Table of Contents

Chapter 1 General

Spectrometer Reset

- After hardware problems, recommended to reset the spectrometer
- Two options:
  - Export ready or complete scan into Topspin and write *ii_restart* into command line
  - Start Macro Manager, go into Bruker folder and then start *ResetSpect* macro

Adjustment of DC-offset (Zipper Artifact)

- Load *RxDcAdjustment* from folder *B_service*
- Run the sequence with *GSAuto*

Removal of Zipper Artifact

- Open *Edit RECO*
- Change *WDW mode* from *NO_WDW* to *SQUARE*
- Change *Start of Wdw maximum* from 0 to 0.05 (experiment with values, this is % of the points that will be cut in the beginning of the FID signal)
- Change *End of Wdw maximum* to 1.

Prescription for Decreasing TE

- Reduce the read matrix (fewer N_x)
- Increase the bandwidth (BW)
- Change length of 180° pulse (and then match the BW of 90° pulse to BW of 180° pulse).
- Sequence details:
  - Increase Fourier acceleration factor
  - Increase zero filling

EPIs

- When changing from single-shot to multi-shot, one has to manually activate the navigator (it is not turned ON automatically)
- For good-quality EPIs need short TE as possible and large bandwidth
- Partial FT acceleration can cause ghosting in EPI scans.

Chapter 2 Useful Macros

ASL_Perfusion_Processing

- Macro for processing ASL perfusion data.
- The macro has a bug in that you have to select the data sequence twice each time you want to perform the ISA analysis.
- In addition, one should be aware that the perfusion analysis uses the most simplistic of models in which blood flow is computed from the difference in relaxation times between global and selective inversion. This model has been surpassed by more advanced models that take into account the kinetics of the tracer through the tissues. There is numerous literature available on this topic, but a good start would be Tofts, Quantitative MRI of the brain.

CalcLinewidth

- Macro for computing the FWHM (full-width-half-maximum) of an FID.
- It has to be executed on a completed spectroscopic sequence, such as *PRESS_waterline.*

DutyCycle

- This macro is used to start the calculation of the maximum gradient utilization on a selected scan, so-called duty-cylce.
- Duty cycle is in this case defined as the percent of time that gradients spend in an active state (i.e, transmitting a field) as a fraction of the total imaging time.
- The duty cycle should never go above 85%.

FastmapScout

- Semi-automatic FASTMAP tool for localized shimming
- Is to be used only for Spectroscopy, not other protocols.

Localized_Spectroscopy_Guide

- This is a script to facilitate the routine acquisition of PRESS and STEAM spectra.

Mapshim

- Macro for performing the shimming protocol based on Fieldmap.
- To be used for DTI-EPI, DSC, FLAI-EPI.

PvStartup

- Macro that determines how PV opens at the startup.
- This macro can be copied and pasted from Bruker into the user's folder for customization.
- For instance, if you change xtip = true (from false), then xtip will open on startup.

QueuedACQ

- Macro for setting up a sequence of scans that will execute automatically, one after another without the need for operator's control.

RecoSeries

- This macro is used to reconstruct a series of images with the same user scaling parameters (*reco_map_slope, reco_map_intercept*) in order to compare the datasets.
- To use this macro properly, you have to:
  - Select the first scan in the series of completed scans.
  - Open the macro by pressing on the *Edit* button
  - Carefully read Pre-conditions and Usage
  - Adjust the *NumScans* to the number of scans in the series you would like to reconstruct with the same scaling parameters.
  - Adjust *WordType* to the word type specified in the completed scans.

ResetSpect

- Macro to reset the spectrometer
- Takes around 45 sec
- See under Spectrometer Reset above for more info.

SubtractImageSeries

Chapter 3 Shimming Strategies

General Principles

Shimming means adjusting the magnetic field gradients such that the static magnetic field inside the sample/animal is as uniform as possible. A good shim is required for many advanced protocols, including Diffusion imaging, Spectroscopy, Arterial-spin labeling, T_2* mapping, fMRI etc.

Various shimming strategies exist within PV5.1:

- 1st order shimming which is is part of the initial adjustments when a new patient/study is created
- 1st and 2nd order GLOBAL shimming using *ADJ_SHIM_1st_2nd_order*
- 1st and 2nd order GLOBAL shimming using *MAPSHIM* macro
- 1st and 2nd order LOCAL shimming using *MAPHIM* macro
- 1st and 2nd order LOCAL shimming using *FASTMAP_scout* macro

How do we measure the quality of the shim? By measuring the width (full-width-half-max or FWHM) of the FID. This is done in the following way:

- Load *PRESS-waterline* sequence from *B_spectroscopy* location
- run Macro *CalcuLinewidth* which measures the linewidth of the water FID signal.

