

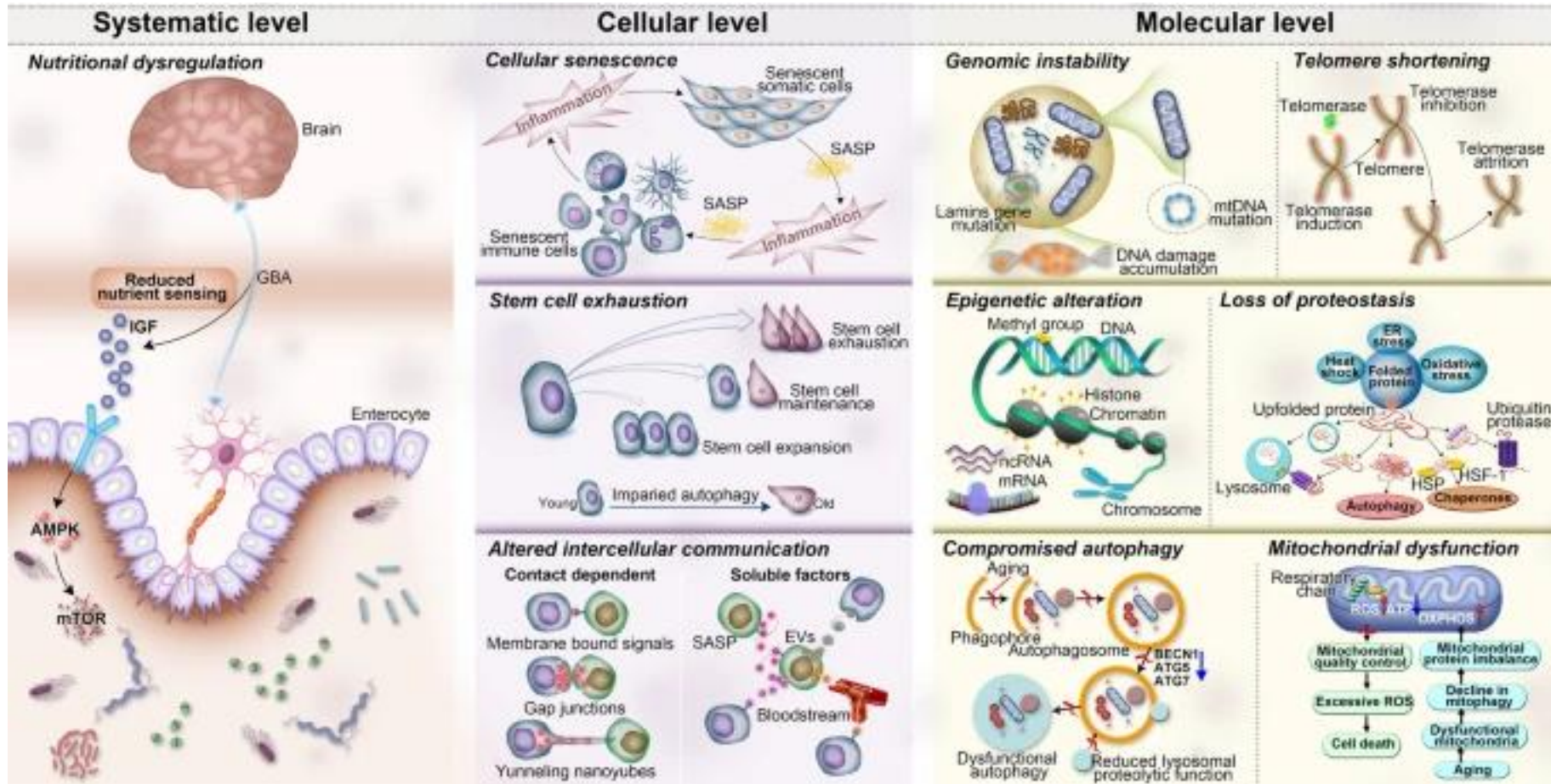
Hands-on AI Regression Model Development (1): Data and Prediction Problem

인공지능 회귀 모델 개발 실습 (1): 데이터 및 예측 문제

Aging

- Process of becoming older
 - Refers mainly to humans
- Biological basis [\[Jin, 2010\]](#)
 - Neither theory appears to be fully satisfactory
 - Two main theoretical categories
 - Genetically programmed
 - Biological timetable, perhaps a continuation of childhood growth and development
 - Damage or error-related
 - Environmental assaults to living organisms

- Hallmarks of aging [\[Guo et al., 2022\]](#)
 - Genomic instability
 - Telomere dysfunction
 - Epigenetic alterations
 - Loss of proteostasis
 - Compromise of autophagy
 - Mitochondrial dysfunction
 - Cellular senescence
 - Stem cell exhaustion
 - Altered intercellular communication
 - Deregulated nutrient sensing

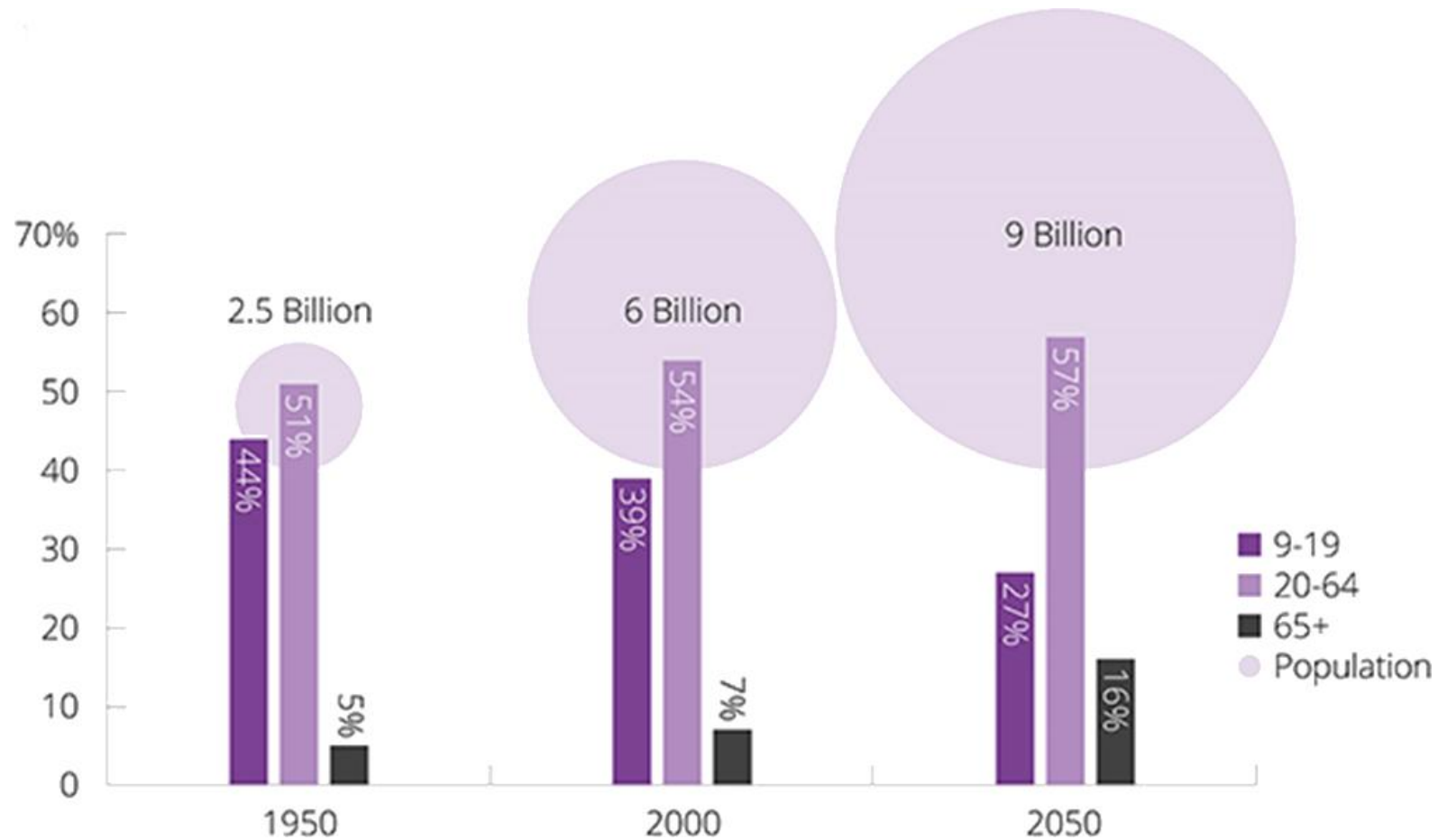


[Guo et al., 2022]

Ten Hallmarks of Aging Subdivided into Three Categories

- Changes by aging
 - Accumulation of a wide variety of molecular and cellular damage over time
 - gradual decrease in physical and mental capacity
 - growing risk of disease
 - death
 - Neither linear nor consistent
 - Only loosely associated with an individual's age in years
 - Often associated with other life transitions such as retirement, relocation to more appropriate housing, and the death of friends and partners

- Population aging
 - Shift in distribution of a country's population towards older ages
 - Increasing median age in a population
 - By 2030, 1 in 6 people in the world will be aged 60 years or over
[\[https://www.who.int/news-room/fact-sheets/detail/ageing-and-health\]](https://www.who.int/news-room/fact-sheets/detail/ageing-and-health)
 - Because of declining fertility rates and rising life expectancy
 - Started in high-income countries and now extended to low- and middle-income countries



[\[http://study-aids.co.uk/dissertation-blog/population-ageing/\]](http://study-aids.co.uk/dissertation-blog/population-ageing/)

Size and Proportion of the Global Population as Related to Age over Time

- Healthy aging [<https://www.who.int/news-room/fact-sheets/detail/ageing-and-health>]
 - Proposed by the World Health Organization (WHO)
 - Importance of an individual's healthspan (years lived in good health) in their lifespan (total years lived) with longevity
 - Related to non-random diversity seen in older age
 - Operationalizes health as functional ability, which results from the interactions of intrinsic capacity and the environments
 - Although some of the variations in older people's health are genetic, most is due to their physical and social environments as well as their personal characteristics

Biological Age

- Two types of age
 - Chronological age
 - Number of years an individual has been alive
 - Unchangeable
 - Biological age
 - How old an individual's cells and tissues appear to be based on their current condition
 - May be reversed

CHRONOLOGICAL AGE

- The number of years that have passed since our birth.
- Cannot be influenced by lifestyle and eating habits.
- Has little relevance to how you feel and function.



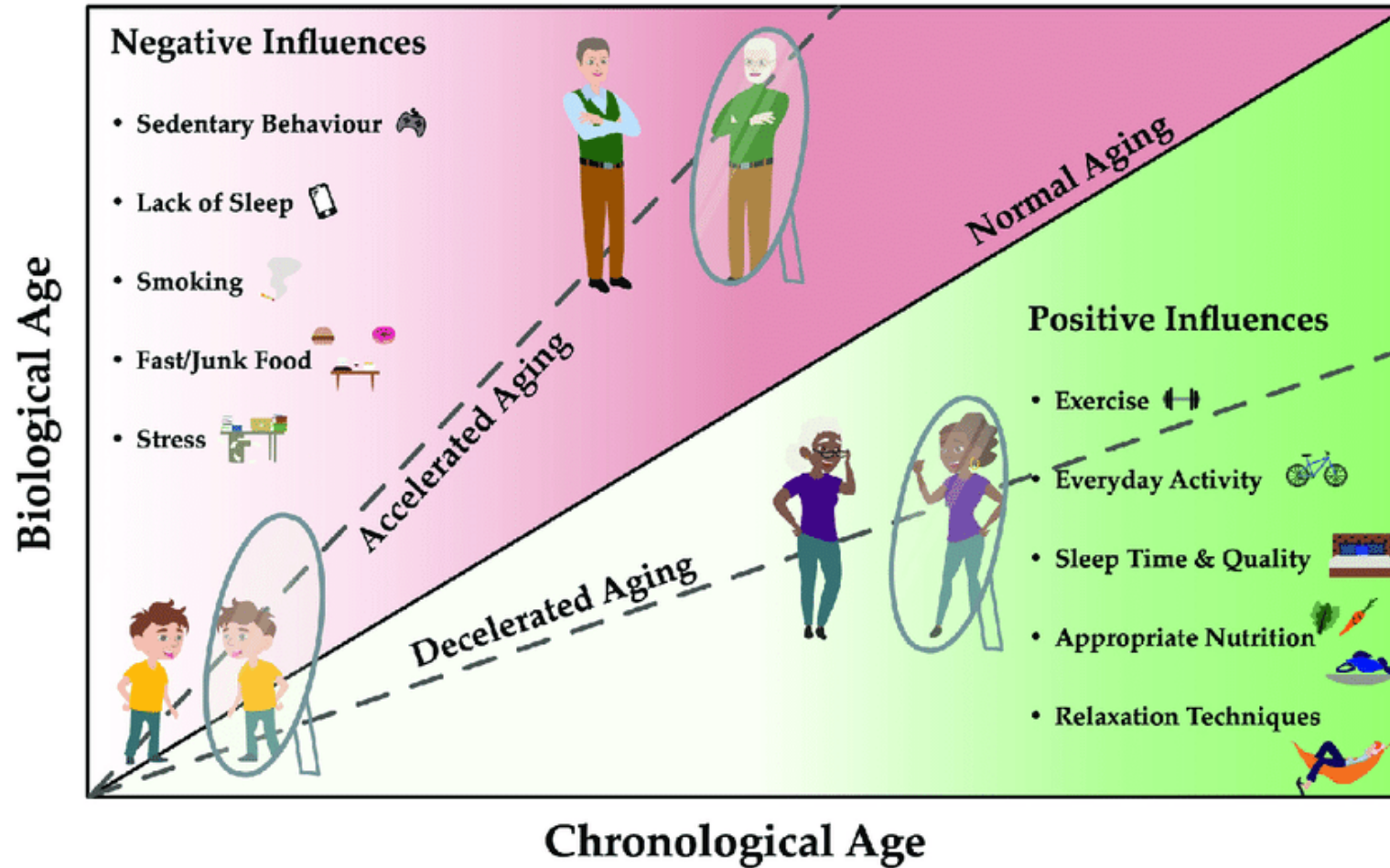
BIOLOGICAL AGE

- How old our cells really are, therefore, our real age
- Can be reversed by attending to your health
- The most important component to the aging process

[<https://rejuvenate.com/truage/>]

Chronological vs. Biological Age

- Departure of biological age from chronological age
 - May exhibit greatly different susceptibilities to age-related diseases and death for individuals of the same chronological age
 - Likely reflective of differences in underlying biological aging processes
- Biological age as a biomarker of aging
 - Individual-level measure of aging that captures inter-individual differences in the timing of disease onset, functional decline, and death over the life course
 - Crucial to enable evaluation of interventions aimed at promoting healthier aging, by providing a measurable outcome



[Haupt et al., 2022]

Factors that Have the Potential to Advance or Delay Aging Processes

- How biological age is determined
 - A combination of numerous potential markers that specifically measures all important aspects of aging processes may be the key to a valid composite biomarker of aging [\[Hartmann et al., 2021\]](#)
 - Routine laboratory
 - Epigenetic
 - Non-epigenetic
 - Physical capability
 - Organ function
 - Cellular senescence

- Commercial biological age testing methods
 - DNA methylation tests
 - Generations
 - 1st generation (2013): Horvath Clock, Hannum Clock
 - » Accurately predicts chronological age
 - 2nd generation (2018-2019): PhenoAge, GrimAge
 - » Assesses health risks (mortality, disease incidence, and health status)
 - 3rd generation (2022+): DunedinPACE
 - » Measures rate of aging
 - » Tracks intervention effects

- Products

- TruDiagnostic - TruAge (<https://www.trudiagnostic.com/>)
- Elysium Health - Index (<https://www.elysiumhealth.com/>)
- Epimorphy - myDNAge (<https://www.mydnage.com/>)
- Clock Foundation - GrimAge Test (<https://clockfoundation.org/>, <https://myagingtests.com/>)
- Tally Health - TallyAge Test (<https://www.tallyhealth.com/>)
- NOVOS - NOVOS Age (<https://novoslabs.com/>)

- Principle

- Measures chemical modifications (methylation) accumulating with age at Cytosine-phosphate-Guanine (CpG) sites across genome: Methylation changes (both hyper- and hypomethylation) → older biological age
- What it measures: Epigenetic changes

- Efficacy

- Most accurate predictor of mortality and disease risk (especially 2nd and 3rd generation clocks)

– Telomere length tests

- Products

- Telomere Diagnostics - TeloYears (<http://teloyears.co/>)
- Life Length - HealthTAV (<https://lifelength.com/>)
- SpectraCell Laboratories - Telomere Test (<https://www.spectracell.com/telomere-genetic-test>)

- Principle

- Measures protective chromosome caps that shorten with age: Shorter telomeres → older biological age
- What it measures: Cellular replication capacity and oxidative stress

- Efficacy

- Direct cellular aging biomarker based on Nobel Prize-backed science (2009)
- High interpersonal variability

– Multi-biomarker blood tests

- Products

- InsideTracker - InnerAge 2.0 (<https://store.insidetracker.com/products/innerage>)
- Thorne - Biological Age Health Panel (<https://www.thorne.com/products/dp/biological-age>)

- Principle

- Analyzes 10-50 blood biomarkers (glucose, cholesterol, inflammation markers, etc.): Elevated inflammatory markers and metabolic dysfunction → older biological age
- What it measures: Current metabolic, cardiovascular, and organ function status

- Efficacy

- Actionable through lifestyle changes
- Cost-effective and accessible
- Higher day-to-day variability

– Microbiome tests

- Products

- Viome - Health Intelligence Test / Full Body Intelligence Test (<https://www.viome.com/>)
- Ombre - Gut Health Test (<https://www.ombrelab.com/>)

- Principle

- Analyzes gut bacteria composition and function: Decreased microbial diversity and altered microbial metabolic function → older biological age
- What it measures: Microbial diversity and metabolic activities

