

Queensland Twin Adolescent Brain Study

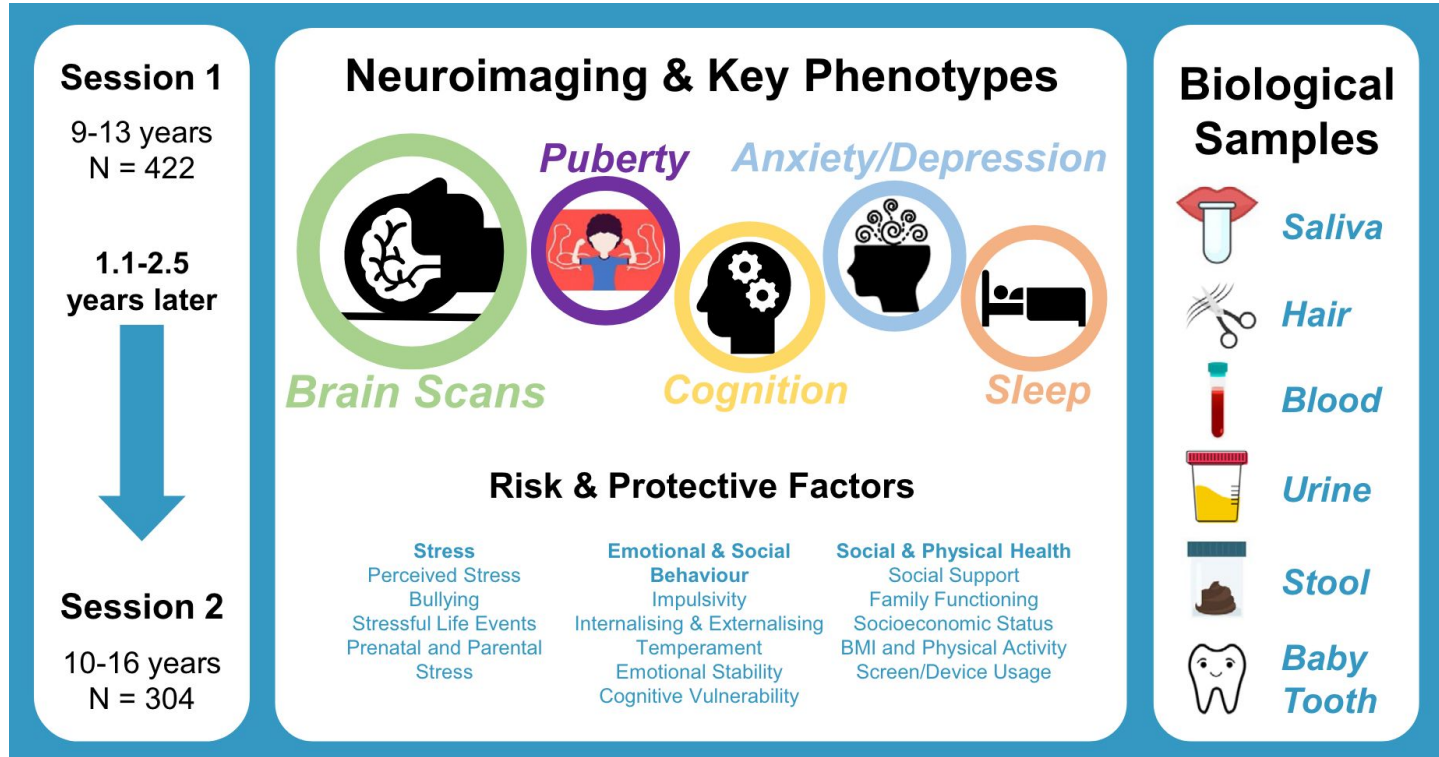
Pitch for a Reproducible Research Tutorial

Goals

1. Develop a template for GitHub repositories
2. Develop an SOP for sharing figures and results
3. Data management and processing training for the informatics team
4. Coding and analysis training for grad students and postdocs
5. Update in-lab documentation

