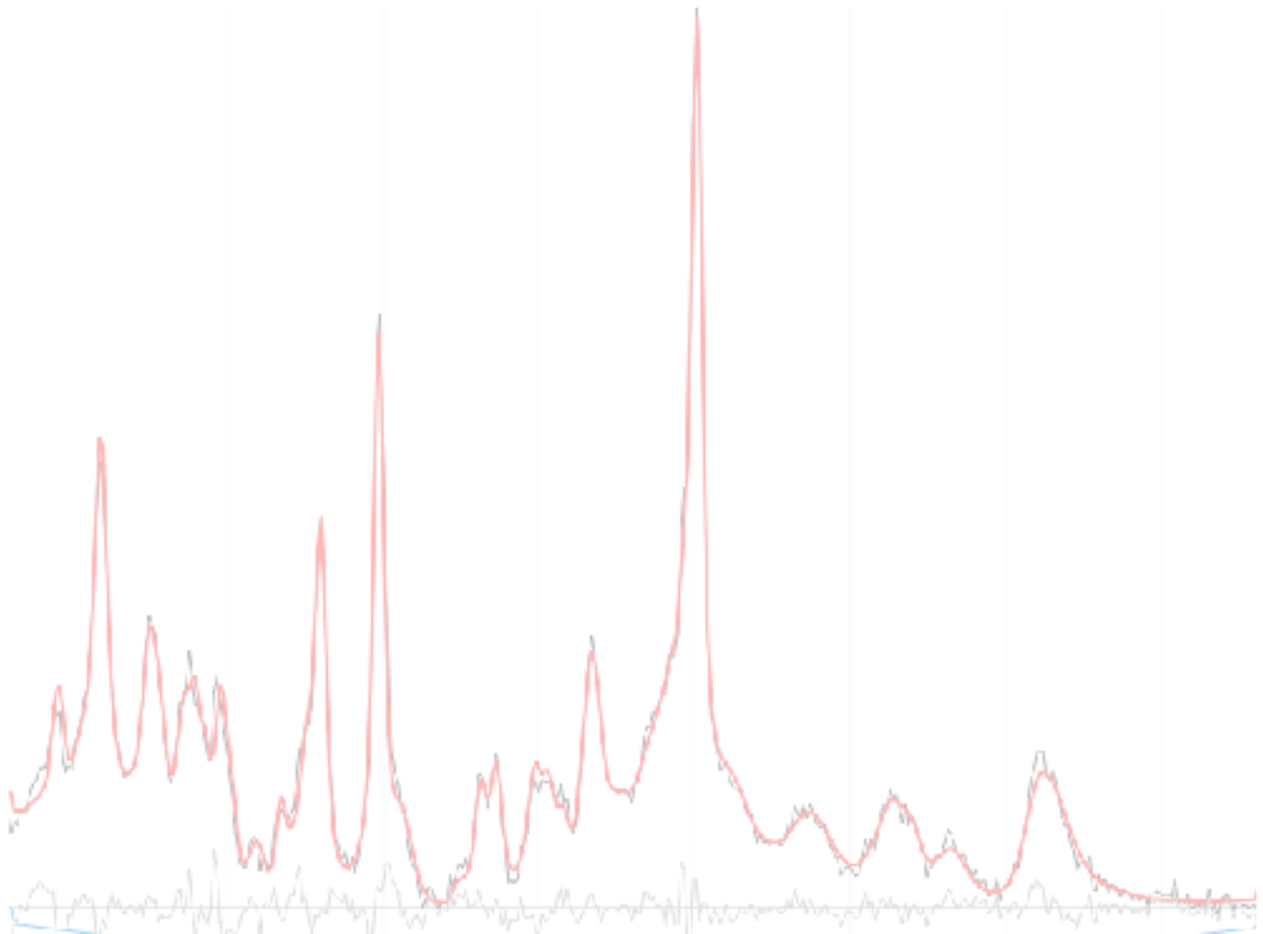
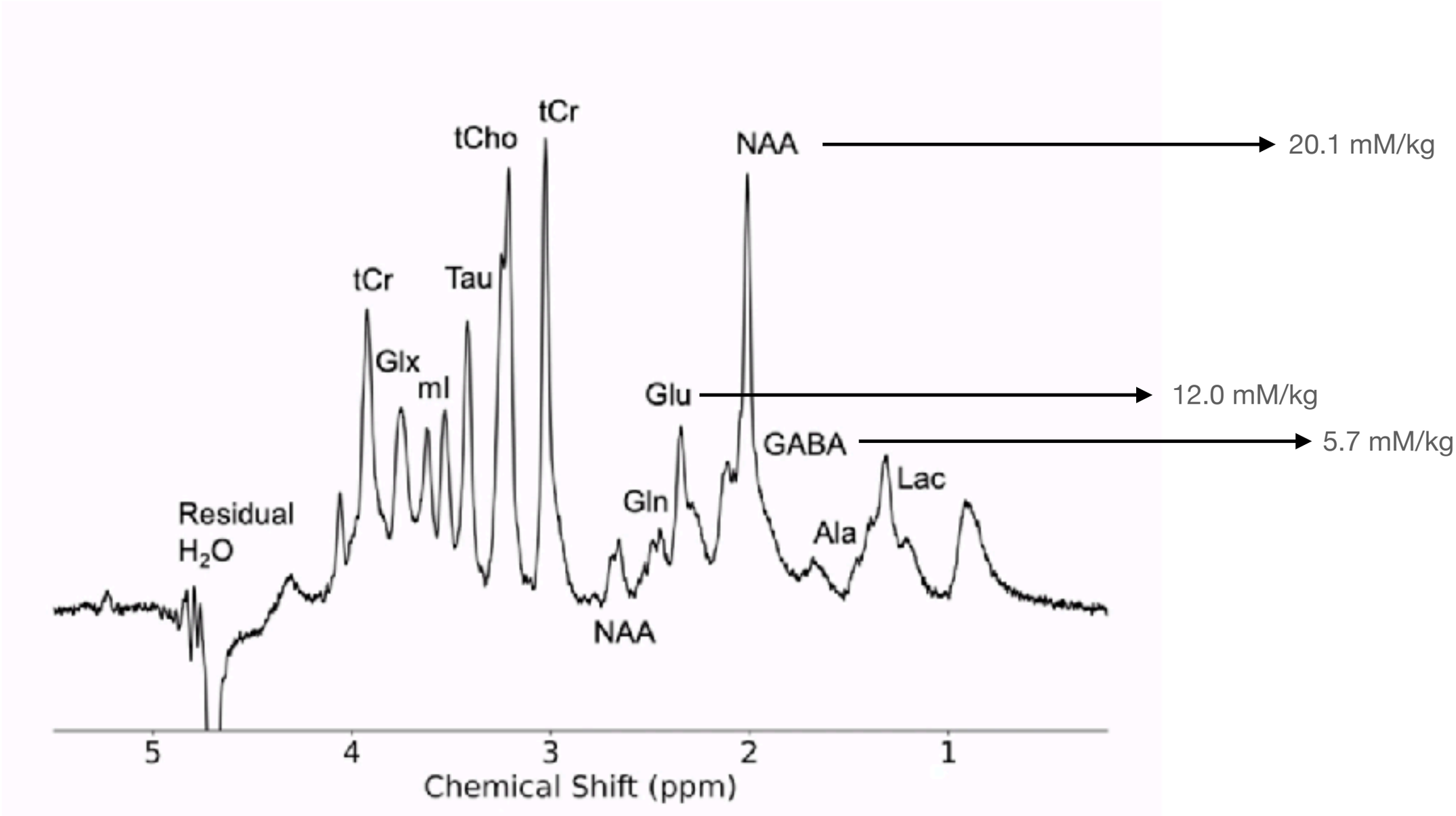
MRS Fitting



