



OHBM 2024
JUNE 23~27, SEOUL, KOREA

OHBM 2024
EDUCATIONAL COURSES

Charting life-course functional connectome using normative modeling



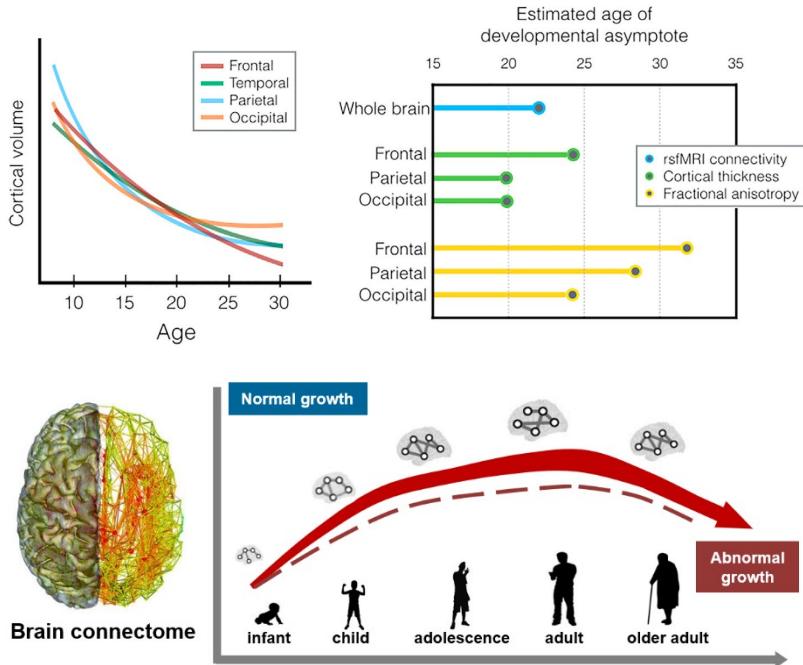
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I have no disclosures.

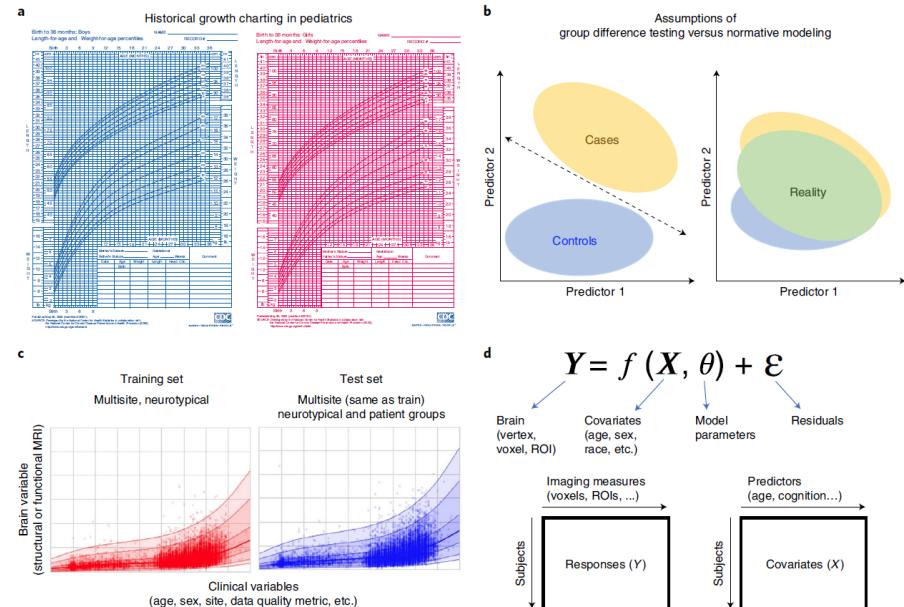
Background

The emergence, development, and aging of the intrinsic connectome architecture throughout the lifespan



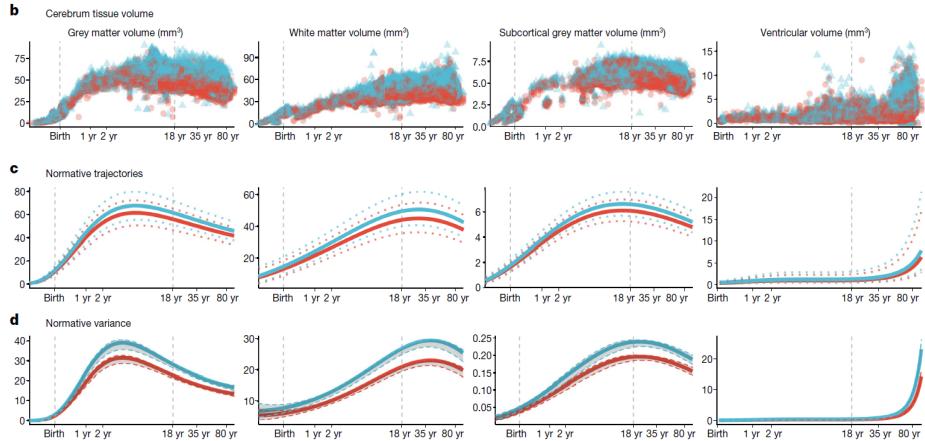
Somerville *et al* (2016) *Neuron*; Zuo *et al* (2017) *Trends Cogn Sci*; Cao *et al* (2017) *Trends Neurosci*; Vogel *et al* (2023) *Nat Rev Neurosci*

The growth chart framework provides an invaluable tool for charting normative reference curves in the human brain



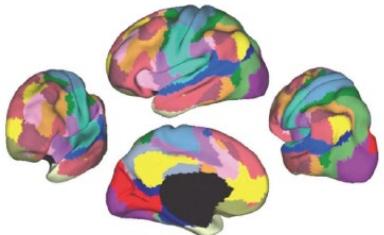
Marquand *et al* (2016) *Biol Psychiatry*; Rutherford *et al* (2022) *Nat Protoc*

Background

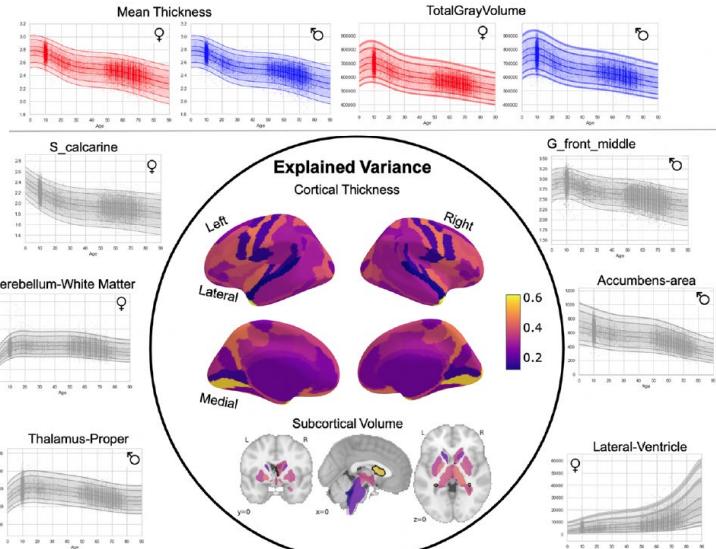


Bethlehem, Seidlitz, White et al (2022) *Nature*

Yeo-17 network parcellation



Rutherford et al (2023) *eLife*



Rutherford et al (2022) *eLife*

The normative growth pattern of the functional brain connectome across the human lifespan