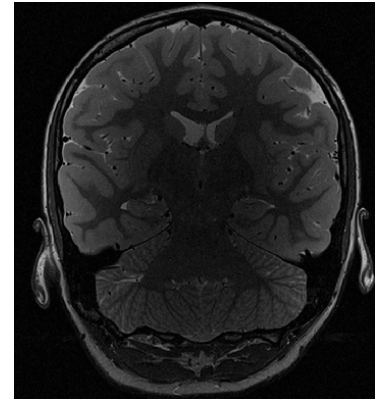
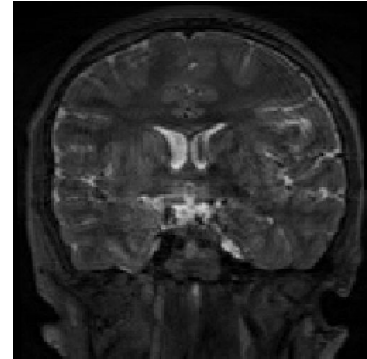
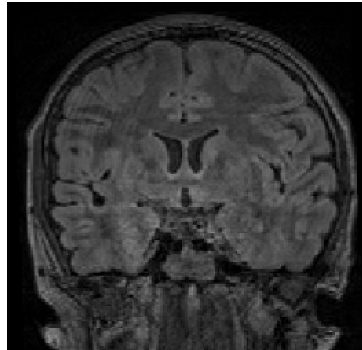
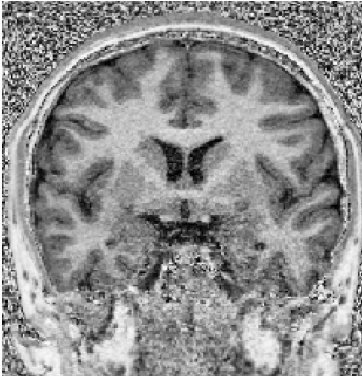
The Queensland Twin Adolescent Brain Dataset

<https://openneuro.org/datasets/ds004146/versions/1.0.4>



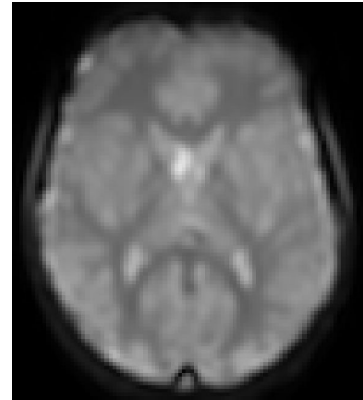
Anatomical MRI

- MP2RAGE (0.8 mm³)
- T2w (1 mm³)
- FLAIR (1 mm³)
- High-resolution limited-FOV T2-weighted turbo spin echo (0.25 x 0.25 x 1 mm) for hippocampal and amygdalar imaging



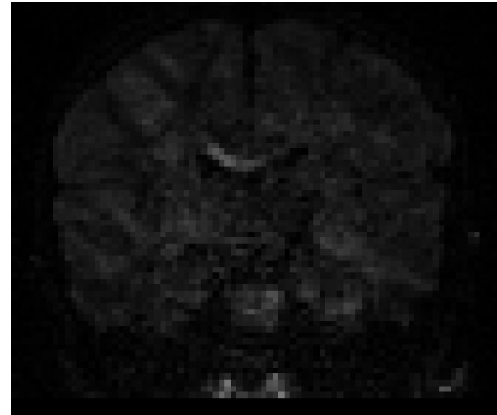
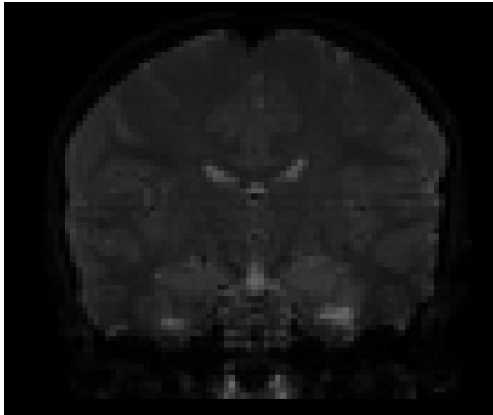
Arterial Spin Labeling

- 1 run
- 1.7 x 1.7 x 4 mm voxels
- Single-PLD PCASL with background suppression
- Separate M0 calibration volumes



