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# Brain clocks capture diversity and disparity in aging and dementia

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111 **Abstract**

112 Brain clocks, which quantify discrepancies between brain age and chronological age, hold  
113 promise for understanding brain health and disease. However, the impact of multimodal diversity  
114 (geographical, socioeconomic, sociodemographic, sex, neurodegeneration) on the brain age gap  
115 (BAG) is unknown. Here, we analyzed datasets from 5,306 participants across 15 countries (7  
116 Latin American countries -LAC, 8 non-LAC). Based on higher-order interactions in brain signals,  
117 we developed a BAG deep learning architecture for functional magnetic resonance imaging  
118 (fMRI=2,953) and electroencephalography (EEG=2,353). The datasets comprised healthy  
119 controls, and individuals with mild cognitive impairment, Alzheimer's disease, and behavioral  
120 variant frontotemporal dementia. LAC models evidenced older brain ages (fMRI: MDE=5.60,  
121 RMSE=11.91; EEG: MDE=5.34, RMSE=9.82) compared to non-LAC, associated with  
122 frontoposterior networks. Structural socioeconomic inequality and other disparity-related factors  
123 (pollution, health disparities) were influential predictors of increased brain age gaps, especially in  
124 LAC ( $R^2=0.37$ ,  $F^2=0.59$ , RMSE=6.9). A gradient of increasing BAG from controls to mild  
125 cognitive impairment to Alzheimer's disease was found. In LAC, we observed larger BAGs in  
126 females in control and Alzheimer's disease groups compared to respective males. Results were  
127 not explained by variations in signal quality, demographics, or acquisition methods. Findings  
128 provide a quantitative framework capturing the multimodal diversity of accelerated brain aging.

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135 **Main**

136 The brain undergoes dynamic functional changes with age<sup>1-3</sup>. Accurately mapping the trajectory  
137 of these changes and how they relate to chronological age is critical for understanding the aging  
138 process, multilevel disparities<sup>4,5</sup>, and brain disorders<sup>1</sup> such as the Alzheimer's disease continuum,  
139 which includes mild cognitive impairment (MCI), and related disorders like behavioral variant  
140 frontotemporal dementia (bvFTD) <sup>6</sup>. Brain clocks or brain age models have emerged as  
141 dimensional, transdiagnostic metrics that measure brain health influenced by a range of factors<sup>7-</sup>  
142 <sup>9</sup>, suggesting that they may be able to capture multimodal diversity<sup>10</sup>. Notably, underrepresented  
143 populations from Latin American countries (LAC) exhibit higher genetic diversity and distinct  
144 physical, social and internal exposomes<sup>11,12</sup> that impact brain phenotypes<sup>4,13,14</sup>. Income and  
145 socioeconomic inequality<sup>15,16</sup>, high levels of air pollution<sup>17</sup>, limited access to timely and effective  
146 healthcare<sup>18</sup>, **increased prevalence of communicable diseases**<sup>19</sup>, rising prevalence of non-  
147 communicable diseases<sup>19,20</sup>, and low education attainment<sup>21,22</sup>, are determinants of brain health in  
148 LAC<sup>18</sup>. Thus, although measuring the brain age gap (BAG) could enhance our understanding of  
149 disease risk and its impact on accelerated aging<sup>23</sup>, there is a lack of research on brain age models  
150 in underrepresented populations with increased socioeconomic and health disparities<sup>18,24,25</sup>.

151

152 Sex and gender differences emerge as critical factors influencing brain changes. Studies on  
153 atrophy in Alzheimer's disease continuum reveal a faster rate of brain atrophy in females than in  
154 males<sup>26</sup>. Moreover, country-level gender inequality is associated to sex differences in cortical  
155 thickness<sup>27</sup>. Structural gender inequality further impacts brain health, with adverse environments  
156 affecting dendritic branching and synapse formation<sup>28</sup>. However, no studies to date have explored  
157 the spectrum of brain age abnormalities, including the effects of demographic heterogeneity across  
158 geographical regions, sexes, and the continuum from brain health to disease. Further, most studies

159 have been conducted with participants from the global north, resulting in a lack of generalization  
160 to underrepresented populations from LAC<sup>24,29-31</sup>.

161  
162 Multimodal machine learning studies show promise in brain aging<sup>23</sup>; however, most rely on  
163 structural MRI, overlooking brain network dynamics. Complex spatiotemporal dimensions can be  
164 tracked with spatial accuracy through functional magnetic resonance imaging (fMRI) and  
165 millisecond precision using electroencephalogram (EEG)<sup>32</sup>. Given the complementary strengths  
166 of fMRI and EEG, it is crucial to cross-validate existing brain clock models using these  
167 techniques. However, no studies have simultaneously applied EEG and fMRI to replicate brain  
168 age effects. Additionally, standard machine learning approaches are less generalizable than deep  
169 learning methods<sup>33</sup>. Brain age indices has been restricted by the predominant use of MRI or PET,  
170 which are less accessible and affordable in LAC, leading to selection biases<sup>34</sup>. EEG offers a  
171 solution due to its cost-effectiveness, portability, and ease of implementation in aging and  
172 dementia<sup>35,36</sup>. However, few studies have combined accessible techniques with deep learning to  
173 develop scalable brain age markers. The application of EEG is hindered by heterogeneity in  
174 recordings, electrode layouts, acquisition systems, processing pipelines, and small sample sizes<sup>37</sup>.  
175 These standardization challenges have impeded the integration of fMRI and EEG in extensive,  
176 multicenter brain age research.

177  
178 We adopted a framework to tackle diversity by including datasets from LAC and non-LAC  
179 regions (n = 5306), utilizing graph convolutional networks (GCN) to functional connectivity of  
180 fMRI and EEG signals. We hypothesized that, across fMRI and EEG imaging, models would  
181 accurately predict BAGs and be sensitive to the impacts of multimodal diversity, including  
182 geographical and sociodemographic effects, sex differences, health disparities, and exposome

183 influences. By testing this hypothesis, we aimed to assess the effectiveness of high-order  
184 interactions and deep learning in predicting brain age differences across diverse and  
185 heterogeneous populations of healthy aging and neurocognitive disorders.

186

## 187 **Results**

188 We employed resting-state fMRI (n = 2953) and EEG (n = 2353) signals separately to evaluate  
189 whether a deep-learning computational pipeline (Fig. 1) captures differences in brain aging across  
190 heterogeneous populations. We included fMRI data from 2953 participants from Argentina, Chile,  
191 Colombia, Mexico, and Peru (LAC) and the USA, China, and Japan (non-LAC). The EEG dataset  
192 involved 2353 participants from Argentina, Brazil, Chile, Colombia, and Cuba (LAC), and Greece,  
193 Ireland, Italy, Turkey, and the UK (non-LAC). Healthy controls, MCI, Alzheimer's disease, and  
194 bvFTD groups were included. We focused on the Alzheimer's disease and bvFTD as these  
195 conditions represent the most common late-onset and early-onset causes of dementia<sup>38,39</sup>. We  
196 included the Alzheimer's disease continuum, which encompasses MCI, to capture the prodromal  
197 stages of the disease<sup>39</sup>. Raw fMRI and EEG signals were preprocessed to remove artifacts and then  
198 normalized. Based on multivariate information theory, we calculated high-order interactions<sup>1</sup>.  
199 Weighted graphs were used as inputs for a graph convolutional deep learning network trained to  
200 predict brain age, employing one model for fMRI and another for EEG.

### 201 **BAG across LAC and non-LAC datasets**

202 We used the fMRI and EEG signals from the control's datasets (i.e., LAC and non-LAC) to train  
203 and test brain-aging models. We employed 80% cross-validation with a 20% hold-out testing split.  
204 As shown in Figs. 2a and 3a, our models predicting brain age obtained adequate goodness of fit  
205 (fMRI:  $R^2 = 0.52$ ,  $p < 0.001$ ,  $F^2 = 1.07$ ; EEG:  $R^2 = 0.45$ ,  $p < 0.001$ ,  $F^2 = 0.83$ ). We implemented  
206 the Root Mean Square Error (RMSE) to evaluate models' fit, obtaining acceptable brain age

207 predictions (fMRI-RMSE = 7.24, EEG-RMSE = 6.45). For both, fMRI and EEG, the main  
208 predictive brain-regional features included hubs in frontoposterior networks (nodes in precentral  
209 gyrus, the middle occipital gyrus, and the superior and middle frontal gyri; Fig. 2a and 3a).  
210 Additional nodes for the fMRI model included the inferior frontal gyri, and the anterior and  
211 median cingulate and paracingulate gyri (Fig. 2a.). For EEG, key nodes also comprised the  
212 superior and inferior parietal gyri and the inferior occipital gyrus (Fig. 3a). Thus, for both fMRI  
213 and EEG the models showed an adequate fit and predictive performance, with key predictive  
214 features involving frontoposterior networks in the brain.

215

### 216 **BAG in non-LAC datasets**

217 Using the same data split ratio, we trained and tested the models in non-LAC datasets. As shown  
218 in Figs. 2b and 3b, our models predicting brain age yielded considerable goodness of fit (fMRI:  
219  $R^2 = 0.40$ ,  $p < 0.001$ ,  $F^2 = 0.67$ ; EEG:  $R^2 = 0.43$ ,  $p < 0.001$ ,  $F^2 = 0.76$ ). RMSE values were also  
220 adequate (fMRI-RMSE = 8.66; EEG-RMSE = 6.54). Mean Directional Errors (MDE) for fMRI  
221 and EEG were 0.69 and 1.07, respectively. For both fMRI and EEG, the main predictive features  
222 included hubs in frontoposterior networks including the superior frontal gyrus (dorsolateral), the  
223 precentral gyrus, and the middle occipital gyrus (Fig. 2b and 3b). Additional critical nodes for the  
224 fMRI model included the inferior and middle frontal gyri, and the anterior and median cingulate  
225 and paracingulate gyri (Fig. 2b). For EEG, key nodes also comprised the superior and inferior  
226 occipital gyri, and the superior parietal gyrus (Fig. 3b). In brief, models trained on non-LAC  
227 datasets exhibited strong fit values and predictive features as in the overall dataset analysis.

