

Team Diffusion

NEUROHACKADEMY

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<https://neurohackademy2024.github.io/diffusion-mri/>

A

Test using QSIprep for
preprocessing
and reconstructing dMRI data

B

Comparing different reconstruction models:
Simple dipy preprocessing vs QSIprep
DTI vs CSD

Diffusion-tensor
imaging

Constrained-spherical
deconvolution

Background documentation

- Basic diffusion MRI
 - Basic physics
 - Isotropy vs Anisotropy
 - DWI vs DTI vs DSI
 - Data Structure
 - Single shell and multi shell
 - Models and measurements
- Introduction to QSI
 - Preprocessing
 - Reconstruction

Files

main

+

Go to file

- > code
- ✓ documentation
- > BIDS
- > HBN_protocols
- ✓ background-diffusion
 - Diffusion Background.pdf
 - README
 - > examples
 - Documentation QSIprep output....
 - setup.md
 - usage.md
 - .DS_Store
 - .gitignore
 - FS_license.txt
 - README.md
 - model_predictions.png

2.09 MB

Diffusion

Motion of molecules
Totally random



<https://github.com/NeuroHackademy2024/diffusion-mri/blob/main/documentation/background-diffusion/Diffusion%20Background.pdf>



GitHub: The nexus of the project



<https://github.com/NeuroHackademy2024/diffusion-mri>

What will you find in our repository?

README

1. Project info
2. Contributors
3. Instructions to run the code

Code

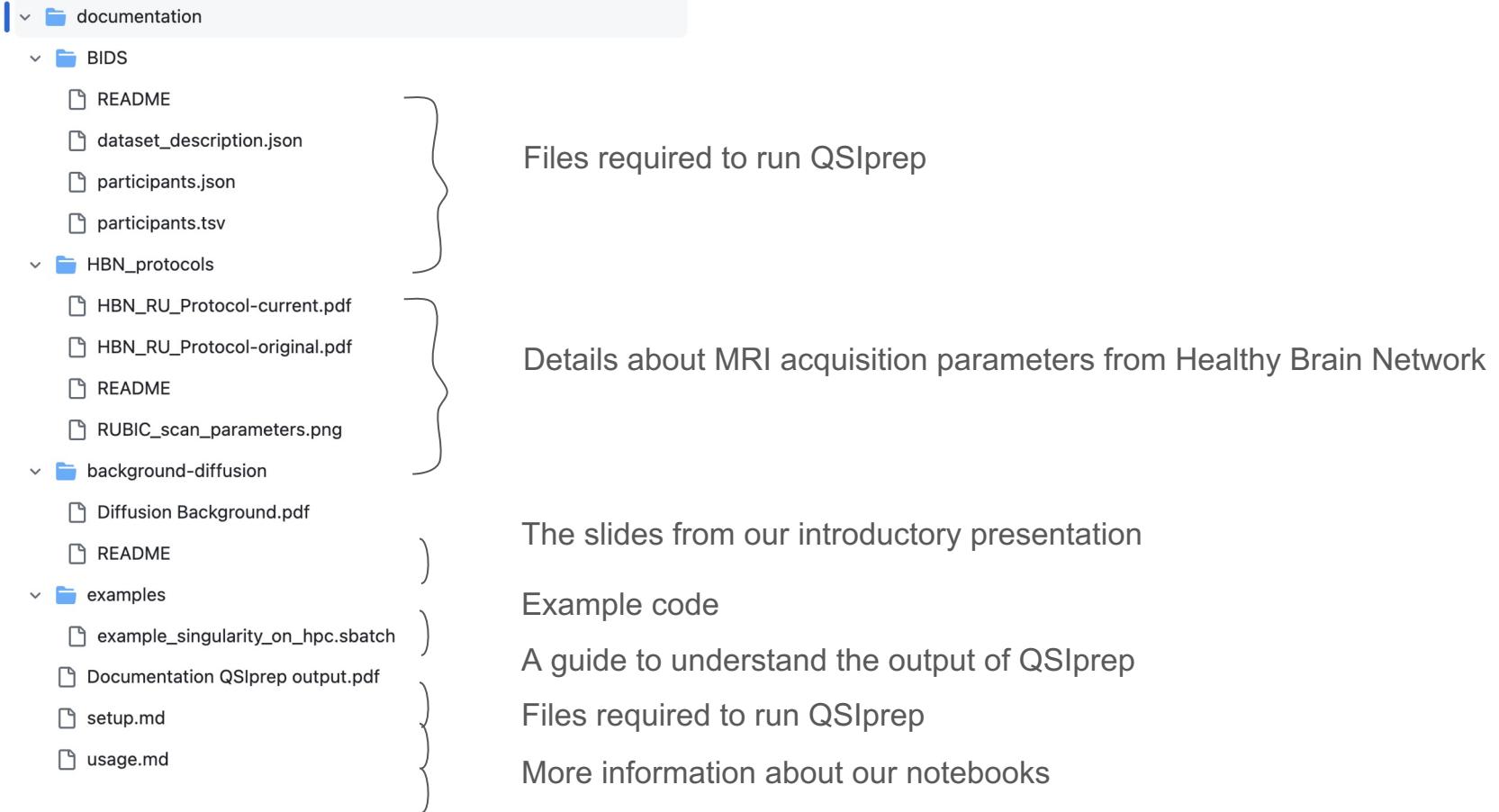
Jupyter notebooks demonstrating how access dMRI data from HBN, then preprocess and reconstruct with QSIprep on JupyterHub

