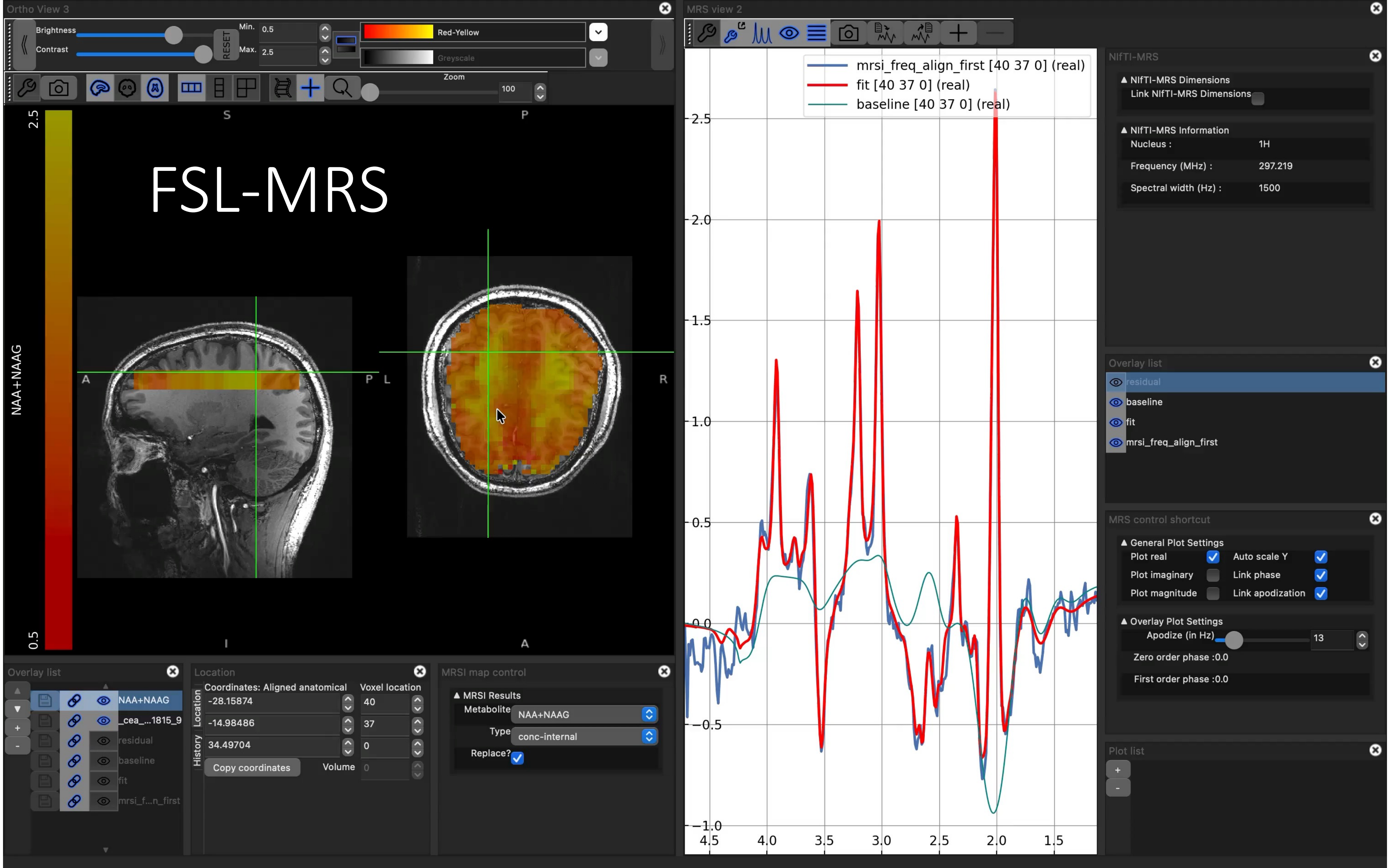
Additional and new FSL tools

- 2 more modalities supported
  - MR Spectroscopy
  - Arterial Spin Labeling
- More tools!
  - Registration: MMORF
  - Segmentation: TrUE-Net
  - Data pipelines: File-tree and FSL-pipe
  - Resting state: PROFUMO
  - Diffusion MRI: BENCH & WHIM

FSL-MRS



Ortho View 3

Min. 0.5
Max. 2.5
Red-Yellow
Greyscale
Zoom 100

Overlay list
- NAA+NAAG
- _cea_...1815_9
- residual
- baseline
- fit
- mrsi_f...n_first

Location
Coordinates: Aligned anatomical
Voxel location

Coordinates: Aligned anatomical	Voxel location
-28.15874	40
-14.98486	37
34.49704	0

Volume 0

MRSI map control
MRSI Results
Metabolite: NAA+NAAG
Type: conc-internal
Replace? ☑

MRS view 2

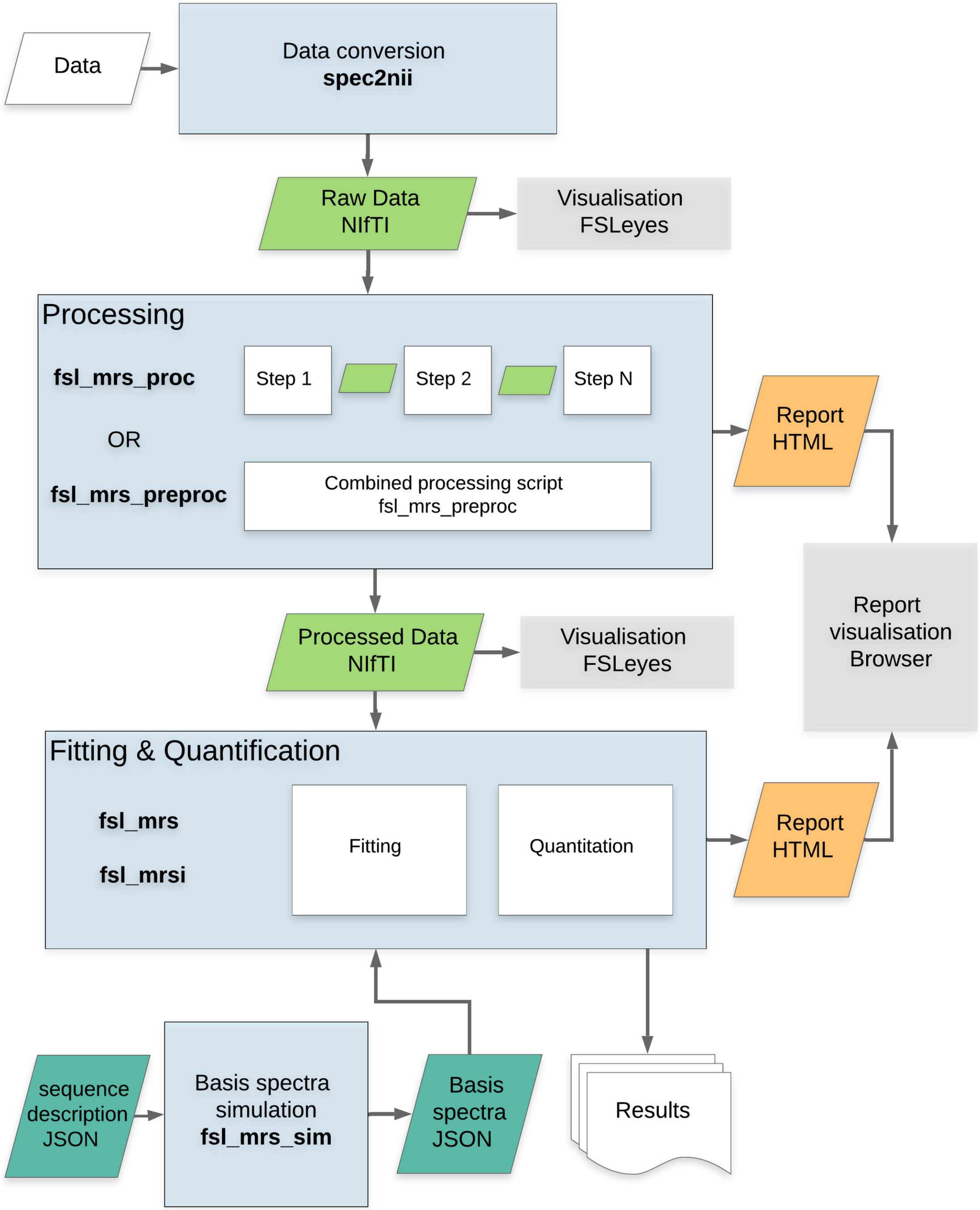
NIfTI-MRS
NIfTI-MRS Dimensions
Link NIfTI-MRS Dimensions ☐
NIfTI-MRS Information
Nucleus : 1H
Frequency (MHz) : 297.219
Spectral width (Hz) : 1500

Overlay list
- residual
- baseline
- fit
- mrsi_freq_align_first

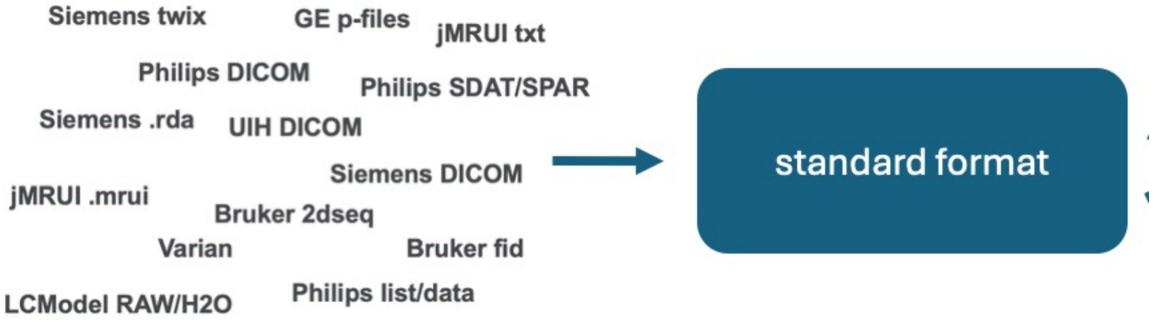
MRS control shortcut
General Plot Settings
Plot real ☑ Auto scale Y ☑
Plot imaginary ☐ Link phase ☑
Plot magnitude ☐ Link apodization ☑
Overlay Plot Settings
Apodize (in Hz) 13
Zero order phase :0.0
First order phase :0.0

