

FAMASITO



FASTMAP Shim Tool

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Abstract

Magnetic resonance spectroscopy (MRS) allows the non-invasive measurement and quantification of chemical compounds from living tissues. This makes MRS a powerful tool for biomedical research and clinical diagnostics of virtually all disorders that possess distinct metabolic signatures.

Varying B_0 conditions, however, lead to line broadening and imperfections of the B_0 magnetic fields can easily render MRS investigations useless. The experimental homogenization of B_0 conditions in a process called B_0 shimming is therefore mandatory for every MR investigation and high quality B_0 shimming is arguably one of the most important ingredients for successful MRS experimentation leading as basis for the reliable extraction of biochemical information.

Gruetter et al. presented in the 1990's an elegant analytical method for the assessment of 3-dimensional B_0 conditions through mapping along selected 1-dimensional column projections in a method called FASTMAP. Adequate B_0 shimming remains a long-standing problem with many commercially available MRI systems and most vendors do not offer FASTMAP-based B_0 shimming routines in their application portfolio despite its unique potential, likely at least in part due to its difficulty of implementation. The FASTMAP Shim Tool (FAMASITO) presented here comprises an installation of the original FASTMAP method for the General Electric EPIC environment along with both experimental and processing modifications for improved accuracy of the determined hardware shim settings and outcome. Macro software and analysis software are provided for optimized B_0 corrections in an efficient and user-friendly one-stop-shop solution. Give it a try!

Contents

Abstract.....	2
Contents.....	3
Introduction	4
I Download and Installation	8
1.1 Download and Preparation	8
1.2 Installation of MR Sequence	8
1.3 Installation of Bash Scripts for Experiment Execution and Shim Hardware Handling	10
1.4 Installation of Analysis Software	13
1.5 Further Downloads: Example Protocols, Calibration and Data	13
II The <i>Shimming</i> Page	14
1.1 General	14
1.2 Data Selection and Visualization	15
1.3 B_0 Field Analysis and Computation of Shim Settings.....	16
1.4 Usage Example: B_0 Shimming of the Human Prefrontal Cortex.....	17
1.5 Running the FAMASITO sequence.....	21
III The <i>Calibration</i> Page	23
2.1. General	24
2.2. Calibration Setup and Execution	24
2.3. Calibration Analysis	25
2.4. Usage Example: Calibration of GE 750MR Shim System	26
IV The <i>Manual</i> Page	27
V The <i>Exit</i> Page.....	27
VI Glossary.....	28
VII Terms of Use and Additional Remarks.....	28
VIII References	29

Introduction

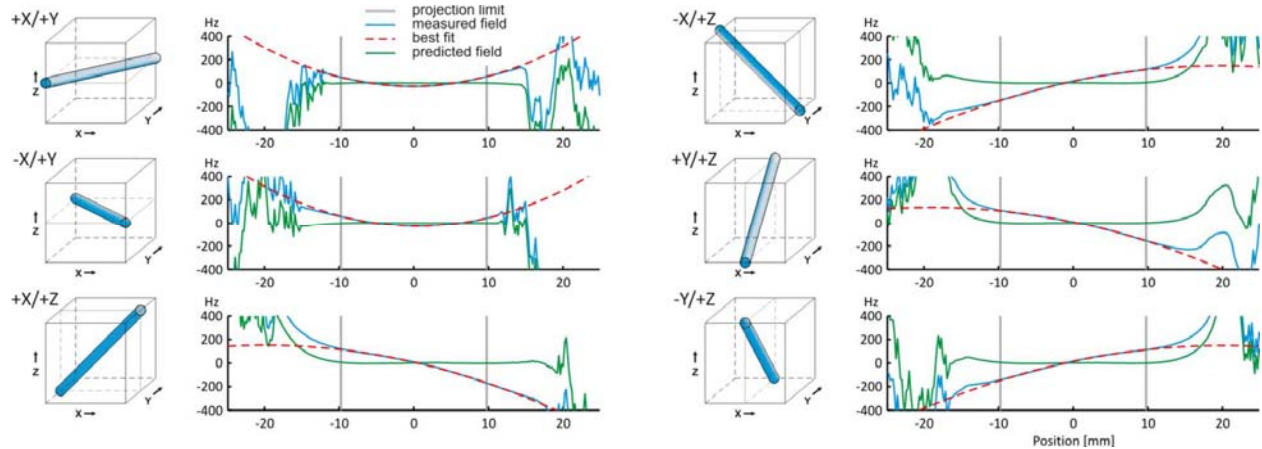
Relevance of B_0 Homogeneity for Magnetic Resonance Investigations

Magnetic resonance imaging (MRI) enables the non-invasive mapping of brain characteristics as different as anatomy, microstructure or function. Magnetic resonance spectroscopy (MRS) allows the chemical analysis of physiological processes *in vivo*. Together these methods provide powerful tools in the life sciences and for clinical diagnostics. However, spatial homogeneity of the static B_0 field is essential with most magnetic resonance imaging (MRI) and spectroscopy (MRS) investigation for meaningful results. In MRI, B_0 inhomogeneity leads to image distortion and signal loss, whereas spatial field variations in MRS causes loss of sensitivity and spectral resolution.

While some MRI artifacts induced by limited B_0 homogeneity can be ameliorated by post-processing, similar corrections are inherently impossible for MRS. The experimental optimization of B_0 homogeneity is therefore mandatory for MRS, and high-level B_0 shimming is arguably one of the most important ingredients for successful metabolic profiling with MRS. Magnetic fields obey the superposition principle and therefore the effective magnetic field present during an MR experiment can be manipulated by addition of correction fields. For a comprehensive review of the origins and flavors of B_0 imperfections as well as the various concepts and specific solutions for their minimization, the reader is referred to the literature [1].

Fast Automatic Shimming Technique by Mapping Along Projections (FASTMAP)

Analytical, or non-iterative, B_0 correction relies on exact knowledge of the B_0 field distribution to be homogenized. In a first step, the B_0 distribution therefore needs to be quantitatively described. However, full 3D mapping of B_0 field conditions can be time consuming. Gruetter et al. presented in the early 1990's an elegant analytical method to determine first and second order spherical harmonic (SH) field terms in cubic volumes from selected B_0 measurements along six selected 1D columns [2, 3]. This 'Fast Automatic Shimming Technique by Mapping Along Projections (FASTMAP) samples the B_0 field distributions to be homogenized along six exemplary, orthogonal column projections only (Figure 1). Basic linear algebra is applied to unambiguously derive the unique solutions for the apparent first and second SH order field imperfections from a set of linear equations that contains the second order polynomial decomposition of the apparent B_0 terms. Given the available B_0 shim system, the B_0 inhomogeneity is then converted to the corresponding correction field to be generated by the active SH shim system at hand.



Concept of FASTMAP field mapping along six selected 1D projections (adopted from Juchem et al., Anal Biochem, 2016 [1]).

FASTMAP is an elegant analytical method that provides a versatile tool for second SH order B_0 homogenization in cubic volumes typical for single-voxel MRS investigations. As such, FASTMAP (and its derivatives [4, 5]) has become the method of choice in several dedicated MR laboratories due to significantly reduced acquisition times compared to B_0 shimming methods that are based on full 3D MRI. Despite the elegance and acquisition efficiency of the FASTMAP technique and, moreover, its introduction approximately 25 years ago, it has not fully prevailed and is typically not the method of choice in the clinic. Among others, the establishment of FASTMAP shimming comprising aspects of MR sequence development, shim and calibration processing as well as hardware shim adjustments is significant and might have hindered its widespread use.

Here, we extend the theoretical FASTMAP concept with specific optimizations and corrections addressing the most significant error sources associated to the experimental application of the theoretical FASTMAP concept. In addition, the comprehensive implementation comprising an MR sequence for B_0 field mapping along projections, a user-software for SH shim analysis and shell scripts for experimental shim current handling is presented. The FASTMAP Shim Tool (FAMASITO) presented here comprises an installation of the original FASTMAP method for the General Electric EPIC environment along with both experimental and processing modifications for improved accuracy of the determined hardware shim settings and outcome. Macro software and analysis software are provided for optimized B_0 corrections in a user-friendly and efficient one-stop-shop solution. FAMASITO is made available to the MR community under a term-limited academic license free of charge.

[Download, Installation and Use](#)

The FAMASITO package consists of three integrated components:

1) FASTMAP sequence in GE's EPIC environment

The scanner installation includes a custom-designed MRI sequence to derive B_0 field information along 6 selected projections (resembling conventional FASTMAP). More specifically, we developed a custom spin-echo pulse sequence in software version DV24 which excites a column

of magnetization along the six required directions, and acquires it at two different echo times in order to obtain the field information.