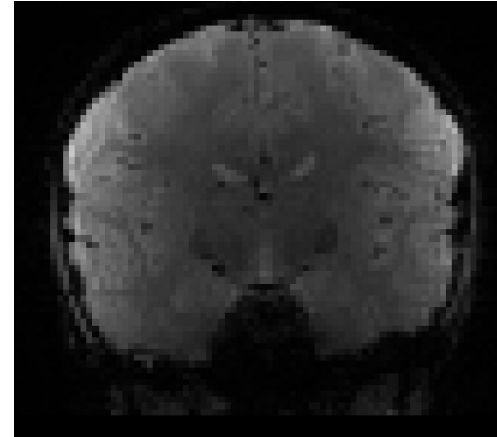
Diffusion MRI

- 4 runs (2 PA, 2 AP)
- 2 mm³ voxels
- B-values of 0, 1000, and 3000
- 80 directions



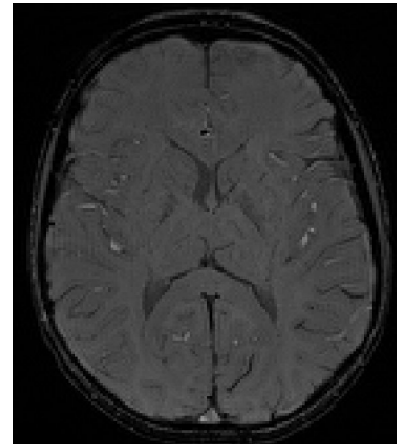
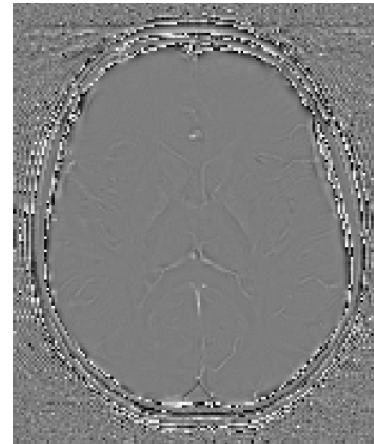
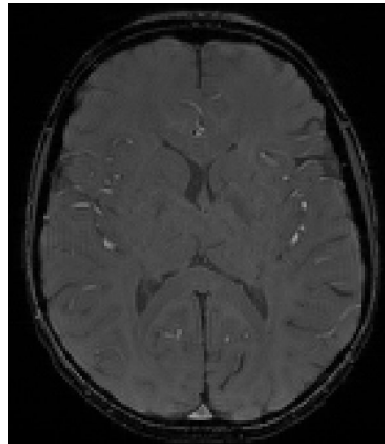
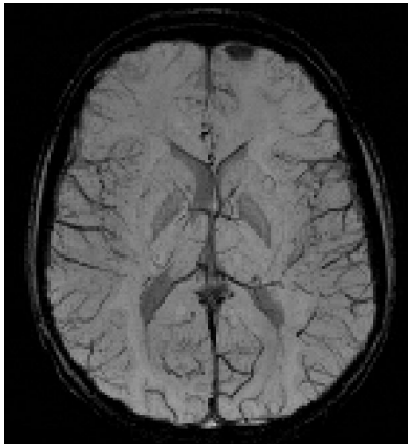
Functional MRI

- 2 runs of resting-state (1 PA, 1 AP) in each session
 - 2 mm³ voxels
 - TR = 0.93 seconds
 - 327 volumes per run
- 1 run of emotional conflict task in session 2
 - 2.4 mm³ voxels
 - TR = 0.8 seconds
 - 837 volumes per run
- 1 run of film viewing task in session 2
 - 2.4 mm³ voxels
 - TR = 0.8 seconds
 - 380 volumes per run



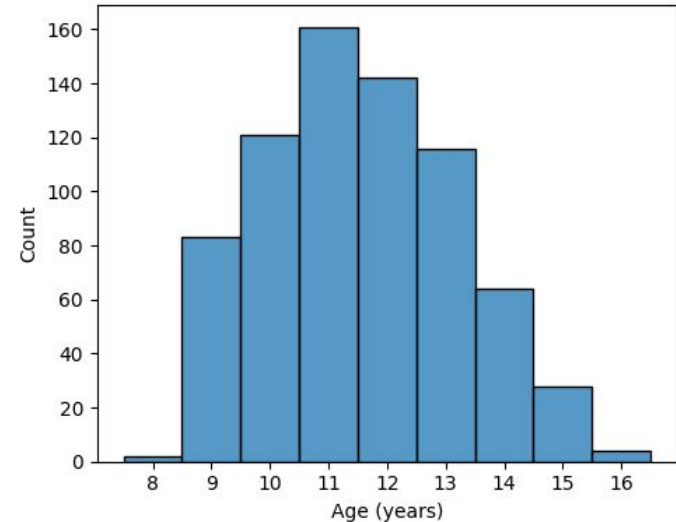
Susceptibility Weighted Imaging

- Single-echo GRE with magnitude and phase reconstruction.
- 1.1 x 1.1 x 2 mm voxels
- Not usable for quantitative susceptibility mapping :(



