# Introduction

## 1 Key features
- 1.1 Data simulator ............................................. 3
- 1.2 Data fitting and visualization ............................. 3

## 2 Methods available
- 2.1 FieldMaps ................................................. 5
- 2.2 T2\_relaxometry ........................................... 5
- 2.3 Processing ............................................... 5
- 2.4 T1\_relaxometry ........................................... 5
- 2.5 Magnetization\_transfer .................................. 6
- 2.6 Diffusion ................................................ 6
- 2.7 QSM ..................................................... 7
- 2.8 UnderDevelopment ....................................... 7
- 2.9 Noise ................................................... 7

## 3 How to install
- 3.1 Citation ................................................. 9
- 3.2 Dependencies ............................................ 9
- 3.3 Zip Download Instructions ................................ 9
- 3.4 Command-Line Instructions .............................. 10
- 3.5 Tests .................................................. 10

## 4 Beginners example with GUI
- 4.1 1. Open matlab .......................................... 11
- 4.2 2. Run startup ........................................... 11
- 4.3 3. Download example data ............................... 11
- 4.4 4. Launch the GUI ........................................ 12
- 4.5 5. Model Selection ...................................... 12
- 4.6 6. Load the data ......................................... 12
- 4.7 7. View the data ......................................... 13
- 4.8 8. Set up the protocol ................................. 13
- 4.9 9. View the data fit in 1 voxel ......................... 13
- 4.10 10. Fit the whole dataset ............................ 13

## 5 Beginners example with batch
- 5.1 1. Open matlab and setup path ....................... 17
- 5.2 2. Generate a batch example ......................... 17
Welcome to qMRLab, a software for quantitative MR image analysis. Please take a look at the following for an overview of what qMRLab can do for you:
qMRLab is an open-source software for quantitative MR image analysis. The main goal is to provide the community with an intuitive tool for data fitting, plotting, simulation and protocol optimization for a myriad of different quantitative models. The modularity of the implementation makes it easy to add any additional modules and we encourage everyone to contribute their favorite recipe for qMR!

1.1 Data simulator

The simulation interface allows end users to easily simulate qMR data and evaluate how well these models perform under known parameters input, determine the most appropriate acquisition protocol and evaluate how fitting constraints impact the results.

1.2 Data fitting and visualization

The data fitting provides a simple interface to import real-world qMR data, fit them using the selected fitting procedure, and visualize the resulting parameter maps. More advanced users could also use the command line tools used in the background by the GUI to include data fitting in their analysis scripts.

Here’s a short video to get you acquainted with the package:
CHAPTER 2

Methods available

2.1 FieldMaps

2.1.1 b1_dam map: Double-Angle Method for B1+ mapping

2.1.2 b0_dem map: Dual Echo Method for B0 mapping

2.2 T2_relaxometry

2.2.1 mwf: Myelin Water Fraction from Multi-Exponential T2w data

2.3 Processing

2.3.1 filter_map: Applies spatial filtering (2D or 3D)
2.4 T1_relaxometry

2.4.1 vfa_t1: Compute a T1 map using Variable Flip Angle

2.4.2 inversion_recovery: Compute a T1 map using Inversion Recovery data

2.5 Magnetization_transfer

2.5.1 qmt_bssfp : qMT using Balanced Steady State Free Precession acquisition

2.5.2 qmt_spgr: quantitative Magnetization Transfer (qMT) using Spoiled Gradient Echo (or FLASH)

2.5.3 mt_sat : Correction of Magnetization transfer for RF inhomogeneities and T1

2.5.4 mt_ratio : Magnetization transfer ratio (MTR)

2.5.5 qmt_sirfse: qMT using Inversion Recovery Fast Spin Echo acquisition

2.6 Diffusion

2.6.1 dti: Compute a tensor from diffusion data

2.6.2 noddi: Neurite Orientation Dispersion and Density Imaging
2.6.3 charmed: Composite Hindered and Restricted Model for Diffusion

2.7 QSM

2.7.1 qsm_sb: Fast quantitative susceptibility mapping

2.8 UnderDevelopment

- Name your Model
- mtv: Macromolecular Tissue Volume

2.9 Noise

2.9.1 denoising_mppca: 4d image denoising and noise map estimation by exploiting

2.9.2 noise_level: Noise histogram fitting within a noise mask
CHAPTER 3

How to install

3.1 Citation

If you use qMRLab in your work, please cite:


Please also cite the reference for the particular module you are using (specified in each model’s page).

