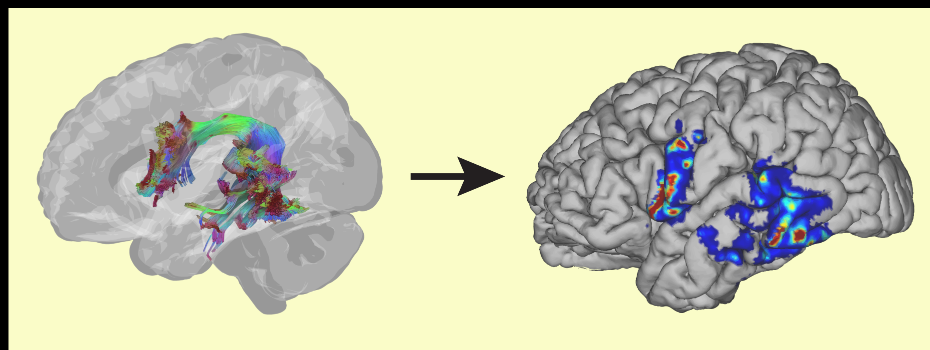
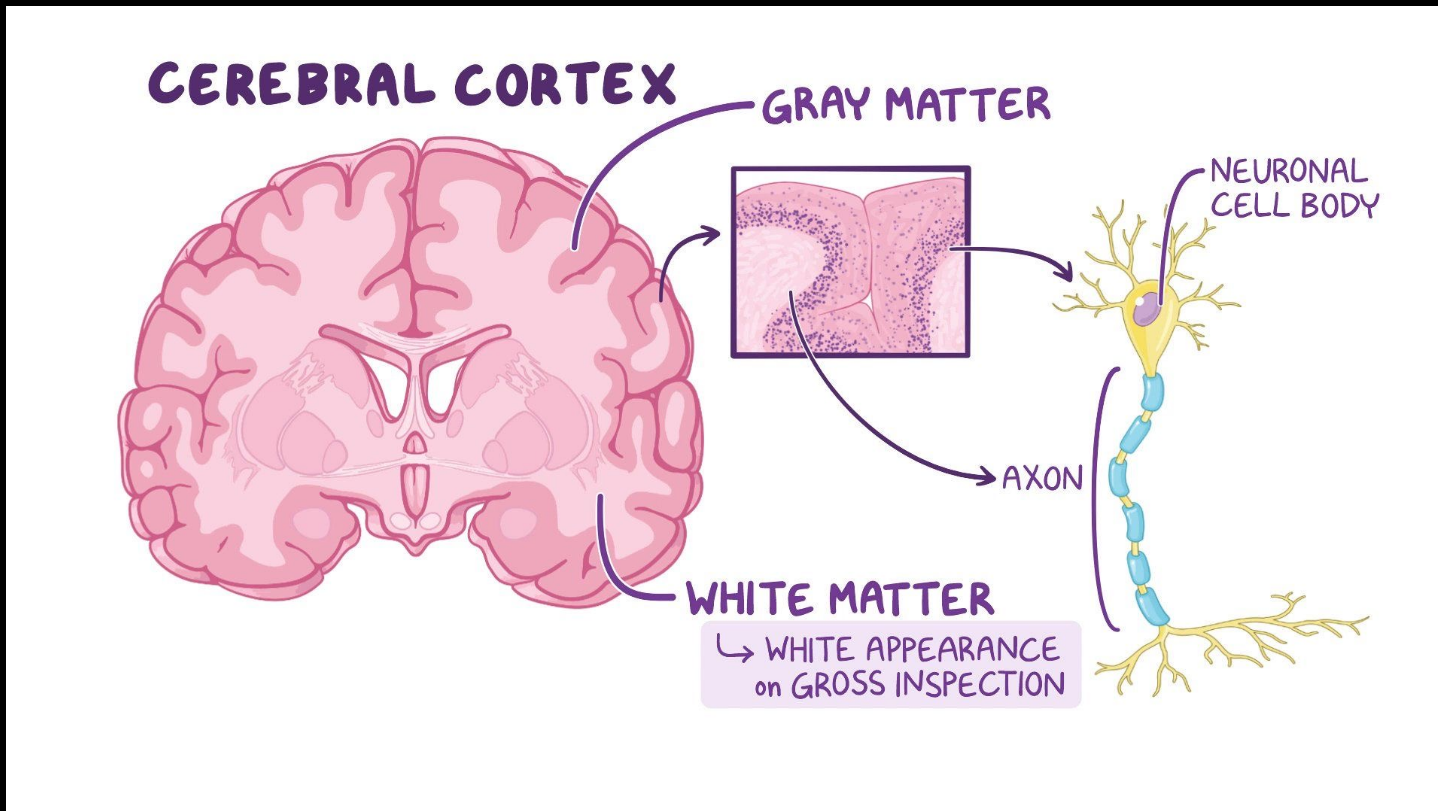
Developmental changes in the white matter-grey matter interface



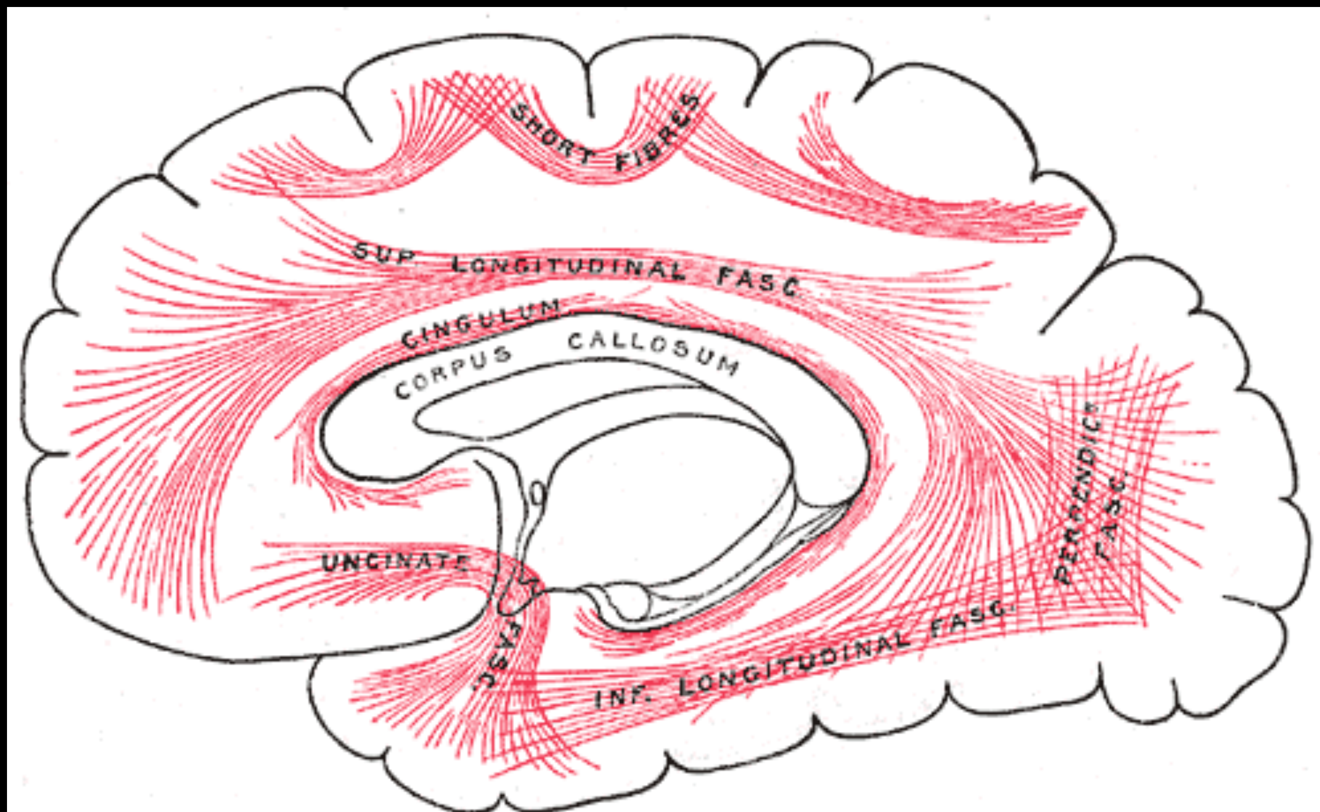
Marc Jaskir
PI: Dr. Theodore Satterthwaite
Spring 2023 Rotation Talk

