

## **Tract-specific white matter microstructure alterations among young adult *APOE ε4* carriers: A replication and extension study**

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1

## Abstract

2 The parahippocampal cingulum bundle (PHCB) connects regions known to be vulnerable to  
3 early Alzheimer's disease (AD) pathology, such as posteromedial cortex and medial  
4 temporal lobe. While AD-related pathology has been robustly associated with alterations in  
5 PHCB microstructure, specifically lower fractional anisotropy (FA) and higher mean  
6 diffusivity (MD), emerging evidence indicates that the reverse pattern is evident in younger  
7 adults at-risk of AD. In one such study, Hodgetts et al. (2019) reported that healthy young  
8 adult carriers of the apolipoprotein-E (*APOE*)  $\epsilon 4$  allele – the strongest common genetic risk  
9 factor for AD – showed higher FA and lower MD in the PHCB but not the inferior longitudinal  
10 fasciculus (ILF). These results are consistent with proposals claiming that heightened neural  
11 activity and connectivity have a significant role in posteromedial cortex vulnerability to  
12 amyloid- $\beta$  and tau spread beyond the medial temporal lobe. Given the implications for  
13 understanding AD risk, here we sought to replicate Hodgetts et al.'s finding in a larger  
14 sample ( $N = 128$ ; 40 *APOE*  $\epsilon 4$  carriers, 88 *APOE*  $\epsilon 4$  non-carriers) of young adults (age  
15 range: 19-33). Extending this work further, we also conducted exploratory analyses using a  
16 more advanced measure of microstructure: hindrance modulated orientational anisotropy  
17 (HMOA). These analyses included an investigation of hemispheric asymmetry in PHCB and  
18 ILF HMOA. Contrary to the original study, we observed no difference in PHCB  
19 microstructure between *APOE*  $\epsilon 4$  carriers and non-carriers. Bayes factors (BFs) further  
20 revealed moderate-to-strong evidence in support of these null findings. *APOE*  $\epsilon 4$ -related  
21 differences in ILF HMOA asymmetry were evident, however, with carriers demonstrating  
22 lower leftward asymmetry. Our findings indicate that young adult *APOE*  $\epsilon 4$  carriers do not  
23 show alterations in PHCB microstructure, as observed by Hodgetts et al., but may show  
24 altered asymmetry in ILF microstructure.

25

26 **Keywords:** *APOE*, Alzheimer's disease, parahippocampal cingulum bundle, inferior  
27 longitudinal fasciculus, diffusion MRI, structural connectivity

28 **1. Introduction**

29 Alzheimer's disease (AD) is a chronic, progressive disease and the most common cause of  
30 dementia (Scheltens et al., 2021). The hallmark pathological features of AD are the  
31 presence of extracellular amyloid- $\beta$ -containing plaques and intracellular tau-containing  
32 neurofibrillary tangles (DeTure & Dickson, 2019; Trejo-Lopez et al., 2021). Although  
33 controversial (Frisoni et al., 2022; Herrup, 2015), the dominant hypothesis in the field – the  
34 amyloid cascade hypothesis – holds that the accumulation of amyloid- $\beta$  peptide is the critical  
35 factor in AD pathogenesis (Selkoe & Hardy, 2016). Amyloid- $\beta$  accumulation follows a  
36 relatively distinct spatiotemporal pattern in the ageing brain, beginning preferentially in  
37 posteromedial regions, including retrosplenial/posterior cingulate cortices and precuneus  
38 (Mattsson et al., 2019; Palmqvist et al., 2017; Villeneuve et al., 2015). Collectively, these  
39 regions are sometimes referred to as posteromedial cortex (Parvizi et al., 2006). The  
40 vulnerability of posteromedial cortex to AD pathology has been linked to its hub-like  
41 properties (Jagust, 2018), in particular its high-levels of baseline metabolic/neural activity  
42 and high intrinsic/extrinsic connectivity (Bero et al., 2012; Buckner et al., 2009; de Haan et  
43 al., 2012). Notably, posteromedial cortex is densely connected with several medial temporal  
44 lobe structures, such as parahippocampal cortex and hippocampus, forming a “posterior  
45 medial” or “extended navigation” network (Murray et al., 2017; Ranganath & Ritchey, 2012).  
46 This broader network is implicated in several inter-related cognitive functions that are  
47 impaired early in AD, such as episodic memory (Rajah et al., 2017), perceptual scene  
48 discrimination (Lee et al., 2006), and spatial navigation (Coughlan et al., 2018). Given this,  
49 there is a pressing need to identify biomarkers that capture the functional and/or structural  
50 integrity of this AD-vulnerable brain network. In this context, the parahippocampal cingulum  
51 bundle (PHCB) – a prominent white matter tract linking posteromedial cortex with the medial  
52 temporal lobe (Bubb et al., 2018; Heilbronner & Haber, 2014; Jitsuishi & Yamaguchi, 2021) –  
53 represents a strong candidate for understanding and characterising connectivity alterations  
54 associated with AD.

56 Increasing evidence indicates that PHCB connectivity is altered in AD. Using diffusion  
57 magnetic resonance imaging (dMRI), a non-invasive method that examines the random,  
58 microscopic movement of water molecules, it is possible to delineate the major white matter  
59 tracts of the brain and evaluate their microstructural properties *in vivo* (Assaf et al., 2019). In  
60 most AD-relevant dMRI studies, white matter microstructure is assessed via measures  
61 derived from the diffusion tensor, notably fractional anisotropy (FA) and mean diffusivity  
62 (MD; Harrison et al., 2020). Low FA and high MD are widely interpreted as representing  
63 poorer microstructural integrity and thus lower connectivity (Yeh et al., 2021), although  
64 multiple biological factors – including neuroinflammation (Kor et al., 2022) – can influence  
65 these measures (Jones, Knösche, & Turner, 2013). Studies comparing AD patients to  
66 cognitively normal older adults using dMRI have reliably observed both lower FA and higher  
67 MD in the cingulum bundle and the PHCB in particular (Acosta-Cabronero et al., 2010;  
68 Bozzali et al., 2012; Choo et al., 2010; Kantarci et al., 2017). In addition, longitudinal  
69 changes in PHCB microstructure – reduced FA, increased MD – have been reported among  
70 AD patients but not cognitively normal older adults (Mayo et al., 2017). Indeed, it has  
71 recently been suggested that PHCB FA constitutes a highly effective biomarker for  
72 differentiating between typical ageing and AD (Dalboni da Rocha et al., 2020).