- Efficacy

- Links gut health to systemic aging
- Provides personalized dietary recommendations
- High interpersonal variability

- Functional near-infrared spectroscopy (fNIRS)-derived tests
 - Products
 - Kernel - BrainAge (<https://www.kernel.com/brainage>)
 - Principle
 - Analyzes brain hemodynamic responses: Altered neurovascular coupling patterns → older biological age
 - What it measures: Functional brain activity patterns
 - Efficacy
 - Non-invasive, quick assessment (7-minute brain activity measurement during video watching)

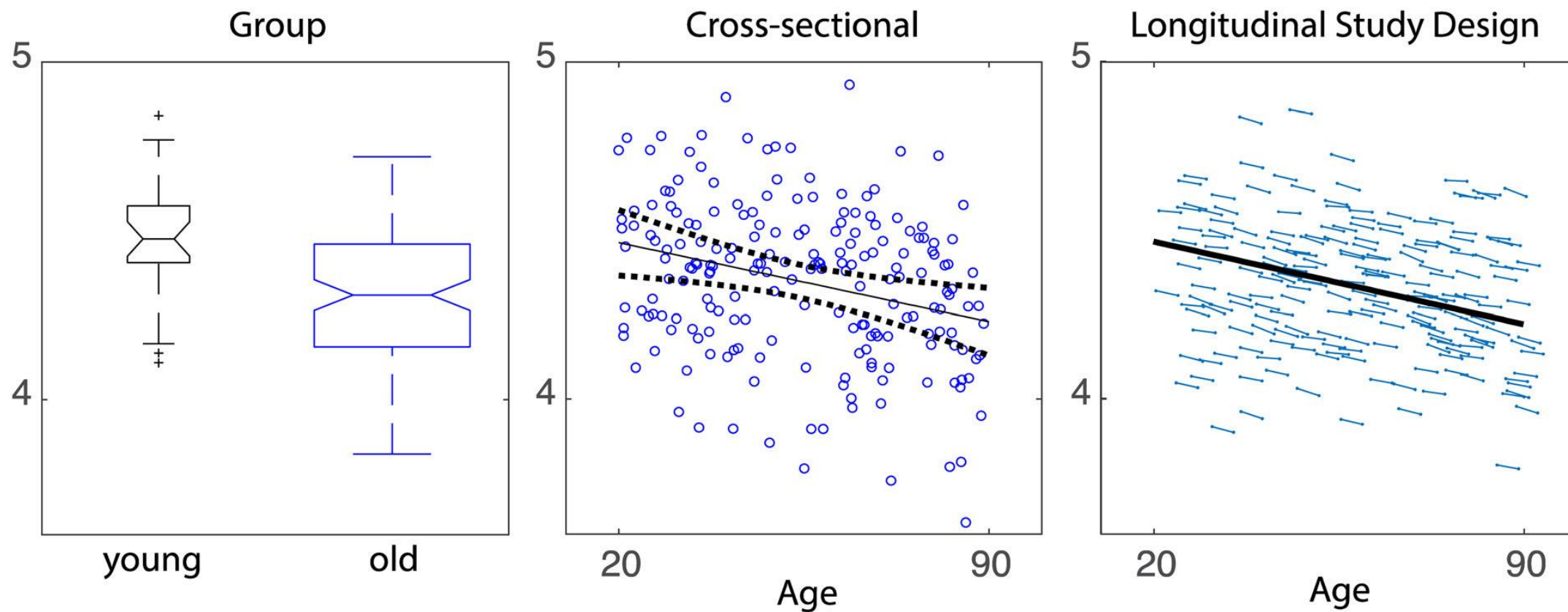


Method	Accuracy for aging	Speed of response	Actionability	Cost	Validation level
DNA methylation	★★★★★	Slow (months)	★★★☆☆	\$\$\$	★★★★★
Telomere length	★★★☆☆	Slow (months-years)	★★☆☆☆	\$\$	★★★★☆
Blood biomarkers	★★★☆☆	Fast (weeks)	★★★★★	\$	★★★★★
Microbiome	★★☆☆☆	Fast (weeks-months)	★★★★☆	\$\$	★★★★☆
fNIRS (brain)	★★☆☆☆	Immediate	★★★☆☆	\$\$\$	★★★☆☆

Comparison of Biological Age Testing Methods

Brain Aging on MRI

- Study designs for assessing age effects
 - Group
 - Age-related differences
 - Cross-sectional
 - Age-related changes
 - Longitudinal
 - Age-related changes
 - Enables to assess the rate of change with inter-individual variability removed



[MacDonald and Pike, 2021]

Study Designs for Assessing Age Effects

Region	Mean (95% Confidence Interval)	
	Cross-sectional Data	Longitudinal Data
Whole brain*	0.33 (0.25-0.41)	0.32 (0.10-0.54)
Temporal lobes*	0.35 (0.20-0.51)	0.68 (0.42-0.93)
Hippocampi*	0.35 (0.13-0.57)	0.82 (0.53-1.11)
Lateral ventricles, mm ³ /y	521 (323-719)	650 (333-968)

[Schhill et al., 2003]

Annual Rates of Brain Volume Changes Based on Cross-Sectional and Longitudinal Data

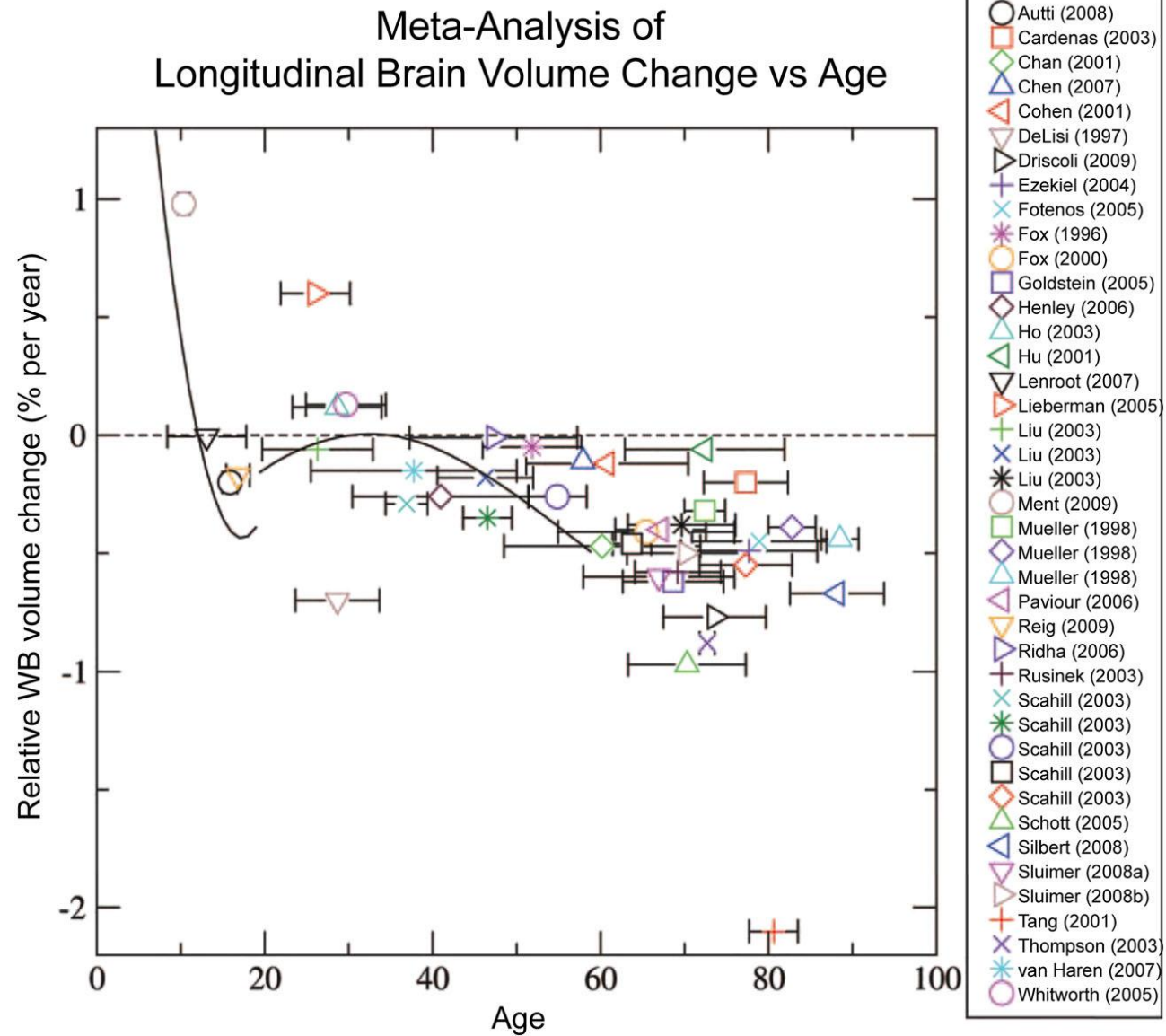
- Morphological changes

- Brain atrophy

- Continuous decline throughout the lifespan
 - With annual reductions of between 0.5% and 1.0% in most brain areas

[Fjell and Walhovd, 2010]

- For both grey matter and white matter
 - In terms of grey matter and white matter volume and cortical thickness
 - Slower rate of shrinkage for white matter [Ge et al., 2002]
 - Highly heterogeneous in the pattern of changes



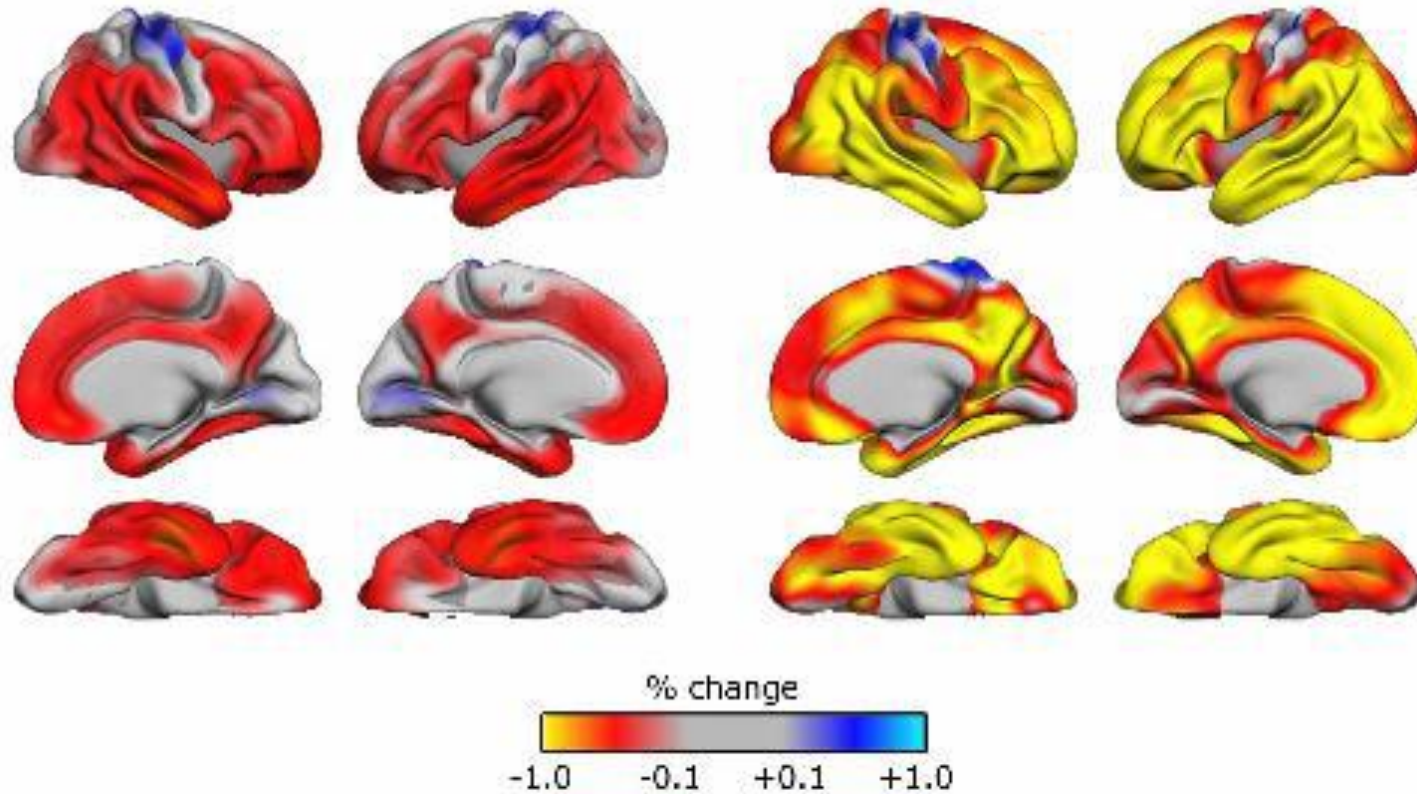
[Hedman et al., 2012]

Whole Brain Volume Changes with Age

Longitudinal changes in cortical thickness

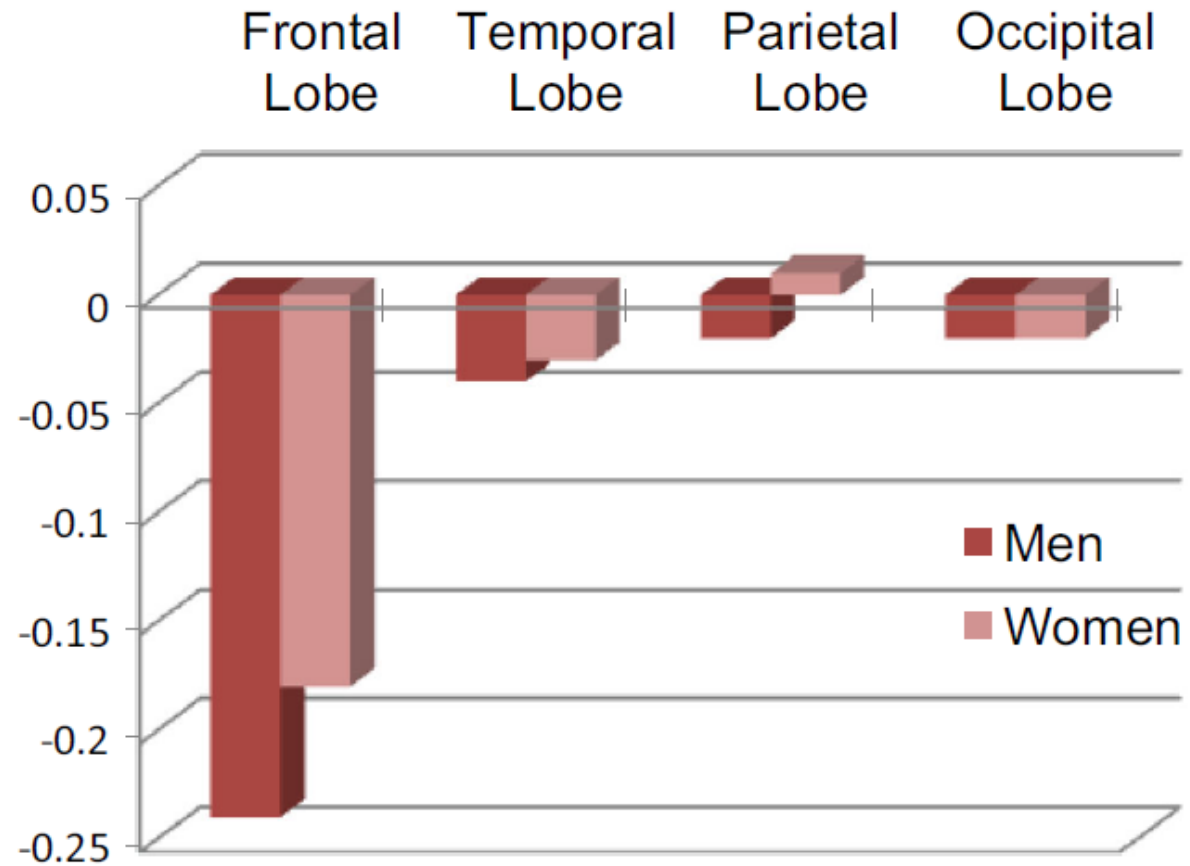
One year

Two years



[Fjell and Walhovd, 2010]

