Supplementary Text

Covariate adjustment. For each feature type, let *j* be the index of a brain region, $j = 1, ..., m$. Let $n = 3418$ be the aggregate training sample size and f_i be an $n \times 1$ vector containing all subjects' hemisphere-averaged values of a given feature. We begin by regressing out the confounding effects of sex, cohort, FreeSurfer version, and of the cohort \times CA interaction. We account for the joint confounding effects of cohort and FreeSurfer version after generating an $n \times 1$ group vector g which assigns a distinct integer to each unique combination of cohort and FreeSurfer version, yielding $N_g = 6$ 'groups' in our training set (Table 1). Let k be an index for each of these groups ($k = 1, ..., N_g$), CA be an $n \times 1$ vector containing the CAs of the subjects, and g_k be an $n \times 1$ vector with entries of 1 for subjects belonging to group k and 0 otherwise. For each feature f_i we fit N_g distinct multiple linear regression models of the form

$$
\boldsymbol{f}_j = \gamma_{0,j,k} + \gamma_{1,j,k} \boldsymbol{g}_k + \gamma_{2,j,k} \boldsymbol{C} \boldsymbol{A} + \gamma_{3,j,k} \boldsymbol{g}_k \odot \boldsymbol{C} \boldsymbol{A} + \boldsymbol{\varepsilon}_{j,k}
$$

For each of k, $\gamma_{0,i,k}$ is the intercept, $\gamma_{1,i,k}$, ..., $\gamma_{3,i,k}$ are regression coefficients, $\varepsilon_{i,k}$ is the residual vector obtained by fitting the regression model to f_i , and $\alpha \odot b$ denotes elementwise multiplication of the elements in \boldsymbol{a} and \boldsymbol{b} , which are of the same dimensions. To note, $\boldsymbol{c}\boldsymbol{A}$ is included as a predictor variable to ensure that its covariance with \boldsymbol{f}_i is not captured in the group-by-CA interaction term, which has been shown to improve model performance and to remove confounding effects (18). Because of this inclusion, each group requires a separate multiple linear regression model to avoid a rank-deficient design matrix. If only the group effect is regressed out, each feature f_i is corrected as

$$
\boldsymbol{f}_j^{(c)} = \boldsymbol{f}_j - \sum_{k=1}^{N_g} (\gamma_{1,j,k}\boldsymbol{g}_k + \gamma_{3,j,k}\boldsymbol{g}_k \odot \boldsymbol{C}\boldsymbol{A})
$$

The intercept $\gamma_{0,k}$ is not subtracted because this would remove the main effect, which is unaccounted for by confounds. To ensure that the covariance of f_i with CA is not removed, the $\gamma_{2,j,k}$ CA term in the regression is not subtracted. The covariate-corrected features $f_j^{(c)}$ are assembled into an $n \times (m+1)$ design matrix

$$
X = \left[1 \; f_1^{(c)} \ldots f_m^{(c)}\right]
$$

where 1 is an $n \times 1$ column vector for the model intercept. Ridge regressions were implemented both across sexes and for each sex. In the former case, the statistical effect of sex on brain features is regressed out; in the latter case, a separate regression model is implemented for each sex. Once the sex effect has been regressed out, a linear regression model $f_i = \alpha_0 + \alpha_1 s + \varepsilon$ is fit, where s is an $n \times 1$ binary variable vector (which codes male subjects as 1 and female subjects as 0.), α_0 is the intercept, α_1 is a linear regression coefficient, and ε is a vector of residuals. We chose this coding scheme to model females as the reference sex group due to their typically slower aging. When the effects of *both* sex and group are regressed out, each feature is corrected according to the equation

$$
\boldsymbol{f}_j^{(c)} = \boldsymbol{f}_j - \sum_{k=1}^{N_g} (\gamma_{1,j,k}\boldsymbol{g}_k + \gamma_{3,j,k}\boldsymbol{g}_k \odot \boldsymbol{C}\boldsymbol{A}) - \alpha_1 \boldsymbol{s}
$$

where $f_j^{(c)}$ is the corrected value of the feature indexed by j.

Supplementary Tables

eTable 1. Formulas for covariate correction procedures, regression objective functions, bias correction, and performance statistics, as well as quantities on which these depend.

