

MRiLab v1.3 User Guide

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Preface

Numerical Magnetic Resonance Imaging (MRI) simulation can improve the understanding and development of new MRI techniques. In this work, a new simulation package named 'MRiLab' has been developed for performing fast three-dimensional (3D) parallel MRI simulation on regular desktop computer. This simulation package is aimed to provide a fast, comprehensive and effective numerical MRI simulation solution with minimum computing hardware requirement.

This manual is aimed to provide a comprehensive introduction to demonstrate the work-flow of simulation, built-in dedicated toolboxes and libraries capable of customizing various aspects of MR simulation experiment. You should become familiar and comfortable with those design functions in MRiLab after reading this User Guide.

It's my pleasure to know that MRiLab can help you in your MR research. Please don't hesitate to leave me feedback about any aspect of MRiLab and/or about this User Guide. All the efforts for improving MRiLab will hopefully help MR researchers including myself for better understanding and improving future MR techniques.

Chapter 1

Introduction

1.1 What is MRiLab

The MRiLab is a numerical MRI simulation package. It has been developed and optimized to simulate MR signal formation, k -space acquisition and MR image reconstruction. MRiLab provides several dedicated toolboxes to analyze RF pulse, design MR sequence, configure multiple transmitting and receiving coils, investigate magnetic field related properties and evaluate real-time imaging technique. The main MRiLab simulation platform combined with those toolboxes can be applied to customize various virtual MR experiments which can serve as a prior stage for prototyping and testing new MR technique and application.

The MRiLab features highly interactive graphical user interface (GUI) for the convenience of fast experiment design and technique prototyping. High simulation accuracy is achieved by simulating discrete spin evolution at small time interval using the Bloch-equation and appropriate tissue model. In order to manipulate large multidimensional spin array, MRiLab employs parallel computing by incorporating latest graphical processing unit (GPU) technique and multi-threading CPU technique. With efficient parallelization, MRiLab can accomplish multidimensional multiple spin species MR simulation at high simulation accuracy and time efficiency, and with low computing hardware cost.

1.2 Obtaining MRiLab

The current MRiLab version (v1.3) is made available online. MRiLab is released as a free software. This means that you are free to use and modify this software as your needs, as long as you acknowledge the original author in any future work. If you find MRiLab useful for the publication of any scientific results, including a line in your acknowledgments section for MRiLab is requested.

MRiLab downloading address:

<http://sourceforge.net/projects/mrilab/>

We also request you to cite this scientific paper:

FANG LIU, JULIA V. VELIKINA, WALTER F. BLOCK, RICHARD KIJOWSKI AND ALEXEY A. SAMSONOV: *Fast Realistic MRI Simulations Based on Generalized Multi-Pool Exchange Tissue Model*, IEEE Trans. Med. Imag., doi: 10.1109/TMI.2016.2620961, 2016.

1.3 Installing and Running MRiLab

To use MRiLab, you need to install Matlab software first. The current MRiLab version was successfully tested under mutiple Matlab versions:

- Matlab R2011a 64-bit Windows
- Matlab R2013a 64-bit Windows
- Matlab R2015a 64-bit Windows
- Matlab R2012b 64-bit Unix

To install MRiLab, you need to download MRiLab source code, then extract the MRiLab root folder, put the folder to any location in you computer. To run MRiLab, start Matlab, then simply run the ‘MRiLab.m’ script under the MRiLab root folder.

The GUIs in MRiLab is developed under Matlab GUI development environment (GUIDE). Majority of the simulation configuration code is programmed using pure Matlab language and Extensible Markup Language (XML). The computing intensive functions are programmed and optimized using MATLAB Executable (MEX) C code. These MEX binaries include GPU computing kernels that interact with GPU devices via NVIDIA Compute Unified Device Architecture (CUDA), and CPU kernels with multi-threading via Open Multi-Processing (OpenMP) for multi-core CPU. Other MEX binaries include several 3D image rendering functions using Visualization Toolkit (VTK). These MEX library binaries have been built under 64-bit Windows and Linux OS system and shipped with MRiLab source code. However, if they are incompatible with your OS system for any reason or if you wish to modify these MEX files for your own good, you need to recompile them from source code.

Before recompiling these MEX files, some dependent packages are required.

1. CMake (required)

CMake is used for cross platform building of these MEX files.

CMake : <http://www.cmake.org/cmake/resources/software.html>

2. IPP or Framework (required)

MRiLab uses Intel Integrated Performance Primitives (IPP) or AMD Framework libraries for large scale matrix manipulation. Please note that Intel IPP isn't a free open source software, however if you are planning to use MRiLab IPP version (i), you can download Intel C Studio XE which includes IPP distribution and follow Intel's non-commercial license for non-commercial usage. As an alternative, MRiLab provides Framework version (f) which uses equivalent Framework libraries. The Framework is released as a free open source software.

Intel IPP : <http://software.intel.com/en-us/intel-ipp>

AMD Framework : <http://framework.sourceforge.net>

3. CUDA (optional)

NVIDIA GPU driver is required for running GPU devices and also for MRiLab to interact with GPU devices. The current MRiLab version only supports GPU cards which support NVIDIA CUDA technique. The GPU card must support CUDA computing capability 2.0 and above. The shipped MEX files in the MRiLab distribution use CUDA libraries from CUDA 7.0.

NVIDIA : <http://www.nvidia.com/page/home.html>

CUDA : http://www.nvidia.com/object/cuda_home_new.html

Although GPU acceleration dramatically improves computational efficiency, the GPU computing mode is also optional. Alternatively, MRiLab provides multi-threading CPU computing mode via OpenMP which requires no additional packages on modern operating system. The CPU kernel provides the same simulation accuracy but with reduced computational efficiency compared to GPU mode.

4. VTK (optional)

The VTK library provides nice functions to render 3D k -space trajectory as well as complex image object in 3D space. The current MRiLab version uses MEX built against VTK 5.10. However, VTK rendering is optional as native Matlab rendering is also provided.

VTK : <http://www.vtk.org>

5. ISMRMRD (optional)

MRiLab supports data conversion from Matlab variables to ISMRMRD, the default data storage format for Gadgetron MRI reconstruction framework. To enable Gadgetron function and allow data conversion to ISM-

RMRD, the user needs to install ISMRMRD.

ISMRMRD : <http://ismrmrd.sourceforge.net/#obtaining-and-installing>

After completing abovementioned dependent packages, you also need to add a few environment variables in your system :

- MATLAB_ROOT : Matlab root folder path
- IPP_ROOT : IPP root folder path if IPP is used
- FRAMEWAVE_ROOT : Framewave root folder path if Framewave is used

Note that the C source code for these MEX files is in /MRiLab/Lib/src folder. To compile and install MEX files

1. Linux Installation

The command lines for compiling the MEX files are

```
mkdir build
cd build
cmake MRiLab/Lib/src
make
sudo make install
```

You also can use cmake-gui for configuration and other building tools (e.g. Eclipse) for building the binaries.

2. Windows Installation

It is recommended to use cmake-gui for generating Visual Studio projects, then build the projects in Visual Studio.

- Step 1 : Locate source folder and build folder in cmake-gui (Figure 1.1)
- Step 2 : Configure and generate Visual Studio projects in cmake-gui (Figure 1.2)
- Step 3 : Build the INSTALL project, compiled MEX binaries will be copied to MRiLab/Lib/bin folder by default (Figure 1.3)

If installation problems do occur in your case, feel free to leave comments on the online supporting forum. For your information, I provide here my development environment (Table 1.1) for the current MRiLab version.

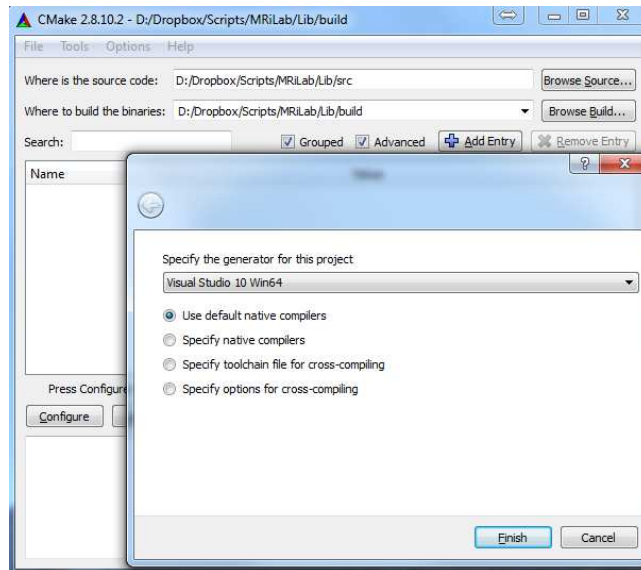


Figure 1.1: The cmake-gui for locating source folder and build folder

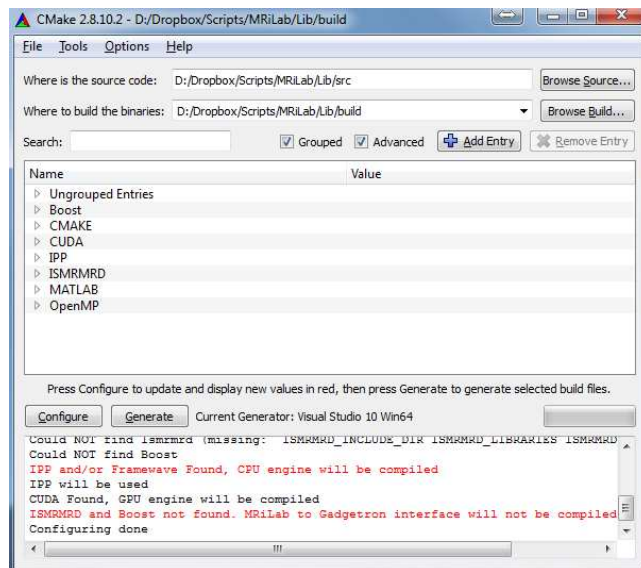


Figure 1.2: The cmake-gui for configuring and building Visual Studio projects

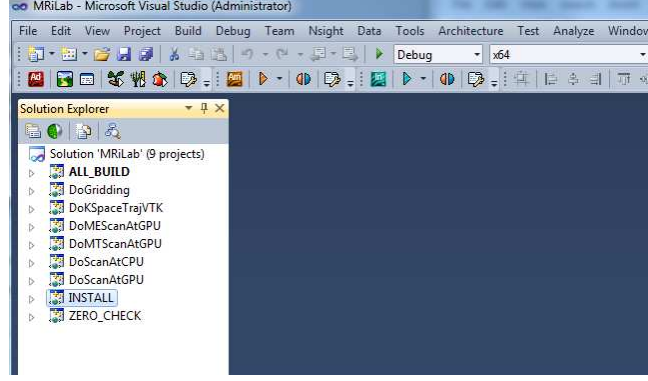


Figure 1.3: Build INSTALL project using Visual Studio

Environment	Desktop	Desktop
Machine	Dell Precision T3500	Dell Precision T3500
CPU	Intel Xeon W3530	Intel Xeon W3530
GPU	NVIDIA Quadro K4000	NVIDIA Quadro K4000
OS	Windows 7 64-bit	Linux Ubuntu 14.04LTS 64-bit
Matlab	Matlab R2015a 64-bit	Matlab R2015a 64-bit
C Compiler	Visual Studio 10 Win64	GCC 4.8.4
VTK	VTK 5.10	VTK 6.3
CUDA	CUDA 7.0.28	CUDA 7.0.28
IPP	Intel IPP 7.0	Intel IPP 7.0
Framewave	AMD Framewave 1.3	AMD Framewave 1.3
ISMRRD	ISMRRD 0.5.0	ISMRRD 0.5.0
Boost	Boost 1.53.0	Boost 1.54.0

Table 1.1: Fang's Computer Environment

Chapter 2

Platform Overview

2.1 MRiLab Simulation Platform

The MRiLab simulation platform consists of

1. A Main Simulation Control Console

The main simulation console (Figure 2.1) behaves analogous to a MR scanner console for graphically adjusting imaging setup and conducting simulation control. Simulation feedback are instantly updated on information panels during simulation.

2. Design Toolboxes

The Design toolboxes (Figure 2.2) provide independent interfaces for analyzing RF pulse (e.g. SLR, non-adiabatic and adiabatic pulse etc.), constructing arbitrary pulse sequence (e.g. SPGR, SSFP and FSE etc.), configuring coil profile and static field (i.e. B1+/- and B0 field), designing imaging object moving track and evaluating spatial specific absorption rate (SAR). Dedicated image display and analysis tools (SpinWatcher, SARWatcher, MatrixUser and arrayShow) are developed and tailored to work with multi-dimensional image array output.

3. Discrete Bloch-equation Solving Kernels

The Bloch-equation solving kernels manipulate tissue spin evolution at discrete time interval with a desired spin model and at a given MR sequence. These kernels are accelerated using Matlab MEX functions that are optimized for running GPU and multi-threading CPU parallel computing techniques. Moreover, these kernels are also capable of preprocessing acquired MR signal and k -space locations prior to desirable image reconstruction. Further image reconstruction with stored k -space data is accomplished in corresponding reconstruction module.

4. Macro Library

MRiLab uses a concept of macros for simplifying experiment design. A

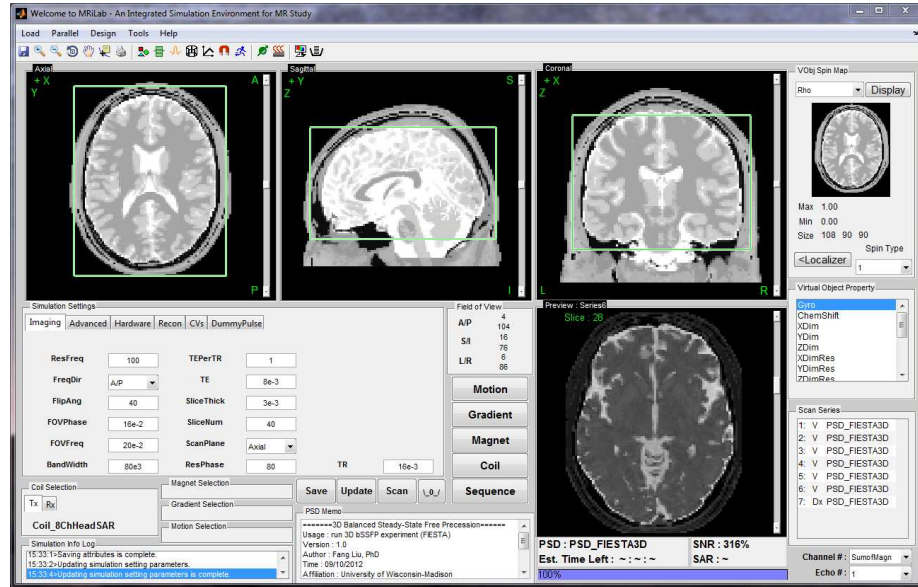


Figure 2.1: The MRiLab Main Simulation Control Console. This control console functions like a MR scanner console for graphically adjusting imaging setup and conducting simulation control.



Figure 2.2: The Shortcut for Function Toolbox on Simulation Control Console. Each icon is associated with an individual toolbox with specific functions.

macro in MRiLab is defined as a programming-free module that can be added, removed and modified in the process of constructing MR sequence, coil profile, magnet field and object moving track, etc. For instance, a Sinc RF pulse (rfSinc) is considered as a RF macro that can be used for constructing a gradient echo sequence, and the attributes of this macro include pulse starting time (tStart), pulse ending time (tEnd) and the time bandwidth product (TBP) etc. MRiLab provides a macro library (Figure 2.3) covering a wide range of macros. Using these predefined macros, you should be able to accomplish most of experimental design work. However, if special macros are needed, MRiLab also provides interfaces to work with user-defined macros. More detailed description for macros is provided in Chapter 5.

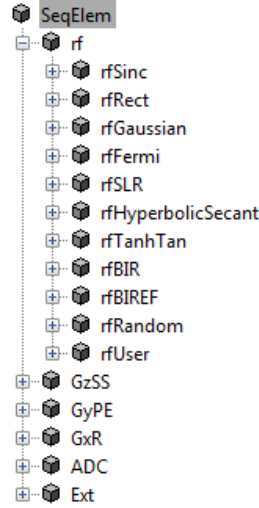


Figure 2.3: The Macro Library Tree Structure in MRiLab. Individual tree nodes under SeqElem root are functional macros that can be used for designing MR sequences. Notice that only RF nodes are unfolded here for display purpose.

MRiLab applies flexible simulation information storage by using XML file system, which simplifies translating simulation across different studies. MRiLab also supports external plugins programmed using either Matlab or C language for creating extendable simulation environment.

2.2 Simulation Workflow

The workflow diagram of MRiLab simulation is shown in Figure 2.4. One typical simulation requires input of :

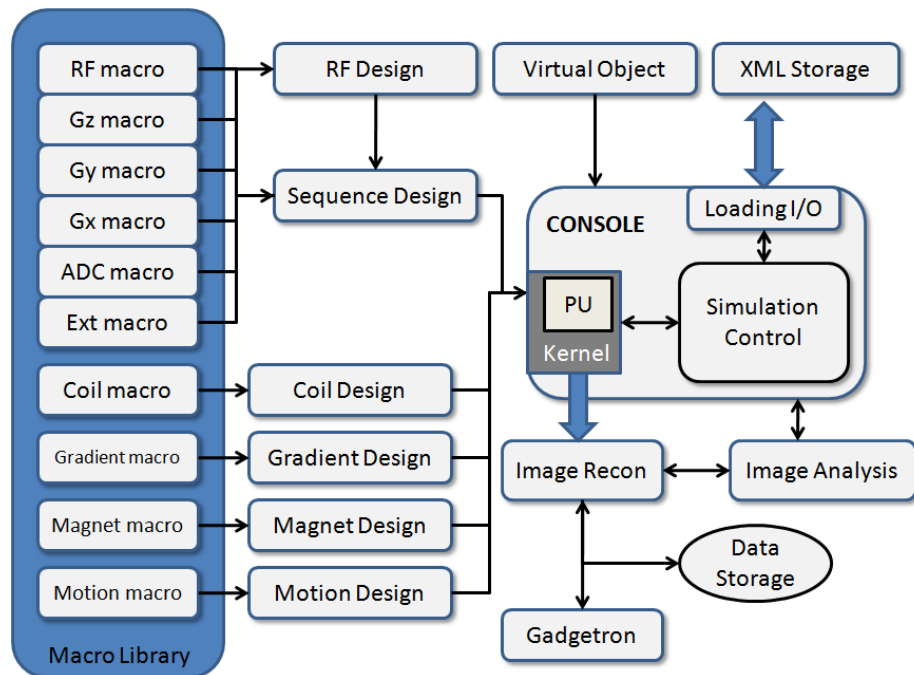


Figure 2.4: MRiLab Workflow Diagram

- Virtual object (VObj) with specific tissue properties including Rho (spin density), T1 and T2 etc.
- MR sequence to drive spin evolution
- B1+/- field for RF transmitting and receiving, default to be uniform field
- Gradient field for spatial encoding, default to be linear gradient
- Magnet field perturbation describing main static field inhomogeneity (dB0), default to be zero
- Motion pattern for describing imaging object movement during real time simulation

The input is configured at the main control console where the user can modify any aspect of the simulation experiment. The main console preprocesses the input information, then translates them into kernel signal, based on which the discrete solving kernel executes each voxel of imaging objects with either GPU or multi-threading CPU acceleration. The acquired MR signal k -space data from the kernel passes to image reconstruction module where either default recon code or external recon tool (e.g. Gadgetron) is applied. The reconstructed image can be analyzed using MRiLab image display tools including :

- MatrixUser : An image display and analysis tool for manipulating multi-dimensional matrix
- SpinWatcher : An analysis tool for analyzing spin evolution behavior within a single voxel
- SARWatcher : An analysis tool for analyzing local spatial SAR distribution
- arrayShow : A Matlab image viewer for the evaluation of multidimensional complex images

2.3 Gradient Echo: Start A Simple Scan

Up to this point, you may wonder how I can start to use MRiLab. Here below is a simple 3D Gradient Echo (GRE) simulation example to gain your first experience of using MRiLab.

- Open MRiLab by running 'MRiLab.m' under the root folder. MRiLab will try to detect available CPU and GPU devices, and initialize the simulation environment. After initialization (typically in couple seconds), MRiLab Main Simulation Control Console will open. Empty Axial, Sagittal, Coronal and Preview views show up. Notice that on the console, several push buttons are disabled at this point, it means more inputs are needed for activating them.

- To simulate images, the virtual object a.k.a. digital phantom is needed. Go to ‘Load’, ‘Load Phantom Example’, choose one of the predefined digital phantoms for the experiment. Several digital phantoms suitable for different experiment purposes are already provided. Here, let’s choose ‘Brain (Standard Resolution 108x90x90)’. After loading this phantom, notice that preview images show up at the top right corner under ‘VObj Spin Map’. The property information of this phantom also show in ‘Virtual Object Property’. Let’s choose ‘Rho’ map from the pop-up menu, and click ‘Localizer’ button to show more image details. Now Axial, Sagittal and Coronal axes are displayed with this 3D digital phantom. **Click ‘Update’ button to accept this phantom loading.** Notice that after updating, all push buttons become enabled.
- Since we want to simulate 3D GRE experiment, we need to load 3D GRE sequence first. Click the ‘Sequence’ button located at the center portion of the console. A SeqList will open where you can choose and load MR sequences. Let’s click ‘Dimension’ pop-up menu and choose ‘3D’. The Category list shows a full list of current available sequence type. Click ‘GradientEcho’, then click ‘PSD_GRE3D’ from the Sequence list. Click ‘Accept’ button to accept and load a 3D GRE sequence. Notice that the ‘Simulation Settings’ tabs on the console update and change to the setting for the current GRE sequence. **Click ‘Update’ button to accept this sequence loading.**
- Under the ‘Imaging’ tab, there are several parameters for imaging control, for instance, Field-of-View in the frequency encoding direction (FOVFreq). We can simply accept the default setting at this moment, however, if you do make any changes, **you need to click ‘Update’ button to update those changes before proceeding to Scan.**
- The final step is to click ‘Scan’ button and wait for the simulation to start. Depending on imaging setting and computing hardware, the simulation will typically finish in a short period of time, the reconstructed image will show in the ‘Preview’ view.

The final result of this 3D GRE experiment should be somewhat similar to this (Figure 2.5).

If you managed to simulate this gradient echo image, congratulations! You have successfully performed your first MRiLab experiment. So you should be prepared for deeper understanding of MRiLab simulation platform by following the rest of this user guide.

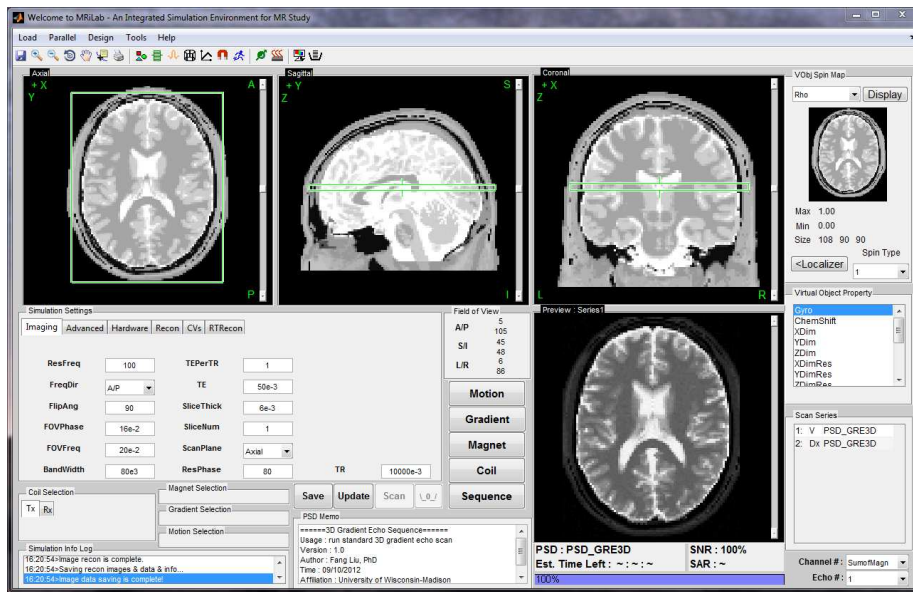


Figure 2.5: The Simulation Result for A 3D GRE Experiment

Chapter 3

Simulation Settings

3.1 Loading Virtual Object

Prior to making any type of simulation in MRiLab, a virtual object has to be loaded first. There are three ways of loading a virtual object: go to menu ‘Load’ and ‘Load Phantom’ to load a user customized phantom in .mat file; go to ‘Load Phantom Example’ to load default phantoms with MR properties mimicking human tissues (e.g. Brain, Cartilage, Fat, etc.); go to ‘Load Phantom from XML’ to load a configurable phantom from XML file (Section 5.3). Note that for the XML loading approach, a VObj XML file needs to be selected through ‘Load Phantom XML’ prior to loading phantom (default phantom XML files are saved in the phantom XML root folder MRiLab/Config/VObj).

If a virtual object is successfully loaded, the geometry of this phantom will show as a preview thumbnail at the top right corner of the console (Figure 3.1). The user can inspect the central slice of phantom property maps (T1, T2 and Rho etc.) using the pop-up menu above the thumbnail. To inspect all slices, the user can click ‘Display’ button to open a separate display window from MatrixUser. If multiple spin species exist in the phantom, the user can also inspect different spin type by using ‘Spin Type’ pop-up menu below the thumbnail. Moreover, a list of complete phantom properties of the virtual object is provided at the ‘Virtual Object Property’ list, the user can check properties by clicking the corresponding items. A complete property list of one virtual object typically include:

- Gyro (rad/s/T) : The gyromagnetic ratio of the spin
- ChemShift (Hz/T) : The chemical shift of the spin
- XDim : The number of voxels in X direction
- YDim : The number of voxels in Y direction
- ZDim : The number of voxels in Z direction

- XDimRes (m) : The voxel size in X direction
- YDimRes (m) : The voxel size in Y direction
- ZDimRes (m) : The voxel size in Z direction
- Type : A descriptive string of the phantom
- TypeNum : The number of spin species
- Rho : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing spin density
- T1 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T1 relaxation time
- T2 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T2 relaxation time
- T2Star (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T2* relaxation time

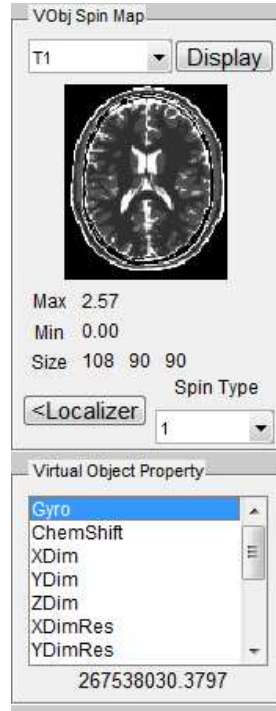


Figure 3.1: A Virtual Object Preview

Optional property for evaluating SAR include:

- ECon (S/m) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing tissue electrical conductivity
- MassDen (kg/m³) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing tissue mass density

MRiLab v1.3 and above introduces new functionality to simulate tissue models with multiple exchanging proton pools. The required properties for performing Magnetization Transfer (MT), Multiple Exchanging water pools (ME), Chemical Exchange Saturation Transfer (CEST) and Generalized Multi-pool exchanging Model (GM) include:

- K (Hz) : A multi-dimensional matrix for describing chemical exchange

The simulation with GM tissue also requires:

- TypeFlag : A flag array for describing proton type (free proton or bound proton)
- LineShapeFlag : A flag array for describing RF saturation line shape

More detailed content about tissue models is available in Chapter 5.3.

To inspect more details of the digital phantom, press the ‘Localizer’ button to populate the thumbnail to the main image display panel. MRiLab provides three image axes to display axial, sagittal and coronal view section of the 3D virtual object, respectively. A scroll bar beside each axes allows to change image slice along the corresponding direction, which serves as an anatomical reference for prescribing simulation parameters. For instance, the location of a green box in each axes indicating current field of view can be adjusted via free hand dragging, and the field of view location is instantly updated at ‘Field of View’ panel upon dragging.

3.2 Loading Sequence

One key feature of MRiLab is to allow simulating a wide range of MR sequences for desirable MR contrast among different tissues. MRiLab provides a sequence loading interface to allow choosing predefined sequences from default MRiLab sequence library, or choosing user customized sequences. MRiLab parses a selected MR sequence and translates the sequence waveform into specific signal which triggers simulation kernel execution. A MR sequence design toolbox is separate from this loading interface and will be explained in detail in Chapter 5.

3.2.1 Loading Predefined Sequence

To open a sequence loading interface (Figure 3.2), click the ‘Sequence’ button located at the center of the main control console. Once the interface is open, the ‘Dimension’ specifies the sequence spatial encoding scheme (2D or 3D). The ‘Category’ provides a list of sequence classes including Gradient Echo, Spin Echo, Inversion Recovery, Fast Spin Echo, Others and User. Upon clicking one sequence category, sequences within the selected category become available in the sequence list on the right. Click a sequence, then press ‘Accept’ to load the selected sequence. pressing ‘Cancel’ button will close the interface without loading any sequence.

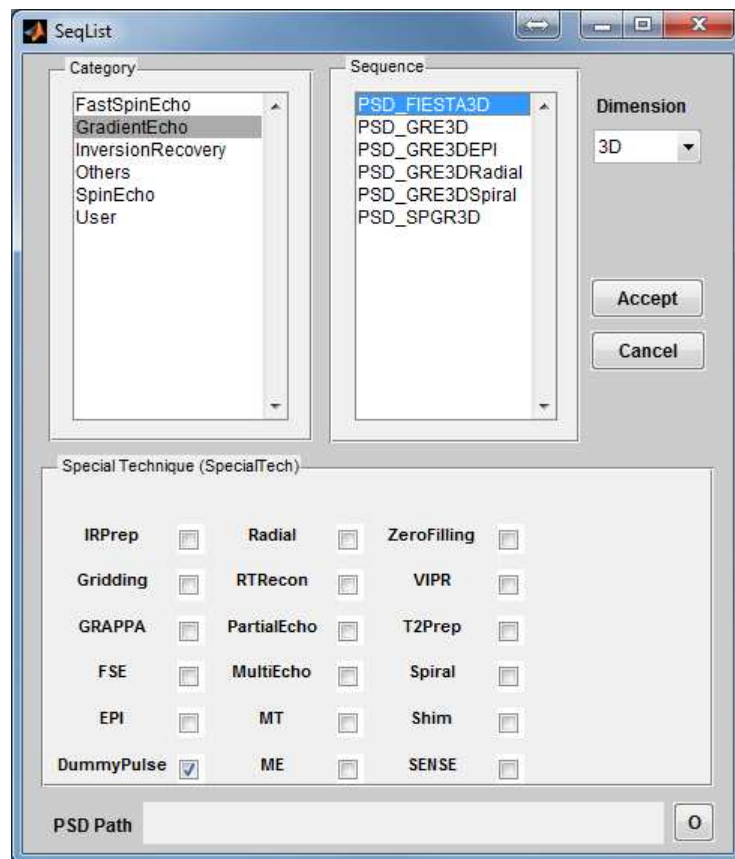


Figure 3.2: The Sequence Loading Interface. A sequence PSD_FIESTA3D from 3D GradientEcho Category is chosen, and DummyPulse special technique is checked by default.

Notice there is a ‘Special Technique (SpecialTech)’ panel below the se-

quence list. If a sequence with special techniques is selected, the corresponding checkboxes beside the special techniques will be chosen. For example, by default PSD_FIESTA3D uses the special techniques called DummyPulse (driving transient steady-state), therefore, by clicking PSD_FIESTA3D, the DummyPulse will be chosen accordingly. However, you can uncheck the checkbox for avoiding DummyPulse module, but this may cause incomplete simulation for PSD_FIESTA3D. It is recommended to keep default selection therefore a complete sequence control is preserved for those default sequences. On the other hand, for sequences which have no special techniques, you can also add special technique module by checking corresponding checkbox. This will load parameter tabs of special techniques on the simulation control console to allow configuration. The special technique strategy enables the ability to reuse ‘capsulized’ module for different sequences.

MRiLab provides a few default sequences under the folder /MRiLab/PSD (follow GE’s naming convention :)), notice the /PSD folder uses the same hierarchical structure scheme as that of the loading interface. Typically a new sequence can be saved anywhere, however it is recommended to save the sequence under those predefined categories under /PSD so they are visible to the loading interface. However, if a customized sequence is not directly visible to the loading interface, it can also be loaded using PSD loading button marked as ‘o’ at the bottom of the loading interface. If PSD loading button is used, loading interface will ignore normal sequence selection.

3.2.2 Predefined Sequences

MRiLab provides a few predefined MR sequences including

1. Fast Spin Echo
 - PSD_FSE3D
A 3D multishot Fast Spin Echo (FSE) sequence with interleaved k -space sampling in Kx-Ky and conventional phase-encoding along Kz.
2. Gradient Echo
 - PSD_FIESTA3D
A 3D balanced Steady State Free Precession (bSSFP) sequence.
 - PSD_SPGR3D
A 3D Spoiled Gradient Echo (SPGR) sequence.
 - PSD_GRE3D
A 3D gradient echo sequence with Cartesian readout.
 - PSD_GRE3DEPI
A 3D gradient echo sequence with multishot Echo Planar Imaging (EPI) readout using interleaved k -space sampling in Kx-Ky and conventional phase-encoding along Kz.

- PSD_GRE3DRadial
A 3D gradient echo sequence with radial readout in Kx-Ky and conventional phase-encoding along Kz, usually referred to as stack-of-stars sequence.
- PSD_GRE3DSpiral
A 3D gradient echo sequence with multishot spiral readout in Kx-Ky and conventional phase-encoding along Kz, referred to as stack-of-spiral sequence.

3. Inversion Recovery

- PSD_IR3D
A 3D Inversion Recovery (IR) sequence with Cartesian readout.

4. SpinEcho

- PSD_SE3D
A 3D Spin Echo (SE) sequence with Cartesian readout.

5. User

- PSD_SPGR3DMT
A 3D SPGR sequence with MT saturation. Note that MT phantom is needed for running this sequence.
- PSD_SPGR3DME
A 3D SPGR sequence for ME tissue model. Note that ME phantom is needed for running this sequence.
- PSD_SPGR3DCEST
A 3D SPGR sequence with off-resonance saturation to perform pulsed CEST saturation. Note that CEST phantom is needed for running this sequence.
- PSD_SPGR3DGM
A 3D SPGR sequence for GM tissue model. Note that GM phantom is needed for running this sequence.

6. Others

- PSD_AFI
A 3D SPGR sequence for performing flip angle mapping using Actual Flip Angle Imaging (AFI) technique [1].
- PSD_T2Prep
A 3D SPGR sequence with an additional T2 preparation section. Note this sequence is aimed to demonstrate the use of multiple ‘Pulses’ structure, thus should NOT be straight-forward used for practical simulation.

3.3 Loading Coil

To simulate multi-transmitting and receiving coil array, MRiLab provides a coil loading interface to allow choosing different coil configurations for Tx (i.e. Transmitting) and/or Rx (i.e. Receiving). MRiLab translates coil configuration and computes a B1+/B1- field accordingly. For multi-transmitting coil, each coil element can be treated separately and receives individual RF signal source. This allows to investigate B1 shimming and multiple RF excitation techniques. For multi-receiving coil, each coil element also connects to an individual signal channel and produces signal according to its specific coil sensitivity. This allows to investigate different coil encoding methods such as parallel imaging. The coil loading interface provides functions to load coil configuration. A coil design toolbox is separate from loading interface and will be explained in detail in Chapter 5.

3.3.1 Loading Predefined Coil

To open a coil loading interface (Figure 3.3), click the ‘Coil’ button located at the center portion of the console. The ‘Category’ list specifies different coil configuration category based on anatomical structure. The ‘Coils’ list beside the ‘Category’ list provides coil configuration within the selected category. Upon clicking a coil configuration, the interface will calculate the coil sensitivity map and display it in the preview axes. The user can specify displaying resolution using the ‘Precision’ with the highest spatial resolution defined as the same resolution of digital phantom. Moreover, the user can specify color map from ‘Jet’, ‘Gray’ or ‘Hot’. Pressing ‘Accept’ will load the selected coil configuration. However, pressing ‘Cancel’ button will close the interface without loading any coil configuration. If an uniform unit coil sensitivity is desired, press ‘Uniform’ button to load that. By default, MRiLab uses an uniform unit coil sensitivity for both RF transmitting and receiving. To indicate coil mode, the user needs to specify ‘Coil Type’ as either Tx for transmitting or Rx for receiving.

MRiLab provides a few default coil configuration under the folder /MRiLab/Config/Coil, notice the /Coil folder uses the same hierarchic structure scheme as that of the loading interface. Typically a new coil configuration can be saved anywhere, however it is recommended to save the coil configuration folder under predefined categories therefore they are visible to the loading interface. However, if a customized coil configuration is not directly visible to the loading interface, it can also be loaded using Coil loading button marked as ‘o’ at the bottom of the loading interface. If Coil loading button is used, loading interface will ignore normal coil selection.

