WM might transfer to lesion-specific localized  
401 effects. Comparing WM and WML across MS patients and healthy participants, T2w WM  
402 hyperintensities showed decreased MT, R1 and R2\* and increased PD compared to healthy WM and  
403 NAWM of MS indicating more pronounced focal damage and structural loss. MPM is also sensitive  
404 to diffuse white matter pathology as NAWM which appears unaffected on conventional MRI can be  
405 differentiated from healthy WM<sup>49</sup>. In particular, demyelination, axonal degeneration, inflammation,  
406 gliosis and edema are exacerbated in MS plaques resulting in higher discrepancy in MPM values  
407 from healthy WM and WML, corroborating findings from other studies using quantitative  
408 relaxometry, MT imaging, and diffusion MRI<sup>50</sup>. However, MS lesions are heterogeneous and present  
409 varying degrees of degeneration, de/re-myelination and inflammation, thus discriminating specific  
410 lesion types remains to be explored<sup>51,52</sup>.

411 Lastly, we hypothesized that MPM measurements might demonstrate more consistency in younger  
412 healthy individuals while displaying greater variability in older populations to acknowledge the  
413 impact of pre-clinical degeneration. Biological age may contribute most to the inter-subject  
414 variability and even be the strongest predictor for pathophysiological changes. Early and late  
415 nonlinear age-dependence have been observed in the lifespan trajectories of quantitative parameters,

416 with distinct patterns in MT mimicking the inverted U-shaped trajectory of human brain myelination  
417 <sup>36</sup> and in  $R2^*$  analogous to the exponential cerebral increase of non-heme iron <sup>53</sup>. Yet, this  
418 relationship may be altered in disease. In multi-center or randomized clinical trials, due to  
419 discrepancy in age distribution of unmatched cohorts, including age as a linear predictor may be  
420 inadequate if one aims to fully capture the true age-related variability when manipulating biomarkers.  
421 It may be recommended to check and correct for non-linear age effects by fitting the response with  
422 age as an independent parameter. For example after fitting with an exponential saturation function,  
423 Ropele et al assessed inter-subject and inter-scanner variability of  $R2^*$  and attributed large  $R2^*$   
424 variations to age suggestive of iron accumulation while scanner differences had a low impact <sup>54</sup>.

#### 425 **4.4 Limitations**

426 Although the sample size is small for robust non-linear models of age-related effects, we report  
427 healthy population MPM data which can serve as control data and such studies are scarce given the  
428 novelty of the protocol. Longitudinal studies are however superior to assess chronological  
429 pathological changes and reduce bias due to the large interindividual variability. Another liability is  
430 that the age and sex distributions of the recruited participants resemble those of typical cohorts of  
431 autoimmune neuroinflammatory diseases with a strong preponderance of women. This may however  
432 become a strength when studying such clinical populations. Indeed, our pipeline considered the  
433 inclusion of WML with MPM and is readily available for upcoming research in diseases like multiple



434 sclerosis and related disorders. Consequently, the recruited population did not permit to have a good  
435 representation of early and late developmental changes occurring in the brain to effectively explore  
436 the impact of aging on quantitative maps and associate it to decline in cognition or motor function.  
437 Moreover, this study was done on a white population, so our results are not necessarily applicable to  
438 other ethnicities. In this study, no visual rating of the WML was attempted as they mostly served to  
439 establish the pipeline and will be further discussed and investigated in a following study to  
440 discriminate MS specific lesions from the WM lesions described in healthy participants which are  
441 likely microangiopathic. Future developments should target improvements in both sensitivity and  
442 specificity of MRI biomarkers, as well as clinical applicability with regards to disease models.

## 443 **5 Conclusion**

444 In conclusion, we present a fast quantitative MPM pipeline at 1.6 mm isotropic resolution, which can  
445 be readily used in a clinical protocol based on manufacturer sequences, along post-processing  
446 methods including standardization of PD maps and healthy brain data acquired with it. The protocol  
447 is anticipated to possess a higher sensitivity in identifying pathological alterations in future  
448 applications in disease<sup>12</sup>. Importantly, previous studies<sup>6,7</sup>, as well as the current study provide  
449 essential reference values and contribute datasets to assist clinical researchers in conducting thorough  
450 power analyses and report effect sizes that carry significance for future investigations in the context  
451 of clinical studies.

452 **Competing interests**

453 H.T is supported by iNAMES - MDC - Weizmann - Helmholtz International Research School for  
454 Imaging and Data Science from NAno to MESo.

455 Q.C is supported by the Chinese Scholarship Council (CSC).

456 C.C has received research support from Novartis and Alexion and is a part of a consortium funded by  
457 the U.S. Department of Defense, unrelated to this study. She also serves as a member of the Standing  
458 Committee on Science for the Canadian Institutes of Health Research (CIHR).

459 D.M has received a research scholarship from the Berlin Institute of Health at Charité, Berlin,  
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461 S.A received speaker's honoraria from Bayer, Alexion, Roche and research grants from Stiftung  
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463 all unrelated to this study.

464 R.R. received speaking honoraria from Roche unrelated to this study.

465 M.S. has received consulting fees from Roche, Pliant therapeutics, and Octave Bioscience all  
466 unrelated to this study. He is named as inventor on a patent describing use of N-acetylglucosamine as  
467 myelination and immunodulating therapy.

468 T.S.H has received research funding from Celgene/bms and speaker honoraria from AbbVie, Bayer,  
469 and Roche both unrelated to this work.

