



ParaVision 6.0.1

- Operating Manual

Version 001

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Contents

1 Software Manual

1.1 Distribution Documents

ParaVision contains the following Distribution documentation:

- The Distribution Note contains information and a list of changes for the ParaVision 6.0.1 distribution. It is described in chapter 1 of the PDF document [ParaVision 6.0.1 Distribution Note and Installation Guide](#).
- The Installation Guide explains the installation and the first start of ParaVision 6.0.1. It is described in chapter 2 of the PDF document [ParaVision 6.0.1 Distribution Note and Installation Guide](#).
- The Migration Guide explains the migration of a user's workplace from an older ParaVision version to version 6.0.1. It is described in chapter 3 (6.0 > 6.0.1) and chapter 4 (5.1 > 6.0.1) of the PDF document [ParaVision 6.0.1 Distribution Note and Installation Guide](#).
- Setting up the correct network configuration for ParaVision 6.0.1 is described in chapter 6.4 of the PDF document [ParaVision 6.0.1 Distribution Note and Installation Guide](#).
- The licenses of the ParaVision software including the TopSpin and Third-Party software licenses can be displayed by clicking the Help > Licenses And Copyrights menu entry in the ParaVision graphical user interface. All the licenses can be found in the installed ParaVision version directory <PvInstDir>/prog/docu/english/pvman/DistrDocs/licenses.

1.2 Examination Card

1.2.1 Overview

To plan or perform an examination the Examination Card as shown in Figure [Examination Card I ▶ 241](#) is used. It consists of four major sub-components. The Geometry Editor at the top allows to view and modify the geometry of an examination. The Slide Show below the Geometry Editor allows to preview acquired data quickly and to select images for the Geometry Editor. The Scan Program Table at the bottom left corner holds the instructions (scan, pause or contrast agent) to be executed for a study. The Parameter Editor at the bottom right corner allows to view and modify instruction parameters and instruction execution details.

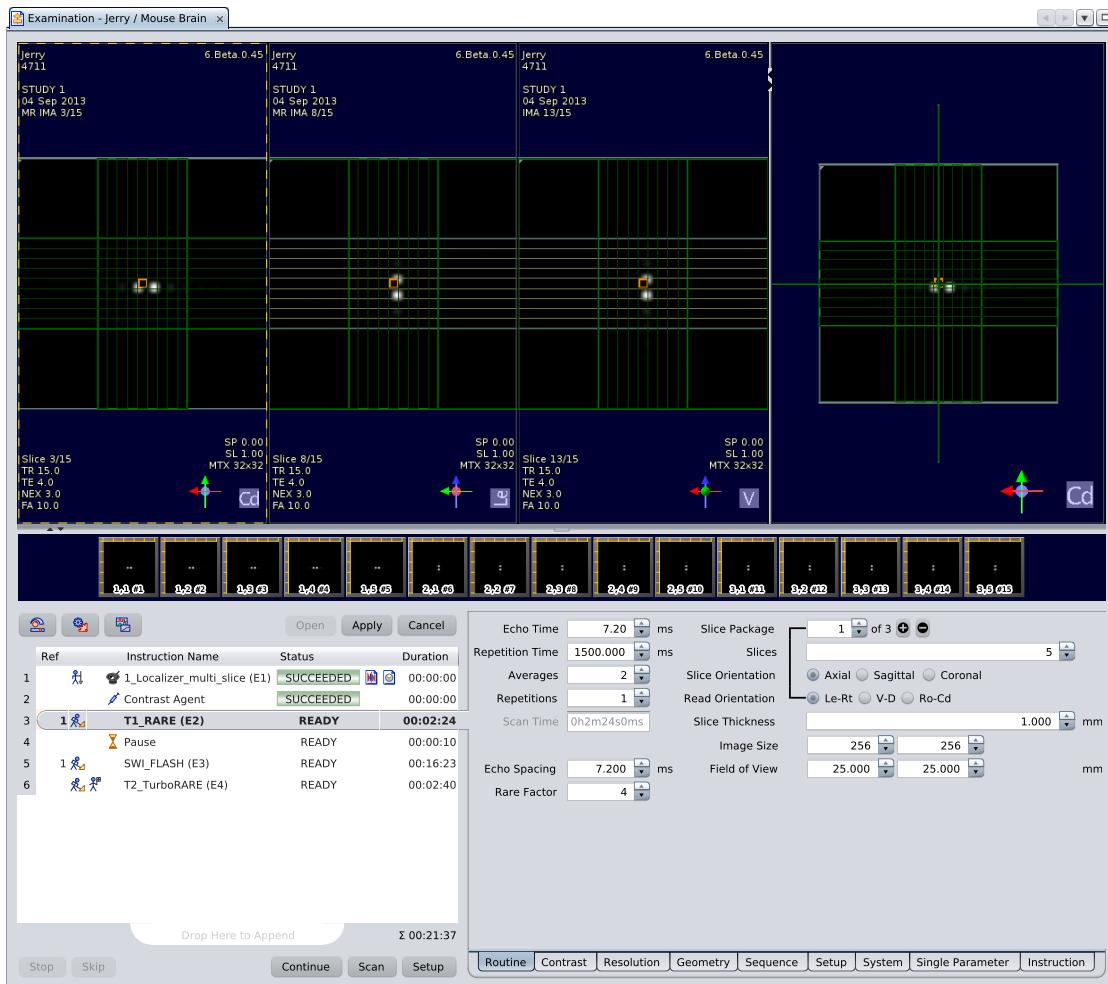


Figure 1.1: Examination Card

1.2.2 Opening the Examination Card for an Existing Study

Goal:

Plan or perform examinations on an already existing study.

- Double click the study to work on in the Workspace Explorer or Dataset Browser.
- The Examination Card is opened for the selected study.

Notice:

If the Examination Card is already open for another study an error message is shown (see Figure [Dialog Examination Card Already Open \[24\]](#)). To overcome this error close the Examination Card and try to open it again.

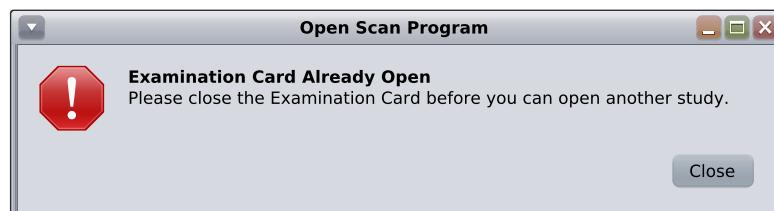


Figure 1.2: Dialog Examination Card Already Open

1.2.3 Closing the Examination Card

Goal:

Stop planning or performing examinations for the current study.

1. Click the cross on the right of the "Examination - ..." tab.
- The Examination Card is closed.

Notice:

- If the option "Window > Options > Examination > Study > Complete at Examination Card Closing" is set to "Ask" the dialog shown in Figure [Dialog Complete Study \[▶ 25\]](#) asks if the study should be completed. On completed studies normally no further examinations are possible.
- The Examination Card cannot be closed, if an acquisition is still running. An information dialog (see Figure [Dialog Examination In Progress \[▶ 25\]](#)) is shown in this case.

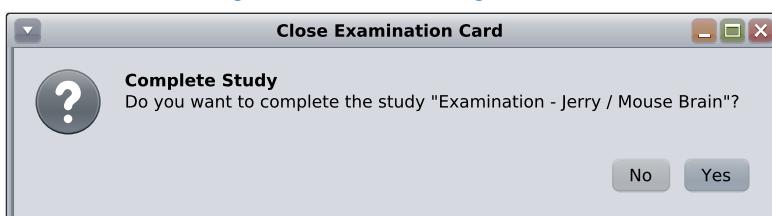


Figure 1.3: Dialog Complete Study

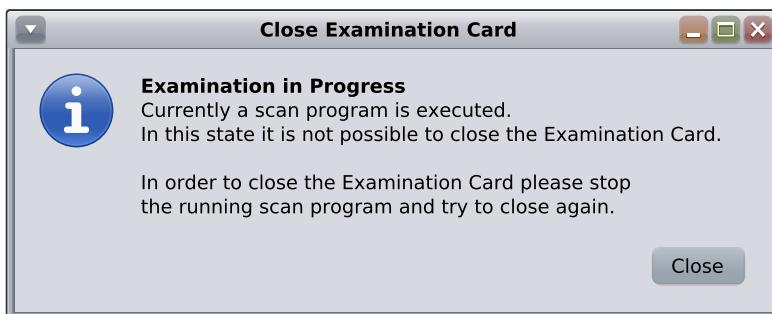


Figure 1.4: Dialog Examination In Progress

1.2.4 Using the Scan Program Table

1.2.4.1 Overview

The Scan Program Table as shown in Figure [Scan Program Table \[▶ 26\]](#) consists of:

The screenshot shows a software interface for managing a scan program. At the top, there are three icons: a wrench (Adjustment Platform), a gear (Processing Platform), and a simulation icon (Simulation Platform). To the right are buttons for "Open", "Apply", and "Cancel". Below this is a table titled "Scan Program Table". The table has columns for "Ref", "Instruction Name", "Status", and "Duration". Row 1 contains "1" and "1_Localizer_multi_slice (E1)" with a green "SUCCEEDED" status bar and a duration of "00:00:00". Row 2 contains "2" and "Contrast Agent" with a green "SUCCEEDED" status bar and a duration of "00:00:00". Row 3 contains "3" and "T1_RARE (E2)" with a yellow "READY" status bar and a duration of "00:02:24". Row 4 contains "4" and "Pause" with a yellow "READY" status bar and a duration of "00:00:10". Row 5 contains "5" and "SWI_FLASH (E3)" with a yellow "READY" status bar and a duration of "00:16:23". Row 6 contains "6" and "T2_TurboRARE (E4)" with a yellow "READY" status bar and a duration of "00:02:40". Below the table, a message says "Drop Here to Append" and shows a total duration of "Σ 00:21:37". At the bottom are buttons for "Stop", "Skip", "Continue", "Scan", and "Setup".

Ref	Instruction Name	Status	Duration
1	1_Localizer_multi_slice (E1)	SUCCEEDED	00:00:00
2	Contrast Agent	SUCCEEDED	00:00:00
3	T1_RARE (E2)	READY	00:02:24
4	Pause	READY	00:00:10
5	SWI_FLASH (E3)	READY	00:16:23
6	T2_TurboRARE (E4)	READY	00:02:40

Figure 1.5: Scan Program Table

- Some buttons in the top left giving quick access to more specialized tools (Adjustment Platform, Processing Platform, Simulation Platform)
- Some buttons in the top right allowing to work with the Parameter Editor ("Open", "Apply", "Cancel")
- Some buttons at the bottom for acquisition control ("Stop", "Skip", "Continue", "Scan", "Setup")
- A table in the center holding the instructions to be executed for a study. The instructions will be executed in the order they are listed in the table (top to bottom). Icons in the table together with tooltips and progress indicators provide status information in a compact manner. The table consists of the following 9 columns:
 - The "Ref" column indicates so called copy references. A number in this column defines the row number from which user selected groups of parameters (Parameter Groups) are copied each time the source scan instruction is modified. In the example shown in Figure [Scan Program Table \[▶ 26\]](#) the instructions in row 3 and 5 (T1_RARE and SWI_FLASH) inherit one or more Parameter Groups from the instruction in row 1 (1_Localizer_multi_slice).
 - The second column may contain icons showing the parametrization status of an instruction.
 - Indicates that the scan instruction has to be parameterized before it can be executed.
 - Indicates that the scan instruction needed parametrization which had been done already.
 - The icon in the third column indicates that the scan instruction has to be started explicitly by the operator. In rows marked with this icon the scan program execution stops until the operator resumes the execution by clicking the "Continue" button.
 - The fourth column may contain icons which indicate special types of instructions.

 Indicates a contrast agent instruction. A contrast agent instruction delays scan program execution for a user defined amount of time, then shows a dialog instructing the operator to administer the contrast agent and close the dialog after the contrast agent has been administered. After the dialog has been closed another user defined delay is performed.

 Indicates a pause instruction. A pause instruction delays scan program execution for a user defined amount of time.

 Marks scan instructions which perform some additional processings or activities. Processings create additional image series while activities do something with existing datasets.

5. The "Instruction Name" column shows the name of the instructions. By default instruction names are derived from the method or protocol name.
6. The "Status" column informs about the status of an instruction. Some instruction statuses are final and will remain after the system has come to rest. Some may only be visible for a short time or not at all (depending on the performance of the workstation).

ABORTED	The instruction execution was interrupted by the user and all cleanup procedures are finished.
ADJUST	An adjustment procedure is running.
ADJUSTED	An adjustment procedure is finished.
FAILED	Scan execution has failed. Data was not successfully acquired.
GSP	A setup pipeline is running.
INTERRUPTED	The instruction was interrupted by the user but not all cleanup procedures are finished yet.
NEW	The instruction is created but not yet initialized.
READY	The instruction is prepared for execution.
RECO	Acquired data is reconstructed.
SCANNING	The data acquisition is running.
SCHEDULED	The instruction execution is queued for execution, but execution has not yet started.
SKIPPED	The instruction was skipped.
SLEEPING	The status of pause or contrast agent instructions while executing the user defined delays.
STOPPED	A setup pipeline was interrupted by the user.
SUCCEEDED	The instruction was successfully executed.

The status string is printed above a three-part progress indicator. The bottom indicator rendered with the lightest color represents the adjustment progress. The middle indicator rendered with a darker color represents the acquisition progress. The indicator at the top rendered with the darkest color represents the progress of the online reconstruction.

7.  The icon in the seventh column marks if acquisition data is available for the scan instruction.
8. Different icons in the eighth column indicate the availability of reconstructed data.
 -  1D image data.
 -  2D image data.
 -  3D image data.
 -  1D spectroscopic data.
 -  2D spectroscopic data.
 -  Data containing spatial and spectroscopic components.
9. The "Duration" column shows the estimated time an instruction will still need to execute. For scan instructions the duration does not contain the time needed for dummy scans.

1.2.4.2 Adding a Scan Instruction

To execute an acquisition a scan instruction is needed. Methods, protocols or scan programs may be added.

Goal:

Execute an acquisition.

1. Select the scan instruction (method/protocol/scan program) to be executed in the Workspace Explorer or the Palette Explorer, drag it into the Scan Program Table and drop it at the desired location.
 - The scan instruction is appended/inserted at the desired location.

Notice:

- Some drop locations may be forbidden (visualized by a special mouse cursor) since new scan instructions must not be inserted above scans which already have been measured.
- Scan instructions may also be dropped from the Dataset Browser on the tab of the Examination Card. In this case the instructions are always appended to the scan program.
- Instructions may also be dropped on the white area (labeled "Drop Here to Append") below the table which allows to append new instructions easily, if empty lines as drop locations are no longer available.

1.2.4.3 Changing the Execution Order

Instructions in the Scan Program Table are always executed consecutively from top to bottom. In order to change the execution order instructions may be moved by drag and drop.

Goal:

Change the order in which instructions are executed.

1. Select the instruction to be moved.
 - The instruction is highlighted.

2. Drag the instruction to the new location and drop it. Invalid drop locations will be visualized by a special mouse cursor.
 - The instruction will be moved from the old location to the new location. In doing so gaps in the scan program will be closed by instructions from below and instructions in the way will be shifted downward.

Notice:

- Only READY instructions can be moved.
- Instructions can only be dropped below non-READY instructions.

1.2.4.4 Duplicating an Instruction**Goal:**

Create an exact clone of an already existing instruction.

1. Select the instruction to be duplicated.
 - The instruction is highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 29\]](#)) and invoke "Duplicate Instruction" or type Ctrl+D on the keyboard.
 - A duplicate of the selected instruction is added below the selected instruction and below all non-READY instructions.

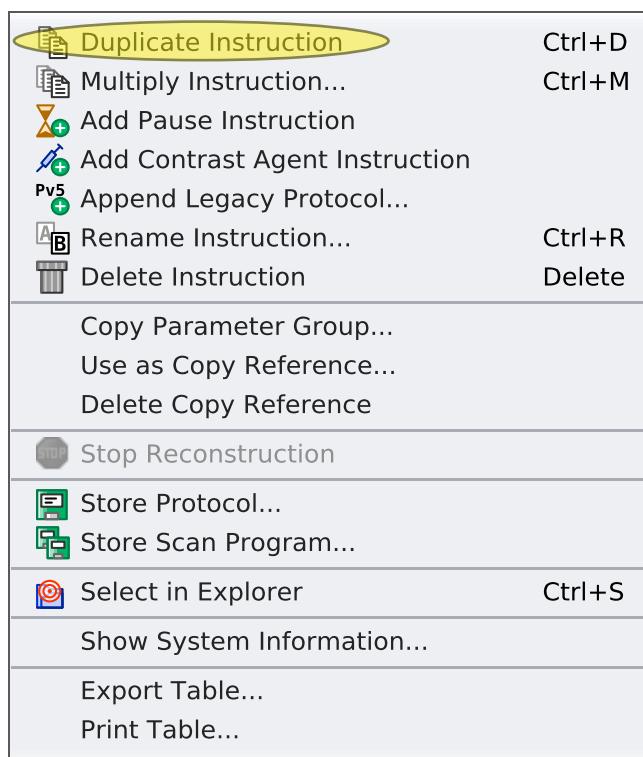


Figure 1.6: Context Menu Examination Card

1.2.4.5 Multiplying an Instruction**Goal:**

Create one or more scan instructions (based on a selected source scan instruction) where one or more parameters are changed in each copy.

1. Select the scan instruction to be multiplied.
 - The instruction is highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 30\]](#)) and invoke "Multiply Instruction".
 - A dialog is opened (see Figure [Dialog Multiply Instruction \[▶ 31\]](#)) allowing to specify the intended parameter variations (see Chapter [Using the Multiply Instruction Dialog \[▶ 31\]](#)). When the "OK" button is clicked, the dialog is closed, the parameter specifications are evaluated and the new scan instructions are appended to the current scan program.

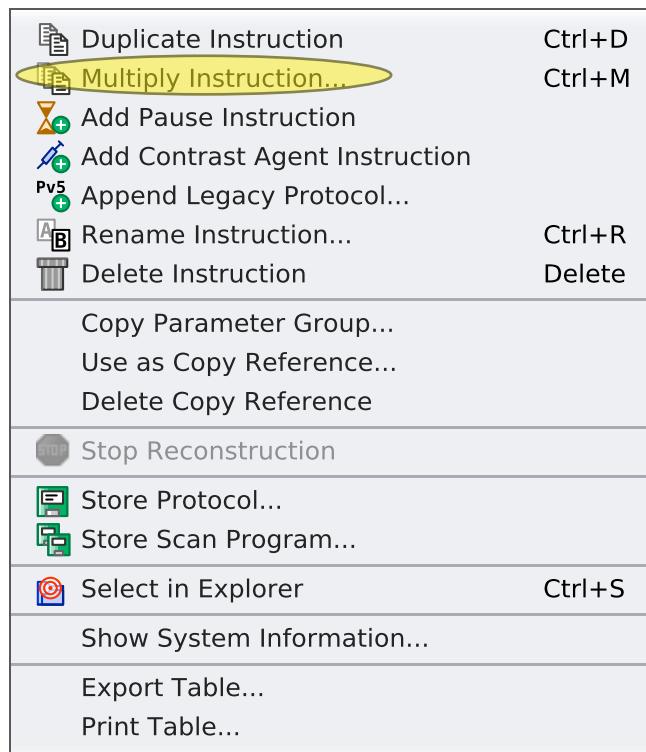


Figure 1.7: Context Menu Examination Card



Figure 1.8: Dialog Multiply Instruction

Notice:

- Like "Duplicate Instruction" (see Chapter [Duplicating an Instruction ▶ 29](#)) "Multiply Instruction" will produce clones of the selected source scan instruction (except for the parameters to be changed in the copies). It is therefore necessary to fully parametrize the source scan instruction (i.e. set all desired parameter values, select prototype mode if base-level parameters should be modified for the copies (see Chapter [Working in Prototype Mode ▶ 64](#)), define processings and activities etc.) before "Multiply Instruction" is invoked.
- When the new scan instructions are created and the specified parameter values are set, it may happen that a desired parameter value cannot be set due to parameter constraints defined by the acquisition method. If this happens a warning message will be logged for the scan instruction (noticeable by a blinking warning icon  in the menu bar) recording which parameter failed to reach its requested value and which value was actually achieved.

1.2.4.5.1 Using the Multiply Instruction Dialog

The main usage of the "Multiply Instruction Dialog" (see Figure [Dialog Multiply Instruction ▶ 31](#)) is to enter/select parameter names and to enter value specifications defining which values should be used for a selected parameter in each of the scans to be created.

The main part of the dialog therefore consists of one or more rows. In each row there is a select button  on the left, followed by two text fields, followed by an add , delete  and preview button  on the right. Each row allows to define one parameter and its value specification.

To define parameters and value specifications the following workflow is recommended:

1. Enter or select the parameter name (see Chapter [Entering>Selecting a Parameter Name ▶ 32](#)).
2. Enter the value specification (see Chapter [Entering a Value Specification ▶ 33](#)).

3. Preview the parameter values resulting from the value specification (see Chapter [Previewing Parameter Values \[35\]](#)).
4. Add a new row for the next parameter if desired (see Chapter [Adding a New Parameter and Value Specification \[36\]](#)).
5. Select the expansion rule (see Chapter [Selecting the Expansion Rule \[37\]](#)).
6. Preview all parameter values resulting from all specifications and the expansion rule (see Chapter [Previewing all Parameter Values \[39\]](#)).
7. Click "OK" to start the creation of the new scan instructions.



Figure 1.9: Dialog Multiply Instruction

Notice:

It is important to remember that changing a parameter value may change other parameters as well due to parameter relations or constraints. The order of the parameter/value specifications is therefore significant (they are applied from top to bottom). Changing the order in which parameters are set will in general not lead to an identical set of parameter values.

1.2.4.5.2 Entering>Selecting a Parameter Name

The multiply instruction dialog only allows to specify values for scalar numeric parameters. It is therefore necessary to enter/select so called fully qualified parameter names (i.e. names which contain array indices or structure members so that the entire expression specifies a simple number).

Goal:

Define a name of a fully qualified numeric parameter.

1. Enter the fully qualified numeric parameter name in the first text field (shortcut for experts) or click the select button to open a selection dialog.

- The selection dialog is opened (see Figure [Dialog Select Qualified Parameter Name \[33\]](#)).
2. In the left "Parameters" column select the desired parameter name from the list (the "Starts With", "Contains" and "Ends With" text fields below the list allow to filter the listed names in order to reduce their number).
 3. In case the selected parameter has a more complex layout (e.g. array or structure) the middle "Qualifications" column will offer all possible qualifications (the "Starts With", "Contains" and "Ends With" text fields below the list again will allow to filter the listed names). The right "Value/Type" column shows the current parameter value (and type) in the source scan.
 4. Click "OK" to choose the selected parameter and close the dialog.
 - The selection dialog is closed and the selected parameter name and its qualification (if present) is copied into the text field to the right of the select button.

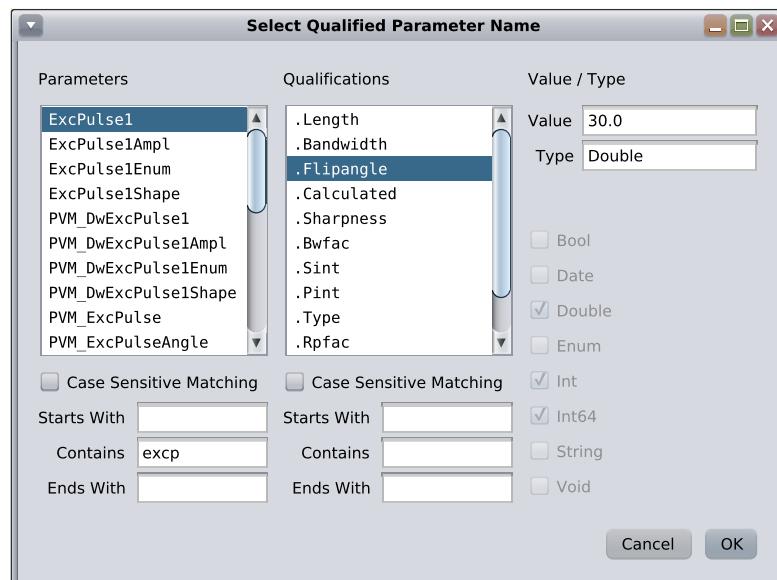


Figure 1.10: Dialog Select Qualified Parameter Name

1.2.4.5.3 Entering a Value Specification

Goal:

Define which values will be used for the selected parameter in each new scan.

1. Enter the value specification using one of the three supported formats described below.

List of comma separated values

Format <number>, <number>, <number>, ...

Example 10.0, 20.0, 30.0

Description The values are taken as entered from the left to the right. Rational numbers use a '.' as decimal separator.

Loop specification with constant increment

Format	[start] : <inc> : [end]
Example	1000:100:2000
Description	A loop creating new values is defined by a start value, an increment and an end value. If the start value or the end value (not both) is omitted the start/end value is replaced by the parameter value of the source scan.

Expression

Format	<loops> # <f(\$p,\$i)>
Example	10#\$p + \$i * 20 5#\$p * Math.pow(2,\$i) 8#100 * Math.sin(\$i * 2 * Math.PI / 8)
Description	An expression specification starts with the number of times the expression is evaluated. A '#' is used to separate the number of repetitions from the expression. The expression itself is an arbitrary function of two variables "\$p" and "\$i". When the expression is evaluated the variable "\$p" is replaced by the value of the parameter in the source scan and the variable "\$i" is replaced by the current loop index (from 1 to the number of repetitions entered before the '#' character). Beside the basic arithmetic operations "+", "-", "*", "/" and braces "(", ")" to change the evaluation order, expressions may also use the constants "Math.PI" (3.141...) and "Math.E" (2.718...) as well as the following elementary functions.
Math.exp(a)	Returns Euler's number e raised to the power of a given value
Math.pow(a,b)	Returns the value of the first argument raised to the power of the second argument
Math.log(a)	Returns the natural logarithm (base e) of the given value
Math.log10(a)	Returns the base 10 logarithm of the given value
Math.sqrt(a)	Returns the positive square root of a value
Math.cbrt(a)	Returns the cube root of a value
Math.sin(a)	Returns the trigonometric sine of an angle (in radians)
Math.asin(a)	Returns the arc sine of a value; the returned angle is in the range -PI/2 through PI/2
Math.sinh(a)	Returns the hyperbolic sine of a value
Math.cos(a)	Returns the trigonometric cosine of an angle (in radians)
Math.acos(a)	Returns the arc cosine of a value; the returned angle is in the range 0.0 through PI.

<code>Math.cosh (a)</code>	Returns the hyperbolic cosine of a value
<code>Math.tan (a)</code>	Returns the trigonometric tangent of an angle (in radians)
<code>Math.atan (a)</code>	Returns the arc tangent of a value; the returned angle is in the range -PI/2 through PI/2
<code>Math.tanh (a)</code>	Returns the hyperbolic tangent of a value

and the following helper functions:

<code>Math.abs (a)</code>	Returns the absolute value of a given value
<code>Math.ceil (a)</code>	Returns the smallest (closest to negative infinity) value that is greater than or equal to the argument and is equal to a mathematical integer
<code>Math.floor (a)</code>	Returns the largest (closest to positive infinity) value that is less than or equal to the argument and is equal to a mathematical integer
<code>Math.max (a, b)</code>	Returns the greater of two given values
<code>Math.min (a, b)</code>	Returns the smaller of two given values
<code>Math.random ()</code>	Returns a random value with a positive sign, greater than or equal to 0.0 and less than 1.0
<code>Math.toDegrees (a)</code>	Converts an angle measured in radians to an approximately equivalent angle measured in degrees
<code>Math.toRadians (a)</code>	Converts an angle measured in degrees to an approximately equivalent angle measured in radians

1.2.4.5.4 Previewing Parameter Values

Goal:

Get an overview which parameter values will be created by a given value specification.

1. Click the preview button .

► A "Parameter Preview" dialog as shown in Figure [Dialog Parameter Preview \[36\]](#) will be opened. The preview shows all parameter values resulting from the provided value specification. For a comma separated list these are simply the entered values. For a loop or an expression specification the values are calculated from the specification.

2. Click "Close" to close the dialog.

► The preview dialog is closed.

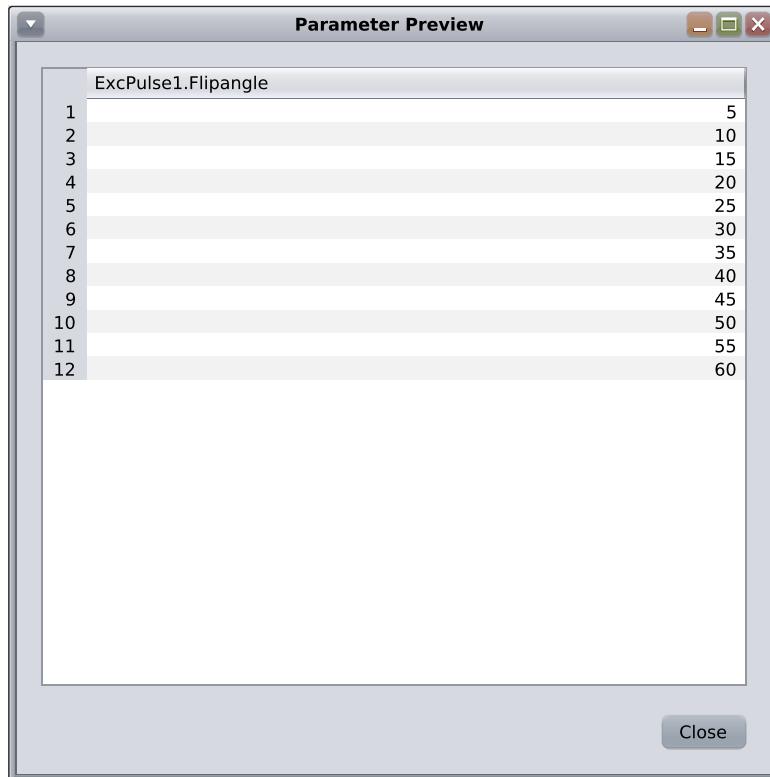


Figure 1.11: Dialog Parameter Preview

1.2.4.5.5 Adding a New Parameter and Value Specification

Goal:

Add a new row allowing to enter another parameter and value specification.

1. Click the add button .
- The new empty row is inserted at the location the add button was clicked. If the add button in the last row was clicked a new empty row is appended at the end. If the add button was clicked on another row this row (and all subsequent rows) is shifted downwards and the new row is inserted at the location the add button was clicked.

1.2.4.5.6 Deleting a Parameter and Value Specification

Goal:

Remove a parameter and its value specification from the "Multiply Instruction" dialog.

1. Click the delete button  in the row to be deleted.
- If the row is empty it is deleted without further inquiry. If it is not empty a confirmation dialog is shown and the row is only deleted if the user gives the permission.

1.2.4.5.7 Deleting all Parameters and Value Specifications**Goal:**

Remove all parameters and their value specifications from the "Multiply Instruction" dialog.

1. Click the delete all button  in the last row.

► A confirmation dialog is shown and all rows are deleted if the user gives the permission.

1.2.4.5.8 Selecting the Expansion Rule**Goal:**

Determine how parameter values are combined if more than one parameter/value specification has been given.

1. Select one of the following items from the "Expansion Rule" combo box.

► The selected expansion rule is used for previewing all parameters and for creating new scans.

Coupled Indices	For each given parameter/value specification a list of candidate values is created. For each new scan the next parameter is taken from each list. Creating new scans stops if one of the lists does not provide further values (see Figure Example - Coupled Indices [▶ 38] for an example).
All Combinations	New scans are created for all possible parameter value combinations (see Figure Example - All Combinations [▶ 39] for an example).

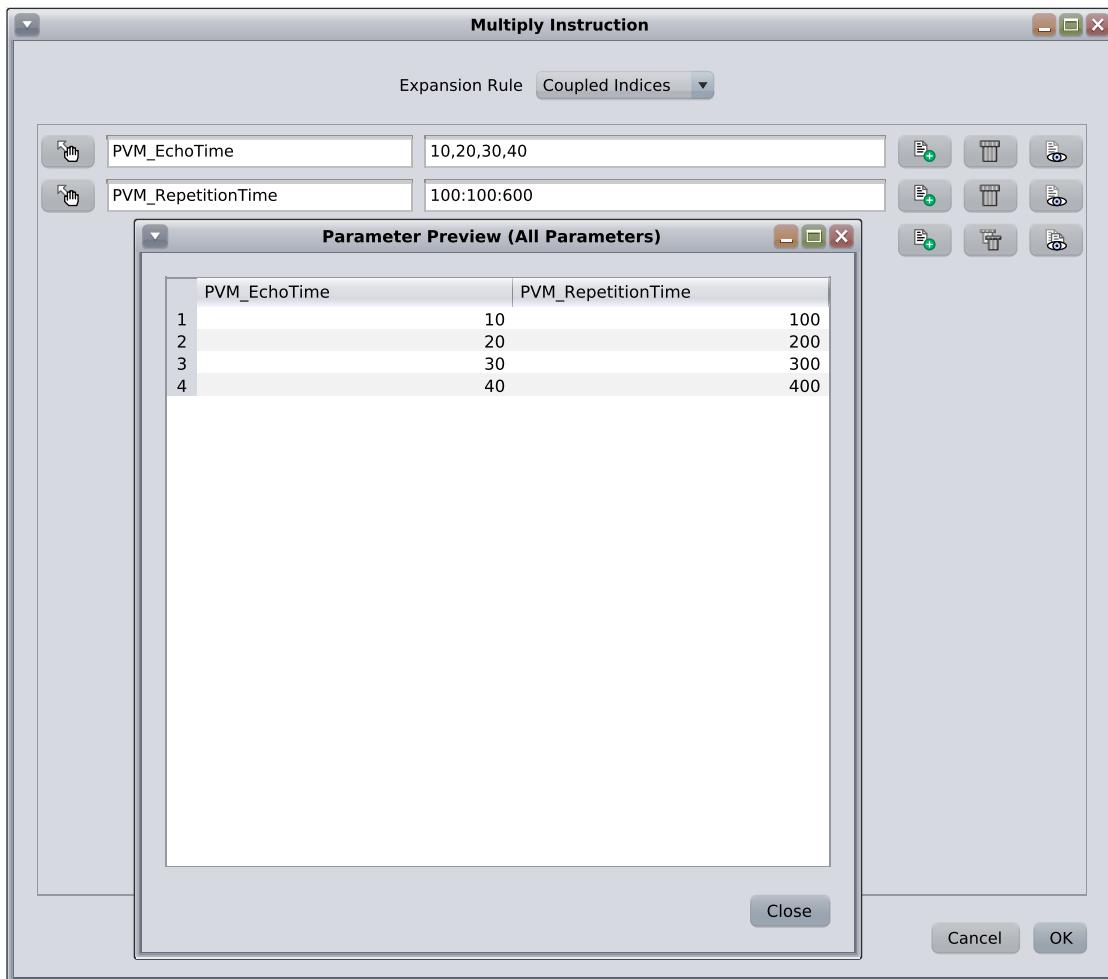


Figure 1.12: Example - Coupled Indices

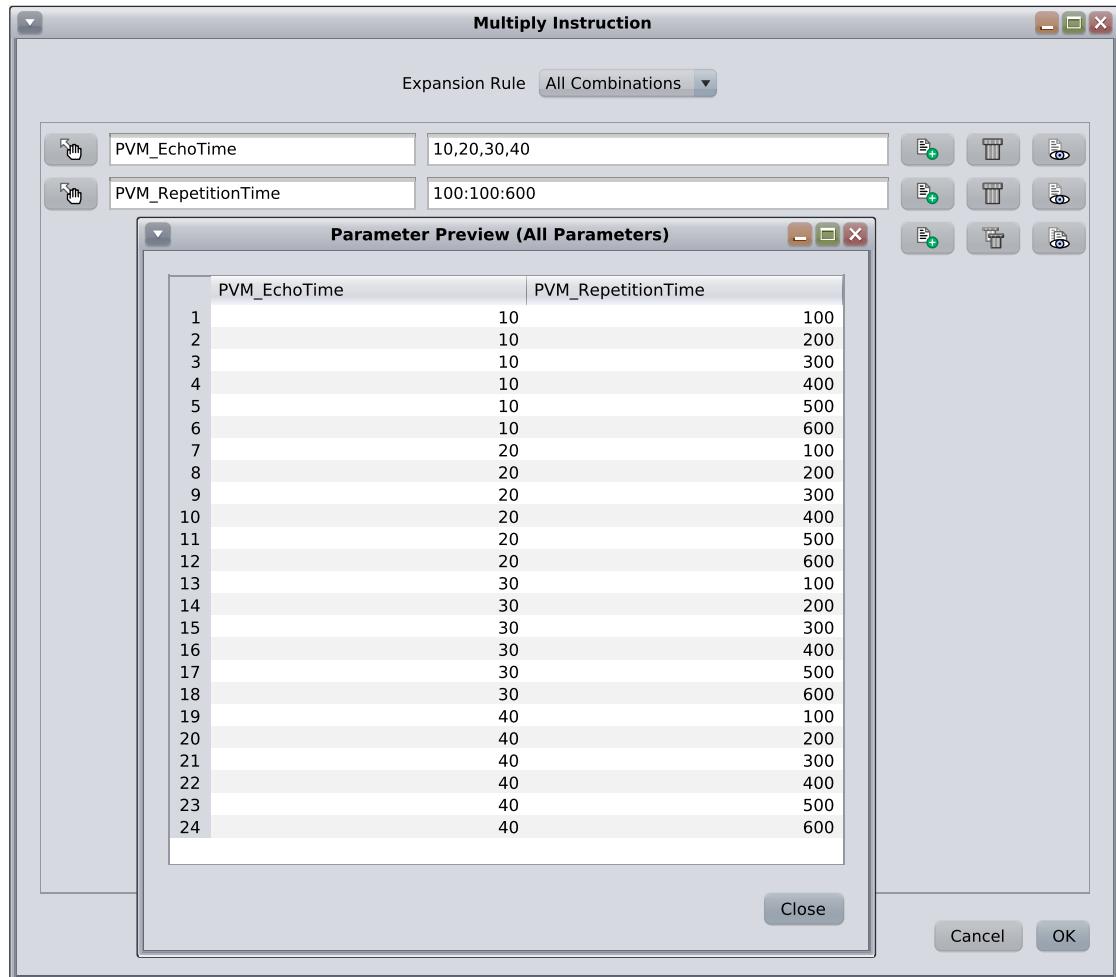


Figure 1.13: Example - All Combinations

Notice:

When using "All Combinations" a huge number of scans can result from even "small" parameter/value specifications. Creating (and later on scanning) a huge number of scans may need a considerable amount of time.

