Functional Connectivity Development Reproducibly Aligns with and Enhances Hierarchical Cortical Organization

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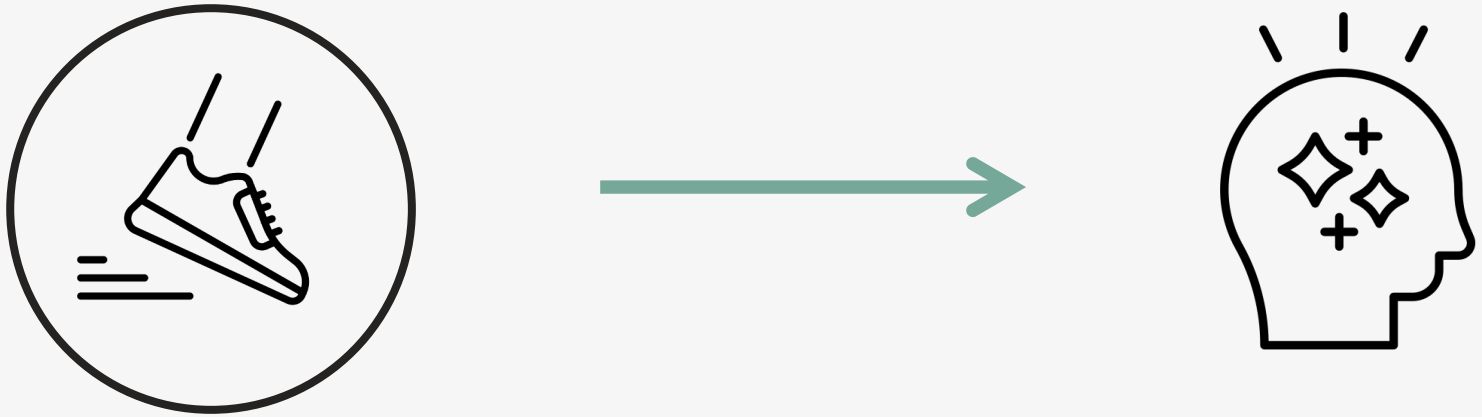
Outline

The Project

The Process

Background



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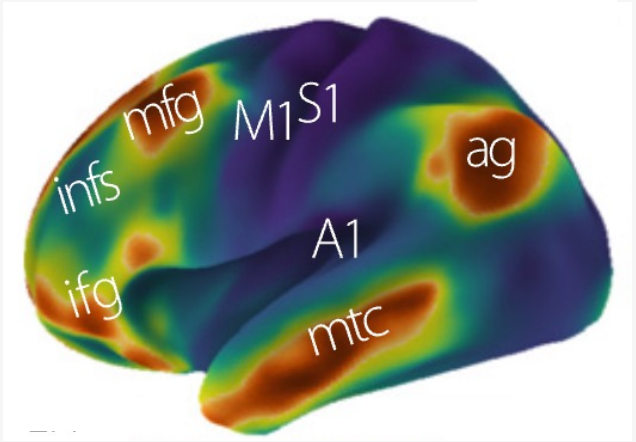

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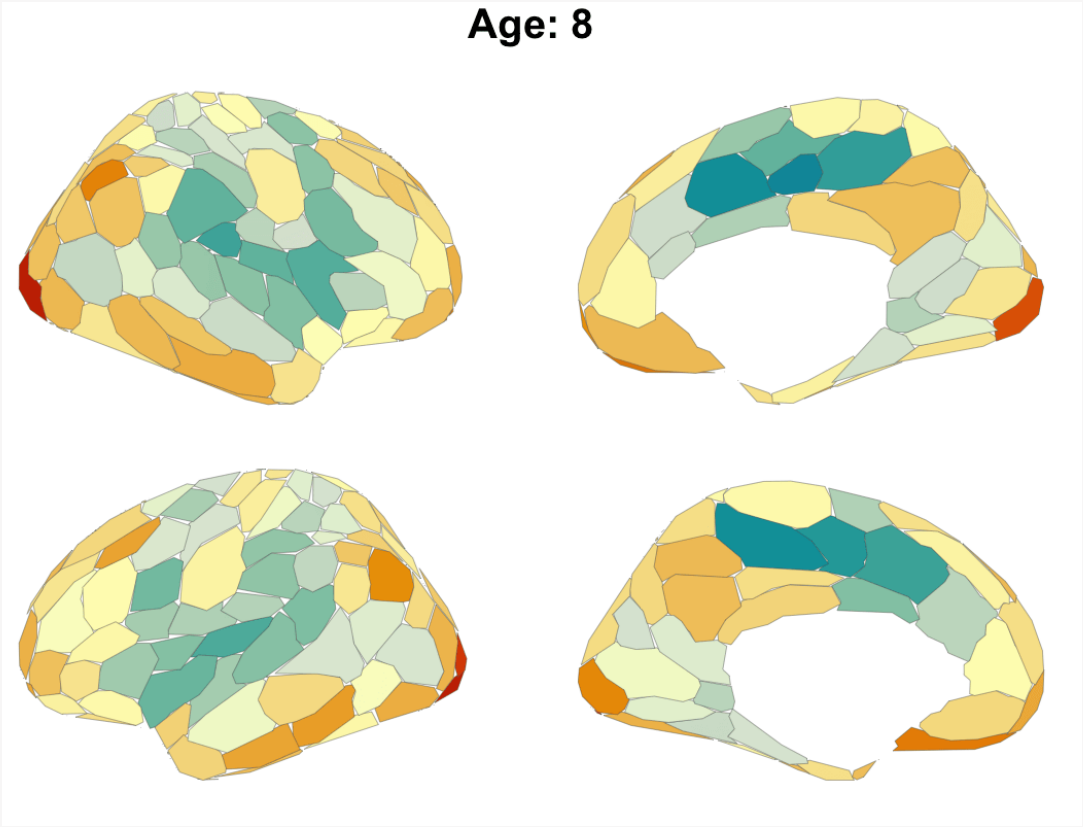

