
Gradient-Modulated PETRA

2019/7/16

Version 1.0.1

Naoharu Kobayashi
Center for Magnetic Resonance Research
Department of Radiology, University of Minnesota

Michael Garwood
Center for Magnetic Resonance Research
Department of Radiology, University of Minnesota

1. Overview

The software package includes MRI pulse sequence and online ICE reconstruction binaries for Pointwise Encoding Time reduction with Radial Acquisition with Gradient Modulation (GM-PETRA). Gradient modulation is applied right after the hard pulse excitation in PETRA, which make it possible to set different bandwidths in excitation and readout. Advantages of using gradient modulation is to improve image blurring due to off-resonance and fast T_2^* decay. Setting a lower bandwidth in excitation can also mitigate the SAR and RF peak power limitations, which are well-known limitations in the ZTE-based sequences including PETRA. Additionally, oversampling in Single Point Imaging (SPI) acquisition, where data sampling around the k-space center is Cartesian point by point, is implemented in the GM-PETRA sequence in this package. The SPI oversampling mitigate the aliasing artifacts that is usually observed when using a smaller FOV relative to the imaging object.

2. Requirements

The current software version supports only the Siemens IDEA version VE11C. Other software versions will also be supported in the future.

The online ICE reconstruction uses Graphics Processing Units (GPUs) with a compute capability 2.0 or higher on MARS. Image reconstruction without GPU is **NOT** supported in the current version. Please confirm that the MARS computer on your system has **at least one GPU**. When you have multiple receive channels, reconstruction time is roughly proportional to the number of GPUs available. 3D non-Cartesian/gridding reconstruction requires relatively large amount of memory on GPUs. We recommend **4 GB (preferably, 6 GB or more)** of VRAM on GPUs for high-resolution image reconstruction.

3. Installation

This software package includes the following files:

- GM-PETRA.pdf (this document)
- nk_petra.exar1
- seq/nk_petra.dll
- seq/nk_petra.so
- seq/nk_ice/nk_params
- ice/nk_iceProgramNonCartesian.ipr
- ice/nk_iceProgramNonCartesian.dll
- ice/nk_iceProgramNonCartesian.evp
- ice/nk_iceProgramNonCartesian.so

To deploy the sequence and ICE binaries on a scanner, switch the Embedded Control into UPDATE mode. You may also need to restart the Protocol Access Server (PAS) by

calling 'ideacmdtool' to put the ICE binaries. Put the sequence binaries (nk_petra.xxx) in:

C:\Medcom\MriCustomer\seq

and the ICE binaries (nk_IceProgramNonCartesian.xxx) in:

C:\Medcom\MriCustomer\ice

After putting the ICE binaries, restart 'MrIrisContainer' to reload nk_IceProgramNonCartesian.so.

The file 'nk_Ice/nk_params' is optional; the ICE program works without it. This file contains an intensity scaling factor in ICE reconstruction. This file is used in ICE, but put the 'nk_Ice' folder in:

C:\Medcom\MriCustomer\seq

The file 'nk_petra.exar1' contains GM-PETRA protocols for sequence test. It has 5 protocols:

nk_petra-gm-test	: test GM-PETRA scan (recommend to run this first)
nk_petra-gm	: GM-PETRA scan
nk_petra-gm-highreso	: high resolution GM-PETRA scan
nk_petra-gm-fsat-highreso	: high resolution GM-PETRA scan with fat sat
nk_petra-highreso	: high resolution PETRA scan (without grad mod)

4. Sequence parameters

GM-PETRA has some restrictions on sequence parameters. In this section, important parameters in GM-PETRA are explained.

4.1 Routine panel

The screenshot shows the 'Routine' panel of the GM-PETRA software interface. At the top, it displays 'TA: 0:10 PM: ISO' and 'Voxel size: 1.0×1.0×1.0mm Rel. SNR: 0.33 : fi'. Below this are tabs for 'Routine', 'Contrast', 'Resolution', 'Geometry', 'System', 'Physio', 'Inline', and 'Sequence'. The 'Routine' tab is active. Parameters are organized into two columns. The left column includes 'Slab group' (1), 'Slabs' (1), 'Dist. factor' (20 %), 'Position' (Isocenter), 'Orientation' (Transversal), 'Phase enc. dir.' (A >> P), 'AutoAlign' (---), and 'Slices per slab' (256). The right column includes 'FoV read' (250 mm), 'FoV phase' (100.0 %), 'Slice thickness' (0.98 mm), 'TR' (4.0 ms), 'TE' (0.05 ms), 'Averages' (1), 'Concatenations' (1), 'Filter' (None), and 'Coil elements' (BC). Five yellow circles with numbers 1 through 5 are placed next to specific parameters: 1 next to Position, 2 next to Orientation, 3 next to Slices per slab, 4 next to Slice thickness, and 5 next to TE.