3.3.2 Predefined Coil

MRiLab provides a few predefined coil configuration including

1. Head

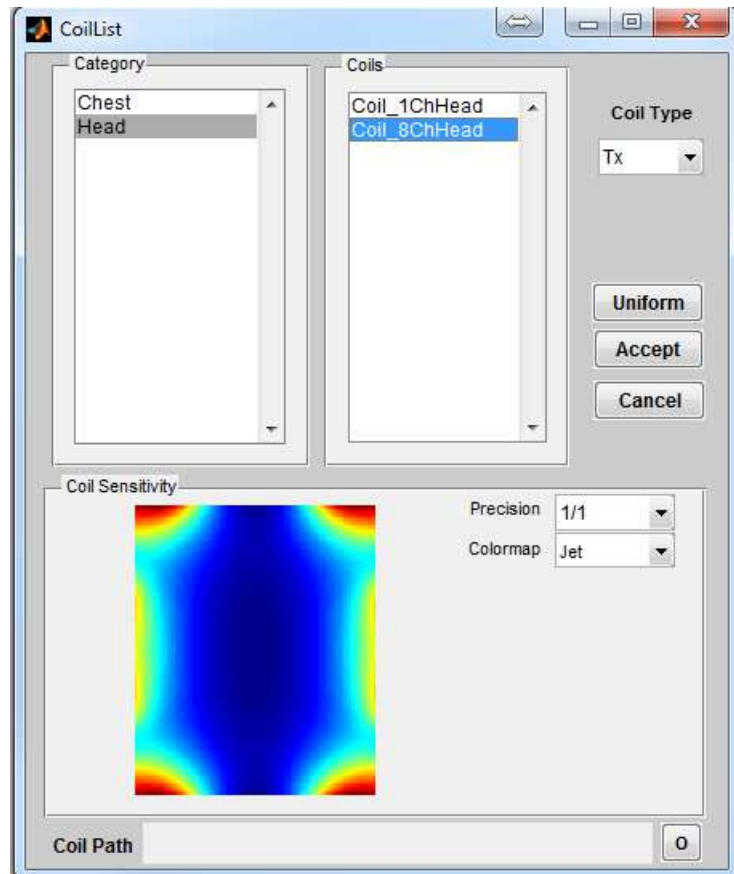


Figure 3.3: The Coil Loading Interface. An eight channel coil configuration Coil.8ChHead from Head Category is chosen, preview image shows the coil sensitivity at the same spatial resolution as that of the chosen digital phantom.

- **Coil.1ChHead**
A coil configuration consists of one single Biot-Savart circle, primarily used for testing purpose.
- **Coil.8ChHead**
A coil configuration consists of 8 Biot-Savart circles, which produces relative flat B1 field in X-Y plane along X direction.
- **Coil.8ChRectHead**
A coil configuration similar to Coil.8ChHead but with rectangle coil element.
- **Coil.8ChHeadSAR**
A coil configuration consists of 8 channels given user input B1 and E1 field by using 'CoilUser', note SAR evaluation requires E1 field which is only supported by 'CoilUser' macro in current MRiLab version.

2. Chest

- **Coil.9ChSurfChest**
A coil configuration consists of 9 Biot-Savart circles, which produces relative flat B1 field in X-Y plane along Y direction at the surface region.

The generated B1 and E1 field is scaled by two factors. 'B1Level' is a linear scale factor for B1. The input B1+ field at a magnitude of B1Level produces nominal flip angle. 'E1Level' is a linear scale factor for E1. When calculating time varying SAR, the input E1+ field is scaled by an number of nominal RF amplitude normalized by E1Level. These two factors are adjustable at parameter list in Chapter 3.8.

3.4 Loading Magnet

Some simulation studies require non-uniform static magnetic field. The situation include studies to investigate susceptibility artifact and to develop robust sequences in related to field inhomogeneity. MRiLab provides a magnet loading interface to allow loading customized B0 field perturbation map (i.e. dB0 map, a map for indicating main field variation). A magnet design toolbox is separate from loading interface and will be explained in detail in Chapter 5.

3.4.1 Loading Predefined Magnet

To open a magnet loading interface (Figure 3.4), click the 'Magnet' button located at the center of the console. The 'Category' list specifies different magnet category based on anatomical structure. The 'Magnet' list beside the 'Category' list provides magnet within the selected category. Upon clicking a magnet file, the interface will compute a dB0 map and display it in the preview axes. Pressing 'Accept' will load the chosen magnet profile. Pressing 'Cancel' button

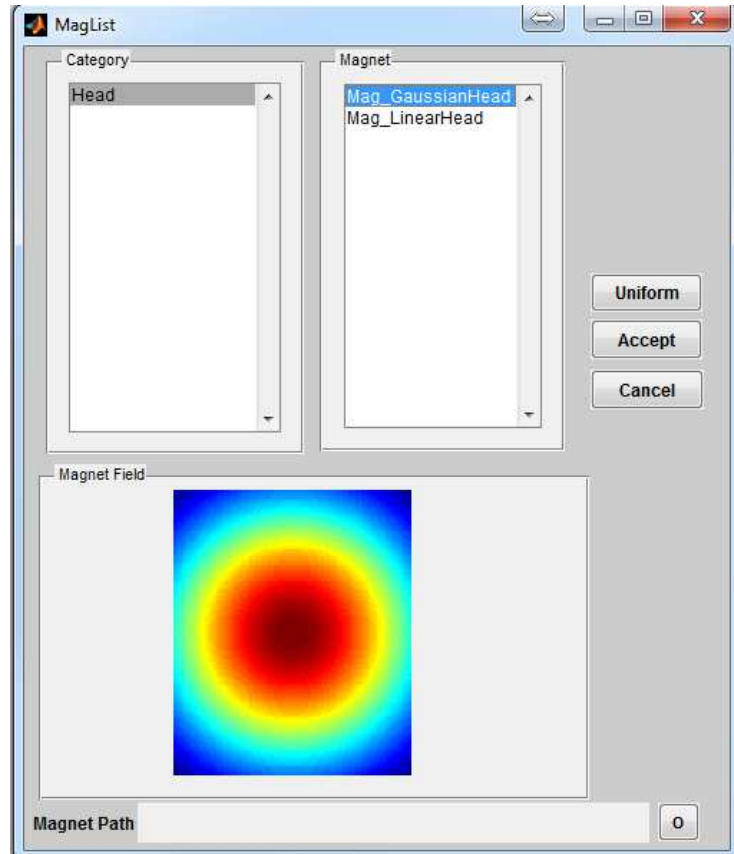


Figure 3.4: The Magnet Loading Interface. A magnet `Mag_GaussianHead` from `Head` Category is chosen, preview image shows the dB0 map in the X-Y plane at the same spatial resolution as that of the chosen digital phantom.

will close the interface without loading any profile. If an uniform B0 field (i.e. zero dB0) is desired, press ‘Uniform’ button to load that. By default, MRiLab uses an uniform B0 field for simulation which is equivalent to the ideal condition without field inhomogeneity across the entire virtual object.

MRiLab provides default magnet profiles in the folder /MRiLab/Config/Mag, notice the /Mag folder uses the same hierarchic structure scheme as that of the loading interface. Typically a new magnet profile can be saved anywhere, however it is recommended to save the magnet profile folder under those predefined categories therefore they are visible to the loading interface. However, if a customized magnet is not directly visible to the loading interface, it can also be loaded using Magnet loading button marked as ‘o’ at the bottom of the loading interface. If loading button is used, loading interface will ignore normal magnet selection.

3.4.2 Predefined Magnet

MRiLab provides two predefined magnet configuration including

1. Head
 - Mag_GaussianHead
A magnet profile produces a Gaussian dB0 field in 3D space.
 - Mag_LinearHead
A magnet profile produces a linear dB0 field in 3D space.

3.5 Loading Gradient

MR spatial encoding is typically performed in a linear fashion. However nonlinear (curved) spatial encoding may serve particular purposes in some MR studies. MRiLab provides a gradient loading interface to load customized 3D nonlinear gradient field. This function can help investigate arbitrary curved gradient field for imaging simulation. With flexible sequence design, nonlinear gradient encoding techniques such as PatLoc can be simulated with minimal efforts in MRiLab. The gradient loading interface provides functions to load nonlinear gradient. A gradient design toolbox is separate from the loading interface and will be explained in detail in Chapter 5.

3.5.1 Loading Predefined Gradient

To open a gradient loading interface (Figure 3.5), click the ‘Gradient’ button located at the center of the console. The ‘Category’ list specifies different gradient category based on the anatomical structure. The ‘Gradient’ list beside the ‘Category’ list provides gradient profile within the selected category. Upon clicking a gradient configuration, pressing ‘Accept’ will load the selected gradient profile. Pressing ‘Cancel’ button will close the interface without loading

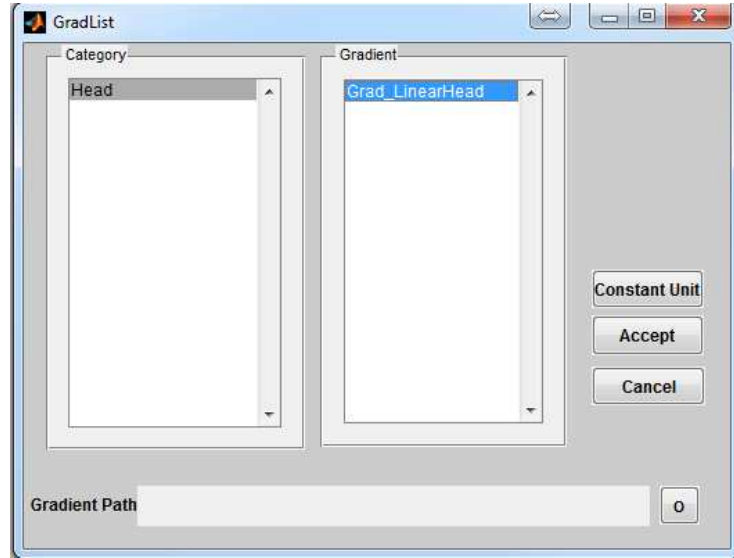


Figure 3.5: The Gradient Loading Interface. A gradient profile `Grad_LinearHead` from `Head` Category is chosen.

any gradient profile. If a constant unit gradient is desired, press ‘Constant Unit’ button to load that. By default, MRiLab uses a constant unit gradient profile in the X, Y and Z direction for gradient simulation. This will maintain a conventional linear spatial encoding in all three spatial dimensions.

MRiLab provides gradient profiles under the folder `/MRiLab/Config/Grad`, notice the `/Grad` folder uses the same hierarchic structure scheme as that of the loading interface. Typically a new gradient profile can be saved anywhere, however it is recommended to save the gradient profile under those predefined categories therefore they are visible to the loading interface. However, if a customized gradient is not directly visible to the loading interface, it can also be loaded using Gradient loading button marked as ‘o’ at the bottom of the loading interface. If Gradient loading button is used, loading interface will ignore normal gradient selection.

3.5.2 Predefined Gradient

MRiLab provides one predefined example of gradient profile

1. Head

- `Grad_LinearHead`

A gradient profile produces constant gradient field with varying gradient value in three dimensions, which can cause image contraction, expansion or shearing etc.

3.6 Loading Motion

MRiLab provides a mechanism to simulate imaging object movement in 3D space. The motion simulation introduces an approach to investigate time varying imaging techniques such as k-t blast and to enable development of real time image reconstruction algorithms. It also helps investigate motion insensitive sequences and test motion artifact at various conditions. The motion loading interface provides functions to load motion trajectory. A motion design toolbox is separate from the loading interface and will be used to design motion pattern in 3D space.

3.6.1 Loading Predefined Motion

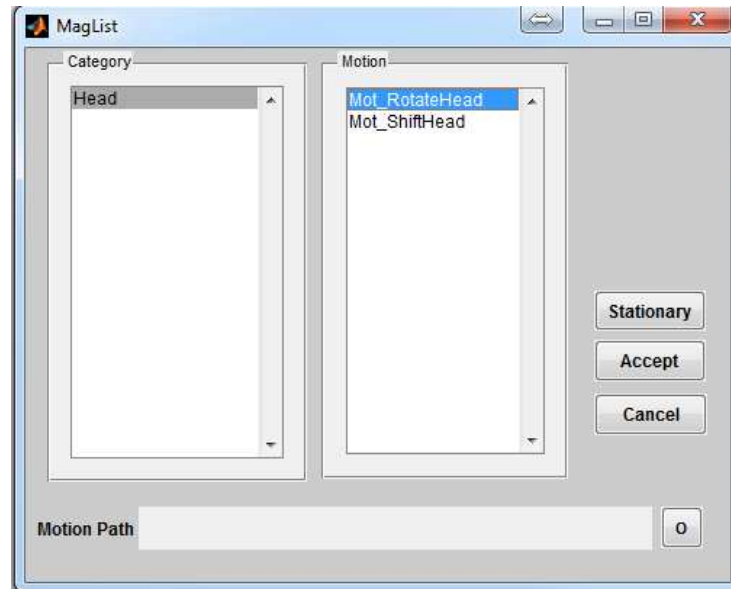


Figure 3.6: The Motion Loading Interface. A motion profile `Mot_RotateHead` from `Head` Category is chosen. This motion profile create object rotation in three dimensions along any user defined axis.

To open a motion loading interface (Figure 3.6), click the ‘Motion’ button located at the center of the console. The ‘Category’ list specifies different motion category based on the anatomical structure. The ‘Motion’ list beside the ‘Category’ list provides motion profile within the selected category. Upon clicking a motion pattern, pressing ‘Accept’ will load the chosen motion profile. Pressing ‘Cancel’ button will close the interface without loading any motion profile. If no motion is needed, press ‘Stationary’ button. By default, no motion is used in MRiLab simulation.

MRiLab provides motion profiles under the folder /MRiLab/Config/Mot, notice the /Mot folder uses the same hierarchic structure scheme as that of the loading interface. Typically a new motion profile can be saved anywhere, however it is recommended to save the motion profile under those predefined categories therefore they are visible to the loading interface. However, if a customized motion is not directly visible to the loading interface, it can also be loaded using Motion loading button marked as ‘o’ at the bottom of the loading interface. If Motion loading button is used, loading interface will ignore normal motion selection.

3.6.2 Predefined Motion

MRiLab provides two predefined examples of motion profile

1. Head

- Mot_RotateHead
A motion profile produces object rotation in 3D space along any user defined axis.
- Mot_ShiftHead
A motion profile produces object translation in any user defined direction.

3.7 Prescribing Scan Parameters

Those loading interfaces provide a mechanism to interpret and convert configuration file into MRiLab parameters. Given a successful loading, the ‘Coil Selection’, ‘Magnet Selection’, ‘Gradient Selection’ and ‘Motion Selection’ fields indicate the current selected configuration. The user can change the configuration by reloading a new configuration file with abovementioned steps. If any of these fields are empty, a default setting will be used. Similar to a real scanner system, MRiLab categorizes scanning parameters into different groups and present them under different tabs in the ‘Simulation Settings’ panel (Figure 3.7). Included in any MR sequences are five typical tabs including Imaging, Advanced, Hardware, Recon and CVs. Additional tabs for special techniques become valid if those techniques are loaded from sequence selection. Below are detailed explanation for each of those parameters.

3.8 Parameter List

Below are a full list of supported simulation parameters in current MRiLab version. Notice that unless otherwise specified, **MRiLab uses International System of Units (i.e. SI units) for all the parameters.**

The image shows a 'Simulation Settings' window with several tabs: Imaging, Advanced, Hardware, Recon, CVs, DummyPulse, and MT. The 'Imaging' tab is selected. It contains a grid of parameters with input fields or dropdown menus. The parameters and their values are as follows:

Parameter	Value	Parameter	Value
ResFreq	40	TEPerTR	1
FreqDir	A/P	TE	8e-3
FlipAng	10	SliceThick	6e-3
FOVPhase	6e-2	SliceNum	1
FOVFreq	6e-2	ScanPlane	Axial
BandWidth	80e3	ResPhase	40
		TR	60e-3

Figure 3.7: The Simulation Settings Panel. The panel contains Imaging, Advanced, Hardware, Recon and CVs tabs, two additional special technique DummyPulse and MT are also added for this sequence.

3.8.1 Imaging

The 'Imaging' tab contains parameters relevant to image resolution, field of view and timing setting etc.

- BandWidth (Hz) : Full receiver bandwidth
- FOVFreq (m) : Field of view in the frequency encoding direction
- FOVPhase (m) : Field of view in the first phase encoding direction
- FlipAng (Degree) : Nominal flip angle of excitation pulse
- FreqDir : Frequency encoding direction
- ResFreq : Number of voxels in frequency encoding direction
- ResPhase : Number of voxels in the first phase encoding direction
- ScanPlane : The scanning plane
- SliceNum : The number of encoding slice
- SliceThick (m) : The thickness of one slice
- TE (s) : The time of echo
- TEPerTR : The number of echoes in multiple echo mode, using a number greater than one requires 'MultiEcho' tab to be loaded
- TR (s) : The time of repetition

3.8.2 Advanced

The ‘Advanced’ tab contains other imaging parameters.

- MasterTxCoil : The master transmitting coil in multi RF transmitting mode
- MultiTransmit : The flag for turning on and off multi RF transmitting mode, default mode is ‘off’ for single RF transmitting
- NEX : The number of excitation
- NoFreqAlias : The flag for avoiding aliasing in frequency encoding direction, default ‘on’ truncates object outside field of view in frequency encoding direction
- NoPhaseAlias : The flag for avoiding aliasing in the first phase encoding direction, default ‘on’ truncates object outside field of view in the first phase encoding direction
- NoSliceAlias : The flag for avoiding aliasing in the second phase encoding (i.e. slice encoding) direction, default ‘on’ truncates object outside field of view in slice encoding direction
- Shim : The flag for choosing shimming mode, manual shimming requires ‘Shim’ tab to be loaded, auto shimming maintain ideal uniform B0 field
- TEAnchor : The flag for choosing TE time offset regarding the excitation RF pulse

3.8.3 Hardware

The ‘Hardware’ tab contains parameters relevant to system hardware setup.

- B0 (T) : Main static magnetic field strength
- B1Level (T) : A linear scale factor for B1. The input B1+ field with magnitude of this number produces nominal flip angle
- E1Level (T) : A linear scale factor for E1. When calculating spatial SAR, the input E1+ field is scaled by a factor of nominal RF amplitude divided by this number
- MaxGrad (T/m) : Maximum allowable gradient strength
- MaxSlewRate (T/m/s) : Maximum allowable gradient slew rate
- MinUpdRate (s) : Minimum update time on generating sequence waveform
- Model : A descriptive string indicating possible real scanner system with similar hardware setting

- NoiseLevel : The level of adjustable noise, the higher the number, the more noise
- SpinPerVoxel : The number of spins in each voxel. Default one spin per voxel will treat $T2^*$ equal to $T2$, **use a number greater than one to simulate $T2^*$ effect based on $T2Star$ input**. Note that simulation time is likely linearly scaled by this number

3.8.4 Recon

The ‘Recon’ tab contains parameters relevant to image reconstruction.

- AutoRecon : The flag for turning on and off automatic image reconstruction after MR signal acquisition
- ExternalEng : The name of a user defined script for image reconstruction
- OutputType : The type of output data including both simulated image and signal, options include ‘MAT’ and ‘ISMRRMRD’, the latter requires ISMRRMRD dependency packages to be installed
- ReconEng : The image reconstruction engine, choosing ‘Default’ uses MRiLab default reconstruction code, choosing ‘External’ uses external engine which requires ExternalEng to be provided
- ReconType : The type of image reconstruction

3.8.5 CVs

The ‘CVs’ tab contains Controllable Variables (CV, again follow GE’s naming convention) which exist in the global scope of sequence design. They are designed for transferring values among multiple MR sequence modules. The user can use them for customized sequence.

- CV1 : Controllable variable 1
- CV2 : Controllable variable 2
- CV3 : Controllable variable 3
- CV4 : Controllable variable 4
- CV5 : Controllable variable 5
- CV6 : Controllable variable 6
- CV7 : Controllable variable 7
- CV8 : Controllable variable 8
- CV9 : Controllable variable 9

- CV10 : Controllable variable 10
- CV11 : Controllable variable 11
- CV12 : Controllable variable 12
- CV13 : Controllable variable 13
- CV14 : Controllable variable 14

3.8.6 SpecialTech

The Special Technique (SpecialTech) contains multiple tabs from which one or more are loaded based on sequence configuration and user choice.

1. DummyPulse

The ‘DummyPulse’ tab are designed to add dummy pulse section prior to image acquisition section. It can be used to skip transient steady state signal.

- DP_Flag : The flag for turning on and off dummy pulse
- DP_FlipAng (Degree) : The flip angle of excitation pulse for dummy pulse
- DP_Num : The number of TRs for dummy pulse
- DP_TR (s) : The time of repetition for dummy pulse

2. EPI

The ‘EPI’ tab contains parameters for performing multi shot interleaved EPI readout.

- EPI_ESP (s) : The echo spacing for EPI
- EPI_ETL : The echo train length for EPI
- EPI_EchoShifting : The flag for turning on and off echo shifting
- EPI_ShotNum : The number of EPI shots, multi shot EPI uses interleaved mode

3. FSE

The ‘FSE’ tab contains parameters for performing multi shot interleaved FSE readout.

- FSE_ESP (s) : The echo spacing for FSE
- FSE_ETL : The echo train length for FSE
- FSE_ShotNum : The number of FSE shots, multi shot FSE uses interleaved mode

4. GRAPPA (:TODO)

The ‘GRAPPA’ tab contains parameters for performing parallel imaging using GRAPPA.

5. Gridding

The ‘Gridding’ tab contains parameters for controlling gridding process in default Non-Cartesian reconstruction. MRiLab uses Voronoi diagram for k -space density compensation, and uses Kaiser-Bessel kernel for gridding. Detailed explanation is beyond the scope of this manual, interested users are referred to literature [2, 3, 4].

- G_Deapodization : The flag for turning on and off kernel deapodization (i.e. dividing reconstructed image with the iFFT of the gridding kernel)
- G_KernelSample : The number of kernel sample point, the more sample points, the better kernel approximation
- G_KernelWidth : The full width of kernel in the unit of gridding grid
- G_OverGrid : The over gridding factor
- G_Truncation : The flag for turning on and off image truncation for reconstructed image

6. IRPrep

The ‘IRPrep’ tab contains parameters for inversion recovery sequence.

- TI (s) : The time of inversion recovery

7. MT

The ‘MT’ tab contains parameters for activating MR sequences running Magnetization Transfer model (MT). In order to perform MT experiment, MT phantom is required.

- MT_Flag : The flag for turning on and off MT simulation

8. ME

The ‘ME’ tab contains parameters for activating MR sequences running Multiple pool spin Exchange model (ME). In order to perform ME experiment, ME phantom is required.

- ME_Flag : The flag for turning on and off ME simulation

9. CEST

The ‘CEST’ tab contains parameters for activating MR sequences running Chemical Exchange Saturation Transfer (CEST). In order to perform CEST experiment, CEST phantom is required.

- CEST_Flag : The flag for turning on and off CEST simulation

10. GM

The ‘GM’ tab contains parameters for activating MR sequences running Generalized Multi-pool exchanging model (GM). In order to perform GM experiment, GM phantom is required.

- GM_Flag : The flag for turning on and off GM simulation

11. RTRecon

The ‘RTRecon’ tab contains parameters for performing real time image reconstruction. Notice that adding RTRecon tab is required to perform real time reconstruction, the user also needs to use the extended real time process to trigger real time image reconstruction at the Ext sequence line. See Section 5.2.7 for more details.

- RTR_Flag : The flag for turning on and off real time reconstruction
- PlotK_Flag : The flag for turning on and off real time k -space plotting
- DelayTime : The delay time for refreshing graphics

12. MultiEcho

The ‘MultiEcho’ tab contains parameters for performing multi echo experiment, the number of echoes much match TEPerTR.

- ME_TEs (s) : An array of multiple echo values

13. PartialEcho (:TODO)

The ‘PartialEcho’ tab contains parameters for performing partial echo in readout.

14. Radial

The ‘Radial’ tab contains parameters for performing 2D radial readout sampling.

- R_AngPattern : The pattern for sampling the angle in k -space
- R_AngRange : The range of sampling angle
- R_SampPerSpoke : The number of sampling points in each spoke
- R_SpokeNum : The number of sampling spokes

15. SENSE (:TODO)

The ‘SENSE’ tab contains parameters for performing parallel imaging using SENSE.

16. Shim

The ‘Shim’ tab contains parameters for performing manual B0 shimming.

- Sh_X : The constant for X term
- Sh_Y : The constant for Y term
- Sh_Z : The constant for Z term
- Sh_ZX : The constant for ZX term
- Sh_ZY : The constant for ZY term
- Sh_Z2 : The constant for Z^2 term
- Sh_XYZ : The constant for XYZ term
- Sh_X2_Y2 : The constant for X^2Y^2 term

17. Spiral

The ‘Spiral’ tab contains parameters for performing multi shot spiral read-out. The 2D spiral design uses a method described in literature [5].

- S.Gradient (T/m) : The desired gradient amplitude
- S.Lamda (1/m/rad) : A constant affecting radial sampling interval in the spiral trajectory
- S.ShotNum : The number of spiral interleaves
- S.SlewRate (T/m/s) : The desired slew rate. Notice that in this approximation, slew rate overshoots the desired value for part of the slew-rate-limited region
- S.SlewRate0 (T/m/s) : The slew rate at the beginning

18. T2Prep

The ‘T2Prep’ tab contains parameters for T2 preparation sequence.

- T2Prep (s) : The preparation time for T2 decay

19. VIPR (:TODO)

The ‘VIPR’ tab contains parameters for performing Vastly Undersampled Isotropic Projection Reconstruction (VIPR) sequence.

20. ZeroFilling

The ‘ZeroFilling’ tab contains parameters for performing image interpolation in the k -space using zero filling.

- ZF_Kz : The zero filling factor in Kz
- ZF_Ky : The number of point in Ky after zero filling
- ZF_Kx : The number of point in Kx after zero filling

3.9 Parallel Computing

The current MRiLab version supports two types of parallel computing mechanisms: GPU based parallel computing using CUDA and multi-threading CPU based parallel computing using OpenMP. As mentioned before, GPU support requires NVIDIA GPU with CUDA capability (shader model 2.0 and above). The OpenMP is, however, supported by most of modern multi core CPU. If both GPU and CPU are available, the user can choose to use one of these two methods. To switch parallel computing methods, go to ‘Parallel’ menu and ‘Select Engine’ and choose available GPU or CPU devices.

Chapter 4

Simulation

4.1 Running Simulation

The MRiLab converts simulation parameters from configuration files into temporary configuration structures during loading process, and uses these structures to organize simulation workflow. The user can check default value of each parameter by placing mouse cursor over selected parameter. The user can modify simulation parameters for desirable simulation design, **to make changes effective, the user needs to press ‘Update’ button located under ‘Simulation Settings’ panel.** The ‘Update’ button not only updates these structures, but also performs a series of pre-scan processes including checking incompatibility error and initializing other necessary simulation variables.

On the left of ‘Update’ button, there is a ‘Save’ button which saves updated configuration structure back into configuration files for later use. **One particular case is that ‘CVs’ need to be updated and saved in order to make changes effective.** This is because ‘CVs’ is one part of the sequence file which needs to be interpreted at the sequence waveform generation module. The sequence memo is also provided at the ‘PSD Memo’ panel. It’s editable and can be saved using ‘Save’ button.

On the right of ‘Update’ button, there is a ‘Scan’ button which activates sequence waveform generation, actual scan process and post-scan process including image reconstruction and data saving. The MRiLab automatically detects parameter changes and set ‘Scan’ button disabled. To enable ‘Scan’ button, simply press ‘Update’ button. Notice that the update process may take some time if heavy initialization is needed. The ‘Simulation Info Log’ is helpful for checking log information about each simulation step. Once simulation setting gets configured properly, the user can press ‘Scan’ button to start scanning.

In MRiLab v1.3, batch scan is also provided. Instead of performing scan

right after configuration, the user can choose to snapshot current configuration in batch basket by pressing 'basket' button on the right side of 'Scan' button. To view queued scans, the user can press 'BatchSim' toolbar icon



Figure 4.1: BatchSim Toolbar Icon

The BatchSim panel (Figure 4.2) gives a list of queued scan tasks, the user can move the order of these scans, delete queued scans and execute them all in one click. The output folder is also adjustable.

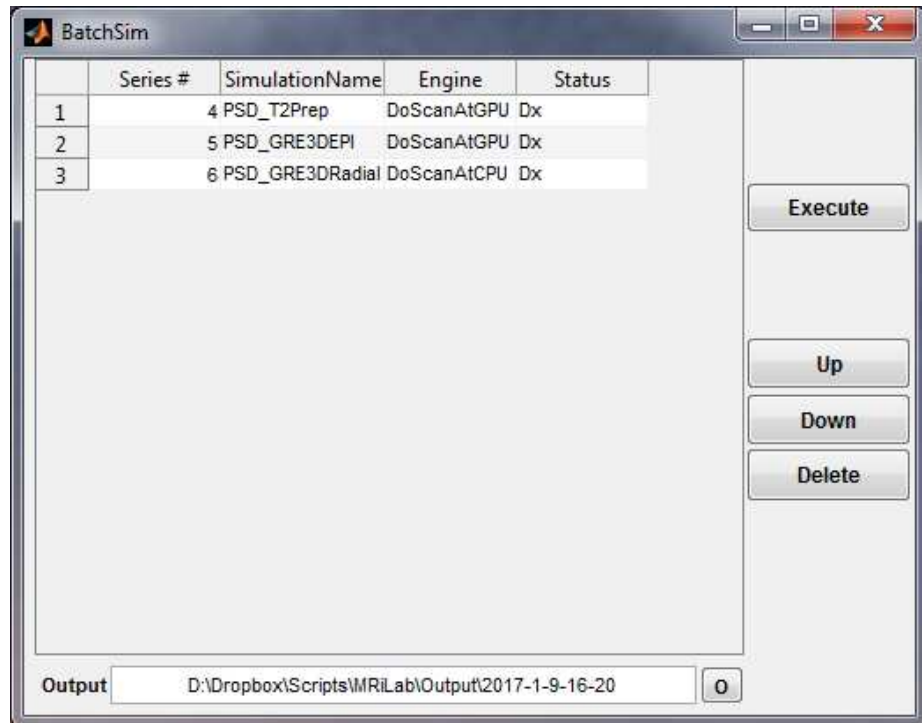


Figure 4.2: A Preview of A BatchSim Panel. This panel shows a list of queued scan tasks.

4.2 Image and SNR

Figure 4.3 demonstrates an example of a series of simulation operated with different sequences. Each sequence is labeled with a unique series number, and



Figure 4.3: A Preview of A Simulated Image. The preview is one slice of simulated image using gradient echo sequence with radial readout and reconstructed without deapodization.

shows in the list at ‘Scan Series’ panel. This series number is also a reference id for saved image and data in the output database (further explain in Chapter 5). There is also a status label on the left of each sequence name. The status labels include:

- Dx : parameter setting and sequence loading
- ... : scanning
- B : queued scan in batch mode
- V : scan complete successfully
- X : scan incomplete or fail

The example (Figure 4.3) shows a series of successful simulation by using PSD_GRE3D, PSD_GRE3DRadial and PSD_FIESTA3D sequences, as well as an incomplete simulation using PSD_FIESTA3D at the second time. The preview axes displays an image preview for series 2 simulated using PSD_GRE3DRadial sequence. The user can switch previews for successful simulation by clicking scan series item. Moreover, the series name is also editable. In this example the series name is kept the same as sequence name, which is not absolutely necessary. If the multiple channel coil for multiple receiving is performed (Figure 4.4), the user can specify display image to a single channel with ‘Channel #’ pop-up menu, or choose ‘SumofMagn’ for summation of image magnitude of all channels or ‘SumofCplx’ for summation of complex image of all channels. If multiple echo is enabled in the sequence, the user can also specify display image to any echo with ‘Echo #’ pop-up menu. Default value of 1 is used for single echo. The preview image provides a quick overview of the simulated images, a further image analysis can be performed with image display and analysis tools in Chapter 6.

At the bottom of the preview axes, there are information for the sequence name, estimated remaining scan time in real time and a scan progress bar. A global relative Signal-to-Noise Ratio (SNR) is also provided and automatic updated in real time. The relative SNR is defined as the ratio of current SNR to the initial SNR calculated upon loading the sequence. The SNR value is calculated using Equation 4.1.

$$SNR = B0 \times RFreq \times RPhase \times RSlice \times \frac{\sqrt{ResFreq \times ResPhase \times SliceNum \times NEX}}{NoiseLevel \times \sqrt{BandWidth}} \quad (4.1)$$

where

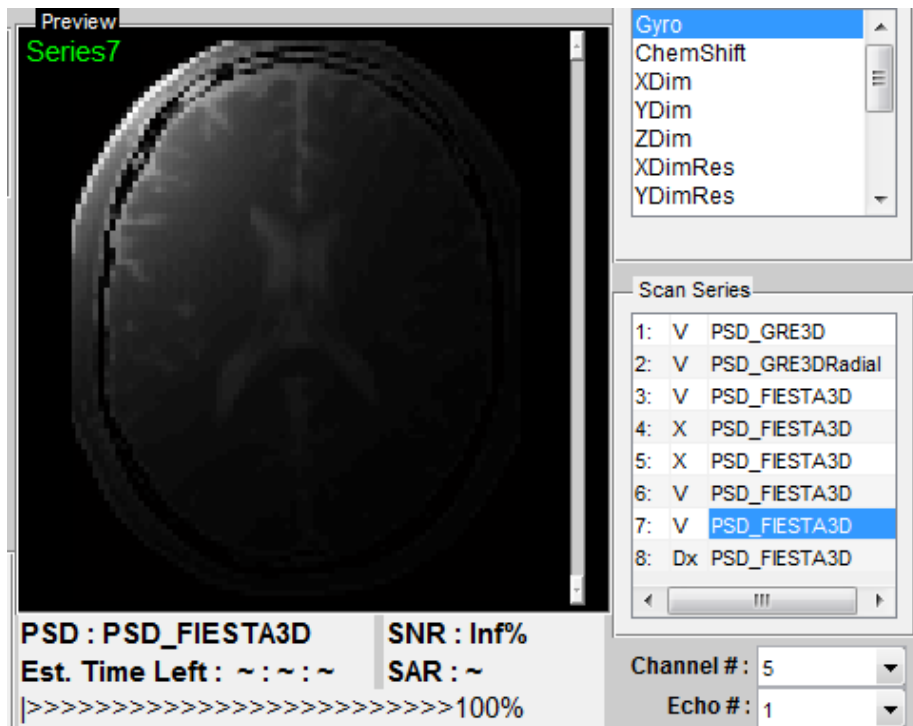


Figure 4.4: A Preview of A Simulated Image with Multiple Receiving. The preview is one slice of simulated image using FIESTA sequence with 8 channel head coil. The image is from the fifth coil channel.

$$\begin{aligned}
RFreq &= \frac{FOVFreq}{ResFreq}; \\
RPhase &= \frac{FOVPhase}{ResPhase}; \\
RSlice &= SliceThick.
\end{aligned} \tag{4.2}$$

To simulate image noise, MRiLab performs a noise adding process to acquired k -space data. The Gaussian noise with zero mean and user-defined standard deviation is added to the complex signal. The standard deviation is determined using Equation 4.3. If no noise is desired, the user can set ‘NoiseLevel’ to zero to get infinite SNR.

$$Noise = \frac{\frac{NoiseLevel}{NoiseRef} \times \sqrt{\frac{BandWidth}{BWRef}}}{\frac{B0}{B0Ref} \times \frac{RFreq \times RPhase \times RSlice}{VolRef} \times \sqrt{\frac{NEX}{NEXRef} \times \frac{ResFreq \times ResPhase \times SliceNum}{ADCRef}}} \tag{4.3}$$

where these reference values are given as:

$$\begin{aligned}
BWRef &= 1e3; \\
NoiseRef &= 1; \\
B0Ref &= 1.5; \\
VolRef &= 1e-9; \\
NEXRef &= 1; \\
ADCRef &= 1e4.
\end{aligned} \tag{4.4}$$

Chapter 5

MRiLab Toolboxes

MRiLab toolboxes consists of several individual GUIs for conducting design task for RF pulse, MR sequence and Coil etc. These toolboxes allow to build and customize project specific MR simulation experiment. This chapter covers the introduction to each toolbox and corresponding macro libraries.

5.1 RF Pulse Design

The RF pulse design toolbox can be activated by pressing ‘RF Design Panel’ toolbar icon located at the top of the main simulation console.