### 228 **BAG in LAC datasets**

229 When trained and tested in the LAC datasets (Figs. 2c and 3c), models demonstrated moderate  
230 goodness of fit indexes but were less precise, as indicated by higher RMSE values (fMRI = 11.91;



231 EEG = 9.82). We observed increased positive biases in the MDE measures compared to the non-  
232 LAC models (fMRI = 3.18; EEG = 5.34). Again, the main features involved frontoposterior  
233 networks. Common nodes for fMRI and EEG included the superior and middle occipital gyri, the  
234 superior and inferior parietal gyri, and the superior and middle frontal gyri (Fig. 2c and 3c). For  
235 EEG, the model also highlighted the precentral gyrus, and the inferior occipital gyrus (Fig. 3c).  
236 Thus, models trained on LAC datasets showed moderate fit and positive biases (older brain age)  
237 in frontotemporal nodes (fMRI and EEG), compared to non-LAC models.

238

### 239 **Cross-regional effects in model generalization**

240 We investigated the effects of cross-region training and testing with data from non-LAC and LAC.  
241 Training with non-LAC data and testing on LAC data led to biases predicting older brain ages  
242 than chronological ages as shown by positive MDE values (Figs. 2d and 3d; fMRI: MDE = 5.60,  
243 RMSE = 9.44; EEG: MDE = 5.24, RMSE = 7.23). On the contrary, training on LAC and testing  
244 on non-LAC resulted in negative age biases predicting younger brain age shown by the MDE  
245 (Figs. 2d and 3d; LAC/non-LAC fMRI: MDE = -2.52, RMSE = 8.41; LAC/non-LAC EEG: MDE  
246 = -2.34, RMSE = 5.69). Sex differences were observed in the BAG when training in the non-LAC  
247 and testing in LAC (Figs. 4a and 4b). Specifically, female participants in LAC exhibited a greater  
248 bias towards older brain age than males (fMRI:  $p = 0.04$ ; EEG:  $p = 0.03$ ). In conclusion, training  
249 with non-LAC data and testing on LAC data resulted in a bias towards predicting older brain ages,  
250 especially for female participants in LAC.

251

### 252 **Accelerated aging in MCI, Alzheimer's disease and bvFTD**

253 We investigated the effects of testing the controls-trained model (80%) on different subsamples,  
254 matched by age, sex, and education, from other groups (i.e., controls non-LAC, controls LAC,

255 MCI, Alzheimer's disease, and bvFTD, Table 1). Permutation subsample analyses with 5000  
256 iterations revealed statistically significant BAGs between the non-LAC and LAC control groups  
257 (Figs. 4a and 4b, fMRI:  $p < 0.01$ ; EEG:  $p < 1e-5$ ). This difference was also observed for  
258 Alzheimer's disease in the fMRI dataset ( $p < 1e-5$ ). Additionally, for fMRI, we found significant  
259 differences between controls from non-LAC and all clinical groups from the same region [MCI  
260 ( $p < 1e-5$ ), Alzheimer's disease ( $p < 1e-5$ ), and bvFTD ( $p < 1e-5$ )]. Similarly, for both fMRI and  
261 EEG, we observed significant differences between controls from LAC and all the clinical groups  
262 [fMRI: MCI ( $p < 1e-5$ ), Alzheimer's disease ( $p < 1e-5$ ), and bvFTD ( $p < 1e-5$ ); EEG: MCI ( $p <$   
263  $1e-5$ ), Alzheimer's disease ( $p < 1e-5$ ), and bvFTD ( $p < 0.01$ )]. Across fMRI and EEG datasets,  
264 both LAC and non-LAC, we observed a gradient of increasing brain age from controls to MCI to  
265 Alzheimer's disease. The MCI groups significantly differed from Alzheimer's disease (fMRI and  
266 EEG:  $p < 1e-5$ ) and bvFTD (fMRI:  $p < 1e-5$ ; EEG:  $p < 0.01$ ), with older brain ages for Alzheimer's  
267 disease and bvFTD. For the fMRI and EEG non-LAC datasets, the Alzheimer's disease group also  
268 showed an older brain age than the bvFTD group ( $p < 0.01$ ). Thus, larger brain age gaps were  
269 observed in LAC compared to non-LAC groups and across clinical groups, with a gradient of  
270 increasing brain age from controls to MCI to dementia.

271

## 272 **Sex differences in neurocognitive disorders**

273 For fMRI, we analyzed the differences between male and female participants with the same  
274 diagnosis for the non-LAC and LAC datasets. There were no significant differences among groups  
275 from non-LAC datasets (Figs 4a and 4b). However, Alzheimer's disease females from LAC  
276 exhibited significantly greater BAGs compared to males (fMRI:  $p < 1e-3$ , EEG:  $p < 0.001$ ). No  
277 other significant effects were observed. We conducted a supplementary analysis incorporating  
278 country-level gender inequality (GII indexes), sex, region (LAC vs. non-LAC), and individual

279 neurocognitive status (HC vs. MCI, Alzheimer's disease, or bvFTD) as predictors of BAGs. The  
280 model demonstrated good performance ( $R^2 = 0.40$ ,  $F^2 = 0.66$ ,  $RMSE = 6.85$ ,  $p < 1e-15$ ) and all  
281 predictors were influential. Having a neurocognitive disorder and being a female living in  
282 countries with high gender inequality – particularly from LAC – were associated with higher  
283 BAGs (Extended Data Fig.1 and Supplementary Table 1). Overall, females with Alzheimer's  
284 disease from LAC exhibited significantly greater brain age gaps compared to males, influenced  
285 by high gender inequality in their countries.

286

### 287 **Exposome determinants of BAGs**

288 We employed gradient boosting regression models to explore the influence of physical and social  
289 exposomes, as well as disease disparity factors on BAGs. Predictors included aggregate country-  
290 level measures of air pollution (PM2.5), socioeconomic inequality (GINI index), and burdens of  
291 communicable, maternal, prenatal, and nutritional conditions, and non-communicable diseases.  
292 We also leveraged the individual neurocognitive status (HC versus Alzheimer's disease, MCI, or  
293 bvFTD). We assessed predictors' importance using a multi-method approach comprising  
294 permutation importance, mean decrease in impurity (MDI), and SHAP values (Fig. 4c). Across  
295 both LAC and non-LAC datasets, the models ( $R^2 = 0.41$ ,  $F^2 = 0.71$ ,  $RMSE = 6.76$ ,  $F = 304.25$ ,  $p$   
296  $< 1e-15$ ) identified neurocognitive disorders (MCI, Alzheimer's disease, or bvFTD) and higher  
297 socioeconomic inequality (GINI index) as the most influential and consistent predictors of  
298 increased BAGs (Fig. 4c). High levels of pollution and burden of non-communicable and  
299 communicable diseases were also predictive of increased BAGs, albeit less impactful. Stratified  
300 models for LAC ( $R^2 = 0.37$ ,  $F^2 = 0.59$ ,  $RMSE = 6.9$ ,  $F = 138.78$ ,  $p < 1e-15$ ) and non-LAC ( $R^2 =$   
301  $0.41$ ,  $F^2 = 0.71$ ,  $RMSE = 6.57$ ,  $F = 135.91$ ,  $p < 1e-15$ ) also showed good performance, with  
302 neurocognitive disorders being the most influential predictor in both. In LAC, higher

303 socioeconomic inequality was the second most consistent and influential predictor of larger BAGs  
304 across the three models. Air pollution and burden of communicable and non-communicable  
305 diseases were also influential. None of these variables was influential predictors in the non-LAC  
306 models. Predictors' estimation coefficients are presented in Supplementary Table 2. In sum,  
307 neurocognitive disorders, followed by macrosocial factors linked to socioeconomic inequality, air  
308 pollution, and health disparities, were influential predictors of increased brain age gaps, especially  
309 in LAC.

310

### 311 **Sensitivity analyses**

312 We performed multiple tests to assess the validity of the results. First, we investigate whether  
313 variations in fMRI or EEG data quality explained the differences in brain age between the non-  
314 LAC and LAC. Subsample permutation tests with 5000 iterations showed no significant  
315 differences between any of the groups for fMRI (Fig. 5a) or EEG (Fig. 5b) data quality metrics.  
316 In addition, a linear regression examining scanner type effects showed that the fMRI data quality  
317 metric did not predict the BAGs ( $R^2 = 0.001$ ,  $p = 0.18$ , Cohen's  $F^2 = 0.001$ , Fig. 5c). To further  
318 test for scanner effects, we implemented a harmonization strategy by normalizing the BAG  
319 variable within each scanner type. We used the min-max scaler to ensure consistent minimum and  
320 maximum values across scanners. Results using this harmonization (Fig. 5d) and our initial  
321 approach were very similar. Additional analyses controlling for datasets collected with eyes open  
322 versus eyes closed protocols revealed no significant differences in BAGs across any groups  
323 (Extended Data Fig. 2).

324

325 We also controlled for effects of age and years of education on fMRI and EEG BAGs by including  
326 them as covariates in the group comparisons. All reported group differences remained significant

327 after covariate adjustment (Supplementary Table 3). Years of education did not change the results  
328 for any analyses. In eight of the nine analyses, age did not have a significant effect. Considering  
329 the chronological age differences between Alzheimer's disease and MCI groups, we performed a  
330 sensitivity analysis using a subset of MCI participants (fMRI:  $n = 254$ , mean age =  $73.287 \pm$   
331  $7.517$ ; EEG:  $n = 52$ , mean age =  $63.231 \pm 6.549$ ) age matched to Alzheimer's disease participants  
332 (fMRI:  $n = 254$ , mean age =  $72.295 \pm 7.530$ ,  $p = 0.13$ ; EEG:  $n = 52$ , mean age =  $62.769 \pm$   
333  $6.302$ ,  $p = 0.71$ ). These results (Extended Data Fig. 3) confirmed those reported for the overall  
334 MCI and Alzheimer's disease datasets (Figs. 4a and 4b). For both fMRI and EEG datasets, we  
335 found significantly larger BAGs in Alzheimer's disease compared to MCI (fMRI:  $p < 1e-5$ ; EEG:  
336  $p < 0.01$ ). For fMRI, these differences were observed in both LAC ( $p < 1e-5$ ) and non-LAC ( $p <$   
337  $1e-5$ ) datasets. We also found differences between MCI participants from LAC vs. non-LAC ( $p <$   
338  $1e-5$ ) and Alzheimer's disease participants from LAC vs. non-LAC ( $p < 1e-5$ ). Thus, controlling  
339 for data quality, scanner effects, age, and education confirmed that the reported effects in brain  
340 age gaps remained the same.