2) Software Tools and Algorithms in GE's EPIC environment

FAMASITO furthermore comprises a series of basic tools and algorithms for experiment execution, file handling, automated shim calibration, and adjustment of shim coil currents, etc. These tools are provided as bash scripts, i.e. text files. Notably, these files can be opened directly with any text editor in case you want to see how we do things.

3) Stand-alone FAMASITO Graphical User Interface for In-Depth Data and Shim Analysis

A stand-alone graphical user interface (GUI) has been developed in MATLAB (MathWorks, Natick, MA, USA) for the detailed analysis, optimization and visualization of 1) FAMASITO projection mapping, 2) FAMASITO B_0 shimming, 3) multi-Rx RF coil performance, and 4) calibration of spherical harmonic coils. The resultant optimized shim adjustments are displayed and written to file for upload and direct application to the B_0 shim hardware by a dedicated bash script.

Before you start

The manual is organized in chapters that resemble the page structure of the software. General aspects and core features, e.g. spectral processing and analysis options, are shared across pages. They are described in full with their first use, and it is, therefore, advisable to read the manual from the beginning. Also of note is the information provided in the last few paragraphs of the manual, especially the call to join us in the fight against multiple sclerosis (MS) as well as some remarks on academic merit and legal aspects of software use.

Overall Structure and Application Pages

Overall, the software is organized by application pages for the determination of optimal B_0 shim settings (i.e. hardware units) based on experimentally acquired data (*Shimming*) and the automated calibration of the shim system at hand (*Calibration*). Selecting the *Manual* page opens a copy of the manual you are currently reading. The *Exit* button saves all FAMASITO settings to a default parameter file and closes the software properly. As such, the *Manual* and *Exit* functionalities do not represent entry points to full pages beyond those previously enumerated.

Notably, once the shim system for the MR scanner at hand has been calibrated, all subsequent use will solely rely on the first *Shimming* page.

Protocol Files

All FAMASITO parameters are saved to file when the software is closed properly via the *Exit* button and automatically reloaded when the software is restarted. This functionality allows users to close the software at any time and to return to the exact same situation very quickly at a later time. Notably, this also includes the FAMASITO page itself, e.g., *Shimming* or *Calibration*. In

addition, the full set of FAMASITO parameters can be saved to a user-specified protocol file (see the *Shimming* page for details).

Units

All spatial dimensions are expressed in centimeters, and angles are expressed in degrees. Frequencies are in Hertz (Hz) or parts-per-million (ppm) depending on the application and indicated with every use. Further units are defined as needed.

Tool Tips

This manual provides detailed explanations on the FAMASITO software. Also, short summaries and reminders on the functionality at hand are added to most entry fields, flags, and buttons as tool tips. This information can be visualized by mousing over the button without clicking it. For further information, feel free to email me.

I Download and Installation

1.1 Download and Preparation

The FAMASITO package can be downloaded as a single zipped file from Columbia's Technology Venture office website:

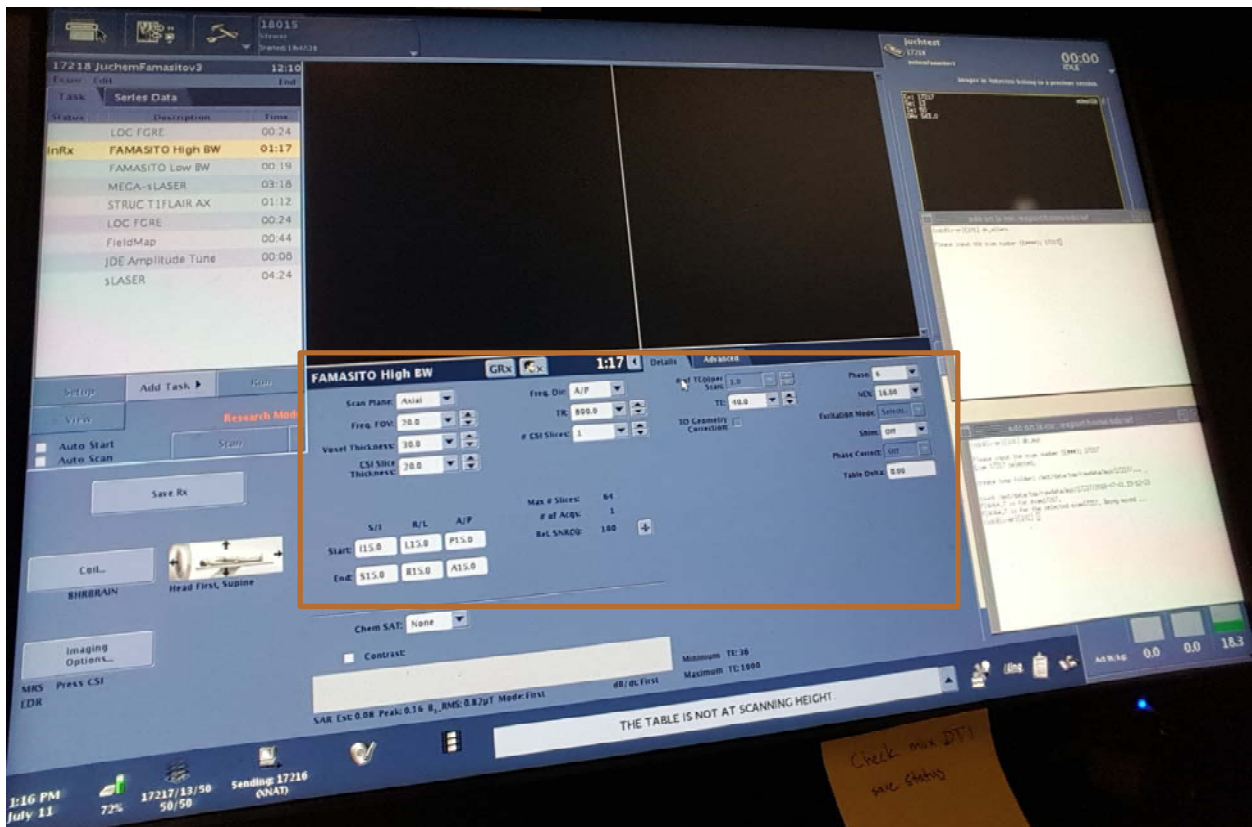
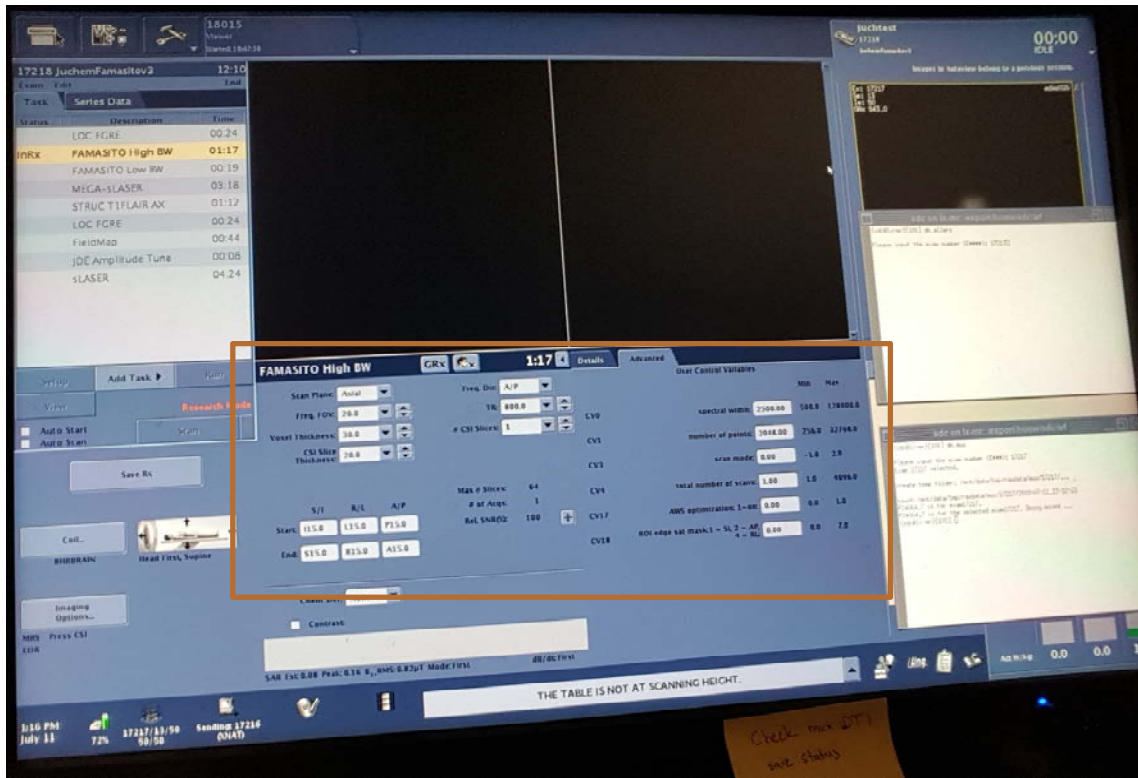
Landheer, K., Juchem, C., FAMASITO: FASTMAP Shim Tool for efficient B_0 shimming. Columbia TechVenture license 17327 (2017). innovation.columbia.edu/technologies/CU17327_famasito

Note that while copies of the MR sequence and the bash scripts for B_0 field mapping and experiment/hardware handling, respectively, need to reside on the console computer, the FAMASITO analysis software can be installed on the console or any other suitable computer. The advantage of an installation on the console computer lies in the efficiency of the B_0 shimming procedure as neither raw data nor resultant text files containing the derived coil current settings need to be copied between computers.