1.2.4.5.9 Previewing all Parameter Values

Goal:

Get an overview which parameter combinations will be used for the scans.

1. Click the preview all button .

- The "Parameter Preview (All Parameters)" dialog (see Figure [Parameter Preview \(All Parameters\) \[40\]](#)) is opened showing all parameter values like they will be used for creating new scans.

	PVM_EchoTime	PVM_RepetitionTime
1	10	100
2	10	200
3	10	300
4	10	400
5	10	500
6	10	600
7	20	100
8	20	200
9	20	300
10	20	400
11	20	500
12	20	600
13	30	100
14	30	200
15	30	300
16	30	400
17	30	500
18	30	600
19	40	100
20	40	200
21	40	300
22	40	400
23	40	500
24	40	600

Figure 1.14: Parameter Preview (All Parameters)

Notice:

This action is only needed if more than one parameter/value specification has been entered.

1.2.4.6 Adding a Pause Instruction

Goal:

Insert an instruction into the scan program which consumes a configurable amount of time.

1. Select the instruction at whose position the pause instruction should be inserted.
 - The instruction is highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 41\]](#)) and invoke "Add Pause Instruction".
 - A pause instruction is inserted at the selected position. The selected instruction and all instructions below are shifted downward one position.

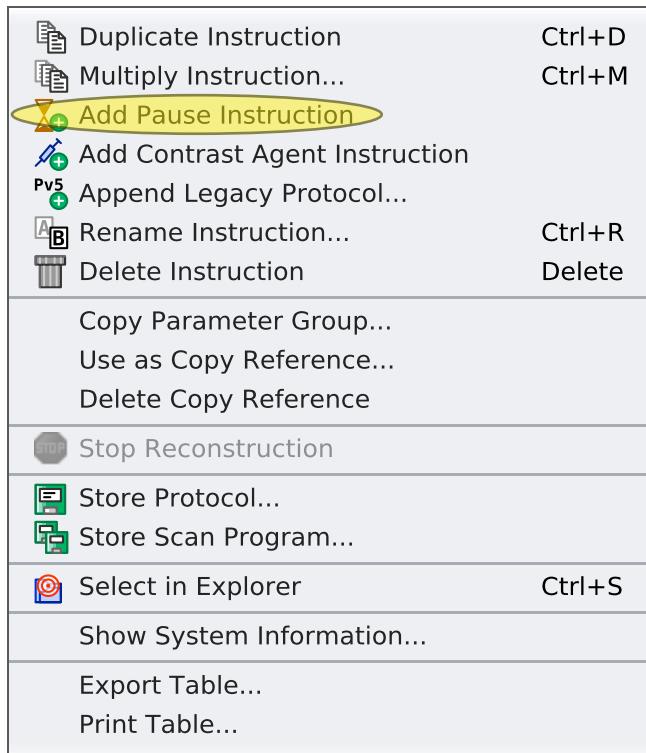


Figure 1.15: Context Menu Examination Card

Notice:

If "Add Pause Instruction" is invoked without a selected instruction, the pause instruction is appended below the last instruction.

1.2.4.7 Adding a Contrast Agent Instruction

Goal:

Insert an instruction into the scan program for contrast agent administration.

1. Select the instruction at whose position the contrast agent instruction should be inserted.
 - The instruction is highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 42\]](#)) and invoke "Add Contrast Agent Instruction".
 - A contrast agent instruction is inserted at the selected position. The selected instruction and all instructions below are shifted downward one position.

Notice:

When executed the contrast agent instruction performs the following operations:

- Count down a configurable amount of time.
- Open a dialog telling the operator to administer the contrast agent now and to close the dialog when contrast agent administration is finished.
- Count down another configurable amount of time after the dialog has been closed.

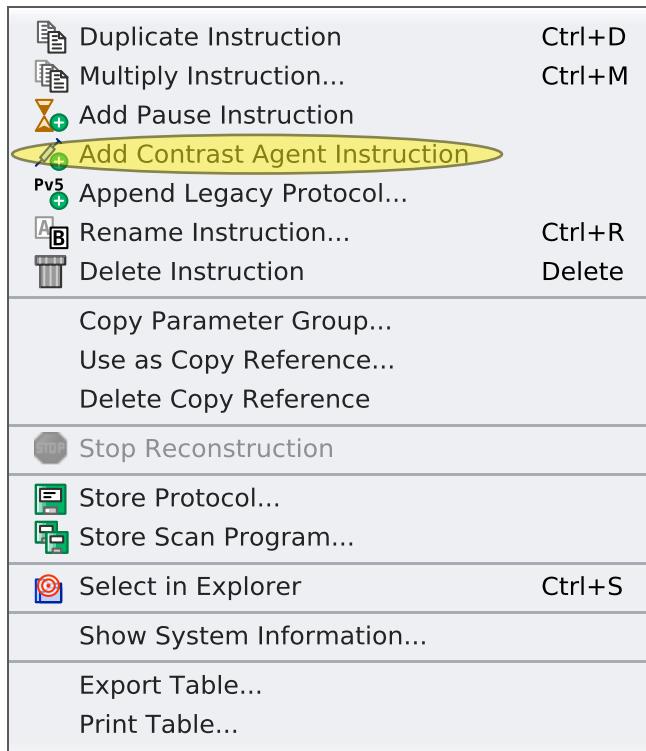


Figure 1.16: Context Menu Examination Card

Notice:

If "Add Contrast Agent Instruction" is invoked without a selected instruction, the contrast agent instruction is appended below the last instruction.

1.2.4.8 Appending a Pre-ParaVision 6 Protocol

Goal:

Use a legacy (pre-ParaVision 6) protocol in ParaVision 6.

1. Open the context menu (see Figure [Context Menu Examination Card \[▶ 43\]](#)) and invoke "Append Legacy Protocol...".
- A file selection dialog (see Figure [Dialog File Selection \[▶ 43\]](#)) is opened allowing the operator to select the protocol file. When the "Open" button is clicked, the dialog is closed and the selected protocol is appended to the scan program.

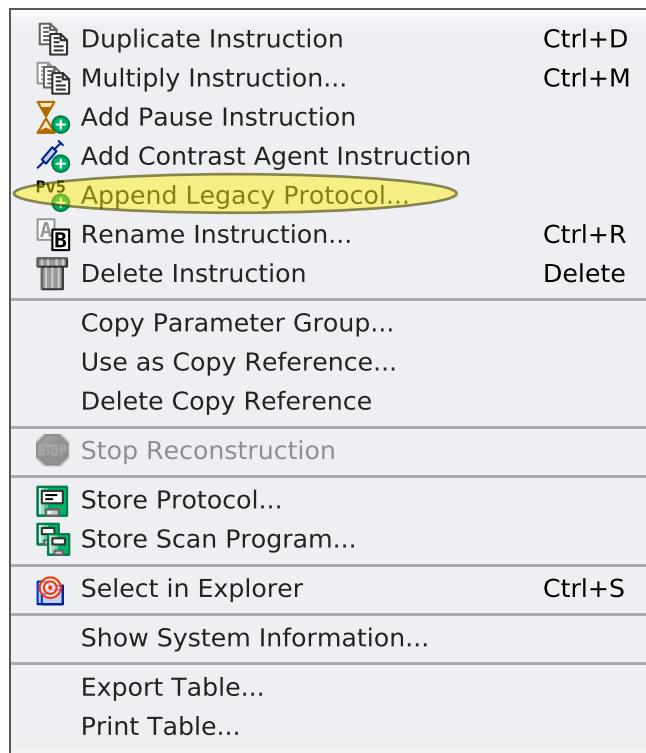


Figure 1.17: Context Menu Examination Card

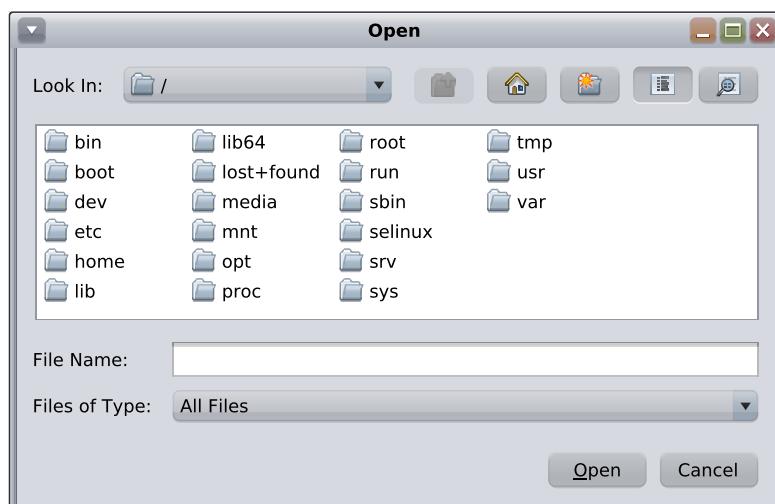


Figure 1.18: Dialog File Selection

Notice:

- A legacy protocol may also be inserted in the current scan program by dragging a protocol from a file browser of the operating system into the scan program.
- Since the methods have been changed for the new software version it cannot be guaranteed that legacy protocols will show the same results (contrast etc.) as in older versions.

1.2.4.9 Renaming an Instruction

Goal:

Give an instruction a different name than the one provided by default.

1. Select the instruction whose name should be changed.
 - The instruction is highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 44\]](#)) and invoke "Rename Instruction..." or type Ctrl+R on the keyboard.
 - A dialog (see Figure [Dialog Rename Instruction \[▶ 44\]](#)) is opened allowing the operator to enter a new name. When the "OK" button is clicked, the dialog is closed and the new name is set.

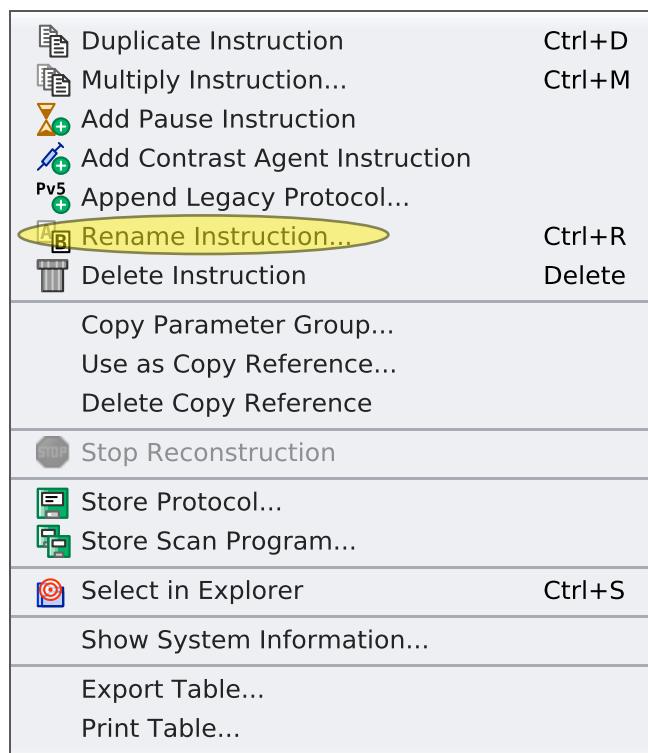


Figure 1.19: Context Menu Examination Card

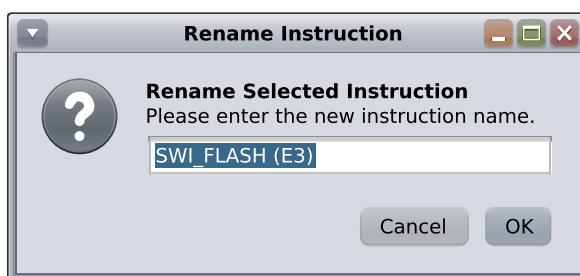


Figure 1.20: Dialog Rename Instruction

1.2.4.10 Deleting an Instruction

Goal:

Delete an instruction which is no longer needed or desired.

1. Select the instruction(s) to be deleted.
 - The instruction(s) is/are highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card ▶ 451](#)) and invoke "Delete Instruction" or use the Delete key on the keyboard.
 - The selected instruction(s) is/are deleted if data has not yet been acquired for the selected instruction(s). If acquired data is available for at least one instruction, a confirmation dialog (see Figure [Dialog: Delete Instruction Confirmation ▶ 451](#)) is shown. The instruction(s) is/are deleted only if the delete operation is confirmed by the operator.

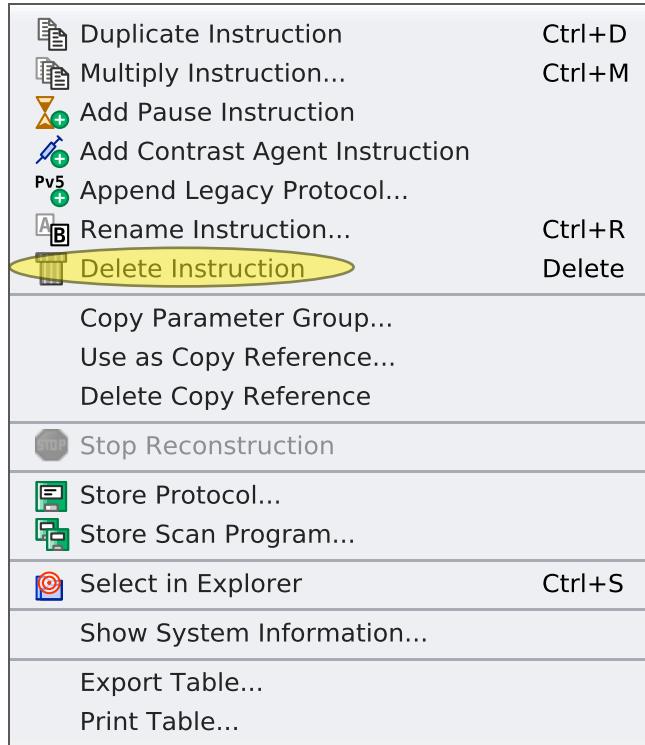


Figure 1.21: Context Menu Examination Card

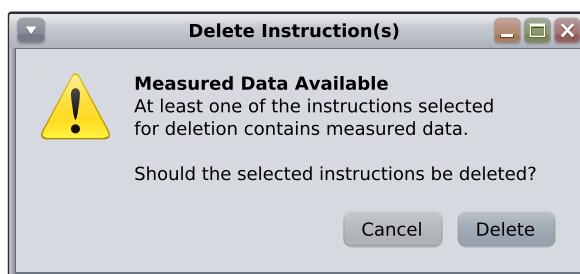


Figure 1.22: Dialog Delete Instruction Confirmation

1.2.4.11 Copying a Parameter Group

Goal:

Immediately copy a group of parameters (e.g. slice geometry) from one scan instruction into other scan instructions.

1. Select the scan instruction from which the parameter values should be taken.
 - The scan instruction is highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 46\]](#)) and invoke "Copy Parameter Group...".
 - A dialog (see Figure [Dialog Copy Parameter Group \[▶ 46\]](#)) is opened allowing the operator to select the destination instruction(s) (which should receive the parameters) and the parameter group to be copied. Clicking "OK" will immediately perform the copy operation.

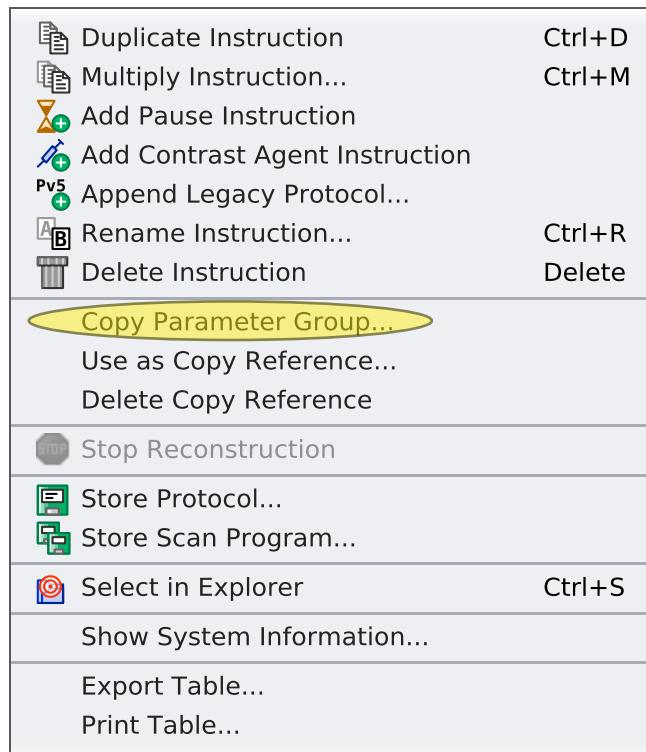


Figure 1.23: Context Menu Examination Card

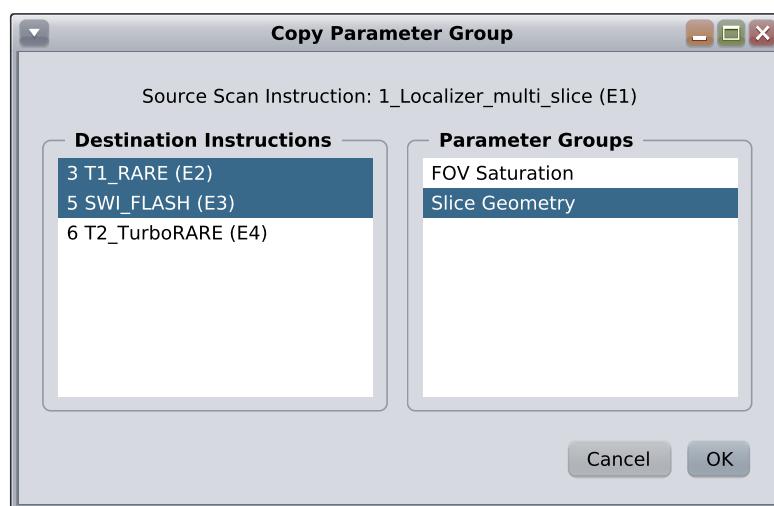


Figure 1.24: Dialog Copy Parameter Group

Notice:

The available parameter groups will depend on the source scan instruction and the selected destination scan instructions.

1.2.4.12 Using a Scan Instruction as Copy Reference

Goal:

Register a scan instruction as the source of a parameter group (e.g. slice geometry) which will be copied into a destination scan instruction every time parameters of the selected parameter group are changed in the instruction registered as a copy reference.

1. Select the scan instruction (copy reference) from which the parameter values should be taken.
 - The scan instruction is highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 47\]](#)) and invoke "Use as Copy Reference...".
 - A dialog (see Figure [Dialog Set Copy Reference \[▶ 48\]](#)) is opened allowing the operator to select the destination instruction(s) (which should receive the parameters) and the parameter group to be copied each time parameters from the selected parameter group are changed in the source instruction. Click "OK" to mark the destination instructions.
 - The destination scan instructions are marked in the "Ref" column with the row index of the source instruction (copy reference).

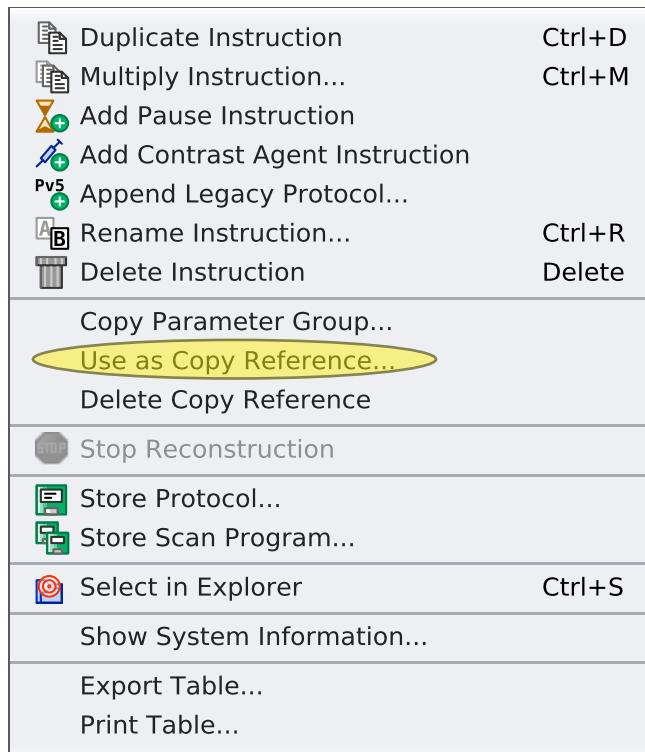


Figure 1.25: Context Menu Examination Card

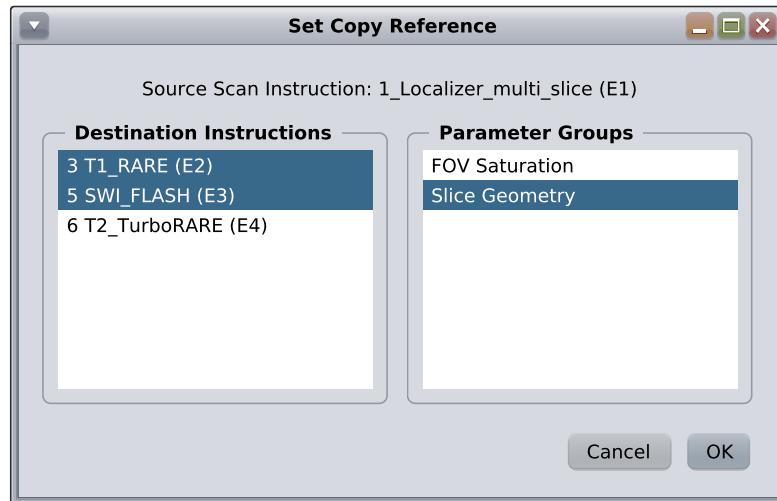


Figure 1.26: Dialog Set Copy Reference

Notice:

- A destination instruction will lose its destination status (indicated by removal of the number in the "Ref" column) if a parameter from the selected parameter group is changed by the operator.
- The available parameter groups will depend on the source scan instruction and the selected destination scan instructions.

1.2.4.13 Deleting a Copy Reference

Goal:

Ensure that a scan instruction no longer receives parameter updates from its copy reference.

1. Select the scan instruction(s) (with a number in its/their "Ref" column) which should lose its/their destination status.
 - The instruction(s) is/are highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 49\]](#)) and invoke "Delete Copy Reference".
 - The number in the "Ref" column is removed. The instruction will no longer receive updates from its former copy reference.

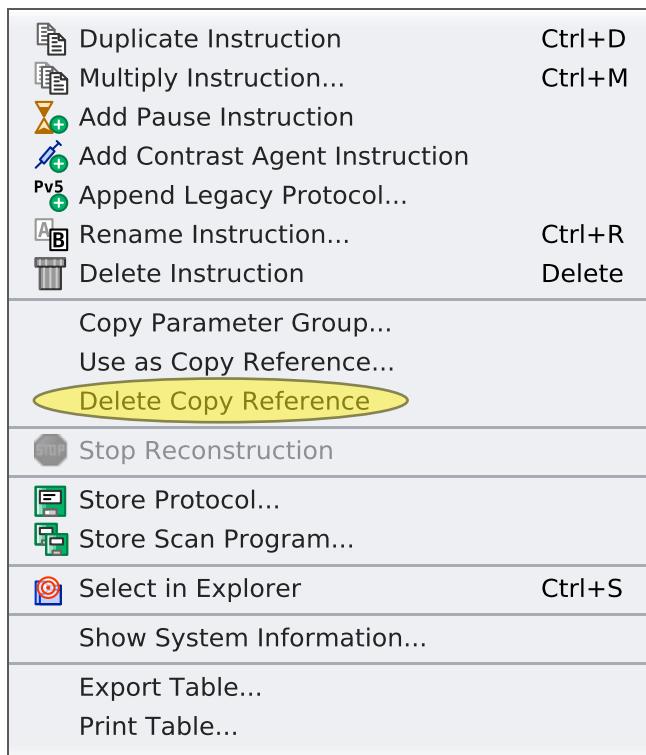


Figure 1.27: Context Menu Examination Card

1.2.4.14 Stopping a Data Reconstruction

Goal:

Stop a data reconstruction still running on a scan instruction.

1. Select the scan instruction for which a running data reconstruction should be stopped.
 - The scan instruction is highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 50\]](#)) and invoke "Stop Reconstruction".
 - The data reconstruction is stopped.

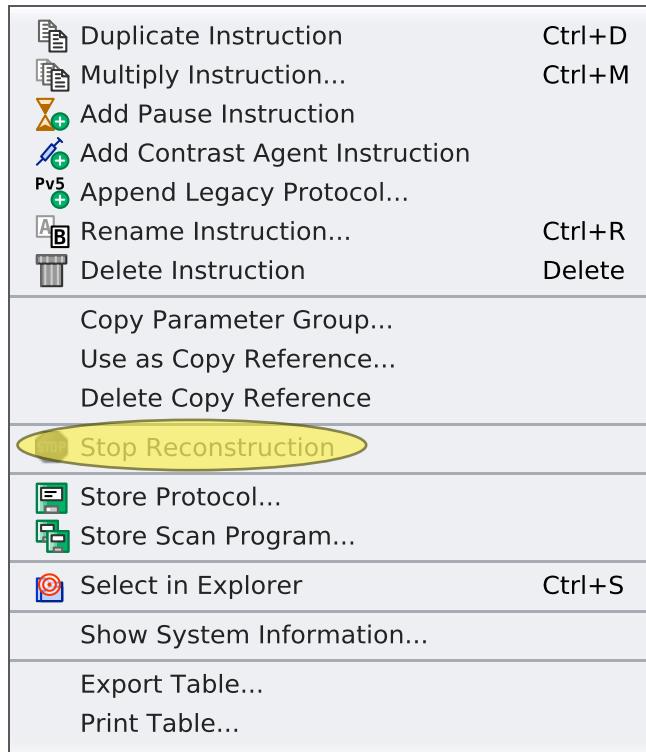


Figure 1.28: Context Menu Examination Card

1.2.4.15 Storing a Protocol

Goal:

Reuse a scan instruction with its current parametrization in other studies.

1. Select the scan instruction to be stored as a protocol.
 - The scan instruction is highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 51\]](#)) and invoke "Store Protocol...".
 - A dialog (see Figure [Dialog Store Protocol \[▶ 51\]](#)) is opened allowing the operator to enter a protocol name and select/enter an object, region and application under which the protocol should be stored. When the "Store" button is clicked, the dialog is closed and the protocol is stored.

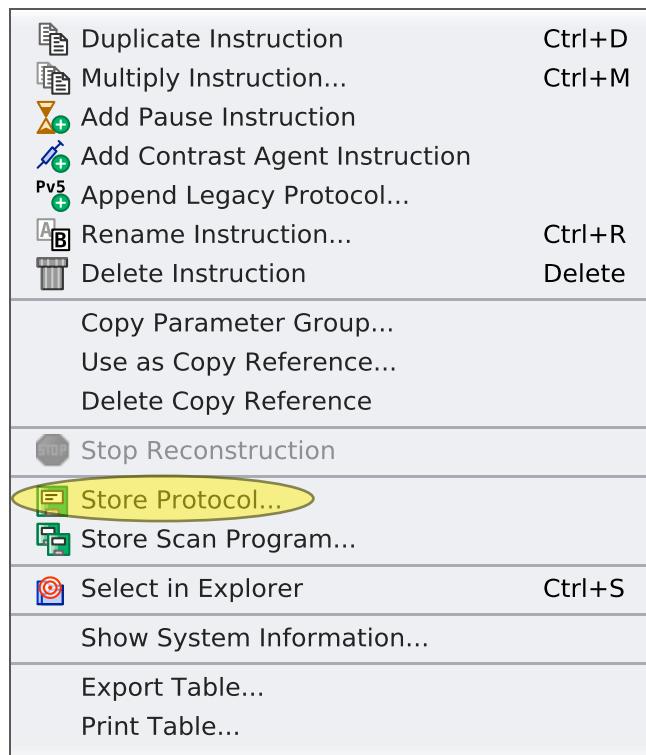


Figure 1.29: Context Menu Examination Card

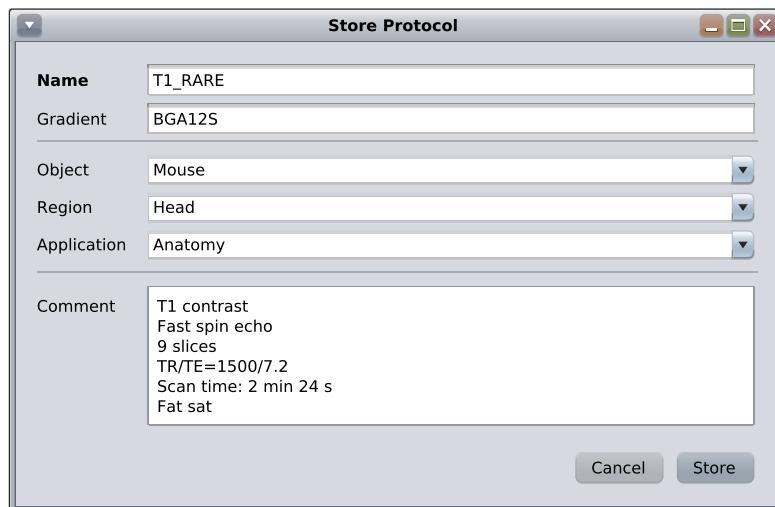


Figure 1.30: Dialog Store Protocol

Notice:

Protocols delivered by Bruker cannot be overwritten (except for protocols stored in the location "AnyObject > AnyRegion > Adjustments").

1.2.4.16 Storing a Scan Program

Goal:

Reuse a collection of instructions with their current parametrizations in other studies.

1. Select the instructions to be stored as a scan program.
 - The instructions are highlighted.

2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 52\]](#)) and invoke "Store Scan Program...".

- A dialog (see Figure [Dialog Store Scan Program \[▶ 52\]](#)) is opened allowing the operator to enter a scan program name and select/enter an object, region and application under which the scan program should be stored. When the "Store" button is clicked, the dialog is closed and the scan program is stored.

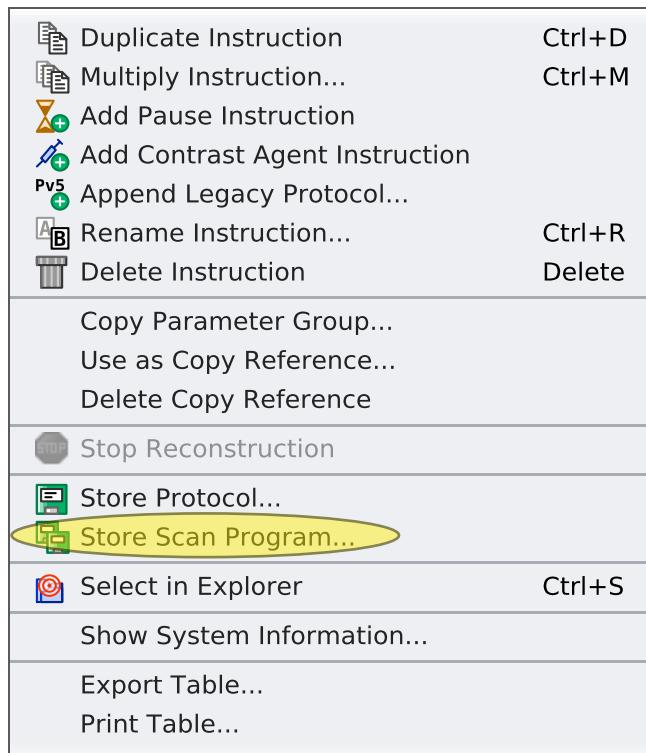


Figure 1.31: Context Menu Examination Card



Figure 1.32: Dialog Store Scan Program

1.2.4.17 Selecting a Scan Instruction in Workspace Explorer or Dataset Browser

Goal:

Select the examination belonging to a scan instruction in the Workspace Explorer or Dataset Browser in order to perform other actions available from these tools.

1. Select the scan instruction to be selected in Workspace Explorer or Dataset Browser.
 - The scan instruction is highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 53\]](#)) and invoke "Select in Explorer" or type Ctrl+S on the keyboard.
 - The examination belonging to the scan instruction is selected in Workspace Explorer and Dataset Browser (if open).