White matter and grey matter



The Partnership in Education and Tara Hoover Design. https://www.thepartnershipineducation.com/resources/nervous-system

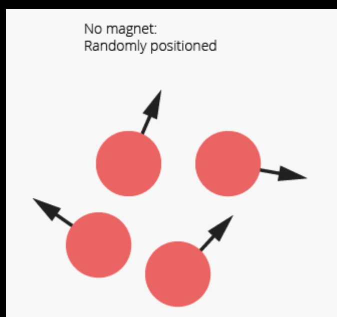
Tracts



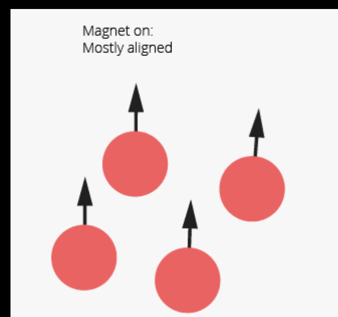
Henry Gray (1918) Anatomy of the Human Body

Magnetic resonance imaging

Hydrogen protons in H_2O

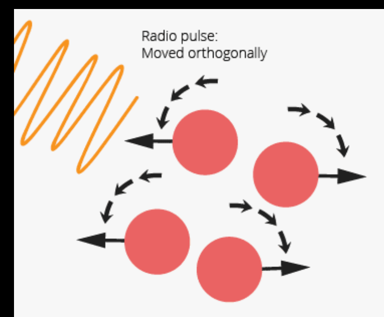


Strong magnetic field applied



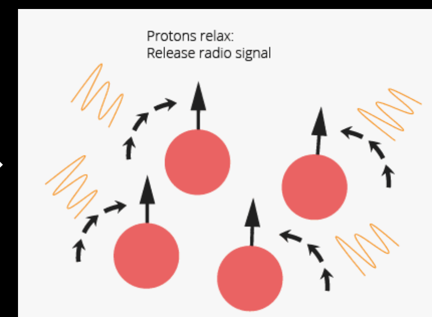
equilibrium energy state

Electromagnetic pulse applied



↑ energy state

Current emitted and measured

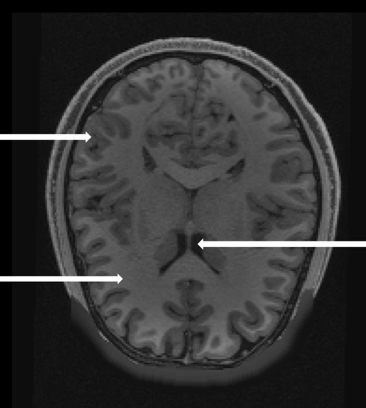


↓ energy state
decaying back towards equilibrium

T1-weighted images encode local energy decay rates of hydrogen protons in H_2O following excitatory electromagnetic pulses

GM

WM

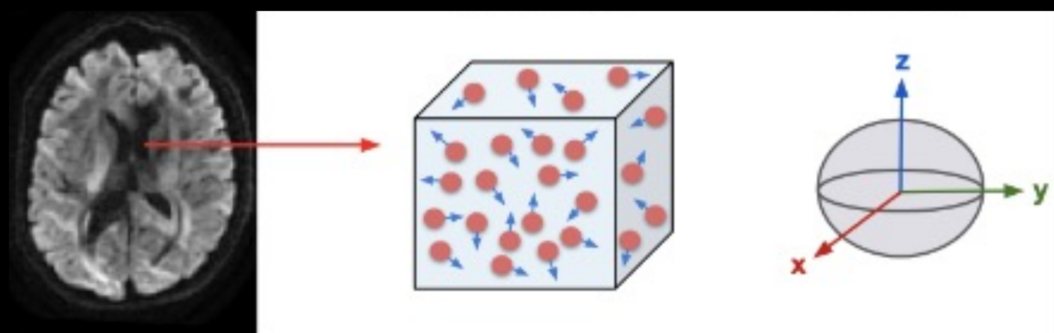


CSF

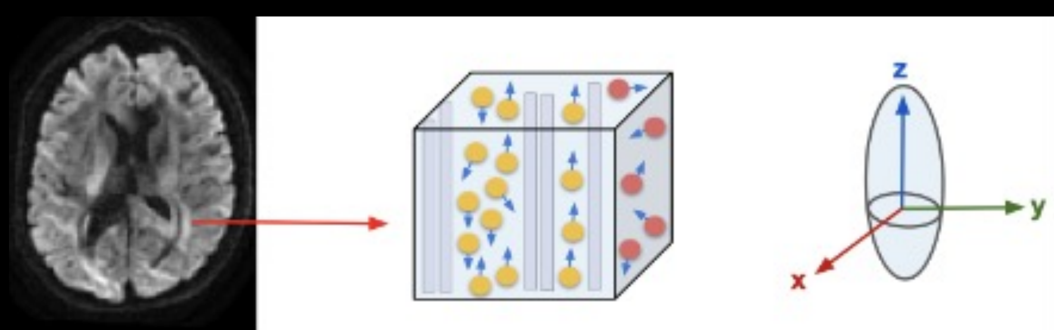
Chandio, B. Q. (2022). Advancing white matter tractometry of the brain using diffusion MRI and machine learning (Unpublished doctoral dissertation). Indiana University.
https://merritt.biochem.med.ufl.edu/about-mri/

Diffusion-weighted imaging

CSF — Isotropic diffusion



WM — Anisotropic diffusion



Diffusion tensor imaging (DTI)

Tensors

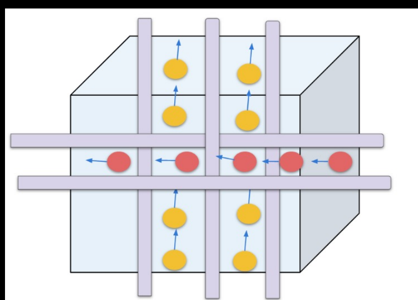
$$D = \begin{pmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{pmatrix}$$

Covariance matrix describing diffusion displacement along the x, y, and z axes

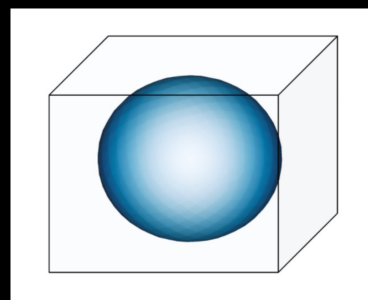
Chandio, B. Q. (2022). Advancing white matter tractometry of the brain using diffusion MRI and machine learning (Unpublished doctoral dissertation). Indiana University.