470 A.U.B is cofounder and holds shares of medical technology companies Motognosis GmbH and  
471 Nocturne GmbH. He is named as inventor on several patents and patent applications describing  
472 methods for retinal image analyses, motor function analysis, multiple sclerosis serum biomarkers and  
473 myelination therapies utilizing N-glycosylation modification. He is cofounder of IMSVISUAL and  
474 has served as member of the board of directors and secretary/treasurer of IMSVISUAL. AUB is now  
475 full-time employee and holds stocks and stock options of Eli Lilly and Company. His contribution to  
476 this work is his own and does not represent a contribution from Eli Lilly.

477 F.P. has received research funding from Biogen, Genzyme, Guthy Jackson Foundation, Merck,  
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491 **Author contributions**

492 H.T: Formal analysis, Data curation, Methodology, Writing - original draft;

493 T.H: Formal analysis, Writing - review & editing;

494 Q.C.: Formal analysis, - review & editing;

495 S.H: Methodology - review & editing;

496 C.C: Data curation, review & editing;

497 P.S: Data curation, review & editing;

498 T.S.H: Data curation, review & editing;

499 S.A: Data curation, review & editing;

500 R.R: Data curation, review & editing;

501 D.M: Data curation, review & editing;

502 M.S: Data curation, review & editing;

503 L.A: Data curation, review & editing;

504 A.U.B: Conceptualization, Supervision, Writing -review and editing;

505 C.F: Data curation, Writing - review & editing;

506 F.P: Conceptualization, Supervision, Writing -review and editing

507

## 508 **Data availability**

509 The analysis pipeline is available at <https://clinicalmpm.github.io/>, including the sequence

510 configuration for Siemens PRISMA scanners. MRI data from this study cannot be shared publicly

511 due to constraints from the European General Data Protection Regulation and its implementation into

512 German laws and required consent from participants.

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				Tables
Number of subjects [n]	27	77	660	
Number of subjects with cerebral WM lesions with a volume above 0.2 mL [n] (percentage)	27 (100%)	20 (26%)	661	
Number of T2w WM hyperintensities, mean $\pm$ SD	86.8 $\pm$ 53.7	41.9 $\pm$ 46.6	662	
T2w hyperintensities volume[mL], mean $\pm$ SD	21.5 $\pm$ 12.2	1.39 $\pm$ 1.63	663	
Age [years], mean $\pm$ SD	50 $\pm$ 9.9	42.1 $\pm$ 14.1		
Total age range [years]	26-65	20-75	664	
Age range for women [years]	26-65	20-75		
Age range for men [years]	44-60	22-68	665	
Female/male [n] (% female)	18F/9M (67%)	60F/17M (77.9%)	666	
Disease course, [n]	RRMS n=22 SPMS n=5	NA	667	
EDSS, median (IQR)	3.0 (2)	NA	668	
Disease duration (since symptom onset) [years], median (IQR)	15.9 (13.2)	NA		

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670

671 **Table 1.** Demographics and clinical characteristics of the participants. MS patients were diagnosed  
672 as RRMS according to revised Mc Donald criteria<sup>19</sup> and as SPMS according to Lublin et al. 2014<sup>55</sup>.

673 Abbreviations: HC= healthy controls, F=female, M=male, WM=white matter, SD = standard  
674 deviation, IQR = interquartile range, RRMS = relapse-remitting multiple sclerosis, SPMS =  
675 secondary progressive multiple sclerosis, EDSS = Expanded Disability Status Scale.

