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Differences between multimodal brain-age and chronological-age are linked to telomere shortening

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Abstract

Telomere shortening is theorized to accelerate biological aging, however, this has not been tested in the brain and cognitive contexts. We used machine learning age-prediction models to determine brain/cognitive age and quantified the degree of accelerated aging as the discrepancy between brain/cognitive and chronological ages (i.e. age gap). We hypothesized these age gaps

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none

are associated with telomere length (TL). Using healthy participants from the ADNI-3 cohort (N=196, Age_{mean}=70.7), we trained age-prediction models using four modalities of brain features and cognitive scores, as well as a 'stacked' model combining all brain modalities. Then, these six age-prediction models were applied to an independent sample diagnosed with mild cognitive impairment (N=91, Age_{mean}=71.3) to determine, for each subject, the model-specific predicted age and age gap. TL was most strongly associated with age gaps from the resting-state functional connectivity model after controlling for confounding variables. Overall, telomere shortening was significantly related to older brain but not cognitive age gaps. In particular, functional relative to structural brain-age gaps, were more strongly implicated in telomere shortening.

Keywords

Brain-age; cognitive-age; telomere; resting-state functional connectivity; structural connectivity; subcortical gray matter; cortical thickness

1. Introduction

Telomeres are nucleoprotein structures that protect the ends of chromosomes (Turner et al., 2019; Zhang et al., 2016). They maintain genomic stability by protecting the genomic DNA from degradation (Giardini et al., 2014). Telomere length (TL) is often proposed as a marker of cellular aging because telomeres are shortened with aging as a result of incomplete DNA replication. The rate at which TL is shortened varies across individuals and is largely attributed to the exposure to DNA replication, oxidative and inflammatory stressors. Thus, TL reflects the cumulative lifetime exposure to these stressors. Naturally, shorter TLs are linked to poor health and increased mortality (Njajou et al., 2009).

Previous research has documented various adverse brain-related outcomes associated with telomere shortening. In terms of gray matter (GM) volume, studies found shorter telomeres linked to significant atrophy, mostly in the subcortical/limbic regions (Jacobs et al., 2014; King et al., 2014; Powell et al., 2018). Findings from brain connectivity studies similarly revealed limbic-related network disruptions in the structural and resting-state functional connectivity modalities (Staffaroni et al., 2018; Yu et al., 2020). However, the accumulated evidence is less consistent on the relationship between TL and cognitive functions. Although some studies showed that shorter TLs were associated with worse cognitive functions (Hägg et al., 2017; Leibel et al., 2020; Ma et al., 2019), many other studies reported the opposite (Lee et al., 2017; Mahoney et al., 2019; Yu et al., 2020) or null associations (Brown et al., 2018; Zhan et al., 2018).

While it has been theorized and shown that telomere shortening is associated with accelerated aging in general (Njajou et al., 2009), this theory has not been tested specifically in the context of brain-aging. It is unclear if the telomere-shortening associated changes in the brain and cognitive domains described earlier reflect accelerated brain-aging, or perhaps age-irrelevant pathophysiological processes. These brain- and cognitive-related changes need not be specific to aging; they can arise as a result of non-aging-related factors. For instance, similar limbic abnormalities were found to be present in youths diagnosed with depression (Redlich et al., 2018) and those with significant psychopathic tendencies (Blair

and Zhang, 2020). Likewise, cognitive impairments were also commonly present in young adults diagnosed with mood disorders (Castaneda et al., 2008).

With the advent of brain-age machine learning prediction methods (Cole and Franke, 2017), we can now put an ‘age’ to an individual’s brain according to certain brain characteristics such as gray matter atrophy, cortical thickness, and connectivity between different regions, and then relate this brain age to variations in TL. If one’s brain-age is older than his/her chronological age, we can infer that the individual is undergoing accelerated brain aging. This difference between brain-age and chronological age have been commonly referred to as the brain age gap. Across the lifespan, accelerated brain aging is linked to other types of aging such as biological aging, older facial appearance (Elliott, et al., 2021), and cognitive decline. Concerning the latter, older adults diagnosed with neurocognitive disorders such as mild cognitive impairment (MCI) and Alzheimer’s disease (AD) were found to possess significantly ‘older’ brain age gaps as compared to their cognitively normal counterparts (Löwe et al., 2016).

One major limitation with many previous brain-age prediction studies was that they trained their age-prediction models solely on one class of brain features (e.g., GM or cortical surface) and this may not adequately capture the effects of aging in the brain. Furthermore, it has been shown that the combination of cortical and functional connectivity features produced more accurate brain-age predictions than either type of features alone (Liem et al., 2017). Hence, in the current study, our brain-age prediction models were derived from four different modalities— resting-state functional connectivity (rsFC), structural connectivity (SC), cortical thickness (CT), and subcortical GM volume (subGM). This will enable us to exploit a far more comprehensive range of age-related brain features in estimating brain age.

In the current study, we used the Alzheimer’s Disease Neuroimaging Initiative (ADNI) dataset to train multimodal brain-age prediction models. We also trained a cognitive-age prediction model in a similar manner. These models were then applied to an independent sample of older adults with MCI to predict their brain- and cognitive-age. Then, we assessed the associations between TL and the brain/cognitive-chronological age gaps. We hypothesized that ‘older’ brain- and cognitive-age gaps were associated with shorter TL. We chose to study individuals with MCI since they are likely to present with lower cognitive scores and atypical brain features such as disrupted white matter microstructure (Yu et al., 2017), resting-state connectivity (Badhwar et al., 2017), and significant GM atrophy (Minkova et al., 2017), as compared to cognitively normal individuals. These abnormalities will translate into larger or more variable brain/cognitive-chronological age deviations, thus making it easier to detect significant associations between brain/cognitive-chronological age gaps and TL.

2. Methods

2.1 Participants

Two independent groups of participants were used in this study. The first group consisted of participants from the Alzheimer’s Disease Neuroimaging Initiative (ADNI). Their data were downloaded from the ADNI’s database (adni.loni.usc.edu). The ADNI was launched

in 2003 as a public-private partnership, led by Principal Investigator Michael W. Weiner, MD. The primary goal of ADNI has been to test whether serial magnetic resonance imaging (MRI), positron emission tomography (PET), other biological markers, and clinical and neuropsychological assessment can be combined to measure the progression of MCI and early AD. For up-to-date information, see www.adni-info.org.