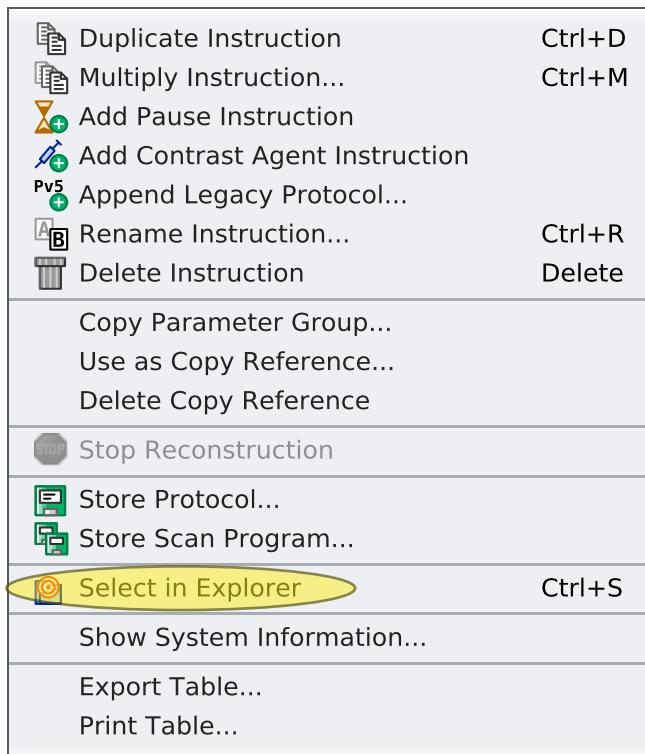


Figure 1.33: Context Menu Examination Card

1.2.4.18 Showing System Information for a Scan Instruction

Goal:

Show information about the system (coils, operation modes etc.) which will be used for scan instruction execution.

1. Select the scan instruction for which system information should be shown.
 - The scan instruction is highlighted.
2. Open the context menu (see Figure [Context Menu Examination Card \[▶ 54\]](#)) and invoke "Show System Information...".
 - A dialog (see Figure [Dialog System Information \[▶ 54\]](#)) is opened presenting the system information.

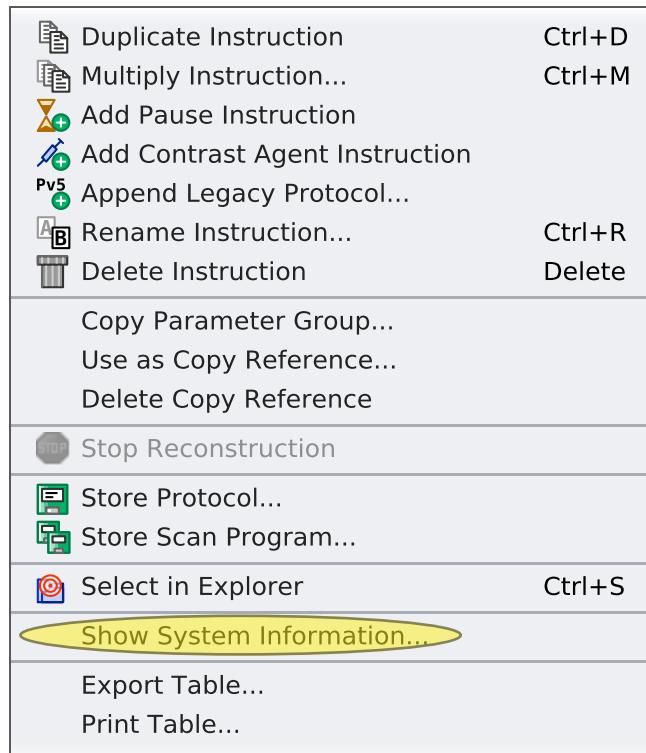


Figure 1.34: Context Menu Examination Card

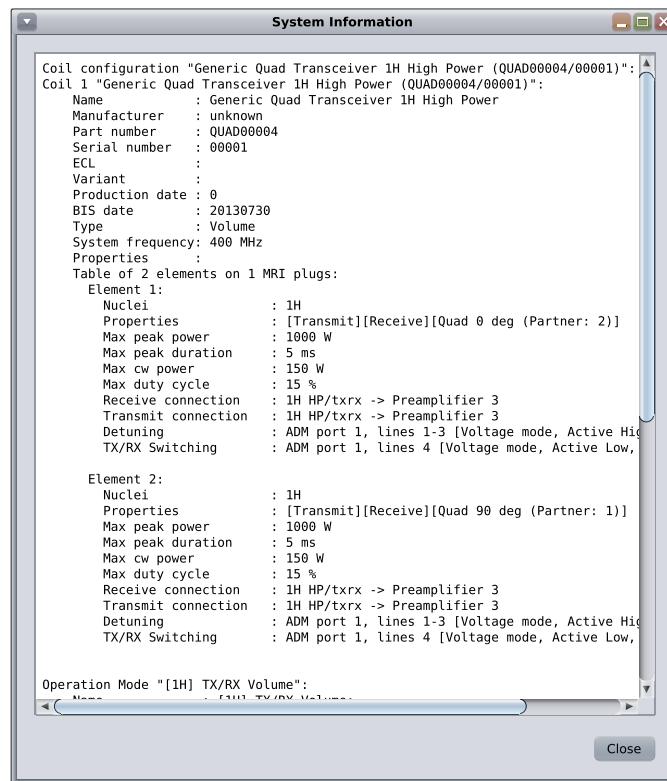


Figure 1.35: Dialog System Information

1.2.4.19 Editing a Scan Instruction

Goal:

Change parameter values of a scan instruction.

1. Double click the scan instruction to be edited or select the scan instruction to be edited and click the "Open" button.
 - The editor for the selected scan instruction is opened, if no other instruction is currently edited. If another instruction is currently edited and has been modified, a dialog (see Figure [Dialog Parameters Changed \[▶ 55\]](#)) is displayed. The dialog allows to save or discard the modifications for the currently edited instruction or to cancel the attempt to edit the new instruction.
2. Modify the parameter values as needed.
3. Click "Apply" to make the changes permanent or click "Cancel" to discard the changes.
 - The editor is closed.

Notice:

- If the edited instruction is the first READY instruction in the scan instruction table, the "Continue" button will be enabled as well while the editor is opened. Clicking "Continue" in this state will apply the changes, close the editor and proceed with the scan program execution.
 - Except for the last two editor cards ("Single Parameter" and "Instruction") the layout and content of the parameter editor cards is defined by the measuring method. Please consult the method documentation for a description of the available parameters and their meaning. The "Single Parameter" editor card (see Figure [Single Parameter Editor \[▶ 56\]](#)) gives access to all parameters defined by the measuring method and is intended for expert use only. The parameter selection offered in the list can be filtered by entering strings into the "Starts With", "Contains" or "Ends With" text fields. Selecting "From Group" allows to restrict the offered parameters to a single parameter group. Complicated struct parameters or arrays may be simplified by entering a "Qualification".
- The "Instruction" editor card (see Figure [Instruction Parameter Editor \[▶ 56\]](#)) allows to define certain aspects of the instruction execution.

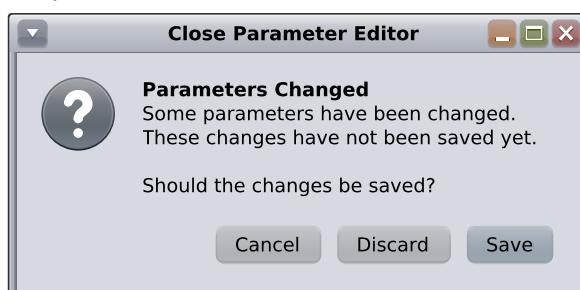


Figure 1.36: Dialog Parameters Changed

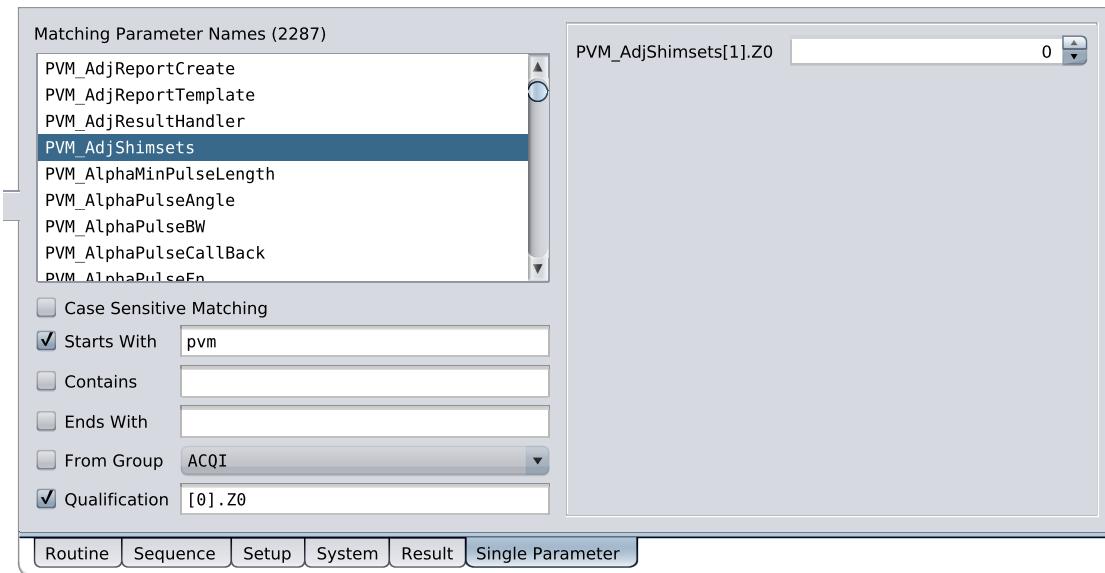


Figure 1.37: Single Parameter Editor

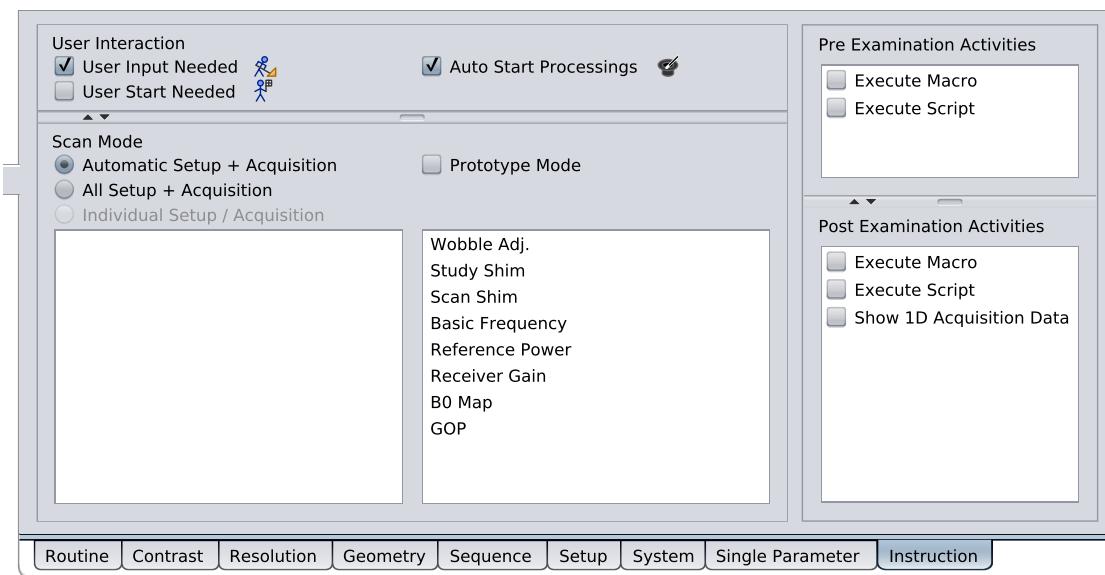


Figure 1.38: Instruction Parameter Editor

1.2.4.20 Editing a Pause Instruction

Goal:

Change parameter values of a pause instruction.

- Double click the pause instruction to be edited or select the pause instruction to be edited and click the "Open" button.
► The editor (see Figure [Pause Instruction Editor \[▶ 57\]](#)) for the selected pause instruction is opened, if no other instruction is currently edited. If another instruction is currently edited and has been modified, a dialog (see Figure [Dialog Parameters Changed \[▶ 57\]](#)) is displayed. The dialog allows to save or discard the modifications for the currently edited instruction or to cancel the attempt to edit the pause instruction. The following properties can be changed for a pause instruction:
"User Input Needed" If checked, the user must edit (and apply) the pause instruction

prior to execution. If unchecked, the pause instruction will automatically be regarded as valid and, therefore, can be executed without further user interaction.

"User Start Needed" If checked, the scan program execution will stop at this pause instruction and the user must click "Continue" in order to proceed with scan program execution. If unchecked, scan program execution will not stop (except for the defined delay) at this instruction (unless "User Input Needed" is checked and the instruction has not been edited yet).

"Time to Wait" The duration of the delay defined in hours, minutes and seconds.

2. Modify the pause properties as needed.
 3. Click "Apply" to make the changes permanent or click "Cancel" to discard the changes.
- The editor is closed.

Notice:

- If the edited instruction is the first READY instruction in the scan instruction table, the "Continue" button will be enabled as well while the editor is opened. Clicking "Continue" in this state will apply the changes, close the editor and proceed with the scan program execution.
- The defaults for pause instructions (used for new pause instructions added to a scan program) can be set via "Window > Options > Examination > Pause Instructions".

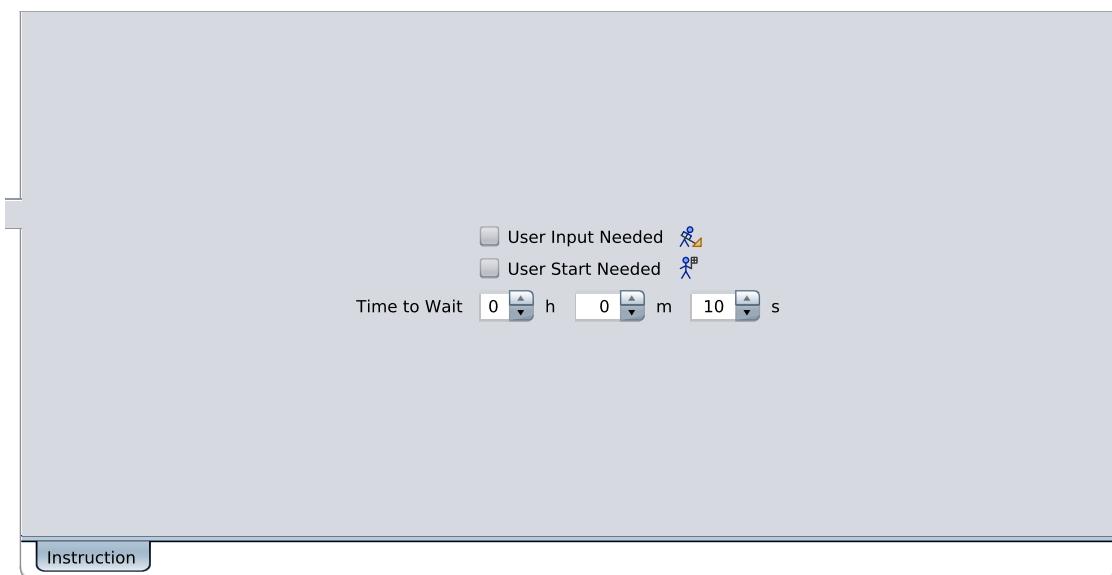


Figure 1.39: Pause Instruction Editor

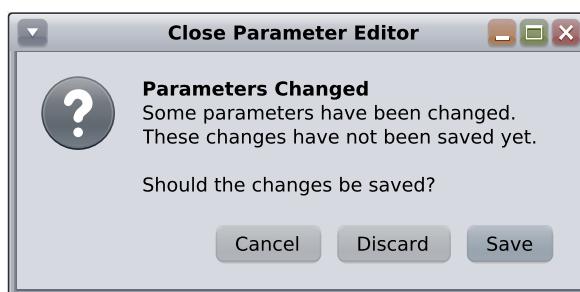


Figure 1.40: Dialog Parameters Changed

1.2.4.21 Editing a Contrast Agent Instruction

Goal:

Change parameter values of a contrast agent instruction.

1. Double click the contrast agent instruction to be edited or select the contrast agent instruction to be edited and click the "Open" button.

► The editor (see Figure [Contrast Agent Instruction Editor \[▶ 59\]](#)) for the selected contrast agent instruction is opened, if no other instruction is currently edited. If another instruction is currently edited and has been modified, a dialog (see Figure [Contrast Agent Instruction Editor \[▶ 59\]](#)) is displayed. The dialog allows to save or discard the modifications for the currently edited instruction or to cancel the attempt to edit the contrast agent instruction. The following properties can be changed for a contrast agent instruction:

"User Input Needed" If checked, the user must edit (and apply) the contrast agent instruction prior to execution. If unchecked, the contrast agent instruction will automatically be regarded as valid and, therefore, can be executed without further user interaction.

"User Start Needed" If checked, the scan program execution will stop at this contrast agent instruction and the user is required to click "Continue" in order to proceed with scan program execution. If unchecked, scan program execution will not stop (except for the defined delays) at this instruction (unless "User Input Needed" is checked and the instruction has not been edited yet).

"Time to Wait Before Contrast Agent Administration" The duration of the delay in hours, minutes and seconds before the dialog requesting the contrast agent administration is shown.

"Time to Wait After Contrast Agent Administration" The duration of the delay in hours, minutes and seconds after the dialog requesting the contrast agent administration has been closed.

2. Modify the contrast agent properties as needed.
3. Click "Apply" to make the changes permanent or click "Cancel" to discard the changes.

► The editor is closed.

Notice:

- If the edited instruction is the first READY instruction in the scan instruction table, the "Continue" button will be enabled as well while the editor is opened. Clicking "Continue" in this state will apply the changes, close the editor and proceed with the scan program execution.
- The defaults for contrast agent instructions (used for new contrast agent instructions added to a scan program) can be set via "Window > Options > Examination > Contrast Agent Instructions".

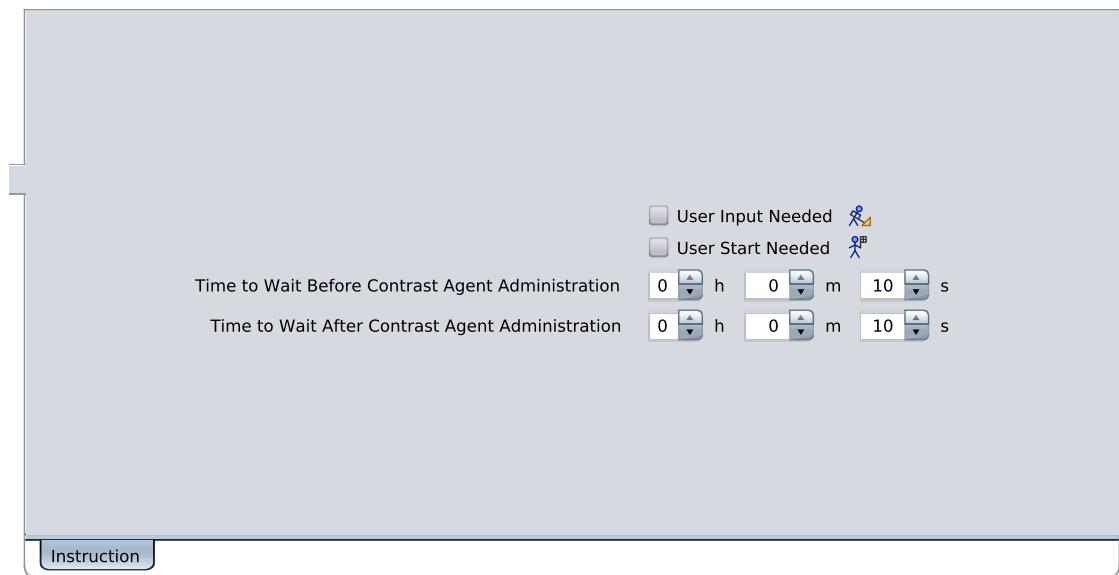


Figure 1.41: Contrast Agent Instruction Editor

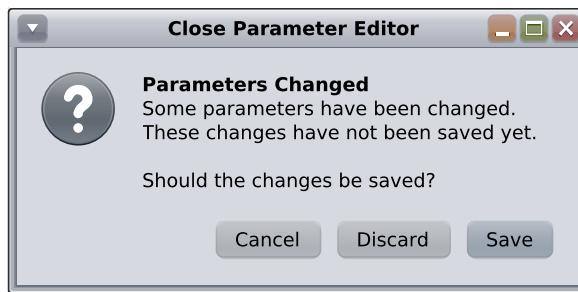


Figure 1.42: Dialog Parameters Changed

1.2.4.22 Specifying User Interaction for a Scan Instruction

Goal:

Determine the required user interaction (user input, user start, automatic processing execution) for a selected scan instruction.

1. Open the parameter editor of the scan instruction for which the user interaction should be modified.
 - The editor for the selected scan instruction is opened.
2. Select the "Instruction" tab.
 - The "Instruction" tab (see Figure [Instruction Parameter Editor \[60\]](#)) is raised.
3. Use the following check boxes to determine how the user is required to interact with the edited scan instruction:
 - "User Input Needed"** If checked, the user will be required to edit (and apply) the scan instruction prior to execution. If unchecked, the scan instruction will automatically be regarded as valid and therefore can be executed without further user interaction.
 - "User Start Needed"** If checked, the scan program execution will stop at this scan instruction and the user is required to click "Continue" in order to proceed with scan program execution. If unchecked, scan program execution will not stop at this instruction (unless "User Input Needed" is checked and the instruction has not been edited yet).

Notice:

The defaults for these check boxes (used for new scan instructions added to a scan program) can be set via "Window > Options > Examination > Scan Instructions".

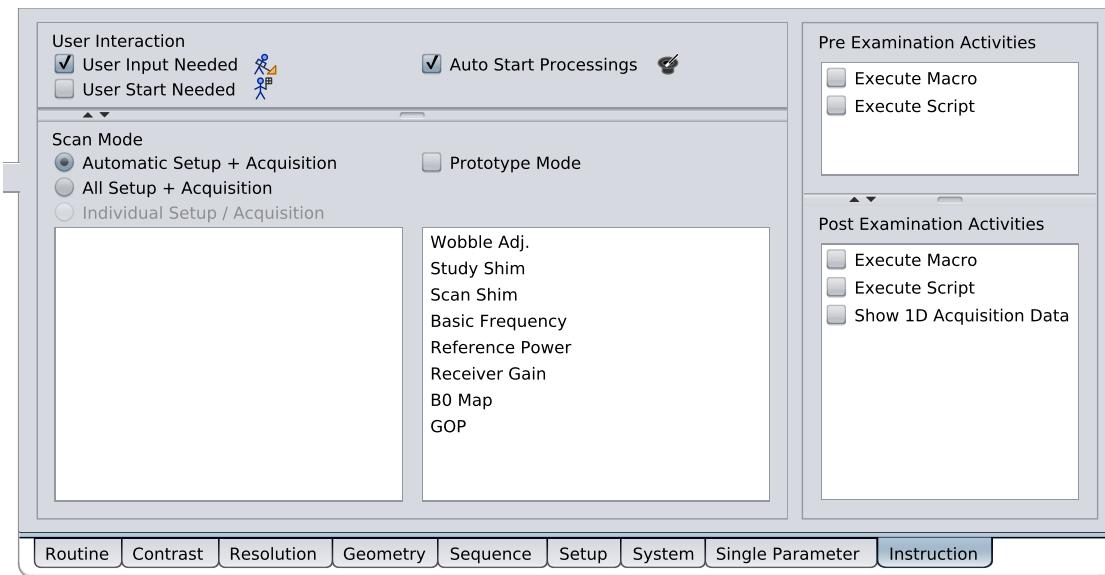


Figure 1.43: Instruction Parameter Editor

1.2.4.23 Specifying Processing Execution

Goal:

Determine if defined processing tasks (tasks creating additional image series, e.g. a second reconstruction) should be automatically executed after a scan instruction has been executed.

1. Open the parameter editor of the scan instruction for which automatic processing execution should be modified.
 - The editor for the selected scan instruction is opened.
2. Select the "Instruction" tab.
 - The "Instruction" tab (see Figure [Instruction Parameter Editor \[▶ 61\]](#)) is raised.

Use the **"Auto Start Processings"** check box to determine whether processing tasks should be automatically executed. If checked, defined processing tasks will be automatically executed for the edited scan instruction. If unchecked, processing tasks are not executed.

Notice:

The default for this check box (used for new scan instructions added to a scan program) can be set via "Window > Options > Examination > Scan Instructions".

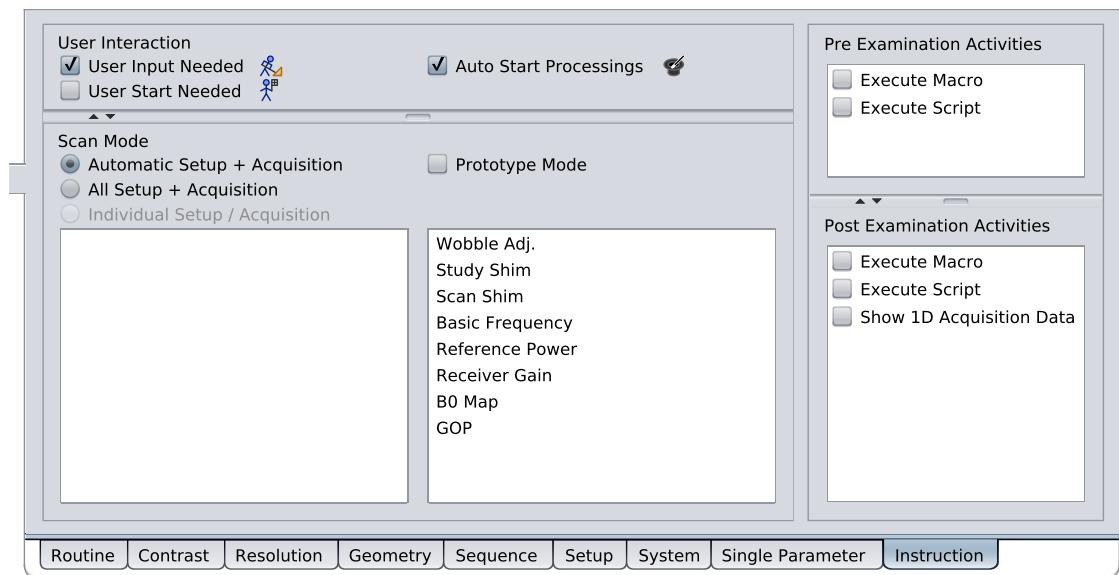


Figure 1.44: Instruction Parameter Editor

1.2.4.24 Specifying Adjustment Execution for a Scan Instruction

By default the system will select the adjustments and their order automatically. So normally there is no need to change this. For special purposes, however, this is possible.

Goal:

Determine which adjustments are executed for a selected scan instruction and in which order they are executed.

1. Open the parameter editor of the scan instruction for which the adjustment execution should be modified.
► The editor for the selected scan instruction is opened.
2. Select the "Instruction" tab.
► The "Instruction" tab (see Figure [Instruction Parameter Editor \[62\]](#)) is raised.
3. Use the lower left part of the "Instruction" tab to change the "Scan Mode" as follows:
"Automatic Setup + Acquisition" The system will automatically execute the needed Adjustments (in the correct order) prior to executing the scan (GOP). This is the default.
"All Setup + Acquisition" All Adjustments available for the scan instruction (apart from the on-demand adjustments) are executed in the correct order prior to executing the scan (GOP) even if they are not needed. It will need additional scan time and should normally be avoided.
"Individual Setup / Acquisition" Adjustment procedures from the right list may be dragged and dropped into the left list for a user defined adjustment setting. The adjustments will be executed in the order of the list (top to bottom). The GOP procedure (the actual scan) may only be used as the last step since it does not make sense to execute adjustments after the scan has already been acquired. Dropping an adjustment on an already existing list entry will replace this list entry with the dropped one. Selected adjustments in the left list can be deleted by using the "Delete" key on the keyboard or the "Delete" action from the lists context menu.

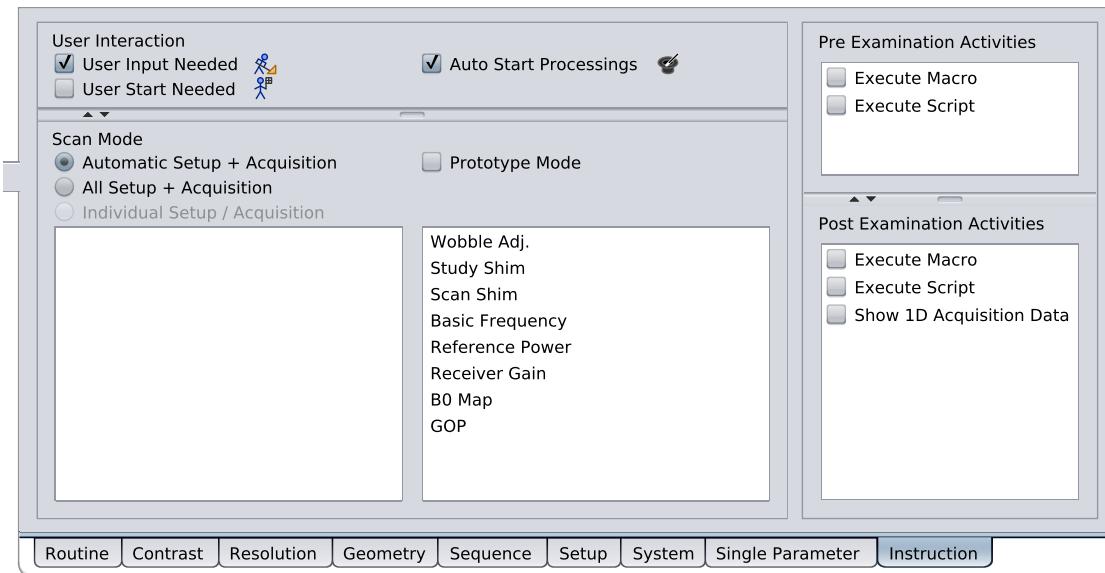


Figure 1.45: Instruction Parameter Editor

1.2.4.25 Executing a Setup Pipeline for a Scan Instruction

Goal:

Execute a setup pipeline for a selected scan instruction in order to change parameters and observe the impact on the signal.

1. Open the parameter editor of the scan instruction for which a setup pipeline should be executed.
 - The editor for the selected scan instruction is opened.
2. Click the "Setup" button to start the setup pipeline.
 - The instruction status changes from READY via SCHEDULED to GSP. When GSP is reached data is acquired. While data is acquired, parameters from the "Setup" parameter card may be changed. Their impact on the signal can be viewed in real-time using the Acq/Reco Display (see Figure [Acq Reco Display \[▶ 63\]](#)) which is automatically opened in the left part of the user interface. The Acq/Reco Display shows the raw data in the top diagram and the reconstructed data in the middle/bottom diagram. The setup pipeline will run endlessly until it is stopped by the operator.
3. Click the "Stop" button below the Scan Program Table or the button in the top right corner of the user interface to stop the setup pipeline.
 - The instruction status changes from GSP via INTERRUPTED to READY.

Notice:

Changing parameters from other (non-"Setup") parameter cards is also possible but the acquisition will automatically stop and start again to make the change effective.

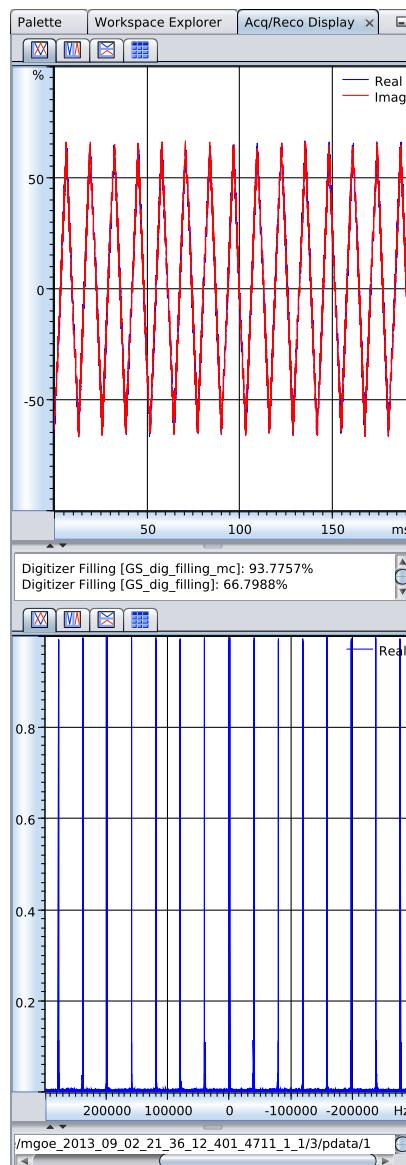


Figure 1.46: Acq Reco Display

1.2.4.26 Executing Instructions/Scan Programs

Goal:

Execute one or more instructions.

1. Click the "Continue" button.

► Execution will start at the first READY instruction and will stop after all parameterized READY instructions which do not require explicit start by the user have been executed.

Notice:

- The "Continue" button will only be enabled if the first ready instruction in the Scan Program Table is already parameterized or if the Parameter Editor is open on the first READY instruction. The "Continue" action will implicitly apply the changes made in the edited instruction.

- If the same instruction should be executed interactively several times, the "Scan" button can be used to start instruction execution. This will create a copy of the first READY instruction and start executing the acquisition afterwards.
- When executing an instruction the status changes will depend on the type of the instruction. For scan instructions the status will change from READY via SCHEDULED, ADJUST (adjustments are executed), SCANNING/RECO (data is acquired and reconstructed) to SUCCEEDED. A FAILED status (usually accompanied by an error dialog) may be reached, if an error occurs during acquisition (possibly caused by demanding timing, gradient duty cycle violation etc.). For pause and contrast agent instructions the status will change from READY via SLEEPING to SUCCEEDED.

1.2.4.27 Working in Prototype Mode

In rare cases it may be desired to change for example a delay in a pulse sequence without changing the method which normally controls the delays. These kinds of changes can be done in the so called prototype mode.

Goal:

Change base-level (e.g. acquisition) parameters independent of the method.

1. Open the parameter editor of the scan instruction for which base-level parameters should be modified.
 - The editor for the selected scan instruction is opened.
2. Select the "Instruction" tab.
 - The "Instruction" tab (see Figure [Instruction Parameter Editor \[▶ 65\]](#)) is raised.
3. Select the "Prototype Mode" option.
 - The "Prototype Mode" option is switched on.
4. Change method (PVM) parameters (if needed).
5. Change base-level parameters. Usually this has to be done on the "Single Parameter" editor card.
6. Click "Apply" to store the changes.
 - The parameter editor is closed.

Notice:

Without the prototype mode, the method always controls the values of the base-level parameters. Modified base-level parameters will be overwritten by the values calculated by the method. When the prototype mode is switched on, modified base level parameters will take precedence over the values calculated by the method. Changed base-level parameters will be lost (even in prototype mode), if method (PVM) parameters are changed after base-level parameters have been changed. For that reason it is important to stick to the workflow described above.

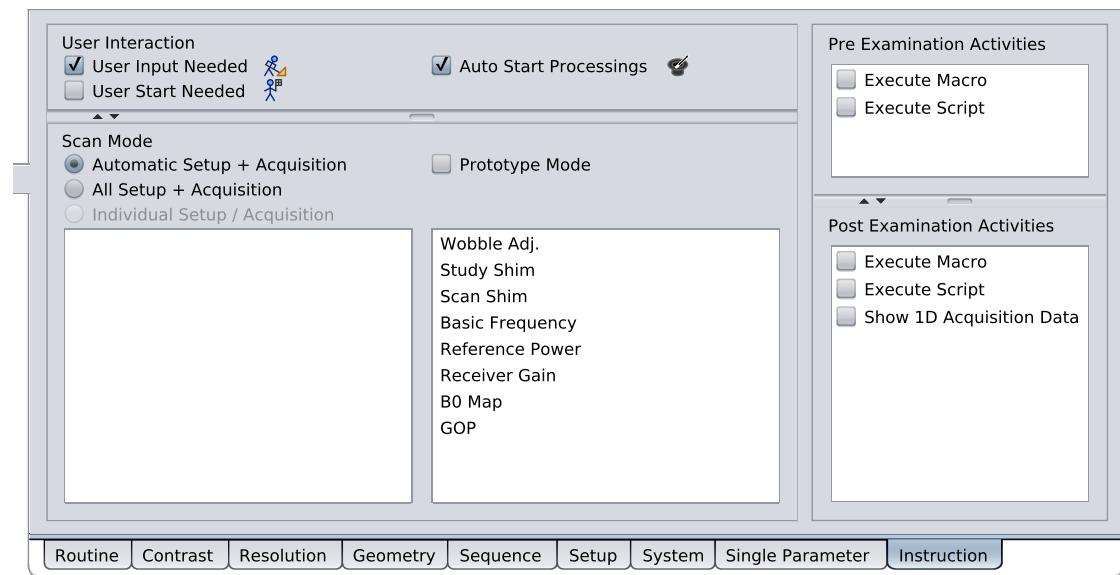


Figure 1.47: Instruction Parameter Editor

1.2.5 Using the Adjustment Platform

1.2.5.1 Overview

Normally the acquisition software will make sure that all adjustments required for a certain scan instruction are automatically performed. For special purposes or when the automatic adjustments did not succeed, adjustments may be executed manually. This can be done from the so called Adjustment Platform. When the Adjustment Platform is active (indicated by the  icon in the tab of the Examination Card) the lower part of the Examination Card is replaced by the Adjustment Table (bottom left) as shown in Figure [Adjustment Table ▶ 66](#) and the Adjustment Parameter Editor (bottom right) as shown in Figure [Adjustment Editor ▶ 66](#).

