

Introduction to qMRLab: An Open-Source Tool for Quantitative MR Image Analysis

Mathieu Boudreau, PhD

Affiliations

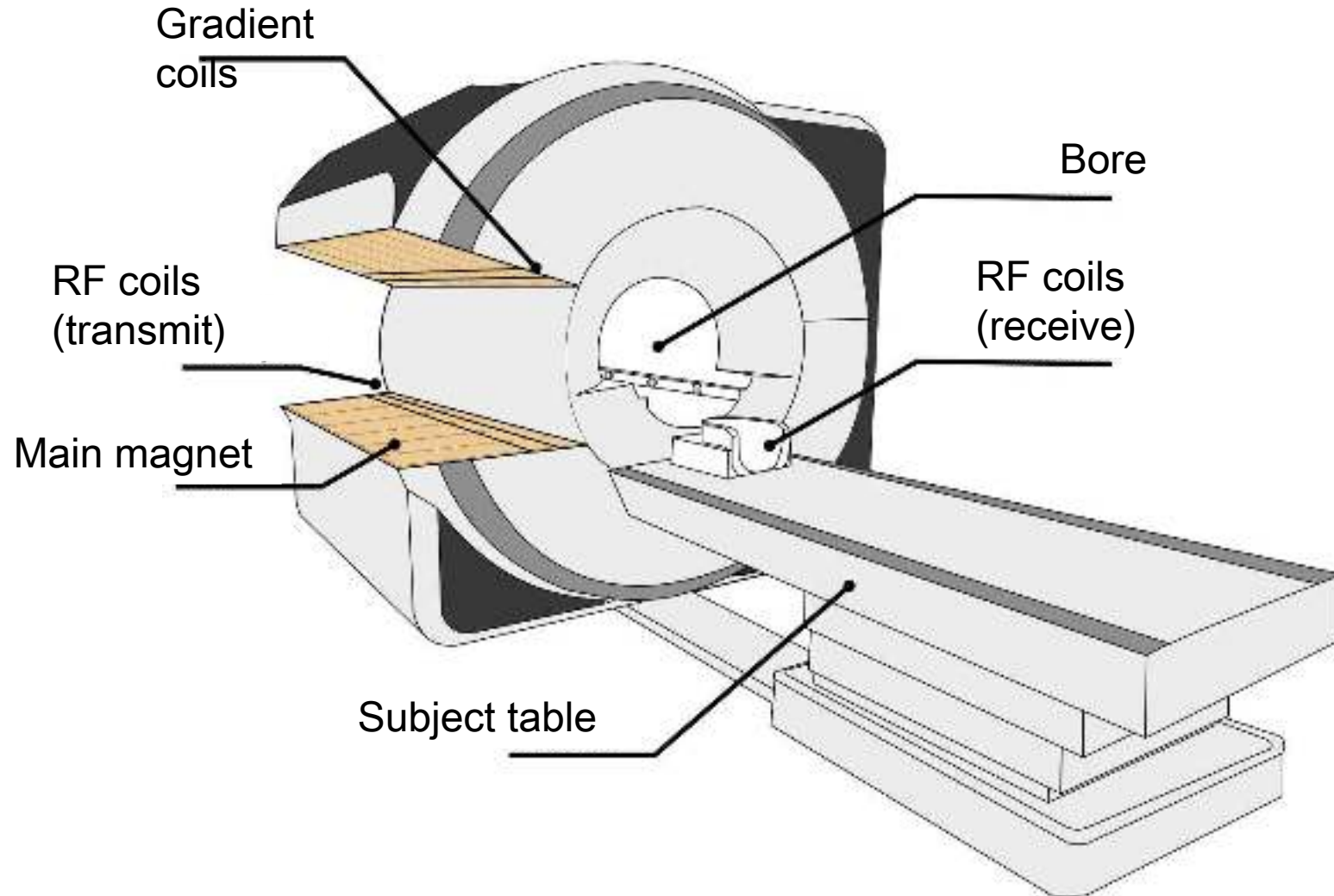
Research Assistant, NeuroPoly, Polytechnique Montréal
MRM Deputy Editor for Scientific Outreach
Lead Editor for Digital Content of MRM Highlights



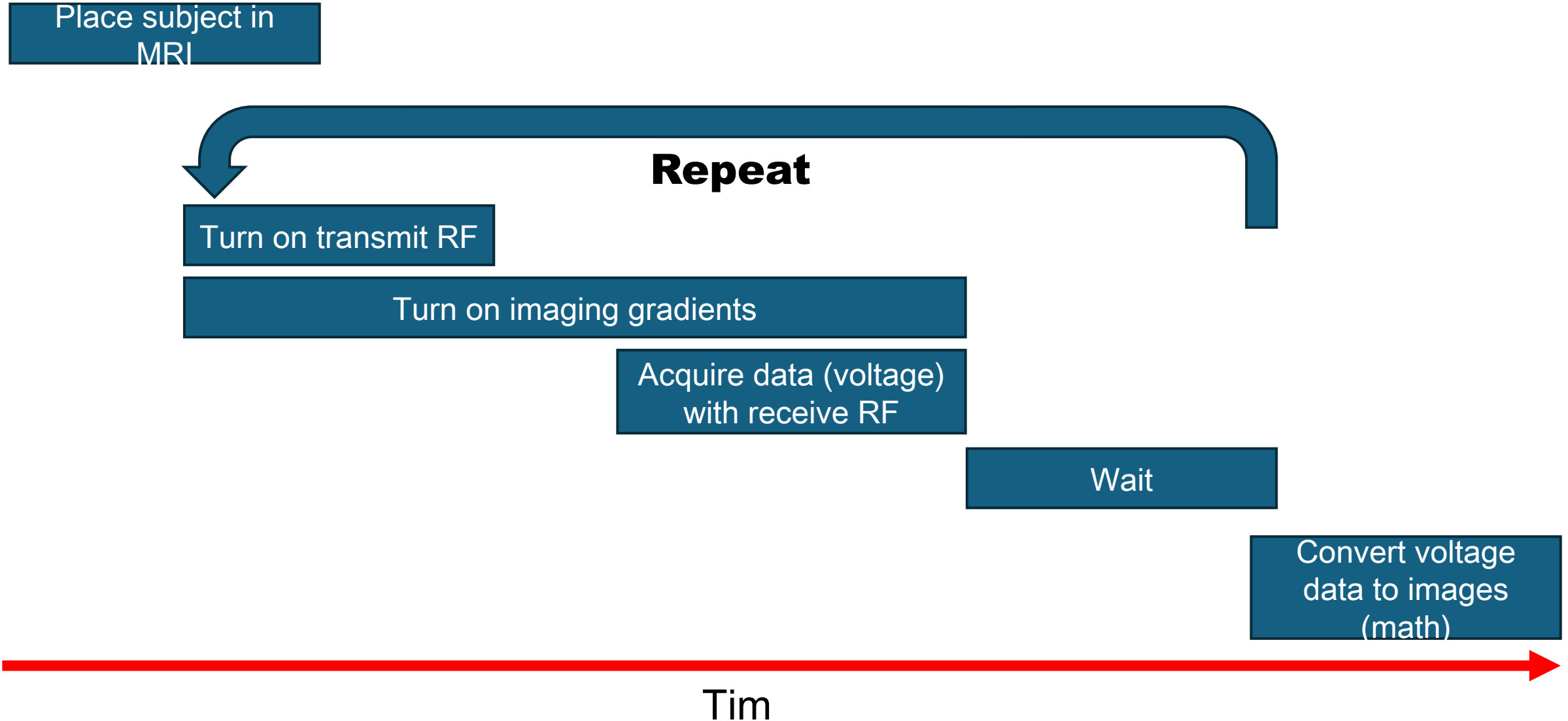
Talk Outline

- MRI Primer
- Quantitative MRI
- Overview of qMRLab
- Quantitative MRI mOOC
- qMRLab Tutorial
- qMRLab application example: ISMRM T_1 challenge
- MRM Highlights

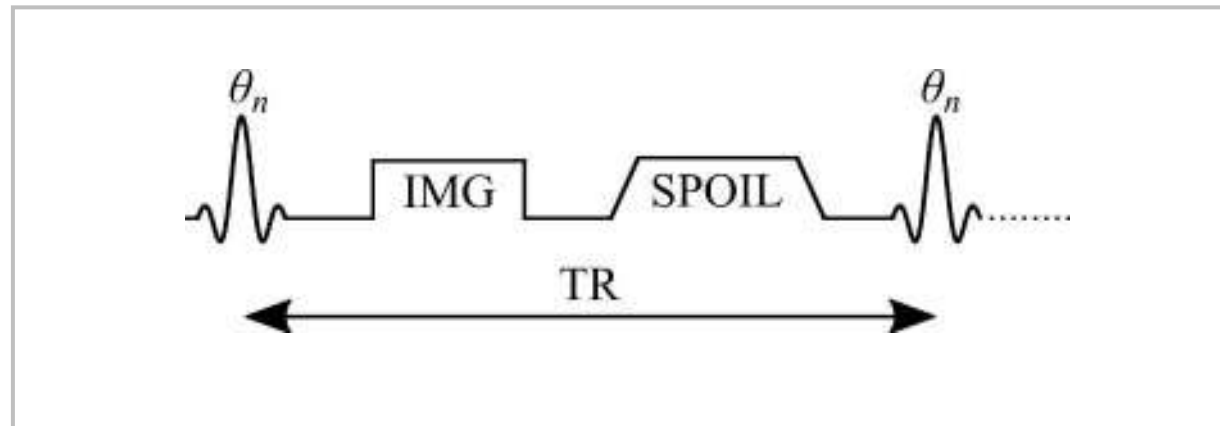
Primer: Magnetic Resonance Imaging (MRI)



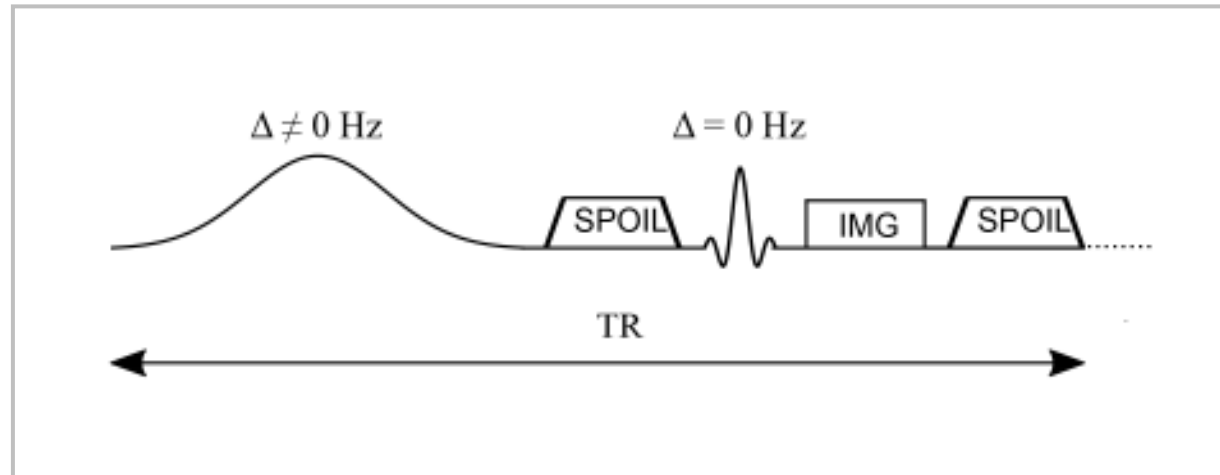
Primer: Magnetic Resonance Imaging (MRI)



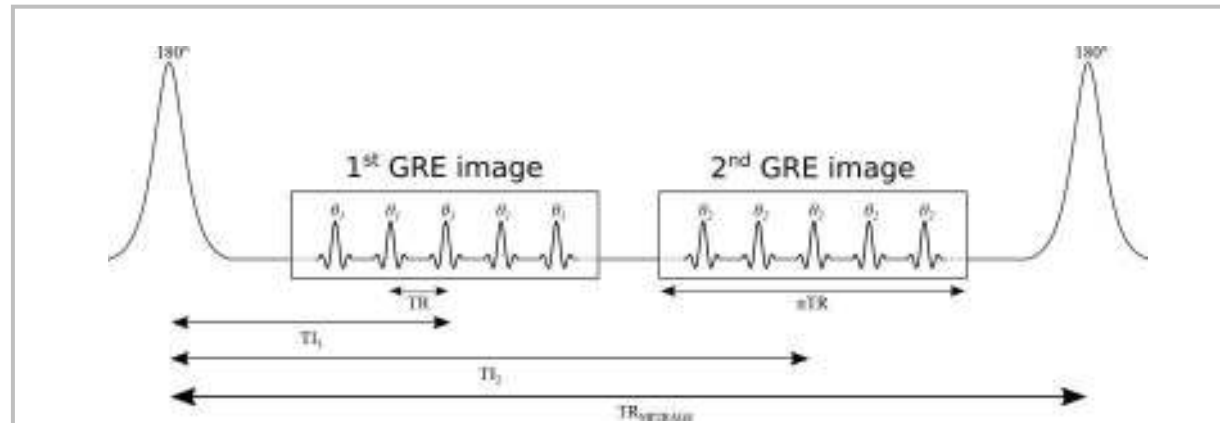
Gradient echo



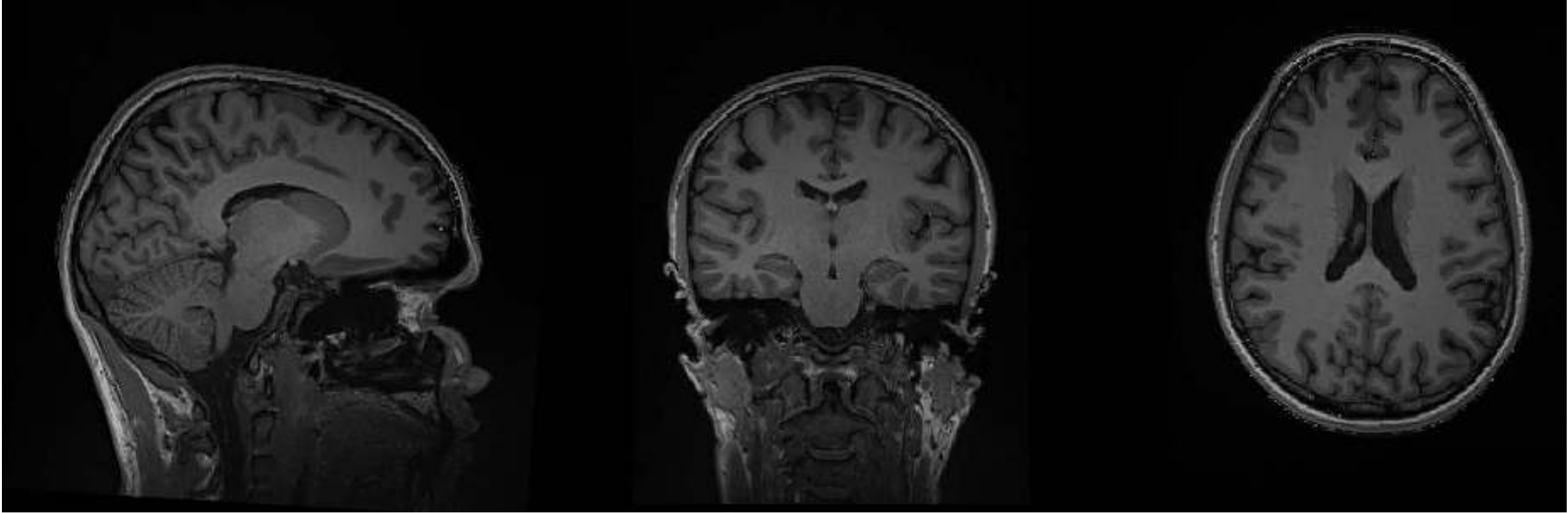
MT-weighted GRE



MP2RA GE



Primer: Magnetic Resonance Imaging (MRI)



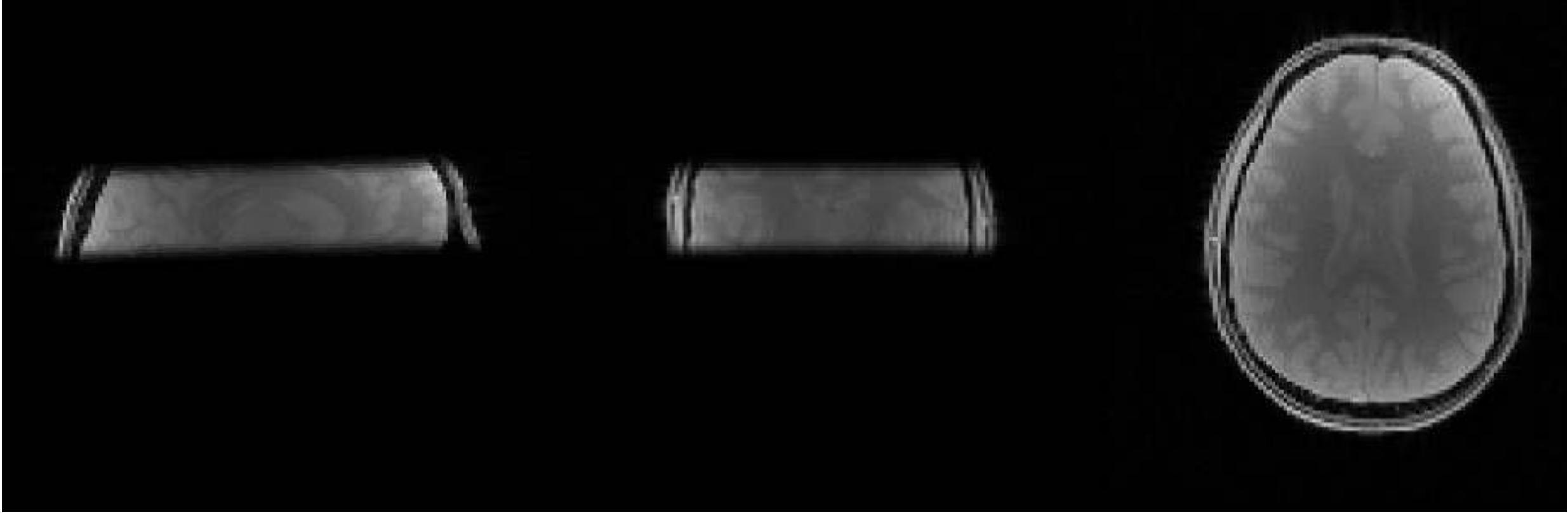
(Pulse Sequence: **MPRAGE**)

Primer: Magnetic Resonance Imaging (MRI)



(Pulse Sequence: **Sagittal TruFISP**)

Primer: Magnetic Resonance Imaging (MRI)



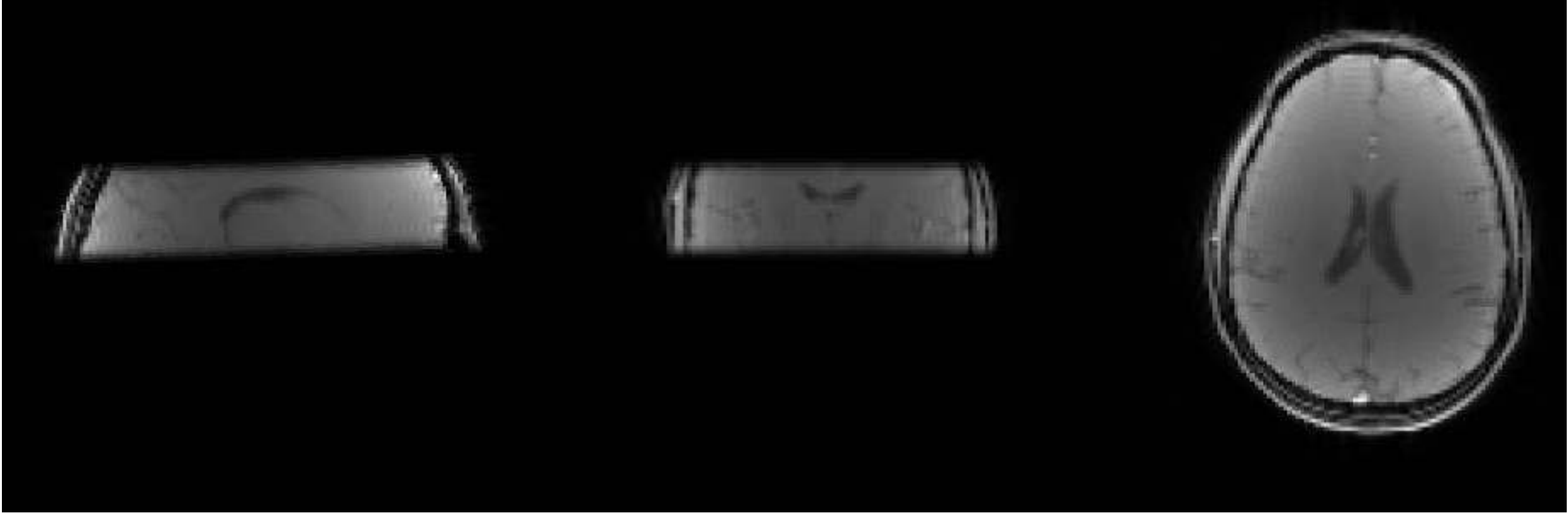
(Pulse Sequence: Gradient Echo, RF flip angle = 3 degree)

Primer: Magnetic Resonance Imaging (MRI)



(Pulse Sequence: Gradient Echo, RF flip angle = 15 degree)

Primer: Magnetic Resonance Imaging (MRI)



(Pulse Sequence: Gradient Echo)

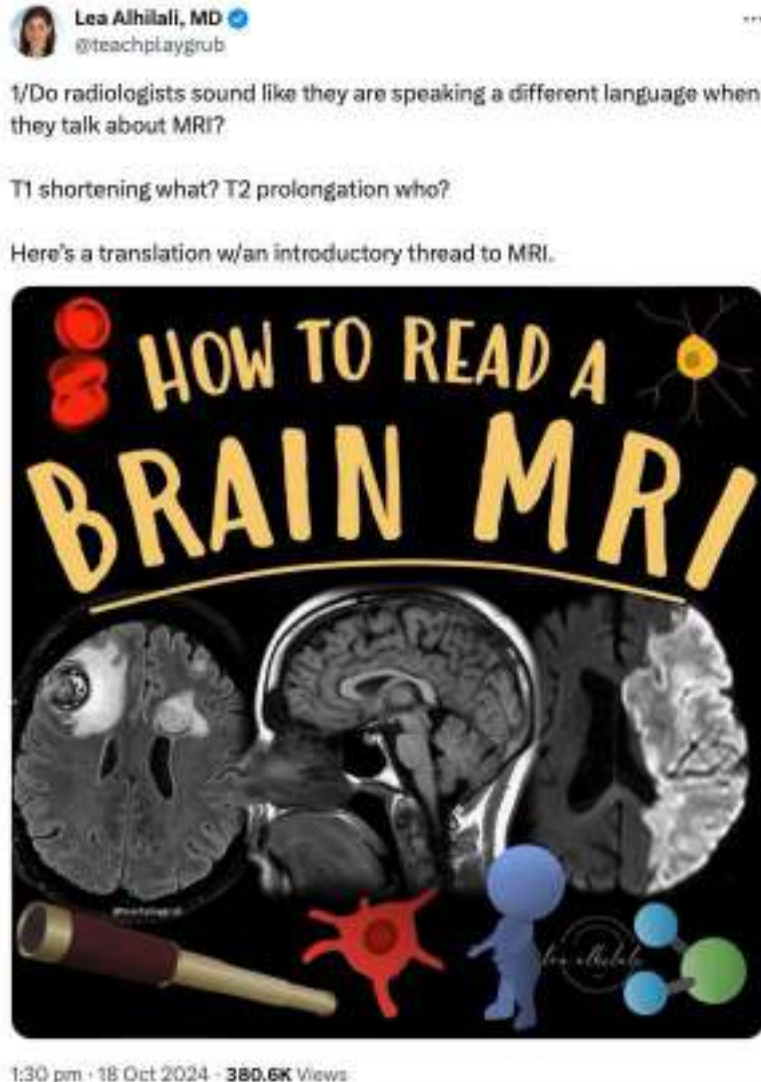
Primer: Magnetic Resonance Imaging (MRI)



(Pulse Sequence: MT-weighted Gradient Echo)

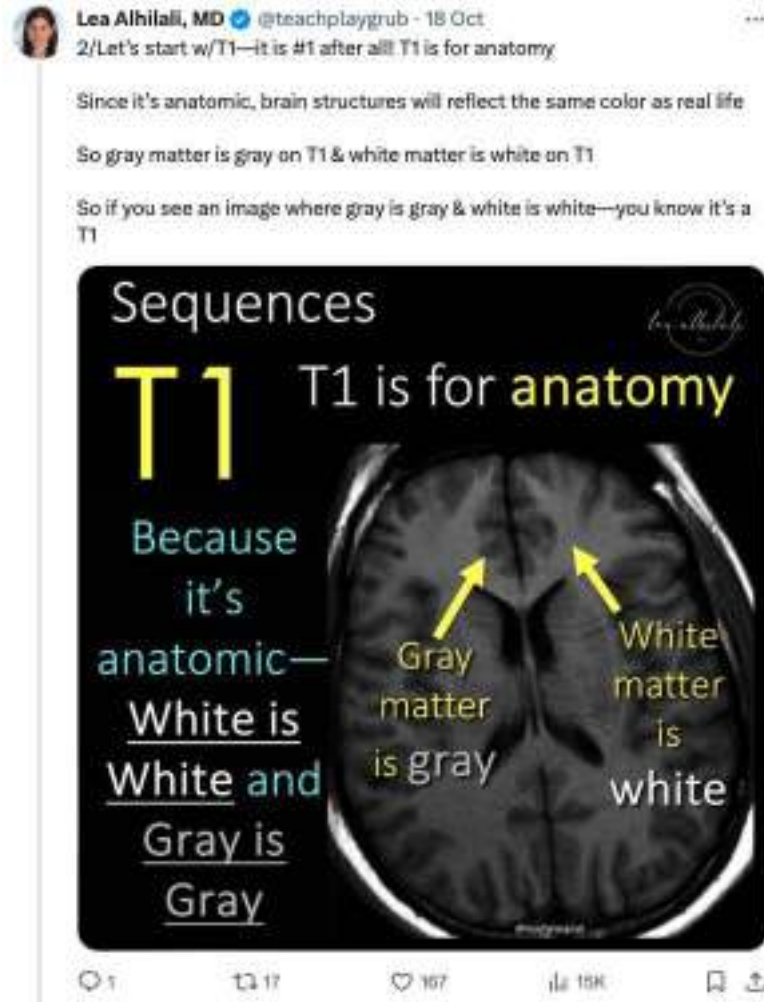
Primer: Interpretation of clinical

MRI images



<https://x.com/teachplaygrub/status/184731426180817306>

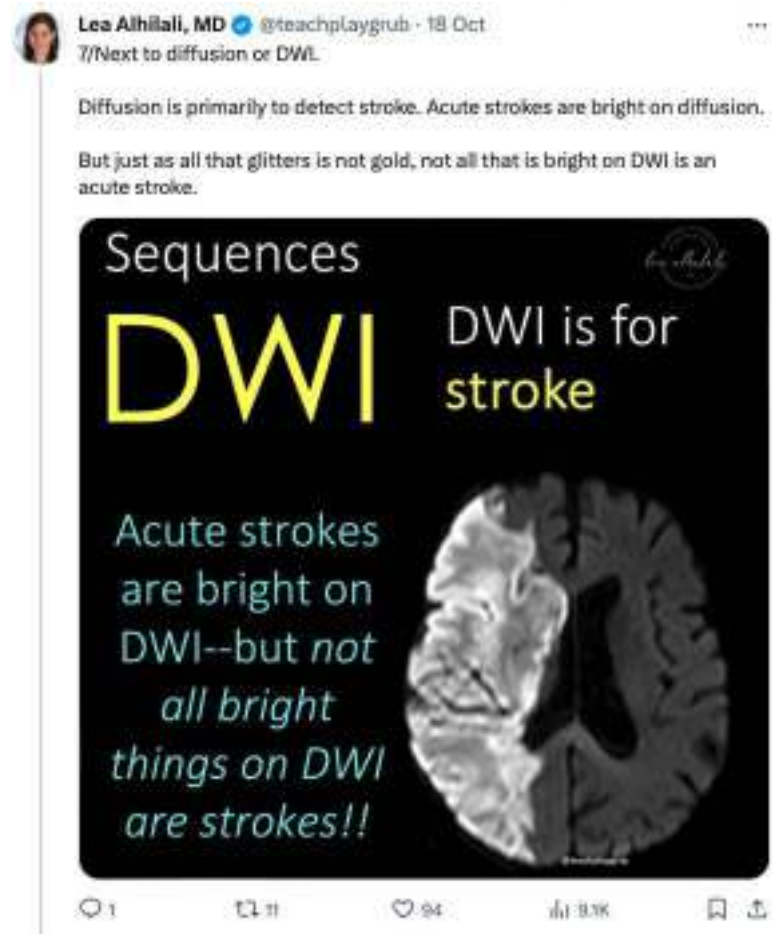
Primer: Interpretation of clinical MRI images



Primer: Interpretation of clinical MRI images



Primer: Interpretation of clinical MRI images



MRI: medical vs measurement applications



The MAGNETOM MR system is not a device with measuring function as defined in the Medical Device Directive (MDD). Quantitative measured values obtained are for informational purposes and cannot be used as the only basis for diagnosis.

Siemens Magnetom Operator's Manual
Print No. MR-05024.640.02.02.24

MRI: medical vs measurement applications

[Code of Federal Regulations]
[Title 21, Volume 8]
[CITE: 21CFR892.1000]



TITLE 21--FOOD AND DRUGS
CHAPTER I--FOOD AND DRUG ADMINISTRATION
DEPARTMENT OF HEALTH AND HUMAN SERVICES
SUBCHAPTER H - MEDICAL DEVICES

PART 892 -- RADIOLOGY DEVICES

Subpart B - Diagnostic Devices

Sec. 892.1000 Magnetic resonance diagnostic device.