73

74 Studies of amnestic mild cognitive impairment (aMCI), a transitional stage between typical  
75 ageing and AD (Albert et al., 2011), further highlight that PHCB alterations precede the  
76 onset of AD dementia. In one region-of-interest (ROI) meta-analysis, for example, Yu et al.  
77 (2017) identified robust alterations in PHCB microstructure (lower FA, higher MD) among  
78 individuals with aMCI. This is congruent with the notion that cingulum bundle alterations  
79 predict cognitive decline in aMCI and may even predict conversion to AD (Gozdas et al.,  
80 2020). Studies combining positron emission tomography and dMRI have also allowed PHCB  
81 changes to be linked directly to AD pathology. For example, amyloid- $\beta$  burden has been  
82 associated with longitudinal changes in white matter microstructure that are consistent with  
83 patterns observed in aMCI and AD (Rieckmann et al., 2016; Song et al., 2018; Vipin et al.,

84 2019). In particular, high levels of cortical amyloid- $\beta$  burden at baseline have been  
85 associated with accelerated decline in PHCB FA and a trend-level increase in PHCB MD  
86 (Rieckmann et al., 2016). In keeping with this tract-specific finding, one recent cross-  
87 sectional study reported that lower FA and higher MD in the PHCB was associated with  
88 greater cortical amyloid- $\beta$  and entorhinal tau burden, especially in those with high levels of  
89 pre-existing pathology (Pichet Binette et al., 2021). It thus appears that PHCB  
90 microstructure is detrimentally impacted over the course of AD, including stages prior to the  
91 onset of dementia symptoms.

92

93 Emerging research indicates, however, that asymptomatic individuals exhibit alterations in  
94 white matter microstructure that run counter to the characteristic AD pattern. Illustrating this  
95 point, several studies have observed higher FA and lower MD in early-stage amyloid- $\beta$   
96 pathology, a pattern that is reversed as pathology further accrues (Collij et al., 2021; Dong et  
97 al., 2020; Wolf et al., 2015). These findings point to a biphasic pattern of microstructure over  
98 the disease course, with a period of high FA/low MD preceding the pattern commonly  
99 observed in patients with aMCI and AD. While increased FA in the context of early AD  
100 pathology could reflect neuroinflammation (Benitez et al., 2021; Dong et al., 2020), there is  
101 evidence that heightened activity and connectivity – including structural connectivity – may  
102 actually precede AD pathology, predisposing individuals to later amyloid- $\beta$  deposition (Bero  
103 et al., 2012; Buckner et al., 2009; de Haan et al., 2012). Support for this proposal can be  
104 found in studies of young adults carriers of the apolipoprotein-E (*APOE*)  $\epsilon$ 4 allele. The *APOE*  
105  $\epsilon$ 4 allele is the strongest common genetic risk factor for AD (Belloy et al., 2019), and is also  
106 associated with a younger age of onset and faster rate of posteromedial amyloid- $\beta$   
107 accumulation (Burnham et al., 2020; Mishra et al., 2018). In line with the notion that this  
108 amyloid- $\beta$  accumulation is related to earlier connectivity changes, a study applying graph  
109 theoretical analysis to dMRI data observed that age was negatively associated with local  
110 interconnectivity in posteromedial regions, but only among *APOE*  $\epsilon$ 4 carriers (Brown et al.,  
111 2011). Higher levels of local interconnectivity in younger adults drove this finding, such that

112 there was a putative *APOE* ε4-related increase in connectivity early in life that was  
113 subsequently followed by a sharper decline later in the lifespan (Brown et al., 2011; see also  
114 Ma et al., 2017). Relatedly, Felsky and Voineskos (2013) further reported higher cingulum  
115 bundle FA in younger *APOE* ε4 carriers compared to younger non-carriers, but lower  
116 cingulum bundle FA in older *APOE* ε4 carriers compared to older non-carriers. Given that  
117 young adults are unlikely to possess significant amyloid-β burden (Jansen et al., 2015),  
118 these findings suggest that early-life structural alterations may precede pathology.

119

120 Consistent with this, Hodgetts et al. (2019) observed higher FA and lower MD among *APOE*  
121 ε4 carriers relative to non-carriers in the PHCB but not the inferior longitudinal fasciculus  
122 (ILF), a tract that connects the occipital lobe to the ventro-anterior temporal lobe (Herbet et  
123 al., 2018). Hodgetts et al. also found that PHCB microstructure was correlated with  
124 posteromedial cortex activity during perceptual scene discrimination, a task that has  
125 previously been shown to elicit heightened activity in young *APOE* ε4 carriers (Shine et al.,  
126 2015) and is sensitive to AD (Lee et al., 2006). Based on the proposal that heightened  
127 neural activity and connectivity can have a significant role in hub-like vulnerability to amyloid-  
128 β (Bero et al., 2012; Buckner et al., 2009; de Haan et al., 2012), it is plausible that such  
129 early-life PHCB alterations may explain why *APOE* ε4 is associated with earlier and faster  
130 posteromedial amyloid-β accumulation (Burnham et al., 2020; Mishra et al., 2018).

131 Moreover, as the spread of tau has been linked to heightened functional connectivity  
132 between posteromedial cortex and the medial temporal lobe (Ziontz et al., 2021) –  
133 presumably mediated by the PHCB (Jacobs et al., 2018) – it is possible that early-life  
134 increases in structural connectivity are also related to elevated tau in *APOE* ε4 carriers  
135 (Therriault et al., 2020).

136

137 In view of the potential implications for understanding the role of *APOE* ε4 in AD risk, we  
138 sought to replicate Hodgetts et al.'s (2019) finding that healthy young adult *APOE* ε4 carriers  
139 demonstrate higher FA and lower MD than non-carriers in the PHCB but not the ILF. We

140 analysed data from an independent data set of young adults, with a total sample over four  
141 times larger than the original study. This replication attempt thus constitutes an important  
142 test of the notion that increased PHCB connectivity, as indexed by higher FA and lower MD,  
143 is evident in young adult *APOE* ε4 carriers, potentially increasing vulnerability to both  
144 amyloid-β accumulation and tau spread.

145

146 We also report additional exploratory analyses that seek to extend this work by incorporating  
147 a more advanced measure of microstructure: hindrance modulated orientational anisotropy  
148 (HMOA; Dell'Acqua et al., 2013). HMOA is regarded as a tract-specific measure of  
149 microstructure and is argued to be more sensitive to alterations in anisotropy than either FA  
150 or MD (Dell'Acqua et al., 2013). As such, we investigated whether *APOE* ε4 is associated  
151 with differences in PHCB and ILF HMOA, complementing the primary (replication) analyses.  
152 In addition, we also assessed whether *APOE* ε4 is associated with asymmetry in PHCB and  
153 ILF HMOA. Recent evidence suggests that AD is characterised by a loss of typical or  
154 “healthy” leftward structural and functional asymmetry in the brain (Banks et al., 2018; Roe  
155 et al., 2021; Tyrer et al., 2020), perhaps as a result of hemispheric differences in  
156 susceptibility to AD pathology (Lubben et al., 2021; Weise et al., 2018). Given the proposal  
157 that early-life *APOE* ε4-related alterations in neural activity and connectivity increase  
158 vulnerability to AD pathology, notably amyloid-β accumulation but perhaps also tau spread, it  
159 is plausible that this allele may be associated with changes in the asymmetry of key white  
160 matter tracts. To our knowledge, no study to date has yet investigated this possibility,  
161 especially in healthy young adults.