Figure 5.1: RF Design Panel Toolbar Icon

5.1.1 RF Design GUI

Figure 5.2 demonstrates an overview of the RF Pulse Design interface. This interface consists of

1. RF and Gradient Pulse Macro Library

The user can use this interface to analyze tissue spin response regarding a selected RF and gradient pulse. To select a RF pulse macro, the user needs to click the macro library tree to unfold the tree structure, and then click a desired RF macro. The properties of the chosen RF macro will show on the left panel under ‘rf:rf name’ tab. The RF memo information is also shown at the ‘rf Memo’ panel below the tree structure. The user can press ‘Execute’ button to start analysis process. MRiLab supports

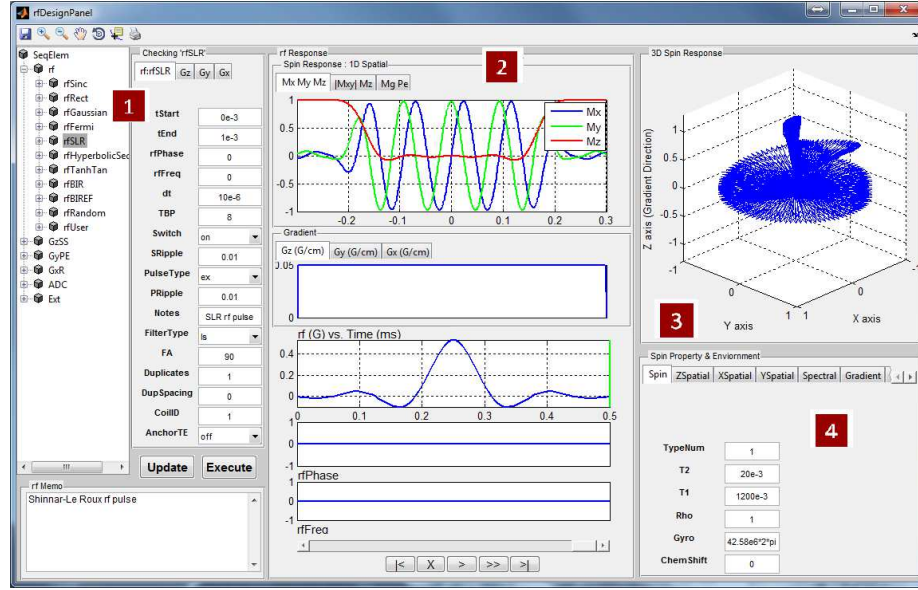


Figure 5.2: RF Design Panel. An example of simulating the slice profile of a linear phase Shinnar-Le Roux RF pulse.

three analysis modes for analyzing 1D spatial RF pulse, 2D spatial RF pulse and Spatial-Spectral RF pulse:

- 1D Spatial Mode

MRiLab assumes a gradient is applied in the Z direction, therefore a constant gradient will be applied if 'Gz' tab is empty (Figure 5.3). To select a 'Gz' gradient, the user needs to choose a gradient macro under 'GzSS'. For example, the 'GzSelective' is a recommended gradient macro typically used for performing slice selection in MRiLab. Once the user selected a gradient macro, the 'Gz:gradient name' tab will become activated and the properties of this gradient macro become accessible and editable. The user can modify macro attributes to meet design goals. To make any modification effective, the user must press 'Update' button before executing the slice profile analysis. Although the library tree contains macros for another gradient line (e.g. GyPE, GxR), they are typically ignored in this mode.

- 2D Spatial Mode

MRiLab assumes a gradient is applied in both the X and Y directions, a constant gradient will be applied if 'Gx' tab or 'Gy' tab is empty. The user can choose any Gx and Gy gradient macros for these two tabs and modify macro attributes to satisfy 2D RF pulse design. To activate 2D pulse analysis, the 'Spat.Flag' under 'XSpatial' tab has

to be turned on (4c). The Gz gradient is typically ignored under this mode.

- Spatial-Spectral Mode

MRiLab assumes a gradient is applied in the Z direction, a constant gradient will be applied if 'Gz' tab is empty. The user can choose any Gz gradient macros for this tab and modify macro attributes to satisfy Spatial-Spectral pulse design. The user can also modify the frequency range and resolution under 'Spectral' tab (4e). To activate Spatial-Spectral pulse analysis, the 'Freq_Flag' has to be turned on (4e). The Gx and Gy gradient are typically ignored under this mode.

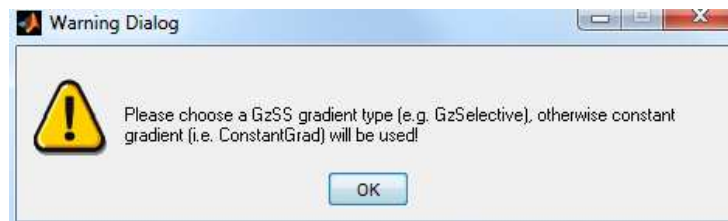


Figure 5.3: A Warning Window for Using Constant Gradient

2. Spin Response

Under 1D Spatial Mode, MRiLab provides three slice profile figures (Figure 5.4) on the 'Spin Response' panel under different tabs. These figures include slice profile regarding

- Mx My Mz : three independent spin component
- |Mxy| Mz : transverse and longitudinal component
- Mg Pe : transverse component magnitude and phase

The horizontal axis is the spin position in units of meters, and the vertical axis is the value of the components in normalized units.

Under 2D Spatial or Spatial-Spectral Mode, MRiLab provides five spin response figures on the 'Spin Response' panel under different tabs. These figures include

- Mx : spin X component
- My : spin Y component
- Mz : spin Z component
- Mag : transverse component magnitude
- Ph : transverse component phase

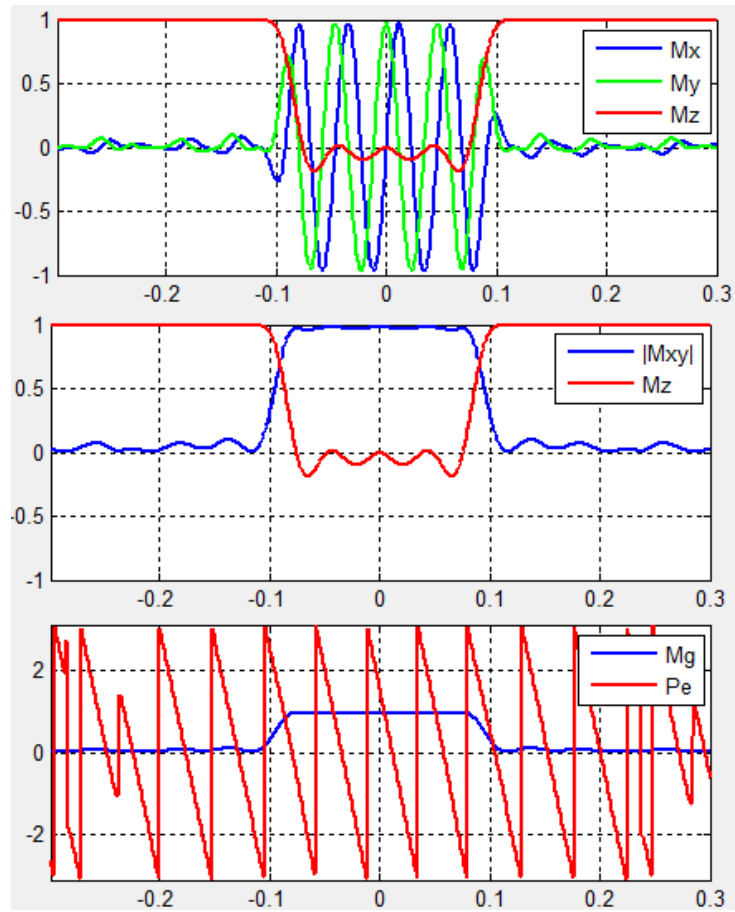


Figure 5.4: A Slice Profile Analysis of A linear phase SLR Pulse

The horizontal axis is the spin position for 2D Spatial mode and the frequency range for Spatial-Spectral mode, and the vertical axis is the spin location in both mode. Notice the units of both axes use spin index for either spatial position or frequency position according to spin property and environment (4c, 4d and 4e).

MRiLab also plots the RF and gradient waveform. In MRiLab, the property of a RF pulse contains RF amplitude (T), RF phase (rad) and RF frequency (Hz). The RF frequency is defined as the spin Larmor frequency minus the laboratory frequency of the RF pulse. Notice that in those figures, for display purpose, the gradient amplitude is in units of G/cm and RF amplitude is in units of G. Both time axes are in units of milliseconds. At the bottom of this interface, there is a group of pushbuttons (Figure 5.5) allowing the user to investigate intermediate spin response during a applied RF and gradient (Figure 5.6).

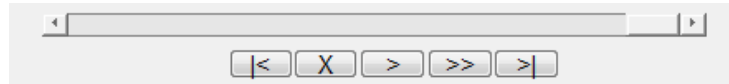


Figure 5.5: The Playback Control Group for Spin Response

- Scroll Bar : Drag the scroll bar to any intermediate time point between beginning and end
- | < : Move to the beginning
- X : Pause animation, notice that the interface can only be closed while animation is paused
- O : Resume animation
- > : Play at normal speed
- >> : Play at double normal speed
- > | : Move to the end

3. 3D Spin Response

MRiLab renders 3D spin response in '3D Spin Response' panel based on different modes. The user can inspect the behavior of spins at specific location under a chosen RF pulse and gradient. The user can use Matlab default graphical tools for interactively changing display view and size (Figure 5.8). To change three-dimensional spin response content reflecting different tabs in 2D spatial mode or Spatial-Spectral model (Figure 5.7), the trick is to simply activate any item of the playback control group (e.g. click the scroll bar).

4. Spin Property and Environment

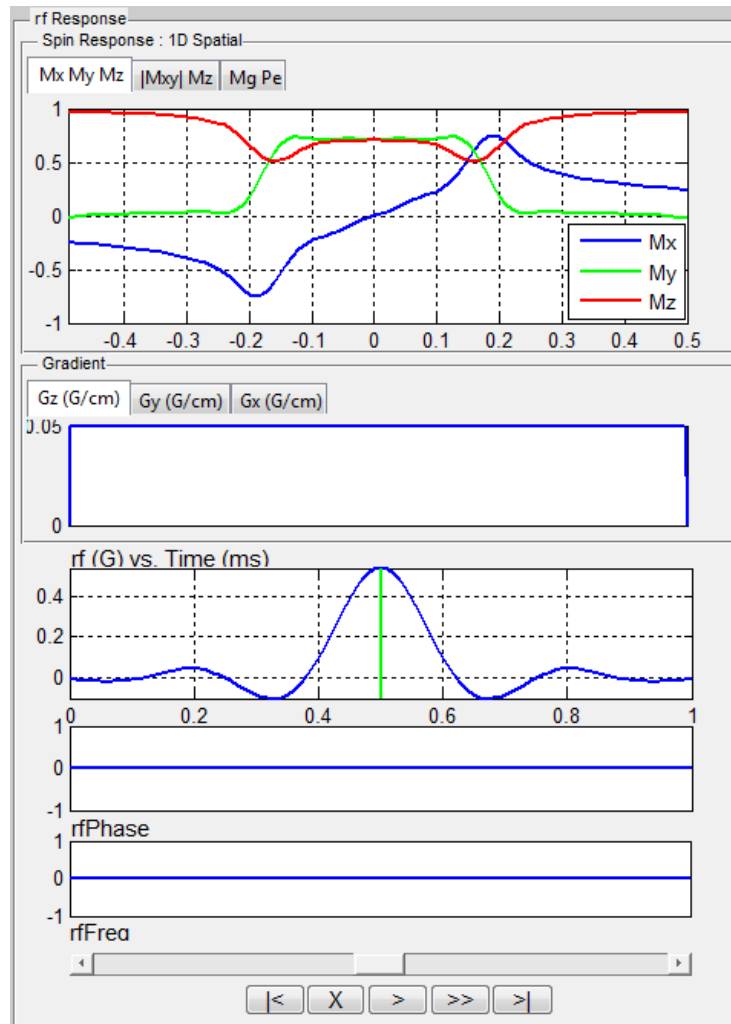


Figure 5.6: An Intermediate Slice Profile in The Middle of RF Pulse

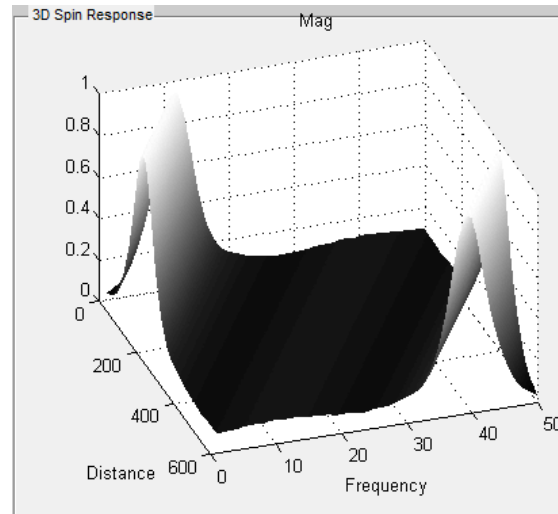


Figure 5.7: The Magnitude of Spin Transverse Component from A Spatial-Spectral Analysis of An Inversion Adiabatic rf Pulse



Figure 5.8: Matlab Default Graphical Tools

The user can modify spin properties and environment to satisfy specific experiment design. The editable properties provided in this interface include:

(a) Spin

- ChemShift (Hz/T): The chemical shift of the spin
- Gyro (rad/s/T): The gyromagnetic ratio of the spin
- Rho : The spin density of the spin
- T1 (s): The longitudinal relaxation time
- T2 (s): The transverse relaxation time
- TypeNum : The number of spin species

(b) ZSpatial

- ZCenter : The index of the central spin in Z direction
- ZSpin : The number of the spins in Z direction
- ZSpinGap (m): The distance between adjacent spins in Z direction

(c) XSpatial

- XCenter : The index of the central spin in X direction
- XSpin : The number of the spins in X direction
- XSpinGap (m): The distance between adjacent spins in X direction
- Spat_Flag: The flag to turn on and off 2D spatial RF analysis

(d) YSpatial

- YCenter : The index of the central spin in Y direction
- YSpin : The number of the spins in Y direction
- YSpinGap (m): The distance between adjacent spins in Y direction

(e) Spectral

- FreqRes : The number of linear frequency sample points
- FreqUpLimit : The upper limit of frequency range
- FreqDownLimit : The lower limit of frequency range
- Freq_Flag: The flag to turn on and off Spatial-Spectral RF analysis

(f) Gradient

- ConstantGrad (T/m): The constant gradient applied when gradient tab is empty

(g) Magnet

- dB0 (T): The main static magnetic field offset

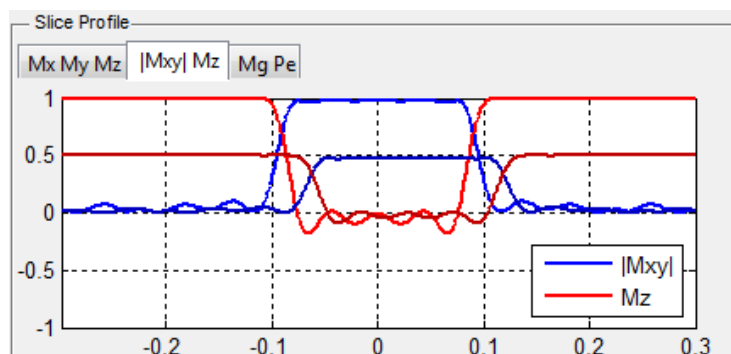


Figure 5.9: A Slice Profile Analysis of Two Spin Species

Figure 5.9 demonstrates a slice profile for two different spin species under the same RF pulse and gradient in 1D spatial mode. To enable slice profile analysis for multiple spin species, the user needs to provide multiple values for T1, T2, Rho and ChemShift in an array, and give the correct number of spin species. The values must be separated with space. For example

- ChemShift = 0 -210
- Rho = 1.0 0.5
- T1 = 1.2 1.0
- T2 = 0.02 0.03
- TypeNum = 2

5.1.2 RF Macro Library

MRiLab uses a concept of macros to simplify experiment design. A RF macro is a predefined module for one type of RF pulse which allows flexible programming-free modification for specific experimental design. MRiLab RF macro library is a collection of RF macros covering from simple RF pulses such as hard pulse, to complex RF pulses such as adiabatic pulses. A specific RF macro to interact with external RF pulse file is also provided to create more extensible pulse design environment. This section will give an introduction to each of the RF macros provided in MRiLab.

rfSinc

A RF macro that creates a Sinc type RF pulse. This macro contains attributes including:

- Apod : Apodization methods including ‘Non’, ‘Hamming’ and ‘Hanning’
- FA (Degree) : Prescribed flip angle

- TBP : The time bandwidth product
- dt (s) : The time interval of RF pulse sample points
- rfPhase (rad) : RF pulse phase
- rfFreq (Hz) : RF pulse frequency
- tStart (s) : RF pulse starting time
- tEnd (s) : RF pulse ending time
- Switch : The flag for turning on and off RF pulse in the RF sequence line
- AnchorTE : The flag for turning on and off TE reference, TE is calculated from this RF pulse if this flag is turned on
- Duplicates : The number of the RF pulse duplicates, used for creating multiple RF pulses with the same shape
- DupSpacing : The time spacing between RF pulse duplicates
- CoilID : The ID of the coil element used with this RF pulse, applied for multiple RF transmitting
- Notes : The notes of the RF pulse

The time dependence of the Sinc RF pulse is given by [6]:

$$B_1(t) = \begin{cases} At_0 \frac{\sin(\frac{\pi t}{t_0})}{\pi t} & -N_L t_0 \leq t \leq N_R t_0 \\ 0 & \text{elsewhere} \end{cases} \quad (5.1)$$

where A is the peak RF amplitude automatically calculated and scaled according to flip angle, t_0 is one-half the width of the central lobe, and the N_L and N_R are the number of zero-crossings to the left and right of the central peak, respectively. In MRiLab, the $N_L \equiv N_R$, thus the Sinc RF pulse is always symmetric. Notice that the The time bandwidth product of a Sinc pulse equals the number of zero-crossings including the start and end. In order to address the discontinuity at the start and end, apodization can be applied using ‘Hamming’ or ‘Hanning’ window as described by:

$$Apodization(t) = \begin{cases} (1 - \alpha) + \alpha \cos(\frac{\pi t}{N t_0}) & -N_L t_0 \leq t \leq N_R t_0 \\ 0 & \text{elsewhere} \end{cases} \quad (5.2)$$

where N equals N_L and N_R . Hamming window uses $\alpha = 0.46$, and Hanning window uses $\alpha = 0.5$. If ‘Non’ is used, apodization is disabled.

rfRect

A RF macro that creates a hard RF pulse. This macro contains attributes including:

- FA (Degree) : Prescribed flip angle
- dt (s) : The time interval of RF pulse sample points
- rfPhase (rad) : RF pulse phase
- rfFreq (Hz) : RF pulse frequency
- tStart (s) : RF pulse starting time
- tEnd (s) : RF pulse ending time
- Switch : The flag for turning on and off RF pulse in the RF sequence line
- AnchorTE : The flag for turning on and off TE reference, TE is calculated from this RF pulse if this flag is turned on
- Duplicates : The number of the RF pulse duplicates, used for creating multiple RF pulses with the same shape
- DupSpacing : The time spacing between RF pulse duplicates
- CoilID : The ID of the coil element used with this RF pulse, applied for multiple RF transmitting
- Notes : The notes of the RF pulse

The time dependence of the hard RF pulse is given by [6]:

$$B_1(t) = \begin{cases} A & |t| \leq \frac{T}{2} \\ 0 & |t| > \frac{T}{2} \end{cases} \quad (5.3)$$

where A is the peak RF amplitude automatically calculated and scaled according to flip angle, T is the width of RF pulse that equals $t_{\text{End}} - t_{\text{Start}}$.

rfGaussian

A RF macro that creates a Gaussian type RF pulse. This macro contains attributes including:

- FA (Degree) : Prescribed flip angle
- dt (s) : The time interval of RF pulse sample points
- rfPhase (rad) : RF pulse phase
- rfFreq (Hz) : RF pulse frequency

- tStart (s) : RF pulse starting time
- tEnd (s) : RF pulse ending time
- Switch : The flag for turning on and off RF pulse in the RF sequence line
- AnchorTE : The flag for turning on and off TE reference, TE is calculated from this RF pulse if this flag is turned on
- Duplicates : The number of the RF pulse duplicates, used for creating multiple RF pulses with the same shape
- DupSpacing : The time spacing between RF pulse duplicates
- CoilID : The ID of the coil element used with this RF pulse, applied for multiple RF transmitting
- Notes : The notes of the RF pulse

The time dependence of the Gaussian RF pulse is given by [6]:

$$B_1(t) = Ae^{-\frac{t^2}{2\sigma^2}} \quad \text{pulse centered at } t = 0 \quad (5.4)$$

where A is the peak RF amplitude automatically calculated and scaled according to flip angle, σ is linearly proportional to the pulse width. Also the Gaussian RF pulse is terminated with a 60-dB attenuation.

rfFermi

A RF macro that creates a Fermi RF pulse. This macro contains attributes including:

- PW : The measure of the pulse width
- FA (Degree) : Prescribed flip angle
- dt (s) : The time interval of RF pulse sample points
- rfPhase (rad) : RF pulse phase
- rfFreq (Hz) : RF pulse frequency
- tStart (s) : RF pulse starting time
- tEnd (s) : RF pulse ending time
- Switch : The flag for turning on and off RF pulse in the RF sequence line
- AnchorTE : The flag for turning on and off TE reference, TE is calculated from this RF pulse if this flag is turned on
- Duplicates : The number of the RF pulse duplicates, used for creating multiple RF pulses with the same shape

- DupSpacing : The time spacing between RF pulse duplicates
- CoilID : The ID of the coil element used with this RF pulse, applied for multiple RF transmitting
- Notes : The notes of the RF pulse

The time dependence of the Fermi RF pulse is given by [6]:

$$B_1(t) = \frac{A}{1 + e^{\frac{|t|-t_0}{\alpha}}} \quad \text{pulse centered at } t = 0 \quad (5.5)$$

where A is the peak RF amplitude automatically calculated and scaled according to flip angle, t_0 is a measure of the pulse width that corresponds to PW, α is a measure of the transition width. The Fermi pulse approximates more to a rectangle pulse with larger t_0 value. Also the Fermi RF pulse is terminated with a 60-dB attenuation.

rfSLR

A RF macro that creates a RF pulse using Shinnar-Le Roux algorithm. This macro contains attributes including:

- PulseType : The type of this SLR pulse, including 'st' (small tip angle pulse), 'ex' (excitation pulse), 'se' (spin-echo pulse), 'sat' (saturation pulse) and 'inv' (inversion pulse)
- FilterType : The type of the applied filter design method, including 'ls' (least squares), 'min' (minimum phase), 'max' (maximum phase), 'pm' (Parks-McClellan equal ripple), and 'ms' (Hamming windowed sinc)
- PRipple : The ripple factor at passband
- SRipple : The ripple factor at stopband
- FA (Degree) : Prescribed flip angle
- TBP : The time bandwidth product
- dt (s) : The time interval of RF pulse sample points
- rfPhase (rad) : RF pulse phase
- rfFreq (Hz) : RF pulse frequency
- tStart (s) : RF pulse starting time
- tEnd (s) : RF pulse ending time
- Switch : The flag for turning on and off RF pulse in the RF sequence line
- AnchorTE : The flag for turning on and off TE reference, TE is calculated from this RF pulse if this flag is turned on

- Duplicates : The number of the RF pulse duplicates, used for creating multiple RF pulses with the same shape
- DupSpacing : The time spacing between RF pulse duplicates
- CoilID : The ID of the coil element used with this RF pulse, applied for multiple RF transmitting
- Notes : The notes of the RF pulse

MRiLab implements a library of Matlab SLR pulse design routines, originally developed by Prof. John Pauly and published online at <http://rsl.stanford.edu/research/software.html>. Thorough explanation of the algorithm is beyond the scope of this manual, users who are interested in the SLR algorithm are referred to literature [6, 7].

rfHyperbolicSecant

A RF macro that creates an adiabatic inversion RF pulse based on hyperbolic secant modulation. This macro contains attributes including:

- Adiab : The adiabatic factor
- MaxB1 (T) : The maximum B1 field
- TBP : The time bandwidth product
- dt (s) : The time interval of RF pulse sample points
- rfPhase (rad) : RF pulse phase
- tStart (s) : RF pulse starting time
- tEnd (s) : RF pulse ending time
- Switch : The flag for turning on and off RF pulse in the RF sequence line
- AnchorTE : The flag for turning on and off TE reference, TE is calculated from this RF pulse if this flag is turned on
- Duplicates : The number of the RF pulse duplicates, used for creating multiple RF pulses with the same shape
- DupSpacing : The time spacing between RF pulse duplicates
- CoilID : The ID of the coil element used with this RF pulse, applied for multiple RF transmitting
- Notes : The notes of the RF pulse

The time dependence of the hyperbolic secant RF pulse is given by [6]:

$$\begin{aligned} A(t) &= A_0 \text{sech}(\beta t) && \text{amplitude modulation} \\ F(t) &= \frac{-\mu\beta}{2\pi} \tanh(\beta t) && \text{frequency modulation} \end{aligned} \quad (5.6)$$

where A_0 is the maximum B1 field corresponding to MaxB1, μ is a dimensionless adiabatic factor corresponding to Adiab, β is an modulation angular frequency. It can be shown that TBP has the relationship with β and μ as

$$TBP = \frac{T\mu\beta}{\pi} \quad (5.7)$$

where T is the pulse width.

To satisfy the Adiabatic Condition, the parameter setting has to meet

$$A_0 \gg \frac{\sqrt{\mu}\beta}{\gamma} \quad (5.8)$$

rfTanhTan

A RF macro that creates an adiabatic inversion RF pulse based on tanh/tan modulation. This macro contains attributes including:

- MaxB1 (T) : The maximum B1 field
- TBP : The time bandwidth product
- dt (s) : The time interval of RF pulse sample points
- rfPhase (rad) : RF pulse phase
- tStart (s) : RF pulse starting time
- tEnd (s) : RF pulse ending time
- Switch : The flag for turning on and off RF pulse in the RF sequence line
- AnchorTE : The flag for turning on and off TE reference, TE is calculated from this RF pulse if this flag is turned on
- Duplicates : The number of the RF pulse duplicates, used for creating multiple RF pulses with the same shape
- DupSpacing : The time spacing between RF pulse duplicates
- CoilID : The ID of the coil element used with this RF pulse, applied for multiple RF transmitting
- Notes : The notes of the RF pulse

The tanh/tan RF pulse is constructed from an adiabatic half passage and its time-reversed adiabatic half passage. The time dependence of the first adiabatic half passage is given by [8]:

$$\begin{aligned} A(t) &= \gamma A_0 \tanh\left(\frac{2\xi t}{T}\right) & 0 \leq t \leq \frac{T}{2} & \text{amplitude modulation} \\ F(t) &= A \frac{\tan(\kappa(1 - \frac{2t}{T}))}{2\pi \tan(\kappa)} & 0 \leq t \leq \frac{T}{2} & \text{frequency modulation} \end{aligned} \quad (5.9)$$

where A_0 is the maximum B1 field corresponding to MaxB1, $\xi = 10$, $\tan(\kappa) = 20$, T is the pulse width. The TBP can be estimated using

$$TBP = \frac{A \cdot T}{\pi} \quad (5.10)$$

rfBIR

A RF macro that creates an adiabatic B1 Independent Rotation (BIR) RF pulse. This macro contains attributes including:

- MaxB1 (T) : The maximum B1 field
- MaxFreq (Hz) : The maximum RF frequency
- Lambda : The λ adiabatic factor
- Beta : The β adiabatic factor
- BIRFlag : The type of BIR pulse, including 'BIR-1', 'BIR-2' and 'BIR-4'
- dt (s) : The time interval of RF pulse sample points
- tStart (s) : RF pulse starting time
- tEnd (s) : RF pulse ending time
- Switch : The flag for turning on and off RF pulse in the RF sequence line
- AnchorTE : The flag for turning on and off TE reference, TE is calculated from this RF pulse if this flag is turned on
- Duplicates : The number of the RF pulse duplicates, used for creating multiple RF pulses with the same shape
- DupSpacing : The time spacing between RF pulse duplicates
- CoilID : The ID of the coil element used with this RF pulse, applied for multiple RF transmitting
- Notes : The notes of the RF pulse

The time dependence of the BIR-1 RF pulse is given by [6]:
Amplitude modulation:

$$A(t) = \begin{cases} \hat{x}A_0\cos(\xi t) & 0 \leq t < \frac{T}{2} \\ \hat{y}A_0\cos(\xi t) & \frac{T}{2} \leq t \leq T \end{cases} \quad (5.11)$$

Frequency modulation:

$$F(t) = \begin{cases} F_0\sin(\xi t) & 0 \leq t < \frac{T}{2} \\ -F_0\sin(\xi t) & \frac{T}{2} \leq t \leq T \end{cases} \quad (5.12)$$

where A_0 is the maximum B1 field corresponding to MaxB1, F_0 is the maximum RF frequency corresponding to MaxFreq. The RF pulse width is $T = \frac{\pi}{\xi}$, and \hat{x} and \hat{y} are unit vectors for indicating RF phase.

The time dependence of the BIR-2 RF pulse is given by [6]:
Amplitude modulation:

$$A(t) = \begin{cases} \hat{x}|A_0\cos(\xi t)| & 0 \leq t < \frac{T}{2} \\ \hat{y}|A_0\cos(\xi t)| & \frac{T}{2} \leq t < T \\ -\hat{y}|A_0\cos(\xi t)| & T \leq t \leq 2T \end{cases} \quad (5.13)$$

Frequency modulation:

$$F(t) = |F_0\sin(\xi t)| \quad (5.14)$$

where A_0 is the maximum B1 field corresponding to MaxB1, F_0 is the maximum RF frequency corresponding to MaxFreq. The RF pulse width is $T = \frac{\pi}{\xi}$, and \hat{x} and \hat{y} are unit vectors for indicating RF phase.

The time dependence of the BIR-4 RF pulse is given by [6]:
Amplitude modulation:

$$A(t) = \begin{cases} A_0\tanh[\lambda(1 - \frac{4t}{T})] & 0 \leq t < \frac{T}{4} \\ A_0\tanh[\lambda(\frac{4t}{T} - 1)] & \frac{T}{4} \leq t < \frac{T}{2} \\ A_0\tanh[\lambda(3 - \frac{4t}{T})] & \frac{T}{2} \leq t < \frac{3T}{4} \\ A_0\tanh[\lambda(\frac{4t}{T} - 3)] & \frac{3T}{4} \leq t \leq T \end{cases} \quad (5.15)$$

Frequency modulation:

$$F(t) = \begin{cases} \frac{\tan(\frac{4\beta t}{T})}{\tan(\beta)} & 0 \leq t < \frac{T}{4} \\ \frac{\tan[\beta(\frac{4t}{T} - 2)]}{\tan(\beta)} & \frac{T}{4} \leq t < \frac{T}{2} \\ \frac{\tan[\beta(\frac{4t}{T} - 2)]}{\tan(\beta)} & \frac{T}{2} \leq t < \frac{3T}{4} \\ \frac{\tan[\beta(\frac{4t}{T} - 4)]}{\tan(\beta)} & \frac{3T}{4} \leq t \leq T \end{cases} \quad (5.16)$$

where A_0 is the maximum B1 field corresponding to MaxB1. The RF pulse width is T . The λ and β are dimensionless constants that describe the degree to which extent the RF pulse satisfies the adiabatic condition.

rfBIREF

A RF macro that creates an adiabatic B1 Independent Refocusing (BIREF) RF pulse. This macro contains attributes including:

- MaxB1 (T) : The maximum B1 field
- MaxFreq (Hz) : The maximum RF frequency
- BIREFFlag : The type of BIREF pulse, including ‘BIREF-1’, ‘BIREF-2a’ and ‘BIREF-2b’
- dt (s) : The time interval of RF pulse sample points
- tStart (s) : RF pulse starting time
- tEnd (s) : RF pulse ending time
- Switch : The flag for turning on and off RF pulse in the RF sequence line
- AnchorTE : The flag for turning on and off TE reference, TE is calculated from this RF pulse if this flag is turned on
- Duplicates : The number of the RF pulse duplicates, used for creating multiple RF pulses with the same shape
- DupSpacing : The time spacing between RF pulse duplicates
- CoilID : The ID of the coil element used with this RF pulse, applied for multiple RF transmitting
- Notes : The notes of the RF pulse

The time dependence of the BIREF-1 RF pulse is given by [6]:
Amplitude modulation:

$$A(t) = \begin{cases} \hat{x}A_0\sin(\xi t) & 0 \leq t < \frac{T}{2} \\ -\hat{x}A_0\sin(\xi t) & \frac{T}{2} \leq t \leq T \end{cases} \quad (5.17)$$

Frequency modulation:

$$F(t) = F_0|\cos(\xi t)| \quad (5.18)$$

where A_0 is the maximum B1 field corresponding to MaxB1, F_0 is the maximum RF frequency corresponding to MaxFreq. The RF pulse width is $T = \frac{\pi}{\xi}$, and \hat{x} is a unit vector for indicating RF phase along the x axis.

The time dependence of the BIREF-2a RF pulse is given by [6]:
Amplitude modulation:

$$A(t) = \hat{x}A_0|\cos(\xi t)| \quad (5.19)$$

Frequency modulation:

$$F(t) = \begin{cases} F_0 \sin(\xi t) & 0 \leq t < \frac{T}{2} \\ -F_0 \sin(\xi t) & \frac{T}{2} \leq t \leq T \end{cases} \quad (5.20)$$

where A_0 is the maximum B1 field corresponding to MaxB1, F_0 is the maximum RF frequency corresponding to MaxFreq. The RF pulse width is $T = \frac{\pi}{\xi}$, and \hat{x} is a unit vector for indicating RF phase along the x axis.

The time dependence of the BIREF-2b RF pulse is given by [6]:
Amplitude modulation:

$$A(t) = \begin{cases} \hat{x} A_0 |\cos(\xi t)| & 0 \leq t < \frac{T}{2} \\ -\hat{x} A_0 \cos(\xi t) & \frac{T}{2} \leq t \leq T \end{cases} \quad (5.21)$$

Frequency modulation:

$$F(t) = \begin{cases} F_0 \sin(\xi t) & 0 \leq t < \frac{T}{4} \\ -F_0 \sin(\xi t) & \frac{T}{4} \leq t < \frac{3T}{4} \\ F_0 \sin(\xi t) & \frac{3T}{4} \leq t \leq T \end{cases} \quad (5.22)$$

where A_0 is the maximum B1 field corresponding to MaxB1, F_0 is the maximum RF frequency corresponding to MaxFreq. The RF pulse width is $T = \frac{2\pi}{\xi}$, and \hat{x} is a unit vector for indicating RF phase along the x axis.

rfRandom

A RF macro that creates a RF pulse with normally distributed pseudo-random amplitude. This macro is used for program testing purpose, however it shows that almost any arbitrary RF pulse could potentially be supported by MRiLab. This macro contains attributes including:

- rfGain : The standard deviation of the normal distribution
- dt (s) : The time interval of RF pulse sample points
- rfPhase (rad) : RF pulse phase
- rfFreq (Hz) : RF pulse frequency
- tStart (s) : RF pulse starting time
- tEnd (s) : RF pulse ending time
- Switch : The flag for turning on and off RF pulse in the RF sequence line

- AnchorTE : The flag for turning on and off TE reference, TE is calculated from this RF pulse if this flag is turned on
- Duplicates : The number of the RF pulse duplicates, used for creating multiple RF pulses with the same shape
- DupSpacing : The time spacing between RF pulse duplicates
- CoilID : The ID of the coil element used with this RF pulse, applied for multiple RF transmitting
- Notes : The notes of the RF pulse

rfUser

If the user has specific RF pulse waveform data saved in a MAT file, the user can easily import the RF file into MRiLab pulse design interface by using 'rfUser' macro. The RF pulse MAT file needs to contain four matrices including 'rfTime' (i.e. RF time points), 'rfAmp' (i.e. RF amplitude), 'rfPhase' (i.e. RF phase) and 'rfFreq' (i.e. RF frequency). All four matrices must have the same size of m-by-n, where m is the number of TR sections and n is the number of RF waveform points. In typical MR sequence, the entire sequence is composed of multiple TR sections. The *i*th TR section uses the *i*th RF pulse stored in the *i*th row of these four matrices. If the number of row is less than the number of TR sections, the last RF pulse will be used for all the remaining TR sections. Notice that if 'rfPhase' and/or 'rfFreq' are not provided, MRiLab initializes them as a value of 0. However, 'rfTime' and 'rfAmp' must be provided. Also note that MRiLab only uses the first RF pulse in the MAT file for pulse analysis in the RF pulse design interface. The 'rfUser' macro contains attributes including:

- rfFile : The path to the file that stores the RF pulse data, quoted using single quotes
- Switch : The flag for turning on and off RF pulse in the RF sequence line
- AnchorTE : The flag for turning on and off TE reference, TE is calculated from this RF pulse if this flag is turned on
- Duplicates : The number of the RF pulse duplicates, used for creating multiple RF pulses with the same shape
- DupSpacing : The time spacing between RF pulse duplicates
- CoilID : The ID of the coil element used with this RF pulse, applied for multiple RF transmitting
- Notes : The notes of the RF pulse

5.1.3 Make New RF Macro

The RF pulse macro library covers several common types of RF pulse waveform. However, comprehensive coverage of existing RF pulses is nearly impossible for almost any pulse sequence design tools. To address this problem in MRiLab, the user can use the 'rfUser' to import RF pulses from files generated by other programs. Another way to import RF pulse is to simply write a RF macro. To create a RF macro, the user should follow the following steps :

1. Write RF macro code

It is strongly recommended to write your own RF macro code based on similar RF macros in the MRiLab macro library, for example, the 'rfRect' macro is coded as:

```
function [rfAmp,rfPhase,rfFreq,rfCoil,rfTime]=rfRect(p)
%Create a hard RF pulse starting from tStart and ending at tEnd
%tStart RF start time
%tEnd RF end time
%FA RF actual flip angle
%dt RF sample time
%rfPhase RF phase
%rfFreq RF off-res freq

tStart=p.tStart;
tEnd=p.tEnd;
FA=p.FA;
dt=p.dt;
rfPhase=p.rfPhase;
rfFreq=p.rfFreq;
rfCoil=p.CoilID;
Duplicates=max(1,p.Duplicates);
DupSpacing=max(0,p.DupSpacing);

rfTime=linspace(tStart,tEnd,ceil((tEnd-tStart)/dt)+1);
rfAmp=ones(size(rfTime)); % Rectangle
rfAmp(1)=0;
rfAmp(end)=0;
rfAmp=DoB1Scaling(rfAmp,dt,FA)*rfAmp; %B1 Scaling

rfPhase=(rfPhase)*ones(size(rfTime));
rfFreq=(rfFreq)*ones(size(rfTime));
rfCoil=(rfCoil)*ones(size(rfTime));
rfPhase(1)=0;
rfPhase(end)=0;
rfFreq(1)=0;
```

```

rfFreq(end)=0;

% Create Duplicates
if Duplicates~=1 & DupSpacing ~=0
    rfAmp=repmat(rfAmp,[1 Duplicates]);
    rfFreq=repmat(rfFreq,[1 Duplicates]);
    rfPhase=repmat(rfPhase,[1 Duplicates]);
    rfCoil=repmat(rfCoil,[1 Duplicates]);
    TimeOffset = repmat(0:DupSpacing:(Duplicates-1)*DupSpacing, ...
        [length(rfTime) 1]);
    rfTime=repmat(rfTime,[1 Duplicates]) + (TimeOffset(:))';
end

end

```

Your macro must start from a function declaration at the beginning, then followed by attribute input section. The 'tStart' and 'tEnd' need to be added for indicating the time scale. It's also strongly recommended to add attribute input 'rfCoil','Duplicates' and 'DupSpacing' for multi-transmitting and multi-echo support.

```

function [rfAmp,rfPhase,rfFreq,rfCoil,rfTime]=rfMacroName(p)
%Create a RF pulse based on user code

tStart=p.tStart;
tEnd=p.tEnd;
rfCoil=p.CoilID;
Duplicates=max(1,p.Duplicates);
DupSpacing=max(0,p.DupSpacing);
...
attribute1=p.attribute1;
attribute2=p.attribute2;
attribute3=p.attribute3;
...