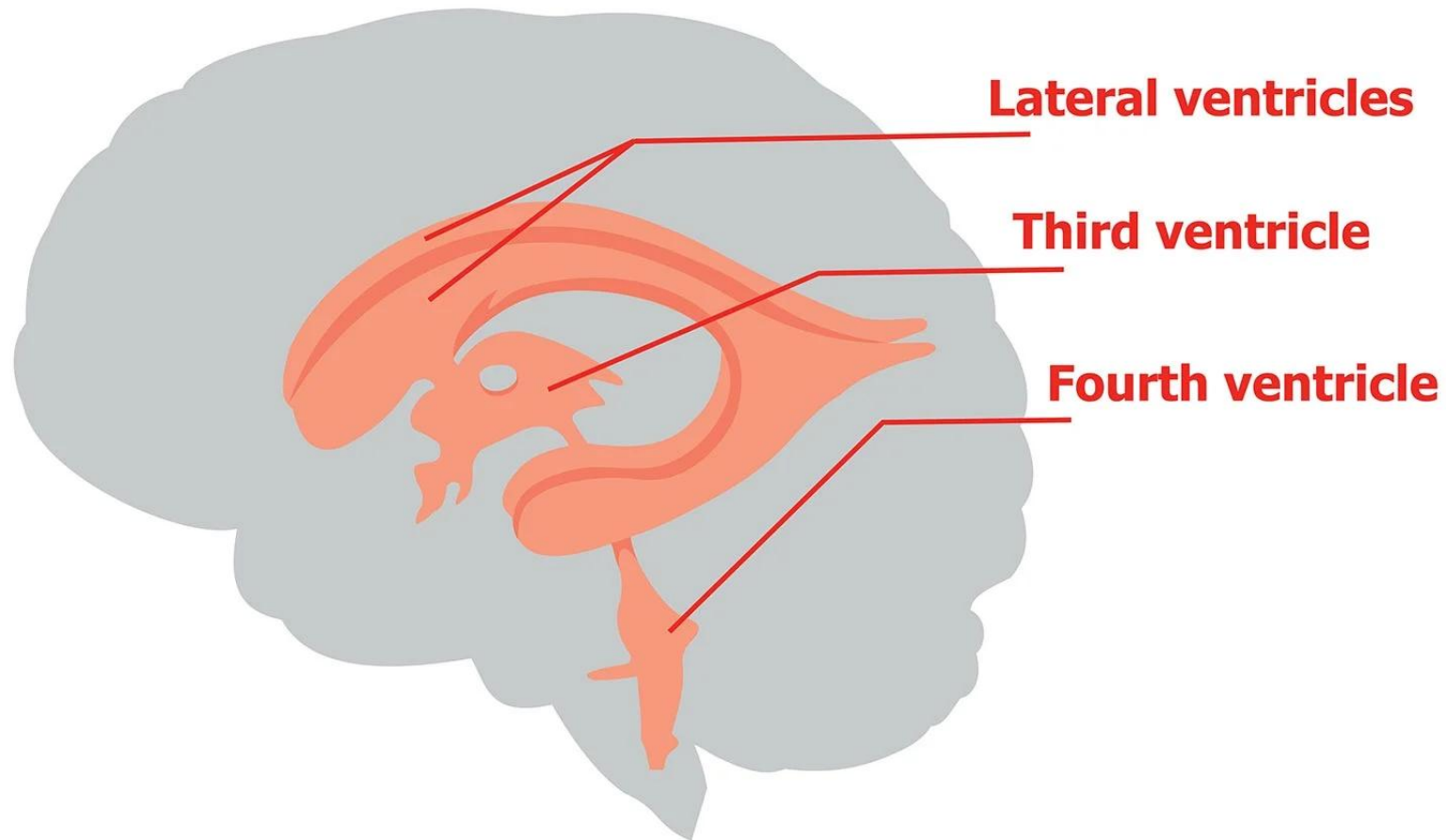
Cortical Thickness Changes over One and Two Years



[DeCarli et al., 2005]

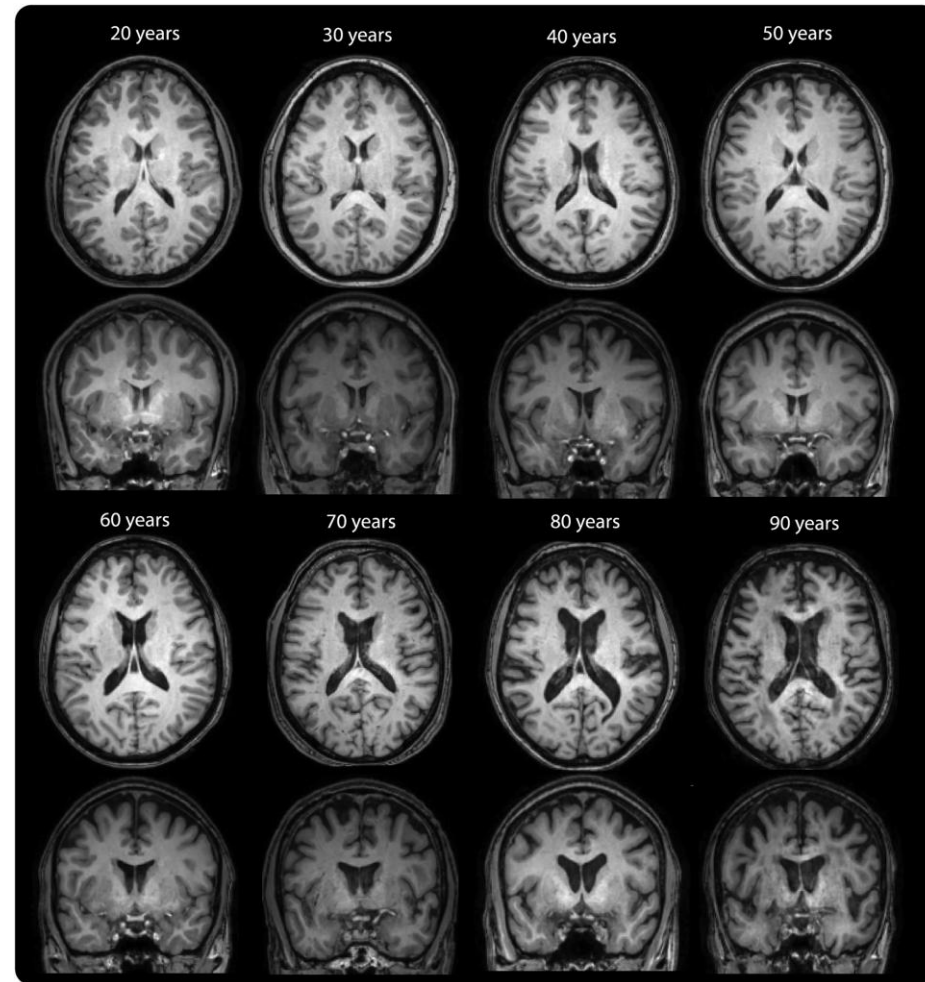
Regional Differences in Yearly Brain Volume Changes

- Changes involving cerebrospinal fluid distribution
 - Ventricular enlargement
 - Sulcal widening
 - Perivascular space dilation
 - Altered cerebrospinal fluid production, absorption, and circulation
 - Cerebrospinal fluid-to-brain volume ratio increases



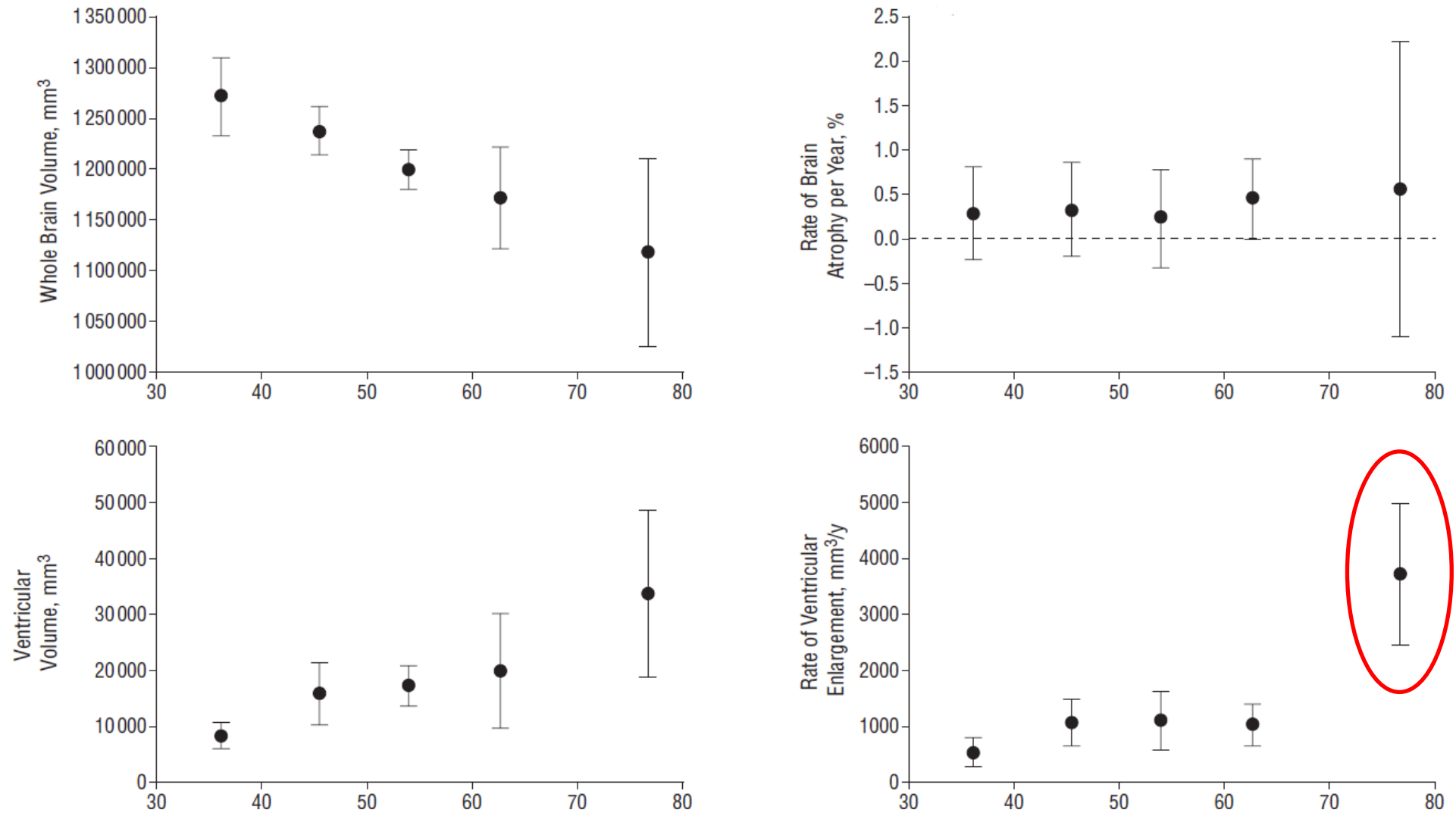
[Fjell and Walhovd, 2010]

Ventricles of the Brain: Two Lateral Ventricles, Third Ventricle, and Fourth Ventricle



[MacDonald and Pike, 2021]

Ventricular Cerebrospinal Fluid Volume Changes with Age



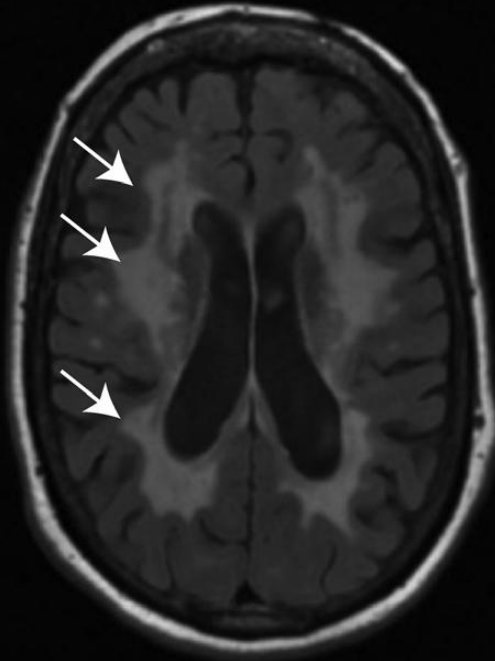
[Schhill et al., 2003]

Cross-sectional and Longitudinal Volume Changes in the Whole Brain and Ventricles

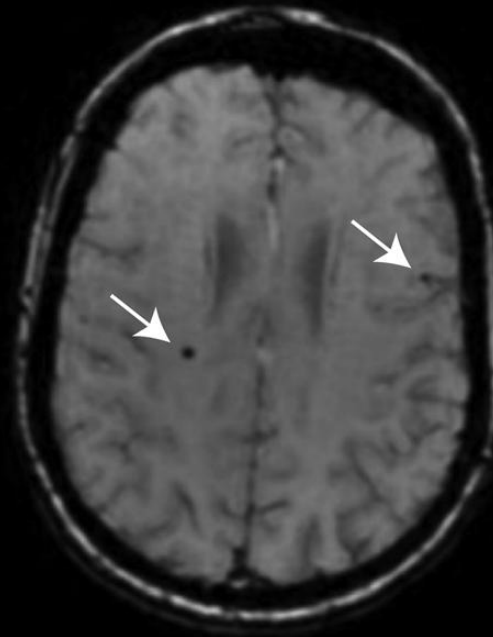
– Accrual of silent lesions

- White matter hyperintensities
 - Focal white matter spots (from a few mm to several cm) that are hyperintense on T2-weighted MRI
- Cerebral microbleeds
 - Hemosiderin deposits (typically <10 mm; visible on specific MRI sequences as small, round or ovoid areas of signal loss, indicating the site of past microbleeding events in the brain tissue) from small hemorrhages caused by rupture of small vessels
- Lacunar infarcts
 - Small noncortical infarcts (typically 3-15 mm) caused by occlusion of a single penetrating branch of a large cerebral artery

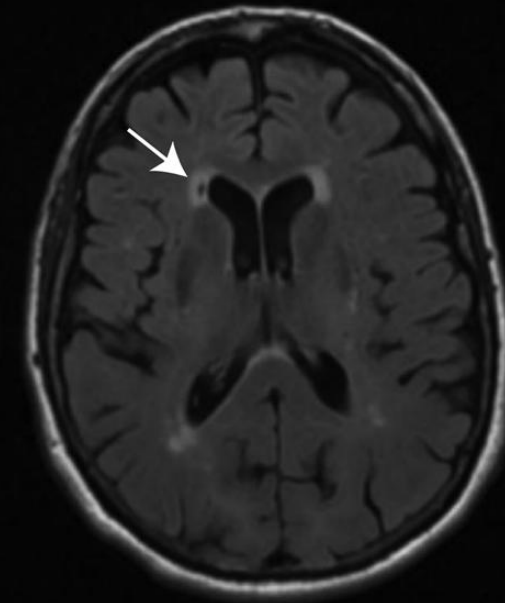
White Matter
Hyperintensities (WMH)



Cerebral Microbleeds (CMB)



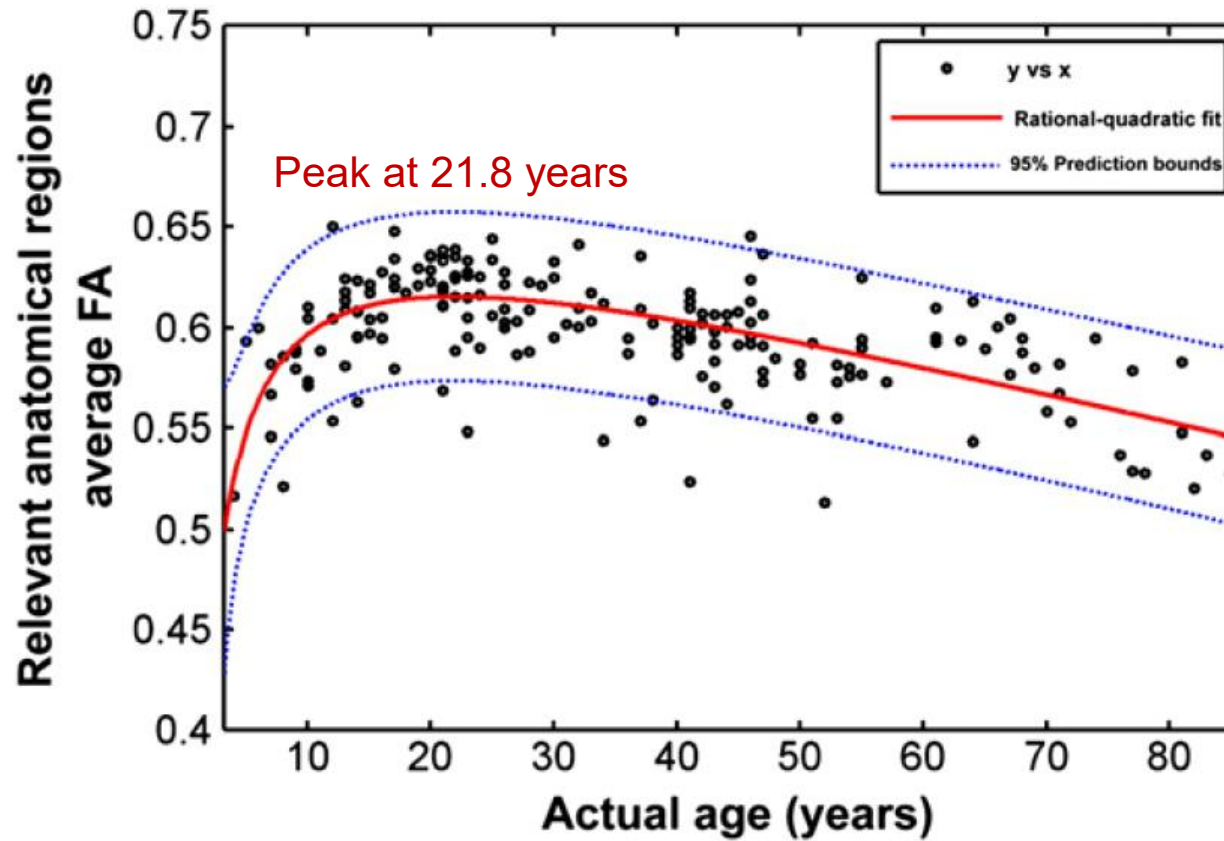
Lacune



[[MacDonald and Pike, 2021]