Therefore, whenever we have to check the quality of the shim, we run the two steps above (collect an FID of water and measure its FWHM).

From experience we know that a good shim for:

- Normal rat brain is below 20 Hz
- Normal mouse brain is below 15 Hz.

Mapshim calibration

- Only has to be performed once by the system administrator.
- Is required in order to perform shimming using MAPSHIM.
- In manual D2-71.
- Load sequence *SVShimCalMap* located in *B_Service* folder. This is a special version of a *Fieldmap* method.
- Change the following parameters (if necessary):
  - *Min Echo Time* = 3 x *PVM_ReiseTime* + *FirstEchoTime*
  - Number of Shim channels: 4
  - Shim radius (should be determined from *TriPilot*)
- Acquire *Fieldmap* with traffic light
- Open Macromanager, run *Mapshim_calib*

Mapshim

- Recommended to EPI acquisitions (DTI-EPI, FLAIR-EPI, DSC-EPI)
- Recommended for T_2* mapping in order to reduce shim-inhomogeneity and thus to be sensitive to the true T_2* effect.

- Requires a Mapshim calibration file (acquired using *SVShimCalMap* method)

Procedure

- Load and run *TriPilot*: 1st order shimming as part of the initial adjustment
- Load *ADJ_SHIM_1st_2nd_order*, run *Acq* →*current adj.* → *Method specific adjustment for the local Field Homogeneity*
- Load *PRESS-waterline* → adjust geometry of the imaging voxel to cover either as much of the brain as possible or region-of-interest → run with traffic light → run Macro *CalcuLinewidth* → record linewidth of the FID (50%). THIS IS THE QUALITY OF SHIMMING WITH 1ST AND 2ND ORDER SHIMS.
- Load *Fieldmap* (either *Fieldmap_rat* or *Fieldmap_mouse*) → Adjust geometry if necessary so that the object is completely enclosed by FOV → Run Macro *Mapshim*, acquire *Fieldmap*.
  Note: *Mapshim* macro can only run on a scan in *Ready* mode, not on a *Completed* scan.
  Note: Resolution of the *Fieldmap* protocol has to be the same in all directions.
- Clone *PRESS-waterline* from before → press *Local* → run with traffic light → run Macro *CalcuLinewidth* → record linewidth of the FID (50%). THIS IS THE QUALITY OF SHIMMING WITH 1ST AND 2ND ORDER SHIMS USING FIELDMAP.
- Clone *PRESS-waterline* from before → run *Acq* →*current adj.* → *Method specific adjustment for the local Field Homogeneity* → run with traffic light → run Macro *CalcuLinewidth* → record linewidth of the FID (50%). THIS IS THE QUALITY OF SHIMMING WITH 1ST, 2ND AND AGAIN 1ST (ITERATED) ORDER SHIMS.

Fastmap

- Use only for spectroscopy, not anything else
- For CSI, can do *Mapshim* with local shimming

Chapter 4 Diffusion

General Principles

Hardware

Procedure

Processing Diffusion Images

Chapter 5 Dynamic Contrast Enhancement (DCE-T1)

General Principles

Hardware

Procedure

Processing DCE Images

Chapter 6 Arterial Spin Label (ASL)

General Principles

Arterial Spin Labeling (or ASL for short) is a technique used for measuring brain perfusion without the use of exogenous contrast agent. This is achieved by magnetically labeling proton spins before they enter, due to perfusion, the imaging slice.

The current implementation of ASL uses a global and a slice-selective inversion of the proton spins. In the global inversion, all spins between the heart and the head should be inverted, so it is important that that part of the body is well within the transmitter coil. In the slice-selective inversion, only the imaging slice + an additional slab is inverted.

An example of ASL perfusion image obtained on a rat brain with our 7T MRI Pharmascan system is given at the end of this Chapter.

Hardware

It is best to use a two-coil configuration for ASL: a large transmitter coil (70 mm ID) and a receiver coil (such as the brain phase-array).