341

## 342 **Discussion**

343 Our study used brain clocks to capture diversity and disparity across LAC and non-LAC datasets  
344 using fMRI and source-space EEG techniques. Despite heterogeneity in signal acquisition and  
345 methods, we captured patterns of brain age modulations in healthy aging from diverse datasets  
346 and participants with MCI, Alzheimer's disease, and bvFTD. Models trained and tested on non-  
347 LAC data showed greater convergence with chronological age. Conversely, models applied to  
348 LAC datasets indicated larger BAGs, suggesting accelerated aging. We observed a gradient of  
349 BAGs from controls to MCI to Alzheimer's disease. Sex differences revealed an increased BAG  
350 in females in control and Alzheimer's disease groups. Most brain clock patterns were

351 independently confirmed and replicated across fMRI and EEG. Aggregate-level macrosocial  
352 factors, including socioeconomic inequality, pollution, and burden of communicable/non-  
353 communicable conditions modulated the BAG, especially in LAC. Variations in signal quality,  
354 demographics, or acquisition methods did not account for the results. The findings offer a  
355 framework that captures the multimodal diversity associated with accelerated aging in various  
356 global settings.

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358 Our results suggest that being from LAC is associated with accelerated aging. The better fit of the  
359 non-LAC compared to the LAC models supports the notion that universal models of brain  
360 phenotypes do not generalize well to underrepresented populations<sup>24,29,40</sup>. Diversity-related factors  
361 associated with different exposome and disease disparities<sup>4,10,24,41</sup> may influence the BAGs in  
362 LAC and non-LAC. Neurocognitive disorders played a crucial role<sup>4,42</sup>. However, structural  
363 socioeconomic inequality, a distinctive characteristic of LAC<sup>15</sup>, increased levels air pollution<sup>43</sup>,  
364 and the burden of non-communicable<sup>19,20</sup> and communicable<sup>18,44</sup> diseases also have an significant  
365 impact on BAGs. The fact that these effects were larger in LAC suggests that underlying  
366 inequalities and adverse environmental and health conditions play a macrosocial, structural  
367 driving role<sup>11</sup> in the observed regional differences. Immigration may also influence brain age  
368 through social determinants of health<sup>45</sup> and genetic diversity. In LAC, tricontinental admixtures  
369 lead to significant ancestral diversity within and across countries<sup>46</sup>, impacting dementia  
370 prevalence and brain phenotypes<sup>41</sup>. Future studies should consider these potential effects in BAGs.

371

372 Selective brain networks were associated with larger BAG in the clinical groups. Both fMRI and  
373 EEG models of BAGs yielded large-scale frontoposterior high-order interactions<sup>1</sup>, consistent with  
374 models of brain age involving long-range connections between frontal, cingular, parietal, and

375 occipital hubs, which may be more vulnerable to aging effects<sup>47-49</sup>. Also consistent with the  
376 cumulative nature of neurobiological changes over time<sup>50</sup>, BAGs increased from controls through  
377 MCI to Alzheimer's disease. A previous deep learning study using MRI and PET in participants  
378 with MCI and dementia also indicated increased brain age associated with disease progression<sup>23</sup>.  
379 Our results point to the brain age of MCI as being an intermediate stage between healthy aging  
380 and dementia<sup>39</sup>, and suggest that both fMRI and EEG markers of brain age may help identify  
381 groups at greater risk of progressing to dementia.

382

383 Sex and gender have been linked to poorer brain health outcomes<sup>27,51</sup>. Larger BAGs in controls  
384 and Alzheimer's disease females from LAC may relate to sex-specific conditions such as  
385 menopause, which involves brain volume reduction and increased amyloid-beta deposition<sup>52,53</sup>.  
386 Females also exhibit disproportionate tau brain burden<sup>54</sup>, pronounced inflammatory  
387 dysregulation<sup>55</sup> and lower basal autophagy<sup>56</sup>, all of which increase Alzheimer's disease risk. Such  
388 sex-specific factors are intertwined with environmental factors and gender inequalities<sup>51</sup>. Females  
389 in countries with higher gender inequality exhibit greater cortical atrophy<sup>27</sup>. Our sex effects were  
390 specific for Alzheimer's disease and LAC, consistent with the impacts of environmental<sup>41</sup> versus  
391 genetic risks<sup>57</sup> in Alzheimer's disease and bvFTD, respectively. Despite advances in gender  
392 equality, women in LAC still face significant obstacles<sup>58</sup> including lower education, less income  
393 and healthcare access, and greater caregiving burden, potentially exacerbating brain health issues  
394 and Alzheimer's disease risk<sup>59,60</sup>. Previous models for brain age have been conducted  
395 predominantly in high-income settings, ignoring sex and gender differences triggered by region-  
396 specific influences<sup>30,31</sup>. Thus, the inclusion of diverse samples can help to better understand the  
397 biological and environmental interaction of sex and gender disparities.

398 Our study had different strengths. We used diverse datasets across LAC and non-LAC including  
399 15 countries, featuring large sample sizes, and replicated results across fMRI and EEG.  
400 Geographical and sex differences modulated brain clocks across fMRI and EEG models, with  
401 more accelerated aging observed in controls and Alzheimer's disease females from LAC,  
402 contributing to the understanding of the effects of sex and diversity in aging. We used an  
403 integrative approach to analyze fMRI and EEG data across a large and geographically diverse  
404 sample. The convergence of two neuroimaging techniques and population heterogeneity enhanced  
405 the generalizability of our findings, making a significant contribution to computational models  
406 that capture diversity<sup>10</sup>. Brain clocks based on high-order interactions capture many risks to brain  
407 health, and thus, offer a new approach to personalized medicine, particularly for underrepresented  
408 populations. Our framework combines multiple dimensions of diversity in brain health, the  
409 Alzheimer's disease continuum and related disorders within a single measure of brain clocks,  
410 which is relevant for global health policies, generalizable computational models, and public health  
411 strategies. Incorporating EEG offers affordable and scalable solutions for disadvantaged settings,  
412 such as those in LAC, compared to traditional neuroimaging techniques<sup>1,35</sup>. Accessible metrics of  
413 accelerated aging can offer personalized assessments of diversity, aging, and neurocognitive  
414 disorders.

415

416 This study has multiple limitations. Our EEG dataset lacks representation from clinical groups in  
417 non-LAC, which may limit the generalizability. This issue is partially mitigated by the consistent  
418 results from the fMRI data, which included MCI, Alzheimer's disease, and bvFTD groups from  
419 both regions. Our BAG approach is unimodal. Future research should adopt multimodal  
420 approaches to deepen our understanding of brain aging across different pathophysiological  
421 mechanisms<sup>1</sup>. We leveraged two independent training and test datasets with fMRI and EEG, with



422 out-of-sample validation yielding consistent results across geographical comparisons, sex effects,  
423 and clinical conditions. These datasets involve multimodal settings and recording parameters,  
424 suggesting that our results are strong across highly variable conditions. However, future research  
425 should include more regions to further validate and strengthen our findings. Additionally, we did  
426 not include individual-level data on gender identity, socioeconomic status, and ethnic  
427 stratification. Future research incorporating these variables could further enrich our understanding  
428 of brain age across diverse populations. Lastly, the sex differences observed between controls  
429 from LAC and non-LAC exhibited moderate effect sizes. Further research should assess sex  
430 differences in other regions.

431  
432 In conclusion, brain clock models were sensitive to the impact of multimodal diversity involving  
433 geographical, sex, macrosocial, and disease-based factors from diverse populations, despite the  
434 heterogeneity in data acquisition and processing. Utilizing an deep learning architecture of the  
435 brain's high-order interactions<sup>1</sup> across fMRI and EEG signals, combined with globally accessible  
436 and affordable data, our study paves the way for more inclusive tools to assess disparities and  
437 diversity in brain aging. These tools can be vital in identifying MCI, Alzheimer's disease and  
438 bvFTD risk factors, as well as to characterizing and staging disease processes. In the future,  
439 personalized medicine approaches could leverage models of BAGs to establish worldwide  
440 protocols for aging and neurocognitive disorders.

441  
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#### 455 **Author Contributions**

456 Conceptualization: AI, SM, SB; Supervision: AI; Methodology and Analyses: SM; Collating data:  
457 RGG, JC, PP; Writing – original draft: AI, SM, SB; Writing – review & editing: all authors.

458

#### 459 **Competing Interest Statement**

460 None of the authors have competing financial or non-financial interests as defined by Nature  
461 Portfolio.

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**Table 1. Demographics for fMRI and EEG datasets**

		Full dataset					
All participants n = 5306		HCs = 3509	MCI = 517	AD = 828	bvFTD = 463		
		fMRI dataset					
Variable		HCs Non-LAC n = 967 LAC n = 477	MCI Non-LAC n = 215 LAC n = 169	AD Non-LAC n = 214 LAC n = 505	bvFTD Non-LAC n = 190 LAC n = 216	Statistics Non-LAC vs. LAC	Post-hoc comparisons
Sex (F:M)	Non-LAC	470:497	114:101	112:102	98:92	$\chi^2 = 2.19$ $p = 0.533$	HC-MCI: $p > 0.05$ HC-AD: $p > 0.05$ HC-bvFTD: $p > 0.05$
	LAC	261:216	84:85	262:243	105:111	$\chi^2 = 2.76$ $p = 0.429$	HC-MCI: $p > 0.05$ HC-AD: $p > 0.05$ HC-bvFTD: $p > 0.05$
Age (years)	Non-LAC	53.55 (13.43)	59.62 (8.77)	76.59 (9.35)	73.14 (8.56)	F = 3.13 $p = 0.47$ $np^2 = 0.02$	HC-MCI: $p > 0.05$ HC-AD: $p > 0.05$ HC-bvFTD: $p > 0.05$
	LAC	65.34 (11.44)	66.53 (8.18)	77.52 (9.35)	73.15 (8.76)	F = 3.62 $p = 0.45$ $np^2 = 0.02$	HC-MCI: $p > 0.05$ HC-AD: $p > 0.05$ HC-bvFTD: $p > 0.05$
Range: [22-91]	Non-LAC	13.15 (5.41)	14.15 (3.41)	13.12 (5.34)	11.16 (3.56)	F = 2.19 $p = 0.49$ $np^2 = 0.02$	HC-MCI: $p > 0.05$ HC-AD: $p > 0.05$ HC-bvFTD: $p > 0.05$
	LAC	12.11 (3.39)	11.52 (6.32)	8.89 (4.34)	7.89 (3.36)	F = 1.31 $p = 0.68$ $np^2 = 0.01$	HC-MCI: $p > 0.05$ HC-AD: $p > 0.05$ HC-bvFTD: $p > 0.05$
		EEG dataset					
		HCs Non-LAC n = 569 LAC n = 1486	MCI LAC n = 133	AD LAC n = 108	bvFTD LAC n = 57	Statistics Non-LAC vs. LAC	Post-hoc comparisons
Sex (F:M)	Non-LAC	470:99	-	-	-	$\chi^2 = 64.62$ $p < 0.001^*$	-
	LAC	954:532	111:22	85:23	39:18	$\chi^2 = 28.05$ $p < 0.001^*$	HC-MCI: $p > 0.05$ HC-AD: $p > 0.05$ HC-bvFTD: $p > 0.05$
Age (years)	Non-LAC	58.98 (12.03)	-	-	-	t = 4.21 $p = 0.07$ $np^2 = 0.02$	-
	LAC	66.74 (13.94)	62.54 (9.98)	78.62 (8.34)	71.05 (9.34)	F = 7.62 $p < 0.001^*$ $np^2 = 0.07$	HC-MCI: $p > 0.05$ HC-AD: $p > 0.05$ HC-bvFTD: $p > 0.05$
Range: [21-92]	Non-LAC	14.85 (4.9)	-	-	-	t = 3.54 $p = 0.08$ $np^2 = 0.01$	-
	LAC	13.92 (3.39)	8.12 (4.34)	10.75 (6.32)	14.38 (5.49)	F = 6.31 $p < 0.001^*$ $np^2 = 0.06$	HC-MCI: $p > 0.05$ HC-AD: $p > 0.05$ HC-bvFTD: $p > 0.05$