162

## 163 **2. Method**

### 164 2.1. Participants

165 Participant data were acquired from a repository at the Cardiff University Brain Research  
166 Imaging Centre. Portions of this data have been published elsewhere (Foley et al., 2017;  
167 Koelewijn et al., 2019). Participants were healthy adults, who were screened via interview or

168 questionnaire for the presence of neuropsychiatric disorders. All were right-handed, had  
169 normal or corrected-to-normal vision, and provided informed consent for their data to be  
170 used in imaging genetics analyses. All procedures were originally reviewed and approved by  
171 the Cardiff University School of Psychology Research Ethics Committee. For the current  
172 study, participants were only included if they completed the requisite MRI scans, had *APOE*  
173 genotype information available, and were aged 35 years or under ( $N = 148$ ). After additional  
174 exclusions were applied – described below (see also Supplementary Figure 1) – the final  
175 sample comprised 128 participants (86 females, 42 males) aged between 19 and 33 years  
176 ( $M = 23.8$ ,  $SD = 3.6$ ).

177

178 Consistent with Hodgetts et al. (2019), the final sample was split into carrier and non-carrier  
179 groups based on the presence/absence of the *APOE*  $\epsilon 4$  allele (Table 1). Participants  
180 carrying both risk-enhancing ( $\epsilon 4$ ) and risk-reducing ( $\epsilon 2$ ) *APOE* alleles were included as part  
181 of the carrier group, as the  $\epsilon 2\epsilon 4$  genotype is associated with higher levels of AD pathology  
182 and risk (Goldberg et al., 2020; Jansen et al., 2015; Reiman et al., 2020). Although *APOE* is  
183 often directly genotyped, as in Hodgetts et al.'s study, here it was inferred from imputed  
184 (1000G phase 1, version 3) genome-wide genetic data (for more detail, see Foley et al.,  
185 2017). Previous research has demonstrated that it is possible to accurately infer *APOE*  
186 genotypes using this method (Lupton et al., 2018; Oldmeadow et al., 2014; Radmanesh et  
187 al., 2014). Overall, the current sample included 40 *APOE*  $\epsilon 4$  carriers (4  $\epsilon 2/\epsilon 4$ , 33  $\epsilon 3/\epsilon 4$ , 3  
188  $\epsilon 4/\epsilon 4$ ) and 88 *APOE*  $\epsilon 4$  non-carriers (4  $\epsilon 2/\epsilon 2$ , 14  $\epsilon 2/\epsilon 3$ , 70  $\epsilon 3/\epsilon 3$ ). An effect size sensitivity  
189 analysis calculated using the *pwr* package (version 1.2-2; Champely, 2018) in R (version  
190 3.6.0; R Core Team, 2019) using RStudio (version 1.3.1093; RStudio Team, 2020) revealed  
191 that the smallest effect size detectable at 80% power was Cohen's  $d_s = 0.575$  ( $1-\beta = .80$ ,  
192 Bonferroni-corrected  $\alpha = .016$ , directional hypothesis). By comparison, even without  
193 correcting the  $\alpha$  level for multiple comparisons, the smallest effect size detectable at 80%  
194 power in Hodgetts et al.'s study was Cohen's  $d_s = 0.931$  ( $1-\beta = .80$ ,  $\alpha = .05$ , directional

195 hypothesis). Basic sample characteristics in this study and in Hodgetts et al.'s study are  
196 compared in Supplementary Table 1.

197

198

**Table 1**

*Basic Sample Characteristics Separated by APOE ε4 Carrier Status.*

	<i>APOE ε4+</i> (n = 40)	<i>APOE ε4-</i> (n = 88)	Statistics
Age (years; <i>M</i> ± <i>SD</i> )	23.9 ±3.3	23.7 ±3.7	$t(84.84) = 0.226, p = .822$ , Cohen's $d_s$ = 0.042, $BF_{10} = 0.206$
Sex (Males/Females; <i>n</i> ) <sup>a</sup>	12/28	30/58	$X^2(1, N = 128) = 0.209, p = .648, \varphi = 0.04$ , $BF_{10} = 0.241$

*Note.* Frequentist null hypothesis significance tests (two-sided Welch's *t*-test for age, chi-square test for sex) revealed no significant difference between *APOE ε4* carriers and non-carriers in terms of age or sex. Effect sizes were also small, while complementary BF analyses provided moderate evidence in support of the null hypothesis of no difference.

Abbreviations: *APOE ε4+* = *APOE ε4* carrier, *APOE ε4-* = *APOE ε4* non-carrier, *M* = mean, *n* = number of participants, *SD* = standard deviation.

<sup>a</sup>Although sex was self-reported, it was checked against chromosomal sex as part of genetic quality control procedures (Foley et al., 2017).

199

200

201 2.2. MRI scan parameters

202 Scanning was conducted on a GE SIGNA HDx 3T MRI system (General Electric Healthcare,

203 Milwaukee, WI) with an eight-channel receive-only head coil. Whole-brain high angular

204 resolution diffusion imaging data (Tuch et al., 2002) were acquired using a diffusion-

205 weighted single-shot echo-planar imaging sequence (TE = 89ms; voxel dimensions = 2.4 x

206 2.4 x 2.4mm; FOV = 230mm x 230mm; acquisition matrix = 96 x 96; 60 slices aligned AC/PC

207 with 2.4mm thickness and no gap). Gradients were applied along 30 isotropic directions

208 (Jones et al., 1999) with *b* = 1200 s/mm<sup>2</sup>. Three non-diffusion-weighted images were

209 acquired with *b* = 0 s/mm<sup>2</sup>. Acquisitions were cardiac-gated using a peripheral pulse

210 oximeter. T1-weighted anatomical images were acquired using a three-dimensional fast

211 spoiled gradient-echo sequence (TR/TE = 7.8/3s; voxel dimensions = 1mm isotropic; FOV

212 ranging from 256 x 256 x 168mm to 256 x 256 x 180mm; acquisition matrix ranging from 256  
213 x 256 x 168 to 256 x 256 x 180; flip angle = 20°). These sequences were similar to those  
214 used by Hodgetts et al. (2019), with only subtle differences between the two studies  
215 (outlined in Supplementary Table 2).

216

217 2.3. dMRI

218 2.3.1. Pre-processing

219 The dMRI data were corrected for motion- and eddy current-induced distortions in  
220 ExploreDTI (version 4.8.6; Leemans et al., 2009), with an appropriate reorientation of the b-  
221 matrix (Leemans & Jones, 2009). Images were registered to down-sampled T1-weighted  
222 images (1.5mm isotropic resolution) to correct for susceptibility deformations (Irfanoglu et al.,  
223 2012). Data were visually checked as part of quality assurance procedures, leading to the  
224 removal of two participants from the analysis due to poor quality data. Consistent with  
225 Hodgetts et al. (2019), the two-compartment free-water elimination procedure was  
226 implemented using in-house MATLAB code (version R2015a; MathWorks, Inc., 2015) to  
227 correct for voxel-wise partial volume artefacts (Pasternak et al., 2009). This procedure has  
228 been shown to improve tract delineation, as well as the sensitivity and specificity of  
229 measures traditionally derived from the diffusion tensor (Pasternak et al., 2009). Free-water  
230 corrected FA and MD maps were then used in further analyses. FA represents the degree to  
231 which diffusion is constrained in a particular direction, ranging from 0 (isotropic diffusion) to 1  
232 (anisotropic diffusion). By contrast, MD ( $10^{-3}\text{mm}^2\text{s}^{-1}$ ) represents the average diffusivity rate.