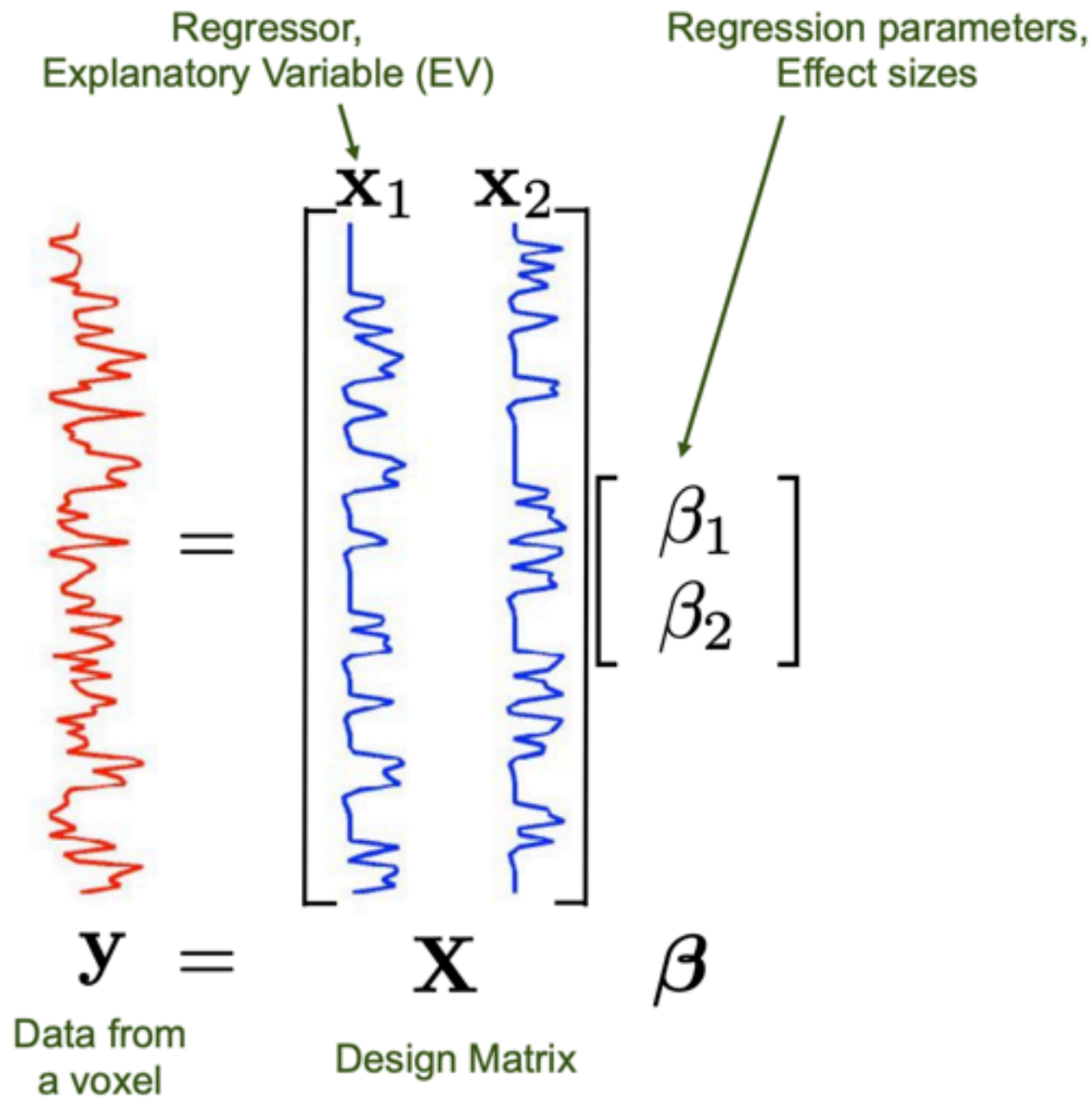
Goal of MRS fitting

Metabolite quantification



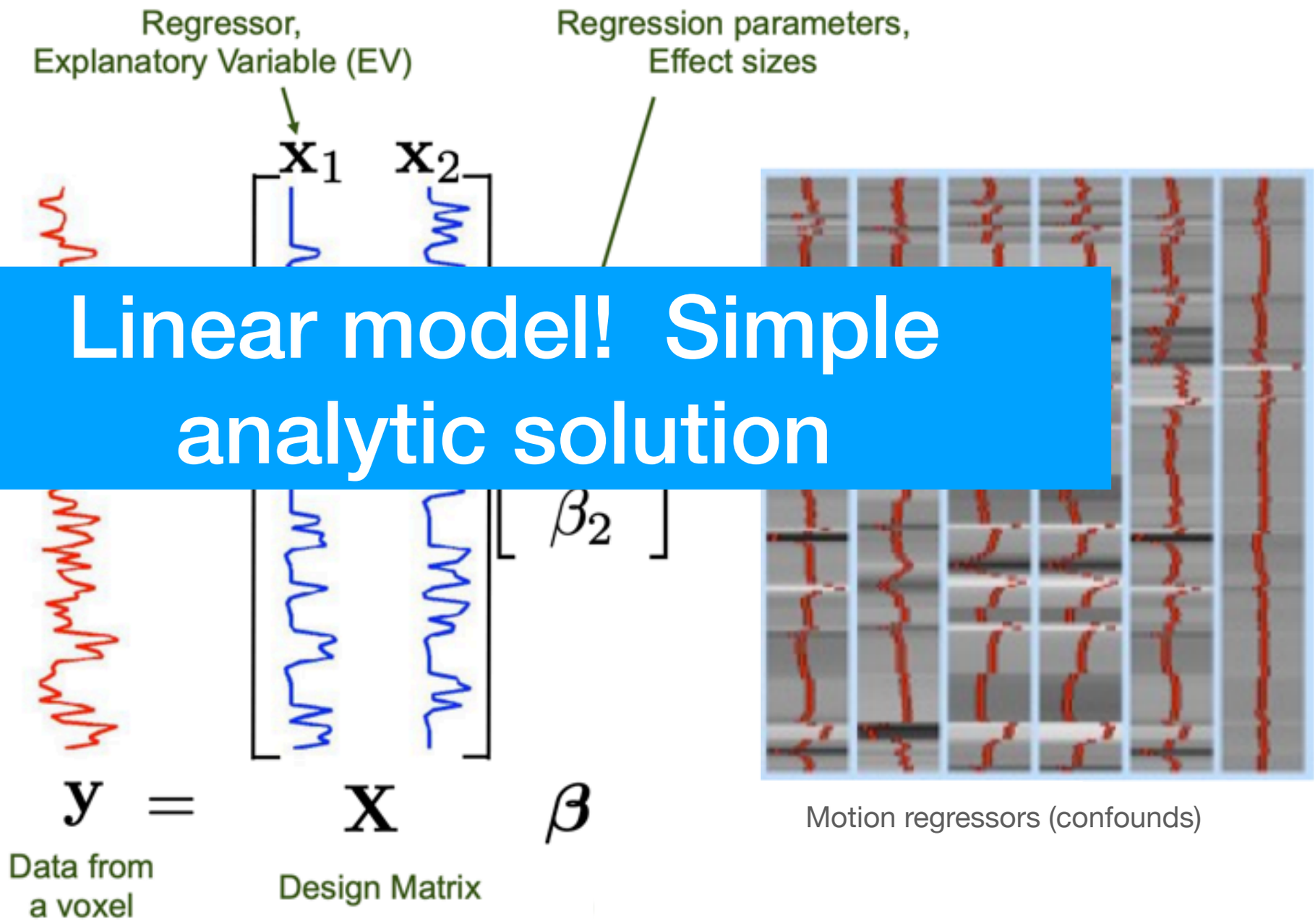
Remember the GLM?

For task FMRI



Remember the GLM?