3.2 Dependencies

- MATLAB_R2014b or later with Optimization Toolbox

or * Octave 4.2.1 or later

3.3 Zip Download Instructions

The latest stable version of qMRLab can be downloaded freely here.

- Extract the downloaded file to the directory you want to install qMRLab.
- Open MATLAB, got to the qMRLab folder and run startup.
- To start a qMRLab session, run qMRLab.
3.4 Command-Line Instructions

If you have git available on a command-line interface (e.g. Terminal on Mac OSX, Git Shell on Windows), the installation can be completed using a few quick commands.

- In the command-line interface, navigate (cd) to the directory that you want to install qMRLab
- Clone the directory:

  ```bash
  git clone https://github.com/neuropoly/qMRLab.git
  ```

- Open MATLAB, got to the qMRLab folder and run `startup`.
- To start a qMRLab session, run `qMRLab`.

3.5 Tests

After installing the software, we recommend you evaluate all the test cases for the software.

To run all tests, from MATLAB or Octave (assuming you are already in the qMRLab directory), execute the following command:

```bash
cd Test/MoxUnitCompatible/
```

and run the following command:

```bash
moxunit_runitests -recursive
```
Beginners example with GUI

This will guide you step by step in processing a sample dataset with the user interface.

4.1 1. Open matlab

4.2 2. Run startup

Go to qMRLab installation folder (note: replace “PATH_QMRLAB” with the actual path)

```
cd PATH_QMRLAB
```

Setup your path (note: you only need to do it once)

```
startup
```

4.3 3. Download example data

In this case we will be working with Variable Flip Angle Data to compute a T1map. The main input data is stored as a 4D volume, where the 4th dimension is different flip angles. For example, in this test dataset, 1 slice at 2 different flip angles were acquired: volume 1 was FA=3degrees and volumes 2 was FA=20degrees, such that VFAData.nii.gz is 128x128x1x2. The other optional inputs are a Mask.nii.gz and a B1Map.nii.gz.

Run this in matlab to get the data:

```
Model=vfa_t1;
downloadData(Model,[])
```

When prompted, select a folder where you would like to put the sample data
4.4 4. Launch the GUI

Type this is matlab to launch the main GUI:

qMRLab

4.5 5. Model Selection

On the top left-hand side pull-down menu, select the method we are going to use, in this case,\textit{vfa}_t1 (\textit{T1}_{relaxometry}): 

At any time, you may use the \textit{Help} button in the \textit{Options} panel to get a description of the model:

For the list of available models, please check \textit{Methods available}.

4.6 6. Load the data

Load the raw data in qMRLab by selecting \textit{Browse} next to \textit{Work Dir}. Select the folder where you have previously saved the sample data (this will load all the data into the correct locations automatically):

For a more detailed description of what the input data should look like, please refer to \textit{4.1 Data format}.
4.7 7. View the data

You can look at your data by clicking View next to the name of the file:

You can browse through slices or volumes of the data files by using arrows and mouse controls. Please refer to 3. Data Viewer.

4.8 8. Set up the protocol

For this dataset, the protocol will be set up by default with the flip angles and TRs:

For your own acquisition, you will have to use an external txt file to load the parameters, please refer to 6.1 Protocol.

4.9 9. View the data fit in 1 voxel

Before fitting the whole volume, it’s a good idea to take a look at your data and how it fits the model. Here, we can visualize the fit in 1 voxel at a time. In the Cursor section, press Select. Then select a voxel in the image and the press View data fit:

A new window will pop-up with the results of the fit in that voxel:

4.10 10. Fit the whole dataset

We can now fit the whole volume by pressing the large Fit Data button.
Chapter 4. Beginners example with GUI
A wait bar will appear while the data is being processed and will automatically when done. From the pull-down menu to the left of the image, it's possible to select the output you would like to view. For example, the T1map:

For more information and to explore other functionality such as the simulations, please visit *Graphical User Interface Usage*.
Beginners example with batch

This will guide you through the steps to create a script that can be used to process sample data. The generated example script can then be used as a guideline to analyze your own data.