The screenshot shows a software interface titled "Adjustment Table". At the top, there are buttons for "Back...", "Open", "Apply", and "Cancel". Below this is a table with the following data:

Context	Config. By	Name	Status
1	Study	Protocol	Wobble Adj.
2	Study	Protocol	Study Shim
3	Scan	Protocol	Scan Shim
4	Study	Protocol	Basic Frequency
5	Study	Protocol	Reference Power
6	Scan	Method	Receiver Gain
7	On Demand	Protocol	B0 Map

At the bottom, there are buttons for "Stop", "Start", and "Setup".

Figure 1.48: Adjustment Table

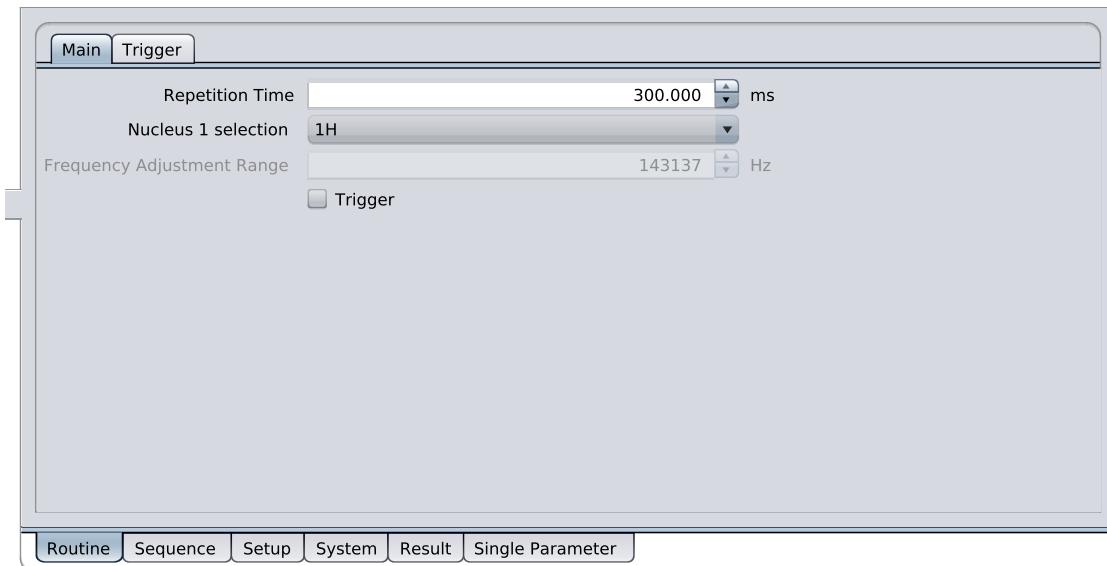


Figure 1.49: Adjustment Editor

- A "Back..." button in the top left allowing to leave the Adjustment Platform.
- Some buttons in the top right allowing to work with the Parameter Editor ("Open", "Apply", "Cancel").
- Some buttons at the bottom for acquisition control ("Stop", "Start", "Setup").
- A table in the center holding the available adjustments. The table consists of the following 4 columns:

1. The "Context" column shows in which context the adjustment is normally executed. The value "Study" indicates that the adjustment is normally executed once for the first scan in a study. "Scan" indicates that the adjustment is executed before each scan. "On Demand" adjustments can only be executed manually in the adjustment platform. They are not executed during normal scan program execution.
2. The "Config. By" column shows the origin of an adjustment. "Protocol" indicates that the adjustment is defined by an own protocol whereas "Method" means that the adjustment is derived from the (reconfigured) method for which the Adjustment Platform was opened.
3. The "Name" column shows the name of the adjustment. A tooltip provides additional information.
4. An icon in the "Status" column provides information about the execution status of the adjustment.
 - No icon indicates, that the adjustment has not yet been executed in its context.
 -  The adjustment is currently executed.
 -  The adjustment has already been executed successfully.
 -  The last execution of the adjustment has failed.

1.2.5.2 Opening the Adjustment Platform

Goal:

Execute adjustments manually.

1. Open the parameter editor for the scan instruction for which the Adjustment Platform should be entered.
 - The scan instruction is opened for editing.
2. Click the  button above the Scan Program Table.
 - The Scan Program Table and the Scan Parameter Editor at the bottom of the Examination Card are replaced by the Adjustment Table and the Adjustment Parameter Editor. The icon shown in the tab of the Examination Card will reflect this change too.

Notice:

To switch back to the scan program, stop a running adjustment (if any), close or apply an open Adjustment Parameter Editor (if any) and click the "Back..." button.

1.2.5.3 Closing the Adjustment Platform

Goal:

Leave the Adjustment Platform and switch back to the scan program.

1. Stop a running adjustment (if any).
 - The adjustment is stopped.
2. Click the "Close" or "Apply" button to leave an open Adjustment Parameter Editor (if any).

- The Adjustment Parameter Editor is closed.
 - The "Back..." button is active.
3. Click the "Back..." button.
- The Adjustment Table and the Adjustment Parameter Editor are replaced by the Scan Program Table and the Scan Parameter Editor.

1.2.5.4 Editing an Adjustment

Goal:

Change adjustment parameters.

1. Double click the adjustment to be edited or select the adjustment to be edited and click the "Open" button.
 - The editor for the selected adjustment is opened, if no other adjustment is currently edited. If another adjustment is currently edited and has been modified, a dialog (see Figure [Dialog Parameters Changed \[▶ 68\]](#)) is displayed. The dialog allows to save or discard the modifications for the currently edited adjustment or to cancel the attempt to edit the new adjustment.
2. Modify the parameter values as needed.
3. Click "Apply" to store the modifications for the current adjustment platform session (until the adjustment platform is left) or click "Cancel" to discard the changes.
 - The editor is closed.

Notice:

- Modifications made (and applied) for a certain adjustment are stored only for the duration of the current adjustment platform session. When the adjustment platform is left (via "Back..." button) and re-entered the parameter values will again have the values defined by the adjustment method or protocol.
 - Closing an adjustment editor with "Apply" will only save the parametrization of the adjustment and not its results. Use one of the "Save Adjustment Result ..." actions from the context menu of the edited adjustment to make adjustment results persistent (see also [Storing Adjustment Results \[▶ 71\]](#)).
 - Except for the last editor card ("Single Parameter") the layout and content of the parameter editor cards is defined by the adjustment. Please consult the adjustment documentation for a description of the available parameters and their meaning.
- The "Single Parameter" editor card (see Figure [Single Parameter Editor \[▶ 69\]](#)) gives access to all parameters defined by the adjustment and is intended for expert use only. The parameter selection offered in the list can be filtered by entering strings into the "Starts With", "Contains" or "Ends With" text fields. Selecting "From Group" allows to restrict the offered parameters to a single parameter group. Complicated struct parameters or arrays may be simplified by entering a "Qualification".

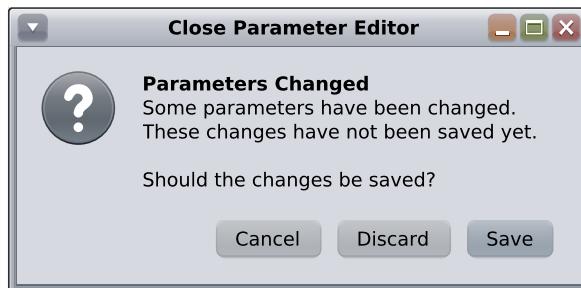


Figure 1.50: Dialog Parameters Changed

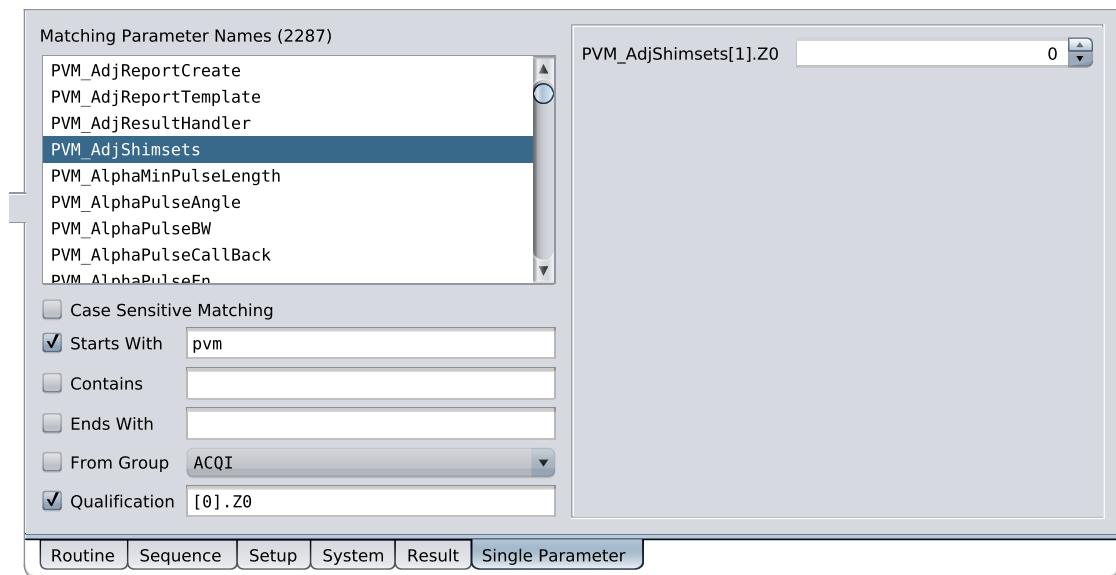


Figure 1.51: Single Parameter Editor

1.2.5.5 Executing a Setup Pipeline for an Adjustment

Goal:

Execute a setup pipeline for a selected adjustment in order to change parameters and observe the impact on the signal.

1. Open the parameter editor of the adjustment for which a setup pipeline should be executed.
 - The editor for the selected adjustment is opened.
2. Click the "Setup" button to start the setup pipeline.
 - The  icon is displayed in the "Status" column. While data is acquired, parameters from the "Setup" parameter card may be changed. Their impact on the signal can be viewed in real-time using the Acq/Reco Display (see Figure [Acq Reco Display \[70\]](#)) which is automatically opened in the left part of the user interface. The Acq/Reco Display shows the raw data in the top diagram and the reconstructed data in the middle/bottom diagram. The setup pipeline will run endlessly until it is stopped by the operator.
3. Click the "Stop" button below the Adjustment Table or the  button in the top right corner of the user interface to stop the setup pipeline.
 - The  "Status" icon is removed.

Notice:

Changing parameters from other (non-"Setup") parameter cards is also possible but the acquisition will automatically stop and start again to make the change effective.

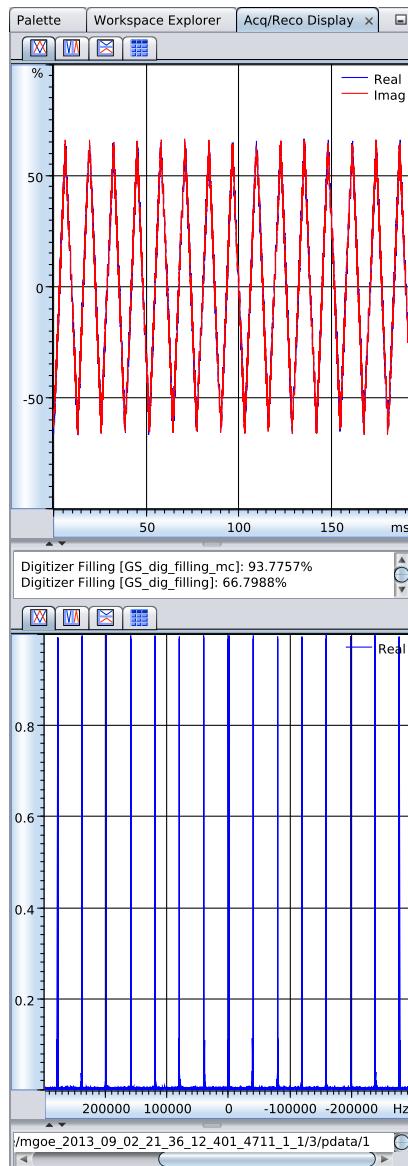


Figure 1.52: Acq Reco Display

1.2.5.6 Executing an Adjustment

Goal:

Execute an adjustment like it is executed during a scan program execution.

1. Open the parameter editor of the adjustment which should be executed.
 - The editor for the selected adjustment is opened.
2. Click the "Start" button to start the adjustment.
 - The  icon is displayed in the "Status" column while the adjustment is in progress. When the adjustment is finished the icon is replaced by the  icon (indicating success) or the  icon (indicating failure).

1.2.5.7 Stopping an Adjustment

Goal:

Stop adjustment execution immediately.

1. Click the "Stop" button below the Adjustment Table or the  button in the top right corner of the user interface.
- The  "Status" icon is removed.

Notice:

Interrupting an adjustment is independent of the way it has been started ("Start" or "Setup").

1.2.5.8 Storing Adjustment Results

Goal:

Reuse the results of an adjustment for other examinations.

1. Open the context menu (see Figure [Context Menu Adjustment Platform \[▶ 71\]](#)) on the currently edited adjustment and invoke one of the "Save Adjustment Result" actions.
 - "**Save Adjustment Result**" The adjustment result parameters from the "Result" parameter card are stored and will be used for the scan instruction for which the adjustment platform has been opened and potentially for all further examinations of the current study (depending on the adjustment).
 - "**Save Adjustment Result for Other Studies**" The adjustment result parameters from the "Result" parameter card are stored and will be used for the scan instruction for which the adjustment platform has been opened and for all further examinations of the current user.
 - "**Save Adjustment Result Globally**" The adjustment result parameters from the "Result" parameter card are stored and will be used for the scan instruction for which the adjustment platform has been opened and for all further examinations of all users.
 - The adjustment result parameters are stored as described above.

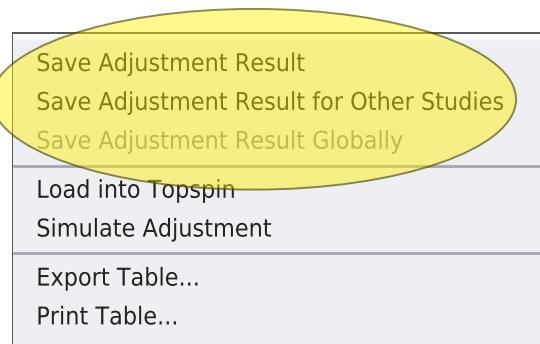


Figure 1.53: Context Menu Adjustment Platform

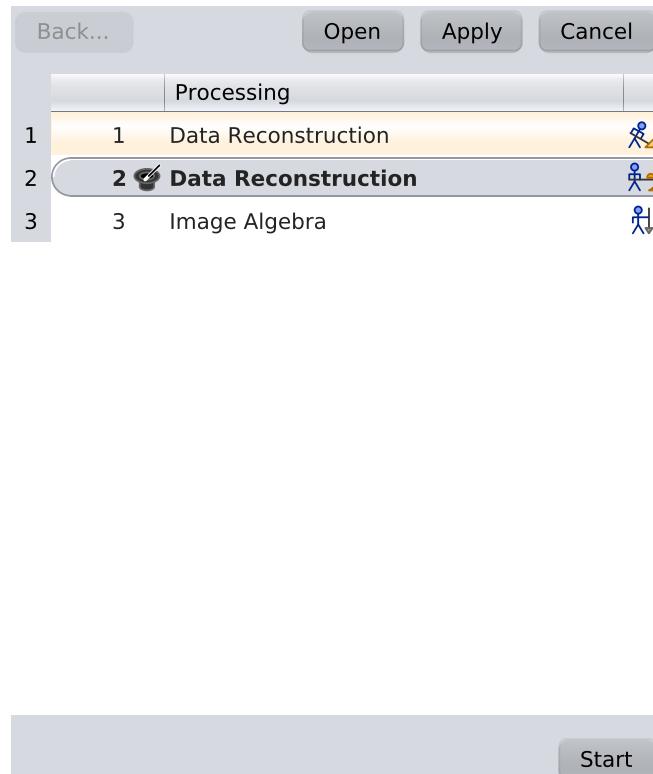
Notice:

- Storing adjustment results globally should be used with care since it will influence the work of all other users of the ParaVision installation.
- The enabled state of the different "Save Adjustment Result" actions is defined by the adjustment. Storing adjustment results for other studies or globally may therefore not be offered for all available adjustments.

1.2.6 Using the Processing Platform

1.2.6.1 Overview

When executing a scan program data is acquired for each scan instruction. In addition to that an image series is normally reconstructed in parallel to the data acquisition. If further image series should be created the Processing Platform can be used. It allows to create new image series for examinations which are already SUCCEEDED or to plan the creation of new image series for examinations which have not yet been done. When the Processing Platform is active (indicated by the  icon in the tab of the Examination Card) the lower part of the Examination Card is replaced by the Processing Table (bottom left) as shown in Figure [Processing Table \[72\]](#) and the Processing Parameter Editor (bottom right) as shown in Figure [Reco Processing Editor \[73\]](#) for the "Data Reconstruction" processing.



The screenshot shows a software interface for managing processing steps. At the top, there are buttons for 'Back...', 'Open', 'Apply', and 'Cancel'. Below this is a table with three columns: a row number, a step number, and a description. The table has four rows:

Processing		
1	1	Data Reconstruction 
2	2  Data Reconstruction 	
3	3	Image Algebra 

Below the table is a large, mostly empty gray area. In the bottom right corner of this area, there is a small button labeled 'Start'.

Figure 1.54: Processing Table

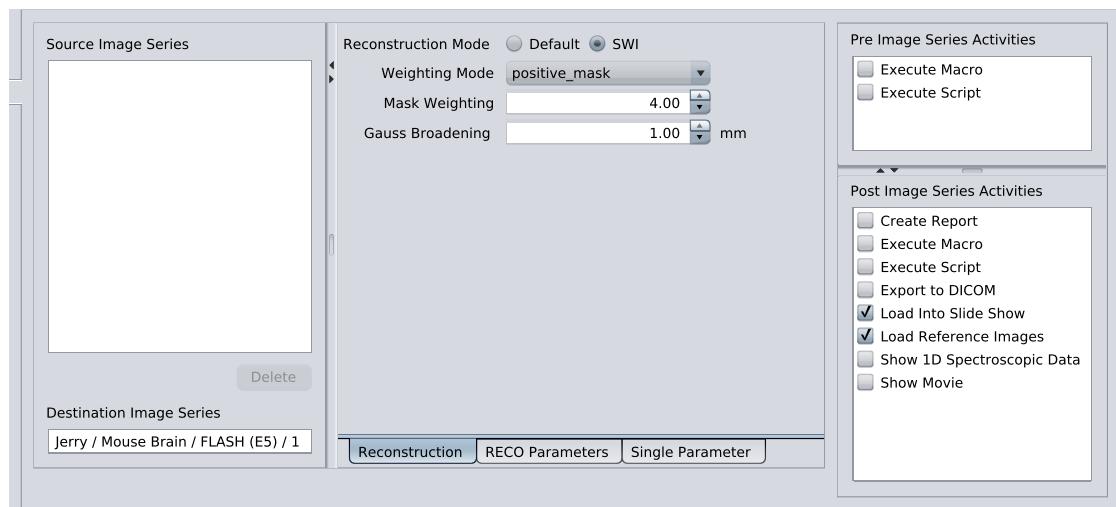


Figure 1.55: Reco Processing Editor

The Processing Table consists of:

- A "Back..." button in the top left allowing to leave the Processing Platform.
- Some buttons in the top right allowing to work with the Parameter Editor ("Open", "Apply", "Cancel").
- A "Start" button at the bottom right allowing to start a processing immediately.
- A table in the center holding the processing tasks. The table consists of the following 4 columns:
 1. The first column shows the number of the image series (PROCNO).
 2. The icon in the second column indicates, if Pre or Post Image Series Activities have been selected for the processing. These will automatically be executed prior or after the processing task.
 3. The "Processing" column shows the type of the processing task.
 4. An icon in the fourth column indicates the status of the processing task.
 - The processing has to be parameterized before it can be executed.
 - The processing has been configured already.
 - The processing is currently edited.
 - The processing is currently executed.
 - The processing has been executed without errors.
 - The execution of the processing failed.

1.2.6.2 Opening the Processing Platform

Normally the raw data acquired during an examination is automatically reconstructed while the examination is performed. If further image series should be created (e.g. by performing another reconstruction or image algebra), these additional image series could be created and parameterized in the so called Processing Platform.

Goal:

Create further image series for an examination.

1. Open the parameter editor for the scan instruction for which the Processing Platform should be entered.
 - ▶ The scan instruction is opened for editing.
2. Click the  button above the Scan Program Table.
 - ▶ The Scan Program Table and the Scan Parameter Editor at the bottom of the Examination Card are replaced by the Processing Table and the Processing Parameter Editor. The icon shown in the tab of the Examination Card will reflect this change too.

Notice:

- To switch back to the scan program, close or apply an open Processing Parameter Editor (if any) and click the "Back..." button.
- Additional image series for an already succeeded examination may also be created at any time using the "Create Image Series..." action from the context menu of the examination in the Workspace Explorer or using the "Create Image Series..." action from the Examination tab in the Dataset Browser.

1.2.6.3 Closing the Processing Platform

Goal:

Leave the Processing Platform and switch back to the scan program.

1. Click the "Back..." button.
 - ▶ The Processing Table and the Processing Parameter Editor are replaced by the Scan Program Table and the Scan Parameter Editor.

1.2.6.4 Duplicating a Processing

Goal:

Create a clone of a selected processing.

1. Select the processing to be duplicated.
 - ▶ The processing is highlighted.
2. Open the context menu (see Figure [Context Menu Processing Platform \[▶ 74\]](#)) and invoke "Duplicate Processing" or type Ctrl+D on the keyboard.
 - ▶ A duplicate of the selected processing is appended.

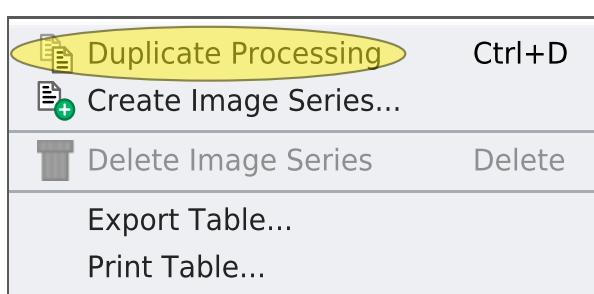


Figure 1.56: Context Menu Processing Platform

1.2.6.5 Creating a new Image Series

Goal:

Create a new image series by executing a processing task.

1. Open the context menu (see Figure [Context Menu Processing Platform \[▶ 75\]](#)) and invoke "Create Image Series...".
 - A selection dialog (see Figure [Dialog Select Processing \[▶ 75\]](#)) is displayed.
2. Select the type of processing to be used to create the new image series and click "OK".
 - The selection dialog is hidden and a new processing is appended.



Figure 1.57: Context Menu Processing Platform

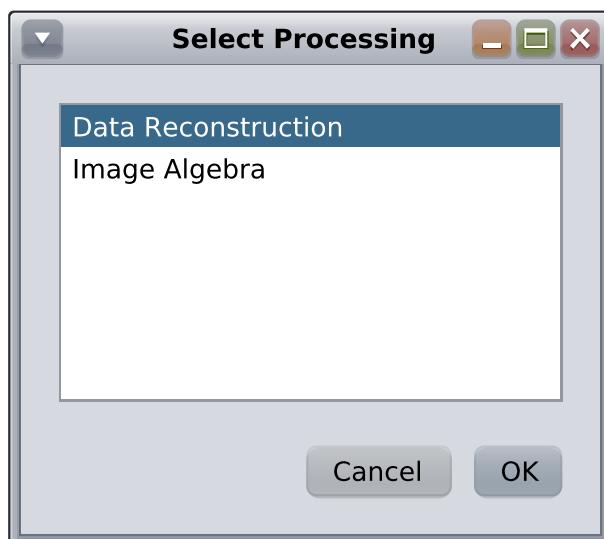


Figure 1.58: Dialog Select Processing

1.2.6.6 Deleting a Processing

Goal:

Delete a processing which is no longer needed or desired.

1. Select the processing(s) to be deleted.
 - The processing(s) is/are highlighted.
2. Open the context menu (see Figure [Context Menu Processing Platform \[▶ 76\]](#)) and invoke "Delete Image Series" or use the Delete key on the keyboard.
 - The selected image series is/are deleted.



Figure 1.59: Context Menu Processing Platform

1.2.6.7 Editing a Processing

Goal:

Change the parametrization of a processing.

1. Double click the processing to be edited or select the processing to be edited and click the "Open" button.
 - The editor for the selected processing is opened.
2. Select the type of processing to be used to create the new image series and click "OK".

Notice:

- A dialog (see Figure [Dialog Parameters Changed \[▶ 77\]](#)) is displayed, if another processing is currently edited and has been modified. The dialog allows to save or discard the modifications for the currently edited processing or to cancel the edit operation.
- Depending on the type of processing the parameter editor will look different.

Figure [Reco Processing Editor \[▶ 77\]](#) shows the editor for the "Data Reconstruction" processing. On the left side of the editor a source image series may be dropped providing the reconstruction parameters to start with (normally not needed). The parameter cards in the center allow the modification of the reconstruction parameters. In the right part of the editor some additional pre- or post-activities can be selected. The selected activities will be executed before ("Pre Image Series Activities") or after ("Post Image Series Activities") the reconstruction is executed. Post image series activities may use the newly created data for their work.

Figure [Image Algebra Processing Editor \[▶ 77\]](#) shows the editor for the "Image Algebra" processing. On the left side of the editor one or more source image series has to be dropped (depending on the selected "Filter" calculating the new image data). The controls in the center allow the "Data Type" and the "Filter" calculating the new image data to be selected. Depending on the filter and the number of source image series, hints may be shown in the bottom line of the editor. In the right part of the editor some additional pre- or post-activities can be selected. The selected activities will be executed before ("Pre Image Series Activities") or after ("Post Image Series Activities") the image algebra is executed. Post image series activities may use the newly created data for their work.

- A standalone version of the Processing Editor can be started from the Workspace Explorer using the "Create Image Series..." or "Edit Processing" context menu entries of the node "Datasets > SUBJECT > STUDY > EXAMINATION > IMAGE SERIES" or from the Dataset Browser via "Image Series > Create Image Series... / Edit Processing".

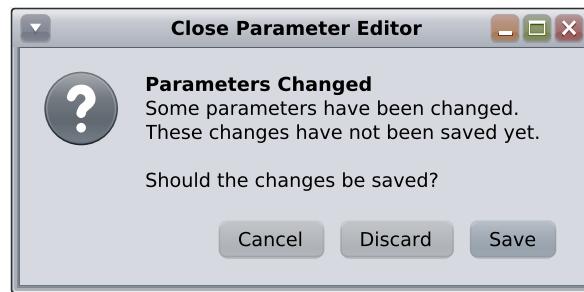


Figure 1.60: Dialog Parameters Changed

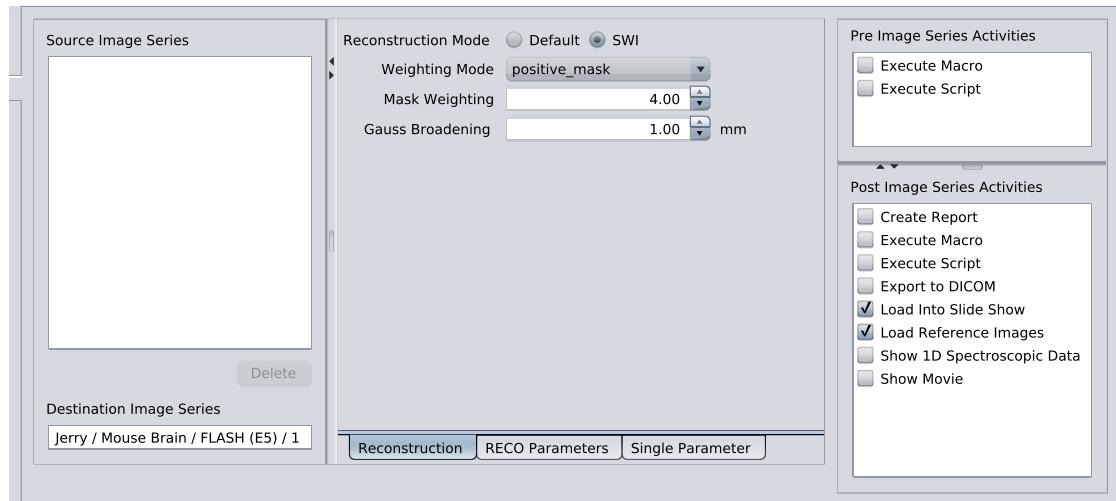


Figure 1.61: Reco Processing Editor

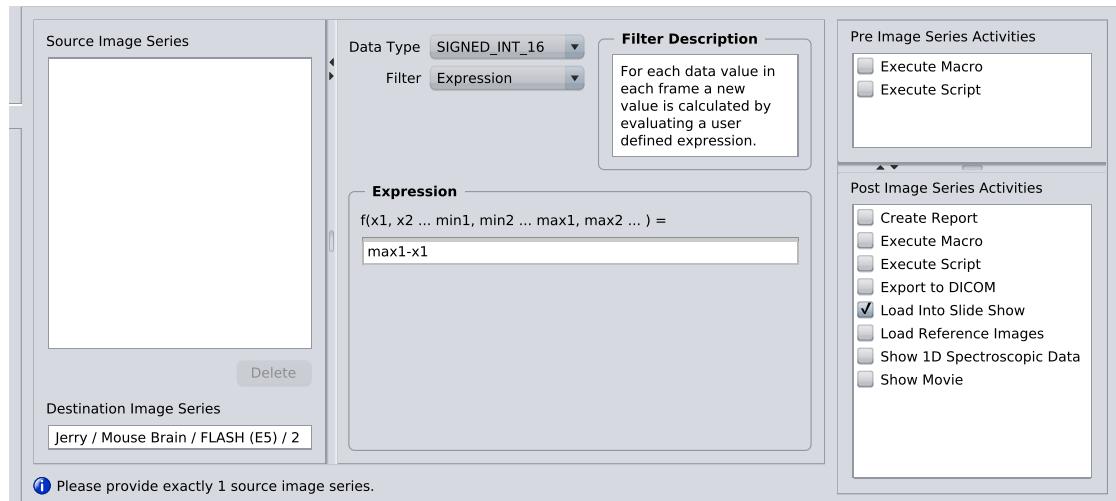


Figure 1.62: Image Algebra Processing Editor

1.2.7 Using the Simulation Platform

1.2.7.1 Overview

Some aspects of the scan execution can be simulated before the actual scan is executed on the spectrometer hardware. The tool allowing to execute these simulations is called the Simulation Platform. Currently a gradient duty cycle simulation and a gradient / HF pulse simulation (GOP simulation) is available.

When the Simulation Platform is active (indicated by the  icon in the tab of the Examination Card) the lower part of the Examination Card is replaced by the Simulation Platform as shown in Figure [Simulation Platform I ▶ 78\].](#) Each available simulation tool is represented by a single tab. To use a certain simulation tool its tab must be selected. A “Start” button usually starts the simulation (see section “Executing a ... Simulation” for details).



Figure 1.63: Simulation Platform

1.2.7.2 Opening the Simulation Platform

Goal:

Execute a gradient duty cycle or GOP simulation.

1. Open the parameter editor for the scan instruction for which the Simulation Platform should be entered.
 - The scan instruction is opened for editing.
2. Click the  button above the Scan Program Table.
 - The Scan Program Table and the Scan Parameter Editor at the bottom of the Examination Card are replaced by the Simulation Platform. The icon shown in the tab of the Examination Card will reflect this change too.

Notice:

- To switch back to the scan program, stop a running simulation (if any) and click the "Back..." button.

1.2.7.3 Closing the Simulation Platform

Goal:

Leave the Simulation Platform and switch back to the scan program.

1. Stop a running simulation (if any).

- ▶ The simulation is stopped and the "Back..." button is enabled again.
2. Click the "Back..." button.
 - ▶ The Simulation Platform is replaced by the Scan Program Table and the Scan Parameter Editor.

1.2.7.4 Executing a Gradient Duty Cycle Simulation

Some examinations will put a high strain on the gradient system. In order to protect the gradients, the spectrometer electronic will interrupt an examination, if the gradient duty cycle limit is exceeded. The examination can be simulated prior to an examination using the so called Gradient Duty Cycle Simulation.

Goal:

Estimate the stress a certain examination will put on the gradients.

1. Open the Simulation Platform.

 - ▶ The Simulation Platform is open..

2. Select the "Gradient Duty Cycle Simulation" tab.

 - ▶ The "Gradient Duty Cycle Simulation" tab is selected as shown in Figure [Gradient Duty Cycle Simulation \[79\]](#).

3. Click the "Start" button to start the simulation.

 - ▶ The "Start" and "Back..." buttons are disabled, the "Stop" button is enabled. While the simulation is running two curves are drawn. One curve shows the current gradient duty cycle at the examination time shown on the x-axis while the other curve shows the maximum duty cycle reached until that time. When the simulation is finished a simulation result is displayed and the "Start" and "Back..." buttons are enabled again (see Figure [Gradient Duty Cycle Simulation \(Finished\) \[80\]](#)).