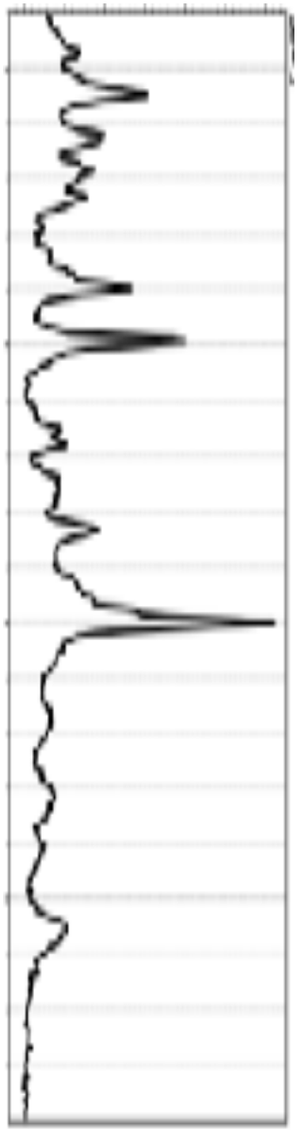
For task FMRI



Linear model! Simple analytic solution

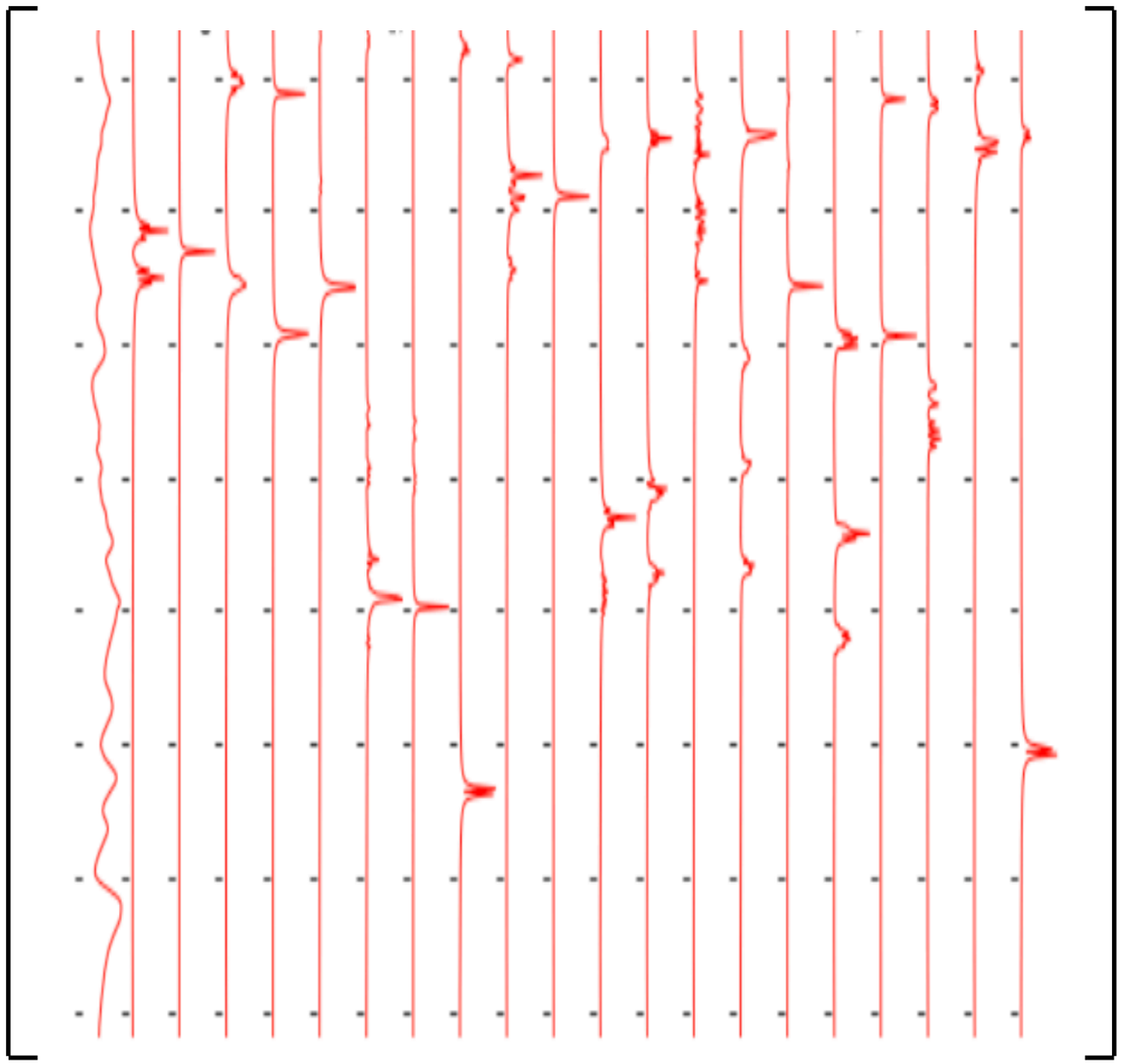
MRS Modelling is also a GLM

Spectrum (complex)



=

Basis (design matrix)



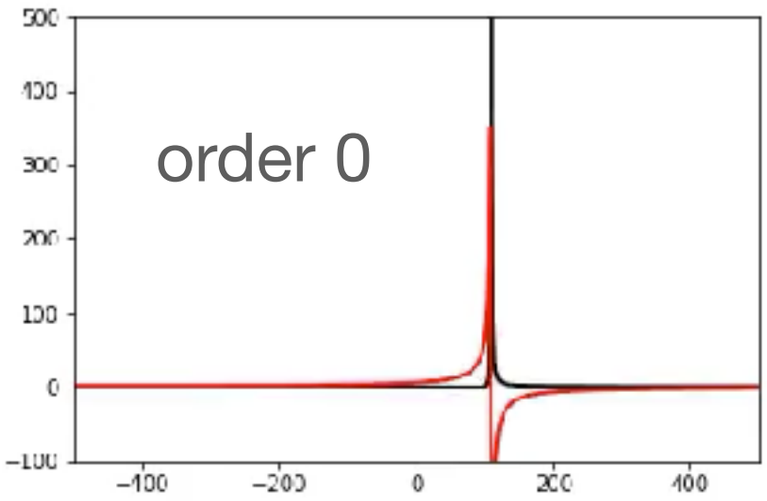
Concentrations

$$\begin{bmatrix} \beta_1 \\ \beta_2 \\ \beta_3 \\ \beta_4 \\ \beta_5 \end{bmatrix}$$