1.2 Installation of MR Sequence

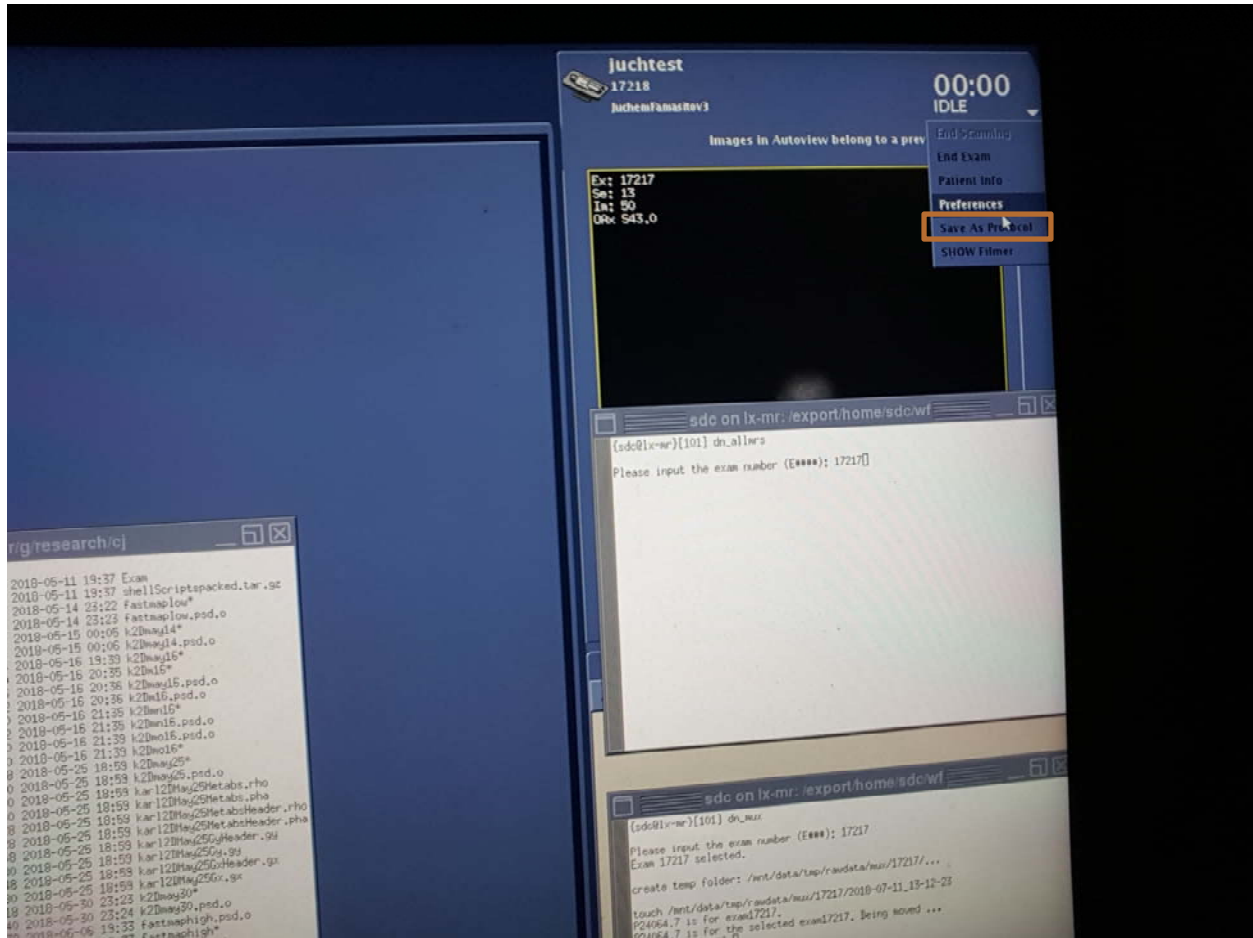
The FASTMAP sequence is written in software version DV24 and provided as compiled library that is installed on your system in line with any other MR sequence installation by

- 1) Place a copy of fastmaphigh and fastmaphigh.psd.o to the directory of your choice (e.g., /usr/g/research/yourinitials)
- 2) Add a stock PRESS sequence, click setup, then in the bottom left click "imaging options". Once a new panel pops up click the "more" in the bottom left corner. A new panel will pop up and in the bottom is a dialog box to the right of "PSD name", which is where the name of the pulse sequence with the absolute file path should be input. For example, if your initials are cj you would put in this box: /usr/g/research/cj/fastmaphigh. Type this in, and press enter. Then press accept and it should exit this window back to the main console window.
- 3) Type in all parameters as follows:



It is recommended to reduce the NEX to 4 (not 16 as displayed) in order to reduce scan time.

4) Save this as a protocol (top right there is an option to save as a protocol). Saving this as a protocol will allow you to load it in later into your desired protocol or experiment.



1.3 Installation of Bash Scripts for Experiment Execution and Shim Hardware Handling

Your installation package includes the following bash scripts which need to all be placed in the same directory of your choice:

`cj_CalibrateFAMASITO` – The script to calibrate FAMASITO

`cj_ClearAllShims` – Sets all first and second order shims to 0 and is called in other scripts

`cj_FAMASITOAcqHigh` – The script which is called to run FAMASITO

`cj_GetLinearShim` – A helper script which is called by `cj_CalibrateFAMASITO`

`cj_SetAllShims` – A script which reads a .txt file with shim currents and applies them

Data Acquisition

After the basic geometry and acquisition parameters for the acquisition of the B_0 field projections have been set, the individual field projections are obtained with FAMASITO as two data sets comprising 6 projections each at a distinct (and somewhat different) echo time. Technically, this is achieved by a macro (*cj_FAMASITOAcqHigh*) which

- 1) sets echo time 1 and runs it and assigns proper name
- 2) sets echo time 2 and runs it and assigns proper name

These two scripts then show up in `/usr/g/mrrow` and have the filenames `P_fastmap_delay_0.7` and `P_fastmap_delay_3000.7`, which are the two files that need to be read in by the FAMASITO software.

Retrieval of Shim Currents

GE provides core functions for the interaction with its shim hardware that we use in our bash macros. Therefore, you need to make sure that these core functions exist on your system and that you have access to them (including a valid license).

The functions we use are called *setNavShimCurrent* and *readNavShimCurrent*. In order to make sure they are present and enabled we should run them. To do so, open a c shell terminal window in the console and call them by typing 'readNavShimCurrent all'. If working properly, the function will retrieve the currently applied shim currents and list them in a channel-specific fashion in absolute units similar to this:

xy 1 mA

x2y2 2 mA

...

Note that this function will only retrieve the second order SH terms. The first order shapes are handled differently. More specifically, they are set and retrieved directly in the linear shim tool from manual prescan.

Also, the function provides measured currents instead of shim settings. While there should be a close correspondence between the applied shim settings (in hardware units and the measure currents, the numbers are not always 100% identical (compare next section).

Adaptation of Macro Paths to Account for Directory Structure on Your Console Computer

Line 52 of the script *cj_CalibrateFAMASITO* should be changed from "`cd /usr/g/research/cj`" to "`cd /yourdirectory`", where `/yourdirectory` is a directory of your choice where you should place all of these associated scripts. Beyond that all that must be done to have the scripts run properly is all be in the same directory.

Direct Application of Shim Currents

In the same vein, you should be able to apply currents to one or more second order shim coils using the *setNavShimCurrent* command. For instance, the command

```
setNavShimCurrent x2y2 1000
```

applies 1000 units of current (corresponding to 25% of your total dynamic range) to the X2-Y2 shim coil. Subsequent retrieval of all second order shim currents via

```
readNavShimCurrent all
```

should provide a number very similar to the applied setting of 1000 mA. Make sure that the underlying functions for hardware interaction are installed on your system

Application of Shim File

In a last step, let's ensure that our scripts are working properly on your system. Bash scripts are started by calling them from a terminal window either by typing their absolute path, e.g. */usr/g/research/cj/MacroName*, or by relative paths, i.e., by going to the respective directory and typing *MacroName*.