A total of 196 participants from the ADNI-3 baseline database who 1) were not diagnosed with dementia or MCI, 2) have valid cognitive test (described in the subsequent section) data, 3) have valid MRI data, and 4) had their rsfMRI scans acquired using single-band EPI sequences were included. Those with rsfMRI scans acquired using only multiband EPI sequences were excluded. These different EPI sequences are not compatible with each other. Most of the participants had at least an rsfMRI scan acquired using a single-band EPI sequence, as opposed to the multiband EPI sequence. Details regarding the criteria for dementia and MCI used in the ADNI are available at <https://adni.loni.usc.edu/wp-content/uploads/2008/07/adni2-procedures-manual.pdf>. Ethical approval for the ADNI study was obtained by the ADNI investigators.

The second group consisted of participants recruited in Singapore (SG dataset) for two different intervention studies (Yu et al., 2021a, 2021b) with identical neurocognitive assessments and MRI acquisition protocols. For the current study, the baseline data from both interventions were combined. These participants were recruited from the same community. The inclusion criteria were 1) aged between 60 and 85 (inclusive), 2) met the criteria for mild cognitive impairment (MCI), 3) able to travel to the intervention venue independently, 4) not presenting with any current neurological conditions, 5) not suffering from any terminal illness and 6) not participating in another interventional study. These participants were diagnosed with MCI (Petersen, 2004) by a consensus panel. Details on the operationalization of the MCI diagnosis are reported in their parent intervention studies. Written informed consent was obtained from these participants prior to their participation. Ethical approvals for both intervention studies were granted by the National University of Singapore Institutional Review Board.

The SG dataset consisted of 121 participants in total. Among the 121 participants, MRI data were acquired from 95. Two subject's MRI data were discarded due to obvious MRI abnormalities and another two were discarded due to excessive head motion during their rsfMRI scans. The remaining 91 participants with valid MRI data were included in the age-prediction analyses. They consisted of 15 single-domain amnesic, 44 single-domain nonamnesic, 12 multiple-domain amnesic and 20 multiple-domain non-amnesic MCI cases. Among scanned sample, 82 had valid TL measurements and were included in the analyses involving TL. The demographic characteristics of the two groups of participants are presented in table 1.

2.2 Cognitive measures

We included all available cognitive measures which are similar or at least comparable in SG and ADNI datasets. These tests were administered either in English or Mandarin in the SG sample, depending on the participant's preference.

The Color Trails Test (CTT) (D'Elia and Satz, 1996) and Trail Making Test (TMT) (Reitan, 1992) were used in the SG and ADNI samples, respectively, to assess divided attention, visual scanning, and processing speed. Both tests are highly similar; the CTT was thought to be a culturally neutral analog of the TMT (D'Elia and Satz, 1996). Although previous studies have observed the non-equivalence of performance in the second parts of the TMT and CTT, these differences were largely attributed to the effect of native language (Lee et al., 2000; Lee & Chan, 2000). To this end, the CTT may be more appropriate for use in the SG sample, which consisted of both English and Mandarin-speaking participants. Each of these tests consisted of two parts. In the first, participants connected a series of numbers that were printed within circles, sequentially from 1 to 25. Subsequently, in the second part participants alternated between choosing numbers in either pink or yellow circles while similarly connecting the numbers from 1 to 25 for the CTT. Whereas in the TMT, participants alternated between numbers and alphabet, in sequential order (i.e., 1-A-2-B-3-C, etc.). Three outcome measures were used in this study—the completion times for both parts, as well as the interference effect (i.e., [part 2 – part 1]/part 1). The CTT has demonstrated good reliability, as well as concurrent and construct validity in the local Singaporean context (Chew et al., 2020).

The Rey Auditory Verbal Learning Test (RAVLT; Rey, 1941) was used to assess verbal immediate and delayed recall, as well as recognition memory. Participants were given a list of 15 unrelated words (list A) to learn and immediately recall aloud over five learning trials (Immediate Recall). Subsequently, an interference list of 15 unrelated words (list B) was presented only once for the participants to learn and recall immediately, following which, the participants were instructed to recall aloud the words from list A. Approximately 30 minutes later, they were again asked to recall aloud the words from list A (Delayed Recall). Finally, they were given a list of 50 words, comprising of list A, list B, and 20 new distractor words, from which to identify the original 15 words (Recognition). The RAVLT have been previously reported to be valid, responsive and reliable in the local context (Shen et al., 2014).

The MMSE (Folstein et al., 1975) was used to assess for general cognitive ability. It was scored on a 30-point scale and consisted of 24 items assessing orientation, attention, calculation, recall, and language. A validated local adaptation (Feng et al., 2012) of the MMSE was administered in the SG sample. In this local adaptation, some of the word stimuli were replaced with more locally and culturally relevant ones.

For these measures, higher scores corresponded to better performance, except for the CTT/TMT outcomes, in which longer completion times and larger interference were associated with worse performance.

2.3 Telomere measurements

Whole blood samples were collected in the morning, upon fasting overnight into vacutainer tubes containing EDTA (lavender colour) and are stored immediately in a mini-fridge (4 °C) and transported within 12 hours of collection into the tubes. Subsequently, they are then centrifuged (2000rpm) for 10 minutes and their plasma is collected into 1.8ml cryo vials for further analysis of stress-related markers. The whole blood cells were then subjected to

genomic DNA extraction using QIA amp DNA blood mini kit (cat.no. 51104) according to the manufacturer's protocol and stored at -80°C . Telomere length was measured using a non-radioactive chemiluminescent telomere length assay kit (Telo TAGGG assay kit, Sigma Aldrich; cat.no.12 209 136 001) to visualize the telomeric DNA repeat sequence TTAAGGG from blood samples. Telomere length measurement involves the digestion of μg of DNA using Hinf I/Rsa I enzymes at 37°C for 2 hours, and run on 0.8% agarose gel. DNA smears were transferred on to the nylon membrane (Amersham Hybond TM-XL) overnight. Transferred DNA fragments are hybridized to a digoxigenin (DIG) labelled probe to validate the telomeric repeats developed by CDP-Star, which is a digoxigenin substrate to capture the imaging by X-ray film. Telomere length was measured by the location of bands based on molecular weight standard, in the white blood cell DNA. Average telomere length is measured between 100 base pairs to 20 kilo base pairs. These TL measurements were measured in 15 batches; TLs from each respective batch were normalised by using the positive control run in each batch. The image processing, detection of DNA smears and, subsequently measurement of telomere length were carried out using TeloTool (Gohring et al., 2014) in MATLAB, as described in a previous study (Rane et al., 2015). The inter-assay coefficients of variability was calculated to be 26.9%