Documentation

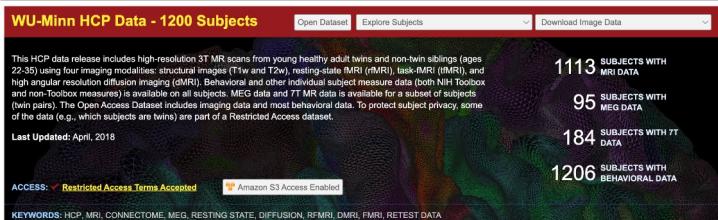
Usability & Interpretability

**** Guidelines for true beginners ****

A hitchhiker's guide through documentation



Data Selection



Minimally preprocessed

Not fully compliant with BIDS format



Child Mind Institute
HEALTHY BRAIN NETWORK

https://fcp-indi.s3.amazonaws.com/index.html#data/Projects/HBN/BIDS_curated/

s3://fcp-indi/data/Projects/HBN/BIDS_curated
sub-NDARAA948VFH
ses-HBNsiteRU
anat
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-HCP_T1w.json
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-HCP_T1w.nii.gz
dwi
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-64dir_dwi.bval
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-64dir_dwi.bvec
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-64dir_dwi.json
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-64dir_dwi.nii.gz
fmap
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-dwi_dir-AP_epi.json
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-dwi_dir-AP_epi.nii.gz
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-dwi_dir-PA_epi.json
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-dwi_dir-PA_epi.nii.gz
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-fMRI_dir-AP_epi.json
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-fMRI_dir-AP_epi.nii.gz
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-fMRI_dir-PA_epi.json
 sub-NDARAA948VFH_ses-HBNsiteRU_acq-fMRI_dir-PA_epi.nii.gz

Downloading the Data

```
[2]: from pathlib import Path
from cloudpathlib import S3Path, S3Client

# Make the path object:
cache_path = Path('/tmp/cache/')

# Just because we have made a cache path object doesn't mean that the directory
# we made exists; here we check if it exists and make the directory if not.
if not cache_path.exists():
    cache_path.mkdir()

# Make the path object for the BIDs data folder:
cache_path = Path('/tmp/cache/data')

if not cache_path.exists():
    cache_path.mkdir()

[3]: from utilities import ls, crawl
import nibabel as nib

[4]: client = S3Client(
    local_cache_dir=cache_path,
    no_sign_request=True)

hbn_base_path = S3Path(
    "s3://fcp-indi/",
    client=client)

[5]: ls(hbn_base_path)
[S3Path('s3://fcp-indi/TEST_DATABASE'), ...]

[6]: #hbn_raw_path = hbn_base_path / "data" / "Projects" / "HBN" / "MRI" / "Site-CBIC"
hbn_raw_path = hbn_base_path / "data" / "Projects" / "HBN" / "BIDS_curated"
#crawl(hbn_raw_path)
#ls(hbn_raw_path)
# The data can be explored under https://fcp-indi.s3.amazonaws.com/index.html#data/Projects/HBN/MRI

[7]: import os
subjects = ["sub-NDARAA948VFH", "sub-NDARAB055BPR"]
#no_subjects = ['sub-NDARAN229MTX', 'sub-NDARAA306NT2']
print(hbn_raw_path)
for subject in subjects:
    sub_path = hbn_raw_path / f"{subject}"
    crawl(sub_path)

s3://fcp-indi/data/Projects/HBN/BIDS_curated ...

[8]: # Define function to download data
def crawl_and_download(s3_sub_path, local_sub_path):
    for item in s3_sub_path.rglob('*'):
        if item.is_file():
            local_file_path = local_sub_path / item.relative_to(s3_sub_path)
            if not local_file_path.parent.exists():
                local_file_path.parent.mkdir(parents=True, exist_ok=True)
            item.download_to(local_file_path)
            print(f'Downloaded {item} to {local_file_path}')

[9]: for subject in subjects:
    sub_path = hbn_raw_path / f"{subject}"
    local_sub_path = cache_path / subject
    crawl_and_download(sub_path, local_sub_path)

Downloaded s3://fcp-indi/data/Projects/HBN/BIDS_curated/sub-NDARAA948VFH/ses-HBNsiteRU/anat/sub-NDA
```