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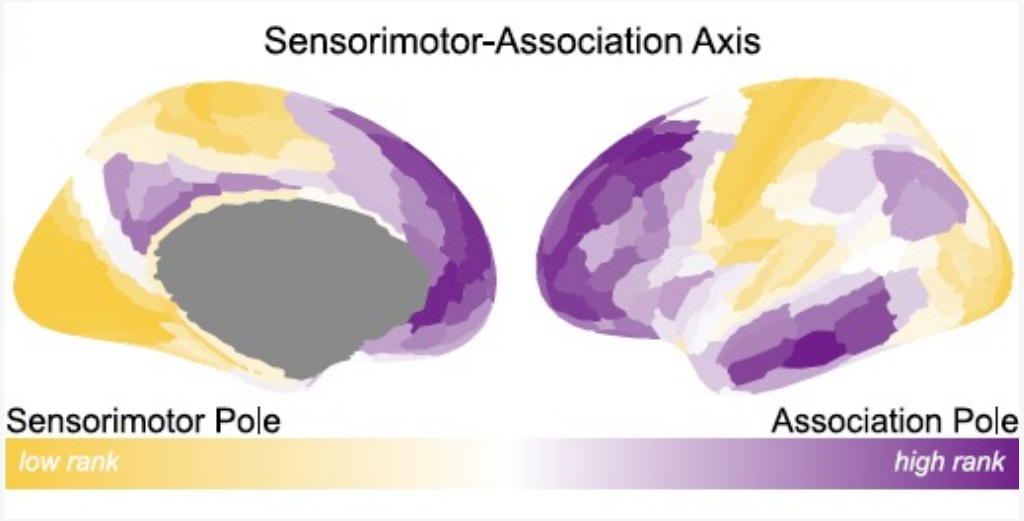
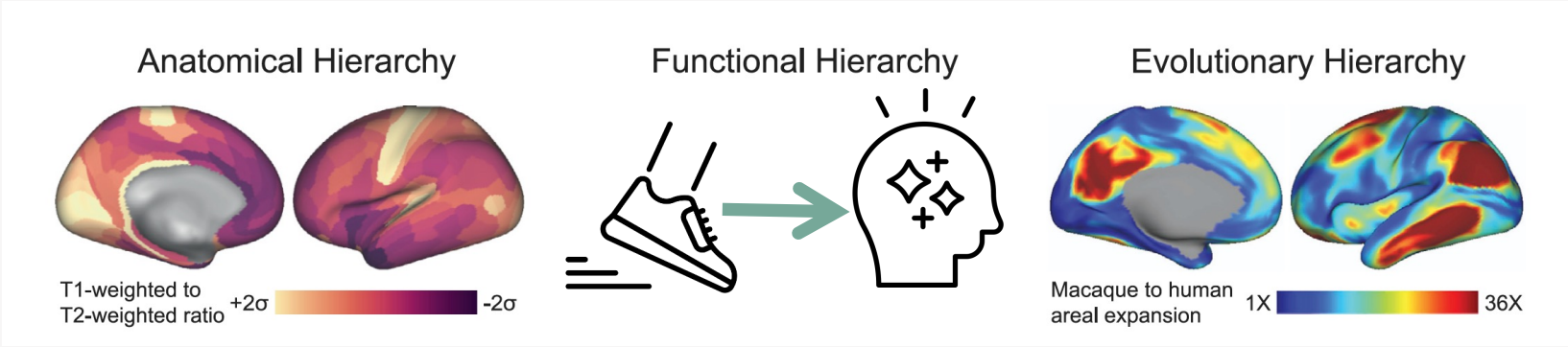
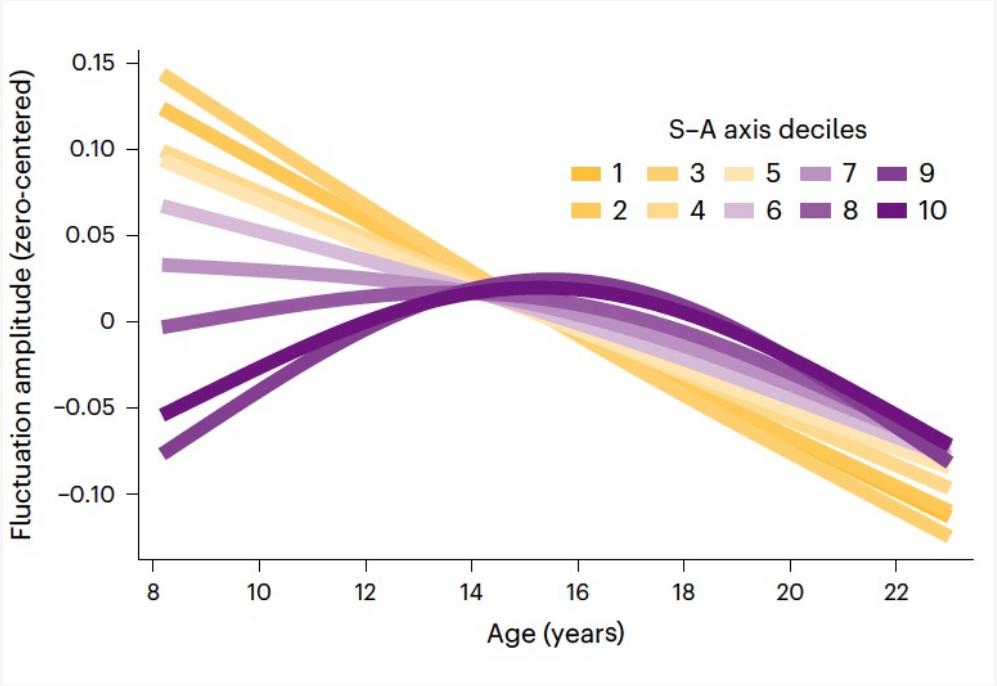
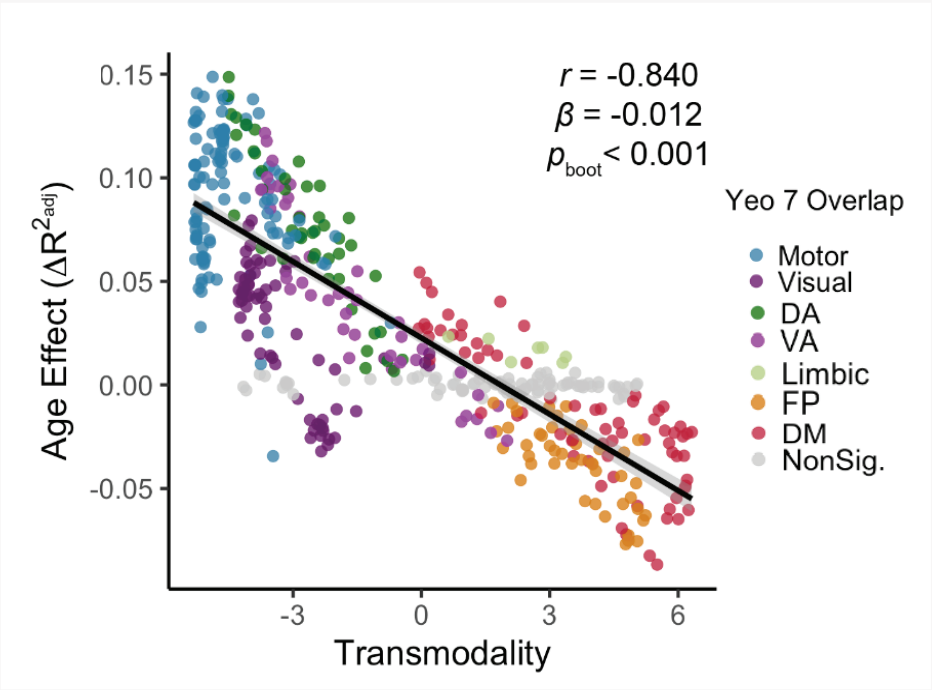




Sydnor, 2021

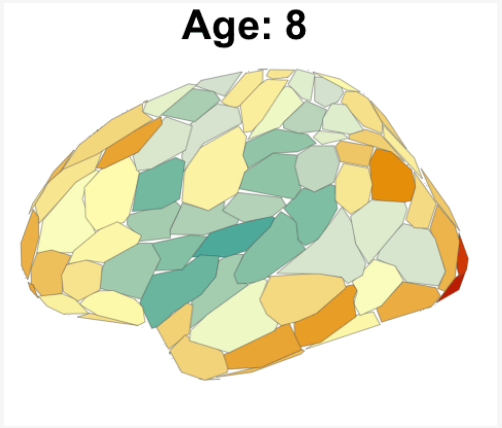
Background



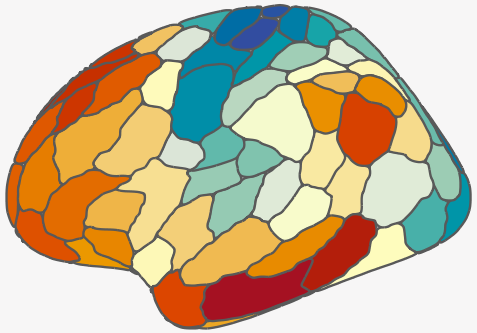


Sydnor, 2021; Pines, 2022

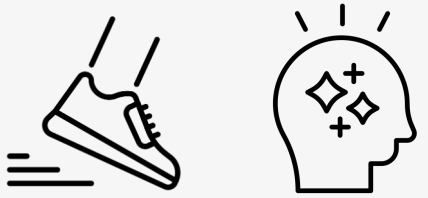
Background



Hierarchical development



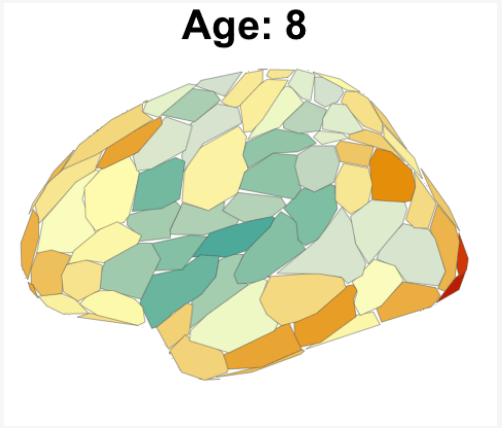
Hierarchical functional connectivity



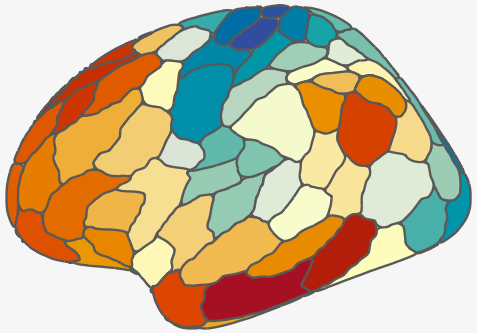
Hierarchical brain functions

Hypothesis: Functional connectivity develops hierarchically across the cortex

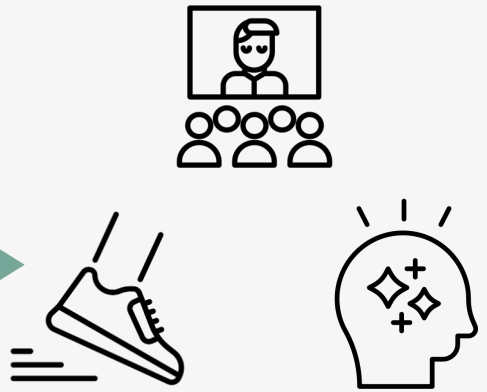
Background



Hierarchical development



Hierarchical functional connectivity



Hierarchical brain functions

Development of functional connectivity diverges across the S-A axis, with unimodal sensorimotor cortices increasing in connectivity and transmodal association cortices tending to weaken in connectivity