2.4 MRI acquisition

Participants in the SG dataset were scanned in a 3-T Siemens Tim Trio scanner at the Clinical Imaging Research Center, Singapore. T1-weighted images were acquired using an MPRAGE protocol (TE=1.90s; TR=2.30s; TI=900ms; 256×256 matrix; 192 sagittal slices; in-plane resolution=1mm; slice thickness=1mm). For the resting-state fMRI, 310 EPI volumes were acquired. (TR = 2.30s; TE = 25ms; 48 axial slices; matrix = 64×64 ; in-plane resolution=3mm; slice thickness=3mm). During the resting-state fMRI scan, subjects were instructed to close their eyes and remain as motionless as possible. Diffusion-weighted images were acquired using a multi-shell High Angular Resolution Diffusion Imaging (HARDI) protocol, consisting of 14 b0 images, 60 diffusion directions at $b = 1000 \text{ s/mm}^2$ and 60 diffusion directions at $b = 3000 \text{ s/mm}^2$ (TE=111ms; TR=6.7s; 84×84 matrix, 48 axial slices, in-plane resolution=3mm; slice thickness=3mm). Details regarding the MRI acquisition protocol in the ADNI sample are available at <http://adni.loni.usc.edu/wpcontent/uploads/2017/07/ADNI3-MRI-protocols.pdf>

2.5 Image processing

The MRI data from both datasets were preprocessed using the same pipeline. T1-weighted images were preprocessed using the CAT12 as implemented in SPM12 within MATLAB. First, the T1-weighted images were corrected for bias-field inhomogeneities. Then, they were segmented into grey matter (GM), white matter (WM), and cerebrospinal fluid (CSF). These GM and WM images were used to estimate spatial normalization deformation fields using the high dimensional Diffeomorphic Anatomic Registration Through Exponentiated Lie Algebra (DARTEL) warping algorithm (Ashburner, 2007) which were applied to segmented images and subsequently modulated. These modulated images were then visually inspected. Finally, the 'volume estimation for ROI' writing option was used to extract region-of-interest (ROI) values from the Neuromorphometrics atlas (<http://>

www.neuromorphometrics.com/). All subcortical GM regions, excluding the cerebellum, were entered into the subsequent analyses.

Estimation of CT and the central surface was carried out using the projection-based thickness method (Dahnke et al., 2013), which consisted of topology correction (Yotter, Dahnke, Thompson, & Gaser, 2011), spherical mapping, and spherical registration (Yotter, Thompson, & Gaser, 2011). After obtaining the segmented images, WM distance was estimated and the local maxima were projected to other GM voxels using a neighbor relationship described by the WM distance (Dahnke et al., 2013). The ‘surface thickness and thickness estimation for ROI’ writing option was used to extract ROI values from the Destrieux atlas (Destrieux et al., 2010). All of these ROI values were subsequently entered into the analyses.

The resting-state functional MRI data were preprocessed using data processing assistant for resting-state fMRI (DPARSF), advanced version (Yan, Wang, Zuo, & Zang, 2016). Briefly, the first 10 volumes were removed to allow for T1 equilibrations effects. Next, the middle slice was used as the reference slice for slice time correction and motion correction realignment. Following this, the corrected images were coregistered to their respective T1-weighted image, and segmented into grey matter, white matter, and cerebrospinal fluid tissue maps using the DARTEL algorithm. Then, nuisance covariates regression, consisting of Friston 24 head-motion parameters, mean white matter and cerebrospinal fluid, and linear detrending was carried out. Global signal regression was also carried out to maximize the associations between functional connectivity and behavioral variables (Li et al., 2019). To further remove the effects of head motion, scrubbing was carried out on volumes with framewise displacement ($FD_{Jenkinson}$) > 0.2mm (Yan et al., 2013). Additionally, participants with excessive head motion, as operationalized by having a mean $FD_{Jenkinson}$ > 0.2mm, were excluded. Next, the images were normalized by DARTEL to MNI space with a voxel size of $3 \times 3 \times 3 \text{ mm}^3$ and smoothed using a 4mm FWHM kernel. A band-pass filter of 0.01 to 0.1Hz was applied to the signal to remove the physiological high-frequency physiological noise and low-frequency drift.

For the network construction, the brainnetome atlas (Fan et al., 2016) was used to parcellate the whole brain into 246 anatomical regions corresponding to the nodes of the network. Previous research has shown rsFC connectivity matrices derived from partial correlations with L2 regularization tend to produce better predictions than connectivity matrices derived from Pearson correlation (Wu et al., 2021). Hence, prior to training the rsFC model, we converted the resting state ROI time-series data into partial correlation matrices with L2 regularization using the FSLNets’ `nets_netmats` function (<http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FSLNets>).

The preprocessing of the diffusion images, tractography, and construction of the structural connectome were carried out using MRtrix3 (Tournier et al., 2019). Briefly, MP-PCA denoising (Veraart et al., 2016) and removal of Gibbs ringing artifacts (Kellner et al., 2016) were carried out on the raw images. Subsequently, they were corrected for motion, eddy currents and susceptibility-induced distortion using the inhomogeneity field maps obtained previously. Following this, bias field correction (Tustison et al., 2010) was carried out.

Next, the GM, WM, and CSF response functions were obtained using the Dhollander (Dhollander and Connelly, 2016) algorithm which are in turn used for estimating fiber orientation distributions (FOD) in the WM, GM and CSF tissues from diffusion data using spherical deconvolution. Then, anatomically-constrained tractography (Smith et al., 2012) was carried out using the WM FOD. This involved the prior preparation of a GM mask from the segmentation of the subject's T1 structural image using FSL FAST, and then using this mask to seed streamlines.