469 Results are presented as mean (SD). Asterisks (\*) indicate an alpha level of  $p < 0.05$ . Demographic data comparing non-LAC and LAC  
470 groups were assessed using unpaired t-tests, while data for pathological groups were analyzed using ANOVAs followed by Tukey post-hoc  
471 pairwise comparisons, except for sex, which was analyzed using Pearson's chi-squared ( $\chi^2$ ) test. Effect sizes were calculated using partial eta  
472 squared ( $\eta^2$ ). Abbreviations: HC = healthy control, MCI = mild cognitive impairment, AD = Alzheimer's disease, bvFTD = behavioral  
473 variant frontotemporal dementia.

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## Figure legends

**Fig. 1. Datasets characterization and analysis pipeline.** Datasets included Latin American countries (LAC) and non-LAC healthy controls (HC, total N = 3509) and participants with Alzheimer’s disease (AD, total N = 828), behavioral variant frontotemporal dementia (bvFTD, total N = 463), and mild cognitive impairment (MCI, total N = 517). The functional magnetic resonance imaging dataset (fMRI, yellow lines) included 2953 participants from LAC (Argentina, Chile, Colombia, Mexico, and Peru) as well as non-LAC (the USA, China, and Japan). The electroencephalography dataset (EEG, blue lines) involved 2353 participants from Argentina, Brazil, Chile, Colombia, and Cuba (LAC) as well as Greece, Ireland, Italy, Turkey, and the UK (non-LAC). Circles represent the number of participants per group, scaled between the number of participants in the largest and smallest groups for each region to facilitate visualization. Line thickness represents the number of participants with fMRI (yellow lines) and EEG (blue lines) per country. The raw fMRI and EEG signals were preprocessed by filtering and artifact removal and the EEG signals were normalized to project them into source space. A parcellation using the automated anatomical labeling (AAL) atlas for both the fMRI and EEG signals was performed to build the nodes from which we calculated the high-order interactions using the  $\Omega$ -information metric. A connectivity matrix was obtained for both modalities, which was later represented by graphs. Data augmentation was performed only in the testing dataset. The graphs were used as input for a graph convolutional deep learning network (architecture shown in the last row), with separate models for EEG and fMRI. Finally, age prediction was obtained, and the performance was measured by comparing the predicted vs. the chronological ages. This figure was partially created using Biorender under Team license.

**Fig. 2. fMRI training and testing the deep learning model in different samples.** (a) Ordinary least squares (OLS) regression comparing chronological age vs. predicted age with the feature importance list for training and testing in the whole sample. (b) Regression comparing chronological age vs. predicted age with the feature importance list for training and testing in the non-LAC dataset. (c) Regression comparing chronological age vs. predicted age with the feature importance list for training and testing in the LAC dataset. For (a), (b) and (c), data point colors indicate the kernel density estimation to provide a visual representation of the density of prediction errors across different values of chronological age. The bars show the brain region feature importance list in descending order, with ring plots and glass brain representations of the most important network-edge connections. (d) Histogram of the prediction error when training in non-LAC dataset and testing in LAC dataset. (e) Violin plot of the distribution and statistical comparison of training and testing with different regions using a permutation test (5000 iterations). (f) Violin plot of the distribution and statistical comparison of testing the models on females and males using a permutation test (5000 iterations). LAC = Latin American countries.

**Fig. 3. EEG training and testing the deep learning model in different samples.** (a) Ordinary least squares (OLS) regression comparing chronological age vs. predicted age with the feature importance list for training and testing in the whole sample. (b) Regression comparing chronological age vs. predicted age with the feature importance list for training and testing in the non-LAC dataset. (c) Regression comparing chronological age vs. predicted age with the feature importance list for training and testing in the LAC dataset. For (a), (b) and (c), data point colors indicate the kernel density estimation to provide a visual representation of the density of prediction

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522 errors across different values of chronological age. The bars show the brain region feature  
523 importance list in descending order, with ring plots and glass brain representations of the most  
524 important network-edge connections. **(d)** Histogram of the prediction error when training in non-  
525 LAC dataset and testing in LAC dataset. **(e)** Violin plot of the distribution and statistical  
526 comparison of training and testing with different regions using a permutation test (5000 iterations).  
527 **(f)** Violin plot of the distribution and statistical comparison of testing the models on females and  
528 males using a permutation test (5000 iterations). LAC = Latin American countries.

529 **Fig. 4. Groups, sex, and macrosocial influences in BAGs.** Violin plots for the distribution of  
530 prediction gaps for different groups and sex effects using **(a)** fMRI and **(b)** EEG datasets. The  
531 statistical comparisons were calculated using subsample permutation testing with 5000 iterations.  
532 **(c)** Associations between macrosocial and disease disparity factors with BAGs were assessed with  
533 a multi-method approach comprising SHAP values, feature importance (mean decrease in  
534 impurity, MDI), and permutation importance. Plots show the mean importance values for each  
535 method, along with their 99% confidence interval, as well as the average R-squared and Cohen's  
536  $f^2$ . \* = Significant predictors. Shaded bars indicate significance across the three methods. LAC =  
537 Latin American countries, HC non-LAC = Healthy controls from non-LAC, HC LAC = Healthy  
538 controls from LAC, MCI = mild cognitive impairment, AD = Alzheimer's disease, bvFTD =  
539 behavioral variant frontotemporal dementia, M = Males. F = Females, \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  
540  $p < 0.001$ .

541 **Fig. 5. Sensitivity analysis.** Violin plots for the distribution of data quality metrics of **(a)** fMRI  
542 and **(b)** EEG datasets. Both panels indicate null results between groups in terms of data quality.  
543 **(c)** Linear regression effects of scanner type, evidencing that the fMRI data quality was not  
544 significantly associated with fMRI BAGs differences. **(d)** fMRI BAG differences across groups  
545 controlling for scanner differences. The statistical comparisons were calculated using subsample  
546 permutation testing with 5000 iterations. LAC = Latin American countries, HC = Healthy controls,  
547 MCI = mild cognitive impairment, AD = Alzheimer's disease, bvFTD = behavioral variant  
548 frontotemporal dementia.

549 **Extended Data Fig. 1. Associations of sex and gender inequality with BAGs.** Multi-method  
550 approach comprising SHAP values, features and permutation importance. Plot shows the mean  
551 importance values for each method, along with their 99% confidence interval, as well as the  
552 average R-squared and Cohen's  $f^2$ . Having a neurocognitive disorder, being female, and living in  
553 countries with larger gender inequality (particularly from LAC), were associated with higher  
554 BAGs. LAC = Latin American countries.

555 **Extended Data Fig. 2. Prediction gaps between fMRI datasets with either eyes open or eyes**  
556 **closed protocols.** No significant differences were observed between participants with open vs.  
557 closed eyes within the same groups (permutation test = 5000 iterations). \*  $p < 0.05$ , \*\*  $p < 0.01$ ,  
558 \*\*\*  $p < 0.001$ . LAC = Latin American countries, OE = open eyes, CE = closed eyes.

559 **Extended Data Fig. 3. BAGs between subsamples of mild cognitive impairment (MCI) and**  
560 **Alzheimer's disease (AD) groups matched by chronological age.** Results were similar to those  
561 reported for the total MCI and Alzheimer's disease datasets in Figs. 4a and b (permutation test =  
562 5000 iterations).

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735

736 **Methods**

737 The total dataset consisted of 5306 participants, with 2953 undergoing fMRI and 2353 EEG  
738 acquisitions. Of these, 3509 were controls, 517 had MCI, 828 Alzheimer's disease, and 463  
739 bvFTD.

740

741 **fMRI dataset**

742 The fMRI study involved 2953 participants from both non-LAC (USA, China, Japan) and LAC  
743 (Argentina, Chile, Colombia, Mexico, Peru), including 1444 healthy controls (HC). Two hundred  
744 fifteen participants met the Petersen criteria for MCI with a 24 MMSE cut-off value, 719 were  
745 diagnosed as probable AD<sup>61</sup>, and 402 fulfilled the diagnostic criteria for bvFTD<sup>62</sup>. LAC  
746 participants were recruited from the Multi-Partner Consortium to Expand Dementia Research in  
747 Latin America (ReDLat, with participants from Mexico, Colombia, Peru, Chile, and Argentina)  
748 <sup>63</sup>. Non-LAC participants were non-Latino individuals from ReDLat, the Alzheimer's Disease  
749 Neuroimaging Initiative (ADNI), and the Neuroimaging in Frontotemporal Dementia (NIFD)  
750 repository. The datasets were matched on sex, age, and years of education (Table 1). Sex  
751 information was determined by self-report. No information regarding gender was inquired. To  
752 ensure data reliability, we excluded subjects who reported a history of alcohol/drug abuse or  
753 psychiatric or other neurological illnesses. No participants reported a history of alcohol/drug  
754 abuse, psychiatric, or other neurological illnesses.

