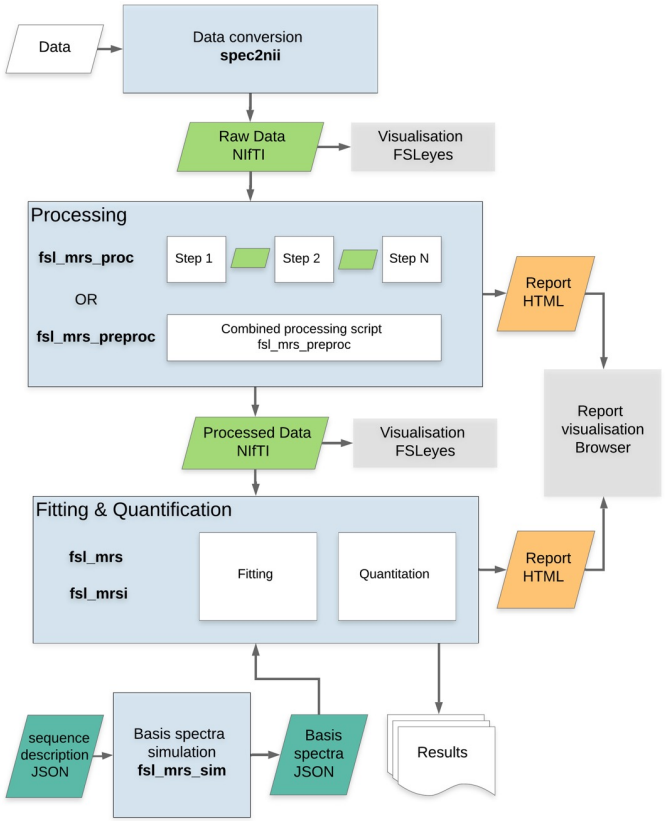
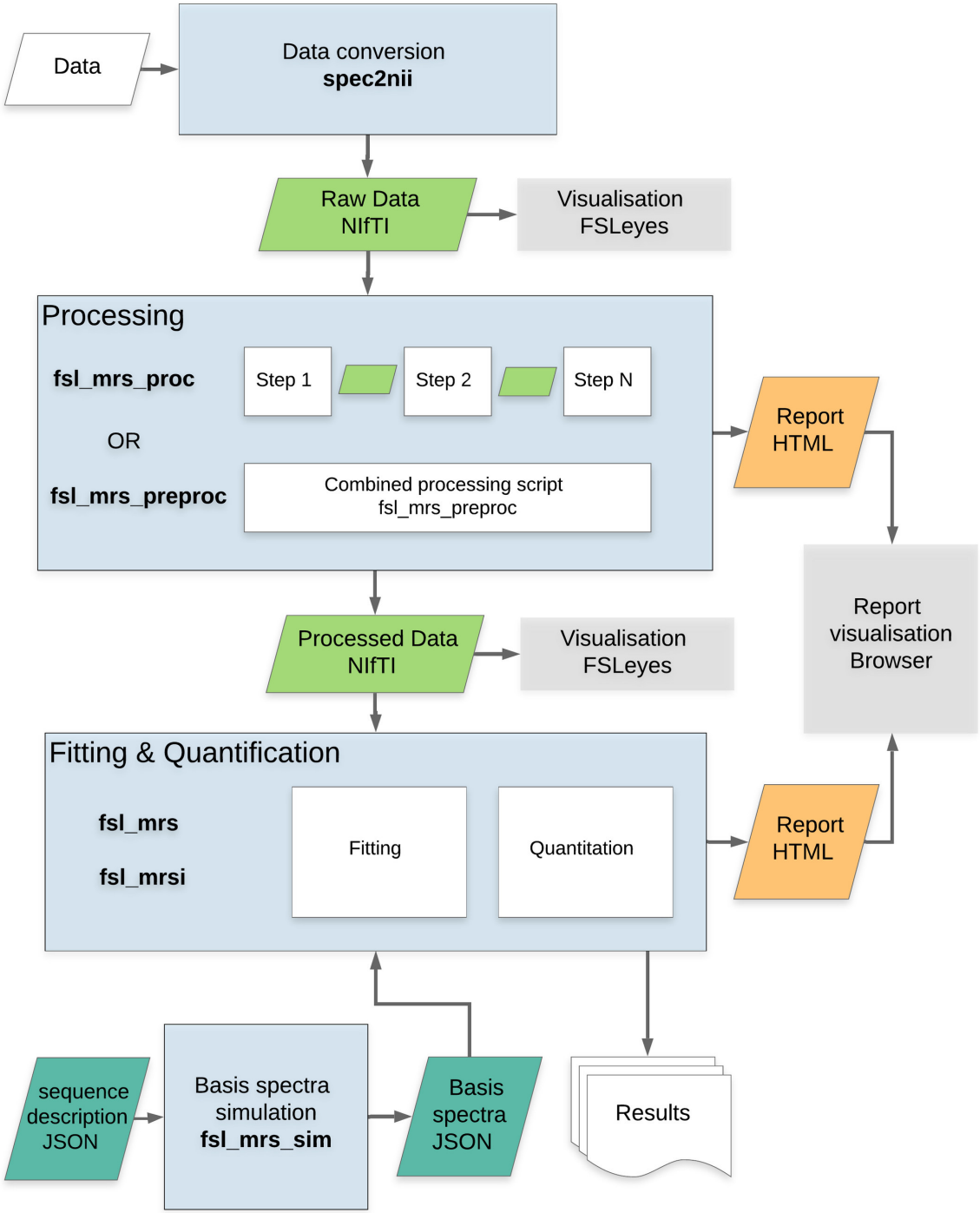
FSL-MRS – Tools for Magnetic Resonance Spectroscopy