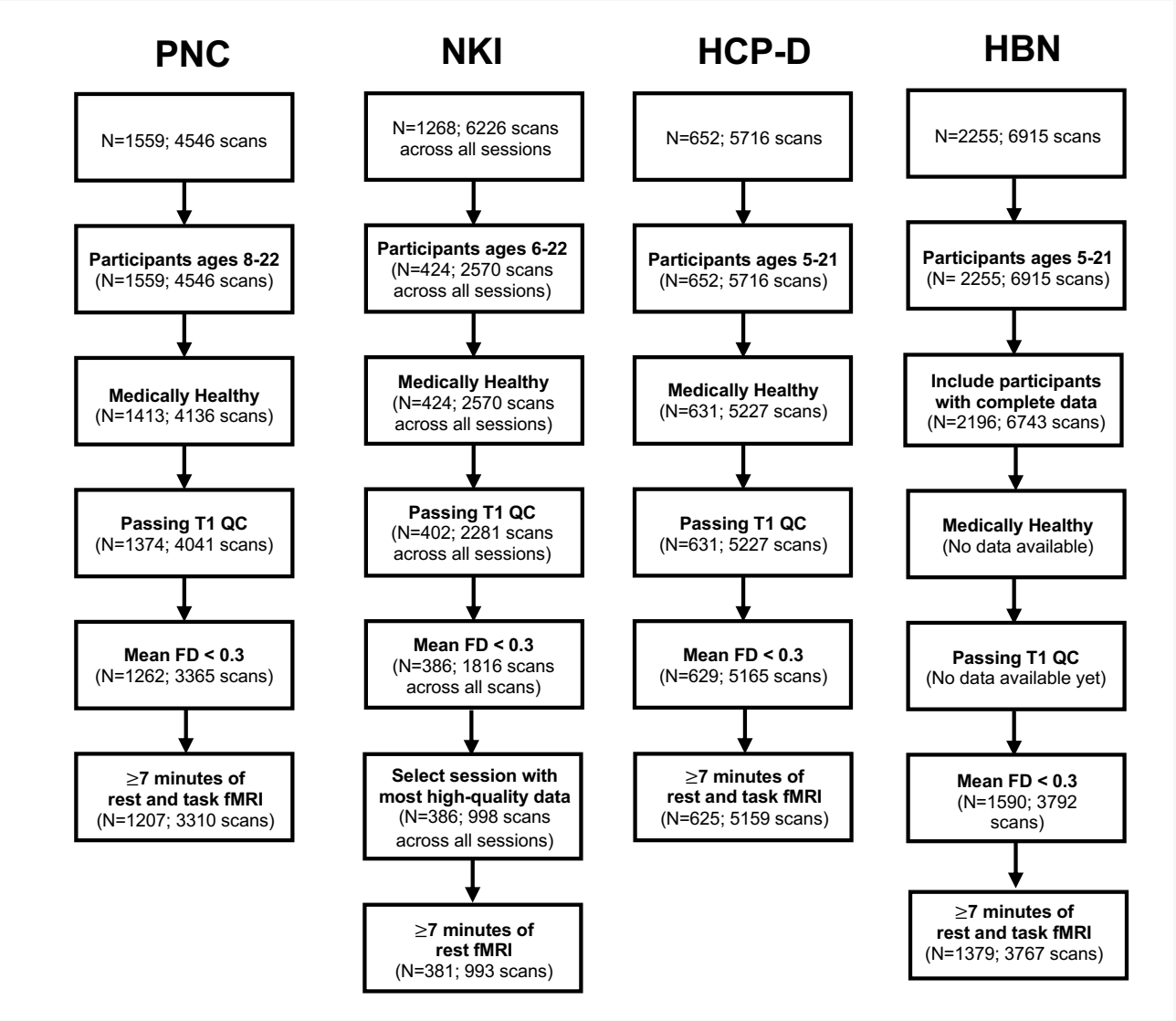
Methods: *Datasets*

PNC: Philadelphia Neurodevelopmental Cohort
HCP: Human Connectome Project: Development
NKI: Nathan Kline Institute-Rockland
HBN: Healthy Brain Network

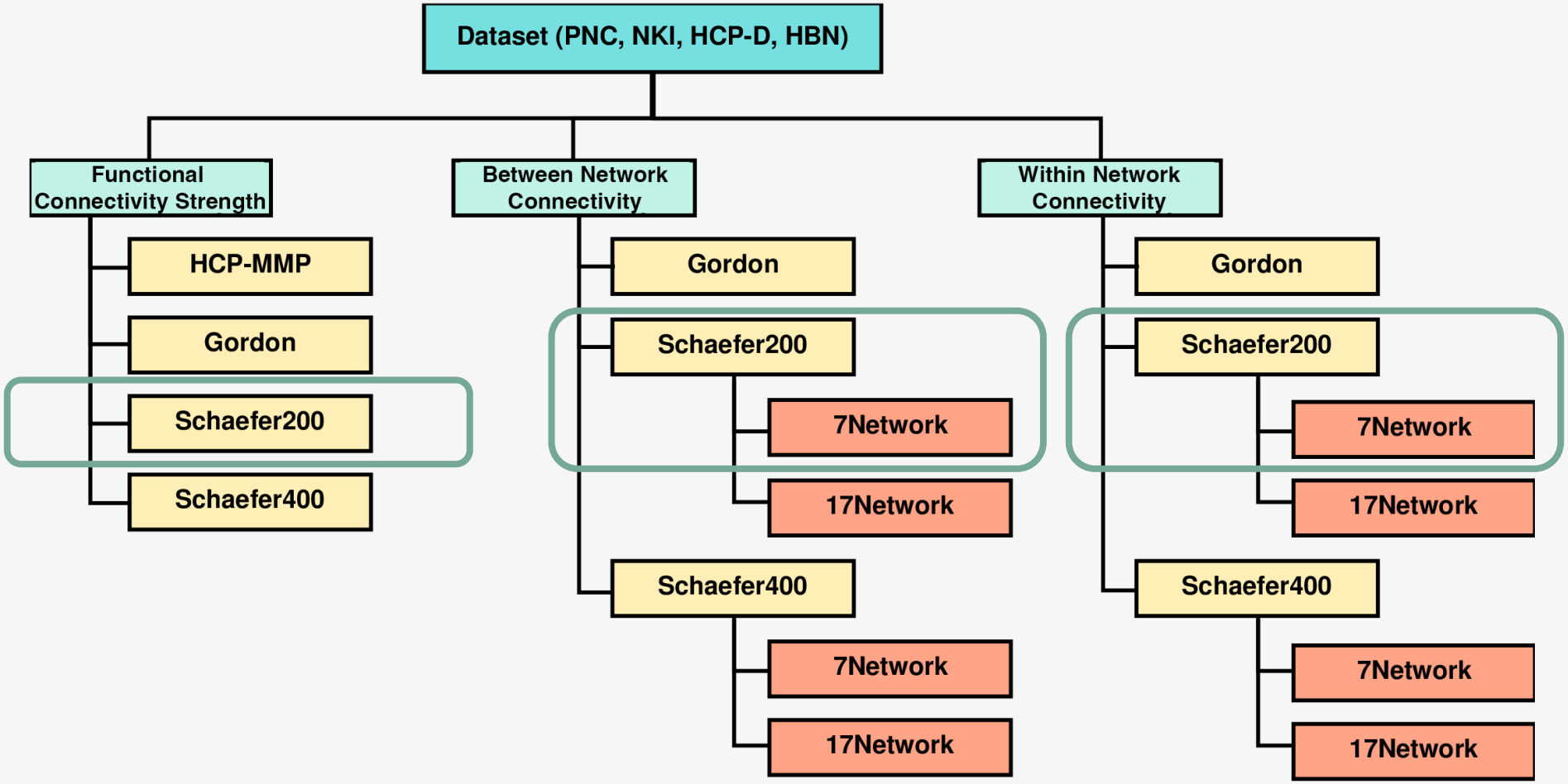
	Discovery
	PNC
N	1207
Age	8-22
Exclusion Criteria	1) presence or hx of abnormal brain struc
fMRI scan type	Rest + Task

Methods:

Sample Selection

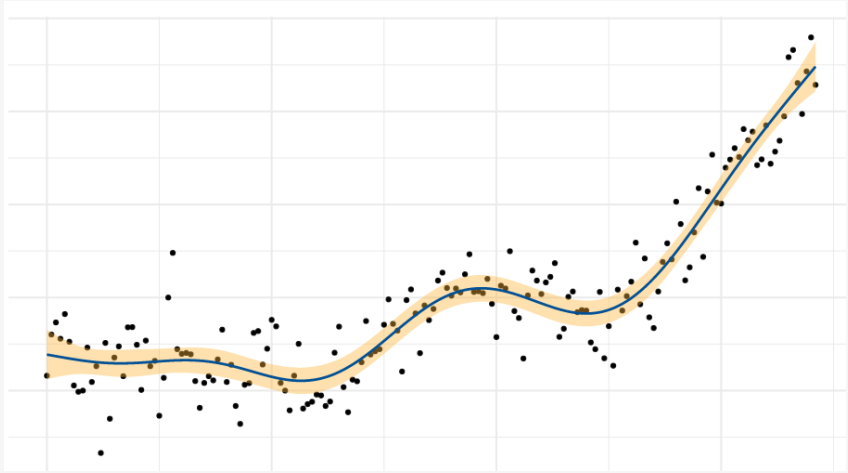


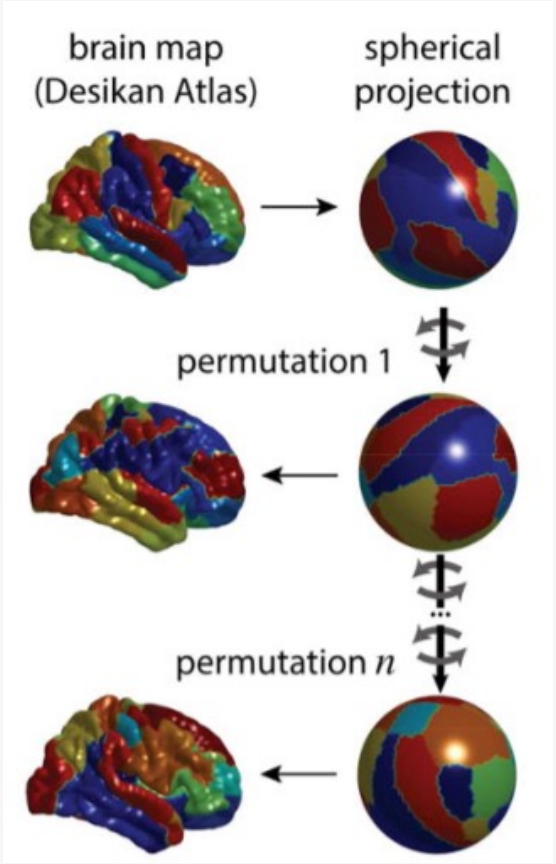
Methods: *Parameters*



Methods: *Modeling Developmental Change*

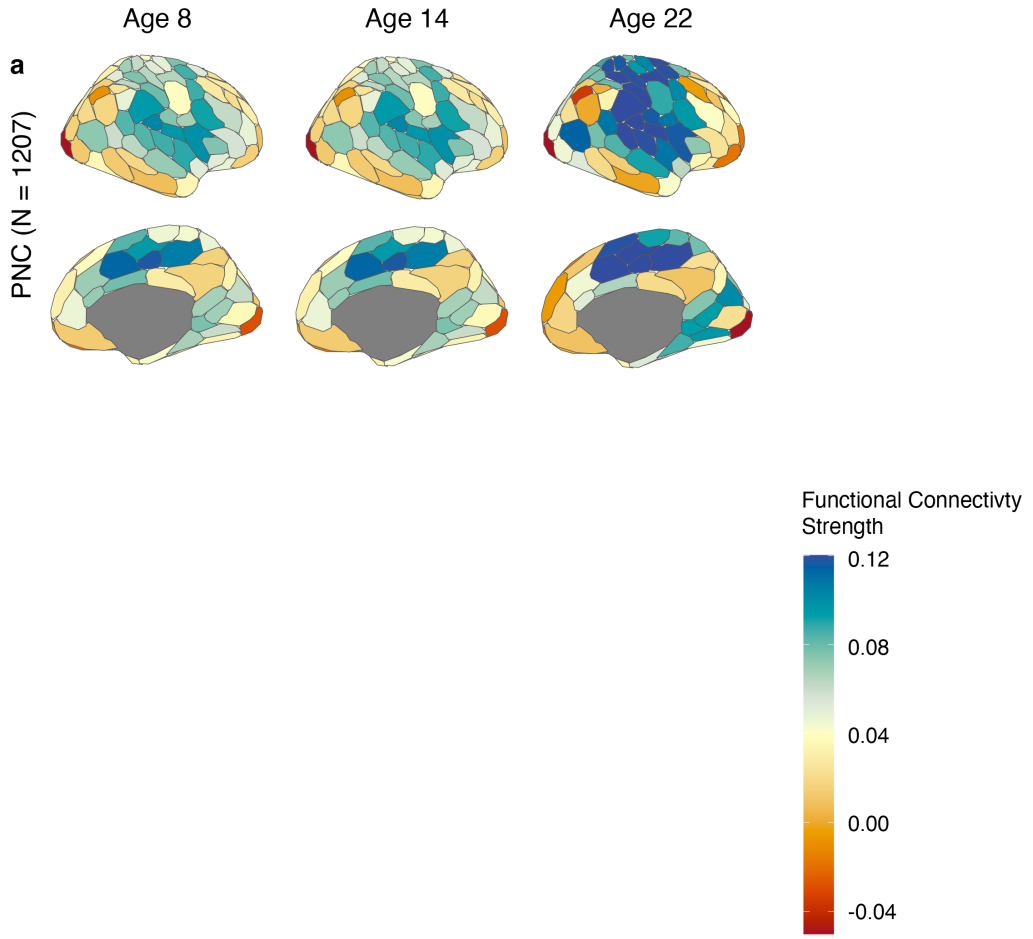
- GAMs
  - **Magnitude of age effect**: change in adjusted R^2 between a full model and reduced model with no age term.
- Spin-based spatial permutation tests





$$Functional\ Connectivity \sim s(age) + \beta_{sex} + \beta_{motion}$$

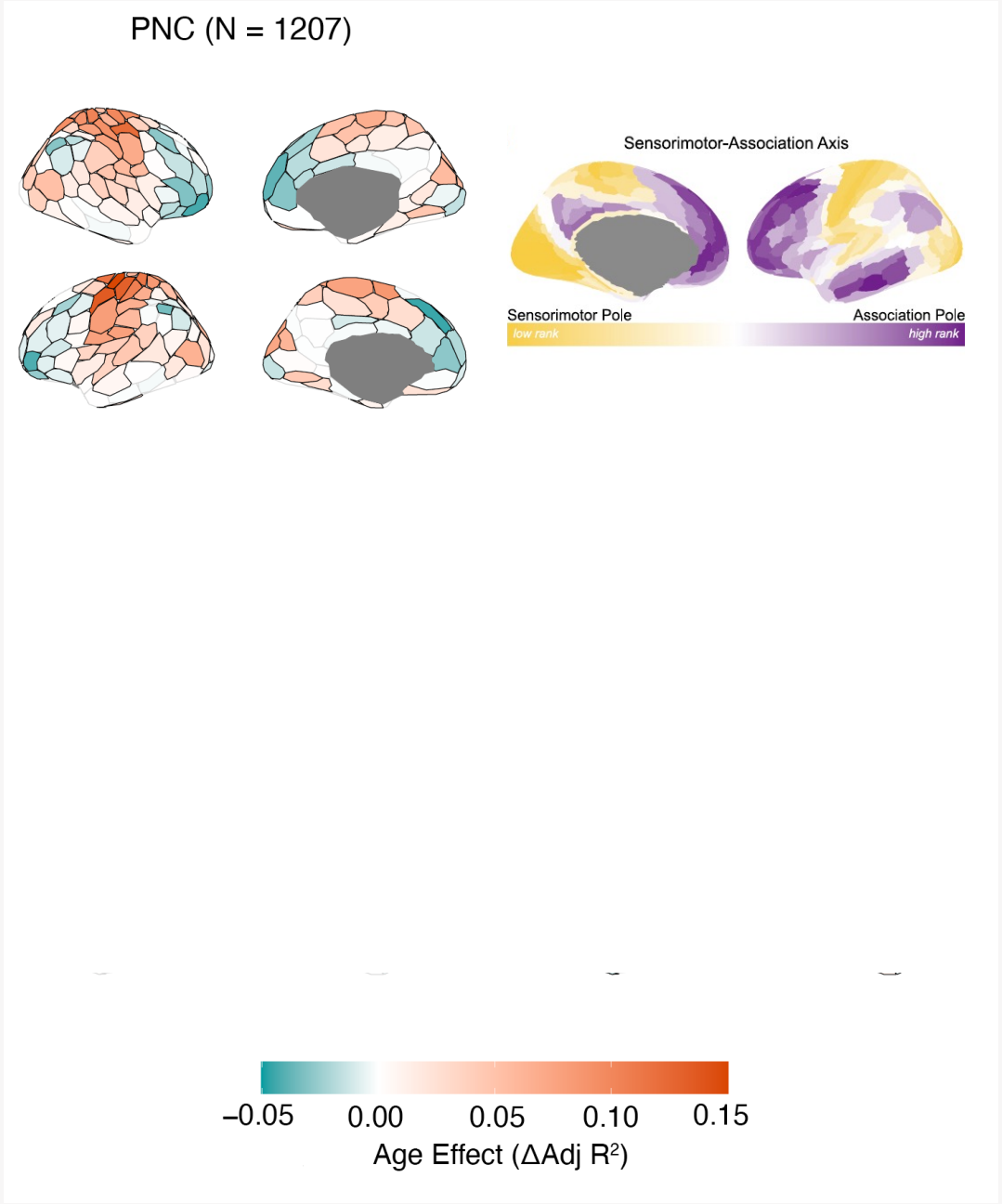
Bloch, 2018; Gavin Simpson, 2022 Physalia GAMs Workshop



Results

The spatial distribution of functional connectivity strength

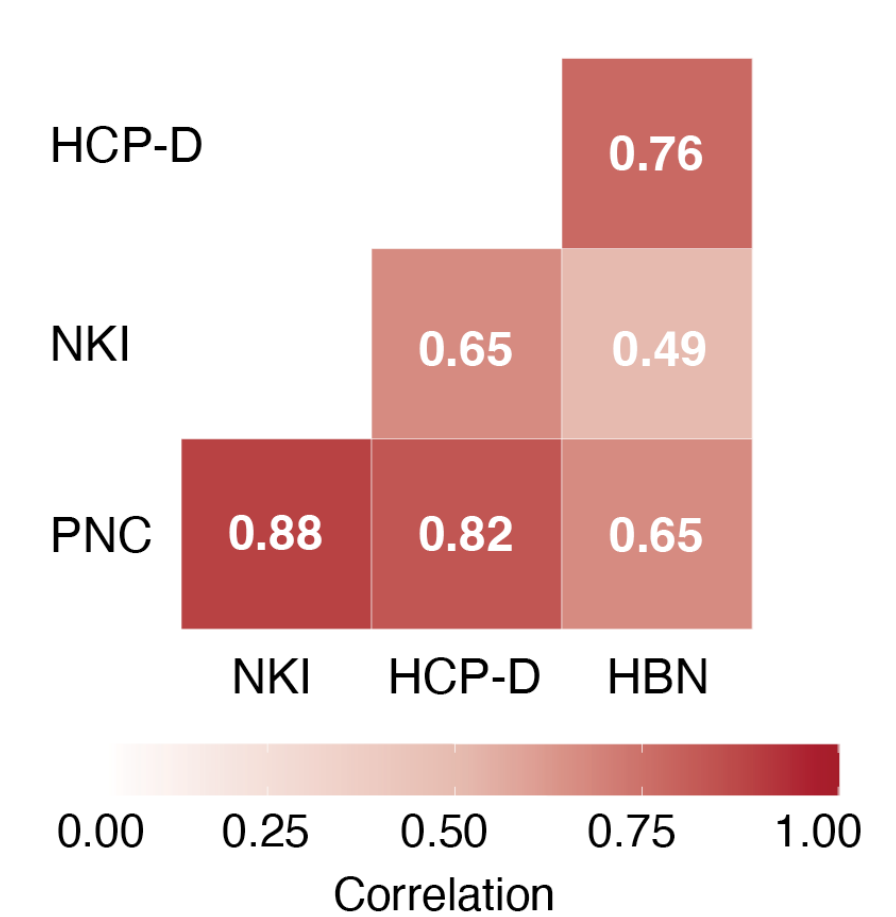
- Resembles the S-A axis
- Is refined with age