755

756 **EEG dataset**

757 The total dataset involved 2353 participants. Controls comprised 1183 participants, including 737  
758 from non-LAC (Turkey, Greece, Italy, United Kingdom, and Ireland) and 446 from LAC (Cuba,  
759 Colombia, Brazil, Argentina, and Chile). The participants presenting with clinical conditions were

760 recruited from a multisite study with harmonized assessments<sup>25,36,63</sup> in LAC (Argentina, Brazil,  
761 Chile, and Colombia). This dataset included 133 patients with MCI, 108 with Alzheimer's disease,  
762 and 57 with bvFTD. The controls datasets were matched on age, sex, and years of education  
763 concerning the clinical groups (MCI, Alzheimer's disease, and bvFTD) (Table 1). Sex information  
764 was determined by self-report. No information regarding gender was inquired. The Petersen  
765 criteria defined the MCI group with a 24 MMSE cut-off value. All individuals with Alzheimer's  
766 disease met the criteria for probable disease following international diagnostic guidelines<sup>61</sup>. The  
767 bvFTD group met the diagnostic criteria for probable bvFTD<sup>62</sup>. No subject in any of the clinical  
768 conditions reported a history of alcohol/drug abuse, psychiatric, or other neurological illnesses.

769

#### 770 **Ethics approval**

771 The local institutions that contributed EEGs and/or fMRIs to this study approved the acquisitions  
772 and protocols (Supplementary Data S1), and all participants signed a consent form following the  
773 declaration of Helsinki. The overall study was approved by the consortium under multiple IRBs  
774 (FWA00028264, FWA00001035, FWA00028864, FWA00001113, FWA00010121,  
775 FWAA00014416, FWA00008475, FWA00029236, FWA00029089, and FWA00000068). Data  
776 collection and analysis posed no risks concerning stigmatization, incrimination, discrimination,  
777 animal welfare, environmental, health, safety, security, or personal concerns. No transfer of  
778 biological materials, cultural artifacts, or traditional knowledge occurred. The authors reviewed  
779 pertinent studies from all countries while preparing the manuscript.

780

#### 781 **fMRI preprocessing**

782 The images were obtained from different scanners and in distinct acquisition settings  
783 (Supplementary Table 4). We included two resting-state recordings, closed and open eyes, to

784 increase the sample size for rs-fMRI data. The type of resting-state recording was controlled by a  
785 dummy variable (open or closed eyes) when employing the functional connectivity metric<sup>64</sup>. The  
786 resting state of fMRI preprocessing was conducted using the *fmriprep* toolbox (version 22.0.2).  
787 Furthermore, additional preprocessing was performed using the toolbox CONN22<sup>64</sup>. The CONN  
788 toolbox preprocessing included smoothing with a Gaussian kernel of 6 x 6 x 6 mm, the signal  
789 denoising through linear regression to account for confounding effects of white matter,  
790 cerebrospinal fluid, realignment, and scrubbing. A band-pass filter (0.008-0.09) Hz was also  
791 applied. After time-series preprocessing, we employed region-of-interest (ROI) analysis based on  
792 the brain regions of the Automated Anatomical Labeling (AAL90) atlas to reduce the  
793 dimensionality of the fMRI data for machine learning algorithms.

794

#### 795 **EEG preprocessing**

796 EEGs were processed offline using procedures implemented in a custom, automatic pipeline for  
797 computing brain functional connectivity in the EEG using a mesh model for multiple electrode  
798 arrays and source space estimation (see Supplementary Table 5 for acquisition parameters). The  
799 pipeline allows for the multicentric assessment of rsEEG connectivity and has been validated in a  
800 large-scale evaluation of connectivity in dementia<sup>65</sup>. Recordings were re-referenced to the average  
801 reference and band-pass filtered between 0.5 and 40 Hz using a zero-phase shift Butterworth filter  
802 of order 8. Data were downsampled to 512 Hz, referenced using the reference electrode  
803 standardization technique (REST), and corrected for cardiac, ocular, and muscular artifacts using  
804 two methods based on Independent Component Analysis (ICA). ICLabel (a tool for classifying  
805 EEG independent components into signals and different noise categories)<sup>66</sup>, and EyeCatch (a tool  
806 for identifying eye-related ICA scalp maps) were used<sup>67</sup>. Data were visually inspected after

807 artifact correction, and malfunctioning channels were identified and replaced using weighted  
808 spherical interpolations.

809

810 EEG normalization: Following guidelines for multicentric studies<sup>37</sup>, EEG was rescaled to reduce  
811 cross-site variability. The normalization was carried out separately for each dataset and consisted  
812 of the Z-score transformation of the EEG time series. The Z-score describes the position of raw  
813 data in terms of its distance from the mean when measured in standard deviation units. The Z-  
814 score transformed EEG connectivity matrices display more prominent interhemispheric  
815 asymmetry and reinforced long-distance connections than unweighted connectivity  
816 representations<sup>65</sup>.

817

818 EEG source space estimation: The source analysis of the rsEEG was conducted using the  
819 standardized Low-Resolution Electromagnetic Tomography method (sLORETA). sLORETA  
820 allows estimating the standardized current density at each of the predefined virtual sensors located  
821 in the cortical gray matter and the hippocampus of a reference brain (MNI 305, Brain Imaging  
822 Centre, Montreal Neurologic Institute) based on the linear, weighted sum of a particular scalp  
823 voltage distribution or the EEG cross-spectrum at the sensor level. sLORETA is a distributed EEG  
824 inverse solution method based on an appropriate standardized version of the minimum norm  
825 current density estimation. sLORETA overcomes problems intrinsic to the estimation of deep  
826 sources of EEG and provides exact localization to test seeds, albeit with a high correlation between  
827 neighboring generators.

828

829 The different electrode layouts were registered onto the scalp MNI152 coordinates. A signal-to-  
830 noise ratio of 1 was chosen for the regularization method used to compute the sLORETA

831 transformation matrix (forward operator for the inverse solution problem). The standardized  
832 current density maps were obtained using a head model of three concentric spheres in a predefined  
833 source space of 6242 voxels (voxel size = 5mm<sup>3</sup>) of the MNI average brain. A brain segmentation  
834 of 82 anatomic compartments (subcortical and cortical areas) was implemented using the  
835 automated anatomical labeling (AAL90) atlas. Current densities were estimated for the 153600  
836 voltage distributions comprising the five minutes of rsEEG (sampled at 512 Hz). The voxels  
837 belonging to the same AAL region were averaged such that a single (mean) time series was  
838 obtained for each cortical region<sup>32,68,69</sup>.

839

#### 840 **High-order interactions**

841 After preprocessing 82 time-series from the AAL brain parcellation for each modality (fMRI and  
842 EEG), we calculated the high-order interactions across triplets composed of a region  $i$  and region  
843  $j$  and a set comprising all the brain regions without  $i$  and  $j$ . To this end, we evaluated high-order  
844 interactions using the organizational information ( $\Omega$ ) metric. It is a multivariate extension of  
845 Shannon's mutual information, which assesses the dominant characteristic of multivariate systems  
846 (i.e., high-order interactions). In this case, to operationalize the Shannon Entropy, we used the  
847 Gaussian copula approximation, which estimates the differential Shannon's entropy from the  
848 covariance matrix of the Gaussian copula transformed data<sup>70</sup>. This is a mixture of a parametric  
849 and a non-parametric approach, as the copula is preserved in a non-parametric way but is then  
850 used to generate Gaussian marginals. The  $\Omega$  quantifies the balance between redundancy and  
851 synergy in high-order interactions among brain regions. By definition,  $\Omega > 0$  implies that the  
852 interdependencies are better described as shared randomness, indicating redundancy dominance.  
853 Conversely,  $\Omega < 0$  suggests that the interdependencies are better explained as collective

854 constraints, indicating synergy dominance. After normalization, its magnitude ranges from -1 to  
855 1. The  $\Omega$  can be expressed as:

$$\Omega(X^n) = (n - 2)H(X^n) + \sum_{j=1}^n [H(X_j) - H(X_{-j}^n)] \quad (1),$$

856 where  $X^n$  is the random vector that describes the system, and  $H$  is the Shannon's entropy. When  
857  $n$  is reduced to three variables ( $x$ ,  $y$ , and  $z$ ),  $\Omega$  can be expressed as

$$\Omega(x, y, z) = H(x, y, z) - H(x, y) - H(x, z) - H(y, z) + H(x) + H(y) + H(z) \quad (2).$$

858 To analyze brain activity,  $z$  can be considered a multivariate time series representing the activity  
859 of all brain regions except for  $x$  and  $y$ . Therefore, *O info* measures how synergistic or redundant  
860 is the relationship between two brain regions concerning the rest of the regions.

861

## 862 **Model input preprocessing**

863 As input to the models, the weighted adjacency matrix corresponding to the  $\Omega$  metric was  
864 converted to a graph. This matrix defines the edges in the graph, where the weight of each edge  
865 reflects the  $\Omega$  value between the corresponding regions. The feature vectors at each graph node  
866 are derived from the O-info matrix; specifically, each node's feature vector is the corresponding  
867 row in the  $\Omega$  matrix. To this end, the connectivity matrices were first converted to tensors using  
868 the PyTorch deep learning library, enabling their efficient manipulation. Subsequently, these  
869 tensors were reshaped, organizing the connectivity data into a structure where each tensor  
870 represented the features of nodes within a graph. This transformation preserved the relational  
871 information from the original matrices, making it accessible for analysis by graph neural networks.  
872 To ensure the integrity of the data, graphs containing NaN values, either in their features or target

873 values, were filtered out. The remaining graphs were then split into training and validation sets  
874 using a stratified split to ensure a balanced representation of age groups in both sets.

### 875 **Data augmentation**

876 We employed augmentation tailored for connectivity matrices to make the model more resilient  
877 to heterogeneity and generalizability. Linear interpolation between matrices corresponding to  
878 neighboring age values was used, in contrast to traditional image augmentation techniques such  
879 as random rotations or crops that are inappropriate for connectivity data.

880 Given two matrices,  $M_1$  and  $M_2$ , representing fMRI or EEG connectivity at ages  $a_1$  and  $a_2$ ,  
881 respectively, the interpolation to produce a matrix for a target age where  $a_1 < a_t < a_2$  was conducted  
882 using the formula:

$$883 \quad M_t = (1 - \alpha)M_1 + \alpha M_2 \quad (3)$$

884 Here,  $\alpha = \frac{a_t - a_1}{a_2 - a_1}$  represents the interpolation factor.

885 This augmentation method enabled the generation of fMRI and EEG connectivity matrices for age  
886 values previously absent in the data set. The derived matrices, through interpolation, ensure a  
887 smooth transition in the fMRI and EEG patterns from one age value to another, thereby  
888 maintaining the inherent physiological significance of the original data—preliminary validation  
889 against a hold-out dataset showed improvements in model fit against dataset heterogeneity. We  
890 included 500 samples with data augmentation only the training datasets for both modalities, half  
891 for the non-LAC and half for the LAC samples.