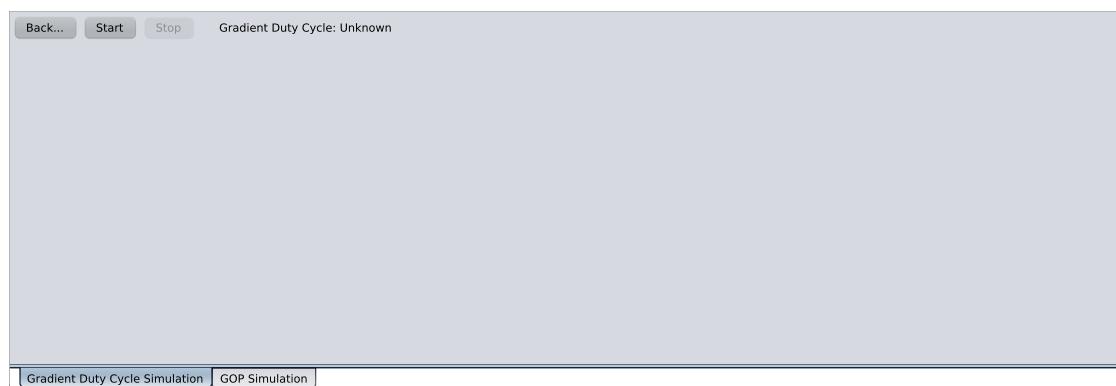


Figure 1.64: Gradient Duty Cycle Simulation

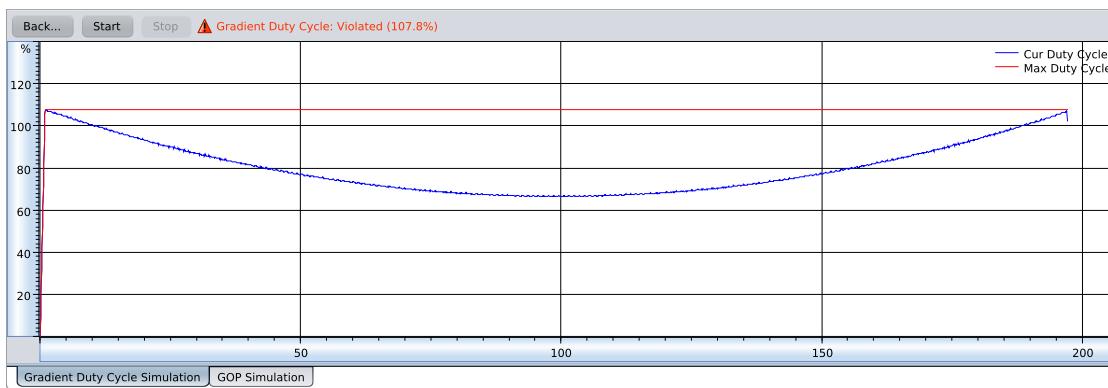


Figure 1.65: Gradient Duty Cycle Simulation (Finished)

Notice:

- To switch back to the scan program, stop a running simulation (if any) and click the "Back..." button.
- Before storing a scan instruction as a protocol it could be useful to perform a duty cycle simulation to make sure that the new protocol will work without causing a gradient duty cycle violation.

1.2.7.5 Stopping a Gradient Duty Cycle Simulation

Goal:

Stop a running gradient duty cycle simulation before it is finished.

1. Click the "Stop" button.
 - The simulation stops.

Notice:

No simulation result is displayed, if a simulation is stopped prematurely because an appropriate maximum duty cycle can only be calculated, if the entire simulation has been completed.

1.2.7.6 Executing a GOP Simulation

When developing methods / pulse programs it is sometimes useful to see a graphical representation of the examination (e.g. gradient / RF pulses) as it would be executed on the spectrometer hardware. The result display of the so called GOP Simulation is exact in every aspect of the examination (e.g. timing, amplitudes, phases etc.).

Goal:

Simulate the examination during developing methods or pulse programs.

1. Open the Simulation Platform.
 - The Simulation Platform is open.
2. Select the "GOP Simulation" tab.
 - The "GOP Simulation" tab is selected as shown in Figure [GOP Simulation \[▶ 81\]](#).
3. Click the "Start" button to start the simulation tool in TopSpin.

- ▶ The "Start" and "Back..." buttons are disabled and the TopSpin window is raised (see Notice if automatic raise failed).
4. Select the channels to be simulated in the dialog presented by TopSpin and click "OK".
- ▶ The simulation is performed. Depending on the complexity of the examination this may take several minutes. After the simulation succeeded the time course of the selected channels is displayed as shown in Figure [GOP Simulation \(Finished\) ↗ 82](#). Buttons from the TopSpin toolbar can now for example be used to zoom into the data or measure durations. When the simulation is finished the "Start" and "Back..." buttons in ParaVision are enabled again.

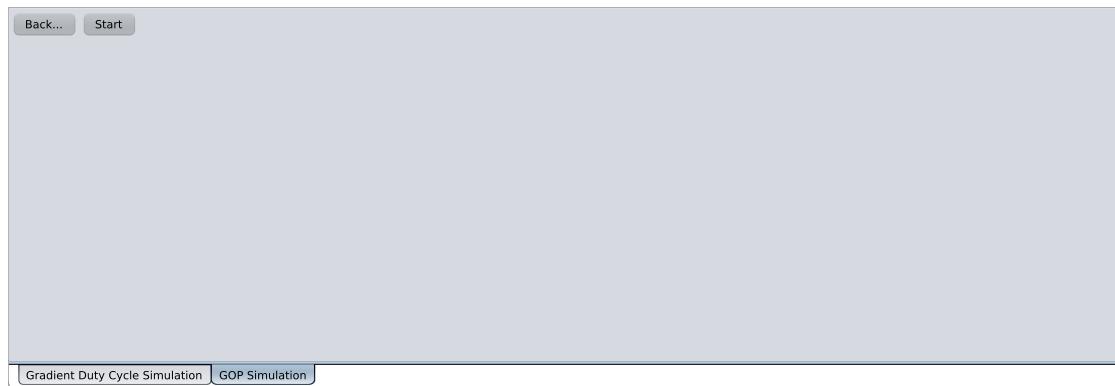


Figure 1.66: GOP Simulation

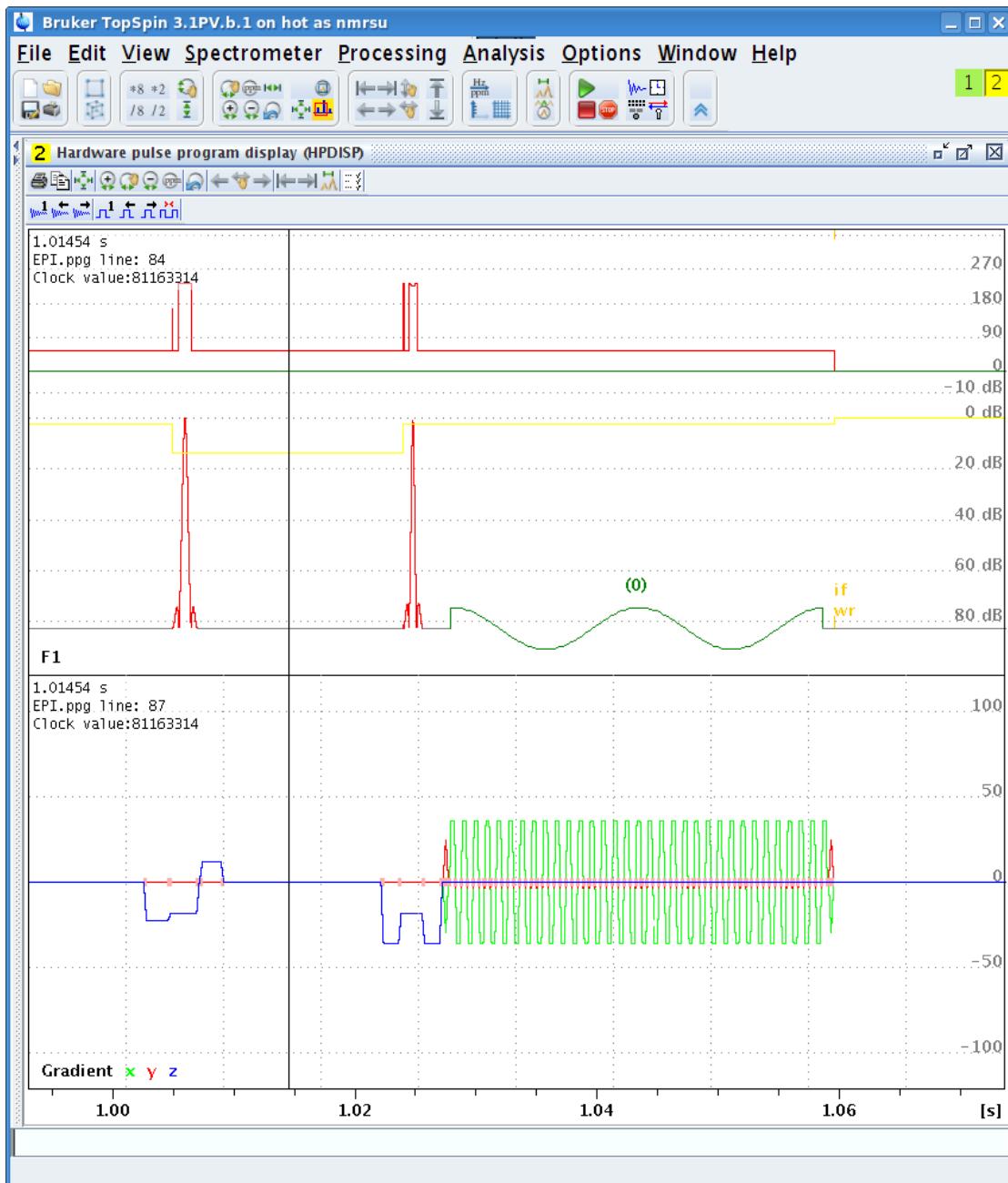


Figure 1.67: GOP Simulation (Finished)

Notice:

- To switch back to the scan program, stop a running simulation (if any) and click the "Back..." button.
- To stop a running GOP simulation enter "kill" into the command line at the bottom of the TopSpin window and press "Return". This will open a dialog presenting all currently running TopSpin commands. Select the line with the "hpdisp" command and click "Kill...".
- The automatic raise of the TopSpin window may not always work reliably (depending on the window manager used by your desktop environment and its configuration). To overcome this inconvenience raise the TopSpin window manually using for example the task bar of your desktop.

1.2.7.7 Stopping a GOP Simulation

Goal:

Stop a running GOP simulation before it is finished.

1. Enter “kill” into the command line at the bottom of the TopSpin window and press “Return”.
 - A dialog presenting all currently running TopSpin commands is opened.
2. Select the line with the “hpdisp” command and click “Kill...”.
 - The simulation stops.

Notice:

No simulation result is displayed, if a simulation is stopped prematurely.

1.2.8 Using the Slide Show

1.2.8.1 Overview

Some scan instructions may produce a huge number of images. In order to get a quick overview or to select individual images for use in other tools the Slide Show (see Figure [Slide Show \[83\]](#)) can be used.

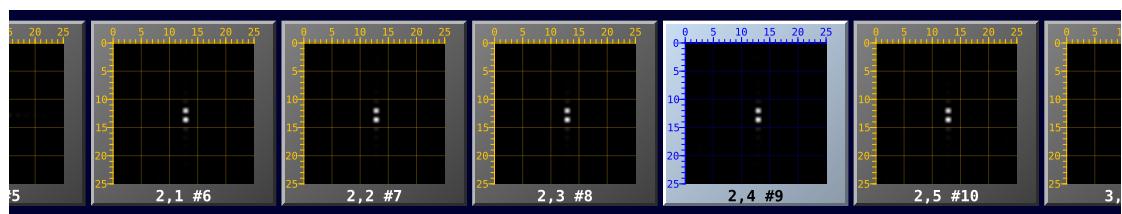


Figure 1.68: Slide Show

1.2.8.2 Loading Images

Goal:

Preview and/or select acquired images.

1. Select the scan instruction whose images should be loaded.
 - The scan instruction is highlighted.
2. Drag and drop the scan instruction into the Slide Show.
 - The images are displayed.

Notice:

- Any image series (e.g. from the Workspace Explorer) may be dragged and dropped into the Slide Show as well.
- A standalone version of the Slide Show can be started from the Workspace Explorer using the "Slide Show" context menu entry of the node "Datasets > SUBJECT > STUDY > EXAMINATION > IMAGE SERIES > 2D/3D Image Data" or from the Dataset Browser via "Image Series > View > Slide Show".

1.2.8.3 Navigating in the Slide Show Using the Mouse Wheel

Goal:

Scroll through all images of a dataset.

1. Turn the mouse wheel while the mouse pointer is located inside the Slide Show.
 - ▶ The images are scrolled to the left/right depending on the direction of rotation.

1.2.8.4 Navigating to Selected Images

Goal:

Navigate to a special image.

1. Open the context menu (see Figure [Context Menu Slide Show \[▶ 84\]](#)) and invoke one of the following "Center ... Slide" actions.

"Center Current Slide" The image currently below the mouse pointer will be centered in the Slide Show.

"Center First Slide" The first image (based on the linear frame index) will be centered in the Slide Show.

"Center Middle Slide" The middle image (based on the linear frame index) will be centered in the Slide Show.

"Center Last Slide" The last image (based on the linear frame index) will be centered in the Slide Show.

- ▶ The selected image is centered in the Slide Show.

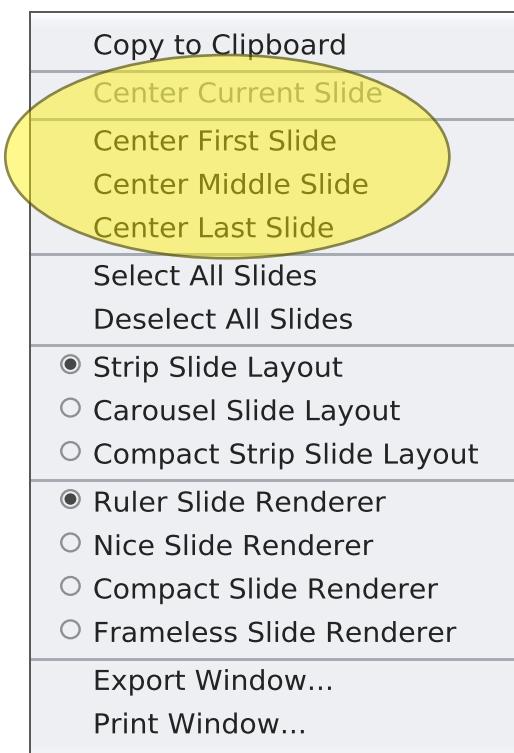


Figure 1.69: Context Menu Slide Show

1.2.8.5 Selecting Images

Goal:

Select one or more images to drag the selected images into the Geometry Editor or Viewing Card.

1. Click the images to be selected or use "Select All Slides" / "Deselect All Slides" from the context menu (see Figure [Context Menu Slide Show \[▶ 85\]](#)).
- The images will be highlighted.

Notice:

The Slide Show supports the so called multiple interval selection (like tables or lists). Pressing the Ctrl key while clicking with the mouse will select/deselect the clicked images. Pressing the Shift key while clicking will extend the selection from the last selection to the new selection.

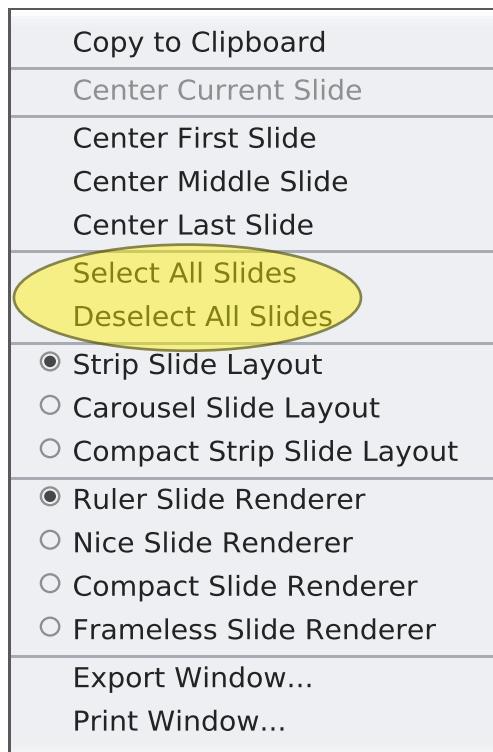


Figure 1.70: Context Menu Slide Show

1.2.8.6 Exporting a Single Image

Goal:

Use a single image in another program (e.g. gimp).

1. Select the image to be exported.
- The image will be highlighted.
2. Open the context menu (see Figure [Context Menu Slide Show \[▶ 86\]](#)) and invoke "Copy to Clipboard".
- The image is copied into the system clipboard and may be imported in another application (e.g. gimp) from the clipboard.

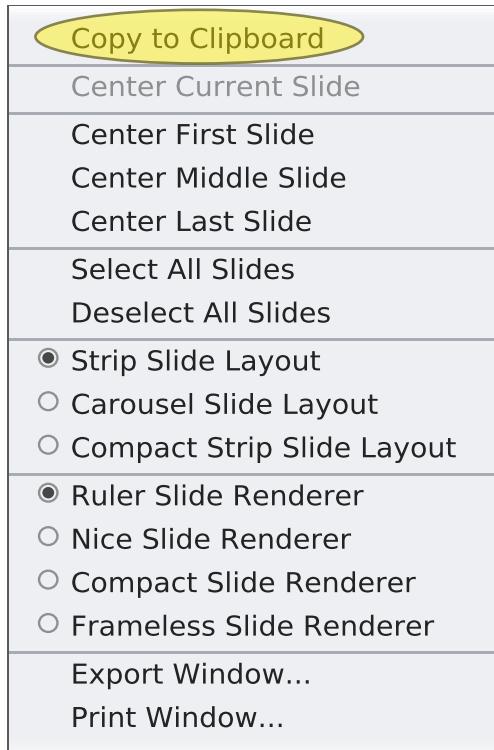


Figure 1.71: Context Menu Slide Show

1.2.8.7 Changing the Slide Show Layout

Goal:

Modify the layout of the slides in the Slide Show.

1. Open the context menu (see Figure [Context Menu Slide Show \[▶ 87\]](#)) and invoke one of the "... Slide Layout" actions.
 - ▶ The selected layout is used for the Slide Show.

Notice:

The default layout can be set in "Window > Options > Slide Show > Renderer and Layout". Changing the default will be come into effect the next time a Slide Show is created.



Figure 1.72: Context Menu Slide Show

1.2.8.8 Changing the Slide Renderer

Goal:

Modify how slides are rendered.

1. Open the context menu (see Figure [Context Menu Slide Show \[▶ 88\]](#)) and invoke one of the "... Slide Renderer" actions.
 - The selected renderer is used for the slides.

Notice:

The default renderer can be set in "Window > Options > Slide Show > Renderer and Layout". Changing the default will be come into effect the next time a Slide Show is created.

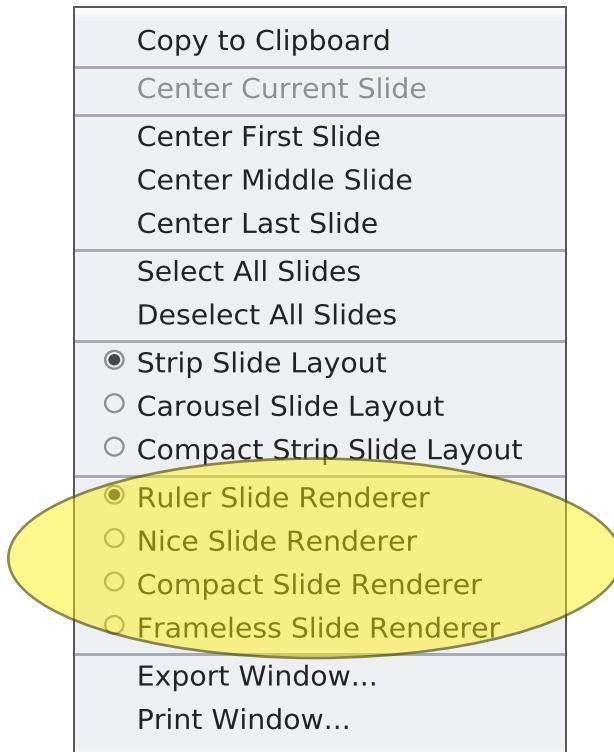


Figure 1.73: Context Menu Slide Show

1.3 Geometry Editor

1.3.1 Overview

The **Geometry Editor**, shown in Figure [Geometry Editor Overview \[▶ 89\]](#) is part of the **Examination Card** and consists of four viewports and the **Geometry Palette**.

It collaborates with the **Parameter Editor** (most importantly with the **Geometry** parameter card) and the **Viewing Palette** (see Chapter [The Palette for Viewing \[▶ 133\]](#)).

The **Geometry Editor** is used to adjust the geometrical properties of the scan going to be acquired by defining and interactively changing geometrical objects such as slice packages, saturation slices, voxels, etc.

Many properties of these objects are represented simultaneously within the viewports, in the **Geometry Palette**, and on the **Parameter Editor's Geometry** card.

All these views are being kept synchronized at all times, and you may choose to make adjustments wherever it's most convenient to you. For instance, if a viewport is cluttered with lots of mutually intersecting objects, object selection by means of the **Geometry Palette** might be faster than trying to click into the viewport.

If an instruction has been opened in the **Parameter Editor**, then the **Geometry Editor** viewports will automatically display geometry objects defined in that instruction. As long as no reference images are present, no interactive changes are possible within the viewports, so either the **Geometry Palette** or the **Routine** card (see Chapter [Routine Card \[▶ 241\]](#)) and **Geometry** card (see Chapter [Geometry Card \[▶ 271\]](#)) in the **Parameter Editor** must be used.

Reference images can be loaded into the left three viewports, to present the geometry to be planned in the context of an image and to work interactively, within the viewport, on the geometry objects. The fourth viewport (at the extreme right) shows a combined 3D view of all current reference images and the geometry objects.

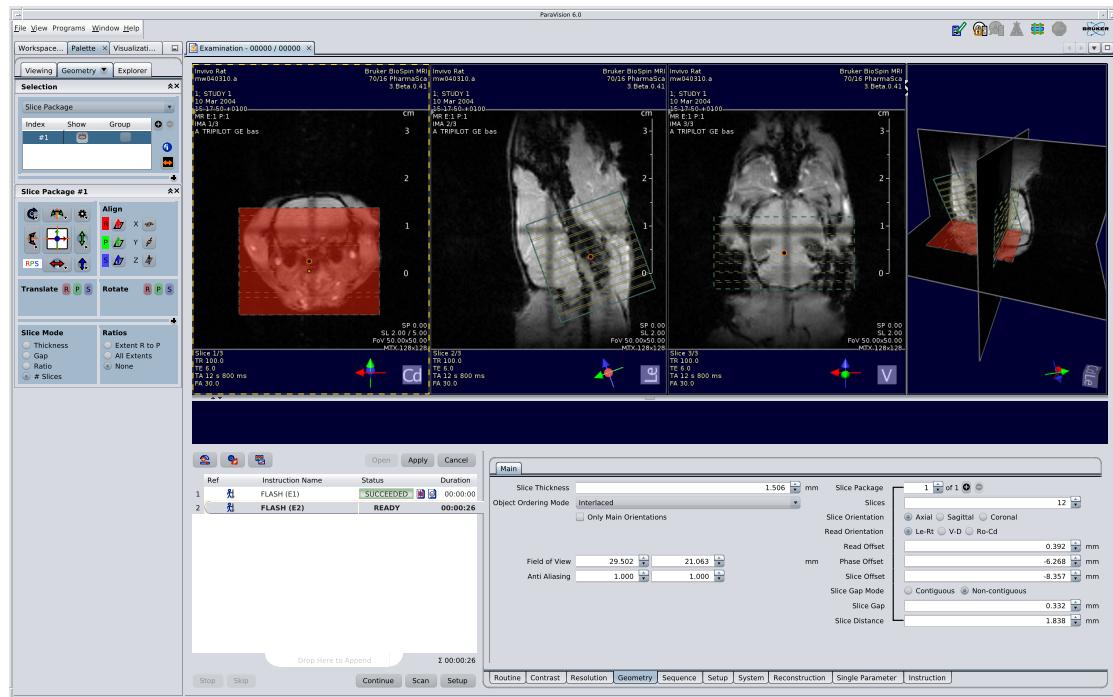


Figure 1.74: Geometry Editor Overview

1.3.2 Common Tasks

This chapter contains concise step-by-step descriptions of the most common tasks involving the **Geometry Editor**. Refer to Chapters **Geometry Palette** and [Geometry Editor Viewports](#) ▶ [114](#) for further details, including illustrations.

1.3.2.1 Load Reference Images

Usually, a first set of reference images is acquired using a localizer scan. Upon completion, these images are loaded automatically into the **Geometry Editor** viewports.

1.3.2.1.1 Load Reference Images Manually

Goal:

Use already acquired images to see the geometry to be planned in context and to be able to work interactively within the Geometry Editor viewports.

Using the Scan Program Table:

1. Drag the desired instruction from the **Scan Program Table** and drop it onto one of the left three **Geometry Editor** viewports.
- Up to three images (if available) from the dropped image series will be loaded. See Chapter [Load a Reference Image Into a Single Viewport](#) ▶ [91](#) for how to load into a single viewport only.

Notices:

- Reconstructed 2D or 3D image data must be available in the instruction to load, i. e., the second last column of the table contains one of the following icons:
 -  2D image data
 -  3D image data
- A warning will be shown on attempts to load reference images which have been acquired as part of a different study than the scan being planned.
- A warning will be shown if the subject coordinate systems of the scan to be planned and the reference images do not match.

Using the Palette:

1. On the Palette, select the tab **Explorer**, then click **Datasets**.
2. Select the desired **Subject**, **Study**, and **Image Series**.
3. Drag the desired image series from the **Palette** and drop it onto one of the left three **Geometry Editor** viewports.
 - Up to three images (if available) from the dropped image series will be loaded. See Chapter [Load a Reference Image Into a Single Viewport \[▶ 91\]](#) for instructions on how to load into a single viewport only.

Notices:

- A warning will be shown on attempts to load reference images which have been acquired as part of a different study than the scan being planned.
- A warning will be shown if the subject coordinate systems of the scan to be planned and the reference images do not match.

Using the Dataset Browser directly:

1. In the main menu, select **Window->Dataset Browser** (see Chapter [Dataset Browser \[▶ 166\]](#) for details).
2. Grab the **Dataset Browser** by its tab and dock it side-by-side with the **Examination Card**.
3. Drag the desired image series from the **Dataset Browser** and drop it onto one of the left three **Geometry Editor** viewports.
 - Up to three images (if available) from the dropped image series will be loaded. See Chapter [Load a Reference Image Into a Single Viewport \[▶ 91\]](#) for instructions on how to load into a single viewport only.

Notices:

- A warning will be shown on attempts to load reference images which have been acquired as part of a different study than the scan being planned.
- A warning will be shown if the subject coordinate systems of the scan to be planned and the reference images do not match.

Using the Dataset Browser via Workspace Explorer:

1. If the **Workspace Explorer** is not already open, select **Window->Workspace Explorer** in the main menu.
2. In the main menu, select **Window->Dataset Browser** (see Chapter [Dataset Browser \[▶ 166\]](#) for details).

3. Right-click the desired image series and select **Select in Explorer** in the context menu.
 - The **Workspace Explorer** will come to the front, with the desired image series selected.
4. Drag the selected node from the **Workspace Explorer** and drop it onto one of the left three **Geometry Editor** viewports.
 - Up to three images (if available) from the dropped image series will be loaded. See Chapter [Load a Reference Image Into a Single Viewport ▶ 91](#) for instructions on how to load into a single viewport only.

Notices:

- A warning will be shown on attempts to load reference images which have been acquired as part of a different study than the scan being planned.
- A warning will be shown if the subject coordinate systems of the scan to be planned and the reference images do not match.

Using the Workspace Explorer:

1. In the main menu, select **Window->Workspace Explorer**.
2. Navigate through the **Datasets** tree to the desired image series folder, **2D Image Data** node, or **3D Image Data** node.
3. Drag the selected node from the **Workspace Explorer** and drop it onto one of the left three **Geometry Editor** viewports.
 - Up to three images (if available) from the dropped image series will be loaded. See Chapter [Load a Reference Image Into a Single Viewport ▶ 91](#) for how to load into a single viewport only.

Notices:

- A warning will be shown on attempts to load reference images which have been acquired as part of a different study than the scan being planned.
- A warning will be shown if the subject coordinate systems of the scan to be planned and the reference images do not match.

1.3.2.1.2 Load a Reference Image Into a Single Viewport

If a reference image series is dropped onto one of the **Geometry Editor** viewports, then **all** viewports will load new images from this series, if available.

Goal:

Load a new reference image into exactly one viewport (and leave the other viewports unchanged).

Use the **Slide Show** in the **Examination Card** as follows:

1. Select any of the options for drag sources already detailed in Chapter [Load Reference Images Manually ▶ 89](#).
2. Instead of dropping into a **Geometry Editor** viewport, drop into the **Slide Show** component located by default below the viewports.
 - Thumbnails of the images available in the image series will be shown.
3. Drag-and-drop an image from the **Slide Show** into one of the left three **Geometry Editor** viewports.
 - The image will be loaded into the drop target viewport. The other viewports will stay unchanged.

4. Optionally, repeat step 3 to load more images into other viewports.

Notices:

- Refer to Chapter [Using the Slide Show \[▶ 83\]](#) for more information about the **Slide Show** component.
- A warning will be shown on attempts to load reference images which have been acquired as part of a different study than the scan being planned.
- A warning will be shown if the subject coordinate systems of the scan to be planned and the reference images do not match.

1.3.2.1.3 Load Reference Images Automatically

Goal:

Create a scan instruction, which loads its results automatically as reference images into the **Geometry Editor** as soon as acquisition and reconstruction are completed.

1. Open the **Processing Platform** for the instruction in question.
2. Double-click the **Data Reconstruction** processing to open the editor.
3. In **Post Image Series Activities**, check **Load Reference Images**.
4. Apply and go back, then save the instruction using its context menu.
 - If the customized scan instruction just created is used in a scan program, then its results will be loaded automatically as reference images into the **Geometry Editor**.

Refer to Chapter [Using the Processing Platform \[▶ 72\]](#) for further details.

1.3.2.2 Work with Reference Images

A large part of the functionality of the **Viewing Palette** (see Chapter [View Tools \[▶ 140\]](#)) is available for working with reference images in the **Geometry Editor**. Likewise, the left three **Geometry Editor** viewports work much in the same way as **Viewing Card** viewports (see Chapter [Viewports \[▶ 134\]](#)).

Notices:

- Number and arrangement of **Geometry Editor** viewports cannot be changed. To work with a large number of images and with arbitrary viewport layouts, use the **Viewing Card**.
- With the exception of creating snapshots (see Chapter [Creating Snapshots \[▶ 162\]](#)), no **Analysis Tools** are available within the **Geometry Editor**. Use the **Viewing Card** (described in Chapter [Viewing Card \[▶ 129\]](#)) instead.

1.3.2.3 Add Slice Packages

Prerequisites:

- An open scan instruction with **READY** status

Goal:

Add a new slice package.

Using the Geometry Palette:

1. In the **Geometry Palette's Selection** section, set the drop-down box at the top to **Slice Package**.
2. In the table below the drop-down box, select the entry representing the slice package to duplicate.

3. Click the  button located to the right of the table to insert a duplicate of the current slice package.
 - A duplicate of the selected slice package is inserted after the current index. The new slice package gets selected automatically.

Notice:

- The  button is disabled if the maximum number of slice packages has been reached.

Using the Parameter Editor:

1. Usually on the **Routine** or **Geometry** card, find the **Slice Package** parameter array group.
2. Optionally adjust the index of the current package to set the insertion index.
3. Click the  button on the same line to insert a new slice package at the current index.
 - A new slice package is created and gets selected automatically.

Notice:

- The  button is disabled if the maximum number of slice packages has been reached.

Using a Geometry Editor Viewport:

Not possible

1.3.2.4 Remove Slice Packages**Prerequisites:**

- An open scan instruction with **READY** status

Goal:

Remove an existing slice package.

Using the Geometry Palette:

1. In the **Geometry Palette's Selection** section, set the drop-down box at the top to **Slice Package**.
2. In the table below the drop-down box, select the entry representing the slice package to remove.
3. Click the  button located to the right of the table to remove the current slice package.
 - The slice package is deleted. The package following it, if any, gets selected automatically. If the last package is removed, then the one preceding it gets the selection.

Notice:

- The  button is disabled if the minimum number of slice packages has been reached.

Using the Parameter Editor:

1. Usually on the **Routine** or **Geometry** card, find the **Slice Package** parameter array group.

2. Optionally adjust the index of the current package.
3. Click the  button on the same line to remove the slice package at the current index.
 - The slice package is deleted. The package following it, if any, gets selected automatically. If the last package is removed, then the one preceding it gets the selection.

Notice:

- The button  is disabled if the minimum number of slice packages has been reached.

Using a Geometry Editor Viewport:

Not possible

1.3.2.5 Select a Slice Package

Prerequisite:

- An open scan instruction

Goal:

Select another slice package.

Using the Geometry Palette:

1. In the **Geometry Palette's Selection** section, set the drop-down box at the top to **Slice Package**.
2. In the table below the drop-down box, select the entry representing the desired slice package.

Notice:

- Only single selection is possible for slice packages. To manipulate multiple slice packages at once, use the grouping feature described in Chapter [Geometry Object Table \[▶ 104\]](#).

Using the Parameter Editor:

1. Usually on the **Routine** or **Geometry** card, find the **Slice Package** parameter array group.
2. Adjust the index spinner to change the currently selected package.

Notice:

- Only single selection is possible for slice packages. To manipulate multiple slice packages at once, use the grouping feature described in Chapter [Geometry Object Table \[▶ 104\]](#).

Using a Geometry Editor Viewport (Reference Image Absent):

1. Move the pointer over the dark green line representing the bounding box of an unselected slice package.
 - The line under the pointer will change to light green.
2. Click the light green line.
 - The slice package is selected; the line will turn to red and slices will be shown in yellow (if any and slice display enabled).

See Chapter [Geometry Editor Viewports \[▶ 114\]](#) for detailed instructions on how to work within viewports. Refer to Chapter [Keyboard Support \[▶ 120\]](#) for information about selecting slice packages by keyboard.

Notices:

- If the viewport is too cluttered, consider setting some objects to invisible, see Chapter [Geometry Object Table \[▶ 104\]](#).
- Only single selection is possible for slice packages. To manipulate multiple slice packages at once, use the grouping feature described in Chapter [Geometry Object Table \[▶ 104\]](#).

Using a Geometry Editor Viewport (Reference Image Present):

In-viewport slice package selection using the mouse is possible, but requires changing geometry object draw styles and is generally discouraged. Preferably use one of the alternatives discussed above or refer to Chapter [Keyboard Support \[▶ 120\]](#) for information about selecting slice packages by keyboard.

1.3.2.6 Deselect Slice Packages

Prerequisites:

- An open scan instruction

Goal:

Clear the current selection.

Using the Geometry Palette:

1. In the **Geometry Palette's Selection** section, set the drop-down box at the top to **Slice Package**.
2. In the table below the drop-down box, click the entry representing the selected slice package (visible by dark blue background) while holding down the <Ctrl> key.

Using the Parameter Editor:

Not possible

Using a Viewport:

Not possible

1.3.2.7 Translate (Move) Slice Packages

Prerequisites:

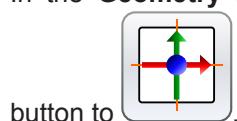
- An open scan instruction with **READY** status and a selected slice package

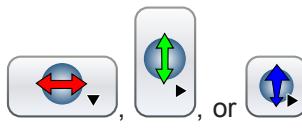
Goal:

Translate the selected slice package.

Using the Geometry Palette, in Subject Coordinate Space:

1. In the **Geometry Palette's Slice Package** section, set the coordinate system toggle





2. Use one of the translation buttons, or or , to bring up a pop-up slider to translate the slice package along the read, phase, or slice axis, respectively.

Notice:

- Moving a slice package may be constrained to some directions or disallowed altogether by the method.

Using the Geometry Palette, in Magnet Coordinate Space:

1. In the **Geometry Palette's Slice Package** section, set the coordinate system toggle



button to .

2. Use one of the translation buttons to move the slice package along the x-axis, y-axis, or z-axis, respectively.

Notice:

- Moving a slice package may be constrained to some directions or disallowed altogether by the method.

Using the Geometry Palette, Relative Translation:

1. In the **Geometry Palette's Slice Package** section, click one of the colored toggle buttons for read , phase , or slice direction, next to the **Translate** heading.

2. Set the value of the spinner that appears to the desired translation in millimeters.

3. Hit <Enter> or click the button to apply, repeat to move again.

Notice:

- Moving a slice package may be constrained to some directions or disallowed altogether by the method.

Using the Geometry Palette, Absolute Translation:

1. In the **Geometry Palette**, expand the **Slice Package** section using the button, so that the **Position** heading is visible.

2. Use one of the spinners to change the slice package position along the read (**R**), phase (**P**), or slice (**S**) axis.