5.1 1. Open matlab and setup path

Open Matlab then go to qMRLab installation folder (note: replace “PATH_QMRLAB” with the actual path)

```
cd PATH_QMRLAB
```

Setup your path (note: you only need to do it once)

```
startup
```

5.2 2. Generate a batch example

To get familiar with the command-line usage, you can automatically generate an example (with sample data) for your model of choice. For example, for inversion_recovery type:

```
model=inversion_recovery; % create an instance of the model
qMRgenBatch(model)
```

When prompted, select the folder where you want to download the data and save the batch example file.

5.3 3. Run the batch

You can run the example directly:
or take a look at the sections independently:

```plaintext
edit inversion_recovery_batch
```

Please refer to `inversion_recovery: Compute a TI map using Inversion Recovery data` to see a batch example and the expected output.

Please refer to `Command-Line Usage` for a more detailed description of the available functions
Usage Guidelines

6.1 Graphical User Interface Usage

This section describes the various features and functionality of the user interface.

6.1.1 1. Startup

Launch matlab from the qMRLab folder. Then load the default setup by typing:

```
startup
```

Then open the GUI by typing:

```
qMRLab
```

6.1.2 2. Interface

When you first launch qMRLab, you will be presented with a blank interface. The interface consists of three columns, or panels. On the left, you have the **Menu** panel, in the center you have the **Main panel**, and on the right, in a separate floating window, you have the **Options** panel.

2.1 Menu Panel

The **Menu panel** is where you can choose the task you want to perform. It is divided in three sections: **Method**, **qMR Data Fit** and **qMR Data Simulator**
2.1.1 Method

At the top, you will find a drop-down menu where you can choose the MR acquisition method that you want to be working with. An updated list of the available methods is here: Methods available

Note that the Main and Options panel will update to the appropriate window according to your selection. If you plan to be working mainly with a particular method, select it from the drop-down menu first, and the click on the Set Default button next to it. Next time you open qMRLab, your preferred method will be selected by default.

Clicking on the Open Options Panel below the method drop-down menu will open the Options panel window and set its position on the right side of the Main panel. This is useful to bring back the Options panel window to the front if it’s hidden behind another window, to reset its position if you have resized the windows, or to reopen it in case you closed it.

2.1.2 qMR Data Fit

Click on the big Fit Data button only when you have selected your data files, set up your protocol and fitting options and are ready to begin the fitting process, which, depending on the size of your data and the method, can take from a few minutes to a couple of hours. The Save Results button will prompt you to save a .mat file with the results of your data fit. Load Results will load previously saved results and display them. Refer to this section 4. Data Fitting for more information.
2.1.3 qMR Data Simulator

The buttons of this menu allow you to choose between different data simulation mode. All Methods that involve a data fitting procedure present at least the following simulations: Single Voxel Curve, Sensitivity Analysis and Multi Voxel Distribution. Clicking on any one of these buttons will bring the corresponding interface in a floating window. When any of these interfaces are opened, clicking on the update button will launch the simulation using the current options (defined in the Options panel). The Save Results button will prompt you to save a .mat file with the current simulation results. Load Results will load previously saved simulation results and display them in the appropriate panel. Refer to this section 5. Simulation for more information.

Single Voxel Curve

The Single Voxel Curve panel is a simple interface to simulate MR data from a single voxel, using the defined MR parameters and protocol. It is the fastest way to evaluate various acquisition protocols, the performance of the model and fitting options. Refer to section 5.1. Single Voxel Curve for more information.

Sensitivity Analysis

The Sensitivity Analysis simulation allows you to systematically vary one MR parameter, over a defined range and number of points, while keeping the others fixed. For each simulated data point, noise is added with a given SNR, and the fit is run multiple times while adding Gaussian noise. This allows you to evaluate the variance of the fit at each point. When the simulation is done, a plot shows any variable input parameters as the independent variable, as well as the mean values and variance of any fitted parameters. Refer to section 5.2. Sensitivity Analysis for more information.