We provide a (random) template shim file (*SampleShimFile.txt*) with the following settings

X = 10

Y = 20

Z = 30

X2-Y2 = 300

ZX = 400

Z2 = 500

ZY = 600

XY = 700

that allows you to get familiar with calling macros and GE's B₀ shim framework. You should be able to apply these (or other) shim currents directly by typing the command: "*cj_SetAllShims SampleShimFile.txt*", and subsequently retrieve the applied current settings either through "*readNavShimCurrent all*" for the 2nd orders, or in manual prescan for the first orders.

It is advisable (and good citizenship) to reset all higher order SH shims before and, more importantly, after your study. To reset all first and second SH shims, call the macro *cj_ClearAllShims* and potentially confirm (close to) zero currents by calling the macro *readNavShimCurrent all*.

1.4 Installation of Analysis Software

The analysis and visualization software is currently distributed as a stand-alone executable program compiled in MATLAB version R2013b for 64-bit Windows®, Apple Macintosh® and Linux® operational systems. The corresponding MATLAB Runtime environment needs to exist to provide the software with the required libraries. Detailed instructions on the installation of the MATLAB Runtime can be found at:

<https://www.mathworks.com/help/compiler/mcrinstaller.html>.

It is important for Linux and Mac users to start the software via the provided shell script, i.e. the file ending with `.sh`, instead of e.g. double-clicking the FAMASITO icon directly. This script opens a terminal window and dynamically links the necessary libraries before the software is started. All these settings are temporary and disappear when the software and the terminal window are closed. The terminal window corresponds to the Matlab command window and all info printouts are delivered to this window.

Step-by-step instructions for starting the FAMASITO software via a shell script on Linux/Mac:

- 1) Place a copy of the provided FAMASITO directory to your computer
- 2) Identify the system's MCR root directory. This is typically something like `/usr/local/MATLAB/R2013b/` on Linux or `/usr/local/MATLAB/R2013b/` on Apple Mac
- 3) Run the shell script file with the MCR root directory as function argument, e.g.
`./run_FAMASITO.sh /usr/local/MATLAB/R2013b/`

if you are currently in the FAMASITO directory or from anywhere via the absolute path:

`/home/juchem/matlab_exe/FAMASITO/run_FAMASITO.sh /usr/local/MATLAB/R2013b/`

If the assigned MCR root directory has been correct, the FAMASITO software will start. You will then find a GUI of the software itself and a terminal window containing information printouts.

- 4) For convenience, I recommend including the MCR root directory information in the shell script itself, thereby rendering its assignment as function argument obsolete and allowing to start FAMASITO by double-clicking the shell script file or a link to it.

To do so, open (a copy of) the shell script and confirm the existence of the paths containing the variable `MCRROOT`. If the paths exist, the software will be able to find the libraries and nothing needs to be changed. If not, adopt the path details after the `MCRROOT` variable to account for the MCR installation details on your computer. Once all paths are correct, calling the shell script alone without function argument will start the software correctly.

1.5 Further Downloads: Example Protocols, Calibration and Data

The download package contains additional files besides those truly needed for the successful installation of B_0 shimming with FAMASITO. These include:

- In vivo scan protocol
- Calibration scan protocol: Calibration

- Template software protocol for FAMASITO GUI
- Example B_0 shim file

For further details on their respective usage, please refer to the appropriate sections.

II The *Shimming* Page

Section 1.1. describes the general setup and use of the *Shimming* page. The data handling and visualization is summarized in section 1.2, followed the computation of SH field terms and translation to hardware shim settings in section 1.3 describing and a selected usage examples employing first and second SH order B_0 shimming of the human prefrontal cortex at 3T.

1.1 General

The *Processing* page (#1, left) is used to load, reconstruct and analyze experimentally acquired FAMASITO data. The resultant B_0 shim settings can be written to file for direct upload and application to the MR scanner employing the `cj_SetAllShims` macro. The page also includes tools for data visualization, data correction and quality management.



Fig. 1.1: Main *Processing* page.

Protocols

Efficient and reproducible B_0 shimming relies on a series of parameter settings and choices, mostly the specific paths to the data, the calibration and resultant shim files. The FAMASITO

software accounts for this by saving the entire parameter selection to protocol files (#2). These protocols can be loaded to restore all parameter settings to previously selected values. While all software and processing parameters are written to file, the decision has been made to exclude larger data structures, thereby keeping the size of the resultant protocol files to a minimum, typically to a few kilobytes. Explicit export options are available to save the data to file. Notably, protocols are saved in MATLAB (.mat) format. Besides convenience, the reloading of tailored protocol files can be used to assure consistent data processing of various experiments throughout a study.

There are two different protocol options: 1) A general default file and 2) user-defined protocols. Parameter settings are inherently saved to a general default file when the software is properly closed via the *Exit* button (#1, rightmost page option) as it is strongly advised to do so. One default parameter file exists for every FAMASITO installation. This background file is shared across users and overwritten every time the software is closed. In addition, parameter settings can be saved to protocol files designated by the user in the protocol section (#2). The *Select*, *Load*, *Save*, and *Delete* functionalities provide handling options for the selected protocol file.

Reset Defaults

This functionality resets all parameters to their default values (#12, left), thereby returning to a meaningful set of starting conditions. This functionality is only rarely applied as in most cases it is more convenient to start from a protocol of a similar experimental setup.

Reset FAMASITO

Processing MRS data requires a multitude of intermediate steps. Sometimes the status of the current data in memory becomes unclear, such as when certain corrections have been applied. The *Reset FAMASITO* button restarts the software (#12, right). All parameter settings are kept, but the data memory is freed, thereby returning to a well-defined starting point.

1.2 Data Selection and Visualization

Experimental FAMASITO field mapping yields two data files that are consistently named *P_fastmap_delay_0.7* and *P_fastmap_delay_3000.7*. These files contain the short and long echo time condition, respectively, and need to be assigned as data set 1 (#3) and data set 2 (#4) in the FAMASITO analysis software either by direct path assignment or file selection via the appropriate *Select* button (#13). The *Derive* functionality (#14) allows easy derivation of file path 1 from file path 2 and vice versa according to the above name convention. Subsequent data loading via the *Load* button (#15) will load the data at hand, combine individual receivers if needed, and compute the resultant individual column traces for both magnitude signal and B_0 field behavior. Note that all parameters are read from the data headers and no manual assignments are necessary. However, the voxel size, ie. the volume over which the B_0 field conditions are to be improved, can be changed after a particular data set has been loaded by direct assignment of the

desired voxel size (#5). The visualization of the Rx-combined amplitude and B_0 frequency information (#7) is typically enough to assess the data quality, voxel placement and the B_0 field behavior both before and after B_0 shimming. However, detailed visualization options are provided for a more detailed analysis of individual (*Single*) or all (*Array*) projections, echo times and receivers (#6, #17). The selection of an amplitude range most suitable for the display at hand, ie. magnitude signal of 1-dimensional readouts or the corresponding B_0 field information, is possible at the lower end of the page (#21). Options include an automated minimum/maximum considering the entire 1D projection at hand (*Global*), an automated minimum/maximum scaling considering the ROI only (*ROI*), as well as direct assignment of user-defined amplitude limits. In addition, the polynomial fitting result of the B_0 field analysis, the predicted outcome after B_0 shimming (i.e. measure minus best fit) as well as vertical green lines indicating the ROI voxel boundaries can be individually enabled or disabled (#22).

1.3 B_0 Field Analysis and Computation of Shim Settings

The application of first (#9, *1st*) or first and second (*1st & 2nd*) analysis of the field behavior in the region-of-interest (ROI) at hand yields the apparent SH field shapes in absolute units of Hz/cmⁿ. A minimum signal-to-noise ratio (SNR) for individual data points can and in most cases should be defined to ensure well-defined phase and resultant B_0 information (#16). A calibration file containing the generated field terms per unit shim setting (or unit current) is therefore needed for the translation of absolute field shapes in the best shim current for their mitigation. The calibration of the MR system's shim system performance needs to be done once (compare next section on *Calibration*) and the resultant text file needs to be made available here (#18). Further settings include the selection of a shim calculation mode (#20) and the potential inclusion of geometry corrections (#10) which should be selected as *Matrix* and *ON*, respectively. The calculation of the SH terms via #9 does not only provide the apparent SH field terms, but also suggests the optimized shim settings in hardware units. These values are displayed and, by pushing button #19 (Save Shim), can be written to a text file (#8) for documentation or direct upload by calling the *cj_SetAllShims* macro.

Notably, every analysis or visualization creates a new figure and excess figures can be easily removed via the Close Figs button without affecting the FAMASITO software itself (#11).

Verbose

FAMASITO can provide detailed information on every processing and analysis step to enable the user to access the processing stream and to evaluate the results obtained at each step. While this information is always available, its display might not always be warranted. A situation-dependent balance exists between the provided level of detail and the risk of overloading the result display. If the *Verbose* flag (#21, left) is selected, detailed information is provided, e.g. for more comprehensive data analysis and experiment debugging. If the flag is not selected, only overview and summary data are shown instead.