Diffusion-weighted imaging

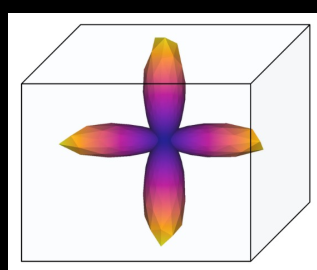
Crossing fibers



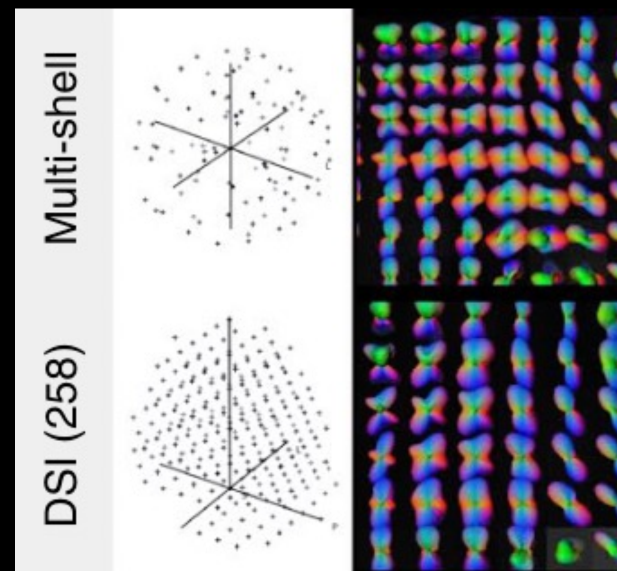
❌ Misleading tensor



✅ Improved accuracy of fiber orientation distributions



High density sampling schemes



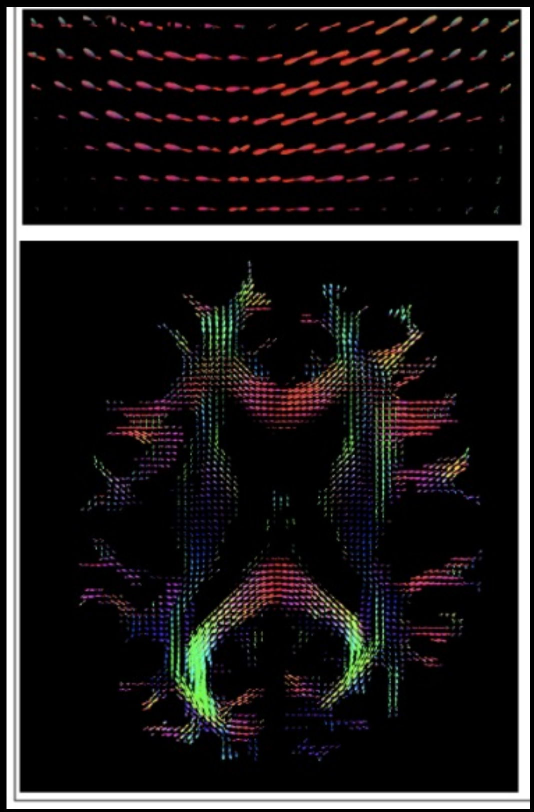
✅ Estimates 3D diffusion probability distribution for each voxel

✅ Confers high angular resolution

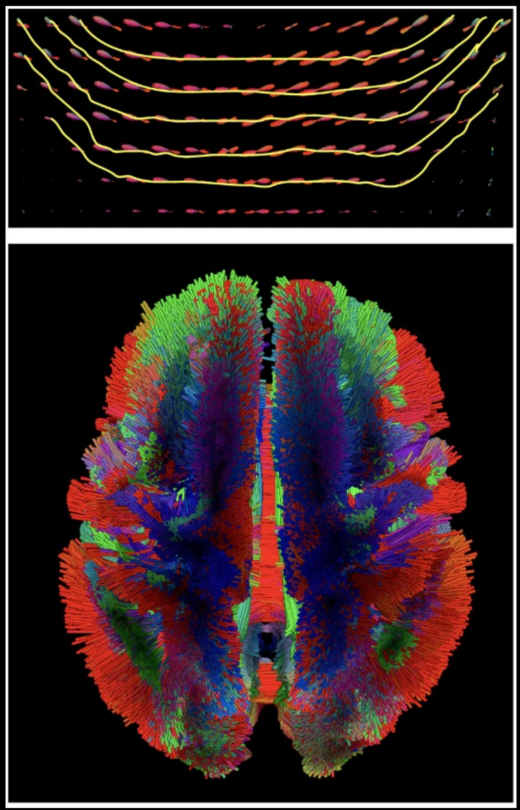
Chandio, B. Q. (2022). Advancing white matter tractometry of the brain using diffusion MRI and machine learning (Unpublished doctoral dissertation). Indiana University.
Cieslak M. (2021). QSIPrep: an integrative platform for preprocessing and reconstructing diffusion MRI data. Nature Methods, 18(7), 775-778. 10.1038/s41592-021-01185-5

Tractography

Fiber orientation distributions



Fiber tracking algorithms



Streamlines

Chandio, B. Q. (2022). Advancing white matter tractometry of the brain using diffusion MRI and machine learning (Unpublished doctoral dissertation). Indiana University.

DSI Studio’s automatic fiber tracking (AutoTrack)

Deterministic fiber tracking

Performs tractography by seeding voxels occupied by HCP-842 tractography atlas streamlines

Randomized parameter saturation

Utilizes random combinations of a wide parameter space for tract generation (step size) and tract termination (anisotropy and angular thresholds) for fiber tracking

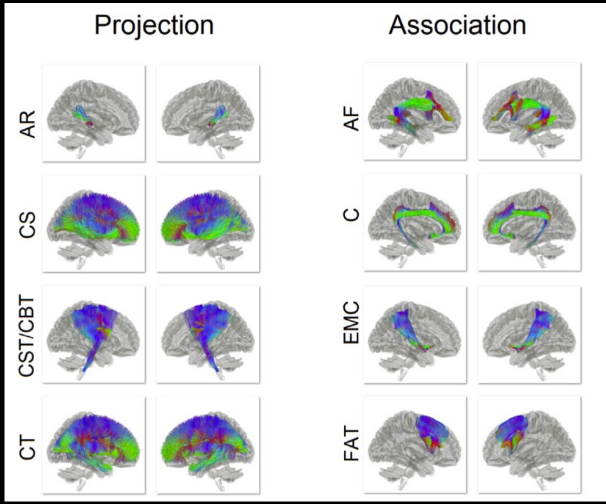
Streamline pruning

Identifies and removes spurious streamlines to improve accuracy

Tract recognition

Determine which of the generated streamlines are the best match to each tract in HCP-842 tractography atlas, discarding all others

HCP-842 tractography atlas
(Yeh 2018)



…
56 tracts

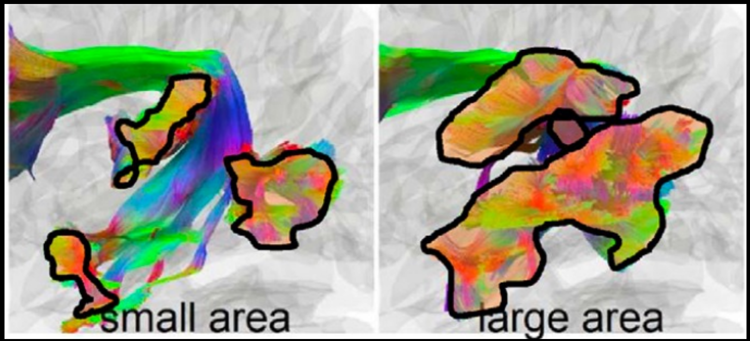
https://dsi-studio.labsolver.org

Yeh F.C. (2018). Population-averaged atlas of the macroscale human structural connectome and its network topology. NeuroImage, 178, 56-68. 10.1016/j.neuroimage.2018.05.027

Motivation

In large-scale neuroimaging datasets spanning early adolescence to young adulthood, no papers to our knowledge have

- applied DSI Studio's AutoTrack to study white matter development
- evaluated age-related changes in the shape characteristics of tract terminals, where white matter interfaces with grey matter