Datasets and imaging quality control

Collecting multi-modal imaging data from 44,030 individuals



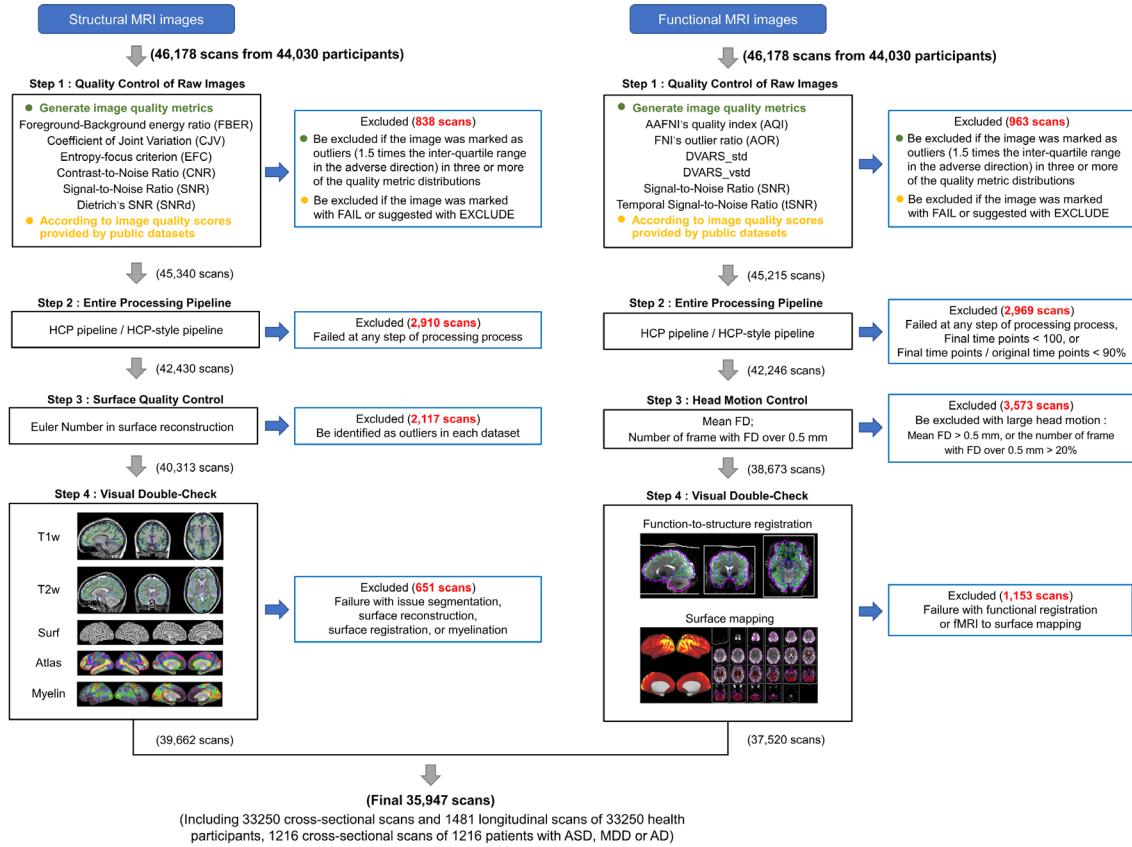
Imaging quality control process

- Four-steps procedure
- Combining automated assessment and expert manual review



The final sample included 34,466 individuals

- ranging in age from 32 postmenstrual weeks to 80 years and from 172 sites
- **33,250 healthy individuals**
- 414 ASD patients
- 622 MDD patients
- 180 AD patients



Datasets and imaging quality control

Collecting multi-modal imaging data from 44,030 individuals



Imaging quality control process

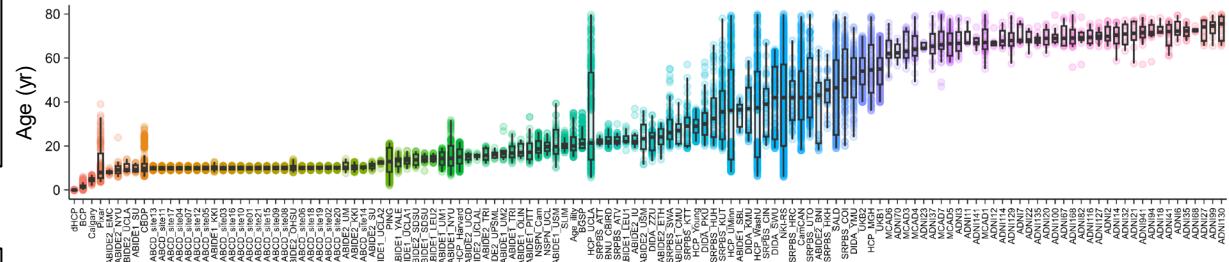
- Four-steps procedure
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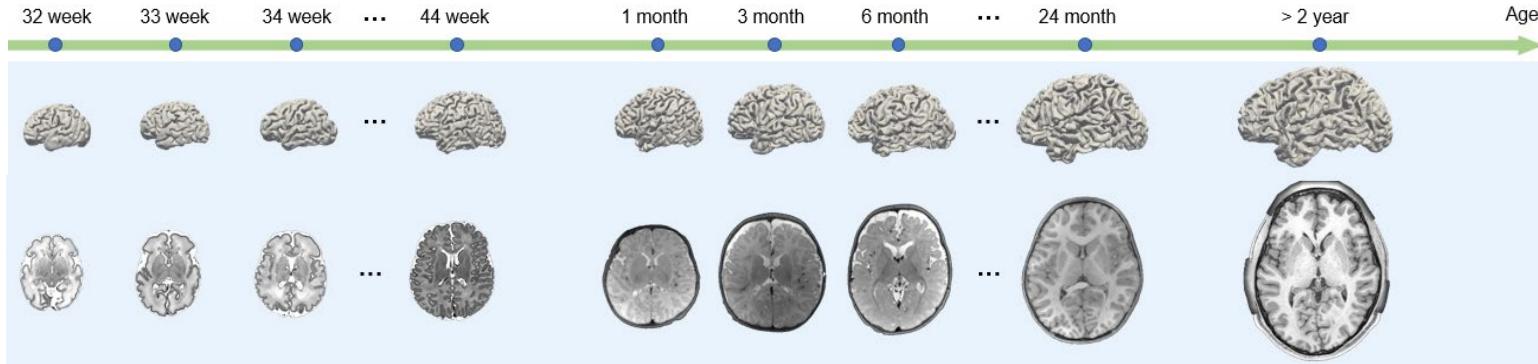
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- **33,250 healthy individuals**
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Aggregated data across 132 sites (after quality control)



Data processing



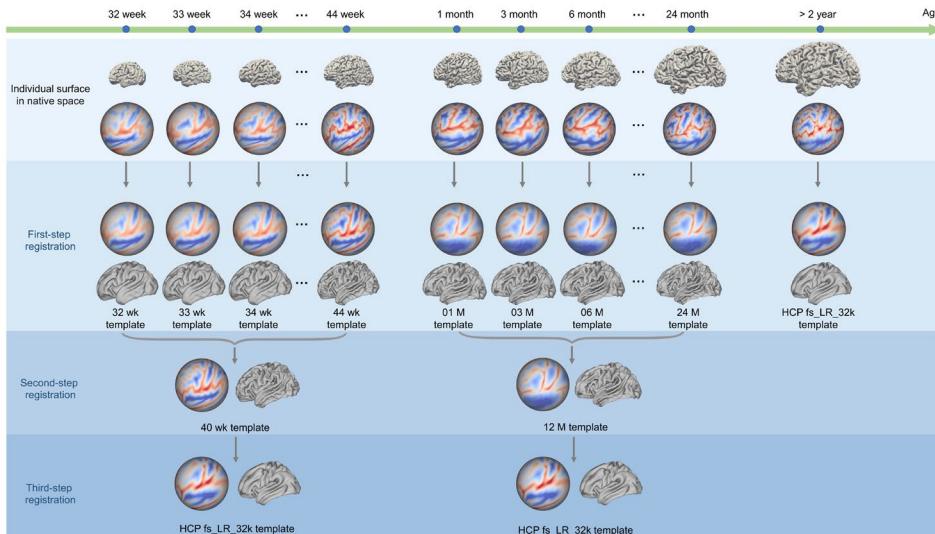
Considerable changes of the human brain in early development

Challenges:

- Lack of a lifespan-appropriate preprocessing pipeline
- Lack of a set of standard template for registration across lifespan
- Lack of a set of functional atlases across lifespan

