

# What is MRI Characterization ?

MRI Characterization is an automatic post-treatment of MRI acquisition which characterizes, by imaging, the radio frequency (RF) coils in term of signal-to-noise ratio (SNR) correlated to a uniform volume located in depth. The main interest is to compare the RF coils on a MRI system to find one that is the most suitable for a study or to compare the MRI systems between themselves. Comparison can be done on Bruker, Siemens, GE or Philips MRI systems. Secondary interest is to realize a quality control of the MRI system + RF coil throughout the time. And the last interest is to find an optimal performance of the MRI system by changing the sequence parameters and/or by changing the configuration of the coil (position, operating mode, etc...).

## Data acquisition

### 1) Phantom

Size, shape and filling of the phantom have a noticeable impact on the SNR in the case of loaded filling. We recommend to compare a set of coils or MRI systems between themselves by using an identical phantom.

The size and shape must mimic the study, the cylinder diameter must fit the biological sample, whereas its length should be greater than the longest coil.

\* Clinical MRI: a sphere of 20 cm diameter for a human head, a bottle of 2 liters (outer diameter: 120 mm, height: 246 mm) for another part of the human body.

\* PreClinical MRI: two cylindrical fillers, simulating a mouse and a rat, have been drawn in SolidWorks (DSS, Concord, MA). The files can be downloaded on the same page than this document to be 3D printed using ABS (Acrylonitrile Butadiene Styrene). The phantoms have 1 mm of thickness, 100 mm of length and have a bottleneck s-bend to avoid presence of air bubbles (see figure 1). The difference between the two phantoms is the diameter which are 30 mm and 50 mm to simulate the mouse and the rat respectively.



*Figure 1: PreClinical phantom*

To reach the in-vivo conditions, we propose a solution of nickel sulfate hexahydrate : 5 g. NaCl, 1,25 g. NiSO<sub>4</sub>, 6H<sub>2</sub>O per liter of water which is commonly used.

### 2) MRI sequence

We opted for a 3D gradient-echo sequence because it is implemented in all MRI systems (no development is necessary), it is broadly employed, and acquisition time is relatively short (~ 5 min.). Some sequence parameters have been optimized - called optimized parameters - to reach a good reproducibility. Modification of these parameters is possible, but the measurement accuracy cannot be ensure. Other parameters - called secondary parameters - can be adapted to the MRI system or study. Modifications of these parameters will be corrected in the SNR measurement

which will allow a comparison.

\* Optimized parameters: TE: 6 ms; TR: 15 ms; Dummy scan number: 40; Spoiler delay: 1ms; excitation pulse delay: 1 ms; Flip angle: 5°; Excitation pulse shape: sinc10H (sinc with ten lobes); Slice orientation: coronal; Read direction: H-F. Encoding step: linear, from the maximum to the minimum value (do not begin at the center of the k-space).

\* Secondary parameters: FOV: centered to the phantom, FOV encloses all the phantom volume with an additional margin in air equal or superior to 20% of the FOV (see Figure 2); Matrix dimension (read\*phase1\*phase2): (256\*128\*128); Readout bandwidth: 50kHz; NEX: 1;

The sequence for Bruker on Paravision 5 with these parameters can be downloaded on the same page than this document.

All filters and post-processing must be turned off before the image reconstruction by FFT. The low flip angle decreases acquisition instability signal and enable to reach faster the steady-state. A matrix dimension greater than  $256^3$  will increase drastically the post-processing time and could incur an overflow of the RAM. We suggest to save these modified sequences in your MRI system to avoid mistakes or omissions for the next acquisition.

The acquisition files have to be converted to DICOM format and compressed into zip or tar format.