V. FSL-MRS tools


Data
Data conversion
spec2nii
Raw Data
NIfTI
Visualisation
FSLeyes
Processing
fsl_mrs_proc
Step 1
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OR
fsl_mrs_preproc
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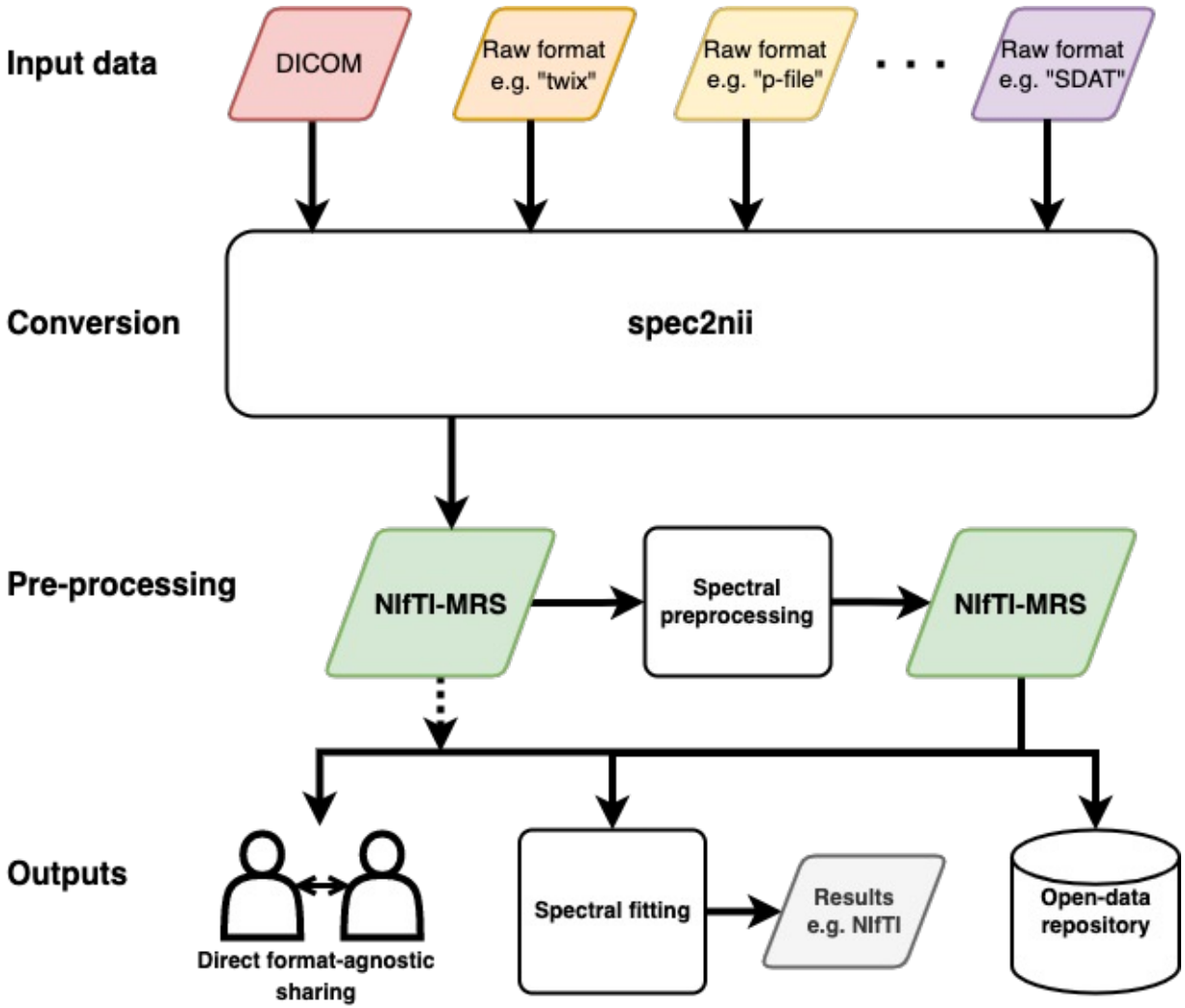
Fitting
Quantitation
Report
HTML
sequence
description
JSON
Basis spectra
simulation
fsl_mrs_sim
Basis
spectra
JSON
Results

Data conversion



https://doi.org/10.1002/mrm.29418

Data conversion

github.com/wtclarke/spec2nii

spec2nii

pypi v0.4.7 | python 3.7 | 3.8 | DOI 10.5281/zenodo.5907960

Currently supported formats

This table lists the currently supported formats. I have very limited experience with Philips and GE formats. Please get in touch if you are willing to help add to this list and/or supply validation data.

Format	File extension	SVS	CSI	Automatic orientation
Siemens Twix	.dat	Yes	No	Yes
Siemens DICOM	.ima / .dcm	Yes	Yes	Yes
Siemens RDA	.rda	Yes	No	Yes (WIP)
Philips	.SPAR/.SDAT	Yes	No	Yes
Philips	.data/.list	Yes	No	Yes
Philips DICOM	.dcm	Yes	No	Yes (WIP)
GE	.7 (pfile)	Yes	Yes	Yes
UIH DICOM	.dcm	Yes	Yes	Yes
Bruker	2dseq	Yes	Yes	Yes
Bruker	fid	Yes	Yes	Yes (WIP)
Varian	fid	Yes	No	No (WIP)
LCModel	.RAW	Yes	No	No
jMRUI	.txt	Yes	No	No
jMRUI	.mrui	Yes	No	No
ASCII	.txt	Yes	No	No

Pre-processing

`fsl_mrs_preproc` – One-stop pre-processing for SVS

`fsl_mrs_proc` – Run individual modular processing steps

- `coilcombine`
- `average`
- `align`
- `ecc`
- `remove`
- `phase`
- …

`fsl_mrs_preproc_edit` – One-stop pre-processing for edited SVS. **Warning**! WIP