```

The main code should deal with calculation for 'rfAmp', 'rfPhase', 'rfFreq' and 'rfTime'. Notice that they should have the same size as 1-by-m where m is the number of RF waveform points.

```

% The main code for user macro
...
rfTime = ...;
rfAmp = ...;
rfPhase = ...;
rfFreq = ...;
...

```


Then you should add several lines to end your macro,

```
% Avoid baseline offset
rfAmp(1)=0;
rfAmp(end)=0;
rfPhase(1)=0;
rfPhase(end)=0;
rfFreq(1)=0;
rfFreq(end)=0;

% Assign coil element index number
rfCoil=(rfCoil)*ones(size(rfTime));

% Create Duplicates
if Duplicates~=1 & DupSpacing ~=0
    rfAmp= repmat(rfAmp,[1 Duplicates]);
    rfFreq= repmat(rfFreq,[1 Duplicates]);
    rfPhase= repmat(rfPhase,[1 Duplicates]);
    rfCoil= repmat(rfCoil,[1 Duplicates]);
    TimeOffset= repmat(0:DupSpacing:(Duplicates-1)*DupSpacing, ...
        [length(rfTime) 1]);
    rfTime= repmat(rfTime,[1 Duplicates]) + (TimeOffset(:))';
end
```

2. Register RF macro

The RF macro file can be placed anywhere as long as the file is included in Matlab search path, however it is recommended to save the file under /MRiLab/Macro/SeqElem/rf for consistent file organization. Besides a RF macro file that performs pulse generation, MRiLab also requires a memo .txt file that accompanies the RF macro with the name 'rfMacroName_Memo'. This file contains information about RF pulse description if necessary.

The customized RF macro needs to be registered in the macro library before using. To register a macro, open file 'SeqElem.xml' under /SeqElem, then add one entry under <rf> category with the proper attribute list. One example could be

```
<rfMacroName
AnchorTE="$2'on', 'off'"
CoilID="1"
DupSpacing="0"
Duplicates="1"
Switch="$1'on', 'off'"
```

```

tEnd="1e-3"
tStart="0"
Notes="A new RF macro"
attribute1="0"
attribute2="0"
attribute3="0" />

```

Notice that in the above example, the first 7 attributes are required for MRiLab, The remaining attributes are optional based on user's choice.

Once the RF macro is coded and registered to the library, the user can use this customized RF macro just like default RF macros in the library.

5.2 MR Sequence Design

The MR Sequence Design toolbox can be activated by pressing 'Sequence Design Panel' toolbar icon located at the top of the main simulation console. The current loaded sequence will show in the MR Sequence Design interface.



Figure 5.10: Sequence Design Panel Toolbar Icon

5.2.1 Sequence Design GUI

Figure 5.11 demonstrates an overview of the MR Sequence Design interface. This interface consists of

1. Macro Library

The Macro Library contains a full set of pulse macros for constructing MR sequence in MRiLab. It covers not only RF macro library as described in above section, but also GzSS, GyPE and GxR gradient macro library, ADC macro library and Ext macro library. The user needs to click the 'SeqElem' root as well as the subsequent nodes to unfold those macros.

2. Sequence Structure

In MRiLab, a MR sequence consists of the following parts :

- CVs : The controllable variables, linked to the 'CVs' tab on the main control console
- Specials : The applied special techniques by default

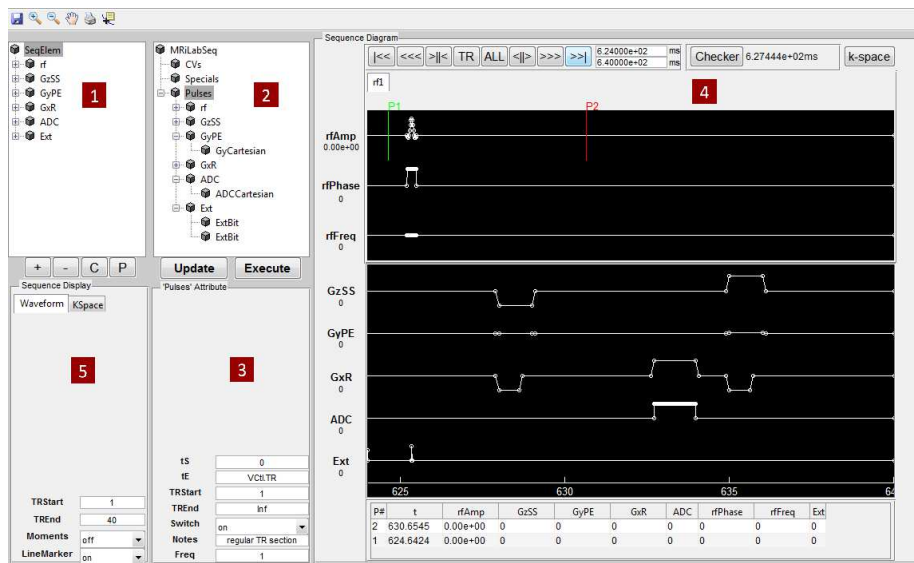


Figure 5.11: Sequence Design Panel. A bSSFP sequence is shown.

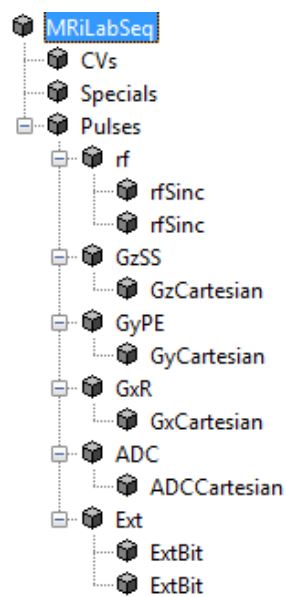


Figure 5.12: An Example of A Typical MR Sequence Structure in MRiLab

- Pulses
 - RF : RF sequence line
 - GzSS : GzSS sequence line
 - GyPE : GyPE sequence line
 - GxR : GxR sequence line
 - ADC : Signal acquisition sequence line
 - Ext : Extended process sequence line

The user can construct desired MR sequence by changing the content of the MR sequence structure. To add a macro into the sequence structure, click one macro in the macro library, then click on the sequence line root (e.g. rf) to which this macro is inserted, then click '+' macro operation button. To delete a macro from the sequence structure, click the unwanted macro at the sequence line, then click '-' macro operation button. To duplicate an existing macro, first click the source macro, then click 'C' macro operation button for copying, click on the sequence line root, then click 'P' macro operation button for pasting. MRiLab requires the pulse macro being operated within its belonging category (e.g. RF pulse can't be added to gradient line). Also empty sequence line is prohibited.



Figure 5.13: Macro Operation Buttons

In MRiLab v1.2 and v1.3, multiple 'Pulses' are allowed in a single sequence structure to enhance design ability for complex MR sequence. For instance, two 'Pulses' can be used to design a MR sequence with two separate sections where one section is for regular image acquisition and the other is for fat saturation which occurs every 5 regular image acquisition sections (Figure 5.14). To add a new 'Pulses', click one 'Pulses' as a source, then click 'C' macro operation button for copying, click on the sequence root 'MRiLabSeq', then click 'P' macro operation button for pasting. The duplicated 'Pulses' will be appended to the end of the sequence structure, from where further modification could be made. Also, removing a selected 'Pulses' can be performed by clicking '-' operation.

The 'Pulses' has several properties:

- tS : The starting time point in TR section, **any waveform timing in this pulse group is relative to this time point**
- tE : The ending time point in TR section, **any waveform timing in this pulse group will be truncated after this time point**

- TRStart : The starting TR number when this pulse group starts to occur
- TREnd : The ending TR number when this pulse group stops to occur
- Freq : The occurrence frequency (e.g. 1 means occurring every TR section, 5 means occurring every 5 TR sections)
- Switch : The flag for turning on and off this pulse group
- Notes : The notes of this pulse group

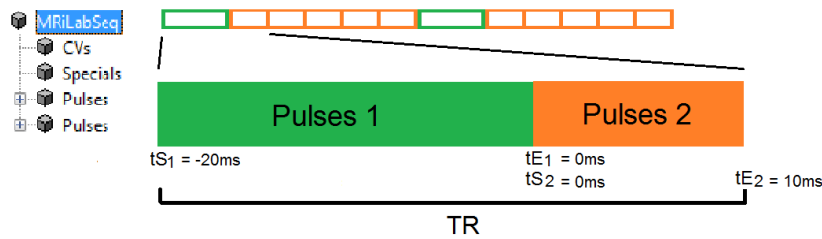


Figure 5.14: A schematic example of a MR sequence containing two pulse groups. Pulses1 is a fat saturation section occurring every 5 TR sections. Pulses2 is a regular image acquisition section occurring every TR section. Note that depending on the occurrence of Pulses1, one TR section could be either Pulses2 or Pulses1+Pulses2.

3. Pulse Attribute

Upon clicking on a pulse macro within a MR sequence structure, the corresponding macro attributes will be shown at the pulse attribute panel down below the sequence structure. The user can edit those attributes to modify the sequence waveform. To make any modification effective, the user must press 'Update' button to update the associated sequence XML file. Pressing 'Execute' button will update and redraw the MR sequence waveform plotting on this interface.

4. Sequence Waveform

The sequence waveform associated with the sequence structure is displayed on the 'Sequence Diagram' panel on the right side of this interface. The user can use the waveform diagram to inspect sequence details and layout. The sequence diagram consists of individual sequence lines corresponding to RF, GzSS, GyPE, GxR, ADC and Ext, respectively. To accommodate multiple RF transmitting, MRiLab provides separate RF sequence lines for each RF source. When 'MultiTransmit' flag is turned on in the main control console and the chosen sequence structure contains multiple RF

pulses for different RF sources (i.e. assign RF pulses to different coil channels by using ‘CoilID’ attribute), the multi-tab will be activated on the ‘rf Source’ panel (Figure 5.15). The user can switch between these tabs for checking individual RF source.

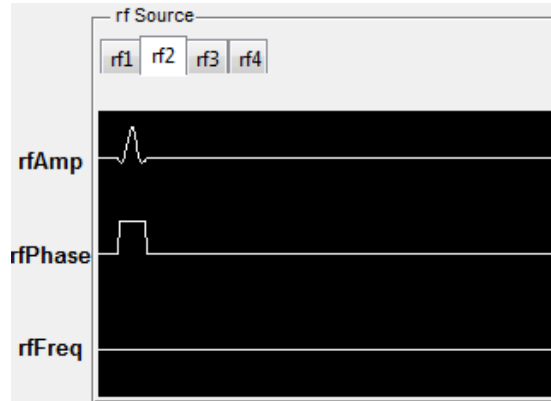


Figure 5.15: An Example of Multiple RF Source. The ‘MultiTransmit’ is turned on and this sequence contains total 4 RF sources. The RF source 2 is chosen and the corresponding RF pulse waveform for coil channel 2 is shown.

Notice that the vertical axes for all sequence lines are normalized and the horizontal axes are in units of milliseconds. MRiLab provides a group of sequence display button (Figure 5.16) to help inspect the sequence waveform details.

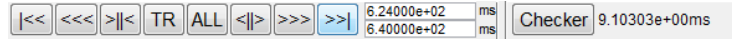


Figure 5.16: The Sequence Display Button.

The sequence display button group consists of :

- Checker : The time checker toggle button
- Time Ruler : Display current time point according to the time checker
- Time Clips : Two editable boxes for defining time range
- |<< : Move sequence waveform to the beginning
- <<< : Move sequence waveform backwards
- >||< : Zoom out
- TR : Display a sequence waveform section with a time interval of TR
- ALL : Display all sequence waveform
- <||> : Zoom in

- >>>: Move sequence waveform forwards
- >> | : Move sequence waveform to the end

The user can use the ‘Checker’ toggle button to display a sequence waveform at any arbitrary time interval (Figure 5.17). First press the ‘Checker’ button, move the mouse cursor into the axes. Notice that the mouse cursor changes to a cross-hair. Move the cross-hair in the axes, the amplitude value for each sequence line will be displayed accordingly on right side of each line with their default units. The user can click on the axes to choose one side of the time slot, then click on the another side. MRiLab will change the sequence view between the chosen time points, and also save time point information in the list at the bottom of this interface. To disable ‘Checker’ function, simply press this button again.

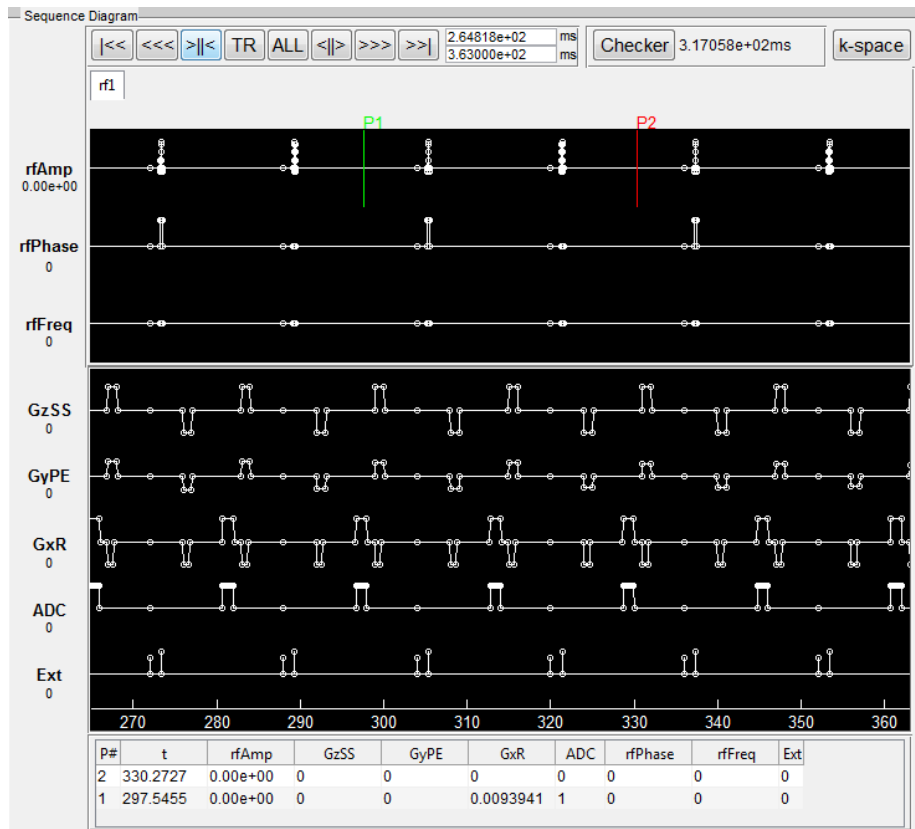


Figure 5.17: A Sequence View with Multiple TRs.

5. Display Control

The ‘Waveform’ tab on the ‘Sequence Display’ contains parameters for controlling sequence waveform display.

- TRStart : The first TR to be displayed
- TREnd : The last TR to be displayed
- Moments (:TODO) : The flag for turning on and off the zeroth moment display for the gradient
- LineMarker : The flag for turning on and off waveform line marker

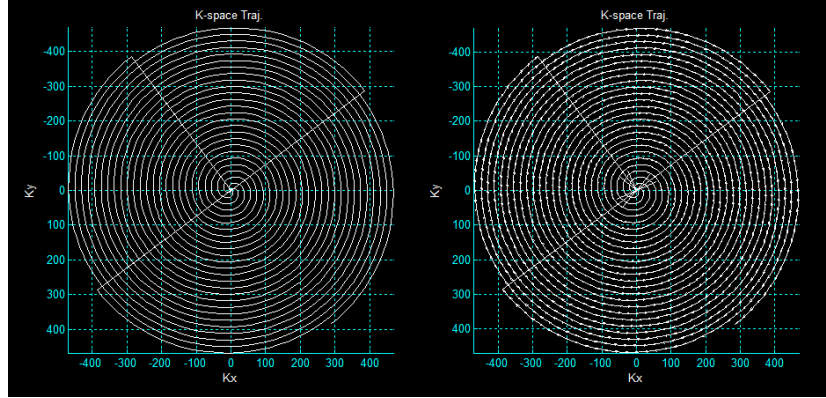


Figure 5.18: Matlab Rendered k -space Trajectory for A Spiral Readout with 4 Interleaves. The left figure is without k -space point rendering. The right figure is with k -space point rendering with the arrows indicating k -space traversing direction.

The ‘KSpace’ tab on the ‘Sequence Display’ contains parameters for controlling k -space trajectory rendering.

- RenderMode : The k -space rendering mode, including ‘Matlab’ (Figure 5.18) and ‘VTK’ (Figure 5.19)
- RenderPoint : The flag for turning on and off k -space point rendering

Notice that in VTK rendering, the k -space line color starts from green and ends to red. If the user uses VTK for k -space rendering, please press keyboard ‘q’ to quit the VTK window before any subsequent simulation. Pressing the quit button on the VTK window under Linux system will force the entire Matlab to close, this is ‘believed’ to be a compatibility bug between Matlab and OpenGL used by VTK.

5.2.2 Virtual Structure

For the convenience of transferring data and configuration information across different modules, MRiLab defined several Matlab structure variables in the global scope. These structures start with ‘V’ standing for ‘Virtual Structure’. Understanding what these structures are and how they work is important to

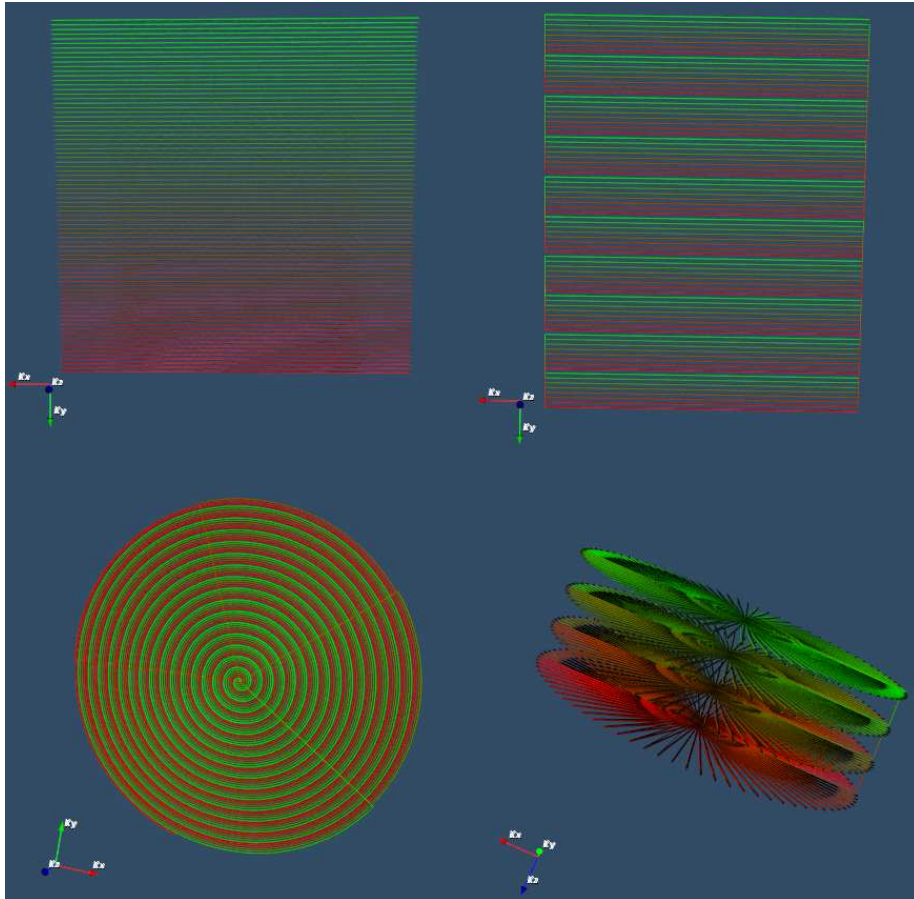


Figure 5.19: VTK Rendered k -space Trajectory Examples. The top left figure shows a typical single slice Cartesian readout. The top right figure shows a single slice multishot EPI readout. The bottom left figure shows a single slice multishot spiral readout. The bottom right figure shows a 3D Stack-of-Stars radial readout.

work with MRiLab and to customize specific experiment design. There are two virtual structures useful for designing MR sequences.

- **VCtl : Virtual Control**
VCtl encapsules all simulation setting parameters in the main control console. For example, the user can use 'VCtl.TE' to reference 'TE' value in the main control console; use 'VCtl.FlipAng' to reference 'FlipAng' value in the main control console. VCtl also allows the user to reference parameters in special techniques if loaded. Another example is that MRiLab uses 'VCtl.TR' in the 'SE' for determining time interval for each TR section. The user can use any legal Matlab syntax combined with VCtl to create desired effect, such as use '2 * VCtl.TR' to indicate twice of 'TR' value.
- **VVar : Virtual Variable**
VVar encapsules loop index variables that MRiLab uses for generating MR sequence waveform. A section of code for generating MR sequence is shown:

```
% MR Sequence Generating Loop
VVar.SliceCount=0;
VVar.PhaseCount=0;
VVar.TRCOUNT=0;
s=1;
j=1;

while s<=VCtl.SecondPhNum
    VVar.SliceCount=s;
    while j<=VCtl.FirstPhNum
        VVar.PhaseCount=j;
        VVar.TRCOUNT=VVar.TRCOUNT+1;

        ...
        %Sequence Generating Code
        ...

        j=j+1;
    end
    j=1;
    s=s+1;
end
```

The user can use the loop index variables in VVar

- VVar.TRCOUNT : The TR section index
- VVar.PhaseCount : The first phase encoding index
- VVar.SliceCount : The second (i.e. slice) phase encoding index

- VCtl.FirstPhNum : The total number of first phase encoding steps
- VCtl.SecondPhNum : The total number of second phase encoding steps

For example, to create 180° RF phase cycling in bSSFP sequence, the user can set the attributes for the excitation RF pulse as

- CV3 : $2\pi/2$
- CV4 : 2
- rfPhase : $\text{rem}(\text{VVar.TRCOUNT}-1, \text{CV4}) * \text{CV3}$

5.2.3 GzSS Macro Library

A GzSS macro is a predefined module for a gradient pulse on the GzSS sequence line. MRiLab GzSS macro library is a collection of GzSS macros covering different gradient pulse types including slice selection and slice phase encoding pulses. Notice that by default the area under the gradient ramp is ignored when calculating k -space. This section will give an introduction to each of the GzSS macros provided in MRiLab.

GzSelective

A GzSS macro that creates a typical slice selective gradient pulse (Figure 5.20). This macro contains attributes including:

- t2Start (s) : Slice selection gradient pulse starting time
- t2End (s) : Slice selection gradient pulse ending time
- tRamp (s) : Gradient pulse ramp time, assume symmetric ramp on both side
- GzAmp (T) : The amplitude of the gradient
- Gz1Sign : The polarity of the prephasing gradient, set 0 for nulling
- Gz2Sign : The polarity of the slice selection gradient, set 0 for nulling
- Gz3Sign : The polarity of the rephasing gradient, set 0 for nulling
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

Notice that both the prephasing gradient and rephasing gradient have half of the area of the slice selection gradient.

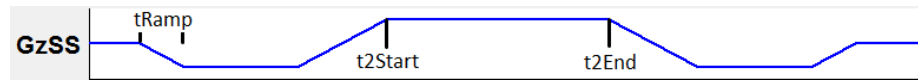


Figure 5.20: GzSelective Waveform

GzSelective2

A GzSS macro that creates a slice selective gradient pulse straddled with crusher gradient (Figure 5.21). This macro contains attributes including:

- $t2Start$ (s) : Slice selection gradient pulse starting time
- $t2End$ (s) : Slice selection gradient pulse ending time
- $tRamp$ (s) : Gradient pulse ramp time, assume symmetric ramp on both side
- $tGz1$ (s) : The duration of the left crusher
- $tGz3$ (s) : The duration of the right crusher
- $Gz1Amp$ (T) : The amplitude of the left crusher
- $Gz2Amp$ (T) : The amplitude of the slice selective gradient
- $Gz3Amp$ (T) : The amplitude of the right crusher
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

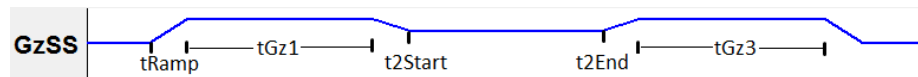


Figure 5.21: GzSelective2 Waveform

GzTrapezoid

A GzSS macro that creates a trapezoid gradient pulse (Figure 5.22) on GzSS sequence line. This macro contains attributes including:

- tStart (s) : The trapezoid gradient pulse starting time
- tEnd (s) : The trapezoid gradient pulse ending time
- tRamp (s) : The trapezoid pulse ramp time, assume symmetric ramp on both side
- sRamp : The sample points on the ramp, use the value of 2 for ignoring the area under the ramp, use above 2 for counting the ramp area
- GzAmp (T) : The amplitude of the gradient
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

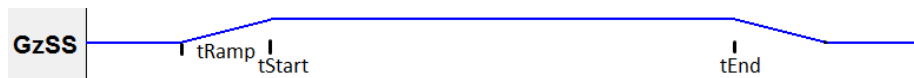


Figure 5.22: GzTrapezoid Waveform

GzAreaTrapezoid

A GzSS macro that creates a trapezoid gradient pulse of specified area (Figure 5.23) on GzSS sequence line. This macro contains attributes including:

- tStart (s) : The trapezoid gradient pulse starting time
- tEnd (s) : The trapezoid gradient pulse ending time
- Area (1/m) : The area under this gradient pulse
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

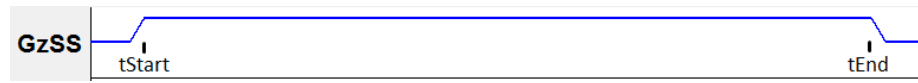


Figure 5.23: GzAreaTrapezoid Waveform

GzAreaTrapezoid2

A GzSS macro that creates a trapezoid gradient pulse of specified area with highest system performance (Figure 5.24) on GzSS sequence line. This macro creates a gradient pulse with nearly shortest pulse width for the given system hardware constraint. This macro contains attributes including:

- tStart (s) : The trapezoid gradient pulse starting time
- Area (1/m) : The area under this gradient pulse
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

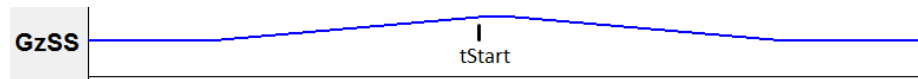


Figure 5.24: GzAreaTrapezoid2 Waveform

GzCartesian

A GzSS macro that creates a Cartesian phase encoding gradient pulse (Figure 5.25) along the slice direction. This macro contains attributes including:

- t1Start (s) : The phase encoding gradient pulse starting time
- t1End (s) : The phase encoding gradient pulse ending time
- t2Start (s) : The rephasing gradient pulse starting time
- t2End (s) : The rephasing gradient pulse ending time
- tRamp (s) : Gradient pulse ramp time, assume symmetric ramp on both side
- Gz1Sign : The polarity of the phase encoding gradient, set 0 for nulling

- Gz2Sign : The polarity of the rephasing gradient, set 0 for nulling
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

Notice that the phase encoding gradient and the rephasing gradient have the same area that is automatically calculated based on the imaging parameters in the main control console.

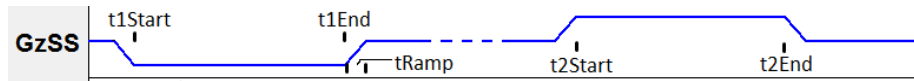


Figure 5.25: GzCartesian Waveform

GzUser

If the user has gradient pulse data saved in a MAT file, the user can easily import the gradient file into MRiLab by using 'GzUser' macro. The gradient pulse MAT file needs to contain two matrices including 'GTime' (i.e. gradient time points) and 'GAmp' (i.e. gradient amplitude). Both matrices must have the same size of m-by-n, where m is the number of TR sections and n is the number of gradient waveform points. In typical MR sequence, the entire sequence is composed of multiple TR sections. The i th TR section uses the i th gradient pulse stored in the i th row of these two matrices. If the number of row is less than the number of TR sections, the last gradient pulse will be used for all the remaining TR sections. The 'GzUser' macro contains attributes including:

- GzFile : The path to the file that stores the gradient pulse data, quoted using single quotes
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

5.2.4 GyPE Macro Library

A GyPE macro is a predefined module for a gradient pulse on the GyPE sequence line. MRiLab GyPE macro library is a collection of GyPE macros covering different gradient pulse types for performing phase encoding. Notice that by default the area under the gradient ramp is ignored. This section will give an introduction to each of the GyPE macros provided in MRiLab.

GyTrapezoid

Similar to GzTrapezoid (Figure 5.22), GyTrapezoid creates a trapezoid gradient pulse on GyPE sequence line. This macro contains attributes including:

- tStart (s) : The trapezoid gradient pulse starting time
- tEnd (s) : The trapezoid gradient pulse ending time
- tRamp (s) : The trapezoid pulse ramp time, assume symmetric ramp on both side
- sRamp : The sample points on the ramp, use the value of 2 for ignoring the area under the ramp, use above 2 for counting the ramp area
- GyAmp (T) : The amplitude of the gradient
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

GyAreaTrapezoid

Similar to GzAreaTrapezoid (Figure 5.23), GyAreaTrapezoid creates a trapezoid gradient pulse of specified area on GyPE sequence line. This macro contains attributes including:

- tStart (s) : The trapezoid gradient pulse starting time
- tEnd (s) : The trapezoid gradient pulse ending time
- Area (1/m) : The area under this gradient pulse
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape

- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

GyAreaTrapezoid2

Similar to GzAreaTrapezoid2 (Figure 5.24), GyAreaTrapezoid2 creates a trapezoid gradient pulse of specified area with highest system performance on GyPE sequence line. This macro creates a gradient pulse with nearly shortest pulse width for the given system hardware constraint. This macro contains attributes including:

- tStart (s) : The trapezoid gradient pulse starting time
- Area (1/m) : The area under this gradient pulse
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

GyCartesian

Similar to GzCartesian (Figure 5.25), GyCartesian creates a Cartesian phase encoding gradient pulse on GyPE sequence line. This macro contains attributes including:

- t1Start (s) : The phase encoding gradient pulse starting time
- t1End (s) : The phase encoding gradient pulse ending time
- t2Start (s) : The rephasing gradient pulse starting time
- t2End (s) : The rephasing gradient pulse ending time
- tRamp (s) : Gradient pulse ramp time, assume symmetric ramp on both side
- Gy1Sign : The polarity of the phase encoding gradient, set 0 for nulling
- Gy2Sign : The polarity of the rephasing gradient, set 0 for nulling
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape

- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

Notice that the phase encoding gradient and the rephasing gradient have the same area that is automatically calculated based on the imaging parameters in the main control console.

GyRadial

A GyPE macro that creates a phase encoding gradient pulse for radial k -space trajectory (Figure 5.26) on GyPE sequence line. This macro contains attributes including:

- t1Start (s) : The prephasing gradient pulse starting time
- t2Middle (s) : The phase encoding gradient pulse middle time
- t3Start (s) : The rephasing gradient pulse starting time
- tRamp (s) : Gradient pulse ramp time, assume symmetric ramp on both side
- Gy1Sign : The polarity of the prephasing gradient, set 0 for nulling
- Gy2Sign : The polarity of the phase encoding gradient, set 0 for nulling
- Gy3Sign : The polarity of the rephasing gradient, set 0 for nulling
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Notes : The notes of the gradient pulse

Notice that both the prephasing gradient and rephasing gradient have half of the area of the phase encoding gradient that is automatically calculated based on the imaging parameters in the main control console. MRiLab requires the ‘Radial’ special technique tab to be loaded for properly configuring the ‘GyRadial’, ‘GxRadial’ and ‘ADCRadial’ macro. The user can set t2Middle value as ‘VCtl.TE’ to acquire the echo signal.

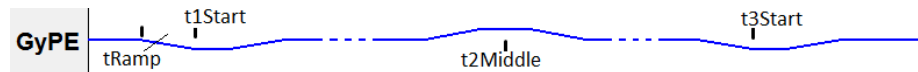


Figure 5.26: GyRadial Waveform

GySpiral

A GyPE macro that creates a phase encoding gradient pulse for spiral k -space trajectory (Figure 5.27) on GyPE sequence line. This macro contains attributes including:

- tStart (s) : The phase encoding gradient pulse starting time
- dt (s) : The time interval of gradient pulse sample points
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Notes : The notes of the gradient pulse

Notice that the area of the phase encoding gradient is automatically calculated based on the imaging parameters in the main control console. MRiLab requires the ‘Spiral’ special technique tab to be loaded for properly configuring the ‘GySpiral’, ‘GxSpiral’ and ‘ADCSpiral’ macro. The user can set tStart value as ‘VCtl.TE’ to acquire the echo signal.

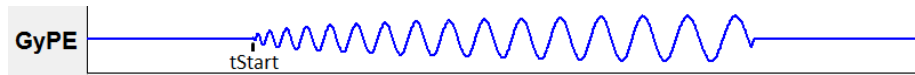


Figure 5.27: GySpiral Waveform

GyFSE

A GyPE macro that creates a FSE phase encoding gradient pulse train (Figure 5.28) on GyPE sequence line. This macro contains attributes including:

- tMiddle (s) : The middle time of the gradient pulse train
- tOffset (s) : The time offset of the gradient pulse
- tGy1 (s) : The duration of the phase encoding gradient
- tGy2 (s) : The duration of the rephasing gradient
- Gy1Sign : The polarity of the phase encoding gradient, set 0 for nulling
- Gy2Sign : The polarity of the rephasing gradient, set 0 for nulling
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Notes : The notes of the gradient pulse

Notice that the phase encoding gradient and the rephasing gradient have the same area that is automatically calculated based on the imaging parameters in the main control console. MRiLab requires the 'FSE' special technique tab to be loaded for properly configuring the 'GyFSE', 'GxFSE' and 'ADCFSE' macro. To satisfy Carr Purcell Meiboom Gill (CPMG) condition and acquire echo signal at the center between two consecutive refocusing RF pulse, the effective TE value must equal $(\text{floor}(\text{FSE_ETL}/2)+1)*\text{FSE_ESP}$. The user can set tMiddle value as 'VCtl.TE' to acquire the echo signal, where the 'VCtl.TE' becomes the effective TE value.

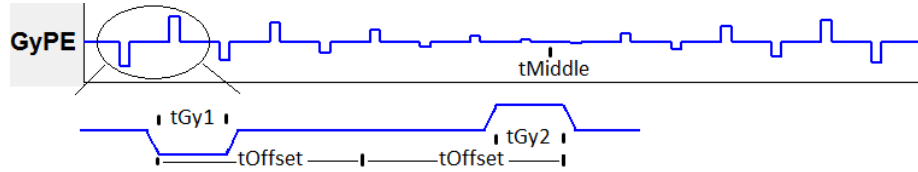


Figure 5.28: GyFSE Waveform

GyEPI

A GyPE macro that creates an EPI phase encoding gradient pulse train (Figure 5.29) on GyPE sequence line. This macro contains attributes including:

- t2Middle (s) : The middle time of the blip gradient pulse train
- t1Start (s) : The prephasing gradient starting time
- Gy1Sign : The polarity of the prephasing gradient, set 0 for nulling
- Gy2Sign : The polarity of the blip gradient train, set 0 for nulling
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Notes : The notes of the gradient pulse

Notice that the area of the prephasing gradient and the blip gradient are automatically calculated based on the imaging parameters in the main control console. MRiLab requires the 'EPI' special technique tab to be loaded for properly configuring the 'GyEPI', 'GxEPI' and 'ADCEPI' macro. The user can set t2Middle value as 'VCtl.TE' to acquire the echo signal, where the 'VCtl.TE' becomes the effective TE value.