Notice:

- Moving a slice package may be constrained to some directions or disallowed altogether by the method.

Using the Parameter Editor:

1. Usually on the **Routine** or **Geometry** card, find the **Slice Package** parameter array group.

2. Use the **Read Offset**, **Phase Offset**, or **Slice Offset** spinners (actual names may vary slightly depending on the method) to translate the slice package along the respective axis.

Notice:

- Moving a slice package may be constrained to some directions or disallowed altogether by the method.

Using a Geometry Editor Viewport, Reference Images Absent:

Not possible

Using a Geometry Editor Viewport, Reference Images Present:

1. Make sure that scaling drag operations have priority, i. e., the toggle button in the lower right corner of the **Geometry Palette's Selection** section is in released state, .
2. Move the pointer over the orange disk representing the centroid of the intersection between slice package and reference image.



► The cursor will change to .

3. Click and drag the package within the reference image plane.

Refer to Chapter [Keyboard Support ▶ 120](#) for information about moving slice packages by keyboard.

Notice:

- Moving a slice package may be constrained to some directions or disallowed altogether by the method.

1.3.2.8 Rotate (Turn) Slice Packages

Prerequisites:

- An open scan instruction with **READY** status and a selected slice package

Goal:

Rotate the selected slice package.

Using the Geometry Palette, in Subject Coordinate Space:

1. In the **Geometry Palette's Slice Package** section, set the coordinate system toggle to .



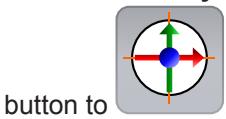
2. Use one of the rotation buttons, , , or , to bring up a pop-up widget to rotate the slice package about the read, phase, or slice axis, respectively.

Notice:

- Rotating a slice package may be constrained to some directions or disallowed altogether by the method.

Using the Geometry Palette, in Magnet Coordinate Space:

1. In the **Geometry Palette's Slice Package** section, set the coordinate system toggle



2. Use one of the rotation buttons to turn the slice package about the x-axis, y-axis, or z-axis.

Notice:

- Rotating a slice package may be constrained to some directions or disallowed altogether by the method.

Using the Geometry Palette, Relative Angles:

1. In the **Geometry Palette's Slice Package** section, click one of the colored toggle buttons

for read **R**, phase **P**, or slice **S** axis, next to the **Rotate** heading.

2. Set the value of the spinner that appears to the desired rotation in degrees.

3. Hit <Enter> or click the button to apply, repeat to turn again.

Notice:

- Rotating a slice package may be constrained to some directions or disallowed altogether by the method.

Using the Geometry Palette, Absolute Angles:

1. In the **Geometry Palette**, expand the **Slice Package** section using the button, so that the **Angles** heading is visible.

2. Use one of the spinners to change the slice package angle about the read (**R**), phase (**P**), or slice (**S**) axis.

Notice:

- Rotating a slice package may be constrained to some directions or disallowed altogether by the method.

Using the Parameter Editor, Main Orientation:

1. Usually on the **Routine** or **Geometry** card, find the **Slice Package** parameter array group.

2. Click one of the **Slice Orientation** radio buttons to set the slice package to the desired main orientation.

Notice:

- Rotating a slice package may be constrained to some directions or disallowed altogether by the method.

Using a Geometry Editor Viewport, Reference Images Absent:

Not possible

Using a Geometry Editor Viewport, Reference Images Present:

1. If the area of intersection between slice package and reference image is very small or very narrow, either zoom in or make sure that rotational drag operations have priority, i.e., the toggle button in the lower right corner of the **Geometry Palette's Selection** section is in pressed state, .
2. Move the pointer over the area of intersection between slice package and reference image.



- The area will light up in red color and the cursor will change to .
3. Click and drag to rotate the package within the reference image plane. Refer to Chapter [Keyboard Support \[▶ 120\]](#) for information about rotating slice packages by keyboard.

Notice:

- Rotating a slice package may be constrained to some directions or disallowed altogether by the method.

1.3.2.9 Resize (Scale) Slice Packages**Prerequisites:**

- An open scan instruction with **READY** status and a selected slice package

Goal:

Resize the selected slice package.

Using the Geometry Palette:

1. In the **Geometry Palette**, expand the **Slice Package** section using the  button, so that the **Extent** heading is visible.
2. Use one of the spinners to resize the slice package in direction of the read (**R**), phase (**P**), or slice (**S**) axis.

Notices:

- Resize operations in slice direction will alter slice thickness, slice gaps, thickness to gap ratio, or the number of slices, depending on the current slice mode, see Chapter [Slice Mode \[▶ 113\]](#).
- Depending on the method, field of view values may be coupled between read and phase axis and/or between slice packages.

Using the Parameter Editor:

1. Usually on the **Routine** or **Geometry** card, find the **Field of View** parameter.
2. Change the value for one of the axes. Depending on the spatial acquisition dimension, the size along one or more axes can only be altered using other parameters.

Notices:

- Resize operations in slice direction will alter slice thickness, slice gaps, thickness to gap ratio, or the number of slices, depending on the current slice mode, see Chapter [Slice Mode \[▶ 113\]](#).
- Depending on the method, field of view values may be coupled between read and phase axis and/or between slice packages.

Using a Geometry Editor Viewport, Reference Images Absent:

Not possible

Using a Geometry Editor Viewport, Reference Images Present:

1. Make sure that scaling drag operations have priority, i. e., the toggle button in the lower right corner of the **Geometry Palette's Selection** section is in released state, .
2. Move the pointer over the boundary of the area of intersection between slice package and reference image.



- The active edge will light up in red color and the cursor will change to .
- 3. Click and drag to resize the slice package in a direction perpendicular to the edge being dragged.

Refer to Chapter [Keyboard Support \[120\]](#) for information about resizing slice packages by keyboard.

Notices:

- Resize operations in slice direction will alter slice thickness, slice gaps, thickness to gap ratio, or the number of slices, depending on the current slice mode, see Chapter [Slice Mode \[113\]](#).
- Depending on the method, field of view values may be coupled between read and phase axis and/or between slice packages.

1.3.2.10 Align Slice Packages

Prerequisites:

- An open scan instruction with **READY** status and a selected slice package
- A reference image being present in the viewport to work in

Goal:

Align either position or orientation of the selected slice package with the reference image in the focused viewport.

Using the Geometry Palette, Align Orientation:

1. Move the mouse pointer over the viewport containing the reference image to align with and hit <Space> to focus that viewport.
2. Click one of the orientational alignment buttons, , , or , to align the slice package orientation with the reference image.
 - The slice package read, phase, or slice axis, respectively, is changed to be perpendicular to the reference image.

Notice:

- If slice package position and/or orientation are constrained by the method, then some alignment operations may be unavailable.

Using the Geometry Palette, Align Position:

1. Move the mouse pointer over the viewport containing the reference image to align with and hit <Space> to focus that viewport.
2. Click one of the positional alignment buttons, , , or , to align the slice package position with the reference image.
 - The slice package center is moved along the reference image x-axis, y-axis, or z-axis, respectively, to the center of the image.

Notice:

- If slice package position and/or orientation are constrained by the method, then some alignment operations may be unavailable.

Using the Parameter Editor:

Not possible

Using a Geometry Editor Viewport:

Not possible

1.3.2.11 Work With Other Geometry Objects

The step-by-step descriptions given for slice packages in the preceding sections are generally valid for other types of geometry objects as well, with the exception of object creation.

Prerequisites:

- An open scan instruction with **READY** status

Goal:

Create another type of geometry object than a slice package.

Using the Parameter Editor, no Objects of Given Type Exist

1. Using the **Parameter Editor**, you first need to locate and (in many cases) enable the parameter array group representing the desired kind of object, for example **Sat Slice** on the **Contrast / Fov Sat** card for saturation slices.
 - If the functionality had first to be enabled, then usually a new object is created and  gets selected automatically. Otherwise, click the  button in the array group header line to insert a new object.

Notices:

- The set of available geometry objects depends on the method in use.
- Applicable constraints may vary among different kinds of geometry objects and for different methods.

Using the Geometry Palette, no Objects of Given Type Exist

Not possible

Using the Parameter Editor, Objects of Given Type Already Exist

1. Locate the parameter array group representing the desired kind of object, for example **Sat Slice** on the **Contrast / Fov Sat** card for saturation slices.
2. Optionally adjust the array group index to set the place of insertion.
3. Click the  button on the same line to insert a new object at the current index.
 - A new object is created and gets selected automatically.

Notices:

- The set of available geometry objects depends on the method in use.
- Applicable constraints may vary among different kinds of geometry objects and for different methods.

Using the Geometry Palette, Objects of Given Type Already Exist

1. Select the desired kind of object from the drop-down box at the top of the **Selection** tab.
2. In the table below the drop-down box, select the entry representing the object to duplicate.
3. Click the  button located to the right of the table to insert a duplicate of the current object.
 - A duplicate of the selected object is inserted after the current index and gets selected automatically.

Notices:

- The set of available geometry objects depends on the method in use.
- Applicable constraints may vary among different kinds of geometry objects and for different methods.

1.3.3 Geometry Palette

The geometry palette consists of two parts:

- A set of tools to manage the collection of geometry objects in the **Selection** section, described in Chapter [Selection Section ▶ 103](#)
- A further set of tools to work on the selected geometry object in a second section, captioned with object type and index. All these will be discussed in Chapter [Slice Package Section ▶ 106](#).

1.3.3.1 Selection Section

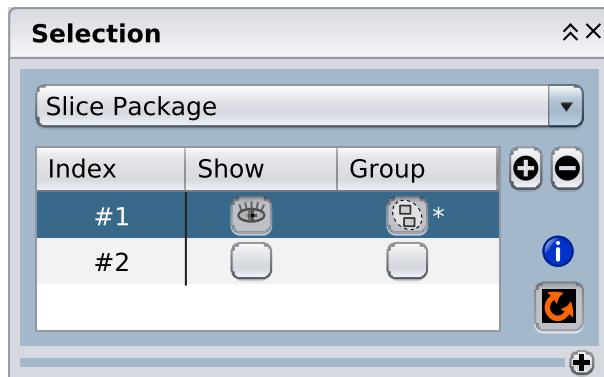


Figure 1.75: Geometry Palette, selection section

Tools to manage the collection of geometry objects, fully described in the remainder of this chapter.

Notice:

- All modifying operations are disabled for scans not in **READY** status.

1.3.3.1.1 Geometry Object Drop-Down Box

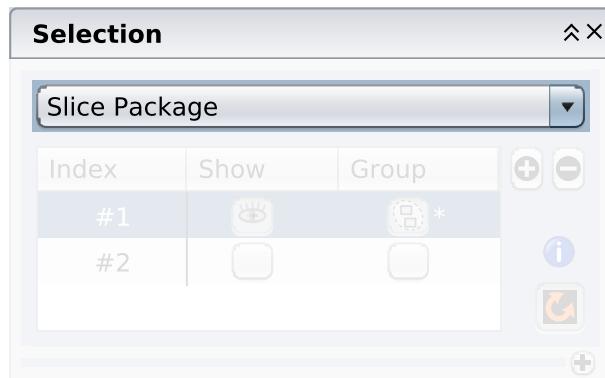


Figure 1.76: Geometry Object Drop-Down Box, only objects of selected type are shown in the Geometry Object Table.

Drop-down box allowing to choose the type of geometry object to work on. Filled in automatically if new kinds of objects (such as saturation slices) are created by means of the **Parameter Editor**. All objects of chosen type are listed in the **Geometry Object Table** below the drop-down box.

1.3.3.1.2 Geometry Object Table

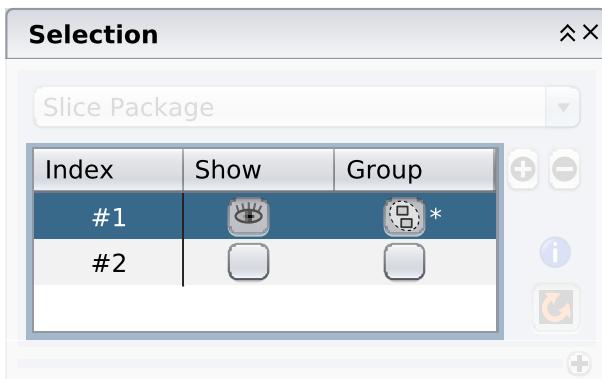


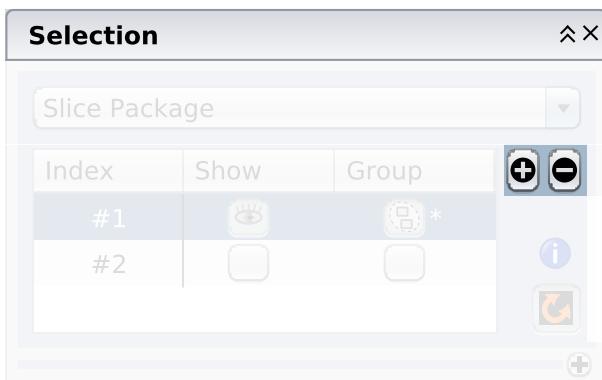
Figure 1.77: Geometry Object Table, a table of all geometry objects with type selected in the Geometry Object Drop-Down Box.

Table listing all geometry objects with type as chosen by the **Geometry Object Drop-Down Box**. The table is composed of the following three columns:

- **Index:** Geometry object index, corresponding to the index into the respective array group in the **Parameter Editor**. Both indices are being held in lockstep. Click into this column to select the corresponding object.
- **Show:** Visibility toggle buttons. New objects are generally visible by default, you might want to set some of them to invisible to clean up cluttered viewports.
- **Group:** Group objects to apply operations to all members at once. Grouping is disabled by default.

Table entries are selected by clicking into the **Index** column and deselected by clicking while holding the **<Ctrl>** key. Only a single object can be selected at any given time, the selected row gets a dark blue background. Properties of the selected object are shown and can be edited in the palette section below, captioned by object type and table index.

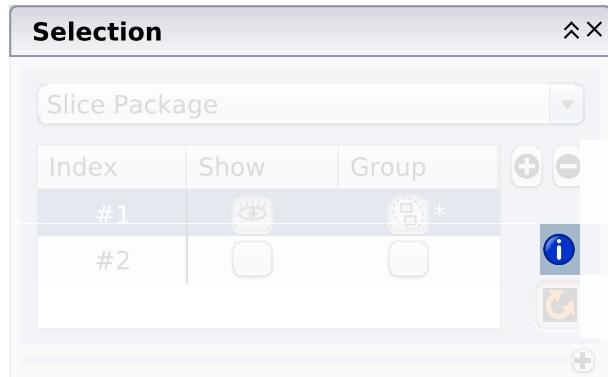
1.3.3.1.3 Add/Remove Buttons



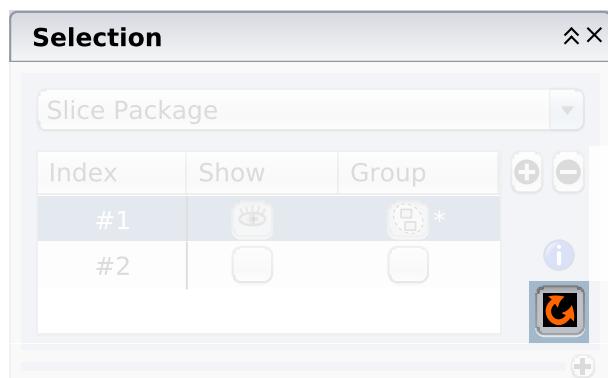
- Insert a duplicate of the selected geometry object at the index after the selection. Disabled if no selection exists or the maximum number of objects of given type has been reached.
- Remove the selected geometry object. Disabled if no selection exists or the minimum number of objects of given type has been reached.

Notice:

- Per-method restrictions for the minimum and maximum number of instances of a given type of geometry object apply.

1.3.3.1.4 Key Binding Information

The **i** button shows a summary of key bindings valid within **Geometry Editor** viewports. Refer to Chapter [Keyboard Support \[120\]](#) for more information.

1.3.3.1.5 Drag Priority Toggle Button

This button toggles picking priority between different sets of drag operations that can be performed on the intersection polygon between geometry object and reference image:

- Drag operations for scaling (at edges) and moving (at center) have priority over rotations. This is the default.
- Drag operations for rotations (whole face) have priority over scaling and translations.

Notice:

- The priorities can also be toggled by means of the middle mouse button while drag operations are active and the pointer is within a viewport.

1.3.3.1.6 Draw Style Drop-Down Boxes

Advanced feature, hidden by default. Click the expansion button, , to show.

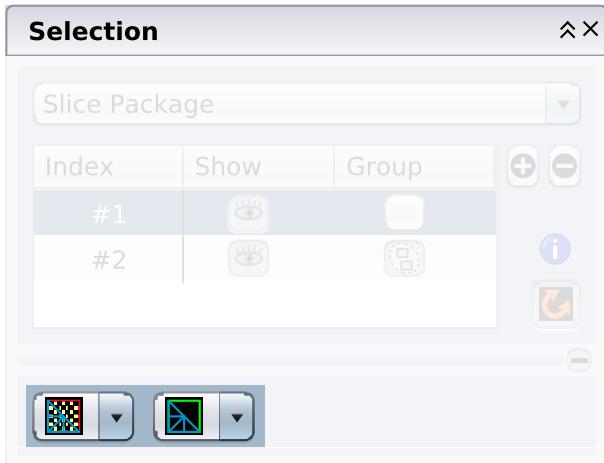


Figure 1.78: Geometry object draw style drop-down boxes

Drop-down boxes allowing to change the draw style for the selected geometry object (left) and unselected geometry objects (right). Two sets of styles are maintained, for the situations without and with reference images.

Available styles for the selected slice package are listed in Chapter [Draw Styles for Selected Slice Package](#) [▶ 125], those for all unselected slice packages are shown in Chapter [Draw Styles for Unselected Slice Packages](#) [▶ 126].

Settings will be discarded and reset to defaults if the instruction is closed. Use the corresponding drop-down-boxes on the **Geometry Editor** page of the **Visualization Preferences** window to set persistent defaults, see Chapter [Default Style](#) [▶ 124].

1.3.3.2 Slice Package Section

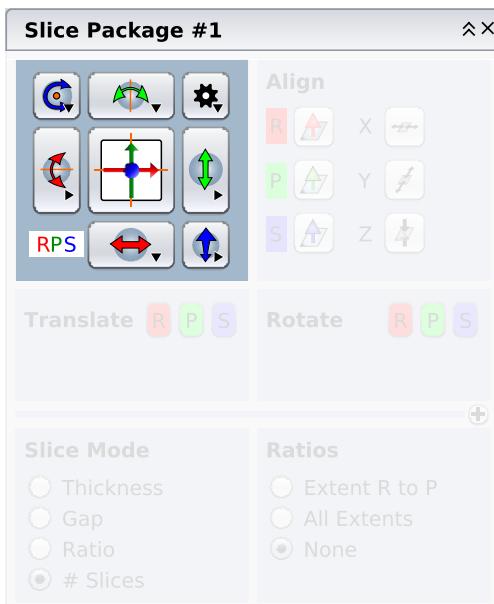


Figure 1.79: Geometry Palette, slice package section

A collection of tools to work on a selected slice package. What will be shown by example of slice packages in the following sections holds generally true for other geometry objects as well. However, many constraints are depending on the combination of method kind and geometry object.

Notices for all following sections:

- The section caption reflects the type and index associated geometry object, so it depends on current context.
- Slice packages cannot be modified if the current scan is not in **READY** status.
- The whole palette section is empty if no slice package is selected.
- Depending on the method, the names of the acquisition coordinate system axes may vary.
- Depending on slice orientation, the read and phase axis control elements may exchange their places.
- The color codes of the acquisition coordinate system axes, read (red), phase (green), and slice (blue) correspond to the coordinate cross shown in all **Geometry Editor** viewports.

1.3.3.2.1 Transform

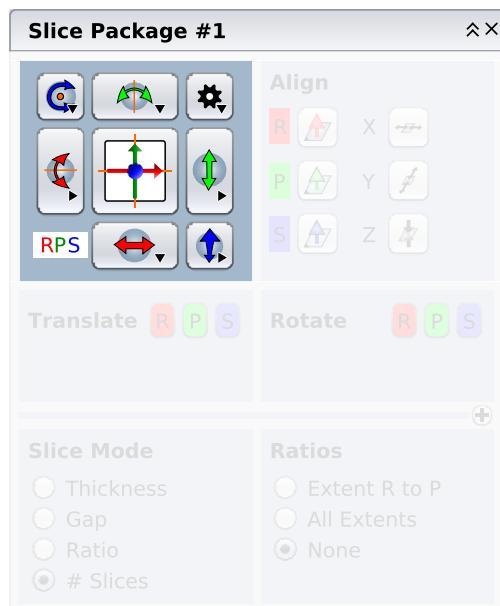


Figure 1.80: Transformation tools

Tools to translate and rotate a slice package either in the subject or in the magnet coordinate system:



- Toggle button to set the current coordinate system either to the acquisition system (RPS, left) or the magnet system (XYZ, right). Effects are limited to the transform panel.



- Rotate slice package about read axis (RPS) or x-axis (XYZ), respectively



- Rotate slice package about phase axis (RPS) or y-axis (XYZ), respectively

-  Rotate slice package about slice axis (RPS) or z-axis (XYZ), respectively
-  Translate slice package along read axis (RPS) or x-axis (XYZ), respectively
-  Translate slice package along phase axis (RPS) or y-axis (XYZ), respectively
-  Translate slice package along slice axis (RPS) or z-axis (XYZ), respectively
-  Brings up a pop-up menu with a few frequently used standard transforms

Notice:

- If slice package position and/or orientation are constrained by the method, then some transform operations may be unavailable.

1.3.3.2.2 Align

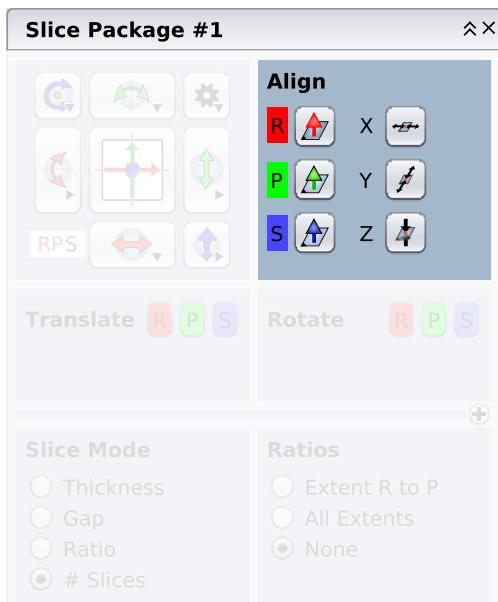


Figure 1.81: Alignment tools

Align either position or orientation of the selected slice package with the reference image in the focused viewport

Orientational alignment (left column):

-  Changes the slice package read axis to be perpendicular to the reference image
-  Changes the slice package phase axis to be perpendicular to the reference image
-  Changes the slice package slice axis to be perpendicular to the reference image

Positional alignment (right column):

- Moves the slice package center along the reference image x-axis, to coincide with the center of the image
- Moves the slice package center along the reference image y-axis, to coincide with the center of the image
- Moves the slice package center along the reference image z-axis, to coincide with the center of the image

Notice:

- If slice package position and/or orientation are constrained by the method, then some alignment operations may be unavailable.

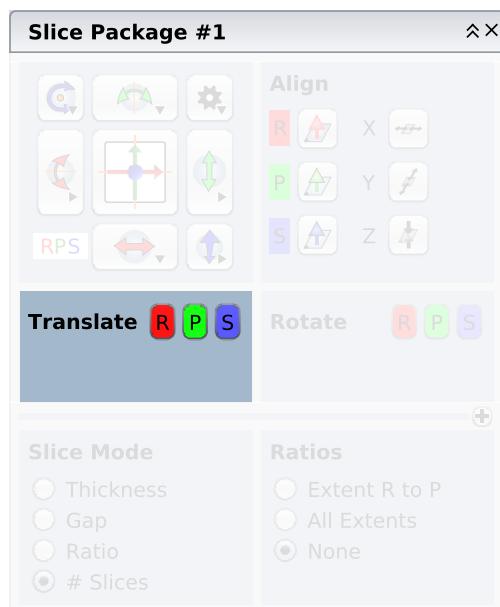
1.3.3.2.3 Translate

Figure 1.82: Relative translation tools

Relative translation along an axis of the acquisition coordinate system

- Initiate relative translation along the read axis
- Initiate relative translation along the phase axis
- Initiate relative translation along the slice axis

Upon clicking, the buttons just described will show a transient spinner where the amount of movement in millimeters can be entered. Hit <Enter> or click the button next to the spinner to apply; repeat to move again.

Notice:

- If the slice package position is constrained by the method, then translation along some or all axes may be unavailable.

1.3.3.2.4 Rotate

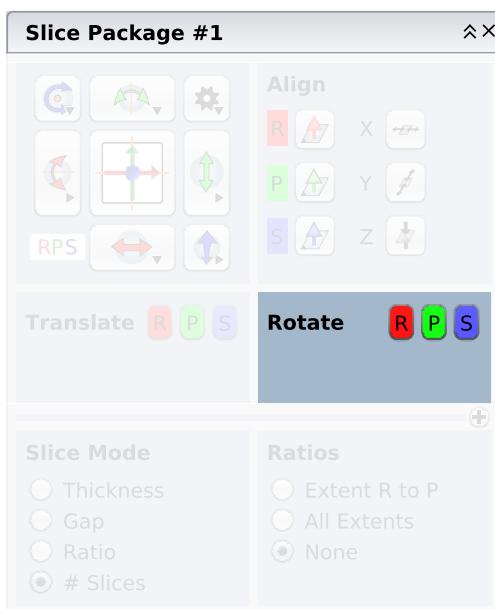


Figure 1.83: Relative rotation tools

Relative rotation about an axis of the acquisition coordinate system

- **R** Initiate relative rotation about the read axis
- **P** Initiate relative rotation about the phase axis
- **S** Initiate relative rotation about the slice axis

Upon clicking, the buttons just described will show a transient spinner where the relative rotation angle in degrees can be entered. Hit <Enter> or click the button next to the spinner to apply; repeat to turn again.

Notice:

- If the slice package orientation is constrained by the method, then rotation about some or all axes may be unavailable.

1.3.3.2.5 Position

Advanced feature, hidden by default. Click the expansion button, , to show.

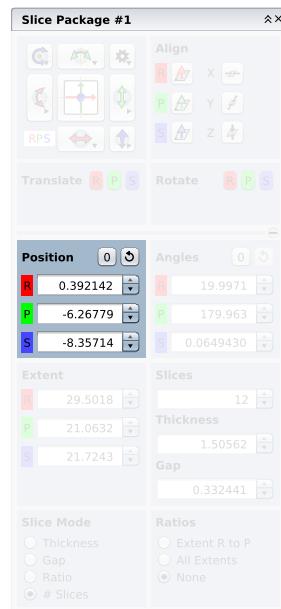


Figure 1.84: Absolute translation tools

- Three spinners showing and allowing changes of the absolute position, in millimeters, in the acquisition coordinate system
- Set position to zero (all axes)
- Revert the position to its initial value

Notice:

- If the slice package position is constrained by the method, then translation along some or all axes may be unavailable.

1.3.3.2.6 Angles

Advanced feature, hidden by default. Click the expansion button, , to show.

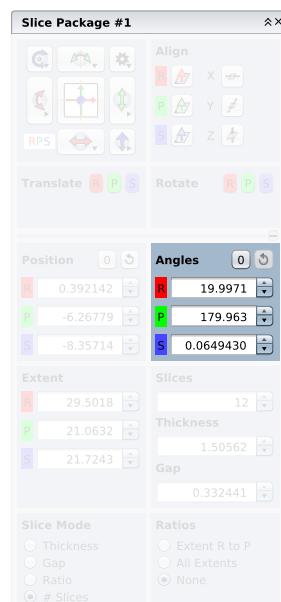


Figure 1.85: Absolute rotation tools

- Three spinners showing and allowing changes of the rotation angles, in degrees, about acquisition coordinate system axes
 - Set angles to zero (all axes)
 - Revert all angles to their initial values

Notice:

- If the slice package orientation is constrained by the method, then rotation about some or all axes may be unavailable.

1.3.3.2.7 Extent

Advanced feature, hidden by default. Click the expansion button, , to show.

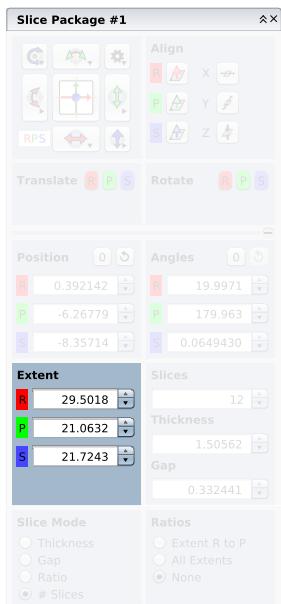


Figure 1.86: Extent modification tools

- Three spinners showing and allowing changes of the slice package extent, in millimeters, in the acquisition coordinate system. Changing the extent in slice direction will change number of slices, slice thickness, or gap, depending on the slice mode.

Notice:

- Extents may be coupled or can be changed independently, depending on the extent ratio mode, see Chapter [Ratios ▶ 114](#).

1.3.3.2.8 Slices, Thickness, and Gap

Advanced feature, hidden by default. Click the expansion button, , to show.

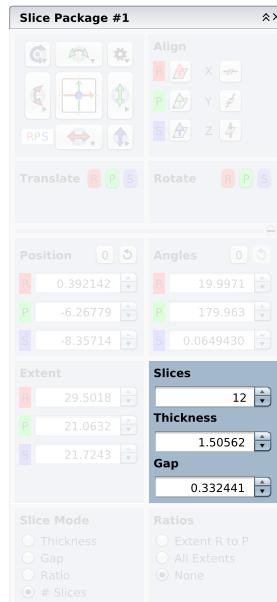


Figure 1.87: Tools to change slice count, slice thickness, and slice gap

Usage of the following tools will lead to changes to the extent in slice direction, the slice gap, or the number of slices, or slice thickness, depending on slice mode.

- **Slices:** Set the number of slices
- **Thickness:** Set the slice thickness
- **Gap:** Set the gap between any pair of slices. Set to zero if there is only a single slice

Notice:

- All values are subject to per-method constraints.

1.3.3.2.9 Slice Mode



Figure 1.88: Slice mode selection tools

Mode for extent changes in slice direction:

- **Thickness:** Adapt slice thickness
- **Gap:** Adapt slice gaps
- **Ratio:** Adapt ratio of slice thickness to slice gap
- **# Slices:** Adapt number of slices

Notices:

- Not all modes are useful in all situations. For example, there is no slice gap if there is only a single slice.
- In **# Slices** mode, the extent in slice direction will be constrained to values leading to an integral number of slices.

1.3.3.2.10 Ratios

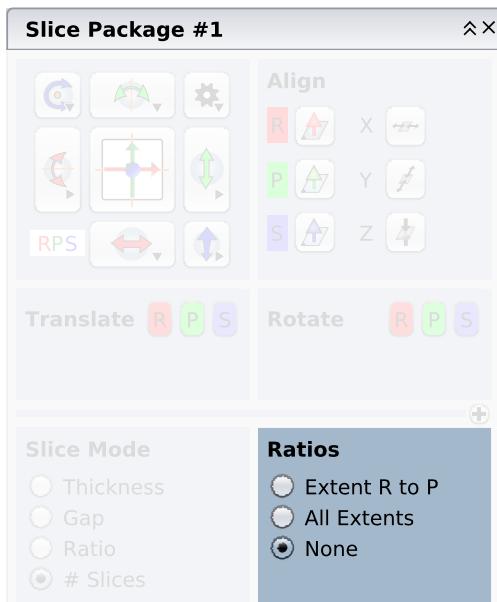


Figure 1.89: Extent ratio mode selection tools

Mode for extent changes:

- **Extent R to P:** Keep ratio of read extent to phase extent
- **All Extents:** Keep ratios between all extents (read, phase, and slice)
- **None:** No extent ratios to keep (let extents change freely)

1.3.4 Geometry Editor Viewports

1.3.4.1 Introduction

The left three **Geometry Editor** viewports are working very similarly to the **Viewing Card** viewports, see Chapter [Viewports ▶ 134](#). The viewport camera view directions are fixed to the reference images used. In contrast, the rightmost viewport presents a hybrid 3D view of all reference images and geometry objects with a camera that can be rotated freely.

Notices:

- Most analysis tools are unavailable within **Geometry Editor** viewports.
- Move the splitter along the left edge of the 3D viewport to distribute screen space between 3D viewports and the three viewports to the left of it.

- Interactive editing of slice packages requires the focused viewport being set to pick mode.

1.3.4.2 Scene without Reference Images

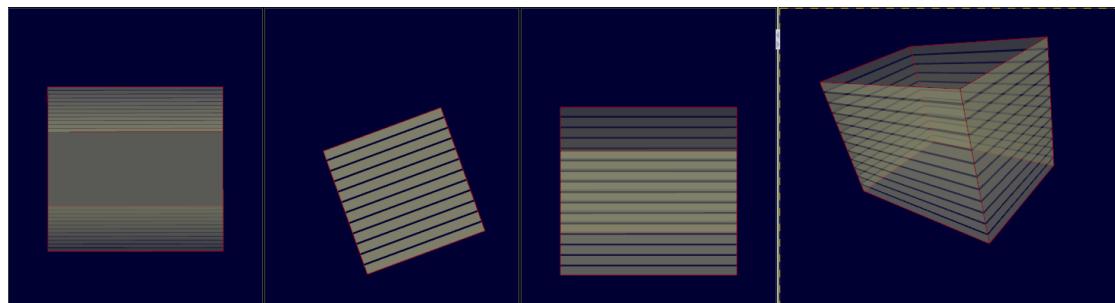


Figure 1.90: Geometry Editor viewports without reference images

- An unselected slice package with bounding box (green).
- An unselected slice package with bounding box (light green) on mouse-over. Click on the wire-frame to select the package.
- A selected slice package with bounding box (red) and three slices (translucent yellow).
- A selected slice package with bounding box (light red) and three slices (translucent yellow) on mouse-over.
- Coordinate cross representing the directions of the selected slice package's acquisition axes: read (red), phase (green), and slice (blue). The arrows point towards more positive values.

Notices:

- Acquisition coordinate axes are color-coded consistently everywhere in the Geometry Editor, within viewports as well as on the geometry palette.

- In-viewport manipulation of slice packages is limited to selection change as long as no reference images are present. Use the **Geometry Palette** instead.

1.3.4.3 Scene with Reference Images

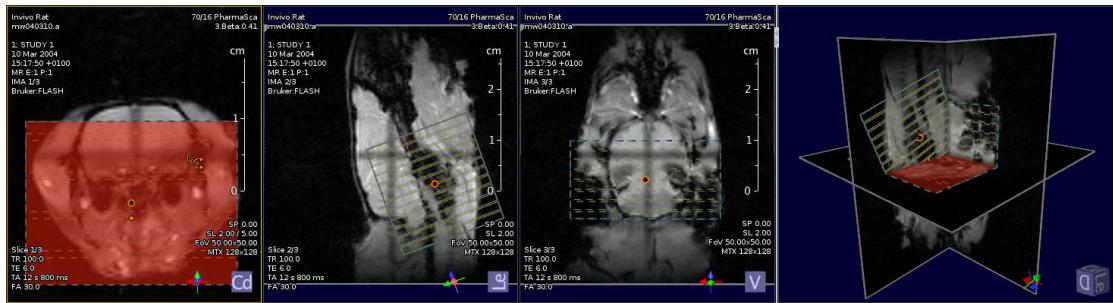
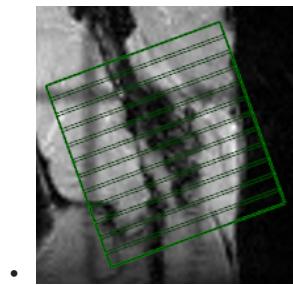


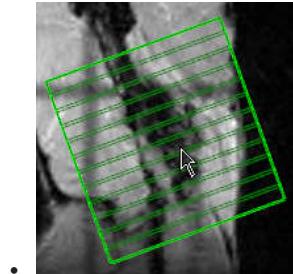
Figure 1.91: Geometry Editor viewports with reference images

The representations of reference images, parameter overlay texts, and 3D orientation cubes are identical to the **Viewing Card**.