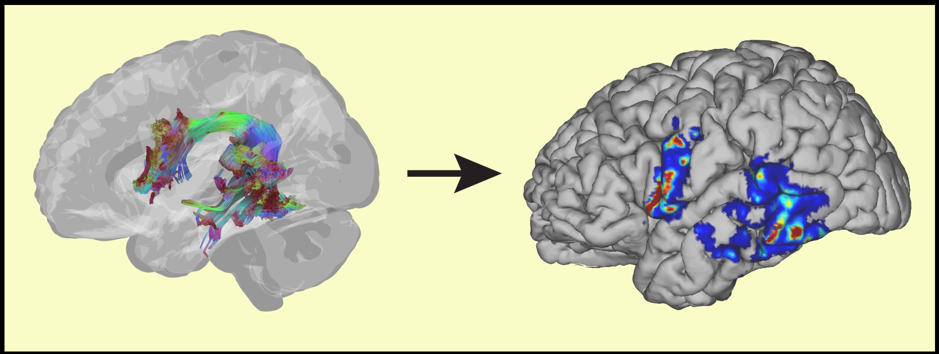


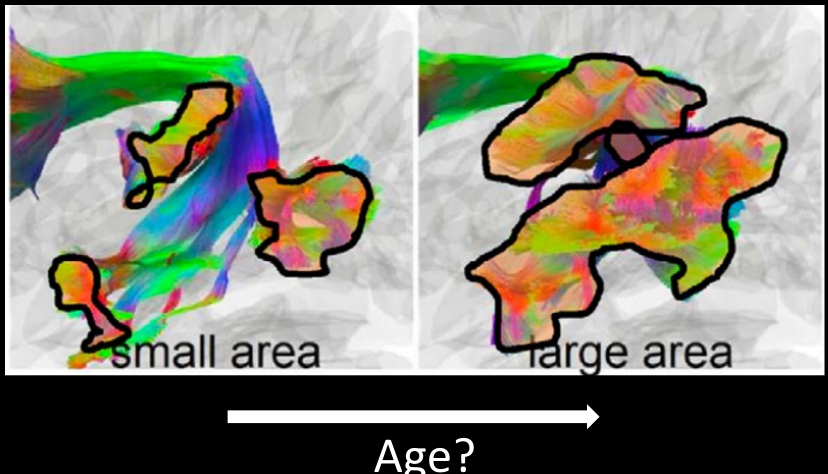
Yeh F.C. (2020). Shape Analysis of the Human Association Pathways. NeuroImage, 223, 117329. 10.1016/j.neuroimage.2020.117329

Goal + Hypothesis

Goal: In a large neuroimaging dataset spanning critical periods of development, 1) visualize how white matter tract reconstructions interface with the cortex ("WM-GM interfaces") and 2) evaluate how these interfaces change over development

Hypothesis: Development is associated with stereotyped changes in the shapes of WM-GM interfaces





Yeh F.C. (2020). Shape Analysis of the Human Association Pathways. NeuroImage, 223, 117329. 10.1016/j.neuroimage.2020.117329

Data + Inclusion criteria

HCP-Development (642 subjects, ages 5-21)

Exclusion criteria

- Incomplete diffusion MRI data
- Poor data quality (T1 neighborhood correlation < 0.6)
- High motion (Mean framewise displacement > 1.0)
- Age outside PNC range (< 8 years old)
- Health conditions (cancer/leukemia, sickle cell anemia, multiple sclerosis, seizures/epilepsy, cerebral palsy, knocked unconscious)