(a) *Identification.* A magnetic resonance diagnostic device is intended for general diagnostic use to present images which reflect the spatial distribution and/or magnetic resonance spectra which reflect frequency and distribution of nuclei exhibiting nuclear magnetic resonance. Other physical parameters derived from the images and/or spectra may also be produced. The device includes hydrogen-1 (proton) imaging, sodium-23 imaging, hydrogen-1 spectroscopy, phosphorus-31 spectroscopy, and chemical shift imaging (preserving simultaneous frequency and spatial information).

(b) *Classification.* Class II (special controls). A magnetic resonance imaging disposable kit intended for use with a magnetic resonance diagnostic device only is exempt from the premarket notification procedures in subpart E of part 807 of this chapter subject to the limitations in § 892.9.

[53 FR 5078, Feb. 1, 1989, as amended at 84 FR 71818, Dec. 30, 2019]

Quantitative MRI

**Adapting the MRI machine to
behave as scientific measurement
device**

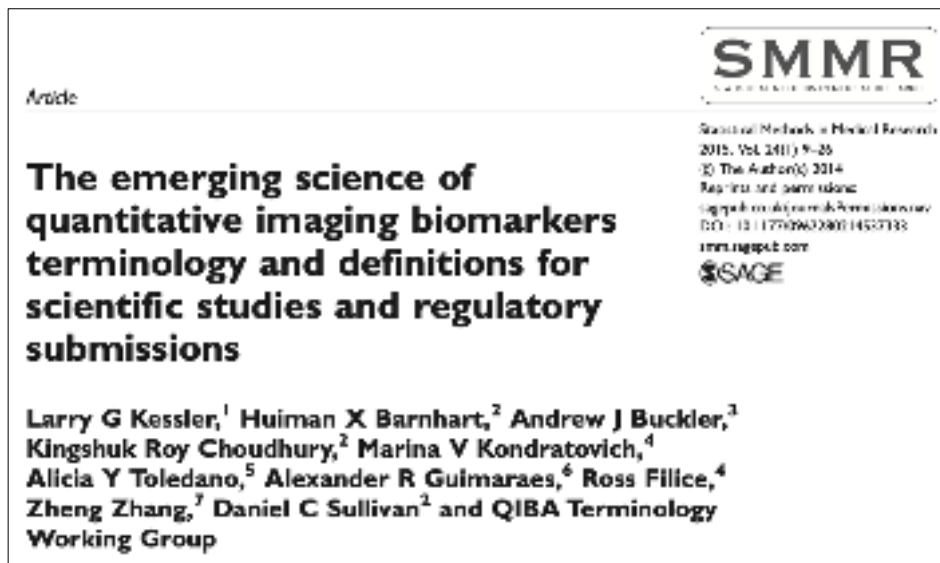
MRI Quantitative Imaging Biomarkers

MRI Parameter	Units	Example Applications
T ₁ (signal recovery time)	ms	Aging, myocarditis, tumors
T ₂ (signal decay time)	ms	Demyelination (MS), ACL injuries
Diffusion coefficients	s·mm ²	Stroke, ALS, emphysema
Flow	cm·s ⁻¹	Aortic dissection, vascular stenosis
Perfusion	mL/100 g /min	Acute stroke, predicting hemorrhages
Magnetization transfer & Chemical exchange	Pool Size Ratio F → unitless Exchange rates k _f & k _r → s ⁻¹	Macromolecules / demyelination (MS), Acute stroke, tumors
Magnetic Susceptibility	ppm	Iron (MS, Alzheimer's, microvascular disease)
Conductivity & permittivity	Conductivity → S·m ⁻¹ (S: “Siemens” → kg ⁻¹ ·m ⁻² ·s ³ ·Amperes ²) Permittivity → F·m ⁻¹ (F: “Farads” → kg ⁻¹ ·m ⁻³ ·s ⁴ ·Amperes ²)	Tumors, thermal ablation planning, MR safety
Temperature	°C	Thermal ablation planning

MRI Field Properties

Electromagnetic field	Units	Example Applications
B₀ (main magnetic field)	Tesla (T), Hz, ppm	Shimming Quantitative Susceptibility Mapping RF pulse offset (e.g., Magnetization transfer & chemical exchange)
B₁⁺ (transmit RF field amplitude)	μT, Volts · m ⁻¹ , normalized units	RF flip angle correction Magnetization transfer RF pulse power correction SAR mapping (MR safety)

Quantitative MRI: Road to Standardization





qMR

Lab

Quantitative MRI. Under one umbrella.

Major Publications

Quantitative Magnetization Transfer Imaging Made Easy with *qMTLab*: Software for Data Simulation, Analysis, and Visualization

JEAN-FRANÇOIS CABANA,¹ YE GU,² MATHIEU BOUDREAU,³ IVES R LEVESQUE,⁴ YAASEEN ATCHIA,⁵ JOHN G. SLED,^{6,7} SRIDAR NARAYANAN,³ DOUGLAS L. ARNOLD,³ G. BRUCE PIKE,^{3,8} JULIEN COHEN-ADAD,⁹ TANGUY DUVAL,⁹ MANH-TUNG VUONG,⁷ NIKOLA STIKOV^{9,10}

¹Department of Medical Physics, University of Montreal, Montreal, QC, Canada

²NeuroRX, Montreal, QC, Canada

³Montreal Neurological Institute, McGill University, Montreal, QC, Canada

⁴Department of Medical Physics, Oncology and RI-MUHC, McGill University, Montreal, QC, Canada

⁵Department of Electrical and Biomedical Engineering, University of Toronto, Toronto, ON, Canada

⁶Hospital for Sick Children, Toronto, ON, Canada

⁷Department of Medical Biophysics, University of Toronto, Toronto, ON, Canada

⁸Department of Radiology, University of Calgary, Calgary, AB, Canada

⁹Institute for Biomedical Engineering, Ecole Polytechnique, Montreal, QC, Canada

¹⁰Montreal Heart Institute, Montreal, QC, Canada

Cabana et al., (2015), *Quantitative magnetization transfer imaging made easy with qMTLab: Software for data simulation, analysis, and visualization*. Concepts Magn. Reson., 44A: 263-277. <https://doi.org/10.1002/cmr.a.21357>



qMRLab: Quantitative MRI analysis, under one umbrella

Agah Karakuzu^{1, 4}, Mathieu Boudreau^{1, 4}, Tanguy Duval¹, Tommy Boshkovski¹, Ilana R. Leppert², Jean-François Cabana⁶, Ian Gagnon¹, Pascale Beliveau⁷, G. Bruce Pike^{2, 5}, Julien Cohen-Adad^{1, 3}, and Nikola Stikov^{1, 4}

¹ NeuroPoly Lab, Institute of Biomedical Engineering, Polytechnique Montreal, Montreal, Canada ² McConnell Brain Imaging Center, Montreal Neurological Institute, McGill University, Montreal, Canada ³ Functional Neuroimaging Unit, CRIUGM, University of Montreal, Montreal, Canada ⁴ Montreal Heart Institute, University of Montreal, Montreal, Canada ⁵ Departments of Radiology and Clinical Neuroscience, Hotchkiss Brain Institute, University of Calgary, Calgary, Canada ⁶ Chaudière-Appalaches Integrated Health and Social Services Center, Sainte-Marie, Canada ⁷ Department of radio-oncology, Research Center of the University of Montreal Hospital Center, Montreal, Canada

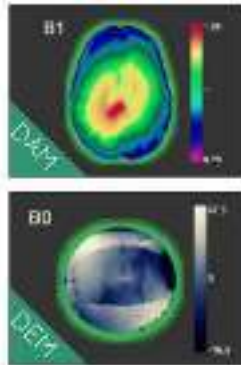
DOI: [10.21105/joss.02343](https://doi.org/10.21105/joss.02343)

Karakuzu et al., (2020), *qMRLab: Quantitative MRI analysis, under one umbrella*. Journal of Open Source Software, 5(53), 2343, <https://doi.org/10.21105/joss.02343>



<https://qmrlab.org>

qMR Lab



Quantitative MRI.
Under one umbrella.

Relaxometry

Diffusion Imaging

Quant. Susceptibility Mapping

Field Mapping

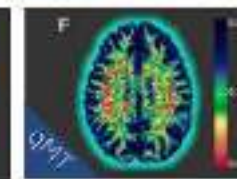
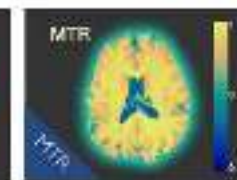
Quant. Magnetization Transfer



Fit.

Simulate.

Visualize.



From scanner

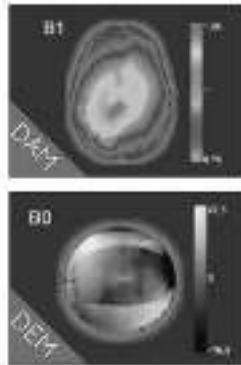
to publication





<https://qmrlab.org>

qMR Lab



Quantitative MRI.
Under one umbrella.

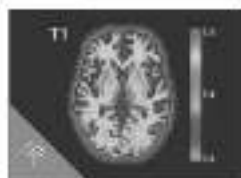
Relaxometry

Diffusion Imaging

Quant. Susceptibility Mapping

Field Mapping

Quant. Magnetization Transfer

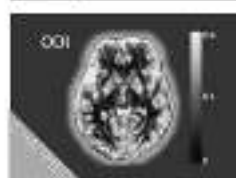
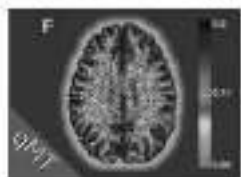


GUI



CLI

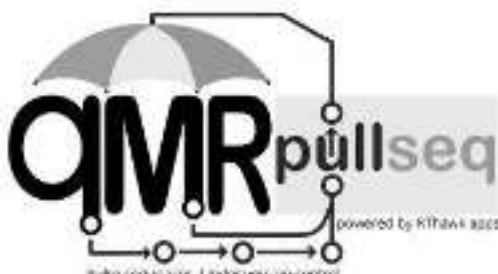
Fit. Simulate. Visualize.



From scanner



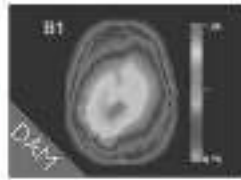
to publication





<https://qmrlab.org>

qMR Lab



Quantitative MRI.
Under one umbrella.

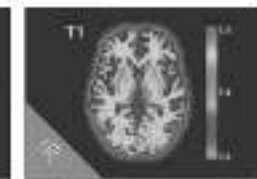
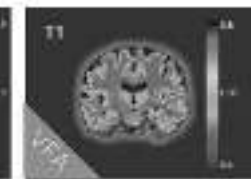
Relaxometry

Diffusion imaging

Quant. Susceptibility Mapping

Field Mapping

Quant. Magnetization Transfer



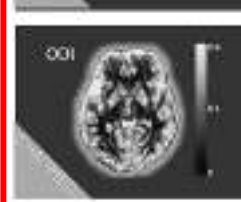
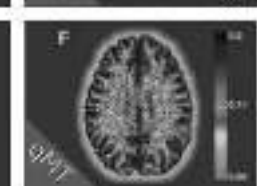
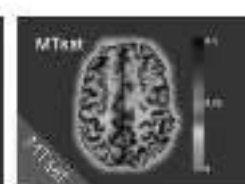
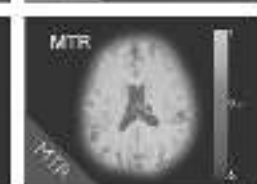
GUI

CLI

Fit.

Simulate.

Visualize.



From scanner

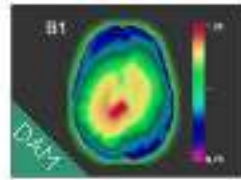
to publication





<https://qmrlab.org>

qMR Lab



Quantitative MRI.
Under one umbrella.

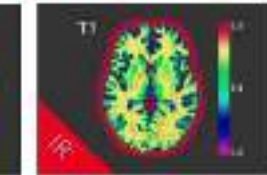
Relaxometry

Diffusion imaging

Quant. Susceptibility Mapping

Field Mapping

Quant. Magnetization Transfer



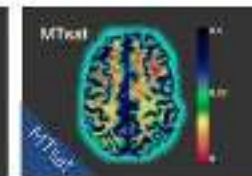
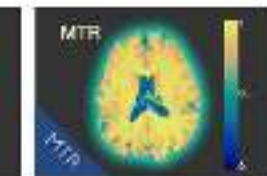
Fit.

Simulate.

Visualize.



From scanner



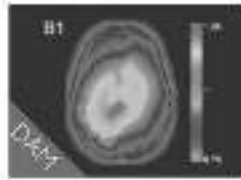
to publication





<https://qmrlab.org>

qMR Lab



Quantitative MRI.
Under one umbrella.

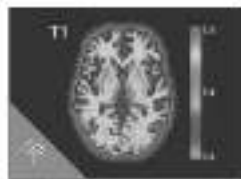
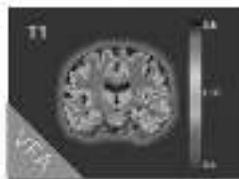
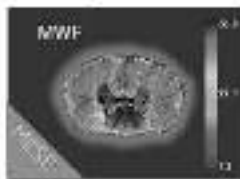
Relaxometry

Diffusion imaging

Quant. Susceptibility Mapping

Field Mapping

Quant. Magnetization Transfer



GUI

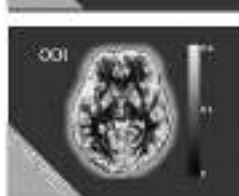
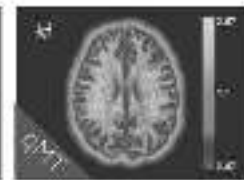
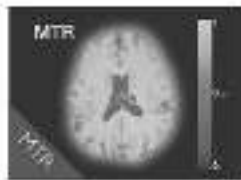


CLI

Fit.

Simulate.

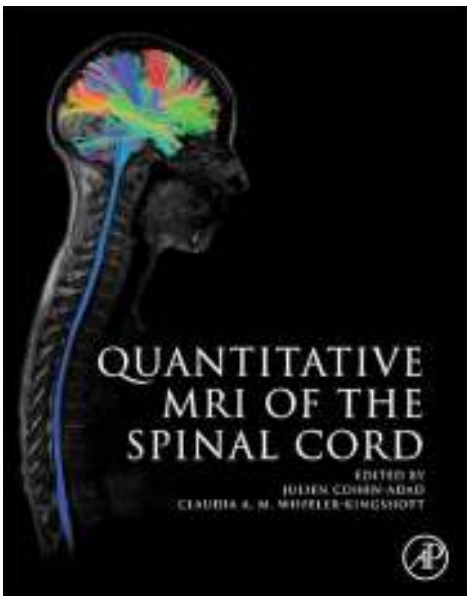
Visualize.



From scanner

to publication





Quantitative MRI mOOC

(mini-Open Online Course)



Quantitative MRI mOOC

Introduction To qMRI >

T1 Mapping >

T2 Mapping >

B1 Mapping >

B0 Mapping >

Magnetization Transfer
Imaging >

MOOC qMRLab



IN THIS ARTICLE ▾

About

What is a mOOC?

Why a book on qMRI?

What sets apart this book?

Can you contribute?

qMRI mOOC

October 7, 2024



Contributions

Authors: Mathieu Boudreau, Alexandre D'Astous, Agah Karakuzu, Katy Keenan, Nikola Stikov, Samuelle St-Onge, Juan Velázquez-Reyes

Editors: Mathieu Boudreau, Julien Cohen-Adad, Benjamin De Leener, Eva-Alonso Ortiz, Nikola Stikov



Quantitative MRI mOOC

Introduction To qMRI

T1 Mapping

Inversion Recovery

Introduction

Signal Modelling

Data Fitting

Benefits and Pitfalls

Other Saturation-Recovery

T1 Mapping techniques

Notebooks

Variable Flip Angle

MP2RAGE

Exercises

T2 Mapping

B1 Mapping

mOOC qMRIlab



Signal Modelling

Inversion Recovery

Mathieu Boudreau

NeuroPoly Lab, Polytechnique Montreal, Quebec, Canada

October 7, 2024

The steady-state longitudinal magnetization of an *inversion recovery* experiment can be derived from the *Bloch equations* for the pulse sequence $\{\theta_{180} - \text{TI} - \theta_{180} - (\text{TR} - \text{TI})\}$, and is given by:

$$M_z(TI) = M_0 \frac{1 - \cos(\theta_{180})e^{-\frac{\text{TI}}{T_1}} - [1 - \cos(\theta_{180})]e^{-\frac{\text{TR}}{T_1}}}{1 - \cos(\theta_{180})\cos(\theta_{90})e^{-\frac{\text{TR}}{T_1}}} \quad (2.1)$$

where M_z is the longitudinal magnetization prior to the θ_{90} pulse. If the in-phase *real* signal is desired, it can be calculated by multiplying Eq. 2.1 by $k \sin(\theta_{90}) e^{-\text{TE}/T_2}$, where k is a constant. This general equation can be simplified by grouping together the constants for each measurements regardless of their values (i.e. at each TI, same TE and θ_{90} are used) and assuming an ideal inversion pulse;

$$M_z(TI) = C(1 - 2e^{-\frac{\text{TI}}{T_1}} + e^{-\frac{\text{TR}}{T_1}}) \quad (2.2)$$

where the first three terms and the denominator of Eq. 2.1 have been grouped together into the constant C . If the experiment is designed such that TR is long enough to allow for full relaxation of the magnetization ($\text{TR} > 5 \cdot T_{11}$), we can do an additional approximation by dropping the last term in Eq. 2.2:


qMRI mOOC

Quantitative MRI mOOC

- Introduction To qMRI
- Basics of MRI and qMRI
- Why MRI Isn't Quantitative (Yet)
- Origins of MRI - A Visual History
- From spin dynamics to images
- Two MRI sequences and two qMRI measurements
- Will qMRI take over the world?

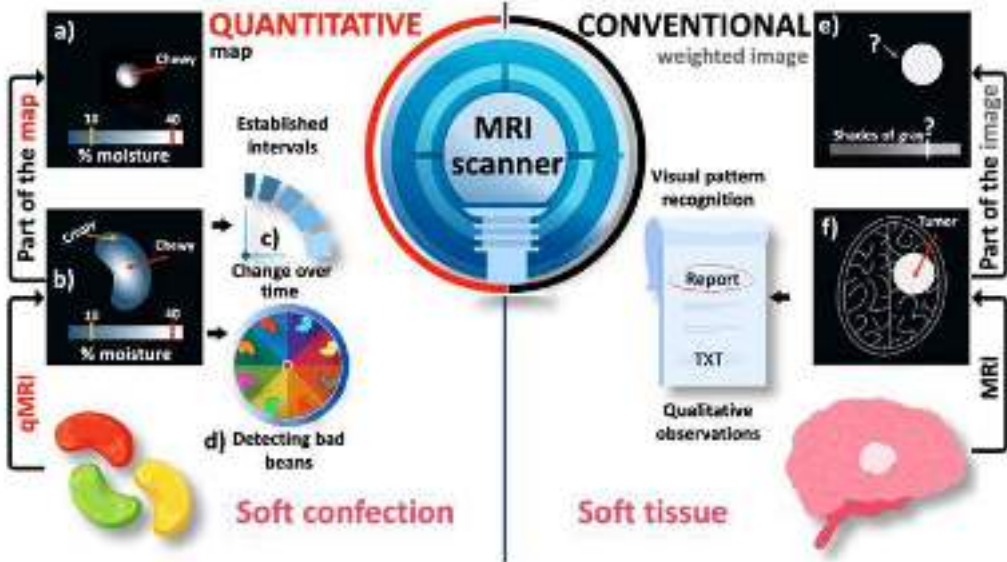


Figure 1: An illustrative comparison between the conventional and quantitative MRI (qMRI). The pixel brightness of conventional MR images is defined in an arbitrary grayscale [e,f]. As a result, only a qualitative pattern recognition is possible when the suspected region (i.e., the tumor) is assessed against the background of the target anatomy (i.e., the brain). On the other hand, quantitative maps spatially resolve a meaningful metric (a,b) to detect changes over time (c) and between different samples (d). On a standardized measurement scale of percent moisture, the texture characteristics of a jellybean (e.g., crispy or chewy) can be objectively determined even from a randomly selected part of the image.

Using the same MRI scanner, it is possible to assign meaningful numbers to the images and this approach turns out to be the most common MRI method in food engineering (Mariette et al., 2012; Ziegler et al., 2003). Fig. 1 illustrates the added value of quantitative MRI (qMRI) when applied to a sample familiar to everyone: a jellybean. The moisturization map indicates that the jellybean has formed a crispy shell while remaining chewy at the center, which is the desired texture Fig. 1b. Given that the level of chewiness is determined by a threshold on a standardized measurement scale, a randomly selected part of the image can be still characterized by comparing selected pixel values against the established threshold Fig. 1. This feature of qMRI

IN THIS ARTICLE

- A sweet jellybean analogy
- A spicy history of NMR and MRI
- A bitter U.S. Supreme Court verdict

- T1 Mapping
- T2 Mapping
- B1 Mapping
- B0 Mapping
- Magnetization Transfer Imaging

<http://qmrlab.org/mooc/>

Quantitative MRI mOOC

Introduction To qMRI >

T1 Mapping >

T2 Mapping >

B1 Mapping >

B0 Mapping ✓

B0 Inhomogeneities >

Dual Echo B0 Mapping ✓

Introduction

Signal Theory

Single Frequency
PopulationMulti-Frequency
Population

Benefits and Pitfalls

Notebooks >

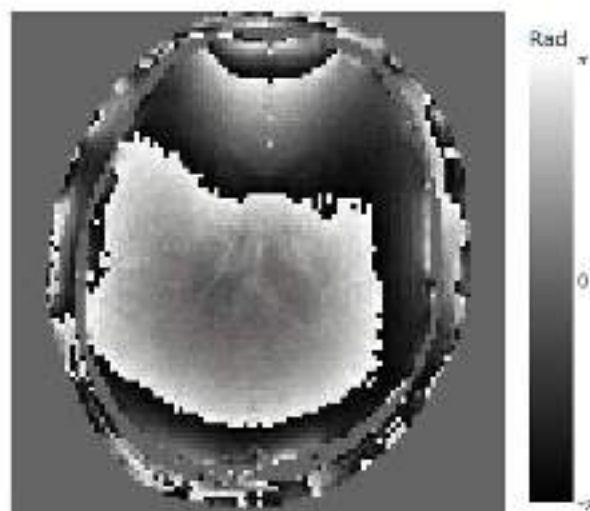
Phase Unwrapping >

Advanced B0 Mapping ✓

the phase is defined over $-\pi$ to π . Phase-wrapping effects will be discussed in more detail in the following section. Wraps can also occur spatially as sharp variations as seen in the following figure. Note that the longer the echo times, the more wraps there are.

Source: Jupyter Notebook

Phase at different echo times



Echo Time (s): 0.02



Figure 5.7: Phase shown at different echo times. The slider can be used to show the phase that would be acquired at different echo times.

Quantitative MRI mOOC

Introduction To qMRI >

T1 Mapping >

T2 Mapping >

B1 Mapping ✓

Double Angle Methods >

Actual Flip Angle
Imaging >

Filtering ✓

Introduction

Filters and smoothing

1D examples

B1 map examples

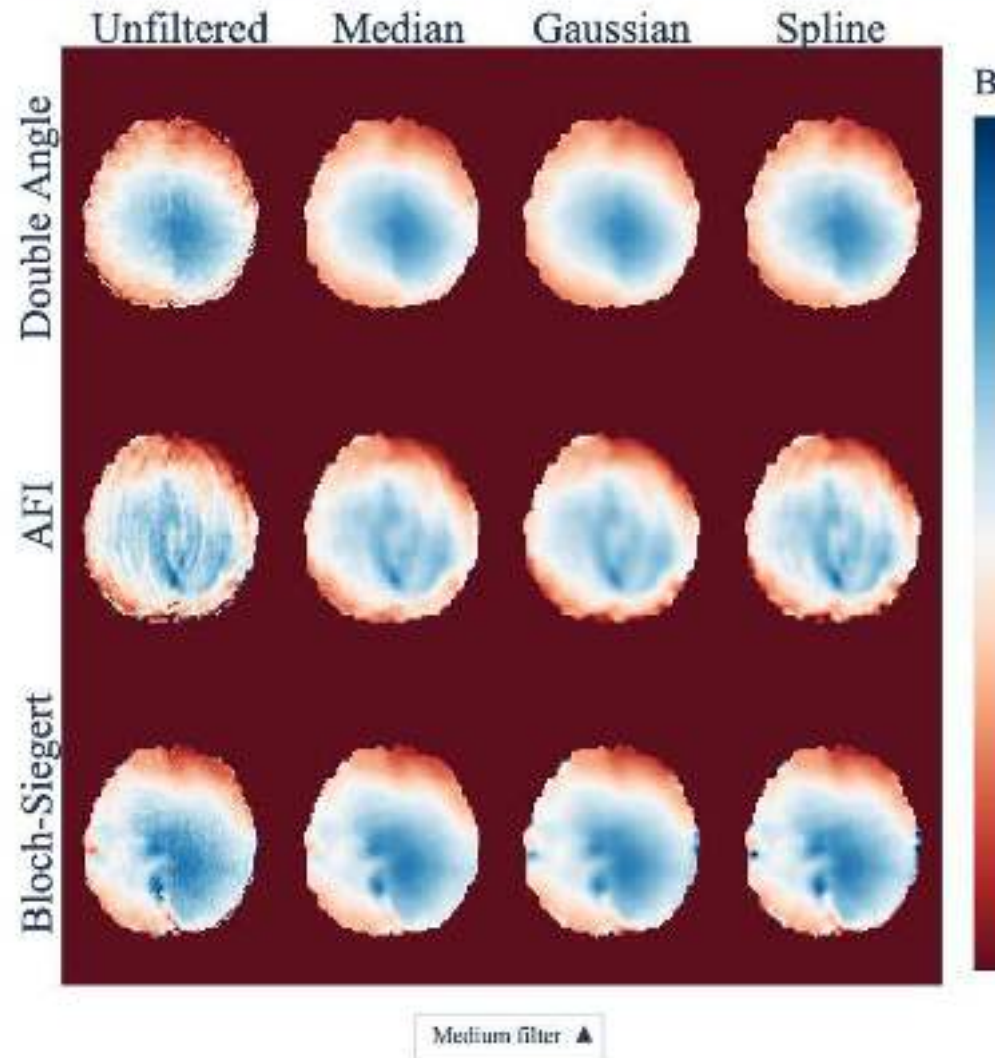
Recommendations,
benefits, and pitfalls

Notebooks >

B0 Mapping >

Magnetization Transfer >

Source: Jupyter Notebook



Quantitative MRI mOOC

Introduction To qMRI >

T1 Mapping >

Inversion Recovery >

Variable Flip Angle >

Introduction

Signal Modelling

Data Fitting

Benefits and Pitfalls

Notebooks >

MP2RAGE >

Exercises

T2 Mapping >

B1 Mapping >

B0 Mapping >

Magnetization Transfer Imaging >

$$M_z(\theta_n) = M_0 \frac{1 - e^{-\frac{TR}{T_1}}}{1 - \cos(\theta_n)e^{-\frac{TR}{T_1}}} \sin(\theta_n) \quad (2.5)$$

where M_z is the longitudinal magnetization, M_0 is the magnetization at thermal equilibrium, TR is the pulse sequence repetition time (Figure 2.7), and θ_n is the excitation flip angle. The M_z curves of different T_1 values for a range of θ_n and TR values are shown in Figure 2.8.

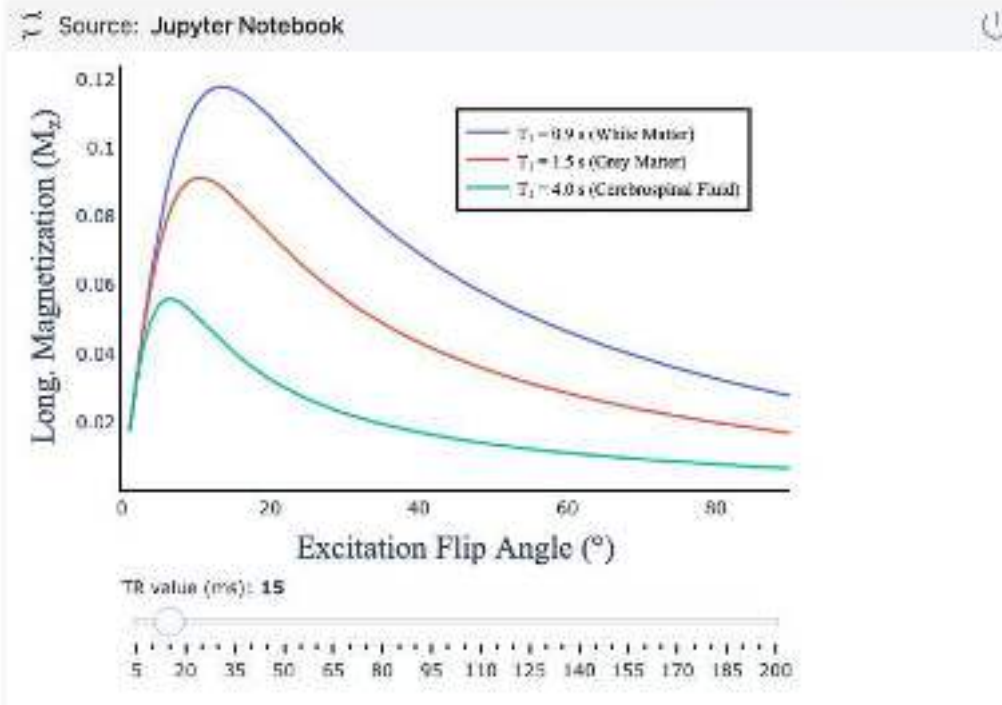


Figure 2.8: Variable flip angle technique signal curves (Eq. 2.5) for three different T_1 values, approximating the main types of tissue in the brain at 3T.


qMRI mOOC

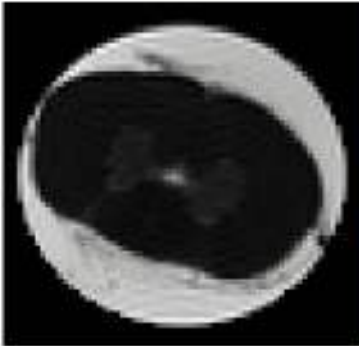
of the signals from both myelin water (MW) and intra/extracellular water (IEW), as follows :

$$S(TE)_{MWI} = S_{MW}e^{-TE/T_{2,MW}} + S_{IEW}e^{-TE/T_{2,IEW}} \quad (3.7)$$

Figure 3.5 presents an example of multi-exponential T_2 fitting applied to an image of the spinal cord. The figure shows the myelin water fraction (MWF) map, which highlights the distribution of myelin water across the spinal cord, as well as the T_2 maps for intra/extracellular water and myelin water. The multi-exponential fitting approach allows for the separation of these components, enhancing tissue characterization in complex structures compared to mono-exponential models. In the following section, we will explain why MWF imaging is a key application of multi-exponential T_2 mapping, and how it provides valuable insights into the microstructure of the spinal cord, highlighting its potential benefits for understanding and diagnosing neurological conditions.