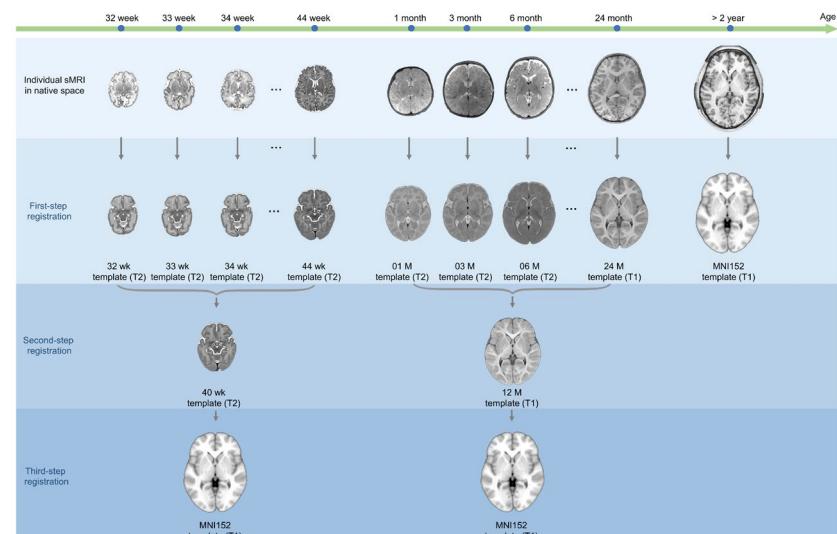
Image registration across the lifespan

Participants aged 32 to 44 postmenstrual weeks



Individual cortical surface registration framework

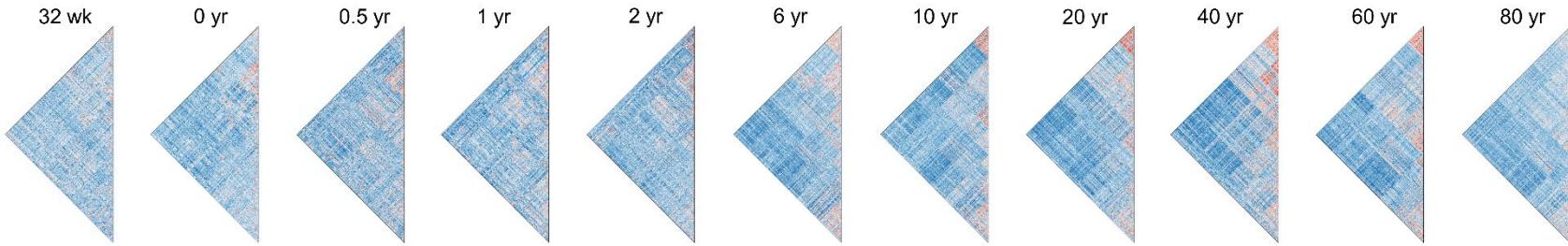
Participants aged 0 to 24 months



Individual volume registration framework

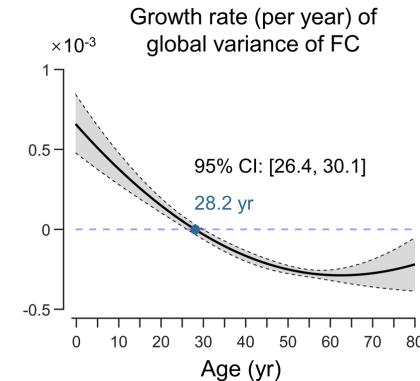
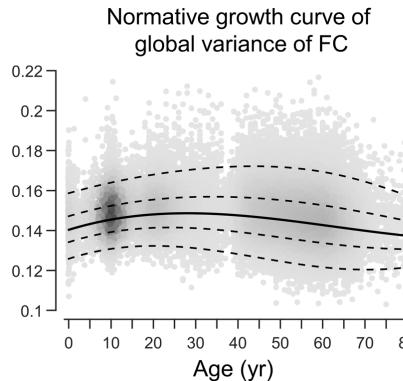
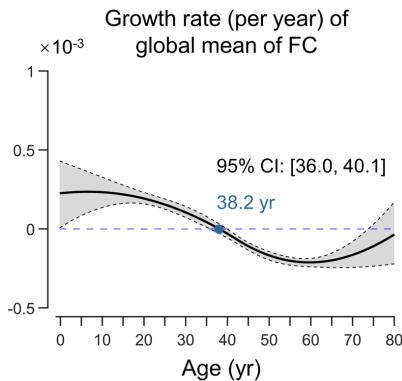
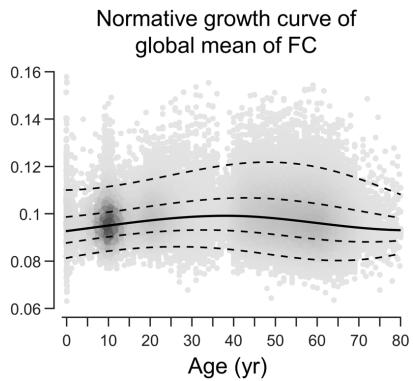
Lifespan normative growth of the global functional connectome

Functional connectome matrices at different growth ages



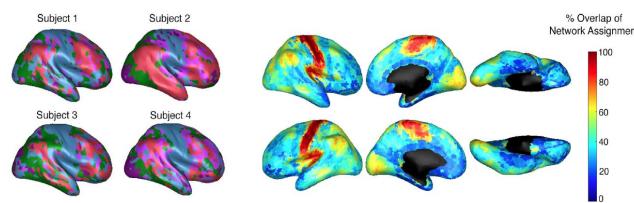
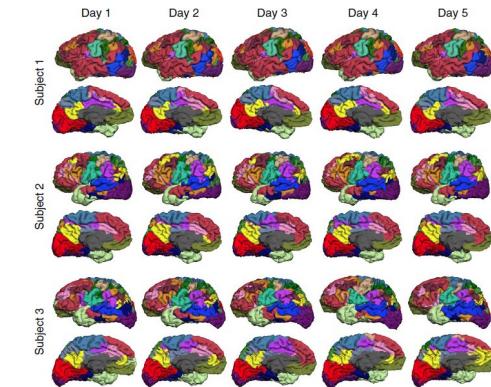
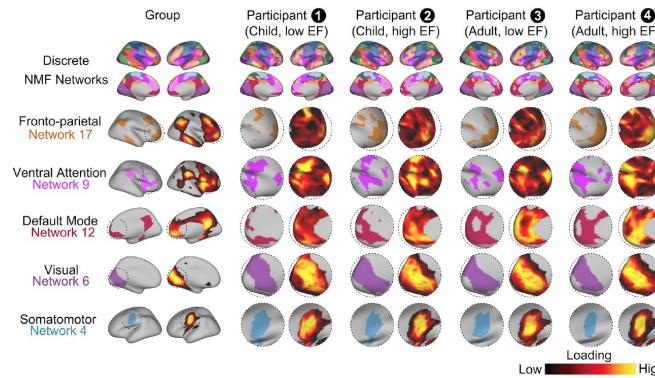
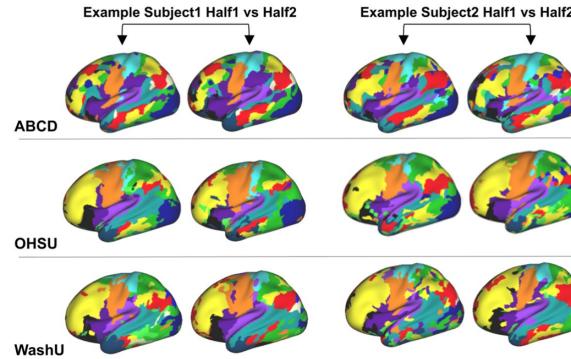
Network size: 4609×4609

Normative models of global functional connectome ($N = 33,250$)



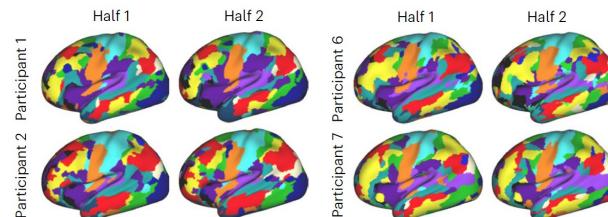
Personalized functional mapping is critical for the entire lifespan

Mutual information calculated between within-subject network maps:



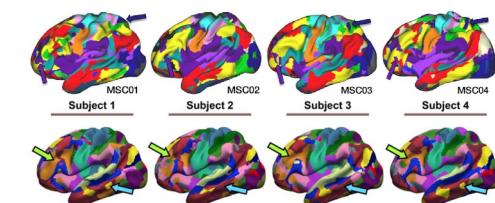
Neonates

Molloy & Saygin (2022) *Neuroimage*;
Moore et al (2024) *Imaging Neurosci*



Children and adolescents

Cui et al (2020) *Neuron*;
Hermosillo et al (2024) *Nat Neurosci*



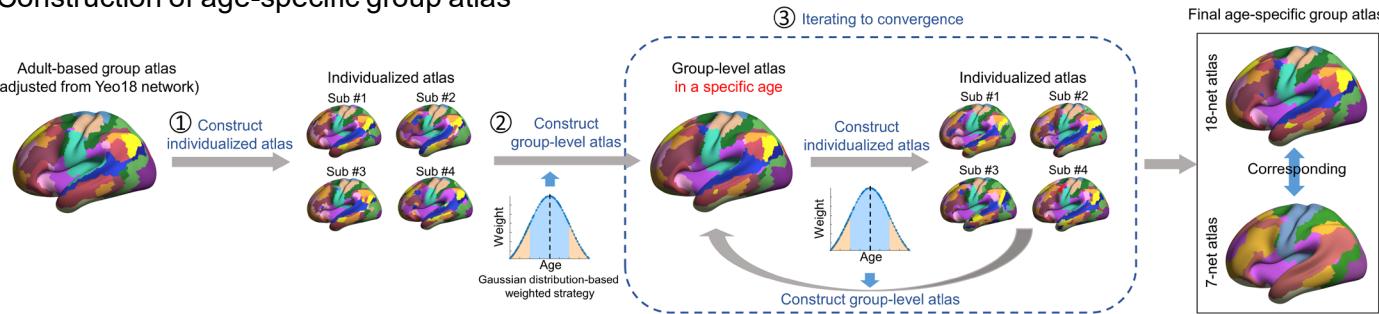
Adults

Wang et al (2015) *Nat Neurosci*;
Gordon et al (2017) *Neuron*;
Kong et al (2019) *Cereb Cortex*

Constructing population-based and individual-based functional atlas

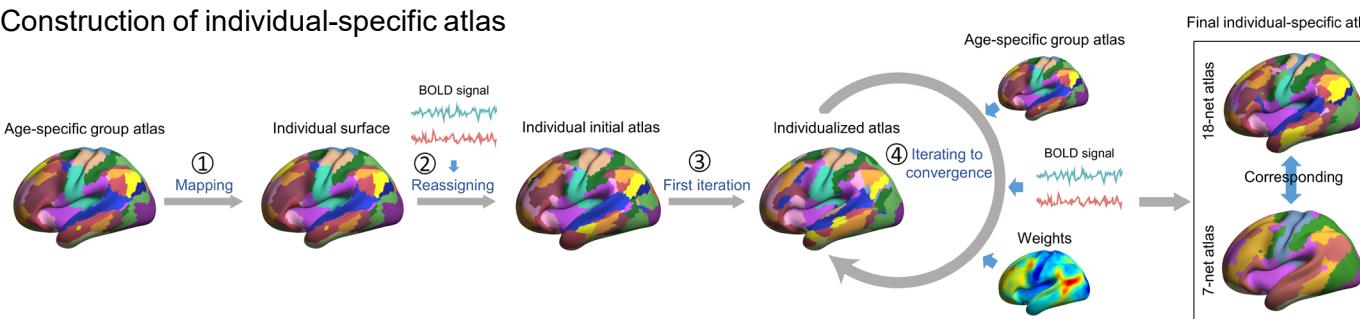
- For **age-specific group atlas**, we developed a Gaussian-weighted iterative age-specific group atlas (GIAGA) generation approach
- For **individual-specific atlas**, we used the individualized atlas approach proposing by Wang *et al* (2015) *Nat Neurosci*

Construction of age-specific group atlas



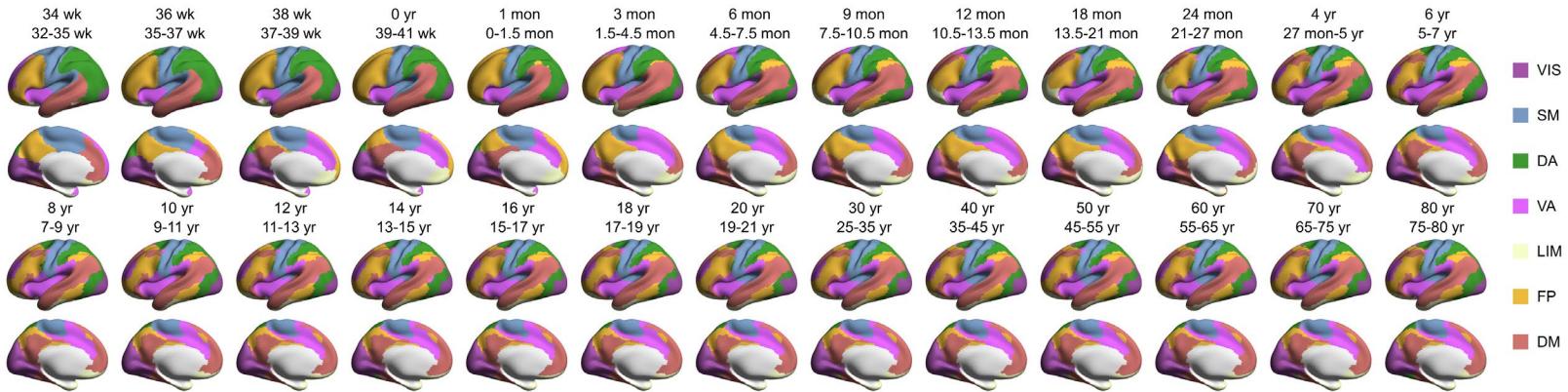
18-net	7-net
VIS_Cent	VIS
VIS_Peri	
SM_A	SM
SM_B	DA
SM_C	VA
DA_A	LIM
DA_B	
VA_A	FP
VA_B	DM
LIM_A	
LIM_B	
FP_A	
FP_B	
FP_C	
DM_A	
DM_B	
DM_C	
DM_D	