GyUser

If the user has gradient pulse data saved in a MAT file, the user can easily import the gradient file into MRiLab by using 'GyUser' macro. The gradient pulse MAT

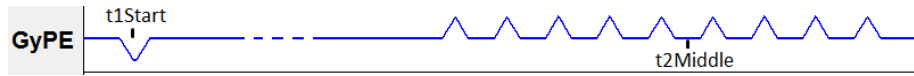


Figure 5.29: GyEPI Waveform

file needs to contain two matrices including ‘GTime’ (i.e. gradient time points) and ‘GAMP’ (i.e. gradient amplitude). Both matrices must have the same size of m -by- n , where m is the number of TR sections and n is the number of gradient waveform points. In typical MR sequence, the entire sequence is composed of multiple TR sections. The i th TR section uses the i th gradient pulse stored in the i th row of these two matrices. If the number of row is less than the number of TR sections, the last gradient pulse will be used for all the remaining TR sections. The ‘GyUser’ macro contains attributes including:

- GyFile : The path to the file that stores the gradient pulse data, quoted using single quotes
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

5.2.5 GxR Macro Library

A GxR macro is a predefined module for a gradient pulse on the GxR sequence line. MRiLab GxR macro library is a collection of GxR macros covering different gradient pulse types for performing frequency encoding. Notice that by default the area under the gradient ramp is ignored. This section will give an introduction to each of the GxR macros provided in MRiLab.

GxTrapezoid

Similar to GzTrapezoid (Figure 5.22), GxTrapezoid creates a trapezoid gradient pulse on GxR sequence line. This macro contains attributes including:

- tStart (s) : The trapezoid gradient pulse starting time
- tEnd (s) : The trapezoid gradient pulse ending time
- tRamp (s) : The trapezoid pulse ramp time, assume symmetric ramp on both side
- sRamp : The sample points on the ramp, use the value of 2 for ignoring the area under the ramp, use above 2 for counting the ramp area

- GxAmp (T) : The amplitude of the gradient
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

GxAreaTrapezoid

Similar to GzAreaTrapezoid (Figure 5.23), GxAreaTrapezoid creates a trapezoid gradient pulse of specified area on GxR sequence line. This macro contains attributes including:

- tStart (s) : The trapezoid gradient pulse starting time
- tEnd (s) : The trapezoid gradient pulse ending time
- Area (1/m) : The area under this gradient pulse
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

GxAreaTrapezoid2

Similar to GzAreaTrapezoid2 (Figure 5.24), GxAreaTrapezoid2 creates a trapezoid gradient pulse of specified area with highest system performance on GxR sequence line. This macro creates a gradient pulse with nearly shortest pulse width for the given system hardware constraint. This macro contains attributes including:

- tStart (s) : The trapezoid gradient pulse starting time
- Area (1/m) : The area under this gradient pulse
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

GxCartesian

A GxR macro that creates a Cartesian frequency encoding gradient pulse (Figure 5.30) on GxR sequence line. This macro contains attributes including:

- t1Start (s) : The prephasing gradient pulse starting time
- t2Middle (s) : The frequency encoding gradient pulse middle time
- t3Start (s) : The rephasing gradient pulse starting time
- tRamp (s) : Gradient pulse ramp time, assume symmetric ramp on both side
- Gx1Sign : The polarity of the prephasing gradient, set 0 for nulling
- Gx2Sign : The polarity of the frequency encoding gradient, set 0 for nulling
- Gx3Sign : The polarity of the rephasing gradient, set 0 for nulling
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Duplicates : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- DupSpacing : The time spacing between gradient pulse duplicates
- Notes : The notes of the gradient pulse

Notice that both the prephasing gradient and rephasing gradient have half of the area of the frequency encoding gradient.

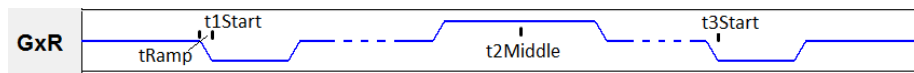


Figure 5.30: GxCartesian Waveform

GxRadial

Similar to GyRadial (Figure 5.26), GxRadial creates a phase encoding gradient pulse for radial k -space trajectory on GxR sequence line. This macro contains attributes including:

- t1Start (s) : The prephasing gradient pulse starting time
- t2Middle (s) : The phase encoding gradient pulse middle time
- t3Start (s) : The rephasing gradient pulse starting time

- **tRamp (s)** : Gradient pulse ramp time, assume symmetric ramp on both side
- **Gx1Sign** : The polarity of the prephasing gradient, set 0 for nulling
- **Gx2Sign** : The polarity of the phase encoding gradient, set 0 for nulling
- **Gx3Sign** : The polarity of the rephasing gradient, set 0 for nulling
- **Switch** : The flag for turning on and off gradient pulse in the sequence line
- **Notes** : The notes of the gradient pulse

Notice that both the prephasing gradient and rephasing gradient have half of the area of the phase encoding gradient that is automatically calculated based on the imaging parameters in the main control console. MRiLab requires the ‘Radial’ special technique tab to be loaded for properly configuring the ‘GyRadial’, ‘GxRadial’ and ‘ADCRadial’ macro. The user can set t2Middle value as ‘Vctl.TE’ to acquire the echo signal.

GxSpiral

Similar to GySpiral (Figure 5.27), GxSpiral creates a phase encoding gradient pulse for spiral k -space trajectory on GxR sequence line. This macro contains attributes including:

- **tStart (s)** : The phase encoding gradient pulse starting time
- **dt (s)** : The time interval of gradient pulse sample points
- **Switch** : The flag for turning on and off gradient pulse in the sequence line
- **Notes** : The notes of the gradient pulse

Notice that the area of the phase encoding gradient is automatically calculated based on the imaging parameters in the main control console. MRiLab requires the ‘Spiral’ special technique tab to be loaded for properly configuring the ‘GySpiral’, ‘GxSpiral’ and ‘ADCsSpiral’ macro. The user can set tStart value as ‘Vctl.TE’ to acquire the echo signal.

GxFSE

A GxR macro that creates a FSE frequency encoding gradient pulse train (Figure 5.31) on GxR sequence line. This macro contains attributes including:

- **t2Middle (s)** : The middle time of the gradient pulse train
- **t1Start (s)** : The prephasing gradient starting time

- Gx1Sign : The polarity of the prephasing gradient, set 0 for nulling
- Gx2Sign : The polarity of the frequency encoding gradient train, set 0 for nulling
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Notes : The notes of the gradient pulse

Notice that the prephasing gradient has half of the area of the frequency encoding gradient that is automatically calculated based on the imaging parameters in the main control console. MRiLab requires the 'FSE' special technique tab to be loaded for properly configuring the 'GyFSE', 'GxFSE' and 'ADCfSE' macro. To satisfy CPMG condition and acquire echo signal at the center between two consecutive refocusing RF pulse, the effective TE value must equal $(\text{floor}(\text{FSE_ETL}/2)+1)*\text{FSE_ESP}$. The user can set t2Middle value as 'VCtl.TE' to acquire the echo signal, where the 'VCtl.TE' becomes the effective TE value.

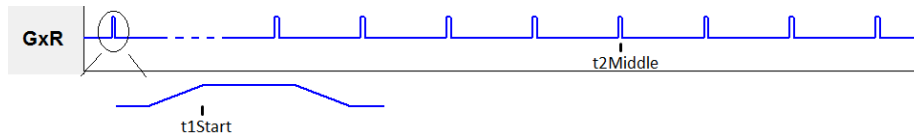


Figure 5.31: GxFSE Waveform

GxEPI

A GxR macro that creates an EPI frequency encoding gradient pulse train (Figure 5.32) on GxR sequence line. This macro contains attributes including:

- t2Middle (s) : The middle time of the frequency encoding gradient pulse train
- t1Start (s) : The prephasing gradient starting time
- Gx1Sign : The polarity of the prephasing gradient, set 0 for nulling
- Gx2Sign : The polarity of the frequency encoding gradient train, set 0 for nulling
- Switch : The flag for turning on and off gradient pulse in the sequence line
- Notes : The notes of the gradient pulse

Notice that the area of the prephasing gradient and the frequency encoding gradient are automatically calculated based on the imaging parameters in the main control console. MRiLab requires the ‘EPI’ special technique tab to be loaded for properly configuring the ‘GxEPI’, ‘GxEPI’ and ‘ADCEPI’ macro. The user can set `t2Middle` value as ‘VCtl.TE’ to acquire the echo signal, where the ‘VCtl.TE’ becomes the effective TE value.

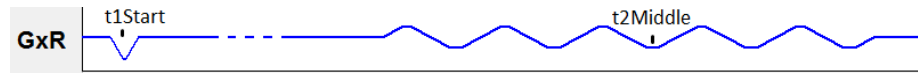


Figure 5.32: GxEPI Waveform

GxUser

If the user has gradient pulse data saved in a MAT file, the user can easily import the gradient file into MRiLab by using ‘GxUser’ macro. The gradient pulse MAT file needs to contain two matrices including ‘GTime’ (i.e. gradient time points) and ‘GAmp’ (i.e. gradient amplitude). Both matrices must have the same size of m -by- n , where m is the number of TR sections and n is the number of gradient waveform points. In typical MR sequence, the entire sequence is composed of multiple TR sections. The i th TR section uses the i th gradient pulse stored in the i th row of these two matrices. If the number of row is less than the number of TR sections, the last gradient pulse will be used for all the remaining TR sections. The ‘GxUser’ macro contains attributes including:

- **GxFile** : The path to the file that stores the gradient pulse data, quoted using single quotes
- **Switch** : The flag for turning on and off gradient pulse in the sequence line
- **Duplicates** : The number of the gradient pulse duplicates, used for creating multiple gradient pulses with the same shape
- **DupSpacing** : The time spacing between gradient pulse duplicates
- **Notes** : The notes of the gradient pulse

5.2.6 ADC Macro Library

An ADC macro is a predefined module for an ADC flag pulse on the ADC sequence line. Signal acquisition starts when ADC flag is 1 and stops when ADC flag is 0. The ADC flag pulse is sampled at certain sampling rate determined by the imaging parameters (default by using ‘BandWidth’) in the main control console. MRiLab ADC macro library is a collection of ADC macros covering different pulse types for performing signal acquisition. This section will give an introduction to each of the ADC macros provided in MRiLab.

ADCBlock

An ADC macro that creates an ADC flag pulse with user defined sampling rate on ADC sequence line. This macro contains attributes including:

- tStart (s) : The ADC starting time
- tEnd (s) : The ADC ending time
- sSample : The number of linear sample points when ADC flag is 1
- Switch : The flag for turning on and off ADC pulse in the sequence line
- Duplicates : The number of the ADC pulse duplicates, used for creating multiple ADC pulses with the same shape
- DupSpacing : The time spacing between ADC pulse duplicates
- Notes : The notes of the ADC pulse

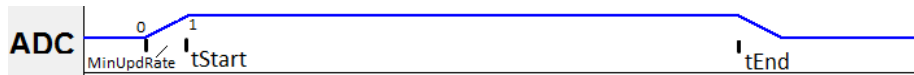


Figure 5.33: ADCBlock Waveform

ADCCartesian

An ADC macro that creates an ADC flag pulse for Cartesian readout on ADC sequence line. This macro contains attributes including:

- tMiddle (s) : The ADC middle time, typically set 'VCtl.TE' for acquiring echo signal
- Switch : The flag for turning on and off ADC pulse in the sequence line
- Duplicates : The number of the ADC pulse duplicates, used for creating multiple ADC pulses with the same shape
- DupSpacing : The time spacing between ADC pulse duplicates
- Notes : The notes of the ADC pulse

ADCRadial

An ADC macro that creates an ADC flag pulse for radial readout on ADC sequence line. This macro needs 'Radial' tab to be loaded. This macro contains attributes including:

- tMiddle (s) : The ADC middle time, typically set 'VCtl.TE' for acquiring echo signal

- Switch : The flag for turning on and off ADC pulse in the sequence line
- Notes : The notes of the ADC pulse

ADCSpiral

An ADC macro that creates an ADC flag pulse for spiral readout on ADC sequence line. This macro needs ‘Spiral’ tab to be loaded. This macro contains attributes including:

- tStart (s) : The ADC starting time, typically set ‘VCtl.TE’ for acquiring echo signal
- Switch : The flag for turning on and off ADC pulse in the sequence line
- Notes : The notes of the ADC pulse

ADCFSE

An ADC macro that creates an ADC flag pulse train for FSE readout on ADC sequence line. This macro needs ‘FSE’ tab to be loaded. This macro contains attributes including:

- tMiddle (s) : The ADC pulse train middle time, typically set ‘VCtl.TE’ for acquiring echo signal
- Switch : The flag for turning on and off ADC pulse in the sequence line
- Notes : The notes of the ADC pulse

ADCEPI

An ADC macro that creates an ADC flag pulse train for EPI readout on ADC sequence line. This macro needs ‘EPI’ tab to be loaded. This macro contains attributes including:

- tMiddle (s) : The ADC pulse train middle time, typically set ‘VCtl.TE’ for acquiring echo signal
- Switch : The flag for turning on and off ADC pulse in the sequence line
- Notes : The notes of the ADC pulse

ADCUser

If the user has ADC pulse data saved in a MAT file, the user can easily import the ADC file into MRiLab by using ‘ADCUser’ macro. The ADC pulse MAT file needs to contain two matrices including ‘GTime’ (i.e. ADC time points) and ‘GAmp’ (i.e. ADC amplitude, use 1 for signal acquisition, 0 for no signal acquisition). Both matrices must have the same size of m-by-n, where m is the

number of TR sections and n is the number of ADC sample points. In typical MR sequence, the entire sequence is composed of multiple TR sections. The i th TR section uses the i th ADC pulse stored in the i th row of these two matrices. If the number of row is less than the number of TR sections, the last ADC pulse will be used for all the remaining TR sections. The ‘ADCUser’ macro contains attributes including:

- ADCFile : The path to the file that stores the ADC pulse data, quoted using single quotes
- Switch : The flag for turning on and off ADC pulse in the sequence line
- Duplicates : The number of the ADC pulse duplicates, used for creating multiple ADC pulses with the same shape
- DupSpacing : The time spacing between ADC pulse duplicates
- Notes : The notes of the ADC pulse

Notice that ‘ADCUser’ macro sets the first and last ADC sample points to 0 regardless of their original value, therefore the signal is not acquired at the first and last time points.

5.2.7 Ext Macro Library

An Ext macro is a predefined module for an Ext flag pulse on the Ext sequence line. MRiLab specifies Ext signal for performing extended real time processes including calculating remaining scan time, manipulating k -space location and triggering object motion etc. Ext macro library only contains ‘ExtBit’ macro, however the ‘Ext’ attribute in this macro triggers different processes.

ExtBit

The ‘ExtBit’ macro (Figure 5.34) creates a triangle blip pulse on Ext sequence line. This macro contains attributes including:

- tStart (s) : The Ext starting time
- Ext : The Ext flag
- Switch : The flag for turning on and off Ext pulse in the sequence line
- Duplicates : The number of the Ext pulse duplicates, used for creating multiple Ext pulses with the same shape
- DupSpacing : The time spacing between Ext pulse duplicates
- Notes : The notes of the Ext pulse

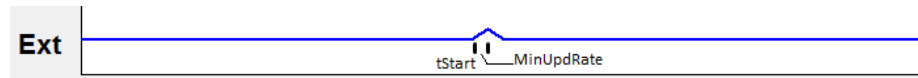


Figure 5.34: ExtBit Waveform

Different Ext flags execute different extended real time processes during run-time scan. These extended processes are implemented using Plugin code in the /MRiLab/Src/Plugin folder. MRiLab reserved several Ext flags for particular purposes.

- 1 : Plugin_ResetK, reset Kx, Ky and Kz to zero
- 2 : Plugin_ReverseK, reverse Kx, Ky and Kz
- 3 : Plugin_LockK, buffer current K space location
- 4 : Plugin_ReleaseK, set K space location to the latest buffered one, used after Plugin_LockK
- 5 : Plugin_Timer, calculate remaining scan time, display it on the main control console
- 6 : Plugin_IdealSpoiler, dephase transverse magnetization of all the spins, set them to zero
- 7 : Plugin_rfRef, buffer current rfPhase value and demodulate signal phase according to this value
- 8 : Plugin_ExecuteMotion, trigger object motion
- 9 : Plugin_RTRecon, trigger real time image reconstruction with currently stored k -space data

5.2.8 Make New Ext Plugin

The user can define Ext flags and use Ext Plugin to create extended real time process. To make your own Ext flag and Plugin code, you should follow the following steps :

1. Write Ext Plugin code

It is strongly recommended to write your Plugin code based on a template like :

```
function Plugin_YourPluginName
%Create a Ext Plugin based on your code
global Vctl      % use Vctl structure, read only
```

```

global VVar      % use VVar structure, read only
global VObj      % use VObj structure, read and write
global VMag      % use VMag structure, read and write
global VCoi      % use VCoi structure, read and write

...
% The main code for your Ext Plugin
...

end

```

As mentioned before, VCtl encapsules all the simulation setting parameters in the main control console. VVar not only encapsules loop index variables that MRiLab uses for generating MR sequence waveform, but also contains variables for temporarily buffering instant sequence line values during runtime. **Do keep in mind, VCtl and VVar are read only, changing values inside these two structures may cause MRiLab crash.**

- VVar.rfAmp (T) : A array with the size of $TxCoilNum \times 1$ for storing current RF amplitude
- VVar.rfPhase (rad) : A array with the size of $TxCoilNum \times 1$ for storing current RF phase
- VVar.rfFreq (Hz) : A array with the size of $TxCoilNum \times 1$ for storing current RF frequency
- VVar.rfCoil : The CoilID of current working coil channel, used in multiple RF transmitting
- VVar.rfRef (rad) : The buffered RF phase, used for demodulating signal phase at ADC
- VVar.GzAmp (T/m) : The current GzSS gradient amplitude
- VVar.GyAmp (T/m) : The current GyPE gradient amplitude
- VVar.GxAmp (T/m) : The current GXR gradient amplitude
- VVar.ADC : The current ADC flag
- VVar.Ext : The current Ext flag
- VVar.t (s) : The current time
- VVar.Kz (1/m) : The current Kz value
- VVar.Ky (1/m) : The current Ky value
- VVar.Kx (1/m) : The current Kx value
- VVar.TRCount : The current TR section index

Notice that there are three new Virtual Structures (VObj, VMag and VCoi) in this template, they store variables about the virtual object, B0 field and coil B1 field which are accessible and editable in Plugin code. **Do keep in mind, do not change the size of the matrices inside these three structures.**

- VObj.Rho : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing spin density
- VObj.T1 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T1 relaxation time
- VObj.T2 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T2 relaxation time
- VObj.Mx : A matrix with the size of $YDim \times XDim \times ZDim \times SpinPerVoxel \times TypeNum$ for describing magnetization in x direction
- VObj.My : A matrix with the size of $YDim \times XDim \times ZDim \times SpinPerVoxel \times TypeNum$ for describing magnetization in y direction
- VObj.Mz : A matrix with the size of $YDim \times XDim \times ZDim \times SpinPerVoxel \times TypeNum$ for describing magnetization in z direction
- VMag.dWRnd (rad/s) : A matrix with the size of $YDim \times XDim \times ZDim \times SpinPerVoxel \times TypeNum$ for describing microscopic resonance frequency variation caused by T2* effect
- VMag.dB0 (T) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing local B0 field variation
- VMag.Gxgrid (m) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing spatial grid in X direction
- VMag.Gygrid (m) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing spatial grid in Y direction
- VMag.Gzgrid (m) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing spatial grid in Z direction
- VCoi.TxCoilmg (T) : A matrix with the size of $YDim \times XDim \times ZDim \times TxCoilNum$ for describing the magnitude of transmitting B1+ field
- VCoi.TxCoilpe (rad) : A matrix with the size of $YDim \times XDim \times ZDim \times TxCoilNum$ for describing the phase of transmitting B1+ field
- VCoi.RxCoilx (T) : A matrix with the size of $YDim \times XDim \times ZDim \times RxCoilNum$ for describing the x component of receiving B1- field

- $V_{Coi.RxCoily}$ (T) : A matrix with the size of $YDim \times XDim \times ZDim \times RxCoilNum$ for describing the y component of receiving B1- field

where ‘TxCoilNum’ is the number of transmitting coil channels, ‘RxCoilNum’ is the number of receiving coil channels.

2. Register Ext Plugin

The user needs to register customized Plugins before MRiLab can use it. To register Plugins and assign Ext flags to them, simply open ‘DoExtPlugin.m’ under /MRiLab/Src/Main folder.

```
function DoExtPlugin
% entry function for extended plugin based on Ext flag
global VVar

switch VVar.Ext
%% System Reserved Ext Flags (Positive)
    case 0 % normal status
        % do nothing
    case 1 % reset K space location
        Plugin_ResetK;
    case 2 % reverse K space location
        Plugin_ReverseK;
    case 3 % lock K space location
        Plugin_LockK;
    case 4 % release K space location
        Plugin_ReleaseK;
    case 5 % calculate remaining scan time
        Plugin_Timer;
    case 6 % ideal spoiler, dephase Mxy
        Plugin_IdealSpoiler;
    case 7 % rfRef, demodulate signal phase referring to RF phase at ADC
        Plugin_rfRef;
    case 8 % trigger object motion
        Plugin_ExecuteMotion;
    case 9 % real time image recon
        Plugin_RTRecon;

%% User Defined Ext Flags (Negative)
% add user defined Ext flags here using case syntax
% e.g.      case -5
%           Plugin_XXX;

end
```

end

Add one more Switch case line, assign a distinct Ext flag, then add user defined Plugin function name under the case line. It is recommended to use negative Ext flag for user defined Plugin to differ from system reserved plugins.

3. Register to refresh GPU device memory

If the customized Plugin function modifies any variables in VObj, VMag or VCoi, the Plugin function needs to be registered for refreshing GPU device memory in case GPU parallel computing method is chosen. Simply open 'DoGPUFetch.m' under /MRILab/Src/Main folder.

```
function DoGPUFetch
% fetch data from GPU?
% VVar.gpuFetch = 1  fetch data from GPU memory to CPU memory
% VVar.gpuFetch = 0  no GPU data fetching
global VVar

switch VVar.Ext
%% System Reserved Ext Flags (Positive)
    case 6 % ideal spoiler, dephase Mxy
        VVar.gpuFetch = 1;
    case 8 % trigger object motion
        VVar.gpuFetch = 1;

%% User Defined Ext Flags (Negative)
% add user defined Ext flags here using case syntax
% e.g.      case -5
%           VVar.gpuFetch = 1;

end
end
```

Add one more Switch case line, assign VVar.gpuFetch equal to 1.

5.2.9 Make New Gradient Macro

The user can make customized gradient macros and use them to create desired k -space trajectory. To make your own gradient macro, you should follow the following steps :

1. Write gradient macro code

It is strongly recommended to write your own gradient macro code based on similar gradient macros in the MRiLab macro library. One template is like :

```
function [GAmp,GTime]=GYourGradientMacroName(p)
%Create a gradient macro based on your code

global VCtl      % use VCtl structure, read only
global VObj      % use VObj structure, read only

% Create attribute list
Duplicates=max(1,p.Duplicates);
DupSpacing=max(0,p.DupSpacing);
...
attribute1=p.attribute1;
attribute2=p.attribute2;
attribute3=p.attribute3;
...

% The main code for your macro
...
GTime = ...;
GAmp = ...;
...

% Avoid baseline offset
GAmp(1)=0;
GAmp(end)=0;

% Create Duplicates
if Duplicates~=1 & DupSpacing ~=0
    GAmp=repmat(GAmp,[1 Duplicates]);
    TimeOffset = repmat(0:DupSpacing:(Duplicates-1)*DupSpacing, ...
        [length(GTime) 1]);
    GTime=repmat(GTime,[1 Duplicates]) + (TimeOffset(:))';
end
end
```

2. Register gradient macro

The gradient macro file can be saved anywhere as long as the file is included in Matlab search path, however it is recommended to save the file under corresponding gradient folder under /SeqElem folder for consistent file organization. The customized gradient macro needs to be registered in the macro library before using. To register the macro, open

file 'SeqElem.xml' under /SeqElem, then add one entry under gradient category with the proper attribute list. One example is

```
<GzGradientMacroName
Switch="$1'on','off'"
DupSpacing="0"
Duplicates="1"
Notes="A new Gz gradient macro"
attribute1="$1'on','off'"
attribute2="0"
attribute3="0" />
```

Notice that in the above example, the first 3 attributes are required for MRiLab, The remaining attributes are optional based on user's choice.

Once the gradient macro is coded and registered to the library, the user can use this customized gradient macro just like default gradient macros in the library.

5.2.10 Load and Edit MR Sequence from XML

To design a sequence in the MR Sequence Design interface, it is recommended to load the sequence into the main control console first and then click toolbar icon to activate the MR Sequence Design interface. This is mainly because imaging parameters necessary for configuring current sequence will also be loaded during the sequence loading process. However, if the interface has already been activated, the user can also use the sequence loading function to load another sequence with current imaging parameters. To load a sequence, click 'Load' menu then click 'Load Sequence File', choose a sequence XML file.

Besides editing sequence structure graphically, the user can also directly edit the sequence XML file using Matlab editor by click 'XML' then 'Edit Seq XML'. After modification, the user needs to save changes for the XML file and then click 'Refresh Seq Tree' to update sequence structure and waveform.

5.2.11 Make New MR Sequence

The user can create a new MR sequence in the MR Sequence Design interface. To create a new sequence, click 'New' then click 'Create Sequence File'. A sequence creation window (Figure 5.35) will show up and ask for new sequence name and notes. To follow MRiLab naming convention, the user is recommended to use 'PSD_' followed by a legal name string that differs from the existing sequences in MRiLab. Then click 'OK' to select a path for storing the sequence XML file. It's strongly recommended to put the sequence under the MRiLab sequence root folder /MRiLab/PSD according to the sequence type so that the

sequence is visible to MRiLab. Finally, MRiLab will create a new sequence XML file based on the content of 'PSD_GRE3D'.

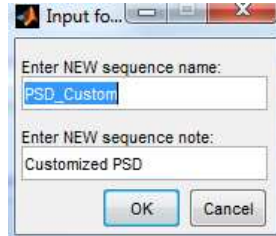


Figure 5.35: The Sequence Creation Window

5.3 Virtual Object Design

To design and optimize MR sequence, the user may need virtual objects with specific geometry and properties according to their experiment purpose. Although MRiLab provides a few phantoms with tissue properties mimicking several human tissue types, the user may still need to define customized virtual object. There are two ways of creating a new virtual object: 1) create phantom .mat file directly; 2) create phantom using MRiLab phantom design tool with XML.

5.3.1 Create Virtual Object Directly

To make a new virtual object using this method, you should follow the following steps :

1. Make Regular Virtual Object

Create a Matlab structure 'VObj'. 'VObj' must contains variables including:

- Gyro (rad/s/T) : The gyromagnetic ratio of the spin
- ChemShift (Hz/T) : A array with the size of $1 \times TypeNum$ for describing the chemical shift of the spins
- XDim : The number of voxels in X direction
- YDim : The number of voxels in Y direction
- ZDim : The number of voxels in Z direction
- XDimRes (m) : The voxel size in X direction
- YDimRes (m) : The voxel size in Y direction
- ZDimRes (m) : The voxel size in Z direction

- Type : A string for describing the type of the spin
- TypeNum : The number of spin species
- ECon (S/m) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing tissue electrical conductivity (optional)
- MassDen (kg/m³) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing tissue mass density (optional)
- Rho : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing spin density
- T1 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T1 relaxation time
- T2 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T2 relaxation time
- T2Star (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T2* relaxation time

Then save the ‘VObj’ structure as a MAT file.

2. Make Virtual Object with Magnetization Transfer (MT) Properties

The current MRiLab version supports two-pool MT model [9] including a free (*f*) water pool and a macromolecule bound (*b*) proton pool. The ‘VObj’ must have the structure like:

- Gyro (rad/s/T) : The gyromagnetic ratio of the spin
- ChemShift (Hz/T) : A array with the size of 1×2 for describing the chemical shift of the spins, free pool first, bound pool second
- XDim : The number of voxels in X direction
- YDim : The number of voxels in Y direction
- ZDim : The number of voxels in Z direction
- XDimRes (m) : The voxel size in X direction
- YDimRes (m) : The voxel size in Y direction
- ZDimRes (m) : The voxel size in Z direction
- Type : A string for describing the type of the spin
- TypeNum : 2
- ECon (S/m) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing tissue electrical conductivity (optional)
- MassDen (kg/m³) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing tissue mass density (optional)
- Rho : A matrix with the size of $YDim \times XDim \times ZDim \times 2$ for describing spin density, Rho_f (free pool) first, Rho_b (bound pool) second

- T1 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times 2$ for describing T1 relaxation time, free pool first, bound pool second
- T2 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times 2$ for describing T2 relaxation time, free pool first, bound pool second
- T2Star (s) : A matrix with the size of $YDim \times XDim \times ZDim \times 2$ for describing T2* relaxation time, free pool first, bound pool second
- K (1/s) : A matrix with the size of $YDim \times XDim \times ZDim \times 4$ for describing MT cross-relaxation rate, the K_{fb} (free pool to bound pool) and the K_{bf} (bound pool to free pool) is the second and third volume at the last dimension, respectively. The cross-relaxation rate to itself for any pool (i.e. K_{ff} and K_{bb}) is assumed to be zero.

Notice that the two-pool MT model needs to satisfy chemical equilibrium described as $Rho_f \times K_{fb} = Rho_b \times K_{bf}$. After making VObj, then save the 'VObj' structure as a MAT file. **Note that the Bloch-equation kernel is executed when the value of any sequence line updates. The time point at which update occurs is referred to as execution point.** To accurately model MT exchange during scan, the user needs to create execution points on the entire RF sequence line. A typical method is to insert a long RF pulse with zero amplitude at the empty portion of the RF sequence line. The interested users are referred to PSD_SPGR3DMT for more information.

3. Make Virtual Object with Multiple Exchanging (ME) Water Pools Properties

The current MRiLab version supports multiple exchanging water pools model with flexible number of water pools. The 'VObj' must have the structure like:

- Gyro (rad/s/T) : The gyromagnetic ratio of the spin
- ChemShift (Hz/T) : A array with the size of $1 \times TypeNumber$ for describing the chemical shift of the spins
- XDim : The number of voxels in X direction
- YDim : The number of voxels in Y direction
- ZDim : The number of voxels in Z direction
- XDimRes (m) : The voxel size in X direction
- YDimRes (m) : The voxel size in Y direction
- ZDimRes (m) : The voxel size in Z direction
- Type : A string for describing the type of the spin
- TypeNum : The number of pools
- ECon (S/m) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing tissue electrical conductivity (optional)

- MassDen (kg/m^3) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing tissue mass density (optional)
- Rho : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing spin density
- T1 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T1 relaxation time
- T2 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T2 relaxation time
- T2Star (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T2* relaxation time
- K (1/s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum^2$ for describing ME exchange rate. To explain the order of the exchange rate at the last dimension, for example, given there are three pools, the exchange rate is ordered as the first pool to itself K_{11} , to the second pool K_{12} , and to the third pool K_{13} , followed by K_{21} , K_{22} , K_{23} , K_{31} , K_{32} and K_{33} . The exchange rate to itself for any pool is assumed to be zero.

Notice that the multiple-pool ME model also needs to satisfy chemical equilibrium analogous to that of MT model. After making VObj, then save the 'VObj' structure as a MAT file. To accurately model ME exchange during scan, the user also needs to create execution points on the entire RF sequence line. A typical method is to insert a long RF pulse with zero amplitude at the empty portion of the RF sequence line. The interested users are referred to PSD.SPGR3DME for more information.

4. Make Virtual Object with Chemical Exchange Saturation Transfer (CEST) Properties

The current MRiLab version supports three-pool CEST model including a free (*f*) water pool, a macromolecule bound (*b*) proton pool and a free CEST (*c*) pool. The 'VObj' must have the structure like:

- Gyro (rad/s/T) : The gyromagnetic ratio of the spin
- ChemShift (Hz/T) : A array with the size of 1×3 for describing the chemical shift of the spins, free pool first, bound pool second, CEST pool last
- XDim : The number of voxels in X direction
- YDim : The number of voxels in Y direction
- ZDim : The number of voxels in Z direction
- XDimRes (m) : The voxel size in X direction
- YDimRes (m) : The voxel size in Y direction
- ZDimRes (m) : The voxel size in Z direction

- Type : A string for describing the type of the spin
- TypeNum : 3
- ECon (S/m) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing tissue electrical conductivity (optional)
- MassDen (kg/m³) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing tissue mass density (optional)
- Rho : A matrix with the size of $YDim \times XDim \times ZDim \times 3$ for describing spin density, free pool first, bound pool second, CEST pool last
- T1 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times 3$ for describing T1 relaxation time, free pool first, bound pool second, CEST pool last
- T2 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times 3$ for describing T2 relaxation time, free pool first, bound pool second, CEST pool last
- T2Star (s) : A matrix with the size of $YDim \times XDim \times ZDim \times 3$ for describing T2* relaxation time, free pool first, bound pool second, CEST pool last
- K (1/s) : A matrix with the size of $YDim \times XDim \times ZDim \times 4$ for describing CEST exchange rate. The order of the exchange rate at the last dimension is K_{fb} , K_{fc} , K_{bf} , and K_{cf} . No exchange between bound pool and CEST pool is assumed.

Notice that the CEST model also needs to satisfy chemical equilibrium analogous to that of MT model. After making VObj, then save the 'VObj' structure as a MAT file. To accurately model CEST exchange during scan, the user also needs to create execution points on the entire RF sequence line. A typical method is to insert a long RF pulse with zero amplitude at the empty portion of the RF sequence line. The interested users are referred to PSD_SPGR3DCEST for more information.

5. Make Virtual Object with Generalized Multi-pool (GM) Exchanging Model Properties

MRiLab v1.3 and above supports generalized multi-pool (GM) exchanging model (Figure 5.36) with flexible number of proton pools. The model consists of free proton pools, all inter-connected by the magnetization exchange pathways, and bound proton pools exchanging with the free proton pools through MT. The free proton pools represent compartments with measurable transverse magnetization (e.g., water, fat, solute proton exchange compounds), while the bound proton pools are used to model semi-solid tissue macromolecular content non-visible on standard MRI (e.g., myelin, muscle fibers, collagen). A particular configuration of the

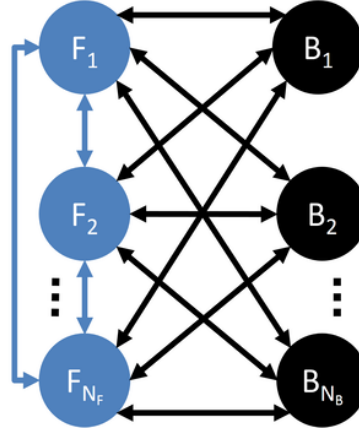


Figure 5.36: Generalized Multi-pool Exchanging Model

generalized model (i.e., number of the pools, their type, and exchange pathways between them) can be chosen along with its parameters (spin density, relaxation times, chemical shift spectra, and exchange rates) to represent a given tissue type. The user can read more about GM model in literature [10].

The ‘VObj’ must have the structure like:

- Gyro (rad/s/T) : The gyromagnetic ratio of the spin
- ChemShift (Hz/T) : A array with the size of $1 \times TypeNumber$ for describing the chemical shift of the spins
- TypeFlag : A array with the size of $1 \times TypeNumber$ for describing the type of each pool, 0 for free pool and 1 for bound pool
- LineShapeFlag : A array with the size of $1 \times TypeNumber$ for describing RF saturation line shape for bound proton pool, 0 for super-Lorentzian and 1 for Gaussian (:ToDo), the flag is ignored for free pool
- XDim : The number of voxels in X direction
- YDim : The number of voxels in Y direction
- ZDim : The number of voxels in Z direction
- XDimRes (m) : The voxel size in X direction
- YDimRes (m) : The voxel size in Y direction
- ZDimRes (m) : The voxel size in Z direction
- Type : A string for describing the type of the spin
- TypeNum : The number of pools
- ECon (S/m) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing tissue electrical conductivity (optional)

- MassDen (kg/m^3) : A matrix with the size of $YDim \times XDim \times ZDim$ for describing tissue mass density (optional)
- Rho : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing spin density
- T1 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T1 relaxation time
- T2 (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T2 relaxation time
- T2Star (s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum$ for describing T2* relaxation time
- K (1/s) : A matrix with the size of $YDim \times XDim \times ZDim \times TypeNum \times TypeNum$ for describing exchange rate. The exchange rate from the i th pool to the j th pool is placed as $K(:, :, :, i, j)$. The exchange rate to itself for any pool is assumed to be zero.