1.4 Usage Example: B₀ Shimming of the Human Prefrontal Cortex

The following analysis corresponds to the example data set that is included in the directory *FST_DemoData* of the FAMASITO download as well as an example calibration file called *calibSlopeMat.txt*.

Make the Provided Protocol File Yours

You can either set the parameters yourself as described in the next sub-section or use the attached FAMASITO protocol file *FST_DemoProtocol.mat* for a kick-start. This section summarizes the suggested steps to adapt a protocol prepared on another computer, e.g. console vs. your PC or provided by someone else as is the case here.

1. Place the protocol file to a suitable directory, typically the study or data directory
2. On the *Shimming* page (#1), identify the protocol file either through the Select button or by assigning the explicit file path on your computer (#2).

Again, protocol files comprise all variables of the FAMASITO parameter space ranging from numeric variables to file paths. As such, direct loading of the protocol file I prepared on my computer will show you the file paths pertaining to my computer. In a first step, you should therefore adapt the protocol to the situation on your computer, i.e. to make it yours, while preserving all other parameters. Here is what you do:

3. Select/mark the protocol file path and copy to clipboard
4. Load my original protocol file. You will notice that all kind of things change on the *Shimming* page as all parameters are overwritten with the values found in the protocol file. Again, that also applies to the protocol file path that is now the one found in the protocol file, i.e. the path where the file was located on my computer.
5. Paste the file location on your computer back to the protocol file entry field to update the file location and *Save*. The protocol file is now yours and the file path is consistent.
6. Update the other file paths and save again under the same or a different name.

Note that this procedure is needed only once. It is generally suggested to make ample use of the protocol functionality and to save application-specific protocols regularly. This not only allows you to comprehensively document your analysis, it also allows easy replication at a later time (on any computer).

Example FAMASITO Shim Procedure

Typical processing for first and second order SH shimming includes the following steps:

- 1) Select/assign the first field map data set *P_fastmap_delay_0.7* of the reference scan *FST_Data_Before* as *Data 1* (#3 of Figure 1.1, compare Figure 1.2. below).

2) Select/assign the second field map data set *P_fastmap_delay_3000.7* scan as *Data 2 (#4)*. The two P files are typically located in the same directory location. If that is the case, the file path of the second file can be easily derived from the path of *Data 1* using the *Derive* functionality. If you push this button, the file path of Data 2 should update resembling the correct location of the file.

3) Select the text file *calibSlopeMat.txt* that contains the calibration information for the shim system at hand (#18). Notably, this file will need to be updated eventually after you have derived the equivalent information for your MR scanner (compare *Calibration* page).

4) Select the result file for the shim outcome *shim_file.txt* (#8). If you don't want to overwrite the provided example shim file, create a copy of the file at hand or modify the file name in the entry field to write to another file.

5) Push the *Load* button to read and reconstruct both data sets (#15). It is generally suggested to keep an eye on the black program window as both processing details as well as error messages are shown there. Here, the experiment details and the shim settings that were applied when the data were acquired are displayed:

Current shim settings:

```
X      = 0 (0.0%)
Z      = 0 (0.0%)
Y      = 0 (0.0%)
X2Y2   = -1 (-0.0%)
ZX     = 0 (0.0%)
Z2     = 0 (0.0%)
ZY     = 0 (0.0%)
XY     = 0 (0.0%)
```

Acquisition details:

```
system:  NYS PSYCHIATRIC INST
method:  FAMASITO Low BW
protocol: JuchemFamasitov3
voxPos:  [-8.0 74.5 0.0]
voxDim:  30 mm
fov:     200 mm
column:  5 mm
sw_h:    15625 Hz
points:  256
TE1:     40.0 ms
TE2:     43.0 ms
delta TE: 3.0 ms
```

Limits of FAMASITO voxel [pts]:

```
Proj. 1: [176 230], 55 of 55 (100.0%)
Proj. 2: [41 95], 55 of 55 (100.0%)
Proj. 3: [94 148], 55 of 55 (100.0%)
Proj. 4: [108 162], 55 of 55 (100.0%)
Proj. 5: [168 223], 56 of 56 (100.0%)
Proj. 6: [33 88], 56 of 56 (100.0%)
```

6) To visualize the magnitude projections of both experiments as 1-dimensional images (Data 1: blue, Data 2: red), select the visualization amplitude range (#21) as *Global* to display the full minimum/maximum amplitude range and push the *Amplitude* button (#7).

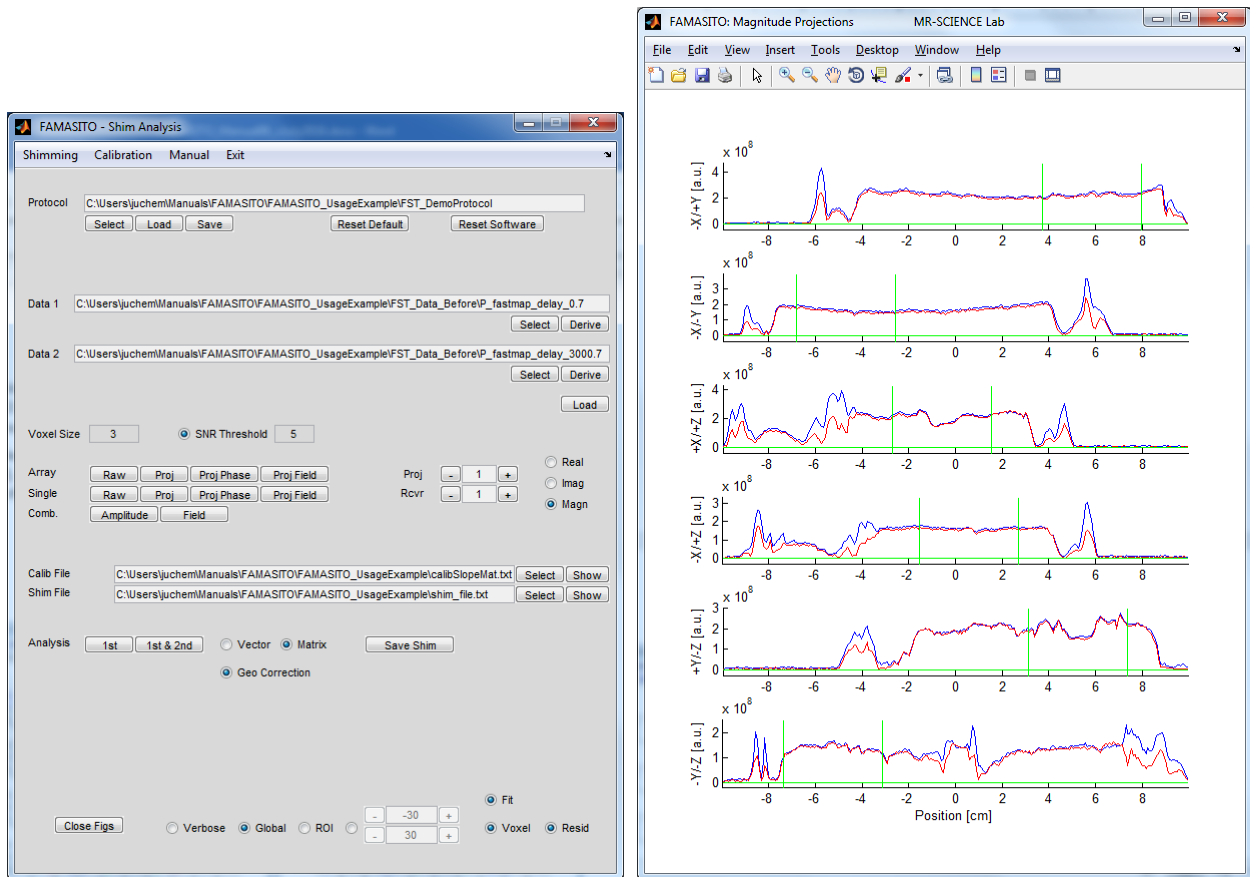


Fig. 1.2: FAMASITO Shim Analysis window (left) and magnitude projections of the shorter-TE *Data 1* in blue and the longer-TE *Data 2* in red (right).

7) Note that the boundaries of the shim voxel position are indicated as vertical green lines.

8) To visualize the B_0 field projections of both experiments as 1-dimensional images (Data 1: blue, Data 2: red), select the visualization amplitude range (#21) as *Global* to display the full minimum/maximum amplitude range and push the *Amplitude* button (#7).

9) Make sure that the visualization of the polynomial fitting functions (#22, *Fit*) and the residual (*Resid*), i.e. the predicted B_0 behavior after shimming, are selected and perform a first and 2nd order shim analysis by pushing the *1st & 2nd* button (#9).