Construction of individual-specific atlas

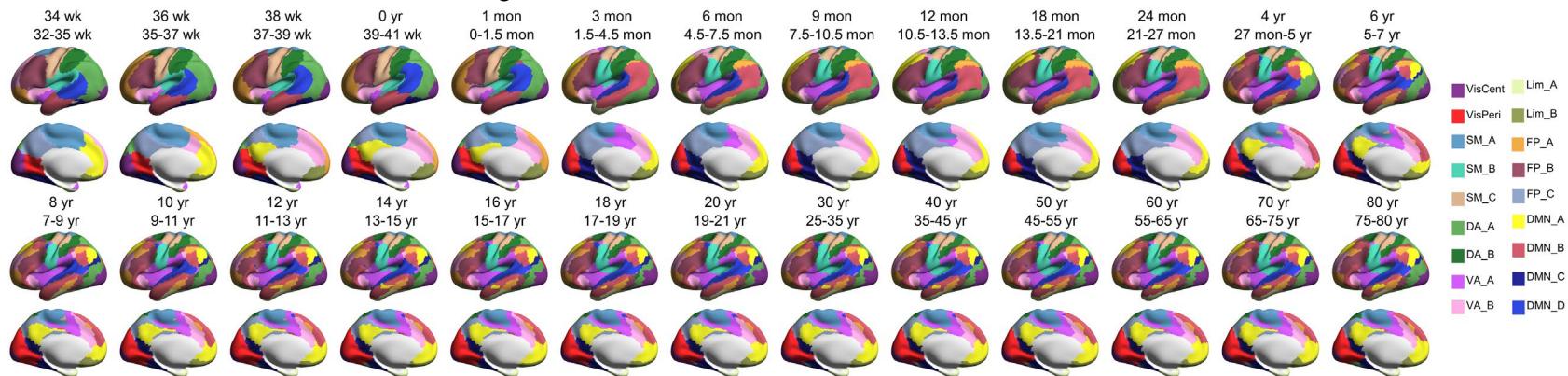


The fine-grained, lifespan-wide suite of system-level atlases

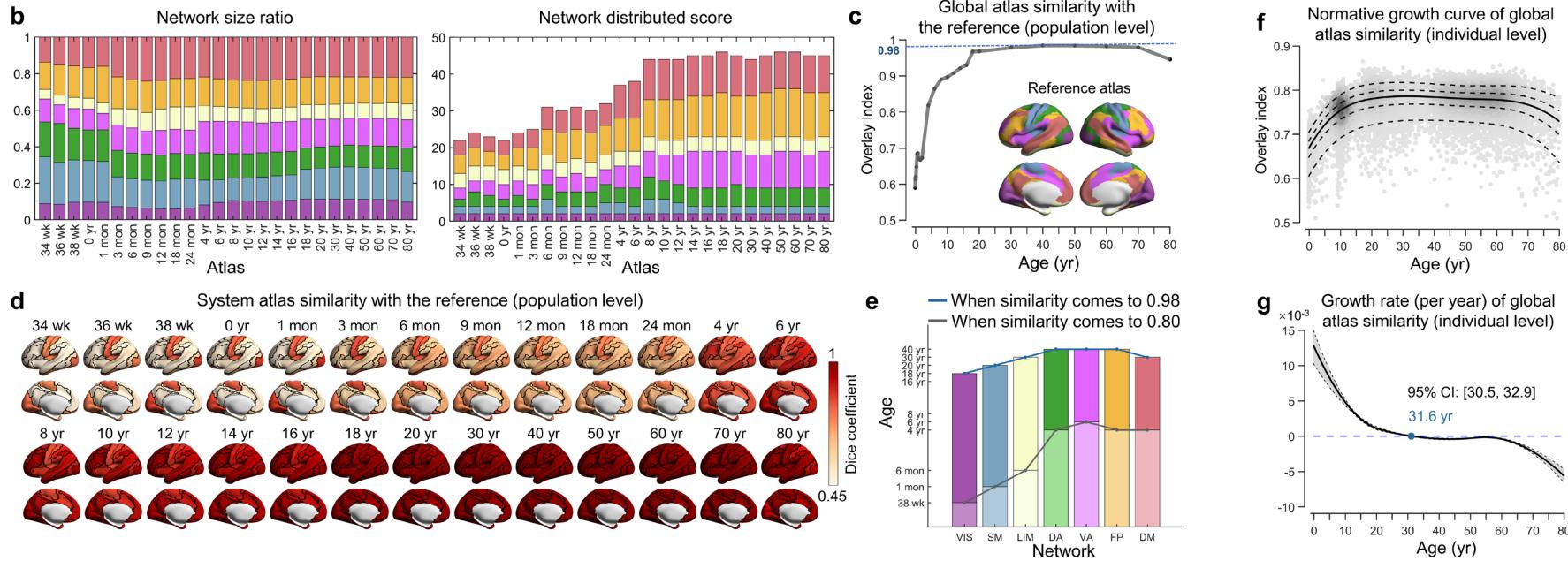
Seven-network functional atlases



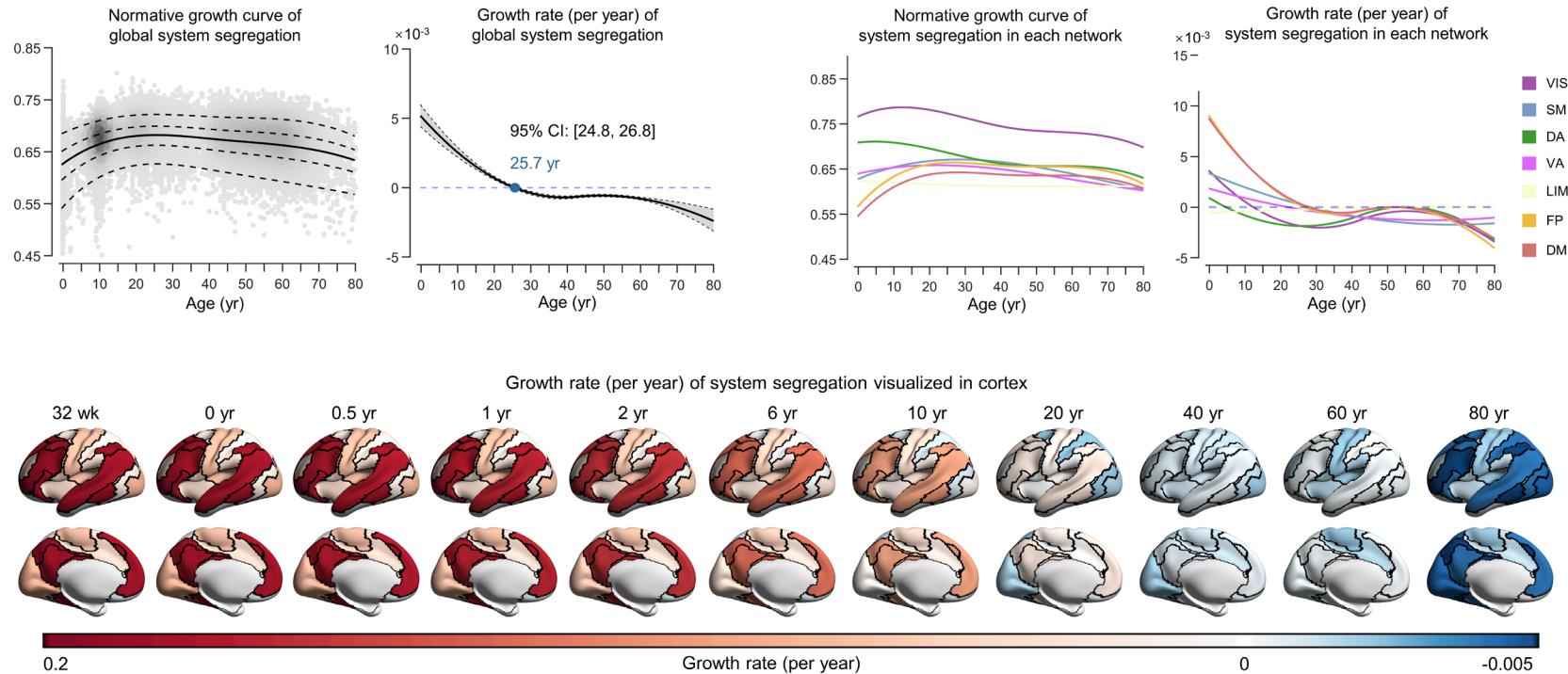
Eighteen-network functional atlases



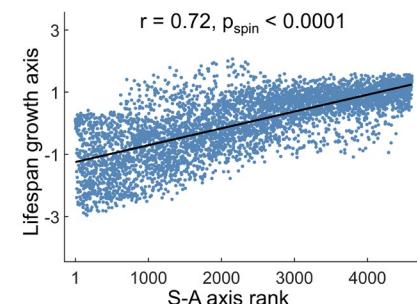
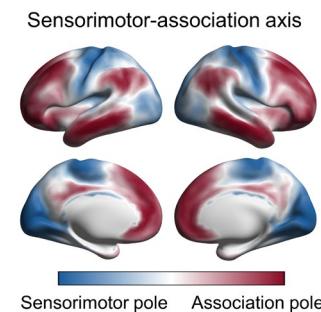
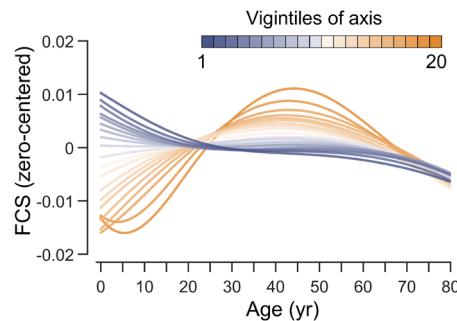
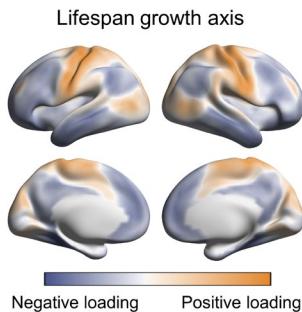
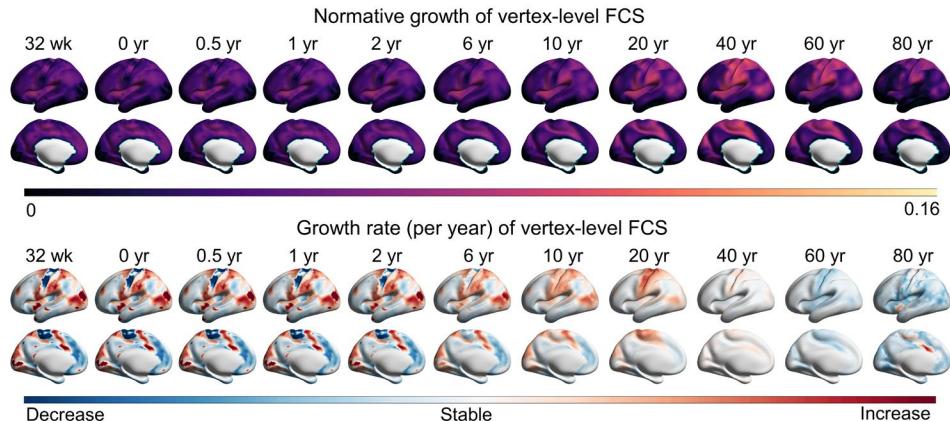
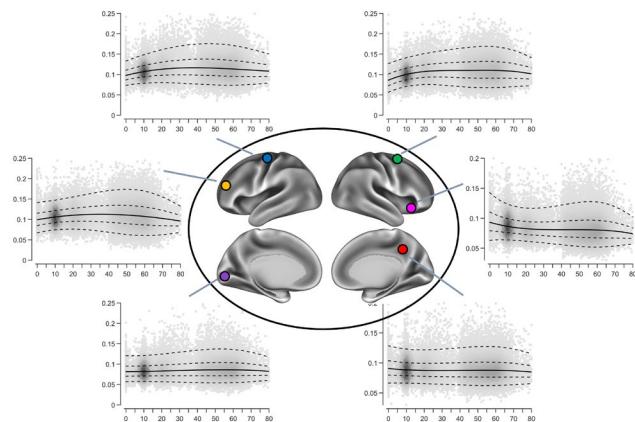
The fine-grained, lifespan-wide suite of system-level atlases



