

## Columbia | Zuckerman Institute Mortimer B. Zuckerman Mind Brain Behavior Institute

## OBJECTIVES

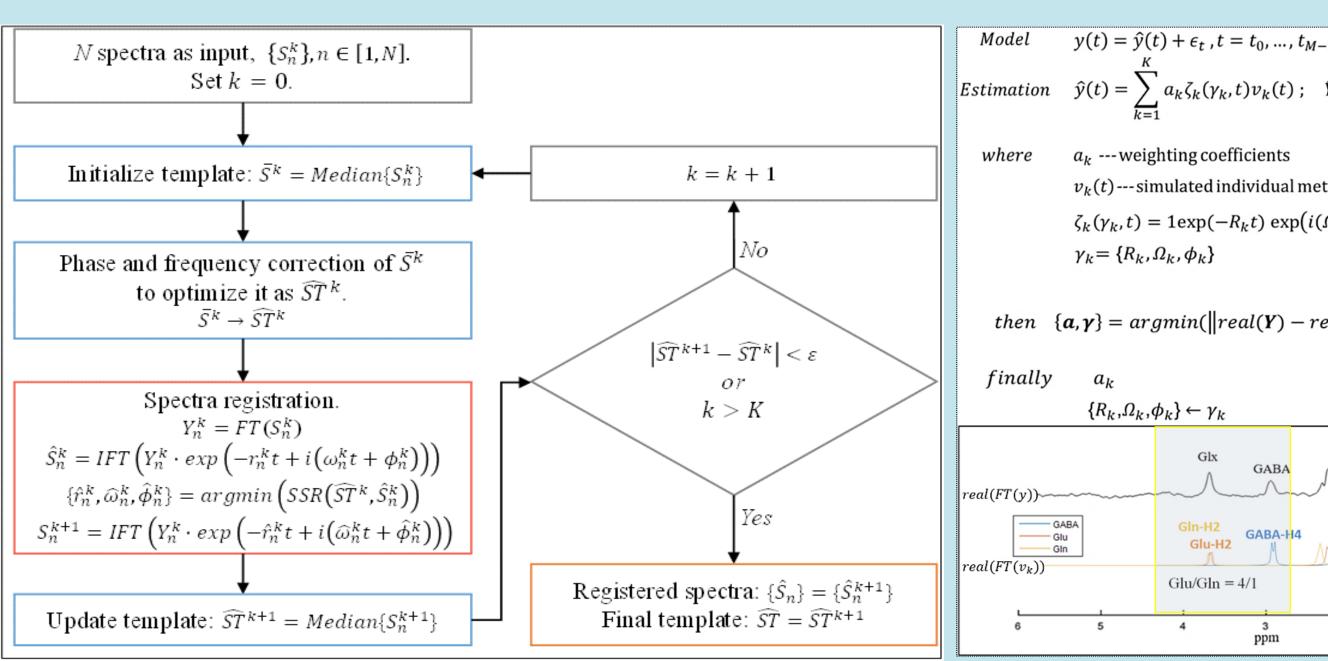
- To develop an open-source toolkit, MRSMouse, for J-difference editing (JDE) spectral processing and analysis in mice.
- To test the performance of MRSMouse toolkit in pre-clinical studies using *in vivo* mouse thalamic spectra acquired at 9.4T
- To further apply MRSMouse toolkit for *in vivo* human studies at 3T and discuss its clinical utility.

## BACKGROUND

- MRS spectral editing studies of mice have been limited due to difficulties in spectrum processing and the lack of a standardized software package for analysis.
- Inspired by the idea of image registration, which has been extensively used for MR image analysis, in this work, we present an automated JDE spectra processing and analysis pipeline built upon the idea of spectrum registration.

### **METHODS**

- **Loading Scanner Raw Data**
- **Initialization**: multi-channel combination, zero-filling, line broadening.
- **Spectrum Registration**: 'On', 'Off', 'On'-Average to 'Off'-Average. 3.
- **4. Preparation for Spectrum Fitting**: 'Off'-Average, 'Diff'-Average, basis set.
- **5. Spectrum Fitting**: 'Off'-Average, 'Diff'-Average, basis set, LCModel.
- **6. Reports:** quality, quantity.