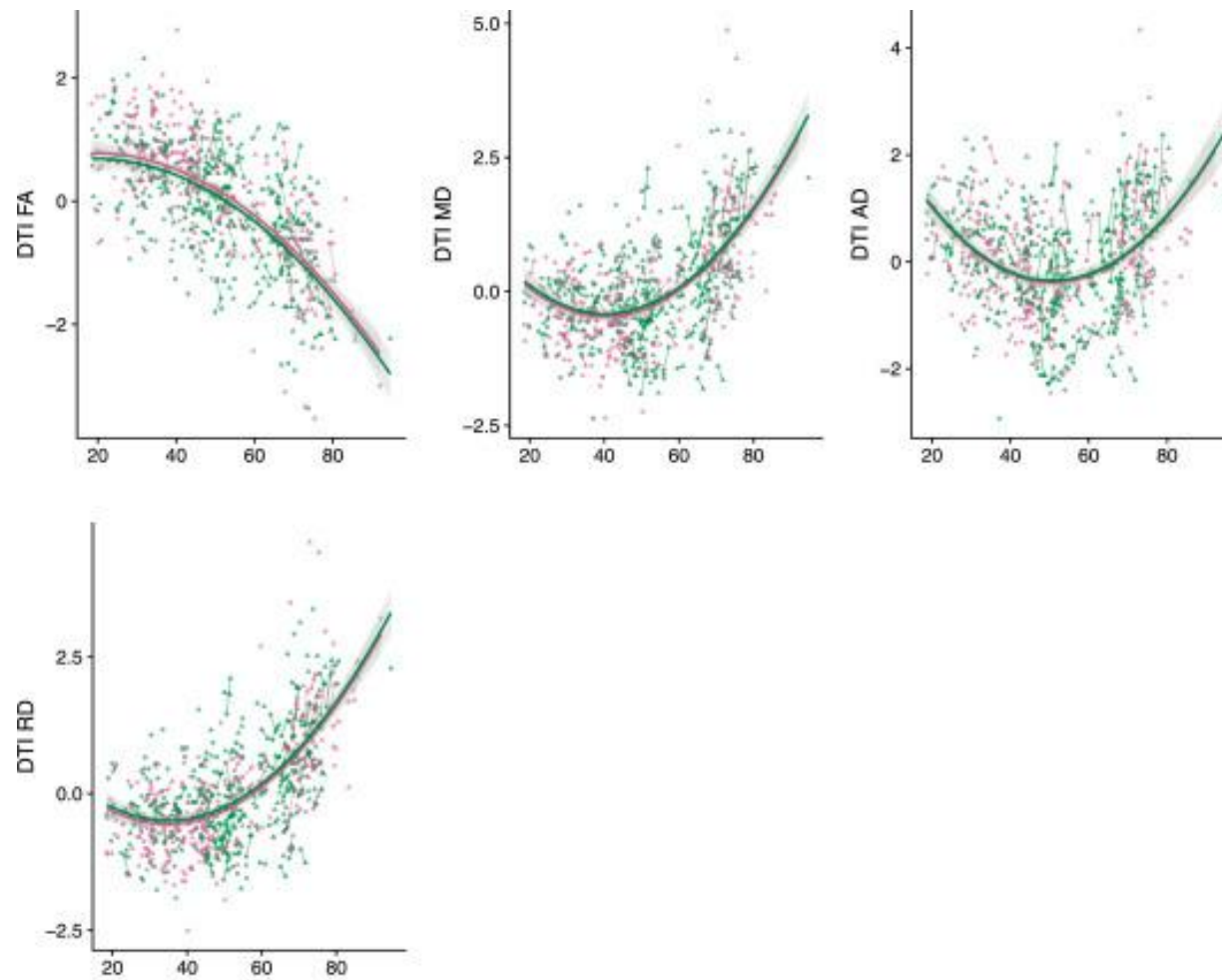
Examples of Silent Lesions

- White matter microstructural changes
 - Anisotropy (fractional anisotropy (FA)) increases and diffusivity (mean/axial/radial diffusivity (MD/AD/RD)) decreases in development [\[Tamnes et al., 2018\]](#), and subsequent anisotropy decreases and diffusivity increases in aging [\[Cox et al., 2016\]](#)
 - With variations in age trajectories between diffusion models [\[Beck et al., 2021\]](#)



[Mwangi et al., 2013]

Nonlinear (Rational-quadratic Fit) Trajectory of FA across the Lifespan

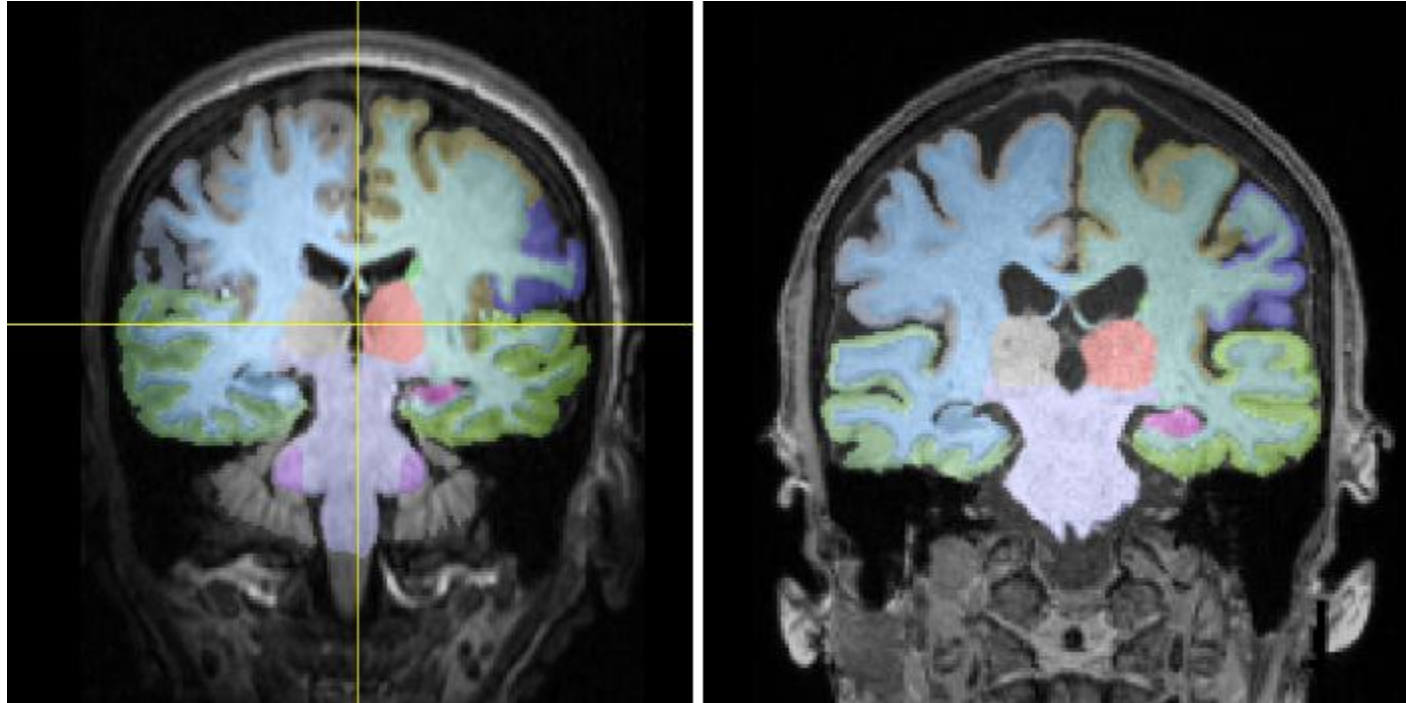


[Beck et al., 2021]

Diffusion Tensor Metrics as a Function of Age

Brain Age

- Biological age estimated from information usually derived from brain MRI data
- Sums up the progression of aging processes in the brain
 - Reflects relatively advanced or delayed brain maturation, while all individuals' brains undergo the general progression such as age-related volumetric changes

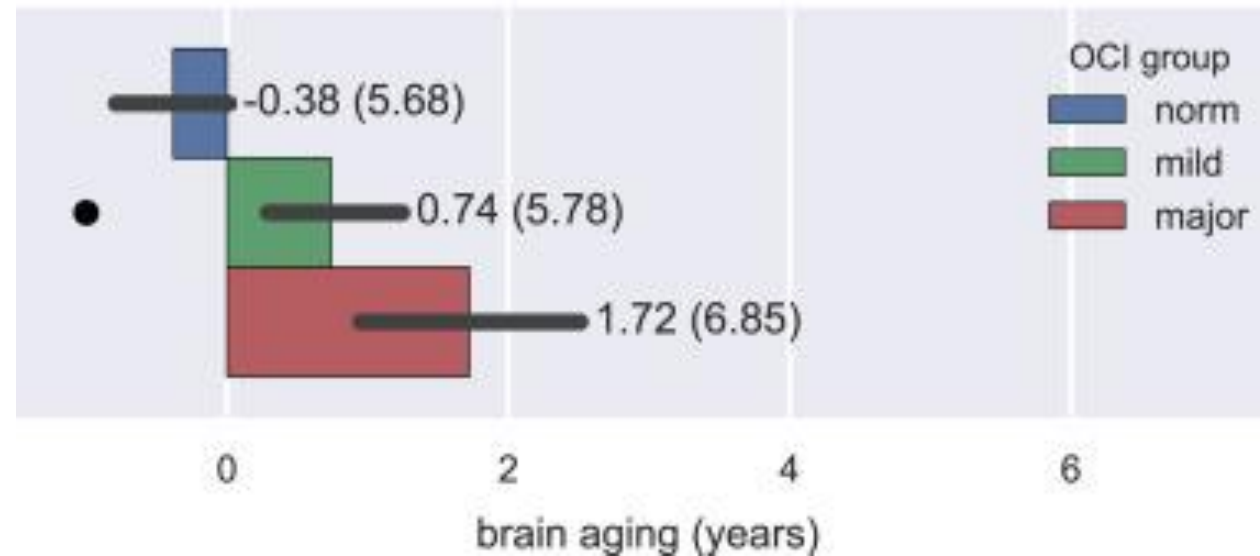


[\[https://www.brainkey.ai/blog/brain-age-how-we-calculate-it-and-what-it-means\]](https://www.brainkey.ai/blog/brain-age-how-we-calculate-it-and-what-it-means)

Typical Brain Images for Young (22 Years) and Old (83 Years) Individuals

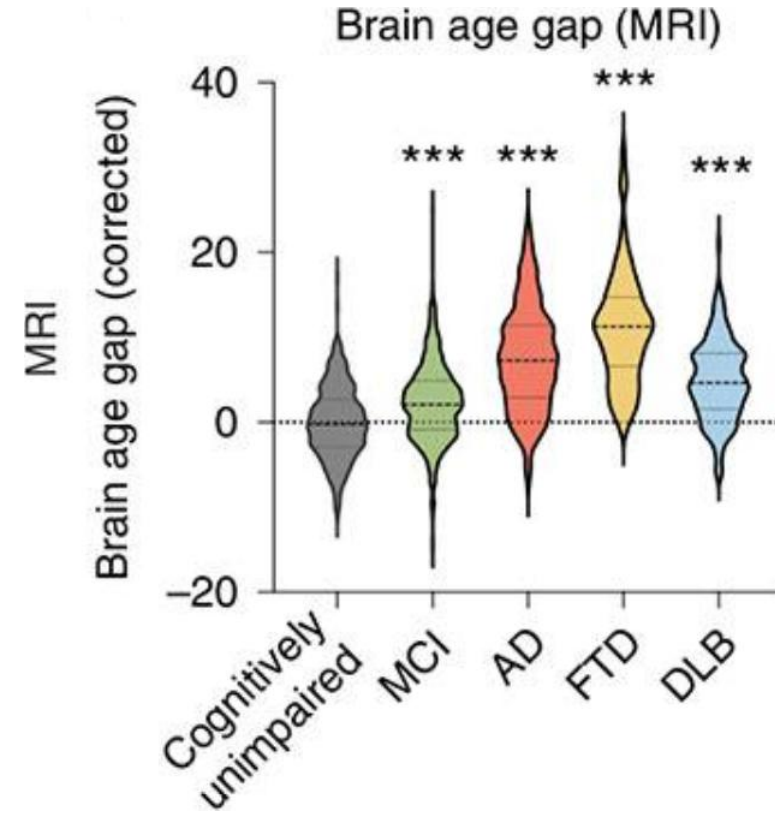
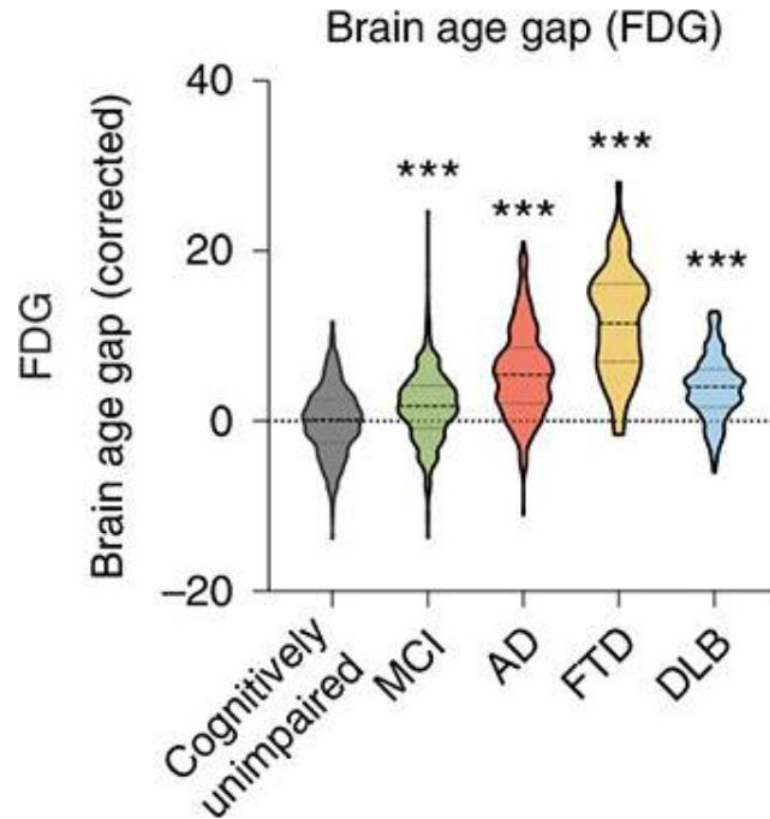
- Brain age gap (BAG, also called brain-predicted age difference, delta, etc.)
 - Difference between brain age and chronological age: $BAG = \text{estimated brain age} - \text{chronological age}$
 - Indicates whether an individual's brain appears to have aged more or less than the population average for their actual chronological age
 - $BAG > 0$: advanced or premature brain aging
 - Related to functional impairment [Liem et al., 2017], brain diseases such as Alzheimer's disease [Yin et al., 2023], Parkinson's disease [Eickhoff et al., 2021], schizophrenia [Nenadic et al., 2017], stroke [Egorova et al., 2019], epilepsy [Sone et al., 2021], and diabetes mellitus [Franke et al., 2013], and mortality [Cole et al., 2017]
 - $BAG < 0$: delayed or resilient brain aging

**Brain aging differences between
objective cognitive impairment (OCI) groups
stacked-multimodal**



[Liem et al., 2017]

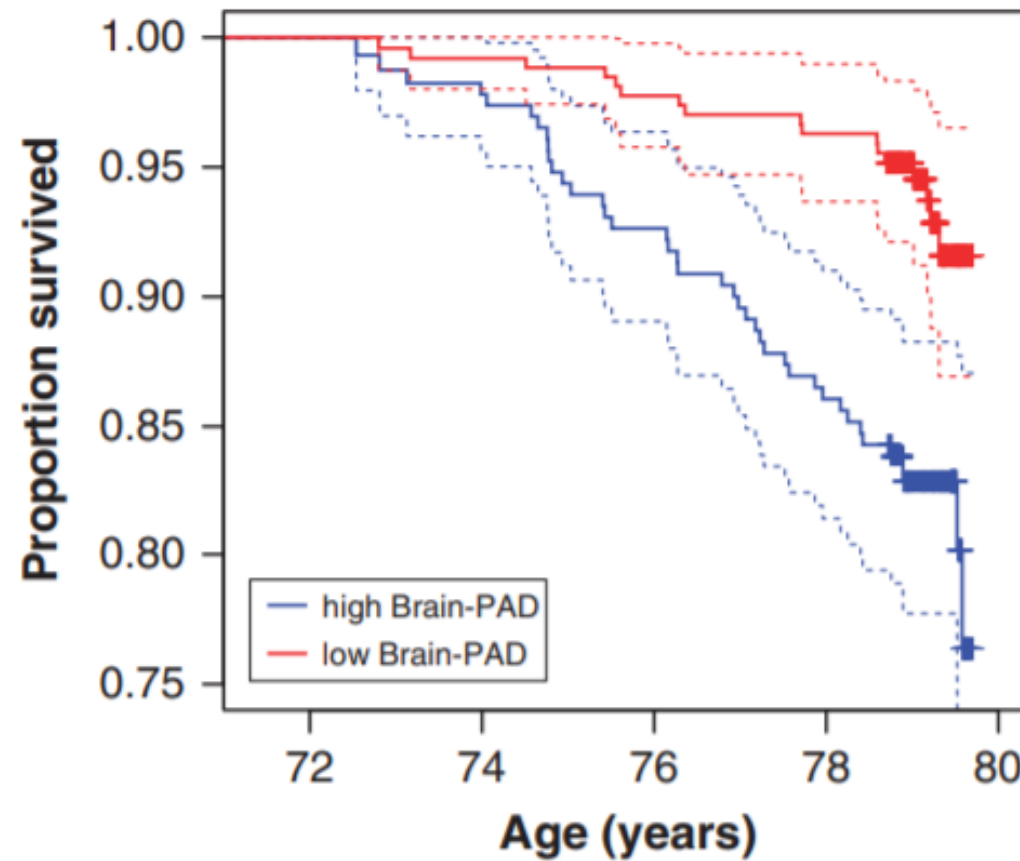
Advanced Brain Aging (BAG > 0) in Cognitive Impairment



MCI, mild cognitive impairment
AD, Alzheimer's disease
FTD, frontotemporal dementia
DLB, dementia with Lewy bodies