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Parameter		MT (%)					
ROI	WM	WML	CGM	DGM	Thalamus	Hippocampus	CSF
Mean (SD)	1.55 (0.05)	1.24 (0.19)	0.85 (0.02)	1.05 (0.04)	1.17 (0.05)	0.83 (0.03)	0.023 (0.007)
SD over voxels	0.28	0.3	0.27	0.24	0.24	0.18	0.020
Median (IQR)	1.6 (0.06)	1.26 (0.27)	0.85 (0.03)	1.03 (0.04)	1.2 (0.07)	0.82 (0.03)	0.017 (0.008)
Intra-subject CoV (%)	18.16	25.23	31.40	22.77	20.23	21.41	89.25
Inter-subject CoV (%)	3.21	15.28	2.78	3.43	4.13	4.12	30.01
2nd - 98th Percentile	1.42 - 1.64	0.91 - 1.57	0.8 - 0.89	0.97 - 1.12	1.07 - 1.26	0.75 - 0.89	0.01 - 0.05
Min - Max (of means)	1.4 - 1.64	0.87 - 1.62	0.79 - 0.89	0.95 - 1.12	1.04 - 1.26	0.73 - 0.91	0.01 - 0.05
		PD (%)					
ROI	WM	WML	CGM	DGM	Thalamus	Hippocampus	CSF
Mean (SD)	69.97 (1.27)	72.91 (2.94)	78.73 (1.10)	77.37 (1.19)	76.53 (1.20)	78.9 (1.27)	100.72 (0.33)
SD over voxels	3.64	4.63	6.5	3.75	4.11	3.24	4.55
Median (IQR)	69.08 (1.84)	72.8 (4.11)	78.81 (1.36)	77.76 (2.05)	76.61 (1.78)	79.14 (1.72)	100.14 (0.23)
Intra-subject CoV	5.20	6.41	8.26	4.84	5.38	4.11	4.52
Inter-subject CoV	1.82	4.03	1.40	1.54	1.57	1.60	0.33
2nd - 98th Percentile	67.67 - 72.22	67.13 - 77.48	76.32 - 80.76	75 - 79.26	74.15 - 78.77	76.47 - 80.82	100.27 - 101.83
Min - Max	66.87 - 72.53	66.24 - 77.56	76.29 - 81.17	74.03 - 79.32	73.78 - 79.09	75.27 - 80.93	100.04 - 101.98
		R1 (s <sup>-1</sup> )					
ROI	WM	WML	CGM	DGM	Thalamus	Hippocampus	CSF
Mean (SD)	0.91 (0.03)	0.81 (0.08)	0.62 (0.01)	0.7 (0.02)	0.73 (0.02)	0.58 (0.02)	0.185 (0.005)
SD over voxels	0.12	0.13	0.1	0.11	0.09	0.07	0.016
Median (IQR)	0.92 (0.04)	0.82 (0.16)	0.61 (0.02)	0.7 (0.03)	0.73 (0.03)	0.57 (0.02)	0.186 (0.009)
Intra-subject CoV	13.62	16.64	16.34	15.59	12.84	11.25	8.71
Inter-subject CoV	2.91	9.29	2.07	2.90	3.41	2.96	2.61
2nd - 98th Percentile	0.85 - 0.96	0.7 - 0.94	0.59 - 0.64	0.67 - 0.74	0.67 - 0.77	0.55 - 0.62	0.17 - 0.19
Min - Max	0.83 - 0.96	0.7 - 0.95	0.58 - 0.64	0.66 - 0.74	0.65 - 0.78	0.54 - 0.62	0.14 - 0.20
		R2* (s <sup>-1</sup> )					
ROI	WM	WML	CGM	DGM	Thalamus	Hippocampus	CSF
Mean (SD)	21.29 (0.56)	18.99 (4.11)	18.01 (0.59)	20.89 (1.07)	20.23 (0.97)	15.92 (0.78)	2.23 (0.67)
SD over voxels	4.23	5.48	9.19	6.44	3.57	3.9	2.06
Median (IQR)	21.06 (0.87)	18.24 (2.27)	16.8 (0.78)	20.24 (1.13)	20.37 (1.09)	15.61(0.84)	1.74 (0.52)
Intra-subject CoV	19.87	25.69	51.03	30.66	17.67	24.44	90.37
Inter-subject CoV	2.64	21.61	3.30	5.11	4.80	4.92	30.03
2nd - 98th Percentile	20.4 - 22.23	15.58 - 29.6	16.96 - 18.96	19.06 - 23.32	18.4 - 22.28	14.63 - 17.71	1.39 - 5.16
Min - Max	20.11 - 22.32	15.44 - 34.94	16.78 - 19.02	18.68 - 24.12	18.27 - 22.61	14.44 - 18.97	1.32- 5.98
		Volume (mL)					
ROI	WM	WML	CGM	DGM	Thalamus	Hippocampus	CSF
Mean (SD)	182.15 (9.52)	1.39 (1.63)	199.85 (11.37)	15.61 (1.45)	5 (0.45)	1.05 (0.9)	18.17 (20.35)
Mean ICV (mL)	2890 (256.05)						

678 **Table 2.** Descriptive statistics for all MPM and volume measurements in white matter (WM), white  
679 matter lesions (WML), cortical grey matter (CGM), deep grey matter (DGM), thalamus,

680 hippocampus and CSF. Values are rounded at 2 decimals. Standard deviation over ROI voxels and  
681 intra-subject coefficient of variation are averaged across participants. Min - Max represent minimum  
682 and maximum of mean ROI values across participants. CSF values were extracted from the lateral  
683 ventricles excluding voxels with T1 values lower than 4s. Please note that PD values are scaled to  
684 100 p.u. normalized by the median CSF value. MT values have been linearly rescaled to reference  
685 values of a MT pulse of  $220^\circ$  for comparison purpose to literature.

686 Abbreviations: SD standard deviation, IQR interquartile range, CoV coefficient of variation, ROI  
687 region of interest, CSF cerebrospinal fluid