233

234 2.3.2. Tractography

235 The RESDORF algorithm was used to identify outliers in the diffusion data (Parker, 2014),  
236 and then tractography was conducted in ExploreDTI using the modified damped Richardson  
237 Lucy spherical deconvolution algorithm (Dell'Acqua et al., 2010). Spherical deconvolution  
238 approaches enable multiple peaks to be extracted in the white matter fibre orientation  
239 density function (fODF) within a given voxel. This allows complex fibre arrangements, such

240 as crossing/kissing fibres, to be modelled more accurately (Dell'Acqua & Tournier, 2019).  
241 The current study and the original study by Hodgetts et al. (2019) both used spherical  
242 deconvolution approaches, although the latter used the constrained spherical deconvolution  
243 algorithm (Jeurissen et al., 2011). While this might lead to subtle differences between the  
244 two studies, the modified damped Richardson Lucy deconvolution algorithm was selected  
245 here because it is considered less sensitive to miscalibration (Parker et al., 2013). To  
246 minimise any further discrepancies between the studies, tracts were reconstructed using the  
247 same parameters used by Hodgetts et al. (fODF amplitude threshold = 0.1; step size =  
248 0.5mm; angle threshold = 60°).

249

250 In-house semi-automated tractography software (Parker et al., 2012) was used to generate  
251 three-dimensional reconstructions of the PHCB and ILF in both hemispheres. The software  
252 was trained on manual reconstructions generated by author R.L. using a waypoint ROI  
253 approach in ExploreDTI, where “SEED”, “AND”, and “NOT” ROIs were used to isolate tract-  
254 specific streamlines (Figure 1). ROIs were placed in the same regions as described by  
255 Hodgetts et al. (2019). Placement was therefore guided by established protocols for the  
256 PHCB (Jones, Christiansen et al., 2013) and the ILF (Wakana et al., 2007), respectively. All  
257 reconstructions generated by the semi-automated software were visually inspected by  
258 authors R.L. and C.J.H. and, where required, manually edited post hoc to remove  
259 erroneous, anatomically implausible fibres. Participants for whom the PHCB and ILF could  
260 not be reconstructed in both hemispheres were removed from analysis ( $n = 18$ ). Thereafter,  
261 measures of microstructure were obtained and averaged across tracts. Although the semi-  
262 automated approach used here differs to that used by Hodgetts et al., larger studies have  
263 shown this to be useful (Foley et al., 2017; Metzler-Baddeley et al., 2019). Furthermore,  
264 during visual inspection, author C.J.H. confirmed that tract reconstruction produced  
265 qualitatively similar outputs to those obtained in the original, to-be-replicated study.

266

267

268 **Figure 1**

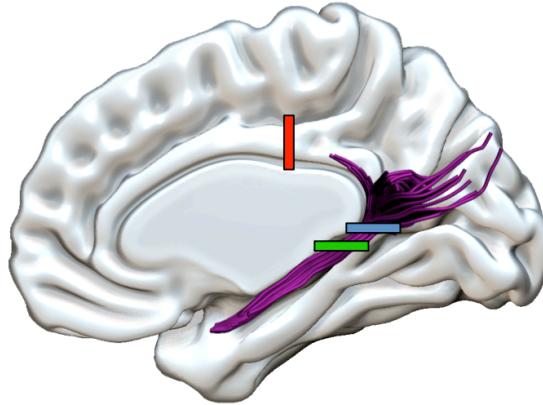
269 *Manual Reconstructions of the PHCB and ILF*

270

271

272

- 273       "SEED"
- 274       "AND"
- 275       "NOT"



276

277



281

282 Note. "SEED", "AND", and "NOT" ROIs used to manually reconstruct the PHCB are  
283 highlighted (*upper panel*). Example tract reconstructions are shown for both the PHCB and  
284 ILF (*lower panel*). The resulting tracts were used to train the semi-automated tractography  
285 software (Parker et al., 2012) and produce tracts for the entire sample. Abbreviations: ILF =  
286 inferior longitudinal fasciculus, PHCB = parahippocampal cingulum, ROI = region of interest.

287

288

289 2.3.3. Tract-based spatial statistics (TBSS)

290 Complementary voxel-wise statistical analysis of the FA and MD data was conducted using  
291 TBSS (Smith et al., 2006). Each participant's free-water corrected FA and MD maps were  
292 first aligned in standard MNI space using nonlinear registration (Andersson et al., 2007a,  
293 2007b). Next, the mean FA images were created and subsequently thinned (threshold = 0.2)  
294 to generate the mean FA skeleton, which represents the centre of all tracts common to the  
295 group. Each participant's aligned FA and MD data were then projected onto the skeleton and  
296 the resulting data carried forward for voxel-wise cross-subject analysis. These analyses  
297 were performed using *randomise* (Winkler et al., 2014), a permutation-based inference tool.

298 For both FA and MD, a general linear model contrasting *APOE* ε4 carriers and non-carriers  
299 (FA: carrier > non-carrier; MD: carrier < non-carrier) was applied (*n* permutations = 1000).  
300 Mirroring Hodgetts et al.'s (2019) example, analyses were first restricted to the PHCB using  
301 an ROI mask [labelled "cingulum (hippo-campus)"] from the John Hopkins University ICBM-  
302 DTI-81 white-matter tractography atlas. An exploratory whole-brain analysis was then  
303 conducted. Statistically significant clusters were extracted from both analyses using  
304 threshold-free cluster enhancement with a corrected *a* level of 0.05 (Smith and Nichols,  
305 2009).

306

307 2.4. Statistical analyses

308 Except for TBSS, all statistical analyses were conducted using R in RStudio. In addition to  
309 common frequentist null hypothesis significance tests, Bayes factors (BFs) were calculated.  
310 BFs quantify the degree to which the observed data favours predictions made by two  
311 models, in this case the null hypothesis and the alternative hypothesis. Consequently, BF  
312 analyses can provide evidence in support of the null (Dienes, 2014). In accordance with the  
313 evidence categories outlined by Lee and Wagenmakers (2013), a  $BF_{+0}$  ( $BF_{10}$  for two-sided  
314 tests) greater than 3 was considered to represent at least moderate evidence for the  
315 alternative hypothesis, whereas a  $BF_{+0}$  less than .33 was considered to represent at least  
316 moderate evidence for the null hypothesis.

317

318 2.4.1. Primary (replication) analyses

319 To test whether *APOE* ε4 carriers showed higher FA and lower MD in the PHCB but not the  
320 ILF, one-sided Welch's *t*-tests were conducted. As in Hodgetts et al. (2019), all tests were  
321 repeated, once with male participants removed and once with ε2 carriers removed. These  
322 additional tests – performed independently of each other – were originally conducted based  
323 on evidence that *APOE* ε4 may have a stronger effect on AD biomarkers in females than  
324 males (Riedel et al., 2016), whereas *APOE* ε2 may have a protective effect on AD  
325 biomarkers (Suri et al., 2013). To ensure that the probability of falsely rejecting the null – the

326 Type I error rate – was not inflated, a Bonferroni correction was applied to the  $\alpha$  level (.05 / 3  
327 = .016). Two BFs were also calculated: a default JZS BF and a replication BF. The default  
328 JZS BF, which uses a default prior distribution and was computed using the *BayesFactor*  
329 package (version 0.9.12-4.2; Morey & Rouder, 2018), examines whether an effect is present  
330 or absent in the data collected in the replication study regardless of the original effect. Here,  
331 one-sided (directional) default JZS BFs were calculated. The replication BF, by contrast,  
332 uses the posterior distribution of the original study as the prior distribution in the replication  
333 study, examining whether the original effect is present or absent in the data collected in the  
334 replication study. This BF was computed using previously published R code (Verhagen &  
335 Wagenmakers, 2014).