Procedure

For best inversion, the neck of the animal should preferably be in the center of the transmitter coil, which means it might be necessary to push the animal a few cm further into the scanner than normal. Note, however, that the automatic adjustment of the transmitter gain will most likely fail due to the low signal strength. In such a case, it is necessary to perform the following procedure:

- Load *ADJ_REFG* from *B_ADJUSTMENTS*
- Go to *Edit Method*
- Change *Receiver Gain* from 10 to 64 (try even bigger gain, if this does not work).
- Change *Initial Attenuation* from 35 dB to 25 dB (check what the usual values are in a previous TriPilot).
- If necessary, also change the *Adjustment Precision* from 3 dB to 2 dB.
- Run Edit Methods → Acq→ Current Adjustments: Protocol ADJ_REFG Adjusting the Reference Pulse Gain

Once the initial adjustment runs to completion, one can proceed with the regular procedure:

- Load *TriPilot*, change the FOV to a large FOV (say 8x8 cm for rat head) in order to cover the head despite positioning the animal further in the scanner (see above). Run with t.l.

- Load *TriPilot*, center the slice around the brain and run with t.l.
- Load *TriPilot-multi*: position all slices through the brain, run with t.l.
- If running *FAIR_EPI*, shimming has to be adjusted according to the Mapshim procedure described in Chapter 3. This is not necessary for *FAIR_RARE* protocol.
- Load either *FAIR_EPI* or *FAIR_RARE* from *MIC_Rat_head_tumor* or *MIC_Mouse_head_tumor*.
- Adjust the geometry to cover the slice of interest. This will in most cases be a slice through the middle of the tumor.
- Setting parameters in *Edit Method*
  - *TR* = 13000 ms, *TE*= 16.6 ms
  - *Effective Spectral Bandwidth*: 350 kHz
  - *Repetition Spacing*: CONST_RECOV
  - *Fair*
    - ✓ *Type of FAIR experiment* = INTERLEAVED2
    - ✓ *TIR setting* = USER_TIR
    - ✓ *TIR Values* = 30 ms, 100 ms, 200 ms, … 2300 ms
    - ✓ *Inversion Slab Thickness* = 4.20 mm
    - ✓ *Slice Package Margin* = 1.5 mm
    - ✓ *IR-Spoiler Duration* = 10 ms
    - ✓ *IR-Spoiler Amplitude* = 40%
  - *RF pulses*
    - ✓ Check BW of all pulses. It should be round 2000 Hz.

- Note that in order to use the post-processing macro, one has to use *Interleved2* as the *Type of FAIR experiment*
- Run the sequence with t.l.

Processing ASL Images

- Start *Macro Manager*
- Run *ASL_Perfusion_Processing*
- Step through the macro by first loading the ASL experiment.
- Select either *Calculate Selective/Calculate Global* T_1 *Map.* Note that there is a bug in the macro so you will have to select each map twice.
- Before selecting *Compute Perfusion Map*, check the T_1 of blood (for reference, see Rane, Swati D, and John C Gore. "Measurement of T1 of Human Arterial and Venous Blood at 7T." Magnetic Resonance Imaging 31, no. 3 (April 1, 2013): 477–479. doi:10.1016/j.mri.2012.08.008).

Chapter 7 Single-voxel Spectroscopy

General Principles

Single-voxel spectroscopy is a technique that enables you to obtain proton spectra from a pre-defined voxel (for instance, in mouse/rat brain). Proton spectra contain information about the concentration of certain metabolites and lipids in tissue.

An example of proton spectra obtained on a mouse brain with our 7T MRI Pharmascan system is given at the end of this Chapter.

The most important part for obtaining good proton spectra is a good shim (magnetic field uniformity). To obtain a good shim, we follow the procedure described under Mapshim in Chapter 3.

The second most important part of Single-voxel spectrometry is to achieve good water suppression. Water proton signal is much bigger than signal from other protons in the body (due to its abundance), so water signal, if left unsuppressed, can dominate over and mask other protons which we are interested in.

This manual will describe two different ways of performing single-voxel spectroscopy imaging:

- Manual adjustments
- Using Macro *Localized_Spectroscopy_Guide*

The two methods are the same in the beginning (i.e., TriPilot and shimming procedure), but differ in the way PRESS-1H is executed (manually or with a macro).

Hardware

No special hardware necessary.