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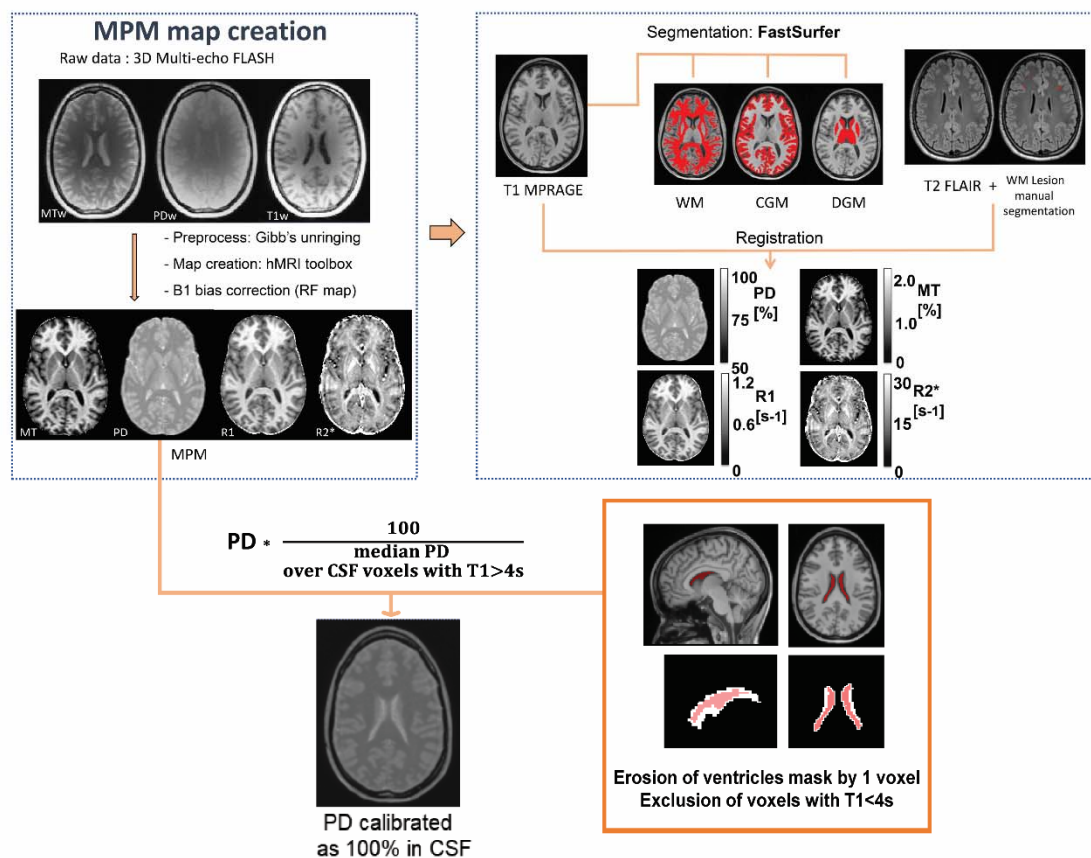
Parameter (a.u)	ROI	Coefficient $\beta$	Confidence Interval (95%)	P-value		
MT (%)	WM	Selected model: linear spline (F=26.18, p<0.001)				
		Intercept	1.085	(0.911, 1.261)	<0.001	
		Age (slope before 55)	-0.022	(-0.056, 0.011)	0.184	
		Age (slope after 55)	-0.154	(-0.2, -0.109)	<0.001	
	CGM	Thalamus	Selected model: quadratic fit (F=6.47, p<0.001)			
			Intercept	1.011	(0.881, 1.142)	<0.001
			Normalized Volume	36.549	(10.827, 62.272)	0.006
			Age	-0.013	(-0.113, 0.088)	0.802
		Hippocampus	Selected model: quadratic fit (F=3.72, p=0.015)			
			Intercept	0.667	(0.599, 0.737)	<0.001
			Age	0.008	(-0.045, 0.061)	0.760
			Age <sup>2</sup>	-0.063	(-0.111, -0.016)	0.010
PD (%)	WM	Selected model: linear fit (F=8.02, p<0.001)				
		Intercept	76.119	(70.539, 81.701)	<0.001	
		Age	0.033	(0.014, 0.054)	0.002	
		Normalized Volume	-46.328	(-77.616, -15.041)	0.004	
	CGM	Thalamus	Selected model: quadratic fit (F=15.39, p<0.001)			
			Intercept	0.659	(0.548, 0.771)	<0.001
			Normalized Volume	1.452	(0.839, 2.064)	<0.001
			Age	-0.081	(-0.127, -0.034)	<0.001
		Hippocampus	Selected model: quadratic fit (F=4.95, p=0.01)			
			Intercept	0.610	(0.608, 0.614)	<0.001
			Age	0.005	(-0.019, 0.029)	0.657
			Age <sup>2</sup>	-0.036	(-0.06, -0.014)	0.003
R1 (s <sup>-1</sup> )	WM	Selected model: quadratic fit (F=15.39, p<0.001)				
		Intercept	0.659	(0.548, 0.771)	<0.001	
		Normalized Volume	1.452	(0.839, 2.064)	<0.001	
		Age	-0.081	(-0.127, -0.034)	<0.001	
	CGM	Thalamus	Selected model: quadratic fit (F=15.39, p<0.001)			
			Intercept	0.659	(0.548, 0.771)	<0.001
			Normalized Volume	1.452	(0.839, 2.064)	<0.001
			Age	-0.081	(-0.127, -0.034)	<0.001
		Hippocampus	Selected model: quadratic fit (F=15.39, p<0.001)			
			Intercept	0.659	(0.548, 0.771)	<0.001
			Normalized Volume	1.452	(0.839, 2.064)	<0.001
			Age	-0.081	(-0.127, -0.034)	<0.001
R2* (s <sup>-1</sup> )	WM	Selected model: linear spline (F=6.50, p<0.001)				
		Intercept	17.314	(14.905, 19.723)	<0.001	
		Age (slope before 55)	0.252	(-0.22, 0.724)	0.290	
		Age (slope after 55)	-0.648	(-1.22, -0.077)	0.027	
	CGM	Thalamus	Selected model: quadratic fit (F=10.17, p<0.001)			
			Intercept	16.796	(16.687, 16.905)	<0.001
			Age	1.127	(0.199, 2.056)	0.018
			Age <sup>2</sup>	-1.772	(-2.702, -0.844)	<0.001
		Hippocampus	Selected model: quadratic fit (F=10.17, p<0.001)			
			Intercept	16.796	(16.687, 16.905)	<0.001
			Age	1.127	(0.199, 2.056)	0.018
			Age <sup>2</sup>	-1.772	(-2.702, -0.844)	<0.001

697 **Table 3.** MPM selected models in white matter (WM), cortical grey matter (CGM), thalamus and  
698 hippocampus. Normalized volume was calculated as structural volume divided by intra-cranial  
699 volume. Age coefficients estimates are given in respective parameter unit per year (a.u/y).