Results

The spatial distribution of functional connectivity strength *age effect*

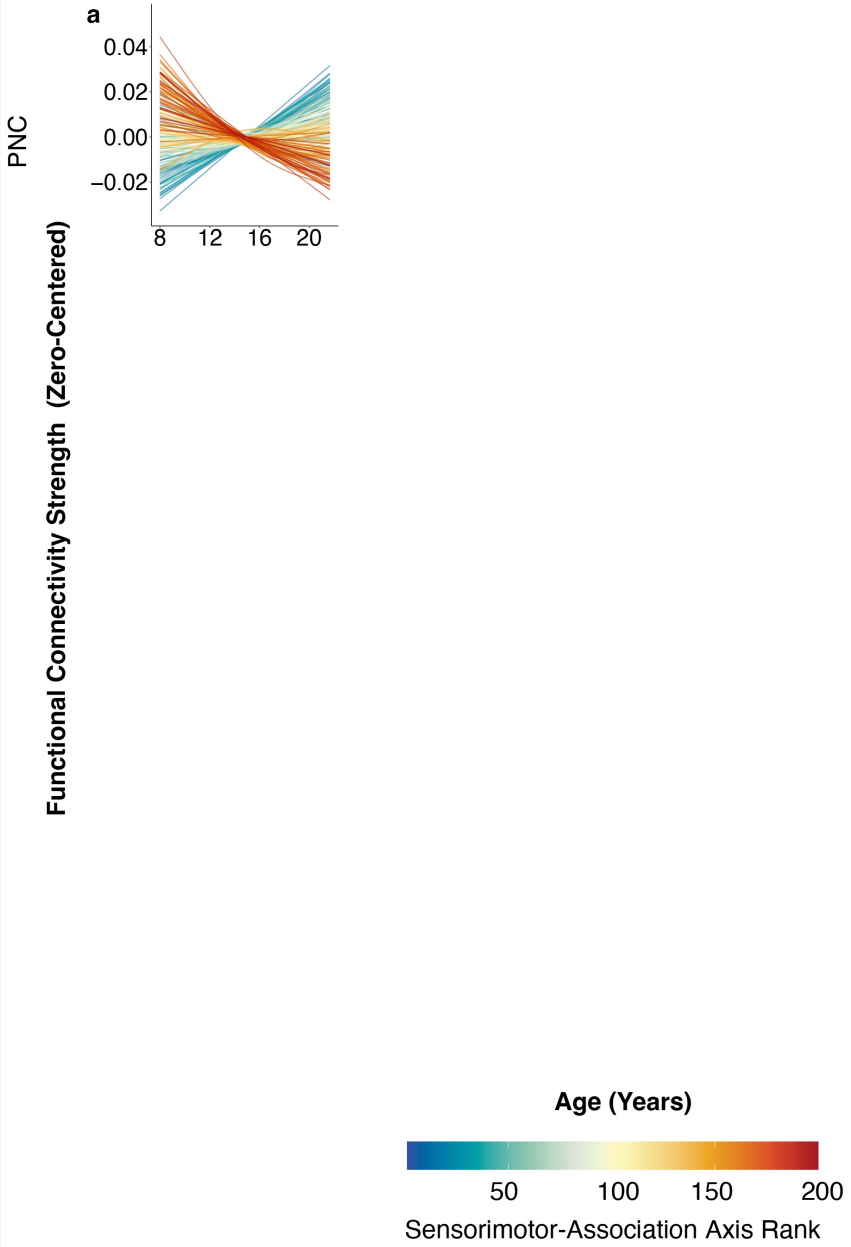
- Resembles the S-A axis



Results

- Spatial correlations between FC strength age effects for each pair of datasets ranged from 0.49-0.88 (mean correlation = 0.71)
- Remarkably high consistency in age effects across the four independent datasets

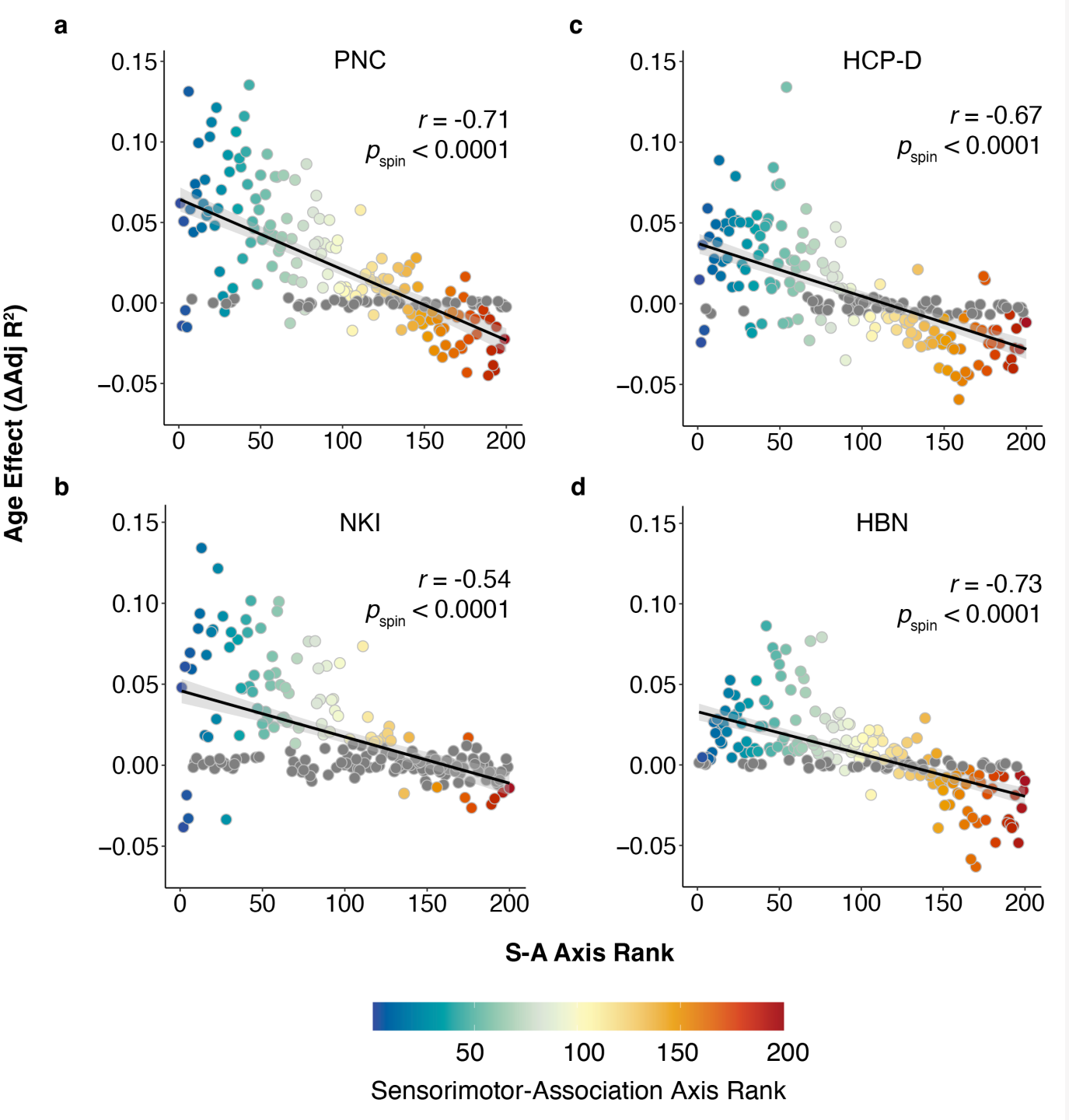
THE PROJECT



Results

- Functional connectivity neurodevelopment exhibits continuously varying patterns of developmental trajectories along the S-A axis.