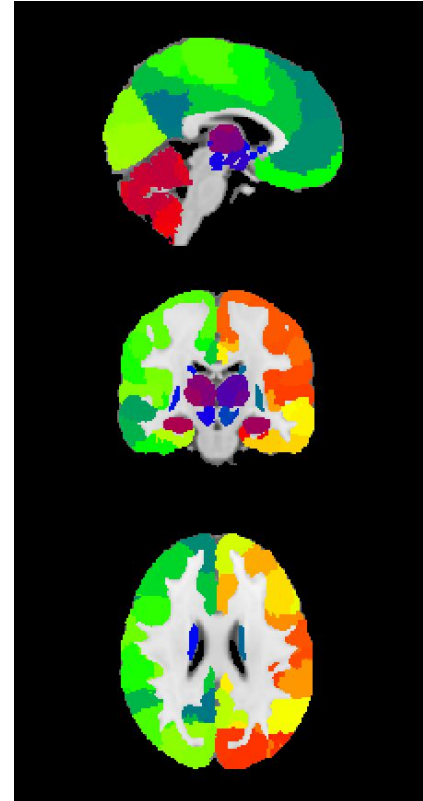
Demographics and Questionnaires (DUA)

- Age, sex, handedness, family ID
- Zygosity, zygosity source, multiple birth status, birth order
- Scales for:
 - Puberty
 - Cognition
 - Anxiety and/or Depression
 - Emotional and Social Behaviours
 - Social Support and Family Functioning
 - Stress
 - Sleep and Physical Health
 - Early Life and Family Demographics
 - Dietary Behaviour
 - COVID-19 Pandemic Specific Assessments