Plot list

FSL-MRS = a complete pipeline



Data conversion



Siemens twix

GE p-files

jMRUI txt

Philips DICOM

Philips SDAT/SPAR

Siemens .rda

UIH DICOM

Siemens DICOM

jMRUI .mrui

Bruker 2dseq

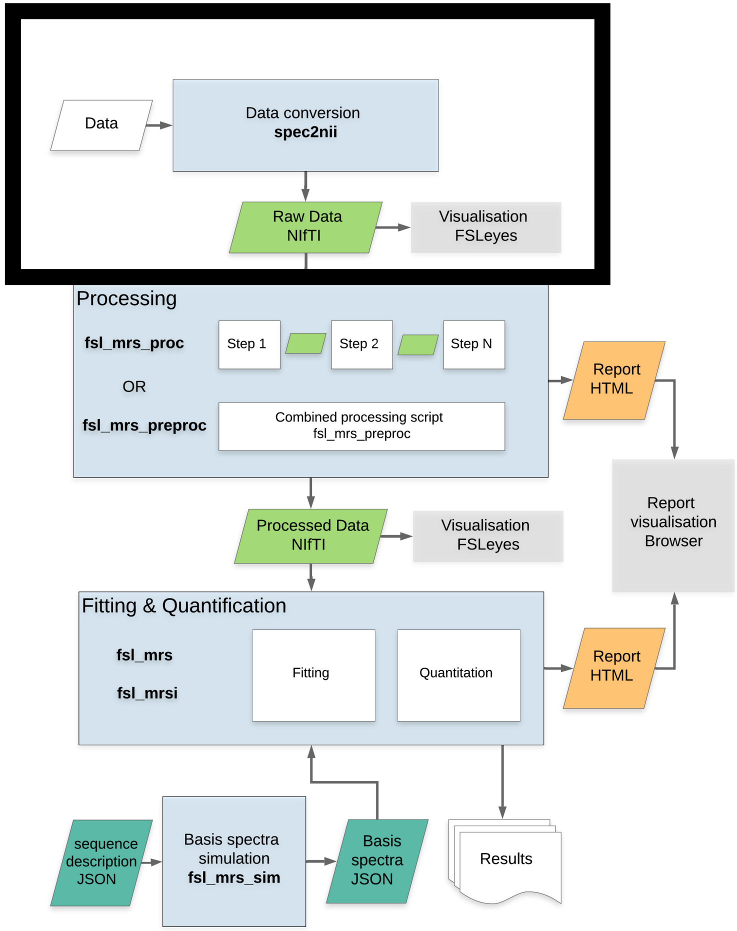
Varian

Bruker fid

LCModel RAW/H2O

Philips list/data

standard format



Data

Data conversion
spec2nii

Raw Data
NIfTI

Visualisation
FSLeyes

Processing

fsl_mrs_proc

Step 1

Step 2

Step N

OR

fsl_mrs_preproc

Combined processing script
fsl_mrs_preproc

Report
HTML

Report
visualisation
Browser

Processed Data
NIfTI

Visualisation
FSLeyes

Fitting & Quantification

fsl_mrs

fsl_mrsi

Fitting

Quantitation

Report
HTML

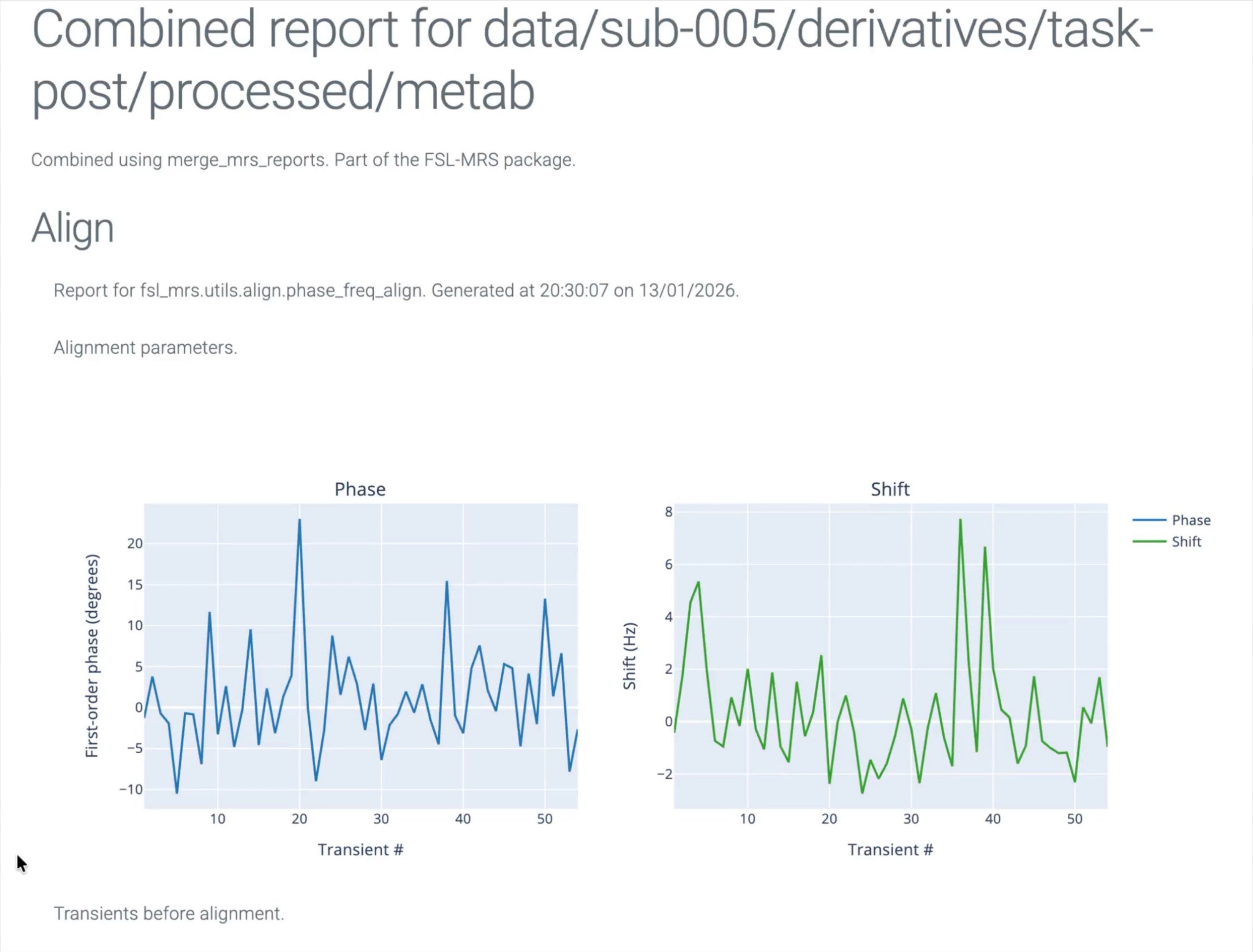
sequence
description
JSON

Basis spectra
simulation
fsl_mrs_sim

Basis
spectra
JSON

Results

Processing



Combined report for data/sub-005/derivatives/task-post/processed/metab

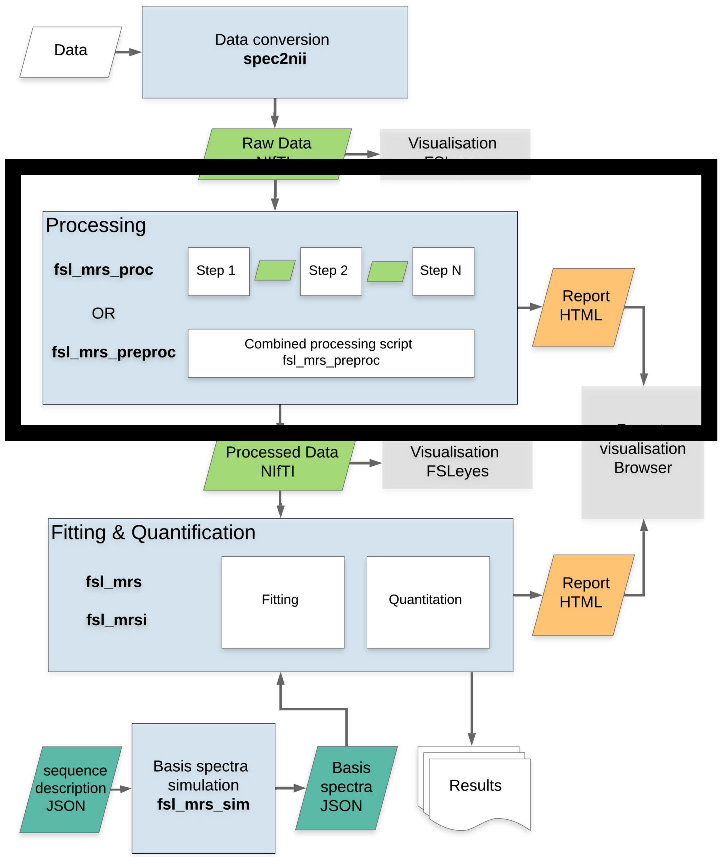
Combined using merge_mrs_reports. Part of the FSL-MRS package.

Align

Report for fsl_mrs.utils.align.phase_freq_align. Generated at 20:30:07 on 13/01/2026.

Alignment parameters.

Transients before alignment.



Data

Data conversion
spec2nii

Raw Data

Visualisation

Processing

fsl_mrs_proc

Step 1

Step 2

Step N

OR

fsl_mrs_preproc

Combined processing script
fsl_mrs_preproc

Report
HTML

visualisation
Browser

Processed Data
NIfTI

Visualisation
FSLeyes

Fitting & Quantification

fsl_mrs

fsl_mrsi

Fitting

Quantitation

Report
HTML

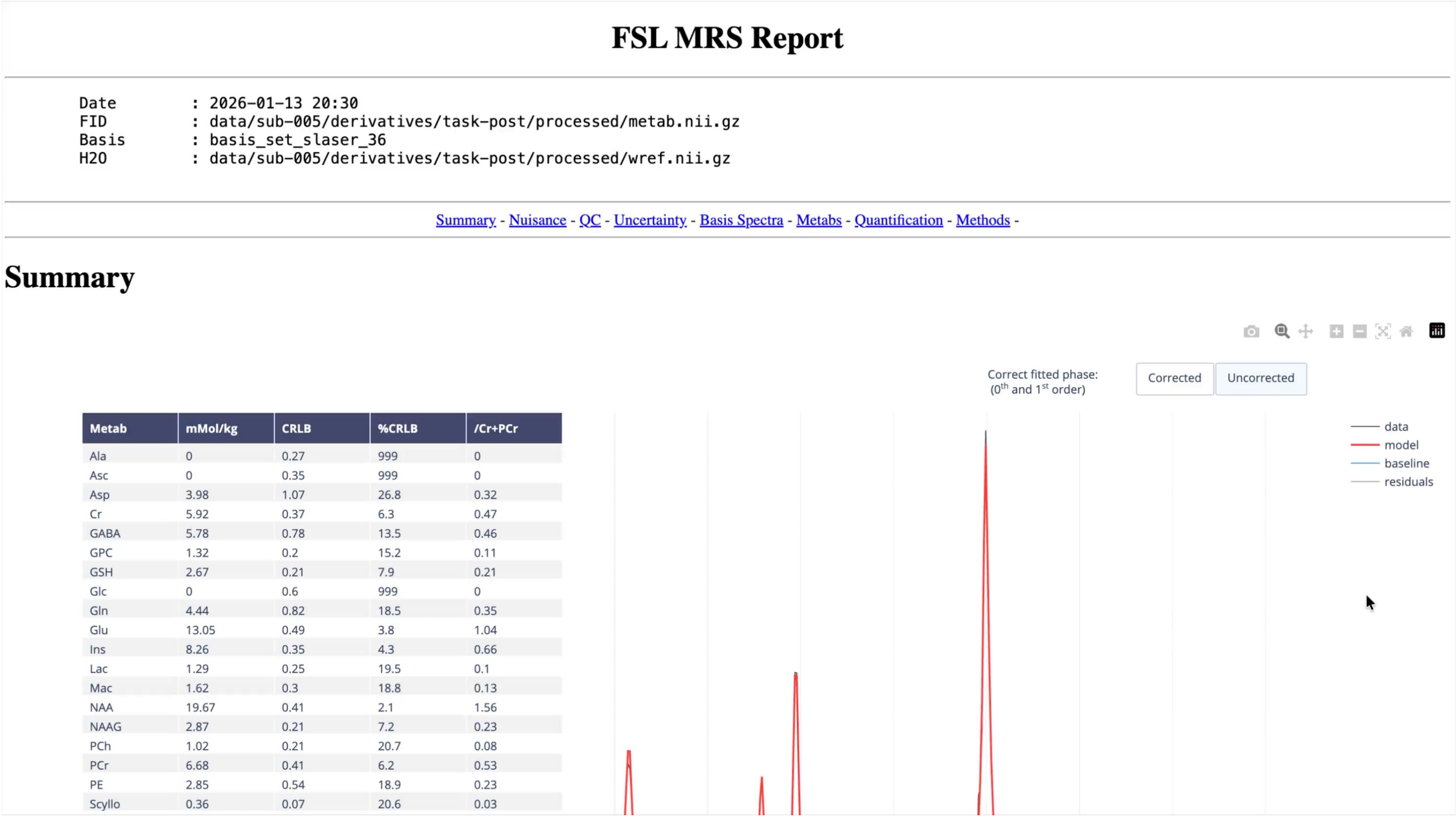
sequence
description
JSON

Basis spectra
simulation
fsl_mrs_sim

Basis
spectra
JSON

Results

Fitting



FSL MRS Report

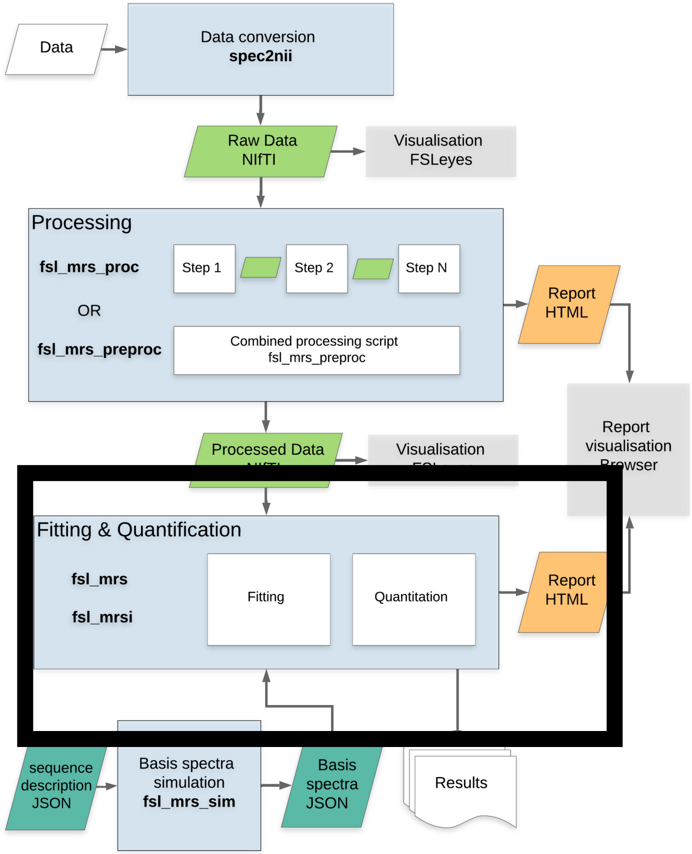
```
Date       : 2026-01-13 20:30
FID        : data/sub-005/derivatives/task-post/processed/metab.nii.gz
Basis      : basis_set_slaser_36
H2O        : data/sub-005/derivatives/task-post/processed/wref.nii.gz
```

Summary - Nuisance - QC - Uncertainty - Basis Spectra - Metabs - Quantification - Methods -

Summary

Correct fitted phase: (0^{th} and 1^{st} order)