Multi Voxel Distribution

The Multi Voxel Distribution is a tool to simulate any number of voxels, where any parameters combination are allowed to be varied simultaneously. You can choose how many voxels to simulate and which parameters are to be normally distributed, with its mean value and variance. The results can be displayed in a number of ways such as distribution histograms, scatter plots of input vs fitted parameters, error histograms, etc. Refer to section 5.3. Multi Voxel Distribution for more information.

2.2 Main Panel

The Main panel is where you can load your data files for fitting and for viewing the resulting parameters maps. This panel changes correspondingly to the Method selected in the Menu panel.

2.3 Options Panel

This is where you can set up all the parameters that are related to the simulation, the fitting and the protocol. The Options panel is displayed in a separate window than the Menu panel or Main panel. This is because each qMR acquisition method has its own particular options, and this window needs to be changed correspondingly. It can also be closed at any time, if it is not currently needed, to provide for a simpler interface. The Options panel consists of three sub-panels: ‘Protocol’, ‘Fitting’, and ‘Options’. At the bottom of all these sub-panels you will find buttons to Reset the changes you made, Save the current settings as a .mat file, Load a .mat file of settings, or go back to the Default settings. Refer to section 6. Options Panel for more information.
2.3.1 Protocol

Here you define the acquisition protocol that you wish to use for simulation, or in the case of data fitting, the protocol you used to acquire the data. See 6.1 Protocol for more information.

2.3.2 Fitting

This is where you set up your fitting options. The fit parameters table lists all the variables that are available for fitting in the current method, a tick box to select which variables are to be held fixed, a starting value and lower/upper bounds. Note that some methods do not have fitting procedures, this table is empty in this case. Depending on the method, additional options may be available. See 6.2. Fitting for more information.

2.3.3 Options

This is where you set up all the options related to the simulations. Depending on the qMR method, different sets of options are available (e.g. the fitting procedure, assumptions of the model, etc). More info in 6.3. Options.

6.1.3 3. Data Viewer

The viewer allows you to navigate through your 5-D dataset easily using arrows:

Use mouse controls to display your volume:
- Middle (shift+) Click and drag  Zoom in/out
- Left Click and drag  Contrast/Brightness
- Right (ctrl+) Click and drag  Pan
- Scroll wheel  Change slice

The viewer provides ROI tools to create and modify a multi-label mask that is overlaid on the image. The Mask in the file browser is loaded automatically, you can delete it using right click on the button label 1. The mask can be hidden/shown using the checkbox on the top (or use spacebar)... make sure the mask is toggle on when you draw it! The mask can have 5 different labels (1-5). Select the label on which you want to operate. One voxel can be attributed only one label (no overlaps between labels). The locker button prevents any modification and overwrite to labels that are not selected. ROI tools such as square or polygon can be converted to mask (right click on an ROI object) and conversely (mask2poly button). Statistics on each label (e.g. volume, mean intensity) can be obtained with mouse over the label number.

Brush tool controls:
- Middle click and drag  Change brush diameter
- Right click  erase
- double click  (smart brush only) Toggle between bright or dark segmentation

Polygon tool controls:
- Click on a line  add a button
- Double click on a point  toggle between a line and a curve
Middle click on a point  delete this intermediary point

6.1.4 4. Data Fitting

qMRLab provides a convenient interface to fit your data and visualize the parameters maps. To ensure that the results are successful, you'll need to define the appropriate protocol, as it was used for data acquisition, and to format your qMR data in the way qMRLab expects it to be.

4.1 Data format

Currently supported file types are .mat and .nii files. Your files should respect the following:

- For .mat files, the name of the file can be anything, but the array it contains should be named appropriately. The list of input names is case sensitive and is specified at the top of the Data dialog box. For example, for a qMT SPGR experiment, MTdata (for the actual MT data array) or R1map/B1map/B0map/Mask respectively for a R1/B1/B0 or Mask file.

![Data format example](image)

Fig. 2: Example of list of inputs for qMT SPGR experiment

- Each model will expect a different format of inputs, but in general, for single slice (2D) imaging, the main data is a 3D array with size \([nx, ny, ndata]\), where \(nx/ny\) is the number of voxels in the x/y direction, and ndata is the number of data points for each voxel. For volume imaging (3D), data is a 4D array with size \([nx, ny, nz, ndata]\), where \(nx/ny/ndata\) are as above, and \(nz\) is the number of voxels (or slices) in the z direction (e.g. in this example MTdata would have several datapoints per voxel).