https://github.com/NeuroHackademy2024/diffusion-mri/blob/main/code/001-get-hbn-data_Ikpo.ipynb

Build QSIPrep Singularity Image

Identify latest version of QSIPrep



TAG

[0.22.1](#)

Last pushed 6 days ago by [matthewcieslak](#)

Digest

[c175102aa4bf](#)

Build image in jupyterhub

```
singularity build ./my-qsi-prep.sif docker://pennbbl/qsiprep:0.22.1
```

QSIPrep: File Structure

Remove fMRI field maps

```
sub-NDARAA948VFH
ses-HBNSiteRU
anat
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-HCP_T1w.json
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-HCP_T1w.nii.gz
dwi
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-64dir_dwi.bval
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-64dir_dwi.bvec
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-64dir_dwi.json
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-64dir_dwi.nii.gz
fmap
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-dwi_dir-AP_epi.json
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-dwi_dir-AP_epi.nii.gz
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-dwi_dir-PA_epi.json
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-dwi_dir-PA_epi.nii.gz
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-fMRI_dir-AP_epi.json
    sub-NDARAA948VFH_ses-HBNSiteRU_acq_fMRI_dir-AP_epi.nii.gz
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-fMRI_dir-PA_epi.json
    sub-NDARAA948VFH_ses-HBNSiteRU_acq_fMRI_dir-PA_epi.nii.gz
    sub-NDARAA948VFH_ses-HBNSiteRU_acq-fMRI_dir-PA_ebo.nii.gz
```