The AAL-90 atlas (Tzourio-Mazoyer et al., 2002) was used to parcellate the whole brain. For each subject, the AAL-90 template was first warped to the subject's native DTI space to obtain the transformations. Then, the warped template was overlaid onto the subject's diffusion tensors for visual inspection of the alignment. The transformations obtained previously were then applied to warp the AAL-90 atlas into the subject's native diffusion space. For the network construction in the subject's native diffusion space, the nodes i and j were thought to be connected by an edge ($e_{ij} = [i, j]$), if at least one reconstructed streamline was found with its two endpoints located within the two nodes, respectively. The edges in the connectivity matrix for each participant were operationalized as the number of streamlines connecting between each pair of regions. Finally, the thresholded matrices were normalized using the Brain Connectivity Toolbox (Rubinov and Sporns, 2010) within MATLAB.

2.6 Statistical analysis

To derive the brain- and cognitive-age prediction models, we trained ridge regression models separately on the five modalities of predictors (i.e., SC, rsFC, CT, subGM, and cognitive test scores) to predict participant's age using the Matlab function 'fitrlinear', within the ADNI dataset. Briefly, we first identified the optimal lambda parameters for the ridge regression models by testing 50 logarithmically-spaced values ranging from 10^{-5} to 10^{-2} in a 5-fold cross-validation (CV) paradigm. In order to minimize overfitting, we selected the largest lambda value that has a mean squared error (MSE) within one standard error of the minimum MSE (Gao et al., 2019). Then we repeated the ridge regression on the full ADNI sample using the selected lambda value to obtain the full-sample ridge regression loadings. Given that the optimal lambda value obtained in the 5-fold CV would vary depending on how participants were shuffled into the five folds, we repeated this process 1,000 times, with participants randomly shuffled into the folds each time. After which, the ridge regression loadings obtained from the full ADNI sample at the end of each iteration were averaged across the 1,000 iterations and these averaged loadings consequently constitute our brain-age (four independent models: SC, rsFC, CT, and subGM) and cognitive-age prediction models.

Next, we also constructed a stacked brain-age model, making use of all four brain modalities. First, we used the ADNI-derived brain-age models (all four modalities) to predict age within the ADNI sample, thus obtaining four sets of age predictions. These four sets of age predictions were then entered as input features into a random forest prediction model to predict participant's age within the ADNI sample. The hyperparameters for this stacked model were tuned automatically via another 5-fold CV using the 'OptimizeHyperparameters', 'auto' option within the 'fitrensemble' function in Matlab. To

quantify the contribution of the different modalities in predicting age, we estimated their prediction importance values.

Consequently, we would have generated five brain-age (i.e. SC, rsFC, CT, subGM, and the stacked model) and one cognitive-age prediction models. These five models were then applied to the SG participant's data to generate age predictions for each model. For each of these models, we assessed the accuracy of these predictions via the root mean square error (RMSE), mean absolute error (MAE), and correlation (Pearson's and Spearman's) between the predicted age and actual age. For every subject, we also computed the discrepancy in predictions (i.e., predicted age - actual age). Then we assessed the associations between these gaps and TL via Pearson's correlations. The age gaps were also compared across modalities using repeated measures analysis of variance (ANOVA). Statistical significance was set at $p < .05$. These analyses were carried out in MATLAB (R2021a) and R 4.0.2. The Matlab and R code for executing the analyses and generating the figures, as well as the preprocessed ADNI data are available at <https://osf.io/vkejr/>.

3. Results

3.1 Characteristics of age-prediction models

The ridge regression coefficients of the cognitive-age prediction model obtained across 1,000 permuted iterations (see figure 1) suggest that the cognitive age-prediction model was largely driven by Total learning, TMT-A, and TMT-B scores. Moving on to the brain-age prediction models, the age-related profiles of SC and rsFC are shown in figure 2c and d. In general, most of the SC connections were negatively associated with increasing age, while frontal-subcortical and subcortical-limbic connections were strengthened with age. In terms of rsFC, the patterns of connectivity were relatively mixed— different sets of connections were weakened and strengthened in relation to increasing age. Next, the age-related cortical profile is shown in figure 2a. In general, there was a mixture of negative and positive loadings, with the former clustered around superior and medial regions of the brain. The age-related subGM profile is shown in figure 2b. All of the subGM regions were negatively loaded, with the largest (absolute) loadings assigned to the bilateral thalamus. Finally, the proportion of predictor importance in the stacked random forest model is shown in figure 2e; the rsFC modality was associated with the largest predictor importance in the random forest model.

3.2 Predictive ability of age-prediction models

We applied ADNI-derived prediction models to the ADNI and SG datasets, and computed their prediction metrics (see figure 3). In terms of the precision (i.e., MAE and RMSE) of age prediction in the SG dataset, the CT and subGM models similarly outperformed the other models, whereas the cognitive model fared the worst. Nevertheless, in terms of the correlation between actual and predicted age in the SG dataset, the cognitive model performed the best, while the rsFC model fared the worst.

3.3 Age gaps and telomere length

The repeated measures ANOVA revealed significant differences between the age-gaps derived from the different age-prediction models (see figure 4). The results of the post-hoc tukey's tests suggest that participants' cognitive age was significantly 'older' than their brain-age estimates from the SC and rsFC models ($p < .001$), their CT-ages were significantly 'older' than their SC- and rsFC ages ($p = .0330$), and their subGM-ages were significantly older than their SC-ages ($p = .004$).

Given that demographical variables such as age, sex, and years of education were likely to confound these associations, we also performed partial correlation tests controlling for these variables. The partial correlation analyses suggest that the age gaps in the rsFC, CT, and stacked model were significantly and negatively correlated with telomere length (see figure 5). If we were to apply a bonferroni correction for the six sets of correlation analyses, only the partial r from the rsFC was statistically significant. On related note, TL was not significantly correlated with age ($r = -.09$, $p = .366$).