- Other files (e.g. in this example R1map/B1map/B0map/Mask) are formatted as \([nx, ny, nz]\).

For a more detailed description of the format required for each input, type this in the matlab window:

```matlab
help Modelname
```

where Modelname is name of the available models (e.g. in this example help SPGR). Alternatively, in the Options panel, you can press on the Help button.

4.2 Fitting Procedure

4.2.1 Single voxel

This is useful when you want to preview the fit of a single voxel (note this option is only available on voxelwise computations)
1. Select the acquisition method of your data using the ‘Method’ drop-down menu in the Menu panel.
2. In the Menu panel, in the ‘Fit qMR data’ panel, enter your study ID in the ‘Study ID’ box (optional).
3. Load your data by clicking the browse button beside the ‘Data:’ line, or enter the full file path to it in the textbox.
4. You can view any of these maps by clicking its View button.

![Image of the Fit qMRI Data interface](image)

Fig. 3: Example of viewing option, in this case R1map used for qMT SPGR

5. Define or load the appropriate protocol in the Options panel (see 6.1 Protocol for details).
6. Define your fitting options in the Options panel (see 6.2. Fitting for details).
7. You can preview the fitted curve for a selected voxel by using the View Data Fit button. Make sure a dataset is loaded by clicking View beside the data file field.
8. Click Select button in the ‘Cursor’ section to activate voxel selection mode, select a voxel to preview and click View Data Fit. You can now see the fitted curve and the parameters computed for that voxel.
4.2.2 Whole dataset

Follow steps 1-6 above, then

7. In the Menu panel, click on **Fit data** to start the fitting process.

8. Once the fitting is done, a temporary file will be saved in the ‘FitResults’ subfolder of the current working directory. You can save the current fit results elsewhere by clicking **Save Results** in the ‘qMR data fit’ section of the Menu panel.

9. Use the controls in the ‘Fit Results’ section to visualize the results (see 4.3 Viewing the fit results for details).

4.3 Viewing the fit results

Once you have finished fitting your qMR data, or when you load previously saved fit results by clicking **Load Results** in the ‘qMR data fit’ section of the Menu panel, the maps will be displayed in the ‘Fit Results’ section. Use controls on the left side of the figure to navigate the maps:

- **Source**: select the parameter map to display
- **View**: select the side from which to view the data (available only on 3D maps)
- **Slice**: navigate through the z direction of the current view (available only on 3D maps)
- **Color Map**: choose the color scheme to use from a set of pre-defined Malab colormaps
- **Range**: Control the colormap min/max values. Clicking ‘Auto’ will set the min/max values using the min/max of the currently displayed image. Top textbox/slider allows you to manually set the Min value, while bottom textbox/slider are for the Max value
- **Open viewer**: open the current data in an external viewer to display simultaneous axial/sagittal/coronal views.
- **Save figure**: save the current figure
- **Histogram**: open a new window with an histogram of the voxels in the currently selected slice (note that zooming in on a particular section while still produce an histogram of the full slice)
- **View data fit**: display raw data + fitted curve of the currently selected voxel (use ‘Cursor’ button to activate voxel selection mode).
- **Pan**: change the cursor mode to ‘Pan’. Click and hold inside the figure to move around. Double click inside the figure to reset view. Clicking again the Pan button will turn off pan mode.
- **Zoom**: change the cursor mode to ‘Zoom’. Click and hold inside the figure to draw a region to zoom in on. Double click inside the figure to reset view. Clicking again the Zoom button will turn off zoom mode.
- **Select**: change the cursor mode to ‘Data Cursor’. Click on a voxel to display info (X/Y is the position of the voxel, index is the value of the map at this point, RGB is the mapped color code).

6.1.5 5. Simulation

5.1. Single Voxel Curve

The Single Voxel Curve simulation interface allows you to simulate qMR data for the defined parameters and protocol. Once the simulation is done, you can also rapidly test the effect of changing fitting options without having to run the simulation again. It is the fastest way to evaluate various acquisition protocols and the performance of the model and
fitting options. A plot of the fitted curve over the actual data will be displayed, and the resulting fitted parameters are compared to the input parameters.