Add other relevant BIDS files

sub-NDARZZ740MLM/

sub-NDARZZ810LVF/

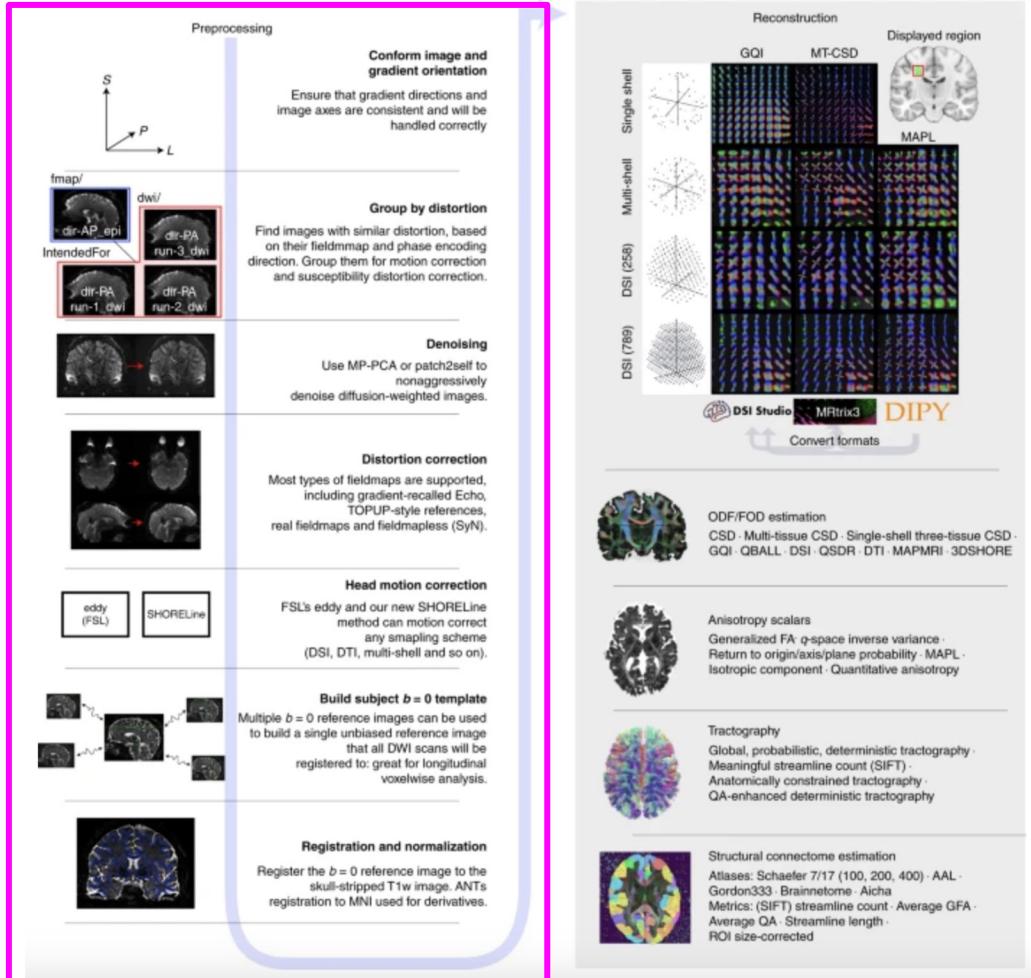
dataset_description.json

QSIPrep Workflows

Based on fMRIPrep

Preprocessing only is the default

BIDS is the foundation



Preprocessing in QSIPrep

diffusion-mri / code / 002_Run_QSI_Prep.sh 

...



aiadipolo Removing comments at the end of each line and moving them to the begin... 

34b4211 · 1 minute ago

 History

Code

Blame

16 lines (14 loc) · 639 Bytes

Raw



```
1 #!/bin/bash
2 SUBJ=$1
3
4 # This script is for running QSIPrep in singularity, on two subjects from the HBN dataset.
5 # Begin by cleaning the environment. We then specify paths to the singularity image, BIDS
6 # formatted dataset, preprocessing output directory, and Freesurfer license.
7 # We also specify that we want to run on a single subject (subjectID) and give the resolution # of the raw data.
8
9 singularity run --cleanenv \
10 ~/diffusion_project/my-qsi-prep.sif \
11 ~./../tmp/cache/data/ \
12 ~/diffusion_project/results/derivatives \
13 participant \
14 --participant-label ${SUBJ} \
15 --output-resolution 1.8 \
16 --fs-license-file ~/FS_license.txt
```

Preprocessing in QSIprep

Options

There may be cases where you want to change the default behavior, particularly in regard to:

- Merging multiple scans from a session
- Denoising and merging images
- Head motion correction
- Using only DWI data (bypassing the T1w workflows)

QSIPrep Preprocessing Output

Organization of the output:

Result_dir

- | dataset_description.json
- | **sub-01.html # Visual quality assessment reports per subject**
- | sub-02.html
- | **sub-01**
 - | **anat #preproc anat data, cross session**
 - | **figures #preproc figure in the html**
 - | **ses-HBNsiteRU #counfounds, transformation matrix, & preproc dwi**
 - | anat
 - | dwi
 - | | **sub-01_ses-xxx_acq-64dir_desc-ImageQC_dwi.csv # Quantitative QA**
- | **sub-02**

QSIPrep Preprocessing Output

Document the guide of html output Figure by Figure (We're the First one!)

Anatomical Processing

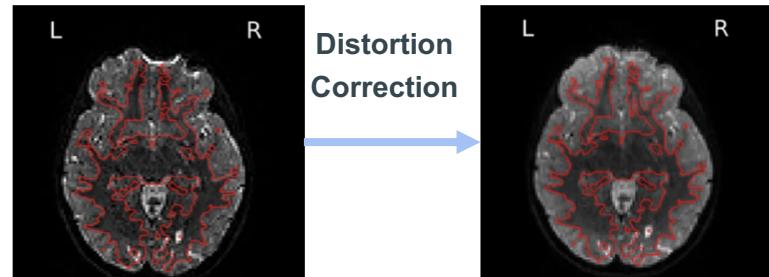
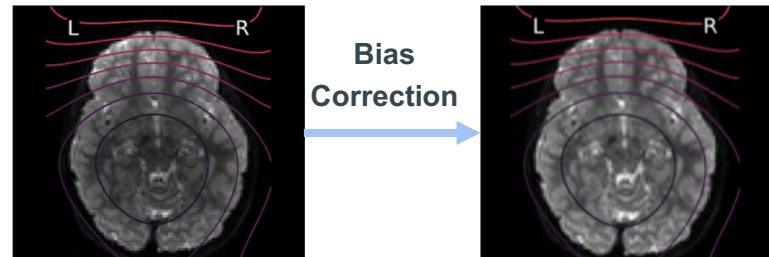
- Brain Mask and Segmentation
- T1w registration to MNI

Denoising

- MP-PCA Noise Denoising
- Bias Field Correction

Diffusion Processing

- b0 reference image
- q space sampling
- Susceptibility Distortion Correction
- Summary Stats



Reconstruction in QSIPrep

Preprocessing

Conform image and gradient orientation
Ensure that gradient directions and image axes are consistent and will be handled correctly

Group by distortion

Find images with similar distortion, based on their fieldmap and phase encoding direction. Group them for motion correction and susceptibility distortion correction.