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702 **Figures and legends**



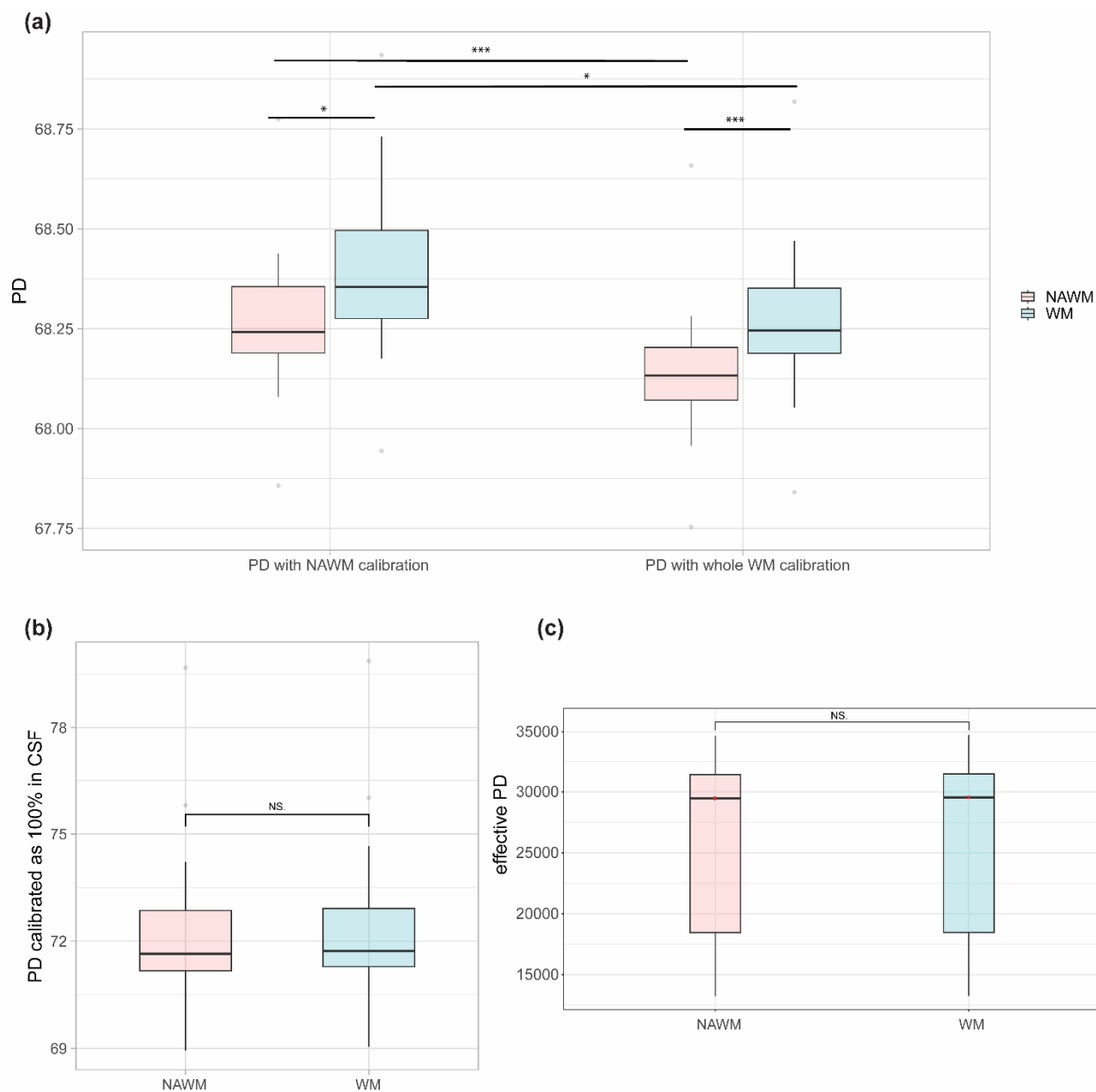
703

704 **Figure 1.**

705 Graphical representation of the MPM pipeline. Raw PDw, MTw, T1w echoes were corrected for  
706 Gibb's artifact before reconstruction with the hMRI toolbox. Receive field inhomogeneities were  
707 corrected using Unified Segmentation. T1-MPRAGE was segmented using Fastsurfer, a deep

708 learning alternative to FreeSurfer, to obtain tissue masks for white matter (WM), cortical grey matter  
709 (CGM) and deep grey matter (DGM). White matter T2 hyperintensities were manually segmented  
710 from T2-FLAIR. All masks were then spatially registered to the quantitative maps. PD maps were  
711 calibrated as 100% in ventricular CSF. Voxels with  $T1 < 4s$  were excluded from the eroded lateral  
712 ventricles mask.

713



714

715 **Figure 2.**

716 **(a)** PD comparison in whole white matter (WM) and normal-appearing white matter (NAWM) of 27

717 MS patients between calibration methods using lesion-filled white matter mask (PD with NAWM

718 calibration) and whole white matter mask (PD with whole WM calibration). Significance levels

719 associated to asterisks:  $p < 0.05$  (\*),  $p < 0.01$  (\*\*),  $p < 0.001$  (\*\*\*)).