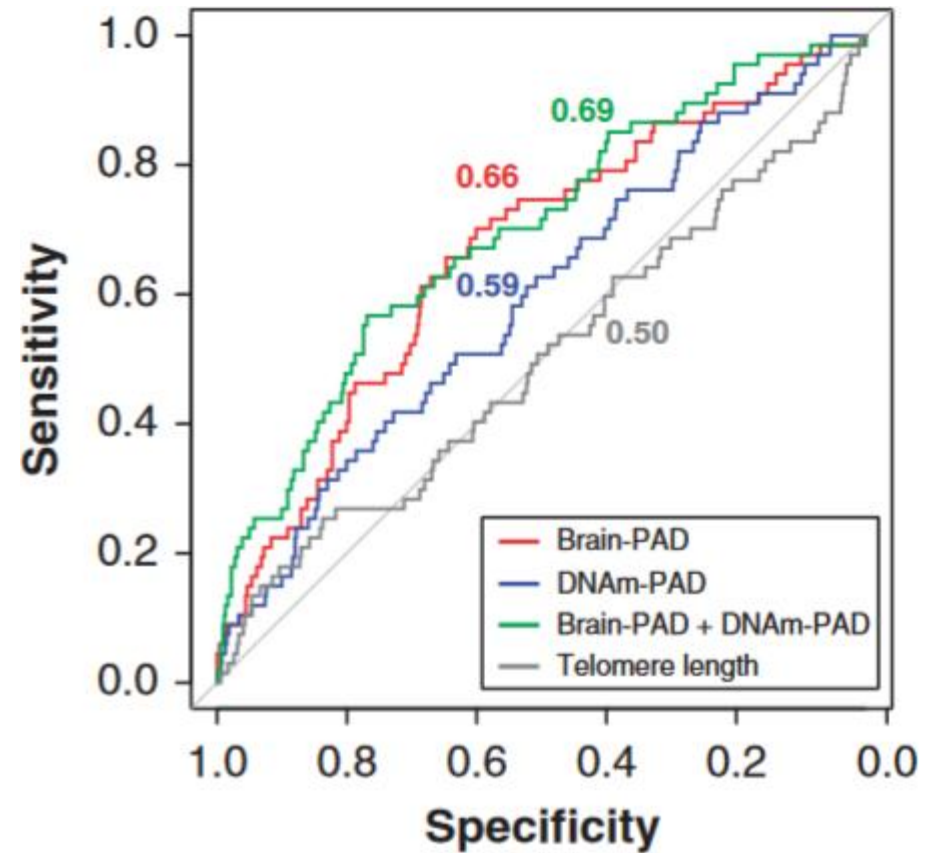
[Lee et al., 2022]

Advanced Brain Aging (BAG > 0) in Brain Diseases



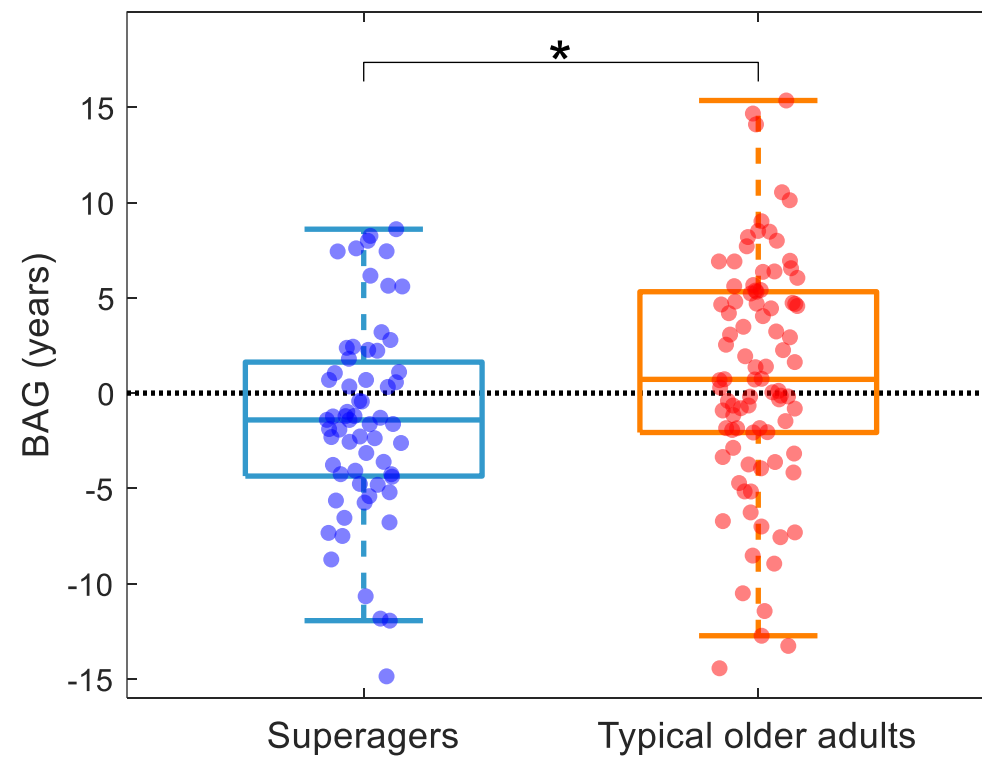
[Cole et al., 2017]

Comparison of Survival Rate: Low BAG vs. High BAG



[Cole et al., 2017]

Receiver Operator Characteristic (ROC) Curves for Four Survival Models



[Park et al., 2025]

Resilient Brain Aging (BAG < 0) in Superaging

Normative Model

- Reference model for population variation [\[Rutherford et al., 2022\]](#)
 - Enables to quantify individual variation against centiles of variation in a reference population
 - Shifts focus away from group-level (e.g., case-control) inferences to the level of an individual
 - The ability to study individual deviations is essential for understanding inter-individual variability and its relation to the onset and progression of clinical conditions

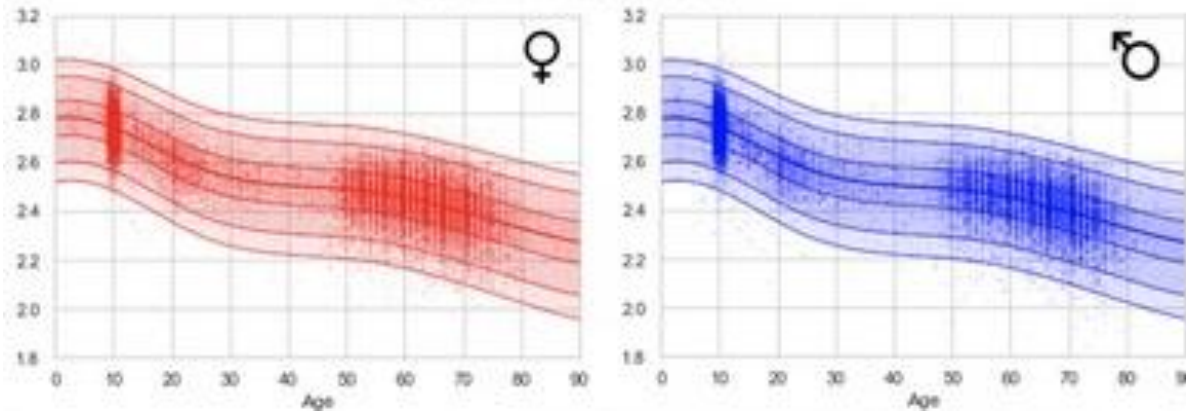
- Framework for mapping population-level trajectories of the relationships between health-related variables while simultaneously preserving individual-level information

[Rutherford et al., 2023]

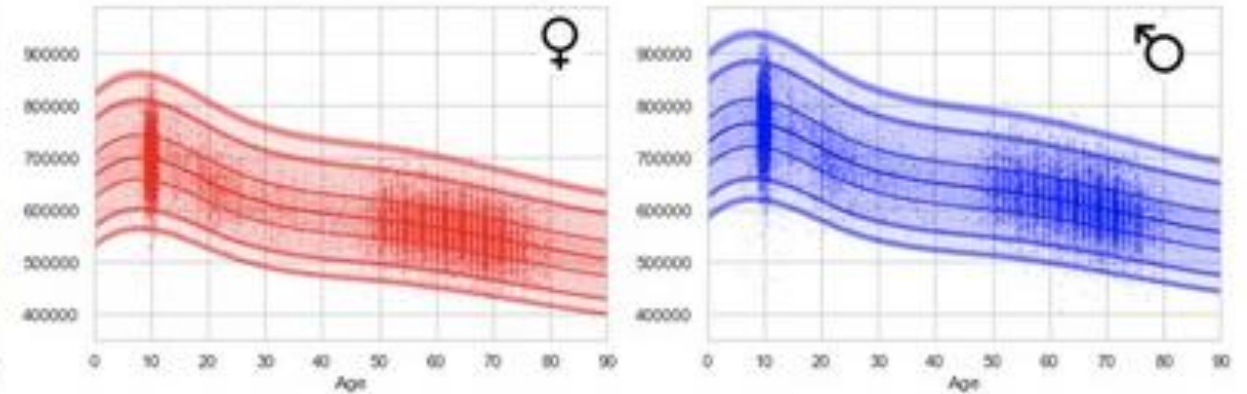
– Health-related variables may involve:

- Demographics (i.e. age and gender)
- Simple (i.e. height and weight) or complex (i.e. brain structure and function, genetics) biological measures
- Environmental factors (i.e. urbanicity, pollution)
- Self-report measures (i.e. social satisfaction, emotional experiences)
- Behavioral tests (i.e. cognitive ability, spatial reasoning)

Mean Thickness



TotalGrayVolume



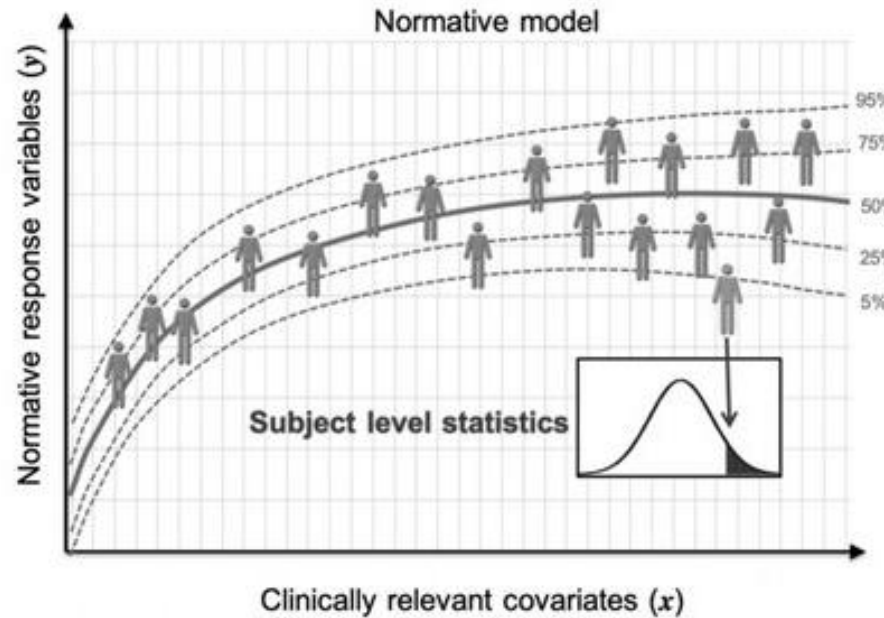
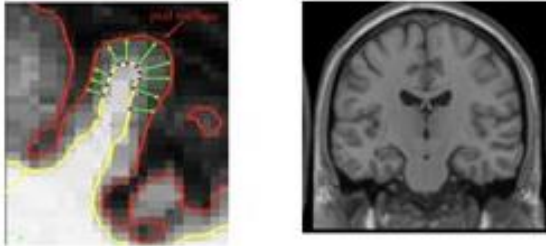
[Rutherford et al., 2022]

Prediction of Cortical Thickness and Subcortical Volume from Age

- Deviation score [\[Rutherford et al., 2023\]](#)
 - Output of a normative model
 - Represents where an individual is in comparison to the population the model was estimated on
 - Positive deviation score: greater cortical thickness or subcortical volume than average
 - Negative deviation score: less cortical thickness or subcortical volume than average
 - Advantageous compared to using raw features in regression and classification tasks

Input

Raw Cortical Thickness



Output

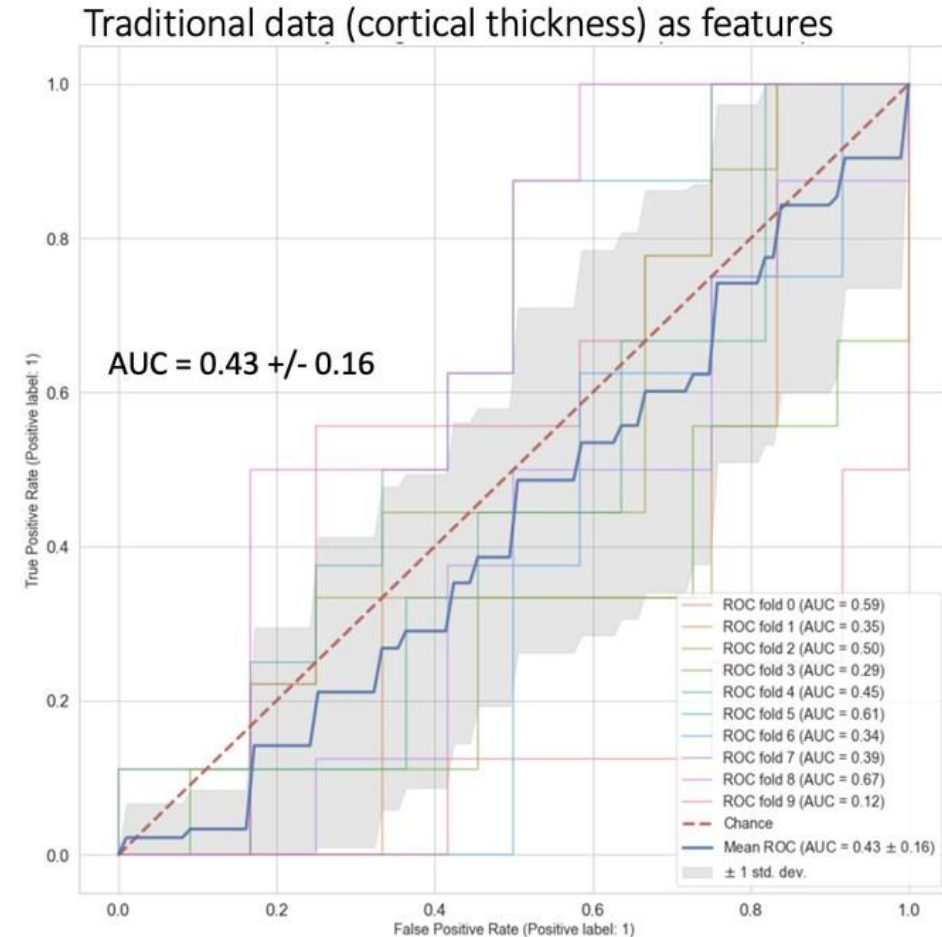
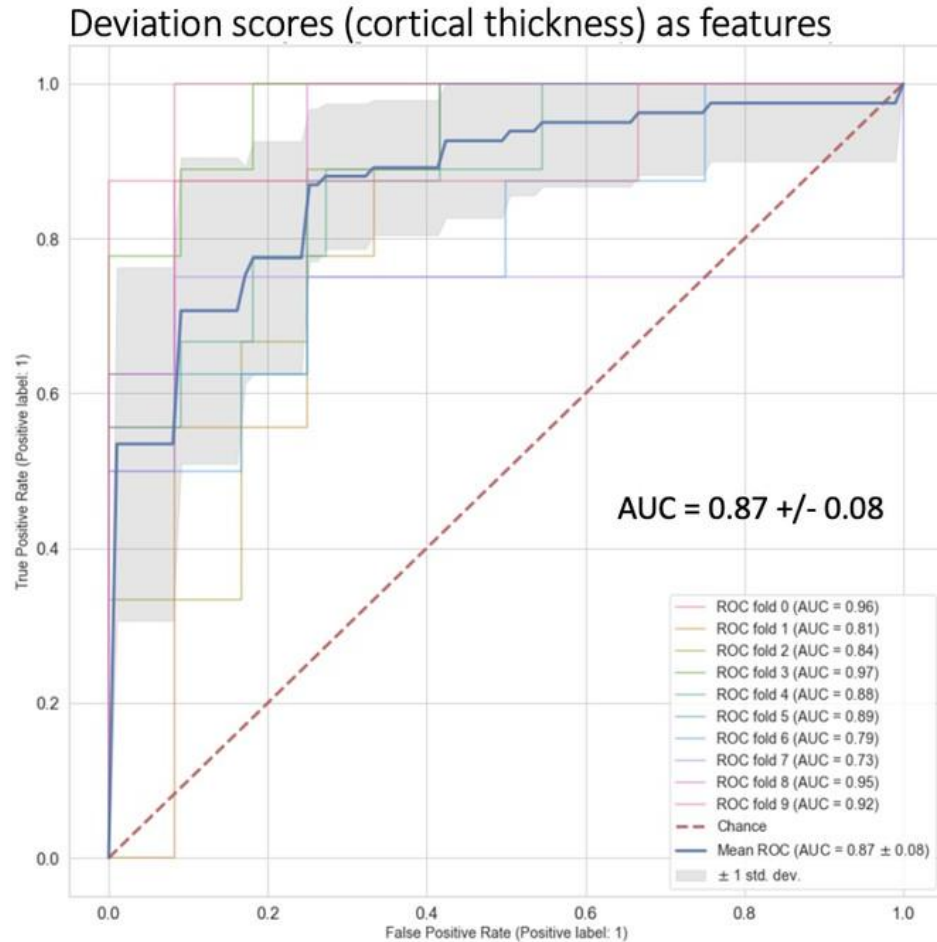
$$z_{nd} = \frac{y_{nd} - \hat{y}_{nd}}{\sqrt{\sigma_d^2 + (\sigma_*^2)_d}}$$

Cortical Thickness
Deviation (Z) Score

[Rutherford et al., 2023]

Normative Model-derived Deviation Scores that Represent Individual-level Deviations

Support Vector Classification: Schizophrenia vs. Controls



[Rutherford et al., 2023]

Comparison of Classification Accuracy between Deviation Scores and Raw Features

- Brain age prediction model as a normative model
 - Describes population-level trajectories of the relationship between brain structure and age
 - Prediction of age from brain structural features
 - Age \sim brain structural features
 - Deviation score
 - BAG = predicted brain age – chronological age

Regression in Machine Learning

- Models the relationship between input features (predictors) and one or more target variables (dependent variables)
- Purpose
 - Understanding the relationship between input features and continuous target variables
 - Predicting continuous target values for new sets of input features

- Supervised learning technique for predicting continuous output values
 - Traditional methods
 - Linear regression: Simple linear regression, multiple linear regression
 - Non-linear regression: Polynomial regression, support vector regression (SVR)
 - Ensemble methods
 - Bagging-based methods: random forests, Extra Trees (extremely randomized trees)
 - Boosting-based methods: AdaBoost (adaptive boosting), gradient boosting machines (GBM), XGBoost (extreme gradient boosting), LightGBM (light gradient boosting machine), CatBoost (categorical boosting)
 - Stacking: combining predictions from multiple models