Denoising

Use MP-PCA or patch2self to nonaggressively denoise diffusion-weighted images.

Distortion correction

Most types of fieldmaps are supported, including gradient-recalled Echo, TOPUP-style references, real fieldmaps and fieldmapless (SyN).

Head motion correction

FSLs eddy and our new SHORELine method can motion correct any sampling scheme (DSI, DTI, multi-shell and so on).

Build subject $b = 0$ template

Multiple $b = 0$ reference images can be used to build a single unbiased reference image that all DWI scans will be registered to: great for longitudinal voxelwise analysis.

Registration and normalization

Register the $b = 0$ reference image to the skull-stripped T1w image. ANTs registration to MNI used for derivatives.

Reconstruction

GQI, MT-CSD, Displayed region, MAPL, Single shell, Multi-shell, DSI (258), DSI (789), DSI Studio, MRtrix, DIPY, Convert formats

ODF/FOD estimation

CSD - Multi-tissue CSD, Single-shell three-tissue CSD - GQI, QBALL, DSI, QSDR, DTI, MAPMRI, 3DSHORE

Anisotropy scalars

Generalized FA/e-space inverse variance · Return to origin/axis/plane probability · MAPL · Isotropic component · Quantitative anisotropy

Tractography

Global, probabilistic, deterministic tractography · Meaningful streamline count (SIFT) · Anatomically constrained tractography · QA-enhanced deterministic tractography

Structural connectome estimation

Atlases: Schaefer 7/17 (100, 200, 400) · AAL · Gordon333 · Brainnetome · Alica · Metrics: (SIFT) streamline count · Average GFA · Average QA · Streamline length · ROI size-corrected

Reconstruction in QSIPrep

diffusion-mri / code / 003_Run_QSI_Recon.sh 

 **aiadipaolo** Pushing changes to 003 script for running qsiprep recon (Thank you Ke... 

Code Blame 20 lines (18 loc) · 656 Bytes

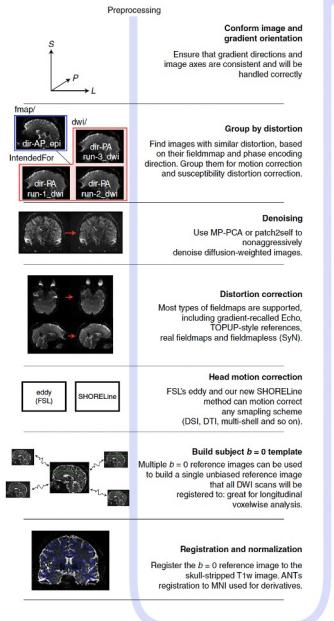
```
1 #!/bin/bash
2 SUBJ=$1
3
4 paths_main="/home/jovyan/diffusion_project"
5 paths_data="${paths_main}/data"
6 paths_derivatives="${paths_main}/results/derivatives"
7 paths_files="${paths_main}/freesurfer"
8
9 #Running QSIPrep reconstruction workflow on two subjects from HBN.
10 singularity run \
11     --bind "${paths_data}:/data" \
12     --bind "${paths_derivatives}:/out" \
13     --bind "${paths_files}:/files" \
14     /home/jovyan/diffusion_project/my-qsi-prep.sif \
15     /data /out participant \
16     --recon-input /out/qsiprep \
17     --recon-only \
18     --recon-spec mrtrix_multishell_msmt_pyafq_tractometry \
19     --participant-label $SUBJ \
20     --fs-license-file /files/license.txt
```