Notice that the GM model needs to satisfy chemical equilibrium analogous to that of MT model. After making VObj, then save the ‘VObj’ structure as a MAT file. To accurately model GM exchange during scan, the user also needs to create execution points on the entire RF sequence line. A typical method is to insert a long RF pulse with zero amplitude at the empty portion of the RF sequence line. The interested users are referred to PSD_SPGR3DGM for more information. **Also notice that the MT, ME and CEST model will be removed in the next MRiLab version and replaced by GM model.**

5.3.2 Create Virtual Object using XML

The Phantom Design toolbox can be activated by pressing ‘Phantom Design Panel’ toolbar icon located at the top of the main simulation console. If a phantom XML file has already been loaded (Chapter 3.1), the loaded phantom will show in the Phantom Design interface.



Figure 5.37: Phantom Design Panel Toolbar Icon

Figure 5.38 demonstrates an overview of the Phantom Design interface. This interface consists of

1. VObj Element Macro Library

The VObj Element Macro Library contains VObj element macros for constructing VObj structure in MRiLab. The user needs to click the ‘VObjElem’ root to unfold subsequent macros.

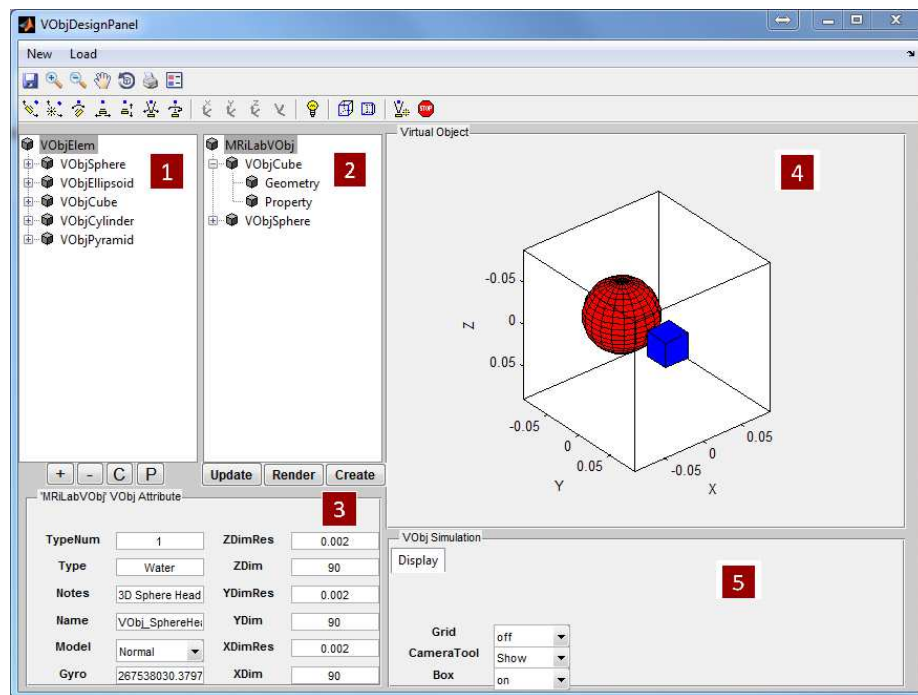


Figure 5.38: Phantom Design Panel

2. VObj Structure

In MRiLab, a VObj structure consists of arbitrary number of VObj elements that are combined to create a digital phantom. The user can construct desired phantom by changing the content within the VObj structure. To add a macro into the VObj structure, the user needs to click one macro in the macro library, then click on the VObj structure root (i.e. MRiLabVObj) to which this macro is inserted, then click '+' macro operation button. To delete a macro from the VObj structure, the user needs to click the unwanted macro, then click '-' macro operation button. To duplicate an existing macro, the user needs to first click the source macro, then click 'C' macro operation button for copying, click on the VObj structure root, then click 'P' macro operation button for pasting. MRiLab doesn't allow empty VObj structure.

3. VObj Element Attribute

Upon clicking on the VObj element macro within the VObj structure, the corresponding macro attributes will be shown at the VObj element attribute panel down below the VObj structure. The user can edit those attributes to modify the VObj element so as to generate different phantom. To make any modification effective, the user must press 'Update' button to update the VObj XML file. Based on this XML file, pressing 'Create' button will generate a .mat phantom file which can then be loaded from 'Load Phantom from XML' or 'Load Phantom'. Pressing 'Render' button will re-render the 3D Object on this interface. For instance, the VObj structure root 'MRiLabVObj' has attributes as follows:

- Name : The name of the VObj structure, recommended to use the naming convention as 'VObj_' followed by the phantom shape and applied anatomy (e.g. VObj.SphereHead)
- Model : The phantom model selection including 'Normal' for regular phantom, 'MT' for two-pool MT phantom, 'ME' for ME phantom and 'GM' for GM phantom. Note that if 'MT', 'ME' or 'GM' model is selected, the exchange rate 'K' must be properly provided in every VObj element macro
- Type : A string for describing the type of the phantom
- Notes : The notes of the phantom
- TypeNum : The number of the spin species
- Gyro (rad/s/T) : The gyromagnetic ratio of the spin
- XDim : The number of voxels in X direction for this phantom
- YDim : The number of voxels in Y direction for this phantom
- ZDim : The number of voxels in Z direction for this phantom
- XDimRes (m) : The voxel size in X direction
- YDimRes (m) : The voxel size in Y direction

- ZDimRes (m) : The voxel size in Z direction
4. 3D VObj Rendering
The 3D object based on the VObj structure is displayed on the ‘Virtual Object’ panel on the right side of this interface.
 5. VObj Rendering Control
The ‘Display’ tab on the ‘VObj Simulation’ panel contains parameters for controlling object display.
 - Grid : Turn on and off grid
 - Box : Turn on and off boundary box
 - CameraTool : Hide or show Matlab camera tool

5.3.3 VObj Element Macro Library

A VObj element macro is a predefined module for creating a VObj element that generates a 3D object with certain MR properties. MRiLab VObj element macro library is a collection of VObj element macros. This section will give an introduction to each of the VObj element macro provided in MRiLab.

VObjSphere

A VObj element macro that creates a sphere object. This macro contains attributes including:

- Notes : The notes of the object
- Color : The display color
- Alpha : The display transparency
- Geometry : The 3D geometry of the object, including
 - Radius (m) : The radius of the sphere
 - CenterX (m) : The X coordinate of the sphere center
 - CenterY (m) : The Y coordinate of the sphere center
 - CenterZ (m) : The Z coordinate of the sphere center
 - FaceNum : The number of the faces for the sphere
- Property : The MR properties of the object, including
 - TypeIdx : An index number of the spin species, used when the phantom has multiple spin species. The index must not exceed the ‘TypeNum’
 - ChemShift (Hz/T) : The chemical shift of the spin for the sphere. Note that for the VObj element with the same ‘TypeIdx’, the ‘ChemShift’ should be kept the same value

- TypeFlag : A flag number for describing the type of the spin, 0 for free pool and 1 for bound pool
- LineShapeFlag : A flag number for describing RF saturation line shape for bound proton pool, 0 for super-Lorentzian and 1 for Gaussian (:ToDo), the flag is ignored for free pool
- ECon (S/m) : A array with size of 1×3 for tissue electrical conductivity (optional)
- MassDen (kg/m^3) : The tissue mass density (optional)
- Rho : The spin density for the sphere
- T1 (s) : The T1 relaxation time for the sphere
- T2 (s) : The T2 relaxation time for the sphere
- T2Star (s) : The T2* relaxation time for the sphere
- K (1/s) : A array with the size of $1 \times \text{TypeNum}$ for describing the exchange rate of the spin, ignored for regular phantom. The rate value must be in the order as the ‘TypeIdx’ pool to the first pool, to the second pool, until to the last pool. The rate to itself for any pool can be set to zero.

VObjEllipsoid

A VObj element macro that creates an ellipsoid object. This macro contains attributes including:

- Notes : The notes of the object
- Color : The display color
- Alpha : The display transparency
- Geometry : The 3D geometry of the object, including
 - RadiusX (m) : The X semi-axis length of the ellipsoid
 - RadiusY (m) : The Y semi-axis length of the ellipsoid
 - RadiusZ (m) : The Z semi-axis length of the ellipsoid
 - CenterX (m) : The X coordinate of the ellipsoid center
 - CenterY (m) : The Y coordinate of the ellipsoid center
 - CenterZ (m) : The Z coordinate of the ellipsoid center
 - FaceNum : The number of the faces for the ellipsoid
- Property : The MR properties of the object, including
 - TypeIdx : An index number of the spin species, used when the phantom has multiple spin species. The index must not exceed the ‘TypeNum’

- ChemShift (Hz/T) : The chemical shift of the spin for the ellipsoid. Note that for the VObj element with the same ‘TypeIdx’, the ‘ChemShift’ should be kept the same value
- TypeFlag : A flag number for describing the type of the spin, 0 for free pool and 1 for bound pool
- LineShapeFlag : A flag number for describing RF saturation line shape for bound proton pool, 0 for super-Lorentzian and 1 for Gaussian (:ToDo), the flag is ignored for free pool
- ECon (S/m) : A array with size of 1×3 for tissue electrical conductivity (optional)
- MassDen (kg/m³) : The tissue mass density (optional)
- Rho : The spin density for the ellipsoid
- T1 (s) : The T1 relaxation time for the ellipsoid
- T2 (s) : The T2 relaxation time for the ellipsoid
- T2Star (s) : The T2* relaxation time for the ellipsoid
- K (1/s) : A array with the size of $1 \times TypeNum$ for describing the exchange rate of the spin, ignored for regular phantom. The rate value must be in the order as the ‘TypeIdx’ pool to the first pool, to the second pool, until to the last pool. The rate to itself for any pool can be set to zero.

VObjCube

A VObj element macro that creates a cube object. This macro contains attributes including:

- Notes : The notes of the object
- Color : The display color
- Alpha : The display transparency
- Geometry : The 3D geometry of the object, including
 - Length (m) : The egde length of the cube
 - CenterX (m) : The X coordinate of the cube center
 - CenterY (m) : The Y coordinate of the cube center
 - CenterZ (m) : The Z coordinate of the cube center
- Property : The MR properties of the object, including
 - TypeIdx : An index number of the spin species, used when the phantom has multiple spin species. The index must not exceed the ‘TypeNum’

- ChemShift (Hz/T) : The chemical shift of the spin for the cube. Note that for the VObj element with the same ‘TypeIdx’, the ‘ChemShift’ should be kept the same value
- TypeFlag : A flag number for describing the type of the spin, 0 for free pool and 1 for bound pool
- LineShapeFlag : A flag number for describing RF saturation line shape for bound proton pool, 0 for super-Lorentzian and 1 for Gaussian (:ToDo), the flag is ignored for free pool
- ECon (S/m) : A array with size of 1×3 for tissue electrical conductivity (optional)
- MassDen (kg/m^3) : The tissue mass density (optional)
- Rho : The spin density for the cube
- T1 (s) : The T1 relaxation time for the cube
- T2 (s) : The T2 relaxation time for the cube
- T2Star (s) : The T2* relaxation time for the cube
- K (1/s) : A array with the size of $1 \times \text{TypeNum}$ for describing the exchange rate of the spin, ignored for regular phantom. The rate value must be in the order as the ‘TypeIdx’ pool to the first pool, to the second pool, until to the last pool. The rate to itself for any pool can be set to zero.

VObjCylinder

A VObj element macro that creates a cylinder object. This macro contains attributes including:

- Notes : The notes of the object
- Color : The display color
- Alpha : The display transparency
- Geometry : The 3D geometry of the object, including
 - Radius (m) : The radius of the cylinder
 - Length (m) : The length of the cylinder
 - CenterX (m) : The X coordinate of the cylinder center
 - CenterY (m) : The Y coordinate of the cylinder center
 - CenterZ (m) : The Z coordinate of the cylinder center
 - FaceNum : The number of the faces for the cylinder
- Property : The MR properties of the object, including

- TypeIdx : An index number of the spin species, used when the phantom has multiple spin species. The index must not exceed the ‘TypeNum’
- ChemShift (Hz/T) : The chemical shift of the spin for the cylinder. Note that for the VObj element with the same ‘TypeIdx’, the ‘ChemShift’ should be kept the same value
- TypeFlag : A flag number for describing the type of the spin, 0 for free pool and 1 for bound pool
- LineShapeFlag : A flag number for describing RF saturation line shape for bound proton pool, 0 for super-Lorentzian and 1 for Gaussian (:ToDo), the flag is ignored for free pool
- ECon (S/m) : A array with size of 1×3 for tissue electrical conductivity (optional)
- MassDen (kg/m³) : The tissue mass density (optional)
- Rho : The spin density for the cylinder
- T1 (s) : The T1 relaxation time for the cylinder
- T2 (s) : The T2 relaxation time for the cylinder
- T2Star (s) : The T2* relaxation time for the cylinder
- K (1/s) : A array with the size of $1 \times TypeNum$ for describing the exchange rate of the spin, ignored for regular phantom. The rate value must be in the order as the ‘TypeIdx’ pool to the first pool, to the second pool, until to the last pool. The rate to itself for any pool can be set to zero.

VObjPyramid

A VObj element macro that creates a pyramid object. This macro contains attributes including:

- Notes : The notes of the object
- Color : The display color
- Alpha : The display transparency
- Geometry : The 3D geometry of the object, including
 - Height (m) : The height of the pyramid
 - Length (m) : The edge length of the pyramid base
 - CenterX (m) : The X coordinate of the pyramid base center
 - CenterY (m) : The Y coordinate of the pyramid base center
 - CenterZ (m) : The Z coordinate of the pyramid base center
- Property : The MR properties of the object, including

- TypeIdx : An index number of the spin species, used when the phantom has multiple spin species. The index must not exceed the ‘TypeNum’
- ChemShift (Hz/T) : The chemical shift of the spin for the pyramid. Note that for the VObj element with the same ‘TypeIdx’, the ‘ChemShift’ should be kept the same value
- TypeFlag : A flag number for describing the type of the spin, 0 for free pool and 1 for bound pool
- LineShapeFlag : A flag number for describing RF saturation line shape for bound proton pool, 0 for super-Lorentzian and 1 for Gaussian (:ToDo), the flag is ignored for free pool
- ECon (S/m) : A array with size of 1×3 for tissue electrical conductivity (optional)
- MassDen (kg/m^3) : The tissue mass density (optional)
- Rho : The spin density for the pyramid
- T1 (s) : The T1 relaxation time for the pyramid
- T2 (s) : The T2 relaxation time for the pyramid
- T2Star (s) : The T2* relaxation time for the pyramid
- K (1/s) : A array with the size of $1 \times \text{TypeNum}$ for describing the exchange rate of the spin, ignored for regular phantom. The rate value must be in the order as the ‘TypeIdx’ pool to the first pool, to the second pool, until to the last pool. The rate to itself for any pool can be set to zero.

5.3.4 Make New VObj XML

The user can also use the VObj loading function to load another VObj XML file. To load a VObj, click ‘Load’ menu then click ‘Load VObj XML File’, choose a VObj XML file. After the VObj XML is loaded, press ‘Render’ to display 3D object.

The user can create a new VObj XML file in the Phantom Design interface. To create a new VObj, click ‘New’ then click ‘Create VObj XML File’. A VObj creation window will show up and ask for new VObj name and notes. To follow MRiLab naming convention, the user is recommended to use ‘VObj_’ followed by the phantom shape and applied anatomy (e.g. VObj_SphereHead), make sure that the new VObj name differs from the existing VObj XML names in MRiLab. Then click ‘OK’ to select a path for storing the VObj XML file. It’s strongly recommended to put the VObj XML under the MRiLab VObj root folder /MRiLab/Config/VObj. Finally, MRiLab will create a new VObj XML file based on the content of ‘VObj_SphereHead’.

5.4 Coil Design

The Coil Design toolbox can be activated by pressing ‘Coil Design Panel’ toolbar icon located at the top of the main simulation console. Depending on the coil mode (i.e. ‘Tx’ or ‘Rx’) highlighted on the ‘Coil Selection’ panel, the loaded coil will show in the Coil Design interface.



Figure 5.39: Coil Design Panel Toolbar Icon

5.4.1 Coil Design GUI

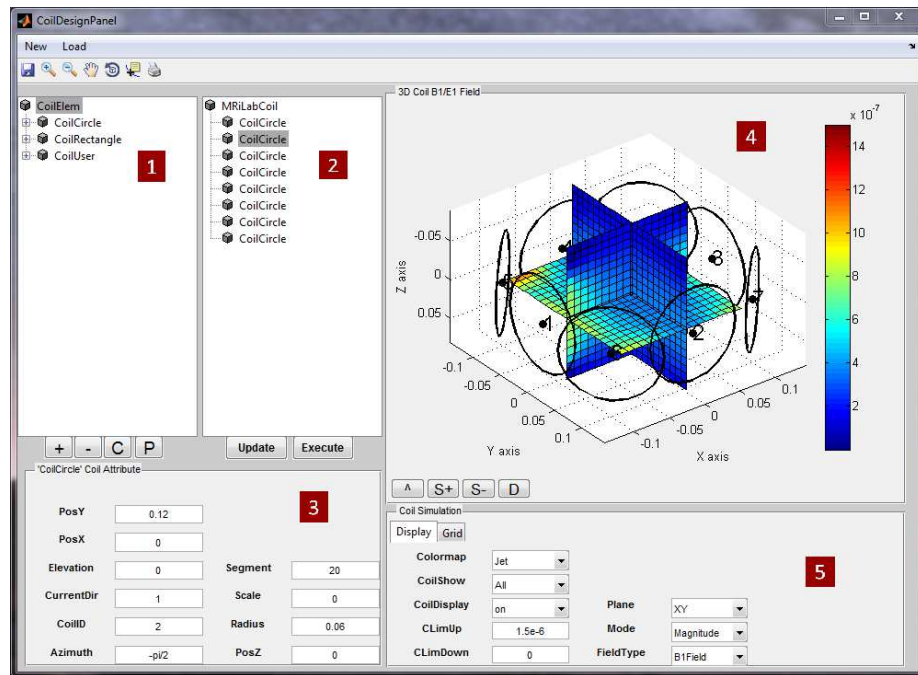


Figure 5.40: Coil Design Panel. An eight channel coil is shown.

Figure 5.40 demonstrates an overview of the Coil Design interface. This interface consists of

1. Coil Element Macro Library

The Coil Element Macro Library contains coil element macros for constructing coil structure in MRiLab. The user needs to click the ‘CoilElem’ root to unfold subsequent macros.

2. Coil Structure

In MRiLab, a coil structure consists of arbitrary number of coil elements that are combined to create desired B1 field and E1 field (only supported by CoilUser). The user can construct desired field by changing the content within the coil structure. To add a macro into the coil structure, the user needs to click one macro in the macro library, then click on the coil structure root (i.e. MRiLabCoil) to which this macro is inserted, then click ‘+’ macro operation button. To delete a macro from the coil structure, the user needs to click the unwanted macro, then click ‘-’ macro operation button. To duplicate an existing macro, the user needs to first click the source macro, then click ‘C’ macro operation button for copying, click on the coil structure root, then click ‘P’ macro operation button for pasting. MRiLab doesn’t allow empty coil structure.

3. Coil Element Attribute

Upon clicking on the coil element macro within the coil structure, the corresponding macro attributes will be shown at the coil element attribute panel down below the coil structure. The user can edit those attributes to modify the coil element so as to generate different field. To make any modification effective, the user must press ‘Update’ button to update the coil file. Pressing ‘Execute’ button will update and redraw the field map on this interface.

4. Coil Field

The coil configuration and B1 (T) and E1 (V/m) field generated based on the coil structure is displayed on the ‘3D Coil B1/E1 Field’ panel on the right side of this interface.

5. Coil Simulation Control

The ‘Display’ and ‘Grid’ tab on the ‘Coil Simulation’ panel contains parameters for controlling field display.

- Colormap : The colormap for the field, includes ‘Jet’, ‘Gray’ and ‘Hot’
- CLimDown (T) : The lower bound of color limits
- CLimUp (T) : The upper bound of color limits
- CoilDisplay : The flag for turning on and off coil display

- CoilShow : The flag for choosing active coil for field display
- Mode : The B1 field display mode, includes ‘Magnitude’, ‘Phase’, ‘Real’ and ‘Imaginary’
- FieldType : The flag to choose B1 field or E1 field, note E1 field only support ‘Magnitude’ display mode
- Plane : The flag for activating field slicing plane, includes ‘XY’, ‘XZ’ and ‘YZ’
- XDimRes (m) : The display spatial resolution in X direction
- YDimRes (m) : The display spatial resolution in Y direction
- ZDimRes (m) : The display spatial resolution in Z direction

MRiLab provides a group of field display button (Figure 5.41) to help inspect field details.



Figure 5.41: The Field Display Button.

The field display button group consists of:

- \wedge : Undock field on active slicing plane (Figure 5.42)
- S+ : Move active slicing plane forwards
- S- : Move active slicing plane backwards
- D : Display field in separate window

5.4.2 Coil Element Macro Library

A coil element macro is a predefined module for creating a coil element that generates B1 and E1 field in three dimensional space. MRiLab coil element macro library is a collection of coil element macros covering simple coil geometries. **Note that in MRiLab v1.3, only ‘CoilUser’ support generation of E1 field from external data file.** This section will give an introduction to each of the coil element macro provided in MRiLab.

CoilCircle

A coil element macro that creates a Biot-Savart coil circle. This macro contains attributes including:

- Azimuth (rad) : The azimuth angle of the circle plane
- Elevation (rad) : The elevation angle of the circle plane

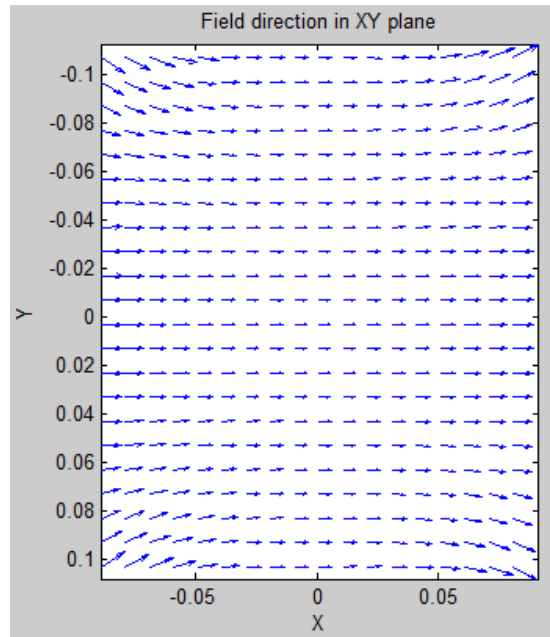


Figure 5.42: An Example of B1 Field on XY Plane.

- Radius (m) : The coil circle radius
- PosZ (m) : The Z position of coil circle center
- PosY (m) : The Y position of coil circle center
- PosX (m) : The X position of coil circle center
- CurrentDir : The current direction in the coil circle, 1 for clockwise, -1 for counterclockwise
- Scale : The scale factor for the B1 field amplitude
- Segment : The number of line segments for approximating circle, MRiLab requires the same 'Segment' for each coil circle
- CoilID : The assigned coil ID, each coil element must have a unique ID

CoilRectangle

A coil element macro that creates a Biot-Savart rectangle coil. This macro contains attributes including:

- Azimuth (rad) : The azimuth angle of the rectangle plane
- Elevation (rad) : The elevation angle of the rectangle plane

- Length (m) : The coil length
- Width (m) : The coil width
- PosZ (m) : The Z position of coil rectangle center
- PosY (m) : The Y position of coil rectangle center
- PosX (m) : The X position of coil rectangle center
- CurrentDir : The current direction in the coil, 1 for clockwise, -1 for counterclockwise
- Scale : The scale factor for the B1 field amplitude
- CoilID : The assigned coil ID, each coil element must have an unique ID

CoilUser

If the user has B1 and E1 field data saved in a MAT file, the user can easily import the field into MRILab coil design interface by using ‘CoilUser’ macro. The B1 field MAT file needs to contain two matrices including ‘B1x’ (i.e. x component of B1 field) and ‘B1y’ (i.e. y component of B1 field). Both of the two matrices must have the same size. The E1 field MAT file needs to contain three matrices including ‘E1x’ (i.e. x component of E1 field), ‘E1y’ (i.e. y component of E1 field) and ‘E1z’ (i.e. z component of E1 field). These three matrices must have the same size. The ‘CoilUser’ macro contains attributes including:

- B1File : The path to the file that stores the B1 field data, quoted using single quotes
- E1File : The path to the file that stores the E1 field data, quoted using single quotes
- Interp : The interpolation method, includes ‘linear’, ‘nearest’ and ‘cubic’
- PosZ (m) : The Z position of coil center (needed for coil display purpose)
- PosY (m) : The Y position of coil center (needed for coil display purpose)
- PosX (m) : The X position of coil center (needed for coil display purpose)
- CoilID : The assigned coil ID, each coil element must have an unique ID

5.4.3 Make New Coil

The user can also use the coil loading function to load another coil. To load a coil, click 'Load' menu then click 'Load Coil File', choose a coil XML file. After the coil is loaded, press 'Execute' to display field.

The user can create a new coil configuration in the Coil Design interface. To create a new coil, click 'New' then click 'Create Coil File'. A coil creation window (Figure 5.43) will show up and ask for new coil name and notes. To follow MRiLab naming convention, the user is recommended to use 'Coil_' followed by the number of coil elements and applied anatomy (e.g. Coil_16ChChest), make sure that the new coil name differs from the existing coil names in MRiLab. Then click 'OK' to select a path for storing the coil XML file. It's strongly recommended to put the coil under the MRiLab coil root folder /MRiLab/Config/Coil according to the coil type so that the coil is visible to MRiLab. Finally, MRiLab will create a new coil XML file based on the content of 'Coil_1ChHead'.



Figure 5.43: The Coil Creation Window

5.5 Magnet dB0 Design

The Magnet dB0 Design toolbox can be activated by pressing 'Magnet Design Panel' toolbar icon located at the top of the main simulation console. The loaded magnet will show in the Magnet dB0 Design interface.



Figure 5.44: Magnet Design Panel Toolbar Icon

5.5.1 Magnet Design GUI

Figure 5.45 demonstrates an overview of the Magnet dB0 Design interface. This interface consists of

1. Magnet Element Macro Library

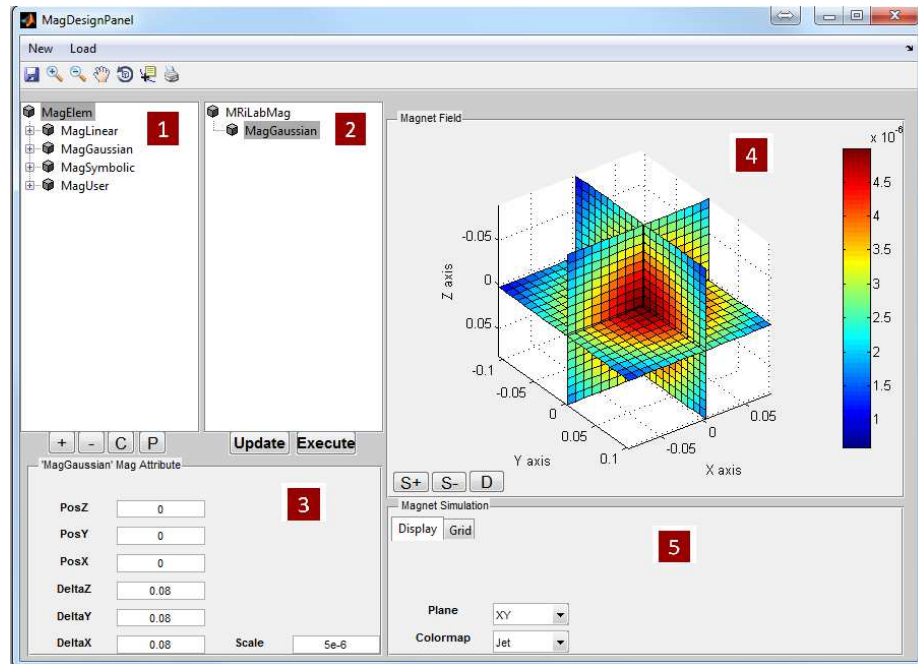


Figure 5.45: Magnet dB0 Design Panel

The Magnet Element Macro Library contains magnet element macros for constructing magnet structure in MRiLab. The user needs to click the 'MagElem' root to unfold subsequent macros.

2. Magnet Structure

In MRiLab, a magnet structure consists of arbitrary number of magnet elements that are combined to create desired dB0 field. The user can construct desired dB0 field by changing the content within the magnet structure. To add a macro into the magnet structure, the user needs to click one macro in the macro library, then click on the magnet structure root (i.e. MRiLabMag) to which this macro is inserted, then click '+' macro operation button. To delete a macro from the magnet structure, the user needs to click the unwanted macro, then click '-' macro operation button. To duplicate an existing macro, the user needs to first click the source macro, then click 'C' macro operation button for copying, click on the magnet structure root, then click 'P' macro operation button for pasting. MRiLab doesn't allow empty magnet structure.

3. Magnet Element Attribute

Upon clicking on the magnet element macro within the magnet structure, the corresponding macro attributes will be shown at the magnet element attribute panel down below the magnet structure. The user can edit those attributes to modify the magnet element so as to generate different dB0 field. To make any modification effective, the user must press ‘Update’ button to update the magnet file. Pressing ‘Execute’ button will update and redraw the dB0 field map on this interface.

4. Magnet Field

The dB0 field (T) generated based on the magnet structure is displayed on the ‘Magnet Field’ panel on the right side of this interface.

5. Magnet Simulation Control

The ‘Display’ and ‘Grid’ tab on the ‘Magnet Simulation’ panel contains parameters for controlling dB0 field display.

- Colormap : The colormap for the dB0 field, includes ‘Jet’, ‘Gray’ and ‘Hot’
- Plane : The flag for activating dB0 field slicing plane, includes ‘XY’, ‘XZ’ and ‘YZ’
- XDimRes (m) : The display spatial resolution in X direction
- YDimRes (m) : The display spatial resolution in Y direction
- ZDimRes (m) : The display spatial resolution in Z direction

MRiLab provides a group of dB0 field display button to help inspect the dB0 field details. The dB0 field display button group consists of:

- S+ : Move active dB0 field slicing plane forwards
- S- : Move active dB0 field slicing plane backwards
- D : Display field in separate window

5.5.2 Magnet Element Macro Library

A magnet element macro is a predefined module for creating a magnet element that generates dB0 field in three dimensional space. MRiLab magnet element macro library is a collection of magnet element macros. This section will give an introduction to each of the magnet element macro provided in MRiLab.

MagLinear

A magnet element macro that creates a linear dB0 field. This macro contains attributes including:

- GradZ (T/m) : The linear gradient of dB0 field in Z direction
- GradY (T/m) : The linear gradient of dB0 field in Y direction
- GradX (T/m) : The linear gradient of dB0 field in X direction
- Scale : The scale factor for the dB0 field

MagGaussian

A magnet element macro that creates a 3D Gaussian dB0 field. This macro contains attributes including:

- PosZ (m) : The Z position of the center
- PosY (m) : The Y position of the center
- PosX (m) : The X position of the center
- DeltaZ (m) : The width of Gaussian function in Z direction
- DeltaY (m) : The width of Gaussian function in Y direction
- DeltaX (m) : The width of Gaussian function in X direction
- Scale : The scale factor for the dB0 field

MagSymbolic

A magnet element macro that creates a dB0 field based on symbolic equation. This macro contains attributes including:

- Equation : An dB0 field equation

The symbolic equation could be any legal Matlab equation using variables 'X', 'Y' and 'Z'. For example, 'X+Y', '2*X.*Y' and '2*sin(X)' etc. Notice that use element operations for variables in the equation. The user needs to fill the equation between a pair of single quotes.

MagUser

If the user has the dB0 field data saved in a MAT file, the user can easily import the dB0 field into MRiLab magnet design interface by using 'MagUser' macro. The dB0 field MAT file needs to contain one matrix 'dB0'. The 'MagUser' macro contains attributes including:

- MagFile : The path to the file that stores the dB0 field data, quoted using single quotes
- Interp : The interpolation method, includes 'linear', 'nearest' and 'cubic'

5.5.3 Make New Magnet

The user can also use the magnet loading function to load another magnet. To load a magnet, click ‘Load’ menu then click ‘Load Magnet File’, choose a magnet XML file.

The user can create a new magnet in the Magnet Design interface. To create a new magnet, click ‘New’ then click ‘Create Magnet File’. A magnet creation window will show up and ask for new magnet name and notes. To follow MRiLab naming convention, the user is recommended to use ‘Mag-’ followed by a legal string and applied anatomy (e.g. Mag.CustomHead), make sure that the new magnet name differs from the remaining magnet names in MRiLab. Then click ‘OK’ to select a path for storing the magnet XML file. It’s strongly recommended to put the magnet under the MRiLab magnet root folder /MRiLab/Config/Mag according to the magnet type so that the magnet is visible to MRiLab. Finally, MRiLab will create a new magnet XML file based on the content of ‘Mag.LinearHead’.

5.6 Gradient Design

The Gradient Design toolbox can be activated by pressing ‘Gradient Design Panel’ toolbar icon located at the top of the main simulation console. The loaded gradient will show in the Gradient Design interface.



Figure 5.46: Gradient Design Panel Toolbar Icon

5.6.1 Gradient Design GUI

Figure 5.47 demonstrates an overview of the Gradient Design interface. This interface consists of

1. Gradient Element Macro Library

The Gradient Element Macro Library contains gradient element macros for constructing gradient structure in MRiLab. The user needs to click the ‘GradElem’ root to unfold subsequent macros.

2. Gradient Structure

In MRiLab, a gradient structure consists of three gradient elements that are combined to create gradient field for GzSS, GyPE and GxR. The user can construct desired gradient field by changing the content within the

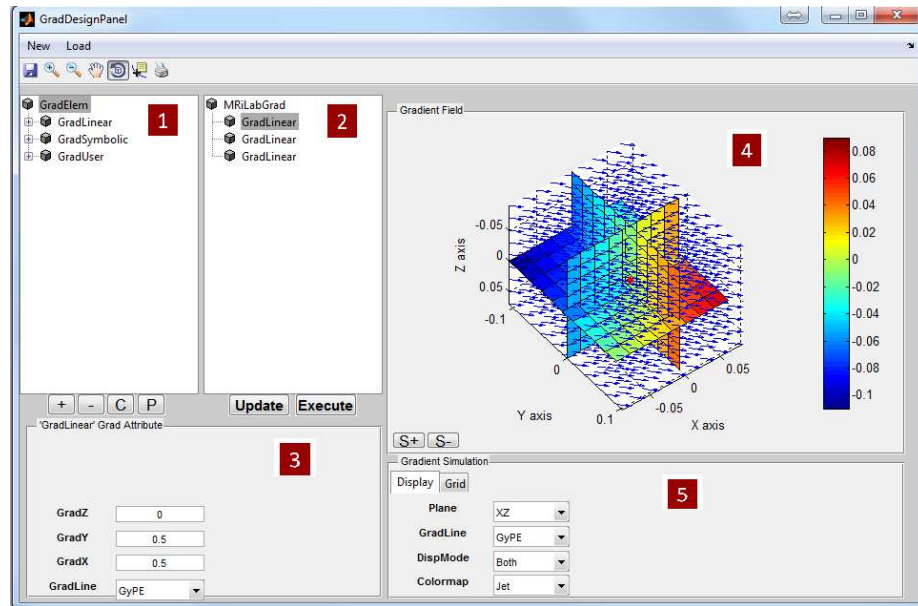


Figure 5.47: Gradient Design Panel

gradient structure. To add a macro into the gradient structure, the user needs to click one macro in the macro library, then click on the gradient structure root (i.e. MRILabGrad) to which this macro is inserted, then click ‘+’ macro operation button. To delete a macro from the gradient structure, the user needs to click the unwanted macro, then click ‘-’ macro operation button. To duplicate an existing macro, the user needs to first click the source macro, then click ‘C’ macro operation button for copying, click on the gradient structure root, then click ‘P’ macro operation button for pasting. MRILab doesn’t allow empty gradient structure, and also requires each of the three gradient sequence lines must have an individual gradient field.

3. Gradient Element Attribute

Upon clicking on the gradient element macro within the gradient structure, the corresponding macro attributes will be shown at the gradient element attribute panel down below the gradient structure. The user can edit those attributes to modify the gradient element so as to generate different gradient field. To make any modification effective, the user must press ‘Update’ button to update the gradient file. Pressing ‘Execute’ button will update and redraw the gradient field map on this interface.

4. Gradient Field

The gradient field is represented using a 3D quiver plot on the ‘Gradient Field’ panel. If a constant unit gradient is used, the regular linear spatial location is applied. However, if non-unit gradient is used, the spatial location could be non-linear with spatial grid deformation. This means the original spatial location will be mapped to a new location in the spatial grid. The transformed spatial grid is represented as three slicing planes on the ‘Gradient Field’ panel. The value (color) of the spatial grid equals to the spatial location in the direction indicated by ‘GradLine’ in ‘Gradient Simulation’ panel.

5. Gradient Simulation Control

The ‘Display’ and ‘Grid’ tab on the ‘Gradient Simulation’ panel contains parameters for controlling gradient field display.