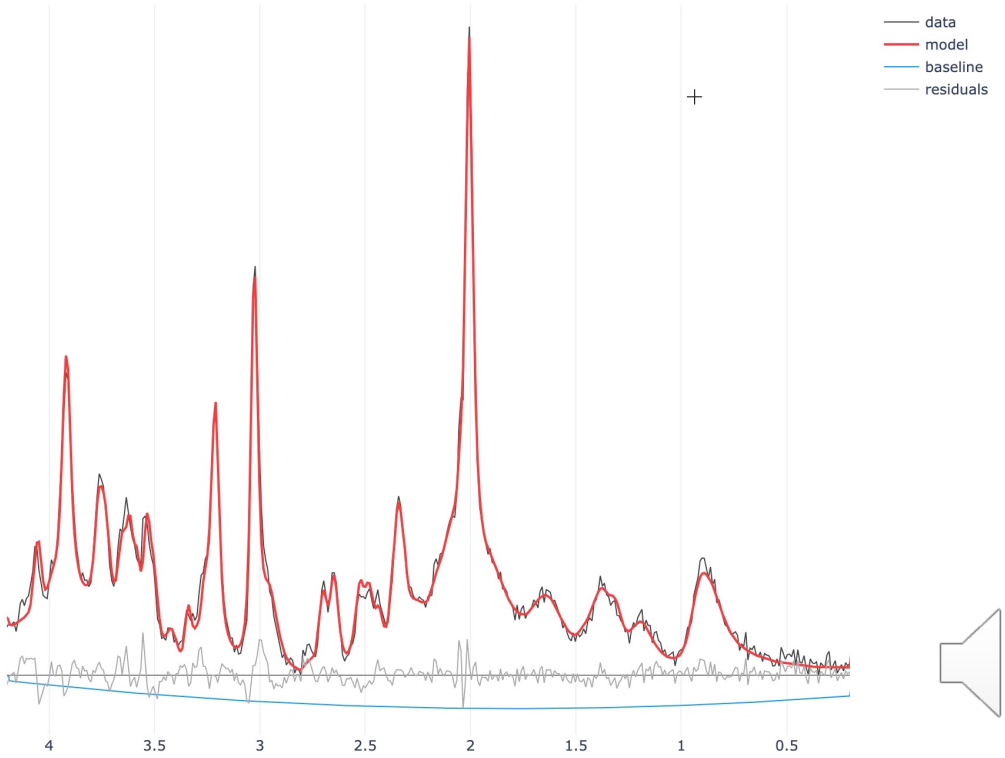
Fitting

Single spectra: `fsl_mrs`

Output: .csv + interactive report

Summary

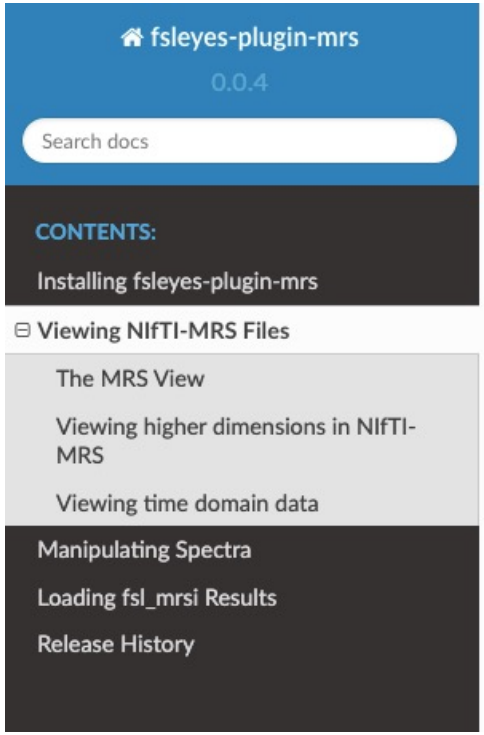
Metab	mMol/kg	%CRLB	/Cr+PCr
Ala	0.22	77.6	0.02
Asc	1.25	50.3	0.11
Asp	1.3	47.4	0.11
Cr	6.96	9	0.61
GABA	1.17	37.9	0.1
GPC	1.54	21.2	0.13
GSH	1.98	13.1	0.17
Glc	0.55	80	0.05
Gln	0.73	52	0.06
Glu	11.2	4.9	0.97
Ins	9.22	4.2	0.8
Lac	0.97	39.2	0.08
Mac	0.87	2.6	0.08
NAA	15.49	2.9	1.35
NAAG	1.72	18.1	0.15
PCh	0.47	56	0.04
PCr	4.54	14	0.39
PE	2.21	25.8	0.19
Scyllo	0.93	15.8	0.08
Tau	2.29	20.6	0.2
Cr+PCr	11.5	3.1	1