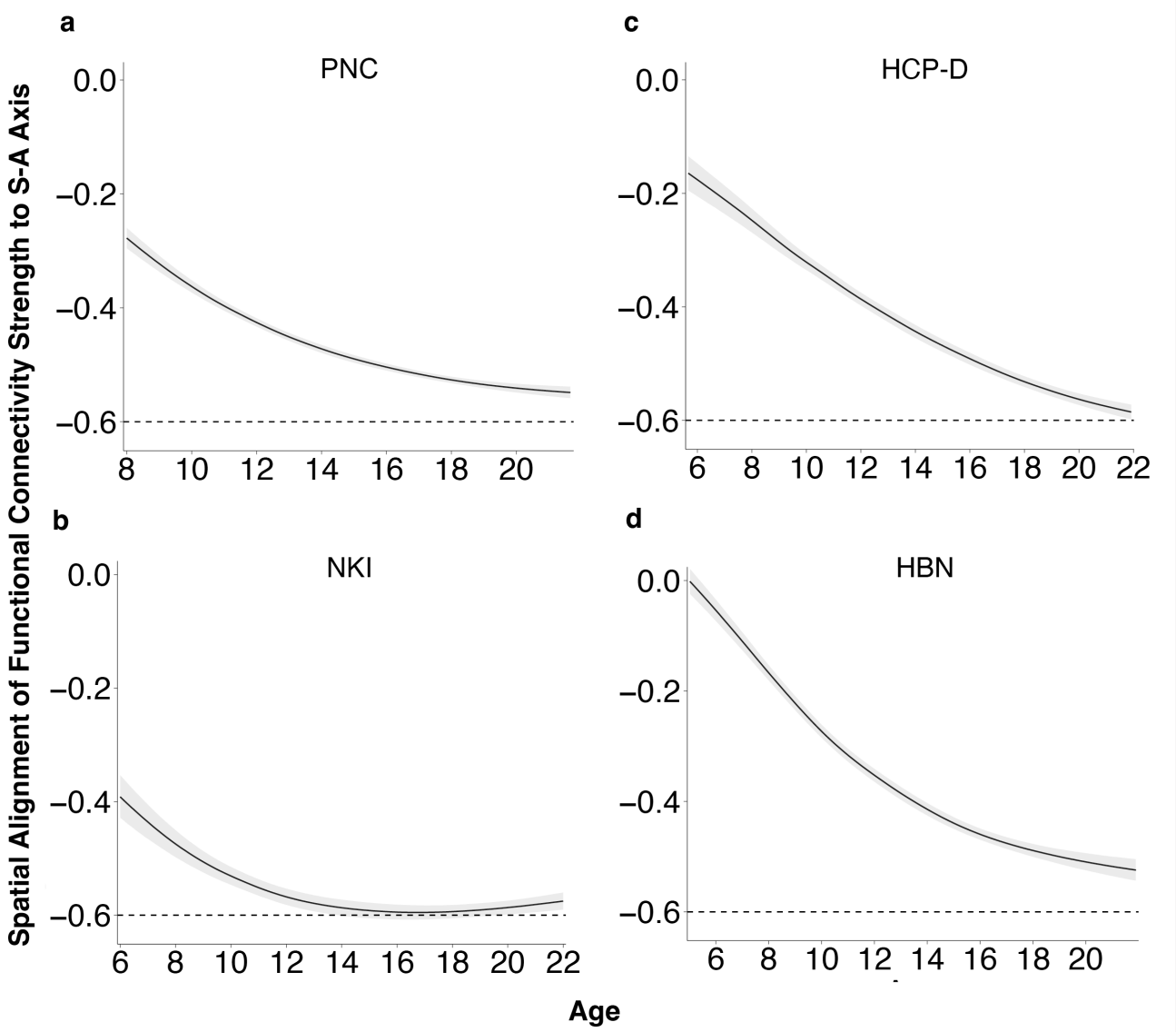
THE PROJECT



Results

- Developmental change in functional connectivity strength significantly aligns with the sensorimotor-association axis

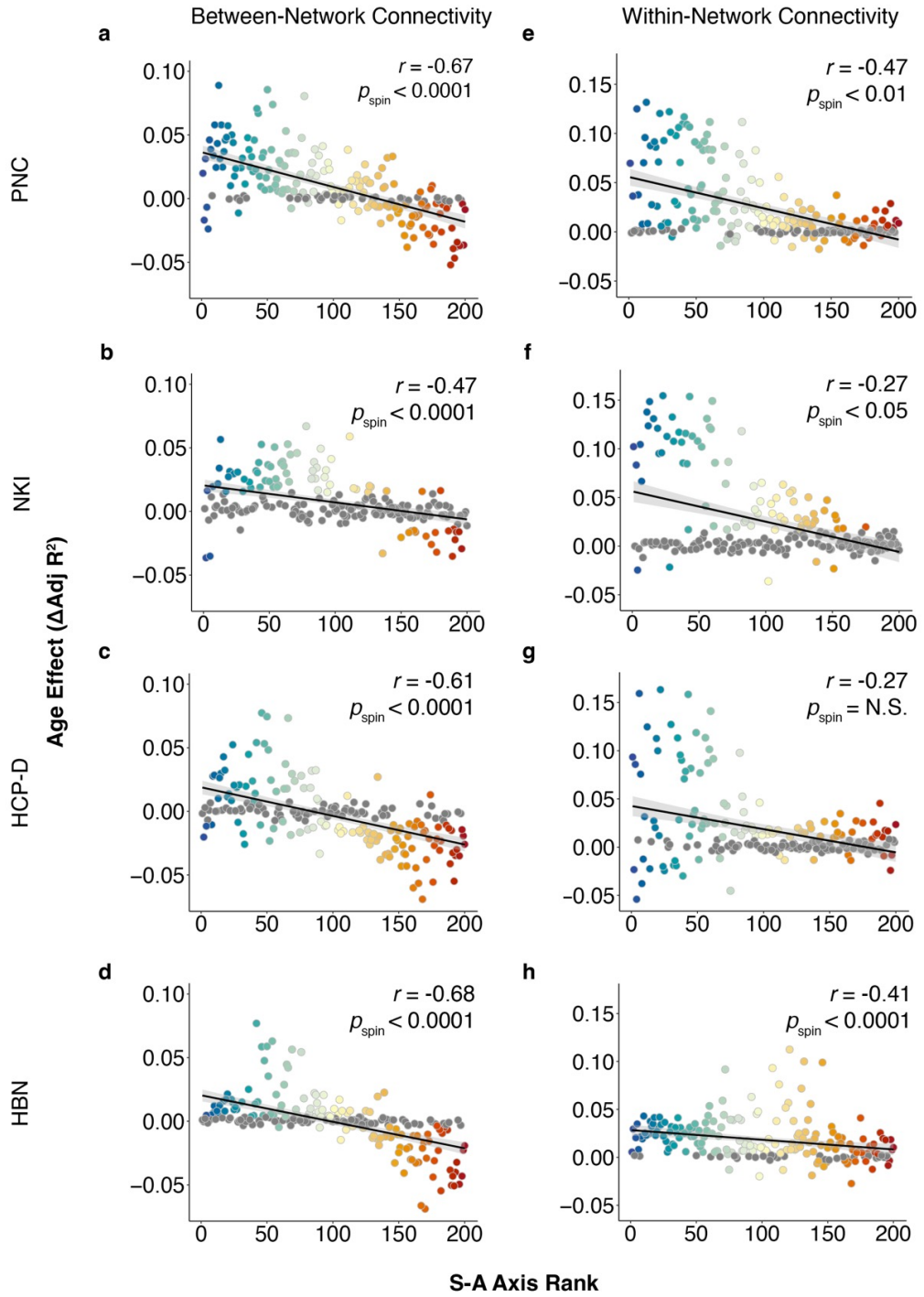
THE PROJECT



Results

- The spatial distribution of functional connectivity strength increasingly aligns with the sensorimotor-association axis with age.

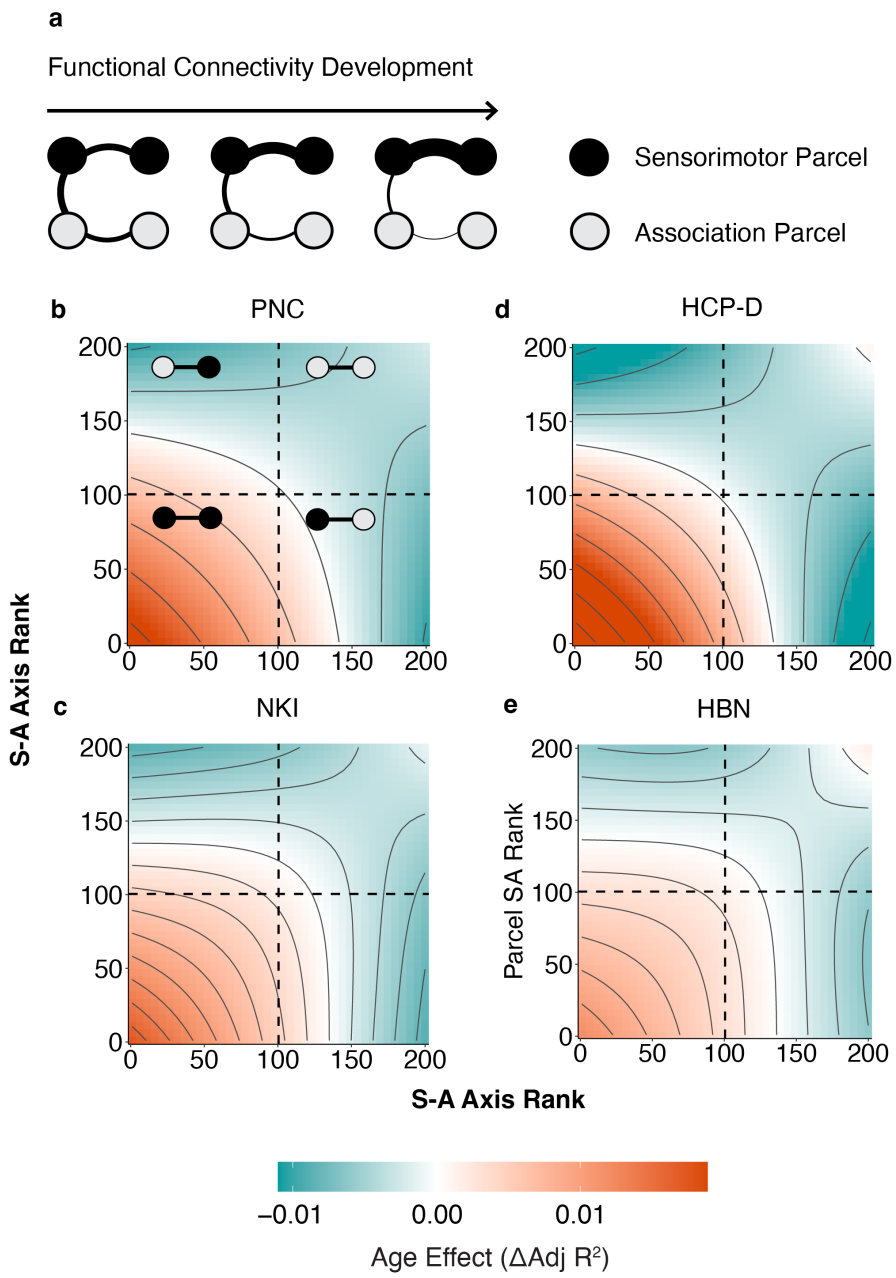
THE PROJECT



Results

- SM cortices generally increase in connectivity
- Association cortices are segregating
  - Segregation is driven by decreases in between-network connectivity.