Procedure

- Load *TriPilot*, run with traffic light (t.l.)
- Load *TriPilot-multi*: position all slices through the brain, run with t.l.
- Load *PRESS-1H* → Define your shimming volume, e.g., a 4x5x6 mm^3 box for mice
- Load *ADJ_SHIM_1st_2nd_order*, run *Acq* →*current adj.* → *Method specific adjustment for the local Field Homogeneity*
- Load *PRESS-waterline* → import geometry from *PRESS-1H* → run with t.l. → run Macro *CalcuLinewidth* → record linewidth of the FID.
- Load *Fieldmap* (either *Fieldmap_rat* or *Fieldmap_mouse*) → Adjust geometry if necessary so that the object is completely enclosed by FOV → Run Macro *Mapshim*, acquire *Fieldmap*.

- Clone *PRESS-waterline* from before → press *Local* and wait for the macro to finish computing the shims → run with t.l. → run Macro *CalcuLinewidth* → record linewidth of the FID.
- Clone *PRESS-waterline* from before → run *Acq* →*current adj.* → *Method specific adjustment for the local Field Homogeneity* → run with t.l. → run Macro *CalcuLinewidth* → record linewidth of the FID

  Now you are ready to go back to the spectroscopy protocol *PRESS-1H* and either proceed with manual adjustments or use the Spectroscopy Macro (Localized_Spectroscopy_Guide).

Manual adjustment of the *PRESS-1H* protocol

- Setting parameters in *Edit Method*
  - *TR* = 2500 ms, *TE*= 6.017 ms (not editable directly)
  - *Number of averages* = 128
  - *Press*
    - ✓ *TE Calculation mode* = MinTE
    - ✓ *Spoiler Duration* should be around 1 ms.
    - ✓ *Spoiler Strength* should be no more than 37% because of Eddy currents.
  - *RF Pulses*
    - ✓ Check BW of all pulses. It should be quite big, around 11 kHz.
    - ✓ The BW of all pulses (excitation, inversion and refocusing must be the same).
    - ✓ *Mao* is a good inversion pulse. If there is not enough power, use *Hermite* pulse.
  - *Spectroscopy*
    - ✓ *Spectral Width* = 11 ppm
    - ✓ *Number of Points* = 2048
  - *Voxel Geometry*
    - ✓ Set already using Geometry Editor
    - ✓ Check that the *Spatial Shift (Fat-Water)* is less than 15% of the voxel size.
  - *Preparation*
    - ✓ WS Pulsegains Mode → Note: flip from *Manual Adjustment* to *Reference Gain* to register the gain settings from the *TriPilot* scan. Then flip back to *Manual Adjustment* because water saturation has to be adjusted manually.
    - ✓ Best water-suppression scheme is *VAPOR*.
  - *Optimize*
    - ✓ *Retro Frequency Lock* = Off
- Setting up the gain of the 90 and 180 degree pulse for water suppression
  - In the *Spectrometer Control Tool*, press on the *Lock* button on the *Transmitter Setting Channel* and then select TPQQ[4] and TPQQ[5]. TPQQ[4] is the gain of the 90 degree pulse and TPQQ[5] is the gain of 180 degree pulse for water suppression.

  - Press *SHIFT GSP* to start a continuous acquisition of the proton spectra without averaging and phase cycling.
  - Keep adjusting first TPQQ[4], and then TPQQ[5] and monitor the size of the water peak. Note: wait a few scans between each adjustment so that the equilibrium is established each time.
  - When water signal is minimal (ie., the amplitude of the noise is comparable to the water signal), then water suppression is optimized.
- Run *PRESS-1H* using t.l. to collect the spectra.

Running PRESS-1H protocol using Macro Localized_Spectroscopy_Guide

- Open the Macro manager
- Start *Localized_Spectroscopy_Guide*
- Press *Wat. Supp.* Under Adjustment.
  - Keep adjusting the *90WS Pulse* and *180WS Pulse* until water signal is as small as the noise level
  - NOTE: The macro automatically reads the initial gains obtained by TriPilot, so there is no need to flip through the *ReferenceGain* in the *Preparation* module. This procedure is only necessary for manual adjustment.
- Change *NA* to 512 (or 256)
- Select *Wat.Supp.* and deselect *Freq.Lock*, *Freq.Lock*, *Sol.Ref.*, and *Edc.Comp.*
- Press *Start*

Processing Spectrometry Data

- Right click on the collected *PRESS-1H* scan and select *Export to TOPSPIN*
- Type: LB, enter 2
- Type: efp (exponential multiplication + FT + phase-correction)
- Type: apk (automatic phase-correction)
  Note: water peak should not be phased.
- See TOPSPIN Users Guide for more detail.