892

### 893 **The architecture of the models**

894 Two Graph Convolutional Networks (GCNs)<sup>71</sup> were designed for this study, specifically tailored  
895 to process graph-structured data. We employed the PyTorch Geometric code library based on the  
896 PyTorch library to develop and train the models. Two models were created, one for the fMRI



897 data and another for the EEG data. Unlike traditional convolutional networks suited for  
898 neuroimaging data, functional connectivity demands a specialized approach since neighboring  
899 data points are not necessarily close in native space (i.e., adjacent brain areas). The GCN employs  
900 adjacency matrices of graphs as inputs comprised of node features. Each node in the graph  
901 aggregates features from its neighbors through a series of operations, including multiplication by  
902 a normalized adjacency matrix, transformation using a weight matrix, and applying an activation  
903 function, here the ReLU<sup>72</sup>. The architecture employed in our work consisted of two Graph  
904 Convolutional layers. The input features (O-info matrix) were passed through the first  
905 convolutional layer, followed by a ReLU activation function and a dropout layer for  
906 regularization. The features were then passed through the second convolutional layer. Finally,  
907 average pooling was used to aggregate the output features. To train the two models, we combined  
908 Mean Squared Error (MSE) as the loss function and the Adam optimizer. Given the variability in  
909 the data and potential model configurations, we implemented a hyperparameter tuning process  
910 using a grid search over specified learning rates and epoch numbers. For each model for the  
911 controls, the data was initially split into 80% for training and validation, and 20% for hold-out  
912 testing. Within the 80% training and validation set, we applied 5-fold cross-validation to  
913 determine the optimal hyperparameters for the model. After determining the best hyperparameters  
914 through this cross-validation process, the final model's performance was evaluated on the  
915 remaining 20% hold-out test set to assess its generalization capability<sup>73</sup>.

916

### 917 **Statistical analyses**

918 Following hyperparameter tuning, each model was retrained using the best hyperparameters on  
919 the training set and evaluated on the test set. For a more comprehensive assessment, the predicted  
920 age values were compared to the actual age values using Pearson's correlation coefficient, R-

921 squared, and Cohen's  $f^2$  effect size for each model<sup>74</sup>. We used the method outlined below to  
922 evaluate if the model was predicting increased or decreased ages concerning the actual  
923 chronological age.

924  
925 The Mean Directional Error (MDE) is a diagnostic metric used to evaluate the prediction accuracy  
926 of the models, specifically focusing on the direction of prediction gaps rather than their magnitude  
927 to detect bias. It is calculated as follows:

$$928 \quad MDE = \frac{1}{n} \sum_{i=1}^n (y_i - \hat{y}_i) \quad (4)$$

929 The function "sign" yields a value of +1 if the prediction is above the actual value, -1 if below,  
930 and 0 if they are equal.  $y_i$  is the real age of subject  $i$  and  $\hat{y}_i$  is the predicted age. An MDE value  
931 close to zero suggests a balanced number of overestimations and underestimations. Positive or  
932 negative values indicate systematic biases in the prediction method, where a positive MDE means  
933 the model generally overpredicts, and a negative MDE indicates underprediction.

934  
935 In our analysis when comparing models, we sought to examine potential regional biases in  
936 predictive accuracy and compare possible sex effects or signal acquisition noise. The statistical  
937 approach involved conducting permutation tests (5,000 subsample iterations each), a non-  
938 parametric statistical test that does not assume a specific distribution of the data, thus offering  
939 flexibility in handling non-normal distributions. Given the nature of the permutation test, our  
940 analysis constituted two-sided tests, assessing the likelihood of observing the obtained difference  
941 under the null hypothesis of no difference between the models. While the permutation test  
942 alleviates the need for normality assumptions, making it resilient to deviations from normal  
943 distribution, it inherently addresses multiple comparison concerns by evaluating the empirical  
944 distribution of the test statistic under the null hypothesis.

945 We compared the adequacy of the models employing the root mean square error (RMSE). This is  
946 a metric to quantify the discrepancies between predicted and observed values in modeling, given  
947 by the formula:

948

$$949 \quad RMSE = \sqrt{\frac{1}{N} \sum_{i=1}^n (y_i - \hat{y}_i)^2} \quad (6)$$

950

951 In this equation,  $y_i$  is the observed value,  $\hat{y}_i$  is the predicted value, and  $N$  is the total number of  
952 observations. RMSE measures the average magnitude of errors between predicted and actual  
953 observations. The squaring process results in a higher weight to outliers, making it a useful  
954 measure to evaluate if a model is robust to outliers.

955 To evaluate feature importance, we employed bootstrapping to assess the significance of  
956 individual nodes (i.e., brain areas) and edges (i.e., connections between brain nodes/regions)  
957 within the graph neural network. With this approach, we executed a two-step process to quantify  
958 the node and its edge's impact on the model's predictions. Initially, the model's output was  
959 calculated with all nodes and its edges present to establish a baseline performance metric.  
960 Subsequently, the analysis was repeated after removing each node and edge at a time, thus  
961 simulating network information absence. The difference in the model's output, with and without  
962 each area and edge was quantified, providing a measure of the network node importance. This  
963 process was repeated across multiple bootstrap testing dataset samples ( $n=5000$ ) to calculate  
964 confidence intervals. Finally, a feature importance list of nodes was generated in descending order  
965 of importance for brain age prediction. This methodological framework allowed for an analysis  
966 of network-level contributions to each model's overall predictive performance.

967 Gradient boosting regression models

968 We used gradient boosting regression models<sup>75</sup> to investigate the impact of factors associated with  
969 the physical and social exposomes, and disease disparities, on BAGs between LAC and non-LAC  
970 populations. As predictors, we included country-level measures of: (i) air pollution (PM2.5  
971 exposure), (ii) socioeconomic inequality (the GINI index)<sup>76</sup>, (iii) the burden of communicable,  
972 maternal, prenatal, and nutritional conditions, and (iv) the burden of non-communicable diseases.  
973 These indicators were sourced from the updated country-specific data provided on the World  
974 Bank's platform (<https://databank.worldbank.org/>). Additionally, individual neurocognitive status  
975 (being controls versus having Alzheimer's disease, MCI, or bvFTD) was included as predictor.  
976 BAGs from fMRI and EEG datasets were the outcomes.

977

978 Models were trained using 90% of the dataset and subsequently tested on an independent 10%  
979 subset, employing a 10-fold cross-validation framework. The cross-validation was repeated 10  
980 times. Within each iteration, estimation coefficients for the predictors, as well as the R-squared,  
981 Cohen's  $f^2$ <sup>77</sup>, and RMSE, were computed. We assessed feature importance using a multi-method  
982 approach incorporating permutation importance, features importance based on the mean decrease  
983 in impurity (MDI), and SHAP values<sup>78</sup>. We provided the mean importance values for each  
984 method, along with their 99% confidence interval, as well as the average R-squared and Cohen's  
985  $f^2$ <sup>77</sup>. Features whose lower confidence interval boundary crosses zero are considered non-  
986 significant. In order to optimize Ridge's hyperparameters, Bayesian optimization was employed.  
987 Following the same multi-method approach, we conducted gradient boosting regressions to  
988 explore the effect of gender inequality and sex on BAGs. As predictors, we included: (i) the  
989 country level gender inequality index (GII), a composite metric measuring reproductive health,  
990 empowerment and the labor market, (ii) sex, (iii) region (LAC vs non-LAC) and (iv) individual

991 neurocognitive status (HC versus Alzheimer's disease, MCI, or bvFTD). BAGs from fMRI and  
992 EEG were the outcomes

993

994 Data quality assessment

995 For the fMRI overall data quality (ODQ) metric, each timeseries was segmented in 20 repetition  
996 time (TR) length to evaluate the temporal signal-to-noise ratio (tSNR)<sup>79</sup>, which is calculated as  
997 the mean fMRI signal divided by its standard deviation within each segment. Segments with tSNR  
998 above a threshold of 50 were classified as high quality<sup>79</sup>. As additional evaluations to consider  
999 overall acquisition quality, we checked the variability of the tSNR segments of all the time series  
1000 in the brain to check for spatial consistency. Lastly, we checked for remaining outliers as signal  
1001 spikes from movement or transient gradient artifacts. Thus, the fMRI ODQ was computed as a  
1002 percentage of good segments considering its tSNR, low spatial variability, and the number of  
1003 segments not having spikes from movement or transient gradient remaining artifacts.

1004 For the EEG data quality assessment, we followed the method proposed by Zhao et al<sup>80</sup>. The EEG  
1005 signals were divided into 1-second segments, and the quality of each segment was evaluated using  
1006 four specific metrics. These metrics included the detection of weak or constant signals based on  
1007 standard deviation, the identification of artifacts through signal amplitude ratios, the presence of  
1008 high-frequency noise, and low correlation between channels. The EEG ODQ was then calculated  
1009 as the percentage of segments exhibiting good quality. A value of 0 indicated that all segments  
1010 were of poor quality, while a value of 100 indicated that all segments were of high quality.

1011

1012 Sensitivity analyses

1013 We examined whether variations in fMRI or EEG data quality explained the differences in brain  
1014 age between the non-LAC and LAC, comparing different groups' fMRI<sup>79</sup> and EEG<sup>80</sup> data quality

1015 metrics, with subsample permutation tests with 5000 iterations for each comparison. In addition,  
1016 we conducted a linear regression to examine the association between the fMRI data quality metrics  
1017 and the BAGs. To further control for scanner effects, we implemented an additional harmonization  
1018 strategy in the fMRI training dataset. This method involves normalizing the BAG variable within  
1019 each scanner type by scaling the data to a fixed range using the min-max scaler<sup>14</sup>. This ensures  
1020 that the minimum and maximum values of the BAG variable are consistent across different  
1021 scanners, thereby reducing variability due to scanner differences. Additionally, we accounted for  
1022 the sign of the BAG after normalization to maintain the interpretability of positive and negative  
1023 values. This procedure adjusts for location and scale differences (e.g., mean and variance) across  
1024 sites, minimizing scanner-related variability.

1025

1026 We used permutation tests (5000 subsample iterations each) to compare the BAGs between  
1027 subsamples of participants undergoing fMRI with open versus closed eyes. We included 124  
1028 controls with closed eyes and 86 with open eyes, 269 Alzheimer's disease with closed eyes and  
1029 164 with open eyes, and 88 bvFTD with closed eyes and 69 with open eyes. Notably, all MCI  
1030 participants underwent fMRI with open eyes. Our findings revealed no significant differences in  
1031 BAGs when analyzing data from open versus closed eyes conditions across all group comparisons  
1032 (permutation test = 5000 iterations).