- ① Slab location can be shifted ONLY along the Z direction (Table positioning mode is forced to ISO).
- ② Oblique orientation is available.
- ③ Slices per slab is fixed to the same value as 'Base resolution' in the 'Resolution' panel (i.e, the image is 3D isotropic). It CANNOT be changed here.
- ④ Slice thickness CANNOT be changed here. The value is (FoV read)/(Base resolution). To change the value, change 'Base resolution' in the 'Resolution' panel.
- ⑤ TE is fixed to minimum (CANNOT be changed).

4.2 Contrast panel -> Common

TA: 0:10 PM: ISO Voxel size: 1.0×1.0×1.0mm Rel. SNR: 0.33 : fi

Routine Contrast Resolution Geometry System Physio Inline Sequence

Common Dynamic

TR 4.0 ms Fat suppr. None ②

TE 0.05 ms

Water suppr. None

MTC

① Magn. preparation None

Flip angle 3.0 deg

SWI

TR 3.3 4.0 10000.0

- ① Non-sel. IR and Non-sel. SR can be used. It is recommended to use them with segmented acquisition (subsection 4.6), otherwise scan time will be too lengthy.
- ② Fat suppression works. Segmented acquisition is recommended with fat suppression (subsection 4.6).

4.3 Resolution panel -> Common

TA: 0:10 PM: ISO Voxel size: 1.0×1.0×1.0mm Rel. SNR: 0.33 : fi

Routine Contrast Resolution Geometry System Physio Inline Sequence

Common Filter Image Filter Rawdata

FoV read 250 mm

FoV phase 100.0 %

Slice thickness 0.98 mm

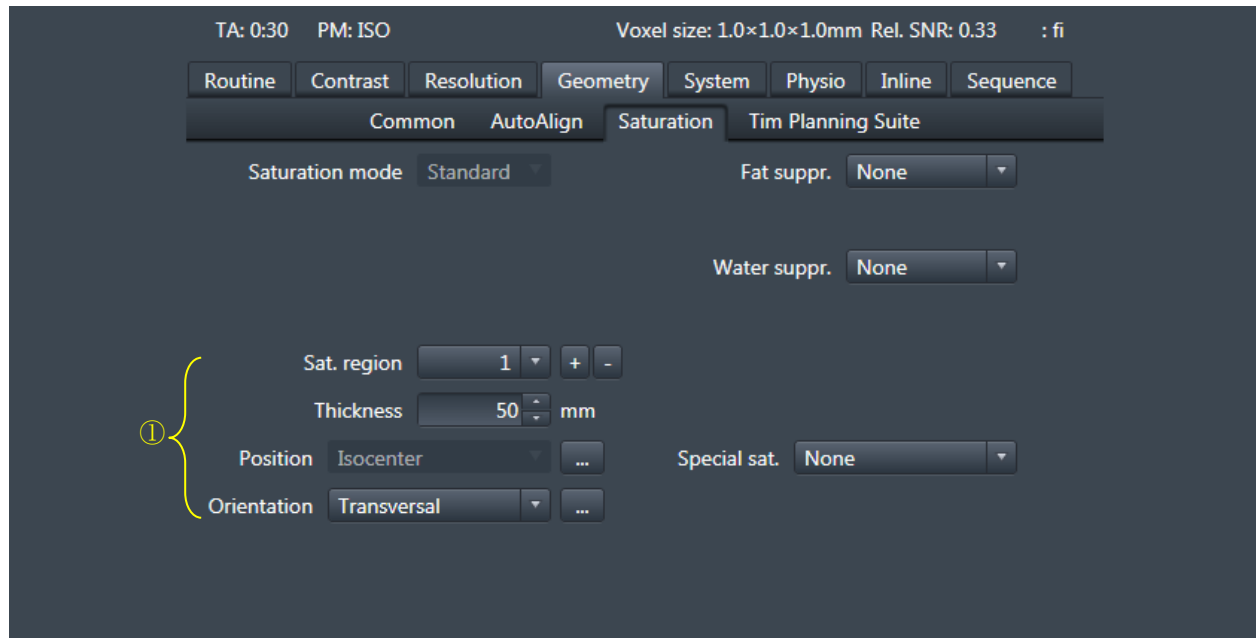
① Base resolution 256

② { Radial views 1024

Radial interleaves 2

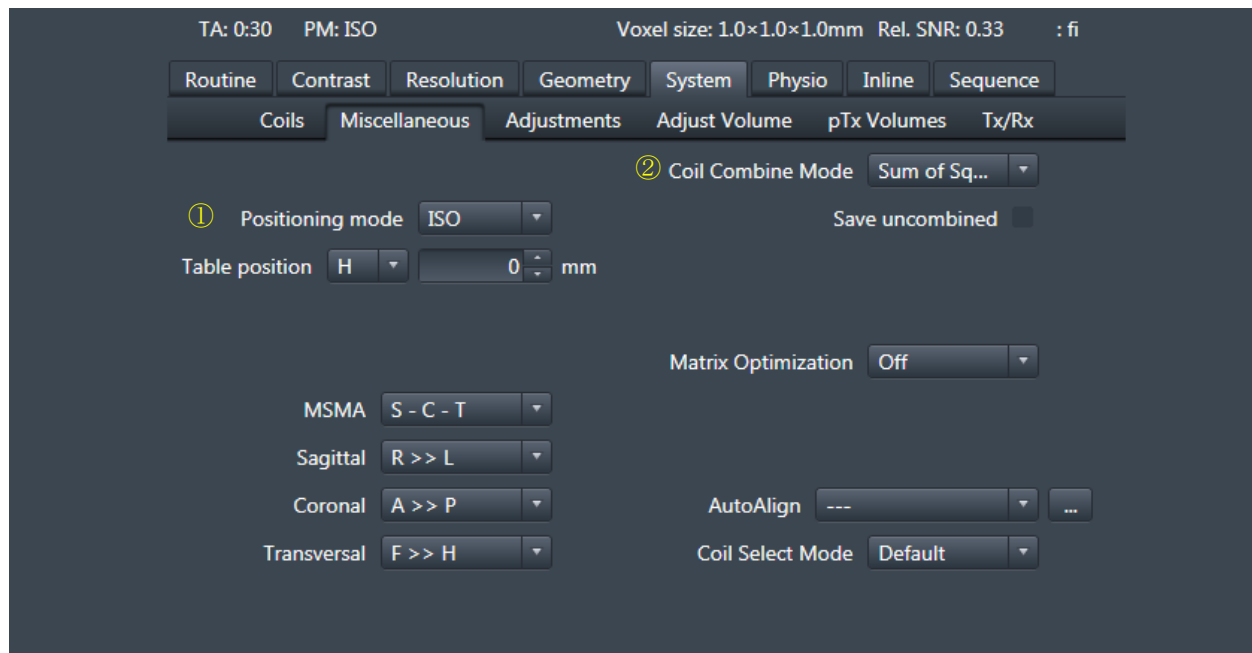
- ① Set Base resolution to change the spatial resolution. 'Slices per slab' in the 'Routine' panel changes accordingly.
- ② The total number of acquisitions (radial and SPI acquisitions) is provided by (Radial views) x (Radial interleaves). Radial interleaves is the number of 3D spirals on a spherical surface in radial acquisition, where each spiral acquires a 3D spherical k-space sparsely.