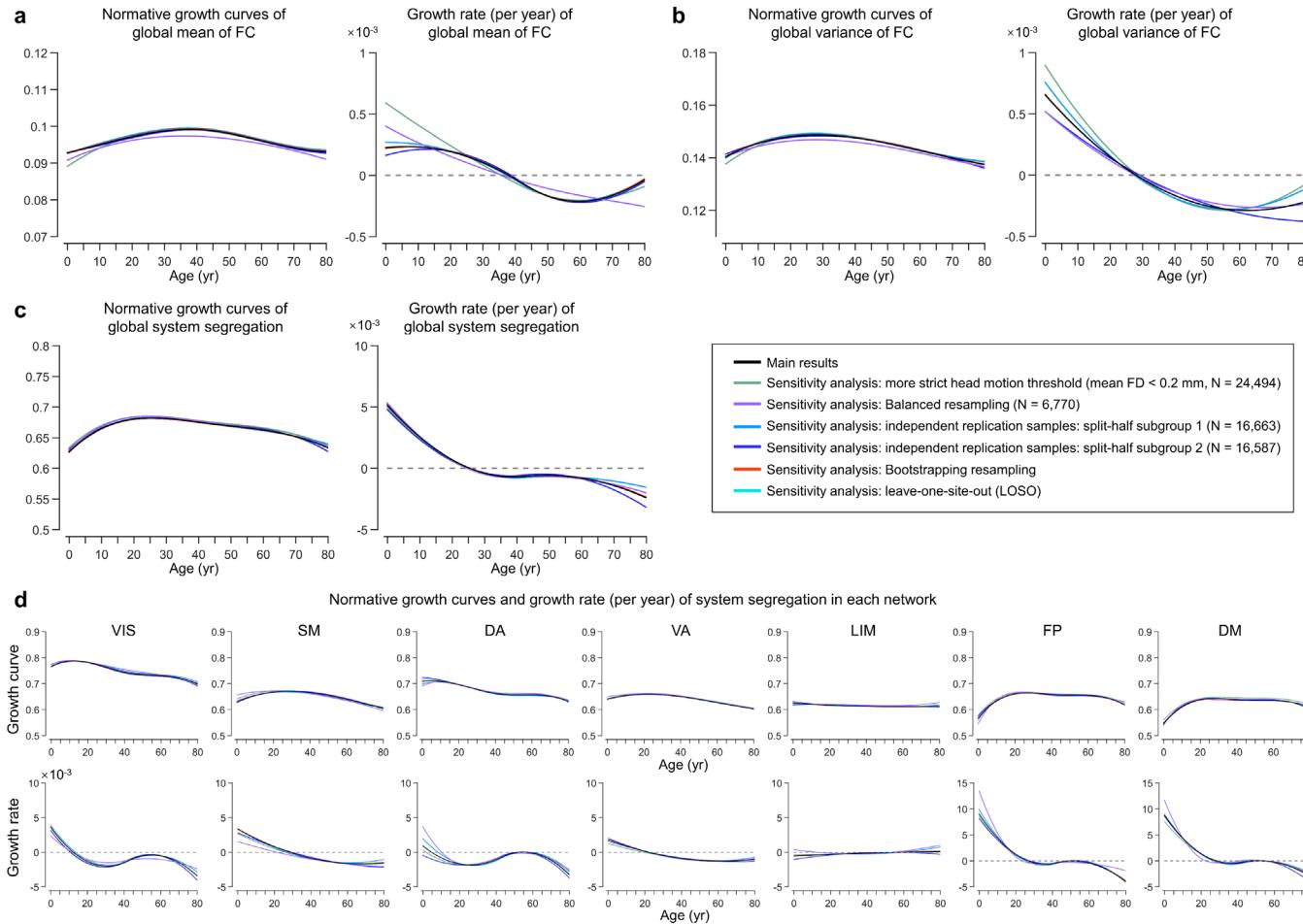
Lifespan growth of system-specific functional segregation



Lifespan growth of regional level functional connectivity



Sensitivity analyses for the lifespan normative growth patterns



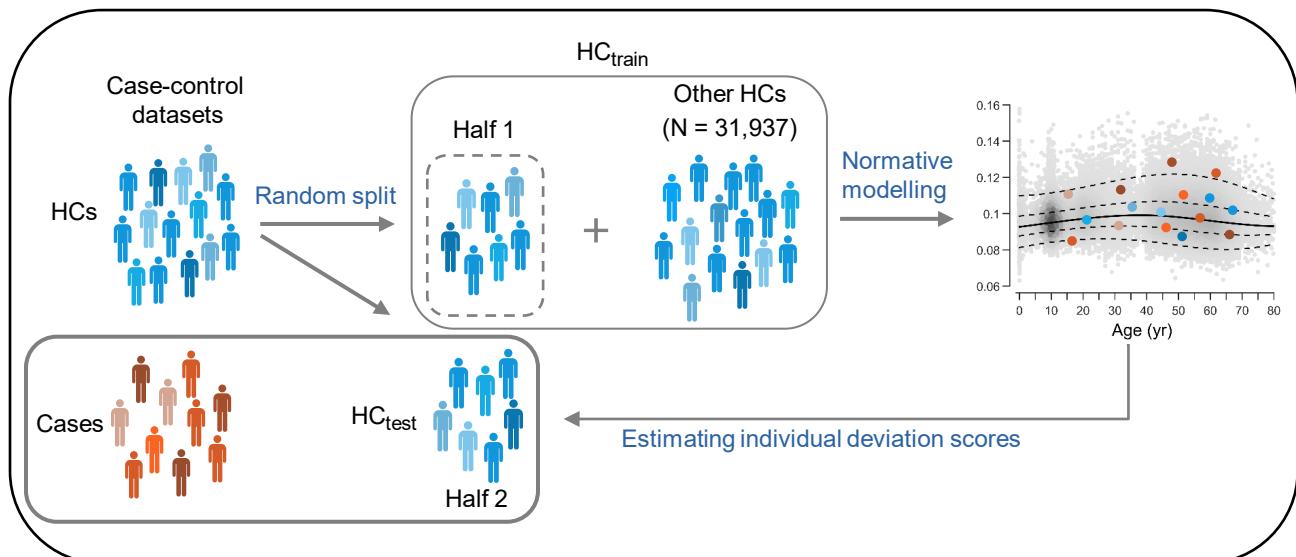
Identifying individual heterogeneity in brain disorders