336

337 2.4.2. Secondary (extension) analyses

338 2.4.2.1. HMOA index

339 It remains to be seen whether *APOE*  $\epsilon 4$ -related differences in PHCB microstructure are  
340 better captured by measures other than FA and MD, which are sensitive to various aspects  
341 of white matter microstructure without being specific to any one (Jones, Knösche, & Turner,  
342 2013). One such measure is HMOA, which is defined as the absolute amplitude of each  
343 fODF lobe (Dell'Acqua et al., 2013). This is normalised using a reference amplitude in order  
344 to create an index bound between zero and one. A value of zero reflects the absence of a  
345 fibre, whereas a value of one reflects the highest fODF signal that can realistically be  
346 detected in biological tissue (Dell'Acqua et al., 2013).

347

348 Given the lack of a directional hypothesis relating to HMOA, two-sided Welch's *t*-tests and  
349 two-sided default JZS BFs were used to identify any differences between *APOE*  $\epsilon 4$  carriers  
350 and non-carriers. In keeping with the primary (replication) analyses described above, these  
351 tests were repeated with males removed and then with  $\epsilon 2$  carriers removed. These  
352 analytical steps were performed independently. A Bonferroni correction was applied to the  
353 nominal  $\alpha$  level (.05 / 3 = .016).

354 2.4.2.2. Hemispheric asymmetry

355 Despite reports linking AD with a loss of leftward structural and functional asymmetry (Banks  
356 et al., 2018; Roe et al., 2021; Tyrer et al., 2020), which may be related to differences in  
357 hemispheric susceptibility to pathology (Lubben et al., 2021; Weise et al., 2018), no study to  
358 our knowledge has yet investigated whether the *APOE* ε4 allele is associated with  
359 asymmetry in PHCB or ILF microstructure. Moreover, considering the proposed interaction  
360 between *APOE* ε4 and sex in the context of AD risk (Riedel et al., 2016), there is also an  
361 interesting question as to whether sex moderates any potential *APOE* ε4-related association  
362 with hemispheric asymmetry. We therefore examined whether HMOA – a more tract-specific  
363 measure – was lateralised to the left or right hemisphere, and whether this was impacted by  
364 *APOE* ε4, sex, or their interaction.

365

366 As with the analyses described previously, the ILF was included as a comparison tract.

367 Lateralisation indices (LIs) were calculated for HMOA in both the PHCB and ILF [LI = (right -  
368 left) / (right + left)]. For any given participant, a negative LI score indicates that HMOA was  
369 higher in the left hemisphere, whereas a positive LI score indicates that HMOA was higher in  
370 the right hemisphere (Zhao et al., 2016). These  $LI_{HMOA}$  scores were subsequently analysed  
371 using robust multiple linear regression, which was carried out via the *lmmrob* function from the  
372 *robustbase* package (version 0.93-7; Maechler et al., 2021). The fitted models were as  
373 follows:

374

375  $LI_{HMOA} \sim APOE \varepsilon 4 \text{ carrier status} \times \text{sex} + \text{age}$  (1)

376

377 LIs were entered as dependent variables. *APOE* ε4 carrier status and sex were treated as  
378 categorical variables and coded using deviation coding. Age – included as a covariate of “no  
379 interest” – was centred and scaled. The interaction between *APOE* ε4 carrier status and sex  
380 was included in the model. Results were deemed statistically significant if the observed *p*  
381 value was smaller than the nominal *α* level of 0.05.

382 2.5. Data and code availability  
383 R code used to analyse and visualise data in the current study is made publicly available via  
384 the Open Science Framework (<https://osf.io/f6jp3/>). Due to the sensitive nature of the data,  
385 the original ethics do not allow for the public archiving of study data (for more information,  
386 see Koelewijn et al., 2019). Access to pseudo-anonymised data may be granted, however,  
387 after the signing and approval of suitable data-transfer agreements. Readers seeking access  
388 through this mechanism should contact Professor Krish D. Singh at the Cardiff University  
389 Brain Research Imaging Centre ([singhkd@cardiff.ac.uk](mailto:singhkd@cardiff.ac.uk)).

390

### 391 **3. Results**

392 3.1. Primary (replication) analyses

393 3.1.1. Effect of *APOE ε4* on PHCB FA and MD

394 FA values for the PHCB – separated by *APOE ε4* carrier status – are shown in Figure 2A.

395 Contrary to our initial hypothesis, PHCB FA was not significantly higher for *APOE ε4* carriers  
396 than non-carriers ( $t(87.559) = -0.606$ ,  $p = .727$ , Cohen's  $d_s = -0.112$ ). Supporting this, BF  
397 analysis produced moderate evidence in favour of the null (default JZS  $BF_{+0} = 0.138$ ,  
398 replication  $BF_{10} = 0.141$ ). Removing males from the analysis did not alter the results in any  
399 meaningful way ( $t(57.685) = 0.045$ ,  $p = .482$ , Cohen's  $d_s = 0.01$ , default JZS  $BF_{+0} = 0.246$ ,  
400 replication  $BF_{10} = 0.168$ ), nor did removing ε2 carriers ( $t(84.459) = -0.923$ ,  $p = .821$ , Cohen's  
401  $d_s = -0.183$ , default JZS  $BF_{+0} = 0.125$ , replication  $BF_{10} = 0.271$ ).

402

403 MD values for the PHCB – separated by *APOE ε4* carrier status – are shown in Figure 2B.

404 Again, contrary to prior expectations, PHCB MD was not significantly lower for *APOE ε4*  
405 carriers than non-carriers ( $t(83.625) = 1.429$ ,  $p = .922$ , Cohen's  $d_s = 0.267$ ). Here, BF  
406 analysis revealed strong evidence in favour of the null (default JZS  $BF_{+0} = 0.092$ , replication  
407  $BF_{10} = 0.057$ ). As with FA, the results for MD did not change substantively after removing  
408 males ( $t(59.729) = 1.515$ ,  $p = .933$ , Cohen's  $d_s = 0.341$ , default JZS  $BF_{+0} = 0.106$ , replication