- Colormap : The colormap for the spatial grid, includes ‘Jet’, ‘Gray’ and ‘Hot’
- Plane : The flag for activating grid slicing plane, includes ‘XY’, ‘XZ’ and ‘YZ’
- GradLine : The flag for activating gradient sequence line, includes ‘GzSS’, ‘GyPE’ and ‘GxR’
- DispMode : The display mode, includes ‘Gradient’, ‘Grid’ and ‘Both’
- XDimRes (m) : The display spatial resolution in X direction
- YDimRes (m) : The display spatial resolution in Y direction
- ZDimRes (m) : The display spatial resolution in Z direction

MRiLab provides a group of grid display button to help inspect the grid details. The grid display button group consists of:

- S+ : Move active grid slicing plane forwards
- S- : Move active grid slicing plane backwards

5.6.2 Gradient Element Macro Library

A gradient element macro is a predefined module for creating a gradient element that generates gradient field in three dimensional space. MRiLab gradient element macro library is a collection of gradient element macros. This section will give an introduction to each of the gradient element macro provided in MRiLab.

GradLinear

A gradient element macro that creates a linear gradient field. This macro contains attributes including:

- GradZ : A constant of gradient field vector in Z direction, 1 for unit gradient
- GradY : A constant of gradient field vector in Y direction, 1 for unit gradient
- GradX : A constant of gradient field vector in X direction, 1 for unit gradient
- GradLine : A gradient sequence line assigned to this gradient field

GradSymbolic

A gradient element macro that creates a gradient field based on symbolic equation. This macro contains attributes including:

- GradZEqu : An equation for gradient field vector in Z direction
- GradYEqu : An equation for gradient field vector in Y direction
- GradXEqu : An equation for gradient field vector in X direction
- GradLine : A gradient sequence line assigned to this gradient field

The symbolic equation could be any legal Matlab equation using variables 'X', 'Y' and 'Z'. For example, 'X+Y', '2*X.*Y' and '2*sin(X)' etc. Notice that use element operations for variables in the equation. The user needs to fill the equation between a pair of single quotes.

GradUser

If the user has gradient field data saved in a MAT file, the user can easily import the gradient field into MRiLab gradient design interface by using 'GradUser' macro. The gradient field MAT file needs to contain one four dimensional matrix 'G' with the size of the fourth dimension equal to 3. $G(:,:,,1)$ is the x component of the gradient vector, $G(:,:,,2)$ is the y component of the gradient vector and $G(:,:,,3)$ is the z component of the gradient vector. The 'GradUser' macro contains attributes including:

- GradFile : The path to the file that stores the gradient field data, quoted using single quotes
- Interp : The interpolation method, includes 'linear', 'nearest' and 'cubic'
- GradLine : A gradient sequence line assigned to this gradient field

5.6.3 Make New Gradient

The user can also use the gradient loading function to load another gradient. To load a gradient, click ‘Load’ menu then click ‘Load Gradient File’, choose a gradient XML file.

The user can create a new gradient in the Gradient Design interface. To create a new gradient, click ‘New’ then click ‘Create Gradient File’. A gradient creation window will show up and ask for new gradient name and notes. To follow MRiLab naming convention, the user is recommended to use ‘Grad.’ followed by a legal string and applied anatomy (e.g. Grad_CustomHead), make sure that the new gradient name differs from the existing gradient names in MRiLab. Then click ‘OK’ to select a path for storing the gradient XML file. It’s strongly recommended to put the gradient under the MRiLab gradient root folder /MRiLab/Config/Grad according to the gradient type so that the gradient is visible to MRiLab. Finally, MRiLab will create a new gradient XML file based on the content of ‘Grad_LinearHead’.

5.7 Motion Design

The Motion Design toolbox can be activated by pressing ‘Motion Design Panel’ toolbar icon located at the top of the main simulation console.



Figure 5.48: Motion Design Panel Toolbar Icon

5.7.1 Motion Design Panel

Figure 5.49 demonstrates an overview of the Motion Design interface. This interface consists of

1. Motion Element Macro Library

The Motion Element Macro Library contains motion element macros for constructing motion structure in MRiLab. The user needs to click the ‘MotElem’ root to unfold subsequent macros.

2. Motion Structure

In MRiLab, a motion structure consists of arbitrary number of motion elements that are combined to create desired motion pattern. The user can construct desired motion pattern by changing the content within the

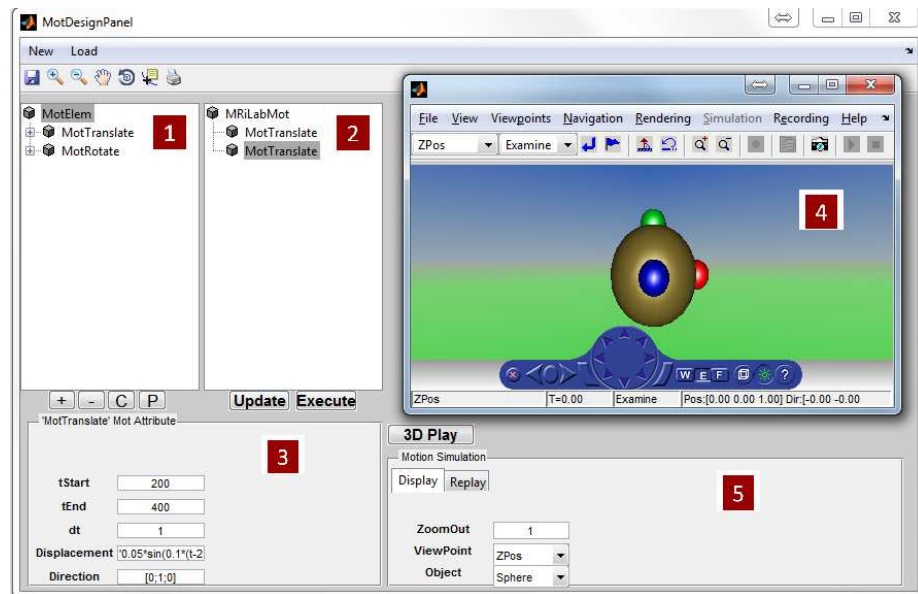


Figure 5.49: Motion Design Panel

motion structure. To add a macro into the motion structure, the user needs to click one macro in the macro library, then click on the motion structure root (i.e. MRiLabMot) to which this macro is inserted, then click '+' macro operation button. To delete a macro from the motion structure, the user needs to click the unwanted macro, then click '-' macro operation button. To duplicate an existing macro, the user needs to first click the source macro, then click 'C' macro operation button for copying, click on the motion structure root, then click 'P' macro operation button for pasting. MRiLab doesn't allow empty motion structure.

3. Motion Element Attribute

Upon clicking on the motion element macro within the motion structure, the corresponding macro attributes will be shown at the motion element attribute panel down below the motion structure. The user can edit those attributes to modify the motion element so as to generate different motion pattern. To make any modification effective, the user must press 'Update' button to update the motion file. Pressing 'Execute' button will update and recalculate the motion track.

4. Motion Tracker

MRiLab uses Matlab Simulink 3D Animation to monitor the movement track of an imaging object in a motion tracker window. To open this

window, the user needs to press ‘3D Play’ button. In the 3D animation, the imaging object is represented as a sphere or ellipsoid attached with three small spheres indicating axis directions (red for x axis, green for y axis and blue for z axis).

5. Motion Simulation Control

The ‘Display’ and ‘Replay’ tab on the ‘Motion Simulation’ panel contains parameters for controlling 3D animation.

- Object : The object model, currently only supports ‘Sphere’
- ViewPoint : A default view point, includes ‘ZPos’, ‘YPos’ and ‘XPos’
- ZoomOut : A factor of view zoom out
- Sample : The sample steps between two adjacent positions during movement
- Repeat : The repeat time of playback

5.7.2 Motion Element Macro Library

A motion element macro is a predefined module for creating a motion element that generates a movement track in three dimensional space. MRiLab motion element macro library is a collection of motion element macros. This section will give an introduction to each of the motion element macro provided in MRiLab.

MotTranslate

A motion element macro that creates translation motion. This macro contains attributes including:

- tStart (s) : The motion starting time
- tEnd (s) : The motion ending time
- dt (s) : The time interval of the motion track sample steps
- Direction : A vector describing translation direction in 3D space
- Displacement (m) : An equation of translation displacement pattern with respect to time

The displacement equation could be any legal Matlab equation using variables ‘t’. For example, ‘2*t’, ‘t+200e-3’ and ‘0.05*sin(0.1*t)’ etc. Notice that the user needs to fill the equation between a pair of single quotes.

MotRotate

A motion element macro that creates rotation motion. This macro contains attributes including:

- tStart (s) : The motion starting time
- tEnd (s) : The motion ending time
- dt (s) : The time interval of the motion track sample steps
- Axis : A vector describing rotation axis in 3D space
- Angle (rad) : An equation of rotation angle with respect to time

The rotation angle equation could be any legal Matlab equation using variables 't'. For example, '2*t', 't+200e-3' and 'sin(0.1*t)' etc. Notice that the user needs to fill the equation between a pair of single quotes.

5.7.3 Make New Motion

The user can also use the motion loading function to load another motion. To load a motion, click 'Load' menu then click 'Load Motion File', choose a motion XML file.

The user can create a new motion in the Motion Design interface. To create a new motion, click 'New' then click 'Create Motion File'. A motion creation window will show up and ask for new motion name and notes. To follow MRiLab naming convention, the user is recommended to use 'Mot_' followed by a legal string and applied anatomy (e.g. Mot_CustomHead), make sure that the new motion name differs from the existing motion names in MRiLab. Then click 'OK' to select a path for storing the motion XML file. It's strongly recommended to put the motion under the MRiLab motion root folder /MRiLab/Config/Mot according to the motion type so that the motion is visible to MRiLab. Finally, MRiLab will create a new motion XML file based on the content of 'Mot_ShiftHead'.

Note that adding motion pattern is required to stimulate motion, the user also needs to use extended real time process to trigger motion at the Ext sequence line. To trigger motion, one or more Ext flag 8 needs to be inserted into Ext line. An accurate motion tracking can be achieved using both small time interval of the motion track sample steps and frequent motion triggering, which typically requires more simulation computing. The interested users are referred to PSD_GRE3D for more information.

5.8 Image Reconstruction

MRiLab provides default image reconstruction code for a few types of Cartesian and Non-Cartesian k -space reconstruction. External reconstruction code is also acceptable.

5.8.1 Default Engine

To choose default reconstruction for Cartesian readout, the user needs to choose 'Cartesian' for 'ReconType' under the 'Recon' tab. The Cartesian reconstruction can be applied to typical Cartesian readout, FSE readout and EPI readout using default gradient macros. To choose default reconstruction for Non-Cartesian readout, the user needs to choose 'NonCart' for 'ReconType'. The corresponding Non-Cartesian reconstruction code can be applied to radial readout and spiral readout. Notice that the Non-Cartesian reconstruction performs 2D gridding process for the Non-Cartesian k -space trajectory using a Kaiser-Bessel kernel, followed by a regular iFFT. The 2D gridding process should also in theory be applicable to other Non-Cartesian readout. Also the 'gridding' tab is required to perform Non-Cartesian reconstruction.

5.8.2 External Engine

If the user uses a special k -space trajectory that requires particular reconstruction code, the user needs to indicate using external reconstruction by changing 'ReconEng' to 'External', and then provides a reconstruction function quoted with a pair of single quotes for 'ExternalEng'. It is recommended to put the external code under /MRiLab/Src/Recon/External, if not, make sure the reconstruction code is in Matlab search path. This setting will simply ignore default reconstruction code and apply external code. It is strongly recommended to write your own reconstruction code based on the template :

```
function DoCustomRecon
%Create an external reconstruction based on your code
global VCtl      % use VCtl structure, read only
global VSig      % use VSig structure, read only
global VImg      % use VImg structure, read and write

% The main code for your reconstruction
...

% Store recon image into VImg structure
VImg.Real = ...;
VImg.Imag = ...;
VImg.Mag = ...;
VImg.Phase = ...;
VImg.Sx = ...;
```

```

VImg.Sy = ...;
...

end

```

Notice that there are two new Virtual Structures (VSig and VImg) in this template, VSig encapsules acquired MR signal. VImg is declared to store reconstructed images. For the structure ‘VSig’, MRiLab provides :

- VSig.Sx : A array storing x (real) component of acquired MR signal
- VSig.Sy : A array storing y (imaginary) component of acquired MR signal
- VSig.Kz (1/m) : A array storing Kz location of k -space trajectory
- VSig.Ky (1/m) : A array storing Ky location of k -space trajectory
- VSig.Kx (1/m) : A array storing Kx location of k -space trajectory

The sample points in these arrays are organized in the order of

Sample points in one readout < Multiple echos < First phase encoding < Second phase encoding < Coil channel < Spin species

For the structure ‘VImg’, MRiLab provides :

- VImg.Real : A matrix for real component of reconstructed complex image with a size of $RYDim \times RXDim \times RZDim \times RxCoilNum \times TEPerTR$
- VImg.Imag : A matrix for imaginary component of reconstructed complex image with a size of $RYDim \times RXDim \times RZDim \times RxCoilNum \times TEPerTR$
- VImg.Mag : A matrix for magnitude of reconstructed complex image with a size of $RYDim \times RXDim \times RZDim \times RxCoilNum \times TEPerTR$
- VImg.Phase : A matrix for phase of reconstructed complex image with a size of $RYDim \times RXDim \times RZDim \times RxCoilNum \times TEPerTR$
- VImg.Sx : A matrix for x (real) component of sorted complex MR signal in Cartesian grid
- VImg.Sy : A matrix for y (imaginary) component of sorted complex MR signal in Cartesian grid

where $RXDim$, $RYDim$ and $RZDim$ are reconstructed image resolution in three spatial directions.

Gadgetron

If the user are interested in using Gadgetron for image reconstruction, MRiLab also provides a simple MEX code to convert acquired data into ISMRMRD file which can be used in Gadgetron process. To activate this function, the user needs to install ISMRMRD dependency packages to properly run compiled interface MEX. I am currently working on improving MRiLab support to Gadgetron recon framework. And I will be very pleased to talk with any MRiLab users who are willing to contribute to improving MRiLab Gadgetron support. Please don't hesitate to contact me. The ISMRMRD relevant code is 'DoToHDF5.m' under /MRiLab/Src/Main and 'DoMatToHDF5' under /MRiLab/Lib/src/interface.

5.9 Simulation Output

MRiLab can save simulation output into two file formats including 'MAT' and 'ISMRMRD'. The user can choose 'OutputType' under 'Recon' tab. If the user choose 'ISMRMRD' format, the 'DoMatToHDF5' MEX has to be functional, if not, MAT file will be saved instead. MRiLab saves simulation output for each series into a folder named by MRiLab's startup time under /MRiLab/Output folder. For MAT file, MRiLab saves:

- SeqXMLFile : Applied sequence XML file
- SeriesName : Series name on the main control console
- VCtl : Virtual Control structure
- VImg : Virtual Image structure
- VSig : Virtual Signal structure

Chapter 6

Image Display and Analysis

MRiLab incorporated a set of image display and analysis tools. They are designed using Matlab GUIDE, and carefully tuned for manipulating multi-dimensional image data in Matlab.

6.1 MagicRightClick

The user can right click on any MRiLab graphical axes to create an individual figure with the identical graphical content.

6.2 MatrixUser

MRiLab incorporated a toolbox called ‘MatrixUser’ for performing image display and analysis. This toolbox can be activated by pressing ‘MatrixUser’ toolbar icon located at the top of the main simulation console.



Figure 6.1: MatrixUser Toolbar Icon

MatrixUser will search through the current output folder and load all image series from this folder into Matlab base workspace. The MatrixUser main window (Figure 6.2) works as a matrix manager for loaded images. The user can choose to display image series by using the pop-up menu. The matrix size, type and value range are calculated and provided on the right side. The user can press ‘MatrixUser’ button to activate MatrixUser display window. Current MatrixUser version supports displaying any valid Matlab multi-dimensional matrix and Matlab structure variable.

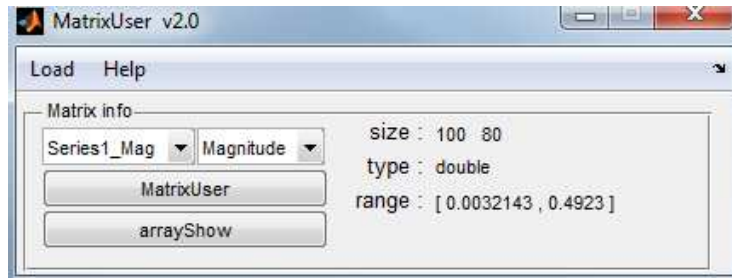


Figure 6.2: MatrixUser Main Window

6.2.1 Data Import

By default, MatrixUser reads Matlab base workspace, scans existing matrices in the Matlab session, then creates a matrix list for tracking matrix content. Once those matrices are updated by the user, MatrixUser will also update the matrix list. Moreover, there are several different approaches to import data from outside Matlab into MatrixUser. The imported matrices will be saved into Matlab base workspace. The import functions are located under 'Load' menu, including:

- Load MAT file

The default Matlab .mat file is natively supported by MatrixUser.

- Load System Clipboard

If image content exists in the system clipboard, it can be converted into a RGB image which contains a three slice matrix with each slice corresponds to an individual Red, Green and Blue channel.

- Load ScreenShot

MatrixUser takes a full screenshot for current monitor and saves it into a RGB image as described above.

- Load from Binary file

Binary data file is supported by MatrixUser. The user needs to properly configure loading parameters (Figure 6.3) according to the matrix size and data type information.

- Load DICOM file(s)

MatrixUser supports loading multiple DICOM files by using a file filter interface (Figure 6.4). The user needs to load DICOM files into the loading interface by selecting desired DICOM files (multiple selection supported). The selected files are listed in the DICOM file list. The user can click any single DICOM file to read associated DICOM header and image preview. To manually create a matrix using DICOM files, choose files from the

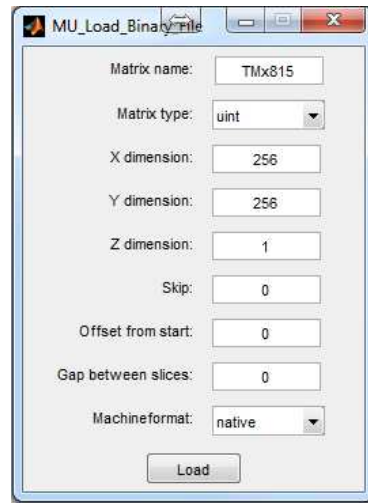


Figure 6.3: MatrixUser Binary File Loading Interface

DICOM file list, press '>>>>>' to push the files into selected DICOM file list, provide a matrix name, press 'Convert' button to create a matrix based on chosen DICOM files. The user can load those created matrices into base workspace by pressing 'Load matrix' button.

- Load DICOM file(s) in Batch

MatrixUser supports loading DICOM files in a batch mode. This function requires the path of the folder containing DICOM files is provided. MatrixUser will try to create separate matrices for DICOM files coming from different image series. A matrix selection interface will provide converted matrices with loading functions.

- Load from NIfTI file

NIfTI file with .nii suffix is supported by MatrixUser.

6.2.2 Window Layout

To activate MatrixUser display window, press 'MatrixUser' button. If the selected matrix contains complex value, four options are available for displaying magnitude, phase, real and imaginary of the matrix. Figure 6.5 demonstrates an overview of the window layout of the MatrixUser display window. The window consists of

1. Matlab Default Toolbar

Matlab toolbar provides basic interactive functions for displaying matrix. These functions include:

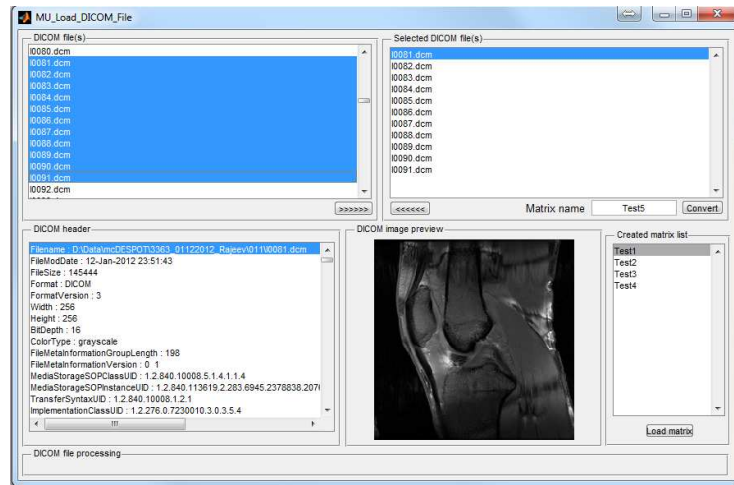









Figure 6.4: MatrixUser DICOM File Loading Interface

-  : Save current image axes into an image file
-  : Zoom in matrix area
-  : Zoom out matrix area
-  : Manually move matrix position
-  : Check individual voxel value and index
-  : Print current figure
-  : Turn on/off color bar

2. MatrixUser Function Library

Most of the matrix analysis functions are represented on function bench panel. MatrixUser groups these functions into categories and dynamically loads them according to the dimension size and compatibility of current display matrix. A multi-tab is used to contain individual function button associated with each function. The tabs under the multi-tab are used to switch between function categories, which include

- Display : Multi-dimensional matrix display functions
- QuickMath : Perform math calculation for current matrix
- Transform : Transform current matrix

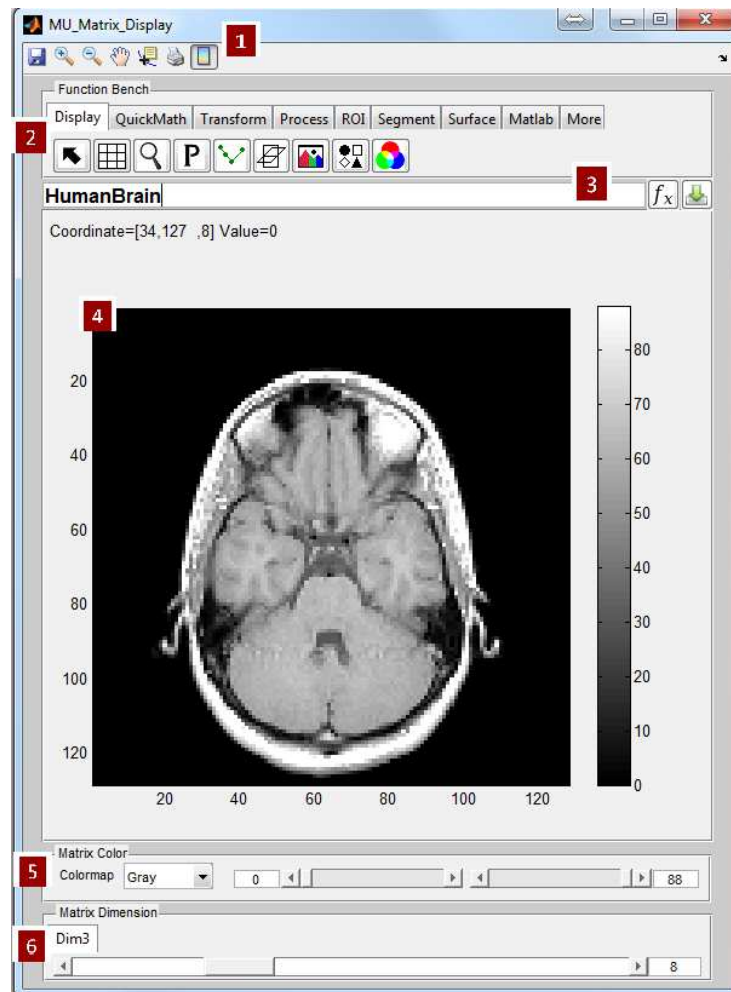




Figure 6.5: MatrixUser Display Window

- Process : Basic matrix processing functions
- ROI : Region-of-Interest functions
- Segment : Segmentation functions
- Surface : Generate surface or mesh plot for current image
- Matlab : Matlab default image tools
- More : Uncategorized functions

3. Matrix Calculator

The matrix calculator consists of three control items, including a matrix expression editbox, an execution button () and a matrix saving button (). Valid matrix calculation expression can be executed in the calculator and updated in the display window, serving as a convenient way to analyze matrix calculation result. Matrix concatenation and recombination can also be done in the calculator, for example, to side-by-side compare multiple 3D matrices (Figure 6.6). Some valid calculation examples are, but not limited to:

- A,B Combines A and B in one row
- A,B;C,D Combines A and B in the first row, C and D in the second row
- A,B;C,zeros(size(C)) Combines A and B in the first row, C in the second row, pad with zero value
- sin(A),cos(B) Calculates voxel-wise sin for A and cos for B, then combine them in one row
- A(:,1:10,:) Extracts submatrix from A and display it

where A, B, C and D are multi-dimensional matrices with proper matrix size. Also note that the source matrices have to stay in the base workspace for being referenced. Pressing the execution button will perform the calculation and save the result as a temporary matrix. The user can also save the temporary matrix into workspace by pressing matrix saving button. The saved temporary matrix will have a ‘_tmp’ suffix by default.

4. Matrix Display Axes

The display axes renders an image for one slice of current matrix. The user can use mouse cursor to inspect the coordinate and value of any voxel. Moving mouse wheel back and forth moves the slice location along current dimension and updates the display axes.

5. Matrix Color Control Group

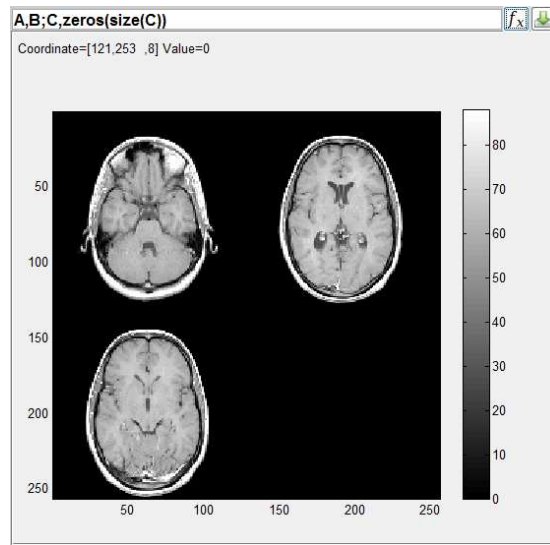


Figure 6.6: MatrixUser Concatenation Example

The matrix color control group provides a set of sliders, editboxes and popup menu which help control image color scheme and contrast. This group consists of

- Colormap Popup Menu: Choose different colormap scheme
- Upper Color Bound Slider (right slider): Slide to control the upper bound of color limits
- Upper Color Bound EditText (right editbox): Edit to control the upper bound of color limits
- Lower Color Bound Slider (left slider): Slide to control the lower bound of color limits
- Lower Color Bound EditText (left editbox): Edit to control the lower bound of color limits





6. Matrix Dimension Control Group

MatrixUser measures the dimension size of the display matrix and assigns one slider and editbox for each dimension that is above 2 (i.e. no slider and editbox for the first and second dimension). These control items are located in individual dimension tab and can be used to switch among slices in current active dimension.

6.2.3 Function Library

1. Display

Matrix display functions are listed under this tab.

-  : Reset matrix display and erase additional display effect
-  : Turn on and off black grid line on the image display axes
-  : Open an instant magnifier which zooms in specific image area
-  : Plot and update a profile curve along a resizable checking line (Figure 6.7)

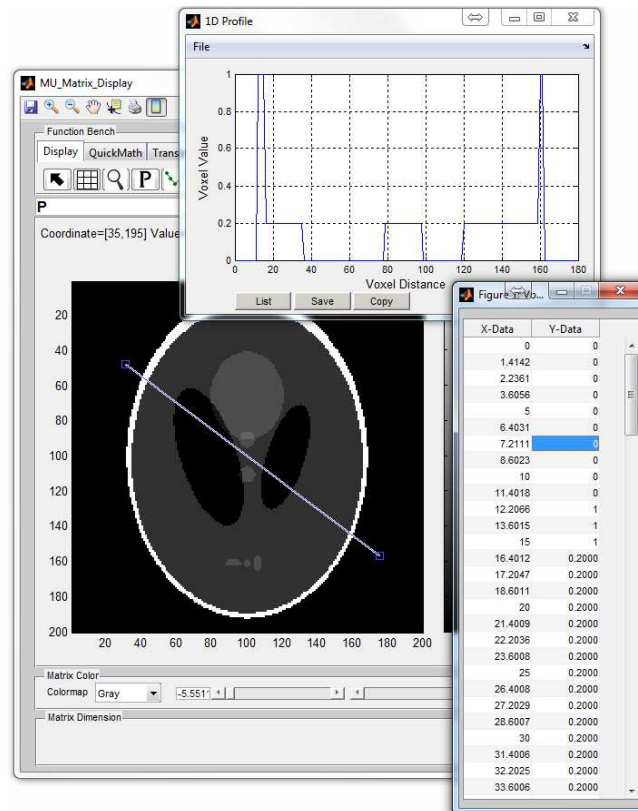



Figure 6.7: An Example of 1D Profile. The user can relocate and resize the profile checking line on the image for inspecting live 1D profile. The buttons on the profile window can list profile data, save the data as 'data.plt' array into workspace or copy the data into clipboard.

-  : Plot and update a profile curve along a matrix dimension (Figure 6.8)

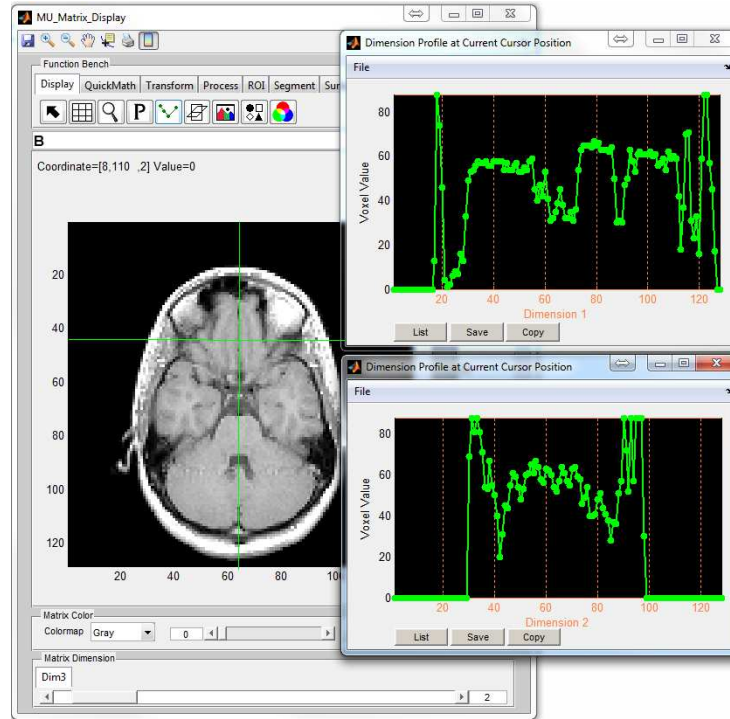








Figure 6.8: An Example of Plotting the First (Column) and Second (Row) Matrix Dimension Profile. The user needs to specify which matrix dimension to plot. The profile curve will update according to current mouse cursor position. The user can pause or resume live updating by right click on main display window.

-  : Open a separate window with two matrix display axes (Figure 6.9) displaying another two orthogonal images. The operation buttons on the second window consists of
 -  : Activate or deactivate localizer line on main display
 -  : Activate or deactivate localizer line on main display
 -  : Switch matrices between main display and second display. This operation simply permutes current matrix into its orthogonal version. The user can save the transformed matrix using ().
-  : Create a RGB image, assign current slice and following two slices to Red, Green and Blue channel, respectively

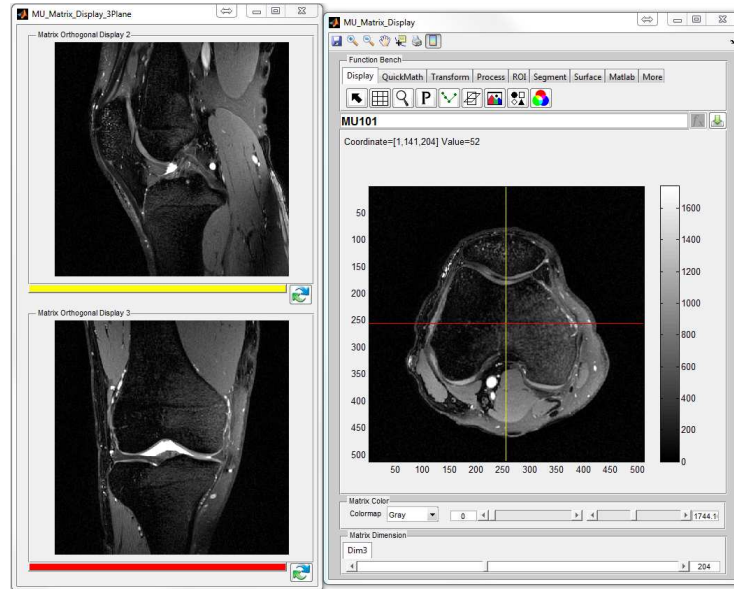





Figure 6.9: 3D Slicer. To change view slice, the user needs to activate localizer line and then click on desired coordinate on the main display window.

-  : Create a montage image using multiple slices (Figure 6.10)
-  : Overlap two matrices with the same matrix size (Figure 6.11), notice that the user can press  to remove foreground matrix from overlapping with background matrix.

2. QuickMath

This function category performs quick math calculation for current matrix. A few commonly used math calculation are provided under this tab. Instead, complex calculation can be performed using matrix calculator as mentioned above.













-  : Calculate absolute value
-  : Calculate negative value
-  : Calculate natural logarithm
-  : Calculate base 10 logarithm
-  : Calculate exponential
-  : Calculate the power of 10









Figure 6.10: Montage Image. An example of creating a 4-by-5 montage image using multiple matrix slices starting from the first slice.

-  : Calculate sine
-  : Calculate cosine
-  : Calculate tangent
-  : Calculate inverse sine
-  : Calculate inverse cosine
-  : Calculate inverse tangent

3. Transform

This function category performs spatial transformation or fast Fourier transform (FFT) to current matrix.

-  : Flip matrix horizontally (along the first dimension)
-  : Flip matrix vertically (along the second dimension)
-  : Flip matrix along slice direction (the third dimension)
-  : Rotate matrix 90 degree in the counter clockwise direction
-  : Rotate matrix 90 degree in the clockwise direction
-  : Rotate matrix certain degree along an axis specified using the rotation axis origin and direction in the 3D space

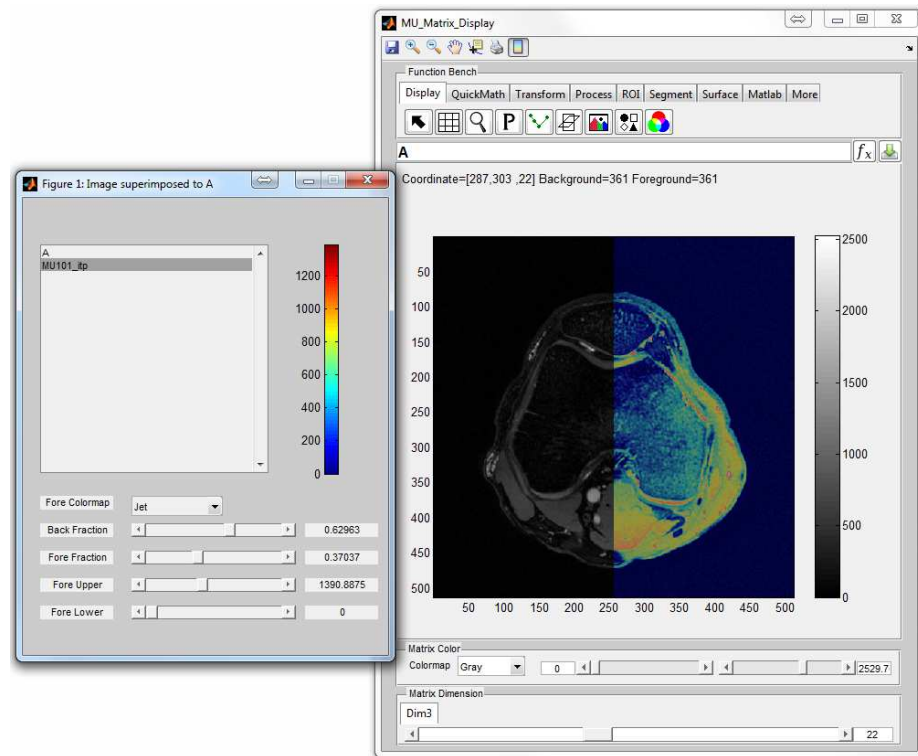









Figure 6.11: An Example of Overlapping Two Matrices. A second window is provided for adjusting overlapping effect. The user can choose to overlap any size compatible matrices from the matrix list. There exist control items to change foreground colormap scheme, to modify image intensity fraction, or to change foreground color limits.

-  : Translate matrix along certain direction
-  : Perform multi-dimensional FFT for current matrix, the user needs to specify up to which dimension to perform FFT.

4. Process

This function category performs basic matrix processing functions.