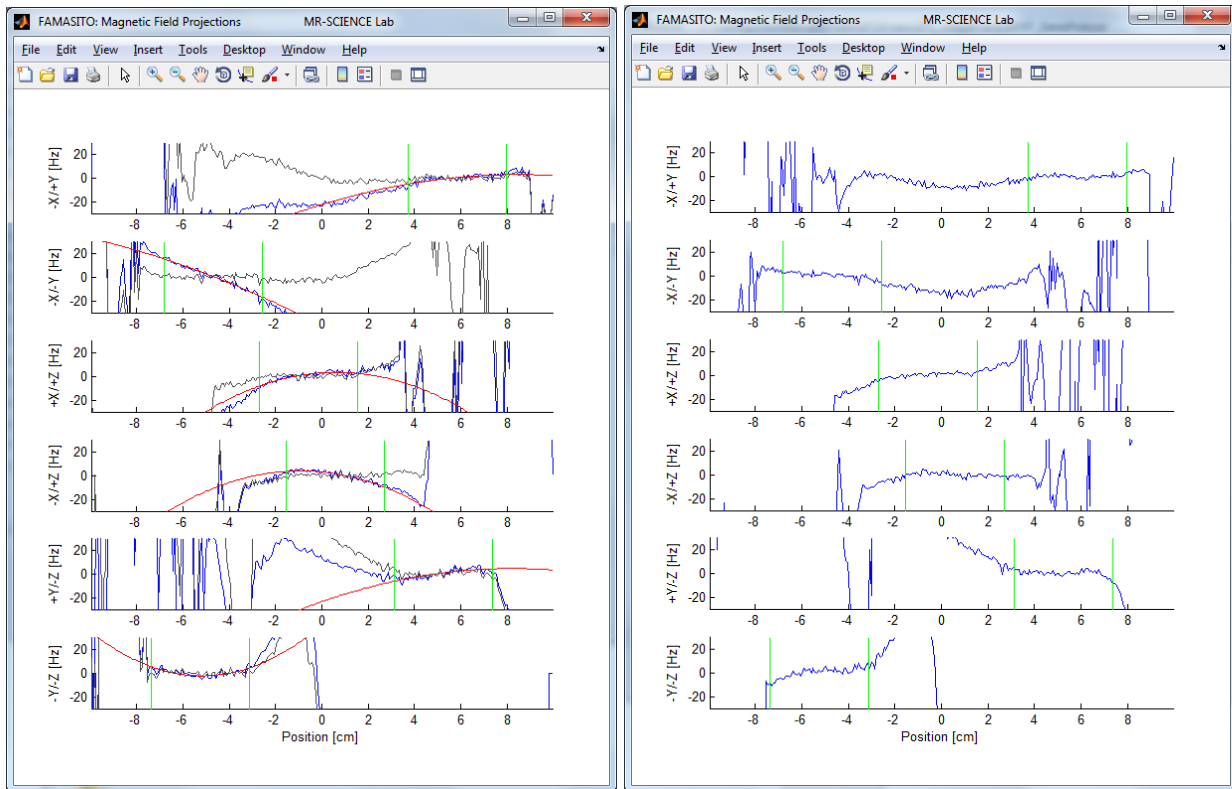


Fig. 1.3: B_0 field projections before (left) and after (right) shimming. Blue: experimental data, red: second-order polynomial fit, gray: predicted outcome as measure minus fit

10) The resultant figure display (Fig. 1.3., left) shows a superposition of the original field map in blue, the best polynomial fit in red and the predicted B_0 behavior in the presence of the derived polynomial terms in gray. The black program window provides 1) the resultant spherical harmonic terms in [Hz/cmⁿ], the necessary shim changes in hardware units as derived from the information found in the calibration file (#18), as well as the resultant optimized shim settings taking into account the applied shim coil currents when the field information was obtained:

```
1st & 2nd order analysis (X, Z, Y, X2-Y2, ZX, Z2, ZY, XY):
[-0.35626 -15.04483 -20.19861 ...
 0.00017 -0.00000 -0.00023 -0.00049 -0.00000] Hz/cm^n
```

Calculated shim changes:

```
X    = 1 (0.3%)
Z    = 16 (5.1%)
Y    = 18 (5.8%)
X2Y2 = -1729 (-43.2%)
ZX   = -2 (-0.1%)
Z2   = 64 (1.6%)
ZY   = 905 (22.6%)
XY   = 49 (1.2%)
```

New / optimized shim settings:

```
X    = 1 (0.3%)
Z    = 16 (5.1%)
```

```
Y      = 18 (5.8%)
X2Y2  = -1730 (-43.3%)
ZX     = -2 (-0.1%)
Z2     = 64 (1.6%)
ZY     = 905 (22.6%)
XY     = 49 (1.2%)
```

11) There are two different ways to apply the optimized second SH order shim settings to the amplifier electronics of the MR scanner, by A) calling the bash script *setNavShimCurrent* on the console computer to apply the second order shims directly as a space-separated list of coil names followed by the respective current settings, or by B) saving the derived shim settings to a previously assigned text file (#8) via the *Save Shim* button (#19). This text file can then be loaded directly by another bash script (*cj_SetAllShims*) on the console to apply the currents to the amplifier hardware. While the latter does not require any explicit typing, the applied shim file must exist on the console computer which signifies one more step if the shim analysis is performed on a computer other than the console computer. In any case, the linear (or first SH order) shim settings have to be entered manually in the GE shim tool as no first-order equivalent to the *setNavShimCurrent* functions exists.

12) The *FST_Data_After* directory contains the data set that has been applied in the presence of the shim settings derived above. The acquisition of the B_0 field conditions in the presence of the optimized shim currents allows direct confirmation of the achieved shim quality. Note that the previously set shim currents now show as applied shims when the data sets are loaded:

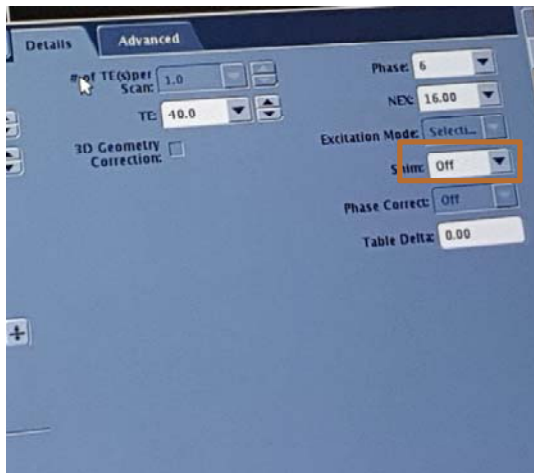
```
Current shim settings:
X      = 1 (0.3%)
Z      = 16 (5.1%)
Y      = 18 (5.8%)
X2Y2  = -1726 (-43.1%)
ZX     = 0 (0.0%)
Z2     = 65 (1.6%)
ZY     = 905 (22.6%)
XY     = 45 (1.1%)
```

As expected the field maps between the vertical green bars are largely horizontal, corresponding to homogeneous B_0 conditions for the shim system at hand. In rare occasions, a single refinement of the linear terms might be beneficial. This is achieved in the equivalent way by a first order shim analysis via the *1st* button (#9) and subsequent application of the derived shim settings as described previously.

1.5 Running the FAMASITO sequence

In order to run the sequence installed in Section 1.2 the sequence must first be loaded from the saved protocol (as set up in Section 1.2). Once the sequence is loaded the voxel should be placed in the desired location (just as a normal spectroscopy voxel would be placed), and with the

desired size. Once positioned hit the “Save Rx” button. Then perform an auto prescan by expanding the tab to the right of the “Save Rx” button. Once auto prescan is completed run the script “cj_FAMASITOAcqHigh”. This will start running the FAMASITO sequence and will take approximately 1 to 2 minutes to run depending on your NEX. Upon completion there will be two files in /usr/g/mrraw: P_fastmap_delay_0.7 and P_fastmap_delay_3000.7. These are the two files which need to be read in by the FAMASITO software. When running spectroscopy, it is then critical to have your voxel the exact same size and location as was shimmed over by FAMASITO. This can be achieved in a variety of ways, one way is by simply writing down the location and size of your voxel that was used for FAMASITO, and transcribing these values into your spectroscopy experiment. It is also critical to turn off auto shim for your subsequent spectroscopy scans, so as to not override the shim parameters. This can be done on the “Details” tab from within your spectroscopy sequence as follows:



III The Calibration Page

The calculation of optimized spherical harmonic (SH) shim settings consists of two steps: 1) The decomposition of the apparent field distribution in a basis of SH fields shapes supported by the shim system, and 2) the translation of the optimized correction field in shim settings for the SH system at hand. While the outcome of the decomposition is a set of field amplitudes in Hz/cmⁿ units, the second step results in a vector of SH coil currents in Ampere or (arbitrary) hardware units.