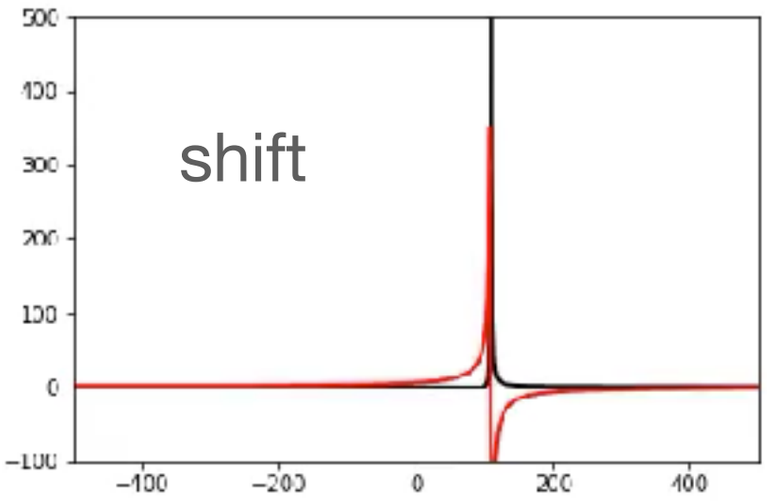
Each metabolite has its own spectrum

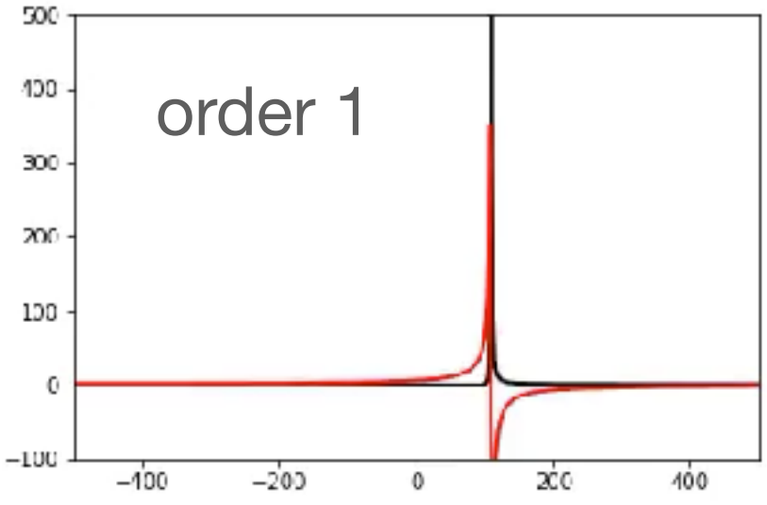
But with "Confound" modelling

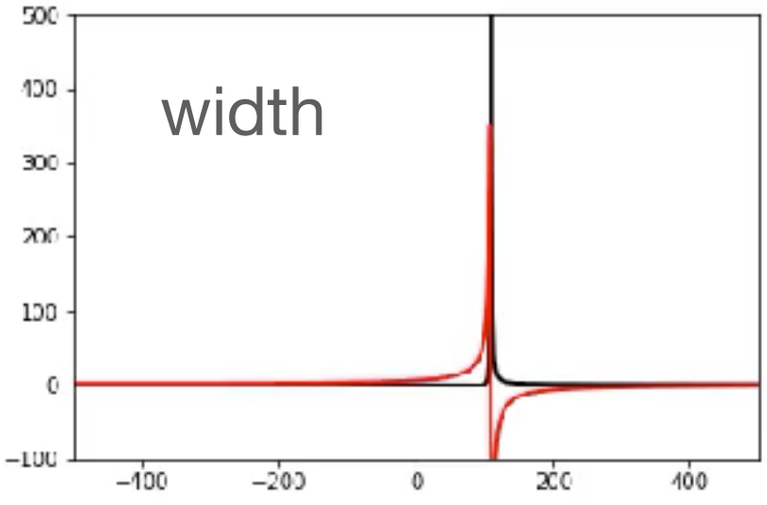
Phase



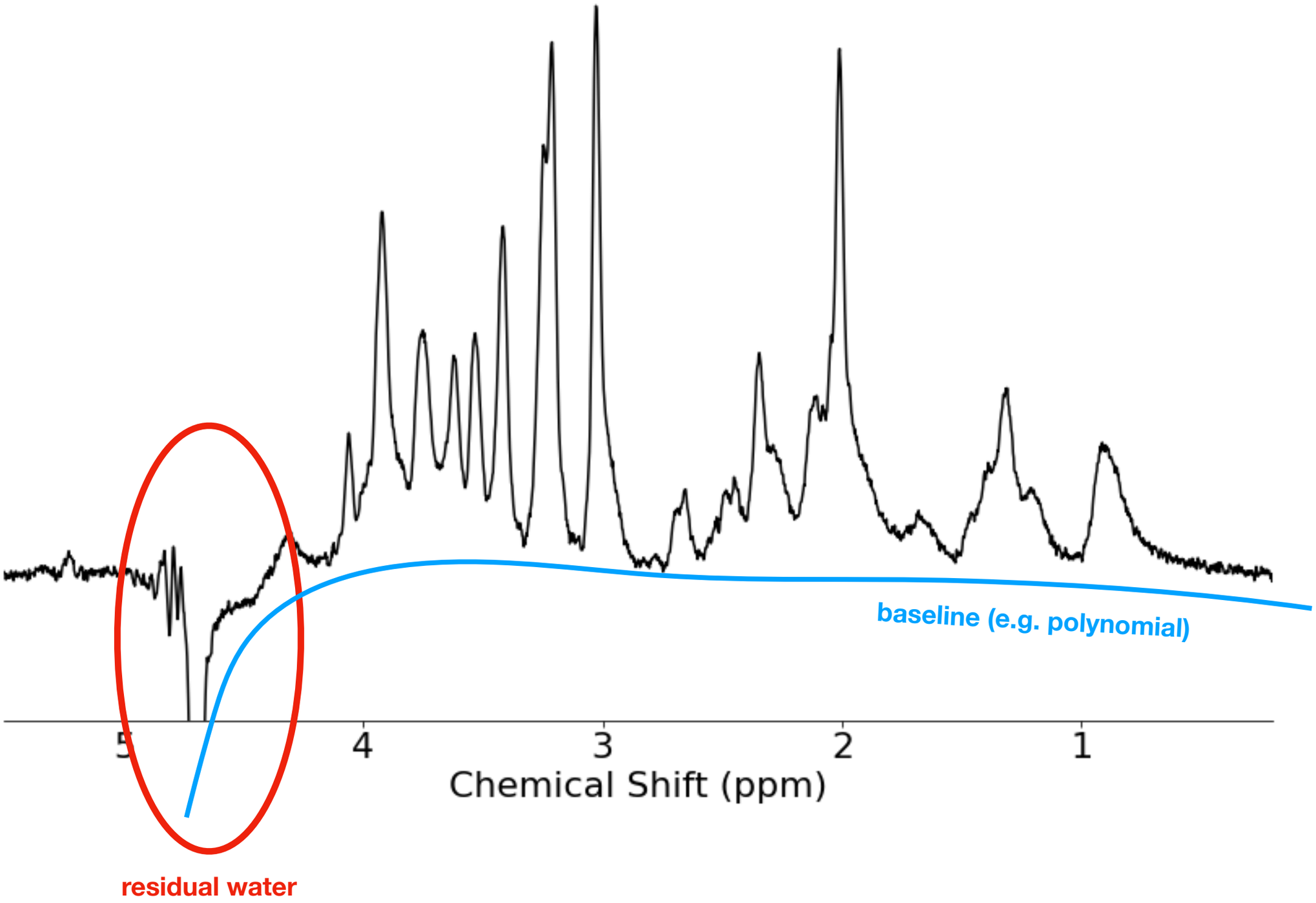
Line shape





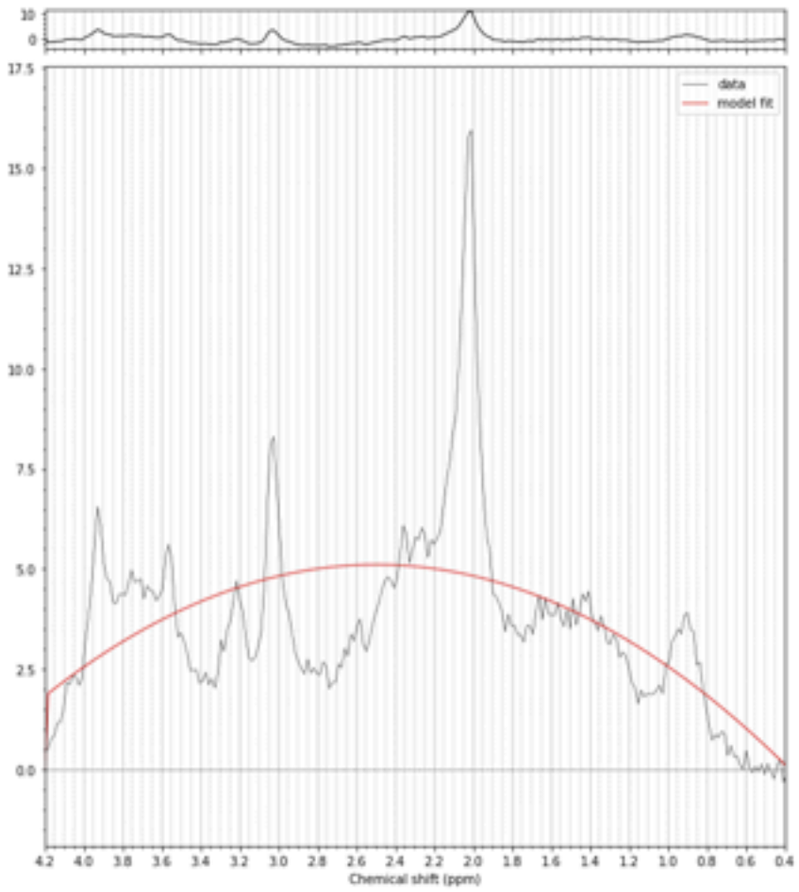


Other confounds (baseline)

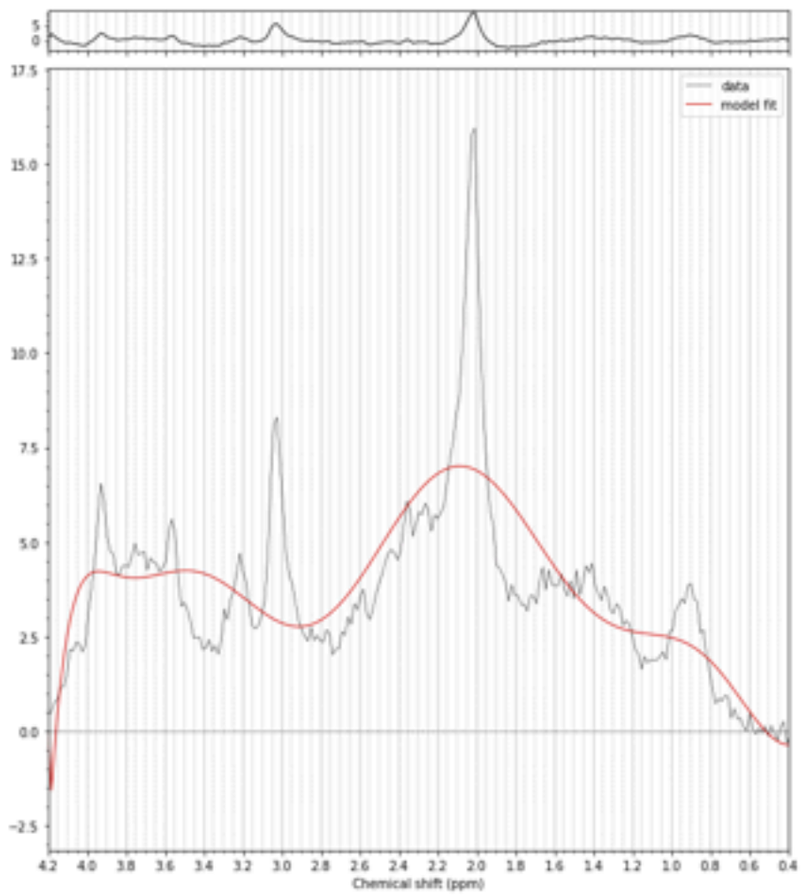


Beware of overfitting!