# MRSMouse **Open-Source Toolkit for J-difference Editing Spectra Processing and Analysis in Mice**

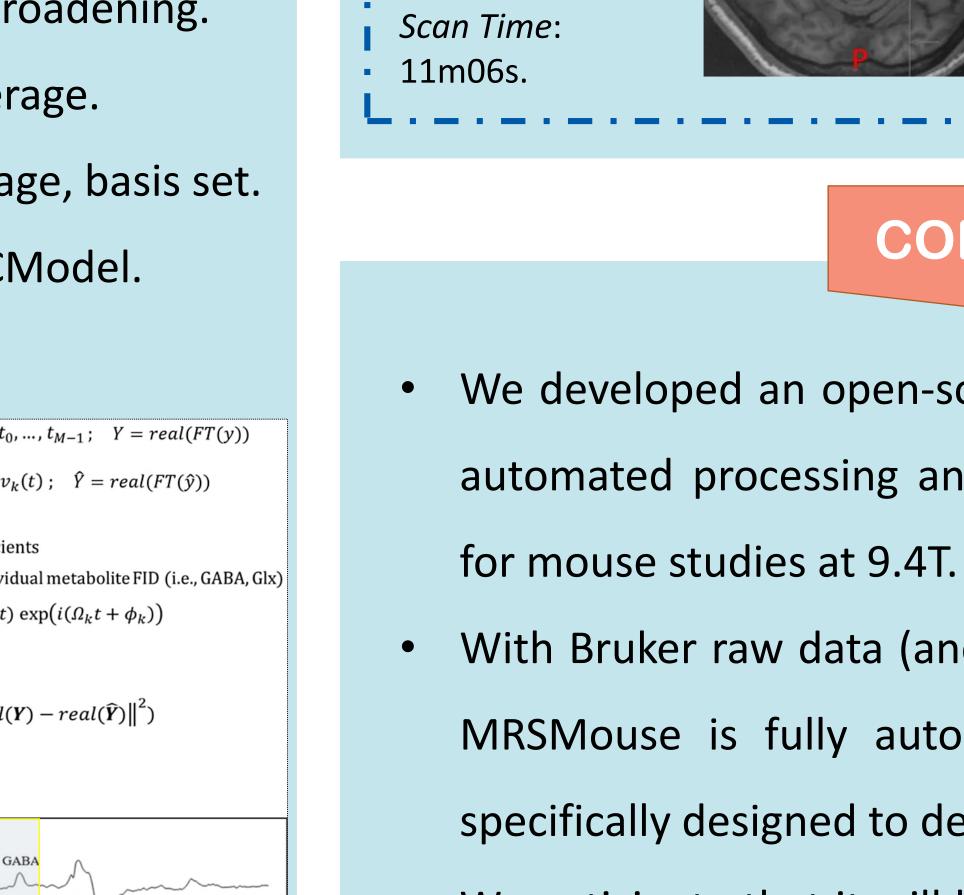
## Jia Guo, Kay C. Igwe, Yanping Sun, Douglas L. Rothman and Scott A. Small

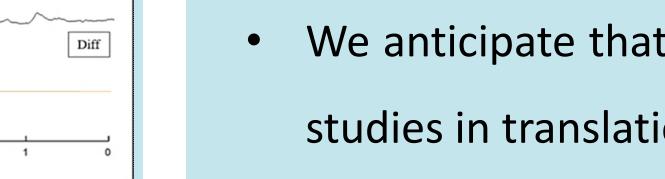
Model  $y(t) = \hat{y}(t) + \epsilon_t$ ,  $t = t_0, \dots, t_{M-1}$ ; Y = real(FT(y))Estimation  $\hat{y}(t) = \sum a_k \zeta_k(\gamma_k, t) v_k(t); \quad \hat{Y} = real(FT(\hat{y}))$  $v_k(t)$  --- simulated individual metabolite FID (i.e., GABA, Glx)  $\zeta_k(\gamma_k, t) = 1 \exp(-R_k t) \exp(i(\Omega_k t + \phi_k))$ then  $\{a, \gamma\} = argmin(\|real(Y) - real(\widehat{Y})\|^2)$  $\{R_k, \Omega_k, \phi_k\} \leftarrow \gamma_k$ 

2

Glu/Gln = 4/1

4





	Amplitude Correction	Mode None -
Cd	LowF 2.7 ppm F HighF 3.1 ppm	Reference average -
0	View Spectra	App
Mart Halle	Off Spectrum	ON Spectrum   O DIFF Spectrum
SP Rt1.48 (SE 1.00 / 2.00)	LowF 0 ppm Hig	phF 5 ppm Scale 1 x
Slice 5/9         Fov 25.00x25.00           Bruker.FLASH         CM	Reset All	Apply
	Target Metabolite Fitting	Reference Metabolite Fitting
	GABA Lower ppm 2.55 Higher ppm 3.5	Cr Lower ppm 2. Higher ppm 3.
	Gtx Lower ppm 3.2	Cho Lower ppm 3.
Rt	Higher ppm 4.2 2HG Lower ppm 3.7	Higher ppm 3.4
<u>o</u> 1	Higher ppm 4.3	Higher ppm 2.
	GSH Lower ppm 2.7 Higher ppm 3.4	Water Higher ppm 5.
SP V3.43 SL 1.00 / 1.61 FeV 25.00x25.00	Apply	Report
Gu	o et al 201	.8. https://or
Cut	5 CT UI., 201	.0. <u>mttp3.//01</u>
Apply to Human 💼		
Scanner: Prisma.		
		1233
Field: 3T.	S T	a X
Region:	62	A COL
		10-20
left hippocampus.		1
Sequence:		
MEGA-PRESS.	H	
	CON this	
TR/TE:	SSE .	and the
2000/80 ms.		the at
Coil:		
Head volume coil	1934	
	1.44	
64 channel.	A	
Voxel Size:		
40 x 20 x 25 mm^3	a sur	EDY
(AP x HF x LR).		R <sup>22</sup> to Template
Averages: 160.		R <sup>A</sup> 2 to
Scan Time:	h /	12- M
	A SECLO	
11m06s		

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LB 10 Hz LowF 0.5 ppm

Mode Off Derivative 2

## CONCLUSION

## **RESULTS - GUI & REPORTS**





We developed an open-source toolkit, MRSMouse, designed for automated processing and analysis of JDE spectra and tailored

With Bruker raw data (and clinical scanner raw data) supported, MRSMouse is fully automated and rater-independent and is specifically designed to deal with low S/N spectra.

We anticipate that it will be a useful tool for the adoption of JDE studies in translational animal (and clinical human) researches.

- Columbia University Taub Institute: Imaging Pilot Grant ICRC Small Imaging Lab: 94/20 Bruker Scanner Zuckerman Institute: MRI Research Seed Grant Zuckerman Institute: Siemens Prisma 3T Scanner Dr. Ray Lee, Siemens Protocol Set-up and Imaging Support
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- Bruker BioSpin

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