Metab	mMol/kg	CRLB	%CRLB	/Cr+PCr
Ala	0	0.27	999	0
Asc	0	0.35	999	0
Asp	3.98	1.07	26.8	0.32
Cr	5.92	0.37	6.3	0.47
GABA	5.78	0.78	13.5	0.46
GPC	1.32	0.2	15.2	0.11
GSH	2.67	0.21	7.9	0.21
Glc	0	0.6	999	0
Gln	4.44	0.82	18.5	0.35
Glu	13.05	0.49	3.8	1.04
Ins	8.26	0.35	4.3	0.66
Lac	1.29	0.25	19.5	0.1
Mac	1.62	0.3	18.8	0.13
NAA	19.67	0.41	2.1	1.56
NAAG	2.87	0.21	7.2	0.23
PCh	1.02	0.21	20.7	0.08
PCr	6.68	0.41	6.2	0.53
PE	2.85	0.54	18.9	0.23
Scyllo	0.36	0.07	20.6	0.03



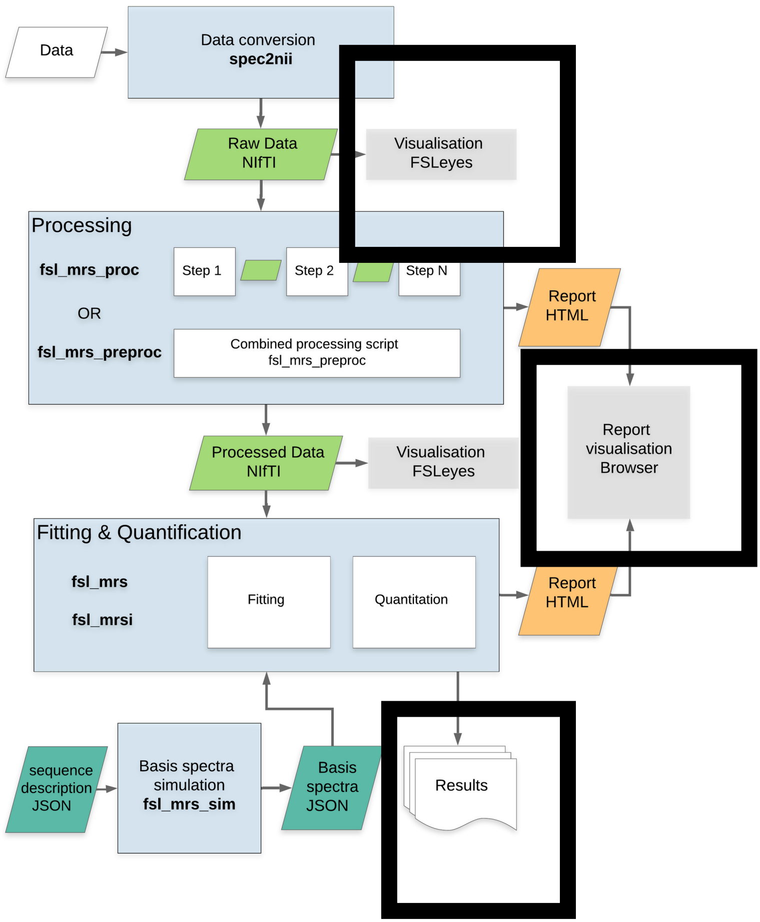
Visualisation & QC

index	NAA
count	18
mean	24.1
std	3.85
min	16.7
25%	22.3
50%	24.3
75%	26.9
max	30.1

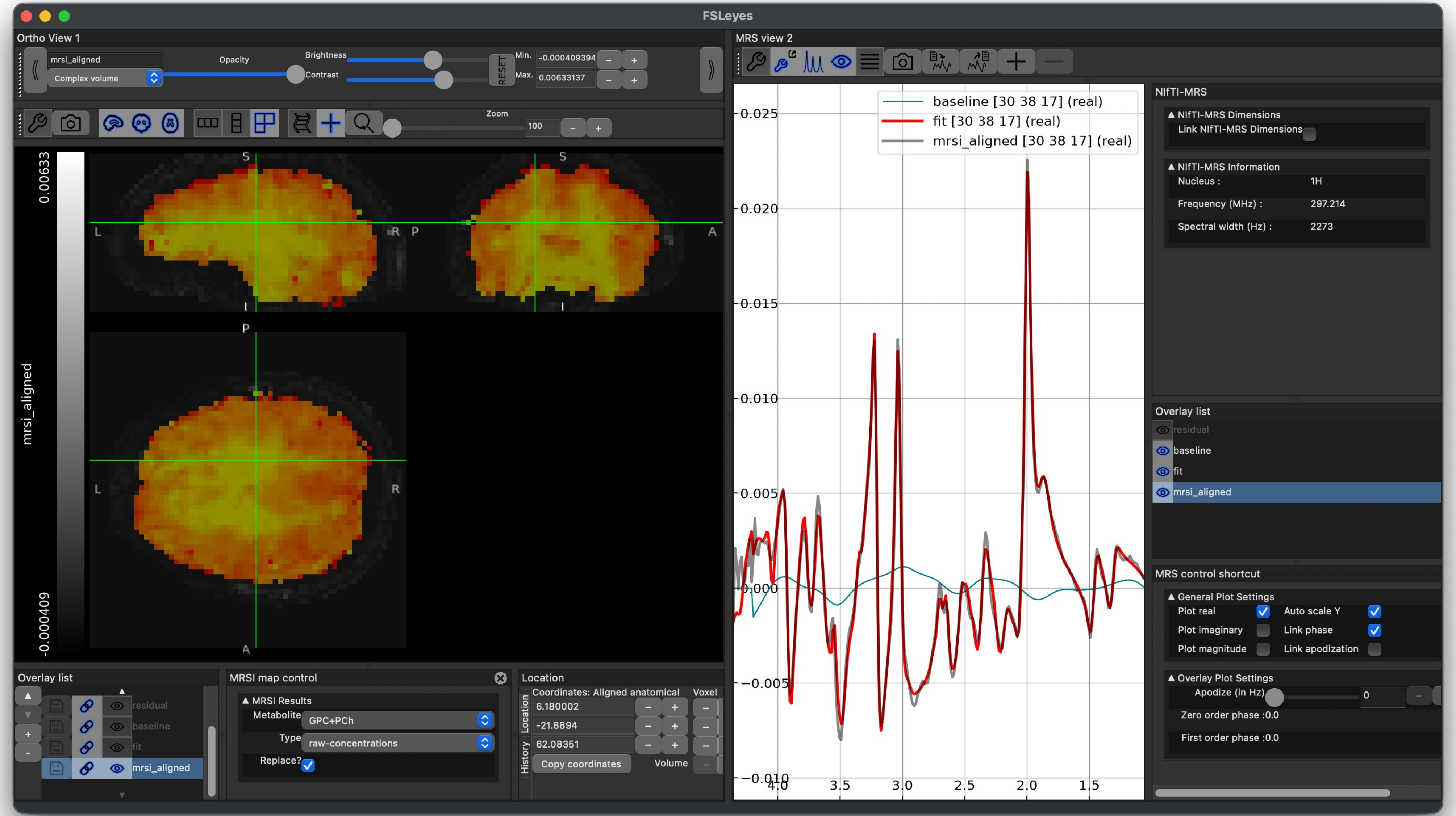
index	FWHM	SNR
count	18	18
mean	13.2	72.8
std	2.95	48.2
min	9.97	9.74
25%	11.5	29
50%	12.6	64.7
75%	13	118
max	22.3	136

F7T_2013_40_738_stim

Average data



High-resolution MRSI – process, fit, and view results



Min. -0.000409394
Max. 0.00633137
Zoom 100

▲ NIfTI-MRS Dimensions
Link NIfTI-MRS Dimensions ☐

▲ NIfTI-MRS Information
Nucleus : 1H
Frequency (MHz) : 297.214
Spectral width (Hz) : 2273

▲ General Plot Settings
Plot real ☑ Auto scale Y ☑
Plot imaginary ☐ Link phase ☑
Plot magnitude ☐ Link apodization ☐

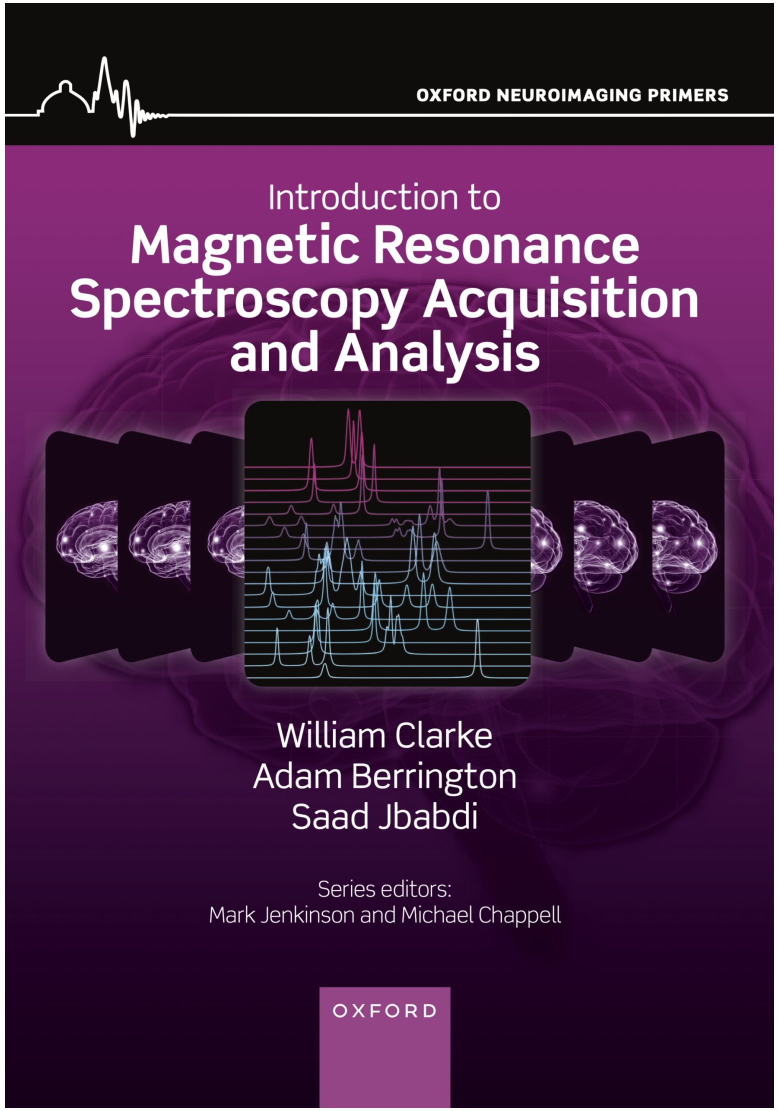
▲ Overlay Plot Settings
Apodize (in Hz) 0
Zero order phase :0.0
First order phase :0.0

▲ MRSI Results
Metabolite GPC+PCh
Type raw-concentrations
Replace? ☑

Coordinates: Aligned anatomical
6.180002
-21.8894
62.08351
Voxel
Volume

Whole brain high-resolution MRSI fitting - Siemens WIP - 28k voxels fit in 30 minutes

Spectroscopy book



OXFORD NEUROIMAGING PRIMERS

Introduction to
Magnetic Resonance Spectroscopy Acquisition and Analysis

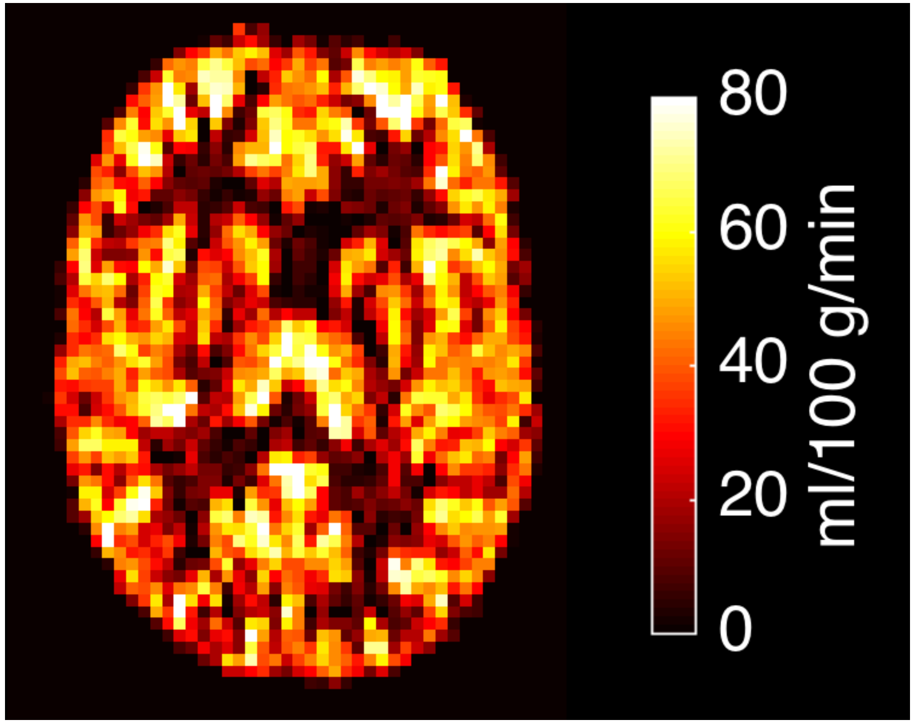
William Clarke
Adam Berrington
Saad Jbabdi