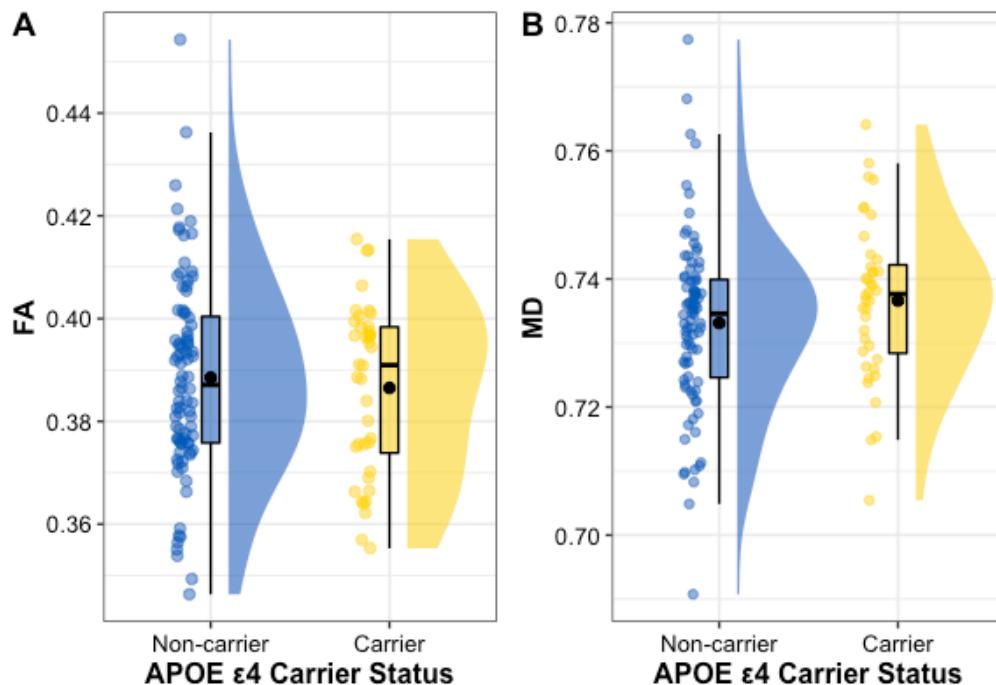
409  $BF_{10} = 0.054$ ) or after removing  $\epsilon 2$  carriers ( $t(79.581) = 1.328, p = .906$ , Cohen's  $d_s = 0.267$ ,  
410 default JZS  $BF_{+0} = 0.103$ , replication  $BF_{10} = 0.1$ ).

411

412

413 **Figure 2**

414 *Differences in PHCB FA and MD Between APOE  $\epsilon 4$  Carriers and Non-Carriers*



425 Note. Differences in (A) PHCB FA and (B) MD ( $10^{-3}\text{mm}^2\text{s}^{-1}$ ) between APOE  $\epsilon 4$  carriers and  
426 non-carriers are shown. Individual data points, each representing a single participant, are  
427 shown alongside boxplots and density plots ("raincloud plots"; Allen et al., 2021). A small  
428 amount of jitter has been added to each data point for clarity. To facilitate interpretation, the  
429 mean value (black circle) and median value (a black line) for each group are both shown.  
430 Abbreviations: FA = fractional anisotropy, MD = mean diffusivity.

431

432

433 3.1.2. Effect of APOE  $\epsilon 4$  on ILF FA and MD

434 The same analysis was conducted on ILF FA and MD. Analysis revealed that ILF FA was  
435 not significantly higher for APOE  $\epsilon 4$  carriers than non-carriers ( $t(86.143) = -0.864, p = .805$ ,  
436 Cohen's  $d_s = -0.16$ ). BF analysis provided moderate-to-strong evidence favouring the  
437 absence of an effect (default JZS  $BF_{+0} = 0.12$ ), as well as anecdotal-to-moderate evidence  
438 favouring the absence of the effect reported by Hodgetts et al. (replication  $BF_{10} = 0.309$ ).

439 This slight discrepancy between BFs is likely because the original to-be-replicated effect was  
440 also small and did not reach the threshold for statistical significance, meaning that the  
441 informed prior used was already more “sceptical” than the default prior. Results remained  
442 largely unchanged when males were removed ( $t(49.129) = -0.069, p = .527$ , Cohen's  $d_s = -$   
443 0.016, default JZS  $BF_{+0} = 0.226$ , replication  $BF_{10} = 0.308$ ) and when  $\epsilon 2$  carriers were  
444 removed ( $t(79.5) = -0.893, p = .813$ , Cohen's  $d_s = -0.179$ , default JZS  $BF_{+0} = 0.126$ ).

445

446 ILF MD was not significantly lower for *APOE*  $\epsilon 4$  carriers than non-carriers ( $t(81.941) = 0.54,$   
447  $p = .705$ , Cohen's  $d_s = 0.101$ ). BFs again provided evidence in support of the null (default  
448 JZS  $BF_{+0} = 0.142$ , replication  $BF_{10} = 0.446$ ). Removing males had no notable impact on the  
449 results ( $t(55.856) = 0.818, p = .792$ , Cohen's  $d_s = 0.187$ , default JZS  $BF_{+0} = 0.144$ ,  
450 replication  $BF_{10} = 0.613$ ) nor did removing *APOE*  $\epsilon 2$  carriers ( $t(75.242) = 0.713, p = .761$ ,  
451 Cohen's  $d_s = 0.145$ , default JZS  $BF_{+0} = 0.137$ ).

452

### 453 3.1.2. TBSS

454 Consistent with the tractography analysis, PHCB-restricted TBSS analysis revealed no  
455 significant differences between *APOE*  $\epsilon 4$  carriers and non-carriers. This was true of both FA  
456 (contrast: carriers > non-carriers) and MD (contrast: carriers < non-carriers). Adopting an  
457 uncorrected  $\alpha$  level of  $p = .005$ , as has been done previously (Hodgetts et al., 2019; Postans  
458 et al., 2014), did not alter this outcome. Exploratory whole-brain TBSS analysis provided  
459 complementary evidence, with no differences evident between *APOE*  $\epsilon 4$  carriers and non-  
460 carriers.

461

## 462 3.2. Secondary (extension) analyses

### 463 3.2.1. Effect of *APOE* $\epsilon 4$ on PHCB and ILF HMOA

464 Analysis revealed no significant difference between *APOE*  $\epsilon 4$  carriers and non-carriers in  
465 terms of PHCB HMOA ( $t(90.357) = -0.399, p = .691$ , Cohen's  $d_s = -0.073$ ). BF analysis also  
466 provided moderate evidence in favour of the null (default JZS  $BF_{10} = 0.215$ ). These results

467 were largely unaffected by the removal of males ( $t(58.33) = 0.445, p = .658$ , Cohen's  $d_s =$   
468 0.10, default JZS  $BF_{10} = 0.258$ ) or the removal of  $\epsilon 2$  carriers ( $t(85.926) = -0.844, p = .401$ ,  
469 Cohen's  $d_s = -0.167$ , default JZS  $BF_{10} = 0.283$ ).

470

471 For completeness, the same analysis was conducted for ILF HMOA. Results revealed that  
472 *APOE*  $\epsilon 4$  carriers and non-carriers did not differ significantly in terms of ILF HMOA  
473 ( $t(94.682) = -0.762, p = .448$ , Cohen's  $d_s = -0.139$ ). BF analysis provided complementary  
474 evidence, largely favouring the null (default JZS  $BF_{10} = 0.251$ ). This remained the case when  
475 males were removed ( $t(48.941) = 0.394, p = .696$ , Cohen's  $d_s = 0.092$ , default JZS  $BF_{10} =$   
476 0.256) and when individuals possessing the  $\epsilon 2$  allele were removed ( $t(84.914) = -0.819, p =$   
477 .415, Cohen's  $d_s = -0.162$ , default JZS  $BF_{10} = 0.279$ ).