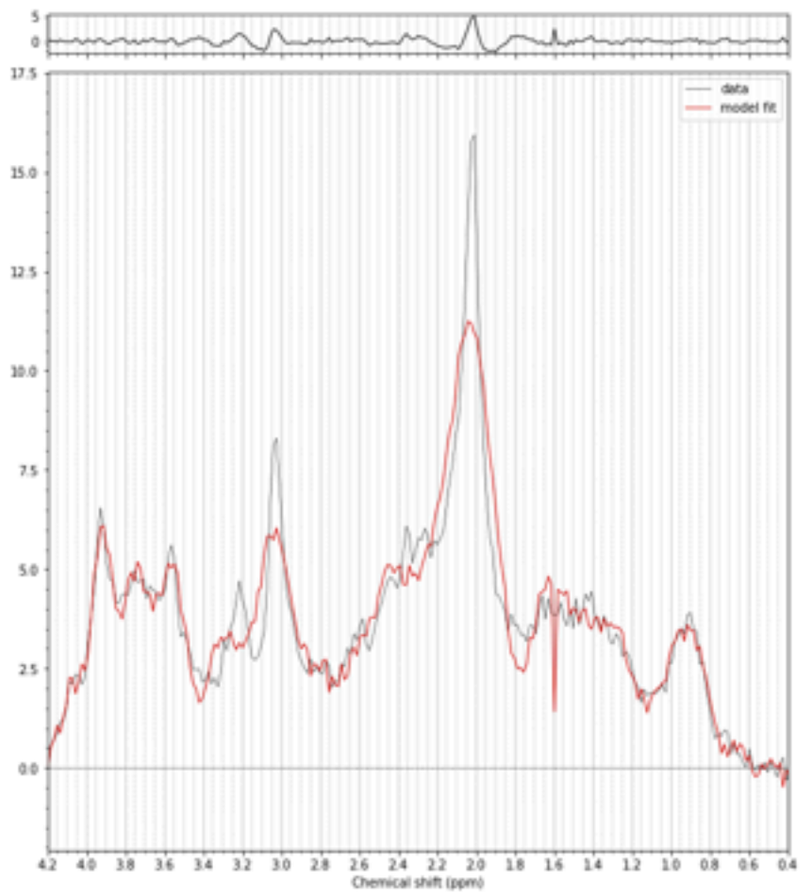
order = 2



order = 10



order = 50



The model

$$S(\nu) = B(\nu) + e^{-j(\Phi_0+\nu\Phi_1)} \sum_{g=1}^{N_g} \sum_{k=1}^{N_m} c_{k,g} \Im \left[m_k(\tau) e^{-\tau(\gamma_g + j\epsilon_g)} \right]$$

- $S(\nu)$: complex Spectrum
- $B(\nu)$: Baseline
- $e^{-j(\Phi_0+\nu\Phi_1)}$: Phase (0th and 1st order)
- $c_{k,g}$: Concentrations
- $m_k(\tau)$: Basis "spectra"
- $e^{-\tau(\gamma_g + j\epsilon_g)}$: Line shifting and broadening

Nonlinear model! Requires Optimisation

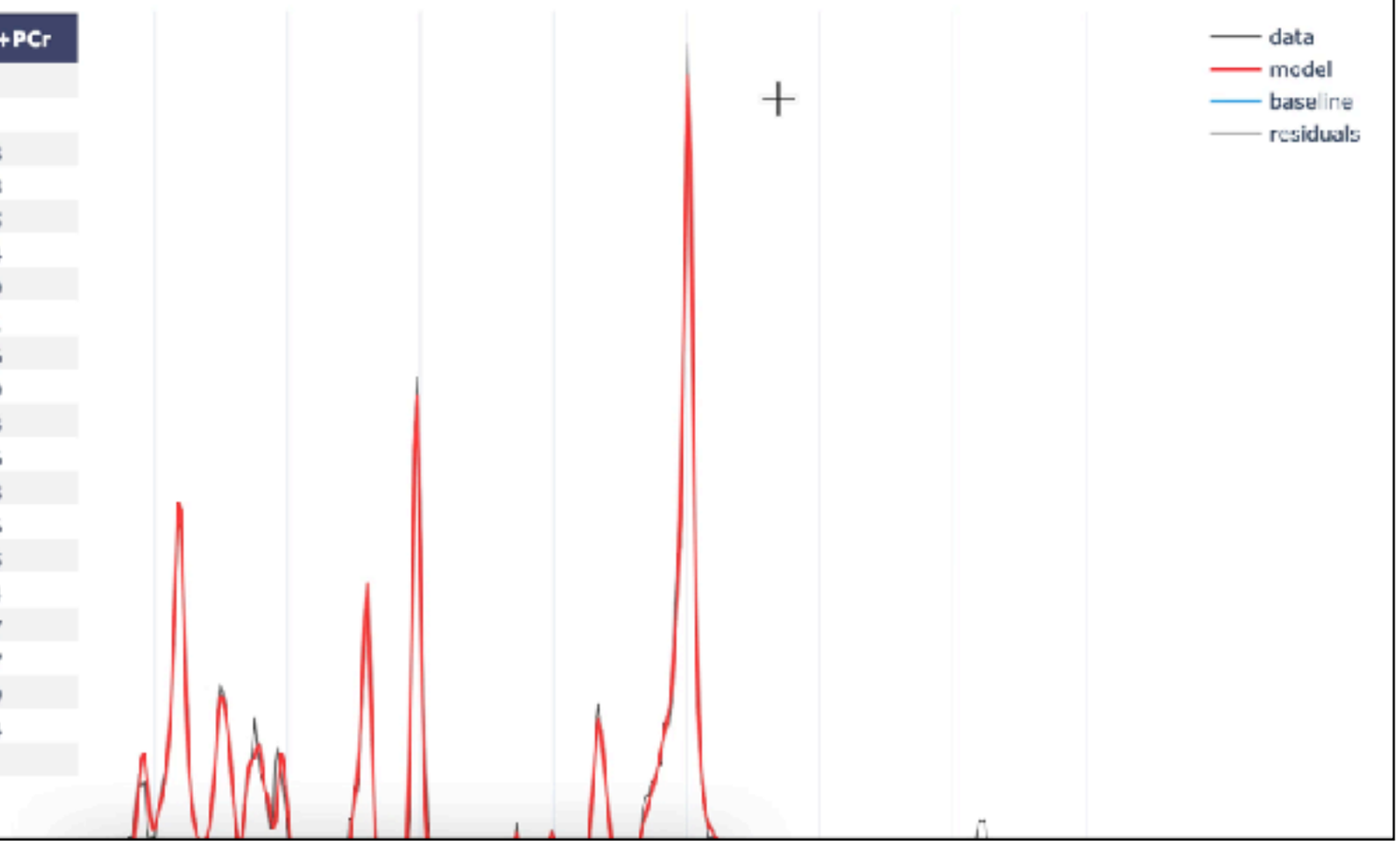
FSL MRS Report

Date : 2021-10-04 22:08
FID : fsl_mrs_proc/metab
Basis : steam_11ms
H2O : fsl_mrs_proc/wref