– Deep learning-based classification

- Feedforward neural network (FNN) / multilayer perceptron (MLP)
- Specialized architectures
 - Convolutional neural network (CNN) for spatial data classification
 - Recurrent neural network (RNN) and long short-term memory (LSTM) for sequential data classification
- Transformer-based models for complex sequential data classification

– Hybrid approaches

- Combining traditional methods with ensemble techniques or neural networks
- Automated machine learning (AutoML) systems incorporating various classification techniques

- Types of regression problems
 - Based on the nature of the relationship
 - Linear regression: modeling linear relationships
 - Nonlinear regression: modeling complex, nonlinear relationships
 - Based on the number of output variables
 - Univariate regression: predicting a single output variable
 - Multivariate regression: predicting multiple output variables simultaneously

- Regression performance
 - Mean absolute error (MAE)
 - Average of absolute differences between predicted and actual values
 - Range: 0 to ∞ (lower is better)
 - In the same unit as the target variable
 - Less sensitive to outliers
 - Mean squared error (MSE)
 - Average of squared differences between predicted and actual values
 - Range: 0 to ∞ (lower is better)
 - Penalizes larger errors more heavily
 - Harder to interpret as being in squared units
 - Sensitive to outliers

– Root mean squared error (RMSE)

- Square root of MSE
- Range: 0 to ∞ (lower is better)
- In the same unit as the target variable
- Still sensitive to outliers, but less than MSE

– R^2 (coefficient of determination)

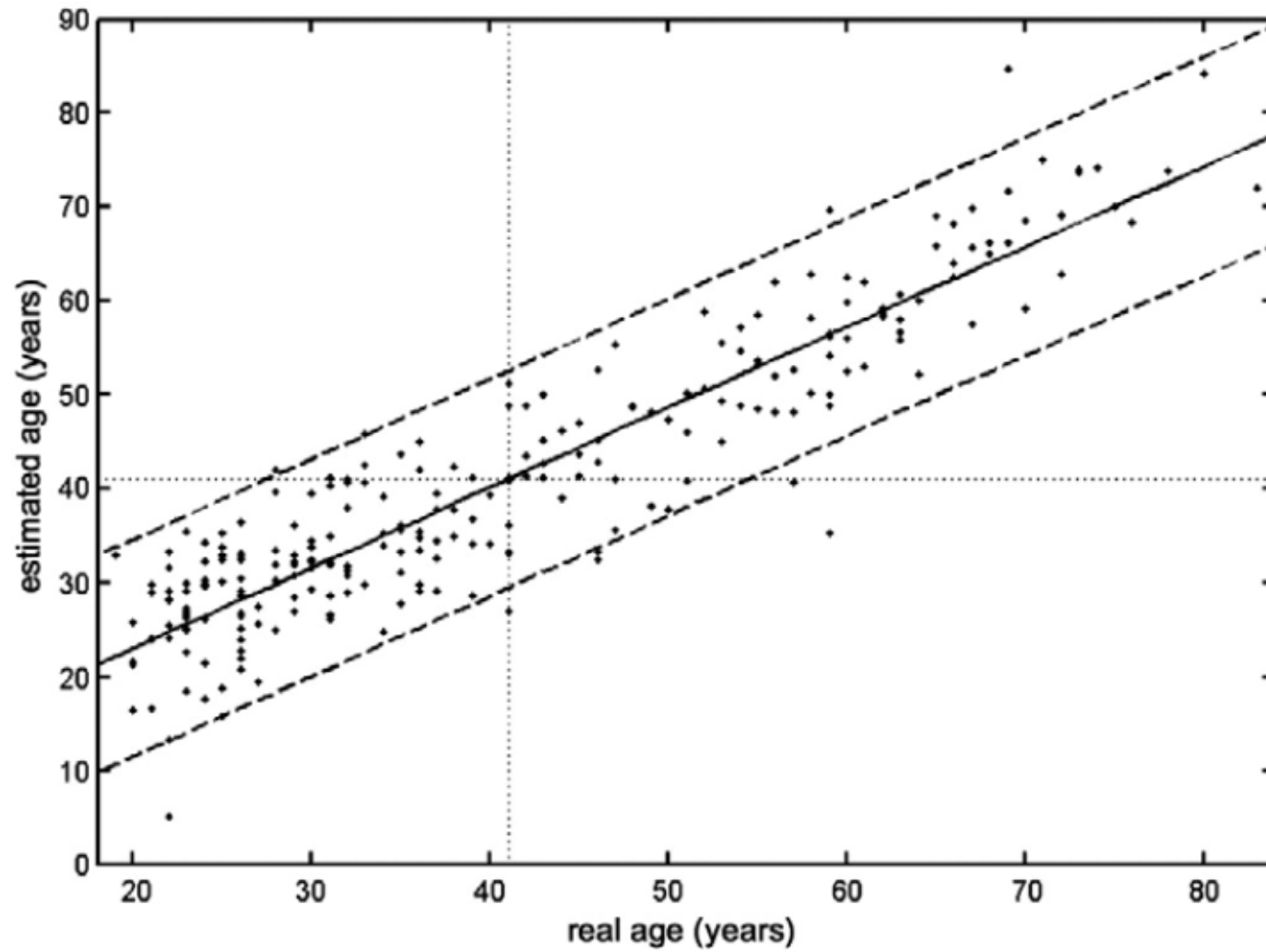
- Proportion of variance in the target variable predictable from input features
 - $R^2 = 1 - (\text{residual sum of squares} / \text{total sum of squares})$
- Range: $-\infty$ (can be negative for poorly fitting models, especially when the model is not fitted with an intercept term) via 0 (just predicting the mean) to 1 (perfect fit)
- Represents the fraction of variance explained by the model
 - $R^2 = 1 - \text{Fraction of Variance Unexplained (FVU)}$

– Correlation coefficient

- Measure of linear correlation between predicted and actual values
- Range: -1 (perfect negative correlation) via 0 (no linear correlation) to 1 (perfect positive correlation)
- Measures strength and direction of linear relationship

Brain Age Prediction

- Process of predicting an individual's biological brain age based on brain features usually extracted from MRI data
- Aims to assess brain health status
 - Life-long, multidimensional, dynamic state consisting of cognitive, emotional, and motor domains underpinned by physiological processes [\[Chen et al., 2022\]](#)



[Franke et al., 2010]

Predicted Brain Age vs. Chronological Age

- Methodology
 - Models chronological age using various brain features
 - Develops brain age prediction models using supervised learning algorithms
- Input data
 - Single or multi-modal brain MRI data, including structural MRI (sMRI), functional MRI (fMRI), and diffusion-weighted MRI (dMRI)
 - Quantitative features such as brain volume, cortical thickness, or white matter integrity

- Applications
 - Assessment of various brain functions, including cognitive and motor functions
 - Early diagnosis of neurodegenerative diseases (e.g., Alzheimer's disease)
 - Development of personalized intervention strategies for brain health improvement

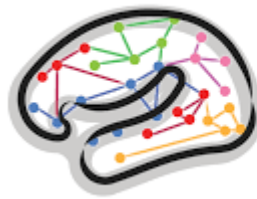
Human Connectome Project (HCP)

- Launched in 2009 as National Institutes of Health Blueprint Grand Challenge
- Project vision
 - To map neural pathways that underlie human brain function
 - To identify functionally distinct brain subdivisions and their relationships

- Project timeline
 - Active phase: 2010-2021 (originally 5 years, extended to 10+ years)
 - Legacy phase: 2021-present (continued data sharing and analysis)
- Research approach
 - Acquires and shares high-quality brain connectivity data
 - Combines multiple imaging modalities (sMRI, fMRI, and dMRI)
 - Links brain structure to function and behavior
 - Provides open data sharing for global research community

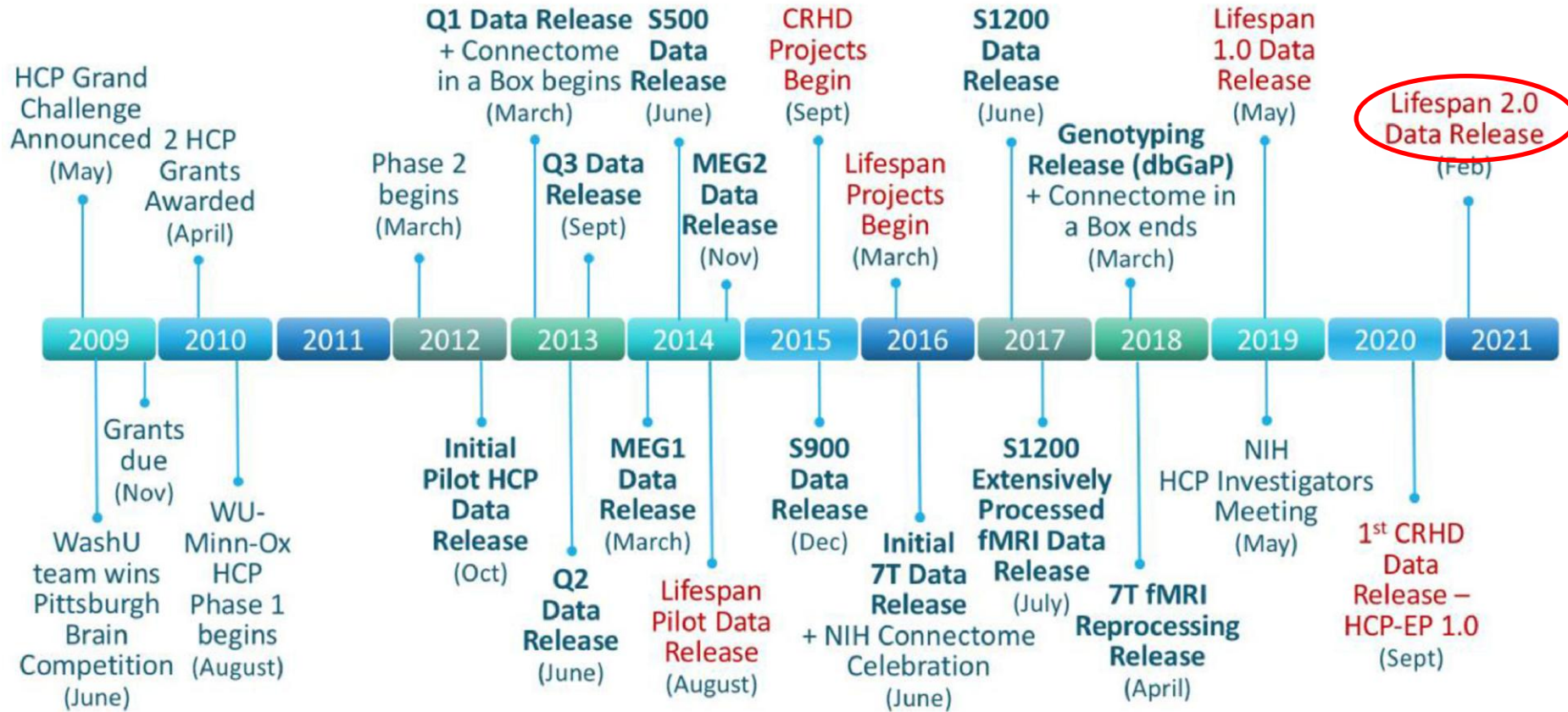
- Major study populations
 - HCP Young Adult (HCP-YA, original study)
 - Age: 22-35 years (healthy adults)
 - Participants: 1,200 subjects (twin pairs and siblings from 300 families)
 - Data collection: 2012-2015
 - Major releases: Q1 → Q3 → S500 → S900 → S1200 (final, 2017)
 - HCP lifespan studies
 - Prenatal: 20-44 weeks post-conception
 - Early childhood: 0-5 years (Baby Connectome Project)
 - Development: 5-21 years (HCP-D, $n = 652$)
 - Aging: 36-100+ years (HCP-A, $n = 725$)
 - Major releases: Lifespan 1.0 (2019) → Lifespan 2.0 (2021)

- HCP disease studies: Connectomes Related to Human Disease (CRHD)
 - Various neurological and psychiatric conditions
 - Neurological conditions: Alzheimer's disease, dementia, epilepsy, frontotemporal degeneration, low vision/blindness
 - Psychiatric conditions: Early psychosis (HCP-EP), treatment-resistant depression (HCP-MDD), anxiety and depression in adolescents (HCP-ADA), disordered emotional states (HCP-DES)
 - Treatment studies: Electroconvulsive therapy, ketamine therapy, sleep deprivation interventions
 - Apply HCP methods to understand brain disorders



HUMAN
Connectome
PROJECT

Human Connectome Project Milestones



[Elam et al., 2021]

Milestones over the HCP Timeline

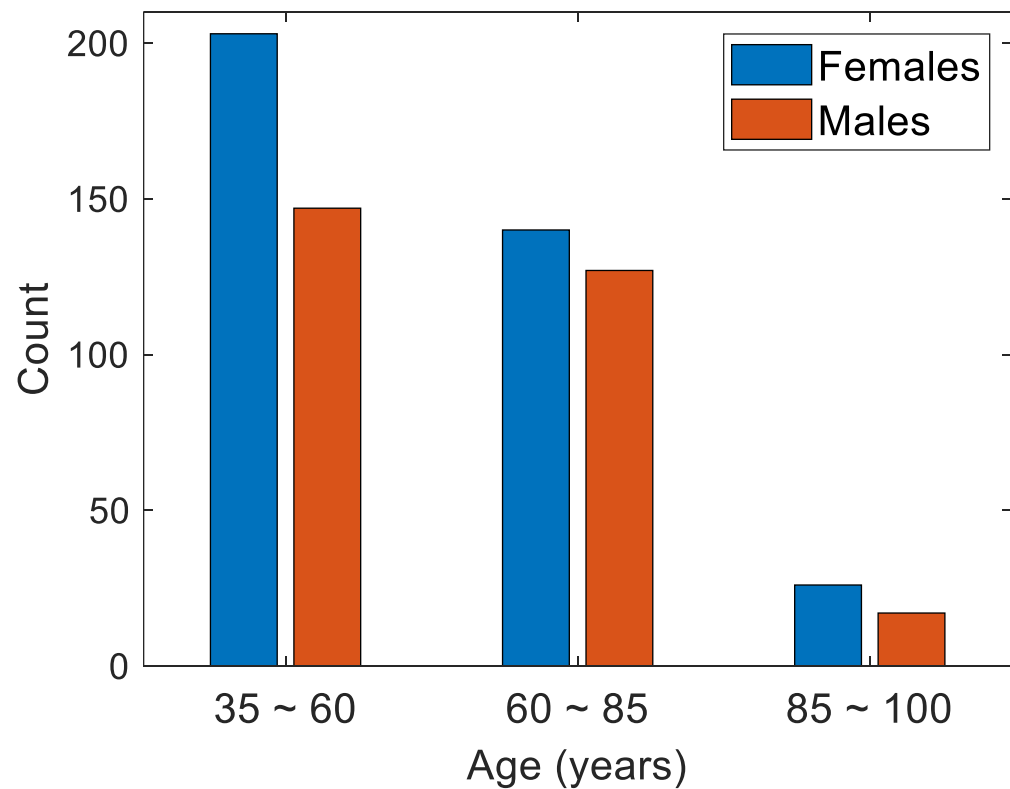
Dataset

- HCP-A dataset ($n = 722$)
 - Training set: $n = 660$
 - Maps from sMRI data: `train/{Brain,GM,WM,CSF}/001-660.nii.gz`
 - Maps from dMRI data: `train/{FA,MD,AD,RD}/001-660.nii.gz`
 - Sex (0 = female, 1 = male): `train/Subjects.csv: Sex`
 - Age (in years): `train/Subjects.csv: Age`

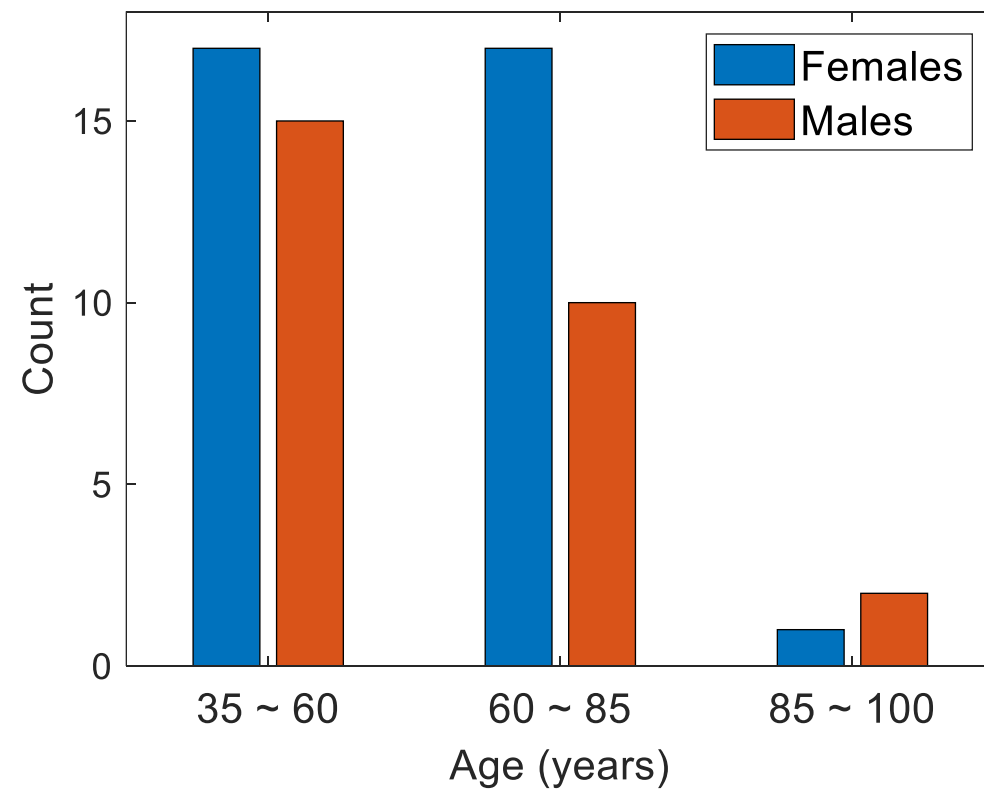
– Test set: $n = 62$

- Maps from sMRI data: `test/{Brain,GM,WM,CSF}/001-062.nii.gz`
- Maps from dMRI data: `test/{FA,MD,AD,RD}/001-062.nii.gz`
- Sex (0 = female, 1 = male): `test/Subjects.csv: Sex`
- Age (in years): hidden