3.4 Supplementary analyses

We repeated all analyses involving the rsFC model, by using the conventional correlation instead of partial correlation rsFC matrices as input features. These results are presented in table S1. Generally, the correlation rsFC matrices produced a model that was slightly more overfitted to the ADNI dataset. This model's produced slightly more accurate age predictions in the ADNI dataset. Not surprisingly, it produced slightly less accurate predictions in the SG sample. Nevertheless, its age-gaps remained significantly correlated with TL, after controlling for age, sex, and years of education

4. Discussion

The current study tested the hypothesis that telomere shortening is linked to older brain and cognitive age gaps. We trained brain-age and cognitive-age prediction models using the ADNI dataset and applied these models to the SG dataset. Our results showed that these age-prediction models were fairly generalizable to the SG dataset; the obtained MAEs were in line with previous findings (Cole and Franke, 2017). Then we correlated the predicted-actual age gaps in each age prediction model with TL. The findings suggested that the predicted-actual age gaps from the cognitive-age model were not significantly correlated with TL, whereas the predicted-actual age gaps obtained from three brain age models were significantly and negatively correlated with TL. In particular, predicted-actual age gaps from the rsFC model showed the highest correlation with TL. Overall, these results suggest telomere shortening is significantly associated with 'older' brain age but not cognitive age.

Using the brain-age prediction approach, we provided novel evidence to show that telomere shortening is linked to 'older' brain age gaps in multiple modalities. It is interesting to note that rsFC brain age gaps are most strongly linked to telomere shortening. These gaps indirectly measure the deviations in the functional connectome in the SG sample from the ADNI sample. To this end, one can infer that telomere shortening is linked to changes in FC. Notwithstanding the cross-sectional nature of this study, which precludes the causal

inferences between telomere shortening and FC changes, we speculate such causal effects can possibly exist in both directions. First, the telomere-associated cellular senescence could have directly led to brain aging (Ain et al., 2018). Alternatively, age-related FC changes in the brain could have resulted in less self-restraint and inhibition (Tsvetanov et al., 2018), and subsequently influencing health-related behaviors. For instance, this could mean more frequent consumption of alcohol and tobacco, or unrestraint eating. These unhealthy behaviors would in turn shorten TL (Puterman et al., 2015).

Relatedly, we observed that the age gaps derived from the structural domains, especially SC, appeared to be less strongly implicated. The relatively different results in the rsFC and SC modalities are not unusual. Although rsFC and SC are related to each other, they are not very strongly coupled. Strong rsFC can thrive in the absence of strong SC since rsFC can rely on indirect structural connections (Damoiseaux, 2017). Furthermore, SC is likely to be more resilient to aging in general. Unlike rsFC networks, SC networks appear to be held together by a consistent set of highly connected and central hubs which remain mostly unchanged across the lifespan (Betzel, et al., 2014), thus ensuring the age-related stability in the SC network topography. Hence, the brain-aging trajectories in the rsFC and SC modalities are likely to diverge to some extent. Contrary to our hypothesis, the cognitive-chronological age gaps were not significantly associated with TL. In fact, these gaps were positively related (though not significantly) to TL, counterintuitively suggesting that telomere shortening was associated with ‘younger’ cognitive functions. This may not be unusual, as there were a handful of studies that showed that shorter TLs were associated with better cognitive functions (Harris et al., 2006; Lee et al., 2017; Liu et al., 2016; Mahoney et al., 2019; Wikgren et al., 2012). Furthermore, it was shown that this counterintuitive increase in cognitive functioning was predicted by telomere-shortening associated SC changes (Yu et al., 2020).

Our multimodal brain-age prediction models were largely consistent with previous research in showing that aging is associated with disrupted structural connections (Betzel et al., 2014) and significant cortical and subcortical GM atrophy (Oh et al., 2014). Amazingly, these ADNI-derived models generalized relatively well to the SG sample despite the different socio-demographics and MRI acquisition protocols in both samples— which is a further testament to the robustness of the brain-age prediction models. Nevertheless, the age-related rsFC profile obtained from the ADNI dataset did not appear to be consistent with previous research in showing an age-related decrease in within-network and increase in between-network connectivity (Damoiseaux, 2017; Zonneveld et al., 2019). Instead, our results suggested the opposite— increased within-network and decreased between-network connectivity. Such an atypical age-related rsFC profile is likely to be the consequence of using partial correlation, as opposed to the conventional correlation rsFC matrices as input features. As Wu et al. (2021) explained, this partial correlation approach removes the shared variance across regions, consequently, the pattern of brain connectivity between regions will be significantly distorted. Although partial correlation matrices would improve the model’s prediction performance, the connectivity profiles obtained from these matrices may not be as interpretable as those of correlation matrices.

On average, we see that the SG sample, consisting of individuals with MCI, had cognitive ages that were older than their chronological ages; this would be largely expected in light of the ‘objective cognitive impairment’ criterion of MCI. Furthermore, education levels were much lower in the SG sample than in the ADNI sample. Given that education constitutes a significant component of cognitive reserve and is strongly associated with cognitive functions (Whalley et al., 2004), the ADNI-derived cognitive age model is likely to overestimate the cognitive age in the SG sample. Next, our results also provided a rare opportunity to compare the pace of aging in the different brain modalities. We showed that cortical age gaps are the ‘oldest’ compared to those of other brain modalities in our MCI sample. Nevertheless, we imagine these results would be largely dependent on the etiology of MCI. For instance, we would expect individuals with MCI due to AD to undergo more rapid subcortical aging as compared to AD-unrelated MCI cases (Yi et al., 2016). In our sample of MCI subjects, the older cortical age gaps may hint at possible vascular-related etiologies (Lee et al., 2018).

Our findings present some important implications for brain-age predictions in general. The significant associations between brain-chronological age gaps and TL are a much-needed validation for brain age predictions in general. These brain age metrics can be used as indices of general brain health (Cole and Franke, 2017) with relative ease. Once a brain-age prediction model has been set up and adequately validated, it can be applied to patients’ MRI scans to obtain their brain-age via largely automated procedures—requiring only very minimal technical expertise. Brain-age is also fairly simple to interpret and can be easily communicated to and understood by patients, unlike the more technical concepts of atrophy, lesions, or brain connectivity. Additionally, our results suggest that brain-age is largely influenced by patterns of rsFC. Given that rsFC is highly susceptible to experience-dependent plasticity (Kelly and Castellanos, 2014), this would open up a whole range of possibilities in using lifestyle or behavioral interventions to ‘reverse’ brain aging to improve brain health in general.

