Background

Brain age prediction using machine learning and neuroimaging techniques has recently gained research momentum, and brain age has emerged as a promising biomarker of cognitive and clinical outcomes in both healthy and clinical populations. The currently available brain age prediction models have limited coverage of the human lifespan, as most of them only cover adulthood.

Objective

- 1. Assess the effects of age range throughout the human lifespan
- 2. Assess the effects of different site harmonization methods
- 3. Establish a minimum sample size requirement for a stable brain age model

Methods

We developed sex-specific brain age models across the human $\int_{a} \int_{a} \frac{1}{2} \int_{a} \frac{1}{2} \frac{1}{2$ lifespan by using brain regional morphometric data from 34,535 8 healthy individuals (53% female) aged 5-90 years. The deidentified data were collated from 87 datasets from Europe, Australia, USA, South Africa, and East Asia; and data use aligned with the policies of the ENIGMA Lifespan Working Group [1].

The regional morphometric features thickness, cortical include cortical surface area, and subcortical volume; and the model development procedures were based on our prior evidence [2]. model was trained by using Each Support Vector Regression with Radial Basis Function Kernel. Hyperparameter tuning was performed by using a grid search in a 10-fold cross-validation scheme across 10 repeats.



We assessed the effects of age range, site harmonization methods (no site correction, linear regression, and combat-GAM), and sample size on the model performance metrics Pearson's correlation coefficient (CORR) and mean absolute error (MAE).







Performance Evaluation of Neuroanatomically-based Brain Age Models Throughout the Lifespan Yuetong (Jordan) Yu^{1,2}, Hao Qi Cui^{1,2}, Ruiyang Ge^{1,2}, Sophia Frangou^{1,2}

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Results

Figure 1. CORR (correlation coefficient between brain predicted age and chronological age) calculated during the repeated crossvalidation with different age ranges. Each curve represents the results obtained from a specific site harmonization method.



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Desikan-Killiany atlas Regional morphometric features include cortical thickness of 68 parcels, surface area of 68 parcels, and 14 subcortical volumes.

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Figure 2. MAE (mean absolute error) calculated during the

References

1. Ruiyang Ge, Yuetong Yu, et al., and Sophia Frangou. Normative Modeling of Brain Morphometry Across the Lifespan Using CentileBrain: Algorithm Benchmarking and Model Optimization. bioRxiv, 2023. 2. Amirhossein Modabbernia, et al., and Sophia Frangou. Systematic evaluation of machine learning algorithms for neuroanatomically-based age prediction in youth. Human Brain Mapping, 2022:43(17), 5126-5140.

Figure 3. The performance of brain age models was evaluated in relation to the sample size, specifically considering an age range of 30 The results presented here were obtained without applying any site correction method to the data.



200 400 600 300,000,200,400,600,300,200,200,200,200,300,320,340,360,360,300,400

Conclusions

We

We

develop recommend to neuroanatomically-based brain age model that incorporates data spanning a minimum of 30 years.

conducting site recommend not harmonization for neuroanatomically-based brain age models.

Performance of neuroanatomically-based brain age models plateaued at sample sizes exceeding 1,000.