Note. BA =biological age, CA =chronological age, f=full, g=group m =number of features, N_g =number of groups, n =number of subjects, r=reduced.

eTable 2. Summary of cognitive assessments available for the Cam-CAN validation sample. For emotional processing, the percentage of correct responses to Ekman's emotion expression task conveys emotional recognition accuracy, which declines with age. For stimuli with negative emotional valence in the emotional memory task, d' indexes memory accuracy (correct rejections vs. correct recognitions). Negative stimuli were selected for this study because negative emotional memory is more affected by age than positive or neutral emotional memories are. Emotional regulation during negatively valanced trials indicates the ability to suppress negative emotions, which is often preserved in typical aging. For executive functioning, the total score on Cattell's fluid intelligence test conveys frontoparietalmediated executive control measured across four subtests. On the hotel test, the time taken on each of five tasks is a measure of complex planning and multitasking ability. The number of correctly interpreted proverbs measures abstraction. For memory, the number of correctly matched unfamiliar faces can index age-related memory decline. The number of correctly recognized famous faces measures semantic recall. In the picture priming task, the word finding time is used to indicate age-related semantic memory decline. The proportion of tipof-the-tongue responses quantifies word finding difficulty, which commonly reflects cognitive decline. Average capacity on the color version of the visual short-term memory task measures working memory span, which often declines with age. For motor functioning, the mean over-compensation time on the force matching task measures sensorimotor integration ability. The mean reaction time on the motor learning task is a measure of motor adaptation. The mean reaction time on the simple task measures automatic response speed, while the mean reaction time on the choice task measures response speed for trials requiring decision-making.

 a_n =sample size

 ${\sf eTable~3}$. Estimated ridge regression coefficients $\hat\beta_j$ and (un)adjusted partial coefficients of determination R_p^2 for the sex-agnostic model to estimate brain age from regional volumes. R_p^2 is expressed as a percentage of the variance, explained by the full model, that is not explained by a reduced model which excludes the variable in question. The model intercept is in units of years (y); the other regression coefficients $\hat\beta_j$ are in units of y × 10³. In accordance with the text, the subscript *j* in $\hat\beta_j$ is used to emphasize that these are *multivariate* regression coefficients. Entries are sorted in descending order by adjusted $\bar{R}_p^2.$

 ${}^{\mathrm{a}}\hat{\beta}_{j}$ =regression coefficient for region j

 ${}^{\text{b}}R_p^2$ =coefficient of partial determination

eTable 4. Relative ability of CA and BA to capture performance within each cognitive domain for Cam-CAN validation sample participants with data available for each cognitive task. For each of CA, BA, and AG, the table lists Spearman's rank correlation coefficient ρ , p -value for the test of the null hypothesis $H_0: \rho = 0$, and df . Also listed are Fischer's z-statistic and p-value for the test of the null hypothesis $H_0: \rho(CA) = \rho(BA)$ of no change in ρ when this measure is computed using CA vs. BA.

 $Note.$ $AG = age$ gap, $BA = biological$ age, $CA =$ chronological age.

 a_{ρ} =Spearman's rank correlation coefficient between task and measure

 $^{\text{b}}p$ = p -value for significance test of ρ

 c d f =degrees of freedom of significance test of ρ

 $^{\tt d}$ z= z -score for the difference between $\rho_{\scriptscriptstyle{CA}}$ and $\rho_{\scriptscriptstyle{BA}}$ for corresponding task

 $ep=p$ -value for significance test of z

 $*_{p} < 0.0013$

Supplementary Figure Captions

eFigure 1. Performance of the sex-agnostic ridge regression model predicting age from regional volumes. Biological ages and age gaps are scatter-plotted against chronological age for the (**A**, **B**) training and (**C**, **D**) test sets. **A**. biological ages in the training set. **B**. age gaps in the training set. **C**. biological ages in the test set. **D**. age gaps for the test set. All quantities are in years. The continuous green line in **A**. and **C**. is for the equation $BA = CA$. The green line in **B** and **D** is for the equation $AG = 0$. Abbreviations: $AG = age$ gap, $BA = biological$ age, $CA =$ chronological age, y=years.

eFigure 2. Adjusted coefficients of partial coefficient of determination \bar{R}^2_p for the 37 structures with the largest \bar{R}^2_p values included in the sex-agnostic ridge regression model estimating age using regional volumes. Plotted are adjusted $\bar R_p^2$ values, expressed as percentages of the total variance \bar{R}^2 explained by the full model that includes all predictors (regions or structures).