The current findings are subjected to two limitations. First, due to the small number of common cognitive tests used in both datasets, we may not have an adequate number of predictors in our cognitive-age model nor were we able to cover the different cognitive domains comprehensively. Second, although the age prediction models had generally demonstrated satisfactory levels of generalizability, it is likely that this generalizability could be higher if the MRI acquisition parameters were identical in both datasets. Third, the differences between the ADNI and SG samples in terms of education levels meant that the brain/cognitive age gap could not be entirely accounted for by accelerated brain aging/degeneration, but could also result from education-related factors implicating brain aging. Fourth, the use of the MCI-only sample in this study meant that these results cannot be generalized to or interpreted within the context of normal aging. It is likely that some disease-related factors, such that those relating to AD or cerebrovascular disease, might have accelerated brain aging and led to telomere shortening; consequently, significant correlations between brain aging and TL could be observed. Speculatively, in the absence of such disease-related factors, such correlations is less likely to be observed.

Verification

We verify that the work described has not been published previously, that it is not under consideration for publication elsewhere, that its publication is approved by all authors and tacitly or explicitly by the responsible authorities where the work was carried out, and that, if accepted, it will not be published elsewhere in the same form, in English or in any other language, including electronically without the written consent of the copyright-holder

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Highlights

- Chronological-age is best predicted by resting-state functional brain connectivity
- Shorter telomeres predict '**older**' brain-age and chronological-age discrepancies
- Shorter telomeres are more strongly linked to functional than structural brain aging

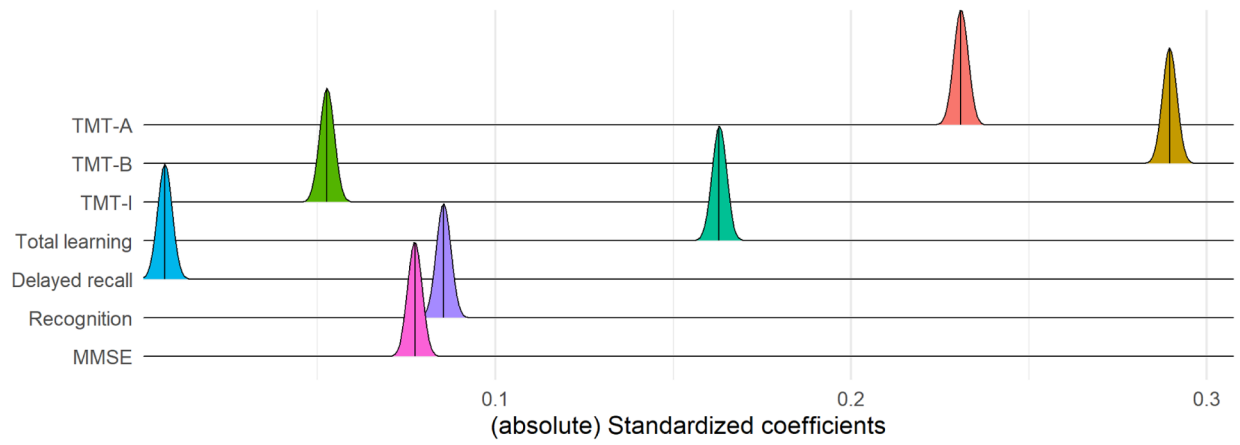


Figure 1.

Ridgeline plot showing the distribution of coefficients in the cognitive-age prediction model, across 1,000 permuted iterations within the ADNI sample. The vertical lines within the ridges represent their respective means. TMT= Trail Making Test; MMSE=Mini-Mental State Exam