720 **(b)** Comparison of PD maps calibrated using CSF signal in normal appearing white matter (NAWM)

721 and whole white matter (WM) regions of MS patients. Using CSF calibration, the mean difference

722 between NAWM and WM is 0.1 p.u, which is of the same order of magnitude as in (a). Standard

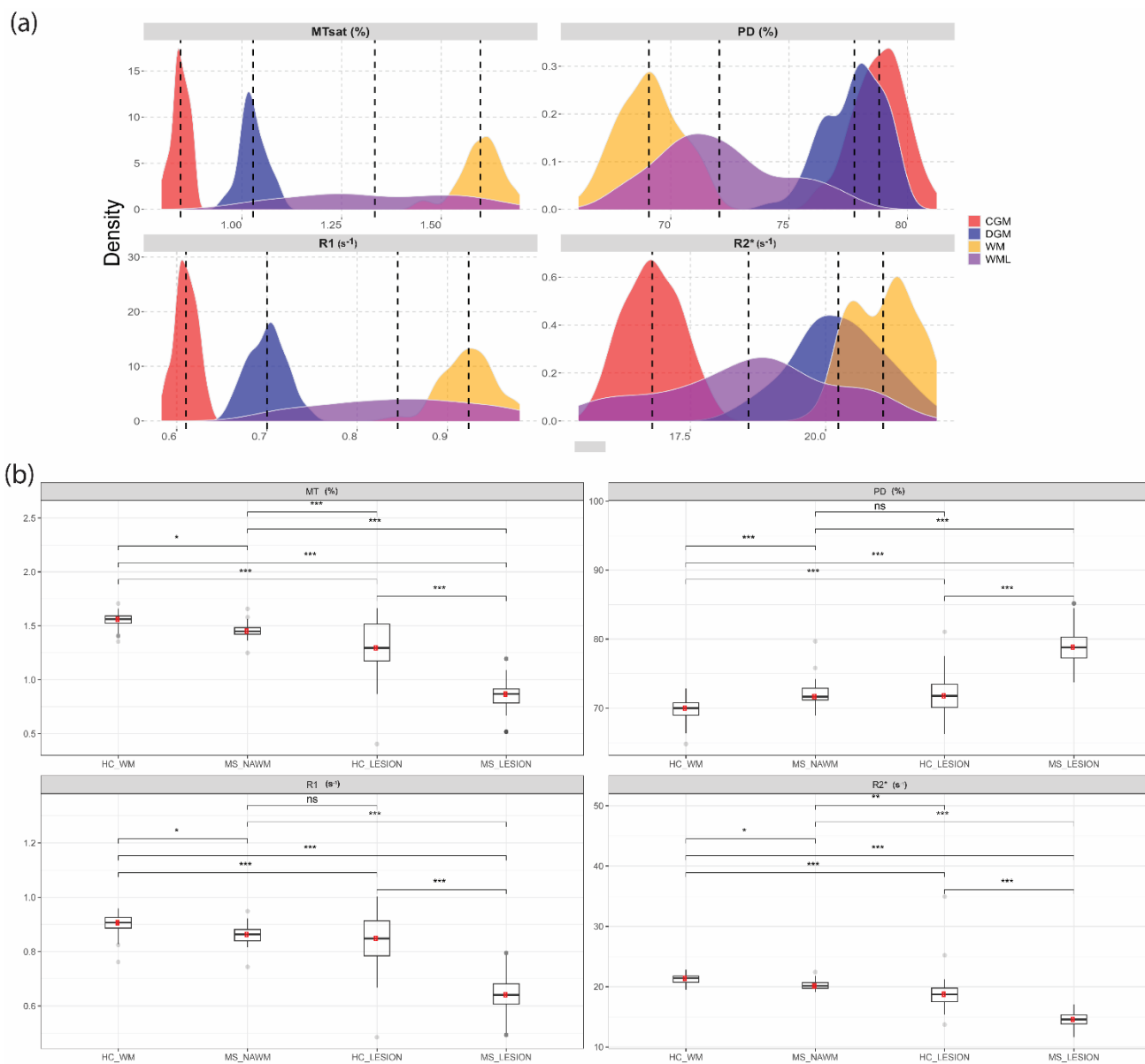
723 deviations are higher resulting in a higher inter-subject coefficient of variation.

724 **(c)** Comparison of non-calibrated PD maps in normal appearing white matter (NAWM) and whole

725 white matter (WM) regions of MS patients

726





727

728 **Figure 3.**

729 **(a)** Histograms of median MPM values distribution across healthy participants in white matter (WM,

730 yellow), white matter lesions (WML, purple), cortical grey matter (CGM, red), deep grey matter

731 (DGM, blue). Dashed lines indicate respective median. For each tissue class except WML, outliers

732 outside the 2-98<sup>th</sup> percentile were removed. WML only included median values of healthy

733 participants with mean volume higher than 0.2mL.