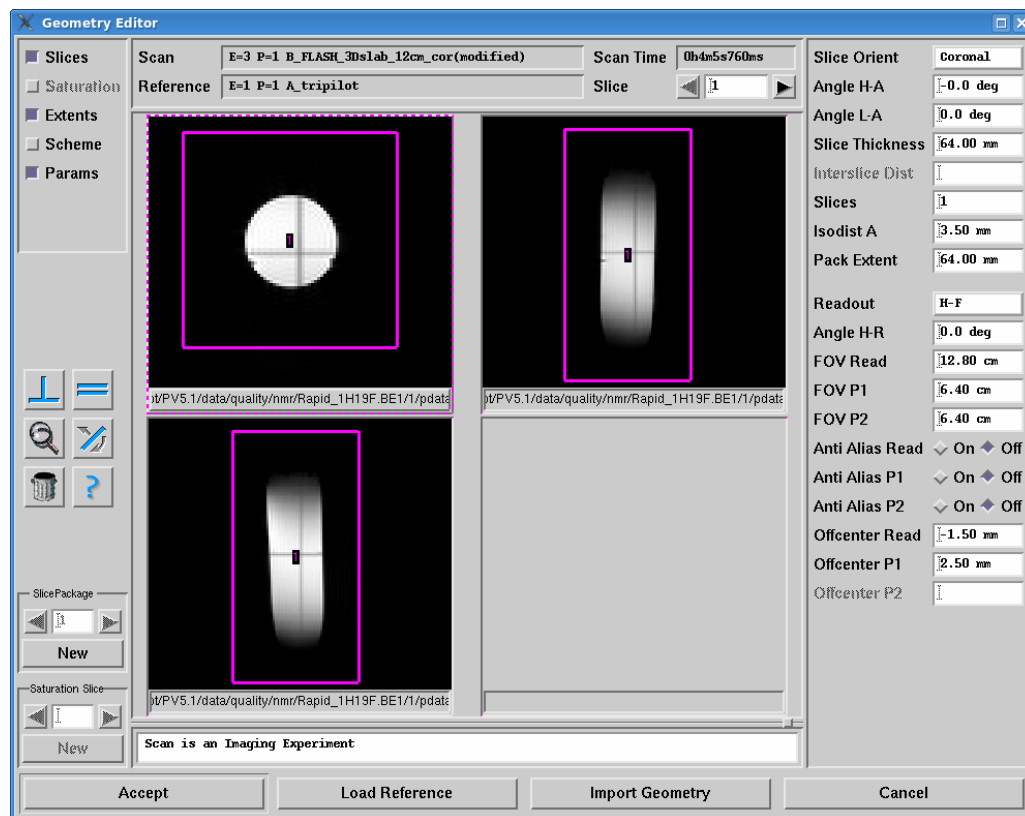


Figure 2: Prescription of the field of view (purple rectangle)

**Special advice for the acquisition on a SIEMENS MRI system:** the Siemens MRI systems modify the raw data of the acquisition by decreasing their dynamic. The noise measurement is skewed and therefore, the SNR measurement is rejected. This modification can be rectify by applying the "ImageScaleFactor" on the raw data to retrieve the original dynamic. To do that, the maximum value (MV) of the raw data must be found and the "ImageScaleFactor" must be set to  $4096/MV$  where  $4096=2^{12}$  is the dynamic range of the receiver. Note that this operation cannot be done after log-out the session.

## Use of MRI Characterization

After creating your account, the home page must look like Figure 3 with three icons below “MRI Characterization”. If it is not the case, go to “My Account” (red circle) and join the group “MRI Characterization”.