<https://qsiprep.readthedocs.io/en/latest/reconstruction.html>

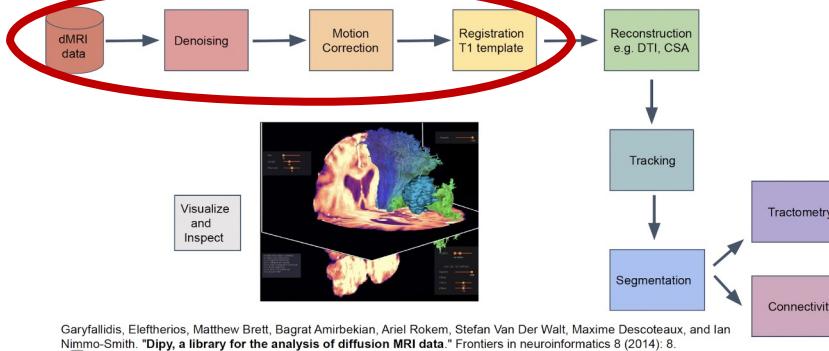
Option	MultiShell	DSI	DTI	Tractography
mrtrix_multishell_msmt_ACT-fast*	Yes	No	No	Probabilistic
mrtrix_multishell_msmt_ACT-hsvs	Yes	No	No	Probabilistic
mrtrix_multishell_msmt_noACT	Yes	No	No	Probabilistic
mrtrix_singleshell_ss3t_noACT	No	No	Yes	Probabilistic
mrtrix_singleshell_ss3t_ACT-hsvs	No	No	Yes	Probabilistic
mrtrix_multishell_msmt_ACT-fast*	No	No	Yes	Probabilistic
pyafq_tractometry	Yes	No	Yes	Both
mrtrix_multishell_msmt_pyafq_tractometry	Yes	No	Yes	Both
amico_noddi	Yes	No	No	None
dsi_studio_gqi	Yes	Yes	Yes*	Deterministic
dsi_studio_autotrack	Yes	Yes	Yes	Deterministic
dipy_mapmri	Yes	Yes	No	Both
dipy_3dshore	Yes	Yes	No	Both
csdsi_3dshore	Yes	Yes	No	Both
reorient_fslstd	Yes	Yes	Yes	None