Chapter 8 Chemical Shift Imaging (CSI)

General Principles

Chemical shift imaging or CSI for short is a technique that enables you to obtain a low-resolution image of certain metabolites and/or lipids in tissue.

CSI is in principle an extension of the single-voxel spectroscopy, with the addition of imaging gradients. However, since the FID signal is now binned into several voxels (instead of single one), the SNR of CSI is much poorer than for Single-voxel spectroscopy. To obtain a sufficient SNR, one therefore has to average over many acquisitions, so that total scan time can be up to 45 min. Take note of this when designing the imaging protocol for your study.

Hardware

Better to use head volume coil than brain surface coil.

Procedure

- *TriPilot*
- *TriPilot_multi*
- Same shimming protocol as described under Mapshim in Chapter 3 and under Procedure in Chapter 7.
- Load *CSI-Rat-Brain* from MIC_Rat_Head_Tumor (or *CSI-Mouse-Brain* from MIC_Mouse_head_Tumor).
- Setting parameters in *Edit Method*
  - *TR* = 1500 ms, *TE*= 16 ms
  - *Number of scans* = 1800
  - *Experimental Mode*: Weighted
  - *RF Pulses*
    - ✓ Check BW of all pulses. It should be round 2800 Hz.
    - ✓ The BW of all pulses (excitation, refocusing and 3rd pulse must be the same).
    - ✓ *Mao* is a good inversion pulse. If there is not enough power, use *Hermite* pulse.
  - *Press*
    - ✓ *TE Calculation mode* = equalize (?)
  - *Spectroscopy*
    - ✓ *Spectral Width* = 10 ppm
    - ✓ *Number of Points* = 1024
  - *Sequence Details*
    - ✓ *Minimum Echo Time* = should be as close to 10ms as possible
    - ✓ *Spoiler Duration* = 2 ms

        - ✓ *Spoiler Strength* = 57 % (why is here spoiler strength allowed to be bigger than 37% which was a recommended max for spectroscopy?)
    - *CSI Inplane Geometry*
        - ✓ *Volume Selection*: Voxel_CSI
        - ✓ *GEO Editor Show*: can flip between FieldOfView and Voxel
    - *Slice Geometry*
        - ✓ *Slice Thickness* = 2mm (for better SNR, but note a bigger partial volume effect!)
    - *Voxel Geometry*
        - ✓ Set already using Geometry Editor
        - ✓ How big can *Spatial Shift (Fat-Water)* be?
    - *Preparation*
        - ✓ WS Pulsegains Mode → Note: flip from *Manual Adjustment* to *Reference Gain* to register the gain settings from the *TriPilot* scan. Then flip back to *Manual Adjustment* because water saturation has to be adjusted manually.
        - ✓ Best water-suppression scheme is *VAPOR*.
        - ✓ *Saturation Slices* ON.
        - ✓ Will have to position saturation slices such that they suppress outer-volume signal from lipids → Procedure for positioning Sat. slices:
          Offset Sat. Slices = Voxel size/2 + Sat. Slice Package Thickness/2

- Setting up the gain of the 90 and 180 degree pulse for water suppression
    - In the *Spectrometer Control Tool*, press on the *Lock* button on the *Transmitter Setting Channel* and then select TPQQ[4] and TPQQ[5]. TPQQ[4] is the gain of the 90 degree pulse and TPQQ[5] is the gain of 180 degree pulse for water suppression.
    - Press *SHIFT GSP* to start a continuous acquisition of the proton spectra without averaging and phase cycling.
    - Keep adjusting first TPQQ[4], and then TPQQ[5] and monitor the size of the water peak. Note: wait a few scans between each adjustment so that the equilibrium is established each time.
    - When water signal is minimal (ie., the amplitude of the noise is comparable to the water signal), then water suppression is optimized.
- Run *CSI-Rat-Brain* or *CSI-Mouse-Brain* using t.l.
- Collecting a reference image for display of spectra:
    - Load *RARE-CSI-reference* (this is a regular RARE sequence)
    - Import *FOV* from *CSI* (make sure that in the CSI inplane geometry the GEO editor shows *FOV*.
    - Change slice thickness to 1mm
    - Run using t.l.

Processing CSI Images

- Use *CSI Visualization Tool*
- Load/drag CSI image and reference image into the appropriate windows
- Scroll through the image to display spectra in each voxel (?)