THE PROJECT



Results

- Edge-level age effects confirm divergent connectivity refinement along the sensorimotor-association axis.

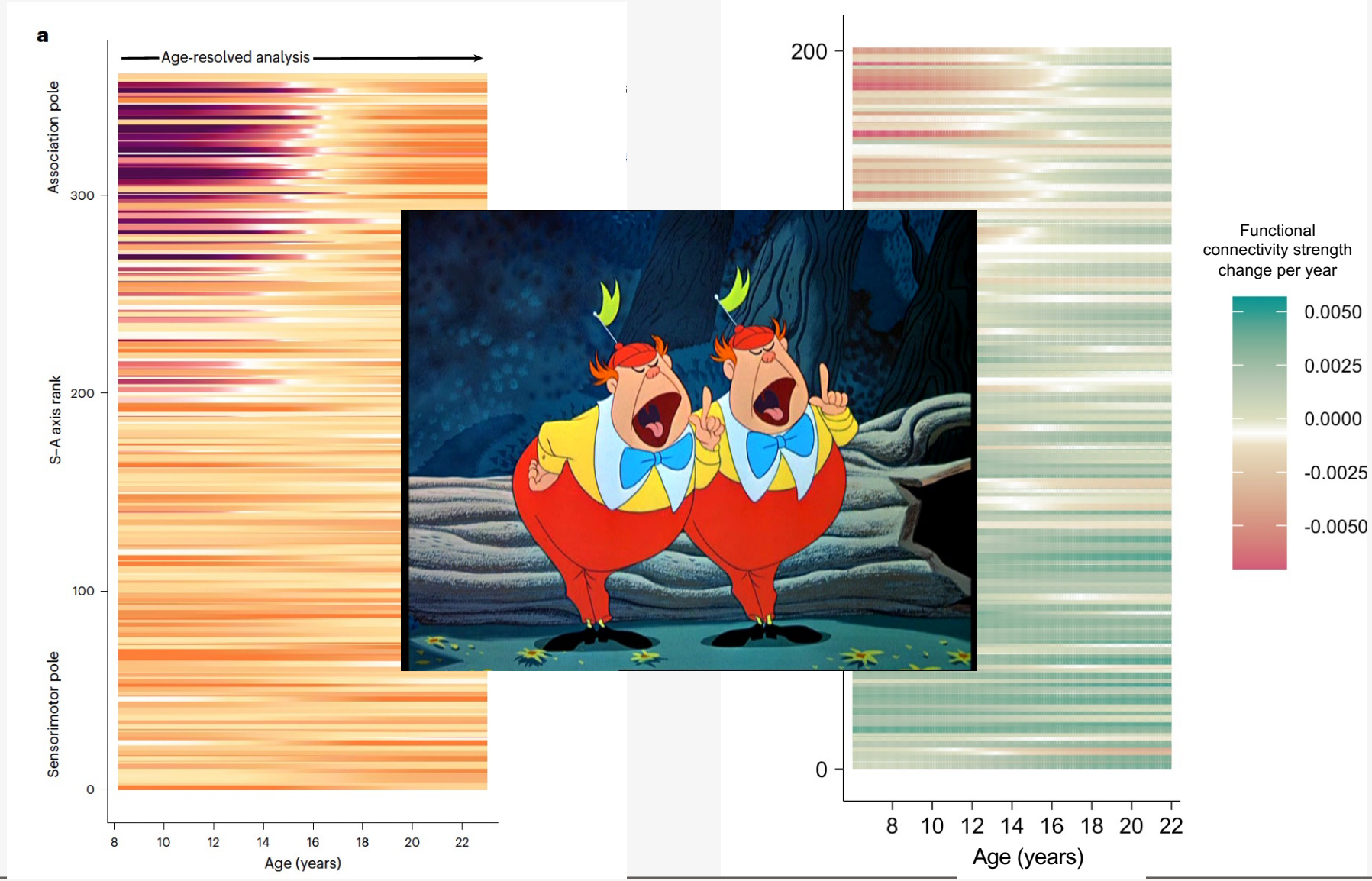
THE PROJECT

Conclusions

- Robust evidence from four large-scale, independent datasets that functional connectivity is refined hierarchically in development along the S-A axis
  - S-A axis encodes the dominant pattern by which cortico-cortical functional connectivity develops
- Differentiation of connectivity across the S-A axis may lead to developmental strengthening of the cortical hierarchy

Future Directions

- Why does association cortex decrease in functional connectivity strength? (especially given that we know association cortices' WM tracts have protracted development/myelination)
- Relationship between functional connectivity strength and ALFF?



Sydnor, 2023

THE PROJECT

Future Directions

- Why does association cortex decrease in functional connectivity strength? (especially given that we know association cortices' WM tracts have protracted development/myelination)
- Relationship between functional connectivity strength and ALFF?
- How do functional and structural brain development jointly shape the cortical hierarchy?

Outline

The Project

The Process

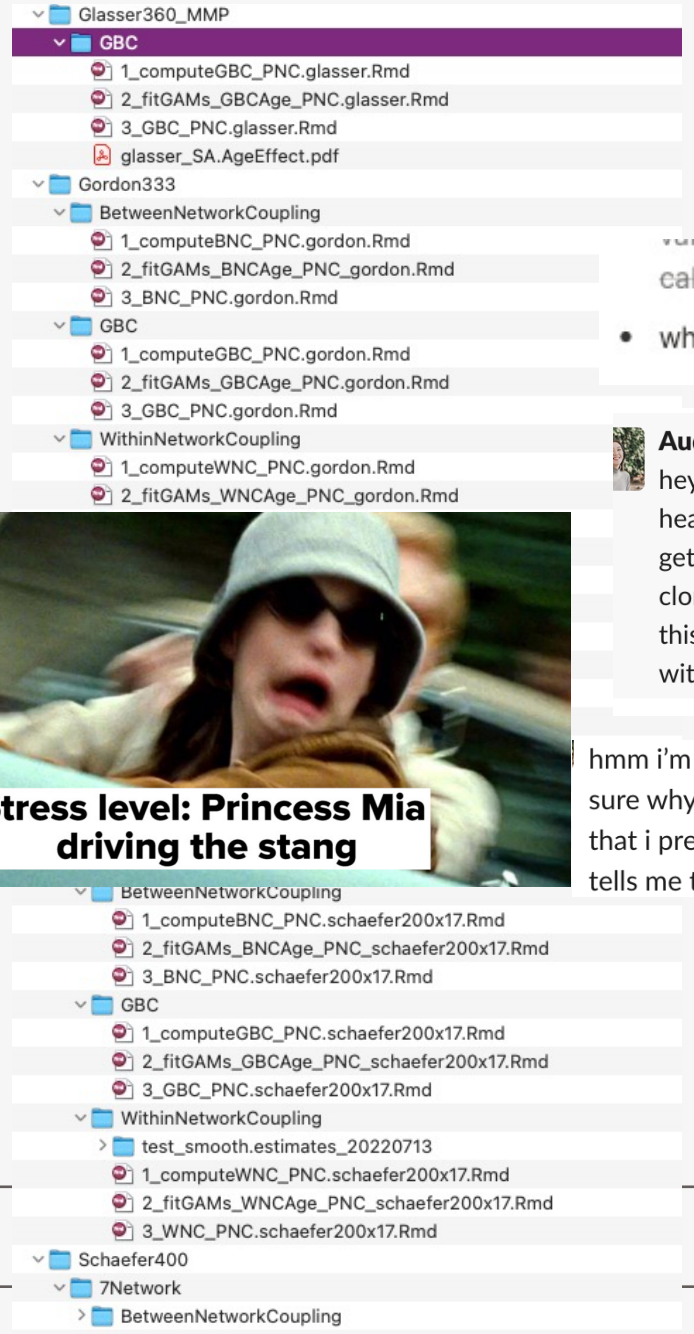
How it started...

How does one write a function

```
for(i in c(1:length(atlases))){
```

I'm confused but idk how to even formulate my question lol

sorry i just finished talking to chenying about building docker containers bc i can't freaking install tidyverse on cubic and docker is a workaround, and my brain is kind of melting 😂



One subfolder of 1 dataset 😬

calls GAM_functions.R)

- why is age the smoothing variable? what exactly does that do?

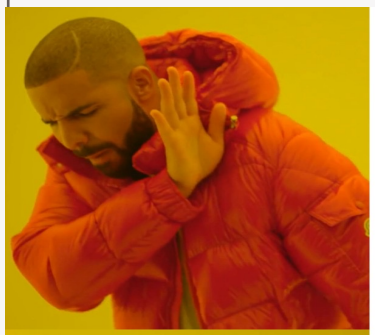
Audrey Luo 2:15 PM
hey sydney! not urgent at all but just wanted to give you a heads up that i'm having the same issues with my datalad get just hanging for a SUPER long time with the PNC clone. i can't datalad get even a single .csv file. Not sure if this is related to issues over the summer. I had no issues with HCP-D!