4.4 Geometry panel -> Saturation



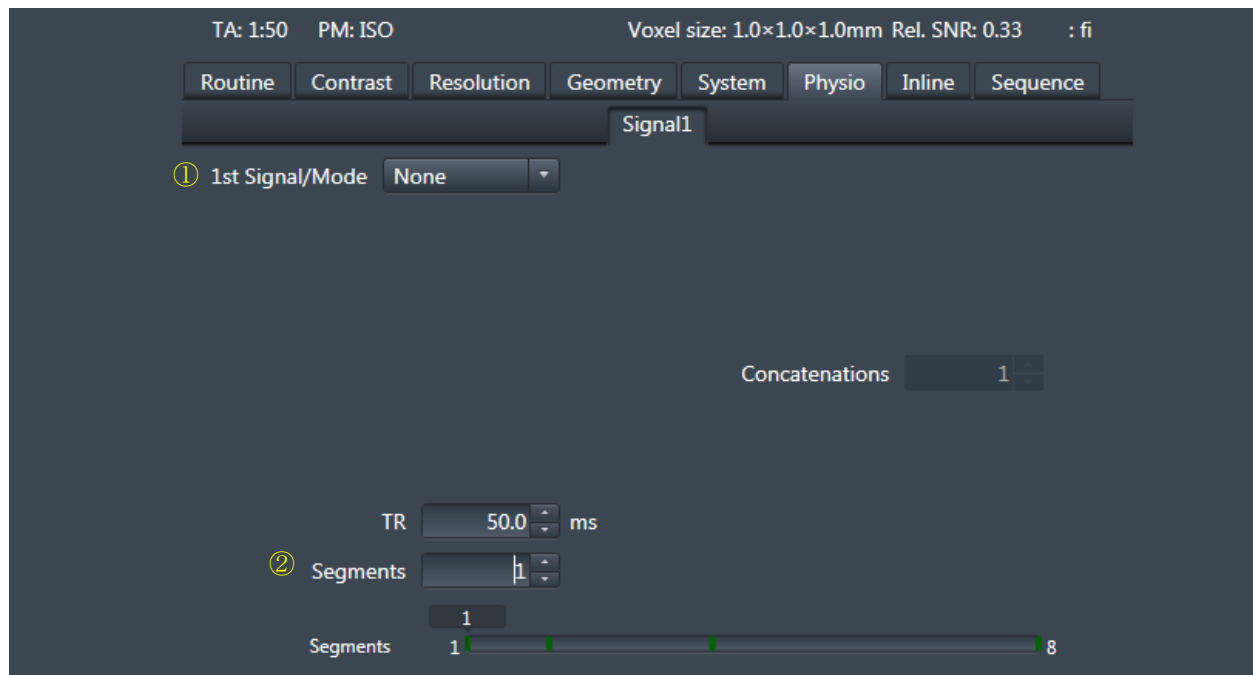
- ① Regional saturation works in the same way as other sequences, but it is strongly recommended to use it with segmented acquisition (4.6). Otherwise, scan time is too lengthy.

4. 5 System panel -> Miscellaneous



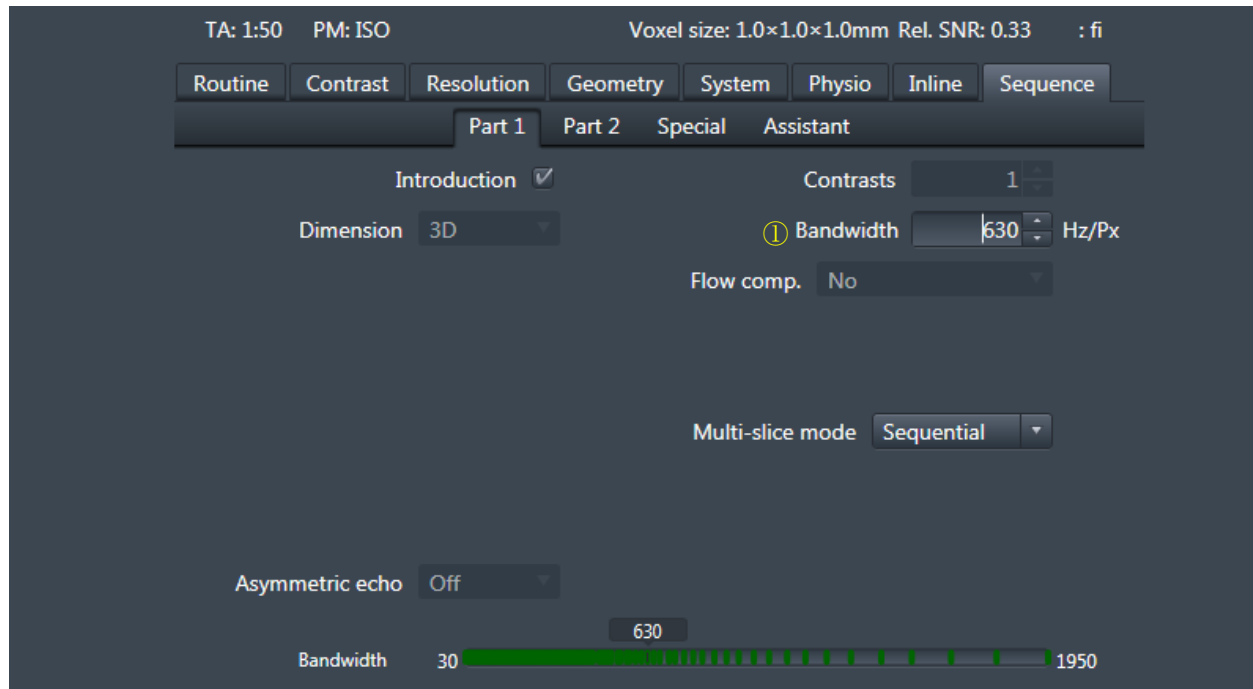
- ① Table positioning mode is fixed to ISO in GM-PETRA, which enables the FOV shift along the Z axis. Keep in mind that the image might not show up on the slice planning window on the console window, if table positioning mode is not consistent with other scans in the study.
- ② Currently, only Sum of Square is available for Coil Combine Mode.