-  : Create binary mask based on given threshold
-  : Perform smoothing operation to current matrix
-  : Perform sharpening operation to current matrix
-  : Perform edge detection to current matrix
-  : Provides various image filters (Figure 6.12)

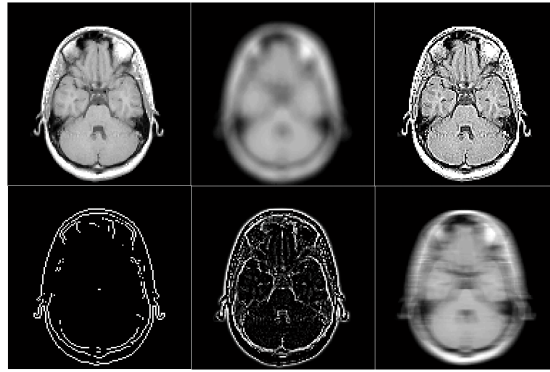



Figure 6.12: Image Filters. An example is shown for applying various image filters.

-  : Add noise to matrix (Figure 6.13)

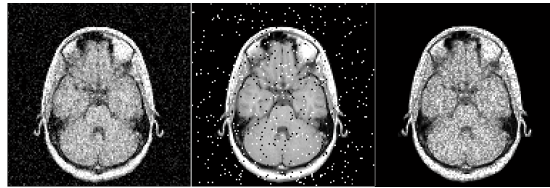









Figure 6.13: Image Noise. An example is shown for applying various image noise.

-  : Replace voxel value for the voxels within certain value range and outside a polygon area. The user needs to draw a polygon first (double click to confirm the polygon).
-  : Replace voxel value for the voxels within certain value range and inside a polygon area. The user needs to draw a polygon first (double click to confirm the polygon).
-  : Replace voxel value for the voxels inside a polygon area. The user needs to draw a polygon first (double click to confirm the polygon).
-  : Replace matrix area with a selected matrix source region. The user needs to draw a free-hand area (source region), drag the free-hand region to target matrix area, then double click to confirm the operation.
-  : Crop current matrix using a rectangle box (double click to confirm the cropping)
-  : Extract parts of current matrix using irregular shape (double click to confirm the extracting)
-  : Resample current matrix by using chosen interpolation method (Figure 6.14). The user can specify sampling factors in x, y and z direction for 3D matrix.

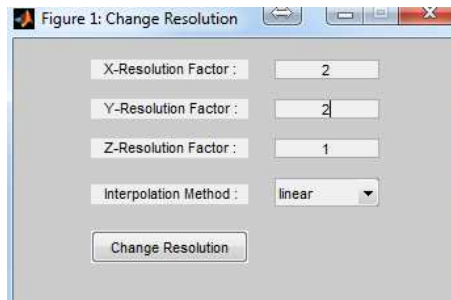










Figure 6.14: Interpolation Window. An example is shown to double spatial resolution in x and y direction by using a linear interpolation.

5. ROI

MatrixUser provides a set of function buttons for performing Region-of-Interest (ROI) analysis (Figure 6.15). To create a ROI, the user needs to click ROI button first, then draw a ROI on the image axes. The statistical measures (i.e. mean, standard deviation and relative standard deviation) for voxels in delineated ROI is calculated and updated with moving ROI position or changing ROI shape. The ROI function buttons consists of

-  : Draw a free hand ROI
-  : Draw a rectangle or square ROI
-  : Draw a circle or ellipse ROI
-  : Draw a polygon ROI
-  : Draw a straight line for measuring distance in units of pixels
-  : Draw a polygon for measuring the interior angles in degrees
-  : Record existing ROI shape and location into a ROI list, allow to redraw selected ROI in multiple image axes. To redraw a existing ROI, the user needs to select a ROI in the list, then press 'Show' button. Note that the copied ROI is no longer resizable and movable.
-  : Plot histogram for current slice (Figure 6.16); if ROIs exist, plot histogram for latest activated ROI

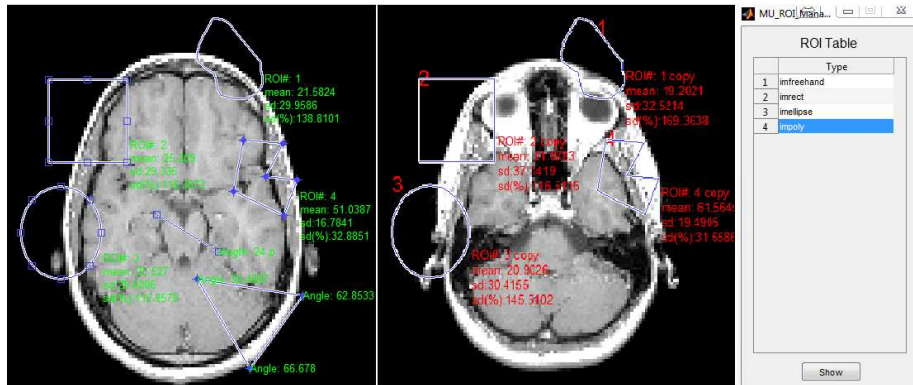





Figure 6.15: Draw Multiple ROIs and Redraw on A Second Image. The source ROIs are in green, copied ROIs are in red.

6. Segment

MatrixUser supports functions for performing multi-slice manual segmentation. To create a segmentation, click segmentation button, then draw a region on the image axes. The user can modify the region location and shape prior to confirming segmentation with double click. The segmentation buttons consists of

-  : Do a free-hand segmentation
-  : Do a circle or ellipse segmentation
-  : Do a polygon segmentation

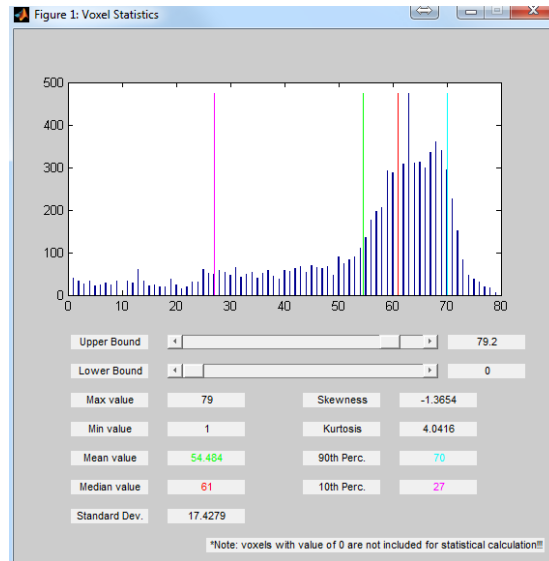












Figure 6.16: Histogram for One Image Slice

-  : Edit segmentation
-  : Save segmentation into a MAT file
-  : Load segmentation from a MAT file

To edit segmented region (Figure 6.17), press  to open a segmentation manager. The manager records the type and location for existing segmented regions. The user can click any region item to inspect the location of the region. To edit chosen region, click 'Edit' button to activate the region outline. Both the shape and mask flag are editable for segmented region. After editing, click 'Update' to conform modification. The user can press  to save current segmentation into a MAT file which contains a mask matrix and a cell array storing segmentation location information. The user can also press  to save the mask matrix into workspace. Pressing  can load previous segmented regions from a saved MAT file. Notice that the user can press  to remove segmentation from overlapping with background matrix.

7. Surface

This function category generates surface or mesh plot for current image.

-  : Create contour plot of current matrix
-  : Create 3D contour plot of current matrix

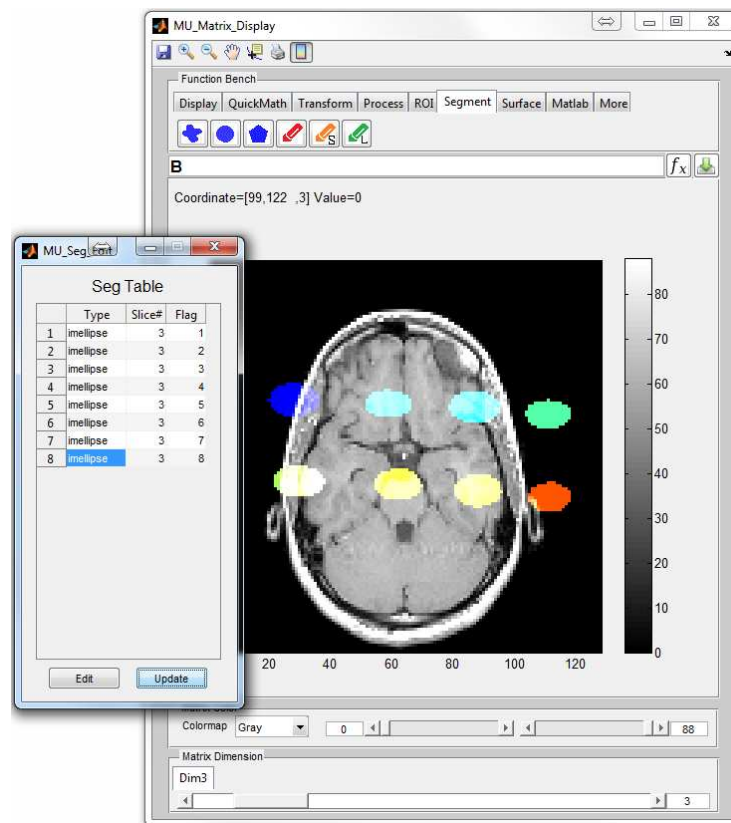















Figure 6.17: Editing Segmentation

-  : Create filled 2D contour plot
-  : Create 3D shaded surface plot
-  : Create surface plot and contour
-  : Create surface plot with colormap based lighting
-  : Create mesh plot
-  : Create mesh plot and contour
-  : Create a curtain around a mesh plot
-  : Create a ribbon plot
-  : Create a waterfall plot
-  : Create pcolor (checkerboard) plot






8. Matlab

Matlab default image tools (Figure 6.18) are tailored for MatrixUser and included in this category.

-  : Perform imtool for current image
-  : Perform immovie for playback current 3D matrix
-  : Perform imcontrast for adjusting image contrast

9. More

Uncategorized functions are categorized under this tab.

-  : Create a 3D graph for rendering current matrix (Figure 6.19)
-  : Perform projection along a given matrix dimension. Support multi-dimensional matrix projection
-  : Perform 3D projection along x, y or z axis with certain angle increment (Figure 6.20)
-  : Reslice 3D matrix at given direction. The user needs to draw a line for indicating the slicing direction with double click for confirmation (Figure 6.21)
-  : Create a movie using current matrix display. Support making movie for overlapped matrices.

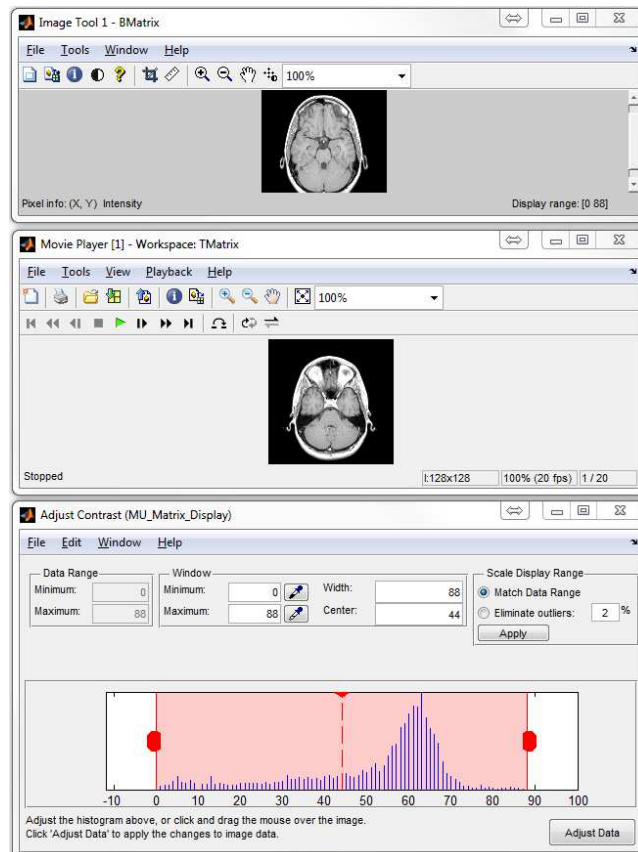


Figure 6.18: Matlab Tools

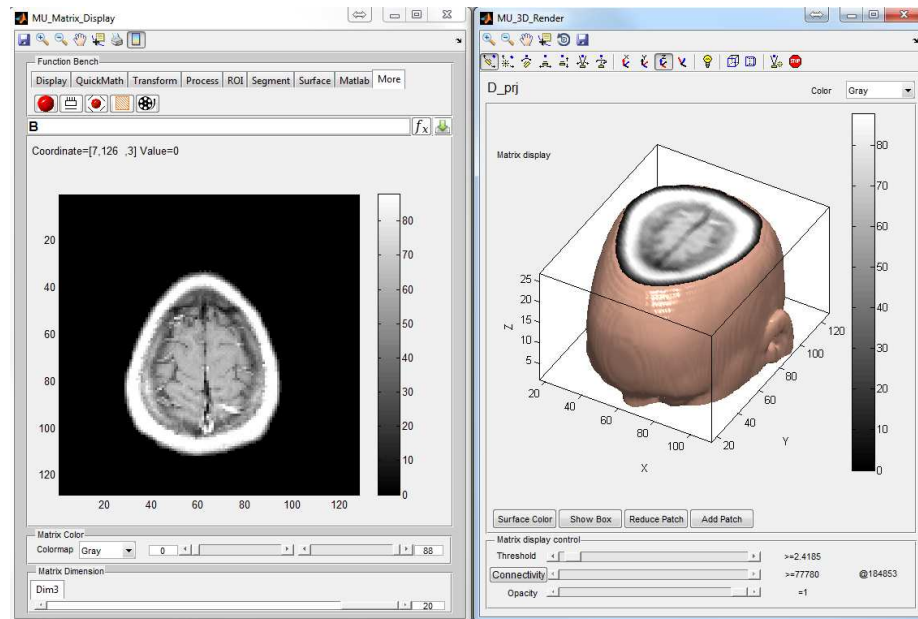


Figure 6.19: An Example of 3D Human Brain Rendering. Control units on the rendering window are provided for fine tuning the renderer. The user can select isosurface threshold, cutoff connectivity threshold (i.e. object with total voxels less than the threshold will be removed from the rendering, '@' is followed by the voxel number of current largest object) and object opacity. A set of pushbuttons are also available for changing surface color, display box and patches. The default Matlab camera toolbar are provided for adjusting the lighting effect.

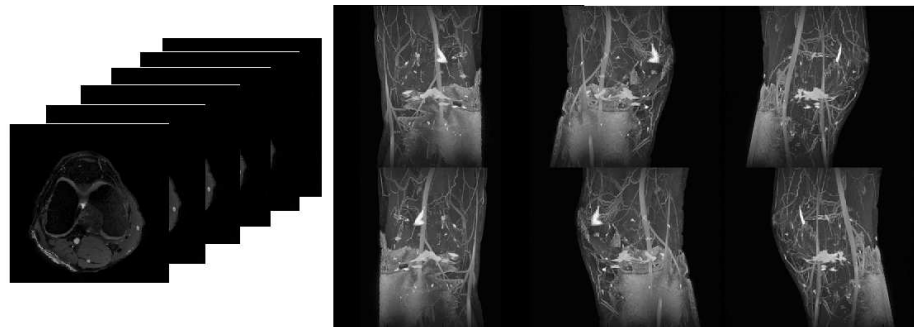


Figure 6.20: 3D Maximum Intensity Projection (MIP). An example of 3D MIP around axial axis of a human knee MRI image stack shows the vascular system of the knee joint.

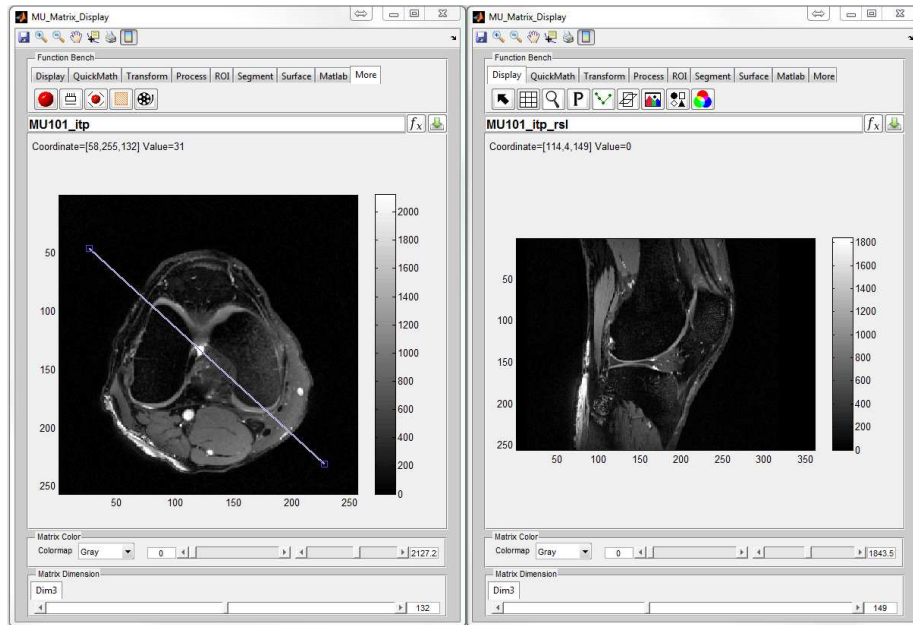


Figure 6.21: Reslice 3D Matrix. An example of 3D reslicing generates a new stack of images in the oblique plane from an axial human knee MRI image stack. Note that the resliced images are extracted from the plane perpendicular to the indicating line on the left window.

6.3 arrayShow

The arrayShow tool is a Matlab image viewer which has been designed for the evaluation of multidimensional complex images. arrayShow is originally designed by Tilman Johannes Sumpf at Biomedizinische NMR Forschungs GmbH. The user can press ‘arrayShow’ button to activate this viewer. Detailed information about arrayShow can be found at http://www.biomednmr.mpg.de/index.php?option=com_content&task=view&id=137&Itemid=43;

6.4 SpinWatcher

The SpinWatcher is designed for monitoring spin evolution behavior within a single voxel at given MR sequence and field environment. This function can be activated by pressing ‘SpinWatcher’ toolbar icon located at the top of the main simulation console.



Figure 6.22: SpinWatcher Toolbar Icon

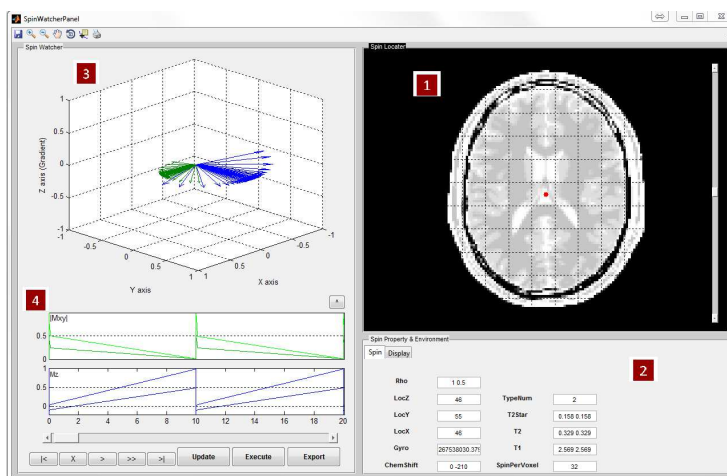



Figure 6.23: SpinWatcher Main Interface

Figure 6.23 demonstrates an overview of the SpinWatcher main interface. This interface consists of

1. Voxel Locator

The default voxel is chosen as the one at the isocenter indicated by a red isocenter marker. However, the user can select any voxel within the virtual

object by using . The slider beside the image can help change image slices.

2. Spin Property and Environment

The spin properties will be automatically updated with a selected voxel. The user can modify the spin properties and environment to meet their own needs. The editable properties provided in this interface include:

(a) Spin

- ChemShift (Hz/T): The chemical shift of the spin
- Gyro (rad/s/T): The gyromagnetic ratio of the spin
- Rho : The density of the spin
- T1 (s): The longitudinal relaxation time
- T2 (s): The transverse relaxation time
- T2Star (s): The T2* relaxation time
- SpinPerVoxel : The number of spins in each voxel, default one spin per voxel will treat T2* equal to T2, use a number above one for simulating T2* effect
- TypeNum : The number of spin species
- LocZ : The Z location of the selected voxel
- LocY : The Y location of the selected voxel
- LocX : The X location of the selected voxel

(b) Display

- WindowSize : The window width of the spin evolution plot
- ISOHighlight : The flag for turning on and off isocenter mark
- Grid : The flag for turning on and off grid line
- Axes : The flag for turning on and off axes label

The SpinWatcher supports monitoring multiple spin species. The user needs to provide an array of multiple values for T1, T2, T2*, Rho and ChemShift, and give the correct number of spin species. The values must be separated with space. For example

- ChemShift = 0 -210
- Rho = 1.0 0.5
- T1 = 1.2 1.0
- T2 = 0.02 0.03
- T2Star = 0.002 0.003

- TypeNum = 2

3. Spin Watcher Window

A 3D spin evolution animation is displayed in the spin watcher window. The 3D animation is controllable using a set of control buttons and sliders

- Scroll Bar : Drag the scroll bar to any intermediate time point between beginning and end
- | < : Move to the beginning
- X : Pause animation, notice that the interface can only be closed while animation is paused
- O : Resume animation
- > : Play at normal speed
- >> : Play at double normal speed
- > | : Move to the end

4. Spin Evolution Plot

SpinWatcher provides two plots for capturing the spin evolution (i.e. $|M_{xy}|$ and M_z) regarding time. Press 'Execute' button to recalculate the spin evolution plot if changes to spin property and environment was made. The settings can be saved into a file by pressing 'Update'. To export temporary variables of spin evolution into Matlab base workspace, press 'Export', the exported variables include :

- Muts : A array for time points
- MxySum : A array for $|M_{xy}|$
- MzSum : A array for M_z
- Mx : x component of magnetization
- My : y component of magnetization
- Mz : z component of magnetization

The user can also undock the spin evolution plot by pressing '^' button.

6.5 SARWatcher

The SARWatcher is a graphical toolbox for monitoring time varying spatial Specific Absorption Rate (SAR) of the virtual object under given experimental design. This function can be activated by pressing 'SARWatcher' toolbar icon located at the top of the main simulation console. **Note that in order to evaluate SAR, transmitting RF coil with E1 field is required.** One example can be found at Coil_8ChHeadSAR.

Figure 6.25 demonstrates an overview of the SARWatcher main interface. This interface consists of



Figure 6.24: SARWatcher Toolbar Icon

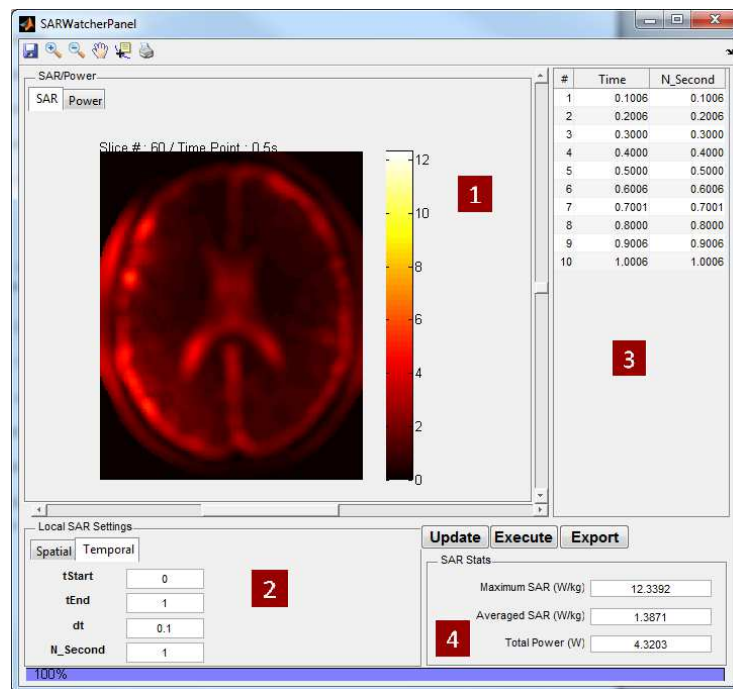


Figure 6.25: SARWatcher Main Interface

1. SAR/Power

The SAR/Power panel displays time varying spatial SAR and power map for the virtual object. The user can choose different time point (horizontal scroll bar) and slice (vertical scroll bar) to inspect map details.

2. Local SAR Settings

The ‘Spatial’ and ‘Temporal’ tab on the ‘Local SAR Settings’ panel contain parameters for controlling SAR and power calculation.

- (a) Spatial

- N_Gram (g): The number to specify averaged N-gram SAR, set to 0 indicating unaveraged spatial SAR

- (b) Temporal

- tStart (s): The starting time to calculate SAR
- tEnd (s): The ending time for SAR calculation
- dt (s): The nominal time interval for SAR calculation
- N_Second (s): The nominal time window for SAR calculation

3. Time Point Table

The Time Point Table contains a list of time point (s) and N_Second (s) in actual SAR calculation, this is because SAR calculation only updates at execution points.

4. SAR Stats

The SAR Stats panel contains overall statistics for calculated SAR and power at given time point.

The user can export the SAR and power map in a separate window by pressing ‘Export’ button. Pressing ‘Update’ button updates any modifications. The spatial SAR and power calculation follows the methods described in literature [11, 12]. The spatial N-gram SAR averaging is implemented using a method described in literature [13].

6.6 SeqConverter

(:TODO) SeqConverter is a graphical toolbox for converting MRiLab MR sequence format to more portable sequence format. This toolbox is still under developing.

Chapter 7

MRiLab Applications

This chapter shows a few examples for demonstrating the applications of MRiLab simulation

7.1 bSSFP with Non-uniform B0

This example (Figure 7.1) simulates the dark banding artifact in bSSFP images arisen from non-uniform B0 field. To perform this simulation, the following steps are needed:

1. Load Brain (Standard Resolution $108 \times 90 \times 90$)
2. Load PSD_FIESTA3D
3. Load Mag_GaussianHead

The user can adjust the ‘FlipAng’, ‘TR’ and ‘TE’ to modify the pattern of the banding artifact.

7.2 Fat Chemical Shift

This example (Figure 7.2) simulates chemical shift artifact at the interface of water and fat in a GRE sequence. To perform this simulation, the following steps are needed:

1. Load Water Fat Phantom ($256 \times 256 \times 32 \times 2$)
2. Load PSD_GRE3D

The user can adjust the ‘BandWidth’ and ‘FreqDir’ to modify the appearance of the chemical shift.

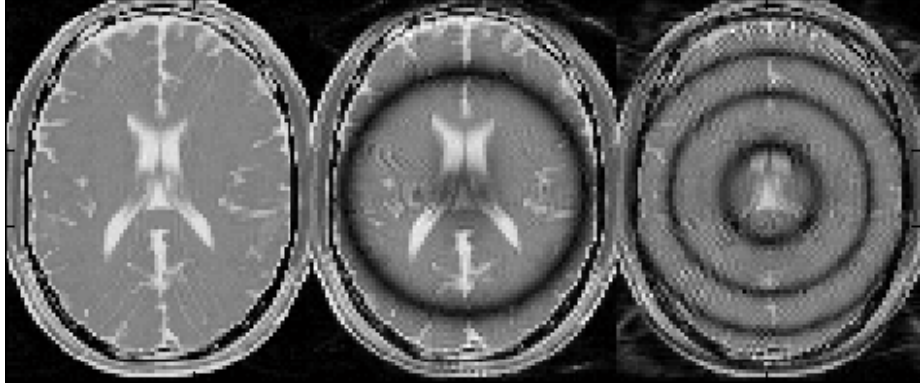


Figure 7.1: Simulated 3D bSSFP brain image of matrix size of $100 \times 80 \times 20$. The circular banding artifact is due to added Gaussian field simulating the main magnet field inhomogeneity. Left: TR/TE=16/8ms, FA=40°; Middle: TR/TE=16/8ms, FA=40°, Gaussian B0 applied; Right: TR/TE=32/16ms, FA=40°, Gaussian B0 applied

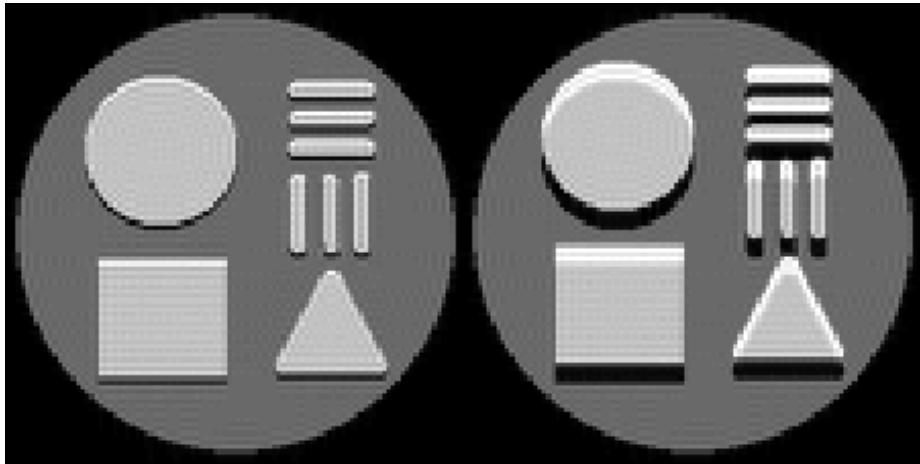


Figure 7.2: Simulated 3D gradient echo image at 3.0T using cartilage-fat phantom showing water fat chemical shift at different readout bandwidth. The simulated in-plane matrix size is 100×100 , TR/TE = 10s/50ms, Axial plane, A/P readout. Left: BW=400Hz/pixel; Right: BW=100Hz/pixel.

7.3 Multi RF Transmitting

This example (Figure 7.3) simulates multiple RF transmitting using a bSSFP sequence. To perform this simulation, the following steps are needed:

1. Load Brain (Standard Resolution $108 \times 90 \times 90$)
2. Load PSD.FIESTA3D
3. Load Coil_8ChHead to Tx
4. Set 'MultiTransmit' to 'on'

The user can adjust the 'B1Level' to modify the actual flip angle, modify the RF pulse using MR sequence Design Toolbox for individual RF source, or modify the coil configuration for generating desired B1+ field.

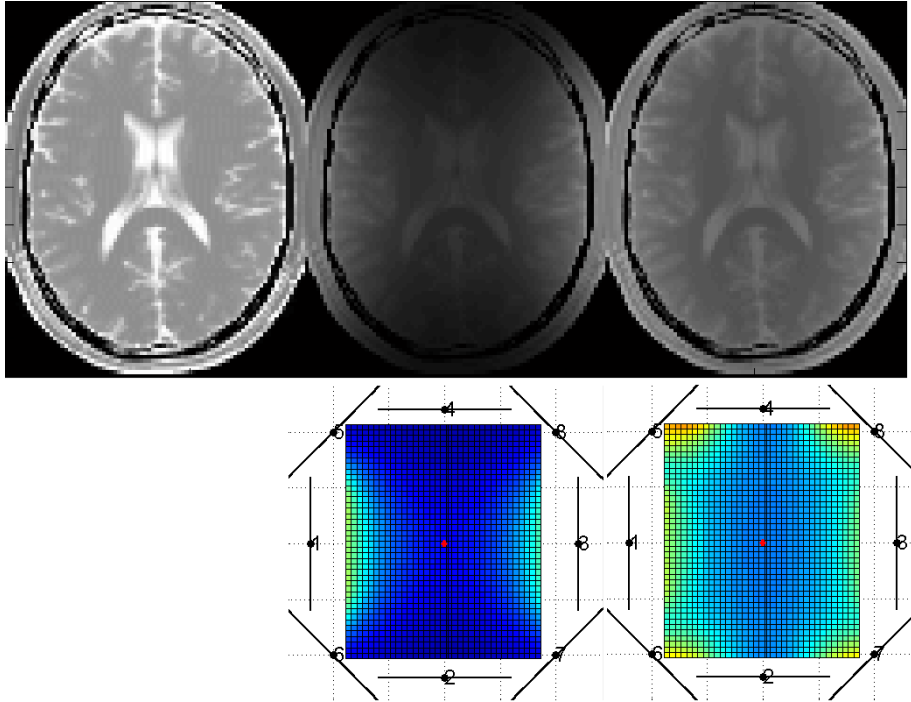


Figure 7.3: Simulated 3D bSSFP brain image of matrix size of $100 \times 80 \times 4$ with different Tx coil configuration. The simulated image uses $FA=40^\circ$, $TR/TE = 16/8ms$. Left: uniform unit B1+ field, RF transmitting from 'MasterTxCoil'; Middle: multi RF transmitting from Coil1 and Coil3; Right: multi RF transmitting from all coil channels

7.4 Multi Receiving Coil

This example (Figure 7.4) simulates multiple receiving using a SE sequence. To perform this simulation, the following steps are needed:

1. Load Brain (Standard Resolution $108 \times 90 \times 90$)
2. Load PSD_SE3D
3. Load Coil_8ChHead to Rx

The user can adjust the coil configuration for generating desired B1- field. All eight channels will be receiving MR signal from the virtual object individually.

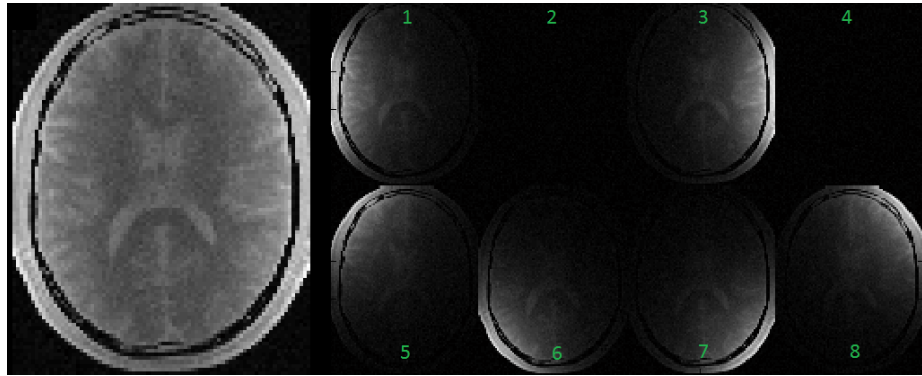


Figure 7.4: Simulated brain spin echo image of matrix size of 100×80 with multi receiving Rx coil. The simulated image uses $FA=90^\circ$, $TR/TE = 10s/10ms$. Left: the combined image using ‘SumofMagn’; Right: individual image for each coil channel, notice that Coil2 and Coil4 receive no signal due to zero B1- field.

7.5 Image Gradient

This example (Figure 7.5) simulates applying non-unit gradient with a 3D SPGR sequence. To perform this simulation, the following steps are needed:

1. Load Brain (Standard Resolution $108 \times 90 \times 90$)
2. Load PSD_SPGR3D
3. Load Grad_LinearHead

The user can adjust the gradient structure for generating desired gradient field. Notice that this applied gradient in GyPE GradLine has a factor of 0.5 in the Y direction. This will cause image contraction in the Y direction.



Figure 7.5: Simulated brain 3D SPGR image of matrix size of $100 \times 80 \times 2$ with non-unit gradient. The simulated image uses $FA=20^\circ$, $TR/TE = 60/8ms$. Left: unit gradient applied; Right: non-unit gradient applied in Y direction.

7.6 Motion Artifact

This example (Figure 7.6) simulates motion artifact with a 3D GRE sequence. To perform this simulation, the following steps are needed:

1. Load Brain (Standard Resolution $108 \times 90 \times 90$)
2. Load PSD_GRE3D
3. Load Mot_ShiftHead

The user can adjust the motion structure to generate different motion track patterns, and/or modify motion triggering in the Ext sequence line to sample object movement.

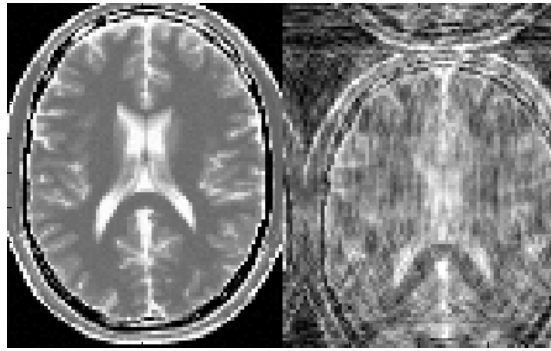


Figure 7.6: Simulated brain GRE image of matrix size of 100×80 with translation motion. The simulated image uses $FA=90^\circ$, $TR/TE = 10s/50ms$, Axial plane, A/P readout. Motion triggering happens one time per TR, and motion lasts for 400s. Left: no motion; Right: translation motion applied.

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Afterword

While MRiLab has been carefully designed and tuned for performing high quality MRI simulation, bugs and misfunctions may still exist. Moreover, several important parts are still missing in MRiLab, including MR spectrum simulation, water diffusion and Eddy-Current simulation etc. I am also working to further optimize solving kernel for better performance and to enhance the compatibility with Gadgetron. The MRiLab project is open to the whole MRI community, any user who are interested to improve MRiLab is more than welcome to do so. I will be pleased if you can leave me feedback and ideas for better enhancing MRiLab functionality. I will also be happy to talk about any kinds of collaboration for future MRiLab development. Please don't hesitate to contact me (leoliuf@gmail.com).