→ Final sample: 572 subjects

Preprocessing

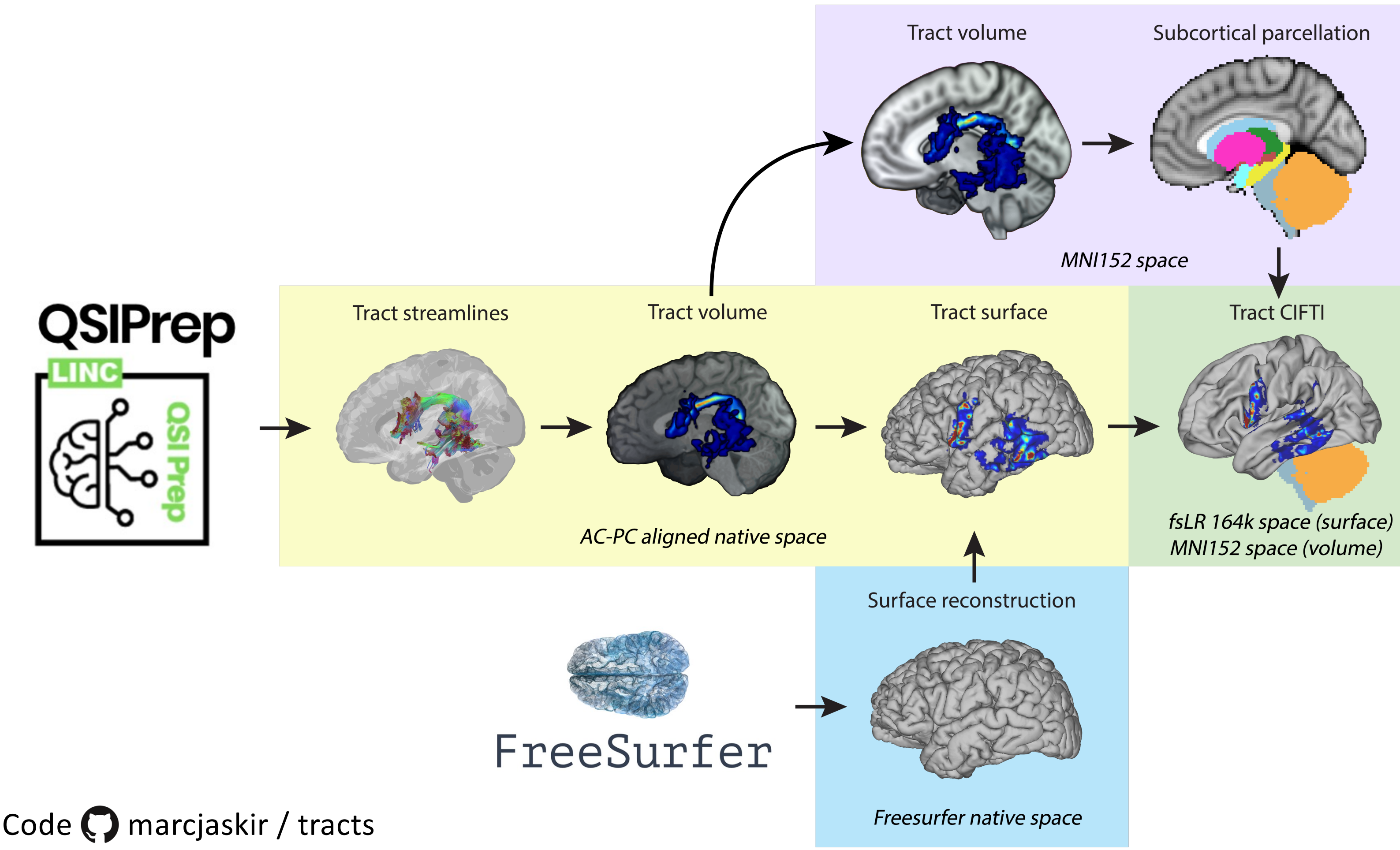
T1w image

fMRIPrep (v20.2.3) including Freesurfer (v6.0.1) surface reconstruction

Diffusion-weighted imaging data

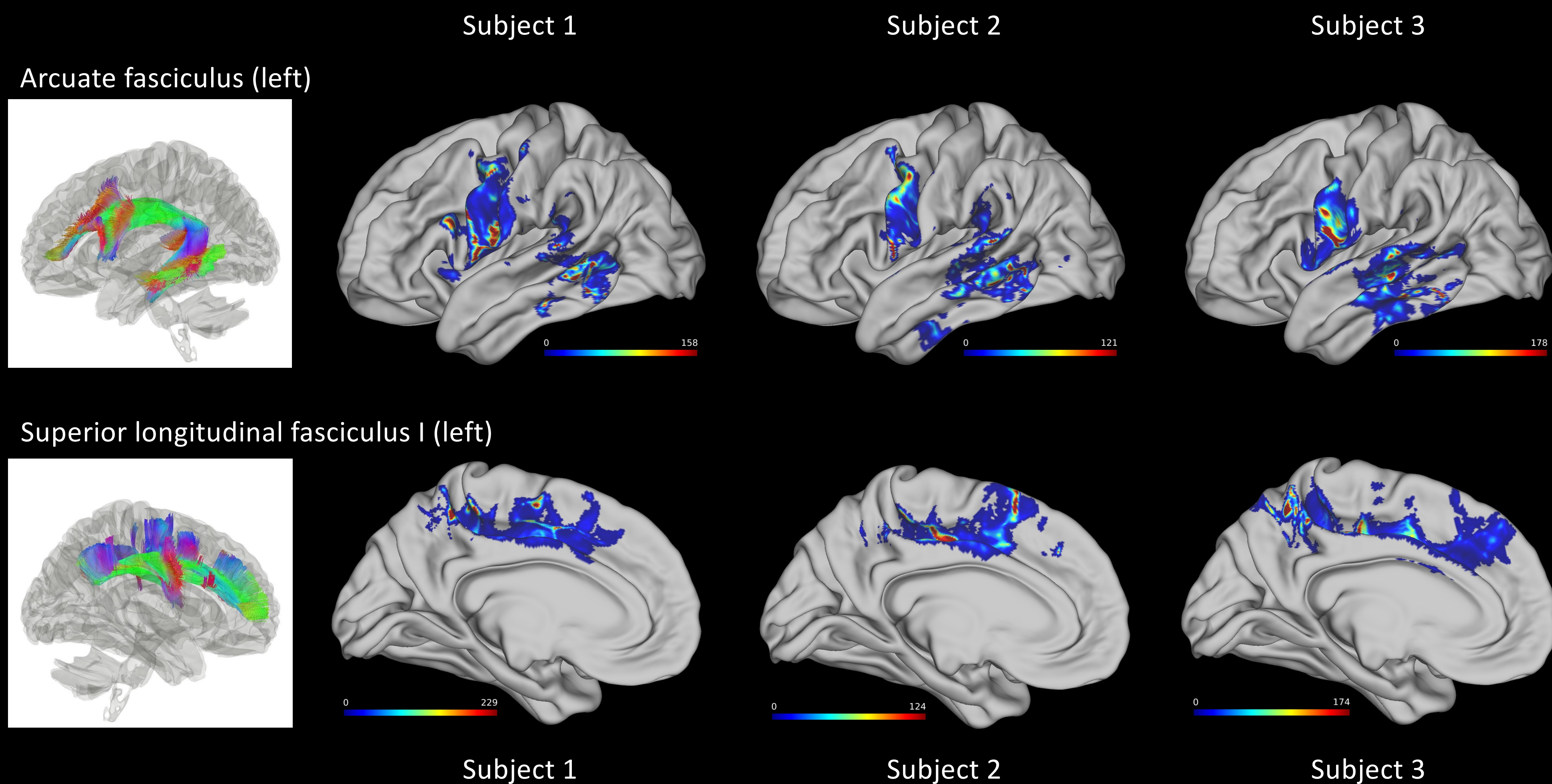
QSIPrep (v0.16.1) with QSIRecon (v0.18.0) workflow, including AutoTrack

Tract-to-surface mapping for visualizing WM-GM interface



Code marcjaskir / tracts

Single-subject tract surfaces

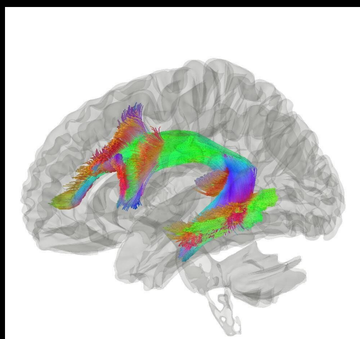


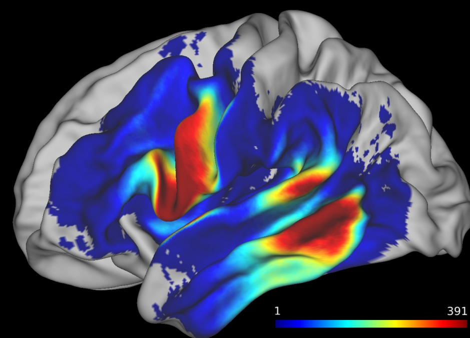
Yeh F.C. (2018). Population-averaged atlas of the macroscale human structural connectome and its network topology. NeuroImage, 178, 56-68. 10.1016/j.neuroimage.2018.05.027

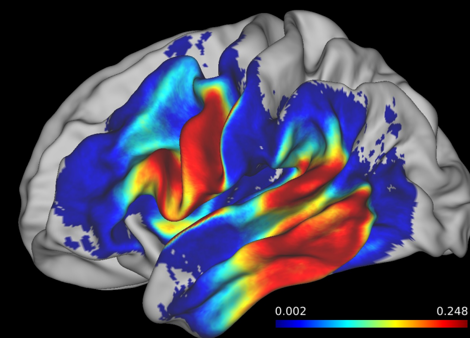
Group tract surfaces

Binarized + Summed | Variance

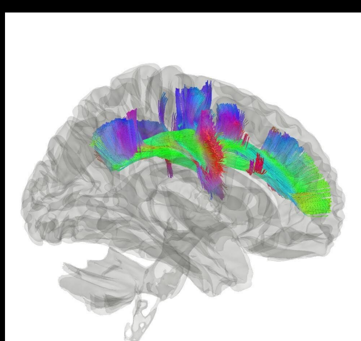
Arcuate fasciculus (left)

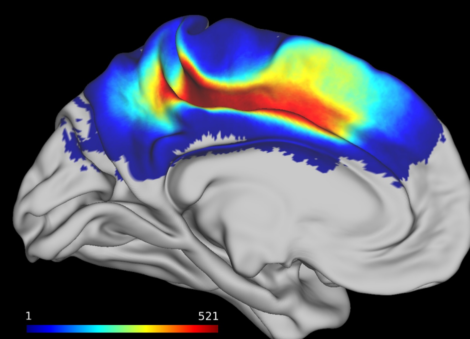


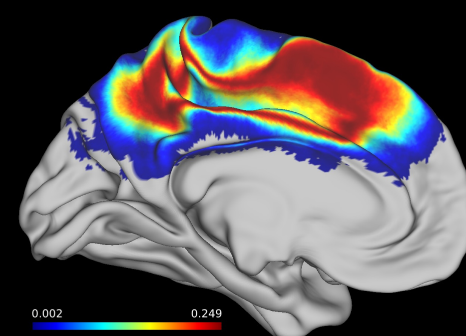




Superior longitudinal fasciculus I (left)







Yeh F.C. (2018). Population-averaged atlas of the macroscale human structural connectome and its network topology. NeuroImage, 178, 56-68. 10.1016/j.neuroimage.2018.05.027

Mass univariate GAMs

ModelArray: An R package for statistical analysis of fixel-wise data

Chenying Zhao[a,b,c,d], Tinashe M. Tapera[a,b,d], Joëlle Bagautdinova[a,b,d], Josiane Bourque[a,b,d], Sydney Covitz[a,b,d], Raquel E. Gur[b,d], Ruben C. Gur[b,d], Bart Larsen[a,b,d], Kahini Mehta[a,b,d], Steven L. Meisler[e], Kristin Murtha[a,b,d], John Muschelli[f], David R. Roalf[b,d], Valerie J. Sydnor[a,b,d], Alessandra M. Valcarcel[g], Russell T. Shinohara[g,h], Matthew Cieslak[a,b,d,1], Theodore D. Satterthwaite[a,b,d,h,1,*]