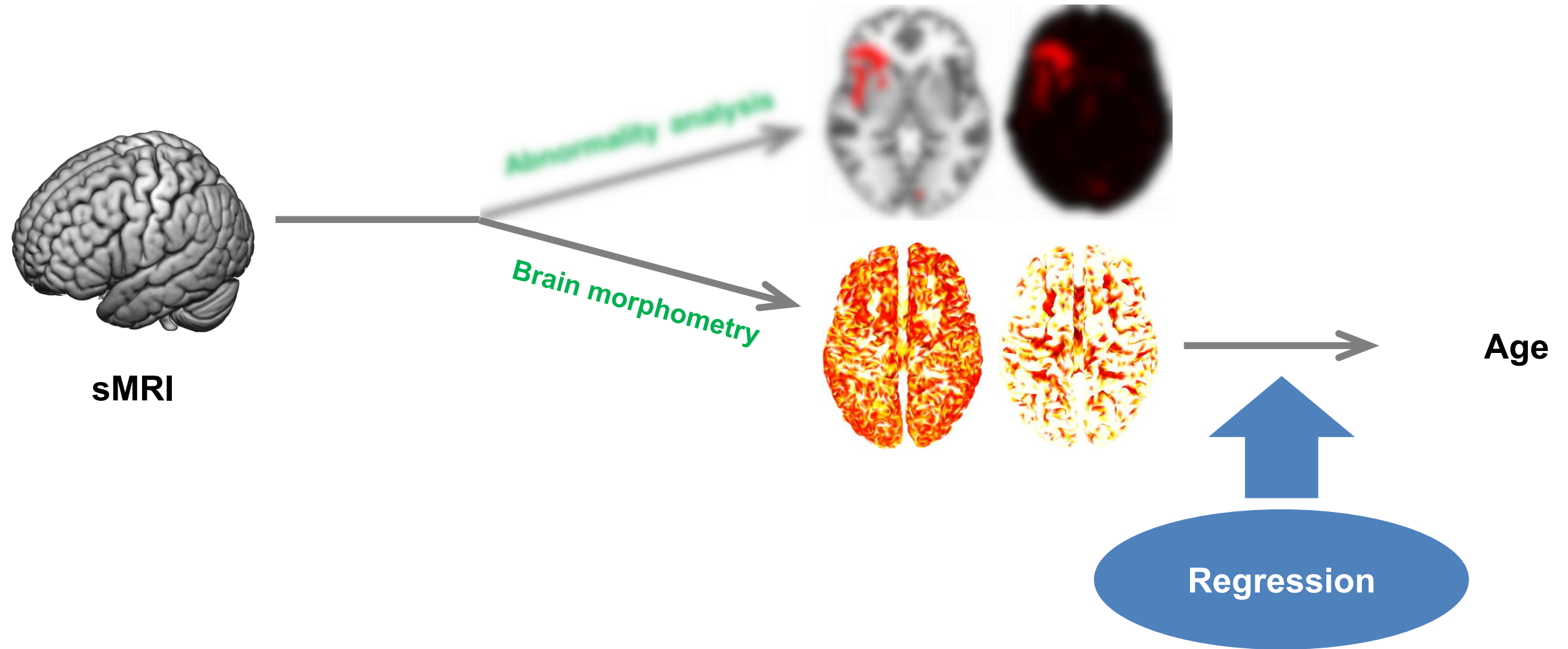
Training set



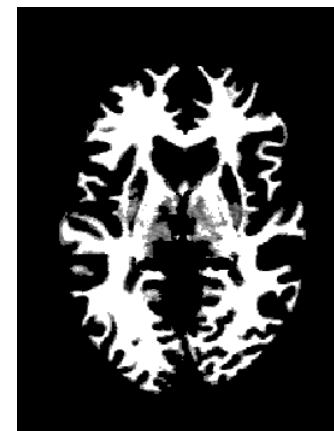
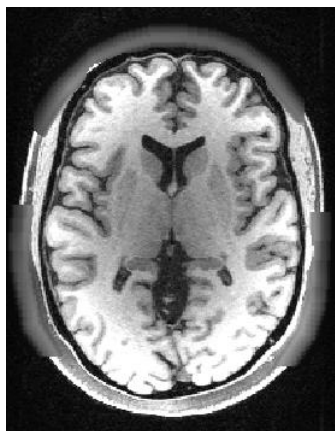
Test set



Distribution of Age and Sex for Training and Test Sets



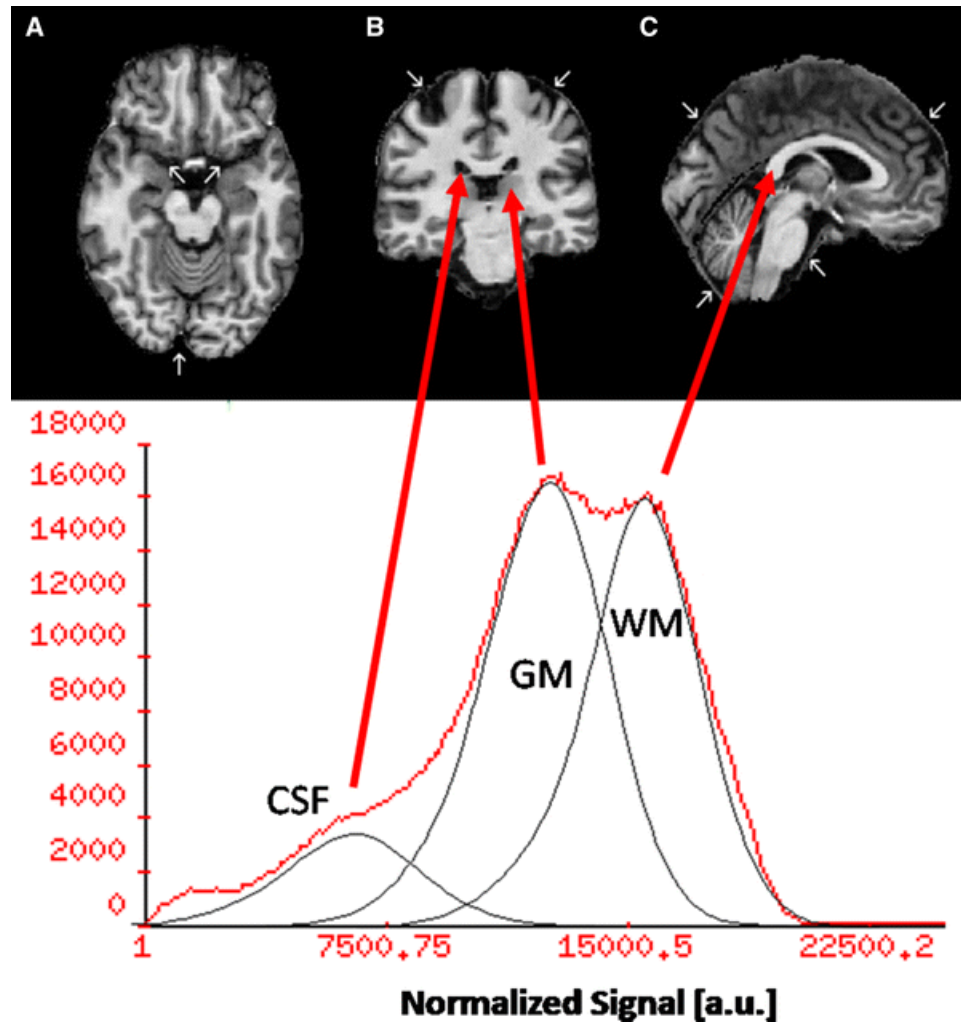
- Preprocessing of sMRI data
 - Correction for intensity non-uniformity (bias field)
 - Segmentation into grey matter, white matter, and cerebrospinal fluid
 - Spatial normalization to the Montreal Neurological Institute (MNI) template brain



Dimensions: $208 \times 300 \times 320$

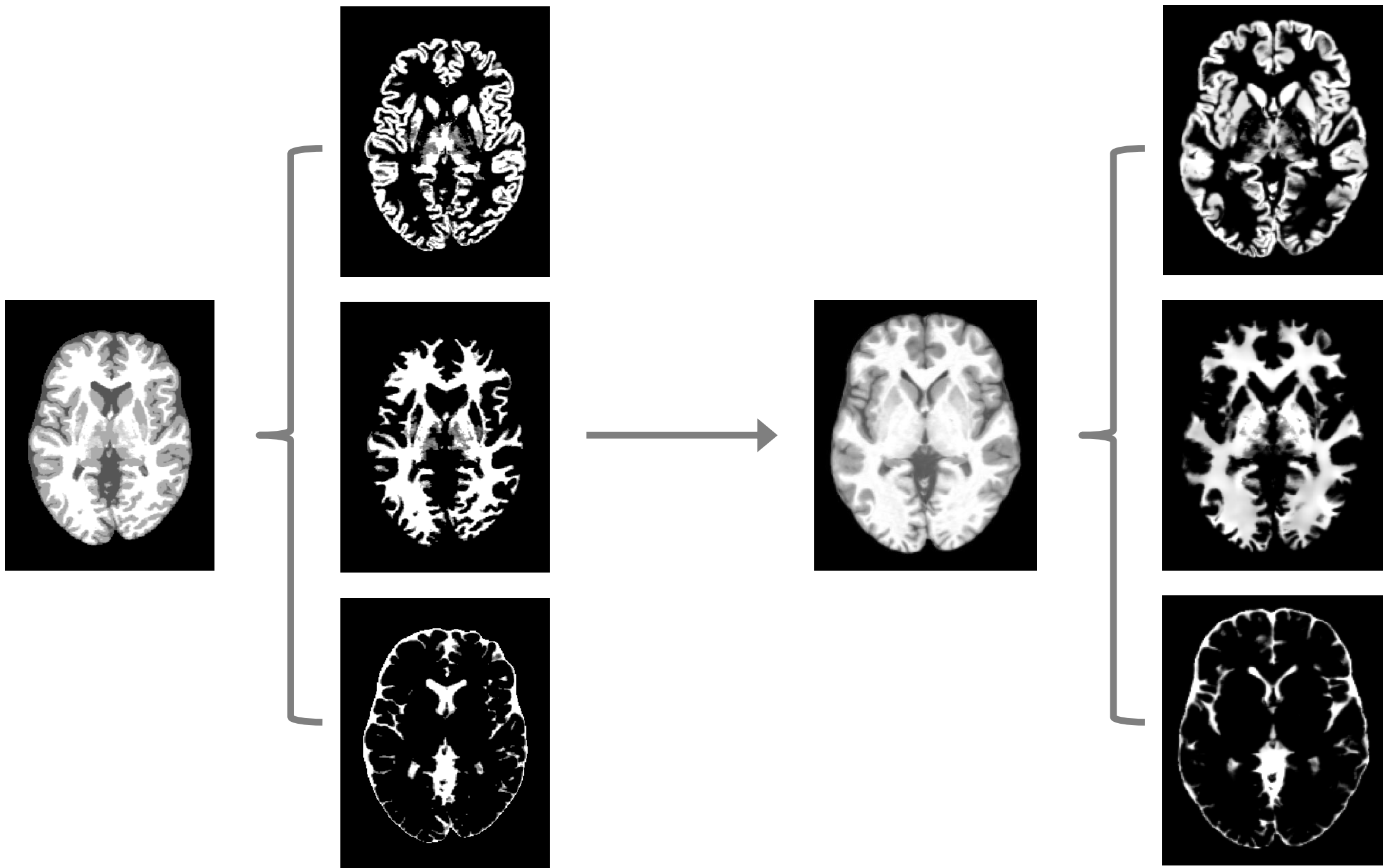
Voxel depth: 32-bit real

Voxel size: $0.8 \text{ mm} \times 0.8 \text{ mm} \times 0.8 \text{ mm}$



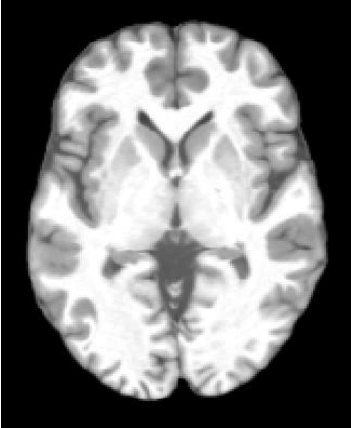
[Helms, 2016]

Segmentation into Different Tissues

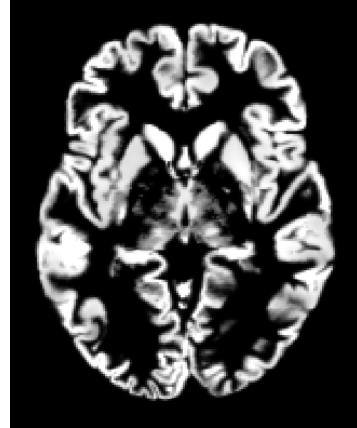


- Maps from sMRI data
 - Brain map in the MNI template brain space
 - Grey matter probability (partial volume fraction) map in the MNI template brain space
 - White matter probability (partial volume fraction) map in the MNI template brain space
 - Cerebrospinal fluid probability (partial volume fraction) map in the MNI template brain space

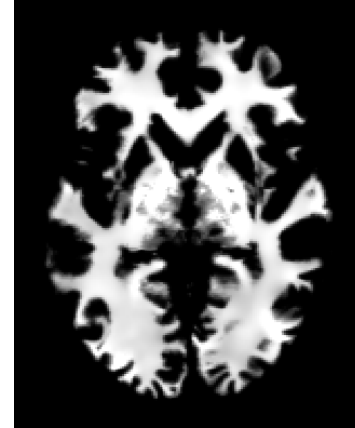
Brain



GM



WM



CSF

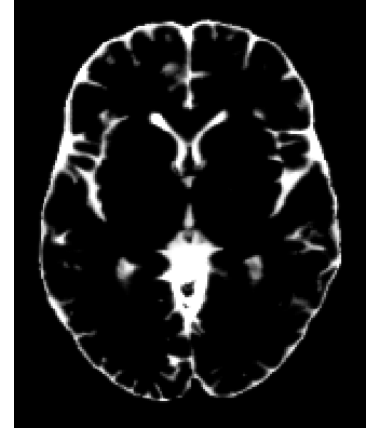
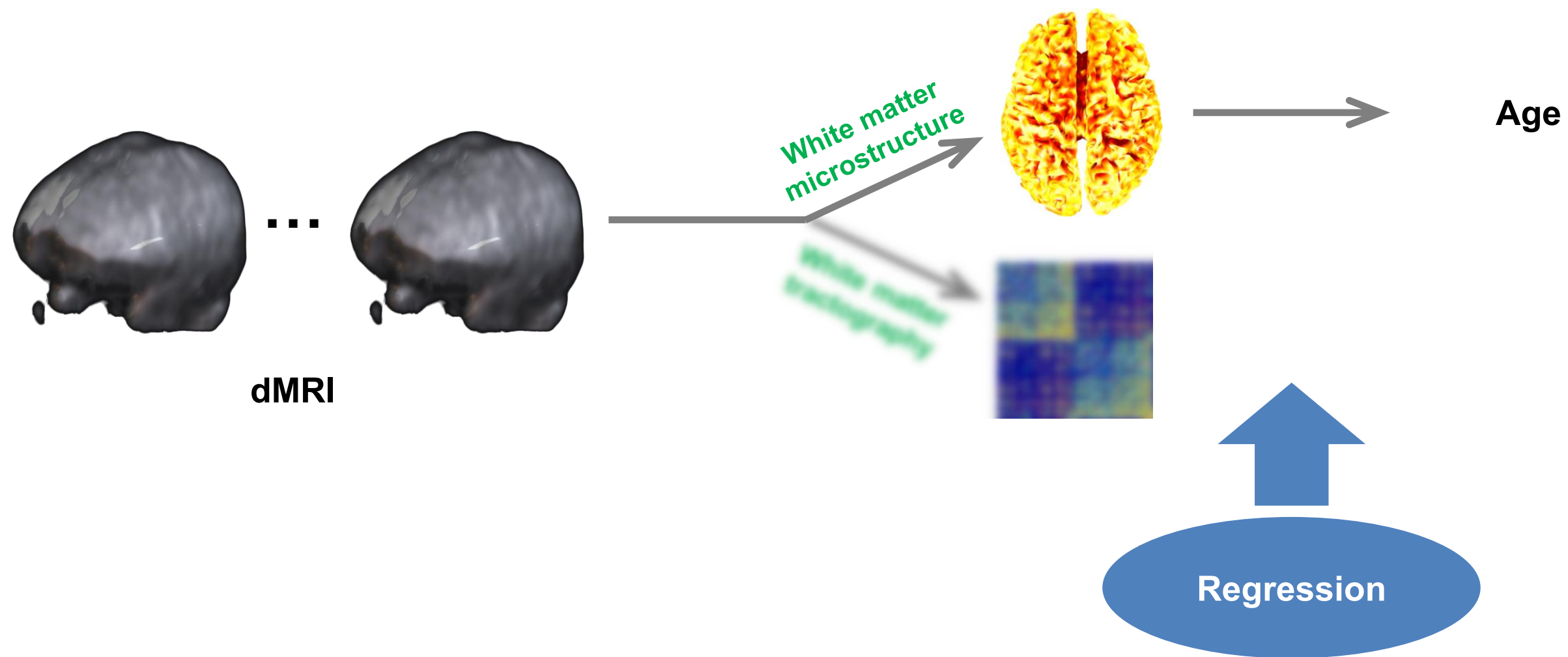