4.6 Physio panel -> Signal1



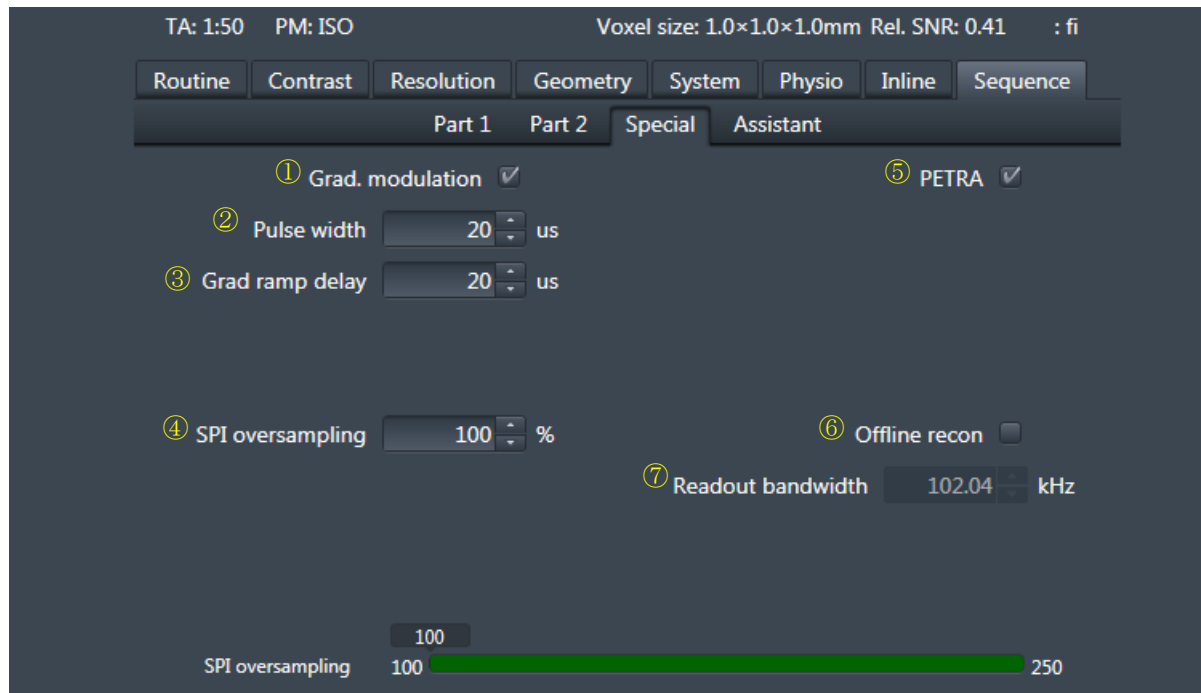
- ① Gated acquisition (ECG, respiratory, etc) works in a similar way to other sequences. Segmented acquisition is highly recommended.
- ② Segments ≥ 2 turns on segmented acquisition. Segmented acquisition is recommended for acquisitions with preparation sequences (IR or SR prep, fat sat and regional sat) and gated acquisition. Currently, solve handlers for segmented acquisition is not implemented well yet. Then, please follow the following procedure when you use segmented acquisition:
 1. Set Base resolution first ; Siemens solve handler for Base resolution has some dependence on Segments. Base resolution should be set before setting Segments.
 2. Set TR to a long value (e.g. 10,000 ms, which will make it possible to turn on prep sequences).
 3. Turn on prep sequences such as IR, SR, fat sat and regional sat or gated acquisition (1st Signal/Mode in this panel ①). When the prep sequence has related parameters (e.g. TI for IR/SR prep and slab thickness for regional sat), set those parameters as well.
 4. Set Segments to the preferred value.
 5. Reset TR to the preferred value.