1033

#### 1034 **Ethics and inclusion statement**

1035 This work involved a collaboration between researchers in multiple countries. Contributors from  
1036 different sites are included as coauthors according to their contributions. Researchers residing in  
1037 LMIC were involved in study design, study implementation, methodological procedure, writing  
1038 and reviewing processes. The current research is locally relevant due to the larger disparities

1039 observed in LAC. Roles and responsibilities were agreed among collaborators ahead of the  
1040 research. Ethics committees approved all research involving participants. To prevent any  
1041 stigmatization, all identifying information has been removed to preserve the privacy of  
1042 individuals. We endorse the Nature Portfolio journals' guidance on LMIC authorship and  
1043 inclusion. Authorship was based on the intellectual contribution, commitment, and involvement  
1044 of each researcher in this study. We included authors born in LMICs and other underrepresented  
1045 countries.

1046  
1047 **Data availability**

1048 All preprocessed data are openly available at: <https://osf.io/8zjf4/>. The fMRI and EEG datasets  
1049 comprise sources (a) currently publicly available for direct download after registration and access  
1050 application, (b) available after contacting the researcher, or (c) accessible after IRB approval of  
1051 formal data-sharing agreement in a process that can last up to 12 weeks. The fMRI sources that  
1052 are publicly available for direct download are the following: Alzheimer's Disease Neuroimaging  
1053 Initiative (ADNI) (USA) ([ida.loni.usc.edu/collaboration/access/appLicense.jsp](http://ida.loni.usc.edu/collaboration/access/appLicense.jsp)), Chinese Human  
1054 Connectome Project (CHCP) (China) ([scidb.cn/en/detail?dataSetId=f512d085f3d3452a9b14689e9997ca94#p2](http://scidb.cn/en/detail?dataSetId=f512d085f3d3452a9b14689e9997ca94#p2)), The frontotemporal  
1055 lobar degeneration neuroimaging initiative (FTLDNI) (USA) ([ida.loni.usc.edu/collaboration/access/appLicense.jsp](http://ida.loni.usc.edu/collaboration/access/appLicense.jsp)), and Japanese Strategic Research Program  
1056 for the Promotion of Brain Science (SRPBS) (Japan) ([bicr-resource.atr.jp/srpbsopen/](http://bicr-resource.atr.jp/srpbsopen/)). The fMRI  
1057 sources available after contacting the researcher include ReDLat USA by contacting Bruce Miller  
1058 at UCSF through [datasharing@ucsf.edu](mailto:datasharing@ucsf.edu). The fMRI sources that require IRB approval and a formal  
1059 data sharing agreement include: ReDLat pros (Argentina, Chile, Colombia, Mexico, Peru) by  
1060 contacting Agustín Ibañez at [agustin.ibanez@gbhi.org](mailto:agustin.ibanez@gbhi.org), Centro de Gerociencia Salud Mental y  
1061 Metabolismo (GERO) (Chile) by contacting Andrea Slachevsky at [andrea.slachevsky@uchile.cl](mailto:andrea.slachevsky@uchile.cl),

1064 ReDLat pre (Argentina) by contacting Agustín Ibañez at agustin.ibanez@gbhi.org, ReDLat pre  
1065 (Peru) by contacting Nilton Custodio at ncustodio@ipn.pe, ReDLat pre (Colombia) by contacting  
1066 Diana Matallana at dianamat@javeriana.edu.co, ReDLat pre (Colombia -II) by contacting Felipe  
1067 Cardona at felipe.cardona@correounivalle.edu.co, ReDLat pre (Mexico) by contacting Ana Luisa  
1068 Sosa at drasosa@hotmail.com, ReDLat pre (Chile) by contacting María Isabel Behrens at  
1069 behrensl@uchile.cl, and ReDLat pre (Chile) by contacting Andrea Slachevsky at  
1070 andrea.slachevsky@uchile.cl. The EEG sources that are publicly available for direct download  
1071 are Centro de Neurociencias de Cuba (CHBMP) (Cuba)  
1072 (www.synapse.org/Synapse:syn22324937). The EEG sources that are available after contacting  
1073 the researcher include BrainLat (Argentina) by contacting Agustina Legaz at  
1074 alegaz@udesa.edu.ar, BrainLat (Chile) by contacting Agustina Legaz at alegaz@udesa.edu.ar,  
1075 Izmir University of Economics (Turkey) by contacting Gorsev Gener at gorsev.yener@ieu.edu.tr,  
1076 Trinity College Dublin (Ireland) by contacting Francesca Farina at  
1077 francesca.farina@northwestern.edu, Universidad de Antioquia (Colombia) by contacting  
1078 Francisco Lopera at floperar@gmail.com, Universidad de Sao Paulo (Brazil) by contacting Mario  
1079 Parra at mario.parra-rodriguez@strath.ac.uk, Universidad de Roma La Sapienza (Italy) by  
1080 contacting Susana Lopez at susanna.lopez@uniroma1.it, University of Strathclyde (UK) by  
1081 contacting Mario Parra at mario.parra-rodriguez@strath.ac.uk, Istanbul Medipol University  
1082 (Turkey) by contacting Tuba Aktürk at takturk@medipol.edu.tr, and Takeda (Chile) by contacting  
1083 Daniela Olivares at danielaolivaresvargas@gmail.com. For additional details, see  
1084 **Supplementary Data S1.**

#### 1085 **Code availability**

1086 The code used to preprocess and analyze the data of this work is available in an Open Science  
1087 Foundation repository at the following address: <https://osf.io/8zjf4/>

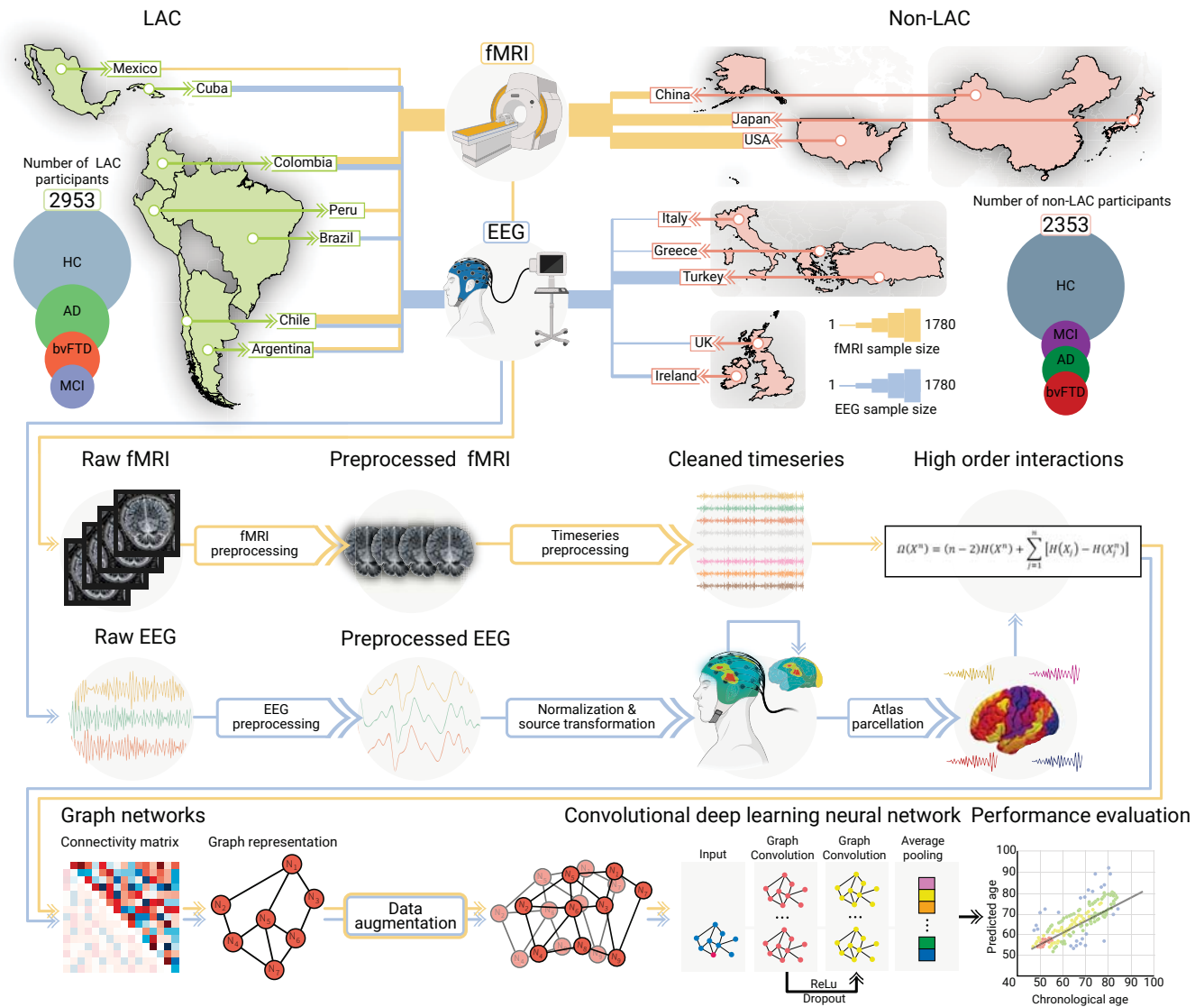


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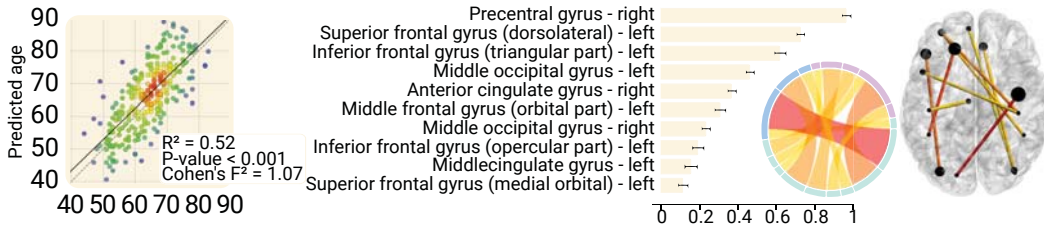
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1143  
  
1144

Datasets characterization (N = 5306)