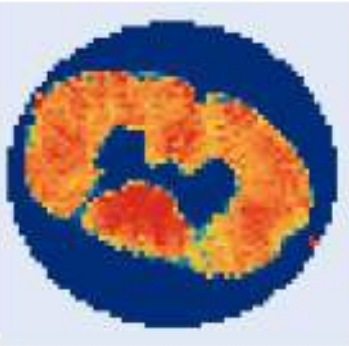
Source: Jupyter Notebook

MET2w



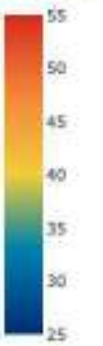
TE: 256 ms ▲

MWF map



MWF ▲

T_2 (ms)



Quantitative MRI mOOC

Introduction To qMRI >

T1 Mapping >

T2 Mapping >

B1 Mapping >

B0 Mapping >

Magnetization Transfer Imaging >

Quantitative Magnetization Transfer >

Introduction

Signal Modelling

Data Fitting

Summary

Notebooks >

Magnetization Transfer Ratio >

Magnetization Transfer Saturation >

Source: Jupyter Notebook

Figure 6.3: Z-spectrum simulated using different absorption lineshapes (Gaussian, Lorentzian, and super-Lorentzian).

Source: Jupyter Notebook

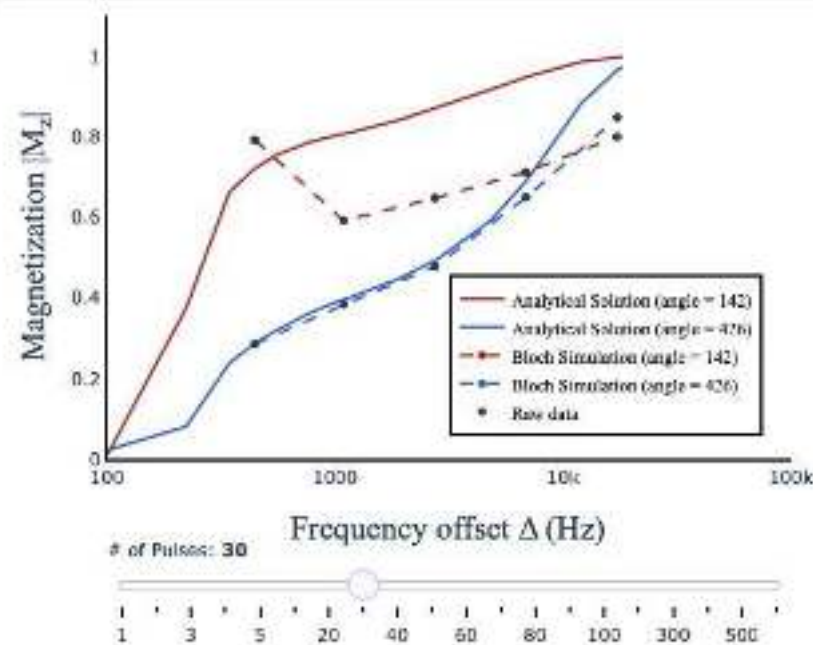


Figure 6.4: Z-spectrum simulated using Bloch simulations (dashed lines) for a number of MT pulses ranging from 1 to 600. Bloch simulations are compared with the Z-spectrum obtained from the analytical solution (solid lines).

References

Show All

1. Sled, J. G., & Pike, G. B. (2000). Quantitative interpretation of magnetization transfer in spoiled gradient echo MRI.



Quantitative MRI mOOC

Introduction To qMRI >

T1 Mapping v

Inversion Recovery v

Introduction

Signal Modelling

Data Fitting

Benefits and Pitfalls

Other Saturation-
Recovery T1 Mapping
techniques

Notebooks >

Variable Flip Angle >

MP2RAGE >

Made with MyST

Click here to view the qMRLab (MATLAB/Octave) code that generated Figure 2.2.

```
% Verbosity level 0 overrides the disp function and suppresses warnings.  
% Once executed, they cannot be restored in this session  
% (kernel needs to be restarted or a new notebook opened.)  
VERBOSITY_LEVEL = 0;  
  
if VERBOSITY_LEVEL==0  
    % This hack was used to suppress outputs from external tools  
    % in the Jupyter Book.  
    function disp(x)  
    end  
    warning('off','all')  
end  
  
try  
    cd qMRLab  
catch  
    try  
        cd ../../../../qMRLab  
    catch  
        cd ../qMRLab  
    end  
end  
  
startup  
clear all  
  
%% Setup parameters  
% All times are in seconds  
% All flip angles are in degrees  
  
params.TR = 5.0;  
params.TI = linspace(0.001, params.TR, 1000);
```



Quantitative MRI mOOC

Introduction To qMRI >

T1 Mapping ▾

Inversion Recovery >

Variable Flip Angle >

MP2RAGE >

Exercises

T2 Mapping >

B1 Mapping >

B0 Mapping >

Magnetization Transfer Imaging >



Exercises

T1 Mapping

Mathieu Boudreau

NeuroPoly Lab, Polytechnique Montreal, Quebec,
Canada

October 7, 2024

Exercise 1

- Using the Plotly figure in the [inversion recovery section](#) that displays the signal curves for white matter, gray matter, and CSF, determine the inversion times that null the signal from each of these tissues.
- In practice, you may not have this type of interactive figure at the scanner. Using the three values nulling inversion time values above, can you find an easy way to approximate the nulling time for any arbitrary T_1 value?
- Assuming that the images acquired at the MRI scanner displays magnitude-only images, at approximately which inversion time will the white matter and grey matter have the lowest contrast?
- Which inversion time would result in the best contrast between white matter and grey matter?

[Discuss on GitHub](#)



qMR

Lab

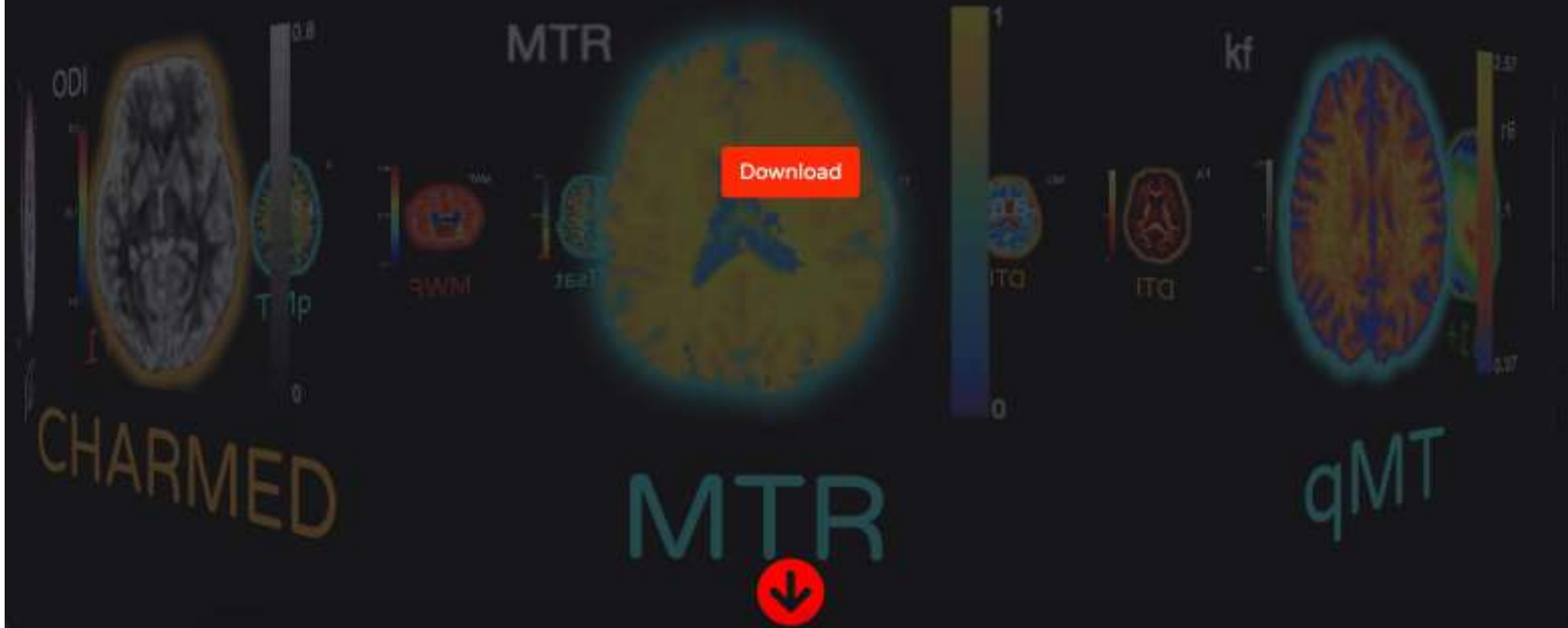
Quantitative MRI. Under one umbrella.

Download

the **qMRLab** software



Quantitative MRI. Under one umbrella.



qMRLab.org

q

 Search or jump to... Pull requests Issues Marketplace Explore

qMRLab / qMRLab Public Edit Pins Unwatch 22 Fork 51 Starred 100

<> Code Issues 54 Pull requests 5 Discussions Actions Projects Wiki Security Insights Settings

master 33 branches 18 tags Go to file Add file Code

 mathieuboudreau Update a few references. ✓ 05e1e62 11 hours ago 829 commits

.github	Env upgrade (#431)	15 months ago
Deploy	Documentation pipeline (#434)	15 months ago
External	Remove documentation from codebase (#428)	15 months ago
Test	Remove documentation from codebase (#428)	15 months ago
src	Fix uncommented line and upgrade Azure tester Ubuntu runners (...)	7 months ago
usr	Remove report bug feature (#432)	15 months ago
.gitattributes	Added fit residuals map	6 years ago
.gitignore	Remove documentation from codebase (#428)	15 months ago
.gitmodules	Add wrappers as submodule (#430)	15 months ago
CHANGELOG.md	V2.4.1 (#405)	2 years ago
CODE_OF_CONDUCT.md	Add code of conduct (#321)	3 years ago
CONTRIBUTING.md	Add code of conduct (#321)	3 years ago
LICENSE	Move	5 years ago

About

Quantitative MRI Made Easy with qMRLab: MRI software for data Simulation, analysis and visualization

[qmrlab.org](#)

analysis mapping mri data-simulation quantitative magnetic-resonance-imaging magnetization relaxometry qmri quantitative-mri

Readme MIT license Code of conduct 100 stars 22 watching 51 forks

Releases 12

<https://github.com/qMRLab/qMRLab>





Installing

the **qMRLab** software

Official Documentation

qMRLab


Quantitative Microscopy Research Lab

Search docs

QMR LAB

Key features

Methods available

Protocols

INSTALLATION

How to install

qMRLab in MATLAB

qMRLab in Octave

qMRLab in Docker

How to cite?

Known issues

GETTING STARTED

Beginner's example with GUI

Beginner's example with CLI

Example datasets

Docs » How to install

Edit on GitHub

How to install



qMRLab in MATLAB

- Minimum required version: R2014b
- Required MATLAB products:
 - Image Processing Toolbox
 - Optimization Toolbox
- Available interfaces:
 - Graphical User interface (GUI)
 - Command Line Interface (CLI)

If you have a MATLAB license, you can easily start using qMRLab:

1. Download the latest stable release [here](#).

qmrlab.readthedocs.io/en/master/install.html

Blog post: SOP for installation



Home · Blog · Users · Developers · Download

Share





0 Comments



Mathieu Boudreau [Follow](#) Author

SOP series: Introduction to qMRLab and installation



Introduction

This qMRLab standard operating procedure (SOP) series is intended to be a step-by-step guide on how to process quantitative MRI data using qMRLab. In this blog post, we'll guide you through installing qMRLab, and upcoming blog posts will provide SOPs for specific qMRLab modules.

qmrlab.org/jekyll/2024/04/17/qmrlab-sop.html

Overview

of the qMRLab **interface**

qMRLab
v2.4.2

Method:
qat_sp...
Open Options Panel

qMR Data Fit
Fit data
Save Results Load Results

qMR Simulator
Multi Voxel Distribution
Sensitivity Analysis
Single Voxel Curve

Fit qMR Data

Path data: Browse

Study ID: Download examples

MTdata

REQUIRED Magnetization Transfer data

View

R1map

REQUIRED Longitudinal relaxation rate (MTA RECOMMENDED)

View

B1 map

Normalized transmit excitation field map (B1+). B1+ is defined as a

View

B0map

B0 field map, used for offset correction (OPTIONAL) (-CHz if not

View

Mask

Binary mask to accelerate the fitting (OPTIONAL)

View

Cannot find required input called MTdata

Fit Results

Source: View

View: A...

3D viewer

Sanity Check
Voxel fit
ROI fit
Statistics
Histogram

Cursor
Select

S
L R
I

(x,y) vol

Vol: 1/1 Time: 1/1 Slice: 1/1

Current file: Web qat_spgr documentation

OptionsGUI

qat spgr options

Protocol

MTData

	Angle	Offset
1	142	443
2	428	443
3	142	1008
4	428	1008
5	142	2732
6	428	2732
7	142	8262
8	428	8262
9	142	17235
10	428	17235

Add

Remove

Move up

Move down

Load

Create

TimingTable

Tmt (s)	0.0102
Ts (s)	0.0030
Tp (s)	0.0015
Tr (s)	0.0100
TR (s)	0.0250

Fit Protocol

Fitting

Var	Fix	Start	Lower	Upper
T		0.0001	0.0000	0.2000
Q		30.1	0.0000	1.00
R1	☒	0.0000	0.0000	1
R1	☒	1	0.0000	1
T2		0.0200	0.0000	0.2000
T2*		1.0000e-05	0.0000e-05	0.0000e-05

Options

MT_Pulse

Shape: gaussian

Sinc TRFA: 4

Bandwidth: 200

Fermi transition (s): 0.000301000

of MT pulses: 100

Model: SvdPkaPP

Uneshape: SuperLorentzian

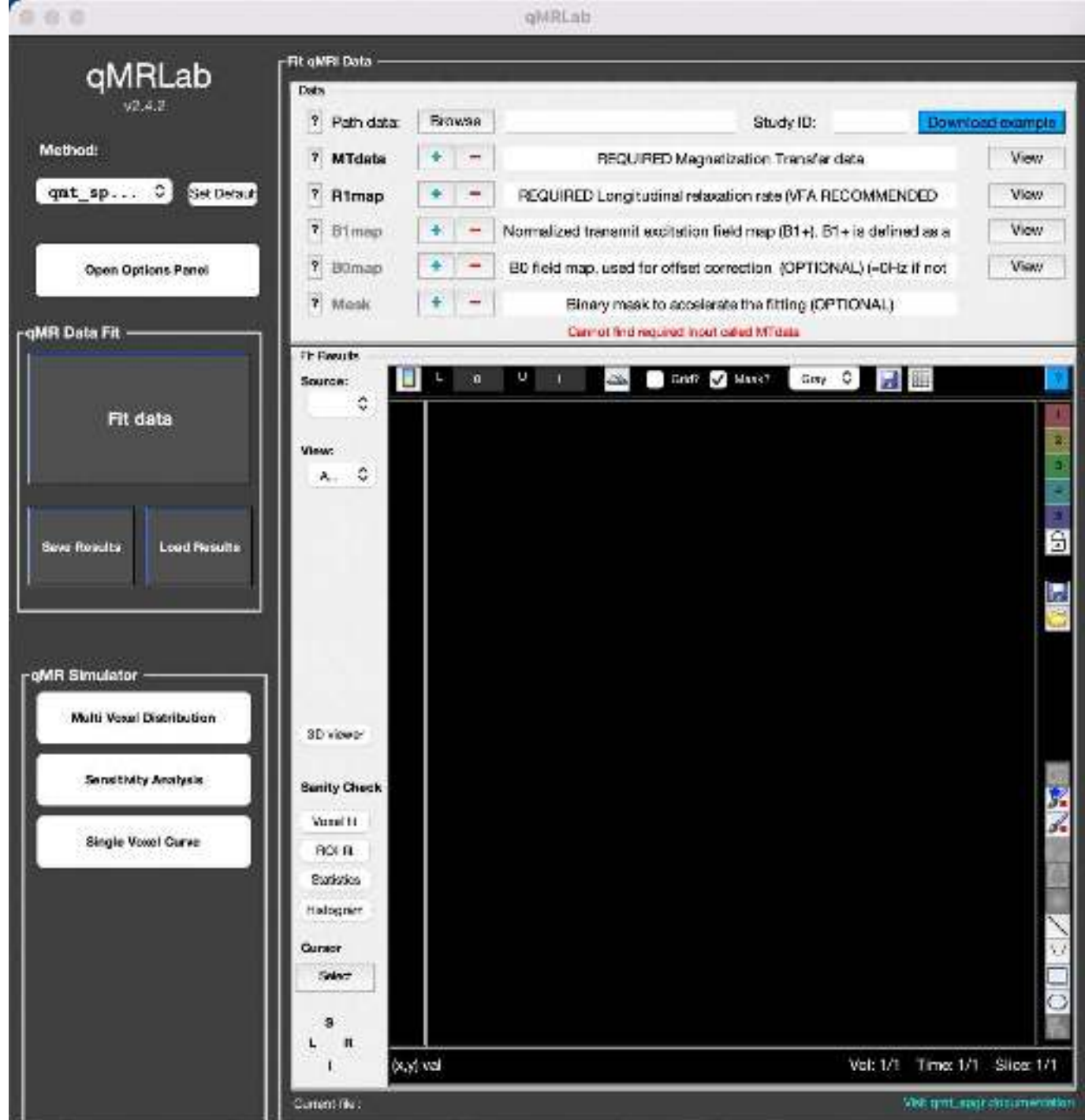
Fitting constraints
☒ Use R1map to constrain R11
☐ R1 R1r = R1f
☐ R1 R1PT2f
R1PT2f = 0.265

Read pulse alpha: 7

Compute Offsets

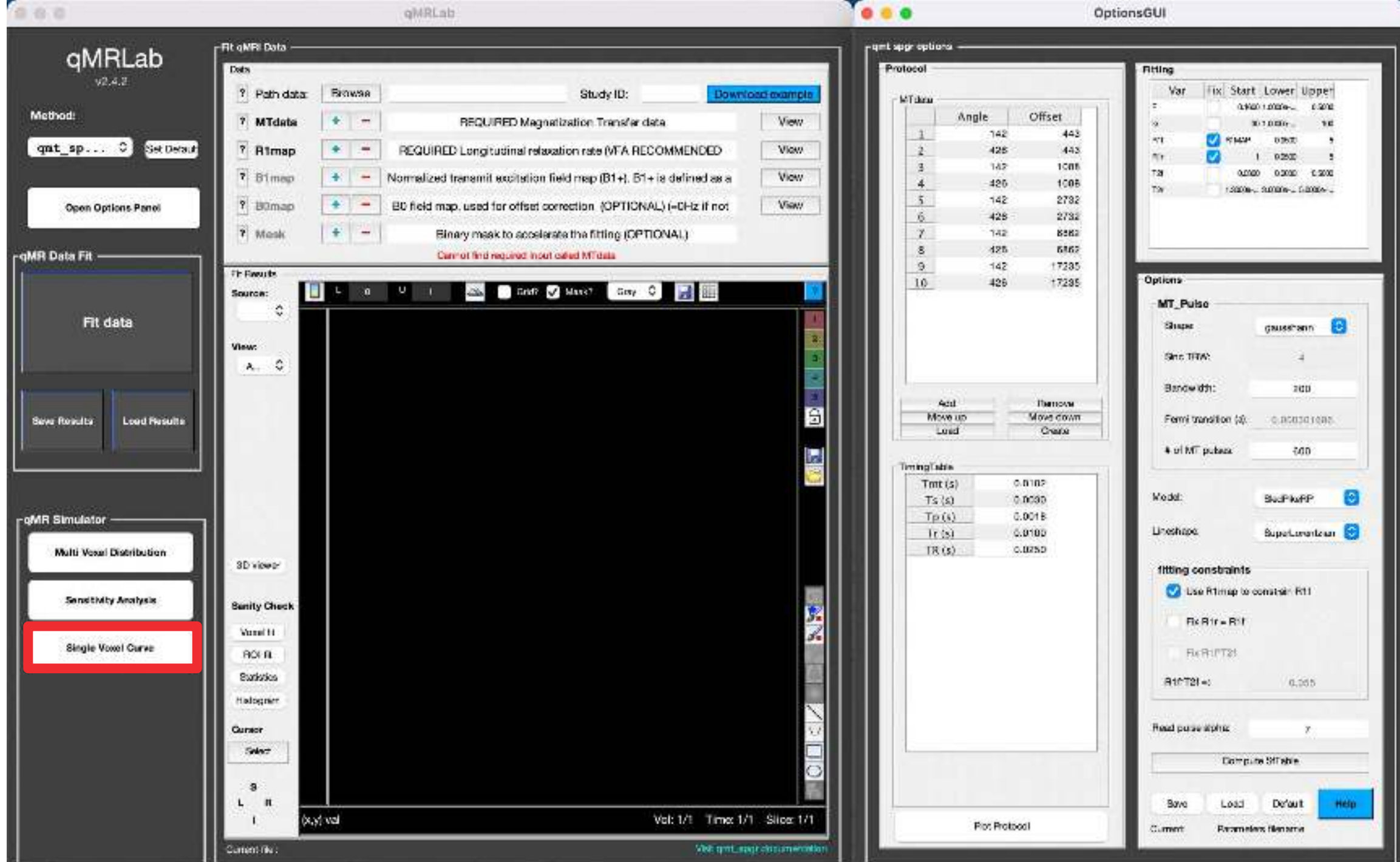
Save Load Default Help

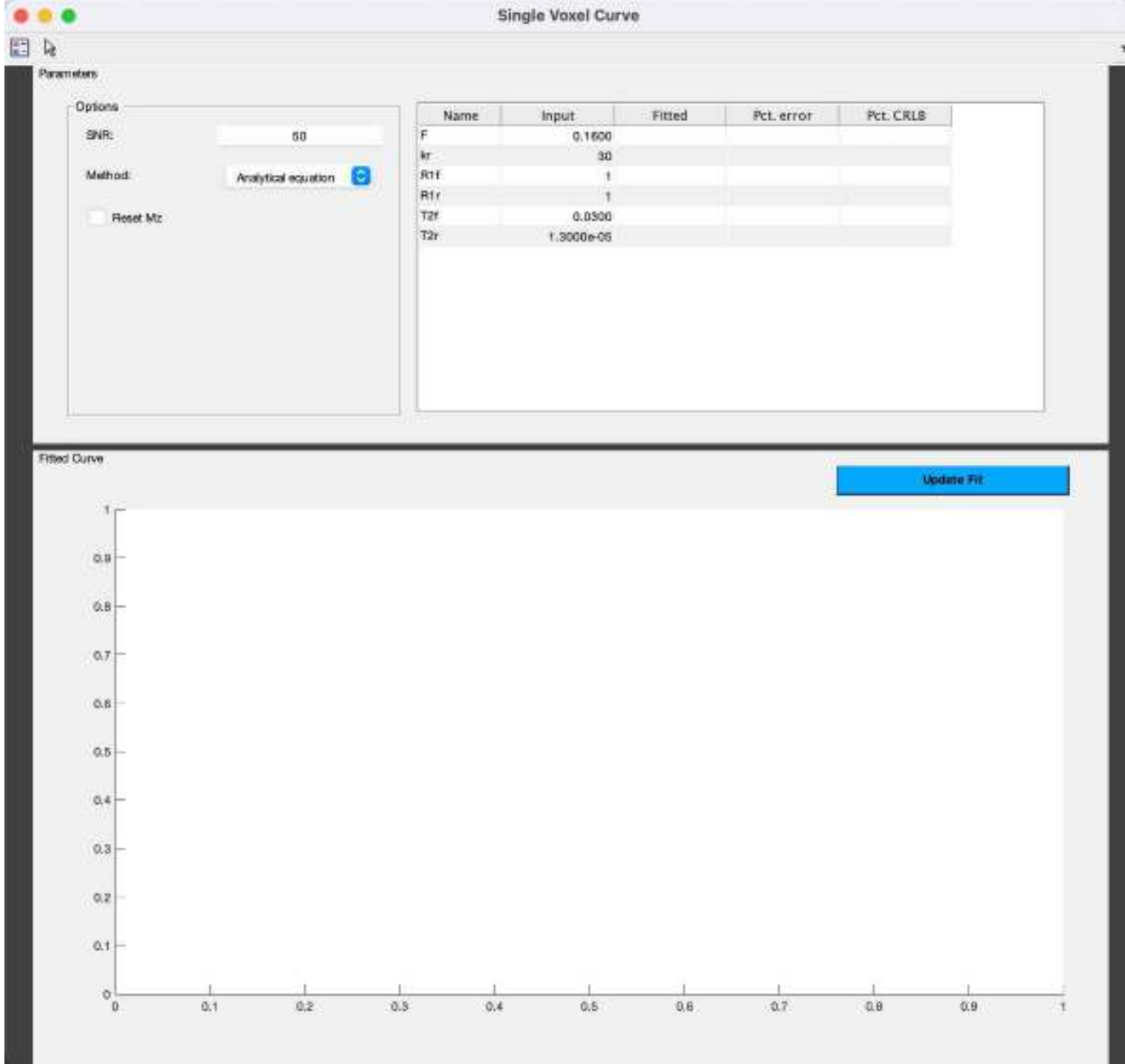
Current Parameters Minima



How to...

simulate and **fit**
a single “voxel” of data





Single Voxel Curve

Parameters

Options

SNR:

1000

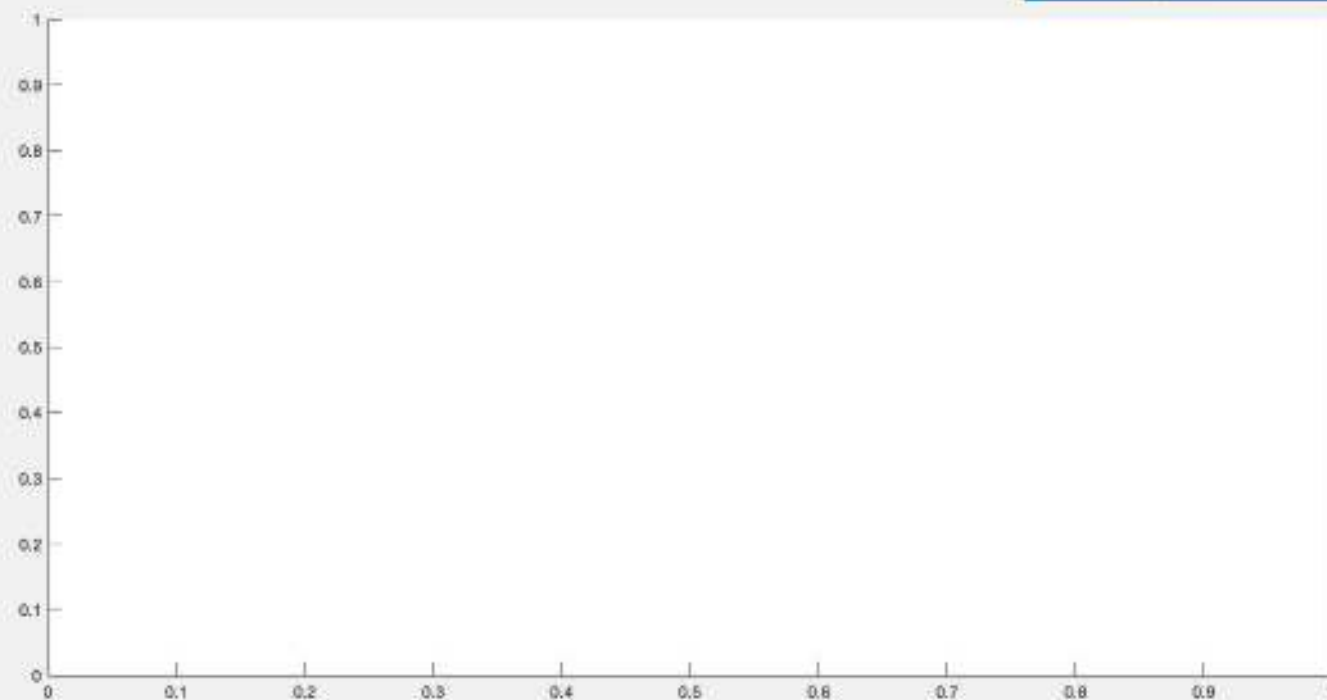
Method:

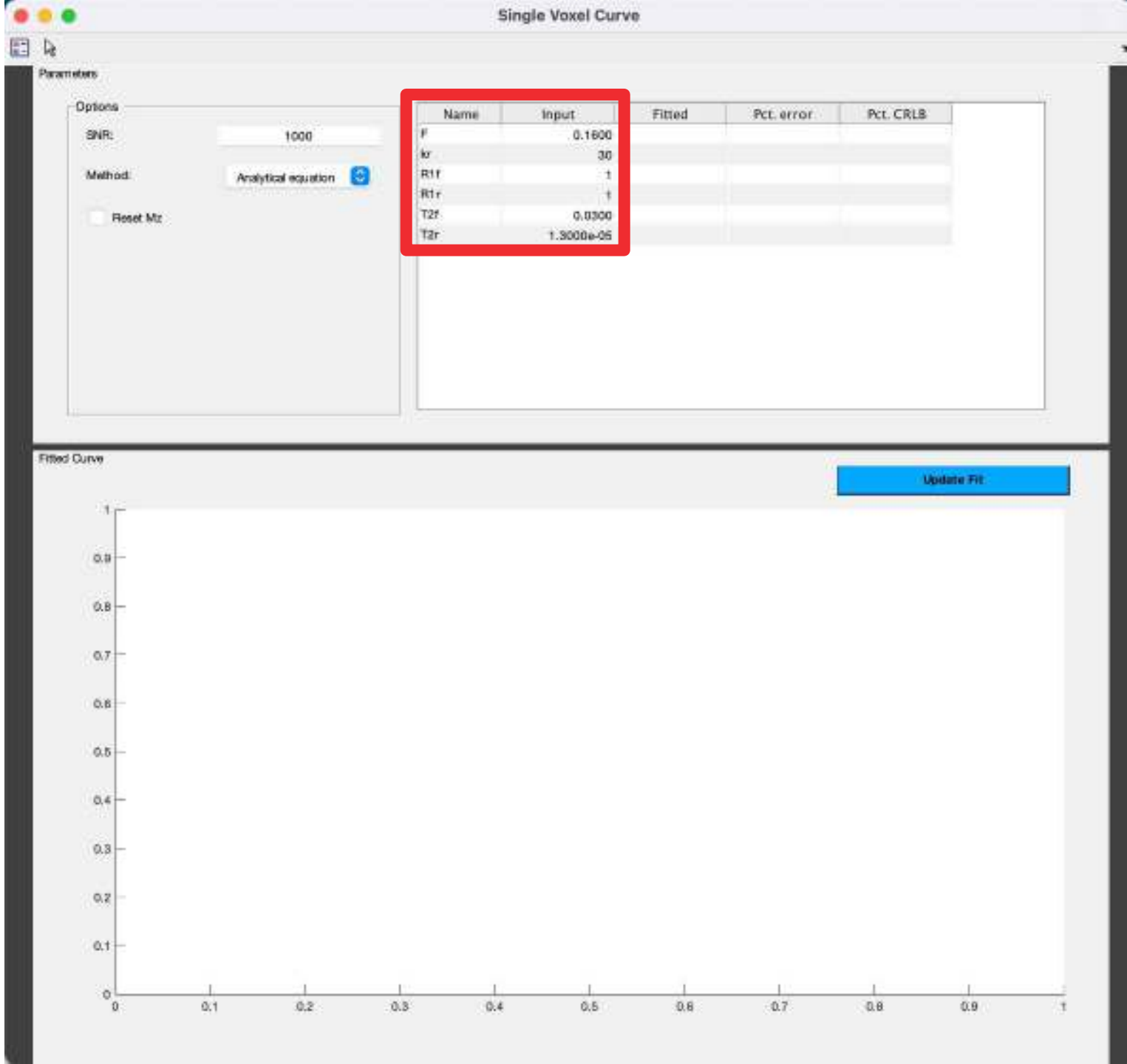
Analytical equation

☐ Reset Mz

Name	Input	Fitted	Pct. error	Pct. CRLB
F	0.1600			
kr	30			
R1f	†			
R1r	†			
T2f	0.0300			
T2r	1.3000e-05			

Fitted Curve

[Update Fit](#)



OptionsGUI

qmt app options

Protocol

MTData

	Angle	Offset
1	142	443
2	425	443
3	142	1085
4	425	1085
5	142	2732
6	425	2732
7	142	6362
8	425	6362
9	142	17235
10	425	17235

AddRemove
Move upMove down
LoadCreate

TimingTable

Tmt (s)	0.0102
Ts (s)	0.0030
Tp (s)	0.0015
Tr (s)	0.0100
TR (s)	0.0250

Plot Protocol

Fitting

Var	Fix	Start	Lower	Upper
c	☐	0.960	1.000e-10	1.000
q	☐	30.1	0.000	100
R1	☒	0.0424	0.000	5
R1	☒	1	0.000	5
T2	☐	0.000	0.000	1.000
T2	☐	1.000e-10	0.000e+00	0.000e+00

Options

MT_Pulse

Shape

gaussian

Gnc TTA:
-4

Bandwidth:

200

Fermi transition (Å):

0.000000000

of MT pulses:

500

Model:

BndPkuAP

Lineshape:

SuperLorentzian

fitting constraints

☒ Use R1map to constrain R11
☐ Rx R1r = R1l
☐ Rx R1PT2l

R1PT2l =:

0.005

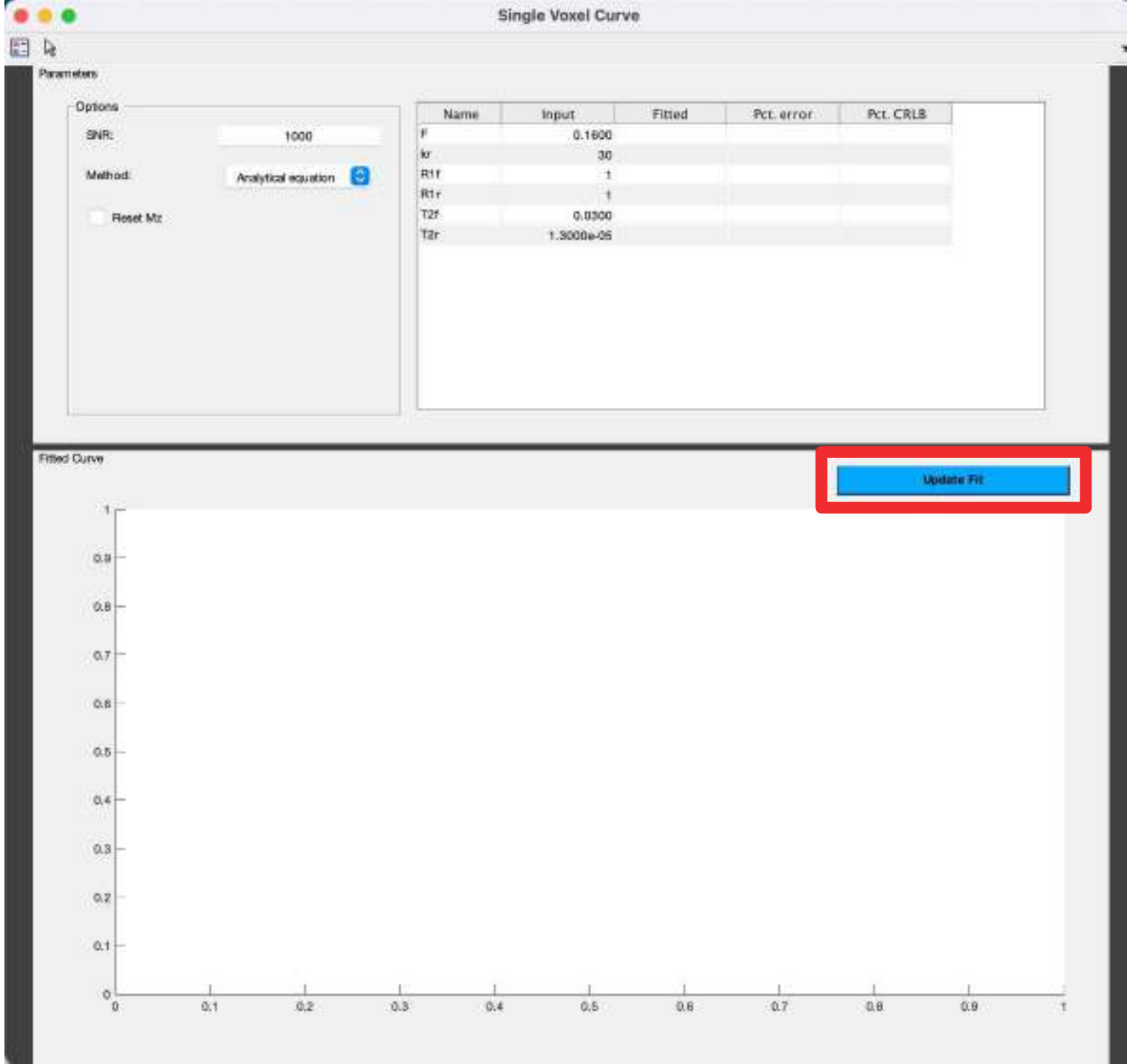
Read pulse alpha:

7

Compute BFF table

SaveLoadDefaultHelp

CurrentParameters filename



Single Voxel Curve

Parameters

Options

SNR:

1000

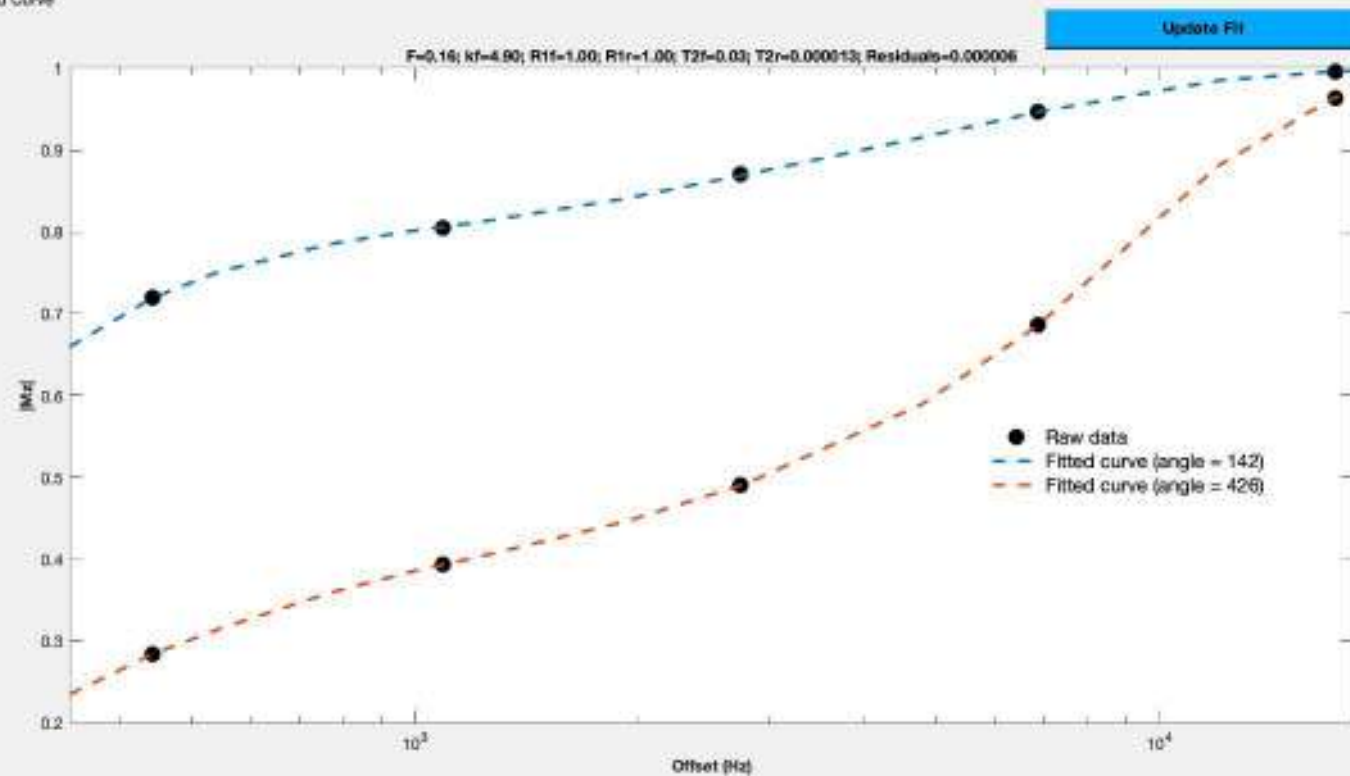
Method:

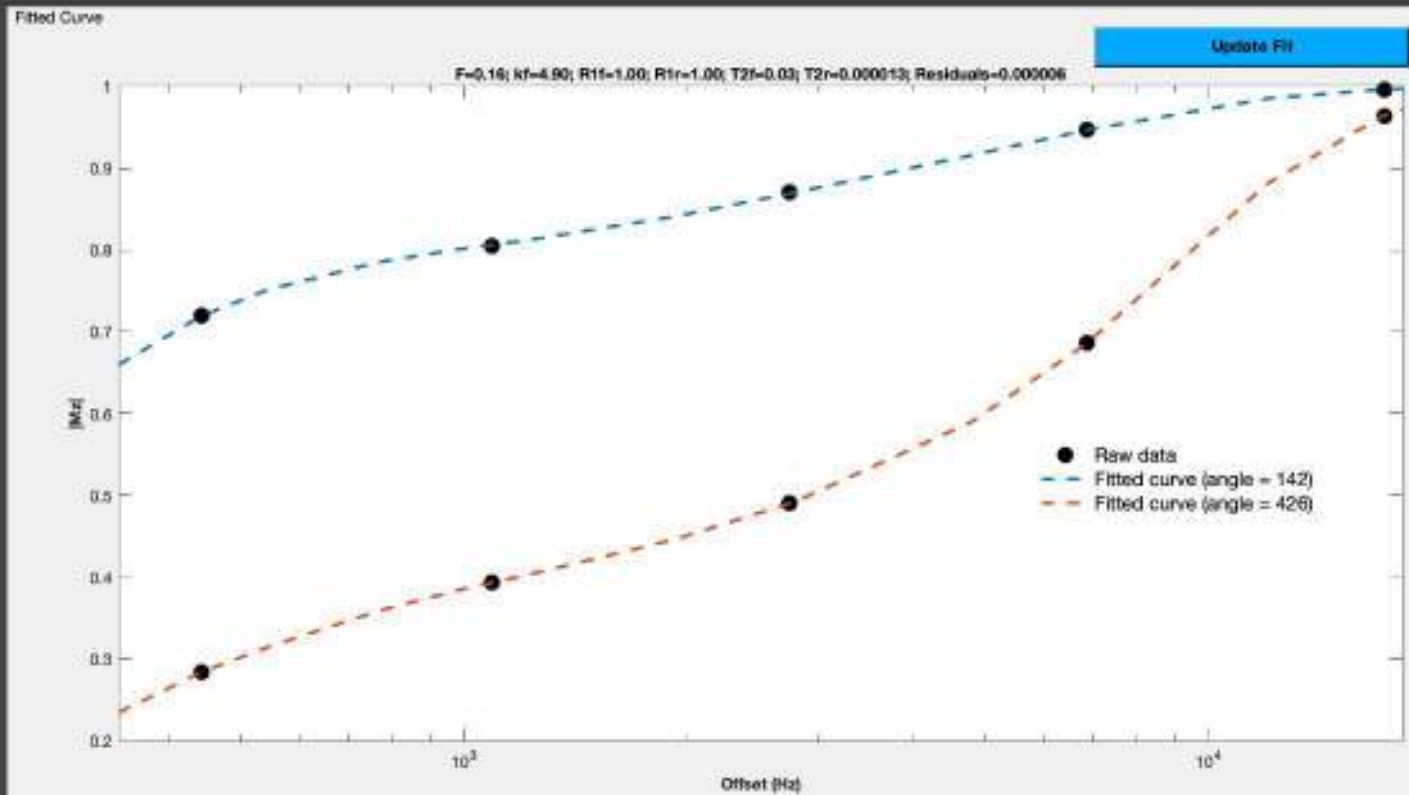
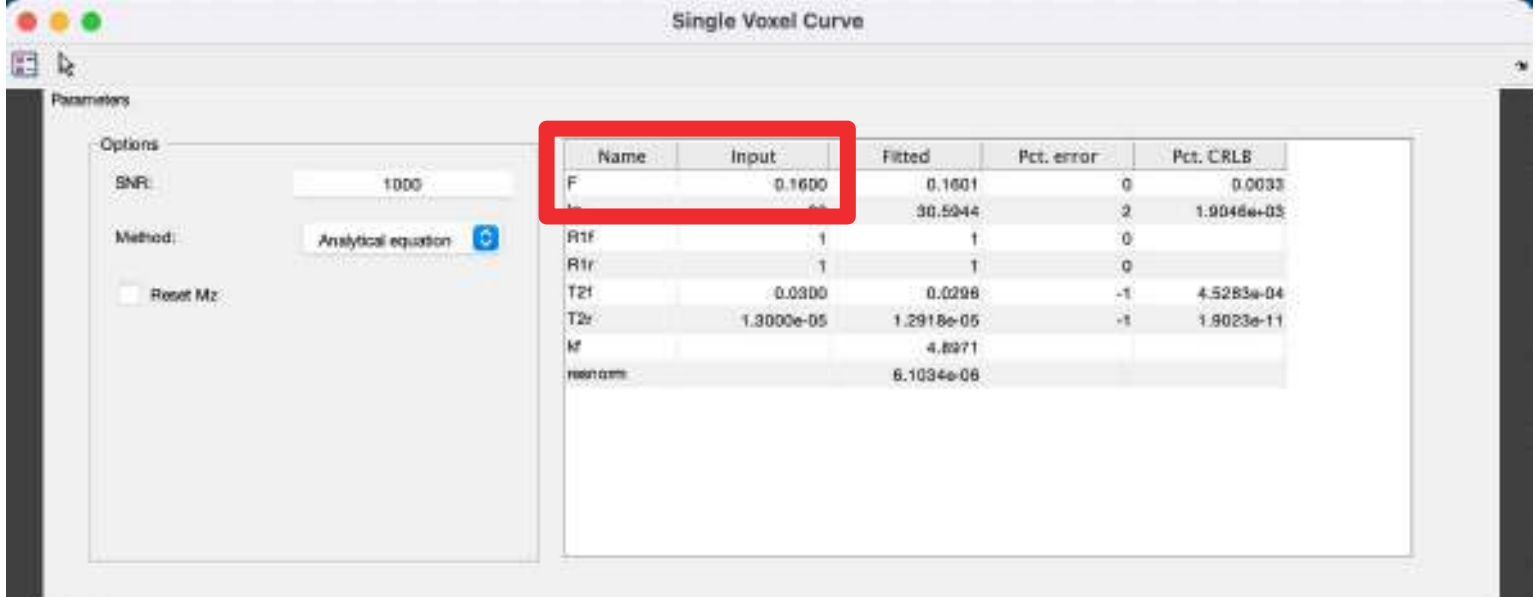
Analytical equation

☐ Reset Mz

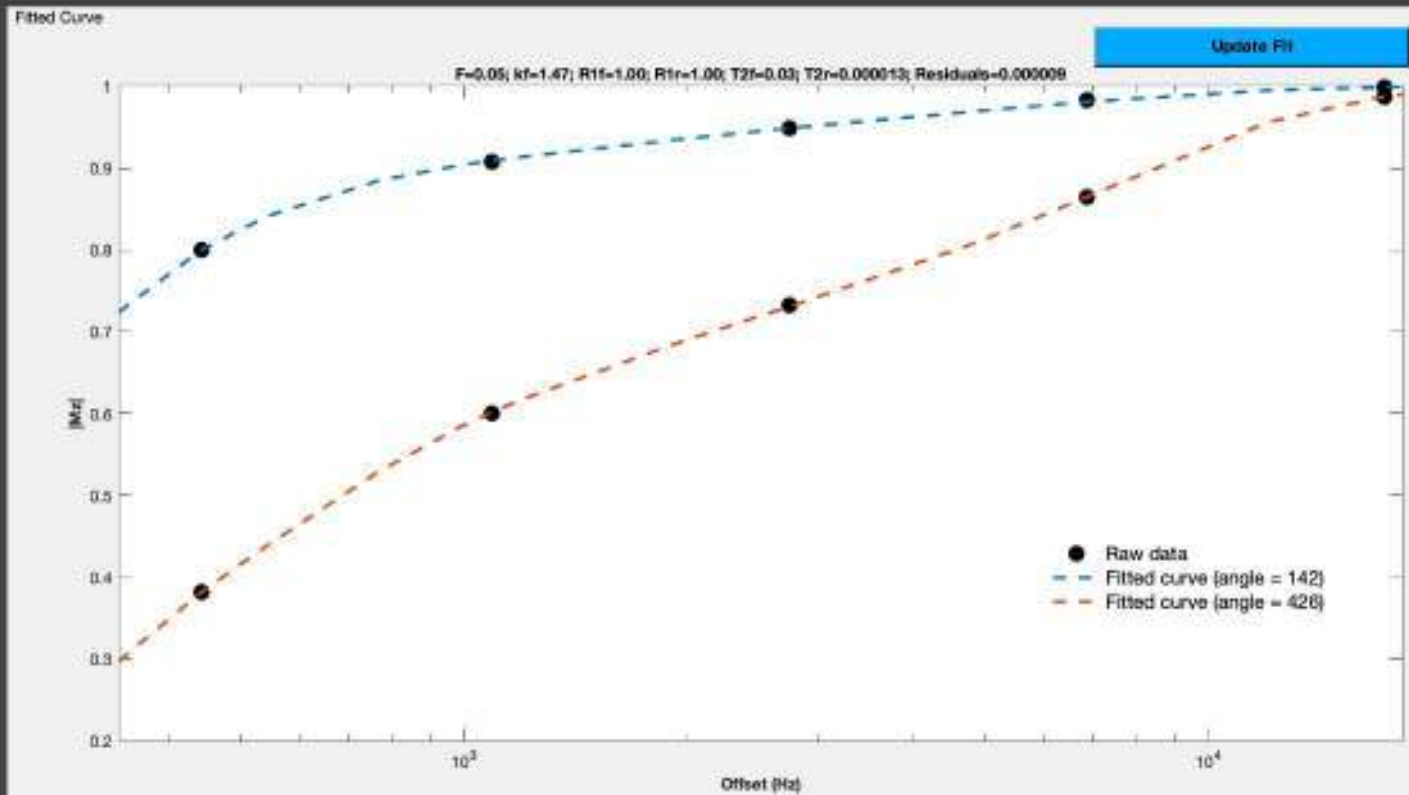
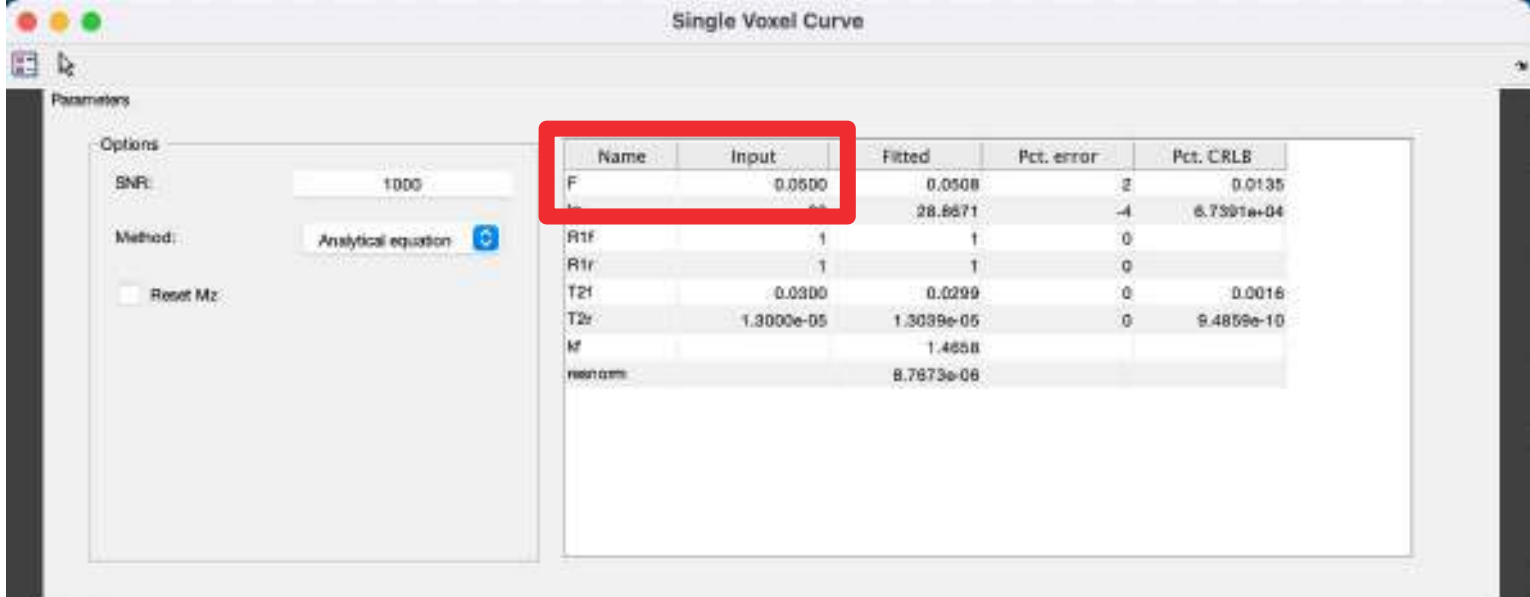
Name	Input	Fitted	Pct. error	Pct. CRLB
F	0.1600	0.1601	0	0.0033
k _r	30	30.5944	2	1.9046e+03
R1f	1	1	0	
R1r	1	1	0	
T2f	0.0300	0.0298	-1	4.5283e-04
T2r	1.3000e-05	1.2918e-05	-1	1.9023e-11
k _f		4.8971		
mean sqm		6.1034e-06		

Fitted Curve

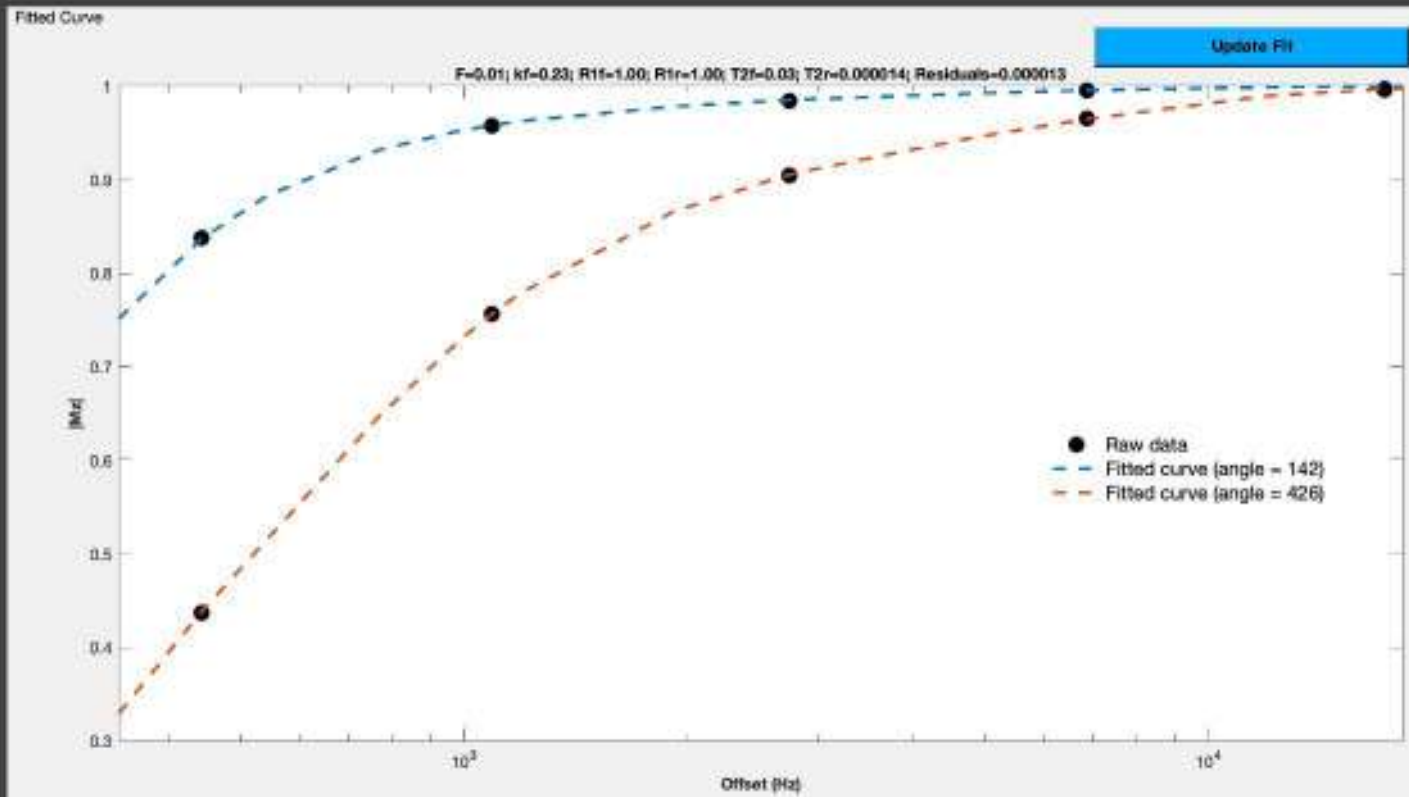
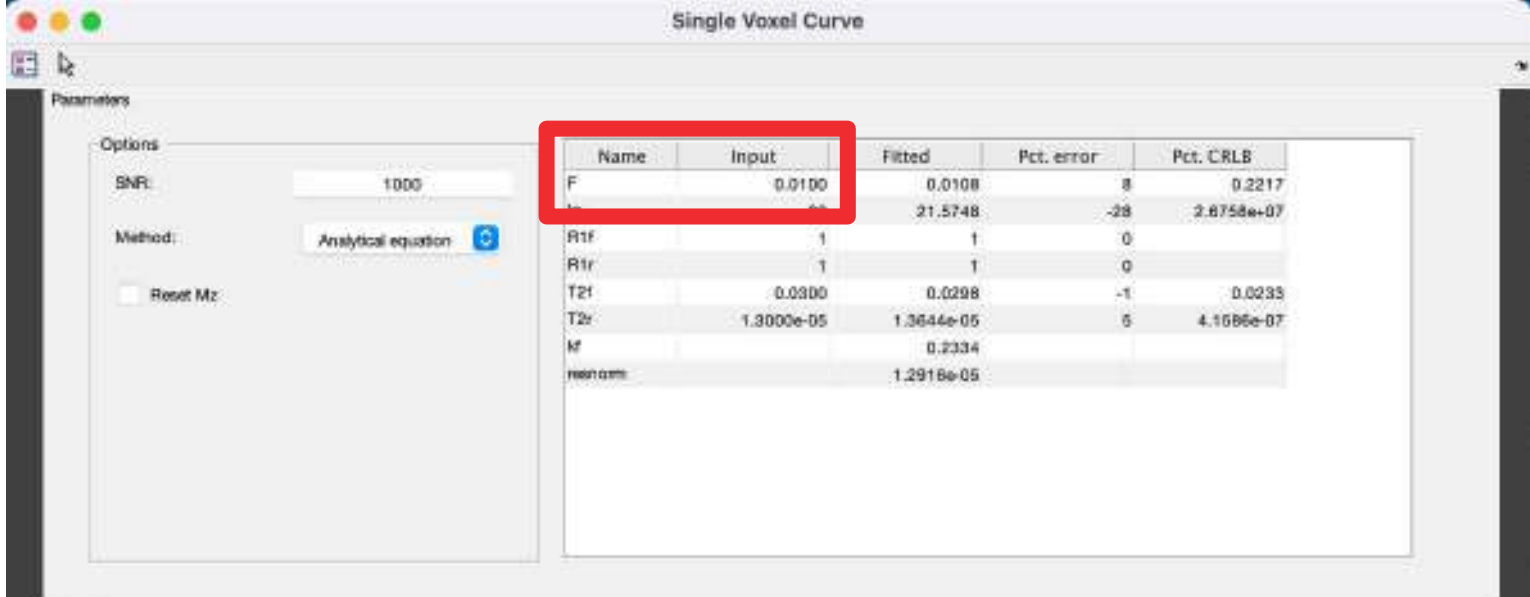