Series editors:
Mark Jenkinson and Michael Chappell

OXFORD

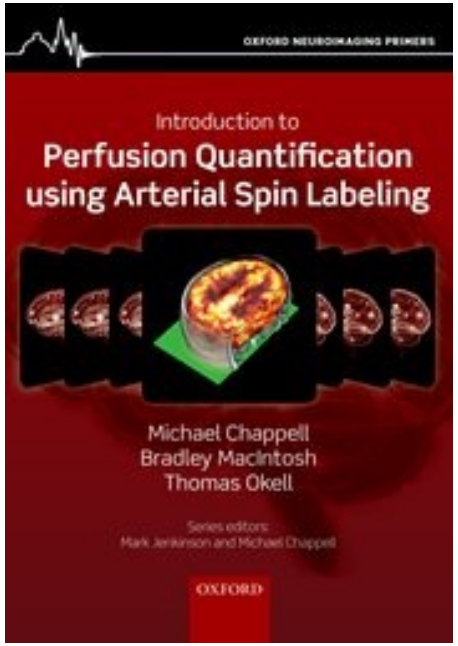
Arterial Spin Labelling

- **Don’t forget physiology:** ASL the one extra thing you should include in your study*
- **Perfusion** is a measurement of delivery of blood to capillary bed
  - Related to nutrient delivery.
  - Altered by task activity.
  - Changes in disease.
- ASL uses blood-water as an endogenous tracer.
  - Non-invasive.
  - Measures **absolute** Cerebral Blood Flow (CBF).
  - Can measure changes separated in time.
- Quick to acquire and easy to quantify
  - 2-5 min scan.
  - Vendor sequences available.
  - Built into FSL: **BASIL.**



*along with all those other ‘just one more thing’…

Arterial Spin Labelling



OXFORD NEUROIMAGING PRIMERS

Introduction to
Perfusion Quantification
using Arterial Spin Labeling

Michael Chappell
Bradley MacIntosh
Thomas Okell

Series editors:
Mark Jenkinson and Michael Chappell

OXFORD

Oxford Neuroimaging Primers:

Introduction to Perfusion Quantification using Arterial Spin Labelling

Based on FSL course materials.

www.neuroimagingprimers.org

Examples using BASIL

FSL: The FMRIB Software Library

BASIL: www.fmrib.ox.ac.uk/fsl/basil

User guide & tutorials for FSL v6.0+

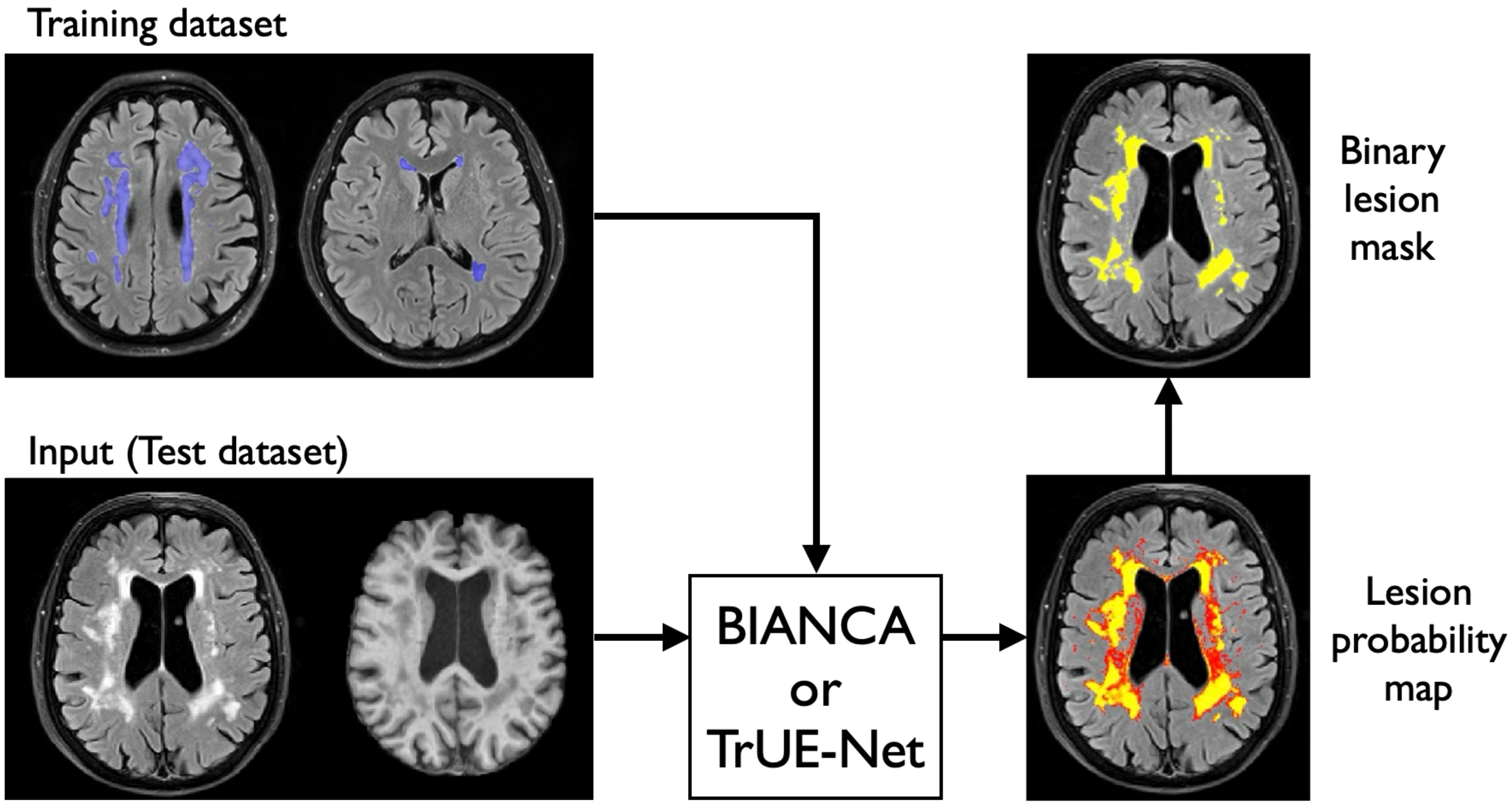
Quantified Imaging

www.quantified-imaging.com

QASL: For clinical research/applications (FDA-cleared)

Lesion/WMH Segmentation in FSL

Two tools now available in FSL!



Training dataset

Input (Test dataset)

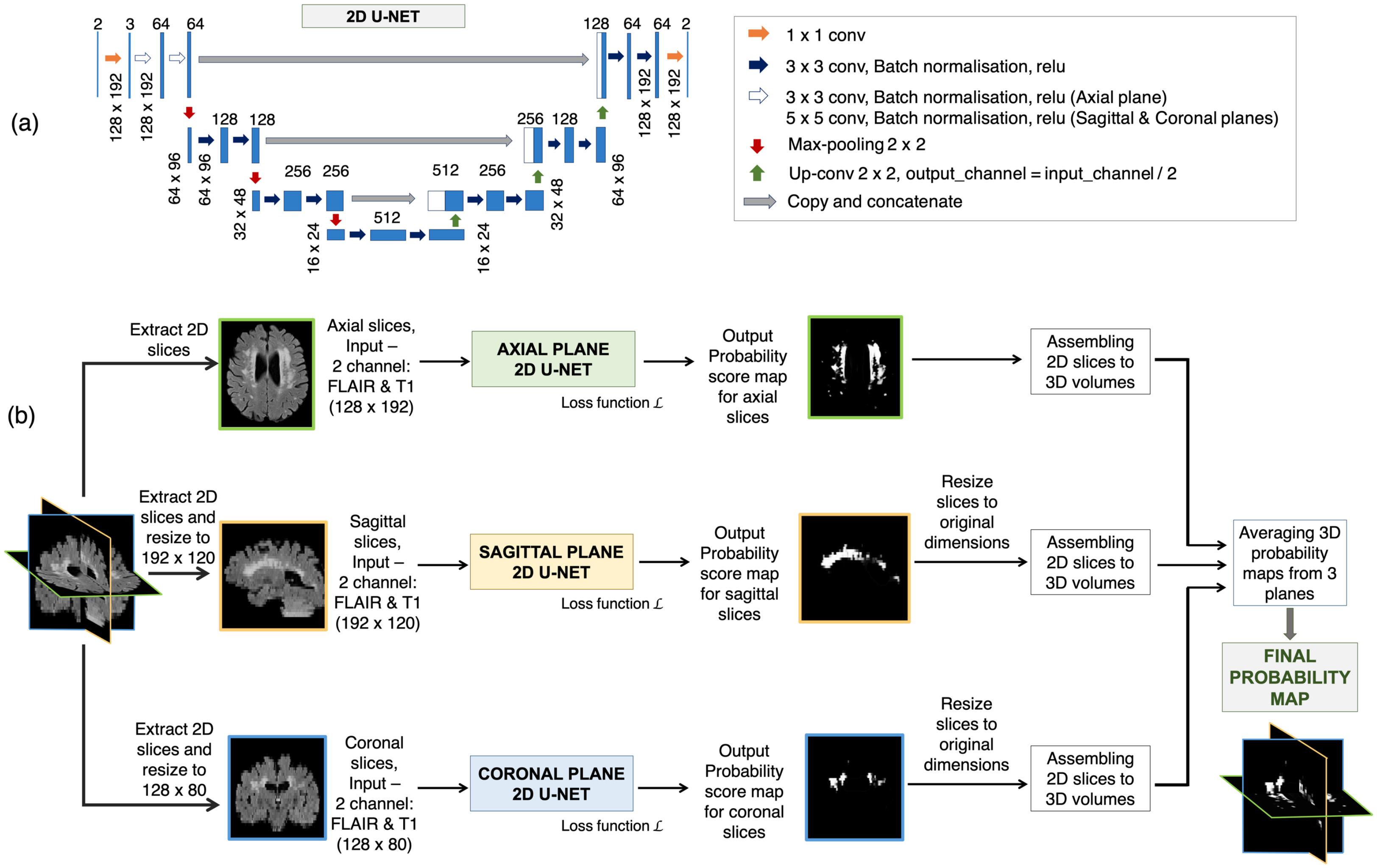
BIANCA
or
TrUE-Net

Binary
lesion
mask

Lesion
probability
map

Triplanar U-Net Ensemble Network (TrUE-Net) is the first deep learning tool in FSL for lesion segmentation

Triplanar ensemble U-Net (TrUE-Net) Methodology



➡ 1 x 1 conv

➡ 3 x 3 conv, Batch normalisation, relu

⇨ 3 x 3 conv, Batch normalisation, relu (Axial plane)
5 x 5 conv, Batch normalisation, relu (Sagittal & Coronal planes)

⬇ Max-pooling 2 x 2

⬆ Up-conv 2 x 2, output_channel = input_channel / 2

⇨ Copy and concatenate

Extract 2D slices → Axial slices, Input – 2 channel: FLAIR & T1 (128 x 192) → **AXIAL PLANE 2D U-NET** (Loss function $\mathcal{L}$) → Output Probability score map for axial slices → Assembling 2D slices to 3D volumes

Extract 2D slices and resize to 192 x 120 → Sagittal slices, Input – 2 channel: FLAIR & T1 (192 x 120) → **SAGITTAL PLANE 2D U-NET** (Loss function $\mathcal{L}$) → Output Probability score map for sagittal slices → Resize slices to original dimensions → Assembling 2D slices to 3D volumes

Extract 2D slices and resize to 128 x 80 → Coronal slices, Input – 2 channel: FLAIR & T1 (128 x 80) → **CORONAL PLANE 2D U-NET** (Loss function $\mathcal{L}$) → Output Probability score map for coronal slices → Resize slices to original dimensions → Assembling 2D slices to 3D volumes

Averaging 3D probability maps from 3 planes

FINAL PROBABILITY MAP

Sundaresan et al., 2021 MEDIA

TrUE-Net vs BIANCA

Similarities

- Designed for WMH
- Supervised (needs training labels or pretrained model)
- Multimodal
- Return lesion probability map