Section 2.1. describes the general setup and use of the *Calibration* page. The characterization of the SH system for the MR scanner at hand is summarized in section 2.2. The third subsection of this chapter contains a selected usage example derived from a recent calibration of first and second order SH shim system on a General Electric 750MR 3T scanner.

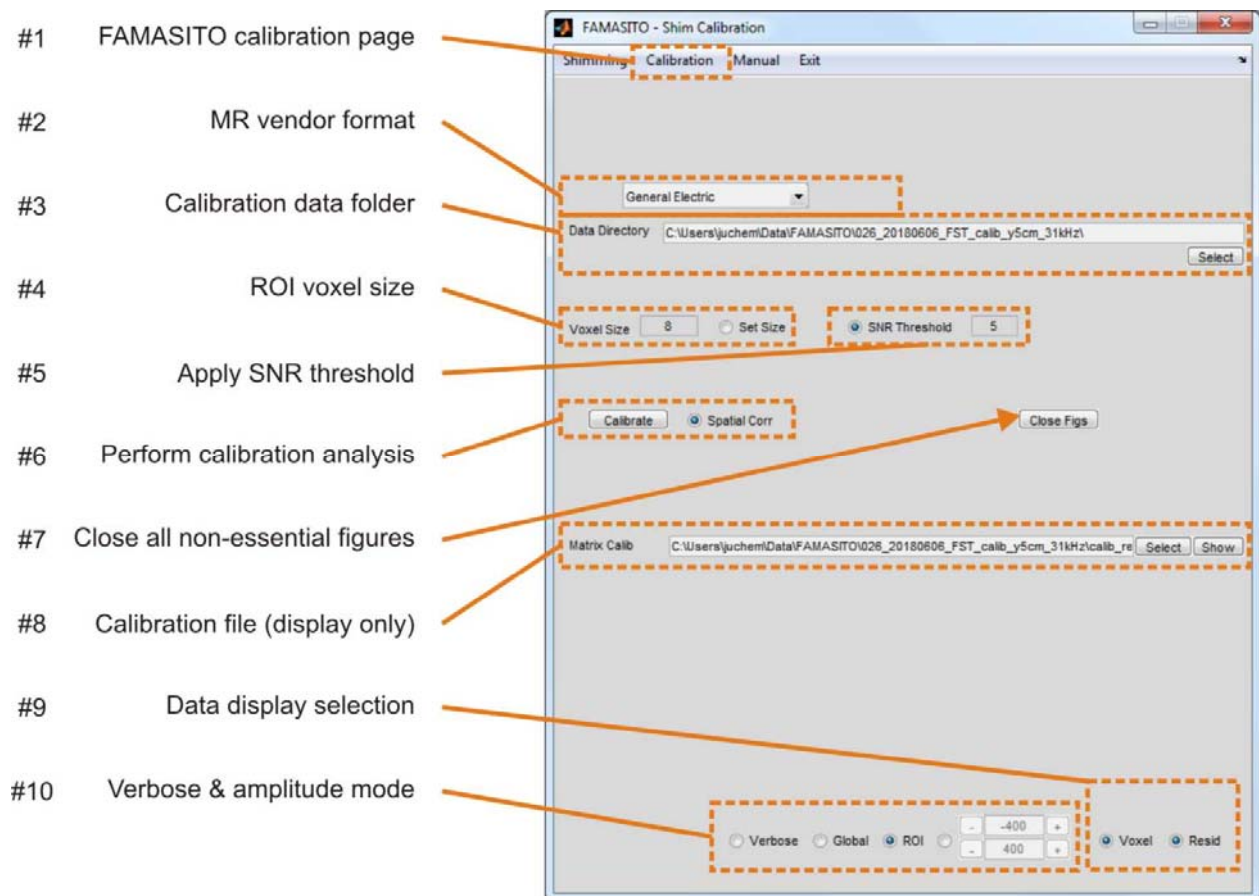


Fig. 2.1: Main Calibration page.

2.1. General

The reliable characterization of the SH shim system serves two purposes and is essential for good B_0 shim performance:

- 1) Characterization of SH field shapes along with their static imperfections, i.e. their cross-terms.
- 2) Determination of the available dynamic range, including the translation factor or link between the applied arbitrary hardware units and the resultant field amplitudes in Hz/cmⁿ.

The resultant calibration matrix in Hz/cmⁿ per 1% of the available dynamic range is used by FAMASITO to translate the optimized SH shim field in a set of SH hardware settings as first described in [6]. The nominal dynamic range of the employed SH coils therefore corresponds to the diagonal elements multiplied by 100. The coils' imperfections (or cross-terms) can be found as off-diagonal elements and should be small for well-designed, constructed and implemented SH coil systems. Note that the derivation of shim settings via the shim system's full correlation matrix minimizes shape imperfections of individual SH channels by other available coils and thereby allows reliable SH B_0 shimming in a one-step process.

2.2. Calibration Setup and Execution

The goal of the SH shim calibration is to determine the available SH field amplitude per employed coil current or hardware setting, i.e. the bang for the buck. To this end, a series of B_0 field maps is acquired for every SH shape at varying shim settings.

BRAIN0 Metabolite Phantom

In principle, every MR phantom of significant size and reasonable T1 and T2 behavior can be used for the calibration of a B_0 shim system. Since all GE sites have been provided a spherical metabolite phantom for MR spectroscopy, the so-called *BRAIN0* phantom, we suggest to use it for the task at hand along with the circular plastic insert for the placement of spherical phantoms. We furthermore suggest to apply the regular GE prescan routine including RF power optimization, iterative first SH order B_0 shimming (*AutoShim*) and a frequency adjustment for general experiment setup.

Calibration Setup and Preparation

The serial application of B_0 shim settings from various SH coils and the subsequent mapping of the apparent B_0 conditions is handled by the macro *cj_CalibrateFAMASITO*. Before the shell script can be executed though, the FAMASITO sequence needs to be loaded and parameter conditions suitable for calibration need to be selected.

Parameter settings that we found suitable on our 3T system are:

method: FAMASITO High BW

voxel position:	[0 4 0] cm, voxel position
voxel dimension:	8 cm, voxel dimension
field-of-view:	20 cm, field-of-view
column width:	5 mm, column width
sweep width:	31250 Hz, sweep width
complex points:	512, complex points
echo time 1:	40.0 ms, echo time 1
echo time 2:	43.0 ms, echo time 2
pw_rf1	2048 us, power of excitation RF pulse
bw_rf1	4160.16 Hz, bandwidth of excitation RF pulse
pw_rf2	2392 us, power of refocusing RF pulse
bw_rf2	3010.03 Hz, bandwidth of refocusing RF pulse

Calibration and Data Handling

Once the overall setup of the calibration experiment has been completed, the full experiment series can be started by calling the *cj_CalibrateFAMASITO* macro. In order to calibrate the system an identical procedure as explained in Section 1.5 (with identical parameters except with NEX = 1) should be performed, except instead of running *cj_FAMASITOAcqHigh* one should run the script *cj_CalibrateFAMASITO*. For the experiment conditions suggested above, the experiment series is expected to take 40 - 45 minutes to complete.

Note that all data is written to the same data directory and labeled in a unique fashion describing the employed SH coil and a serial number of the shim setting. The calibration analysis itself is done with the FAMASITO GUI software and, if not installed on the console computer, the data directory containing the acquired calibration data needs to be copied to a computer that has FAMASITO installed.

2.3. Calibration Analysis

Linear regression of the applied percentage of the available dynamic range (in [%]) and the SH field amplitude (in [Hz/cmⁿ]) then reveals the desired calibration information. The detailed description of the do's and don'ts of a high-quality B₀ shim calibration is beyond the scope of this manual. Feel free to contact me directly for more information.

The calibration information is reported as a quadratic 8x8 matrix in Hz/cmⁿ for 1% of the dynamic range capable of describing SH shim systems of up the second order. SH orders in FAMASITO are consistently structured in ascending order n with terms listed from -n to n. Rows one to three reflect the linear gradients X (m=1), Z (m=0) and Y (m=-1) and their effects on the other SH shapes,

followed by the second order terms X2-Y2 (m=2), ZX (m=1), Z0 (m=0), ZY (m=-1) and XY (m=-2). An ideal coil system would have non-zero entries only along the matrix' diagonal representing the field amplitude that is generated per % of it dynamic range. In reality, however, the shapes of individual coils do not fully resemble the target shape at hand, reflected by non-zero off-diagonal values. The purpose of a full calibration matrix describing all self- and cross-terms instead of the self-terms only is the consideration and compensated in a single-step process.