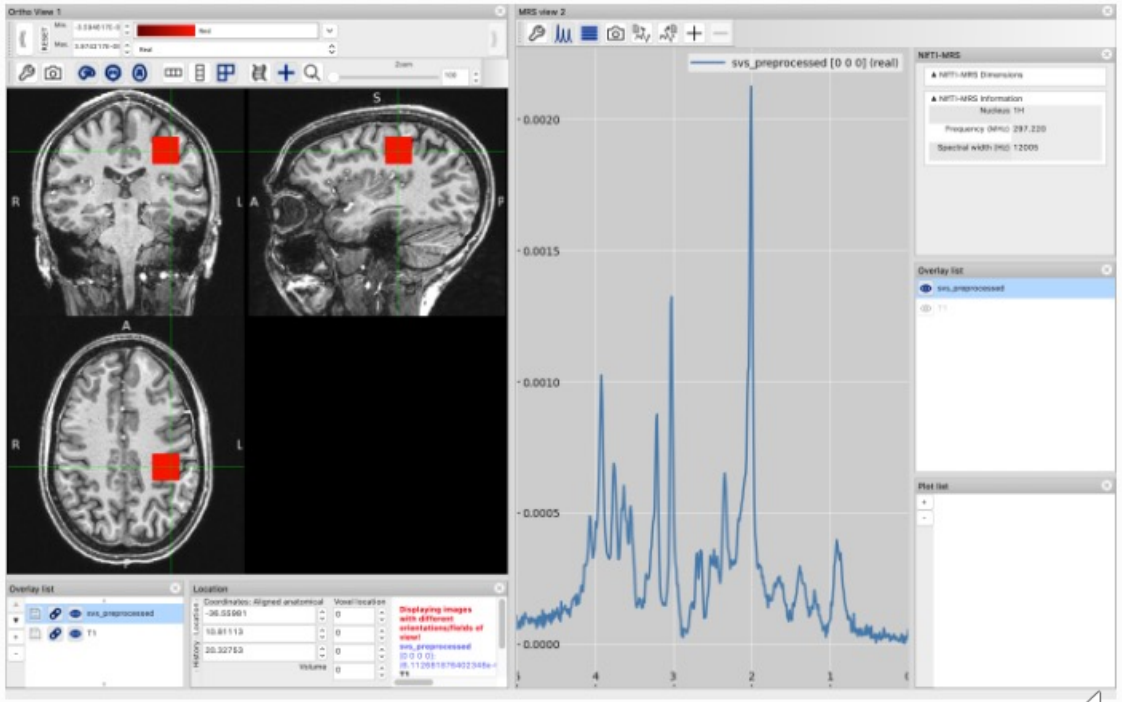


Fitting

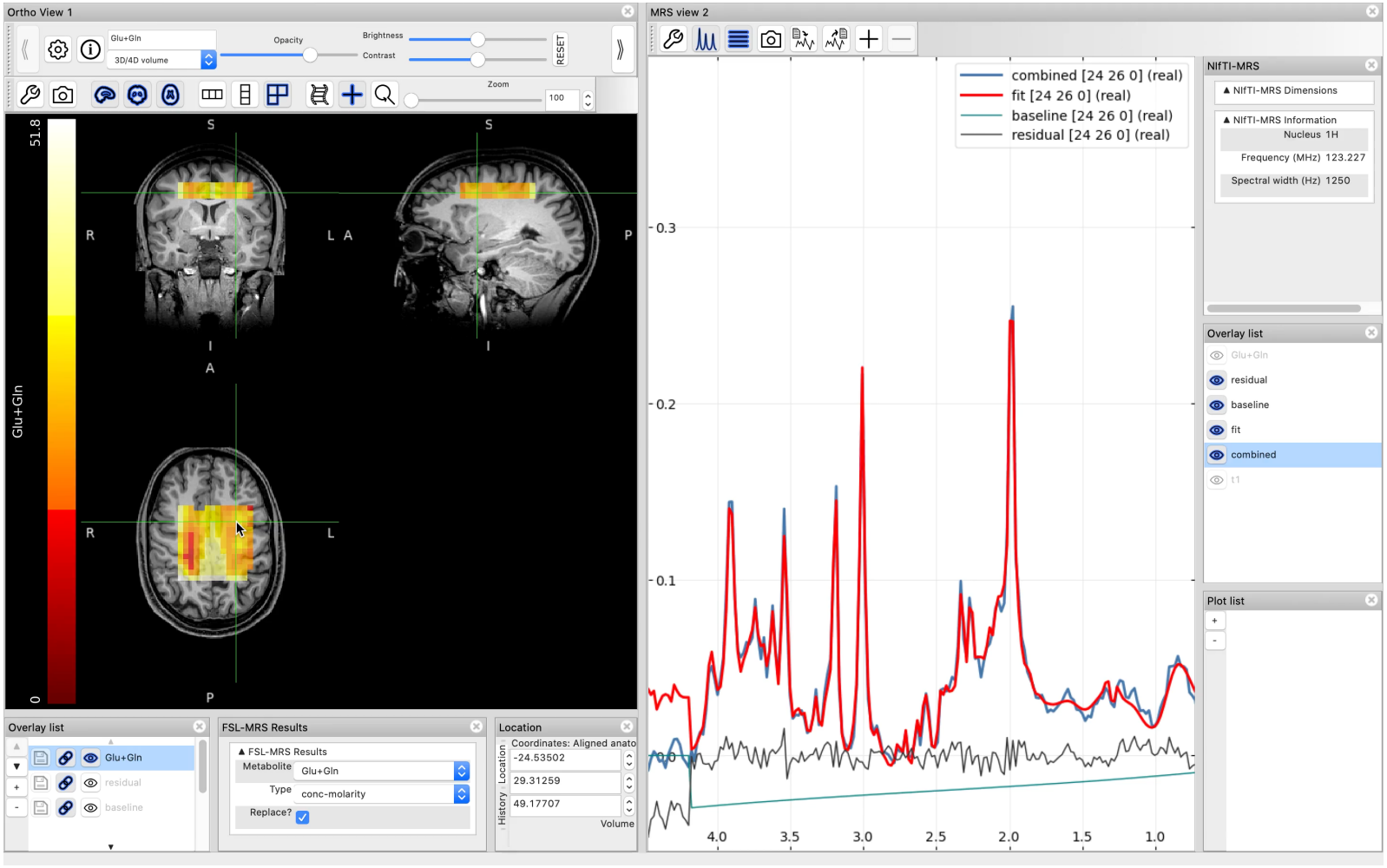
MRSI: `fsl_mrsi`

Output: NIfTI files (.nii), to be viewed in fsleyes…





Visualisation