F = 0.16



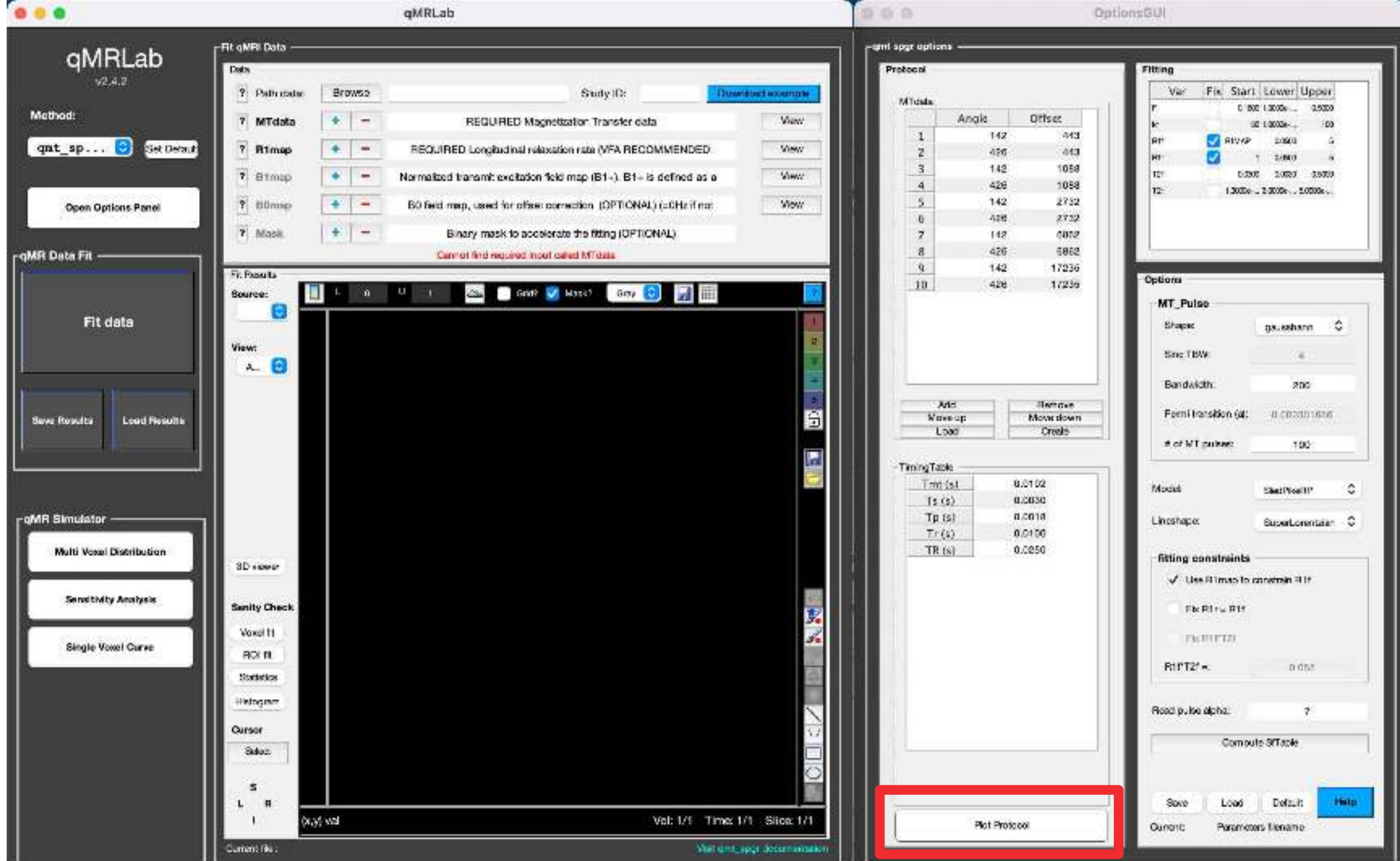
F = 0.05

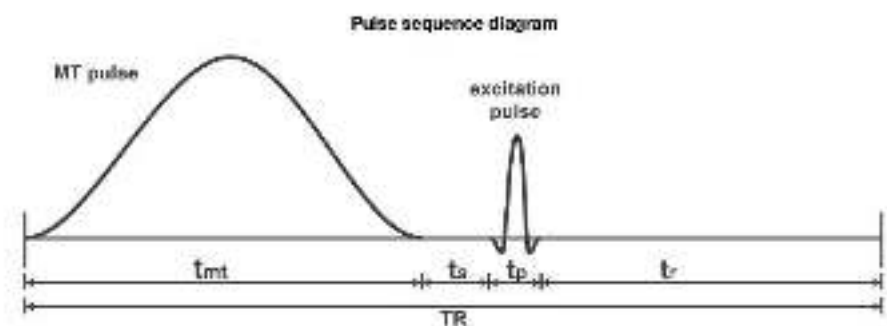
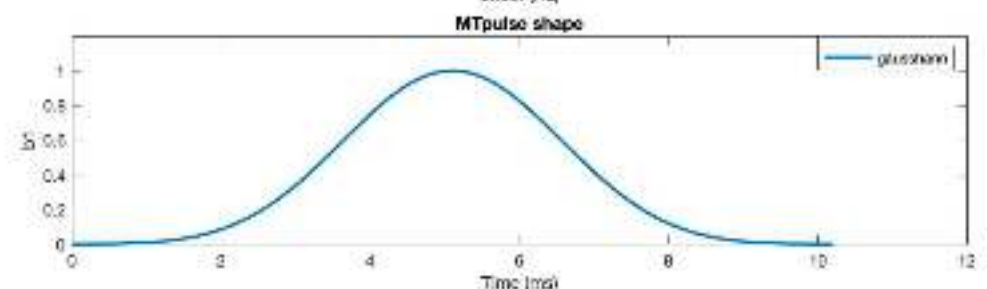
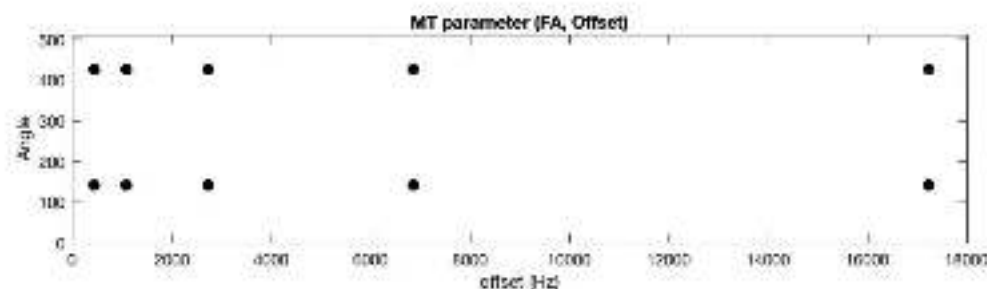


F = 0.01

Other options:

view and **edit** protocol





OptionsGUI

—gmt exp options—

Protocol

MTdata

	Angle	Offset
1	142	445
2	425	445
3	142	1085
4	425	1085
5	142	2732
6	425	2732
7	142	6362
8	425	6362
9	142	17335
10	425	17335

Add Remove
Move up Move down
Load Create

Fitting

Var	Fix	Start	Lower	Upper
F		0.0001 0.0001	0.000	0.000
W		20 1.0000	15	
MT	☒	0.0001	0.000	5
TR	☒	1	0.000	5
TR		0.0001 0.000	0.000	0.000
FA		1.0000 0.0000	0.0000	

Options

MT_Pulse

Shape: gaussian

Sine TSW: 1

Bandwidth: 200

Fermi transition (s): 0.0001 0.000

of MT pulses: 100

Model: RedWood

Lineshape: SuperGaussian

fitting constraints

☒ Use R1 map to constrain R1

☐ Fix R1r = R1f

☐ Fix R1^T2f

R1^T2f = 0.015

Read pulse shape: T

Compute STable

Save Load Default Help

Current Parameters/Results

Plot Protocol

Single Voxel Curve

Parameters

Options

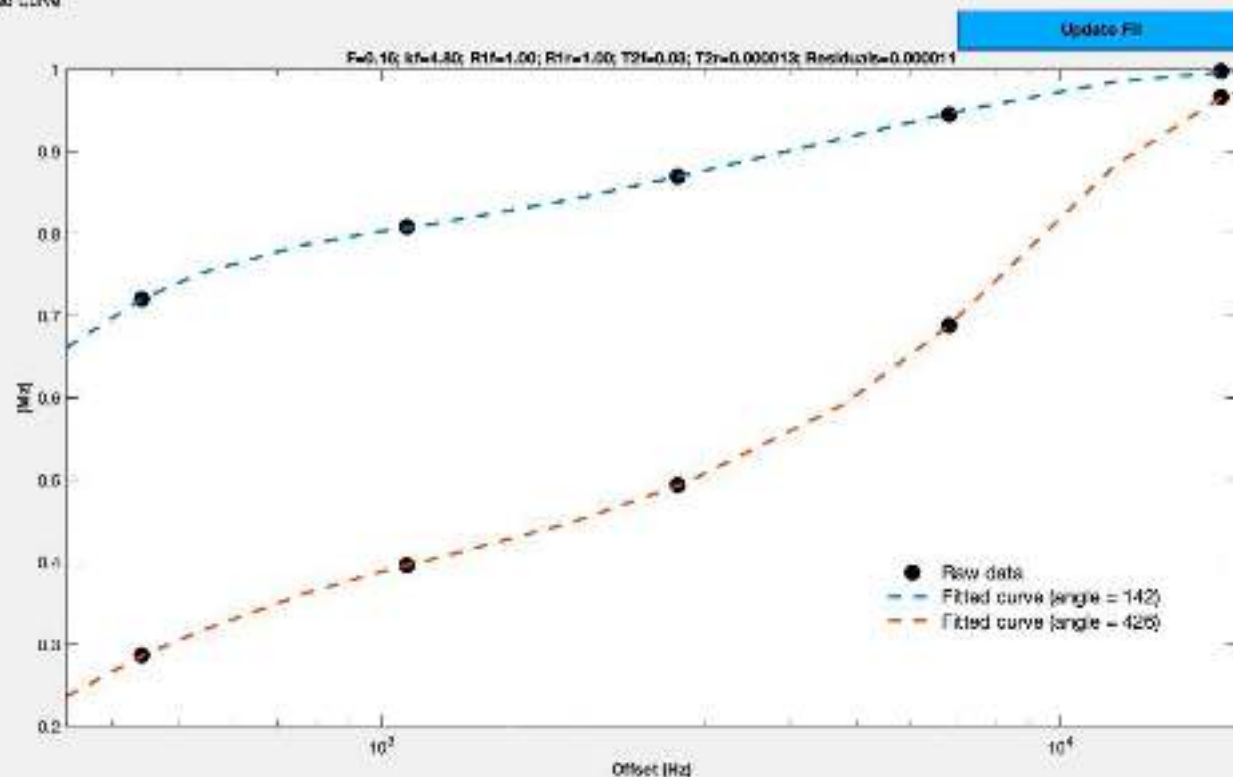
Shift 1000

Method Analytical eq. of...

☐ Fixed Mz

Name	Input	Fitted	Pct. error	Pct. CRLB
F	0.1600	0.1584	-1	0.0038
α	30	30.3167	1	1.2048e-03
R1f	1	1	0	
R1r	1	1	0	
T2f	0.0300	0.0288	-1	4.5068e-04
T2r	1.3000e-05	1.2847e-05	0	1.3023e-11
σ		4.8035		
norm		1.1252e-05		

Fitted Curve



OptionsGUI

gmit app options

Protocol

MTData

	Angle	Offset
1	142	440
2	426	440
3	142	1058
4	426	1058
5	142	2732
6	426	2732
7	142	5852
8	426	5852
9	142	17215
10	426	17215

Add
 Move up
 Load

Remove
 Move down
 Create

Timing Table

Tmt (s)	0.0100
Ts (s)	0.0050
Tp (s)	0.0018
T+ (s)	0.0100
TR (s)	0.0250

Not Protocol

Fitting

Var	Fix	Start	Lower	Upper
F		0.1600	0.0000	0.5000
α		30.0000	0.0000	100
R1f	☒	R1f/R1r	0.0000	5
R1r	☒	1	0.0000	5
T2f		0.0300	0.0000	0.0500
T2r		1.3000e-05	0.0000e-05	5.0000e-05

Options

MT_Pulse

Shape: gaussian

Sinc TBW: 3

Bandwidth: 200

Fermi transition (K): 0.00001658

of MT pulses: 100

Model: SkelTweeIT

Linshape: SuperLorentzian

fitting constraints

☒ Use R1map to constrain R1f☐ Fix R1r = R1f☐ Fix R1f/T2f

T1/T2f = 0.055

Read pulse alpha: 7

Compute SRTake

Save

Load

Default

Help

Current

Parameters filename

Single Voxel Curve

Parameters

Options

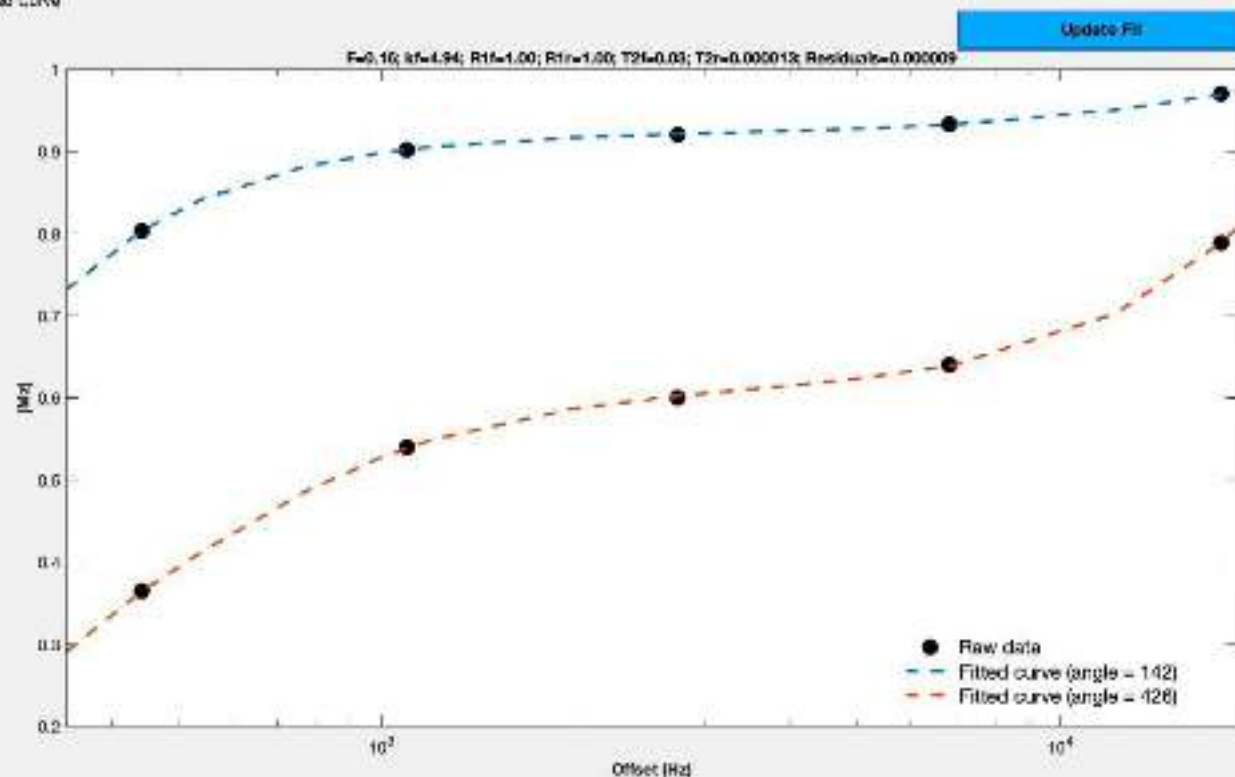
Shift 1000

Method Analytical eq. of...

☐ Reset fit

Name	Input	Fitted	Pct. error	Pct. CRLB
F	0.1000	0.1588	1	0.0034
α	30	31.1531	4	1.5570e-04
R1f	1	1	0	
R1r	1	1	0	
T2f	0.0300	0.0300	0	1.7106e-04
T2r	1.3000e-05	1.2952e-06	0	1.4931e-11
σ		4.9394		
varnorm		2.1050e-06		

Fitted Curve



OptionsGUI

gmit app options

Protocol

MTData

	Angle	Offset
1	142	443
2	426	443
3	142	1058
4	426	1058
5	142	2732
6	426	2732
7	142	6852
8	426	6852
9	142	17215
10	426	17215

Add
Move up
LoadRemove
Move down
Create

Timing Table

Tmt (s)	0.0100
Ts (s)	0.0050
Tp (s)	0.0018
T+ (s)	0.0100
TR (s)	0.0250

Not Protocol

Fitting

Var	Fix	Start	Lower	Upper
F		0.100	1.000e-10	0.5000
α		30	1.000e-10	100
R1f	☒	R1f/RP	0.000	5
R1r	☒	1	0.000	5
T2f		0.030	0.000	0.5000
T2r		1.000e-5	1.000e-10	5.000e-5

Options

MT_Pulse

Shape: gaussian

Sinc TBW: 1

Bandwidth: 200

Fermi transition (K): 0.000001658

of MT pulses: 100

Model: Skel/Yeall/P

Lineshape: Gaussian

fitting constraints

☒ Use R1map to constrain R1f☐ Fix R1f = R1r☐ Fix R1f/T2f

R1f/T2f = 0.055

Read pulse alpha: 7

Compute STable

Save

Load

Default

Help

Current

Parameters filename

How to...

download a **demo** dataset



Method:

qat_sp...

[Open Options Panel](#)

qMR Data Fit

Fit data

[Save Results](#)[Load Results](#)

qMR Simulator

[Multi Voxel Distribution](#)[Sensitivity Analysis](#)[Single Voxel Curve](#)

Fit qMR Data

Path data: Study ID: [Download example](#)

MTdata REQUIRED Magnetization Transfer data [View](#)

R1map REQUIRED Longitudinal relaxation rate (N/A RECOMMENDED) [View](#)

B1map Normalized transmit excitation field map (B1+). B1+ is defined as a [View](#)

B0map B0 field map, used for offset correction (OPTIONAL) 0-0Hz if not [View](#)

Mask Binary mask to accelerate the fitting (OPTIONAL)

Cannot find required input called MTdata

Fit Results

Source:

View:

A...

3D viewer

Sanity Check

[Voxel fit](#)[ROI fit](#)[Statistics](#)[Histogram](#)

Cursor

[Select](#)S
L R
I

(1,1,1) 0

Vol: 1/1 Time: 1/1 Slice: 1/1

Current file:

[View qMRLab documentation](#)

qMR app options

Protocol

MTdata

	Angle	Offset
1	142	413
2	425	413
3	142	1085
4	425	1085
5	142	2732
6	425	2732
7	142	6562
8	425	6562
9	142	17235
10	425	17235

[Add](#)[Move up](#)[Load](#)[Remove](#)[Move down](#)[Create](#)

TimingTable

Tmt (s)	0.0102
Ts (s)	0.0080
Tp (s)	0.0015
Tr (s)	0.0100
TR (s)	0.0250

Fit Protocol

Fitting

Var	Fix	Start	Lower	Upper
F		0.000 1.000e-		0.020
k		35 1.000e-		100
m	☒	R1/RP	0.000	5
R1	☒	1	0.000	5
T2		0.000 0.020	0.020	0.020
T2*		1.000e- 1.000e-	1.000e-	1.000e-

Options

MT_Pulse

Shape:

Sinc TRW:

Bandwidth:

Form factor (d):

of MT pulses:

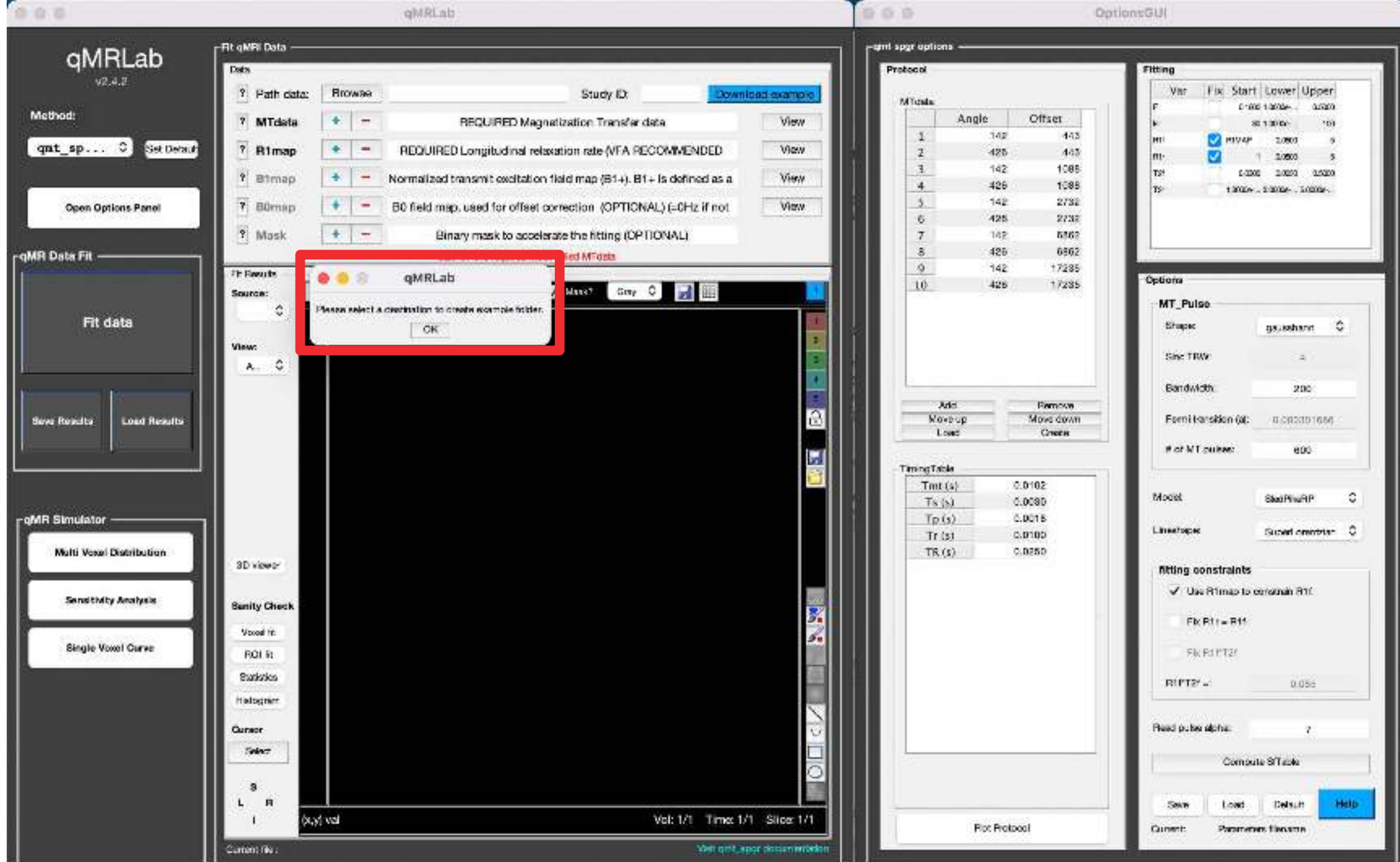
Model:

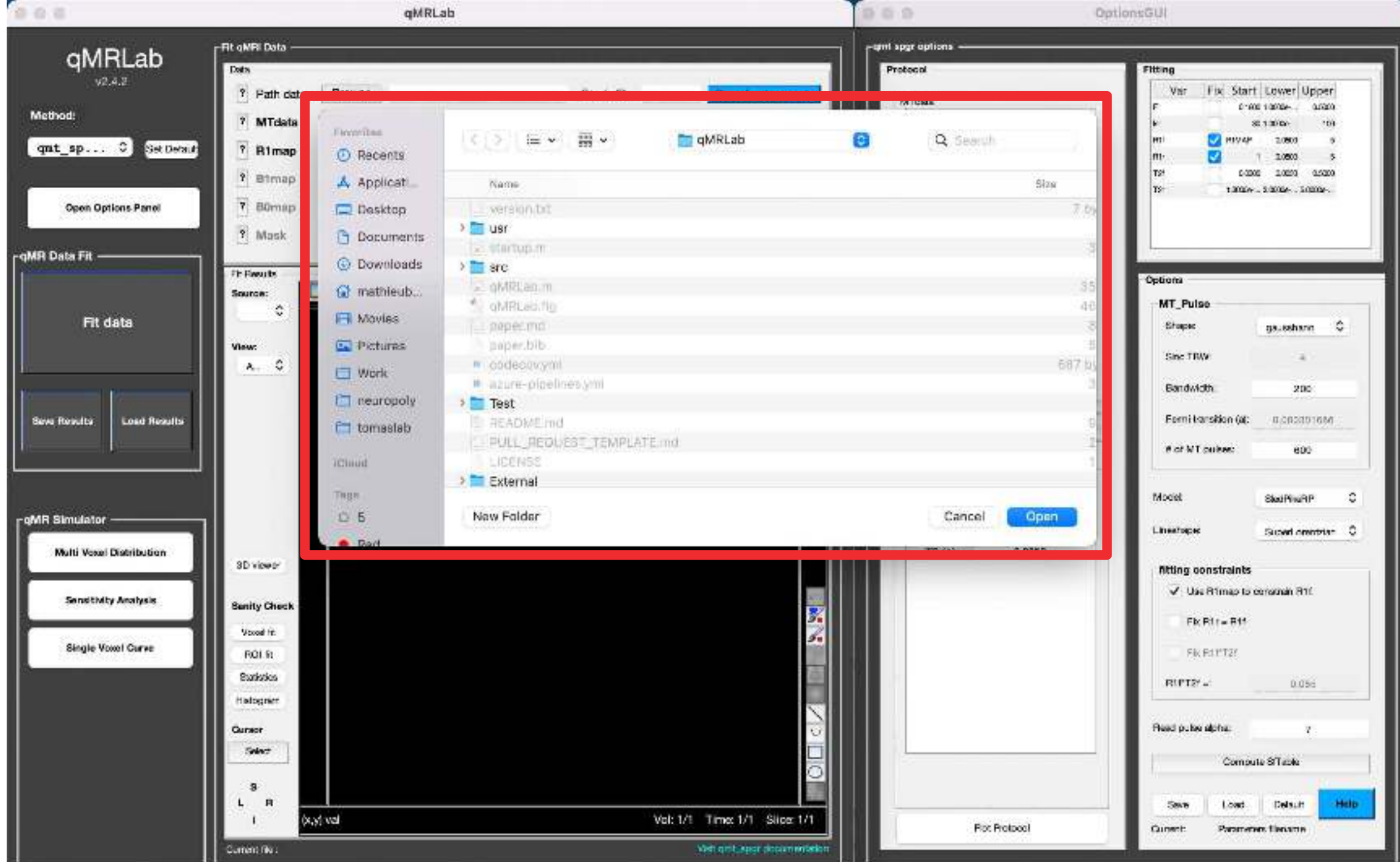
Line shape:

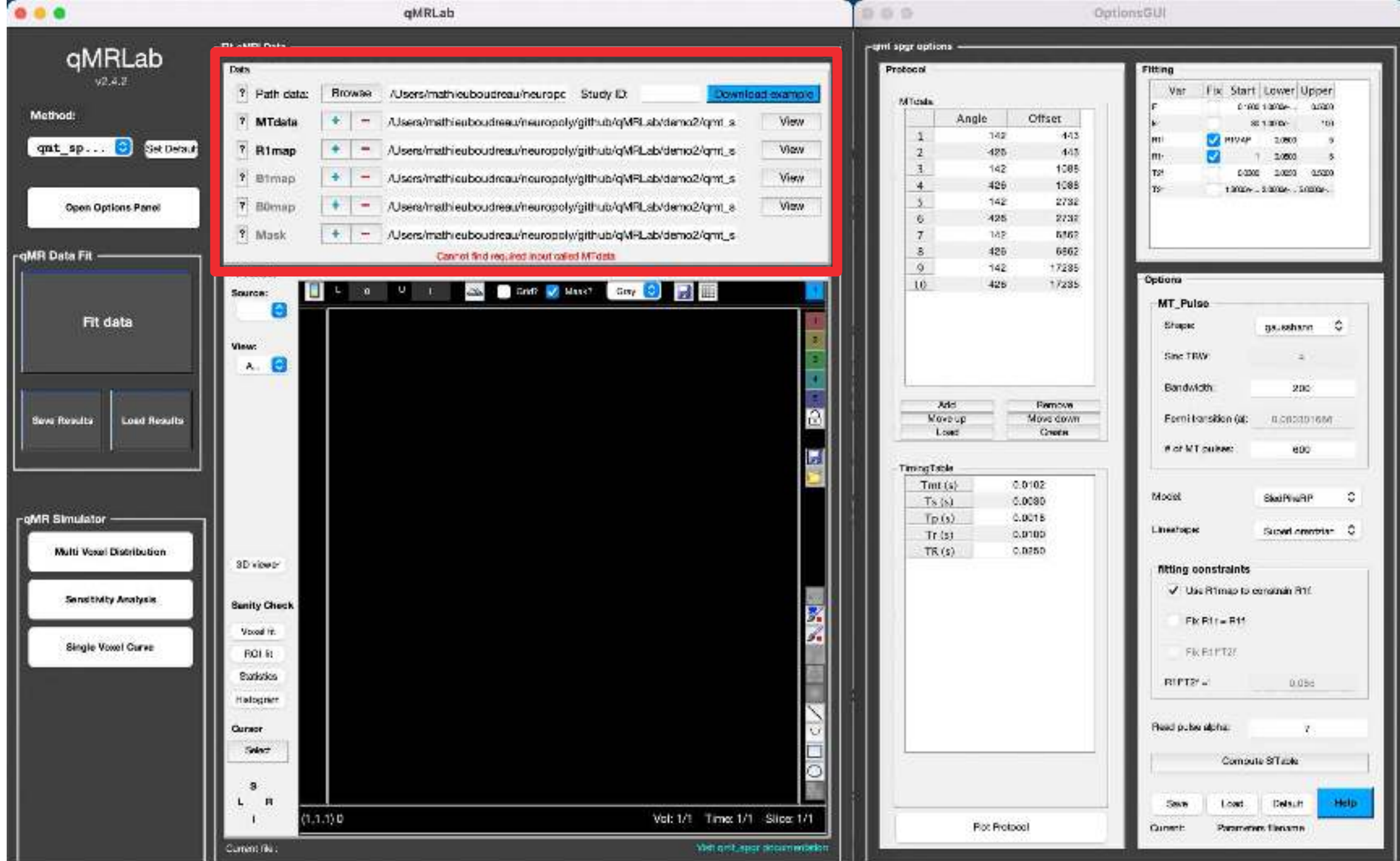
Fitting constraints

☒ Use R1map to constrain R1☐ Fix R1 = R11☐ Fix R1/T2*R1/T2* = Read pulse alpha: [Compute S/Tdata](#)[Save](#) [Load](#) [Default](#) [Help](#)

Current: Parameters: Functions







How to...

visualize loaded datasets



Method:

qmt_sp...   Open Options Panel

qMR Data Fit

Fit data

Save Results

Load Results

qMR Simulator

Multi Voxel Distribution

Sensitivity Analysis

Single Voxel Curve

Fit qMR Data

Data

Path data:		/Users/mathieuboudreau/neuropr	Study ID:	
MTdata	 	/Users/mathieuboudreau/neuropr/github/qMRLab/demo2/qmt_s		View
R1map	 	/Users/mathieuboudreau/neuropr/github/qMRLab/demo2/qmt_s		View
B1map	 	/Users/mathieuboudreau/neuropr/github/qMRLab/demo2/qmt_s		View
B0map	 	/Users/mathieuboudreau/neuropr/github/qMRLab/demo2/qmt_s		View
Mask	 	/Users/mathieuboudreau/neuropr/github/qMRLab/demo2/qmt_s		View

Fit Results

Source:

B... 