Case-control datasets:

for ASD ($N_{ASD} = 414$; $N_{HC} = 591$)

for MDD ($N_{MDD} = 622$; $N_{HC} = 535$)

for AD ($N_{AD} = 180$; $N_{HC} = 187$)



This process was iterated 100 times, generating 100 models and 100 sets of deviation scores

High reproducibility was observed among the 100 repetitions (mean $R > 0.95$, mean MSE < 0.1 of the growth curves) and the 100 sets of deviation scores (mean $R > 0.97$, mean MSE < 0.2)

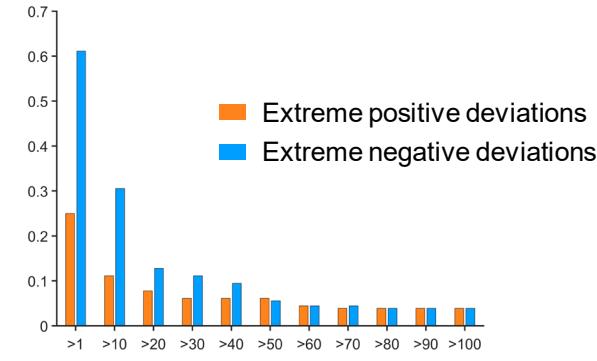
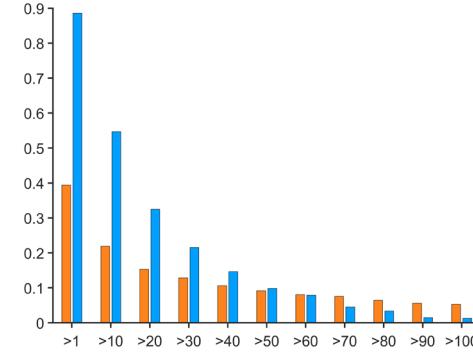
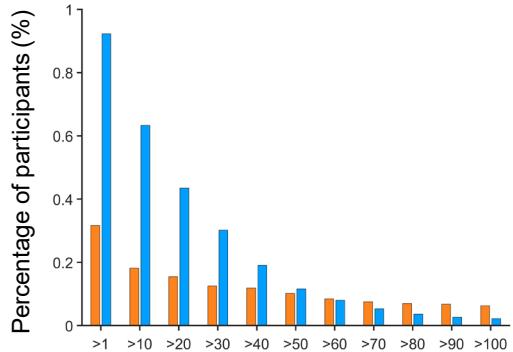
Identifying individual heterogeneity in brain disorders

ASD

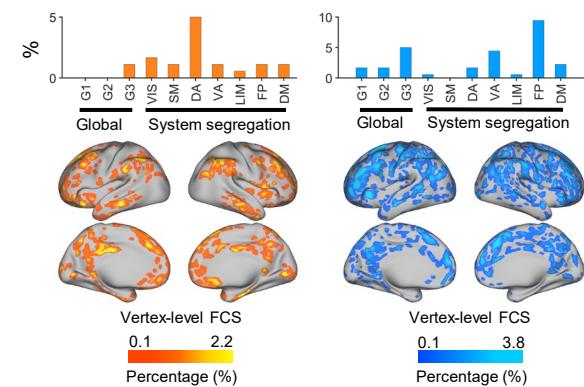
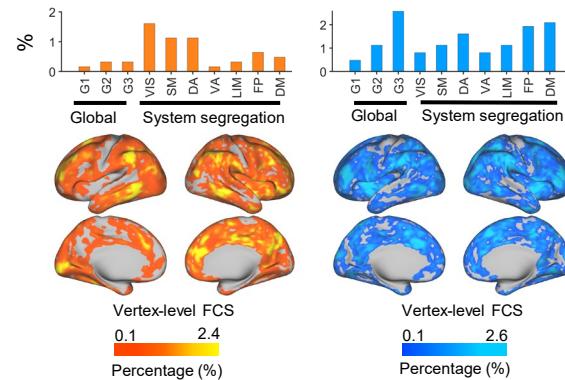
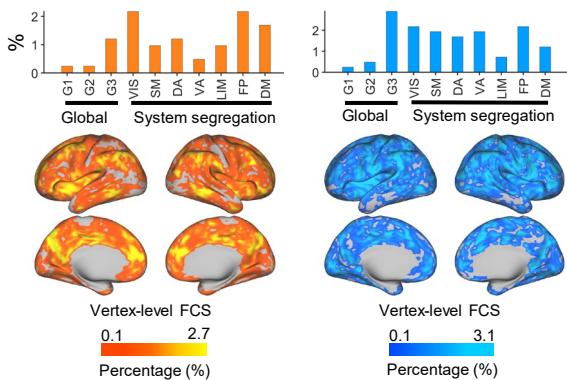
MDD

AD

The percentage of participants with extremely deviations under different number of functional metrics