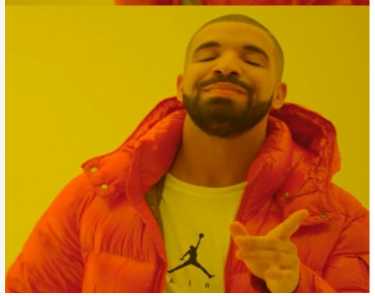
hmm i'm still having problems with installing datalad! not sure why it's giving me so many issues this time. i'm seeing that i previously did `sudo apt-get install datalad` which tells me that "EnvironmentNotWritableError: The current

Audrey Luo 4 months ago
ahh @Sydney Covitz datalad get is just hanging again - similar to my issues before 😞 couldn't even get a csv file. i wouldn't have to use git annex like last time with pnc right? (edited)

THE PROCESS

How it's go



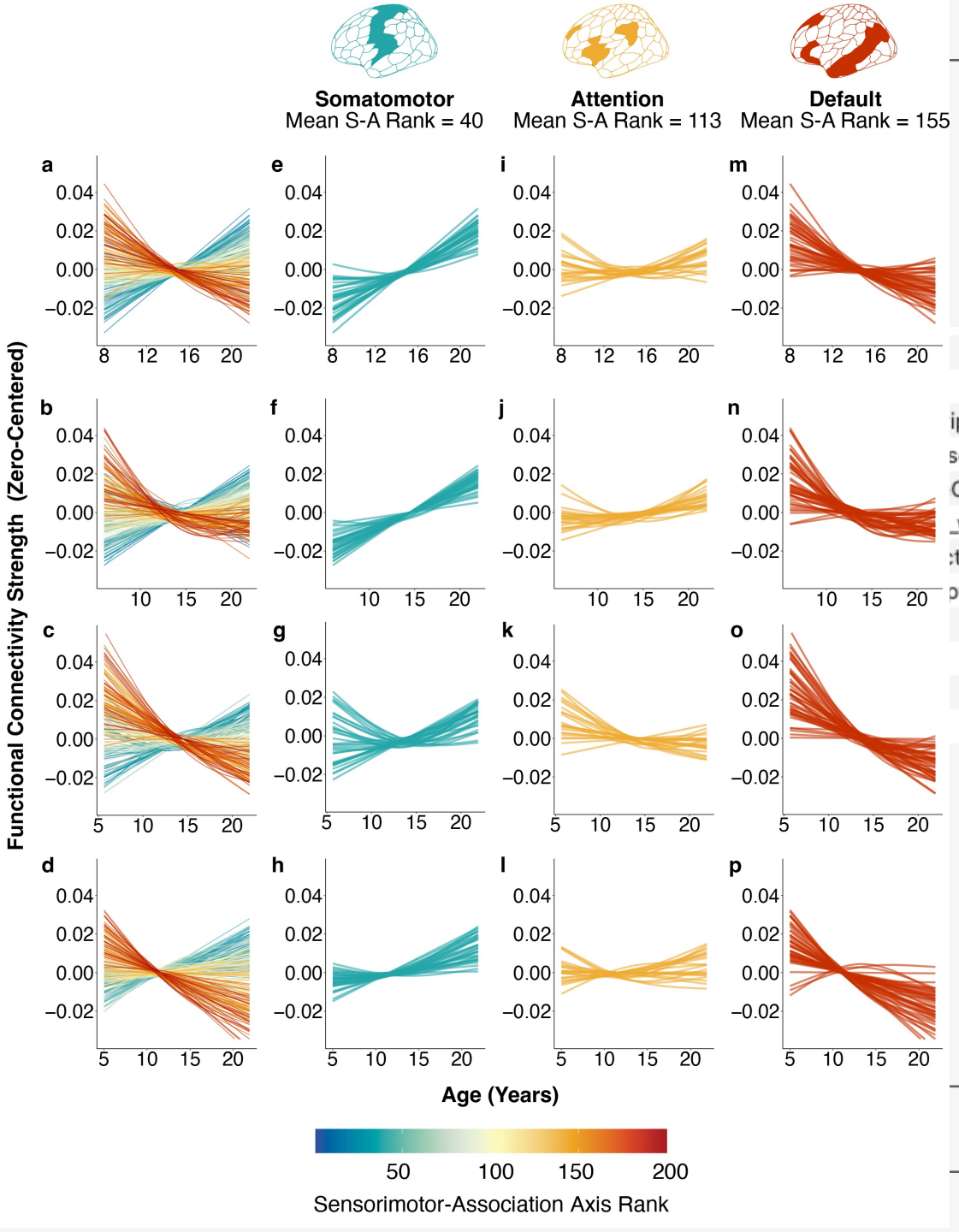



```
# Function for estimating GAM smooths based on model-predic
# @param parcel.labels A vector of parcel labels
# @param metric A character string of connectivity metric (
# @param atlas_name A character string of atlas
# @param network_parcellation A character string for schaef
# @param dataset_name A character string of dataset (e.g. "
estimate_GAMsmooths <- function(parcel.labels, metric, atla
  parcel.labels <- parcel.labels$label
  gam.smooths <- matrix(data=NA, ncol=7) #empty matrix to s
  colnames(gam.smooths) <- c("age","fit","se.fit","selo","s

  for(row in c(1:length(parcel.labels))){ #for each region

    region <- parcel.labels[row] #get the region name
    GAM.SMOOTH <- gam.predsmooth(measure = metric, atlas =

    preddata <- as.data.frame(GAM.SMOOTH[3]) #get predicted
    preddata$index <- rep(x=row, 1000) #region index
    preddata$label <- rep(x=GAM.SMOOTH[1], 1000) #label
    gam.smooths <- rbind(gam.smooths, preddata)
```



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tFigures_withCovbat.Rmd
pts

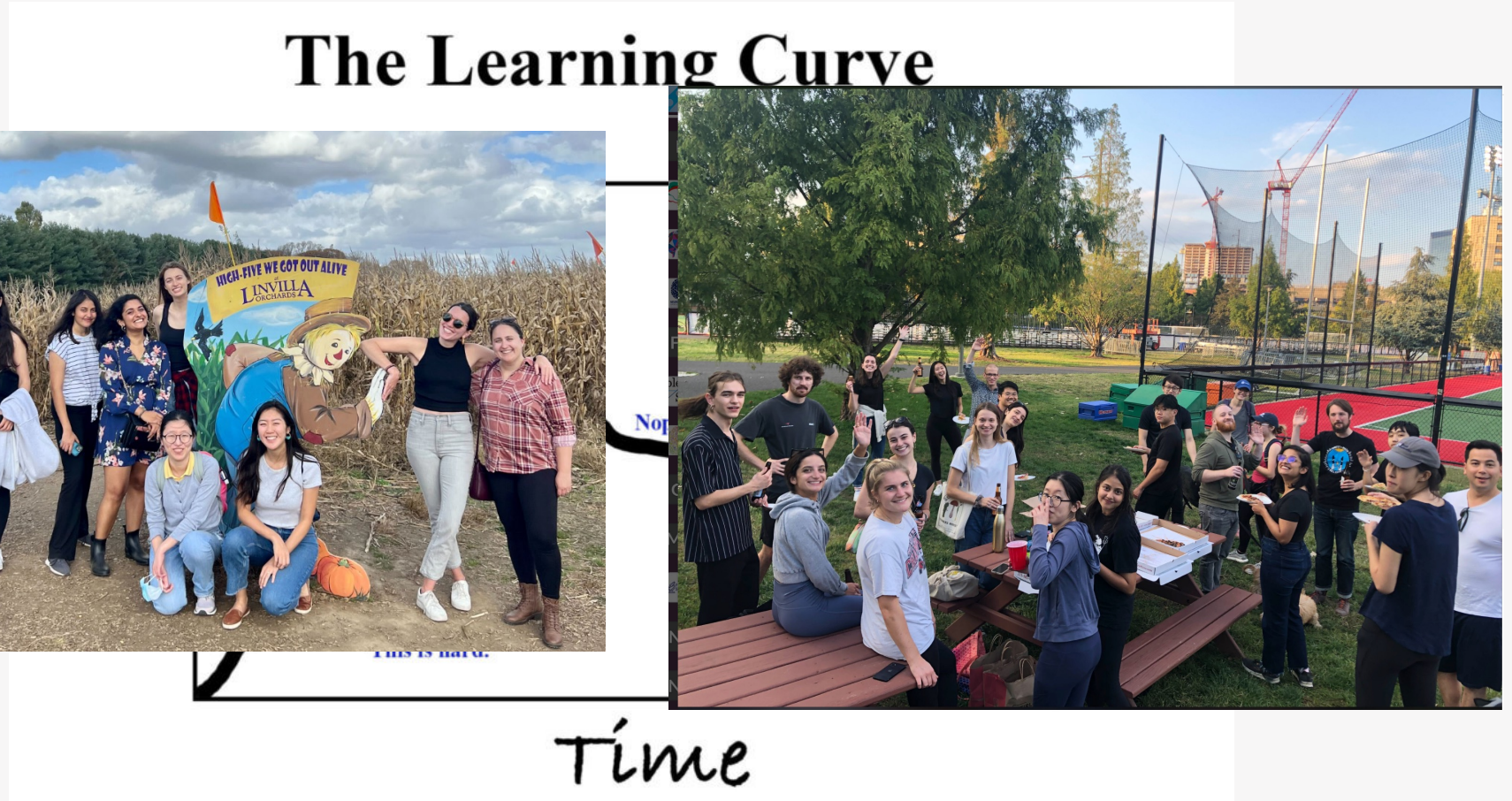
THE PROCESS

How it’s going

How it's going

- Didn't know how to write a function or the benefits of writing functions…so wild
- How to organize a project folder for analyses in 4 different datasets
  - How to organize project for even 1 dataset lol
- Submitting jobs in R – didn't know how to do it, didn't know people who've done it in our lab. But I'm an R girl
- Github, Docker, Singularity
- Covbat harmonization
- Importance of sample selection and doing it early/clearly
- Preregistration
- Writing the manuscript
  - Importance of reading
  - Consolidating and writing concisely with clear narrative and framework + putting my money on the table for interpretations/conclusions/what to include (i.e. middle axis discussion), being ok with being told I'm wrong (lol)

How it's going



Acknowledgements

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- Golia Shafiei
- Taylor Salo
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  Andrew Chen and Fengling Hu