View:

A... 

3D view:

Sanity Check

Voxel fit

R1 fit

Statistics

Histogram

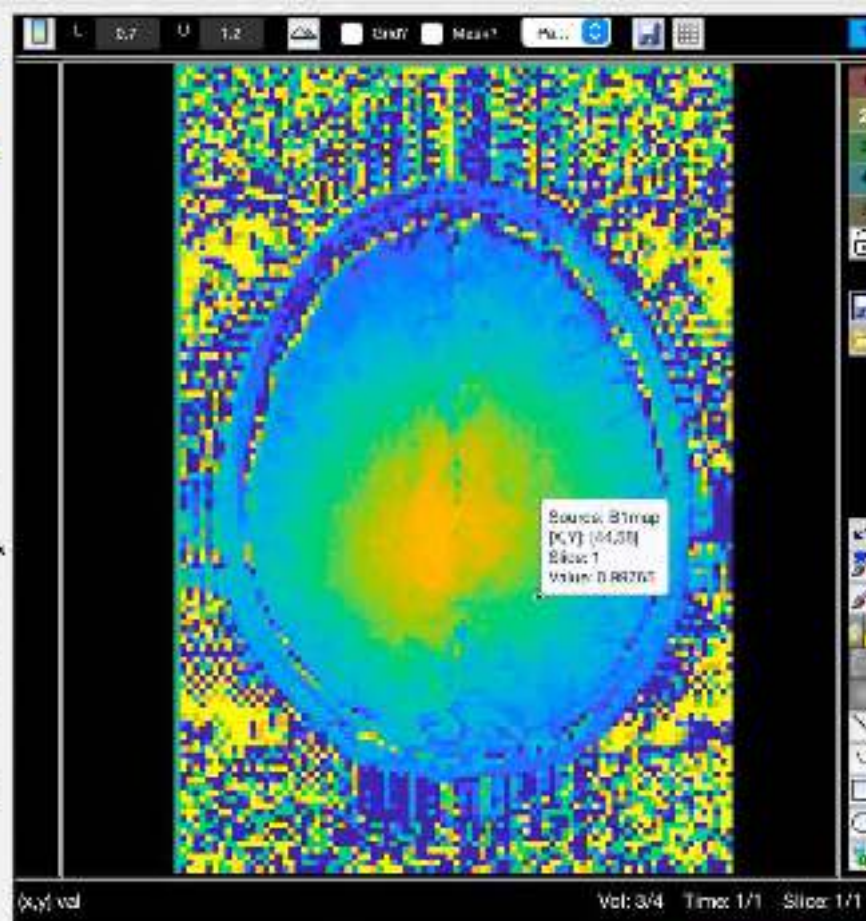
Cursor

Select

A

L R

P



Current file:

[Web qmt_spr documentation](#)

qmt_spr options

Protocol

-MTdata

	Angle	Offset
1	142	443
2	425	443
3	142	1085
4	425	1085
5	142	2732
6	425	2732
7	142	6262
8	425	6262
9	142	17235
10	425	17235

Add

Move up

Load

Remove

Move down

Create

Timing Table

Tmt (s)	0.0105
Ts (s)	0.0030
Tp (s)	0.0015
Tr (s)	0.0100
TR (s)	0.0250

Plot Protocol

Fitting

Var	Fix	Start	Lower	Upper
P		0.100	1.000e-	0.500
K		00	1.000e-	100
RH	☒	nrvap	0.000	5
R1	☒	1	0.000	5
T2*		0.000	0.000	0.000
T2		1.000e-	0.000e-	0.000e-

Options

MT_Pulse

Shape: gaussian 

Sinc TRW: 0

Bandwidth: 200

Fermi iteration (q): 0.00301656

of MT pulses: 600

Model: SteadRP Lineshape: SuperLorentzian 

fitting constraints

☒ Use R1map to constrain R1f☐ Fix R1 to R1f☐ Fix R1/T2*

R1/T2* = 0.050

Read pulse alpha: 7

Compute STable

Save

Load

Default

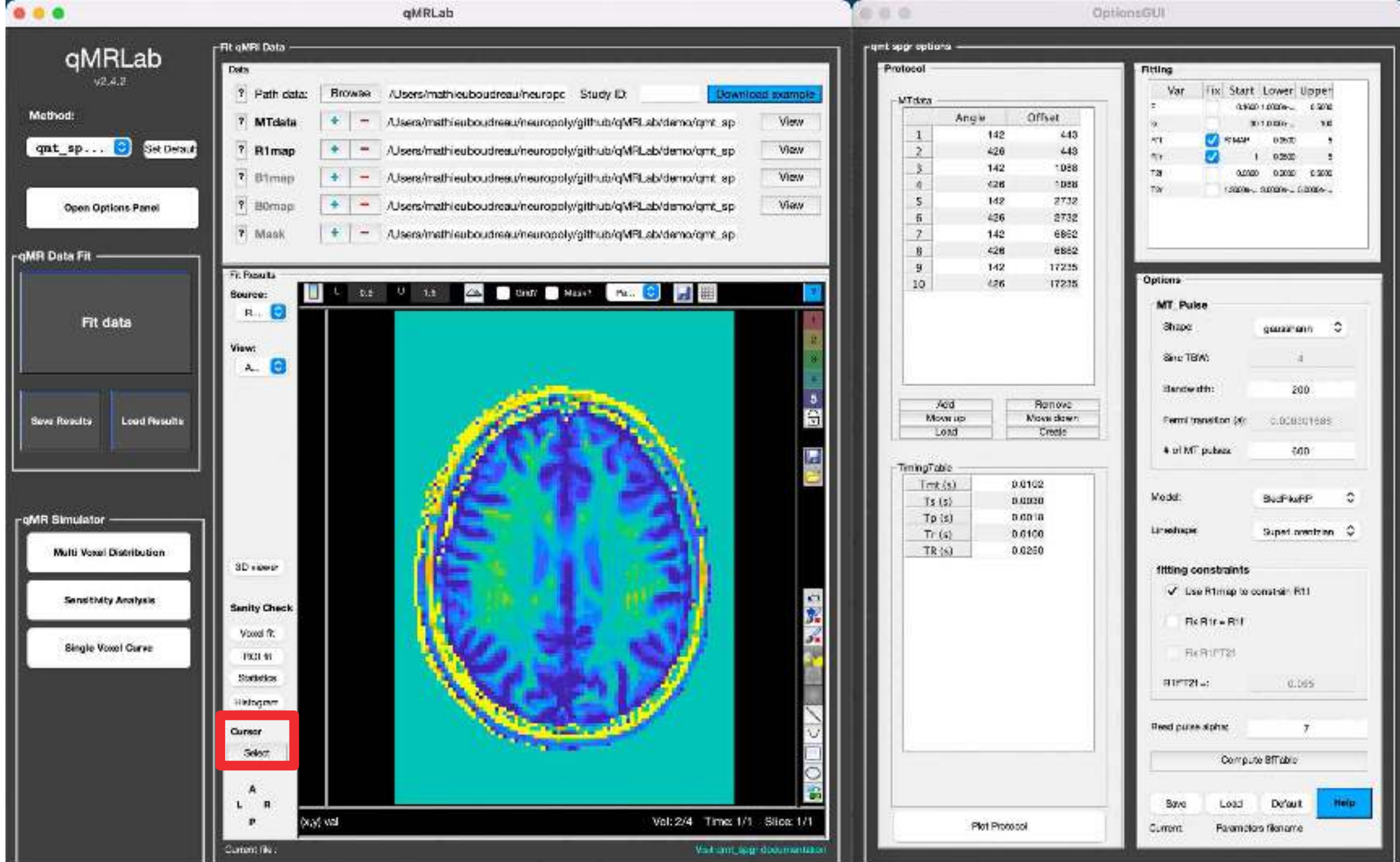
Help

Current

Parameters filename

How to...

verify the fit of a single voxel





Method:

qmt_sp...   Set Default

qMR Data Fit

Fit data

Save Results

Load Results

qMR Simulator

Multi Voxel Distribution

Sensitivity Analysis

Single Voxel Curve

Fit qMR Data

Data

Path data:		/Users/mathieuboudreau/neuropc	Study ID:		
MTdata	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			
R1map	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			
B1map	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			
B0map	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			
Mask	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			

Fit Results

Source:

R... 

View:

A... 

3D viewer

Sanity Check

Voxel fit

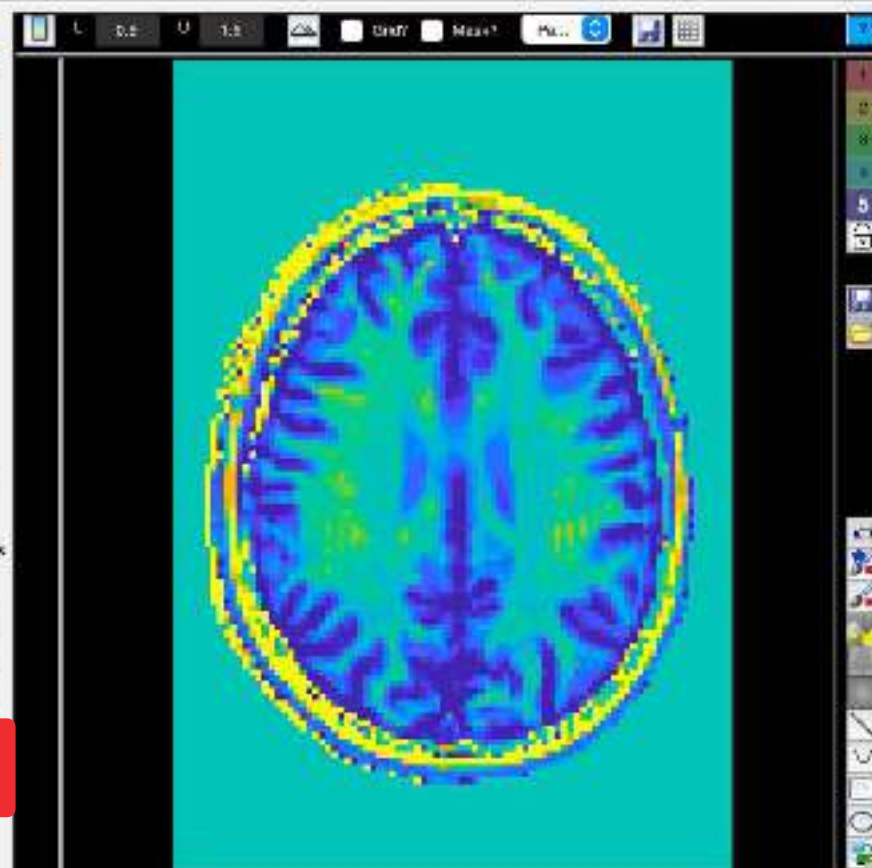
FOI fit

Statistics

Histogram

Cursor

Select

A
L R
P

(x,y) val

Vol: 2/4 Time: 1/1 Slice: 1/1

Current file:

[View qmt_app documentation](#)

qmt_app options

Protocol

MTdata

	Angle	Offset
1	142	443
2	426	443
3	142	1088
4	426	1088
5	142	2732
6	426	2732
7	142	6882
8	426	6882
9	142	17235
10	426	17235

Add

Move up

Load

Remove

Move down

Create

TimingTable

Tmt (s)	0.0102
Ts (s)	0.0030
Tp (s)	0.0010
Tr (s)	0.0100
TR (s)	0.0250

Plot Protocol

Fitting

Var	Fix	Start	Lower	Upper
T		0.00010000000000000000	0.0000	0.0000
q		0.10000000000000000000	0.0000	0.0000
R1	☒	0.00000000000000000000	0.0000	0.0000
R1	☒	1	0.0000	0.0000
T2		0.0000	0.0000	0.0000
T2		1.00000000000000000000	0.00000000000000000000	0.00000000000000000000

Options

MT_Pulse

Shape: gaussian 

Sinc TBA: 1

Bandwidth: 200

Firmi transition (K): 0.000001588

of MT pulses: 100

Model: BudFickPP Lineshape: Super resolution 

fitting constraints

☒ Use R1map to constrain R1f☐ R1 R1f = R1f☐ R1 R1f T2f

R1f T2f =: 0.005

Read pulse alpha: 7

Compute BTable

Save

Load

Default

Help

Current

Parameters filename



Method:

qmt_sp...

Open Options Panel

qMR Data Fit

Fit data

Save Results

Load Results

qMR Simulator

Multi Voxel Distribution

Sensitivity Analysis

Single Voxel Curve

Fit qMR Data

Data

Path data:		/Users/mathieuboudreau/neuro...	Study ID:	Download example
MTdata		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp		View
R1map		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp		View
B1map		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp		View
B0map		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp		View
Mask		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp		View

Fit Results

Source:

R...

View:

A...

3D viewer

Sanity Check

Voxel fit

FOI fit

Statistics

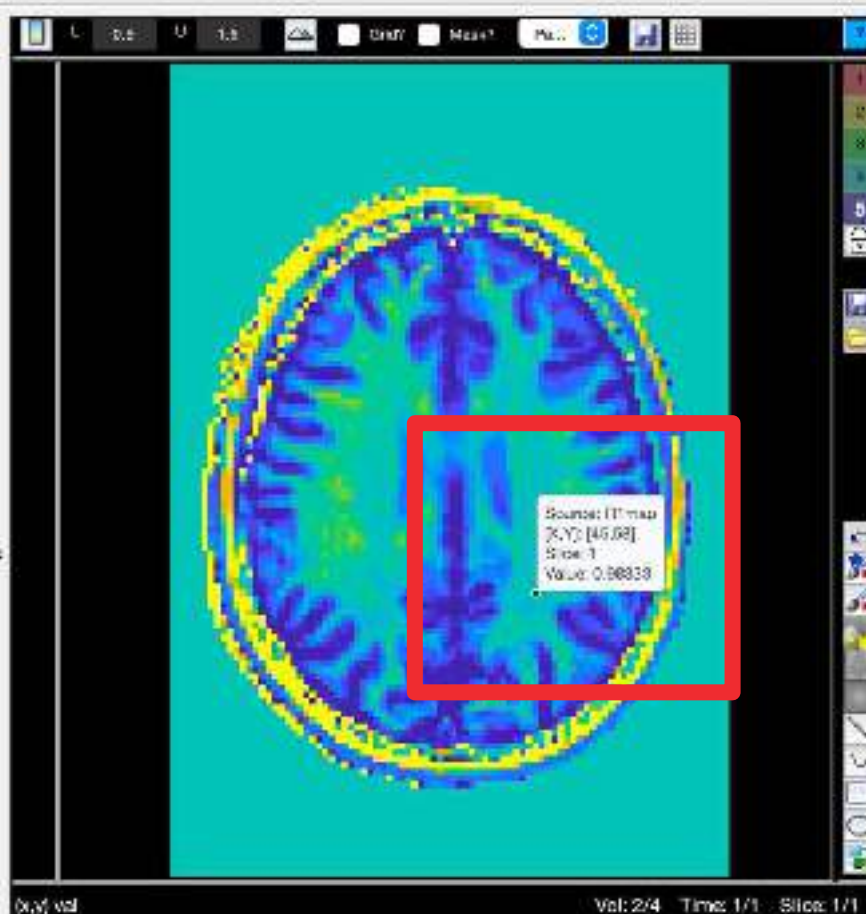
Histogram

Cursor

Select

A
L R
P

Current file:



Visit qmt_app documentation

qmt_app options

Protocol

MTData

	Angle	Offset
1	142	443
2	426	443
3	142	1088
4	426	1088
5	142	2732
6	426	2732
7	142	6882
8	426	6882
9	142	17235
10	426	17235

Add

Move up

Load

Remove

Move down

Create

TimingTable

Tmt (s)	0.0102
Ts (s)	0.0030
Tp (s)	0.0010
Tr (s)	0.0100
TR (s)	0.0250

Plot Protocol

Fitting

Var	Fix	Start	Lower	Upper
T		0.0001 0.000...	0.000	0.000
q		0.1 0.000...	0.0	0.0
R1	☒	0.142	0.000	0.0
R1	☒	1	0.000	0.0
T2		0.000	0.000	0.000
T2		1.0000e-0...	0.0000e-0...	0.0000e-0...

Options

MT_Pulse

Shape	gaussian
Sinc TBA	1
Bandwidth	200
Fermi transition (K)	0.0000015885
# of MT pulses	100

Model	BudFickPP
Lineshape	Super resolution

fitting constraints

☒ Use R1map to constrain R11☐ R1 R11 = R11☐ R1 R11 T21

R1 T21 = 0.065

Red pulse alpha 7

Compute BTable

Save Load Default Help

Current Parameters filename



Method:

qmt_sp...

Open Options Panel

qMR Data Fit

Fit data

Save Results

Load Results

qMR Simulator

Multi Voxel Distribution

Sensitivity Analysis

Single Voxel Curve

Fit qMR Data

Data

Path data:		/Users/mathieuboudreau/neuro...	Study ID:	Download example
MTdata		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp		View
R1map		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp		View
B1map		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp		View
B0map		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp		View
Mask		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp		

Fit Results

Source:

R...

View:

A...

3D viewer

Sanity Check

Voxel fit

ROI fit

Statistics

Histogram

Cursor

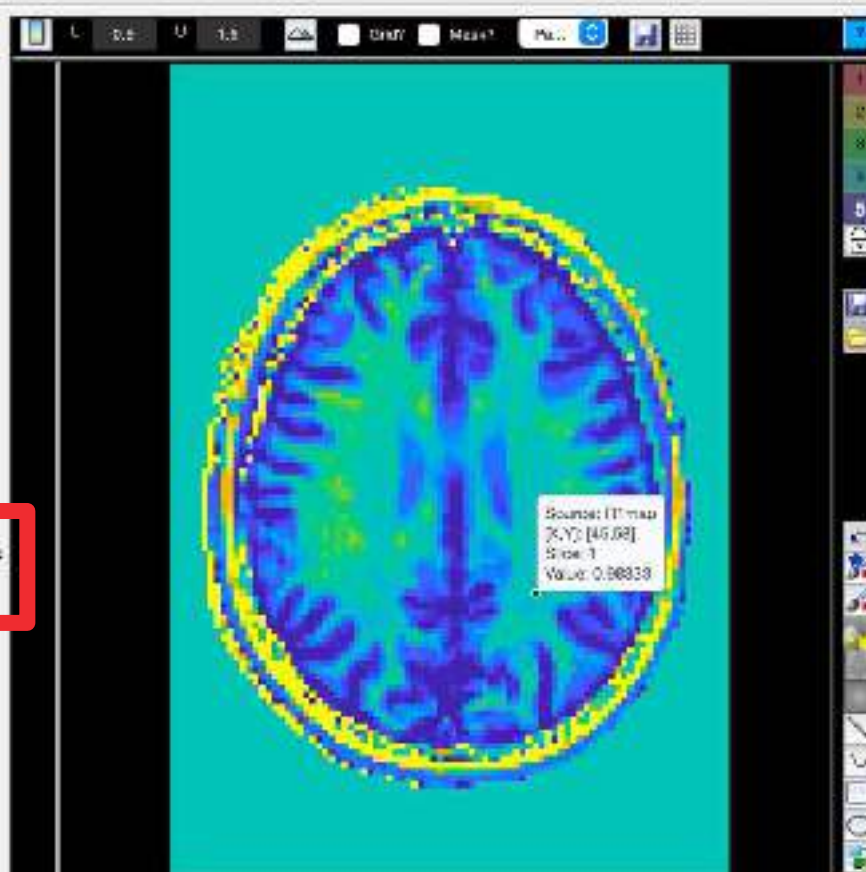
Select

A

L

R

P



(x,y) val

Vol: 2/4 Time: 1/1 Slice: 1/1

Current file:

[View qmt_app documentation](#)

qmt_app options

Protocol

MTData

	Angle	Offset
1	142	443
2	426	443
3	142	1088
4	426	1088
5	142	2732
6	426	2732
7	142	6882
8	426	6882
9	142	17235
10	426	17235

Add

Move up

Load

Remove

Move down

Create

TimingTable

Tmt (s)	0.0102
Ts (s)	0.0030
Tp (s)	0.0010
Tr (s)	0.0100
TR (s)	0.0250

Plot Protocol

Fitting

Var	Fix	Start	Lower	Upper
T		0.0001	0.0000	0.5000
Ts		0.010000		1.0
R1	☒	0.142	0.0000	1
R1	☒	1	0.0000	1
T2		0.0000	0.0000	0.0000
T2		1.000000	0.000000	0.000000

Options

MT_Pulse

Shape	gaussian
Sinc TBA	1
Bandwidth	200
Fermi transition (K)	0.000001588
# of MT pulses	100