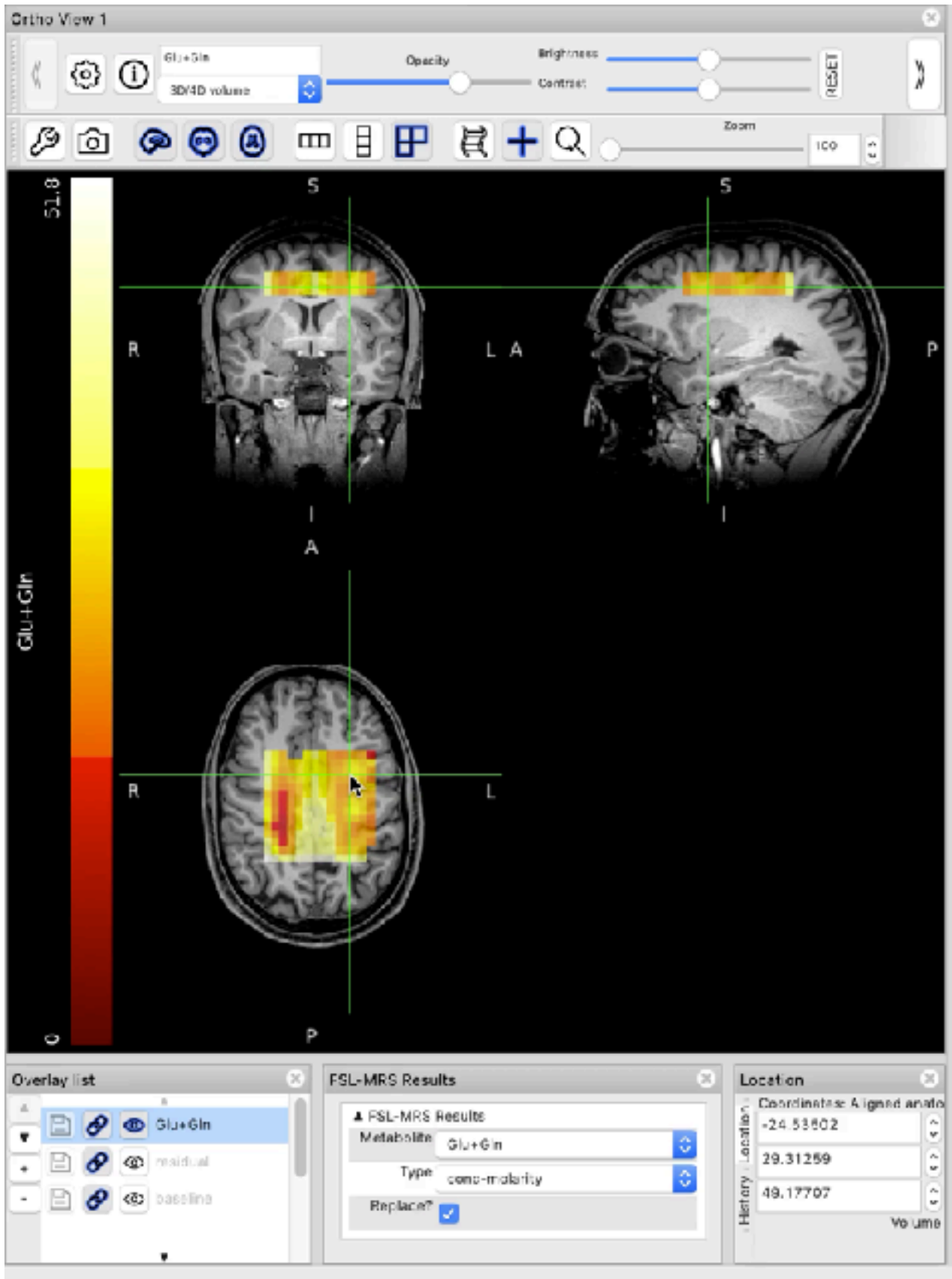
Summary - Nuisance - QC - Uncertainty - Real/Imag - Metabs - Quantification - Methods

Summary

Metab	mMol/kg	CRLB	%CRLB	/Cr+PCr
Ala	0	0.33	999	0
Asc	1.55	0.6	36.3	0.1
Asp	3.03	0.96	31.7	0.18
Cr	10.64	0.88	8.3	0.63
GABA	2.58	0.46	17.6	0.15
GPC	2.38	0.38	16.1	0.14
GSH	3.15	0.29	9.2	0.19
Glc	0.12	0.75	600.7	0.01
Gln	0.98	0.58	59.8	0.06
Glu	16.56	0.59	3.5	0.99
Ins	13.87	0.49	3.5	0.83
Lac	1.02	0.32	31.2	0.06
Mac	1.35	0.04	3	0.08
NAA	22.75	0.62	2.7	1.36
NAAG	2.5	0.32	12.6	0.15
PCh	0.7	0.41	58.9	0.04
PCr	6.15	0.83	13.5	0.37
PE	2.8	0.63	22.3	0.17
Scyllo	1.44	0.15	10.2	0.09
Tau	4.05	0.54	13.4	0.24
Cr+PCr	16.79	0.49	2.9	1



Using FSLeyes (MRS plugin)

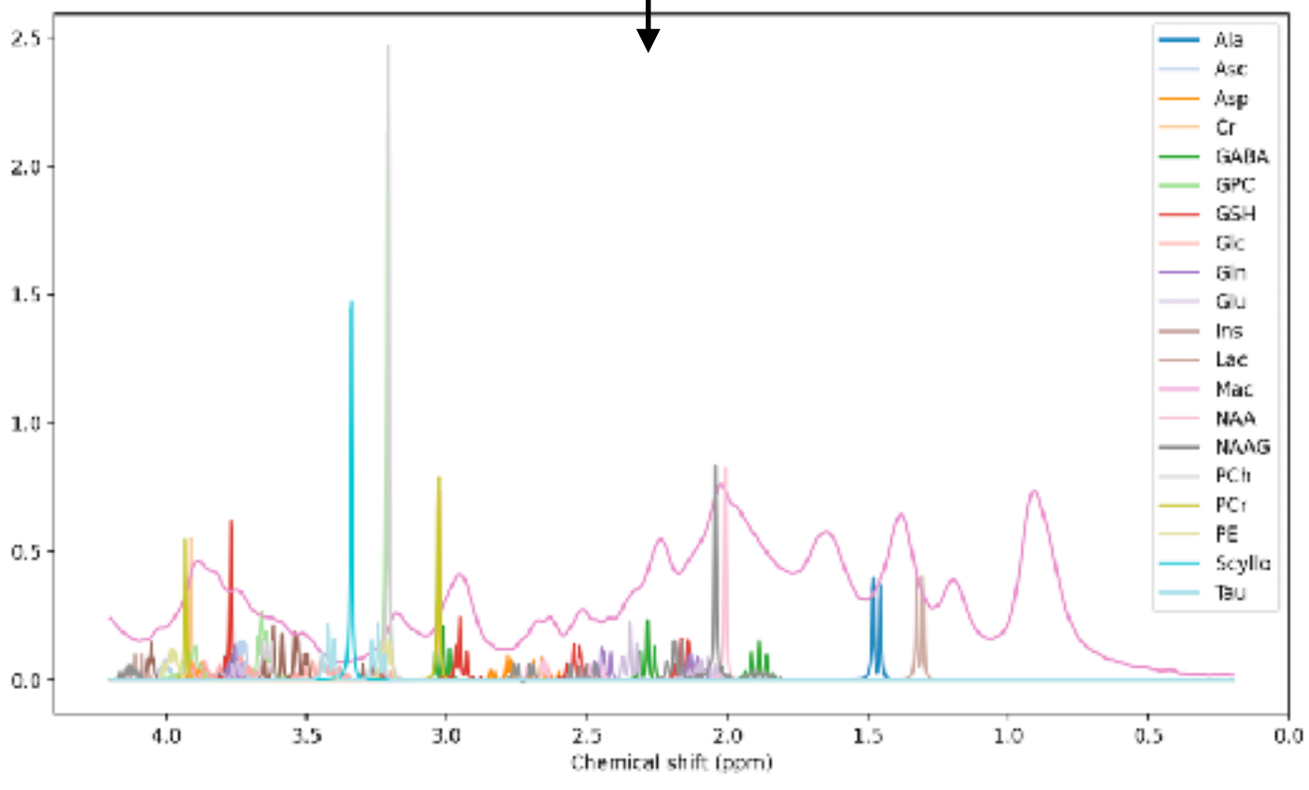


How to get the basis (design matrix)?

Spin system
(metabolite)

Sequence
(Gradients and RF pulses)