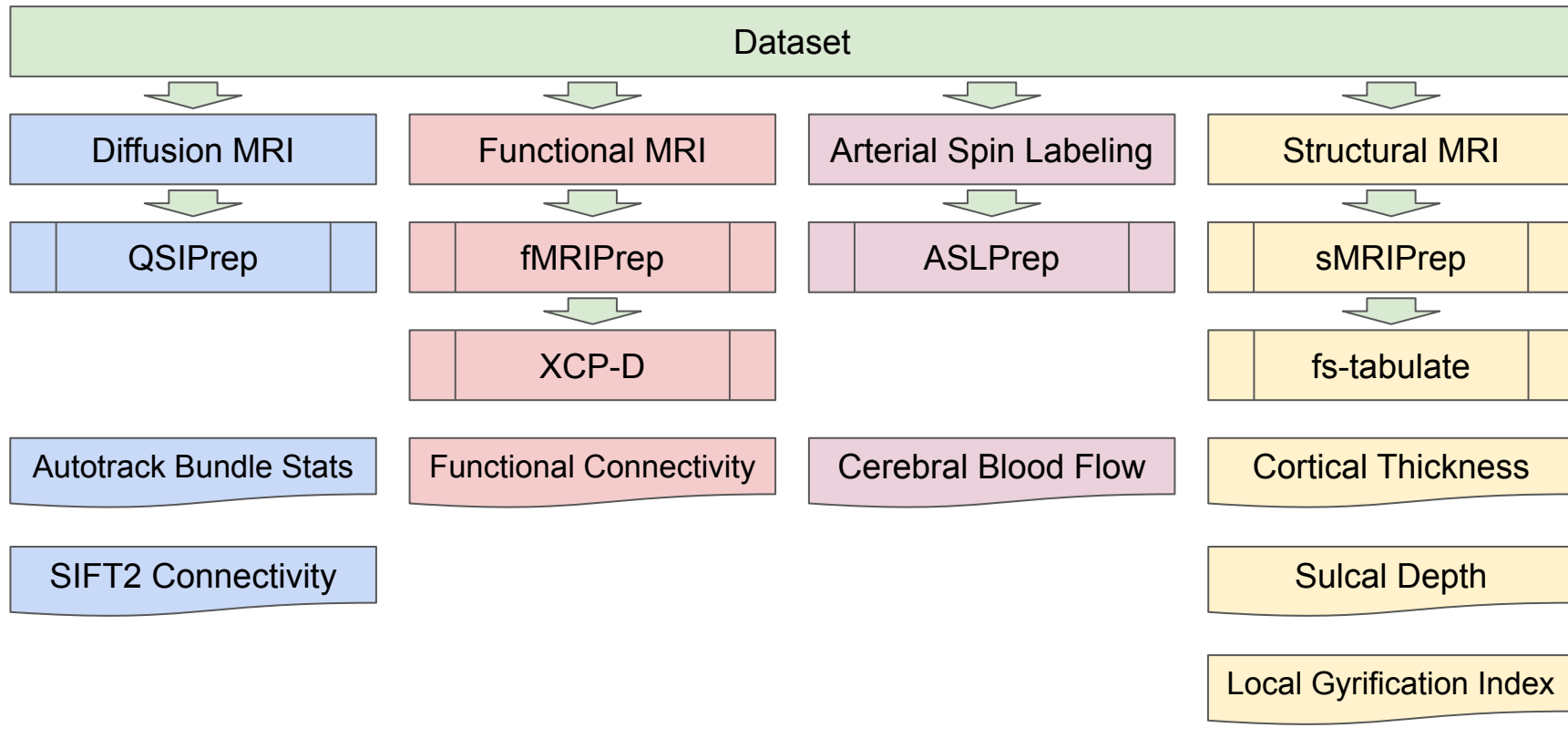


4S: Schaefer Supplemented with Subcortical Structures

- Matt and I combined the Schaefer cortical atlases (100 - 1000 parcels) with 56 subcortical regions drawn from the CIT168 subcortical atlas, the Diedrichsen cerebellar atlas, and HCP atlases for hippocampus, amygdala, and thalamus.
- 4S is integrated into XCP-D and ASLPrep.
- It's almost integrated into QSIPrep and fs-tabulate.



Processing Plan



Analysis Ideas

Demographics (DUA)

Questionnaires (DUA)

4S Edge-Wise Data

Functional Connectivity

SIFT2 Connectivity

4S Node-Wise Data

Autotrack Bundle Stats

Cerebral Blood Flow

Cortical Thickness

Sulcal Depth

Local Gyrification Index

- Baseline vs. follow up
- Twins vs. unrelated
- Monozygotic vs. dizygotic twins

- Predict phenotypes
- Replicate Sydnor 2023?

- Voxel-wise data analyses
- Multimodal tensor decomposition (e.g., PARAFAC)

Dataset as reproducible research training

Version 1: Informatics (for informatics team and anyone interested)

1. Download data from OpenNeuro as Datalad dataset.
2. Curate dataset with CuBIDS.
3. Perform quality control and select sample for each modality.
4. Run pre- and post-processing pipelines with BABS.
5. Deploy derivatives to G-Node GIN.
6. Archive data on PMACS.

Dataset as reproducible research training, continued

Version 2: Analysis (for grad students and postdocs)

1. Clone derivatives.
2. Aggregate analysis data.
3. Write readable R and/or Python code to perform analyses and generate figures.
4. Code version control on GitHub.
5. Reproducibilibuddy analysis.
6. Upload results to G-Node GIN, FigShare, etc.

I've started drafting a repository:

<https://github.com/PennLINC/multimodal-qtab>

Feel free to open issues or PRs

```
multimodal-qtab/
├── LICENSE
├── README.md
├── analysis
│   ├── README.md
│   └── generate_figure_01.ipynb
├── analysis_plan
│   └── README.md
├── data
│   ├── README.md
│   └── demographics.tsv
├── figures
│   ├── README.md
│   └── figure_01.svg
├── manuscript
│   ├── README.md
│   └── manuscript.tex
├── processing
│   ├── README.md
│   ├── download_dataset.sh
│   ├── download_singularity.sh
│   ├── fix_rawdata.sh
│   ├── run_aslprep.sh
│   ├── run_fmriprep.sh
│   └── run_smriprep.sh
└── python_requirements.txt
```