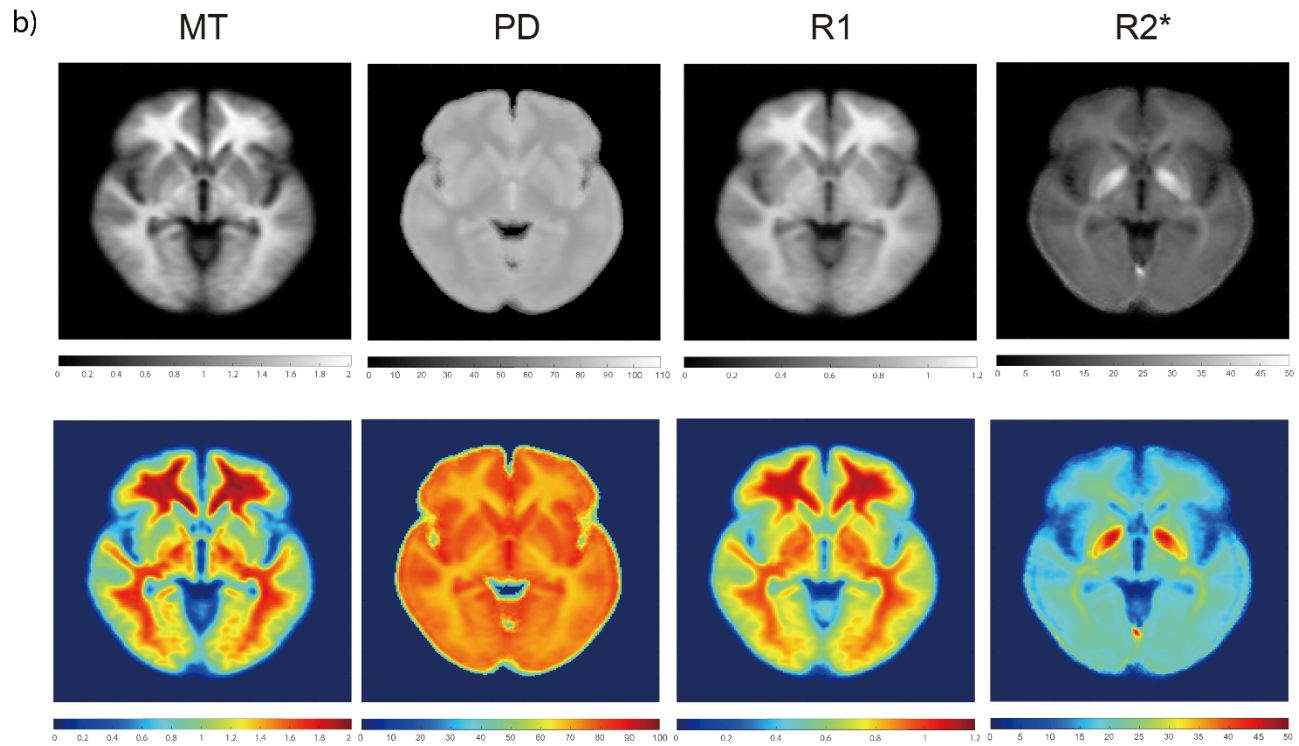
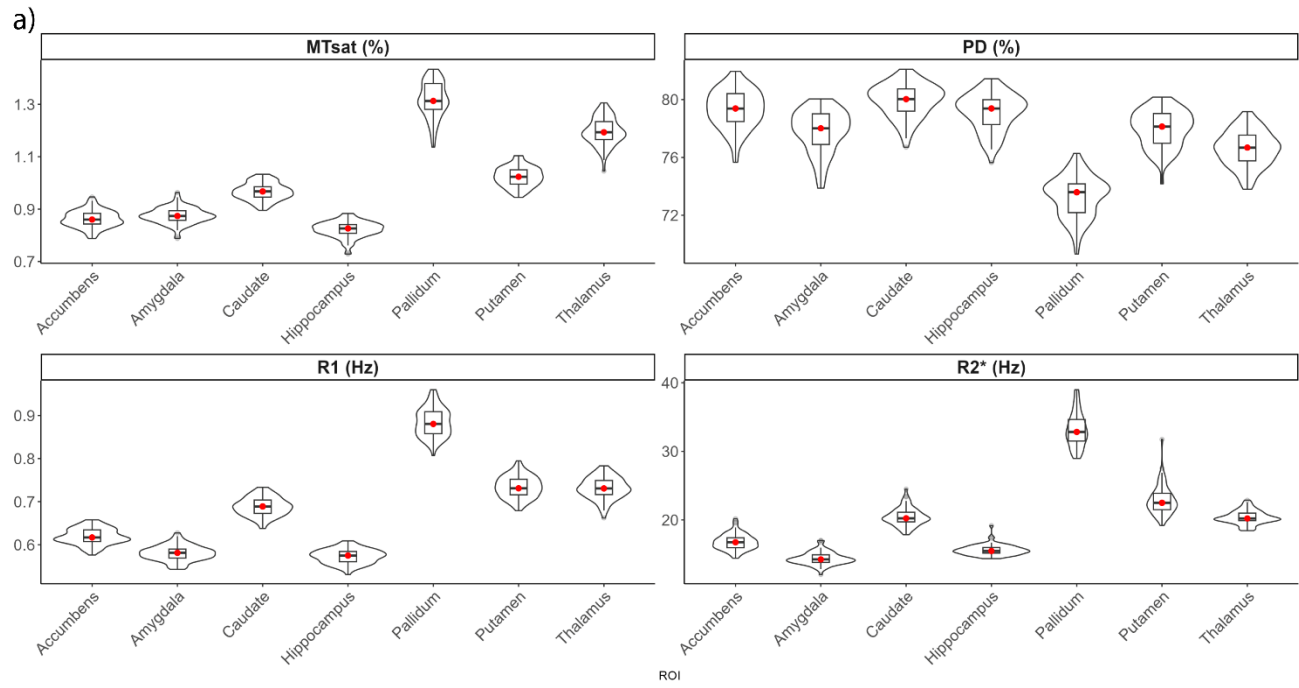
734 **(b)** MPM comparison of white matter lesions in MS patients (MS\_LESION) and HC T2w white

735 matter hyperintensities (HC\_LESION) against healthy white matter (HC\_WM) of healthy controls

736 and normal appearing white matter of MS patients (MS\_NAWM, free of lesions). Significance levels

737 associated to asterisks:  $p < 0.05$  (\*),  $p < 0.01$  (\*\*),  $p < 0.001$  (\*\*\*)).