478

### 479 3.2.2. Hemispheric asymmetry in PHCB and ILF HMOA

480 In terms of hemispheric asymmetry, analysis revealed that HMOA was higher in the right ( $M$   
481 = .234,  $SD = .015$ ) than the left ( $M = .224, SD = .018$ ) PHCB ( $t(127) = -6.631, p < .001$ ,  
482 Cohen's  $d_z = -0.586$ , default JZS  $BF_{10} > 100$ ). Nevertheless, for PHCB  $LI_{HMOA}$ , there was no  
483 significant association with *APOE*  $\epsilon 4$  ( $b < -.001, p = .911$ ), sex ( $b = -.002, p = .743$ ), or their  
484 interaction ( $b = -.008, p = .558$ ). Consequently, we observed no evidence indicating that  
485 *APOE*  $\epsilon 4$ , sex, or their interactions influenced hemispheric asymmetry in PHCB  
486 microstructure.

487

488 The same analysis was conducted on ILF microstructure. HMOA was higher in the left ( $M =$   
489 .302,  $SD = .027$ ) than the right ( $M = .293, SD = .029$ ) hemisphere ( $t(127) = 3.778, p < .001$ ,  
490 Cohen's  $d_z = 0.334$ , default JZS  $BF_{10} = 74.09$ ). Examining whether this hemispheric  
491 asymmetry was influenced by *APOE*  $\epsilon 4$ , sex, or their interaction, LIs were again calculated  
492 and analysed. In the case of ILF  $LI_{HMOA}$ , there was a significant association with *APOE*  $\epsilon 4$  ( $b$   
493 = 0.027,  $p = .005$ ) but not with sex ( $b = 0.014, p = .156$ ) or their interaction ( $b = 0.007, p =$

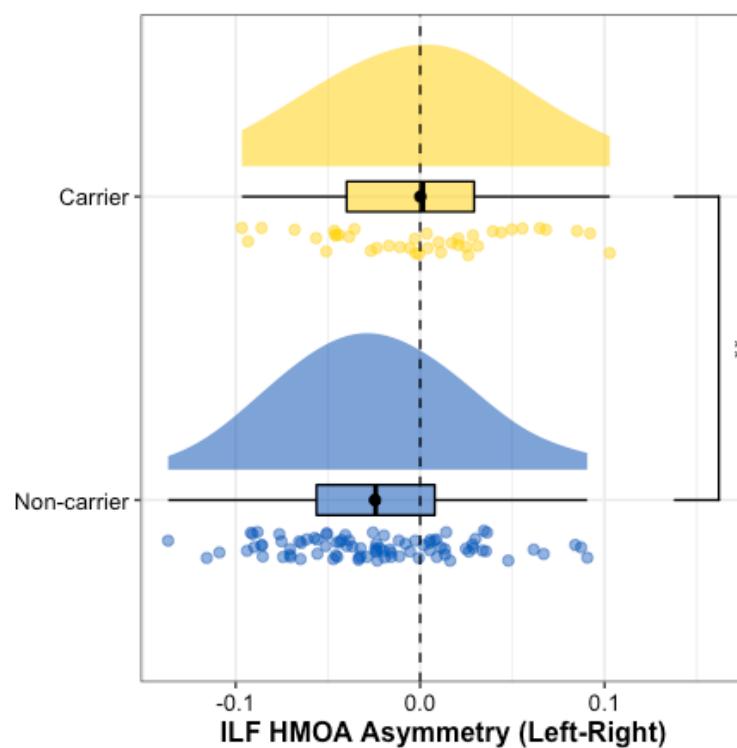
494 .674). Figure 3 highlights the group-level differences in ILF  $LI_{HMOA}$ . As shown, this was driven  
495 by reduced leftward asymmetry in this tract among *APOE*  $\epsilon 4$  carriers than non-carriers.

496

497

498 **Figure 3**

499 *Difference in ILF  $LI_{HMOA}$  Between *APOE*  $\epsilon 4$  Carriers and Non-Carriers*



513 Note. Differences in ILF  $LI_{HMOA}$  between *APOE*  $\epsilon 4$  carriers and non-carriers are shown.  
514 Negative values indicate that HMOA was higher in the left hemisphere, whereas positive  
515 values indicate that HMOA was higher in the right hemisphere. Zero – highlighted by a  
516 dashed line – indicates no asymmetry. Individual data points, each representing a single  
517 participant, are shown alongside boxplots and density plots (“raincloud plots”; Allen et al.,  
518 2021). A small amount of jitter has been added to each data point for clarity. To facilitate  
519 interpretation, the mean value (black circle) and median value (a black line) for each group  
520 are both shown. Abbreviations: HMOA = hindrance modulate orientation anisotropy, LI =  
521 lateralisation index.

522

523

524 **4. Discussion**

525 In this study, we aimed to replicate Hodgetts et al.’s (2019) findings that healthy young

526 *APOE*  $\epsilon 4$  carriers show higher FA and lower MD than non-carriers in the PHCB but not the

527 ILF. Such a pattern would be in line with suggestions that individuals with pre-existing  
528 “hyper-connectivity” between posteromedial cortex and the medial temporal lobe may be  
529 more vulnerable to amyloid- $\beta$  accumulation (Buckner et al., 2009; Bero et al., 2012; de Haan  
530 et al., 2012) and/or tau spread (Jacobs et al., 2018; Ziontz et al., 2021). Extending this work,  
531 we also conducted analyses on HMOA, a measure that is proposed to be more sensitive to  
532 alterations in tract microstructure than FA or MD (Dell’Acqua et al., 2013). This included an  
533 investigation into hemispheric asymmetry in PHCB and ILF HMOA, as prior reports indicate  
534 that AD impacts brain asymmetry (Banks et al., 2018; Roe et al., 2021; Tyrer et al., 2020).

535

536 In contrast to the original study, we did not observe higher FA or lower MD in the PHCB of  
537 young *APOE*  $\epsilon$ 4 carriers compared to non-carriers. Rather, we found: no statistically  
538 significant effects in the expected direction (all  $ps \geq .482$ ); relatively small effect sizes  
539 (Cohen’s  $d_s$  range from -0.183 to 0.341); and BFs providing evidence in favour of the null  
540 (default JZS  $BF_{+0}$  range from .092 to .246, replication  $BF_{10}$  range from .054 to .273).

541 Crucially, these BFs represent moderate-to-strong evidence in support of the null hypothesis  
542 (Lee & Wagenmakers, 2013). As such, we not only failed to replicate the effect reported by  
543 Hodgetts et al. (2019), but also found evidence against the presence of such an effect.