Model	BudFickPP
Lineshape	Super resolution

fitting constraints

☒ Use R1map to constrain R11☐ R1 R11 = R11☐ R1 R11 T21

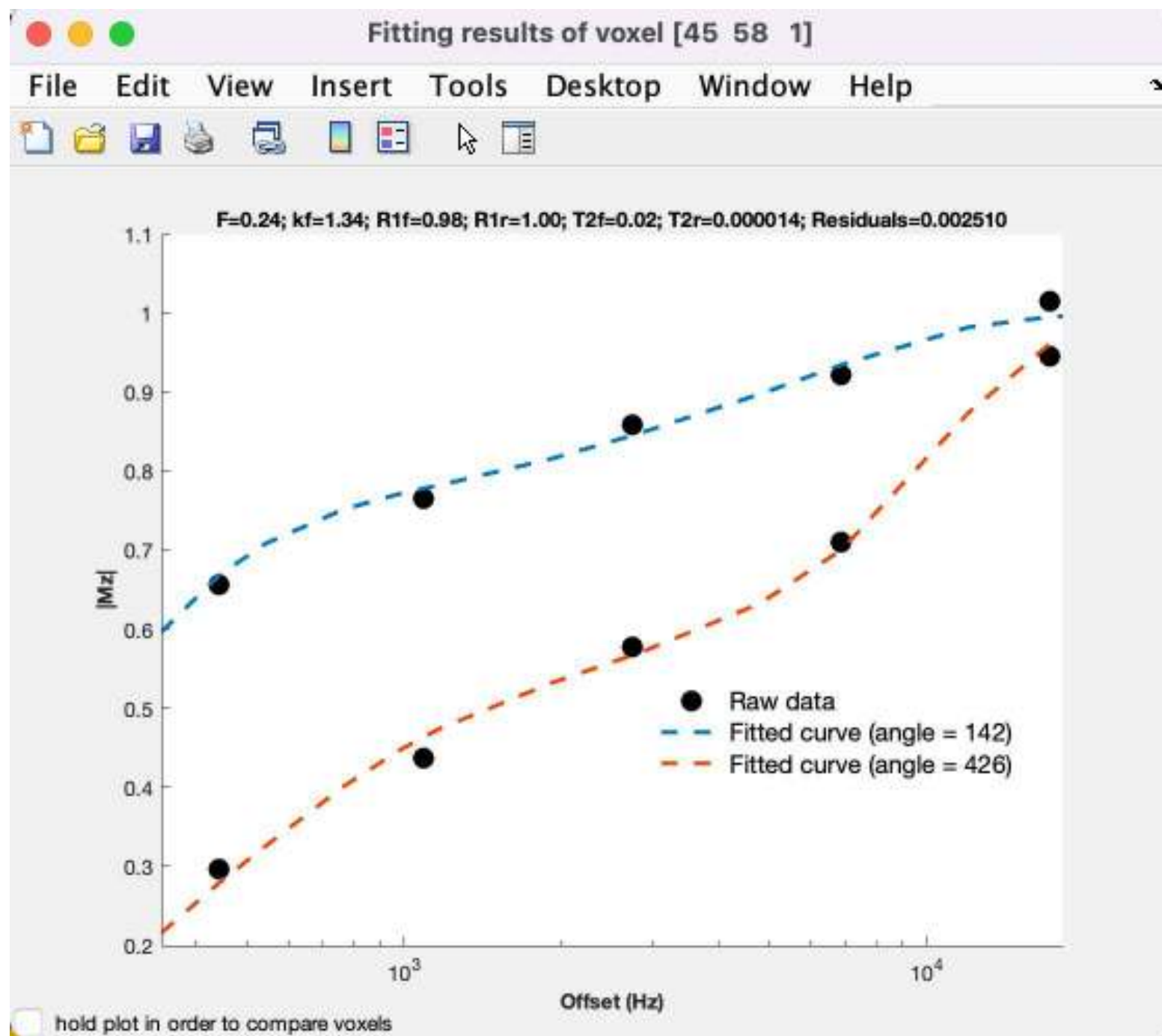
R1 T21 = 0.065

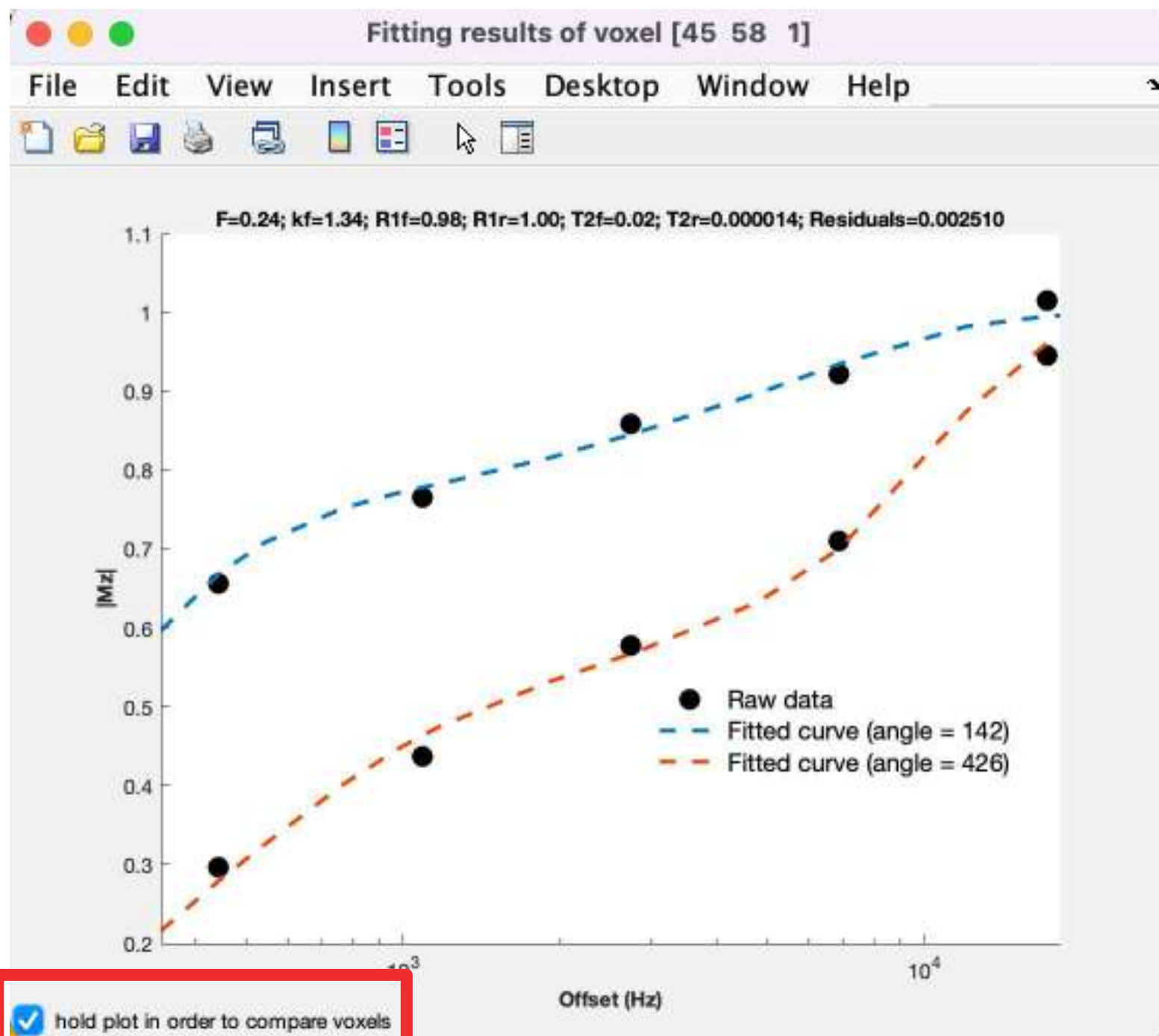
Red pulse alpha 7

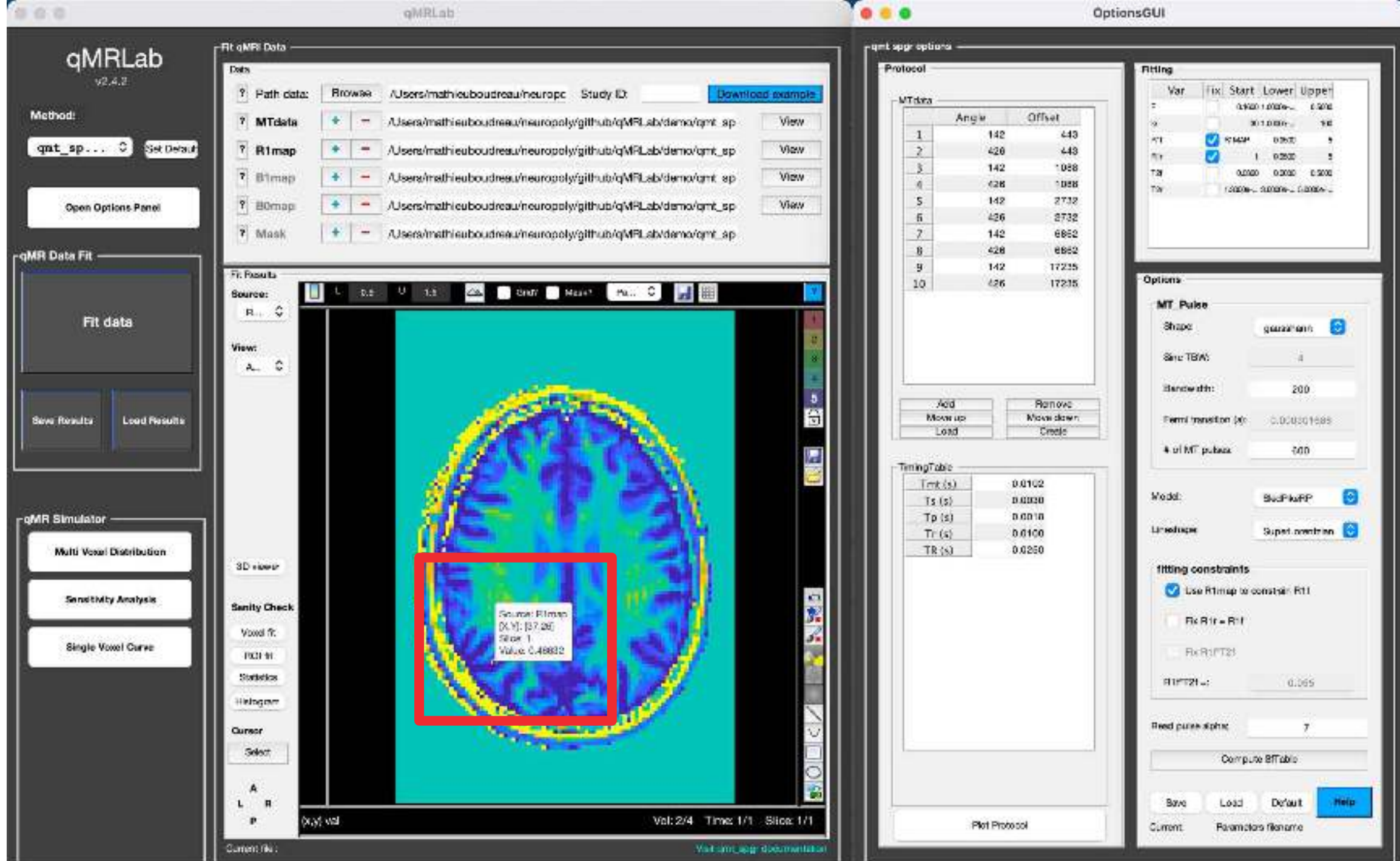
Compute BTable

Save Load Default Help

Current Parameters filename







qMRLab
v2.4.2

Method:
qmt_sp...
Open Options Panel

qMR Data Fit
Fit data
Save Results Load Results

qMR Simulator
Multi Voxel Distribution
Sensitivity Analysis
Single Voxel Curve

Fit qMR Data

Path data: Browse /Users/mathieuboudreau/neuropc Study ID: Download examples

MTdata

+

-

/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp

View

R1map

+

-

/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp

View

B1map

+

-

/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp

View

B0map

+

-

/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp

View

Mask

+

-

/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp

View

Fit Results

Source: R1map

View: A

3D viewer

Sanity Check

Voxel fit

Statistics

Histogram

Cursor

Select

A

L

R

P

Source: R1map
(X,Y): [37,26]
Slice: 1
Value: 0.48832

(x,y) val

Val: 2/4 Time: 1/1 Slice: 1/1

Current file: [View qmt_app documentation](#)

OptionsGUI

qmt_app options

Protocol

MTdata

	Angle	Offset
1	142	443
2	426	443
3	142	1088
4	426	1088
5	142	2732
6	426	2732
7	142	6862
8	426	6862
9	142	17235
10	426	17235

Add

Move up

Load

Remove

Move down

Create

TimingTable

Tmt (s)	0.0102
Ts (s)	0.0020
Tp (s)	0.0010
Tt (s)	0.0100
TR (s)	0.0250

Plot Protocol

Fitting

Var	Fix	Start	Lower	Upper
T		0.00010000...	0.000	0.500
q		30.10000...	0.0	9.0
R1	☒	0.1444	0.000	1
R1	☒	1	0.000	1
T2		0.0000	0.000	0.200
T2		1.0000...	0.0000...	0.0000...

Options

MT Pulse

Shape: gaussian

Sinc TBA: 1

Bandwidth: 200

Fermi transition (K): 0.00001588

of MT pulses: 100

Model: SudPikAPP

Uneshape: Super-resolution

fitting constraints

☒ Use R1map to constrain R1

☐ R1 R1t = R1t

☐ R1 R1T2

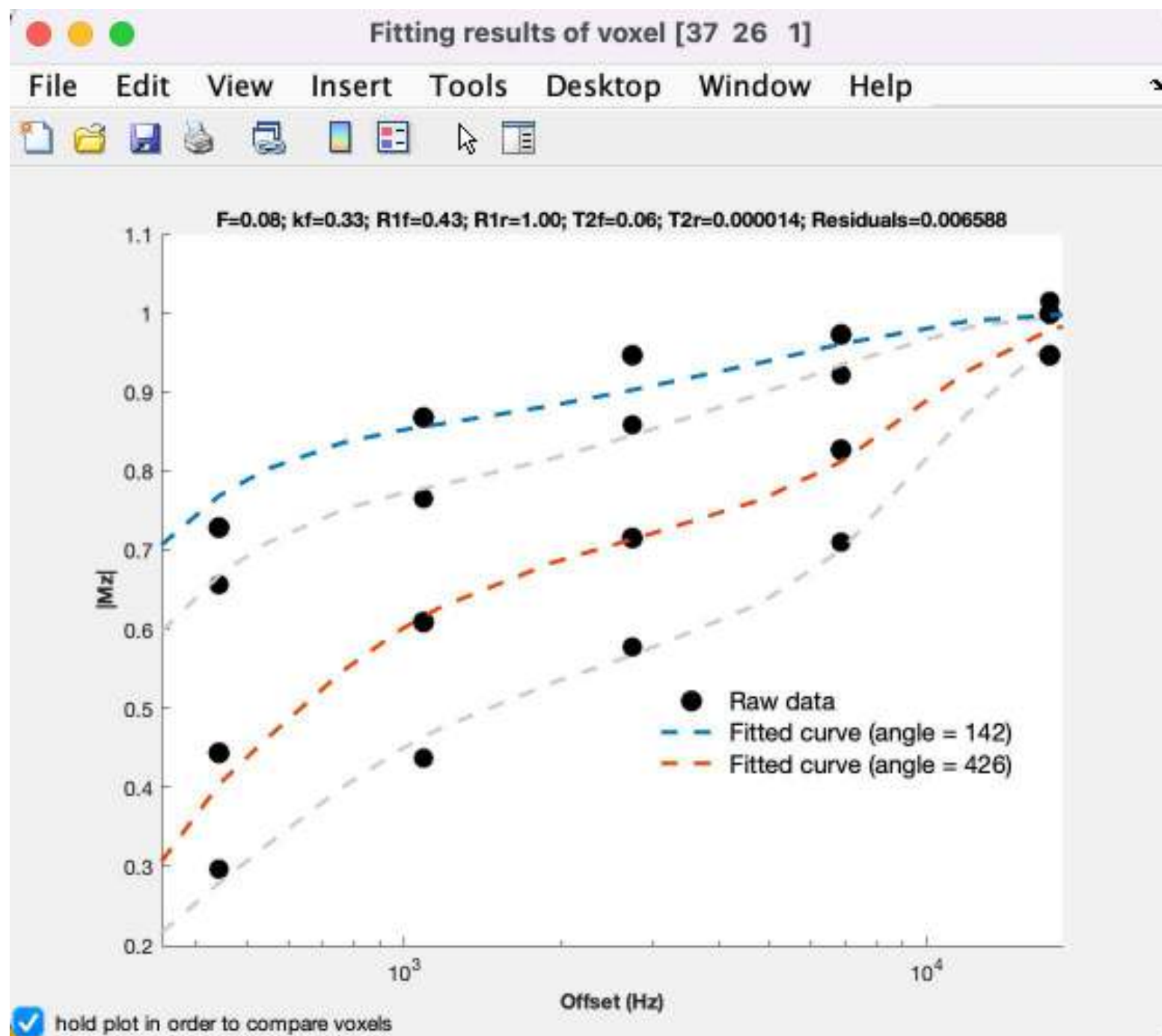
R1T2T1 = 0.065

Read pulse alpha: 7

Compute BTable

Save Load Default Help

Current Parameters filename



How to...

fit an entire dataset

Method:

qmt_sp...  

Open Options Panel

qMR Data Fit

Fit data

Save Results

Load Results

qMR Simulator

Multi Voxel Distribution

Sensitivity Analysis

Single Voxel Curve

Fit qMR Data

Data

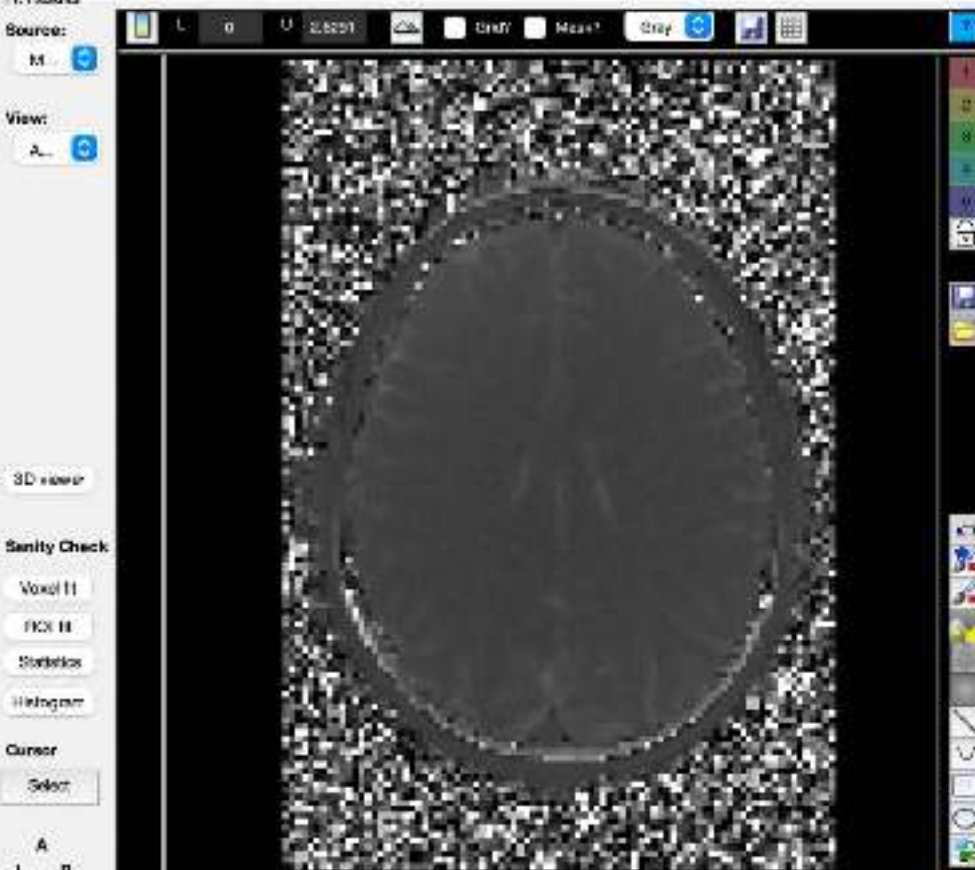
Path data:		/Users/mathieuboudreau/neuropoly	Study ID:	 Download example	
MTdata	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			 View
R1map	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			 View
R2map	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			 View
R3map	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			 View
Mask	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			 View

Fit Results

Source:

M 

View:

A 

3D view

Sanity Check

Voxel H

ROI H

Statistics

Histogram

Cursor

Select

A

L R

P

(x,y) val

Vol: 1/4 Time: 1/10 Slice: 1/1

Current file:

[View qmt_spr documentation](#)

qmt_spr options

Protocol

-MTdata

	Angle	Offset
1	142	443
2	425	443
3	142	1085
4	425	1085
5	142	2732
6	425	2732
7	142	6262
8	425	6262
9	142	17235
10	425	17235

Add
Move up
LoadRemove
Move down
Create

Timing Table

Tint (s)	0.0102
Ts (s)	0.0090
Tp (s)	0.0015
Tr (s)	0.0100
TR (s)	0.0260

Fit Protocol

Fitting

Var	Fix	Start	Lower	Upper
F		0.000 1.000	0.000	0.000
k		80 1.000	100	100
m	☒	R1/R2	0.000	5
R1	☒	1	0.000	5
T2*		0.000 0.000	0.000	0.000
T2		1.000	0.000	1.000

Options

MT Pulse

Shape: Sinc BW: Bandwidth: Pulse duration (s): # of MT pulses: Model: Line shape:

Fitting constraints

☒ Use R1map to constrain R1f☐ Fix R1 to R1f☐ Fix R1/T2*R1/T2* = Read pulse alpha:

Compute 2T table

Save

Load

Default

Help

Current

Parameters filename

qMRLab
v2.4.2

Method:
qmt_sp... Set Default

Open Options Panel

qMR Data Fit

Fit data

Save Results Load Results

qMR Simulator

Multi Voxel Distribution

Sensitivity Analysis

Single Voxel Curves

Fit qMRI Data

Data

Path data: Browse /Users/mathieuboudreau/neuropoly Study ID: Download example

MTdata + - /Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp View

R1map + - /Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp View

R1map + - /Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp View

R2map + - /Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp View

Mask + - /Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp

Fit Parameters

Source

M

View

A

3D viewer

Sanity Check

Voxel H

ROI H

Statistics

Histogram

Cursor

Select

A

L R

P

(x,y) val

Vol: 1/4 Time: 1/10 Slice: 1/1

Current file: [View qmt_appr documentation](#)

Parallel Processing

Would you like to start a parallel pool with 8 cores?

Yes No

OptionsGUI

qmt_appr options

Protocol

MTdata

	Angle	Offset
1	142	443
2	425	443
3	142	1085
4	425	1085
5	142	2732
6	425	2732
7	142	6262
8	425	6262
9	142	17235
10	425	17235

Add

Move up

Load

Remove

Move down

Create

Timing Table

Tmt (s)	0.0102
Ts (s)	0.0090
Tp (s)	0.0018
Tr (s)	0.0100
TR (s)	0.0260

Fit Protocol

Fitting

Var	Fix	Start	Lower	Upper
F		0.000 1.000	0.000	
k		80 1.000	100	
m1	☒	R1/R2	0.000	5
R1	☒	1	0.000	5
T2*		0.000 0.020 0.020		
T2		1.000 1.000 1.000		

Options

MT_Pulse

Shape: gaussian

Sinc BW:

Bandwidth: 200

Parm Iteration (s): 0.00301656

of MT pulses: 600

Model: SledPilot

Linehape: Scaled gaussian

Fitting constraints

☒ Use R1map to constrain R1f

☐ Fix R1 to R1f

☐ Fix R1/T2*

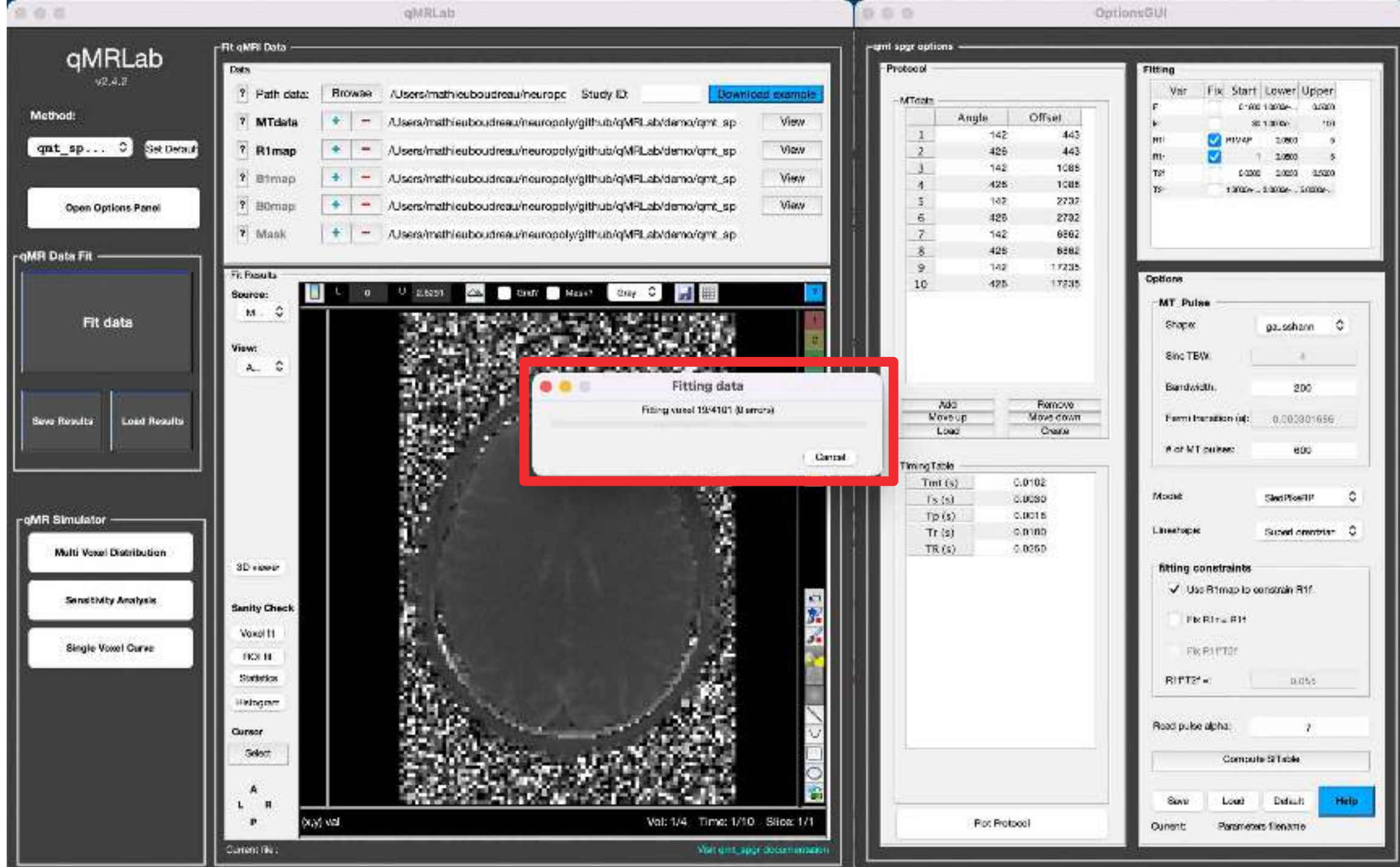
R1/T2* = 0.055

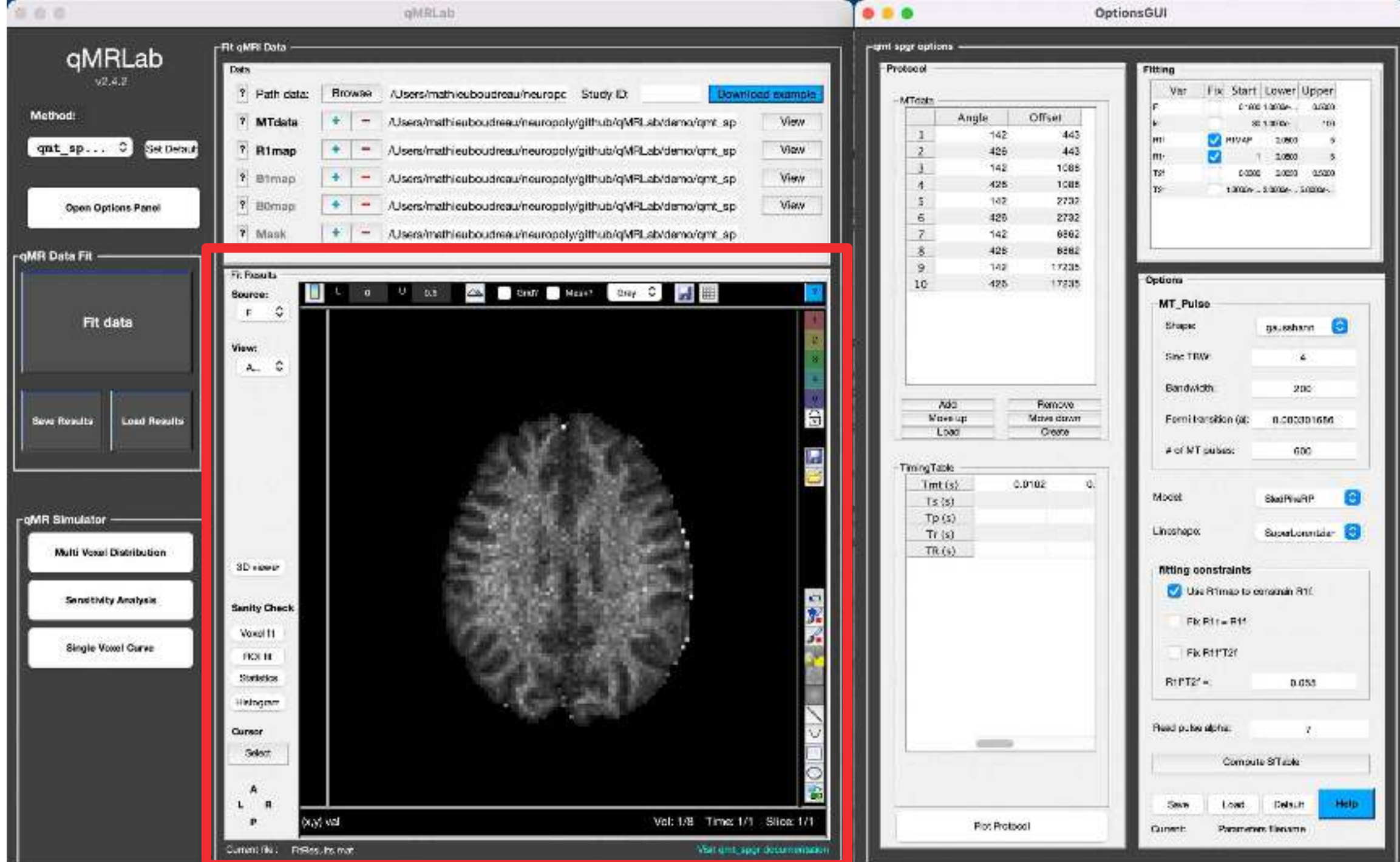
Read pulse alpha: 7

Compute QTable

Save Load Default Help

Current Parameters filename







Method:

qmt_sp...

qMR Data Fit

Fit data

Save Results

Load Results

qMR Simulator

Multi Voxel Distribution

Sensitivity Analysis

Single Voxel Curve

Fit qMR Data

Data

Path data:	Browse	/Users/mathieuboudreau/neuro...	Study ID:		
MTdata		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			
R1map		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			
R1map		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			
R2map		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			
Mask		/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp			

Fit Results

Source:

F

View:

A...