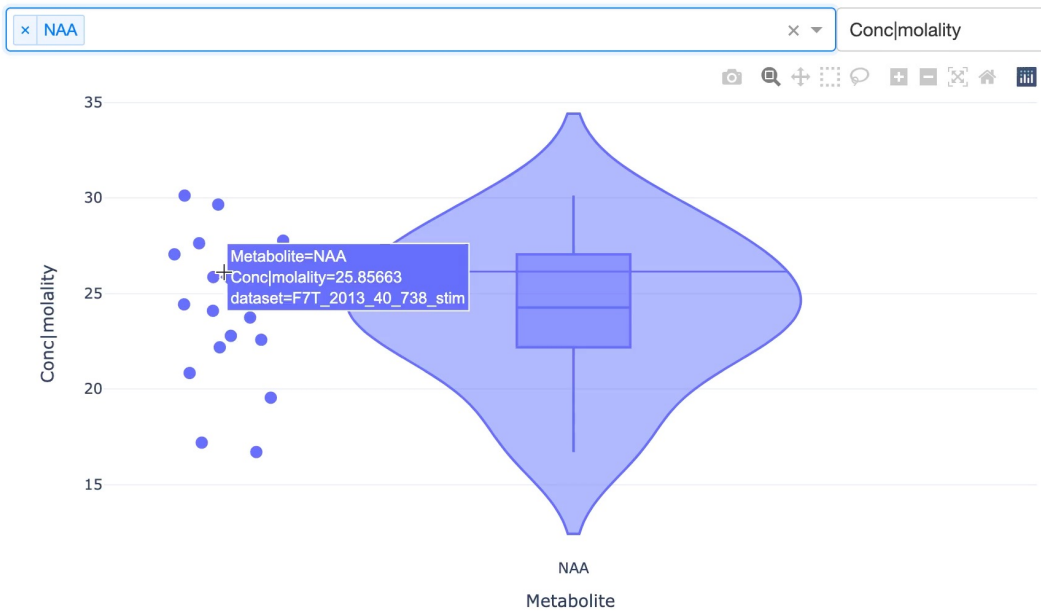
+ basic viewer: `mrs_tools vis my_data.nii.gz`

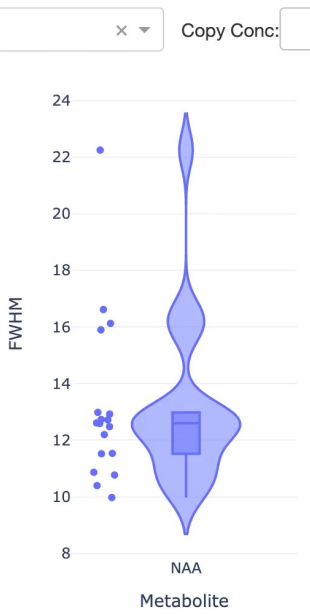
Other tools

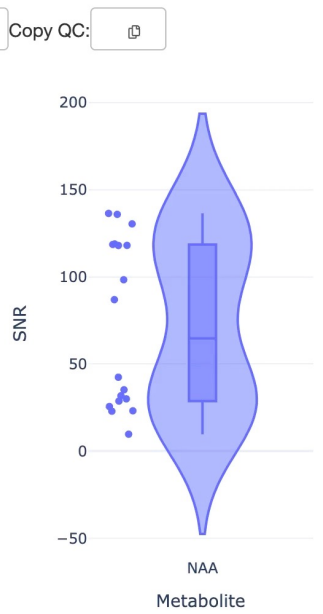
1. Simulation of basis spectra: `fsl_mrs_sim`
2. Basis spectra manipulation: `basis_tools`
3. Data manipulation: `mrs_tools`
4. Tissue segmentation: `svs_segment, mrsi_segment`
5. Summary statistics: `fsl_mrs_summarise`