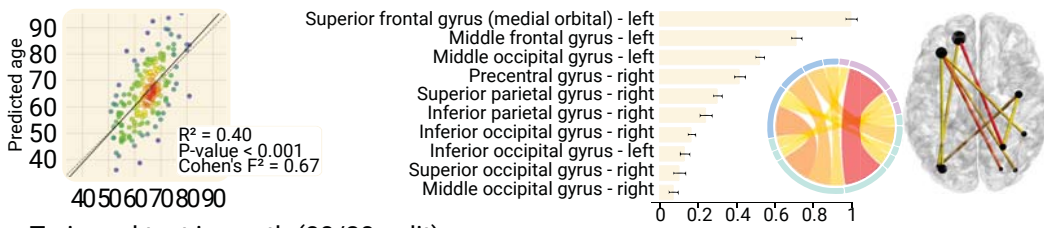




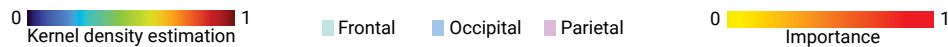
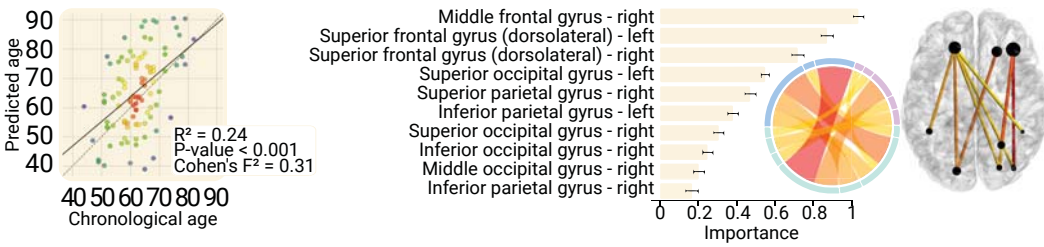
a. Train and test in north and south (80/20 split)



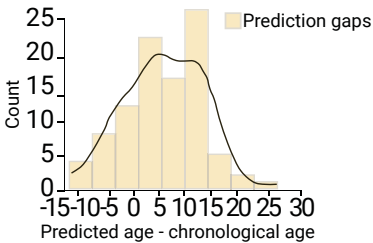
b. Train and test in north (80/20 split)



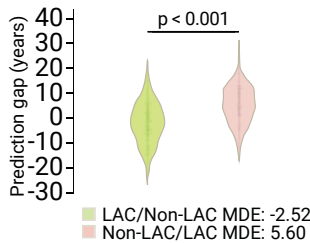
c. Train and test in south (80/20 split)



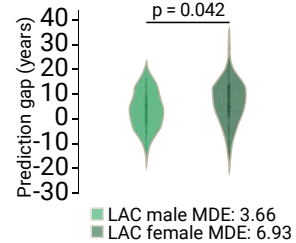
d. Train north and test south



e. Fit error comparison



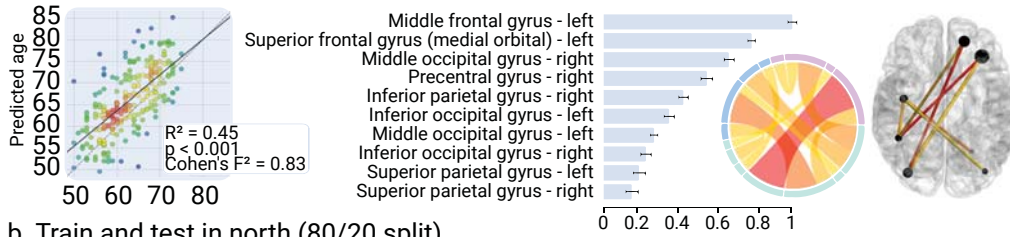
f. Sex differences



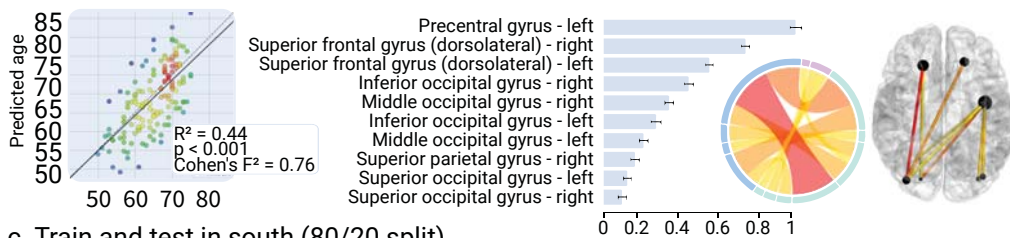


EEG

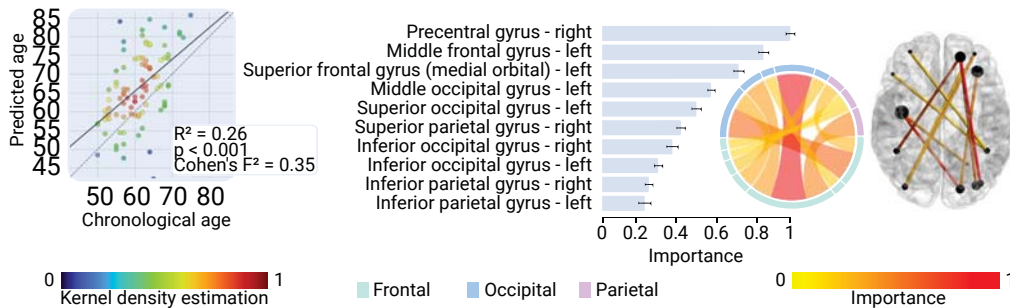
a. Train and test in north and south (80/20 split)



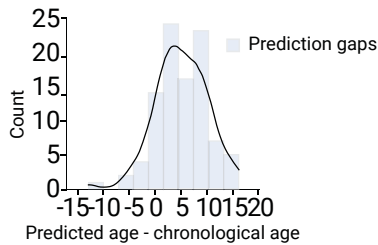
b. Train and test in north (80/20 split)



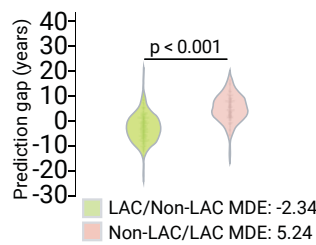
c. Train and test in south (80/20 split)



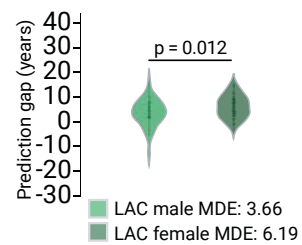
d. Train north and test south



e. Fit error comparison

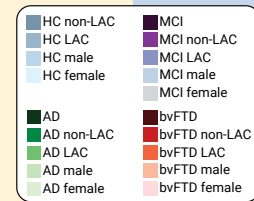
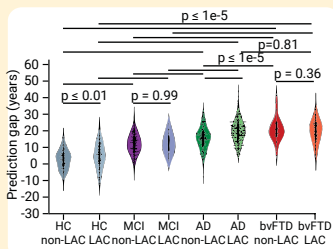


f. Sex differences

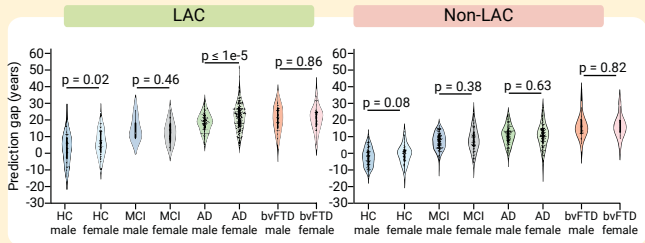


a. fMRI

Prediction gap by region

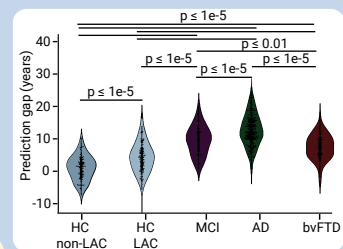


Prediction gap by gender

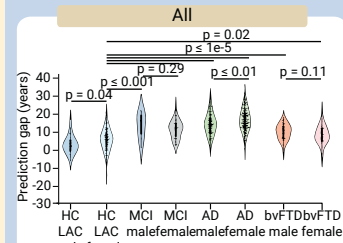


b. EEG

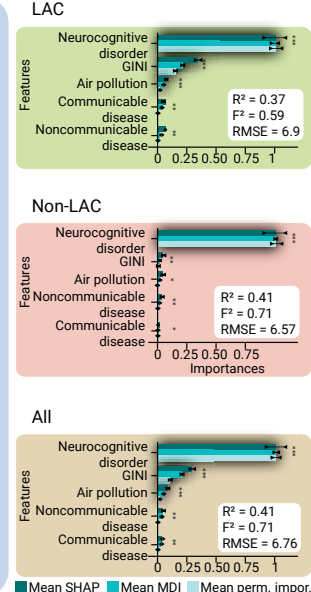
Prediction gap by region



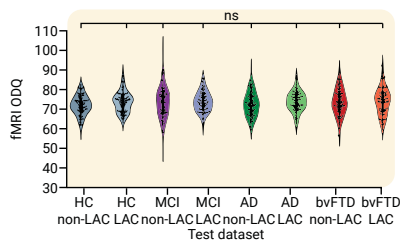
Prediction gap by gender



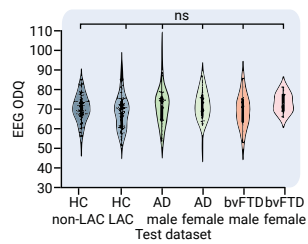
c. Exploratory analysis



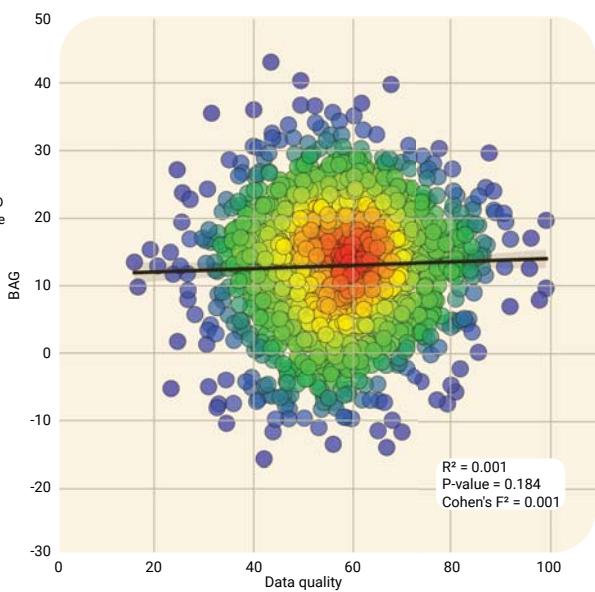
a. fMRI data quality



b. EEG data quality



c. fMRI prediction gap by data quality



d. fMRI prediction gap controlling by scanner