2.4. Usage Example: Calibration of GE 750MR Shim System

FAMASITO performs the calibration analysis in a fully automated fashion. All you need to do is place all calibration data in a directory and let the software know where to find it (#3). Low signal-to-noise data points have poorly defined phases that lead to large frequency (or B_0) errors. FAMASITO therefore includes an option to disregard data points along the spatial projection for which a threshold SNR value is not reached (#5). This criterion does not affect adequate data and it is therefore recommended to always use it, e.g. employing a moderate SNR threshold of 5. Note that the voxel size considered for the FAMASITO calibration analysis is read from file unless specified otherwise (#4). Pushing the *Calibrate* button will cycle through all shim conditions of all shim coils, perform a field analysis and write the resultant calibration information to a newly generated (directory and) file *./calib_results/calibSlopeMat.txt*. A display option (#8) is available on this page to visualize the calibration at hand or other calibration files.

The calibration file *calibSlopeMat.txt* of the GE 750MR shim system used to derive the data set at hand reads:

```
*** FAMASITO calibration matrix ***
2.99076628 0.00102619 -0.00271720 -0.00006777 -0.00011251 -0.00009094 -0.00010604 -0.00004144
-0.00077692 2.95039347 -0.00065498 0.00001312 0.00020962 0.00000569 -0.00014366 0.00004495
0.00078216 0.00209467 2.99013865 -0.00021390 0.00011158 0.00116888 0.00013278 0.00000326
0.00558694 -0.01267935 -0.09209224 -0.01256043 0.00003529 0.00011027 -0.00013671 -0.00002745
0.01131226 0.00739102 0.00195311 0.00004867 -0.02950131 0.00003475 -0.00011325 -0.00001215
-0.00634372 0.02668335 -0.08713253 0.00010993 0.00003269 -0.07728182 -0.00023330 0.00001639
-0.00355707 -0.00237073 0.01106653 -0.00003657 -0.00011193 0.00041494 -0.02966632 0.00004951
-0.00232611 -0.01319967 0.00645467 0.00001209 0.00008613 0.00002926 -0.00001570 -0.01265217
```

The results of the linear regression analysis leading to the above calibration matrix are furthermore compiled in SH coil-specific summary figures and saved to file to allow quality control. For instance, the fields generated by the Z2 coil can be found in the file *fhCalibLinRegZ2.fig*. The data points defining the coil at hand, here Z2, should show a highly linear behavior and the linear regression curve should be correspondingly well-defined. If the data points of the target (or self) term are found to spread considerably, the quality of the calibration experiments as well as the voxel size and positioning should be assessed and corrected if needed. Note that the slope of the self-term Z2 regression analysis, here $-0.07728182 \text{ Hz/cm}^2$, can be found along the diagonal of the calibration matrix along with all other cross-terms. The application of a positive current to the Z2 coil leads to a negative Z2 field shape, i.e. the polarity of the coil is apparently reversed. The Z2 coil at hand furthermore induces some Z and Y cross-terms, whereas all other interactions can be considered negligible.

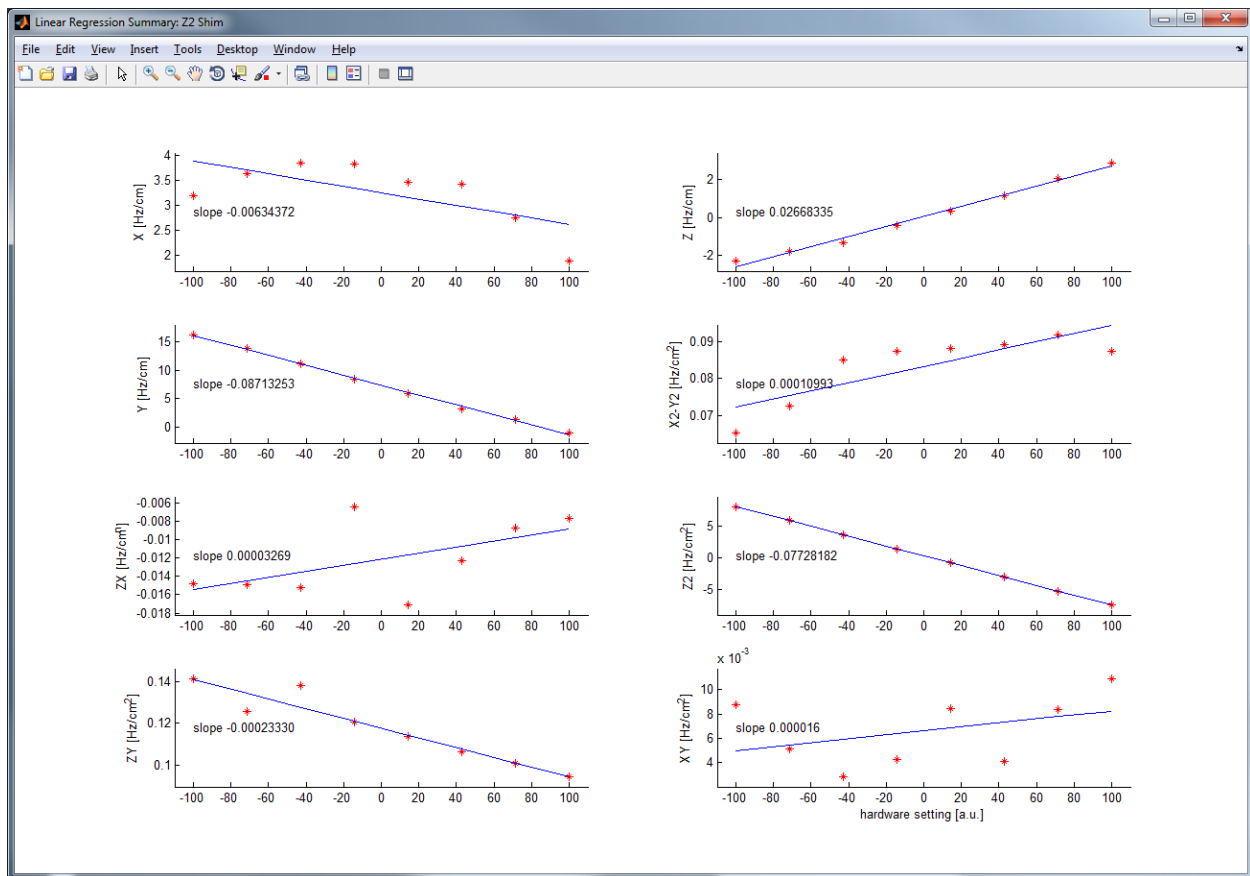


Fig. 2.2: Example self- and cross-term analysis of Z2 shim coil.

IV The Manual Page

The *Manual* tab of the FAMASITO window does not switch to other pages but opens the software manual that you are currently reading. You can place the PDF file of the manual that comes with the software anywhere on your computer. The first time you press the *Manual* tab, you are prompted to select the file location. This location is remembered by the software and the manual will be opened immediately with subsequent use.

V The Exit Page

The *Exit* tab saves all current parameters to a default protocol file and subsequently closes the program. This procedure allows FAMASITO to reopen in the page that has been used last with all parameter settings as selected previously. Note that explicitly loading a specific protocol on the *Data* page is always possible.

VI Glossary

FASTMAP	Fast mapping along projections
FAMASITO	FASTMAP Shim Tool

VII Terms of Use and Additional Remarks

Purpose and Liability

The FAMASITO software is meant for research purposes only. Neither the creators nor Columbia University assume any responsibility of any kind. Please refer to the license agreement for further details.

Data Reading Routines Provided by General Electric

The FAMASITO analysis software uses basic routines for file header and raw data reading that were provided to us by General Electric. Written permission has been obtained for the use and incorporation in FAMASITO.

Legal and Academic Concerns

The FAMASITO method consisting of MR sequence, bash scripts and analysis software are made publically available under a term-limited license. They can be used free of charge in a non-commercial academic setting with the understanding that

1) It is referenced properly in any publication for which it has been used:

Landheer, K., Juchem, C., FAMASITO: FASTMAP Shim Tool for efficient B_0 shimming. Columbia TechVenture license 17327 (2017). innovation.columbia.edu/technologies/CU17327_famasito

2) The creators Karl Landheer, Ph.D., and Christoph Juchem, Ph.D., are offered authorships on the first two publications for which the methods have been used.

Join Us in the Fight against Multiple Sclerosis

The National Multiple Sclerosis Society (NMSS) and patient advocate groups such as the Nancy Davis Foundation (*Erase MS*) provide instrumental support for MS patients and researchers aiming to end this devastating disease. While we do not ask for monetary contributions for ourselves, we encourage you to consider a donation to these organizations. If you chose to support their invaluable efforts based on the free use of the FAMASITO software, please assign *Juchem Laboratory* as the occasion of the donation.

<http://www.nationalmssociety.org/Donate>

<http://www.erasems.org/donate/>

Questions and Feedback

The development of the FAMASITO software is still a work in progress. Questions and feedback are always welcome to help us to further tailor it to the needs of its users:

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