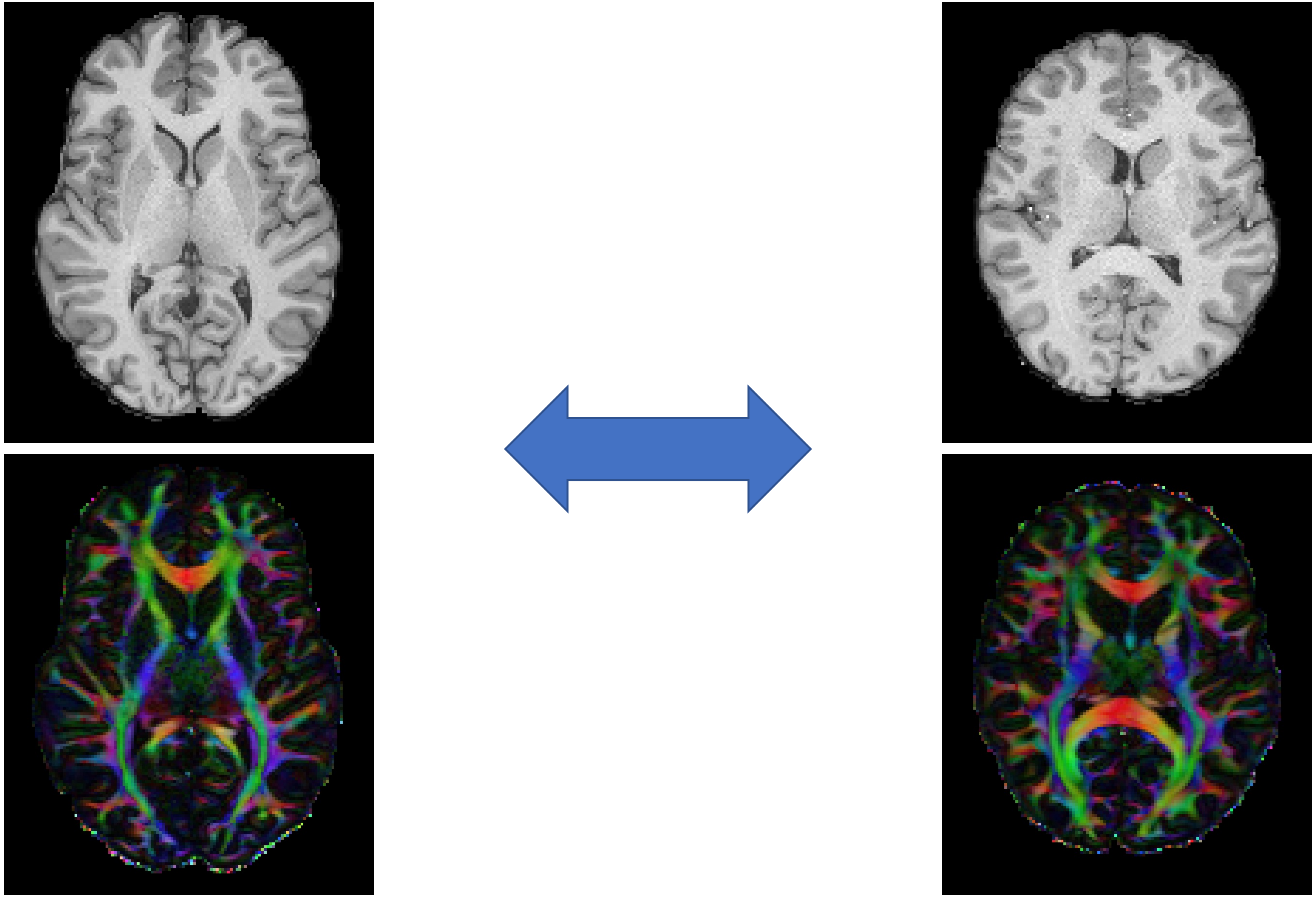
Differences

- TrUE-Net is better at detecting small deep WM lesions
- Possibility for TrUE-Net to fine-tune an existing model
- Promising results of TrUE-Net on different types of lesions
- TrUE-Net is available in FSL but needs add-on module to install in FSL
- GPU needed for TrUE-Net best performance (essential for training and fine tuning)
- BIANCA more widely used (e.g. UK Biobank), TrUE-Net newer, less tested.

MMORF

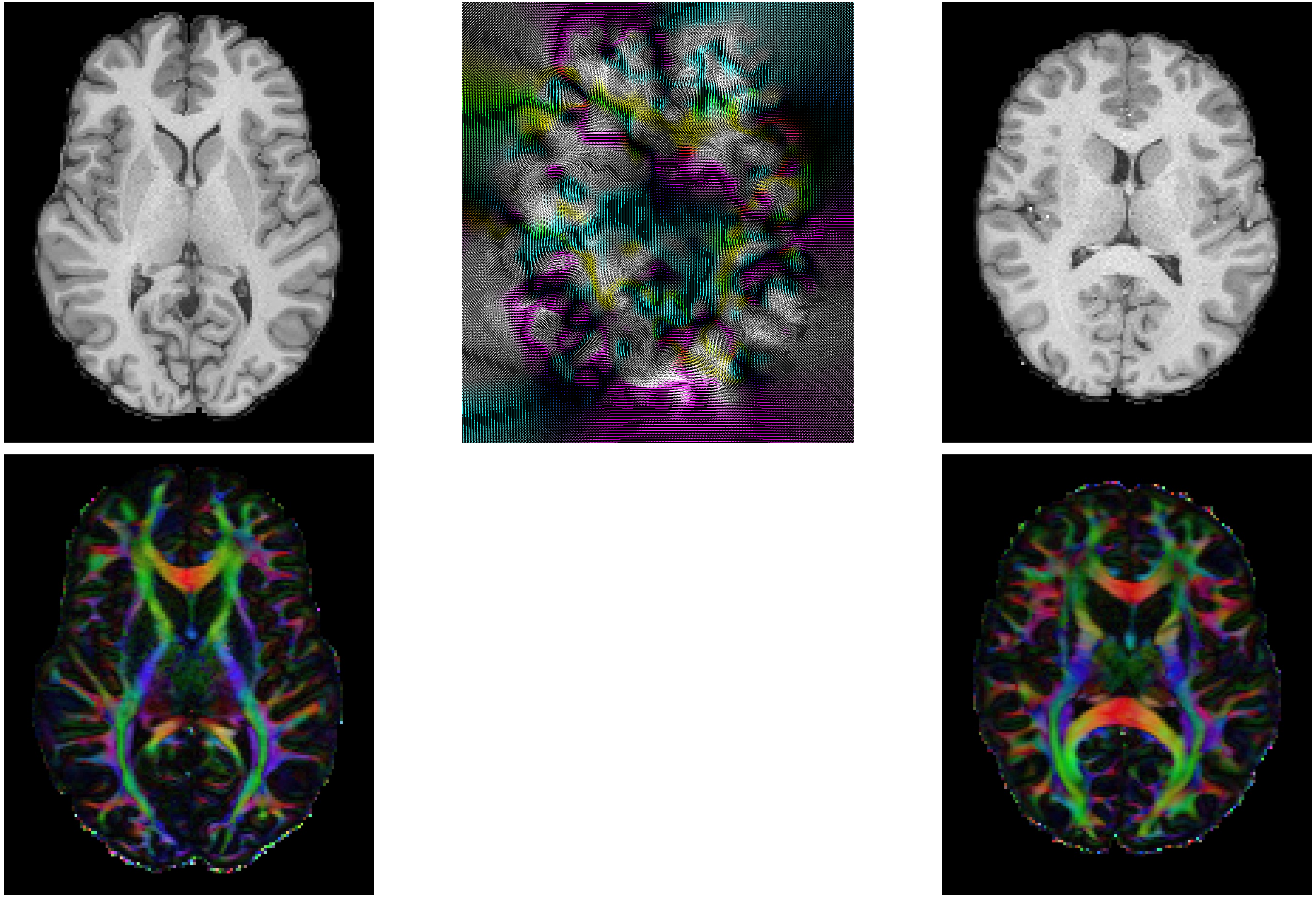
FSL’s MultiMOdal Registration Framework

Multimodal registration:



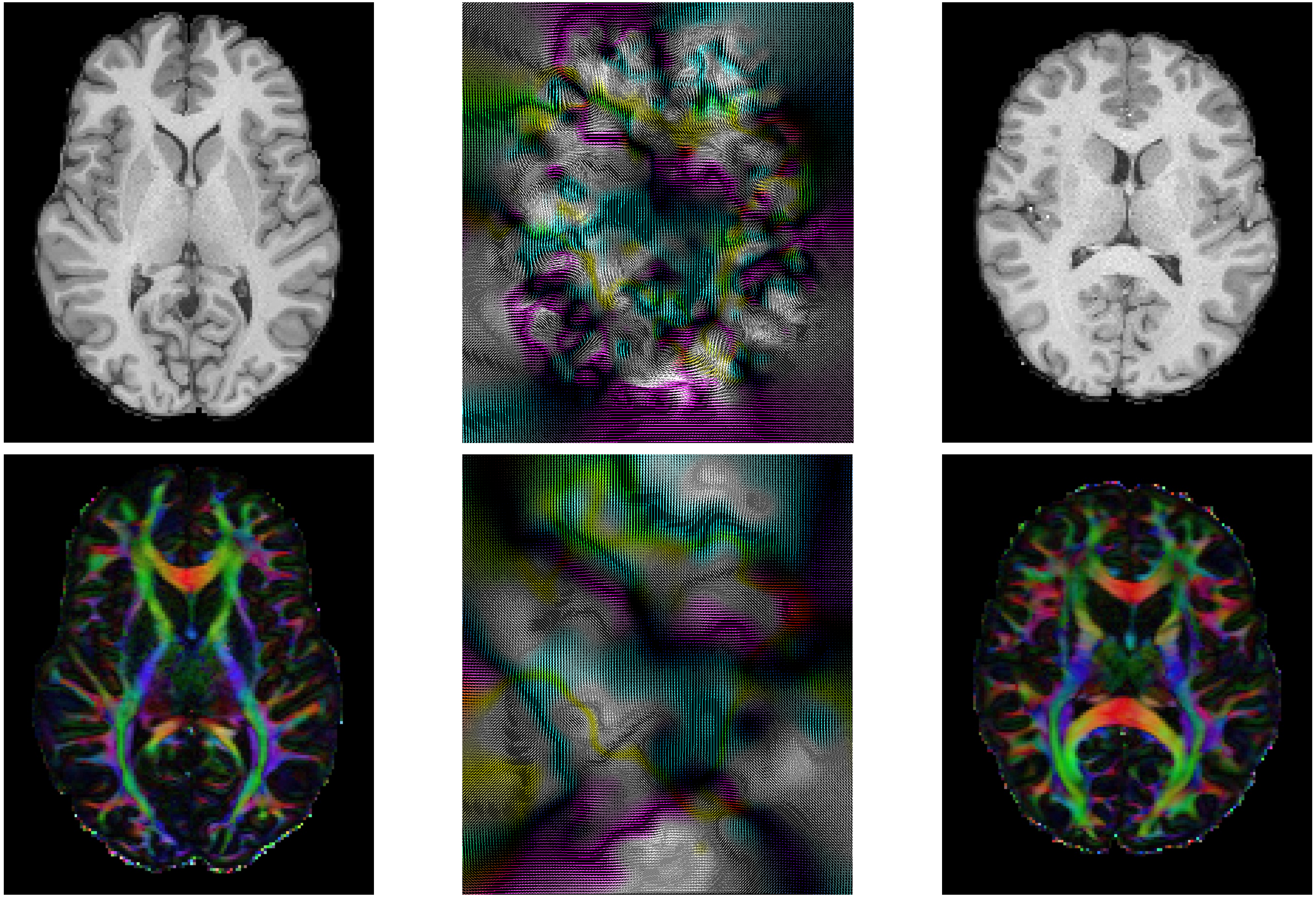
Frederik Lange

Multimodal registration:



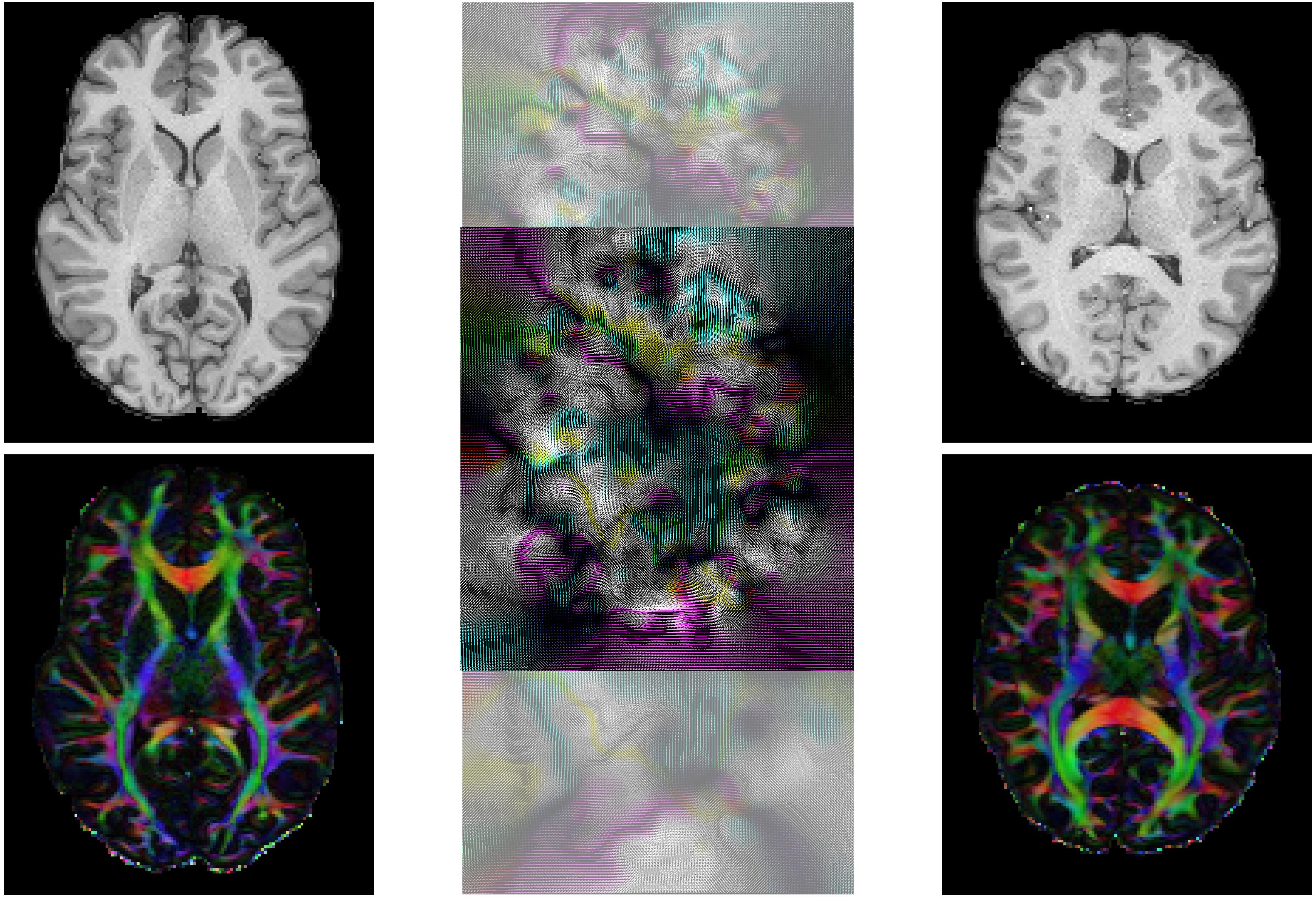
Frederik Lange

Multimodal registration:



Frederik Lange

Multimodal registration:



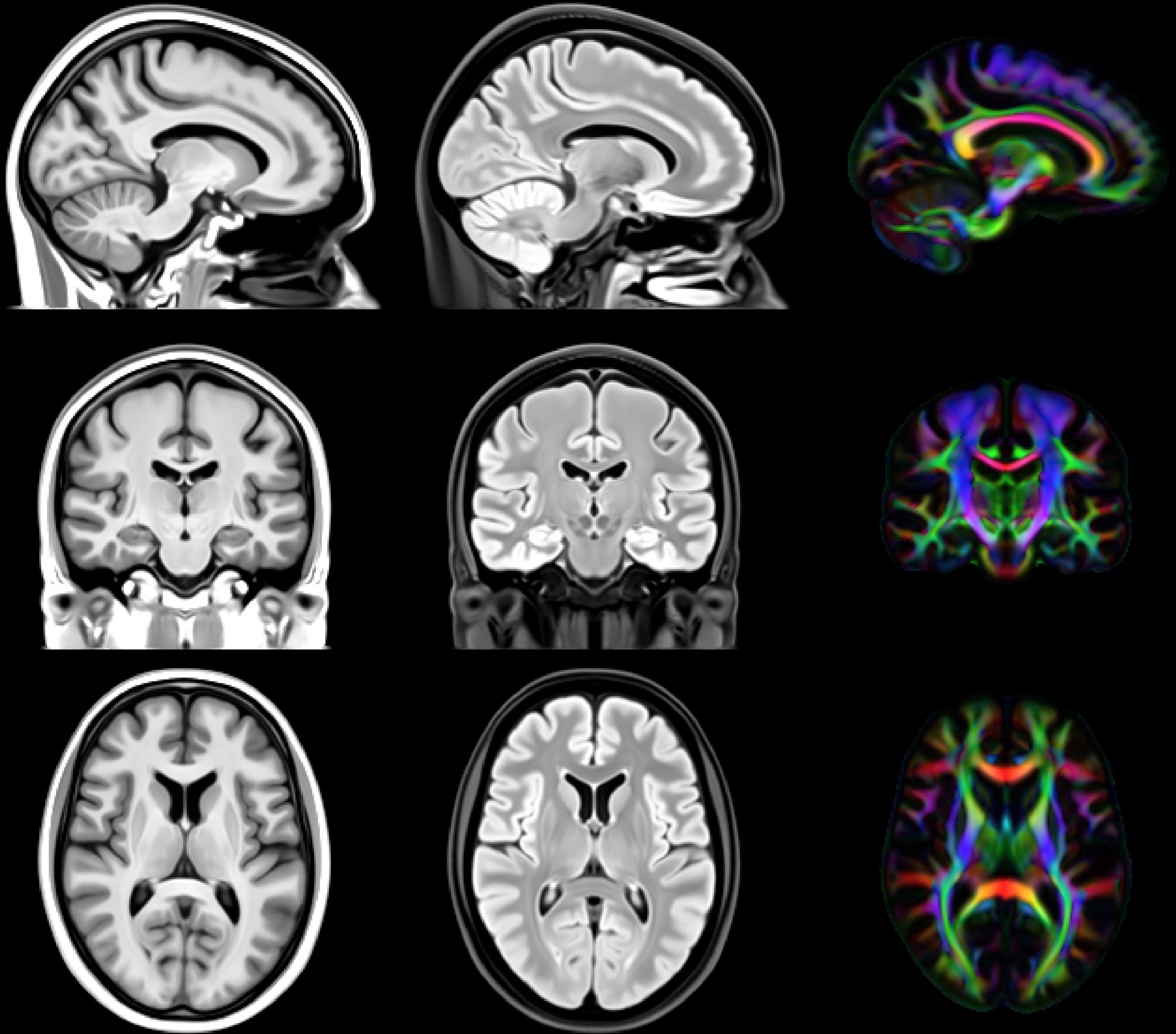
Frederik Lange

Potential Advantages of MMORF

- Better overall accuracy (with less distortion)
  - More modalities = more information driving alignment
- Single warp for multimodal datasets
  - No need to register each modality individually
  - Within-subject correspondence across modalities maintained in standard space
- Structural analyses (VBM, TBM, segmentation propagation)
  - Benefits from MMORF's anatomically plausible regularisation
- Voxelwise diffusion analyses
  - When driving registration with DTI
- Fixelwise diffusion analyses
  - Using the new WHIM tool from Hossein Rafipoor

Oxford Multimodal Template (OMM-1)

- 240 UKB individuals
- 50-55 YOA
- 50% female
- T1w, T2 FLAIR, DTI modalities
- A new standard for multimodal imaging analysis
- Unifying volumetric analysis space across modalities in UKB
- Available in FSL 6.0.7.6 and up

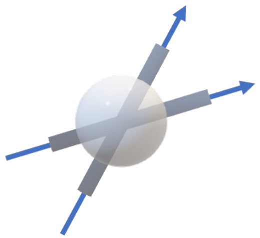


Arthofer C. et al; Internally-consistent and fully-unbiased multimodal MRI brain template construction from UK Biobank: Oxford-MM bioRxiv 2023.11.30.569378; https://doi.org/10.1101/2023.11.30.569378

WHIM

(White matter Hierarchical Model)

Ball & Sticks Model

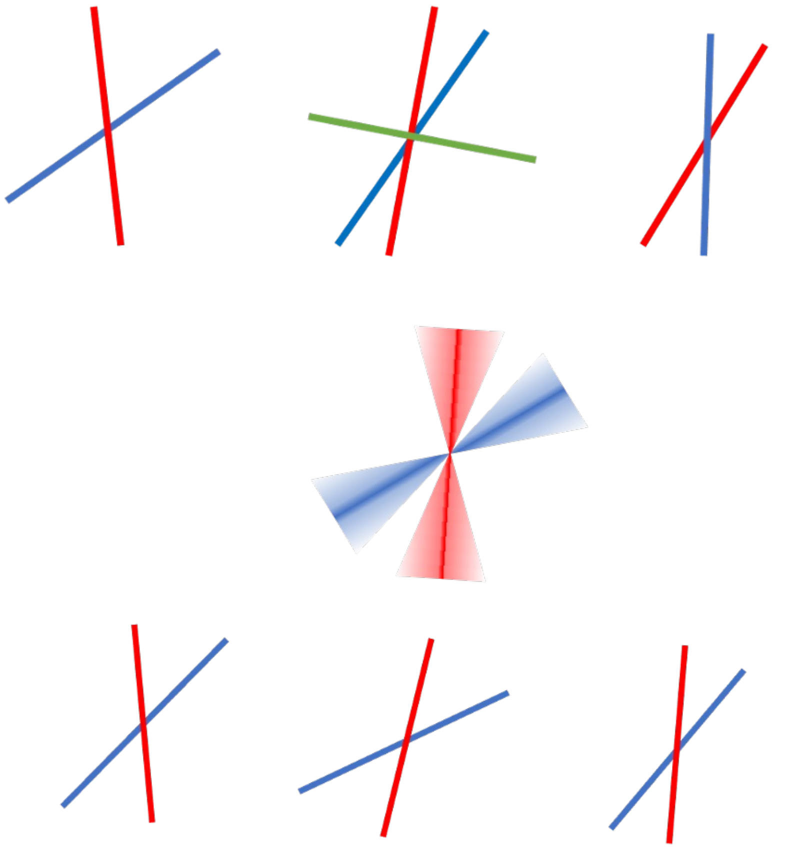


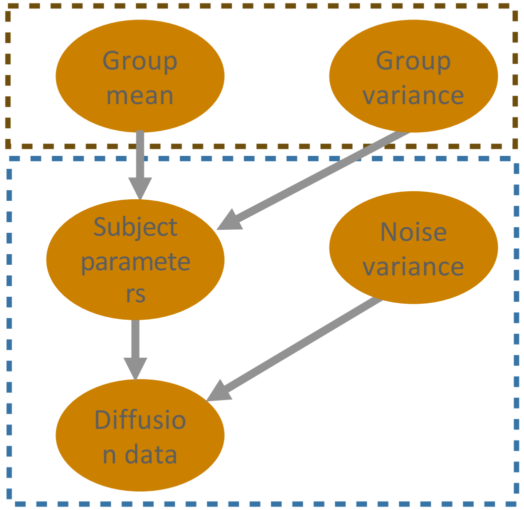
🟦 Fibre 1
🟥 Fibre 2
🟩 Fibre 3

Subject 1

Subject 2

Subject 3





Group parameters
(Template)

Group mean

Group variance

Subject parameters

Noise variance

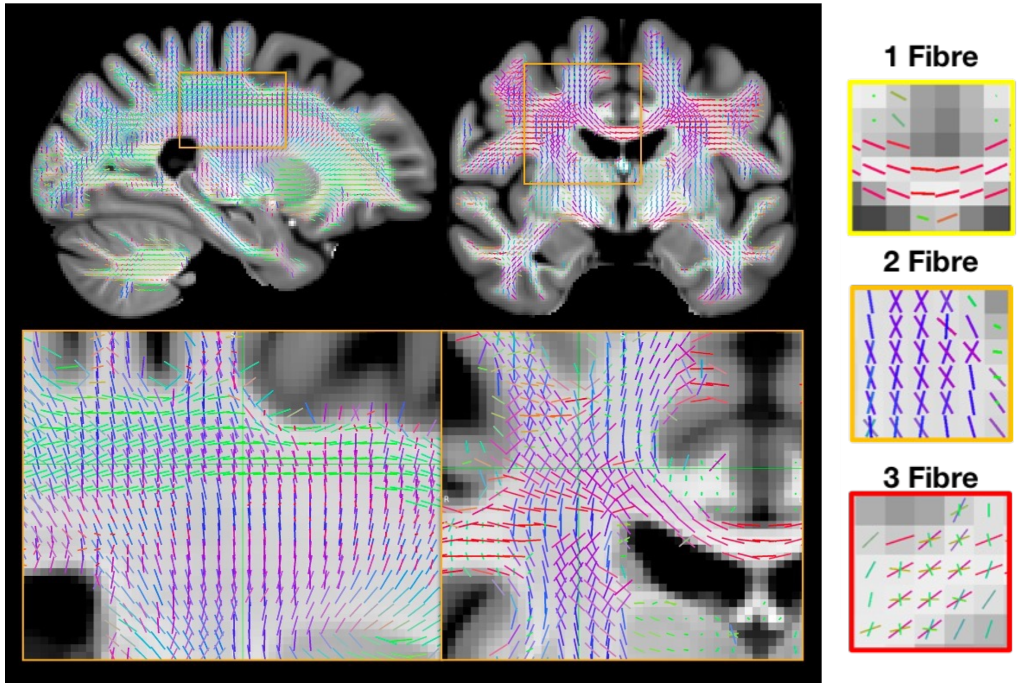
Diffusion data

Subject
parameters

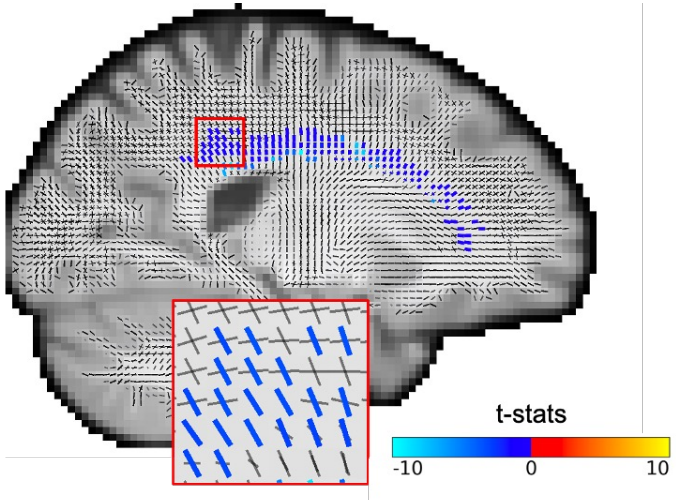
WHIM

(White matter Hierarchical Model)