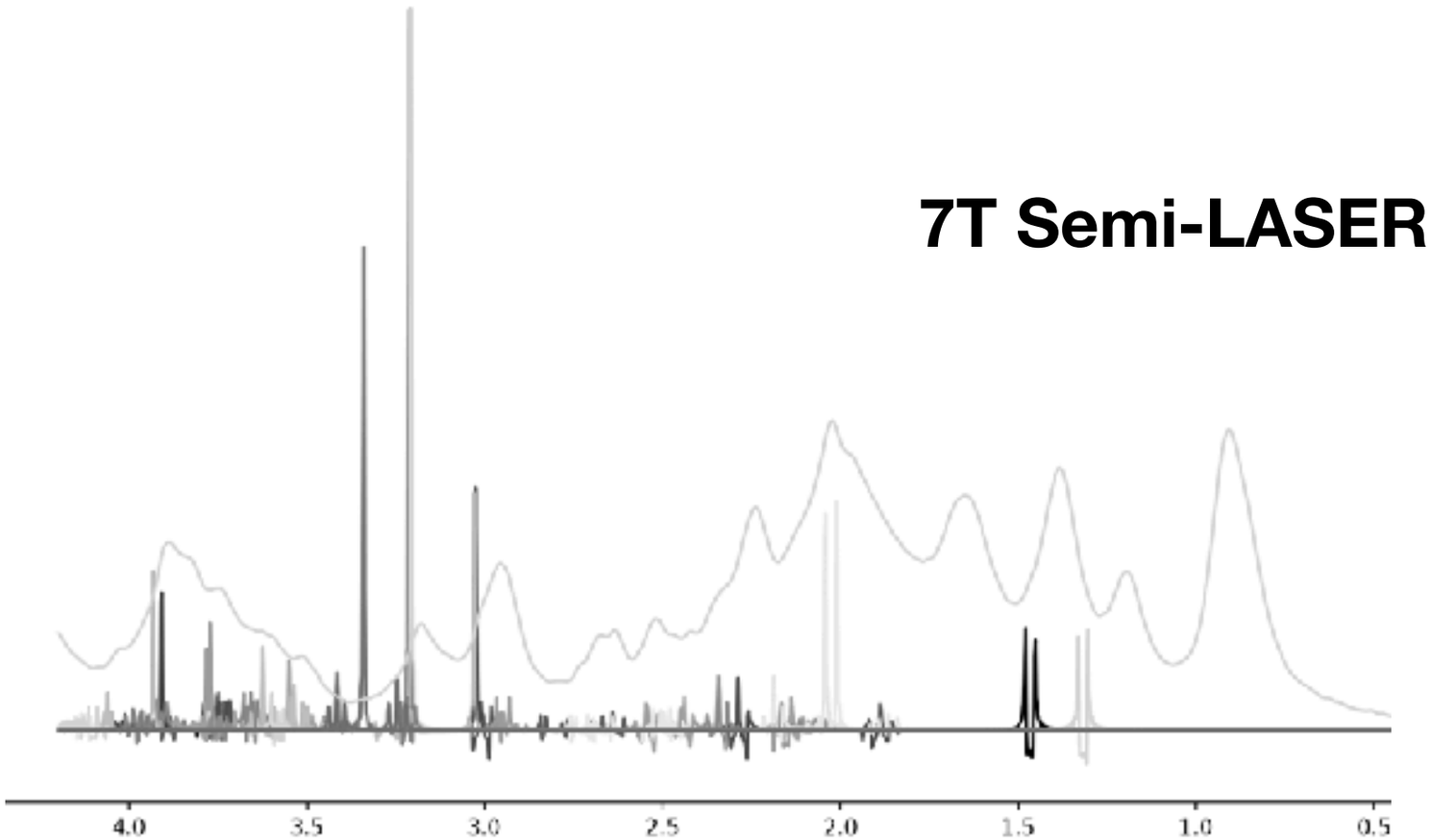
Density Matrix
Simulator

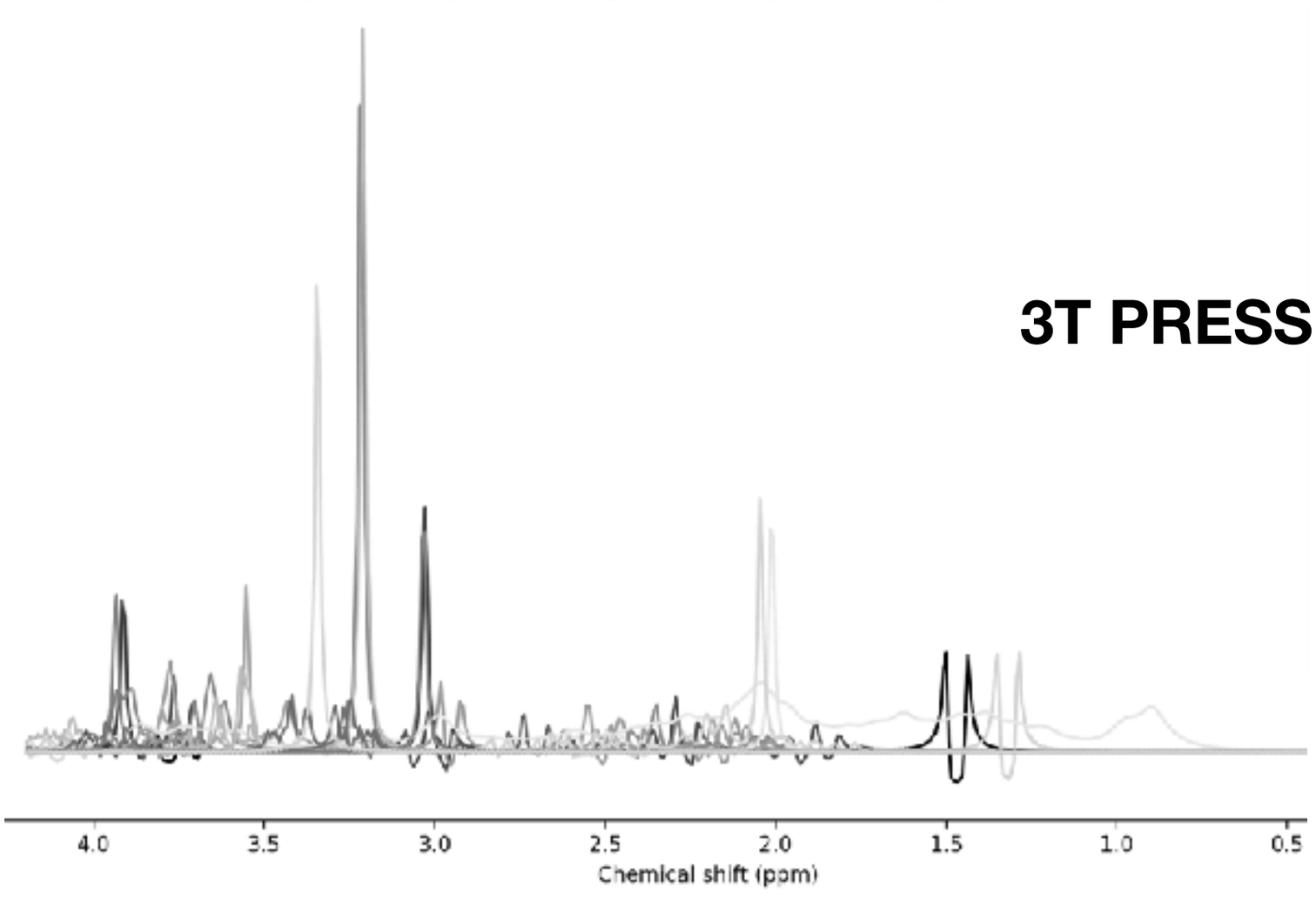


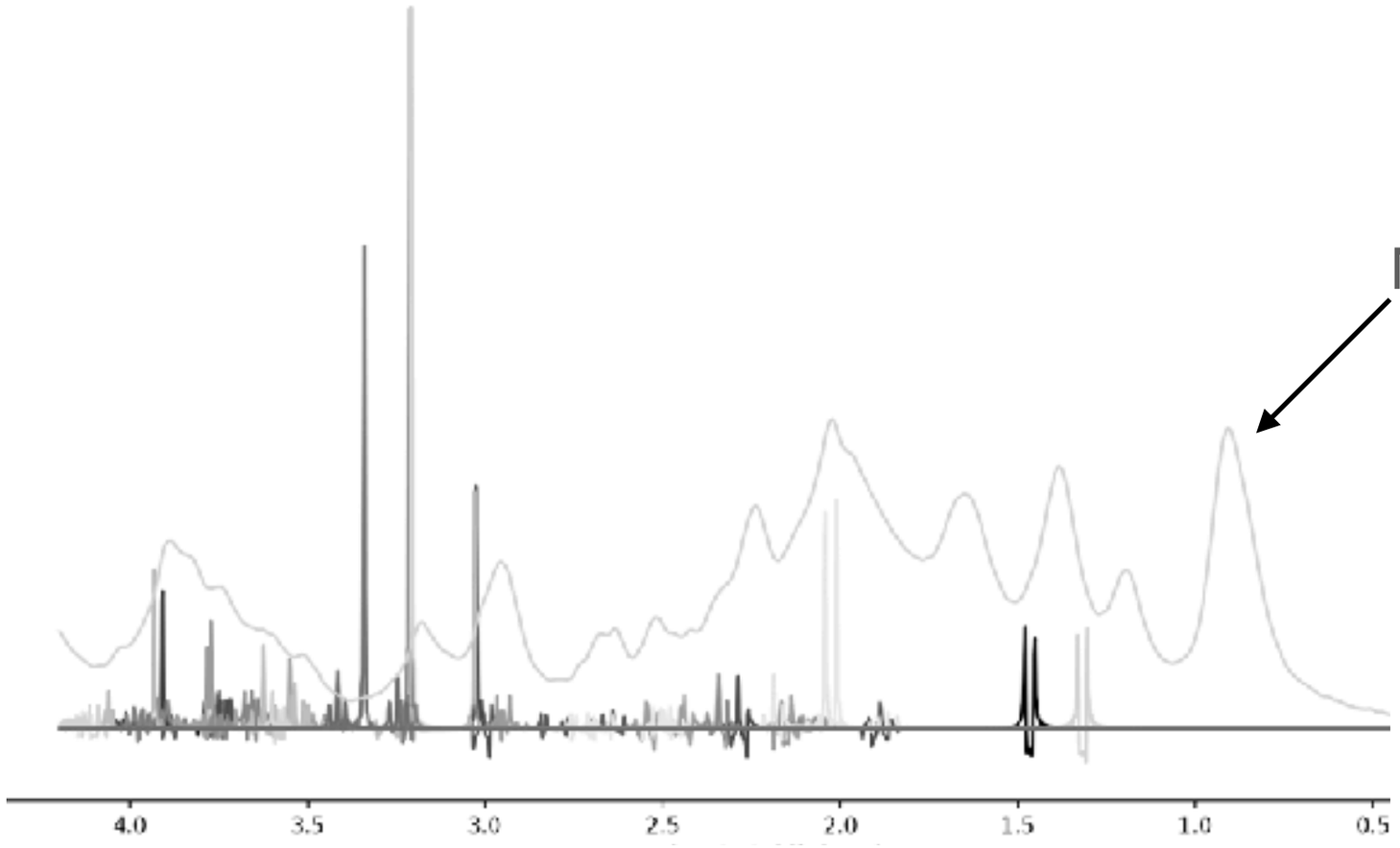
Metabolites in FSL-MRS

System	Name in simulator	System	Name in simulator
acetate	Ace	water	H2O
alanine	Ala	myo-inositol	Ins
ascorbic acid	Asc	lactate	Lac
aspartic acid	Asp	N-acetyl aspartate	NAA
citrate	Cit	(NAA) glutamate	NAAG
creatine	Cr	phosphocholine	PCh
ethanol	EtOH	phosphocreatine	PCr
γ-aminobutyric acid[1]	GABA	phosphorylethanolamine	PE
γ-aminobutyric acid[2]	GABA_gov	phenylalanine	Phenyl
glycerophosphocholine	GPC	scyllo-Inositol	Scyllo
glutathione[2]	GSH	serine	Ser
glutathione[3]	GSH_v2	taurine	Tau
glucose	Glc	tyrosine	Tyros
glutamine	Gln	beta-hydroxybutyrate	bHB
glutamate	Glu	2-HG[4]	bHG
glycine	Gly		

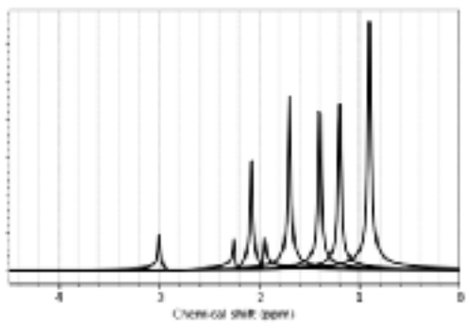
https://open.win.ox.ac.uk/pages/fsl/fsl_mrs


7T Semi-LASER
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5

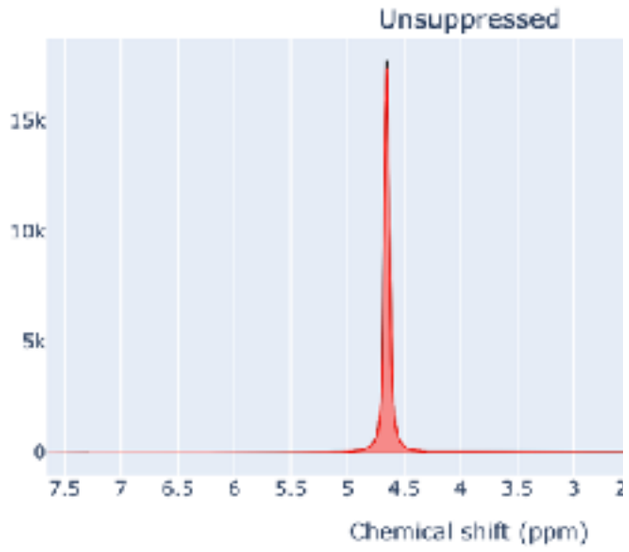

3T PRESS
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
Chemical shift (ppm)

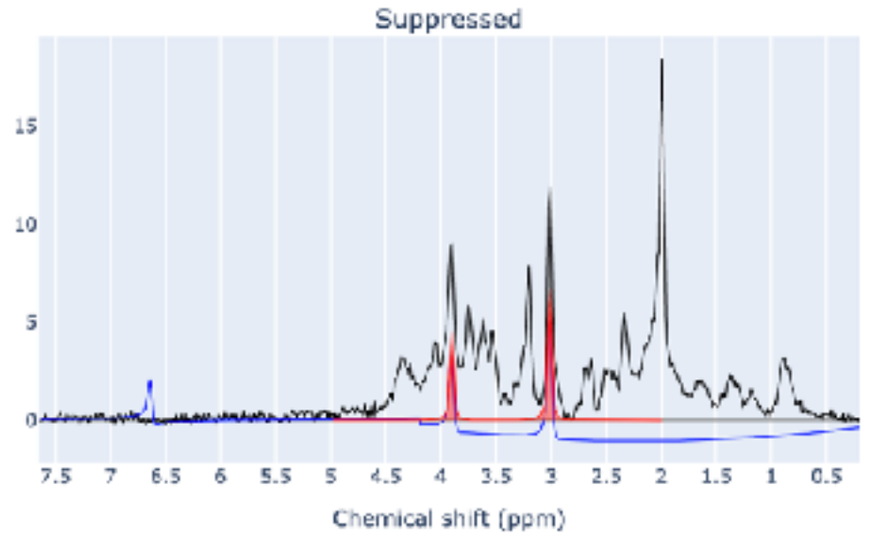


- Measured (with a similar sequence)
- Simulated (approximate)

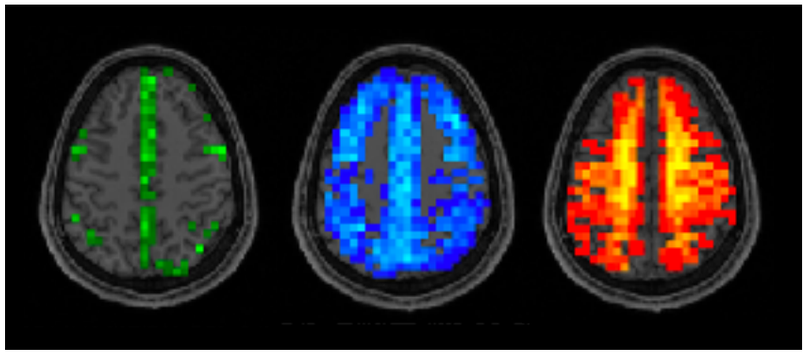


Quantitation
Calibrated measurements





- Water reference data