544 There are several plausible explanations for this, although they are not necessarily mutually  
545 exclusive.

546

547 First, it could be the case that Hodgetts et al.’s (2019) findings were false positives (see also  
548 Dell’Acqua et al., 2015). Hodgetts et al.’s study included just 15 participants in the *APOE*  $\epsilon$ 4  
549 carrier and non-carrier groups and, as such, was likely underpowered to detect an effect of  
550 the magnitude one might expect from this common genetic variant, especially in early  
551 adulthood (Henson et al., 2020). Given that low statistical power reduces the probability that  
552 an observed effect represents a true effect (Button et al., 2013), it is possible that the effects  
553 reported by Hodgetts et al. were false positives, although it is unclear how this relates the  
554 their observation that PHCB microstructure correlated with posteromedial cortex activity

555 during perceptual scene discrimination (see also Shine et al., 2015). The BF analyses  
556 conducted here provide complementary support for this assertion, demonstrating that the  
557 observed data favour the null. Taken at face value, this interpretation casts doubt on the  
558 notion that increased connectivity between posteromedial cortex and the medial temporal  
559 lobe – mediated by individual differences in PHCB microstructure – represents a pre-existing  
560 *APOE ε4*-related trait enhancing vulnerability to amyloid-β accumulation and/or tau spread.

561

562 Alternatively, it could be the case that Hodgetts et al. (2019) observed a true effect, but its  
563 magnitude was exaggerated. Effect size inflation is most likely to occur in studies with small  
564 sample sizes, a phenomenon referred to as the “winner’s curse” (Button et al., 2013). If true,  
565 the analysis reported in this replication attempt might itself be underpowered to detect the  
566 effect of *APOE ε4* on PHCB FA and MD, thereby constituting a Type II error or false  
567 negative. Such an explanation would help to reconcile the observed findings with prior  
568 results indicating that *APOE ε4* does have an impact on posteromedial connectivity early in  
569 life (Brown et al., 2011; Felsky & Voineskos, 2013; Hodgetts et al., 2019). While this cannot  
570 currently be ruled out, it should be noted that an effect size sensitivity analysis revealed that  
571 the smallest effect size detectable at 80% power in the current study was Cohen’s  $d_s = 0.57$ .  
572 In addition, the BF analyses conducted here indicated that the observed data provided  
573 moderate-to-strong evidence in favour of the null, as opposed to simply providing  
574 inconclusive evidence. This shows that, even with the current sample size, our findings have  
575 relatively high evidential value (Dienes, 2014).

576

577 Another potential explanation is that the *APOE ε4* carriers and non-carriers included in the  
578 two studies differed in other AD-relevant factors. It is well established that while *APOE ε4*  
579 carriers are at increased risk of developing AD relative to non-carriers, not all go on to  
580 develop the disease (Liu et al., 2013). In fact, only ~50% of individuals with AD possess one  
581 or more copies of the *APOE ε4* allele (Karch et al., 2014), highlighting the importance of  
582 other factors – genetic and environmental – in disease risk/protection (Jagust & Mormino,

583 2011; Silva et al., 2019). Following this line of reasoning, it is possible that – due to sampling  
584 variation – the *APOE ε4* carrier and non-carrier groups included in the two studies differed in  
585 their overall AD risk profiles, with potential implications for white matter microstructure. This  
586 would at least partly explain why we failed to replicate the effect originally reported by  
587 Hodgetts et al. (2019). Nevertheless, it is important to recognise that this remains an open  
588 question, and large-scale dMRI studies are required to test this possibility.

589

590 Regarding the asymmetry of PHCB microstructure, we found that HMOA was higher in the  
591 right hemisphere. This is consistent with some previous reports using diffusion tensor  
592 metrics (Metzler-Baddeley et al., 2012; Powell et al., 2012), although certainly not all (Lebel  
593 et al., 2012; Thiebaut de Schotten et al., 2011). Prior research has suggested that while left-  
594 hemispheric networks exhibit increased nodal efficiency in brains areas supporting  
595 language, right-hemispheric networks exhibit increased nodal efficiency in brain areas  
596 related to episodic memory (Caeyenberghs & Leemans, 2014). This potentially highlights a  
597 functional role for the observed rightward asymmetry in PHCB microstructure. However, we  
598 did not observe an effect of *APOE ε4* or sex on the degree of PHCB asymmetry.

599

600 A different pattern emerged in the analysis of ILF microstructure, with HMOA characterised  
601 by leftward asymmetry. As with the PHCB, this finding is consistent with a number of studies  
602 examining asymmetry in ILF volume and diffusion tensor-derived measures of  
603 microstructure (Banfi et al., 2019; Panesar et al., 2018; Thiebaut de Schotten et al., 2011).  
604 We also observed that the degree of asymmetry in this tract was associated with *APOE ε4*  
605 carrier status, such that asymmetry was lower in carriers relative to non-carriers, mirroring to  
606 some extent the loss of leftward asymmetry in AD (Banks et al., 2018; Roe et al., 2021;  
607 Tyrer et al., 2020). The ILF connects occipital and ventro-anterior temporal lobe (Herbet et  
608 al., 2018), underpinning a network involved in representing item information, including  
609 semantic and perceptual information (Murray et al., 2017; Ranganath & Ritchey, 2012).  
610 Recent research suggests that complex item discrimination is impaired in AD risk (Fidalgo et

611 al., 2016; Mason et al., 2017), which has in turn been linked to the structure and function of  
612 components within this network (Berron et al., 2018; Olsen et al., 2017; Reagh et al., 2016).  
613 Indeed, complex item discrimination has been proposed as a useful measure for the  
614 detection of early AD (Gaynor et al., 2019). In addition, a recent study of young adult *APOE*  
615  $\epsilon 4$  carriers in the Human Connectome Project failed to replicate enhanced intrinsic functional  
616 connectivity between posteromedial cortex and the medial temporal lobe, as observed  
617 previously (Filippini et al., 2009), but found heightened activity in left hemisphere regions  
618 connected by the ILF during face encoding (Mentink et al., 2021), possibly suggestive of a  
619 lifelong neural inefficiency (Jagust & Mormino, 2011). Future research should seek to  
620 replicate further the effect of *APOE*  $\epsilon 4$  on reduced structural (and functional) left hemispheric  
621 asymmetry, especially given potential implications for later life cognition (Jiang et al., 2021;  
622 Maass et al., 2019).

623

624 **5. Summary**

625 In this study, we failed to replicate Hodgetts et al.'s (2019) finding that, relative to non-  
626 carriers, healthy young adult *APOE*  $\epsilon 4$  carriers show higher FA and lower MD in the PHCB  
627 but not the ILF. Rather, the observed data strongly supported the null hypothesis of no  
628 difference. Our findings thus suggest that young adult *APOE*  $\epsilon 4$  carriers do not show  
629 alterations in PHCB microstructure that might enhance vulnerability – via excessive  
630 connectivity-dependent neuronal activity – to amyloid- $\beta$  accumulation and/or tau spread.  
631 Nevertheless, marked patterns of hemispheric asymmetry were evident in PHCB and ILF  
632 microstructure, although only the latter was associated with *APOE*  $\epsilon 4$  carrier status. Given  
633 the potential implications for later life cognition, our study highlights an important area for  
634 future research seeking to understand how this AD risk factor impacts neural and cognitive  
635 efficiency years prior to the onset of clinical symptoms.

636

637

638

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640

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