ModelArray facilitates mass univariate stats for voxel- and vertex-level data

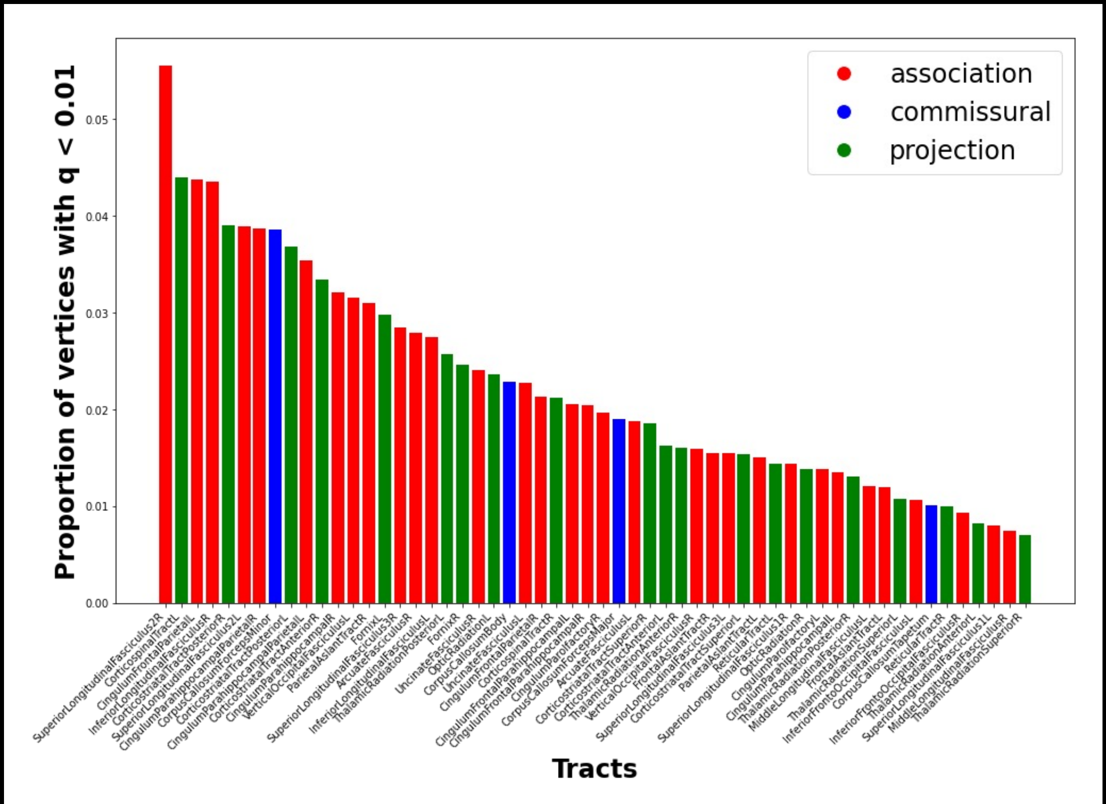
Generalized additive models (GAMs) were fit to binary tract CIFTIs:

voxel/vertex (0 = No Streamline, 1 = Streamline) ~ s(age) + sex + motion

→ Unpenalized fixed degrees of freedom model with 2 knots

Mass univariate GAMs

Tracts ordered by highest proportion of vertices/voxels with significant effect of age (FDR-corrected p-values < 0.01)

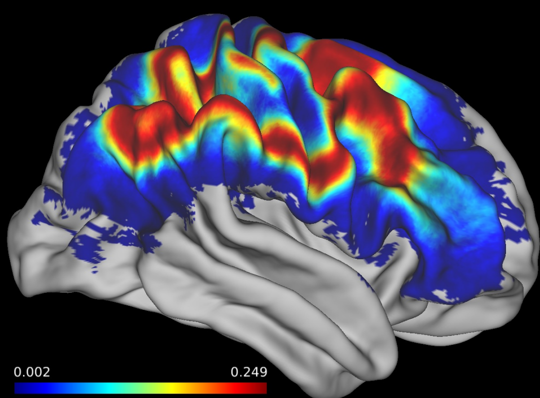


Top 2 tracts by proportional age effects

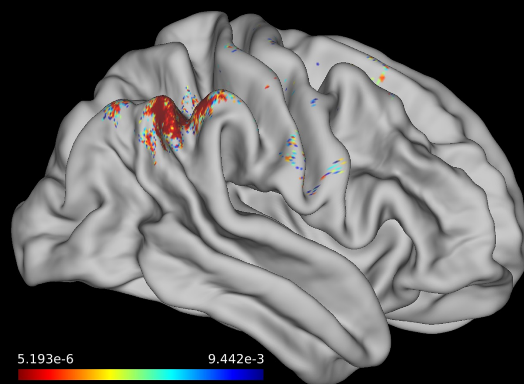
1. Superior longitudinal fasciculus II (right)
2. Corticospinal tract (left)

Mass univariate GAMs

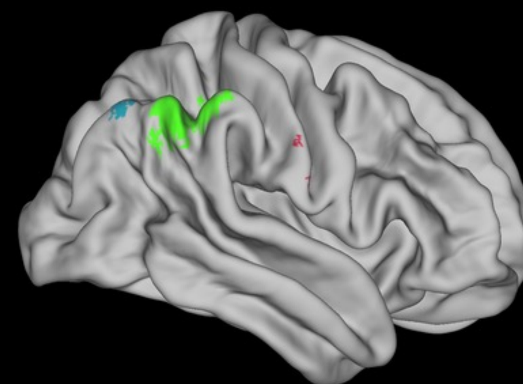
Variance



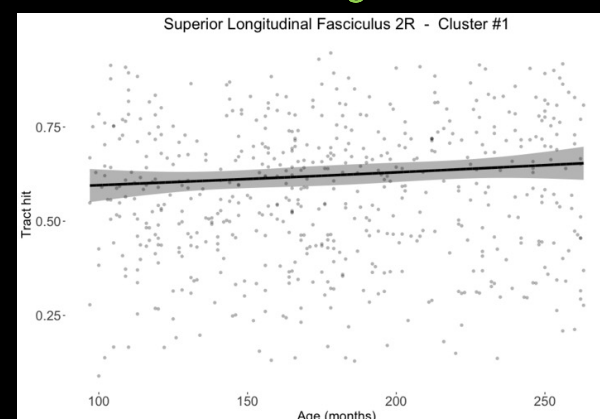
Age
FDR-corrected p-values < 0.01



Clustered p-value surface



GAM refit to largest cluster

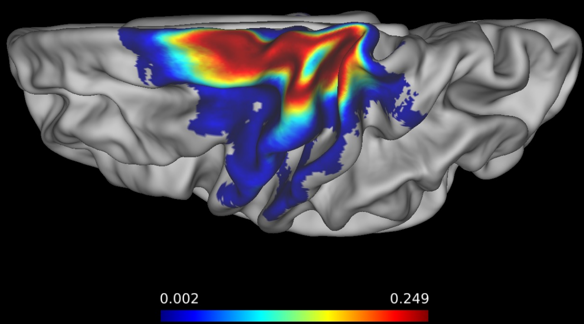


Top 2 tracts by proportional age effects

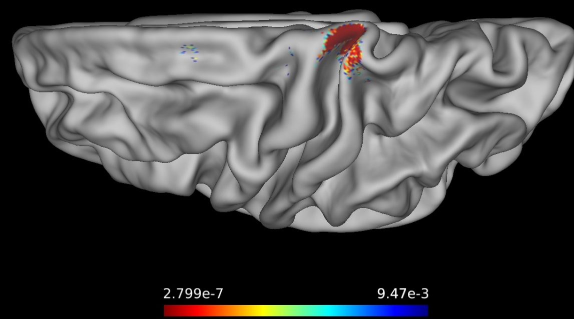
1. Superior longitudinal fasciculus II (right)
2. Corticospinal tract (left)