Testing reconstruction models

QSI Prep

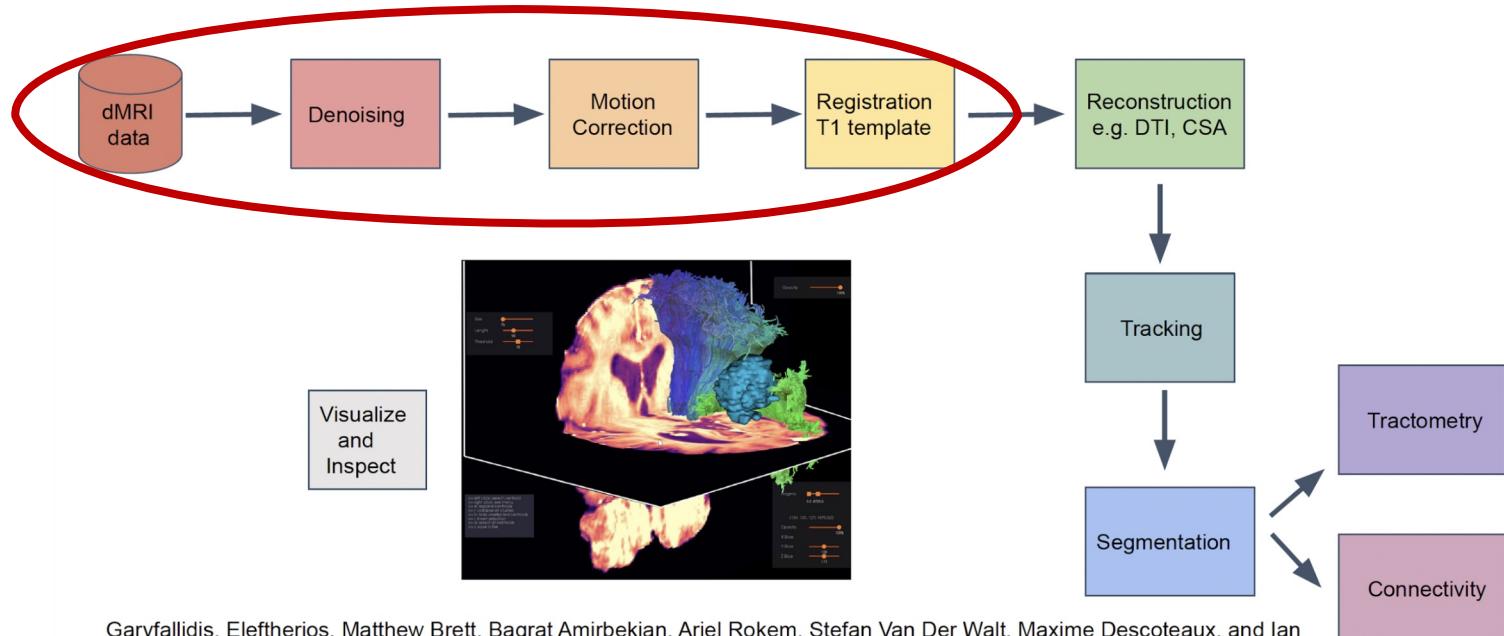


Simple preprocessing



Testing reconstruction models

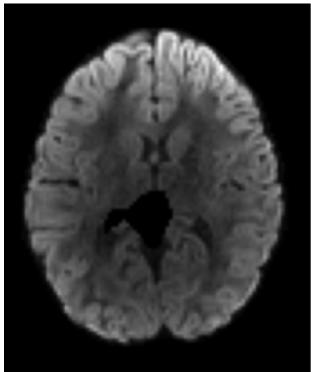
Simple preprocessing



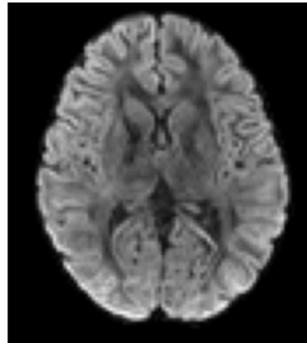
Garyfallidis, Eleftherios, Matthew Brett, Bagrat Amirbekian, Ariel Rokem, Stefan Van Der Walt, Maxime Descoteaux, and Ian Nimmo-Smith. "Dipy, a library for the analysis of diffusion MRI data." *Frontiers in neuroinformatics* 8 (2014): 8.

Approach comparisons

Simple preproc

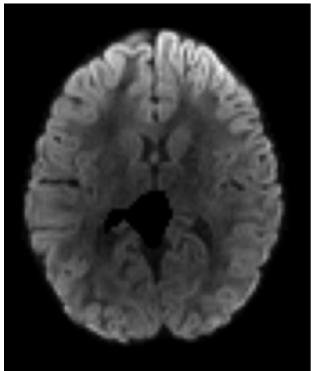


QSI prep data

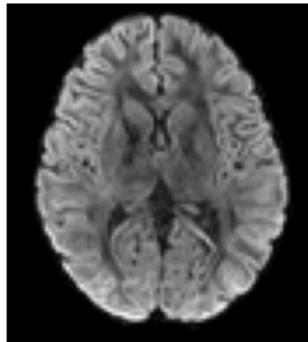


Approach comparisons

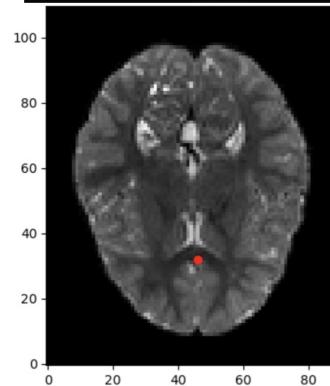
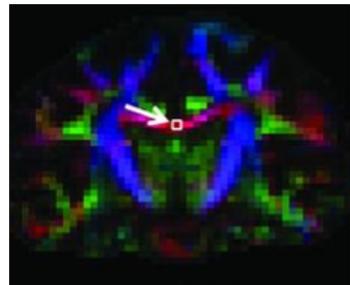
Simple preproc



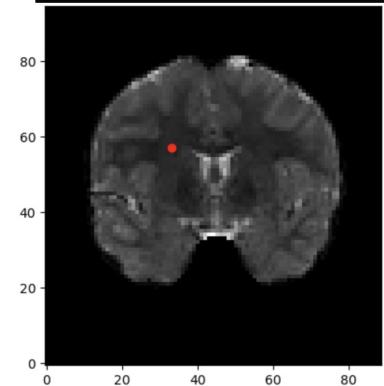
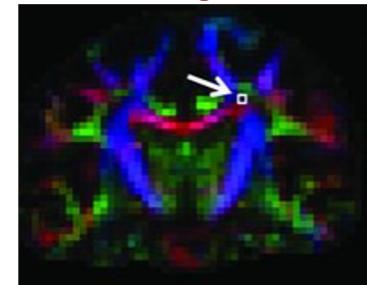
QSI prep data