738



739

740 **Figure 4.**

741 **(a)** Boxplots and density distribution comparison of median MT, PD, R1 and R2\* values in thalamus,

742 caudate, globus pallidus (Pallidum), putamen, amygdala, hippocampus, nucleus accumbens

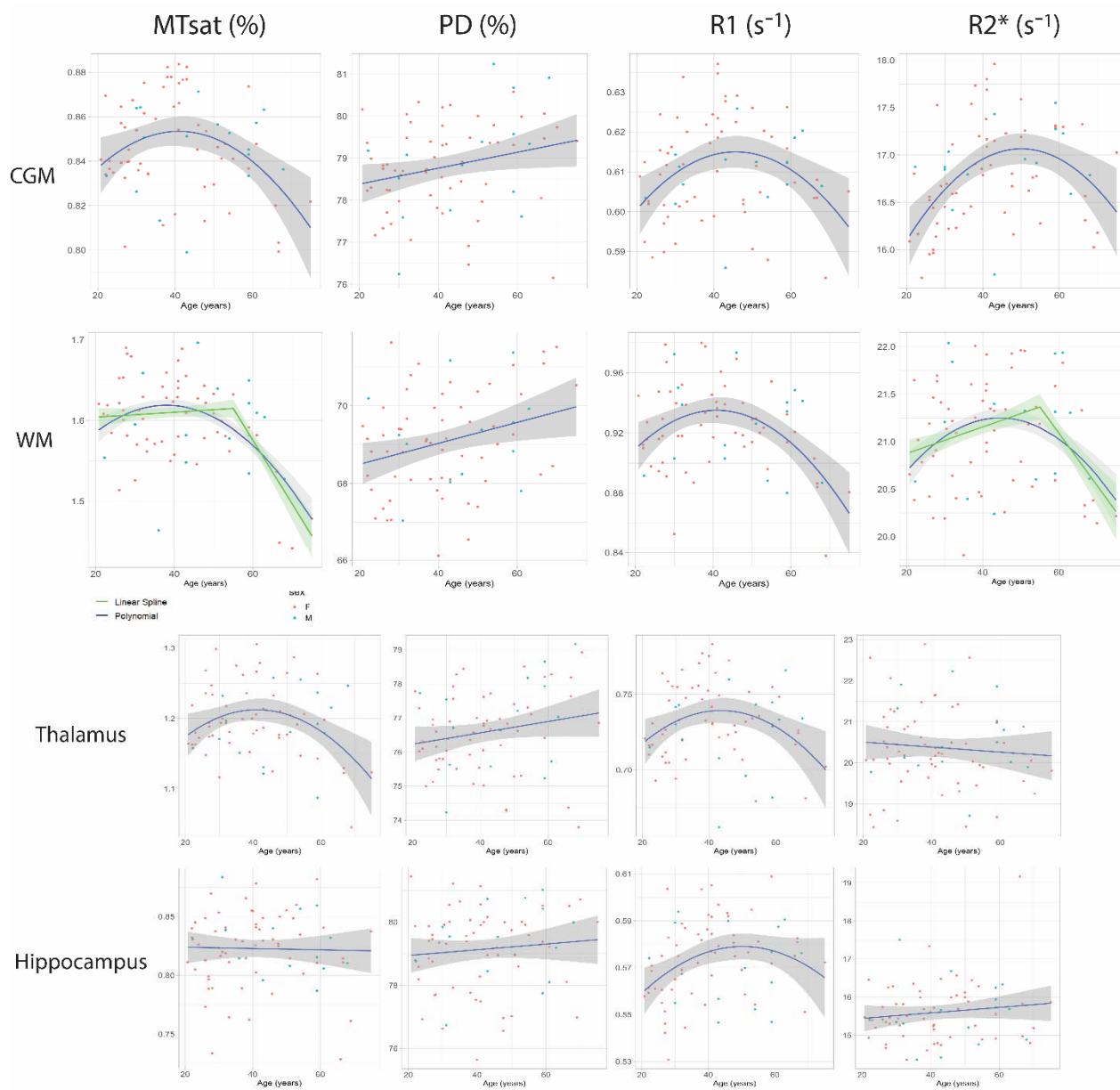
743 (Accumbens).

744 **(b)** Greyscale and RGB-colored slice examples of population averaged quantitative maps showing

745 globus pallidus caudate putamen and thalamus. In particular, the globus pallidus shows higher R2\*,

746 R1, MT and lower PD values.

747



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749 **Figure 5.** Scatterplots and fitted trajectories (blue) for the described ROIs. Green curve shows the  
750 linear spline with a cut-off of 55y when it performed better than the other models. Orange curve  
751 displays the cubic model which performed equally well but not significantly better than a linear  
752 regression in caudate nucleus and putamen. Red and green dots represent women and men  
753 respectively.