1. Select the acquisition method of your qMR data using the ‘Method’ drop-down menu in the *Menu* panel.
2. In the *Menu* panel, click on **Single Voxel Curve** to display the interface in the *Main* panel.
3. Using the *Options* panel, define or load the protocol you wish to use (see section 5.1).
4. Using the *Options* panel, define or load your initial fitting options (see section 5.2).
5. Using the *Options* panel, define or load your simulation parameters (see section 5.3).
6. In the *Menu* panel, click on the big **Simulate data** button. A progress bar will appear to show the progression of the simulation. Clicking **Cancel** in the progress bar window will stop the current simulation.
7. Once the simulation is done, the results are displayed in the *Main* panel.
8. If you want to see the effect of changing fitting options, use the *Options* panel to make your changes. Then, in the *Main* panel inside the ‘Simulation Fit Results’ panel, click on **Update Fit**. Clicking this button without changing fitting options will also generate a new noisy data distribution and recalculate the fitted curve.
9. Once the fitting is done, a temporary file (SimCurveTempResults) will be saved in the ‘SimResults’ subfolder of the current active method (e.g. *qMTLab/SPGR/SimResults/*). You can save the current simulation results by clicking **Save Results** in the ‘qMR Data Simulator fit’ section of the *Menu* panel. You can later load it using the **Load Results** button.

### 5.2. Sensitivity Analysis

The Sensitivity Analysis simulation allows you to systematically vary one parameter, over a defined range and number of points, while keeping the others fixed. For each simulated data point, noise is added with a given SNR, and the fit is run multiple times while adding gaussian noise. This allows you to evaluate the variance of the fit at each point. When the simulation is done, a plot shows any variable input parameters as the independent variable, as well as the mean values and variance of any fitted parameters.

1. Select the acquisition method of your data using the ‘Method’ drop-down menu in the *Menu* panel.
2. In the *Menu* panel, click on **Sensitivity Analysis** to display the interface in the *Main* panel.
3. Using the *Options* panel, define or load the protocol you wish to use (see section 5.1).
4. Using the *Options* panel, define or load your fitting options (see section 5.2).
5. Using the *Options* panel, define or load your simulation parameters (see section 5.3). The parameters defined here are used as the fixed parameters values as one parameter at a time is systematically varied during the simulation process.
6. In the *Main* panel, use the ‘Parameters variation’ table to define your analysis settings. Select the parameters that are to be varied by setting a mark in the appropriate checkbox, set the minimum and maximum values for this parameter under the column ‘Min’ and ‘Max’, and the size of the incrementing step under ‘Step’. Set the number of times you want to add noise and fit for each data point by entering an integer value in the ‘# of runs’ box. These settings can be saved, retrieved or reset to their initial settings using the ‘Save’, ‘Load’ and ‘Reset’ buttons respectively.
7. In the *Menu* panel, click on the big **Simulate data** button. A progress bar will appear to show the progression of the simulation. Clicking **Cancel** in the progress bar window will stop the current simulation.
8. Once the simulation is done, the results are displayed in the ‘Plot Results’ section in the Main panel. Using the ‘x axis’ and ‘y axis’ dropdown menu, you can change the independent/dependant parameters respectively. The parameters that have been varied will be available under the ‘x axis’ menu, while all the model parameters will be available under the ‘y axis’ menu.
Fig. 5: Example result of simulation in 1 voxel. Remember to set options in ‘Options’ panel
9. A temporary file (SimVaryTempResults) will be saved in the ‘SimResults’ subfolder of the current active method (e.g. qMTLab/SPGR/SimResults/). You can save the current simulation results by clicking **Save Results** in the ‘qMT Data Simulator fit’ section of the **Menu panel**. You can later load it using the **Load Results** button.

![SimVary Interface](image)

**Fig. 6:** Example of sensitivity analysis of the F parameter for qMT

### 5.3. Multi Voxel Distribution

The Multi Voxel Distribution is a tool to simulate any number of voxels, where any combination of parameters are allowed to be varied simultaneously. You can choose how many voxels to simulate and which parameters are to be normally distributed, with its mean value and variance. The results can be displayed in a number of ways such as distribution histograms, scatter plots of input vs fitted parameters, error histograms, etc.