Mass univariate GAMs

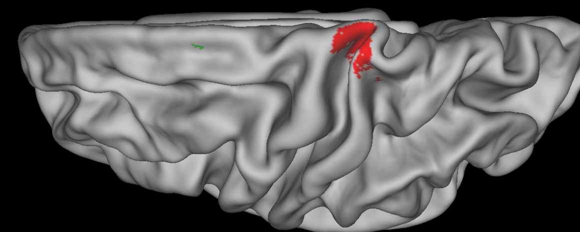
Variance



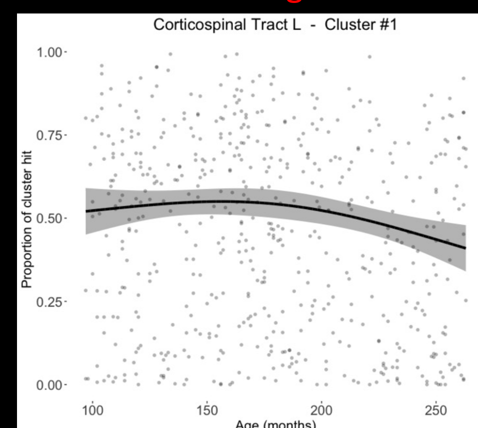
Age
FDR-corrected p-values < 0.01



Clustered p-value surface



GAM refit to largest cluster



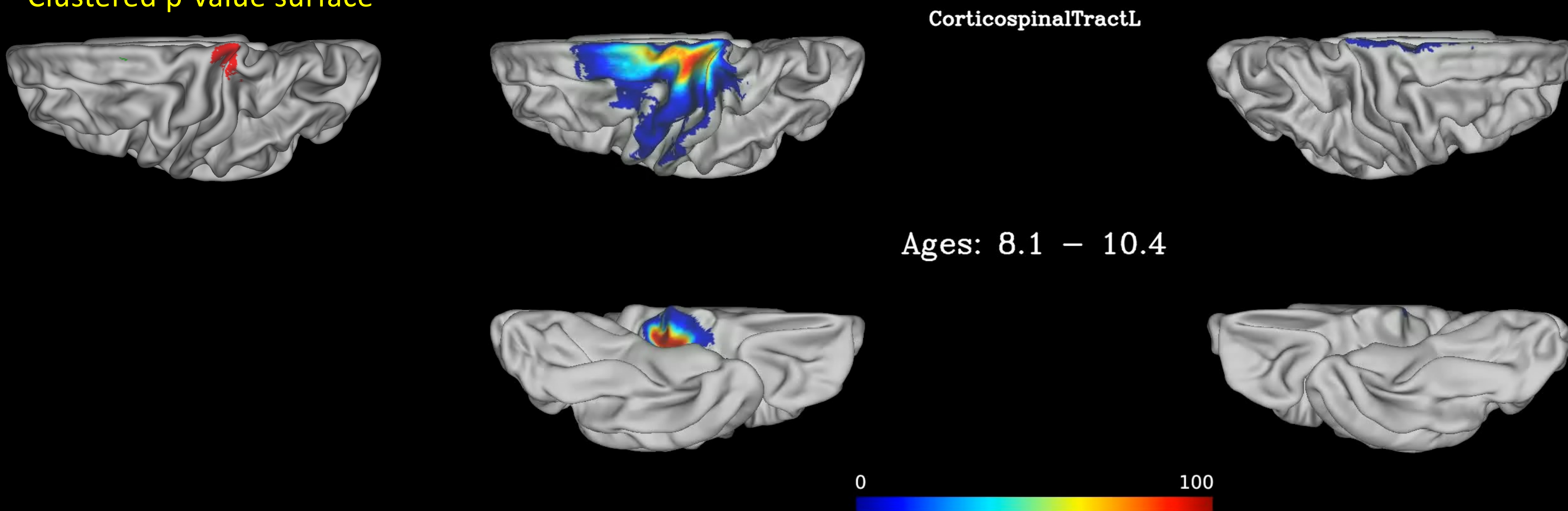
Top 2 tracts by proportional age effects

1. Superior longitudinal fasciculus II (right)
2. Corticospinal tract (left)

Mass univariate GAMs

Changes in tract-to-surface maps over development

Clustered p-value surface

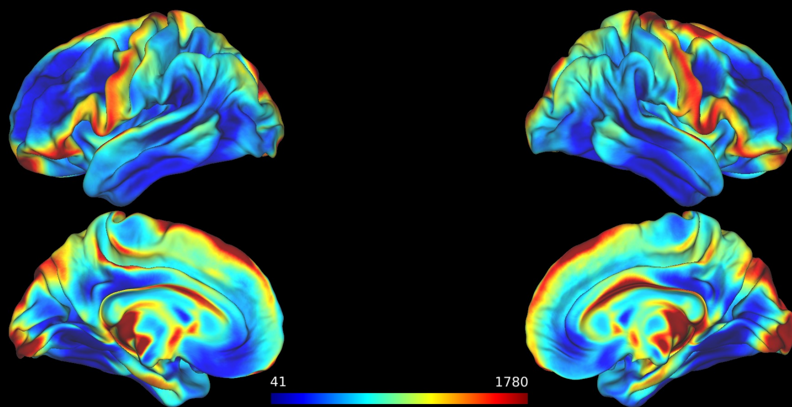


Top 2 tracts by proportional age effects

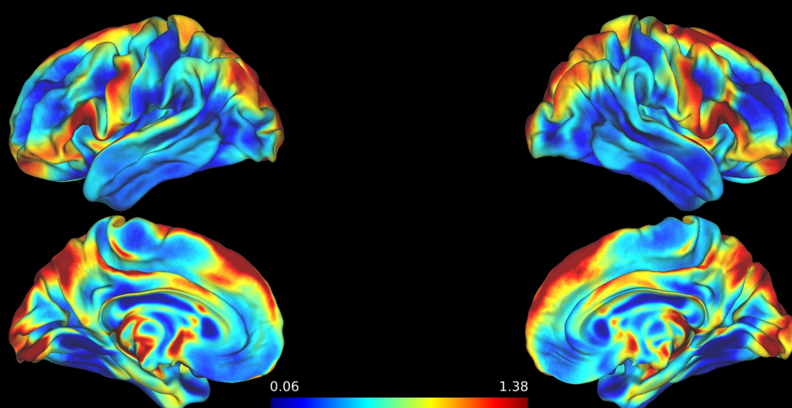
1. Superior longitudinal fasciculus II (right)
2. Corticospinal tract (left)