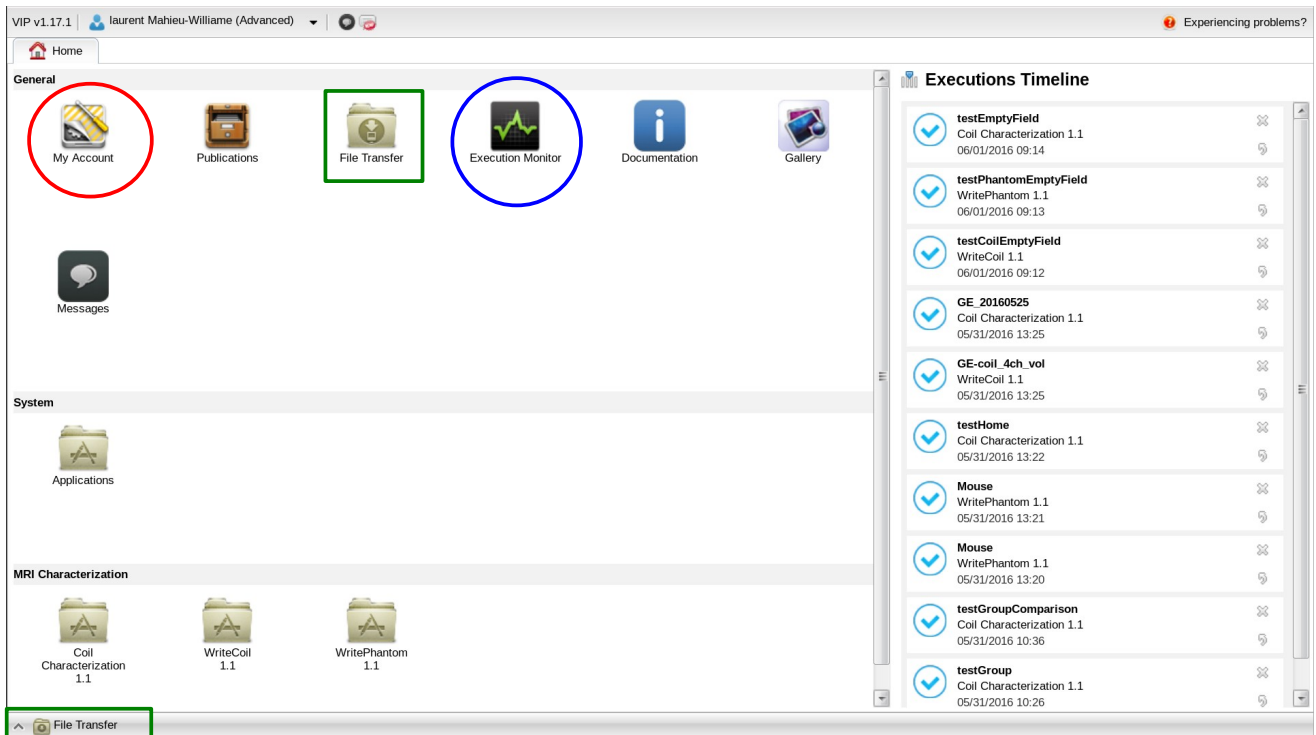


Figure 3: Home Page.

### 1) Create the coil file(s)

The program needs to know which coil you used to acquire the specific data. Click on the “WriteCoil” icon to create the first coil and inquire the different fields:

- Execution name\*:** is the identification of the process. Example: “WriteCoil\_Rapid\_Quad\_4cm”.
- coilName\*:** is the nickname of the coil. Avoid a too long name and some special characters (space, slash, backslash, accent, point). Example: “Rapid\_Quad\_4cm”.
- geometry\*:** Specify the geometry of the coil: “volume” or “surface”. The treatment is slightly different.
- homeDir\*:** specify the home directory: “/vip/Home” for a private characterization or “vip/MRI Coil Characterization (group)” for a multicentric comparison.
- numberOfActiveElement:** indicate the number of active elements only for array coils. This is an important field which determines if the measure of SNR is valid or not. We advice to set this number in the nick name of the coil. If you modify the number of active element in the configuration coil of the experiment, you must create another nickname. In the case of a single-channel coil, fill-in “1” even in the case of quadrature coil.
- constructor:** the constructor of the coil.
- mode:** specify if the coil is in transmission/reception mode or only in reception mode by writting “Tx/Rx” or “Rx” respectively.
- Uncertainty (%):** is the uncertainty of the SNR measurement in %. By default, this value is set to 5% for volume coils (quadrature and bird cage) and 10% for surface coils (single loop). These values have been found on two Bruker preclinical MRI at 4.7T and 7T. The uncertainty depends on the MRI and the coil, see below to the section “6) Uncertainty measurement” to measure your own

uncertainty.

**i) serialNumber:** to identify the coil if there is a confusion on the nickname.

The fields marked with an asterisk are mandatory for the post-treatment. We advice to save it by clicking the "Save Inputs" button on the right of the "Launch" button. Click on the "Launch" button to execute the creation of the coil file. If a modification or a similar creation is required by changing the geometry or changing the number of active element of an array coil, click on the "Save Inputs" button on the left of the "Examples" button on the upper-right of the windows. Change the nickname to create another coil, keep the same nickname to overwrite the previous coil. Repeat this section for all the coils.

## **2) Create the phantoms**

In the case of loaded sample, the comparison between the coils can be done only on the same phantom. Click on the "WritePhantom" icon to create the first phantom and inquire the different fields:

**a) Execution name\*:** is the identification of the process. Example: "WritePhantom\_Mouse".

**b) phantomName\*:** is the nickname of the phantom. Avoid a too long name and some special characters (space, slash, backslash, accent, point). Example: "Mouse".

**c) homeDir\*:** specify the home directory: "/vip/Home" for a private characterization or "vip/MRI Coil Characterization (group)" for a multicentric comparison.




**d) description:** Specify the filling of the phantom. Example: "Mouse 50mL - 1,25 g. NiSO<sub>4</sub> x 6H<sub>2</sub>O + 5 g. NaCl per liter of water".