Parallel fibers

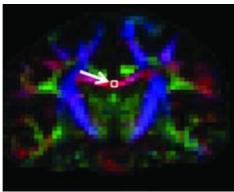


Crossing fibers



Approach comparisons: Simple vs QSI

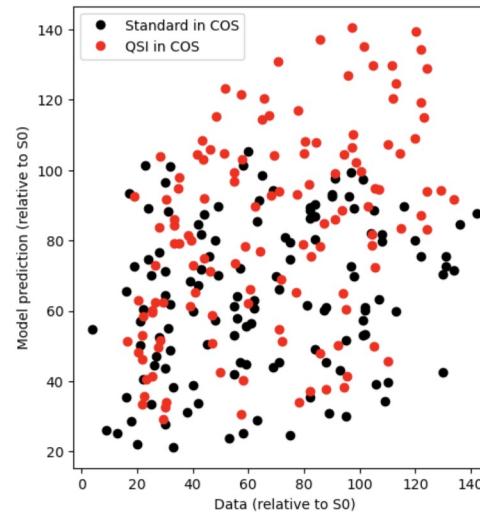
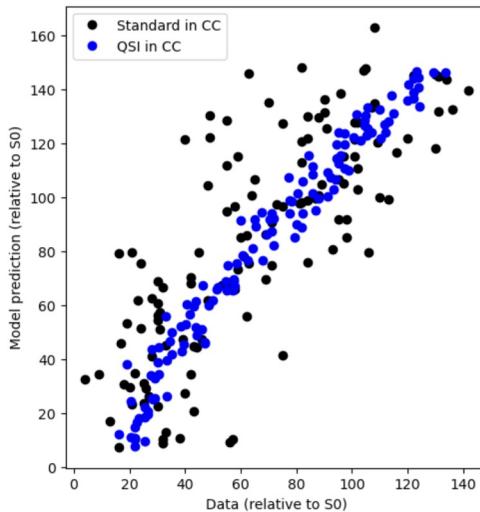
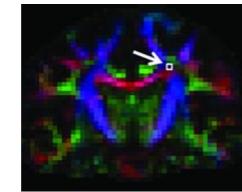
Parallel fibers



K-fold cross-validation

QSI vs Simple

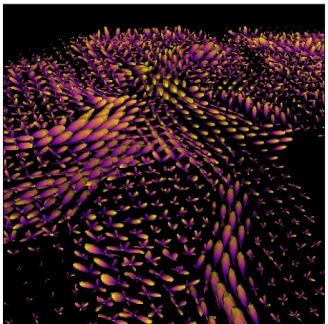
Crossing fibers



Comparing DTI vs CSD

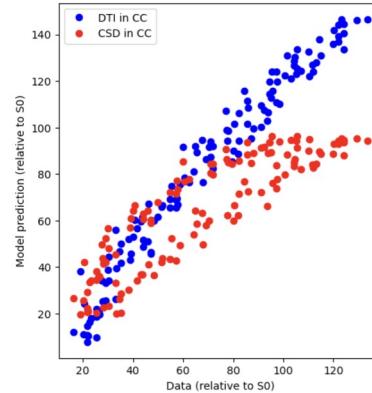
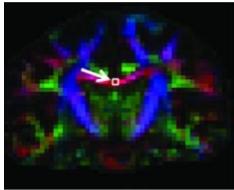


Diffusion
Tensor
Imaging
(DTI)

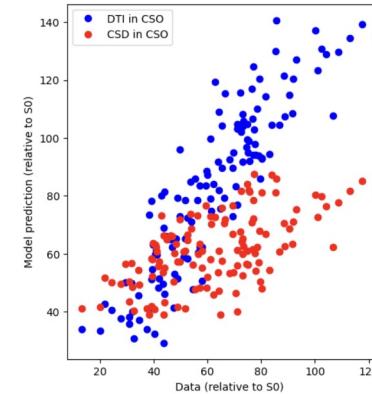
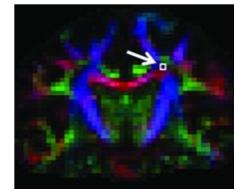


Constrained
Spherical
Deconvolution
(CSD)

Parallel fibers



Crossing fibers



Aims

A

Test using QSIprep for
preprocessing
and reconstructing dMRI data

✓
~

B

Comparing different reconstruction models:

Simple preproc vs QSIprep
Models DTI vs CSD

✓
✓



Pinboard

@Pinboard



The Programmers' Credo: we do these things not because they are easy, but because we thought they were going to be easy

BIG TAKE-AWAYS

- Do not work on a script in parallel within a git repo
- BIDS validation:
Have the `data_description.json`
- Relevance of documentation!
Bug in QSIprep:
 - or `_` for the argument flags
- In Bash, don't include spaces or comments after back-slash (`\`)
- Limitations in running dipy visualization function in JupyterLab



THANK YOU!