Creates a group level
white matter Fibre Template

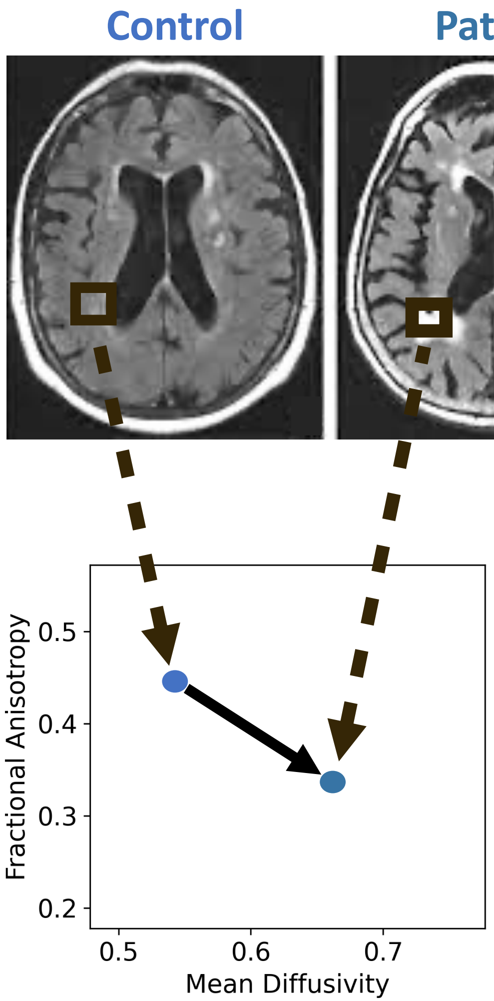


Allows for:
Fibre specific statistical inference
within each voxel across subjects



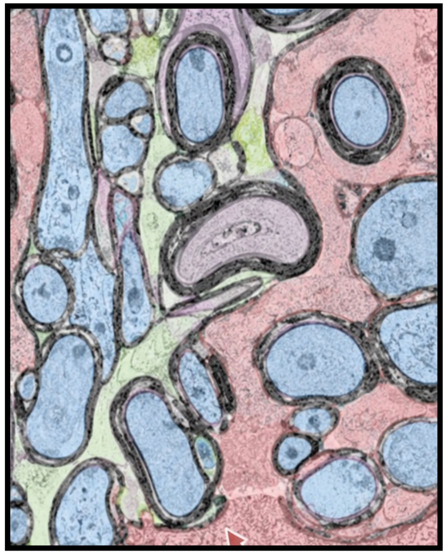
BENCH

(Bayesian EstimatioN of Change)

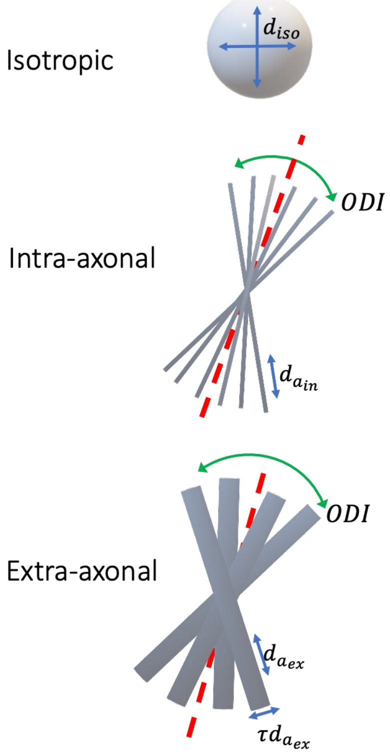


FA ↓, MD↑
What does this mean?

Tissue Microstructure

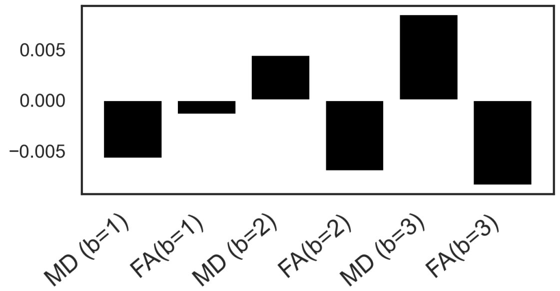


Biophysical Modelling

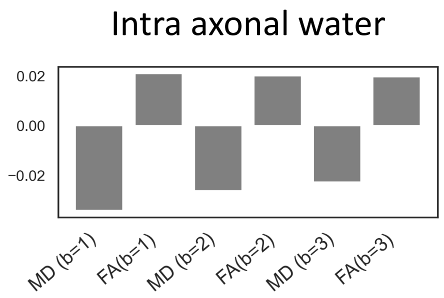


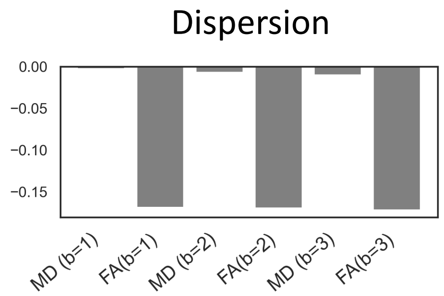
BENCH compares change fingerprints

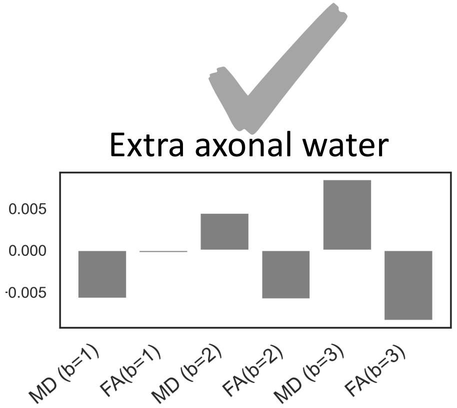
Actual Change:



Change Models:

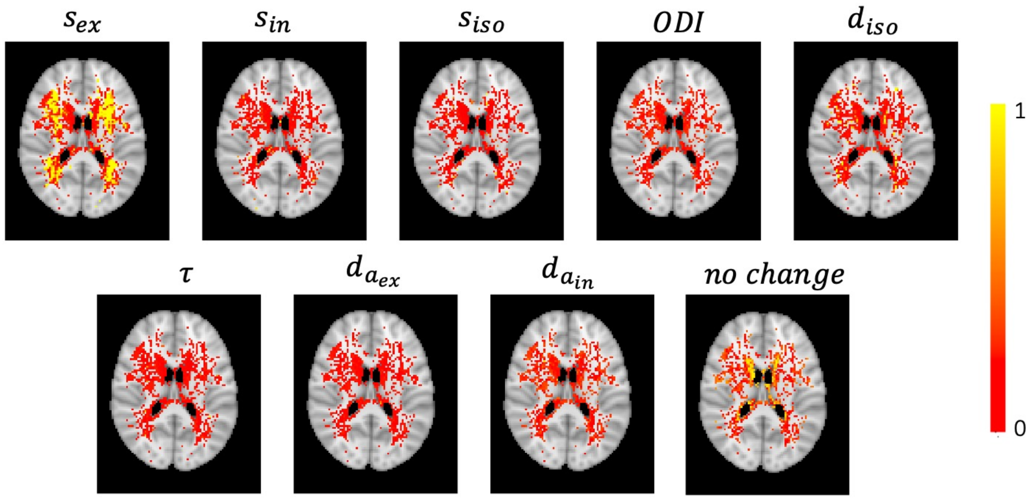

Intra axonal water


Dispersion


Extra axonal water

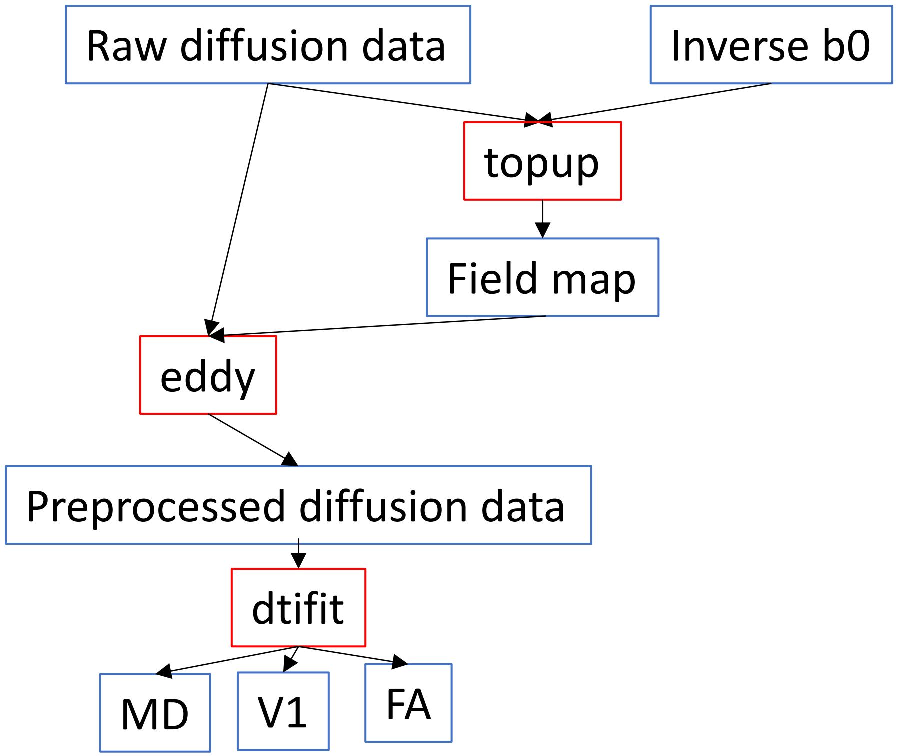
BENCH Output:

Probability of change in each parameter between two groups



File-tree and FSL-pipe

Pipelines



Visualisation (Quality Control)

File tree

HCP_directory.tree

/Users/paulmc/Data/HCP_Structural_Q1200

- ☐ T1w_32k/very_inflated
- ☐ T1w_32k/white
- ☑ T1w_acpc_dc
- ☐ T1w_acpc_dc_restore
- ☐ T1w_acpc_dc_restore_brain
- ☐ T1w_brainmask
- ☐ T1w_native/inflated
- ☐ T1w_native/mid
- ☐ T1w_native/pial
- ☐ T1w_native/spec
- ☐ T1w_native/very_inflated
- ☑ T1w_native/white
- ☐ T1w_restore

hemi <all>
space native
subject <any>

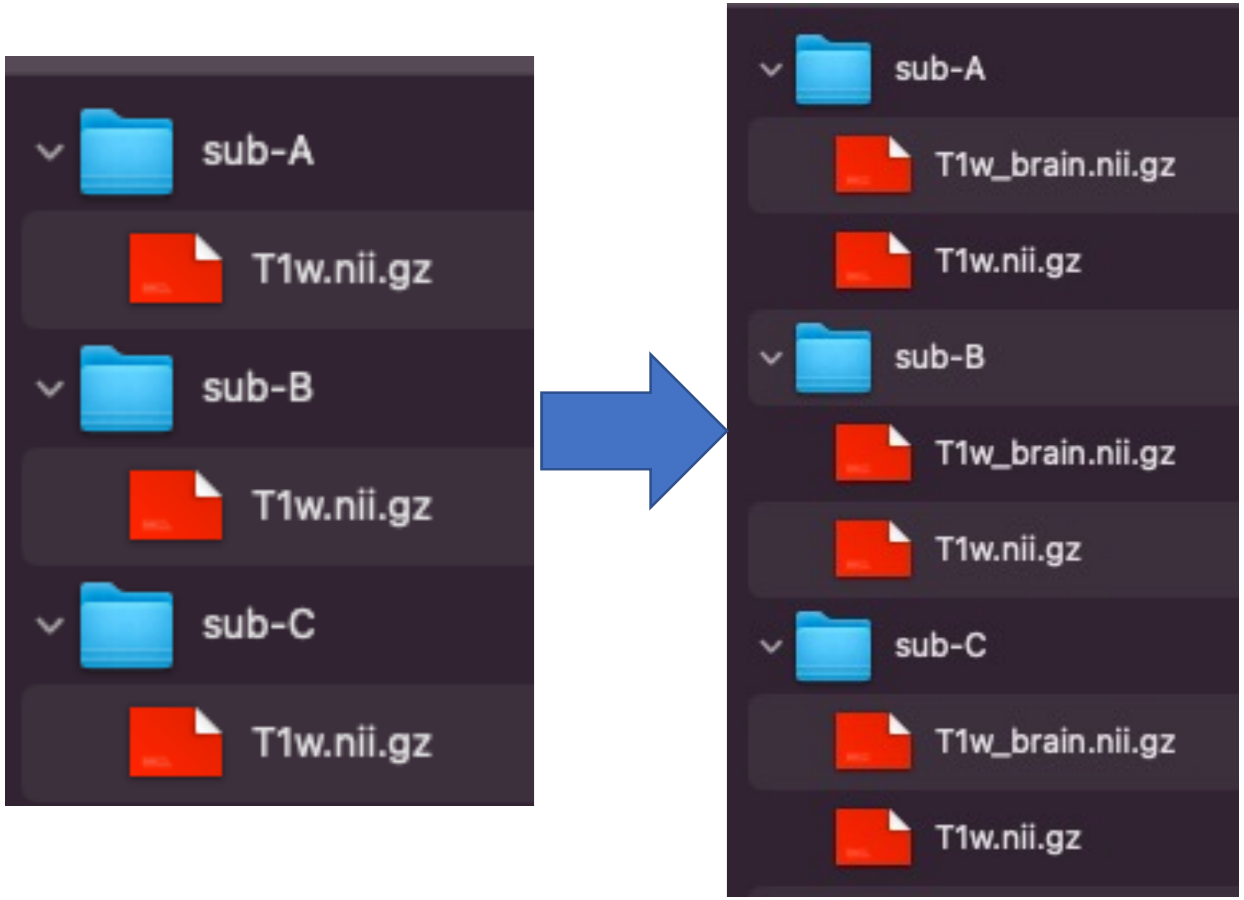
subject	T1w_acpc_dc	T1w_native/white[hemi=L]	T1w_native/white[hemi=R]	Notes
115017	✓	✓	✓	
120717	✓	✓	✓	
121618	✓	✓	✓	
121719	✓	✓	✓	
131924	✓	✓	✓	
134021	✓	✓	✓	
154330	✓	✓	✓	
160123	✓	✓	✓	
207426	✓	✓	✓	
382242	✓	✓	✓	
495255	✓	✓	✓	
536647	✓	✓	✓	