**e) T2 (ms):** indicate the spin-spin relaxation time for a prospective correction.

**f) T1 (ms):** indicate the spin-lattice relaxation time for a prospective correction.

The fields marked with an asterisk are mandatory for the post-treatment. We advice to save it by clicking the "Save Inputs" button on the right of the "Launch" button. Click on the "Launch" button to execute the creation of the phantom. If a modification or a similar creation is required, click on the "Save Inputs" button on the left of the "Examples" button on the upper-right of the windows. Change the nickname to create another phantom, keep the same nickname to overwrite the previous phantom. Repeat this section for all the phantoms.

## **3) Upload the DICOM acquisition file(s)**

The acquisition file has to be converted to DICOM format and compressed into zip or tar format. Click on "File Transfer" icon (green square in the Figure 3) or on the bar at the lower-left of the home page (green rectangle in the Figure 3). Go to the following folder: "/vip/Home/caractRF/inputs/data/" and click on the upload icon  for a single file or on the upload multiple data icon  for a set of files. Click on the refresh icon  to see it.

## **4) Execute the main program**

Click on the "RF Characterization" and inquire the different fields:

**a) Execution name\*:** is the identification of the process to visualize it and to recognize it if modification is required. Example: Execution\_2016-02-23.

**b) Coil\*:** click on the magnifying glass button to select the coil you created and with which you acquired the data. The coil folder is located at "/vip/Home/caractRF/inputs/coil/".




**c) Phantom\*:** click on the magnifying glass button to select the phantom you created and with




which you acquired the data. The phantom folder is located at `"/vip/Home/caractRF/inputs/phantom/"`.

**d) Data\*:** click on the magnifying glass button to select the data. The data folder is located at `"/vip/Home/caractRF/inputs/data/"`.

**e) homeDir\*:** specify the home directory: `"/vip/Home"` for a private characterization or `"/vip/MRI Coil Characterization (group)"` for a multicentric comparison.

All the fields are mandatory. A multiple execution is feasible by clicking on the "plus" button in front of the coil, phantom, and data fields. The correspondence between the coil, the phantom and the data are in order. The first line of the coil correspond to the first line of the phantom and data, etc... **Do not replicate the "homeDir" field!** We advice to save it by clicking the "Save Inputs" button on the right of the "Launch" button. Click on the "Launch" button to execute the main program. If a rerun is required, click on the "Save Inputs" button on the left of the "Examples" button on the upper-right of the windows.

You can visualize in real time the progress of the post-processing by clicking on the "Execution monitor" icon  in the home page (blue circle in the Figure 3). Right click on your execution and click on "View Execution", a window appear with the progress bar. Click on this tiny icon  on the upper-left to see an histogram of the execution(s). Green color tells that it is running. Click here  to watch a debugging message.

When everything went well, the color of the histogram change into blue. Download the report file at the location `"/vip/Home/caractRF/outputs/reportFiles/"`. Click on refresh button . Select the report files and click on the download icon . The files are ready to be downloaded on the lower-right below the "Pool transfer", click on the second download icon .

## 5) Multicenter comparison

In the case of a multicenter comparison is required, change all the root paths of `"/vip/Home/*"` by `"/vip/MRI Coil Characterization (group)/*"`. To have the permission to write in this group, you have to change your status from beginner to advanced. To do that, an individual certification of GRID2-FR must be requested through the CNRS website: <https://igc.services.cnrs.fr/usercert/?CA=GRID2-FR&lang=fr>. Your organism and laboratory must be referenced in the GRID2-FR.

## 6) Uncertainty measurement

We propose a reproducibility study on different kind of coils (volume, surface, and array coil) to evaluate the error on the SNR measurement. Acquire 9 scans, between each acquisition, the coil is removed from the magnet, and the phantom is removed from the coil. All the automatic adjustments have to be performed after each new scan. Execute the main program on the 9 scans and note the SNR values. The uncertainty is defined as:

$$Uncert = \frac{SNR_{max} - SNR_{min}}{\overline{SNR}} * 100$$

where  $SNR_{max}$  is the maximal value,  $SNR_{min}$  is the minimum value, and  $\overline{SNR}$  is the average.

## 7) Additional Information

The main results of all the executions are saved in the folder: `"/vip/Home/caractRF/comparison"` as a Matlab structure (file ".mat"). Use the command "load" to read the structure in the Matlab Editor. The 3D matrix of the acquisition is not saved.

The Latex source file called "temp-sources.tgz" containing all the figures can be downloaded from the following folder "/vip/Home/caractRF/outputs/sources/". At each new execution, this file is overwritten.

## **Acknowledge**

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