Tools can also be run through interactive Python API

FSL-MRS: Single voxel MRS results summary







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

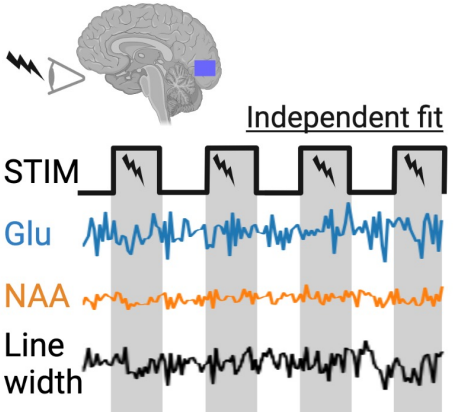
index	FWHM	SNR
count	18	18
mean	13.2	72.8
std	2.95	48.2
min	9.97	9.74
25%	11.5	29
50%	12.6	64.7
75%	13	118
max	22.3	136

F7T_2013_40_738_stim

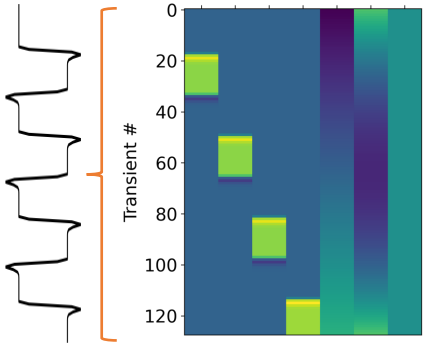
Average data

New: Dedicated fMRS (+ dMRS) fitting

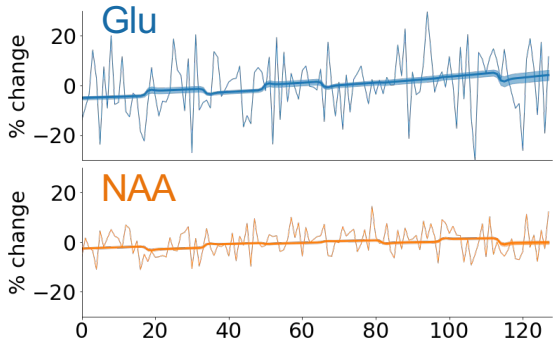
Block-design visual stimulation + MRS in V1



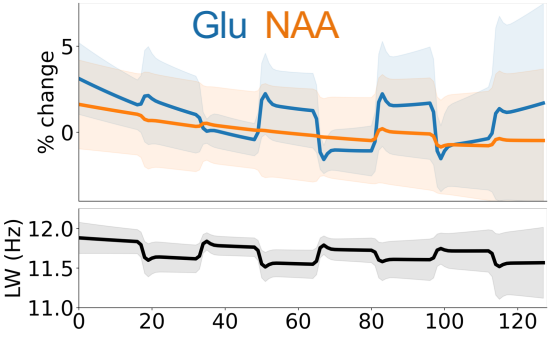
Modelled with fMRI-style GLM



First-level fits



Second-level group analysis in FLAMEO



Mean activation statistics

	Effect(%)	SD(%)	z	p
NAA+NAAG	-00.05	00.2	-0.32	0.373
PCh+GPC	+00.37	00.8	+0.46	0.321
Cr+PCr	+00.13	00.2	+0.56	0.286
Glu	+01.69	00.8	+1.93	**0.027**
Lac	+01.29	05.6	+0.23	0.411

See github.com/wtclarke/fsl_mrs_fmrs_demo and

bioRxiv
THE PREPRINT SERVER FOR BIOLOGY
doi.org/10.1101/2023.06.15.544935

Please Update!

FSL-MRS Release History

This document contains the FSL-MRS release history in reverse chronological order.

2.1.12 (Thursday 10th August 2023)

- Implemented more testing of *fsl_mrs_proc* routines.
- Fixed further bugs in *fsl_mrs_proc unlike*.
- Fixed issues in the example notebooks distributed with FSL-MRS.

Instructions on fsl-mrs.com

```
conda update -c conda-forge -c defaults \
-c https://fsl.fmrib.ox.ac.uk/fsldownloads/fslconda/public/ \
fsl_mrs
```