[filetree] T1w_native/white[hemi=R]
[filetree] T1w_native/white[hemi=L]
[filetree] T1w_acpc_dc

Coordinates: MNI152	Voxel location
29.92672	86
-66.52511	85
0.09999877	103
Volume	0

[filetree] T1w_native/white[hemi=R]
[no vertex]
[filetree] T1w_native/white[hemi=L]
[no vertex]
[filetree] T1w_acpc_dc
[86 85 103]: 1017.4098510742188

File-tree: describing your directory structure



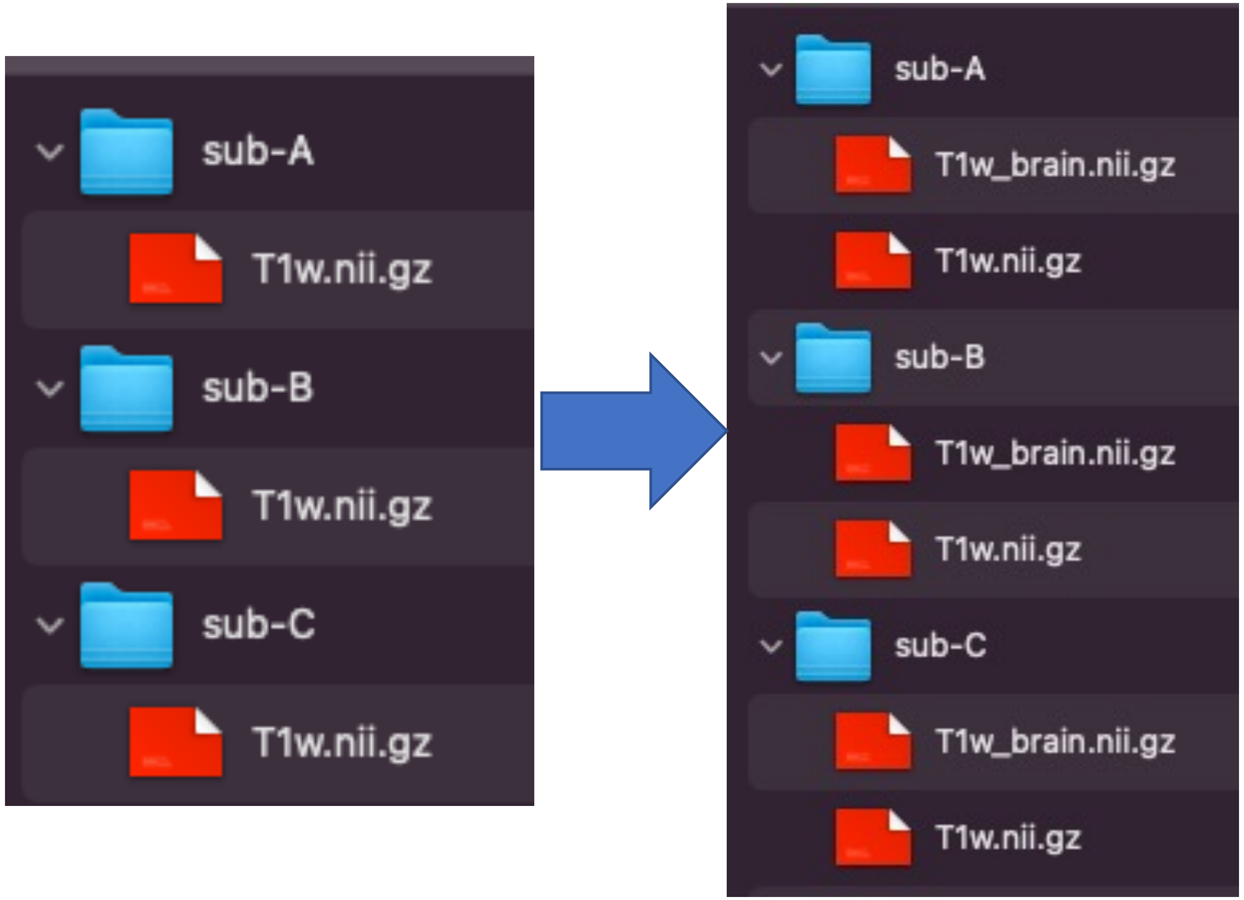
```
sub-A
    T1w.nii.gz
sub-B
    T1w.nii.gz
sub-C
    T1w.nii.gz
```

```
sub-A
    T1w_brain.nii.gz
    T1w.nii.gz
sub-B
    T1w_brain.nii.gz
    T1w.nii.gz
sub-C
    T1w_brain.nii.gz
    T1w.nii.gz
```

data.tree

```
sub-{subject}
        T1w.nii.gz
```

File-tree: describing your directory structure



data.tree

```
sub-{subject}
        T1w.nii.gz
        T1w_brain.nii.gz
```

File-tree: describing your directory structure

Visualisation
(Quality Control)

HCP_directory.tree

/Users/paulmc/Data/HCP_Structural_Q1200

☐ T1w_32k/very_inflated
☐ T1w_32k/white
☑ T1w_acpc_dc
☐ T1w_acpc_dc_restore
☐ T1w_acpc_dc_restore_brain
☐ T1w_brainmask
☐ T1w_native/inflated
☐ T1w_native/mid
☐ T1w_native/pial
☐ T1w_native/spec
☐ T1w_native/very_inflated
☑ T1w_native/white
☐ T1w_restore

hemi <all>
space native
subject <any>

subject	T1w_acpc_dc	T1w_native/white[hemi=L]	T1w_native/white[hemi=R]	Notes
115017	✓	✓	✓	
120717	✓	✓	✓	
121618	✓	✓	✓	
121719	✓	✓	✓	
131924	✓	✓	✓	
134021	✓	✓	✓	
154330	✓	✓	✓	
160123	✓	✓	✓	
207426	✓	✓	✓	
382242	✓	✓	✓	
495255	✓	✓	✓	
536647	✓	✓	✓	

[filetree] T1w_native/white[hemi=R]
[filetree] T1w_native/white[hemi=L]
[filetree] T1w_acpc_dc

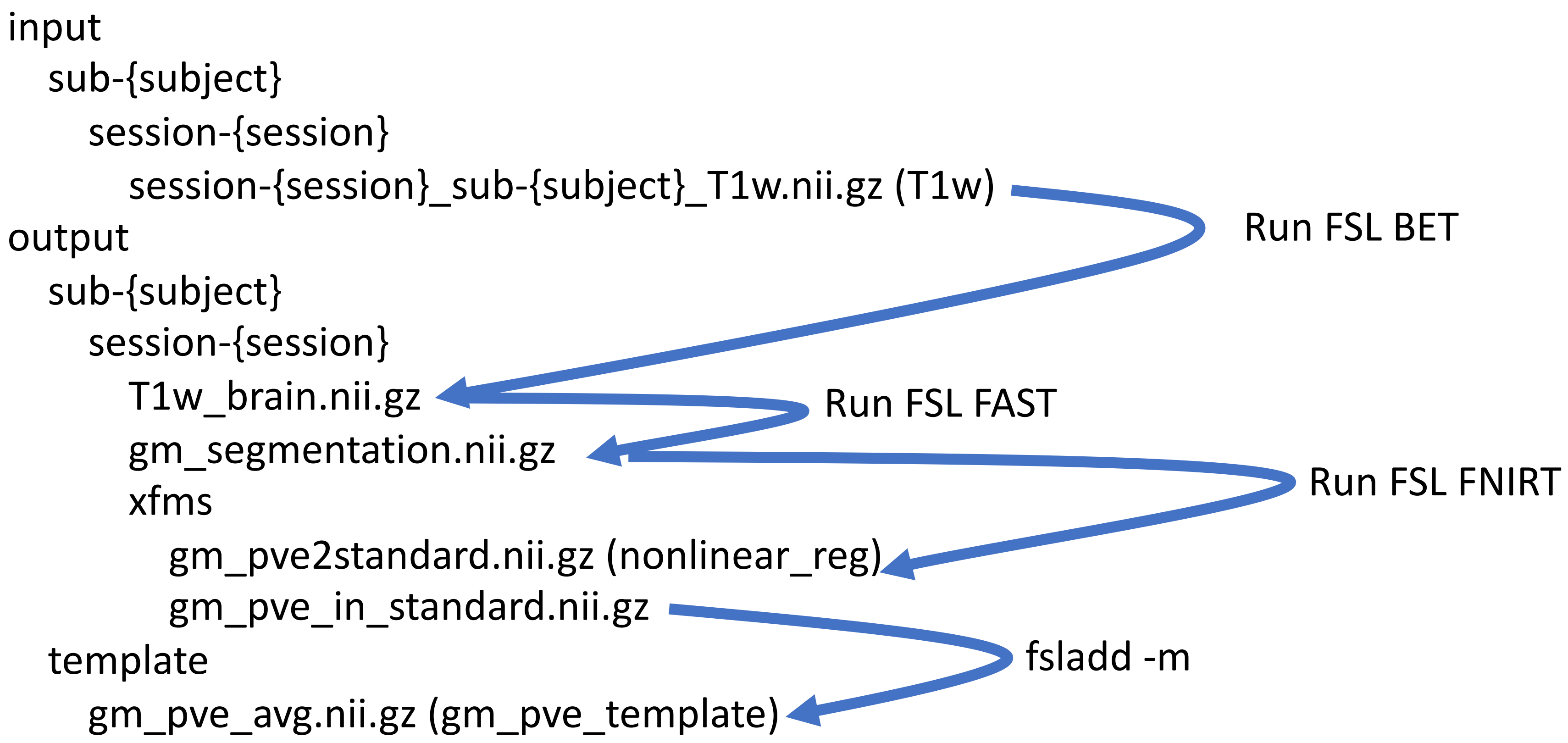
Coordinates: MNI152	Voxel location
29.92672	86
-66.52511	85
0.09999877	103
Volume	0

[filetree] T1w_native/white[hemi=R]
[no vertex]
[filetree] T1w_native/white[hemi=L]
[no vertex]
[filetree] T1w_acpc_dc
[86 85 103]: 1017.4098510742188

FSL pipeline tools

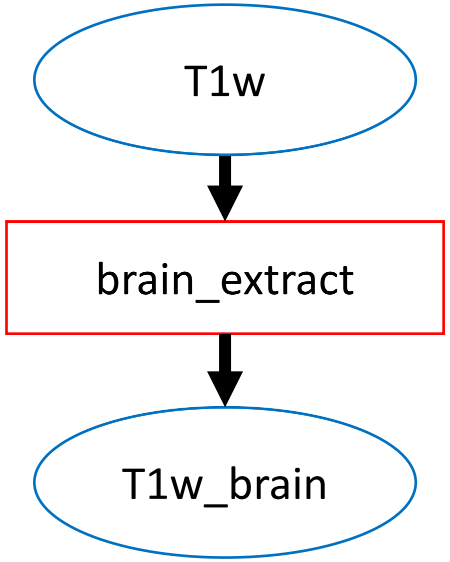
File-tree describes the directory structure

FSL-pipe describes how these files are produced



```
input
  sub-{subject}
    session-{session}
      session-{session}_sub-{subject}_T1w.nii.gz (T1w)
output
  sub-{subject}
    session-{session}
      T1w_brain.nii.gz
      gm_segmentation.nii.gz
      xfms
        gm_pve2standard.nii.gz (nonlinear_reg)
        gm_pve_in_standard.nii.gz
  template
    gm_pve_avg.nii.gz (gm_pve_template)
```

FSL-pipe: Defining individual jobs



defines directions of arrows

```
@pipe
def brain_extract(T1w: In, T1w_brain: Out):
      run(f“bet {T1w} T1w_brain”)
```

Actual command to be run

Conclusions

- Just define jobs/recipes
  - FSL-pipe will determine in which order they should run
- Smart restart (only failed jobs are rerun)
- Users can run part of the pipeline
- Jobs can be run locally or on cluster
- Update input/output directory structure using file-tree
  - Same pipeline works for single-session or multi-session data
- Documentation & tutorial
  - https://tinyurl.com/file-tree
  - https://tinyurl.com/fsl-pipe