3D view

Sanity Check

Voxel H

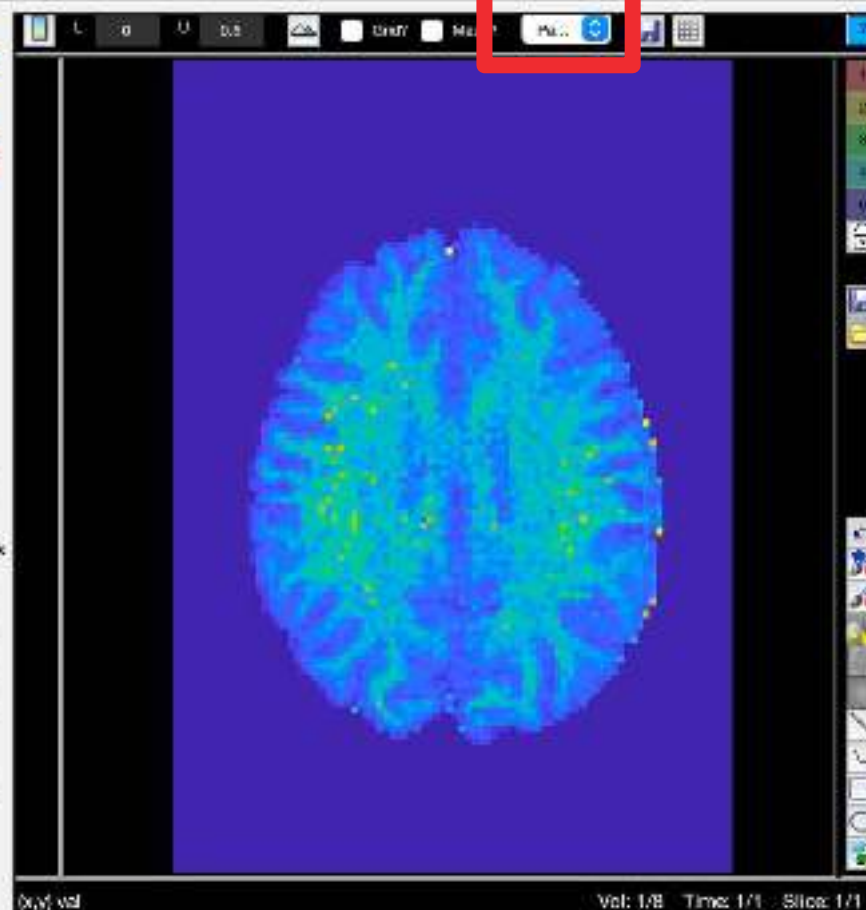
ROI H

Statistics

Histogram

Cursor

Select

A
L R
P

Current file: D:\Res..._hs.mat

[Visit qmt_appr documentation](#)

qmt_appr options

Protocol

-MTdata

	Angle	Offset
1	142	443
2	425	443
3	142	1085
4	425	1085
5	142	2732
6	425	2732
7	142	6262
8	425	6262
9	142	17235
10	425	17235

Add

Move up

Load

Remove

Move down

Create

TimingTask

Tmt (s)	0.0102	0.
Ts (s)		
Tp (s)		
Tr (s)		
TR (s)		

Plot Protocol

Fitting

Var	Fix	Start	Lower	Upper
F		0.000 1.000	-	0.020
k		80 1.000	-	100
m	☒	R1/R2	0.000	5
R1	☒	1	0.000	5
T2		0.000 0.020	0.000	0.020
T2'		1.000	0.000	5.000

Options

MT_Pulse

Shape:	gaussian
Sinc TRW:	4
Bandwidth:	200
Form factor (a):	0.00001666
# of MT pulses:	600

Model:

Line shape:

Fitting constraints

☒ Use R1map to constrain R1☐ Fix R1 = R11☐ Fix R1/T2'

R1/T2' = 0.053

Read pulse alpha: 7

Save

Load

Default

Current: Parameters: Parameters



Method:

qmt_sp...

qMR Data Fit

Fit data

Save Results

Load Results

qMR Simulator

Fit qMR Data

Data

Path data:		/Users/mathieuboudreau/neurosp	Study ID:	
MTdata		/Users/mathieuboudreau/neurosp/github/qMRLab/demo/qmt_sp		
R1map		/Users/mathieuboudreau/neurosp/github/qMRLab/demo/qmt_sp		
R1map		/Users/mathieuboudreau/neurosp/github/qMRLab/demo/qmt_sp		
R2map		/Users/mathieuboudreau/neurosp/github/qMRLab/demo/qmt_sp		
Mask		/Users/mathieuboudreau/neurosp/github/qMRLab/demo/qmt_sp		

Fit Results

Source:

F

View:

A

3D view

Sanity Check

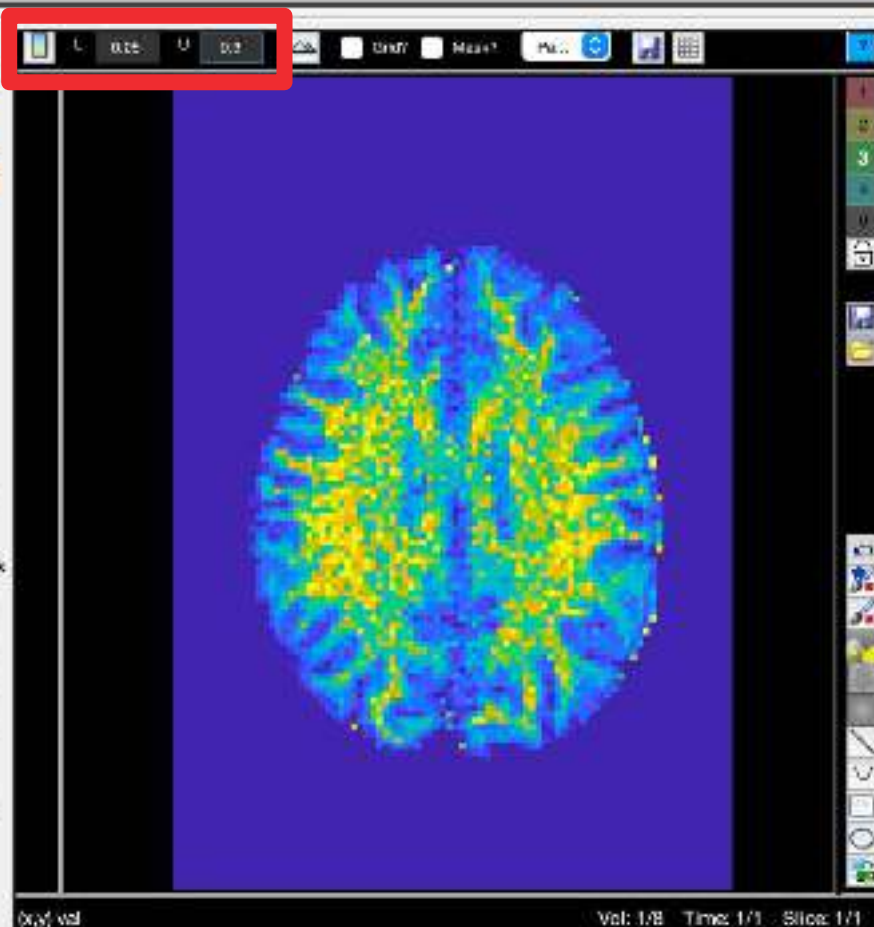
Voxel H

ROI H

Statistics

Histogram

Cursor

A
L R
P

Current file: fitRes_hb.mat

[View qmt_spr documentation](#)

qmt spr options

Protocol

-MTdata

	Angle	Offset
1	142	443
2	425	443
3	142	1085
4	425	1085
5	142	2732
6	425	2732
7	142	6362
8	425	6362
9	142	17235
10	425	17235

Add

Move up

Load

Remove

Move down

Create

TimingTask

Tmt (s)	0.0102	0.
Ts (s)		
Tp (s)		
Tr (s)		
TR (s)		

Fit Protocol

Fitting

Var	Fix	Start	Lower	Upper
F		0.000 1.000	-	0.020
k		80 1.000	-	100
m	☒	R1/R2	0.000	5
R1	☒	1	0.000	5
T2		0.000 0.020	0.000	0.020
T2'		1.000	0.000	0.000

Options

MT_Pulse

Shape: gaussian

Sinc TRW: 4

Bandwidth: 200

Fermi position (x): 0.00001656

of MT pulses: 600

Model

SkatPwRP

LineShape:

SuperLorentzian

Fitting constraints

☒ Use R1map to constrain R1☐ Fix R1 = R1'☐ Fix R1/T2'

R1/T2' = 0.055

Read pulse alpha:

7

Save

Load

Default

Current: Parameters: fitRes_hb.mat

qMRLab
v2.4.2

Method:
qmt_sp...
Open Options Panel

qMR Data Fit
Fit data
Save Results Load Results

qMR Simulator
Multi Voxel Distribution
Sensitivity Analysis
Single Voxel Curves

Fit qMRI Data

Path data: /Users/mathieuboudreau/neuropoly/ Study ID: Download example

MTdata

R1map

R1map

R2map

Mask

Fit Results

Source:
✓ F
kr
R1f
R1f
T2f
T2f
kr
norm

3D viewer

Sanity Check
Voxel H
ROI H
Statistics
Histogram

Cursor
Select
A
L R
P

(x,y) val

Vol: 1/8 Time: 1/1 Slice: 1/1

Current file: FResults.mat

OptionsGUI

qmt apgr options

Protocol

MTData

TimingTask

Fit Protocol

Fitting

Options

Model: SkatPwRP

LineShape: SuperLorentzian

Fitting constraints

Read pulse alpha: 7

Compute SFTask

Save Load Default Help

Current: Parameters: FitResults

	Angle	Offset
1	142	443
2	425	443
3	142	1085
4	425	1085
5	142	2732
6	425	2732
7	142	6362
8	425	6362
9	142	17235
10	425	17235

Var	Fix	Start	Lower	Upper
F		0.000000000	0.0000	
k		80.000000000	100	
m1	✓	R1MAP	0.0000	5
m1	✓	1	0.0000	5
T2f		0.0000	0.0000	0.0000
T2f		1.0000e-1	0.0000e-1	0.0000e-1

MT_Pulse

Shape: gaussian

Sinc TRW: 4

Bandwidth: 200

Fermi kernal (k): 0.000001656

of MT pulses: 600

TimingTask

Tmt (s): 0.0102

Ts (s):

Tp (s):

Tr (s):

TR (s):

Fitting constraints

Use R1map to constrain R1f

Fix R1f = R1f

Fix R1f/T2f

R1f/T2f = 0.053

Read pulse alpha: 7

Compute SFTask

Save Load Default Help

Current: Parameters: FitResults



Method:

qmt_sp...  

qMR Data Fit

Fit data

Save Results

Load Results

qMR Simulator

Multi Voxel Distribution

Sensitivity Analysis

Single Voxel Curve

Fit qMR Data

Data

Path data:		/Users/mathieuboudreau/neuropc Study ID:	
MTdata	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp	
R1map	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp	
B1map	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp	
B0map	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp	
Mask	 	/Users/mathieuboudreau/neuropoly/github/qMRLab/demo/qmt_sp	

Fit Results

Source:

T2* 

View:

A_ 

3D viewer

Sanity Check

Voxel H

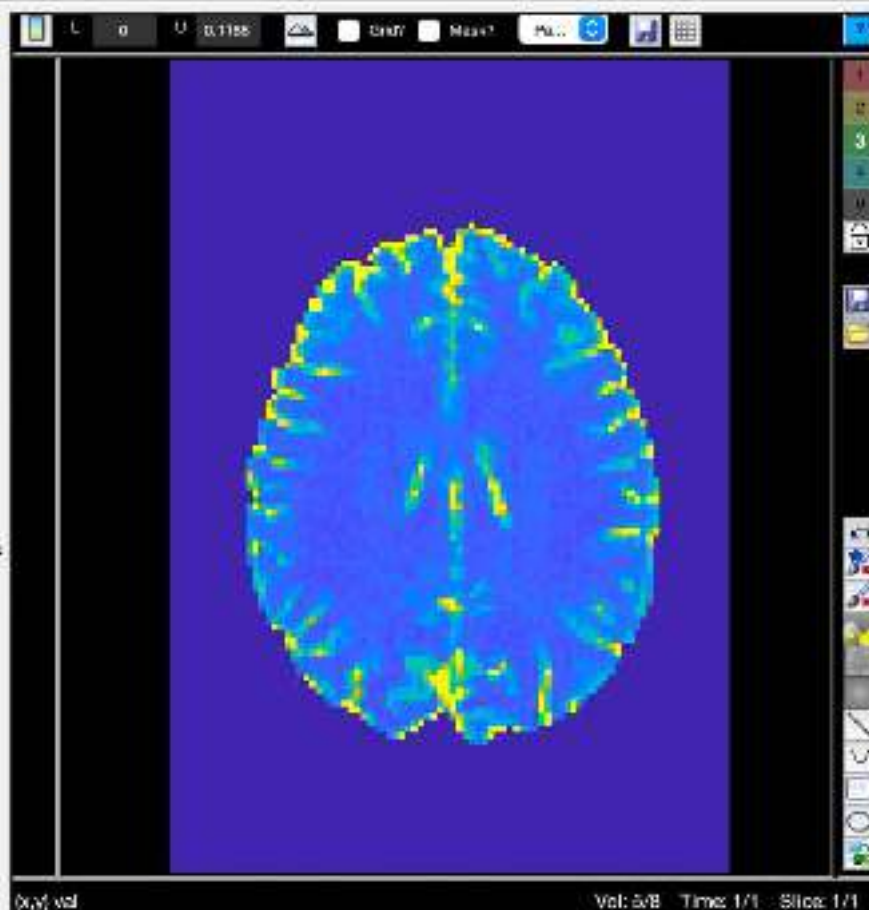
ROI H

Statistics

Histogram

Cursor

Select

A
L R
P

Current file: fitRes_hb.mat

[View qmt_spr documentation](#)

qmt spr options

Protocol

-MTdata

	Angle	Offset
1	142	443
2	425	443
3	142	1085
4	425	1085
5	142	2732
6	425	2732
7	142	6262
8	425	6262
9	142	17235
10	425	17235

Add

Move up

Load

Remove

Move down

Create

TimingTable

Tmt (s)	0.0102	0.
Ts (s)		
Tp (s)		
Tr (s)		
TR (s)		

Fit Protocol

Fitting

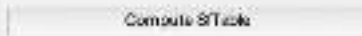
Var	Fix	Start	Lower	Upper
F		0.000 1.000	-	0.020
k		80 1.000	-	100
m	☒	R1/R2	0.000	5
R1	☒	1	0.000	5
T2*		0.000 0.020	0.000	0.020
T2		1.000	0.000	0.000

Options

MT_Pulse

Shape: Sinc TRW: Bandwidth: Form factor (d): # of MT pulses: Model: Line shape:

Fitting constraints

☒ Use R1map to constrain R1☐ Fix R1 = R1f☐ Fix R1/T2*R1/T2* = Read pulse alpha: 

Save

Load

Default

Help

Current: Parameters: fitRes_hb.mat

Other options:

command line interface (**CLI**)

scripting and **batch** demos

```

1 % This n-file has been automatically generated using qMRgenBatch(qmt_spgr)
2 % Command Line Interface (CLI) is well-suited for automatization
3 % purposes and Octave.
4 %
5 % Please execute this n-file section by section to get familiar with batch
6 % processing for qmt_spgr on CLI.
7 %
8 % Demo files are downloaded into qmt_spgr_data folder.
9 %
10 % Written by: Agah Karakuzu, 2017
11 % =====

```

qmt_spgr_batch.m

%% I- DESCRIPTION

```

14 qMRInfo('qmt_spgr'); % Describe the model
15

```

%% II- MODEL PARAMETERS

```

17 %%      a- create object
18

```

```

19
20 Model = qmt_spgr;
21

```

```

22 %%      b- modify options
23

```

```

23 %      |- This section will pop-up the options GUI. Close window to continue.
24 %      |- Octave is not GUI compatible. Modify Model.options directly.
25

```

```

26 Model = Custom_OptionsGUI(Model); % You need to close GUI to move on.
27

```

%% III- FIT EXPERIMENTAL DATASET

```

28 %%      a- set protocols via gui
29

```

```

30 Angle = [142.0000; 426.0000; 142.0000; 426.0000; 142.0000; 426.0000; 142.0000; 426.0000; 142.0000; 426.0000];
31 % Angle is a vector of [10X1]

```

```

32 Offset = [443.0000; 443.0000; 1088.0000; 1088.0000; 2732.0000; 2732.0000; 6862.0000; 6862.0000; 17235.0000; 17235.0000];
33 % Offset is a vector of [10X1]

```

```

34 Model.Prot.MTdata.Mat = [ Angle Offset];
35

```

```

36 Tn1 = 0.8102;
37 Ts = 0.003;
38 Tp = 0.0018;
39 Tr = 0.01;
40 TR = 0.025;

```

```

41 Model.Prot.TimingTable.Mat = [ Tn1 Ts Tp Tr TR ];
42

```

```

43 %%      b- load experimental data
44

```

```

44 %      |- qmt_spgr object needs 5 data input(s) to be assigned:
45 %      |- MTdata
46 %      |- Rmap
47 %      |- Bmap
48 %      |- B0map
49 %      |- Mask

```

```

50
51 data = struct();
52

```

Recent work using qMRLab: ISMRM T₁ Reproducibility Challenge

Received: 17 October 2023 | Revised: 21 March 2024 | Accepted: 23 March 2024

DOI: 10.1002/mrm.30111

TECHNICAL NOTE

Magnetic Resonance in Medicine

Repeat it without me: Crowdsourcing the T₁ mapping common ground via the ISMRM reproducibility challenge

Mathieu Boudreau^{1,2} | Agah Karakuzu¹ | Julien Cohen-Adad^{1,2,3,4,5} |
Ecem Bozkurt⁶ | Madeline Carr^{7,8} | Marco Castellaro⁹ | Luis Concha¹⁰ |
Mariya Doneva¹¹ | Seraina A. Dual¹² | Alex Ensworth^{13,14} | Alexandru Foias¹ |
Véronique Fortier^{15,16} | Refaat E. Gabr¹⁷ | Guillaume Gilbert¹⁸ |
Carri K. Glide-Hurst¹⁹ | Matthew Grech-Sollars^{20,21} | Siyuan Hu²² |
Oscar Jalnefjord^{23,24} | Jorge Jovicich²⁵ | Kübra Keskin⁶ | Peter Koken¹¹ |
Anastasia Kolokotronis^{13,26} | Simran Kukran^{27,28} | Nam G. Lee⁶ | Ives R. Levesque^{13,29} |
Bochao Li⁶ | Dan Ma²² | Burkhard Mädler³⁰ | Nyasha G. Maforo^{31,32} |
Jamie Near^{33,34} | Erick Pasaye¹⁰ | Alonso Ramirez-Manzanares³⁵ | Ben Statton³⁶ |
Christian Stehning³⁰ | Stefano Tambalo²⁵ | Ye Tian⁶ | Chenyang Wang³⁷ |
Kilian Weiss³⁰ | Niloufar Zakariaci³⁸ | Shuo Zhang³⁰ | Ziwei Zhao⁶ |
Nikola Stikov^{1,2,39} | on behalf of the ISMRM Reproducible Research Study Group and
the ISMRM Quantitative MR Study Group

<https://doi.org/10.1002/mrm.30111>

Dashboard





Paper is not enough: Crowdsourcing the T_1 mapping common ground via the ISMRM reproducibility challenge

*Mathieu Boudreau^{1,2}, *Agah Karakuzu¹, Julien Cohen-Adad^{1,3,4,5}, Ecem Bozkurt⁶, Madeline Carr^{7,8}, Marco Castellaro⁹, Luis Concha¹⁰, Mariya Doneva¹¹, Seraina A. Dual¹², Alex Ensworth^{13,14}, Alexandru Foias¹, Véronique Fortier^{15,16}, Refaat E. Gabr¹⁷, Guillaume Gilbert¹⁸, Carri K. Glide-Hurst¹⁹, Matthew Grech-Sollars^{20,21}, Siyuan Hu²², Oscar Jalnefjord^{23,24}, Jorge Jovicich²⁵, Kübra Keskin⁶, Peter Koken¹¹, Anastasia Kolokotronis^{13,26}, Simran Kukran^{27,28}, Nam. G. Lee⁶, Ives R. Levesque^{13,29}, Bochao Li⁶, Dan Ma²², Burkhard Mädler³⁰, Nyasha Maforo^{31,32}, Jamie Near^{33,34}, Erick Pasaye¹⁰, Alonso Ramirez-Manzanares³⁵, Ben Statton³⁶, Christian Stehning³⁰, Stefano Tambalo²⁵, Ye Tian⁶, Chenyang Wang³⁷, Killian Weiss³⁰, Niloufar Zakariaei³⁸, Shuo Zhang³⁹, Ziwei Zhao⁶, Nikola Stikov^{1,2,39}

*Authors MB and AK contributed equally to this work

¹NeuroPoly Lab, Polytechnique Montréal, Montreal, Quebec, Canada, ²Montreal Heart Institute, Montreal, Quebec, Canada, ³Unité de Neuroimagerie Fonctionnelle (UNF), Centre de recherche de l'Institut Universitaire de Gériatrie de Montréal (CRJUGM), Montreal, Quebec, Canada, ⁴Mila - Quebec AI Institute, Montreal, QC, Canada, ⁵Centre de recherche du CHU Sainte-Justine, Université de Montréal, Montreal, QC, Canada, ⁶Magnetic Resonance Engineering Laboratory (MREL), University of Southern California, Los Angeles, California, USA, ⁷Medical Physics, Ingham Institute for Applied Medical Research, Liverpool, Australia, ⁸Department of Medical Physics, Liverpool and Macarthur Cancer Therapy Centres, Liverpool, Australia, ⁹Department of Information Engineering, University of Padova, Padova, Italy, ¹⁰Institute of Neurobiology, Universidad Nacional Autónoma de México Campus Juriquilla, Querétaro, México, ¹¹Philips Research Hamburg, Germany, ¹²Department of Radiology, Stanford University, Stanford, California, United States, ¹³Medical Physics Unit, McGill University, Montreal, Canada, ¹⁴University of British Columbia, Vancouver, Canada, ¹⁵Department of Medical Imaging, McGill University Health Centre, Montreal, Quebec, Canada, ¹⁶Department of Radiology, McGill University, Montreal, Quebec, Canada, ¹⁷Department of Diagnostic and Interventional Imaging, University of Texas Health Science Center at Houston, McGovern Medical School, Houston, Texas, USA, ¹⁸MR Clinical Science, Philips Canada, Mississauga, Ontario, Canada, ¹⁹Department of Human Oncology, University of Wisconsin-Madison, Madison, Wisconsin, USA, ²⁰Centre for Medical Image Computing, Department of Computer Science, University College London, London, UK, ²¹Lynholm Department of Neuroimaging, National Hospital for Neurology and Neurosurgery, University College London Hospitals NHS Foundation Trust, London, UK, ²²Department of Biomedical Engineering, Case Western Reserve University, Cleveland, Ohio, USA, ²³Department of Medical Radiation Sciences, Institute of Clinical Sciences, Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden, ²⁴Biomedical Engineering, Sahlgrenska University Hospital, Gothenburg, Sweden, ²⁵Center for Mind/Brain Sciences, University of Trento, Italy, ²⁶Hôpital Maisonneuve-Rosemont, Montreal, Canada, ²⁷Neuroengineering, Imperial College London, UK, ²⁸Radiotherapy and Imaging, Institute of Cancer Research, Imperial College London, UK, ²⁹Research Institute of the McGill University Health Centre, Montreal, Canada, ³⁰Clinical Science, Philips Healthcare, Germany, ³¹Department of Radiological Sciences, University of California Los Angeles, Los Angeles, CA, USA, ³²Physics and Biology in Medicine IDP, University of California Los Angeles, Los Angeles, CA, USA, ³³Douglas Brain Imaging Centre, Montreal, Canada, ³⁴Sunnybrook Research Institute, Toronto, Canada, ³⁵Computer Science Department, Centro de Investigación en Matemáticas, A.C., Guanajuato, México, ³⁶Medical Research Council, London Institute of Medical Sciences, Imperial College London, London, United Kingdom, ³⁷Department of Radiation Oncology - CNS Service, The University of Texas MD Anderson Cancer Center, Texas, USA, ³⁸Department of Biomedical Engineering, University of British Columbia, British Columbia, Canada, ³⁹Center for Advanced Interdisciplinary Research, St. Cyril and Methodius University, Skopje, North Macedonia

Abstract



Paper is not enough: Crowdsourcing the T_1 mapping common ground via the ISMRM reproducibility challenge

*Mathieu Boudreau^{1,2}, *Agah Karakuzu¹, Julien Cohen-Adad^{1,3,4,5}, Ecem Bozkurt⁶, Madeline Carr^{7,8}, Marco Castellaro⁹, Luis Concha¹⁰, Mariya Doneva¹¹, Seraina A. Dual¹², Alex Ensworth^{13,14}, Alexandru Foias¹, Véronique Fortier^{15,16}, Refaat E. Gabr¹⁷, Guillaume Gilbert¹⁸, Carri K. Glide-Hurst¹⁹, Matthew Grech-Sollars^{20,21}, Siyuan Hu²², Oscar Jalnefjord^{23,24}, Jorge Jovicich²⁵, Kübra Keskin⁶, Peter Koken¹¹, Anastasia Kolokotronis^{13,26}, Simran Kukran^{27,28}, Nam. G. Lee⁶, Ives R. Levesque^{13,29}, Bochao Li⁶, Dan Ma²², Burkhard Mädler³⁰, Nyasha Maforo^{31,32}, Jamie Near^{33,34}, Erick Pasaye¹⁰, Alonso Ramirez-Manzanares³⁵, Ben Statton³⁶, Christian Stehning³⁰, Stefano Tambalo²⁵, Ye Tian⁶, Chenyang Wang³⁷, Kilian Weiss³⁰, Niloufar Zakariaei³⁸, Shuo Zhang³⁹, Ziwei Zhao⁶, Nikola Stikov^{1,2,39}

* Authors MB and AK contributed equally to this work

¹NeuroPoly Lab, Polytechnique Montréal, Montreal, Quebec, Canada, ²Montreal Heart Institute, Montreal, Quebec, Canada, ³Unité de Neuroimagerie Fonctionnelle (UNF), Centre de recherche de l'Institut Universitaire de Gériatrie de Montréal (CRIUGM), Montreal, Quebec, Canada, ⁴Mila - Quebec AI Institute, Montreal, QC, Canada, ⁵Centre de recherche du CHU Sainte-Justine, Université de Montréal, Montreal, QC, Canada, ⁶Magnetic Resonance Engineering Laboratory (MREL), University of Southern California, Los Angeles, California, USA, ⁷Medical Physics, Ingham Institute for Applied Medical Research, Liverpool, Australia, ⁸Department of Medical Physics, Liverpool and Macarthur Cancer Therapy Centres, Liverpool, Australia, ⁹Department of Information Engineering, University of Padova, Padova, Italy, ¹⁰Institute of Neurobiology, Universidad Nacional Autónoma de México Campus Juriquilla, Querétaro, México, ¹¹Philips Research Hamburg, Germany, ¹²Department of Radiology, Stanford University, Stanford, California, United States, ¹³Medical Physics Unit, McGill University, Montreal, Canada, ¹⁴University of British Columbia, Vancouver, Canada, ¹⁵Department of Medical Imaging, McGill University Health Centre, Montreal, Quebec, Canada, ¹⁶Department of Radiology, McGill University, Montreal, Quebec, Canada, ¹⁷Department of Diagnostic and Interventional Imaging, University of Texas Health Science Center at Houston, McGovern Medical School, Houston, Texas, USA, ¹⁸MR Clinical Science, Philips Canada, Mississauga, Ontario, Canada, ¹⁹Department of Human Oncology, University of Wisconsin-Madison, Madison, Wisconsin, USA, ²⁰Centre for Medical Image Computing, Department of Computer Science, University College London, London, UK, ²¹Lynholm Department of Neuroimaging, National Hospital for Neurology and Neurosurgery, University College London Hospitals NHS Foundation Trust, London, UK, ²²Department of Biomedical Engineering, Case Western Reserve University, Cleveland, Ohio, USA, ²³Department of Medical Radiation Sciences, Institute of Clinical Sciences, Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden, ²⁴Biomedical Engineering, Sahlgrenska University Hospital, Gothenburg, Sweden, ²⁵Center for Mind/Brain Sciences, University of Trento, Italy, ²⁶Hôpital Maisonneuve-Rosemont, Montreal, Canada, ²⁷Bioengineering, Imperial College London, UK, ²⁸Radiation Therapy and Imaging, Institute of Cancer Research, Imperial College London, UK, ²⁹Research Institute of the McGill University Health Centre, Montreal, Canada, ³⁰Clinical Science, Philips Healthcare, Germany, ³¹Department of Radiological Sciences, University of California Los Angeles, Los Angeles, CA, USA, ³²Physics and Biology in Medicine IDP, University of California Los Angeles, Los Angeles, CA, USA, ³³Douglas Brain Imaging Centre, Montreal, Canada, ³⁴Sunnybrook Research Institute, Toronto, Canada, ³⁵Computer Science Department, Centro de Investigación en Matemáticas, A.C., Guanajuato, México, ³⁶Medical Research Council, London Institute of Medical Sciences, Imperial College London, London, United Kingdom, ³⁷Department of Radiation Oncology - CNS Service, The University of Texas MD Anderson Cancer Center, Texas, USA, ³⁸Department of Biomedical Engineering, University of British Columbia, British Columbia, Canada, ³⁹Center for Advanced Interdisciplinary Research, Sa. Cyril and Methodius University, Skopje, North Macedonia

What is MRM Highlights?

**MAGNETIC RESONANCE
IN MEDICINE**

ISMIRM

ONE
COMMUNITY
FOR CLINICIANS
AND SCIENTISTS



<https://blog.ismrm.org/category/highlights/>

Three Pillars of Highlights



Monthly Interviews



Annual Magazine



ISMRM Afterparty

<https://blog.ismrm.org/category/highlights/>

Q&A Interviews

<https://blog.ismrm.org/category/highlights/>



**Q&A with Berk Silemek
and Lukas Winter**



**Q&A with Hannah
Scholten and Herbert
Köstler**



**Q&A with Moritz
Blumenthal and Martin
Uecker**



**Q&A with Ayse Sila
Dokumaci and David
Carmichael**



**Q&A with Julien Songeon
and Antoine Klauser**



**Q&A with Layla Tabea
Riemann and Ariane
Fillmer**



**Q&A with Agah Karakuzu
and Nikola Stikov**



**Q&A with Yaël Balbastre
and Martina F. Callaghan**



**Q&A with Joseph Woods
and Divya Bolar**



**Q&A with Kyle Gilbert and
Corey Baron**



**Q&A with Jakob Assländer
and Daniel Sodickson**



**Q&A with Jianpan Huang
and Kannie WY Chan**



**Q&A with Antonio Tristán-
Vega and Santiago Aja-
Fernández**



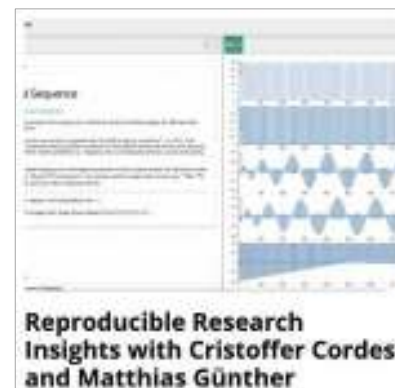
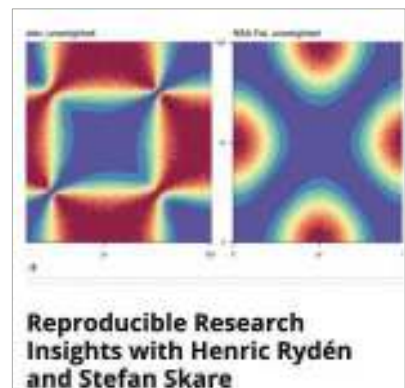
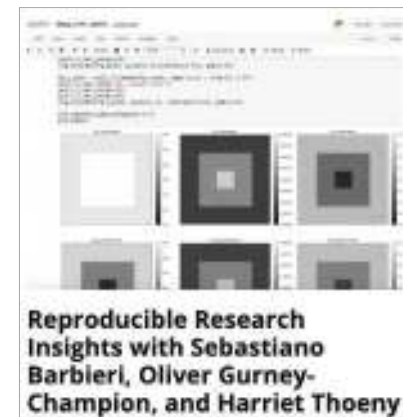
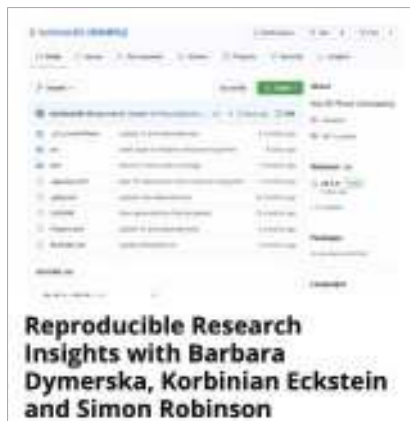
**Q&A with Aaron T. Hess
and Mark Chiew**



**Q&A with Christopher
Rowley and Christine
Tardif**

Reproducible Research Insights

<https://blog.ismrm.org/category/highlights/>



Acknowledgements

qMRLab contributors

Agah Karakuzu

Alexandre D'Astous

Benjamin De Leneer

Bruce Pike

Eva Alonso-Ortis

Gabriel Berestovoy

Ian Gagnon

Ilana Leppert

Ives Levesque

Harris Nami

Juan Velazquez-Reyes

Jean-François Cabana

John Sled

Julien Cohen-Adad

Nadia Blostein

Manh-Tung Vuong

Matteo Mancini

Nikola Stikov

Pascale Beliveau

Samuelle St-Onge

Tanguy Duval

Tommy Boshkovski

Ye Gu

Zaki Ahmed

NeuroPoly Lab