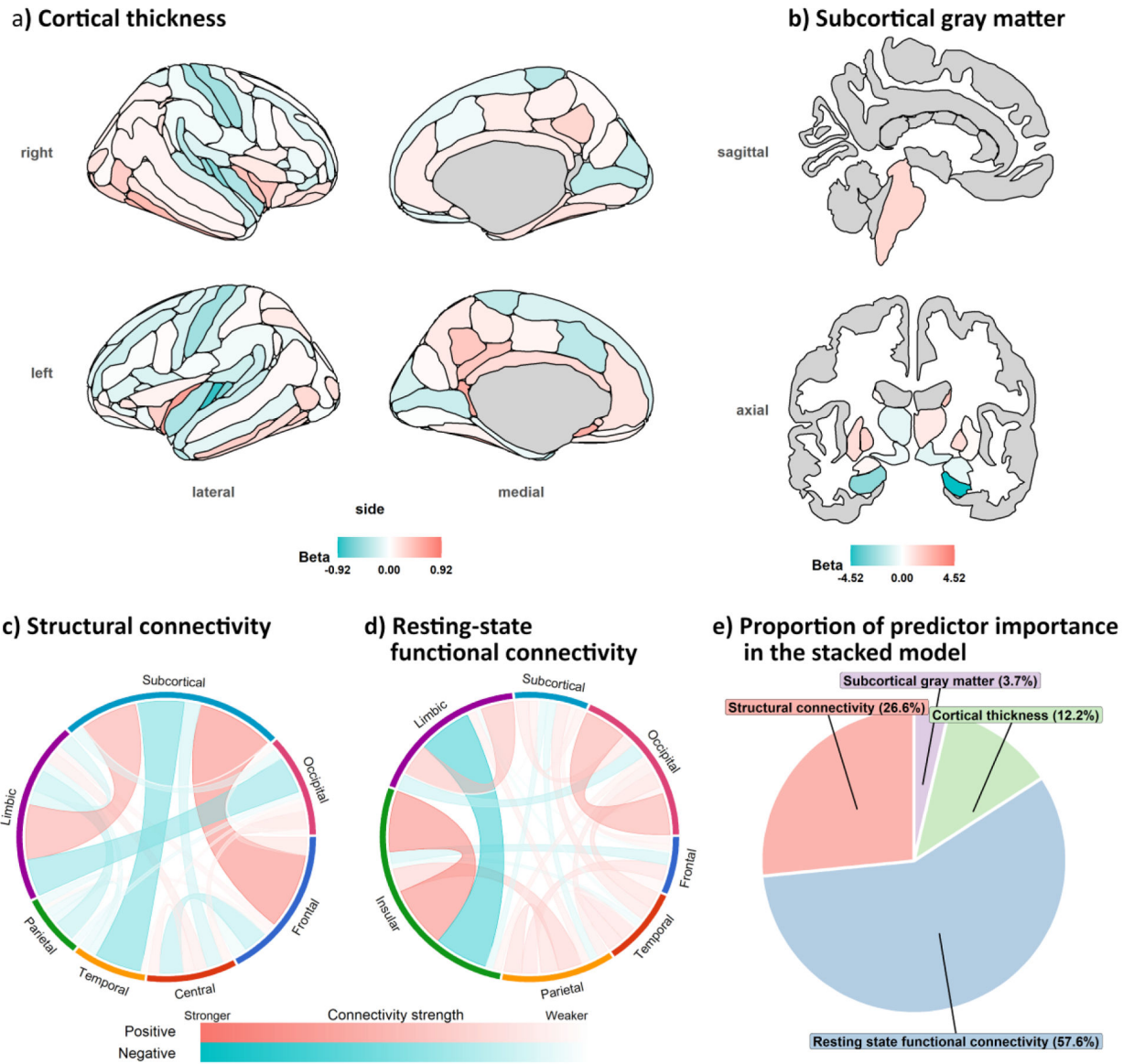


Figure 2. Averaged ridge regression loadings across the 1000 permuted iterations in the a) cortical thickness b) subcortical gray matter, c) structural connectivity and d) resting state connectivity age prediction models. e) predictor importance in the stacked model. Note. the left and right nucleus accumbens regions which have the loadings of -0.29 and -0.33 , respectively, could not be shown together with the other subcortical brain regions within the same sagittal and axial slice in b).

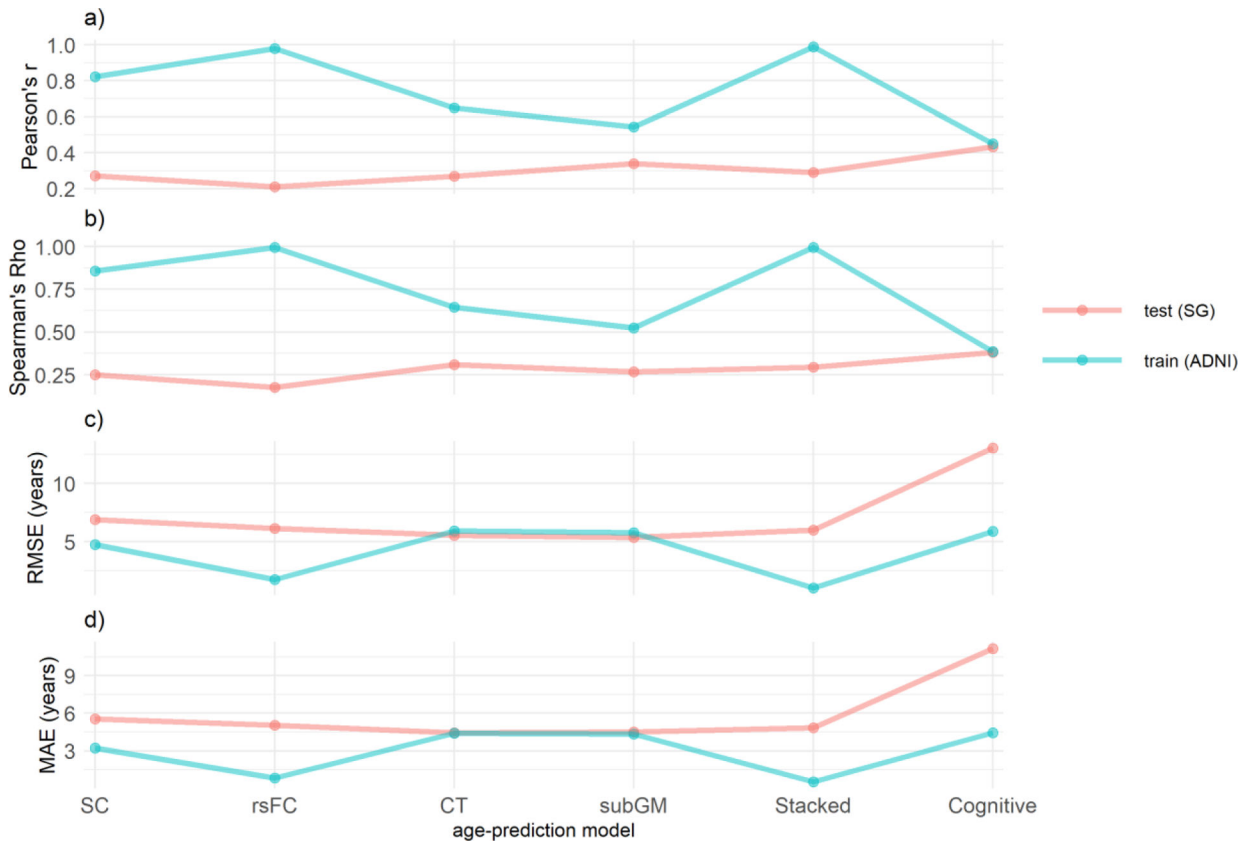


Figure 3. Accuracy of age-prediction models as quantified by a) Pearson's r , b) Spearman's Rho , c) root mean square error and d) mean absolute error. SC= structural connectivity; rsFC = resting state functional connectivity; CT= cortical thickness; subGM= subcortical gray matter.