Chapter 9 Intragate

General Principles

Intragate is a special technique that enables one to acquire multislice cardiac images without the need for an external trigger to control data acquisition. Instead, a so-called retrospective gating technique is used. This technique collects a large number of images irrespective of the cardiac cycle and then uses a navigator to correlate the measured signal with the heart motion.

The navigator signal can be obtained from the imaging slice or from a saturation slice, which can be positioned independently of the imaging slice. Both, blackblood and bright blood contrast can be generated.

The method is particularly useful for measuring cardiac output and wall thicknesses in healthy and infarcted hearts. Due to the averaging aspect of the retrospective gating technique, it is not useful for investigations of arrhythmia.

Hardware

Use rat/mouse body coil.
Note: we have tested the 20 mm loop coil and positioned it on top of the heart, but the scan quality was poor due to the small penetration depth.

Procedure

- When creating the patient, choose the position for the animal as *prone*, not *supine*.
- *TriPilot_ig*
- *TriPilot_ig*, but this time position the 3 slices through the middle of the heart.
- *TriPilot_ig_multi*, position the slices so that they cover the entire heart.
- *IG_FLASH_cine*
  - Position slices appropriately through the apex of the heart for 4-chamber view (see pics).
  - Matrix = 320 x 320, FOV = 50 x 50 mm.
  - For better SNR, increase number of repetitions.
  - Be careful not to shorten TR too much because of duty cycle. Run Duty Cycle macro, if necessary.
- *IG_cineFLASH_blackblood*
  - Sat. slice located across top of the heart (atrium and aorta) to saturate inflowing blood → Location of navigator: In ParallelSatSlice, NexttoSlice1
  - Scheme: reverse sequential
  - Echo time = 1.487 ms, TR = 40.0 ms, NA = 100.

- *IG_cineFLASH_brightbloodInflow*
  - Sat. slice located on top of the slices to see only the inflowing blood → the flip angle of the navigator signal should be small → Location of navigator: In ParallelSatSlice, Centered →
  - Scheme:
  - Echo time = ms, TR = ms.
- *IG_cineFLASH_AllBlood*
  - Start with balckblood sequence
  - Sat. slice located in an oblique slice far away from the heart, but still in location where you have cardiac movement → the flip angle of the navigator signal should be reduced a little (but not too much, so that the navigator signal is not too small) → Location of navigator: In ObliqueSatSlice →
  - Scheme:
  - Echo time = 1.487 ms, TR = 40 ms, NA = 100.

Processing Cardiac Images

Chapter 10 Ultra Short TE (UTE)

General Principles

Ultra short TE sequence (UTE for short) is a pulse sequence with very short (on the order of 10s of us) echo times (TE). This makes it a useful method for capturing signal from short T_2 components, such as liver and lung parenchyma, tendons, ligaments and periosteum. There are two versions of UTE, a 2D and a 3D technique. Shorter echo times are achievable with the 3D sequence.

Hardware

No special hardware necessary.

Procedure

- *TriPilot* or *TriPilot_ig* for imaging moving organs, such as lungs. *TriPilot_ig* is basically a regular TriPilot with lots of averaging to remove the artifacts due to motion.
- *TriPilot_multi*
- Same shimming protocol as described under Mapshim in Chapter 3 and under Procedure in Chapter 7.
- Load *UTE_3D* from *B_TEMPLATES*
- Setting parameters in *Edit Method*
  - *TR* = 11 ms, *TE* = 13 us
  - *Number of projections* = 51360
  - *RF Pulses*
    - ✓ *Excitation Pulse Shape*: bp (Block pulse)
    - ✓ *Bandwidth*: 200 kHz (the larger the BW, the shorter the TE)
    - ✓ *Flip Angle*: can play with flip angle to manipulate contrast
  - *Sequence Details*
    - ✓ *Effective Spectral BW* < RF pulse BW, so around 100 kHz
  - *In-plane Geometry*
    - ✓ *Field of View* important to cover the entire object
    - ✓ *Matrix Size* = 128x128x128 (now, after the upgrade, we can try a bigger matrix, such as 256x256x256 since we have more memory).
  - *Preparation*
    - ✓ *Trigger Module*: Off (no need to trigger when using such a short TR).
- In order to obtain image of the short T_2 components only, do the following:
  - Run *UTE_3D* with short TE (13 us), clone, and then run again with longer TE (11 ms). Note: the image with long TE will be identical to the

one at short TE except that all the short T_2 components will be de-phased so there will be no MR signal from these components.

- Subtract the two images. The difference is image of the short T_2 components.

Processing UTE Images