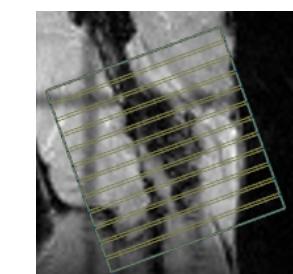
The primary visual elements to work on are the polygonal intersections between slice packages and reference images, these will be called "intersection polygons" from now on.



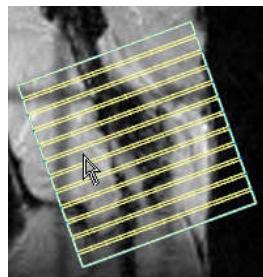
- **Unselected** intersection polygon in passive state. The intersection of the bounding box is drawn as wide, light green line, while intersections of slices are shown as thin dark green lines. Lines are dashed if intersections are oblique.



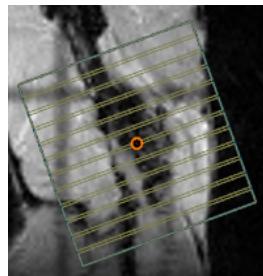
- **Unselected** intersection polygon on mouse-over. Line colors are brighter.



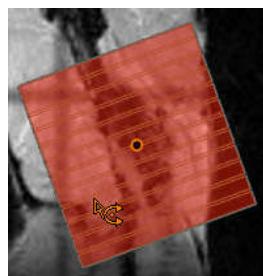
- **Selected** intersection polygon in passive state. Drag operations are disabled. The intersection of the bounding box is drawn as wide, blue line, while intersections of slices are shown as thin yellow lines. Lines are dashed if intersections are oblique.



- **Selected** intersection polygon on mouse-over. Click into the polygon to enable drag operations.



- **Selected** intersection polygon with drag operations enabled, no mouse-over. Can be distinguished from the case with disabled drag operations by the polygon center shown as orange circle.



- **Selected** intersection polygon on mouse-over, with drag operations enabled. Red drag highlights are context sensitive, see Chapters [In-Plane Translation](#) [▶ 118], [In-Plane Rotation](#) [▶ 119], and [Scaling](#) [▶ 120] for further usage details.

- ○ Projected center of rotation for in-plane rotation of the slice package, rendered as small orange disk if scaling drag operations have precedence. May coincide with the center of the intersection polygon.

- ○ Projected center of rotation for in-plane rotation of the slice package, rendered as large orange disk if translation and rotation drag operations have precedence. May coincide with the center of the intersection polygon.

- ○ Center of the intersection polygon, usable for in-plane translation, drawn as orange circle.



- Coordinate cross representing the directions of the selected slice package's acquisition axes: read (red), phase (green), and slice (blue). The arrows point towards more positive values.



- Orientation cube visualizing the axis directions of the subject coordinate system. See Chapter [Subject Coordinate Systems](#) [▶ 127] for details.

Notices:

- Acquisition coordinate axes are color-coded consistently everywhere in the **Geometry Editor**, within viewports as well as on the **Geometry Palette**.
- It is possible to interact with intersection polygons in all four viewports.
- If an intersection polygon overlaps a viewport edge, shift the view or zoom out to see it all.
- If working with three mutually perpendicular, intersecting reference images, operations which are not possible in one viewport (such as rotation about an axis not perpendicular to the image) can often easily be done in another viewport.
- If reference image and slice package do not intersect, then either try working in another viewport, use the **Geometry Palette** or the **Parameter Editor** to modify the slice package, or use other reference images.

1.3.4.3.1 In-Plane Translation

Goal:

Displace the slice package within the image plane by dragging the intersection polygon.

Prerequisites:

- An open scan instruction with **READY** status, a reference image in the focused viewport, and a selected slice package
- A selected intersection polygon with drag operations enabled, see Chapter [Scene With Reference Images \[▶ 116\]](#)
- Drag operation precedence toggle button released, 

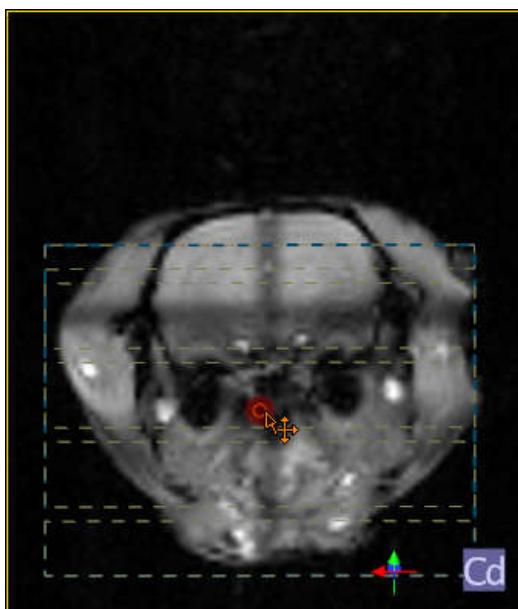


Figure 1.92: Red drag zone and orange cursor for translation

1. If the pointer is located over the intersection polygon center (orange circle), then the center gets a translucent red marker and the pointer changes to the move cursor,



. Click and drag to translate the slice package on the image plane.

or

1. Use the arrow keys to translate by one screen pixel. Move by 10 pixels instead if <CapsLock> is on. Zoom in to move with higher precision.

Notice:

- Moving a slice package may be constrained to some directions or disallowed altogether by the method.

1.3.4.3.2 In-Plane Rotation

Goal:

Rotate the slice package about an axis perpendicular to the image plane by dragging the intersection polygon.

Prerequisites:

- An open scan instruction with **READY** status, a reference image in the focused viewport, and a selected slice package
- A selected intersection polygon with drag operations enabled, see Chapter [Scene With Reference Images \[116\]](#)

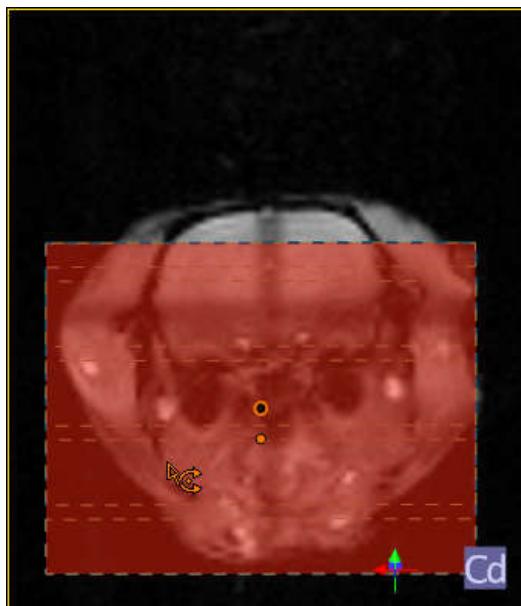


Figure 1.93: Red drag zone and orange cursor for rotation

1. If the pointer is located over the intersection polygon, the whole face of the polygon gets a



translucent red marker and the pointer changes to the rotation cursor, . Click and drag to rotate the slice package about an axis perpendicular to the image plane.

or

1. Use the <PageUp> and <PageDown> keys to rotate by 1 degree counter-clockwise or clockwise, respectively. Rotate by 10 degrees instead if <CapsLock> is on.

Notices:

- If the intersection polygon is very small or very narrow, either zoom in or make sure that rotational drag operations have priority, i.e., the toggle button is in pressed state, .
- Rotating a slice package may be constrained to some directions or disallowed altogether by the method.

1.3.4.3.3 Scaling

Goal:

Resize the slice package by dragging an edge of the intersection polygon.

Prerequisites:

- An open scan instruction with **READY** status, a reference image in the focused viewport, and a selected slice package
- A selected intersection polygon with drag operations enabled, see Chapter [Scene With Reference Images \[▶ 116\]](#)
- Drag operation precedence toggle button released, 
- Drag operation precedence toggle button released, 

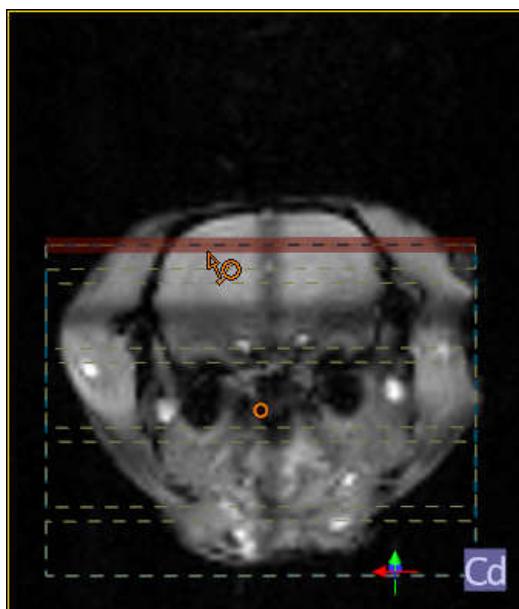


Figure 1.94: Red drag zone (one edge in current use as example) and orange cursor for scaling

1. If the pointer is located over the edge of the intersection polygon, then that edge gets a



translucent red marker and the pointer changes to the resize cursor, . Click and drag the edge to resize the slice package.

or

1. Use the arrow keys while holding down <Shift> to scale by one screen pixel. Resize by 10 pixels instead if <CapsLock> is on. Zoom in for higher precision.

Notices:

- In an oblique setting, the extent in direction of more than one acquisition axis may be changed.
- Depending on the method, field of view values may be coupled between read and phase axis and/or between slice packages.

1.3.4.4 Keyboard Support

Goal:

Focus a viewport by keyboard.

1. Place the pointer over the desired viewport.

2. Hit <Space>, or click the middle mouse button.
 - The viewport under the pointer will get focused (visible by a continuous yellow border).

Notice:

- The above work-flow is handy, in that it does not change any selections within the viewport (in contrast to clicking into the viewport using the left mouse button).

Goal:

Select an object by keyboard.

Prerequisites:

- An open scan instruction
- Focused viewport in pick mode (yellow border and arrow cursor)

Keys	Effect
<Tab>	Select the next slice package.
<Shift>+<Tab>	Select the previous slice package.

The selection will navigate through all indices within all kinds of objects listed in the drop-down box at the top of the **Selection** section of the **Geometry Palette**, wrapping around if needed.

Goal:

Manipulate a slice package by keyboard.

Prerequisites:

- An open scan instruction with **READY** status
- A focused viewport in pick mode (yellow border and arrow cursor)
- A selected slice package
- Drag operations must be enabled: Make sure any of the red mouse-over markers is visible, or the intersection polygon center is shown as orange circle .

Keys	Effect
<Left>, <Up>, <Right>, <Down>	Translate selected slice package left, up, right, or down by one screen pixel.
<Shift>+<Left>, <Shift>+<Right>	Grow or shrink selected slice package in horizontal direction, by one screen pixel.
<Shift>+<Up>, <Shift>+<Down>	Grow or shrink selected slice package in vertical direction, by one screen pixel.
<PageUp>, <PageDown>	Rotate selected slice package by 1 degree, counter-clockwise or clockwise.
<CapsLock>	Multiply per-keystroke increment by a factor of 10 while on.

Notices:

- All keyboard operations in the table above are available simultaneously, regardless of which drag operation is currently enabled (e. g., it is also possible to translate or scale the intersection area while its whole face is painted red and the rotation cursor is shown).
- Manipulations may be constrained by the method.

- Zoom in to increase precision of translation and scaling: Their increments are based on screen pixels.

1.3.4.5 Using the 3D Viewport

This is the rightmost viewport of the **Geometry Editor**. No reference images can be dropped here, but all images present in the other three viewports are shown together.

To facilitate the interpretation of the whole situation, switch the 3D viewport to rotate mode and drag to view the scene from an arbitrary direction. Return to pick mode to modify intersection polygons.

If reference images are present, it may be worthwhile to change the draw style for the selected slice package, see Chapter [Draw Style Drop-Down Boxes ▶ 1061](#), from invisible



(default) to surrounding shape as wire-frame , or to show the bounding box .

Notice:

- Per-viewport draw styles are not supported, changes to draw styles always affect the scene in **all** viewports.

1.3.5 Geometry Editor Preferences

1.3.5.1 Introduction

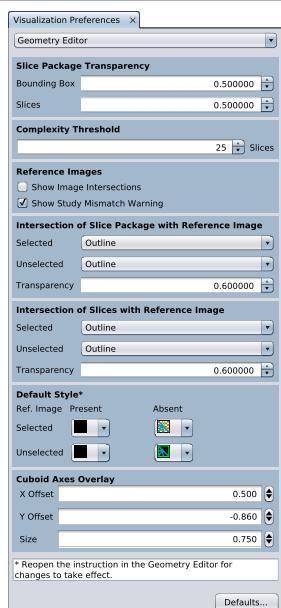


Figure 1.95: Factory defaults of Geometry Editor preferences

Less frequently used **Geometry Editor** settings, located on the **Geometry Editor** page of the **Visualization Preferences** window

1.3.5.2 Slice Package Transparency

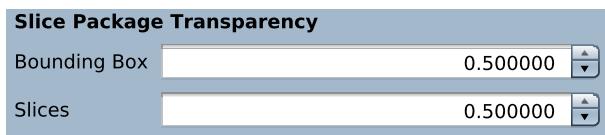


Figure 1.96: Geometry Editor preferences, transparency settings

- **Bounding Box:** transparency of cuboid package bounding box, if its style is set to translucent
- **Slices:** transparency of slices, if their style is set to translucent

Notice:

- Values range from 0.0 (opaque) to 1.0 (transparent)

1.3.5.3 Complexity Threshold



Figure 1.97: Geometry Editor preferences, complexity threshold

Maximum number of slices to render as individual objects. Only the center slice is shown if the slice count exceeds this limit.

1.3.5.4 Reference Image Settings



Figure 1.98: Geometry Editor preferences, reference image settings

- **Show Image Intersections** traces all mutual intersections of reference images in all viewports with gray lines, if enabled.
- **Show Study Mismatch Warnings** warns about reference images acquired in a study different from the current study, if enabled. The reason for issuing warnings lies in potential differences in subject positions.

1.3.5.5 Intersection of Slice Package with Reference Image

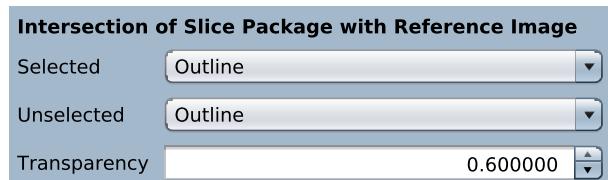


Figure 1.99: Geometry Editor preferences, settings of intersection of slice package with reference image

Draw style for the intersection polygon of the whole slice package with the reference image:

- **Selected:** style for the selected slice package
- **Unselected:** style for all unselected slice packages
- **Transparency:** transparency if style is set to **Translucent**

Style	Description
Invisible	Do not show slice package intersection at all
Outline	Draw outline of slice package intersection polygon as wire-frame
Outline High Contrast	Draw outline of slice package intersection polygon as wire-frame with high contrast
Translucent	Render slice package intersection polygon translucently
Opaque	Render slice package intersection polygon opaque

1.3.5.6 Intersection of Slices with Reference Image

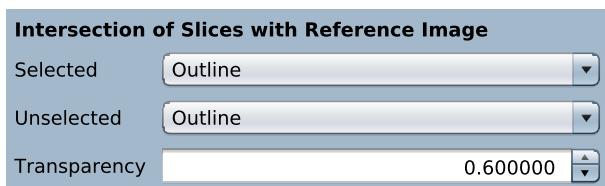


Figure 1.100: Geometry Editor preferences, settings of intersections of slices with reference image

Draw style for the intersection polygons of individual slices with the reference image

Style	Description
Invisible	Do not show slice intersection at all
Center Line	Draw slice intersection as single line, ignoring thickness
Center Line High Contrast	Draw slice intersection as single line with high contrast, ignoring thickness
Outline	Draw outline of slice intersection polygon as wire-frame
Outline High Contrast	Draw outline of slice intersection polygon as wire-frame with high contrast
Translucent	Render slice intersection polygon translucently
Opaque	Render slice intersection polygon opaque

1.3.5.7 Default Style



Figure 1.101: Geometry Editor preferences, default style of intersection polygon

- Upper left: Style of selected slice package with reference image present; refer to Chapter [Draw Styles for Selected Slice Package \[▶ 125\]](#) for a list of styles.
- Upper right: Style of selected slice package with reference image absent; see Chapter [Draw Styles for Selected Slice Package \[▶ 125\]](#) for a list of styles.

- Lower left: Style of unselected slice package with reference image present; Chapter [Draw Styles for Unselected Slice Packages ▶ 126](#) contains a list of styles.
- Lower right: Style of unselected slice package with reference image absent; styles are listed in Chapter [Draw Styles for Unselected Slice Packages ▶ 126](#).

The values set here are used as defaults which are applied every time an instruction is opened or a reference image is loaded or unloaded. The corresponding drop-down boxes on the **Geometry Palette**, covered by Chapter [Draw Style Drop-Down Boxes ▶ 106](#), are always preset accordingly and may be used to temporarily fine-tune a setting.

1.3.5.7.1 Draw Styles for Selected Slice Packages

Icon	Surrounding Shape (blue)	Bounding Box (red)	Slices (yellow)
	Opaque surface	Visible	Invisible
	Opaque surface	Invisible	Invisible
	Translucent surface	Visible	Invisible
	Translucent surface	Invisible	Invisible
	Edges only (wire-frame)	Visible	Opaque boxes
	Edges only (wire-frame)	Visible	Translucent boxes
	Edges only (wire-frame)	Visible	Edges only (wire-frame)
	Edges only (wire-frame)	Visible	Invisible
	Edges only (wire-frame)	Invisible	Opaque boxes
	Edges only (wire-frame)	Invisible	Translucent boxes
	Edges only (wire-frame)	Invisible	Edges only (wire-frame)
	Edges only (wire-frame)	Invisible	Invisible
	Invisible	Visible	Opaque boxes

Icon	Surrounding Shape (blue)	Bounding Box (red)	Slices (yellow)
	Invisible	Visible	Translucent boxes
	Invisible	Visible	Edges only (wire-frame)
	Invisible	Visible	Invisible
	Invisible	Invisible	Opaque boxes
	Invisible	Invisible	Translucent boxes
	Invisible	Invisible	Edges only (wire-frame)
	Invisible	Invisible	Invisible

Notice:

- The surrounding shape differs from the bounding box only for cylinders and ellipsoids.

1.3.5.7.2 Draw Styles for Unselected Slice Packages

Icon	Surrounding Shape (blue)	Bounding Box (light green)	Slices (dark green)
	Opaque surface	Visible	Invisible
	Opaque surface	Invisible	Invisible
	Edges only (wire-frame)	Visible	Opaque boxes
	Edges only (wire-frame)	Visible	Edges only (wire-frame)
	Edges only (wire-frame)	Visible	Invisible
	Edges only (wire-frame)	Invisible	Opaque boxes
	Edges only (wire-frame)	Invisible	Edges only (wire-frame)

Icon	Surrounding Shape (blue)	Bounding Box (light green)	Slices (dark green)
	Edges only (wire-frame)	Invisible	Invisible
	Invisible	Visible	Opaque boxes
	Invisible	Visible	Edges only (wire-frame)
	Invisible	Visible	Invisible
	Invisible	Invisible	Opaque boxes
	Invisible	Invisible	Edges only (wire-frame)
	Invisible	Invisible	Invisible

Notice:

- The surrounding shape differs from the bounding box only for cylinders and ellipsoids.

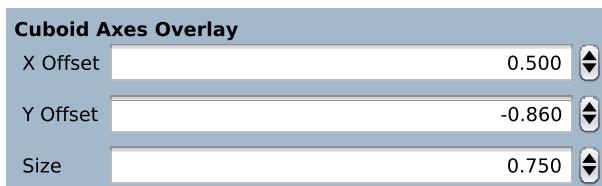
1.3.5.8 Cuboid Axes Overlay

Figure 1.102: Geometry Editor preferences, settings of cuboid axes overlay



Change placement and size of the acquisition axes cross, . Set size to zero to hide completely.

1.3.6 Subject Coordinate Systems

The orientation of reference images is expressed in one of several subject coordinate systems depending on the subject specimen.

1.3.6.1 Subject Coordinate System for Rodents

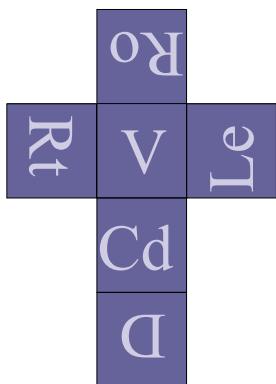


Figure 1.103: Subject coordinate system for Rodent specimen

The **Rodent** subject coordinate system used for quadrupeds has the following axes:

Label	Axis
V	Ventral
D	Dorsal
Le	Left
Rt	Right
Cd	Caudal
Ro	Rostral

1.3.6.2 Subject Coordinate System for Primates

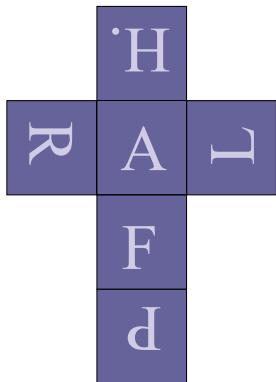


Figure 1.104: Subject coordinate system for Primate and Unknown specimens

The **Primate** subject coordinate system used for bipeds has the following axes:

Label	Axis
A	Anterior
P	Posterior
L	Left
R	Right

Label	Axis
H	Head
F	Foot

This coordinate system is also used for subject specimen **Unknown**.

1.3.6.3 Subject Coordinate System for Materials

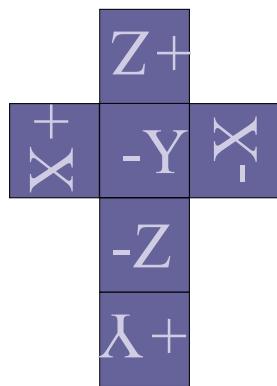


Figure 1.105: Subject coordinate system for Material specimen

XYZ subject coordinate system used for subject specimen **Material**.

1.4 Viewing Card

1.4.1 Overview

To display images from an acquired or imported dataset, the Viewing Card is used, see Figure [The Viewing Card \[▶ 130\]](#). To compare images from different datasets, images from those datasets can either be displayed in a single Viewing Card or a separate Viewing Card can be used for each dataset.

A Viewing Card contains one or more viewports, in each of which one image and additional information about that image can be displayed (see also Chapter [Viewports \[▶ 134\]](#)).

When a Viewing Card is displayed in the foreground, the Palette offers corresponding View Tools (see Chapter [Overview \[▶ 140\]](#)) for adapting the image display, and for navigating through the dataset. The Palette also offers Analysis Tools for quantitative image analysis (see Chapter [Analysis Tools \[▶ 150\]](#)).

The most commonly used View Tools are also accessible in interactive mode directly on the viewports (see Chapter [Using View Tools Interactively on a Viewport \[▶ 141\]](#)).

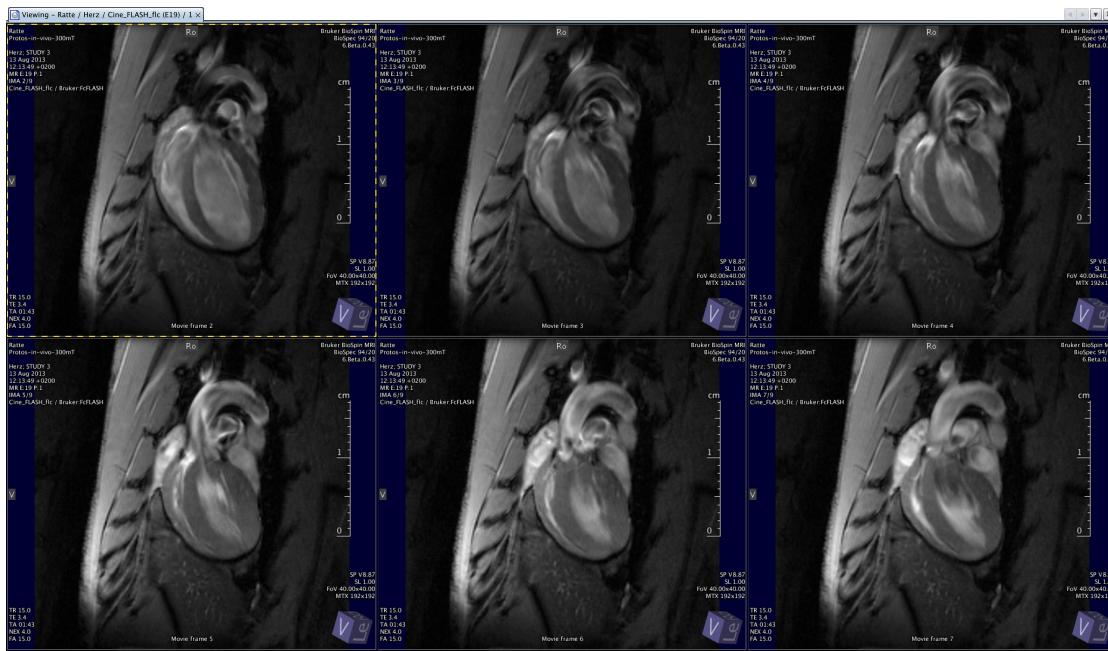


Figure 1.106: The Viewing Card

1.4.1.1 Open Images from Completed Studies

Goal:

View images from a study that is stored in the database.

Using the Dataset Browser:

1. In the main menu, select Window->Dataset Browser (see Chapter [Dataset Browser](#) ▶ [166](#) for details about the Dataset Browser).
2. Select the desired image series and double-click it, or press the button "View".
► A Viewing Card opens, showing an initial selection of images from the dataset, using the default viewport layout.

Using the Palette:

1. On the Palette, select the Tab "Explorer", then click "Datasets".
2. Select the desired Subject, Study, and Image Series.
3. Double-click the desired Image Series, or right-click and in the context menu select "View".
► A Viewing Card opens, showing images from the selected dataset.

1.4.1.2 Open Images from the Active Study

Goal:

Starting from a situation where the Examination Card is in the foreground, view images acquired during the active study.

1. On the Palette, select the Tab "Explorer", then click "Datasets".
► A list of datasets is displayed that corresponds to the active study.

2. Double-click the desired dataset, or right-click and in the context menu select "View".
 - A Viewing Card opens, showing an initial selection of images from the dataset using the default viewport layout.

Notice:

The newly opened Viewing Card covers the Examination Card. To continue the examination after viewing the images, above the Viewing Card click on the Tab "Examination" to bring the Examination Card back to the foreground.

1.4.1.3 Open Images in an existing Viewing Card

Goal:

View images using a Viewing Card that is already open.

Using the Dataset Browser:

1. In the main menu, select Window->Dataset Browser and in the Dataset Browser select the desired Image Series.
2. Drag and drop the Image Series onto the Tab of the existing Viewing Card (see Figure [Drag and Drop an Image Series to a Viewing Card \[▶ 131\]](#)).
 - The images in the viewports of the Viewing Card are replaced with the images from the new Image Series.

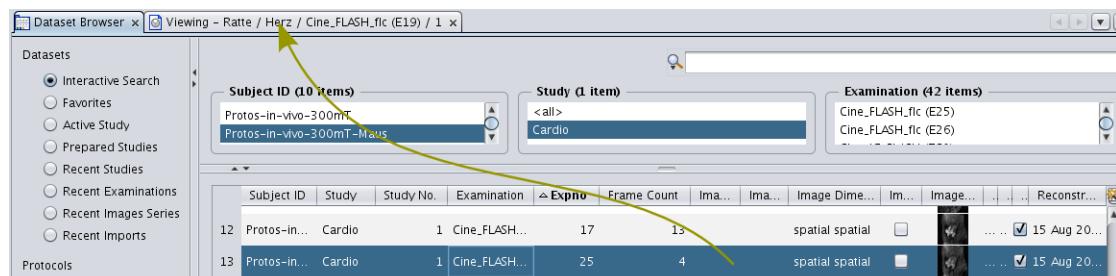


Figure 1.107: Drag and Drop an Image Series to a Viewing Card

Using the Palette:

1. On the Palette, select the Tab "Explorer", then click "Datasets" and select the desired Subject and Study.
2. Drag and drop the desired image series onto the Tab of the existing Viewing Card
 - The images in the viewports of the Viewing Card are replaced with the images from the new Image Series.

Notice:

If there are less images in the new Image Series than there are viewports on the Viewing Card, the extra viewports are cleared.

1.4.1.4 Compare Images from Different Datasets

Goal:

Display images from two different datasets in the same Viewing Card for comparison.

1. Open the images from the first dataset in a new Viewing Card.
2. On the Palette, select the Tab "Explorer", then click "Datasets" and select Subject and Study to match the second dataset.

- A list of Image Series from the second dataset is displayed.
3. Drag and drop the desired Image Series into a viewport of the Viewing Card (see Figure [Drag and Drop an Image Series To a Viewport \[▶ 132\]](#)).
 - The image in that viewport is replaced by one image from the Image Series of the second dataset. 4. To display additional images from the second dataset, use viewport advance as described in Chapter [Navigating Through a Dataset \[▶ 142\]](#).

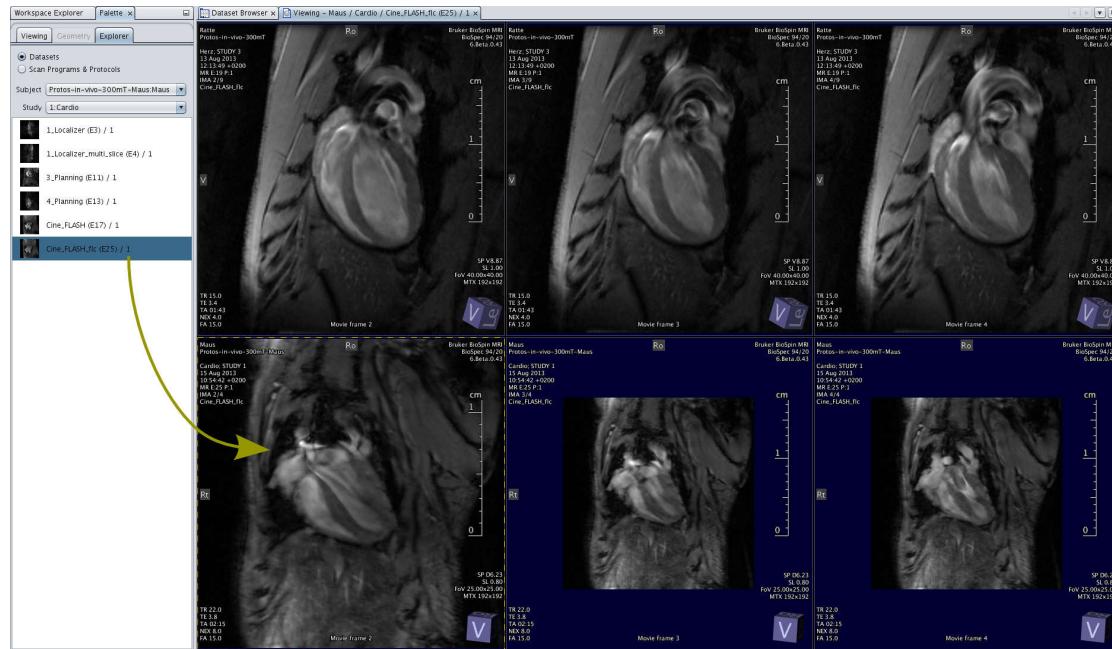


Figure 1.108: Drag and Drop an Image Series To a Viewport

Caution:

Images from different datasets usually have different scaling, contrast and slice orientation, etc. For example, in Fig. [Drag and Drop an Image Series To a Viewport \[▶ 132\]](#), the upper row shows images acquired in a rat, the lower row shows images acquired in a mouse. After dropping the mouse image, its scaling is set such that viewport 4 is filled, and the rat and the mouse appear to have similar size. Use viewport state copy (see Chapter [Copying a Viewport State \[▶ 138\]](#)) to ensure that scaling and image Lookup Table are equal, as demonstrated in viewports 5 and 6 of the figure.

Notice:

Image comparisons are not limited to two datasets, each viewport can hold an Image Series from a different dataset.

1.4.1.5 Open Images Directly on the Examination Card

Goal:

View images from the active study directly on the Examination Card, without switching to a Viewing Card.

1. Select a scan with available image data from the Scan Program Table (see Chapter [Examination Card \[▶ 23\]](#)) or select a dataset from the Palette Explorer.
2. Using the mouse, drag and drop it into one of the viewports at the top of the Examination Card.
 - The target viewport and the viewports to the right are filled with images from the selected dataset.

This is particularly useful for planning a new scan geometry based on one of the previous scans.

The viewports on the Examination Card provide most of the View Tools as those on the Viewing Card, including interactive mode and the use of the Palette. However, to display more than three images simultaneously, use the Viewing Card.

1.4.2 The Palette for Viewing

When a Viewing Card is open, or a viewport on the Examination Card is selected, the Palette for Viewing can be used to access View Tools and Analysis Tools.

1. If the Palette is not visible, in the main menu select Window->Palette.
 - The Palette is opened, containing several different tabs.
2. Switch the Palette to the "Viewing" tab.
 - The Palette for Viewing is displayed (see Fig. [The Palette for Viewing \[▶ 133\]](#))

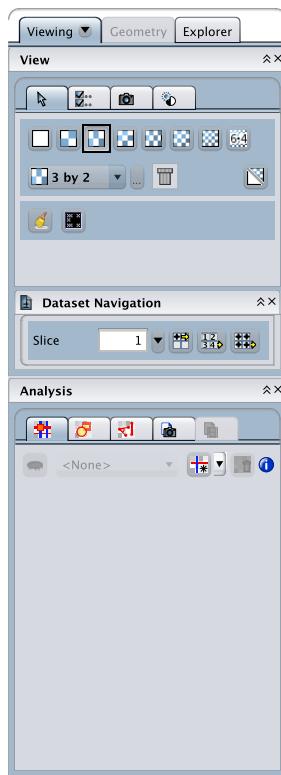


Figure 1.109: The Palette for Viewing

The Palette for Viewing contains two categories of tools, "View" (see Chapter [View Tools \[▶ 140\]](#)) and "Analysis" (see Chapter [Analysis Tools \[▶ 150\]](#)).

1.4.2.1 Using the Palette to Access Viewing Tools

Goal:

With a Viewing Card in the foreground, locate tools for changing the viewport layout, for adjusting the image display and for image analysis.

1. On the Palette, select the Tab "Viewing".

- If the Viewing Tab is empty and you would like to access tools for adjusting the image display, click the black triangle on the Viewing Tab and check the box "View" (see Figure [Activate View Tools and Analysis Tools \[▶ 134\]](#))
- If the Viewing Tab is empty and you would like to access tools for image analysis, click the black triangle on the Viewing Tab and check the box "Analysis".
⇒ On the Panels "View" and "Analysis", a number of tools are available.



Figure 1.110: Activate View Tools and Analysis Tools

The individual tools are described in detail below. Each tool can also be displayed in a separate Panel using the undock ↗ arrow, see Figure [The Palette for Viewing \[▶ 133\]](#). In this Figure, the Dataset Navigation Tool is undocked. To reverse the undocking, simply close the respective Panel.