Across tracts

Across tract sum
All tracts
All subjects

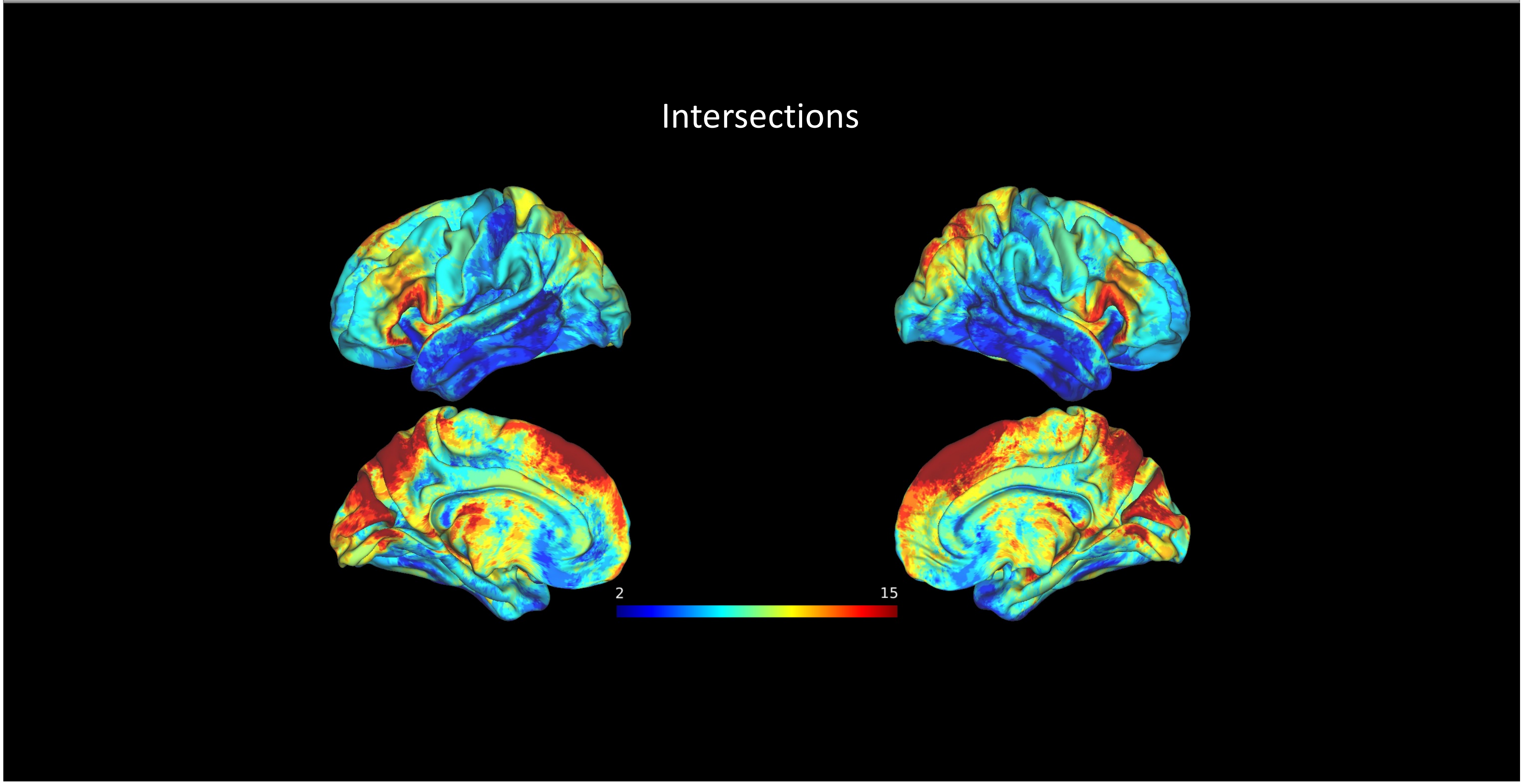


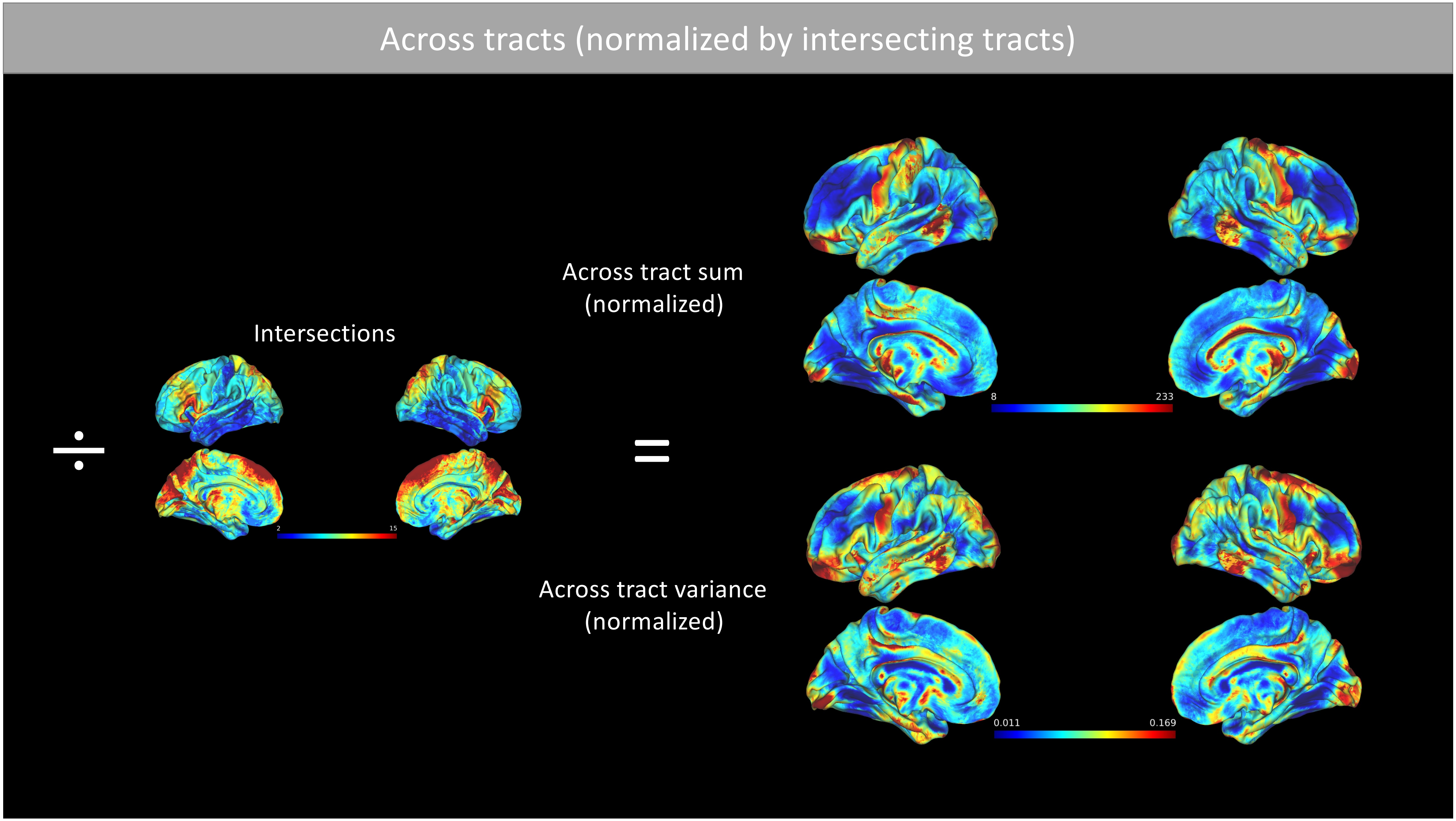
Across tract variance
All tracts
All subjects



Across tract sum (subcortex)

Tract intersections




Across tracts (normalized by intersecting tracts)
Intersections
2
15
÷
=
Across tract sum
(normalized)
8
233
Across tract variance
(normalized)
0.011
0.169

Conclusions + Next Steps

Conclusions

- Based on preliminary evidence, there are stereotyped developmental changes in WM-GM interface topography
- Tract-to-surface mapping may be a useful method for linking the structural connectome to cortical network organization

Next steps

- Across all tracts, sort p-value clusters for “age” predictor by size/mass

  → Localize most pronounced developmental changes in WM-GM interface
- Relate tract-to-surface density/variance across tracts with whole-brain maps of interest (e.g. S-A axis, evolutionary expansion, individual myelin maps)

Acknowledgements

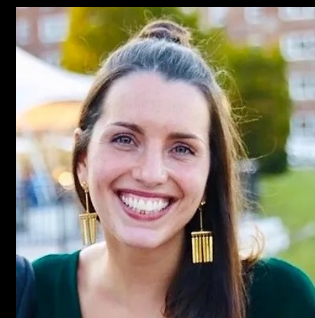
Dr. Ted Satterthwaite

Principal Investigator

Dr. Matthew Cieslak

Director of Neuroinformatics

Dr. Val Sydnor



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& Software Engineer

PennLINC

LINC
lifespan
informatics &
neuroimaging
center