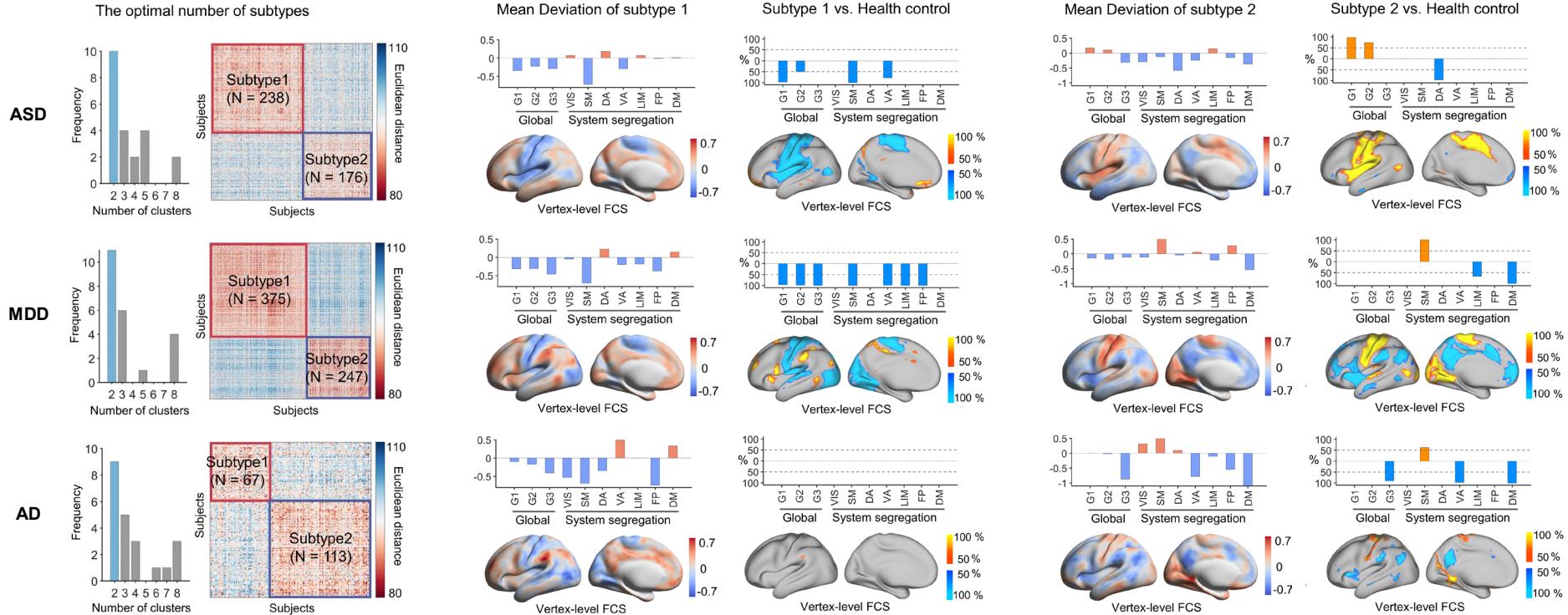


The percentage of extreme FC deviations of global, system, and vertex levels



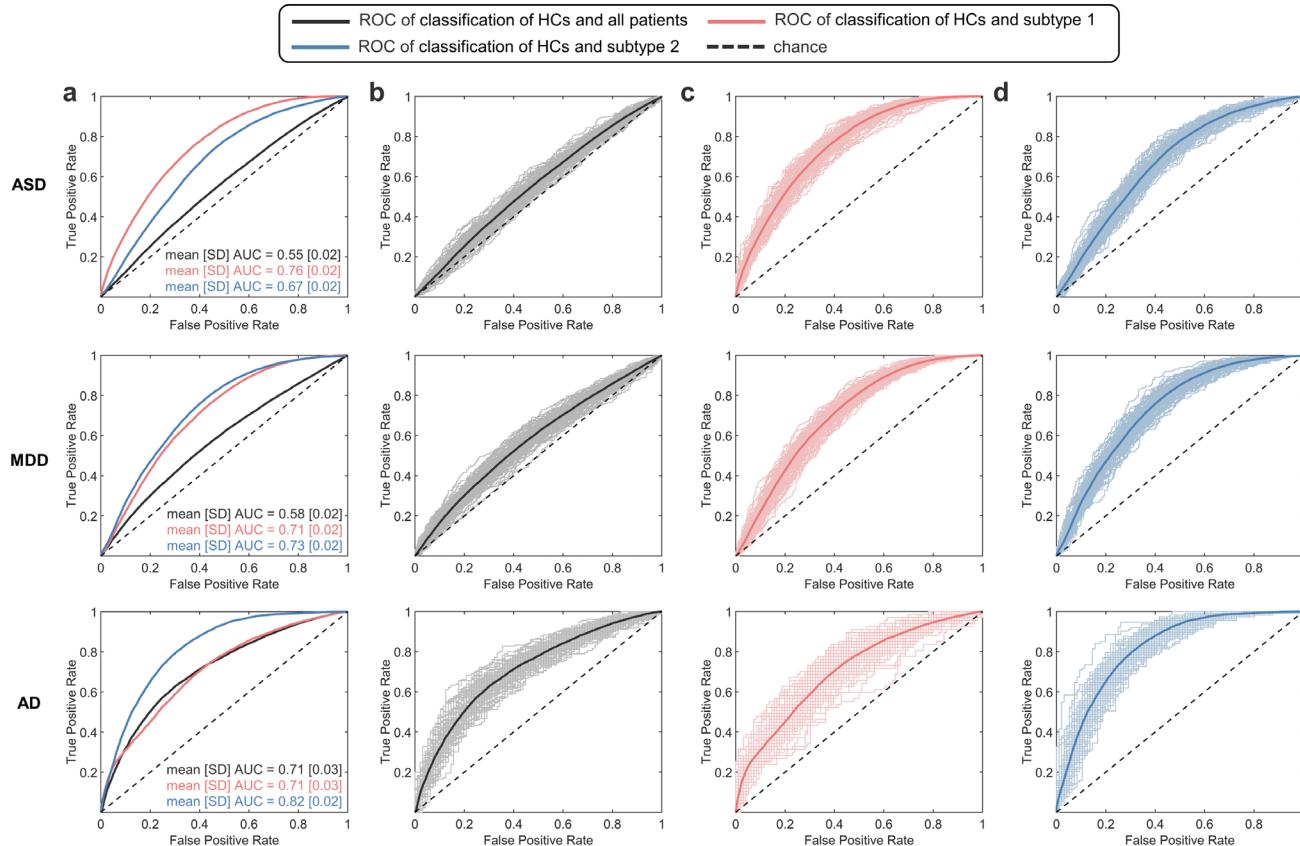
Identifying individual heterogeneity in brain disorders

Subtyping analysis



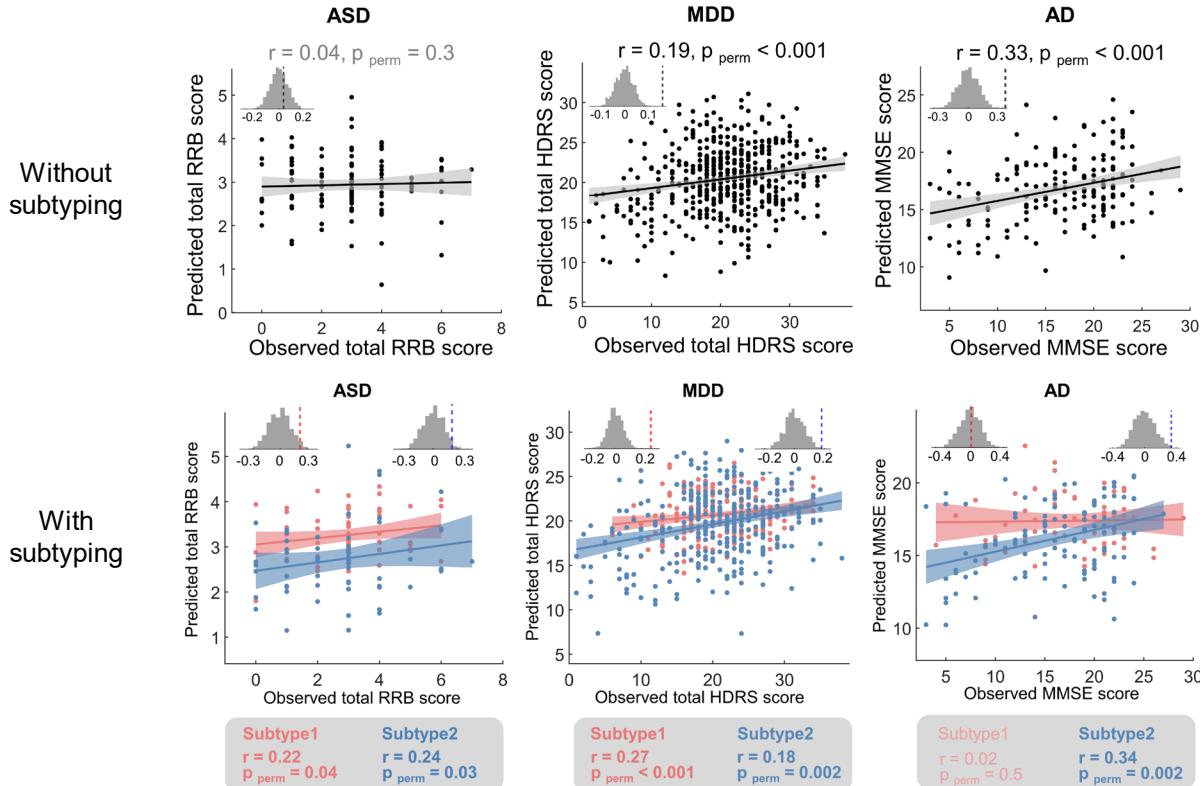
Identifying clinical relevance in brain disorders

Classification analysis



Identifying clinical relevance in brain disorders

Prediction analysis



Summary

- The global mean and variance of functional connectivity show continuous nonlinear changes across the lifespan, peaking in the late of fourth decade and the late of third decade, respectively.
- The default mode and frontoparietal networks undergo more rapid development of system segregation during infancy, childhood, and adolescence, peak later, and decline precipitously during aging.
- The lifespan growth pattern of regional FCS is constrained by its position along the S-A axis, highlighting the role of the S-A axis as a key organizational principle that influences cortical development and aging.
- The connectome-based normative model is useful in capturing individual heterogeneity within the clinical populations, underscoring its potential to advance our understanding of neuropsychiatric disorders.

For more details on this study, please refer to the preprint available at:

<https://www.biorxiv.org/content/10.1101/2023.09.12.557193v2>

Code example

https://github.com/predictive-clinical-neuroscience/NM_educational_OHBM24/tree/main/slot4_Sun

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The Age_ility Project,
The Baby Connectome Project,
The Brain Genomics Superstruct Project,
The Calgary Preschool MRI Dataset,
The Cambridge Centre for Ageing and Neuroscience Dataset,
The Connectivity-based Brain Imaging Research Database,
The Children Brain Development Project,
The Developing Human Connectome Project,
The Disease Imaging Data Archiving: major depressive disorder Working Group
The Human Connectome Project,
The Lifespan Human Connectome Project,
The Multi-center Alzheimer Disease Imaging (MCADI) Consortium,
The Nathan Kline Institute-Rockland Sample Dataset,
The Neuroscience in Psychiatry Network Dataset,
The Pediatric Imaging, Neurocognition, and Genetics Data Repository,
The Pixar Dataset,
The Strategic Research Program for Brain Sciences Dataset,
The Southwest University Adult Lifespan Dataset,
The Southwest University Longitudinal Imaging Multimodal Brain Data Repository,
The UK Biobank Brain Imaging Dataset,

Thanks!