1. Select the acquisition method of your qMR data using the ‘Method’ drop-down menu in the **Menu panel**.
2. In the **Menu panel**, click on **Multi Voxel Distribution** to display the interface in the **Main panel**.
3. Using the **Options panel**, define or load the protocol you wish to use (see section 5.1).
4. Using the **Options panel**, define or load your fitting options (see section 5.2).
5. Using the **Options panel**, define or load your simulation parameters (see section 5.3). The parameters defined here are used as the fixed parameters values for parameters that are not selected to be varied.
6. In the **Main panel**, use the ‘Parameters distribution’ table to define your distribution settings. Select the parameters that are to be varied by setting a mark in the appropriate checkbox, set the mean and standard deviation values for this parameter under the column ‘Mean’ and ‘Std’ respectively. Set the number of voxels you want to...
simulate by entering an integer value in the ‘# of voxels’ box. These settings can be saved, retrieved or reset to their initial settings using the Save, Load and Reset buttons respectively.

7. Click on Get Parameters in the ‘Parameters distribution’ section to generate a set of normally distributed parameters using the current settings. You can look at the distribution in the ‘Plot Results’ section, by choosing ‘Input parameters’ under the ‘Plot type’ dropdown menu. Select the parameters you want to look at with the ‘x axis’ dropdown menu. You can generate a new set of random values by clicking on the Get Parameters button again.

8. In the Menu panel, click on the big Simulate data button. A progress bar will appear to show the progression of the simulation. Clicking Cancel in the progress bar window will stop the current simulation.

9. Once the simulation is done, the results are displayed in the ‘Plot Results’ section in the Main panel. Using the ‘Plot type’ dropdown menu, choose what plot you want to view. Plot types are defined below.

10. A temporary file (SimRndTempResults) will be saved in the ‘SimResults’ subfolder of the current active method (e.g. qMTLab/SPGR/SimResults/). You can save the current simulation results by clicking ‘Save Results’ in the ‘qMT Data Simulator fit’ section of the Menu panel. You can later load it using the ‘Load Results’ button.

Plot types

Different plot types are available to analyze your simulation results. Depending on the plot type, available selections under ‘x axis’ and ‘y axis’ dropdown menus will change accordingly.

- **Input parameters**: Histogram of initial input parameters distribution.
- **Fit results**: Histogram of fitted parameters distribution.
- **Input vs. Fit**: Scatter plot of input parameter value vs fitted value.
- **Error**: Histogram of the error distribution. Error is defined as: Fit-Input
- **Pct error**: Histogram of the percentage error distribution. Percentage error is defined as: 100×(Fit-Input)/Input
- **MPE**: Bar graph of the mean percentage error, defined as: 100/n ((Fit-Input)/Input), where n is the number of simulated voxels.
- **RMSE**: Bar graph of the root mean squared error, defined as: (1/n(Fit-Input)^2), where n is the number of simulated voxels.
- **NRMSE**: Bar graph of the normalized root mean squared error, defined as RMSE/(max(Input)-min(Input)) , where max(Input) is the maximum value in the input parameter distribution, and min(Input) is the minimum value.

6.1.6 6. Options Panel

Each qMR acquisition method has its own particular options for simulation, protocol and fitting. These options can be modified by using the Options panel. The Options panel consists of three sub-panels of options: ‘Protocol’, ‘Fitting’ and ‘Options’. At the bottom of all these sub-panels you will find buttons to Reset the changes you made, Save the current settings as a .mat file, Load a .mat file of settings, or go back to the Default settings. The Help button will open the help for the particular model.