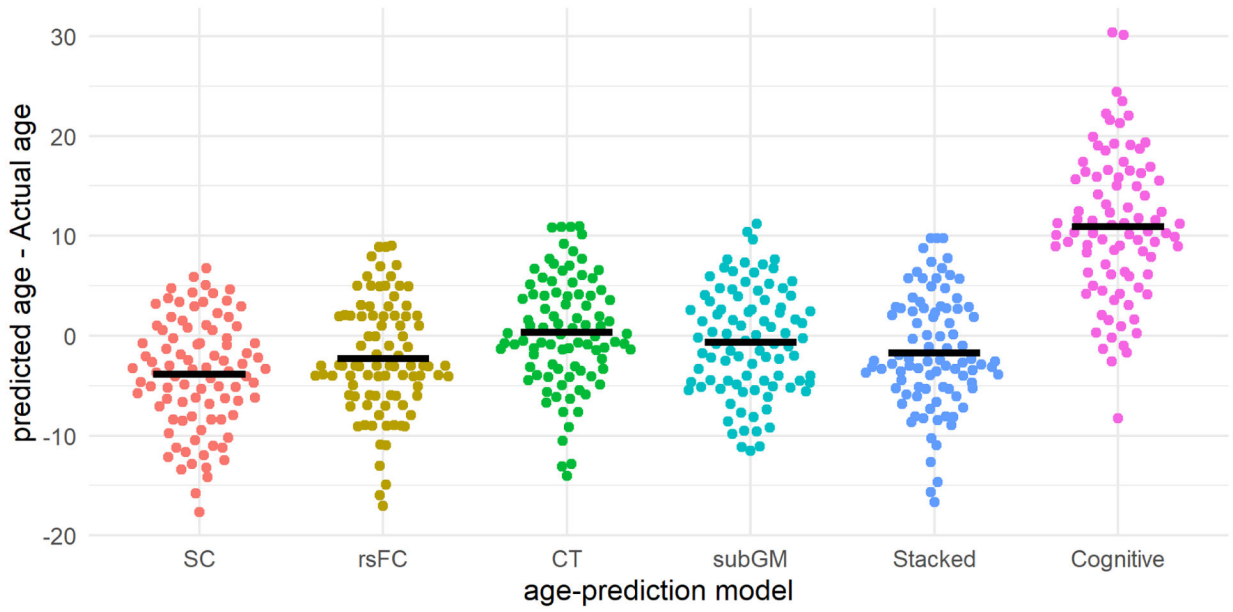


Figure 4. Beehive plots showing the distribution of predict-actual age gaps across the different age-prediction models. The thick black lines represent the mean predict-actual age discrepancies in their respective age-prediction models. SC= structural connectivity; rsFC = resting state functional connectivity; CT= cortical thickness; subGM= subcortical gray.

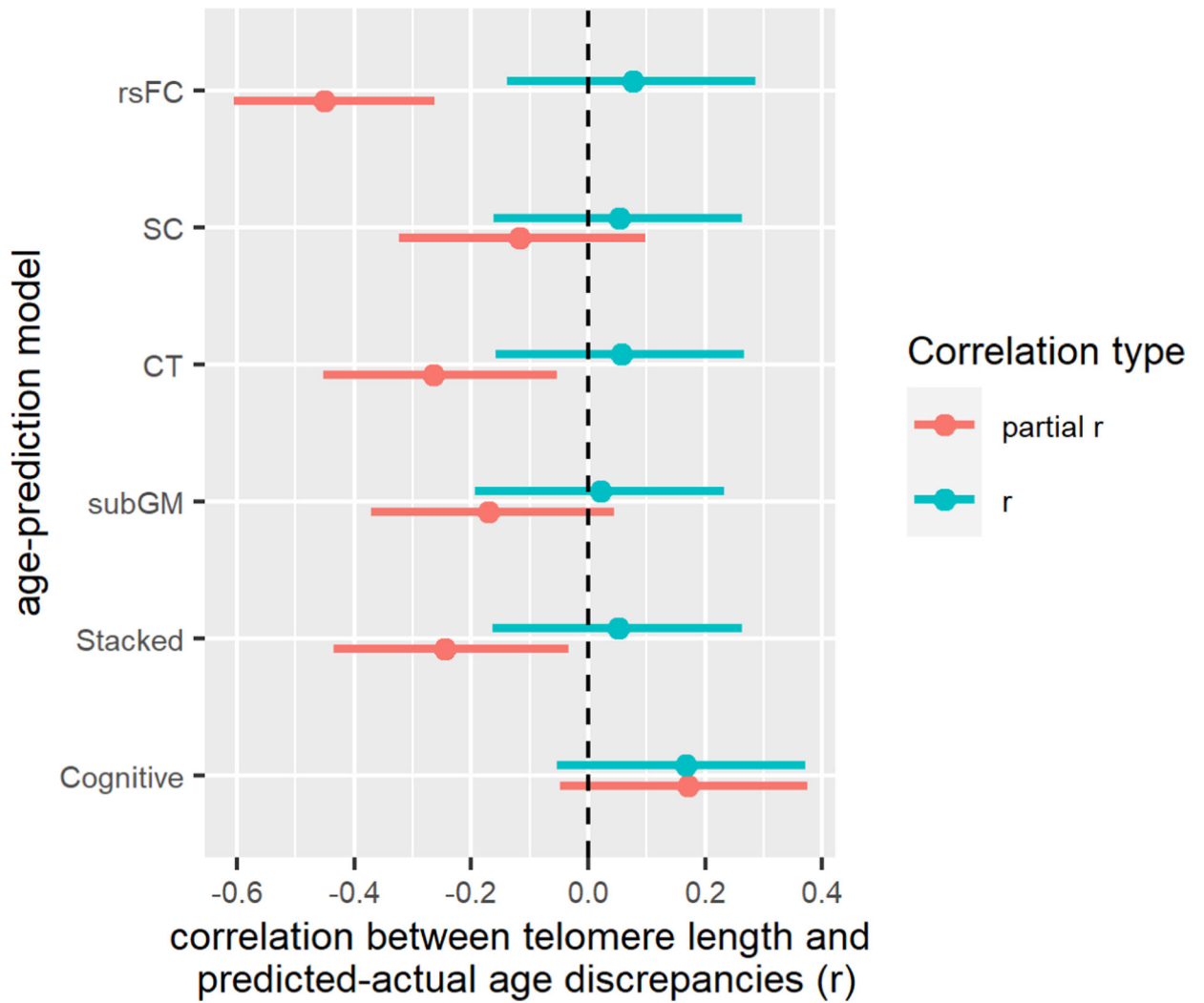


Figure 5. Forest plots showing the correlations between telomere length and predicted-actual age gaps from the different age-prediction models. Note. ‘partial r’ is controlled for age, sex and years of education. The error bars represent the 95% confidence intervals of the correlation coefficients. SC= structural connectivity; rsFC = resting state functional connectivity; CT= cortical thickness; subGM= subcortical gray matter.

Table 1.

demographical characteristics of both groups of participants

Dataset	ADNI (N=196)	SG (N=91)
Mean age (SD)	70.7 (6.5)	71.3 (5.7)
% females	60%	76%
Mean years of education (SD)	16.9 (2.2)	5.1 (4.2)
Mean MMSE score (SD)	29.0 (1.1)	25.3 (3.3)

Note. SD= standard deviation; MMSE=mini-mental state examination.

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