4.7 Sequence panel -> Part1



- ① Bandwidth (Hz/px) determines the readout bandwidth after gradient ramp, which is given by (Hz/px) x (Base resolution); the readout bandwidth shows up in 'Readout bandwidth' at the right bottom in 'Sequence -> Special'. Low bandwidth/Hz/px may result in ramp down of the gradient after excitation. The readout bandwidth based on Hz/px is valid ONLY with gradient modulation. Hz/px is ignored when running PETRA without gradient modulation, in which the readout bandwidth is determined based on pulse width of the excitation hard pulse.

4.8 Sequence panel -> Special



- ① Switch GM-PETRA and PETRA. Keep in mind that this PETRA (without gradient modulation) is different from the Siemens product PETRA. For PETRA, excitation and readout bandwidths are common and takes the value in 'Readout bandwidth' at the right bottom in this panel (⑦).
- ② Pulse width is pulse duration of the excitation hard pulse [us]. This determines the excitation bandwidth; a shorter pulse width results in a broader excitation bandwidth.
- ③ In GM-PETRA, the gradient start ramping up/down after the excitation hard pulse and the following T/R switching delay (typically 20 us). Grad ramp delay is an extra delay time from the end of the T/R switching delay to the start of the gradient ramp. The Rx gate opens at the beginning of Grad ramp delay. Empirically, the default setting of 20 us is a safe setting in most coils.
- ④ SPI oversampling is the oversampling factor in SPI acquisition around the k-space center. 100% is Nyquist sampling. When FOV is comparable to or smaller than the imaging object, SPI oversampling >100% is recommended to avoid aliasing artifacts that is commonly seen in PETRA.
- ⑤ This check box cannot be turned off – the sequence only runs as PETRA or GM-PETRA.
- ⑥ Checking this box turns off online ICE image reconstruction. When the ICE recon is turned off, the ICE program outputs an empty dicom image which has zero values in all image pixels. DO NOT check this box, unless you can reconstruct data offline.
- ⑦ Readout bandwidth is the bandwidth after gradient ramping in GM-PETRA, which is given by (Hz/px) x (Base resolution). With PETRA (without gradient modulation), this value is the excitation/readout bandwidth obtained from the excitation hard pulse width.

5. ICE program

Online ICE reconstruction does not require manual parameter settings. However, when dynamic range of the output DICOM image is not proper, one can scale the signal intensities by changing the '\$SignalAmpl3D' parameter in 'C:/Medcom/MriCustomer/seq/nk_Ice/nk_params' (default value is 1.0). The 'nk_params' can be edited with a text editor (e.g. Notepad on the console computer). After changing this parameter value, you can run ICE reconstruction from Twix without running the sequence again.

One limitation of the ICE processing is VRAM on GPUs. One functor in the ICE processing pipeline checks if VRAM is large enough to reconstruct an image before the sequence starts. When the memory demand exceeds the limit, the sequence won't start running. When MARS is busy for processing data from previous scans, the sequence may start running without the VRAM check. However, image reconstruction will fail if the memory demand exceeds the limit. Turning on the 'offline recon' check box in 'Sequence -> Special' skips the VRAM check and thus make it possible to run the sequence regardless of VRAM on GPUs, but the ICE program outputs an empty image in DICOM.

Image reconstruction time is dependent on the number of receive channels, the total number of radial projections, matrix size, the number of GPUs and the GPU's computational power. Reconstruction of a high resolution scan dataset (for example, 32 receive channels, 100k radial projections and 512 cube matrix) may take time comparable to the scan time (5-10 min).

It should not happen, but if the ICE program failed in the GPU processes, you may need to restart MrIrisContainer, because failure in the GPU processes might result in memory leak on VRAM. You can figure out if memory is leaking on GPUs by calling 'nvidia-smi' on MARS.

6. Contact

In a case that you see any bug or abnormal functioning in the pulse sequence or ICE program, please contact Naoharu Kobayashi at nkobayas@umn.edu by email. In such cases, if you can provide us the detailed information (e.g, the protocol you see the issue, raw data and system log), it will be helpful for debugging.