- Ref metabolite (e.g. tCr)
- Tissue partial volume (FAST)



- Relaxation parameters (typically from literature)

```
STANDARD_T1 = { '3T':{'H2O_WM':0.97, # Ref: 1-6
                      'H2O_GM':1.50, # Ref: 1-6
                      'H2O_CSF':4.47, # Ref: 4
                      'METAB':1.29}, # Ref: 2, 7-9
                '7T':{'H2O_WM':1.21, # Ref: 1-6
                      'H2O_GM':2.05, # Ref: 1-6
                      'H2O_CSF':4.43, # Ref: 4
                      'METAB':1.43}} # Ref: 2, 7-9

STANDARD_T2 = { '3T':{'H2O_WM':0.073, # Ref: 1,3,10-11
                      'H2O_GM':0.080, # Ref: 1,3,10-11
                      'H2O_CSF':2.030, # Ref: 12
                      'METAB':0.194}, # Ref: 7-9,13-15
                '7T':{'H2O_WM':0.055, # Ref: 1,3,10-11
                      'H2O_GM':0.050, # Ref: 1,3,10-11
                      'H2O_CSF':1.050, # Ref: 12
                      'METAB':0.131}} # Ref: 7-9,13-15
```

Summary

- MRS fitting similar to GLM but with nonlinear dependences
- Fitting concentrations and confounds
- "Design Matrix" depends on precise MR sequence description and chemical structure of metabolites
- Important to visualise the fitting (details matter)
- Quantitation requires additional information (partial volume and relaxation)