Image specifications:

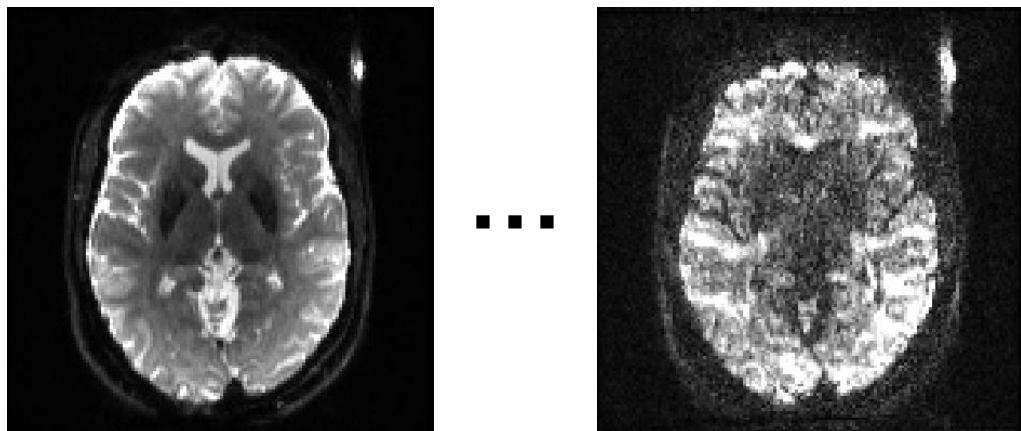
Dimensions: $79 \times 95 \times 79$

Voxel size: $2.0 \text{ mm} \times 2.0 \text{ mm} \times 2.0 \text{ mm}$

Maps from sMRI Data



- Processing of dMRI data
 - Correction for head motion, eddy current-induced distortion, and susceptibility artifact (B0 inhomogeneity-induced distortion)
 - Diffusion tensor modelling
 - Computation of diffusion tensor metrics
 - Spatial normalization to the MNI template brain

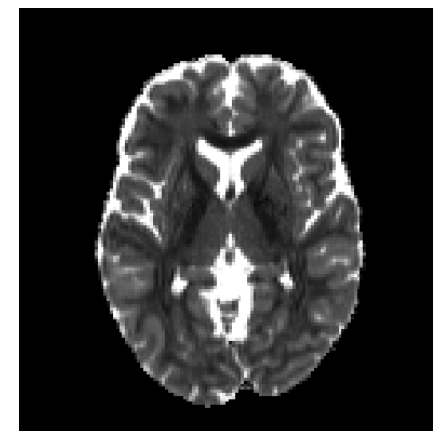
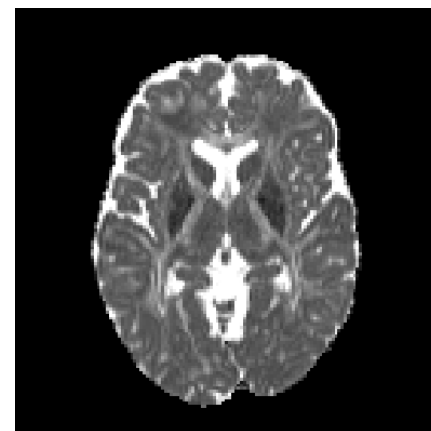
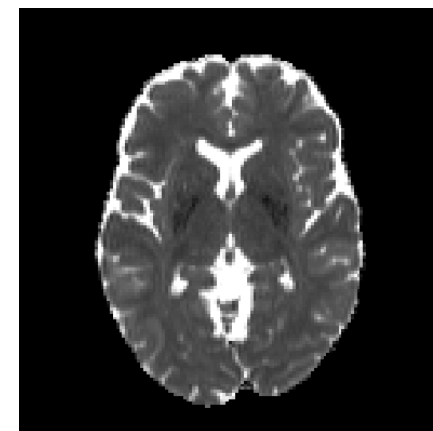
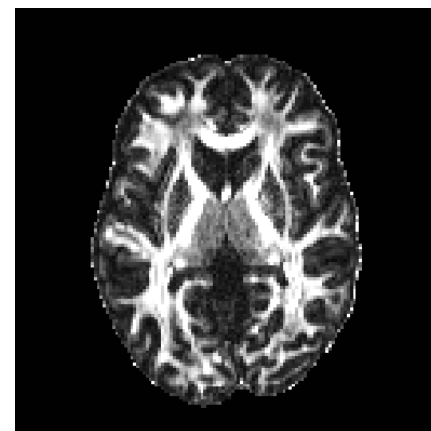


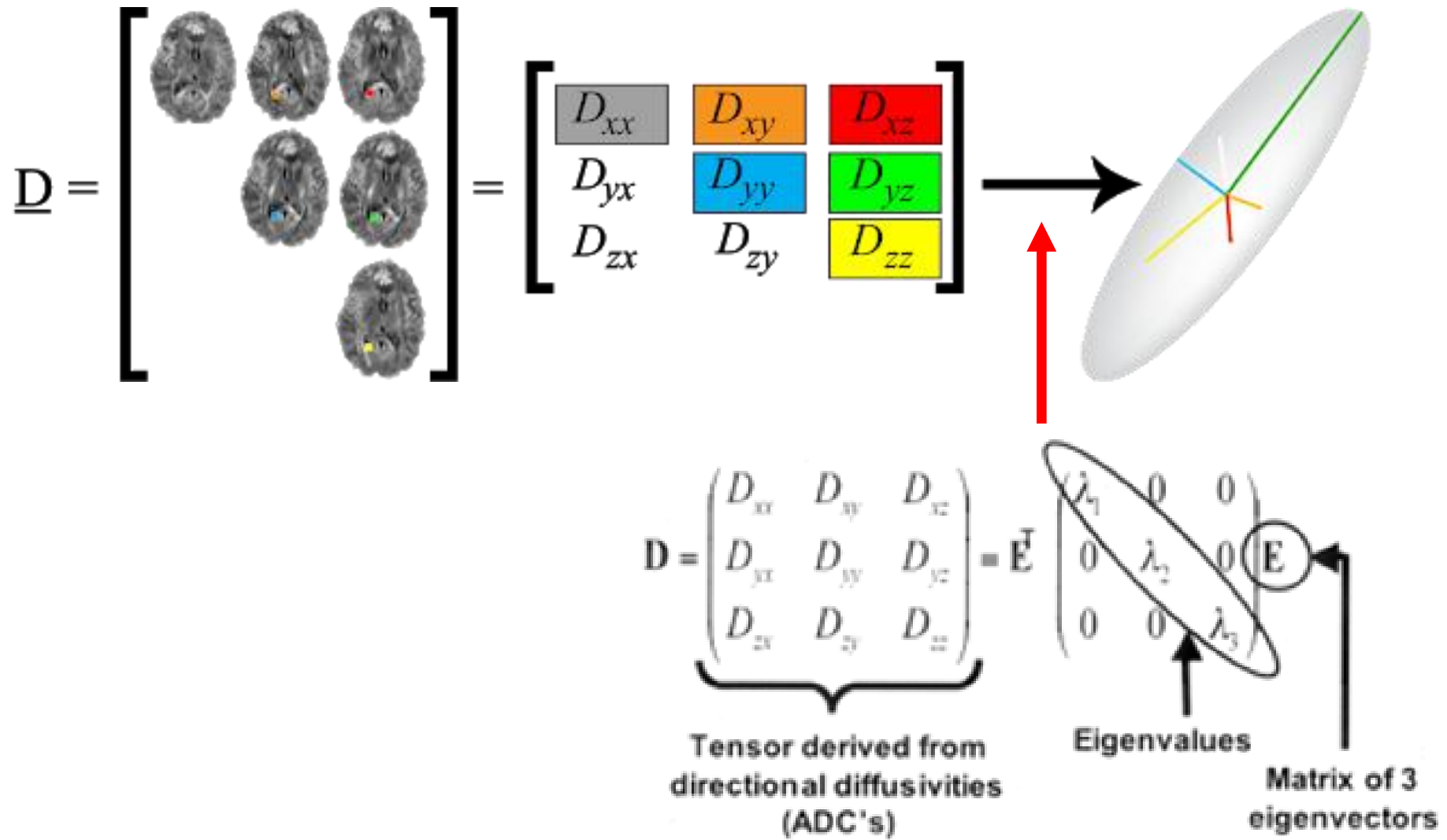
99 volumes:

Dimensions: $140 \times 140 \times 92$

Voxel depth: 32-bit real

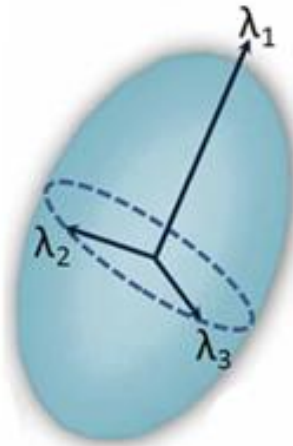
Voxel size: $1.5 \text{ mm} \times 1.5 \text{ mm} \times 1.5 \text{ mm}$



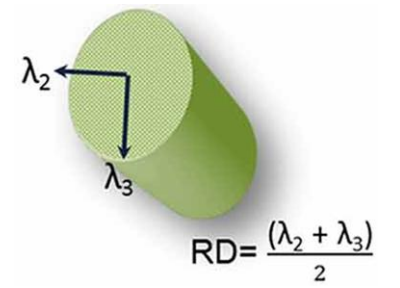
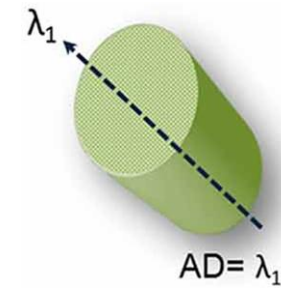
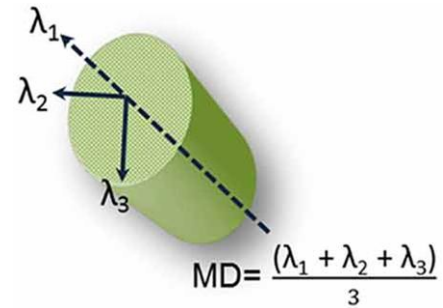


[<https://www.blog.brainsightai.com/post/from-dti-to-hardi>]

Diffusion Tensor Modeling

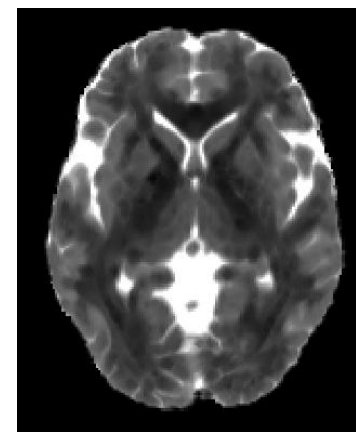
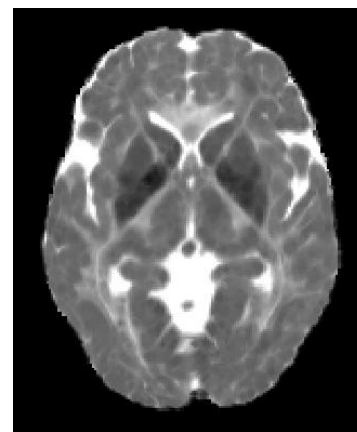
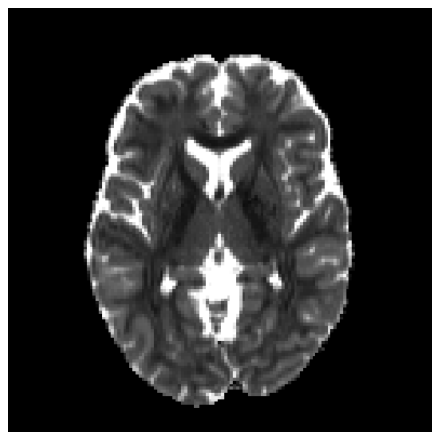
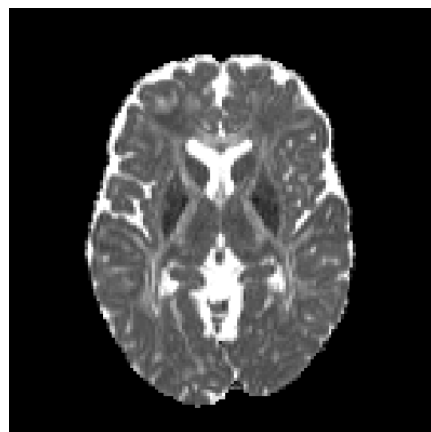
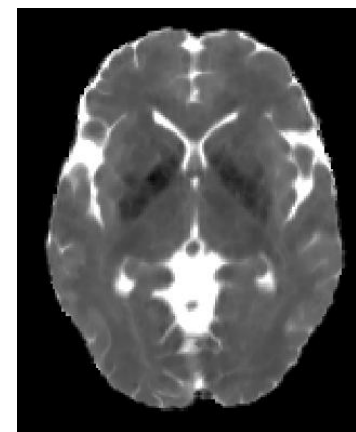
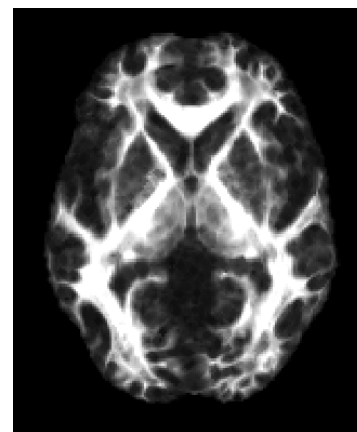
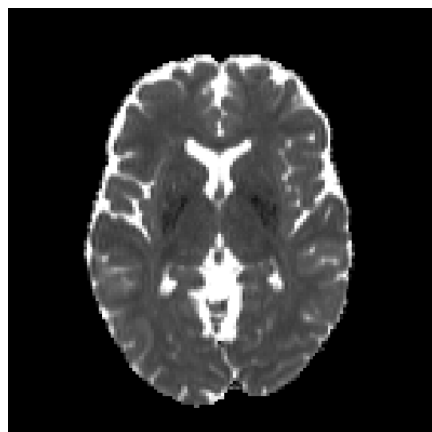
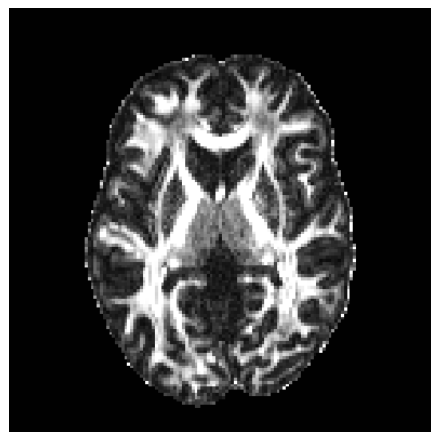


$$FA = \sqrt{\frac{1}{2}} \cdot \frac{\sqrt{(\lambda_1 - \lambda_2)^2 + (\lambda_2 - \lambda_3)^2 + (\lambda_3 - \lambda_1)^2}}{\sqrt{(\lambda_1)^2 + (\lambda_2)^2 + (\lambda_3)^2}}$$



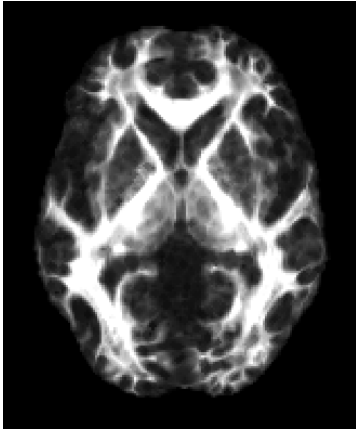
[DeSouza et al., 2016]

Computation of Diffusion Tensor Metrics

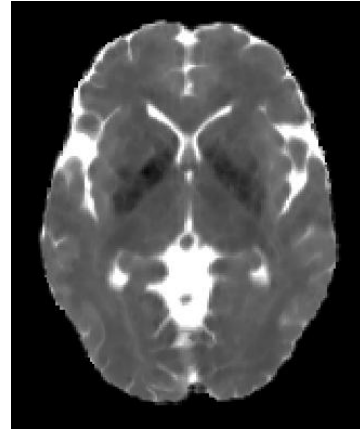


- Maps from dMRI data
 - Fractional anisotropy (FA) map in standard space
 - Mean diffusivity (MD) map in standard space
 - Axial diffusivity (AD) map in standard space
 - Radial diffusivity (RD) map in standard space

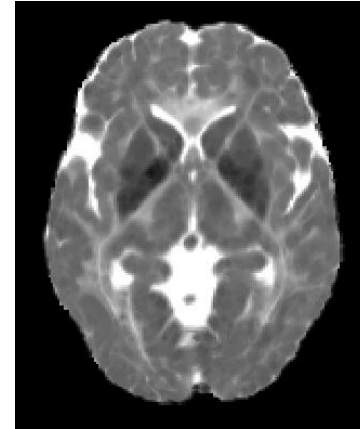
FA



MD



AD



RD

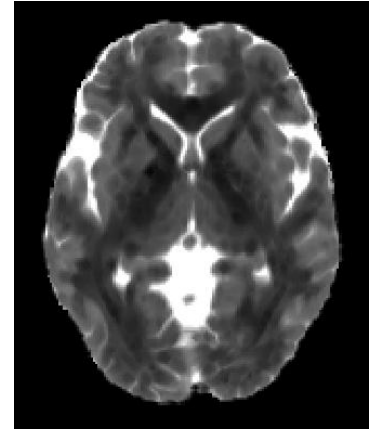


Image specifications:

Dimensions: $79 \times 95 \times 79$

Voxel size: $2.0 \text{ mm} \times 2.0 \text{ mm} \times 2.0 \text{ mm}$

Maps from dMRI Data

- Target variable
 - Age (in years)
- Brain age prediction performance
 - MAE for the test set ($n = 62$)
 - Average of absolute differences between predicted and actual ages across the test set
 - Ranges from 0 to ∞ (lower is better)