6.1 Protocol

The ‘Protocol’ panel is where you define all options relating to the acquisition sequence. These options are specific for each method. For all methods, you will find (at the top of the protocol panel) input text fields corresponding to the independent variables. You will need to load a previously saved text (.txt) file with the required options and format.
Fig. 7: Example of MultiVoxel Distribution (option: Input parameters)
Fig. 8: Example of *Options* panel for qMT SPGR and Inversion Recovery

### 6.1. Graphical User Interface Usage
by using the **Load** button. Press the **Help** button in this panel to see the format expected by each of the models in the **Protocol** section

For example, the *vfa_t1* model is expecting

**Protocol**

**VFAData Array [nbFA x 2]:** [FA1 TR1; FA2 TR2; ...] flip angle [degrees] TR [s]

Which means a text file where each row is a different flip angle, 1st column is the flip angle in degrees, 2nd is the TR in sec, e.g.:

<table>
<thead>
<tr>
<th>Angle</th>
<th>TR</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>0.015</td>
</tr>
<tr>
<td>20</td>
<td>0.015</td>
</tr>
</tbody>
</table>

### 6.2. Fitting

The ‘Fitting’ panel is where you determine the upper, lower and starting points of your parameters. You can also select which parameters should be kept fixed for the fitting.

### 6.3. Options

The ‘Options’ panel is where you specify the properties of the model and the fitting. For example, the assumptions/type of model (e.g. for SPGR, the SledPikeRP or Yarnykh model), type of images (magnitude or magnitude/phase for Inversion Recovery), etc.

### 6.1.7 7. Tutorial

See the video here:

### 6.2 Command-Line Usage

#### 6.2.1 General structure

The models are objects, each with a set of properties and generic functions. Before interacting with a model, it must first be instantiated, e.g.

```python
model=charmed
```

#### 6.2.2 General commands

- `qMRInfo(model)` : Print the help for the ‘model’ object
- `qMRusage(model)` : Print the methods of ‘model’ and examples of how to interact with them
- `qMRgenBatch(model)` : Generate a batch example script for ‘model’ (will automatically download test data)
6.2.3 Model structure

All models have the following properties:

- **MRIinputs**: Names of input data
- **voxelwise**: Whether the fit is voxelwise [1] or a matrix operation [0]
- **xnames**: Names of output data
- **Prot**: structure containing the protocol parameters
- **buttons**:
- **Options**: options specific to the model (e.g. linear or non-linear fir for VFA-T1)

And functions:

- **equation**:

  ```
  Compute MR signal
  USAGE: 
  Smodel = Model.equation(x)
  INPUT:
  x: [struct] OR [vector] containing Model output parameters
  ```

- **fit**:

  ```
  Fit experimental data 
  USAGE: 
  FitResults = Model.fit(data)
  INPUT:
  data: [struct] containing input data IN ORDER as in MRinuts 
  NOTE: data are 1D. For 4D datasets use FitData(data,Model)
  ```

- **plotModel**:

  ```
  Plot model equation (and fitting)
  USAGE: 
  Model.plotModel(obj, x)
  Model.plotModel(obj, x, data)
  INPUT:
  x: [struct] OR [vector] containing Model output parameters 
  data: [struct] containing input data in ORDER as in MRinuts
  ```

Most models have these additional functions:

- **Sim_Sensitivity_Analysis**:

  ```
  Simulates sensitivity to fitted parameters:
  (1) vary fitting parameters from lower (lb) to upper (ub) bound in 10 steps 
  (2) run Sim_Single_Voxel_Curve Nofruns times
  (3) Compute mean and std across runs
  USAGE: 
  SimVaryResults = Model.Sim_Sensitivity_Analysis(OptTable, Opt);
  INPUT:
  ```
OptTable: [struct] nominal value and range for each parameter.
   st: [vector] nominal values for output parameters
   fx: [binary vector] do not vary this parameter?
   lb: [vector] vary from lb...
   ub: [vector] up to ub
Opt: [struct] Options of the simulation

• Sim_Single_Voxel_Curve:

Simulates Single Voxel curves:
   (1) use equation to generate synthetic MRI data
   (2) add rician noise
   (3) fit and plot curve
USAGE:
   FitResults = Model.Sim_Single_Voxel_Curve(x)
   FitResults = Model.Sim_Single_Voxel_Curve(x, Opt, display)
INPUT:
   x: [struct] OR [vector] containing fit results
   display: [binary] 1=display, 0=nodisplay

Please type the following to see the specific usage of the model you are interested in

qMRusage(model)

Or the batch example associated with your model located here Methods available
CHAPTER 7

Indices and tables

- genindex
- modindex
- search