1.4.3 Viewports

1.4.3.1 Overview

In each viewport, a single image is displayed, overlaid with additional information about the image. Figure [Viewport Displaying a 2D Image \[▶ 135\]](#) shows an example with an image from a rat heart dataset. The image overlay consists of:

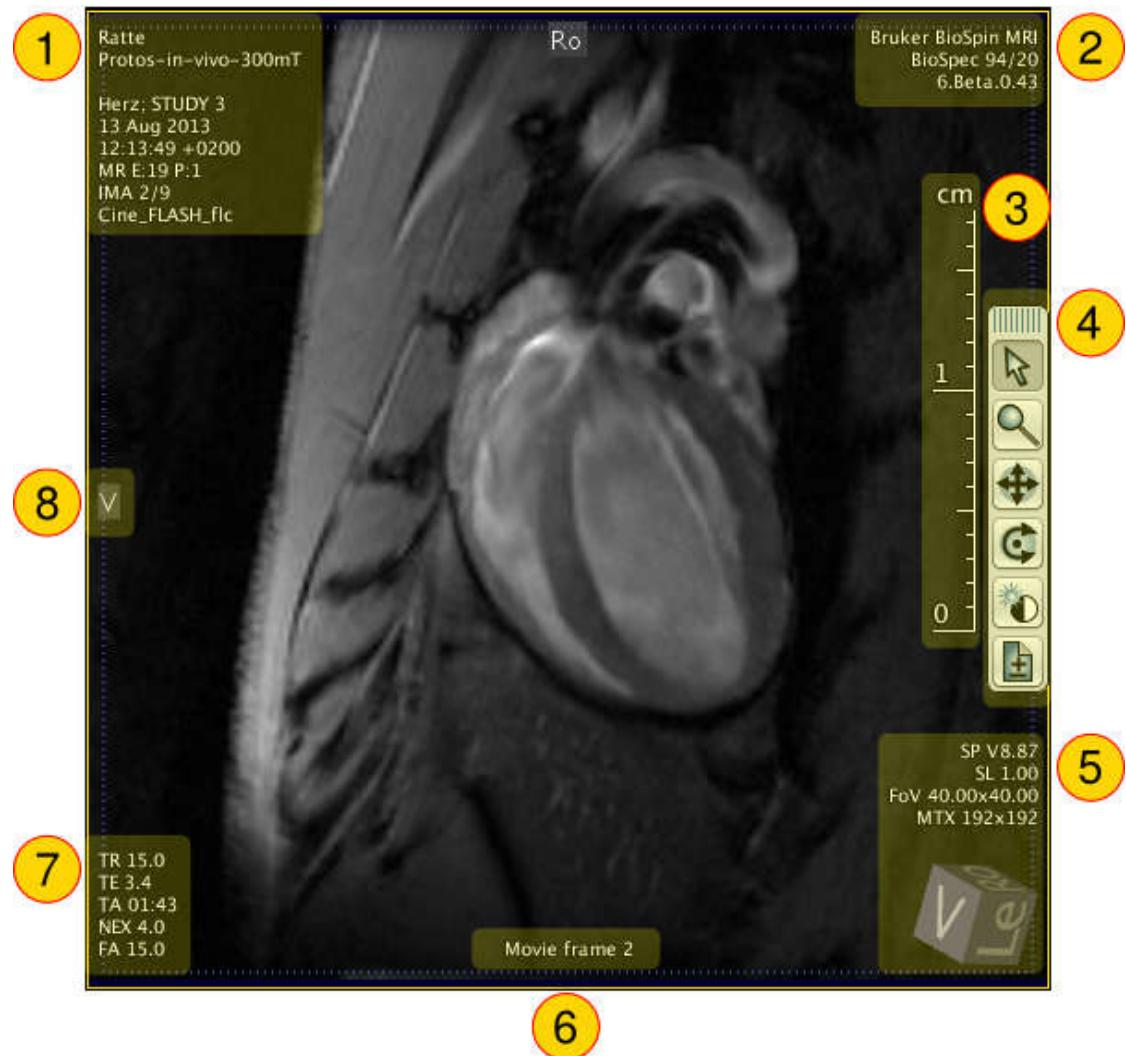


Figure 1.111: Viewport Displaying a 2D Image

1 Top left: Subject and study information:

- Subject name
- Subject ID
- Study ID, study number
- Study date and time
- Imaging Modality, EXPNO, PROCNO, Frame number
- Acquisition protocol name

2 Top right: Infrastructure information:

- Institution
- Acquisition station
- Acquisition software version

3 Center right:

Image scale, giving an impression of the actual size of the object. Note: To measure distances accurately, use the Measurement Tool (see Chapter [Performing Measurements on an Image](#) [▶ 159]).

4 Center right: Viewport Toolbar

- Pick mode: Select viewports
- Zoom mode: Change zoom factor
- Pan mode: Move image inside the viewport
- Roll mode: In-plane rotation of the image
- Map mode: Adjust image brightness and contrast
- Navigation mode: Navigate through the dataset

5 Bottom right: Geometry information (in units mm)

- Slice position (SP): Slice shift from the isocenter in slice direction. In the example (Figure [Viewport Displaying a 2D Image ▶ 135](#)), the slice is shifted in ventral (V) direction by 8.87 mm.
- Slice thickness/slice distance (SL): In the example, the slice thickness is 1.00 mm. In a multislice experiment, with a slice thickness of 1.50 mm and a slice gap of 1.00 mm, this would read "SL 1.50/2.50".
- Field of view (FoV): FoV in read direction x FoV in phase encoding direction.
- Image matrix (MTX): Image size in read x phase directions. Note: This is the size of the reconstructed image, which is not necessarily equal to the acquisition matrix (e.g., for partial Fourier or anti-aliasing acquisitions).
- Slice orientation: The slice orientation is visualized by a 3D cube aligned with the subject coordinate system. On the faces of the cube, the subject coordinate directions are displayed. In the example, the slice is oblique, tilted from an initial coronal orientation to the subject's left (Le) and a little to the subject's head (Ro). For further information on different subject coordinate systems refer to Chapter [Subject Coordinate Systems ▶ 127](#).

6 Bottom center: Frame description.

This is a method specific description and not used in all methods. In the example, the description contains information about the movie frame number in the heart cycle.

7 Bottom left: Selected acquisition parameters

- Repetition time (TR), in ms
- Echo time (TE), in ms
- Total acquisition time (TA)
- Number of averages (NEX), only displayed if NEX>1
- Flip angle (FA), in degrees

8 Center left and top center: Subject Coordinate Labels

These labels show how the image is oriented with respect to the subject coordinate system, in addition to the 3D cube. Especially for the standard orientations (axial, sagittal, coronal) they are useful, because in these cases the 3D cube only shows one face. For oblique orientations, the labels at the image border correspond to the closest standard orientation, and the 3D cube is the more detailed display.

Notice:

Depending on viewport dimensions and font size, parts of the image overlay information may be invisible. In this case, to see all overlay texts, enlarge the viewport, switch the viewport to full size (see Chapter [Changing Number and Arrangement of Viewports ▶ 137](#)), or reduce the font size. To access the font size setting, in the main menu select Window->Visualization Preferences, then, in the drop-down menu of the Visualization Preferences dialog, select "Overlay Graphics".

1.4.3.2 Changing Number and Arrangement of Viewports

Goal:

Change the number and arrangement of images that can be displayed simultaneously on one Viewing Card.

1. Use the Palette to access the View Tools, then select the tab with the  symbol.

 - The Viewport Layout tool opens, see Figure [The Viewport Layout Tool \[▶ 137\]](#).

2. From the drop-down menu, select one of the predefined viewport layouts.

 - The viewport arrangement on the Viewing Card in the foreground changes to the selected layout.

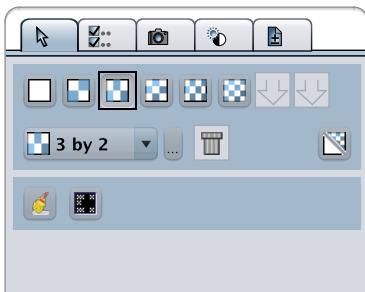


Figure 1.112: The Viewport Layout Tool

To add individual layouts, up to 9 by 9 viewports, use the button .

For quick access to frequently used layouts, drag a layout from the drop-down menu to the quick access fields  above the drop-down menu. To remove a layout from the quick access fields, drag it onto the recycle bin symbol , or right-click it, and from the context menu select “Remove”.

The layout in bold font is used as default layout when a new Viewing Card is opened. In the quick access fields, the default layout is marked by a black border.

Notice:

When increasing the number of viewports, the new viewports are not filled automatically, e.g., with images of adjacent slices.

Notice:

To display a single viewport at full size in a Viewing Card, on the Viewport Layout tool click the button . Click it again to switch back to the previous viewport layout.

Notice:

Both the layout currently in use on the Viewing Card in the foreground (quick access button appears pressed) and the default layout cannot be removed.

1.4.3.3 Changing the Default Viewport Layout

Goal:

Change the default viewport layout, initially set to a 3 by 2 layout.

1. Use the Palette to access the View Tools, then select the Viewport Layout tab .

 - In the drop-down menu, the default layout is displayed in bold font.

2. Click the button .
3. Choose a layout from the list or create a new individual layout.

4. Select the desired layout and click "Set as Default".

Notice:

The new default layout will be used in all Viewing Cards that are opened after the default was changed. Viewing Cards that are already open will keep their individual layouts.

Notice:

To set a layout from a quick access field as the default viewport layout, right-click it, and from the context menu select "Set as Default".

1.4.3.4 Viewport State and its Aspects

The Viewport State determines how a reconstructed image is presented in the viewport. A Viewport State is characterized by three aspects:

1. The Lookup Table determines how the numerical values are mapped to gray levels or colors.
2. The Camera Position determines the geometrical perspective used for projecting the image.
3. The Parameter Overlay. If active, the image overlay as described above is displayed in the viewport.

The Lookup Table and Camera Position aspects can be changed with the View Tools described in detail below. The Parameter Overlay can be switched on and off as follows:

1. On the Viewing Card, select a viewport by left-clicking it.
 - A yellow frame appears around the selected viewport.
2. Click the right mouse button.
 - A context menu appears.
3. In the context menu, check or uncheck the option "Parameter Overlay".

1.4.3.5 Copying a Viewport State

Goal:

Set the Viewport State to match the state of another viewport.

1. Select the viewport with the desired source Viewport State and then click the right mouse button.
2. In the context menu, select "Copy State".
 - The Viewport State is copied.
3. Select the target viewport and click the right mouse button.
4. In the context menu, select "Paste State".
 - By default, all aspects of the source Viewport State are transferred to the target viewport.

Notice:

To specify which aspects are copied during copy & paste, see Chapter [Configuring Viewport State Transfer \[▶ 140\]](#).

Goal:

Paste a Viewport State to several viewports at once.

Several viewports can be selected as a target for subsequent Viewport State paste operations. A target viewport is marked by a blue dot on the bottom right, as illustrated as (1) in Figure [Viewport Selected as Target \[▶ 139\]](#).

To select arbitrary viewports as targets:

1. Move the mouse close to any border of a viewport until a blue dotted frame appears (see Figure [Viewport Displaying a 2D Image \[▶ 135\]](#)).
2. Hold the “Ctrl” key and click the left mouse button.
 - A blue dot appears on the bottom right of each viewport selected as target (see (1) in Figure [Viewport Selected as Target \[▶ 139\]](#)).
3. Repeat steps 1 and 2 for other desired viewports.

To select a rectangular range of viewports as targets:

1. Move the mouse close to the border of the viewport on the top left of the desired range until a blue dotted frame appears.
2. Click and hold the left mouse button and drag the mouse over the desired range of viewports.
 - On each viewport in the desired rectangle, a blue dot appears on the bottom right.
3. Release the mouse button.



Figure 1.113: Viewport Selected as Target

Notice:

Viewport States can also be copied among viewports on different Viewing Cards.

1.4.3.6 Configuring Viewport State Transfer

Goal:

Determine which aspects of the Viewport State are copied when using Viewport State copy & paste, and when navigating through slices in the viewport.

1. Use the Palette to access the View Tools, then select the Viewport State tab .
 - The Viewport State tool opens, see Figure [The Viewport State Tool \[140\]](#).
2. To configure the Viewport State transfer for dataset navigation or for copy & paste, select the respective tab.
3. Check the boxes of the Viewport State aspects you would like to be transferred.
 - In subsequent navigation steps/copy & paste operations, the selected Viewport State aspects are transferred.

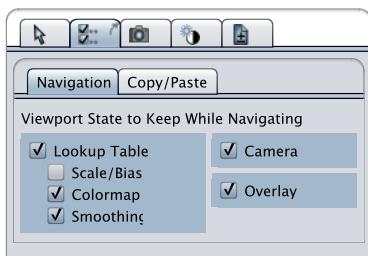


Figure 1.114: The Viewport State Tool

1.4.3.7 Clearing Viewports

Goal:

Clear the contents of a single viewport.

1. On the desired viewport, click the right mouse button.
2. In the context menu, select " Clear Viewport".
 - The selected viewport is cleared.

Goal:

Clear all viewports.

1. Use the Palette to access the View Tools, then select the Viewport Layout tab .
2. Click the button - All viewports are cleared.

1.4.4 View Tools

1.4.4.1 Overview

The following View Tools are available on the Palette:

Symbol	Function
	Change number and arrangement of viewports (see Chapter Changing Number and Arrangement of Viewports [▶ 137])
	Define which parts of the Viewport State are to be kept while navigating and to be transferred in copy & paste (see Chapter Configuring Viewport State Transfer [▶ 140])
	Zoom, pan, and roll image inside the viewport (see Chapter Zooming, Panning and Rotating the Image [▶ 145])
	Adjust image lookup table, brightness, contrast, and smoothing (see Chapters Adjusting Image Contrast and Brightness [▶ 143] and Changing the Color Map and Image Smoothing [▶ 145])
	Navigate through the dataset and fill viewports with multiple images (see Chapter Navigating Through a Dataset [▶ 142])

The following interactive modes are available directly on the viewports:

Symbol	Function
	Pick mode: Select viewports
	Zoom mode: Change zoom factor (see Chapter Zooming, Panning and Rotating the Image [▶ 145])
	Roll mode: In-plane rotation of the image (see Chapter Zooming, Panning and Rotating the Image [▶ 145])
	Rotate mode: Free rotation of image or volume (only available in the 3D viewport on the Examination Card and in Advanced Viewing, see Chapter 3D Image Viewing [▶ 177]).
	Pan mode: Move image inside the viewport (see Chapter Zooming, Panning and Rotating the Image [▶ 145])
	Map mode: Adjust image brightness and contrast (see Chapter Adjusting Image Contrast and Brightness [▶ 143])
	Navigation mode: Navigate through the dataset (see Chapter Navigating Through a Dataset [▶ 142])

1.4.4.2 Using View Tools Interactively on a Viewport

Goal:

On an open Viewing Card, navigate through the dataset and change the image display directly on the viewport.

1. On the Viewing Card, select a viewport by left-clicking it.
 - A yellow frame appears around the selected viewport.
2. Move the mouse close to the right image border or press the "Esc" key.
 - The viewport Toolbar appears at the right border of the viewport (see Figure [Viewport Toolbar \[▶ 142\]](#)).
3. Select one of the icons representing a View Tool (see [Overview \[▶ 140\]](#) for an overview of available Tools).

- The viewport is now in interactive mode and the mouse pointer changes to represent the selected View Tool.
4. Left-click and drag the mouse to adjust the image display corresponding to the selected View Tool (see also Chapter [Navigating Through a Dataset \[▶ 142\]](#), Chapter [Adjusting Image Contrast and Brightness \[▶ 143\]](#), and Chapter [Zooming, Panning and Rotating the Image \[▶ 145\]](#) below).
 5. To leave interactive mode, choose the arrow (pick mode) from the viewport Toolbar or press the "Esc" key again.



Figure 1.115: Viewport Toolbar

Notice:

The viewport Toolbar can be moved to any viewport border by dragging it with the mouse. If the current position of the viewport Toolbar is unknown, use the "Esc" key to make it appear.

Notice:

On a selected viewport, an interactive View Tool can be activated directly by pressing the number key corresponding to the tool position on the viewport Toolbar. For example, by pressing the "2" key, the Zoom mode is activated. By pressing <Ctrl>-2, the Zoom mode is activated on all viewports of the active Viewing Card.

1.4.4.3 Navigating Through a Dataset

Goal:

Display one or more specific images from a dataset.

Image datasets are organized in categories. For example in a multi-slice, multi-echo (MSME) dataset, the images differ in slice position and echo time (see Figure [Categories \[▶ 142\]](#)). You can thus navigate along the category dimensions "Echo" and "Slice" as well as choose specific frames directly.

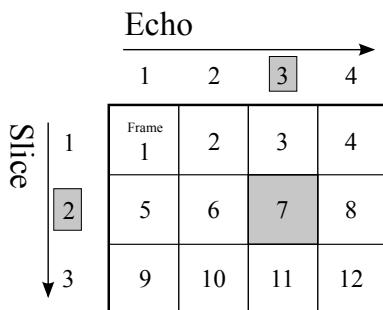


Figure 1.116: Categories

Using the Palette:

1. On the Viewing Card, select a viewport by left-clicking it.
2. Use the Palette to access the View Tools, then select the Dataset Navigator tab .
 - The Dataset Navigation Tool is displayed, see Figure [The Dataset Navigation Tool \[▶ 143\]](#). The exact appearance depends on the category structure of the dataset.
3. Specify the frame number or use the drop-down menus to select a specific image to be displayed in the selected viewport.

- The desired image is displayed in the selected viewport.

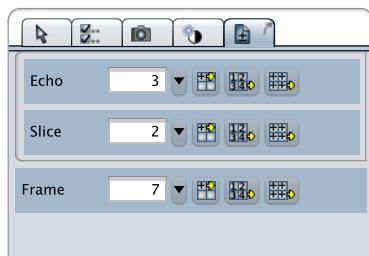


Figure 1.117: The Dataset Navigation Tool

To display the image following the current viewport's image in the viewport next to it, use the button in the desired category. The current viewport will advance left to right, row-wise, wrapping around from bottom right to top left viewport.

Use the button to fill viewports row-wise, starting with the current viewport and the first image within the category.

To fill viewports row-wise, starting with the current viewport and image, use the button. Click it repeatedly to page through the images in the selected category.

Using interactive Navigation mode:

1. On the viewport Toolbar (see [Using View Tools Interactively on a Viewport \[▶ 141\]](#)), select Navigation mode .
- An overlay appears on the image (see Figure [Interactive Tool Navigate Dataset \[▶ 143\]](#)) showing the frame number and category number of the current image.
2. To display a specific image, click the arrows next to the image number, point the mouse over the image number and move the mouse wheel, or drag horizontally over the rectangle between the arrows.



Figure 1.118: Interactive Tool Navigate Dataset

Notice:

To view a dataset or one of its categories as a movie, use the Movie Player (see Chapter [Displaying Images As A Movie \[▶ 146\]](#)).

1.4.4.4 Adjusting Image Contrast and Brightness

Goal:

Adjust brightness and contrast of the image in the selected viewport.

Using the Palette:

1. Access the View Tools and select the Lookup Table and Smoothing tool

- The Lookup Table tool is displayed, (see Figure [The Brightness Contrast Tool \[▶ 144\]](#)), showing the mapping of image values on the horizontal axis onto gray values on the vertical axis.
2. To adjust brightness and contrast change the Lookup Table function by dragging it with the mouse. Figure [Increasing The Brightness \[▶ 144\]](#) shows an example of how to change the function to brighten an image, the function in Figure [Increasing The Contrast \[▶ 144\]](#) results in a higher image contrast.

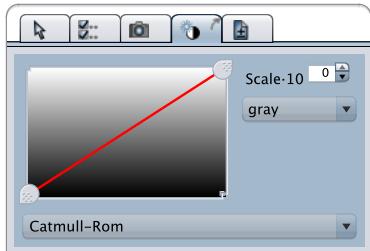


Figure 1.119: The Brightness Contrast Tool

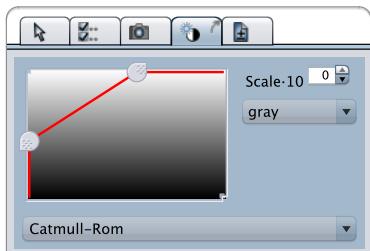


Figure 1.120: Increasing The Brightness

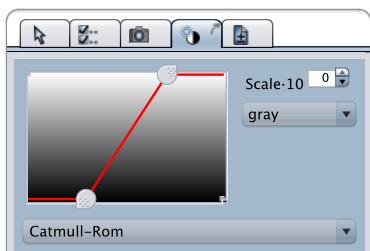


Figure 1.121: Increasing The Contrast

Using interactive Map mode:

1. On the viewport Toolbar (see Chapter [Using View Tools Interactively on a Viewport \[▶ 141\]](#)), select Map mode .
2. Click on the selected viewport and drag the mouse up/down to increase/decrease image brightness. Drag the mouse left/right to decrease/increase image contrast.

Notice:

Image brightness and contrast are not saved with the image. If, in the same viewport, you navigate to another image, by default the Lookup Table function will be adapted to optimize the display of the new image. You can change this behavior by configuring the viewport state transfer, such that the Lookup Table function is kept during dataset navigation (see Chapter [Configuring Viewport State Transfer \[▶ 140\]](#)).

1.4.4.5 Changing the Color Map and Image Smoothing

Goal:

Change the color representation of image values.

1. Use the Palette to access the View Tools, then select the Lookup Table and Smoothing tool .
2. In the drop-down menu on the upper right, choose a color map
 - The background of the Lookup Table and the image in the selected viewport reflect the new color map.

Goal:

Change the smoothing filter used for image display.

Because the resolution of the viewport usually differs from the resolution in the experiment, the acquired images need to be interpolated (smoothed) to match the viewport resolution. To change the smoothing filter:

1. Use the Palette to access the View Tools, then select the Lookup Table and Smoothing tab .
2. In the drop-down menu at the bottom choose the desired smoothing filter or choose "Nearest" to switch off image smoothing.

1.4.4.6 Zooming, Panning and Rotating the Image

Goal:

Zoom in on a detail of an image, move around a zoomed image, or perform an in-plane rotation of the image.

Using the Palette:

1. Access the View Tools, then select the Camera tab .
- The Camera Tool is displayed, see Figure [The Camera Tool \[145\]](#).

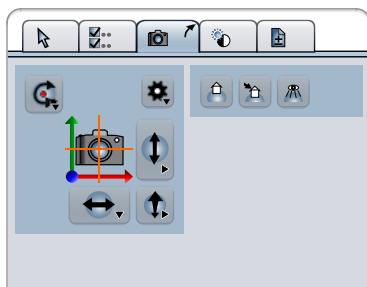


Figure 1.122: The Camera Tool

- To zoom in/out of the image: Click and hold the left mouse button on the symbol  and drag the mouse down/up.
- To move the image up/down: Click and hold the left mouse button on the symbol  and drag the mouse up/down.
- To move the image left/right: Click and hold the left mouse button on the symbol  and drag the mouse left/right.

- To rotate the image clockwise/counter-clockwise: Click and hold the left mouse button on the symbol  and drag the mouse right/left.

Using interactive modes:

- On the viewport Toolbar (see Chapter [Using View Tools Interactively on a Viewport ▶ 141](#)), select:

Symbol	Function
	Click on the selected viewport and drag the mouse down/up to zoom in/out of the image.
	Click on the selected viewport and drag the mouse to move the image in the desired direction.
	Click on the selected viewport and drag the mouse to roll the image into the desired orientation.

1.4.4.7 Displaying Images As A Movie

In dynamic MRI examinations, acquired images represent a time course, for example in Cine imaging of the heart. To display these images as a movie, the Movie Player is used (see Figure [The Movie Player ▶ 146](#)).

The Movie Player can also be used to display images from a multislice or 3D experiment and thus virtually move through the subject to get an impression of the overall anatomy.

Generally, any image category (see Chapter [Navigating Through a Dataset ▶ 142](#)) can be rendered as a movie, e.g. movie frames and slices, but also echoes, diffusion weightings, etc.

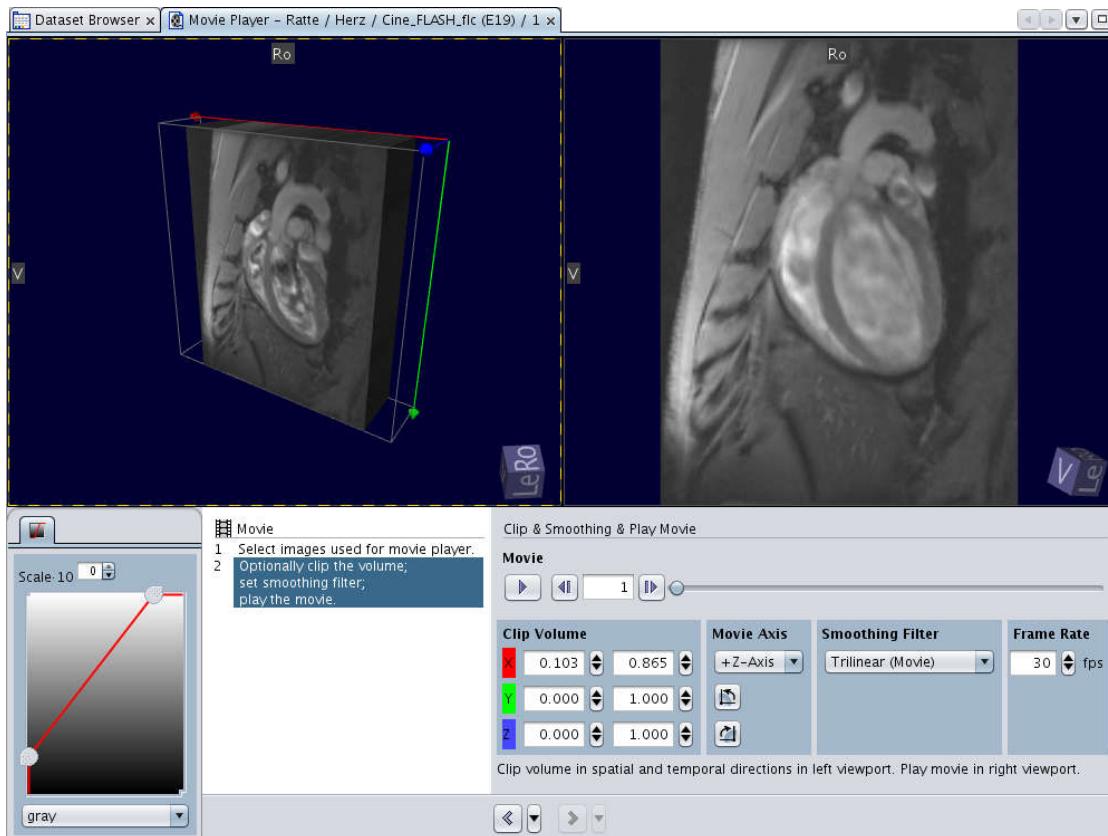


Figure 1.123: The Movie Player

The Movie Player contains two viewports: A 3D viewport on the left hand side, in which all images selected for the movie are rendered as a 3D volume, and a 2D viewport on the right hand side, in which the movie is played.

In the bottom row, a Color Mapping Panel and a two-step dialog are displayed. In Step 1, a set of images to be included in the movie can be specified. In Step 2, the selected images can be prepared and the movie can be started.

Goal:

Open an Image Series in the Movie Player using the Dataset Browser.

1. In the Dataset Browser, locate the desired Image Series.
2. Click the black triangle on the right of the button “View” (see Figure [Start Movie Player From Dataset Browser \[▶ 147\]](#)).
3. Select “Movie Image Data”. If this menu item is not available, the image series cannot be displayed as a movie (e.g. when all slice packages contain only a single slice).
 - A new Movie Player Card will open.

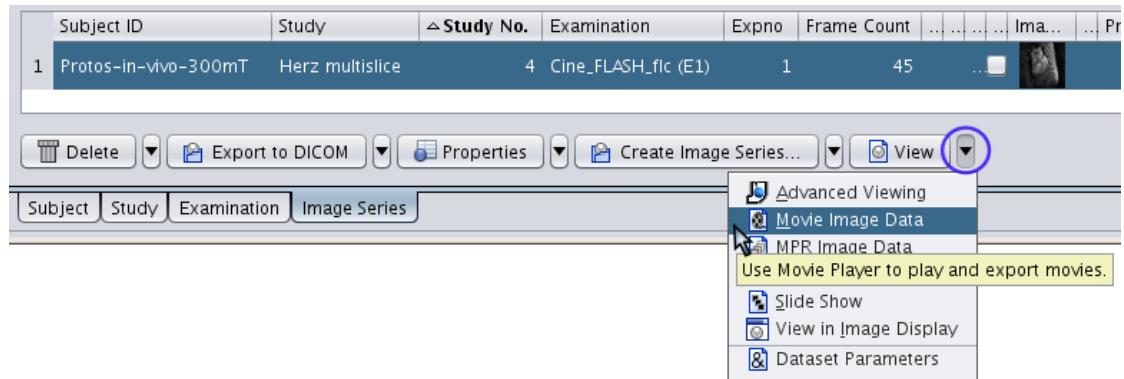


Figure 1.124: Start Movie Player From Dataset Browser

Goal:

Open images in the Movie Player using the Palette.

1. In the Palette Explorer, click “Datasets” and locate the desired Image Series.
2. Right-click the desired Image Series and select “Movie Image Data” (see Figure [Start Movie Player From the Palette \[▶ 148\]](#)).
 - A new Movie Player Card will open.

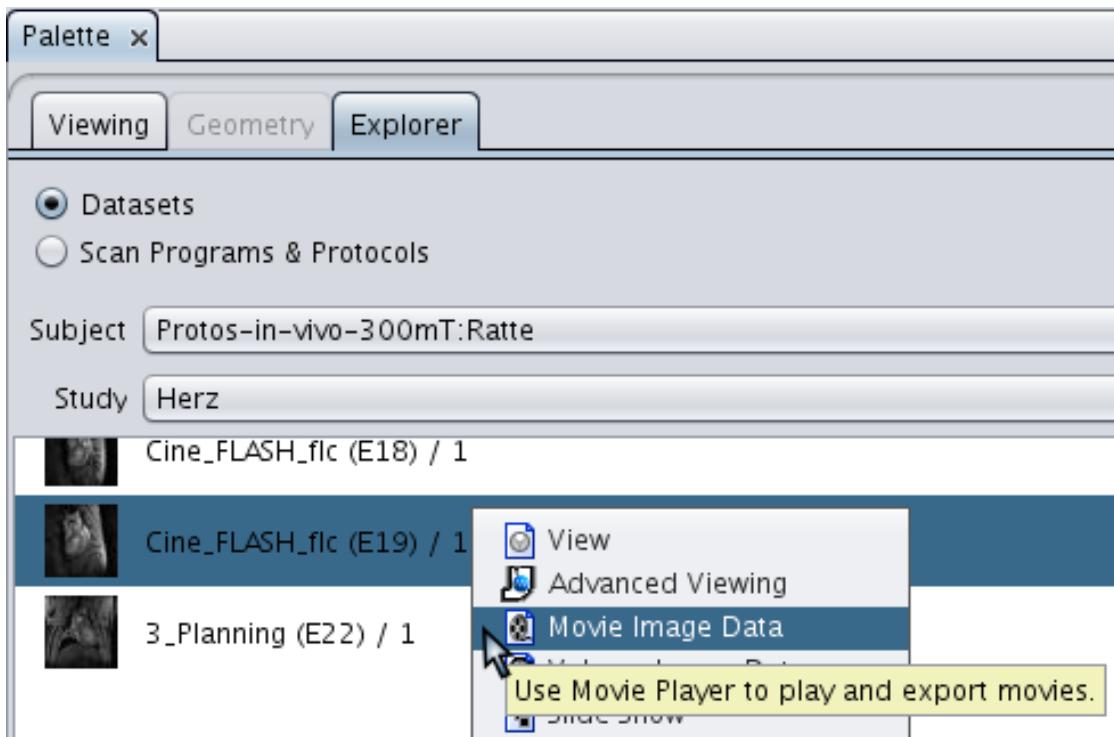


Figure 1.125: Start Movie Player From the Palette

Goal:

Select specific images from the Image Series to display in a movie (Step 1).

1. On the bottom right of the Movie Player Card, in the image selection dialog, specify the images to include into the movie from the different categories (see Figure [Select Images to Include in The Movie \[148\]](#)). From the drop-down menu, select
 - to include only a single image from the given category
 - to include a range of images from the given category
 - to include all images of the given category
 - The total number of images to load is displayed.
 2. To change the order of the image categories in the movie, click the category panel on the very left and drag it to the desired position (see Figure [Change the Category Order \[149\]](#)). The category at the top is the “fastest”, i.e., it is traversed first in the movie.
 3. Click “Load”, then click the button .
- The selected images are displayed as a 3D volume in the left hand viewport of the Movie Player and the dialog for Step 2 is displayed.

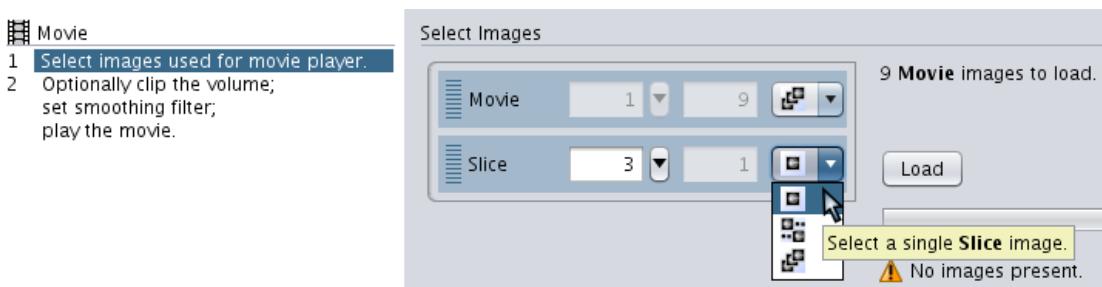


Figure 1.126: Select Images to Include in The Movie

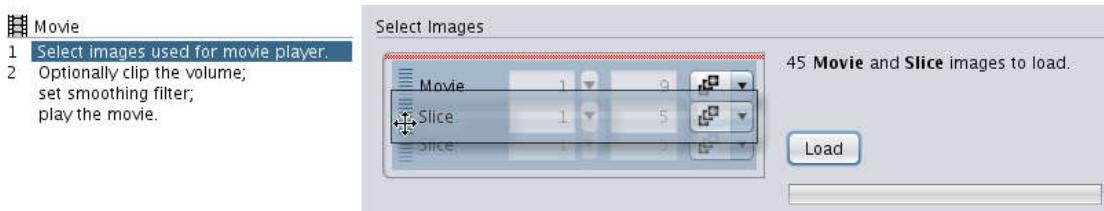


Figure 1.127: Change the Category Order

Notice:

If there is only a single image category, e.g. single slice Cine, the complete set of time frames is chosen automatically and you are directed directly to Step 2. In case you want to manually select a subset of images for the movie, click the button to switch back to the image selection dialog (Step 1).

Notice:

Depending on graphics hardware capabilities, the number of movie frames (i.e., the total number of images to load) is restricted. The number of images is also constrained by the amount of free graphics memory. A large number of Movie Player or Volume Viewer instances being open at the same time will consume significant quantities of memory.

Goal:

Play a movie of the selected images, with optional clipping and smoothing (Step 2).

The selected images are displayed as a 3D volume in the left hand viewport with a local coordinate system indicated by a red, green and blue axis.

1. To clip the display range, in the Clip Volume panel adjust the range along the three axes (see Figure [Clip, Smooth and Play a Movie \[149\]](#)).
 - In the left hand viewport of the Movie Player, the 3D volume is clipped accordingly.
2. To smooth the movie frames, spatially as well as temporally, choose a filter from the Smoothing Filter panel. To switch off spatial and temporal smoothing, select “Nearest (Movie)”.
3. To play the movie, in the Movie panel click the button .
 - In the right hand viewport of the Movie Player, the movie is played.
4. To change the playback speed (frame rate), on the Movie panel use the button .

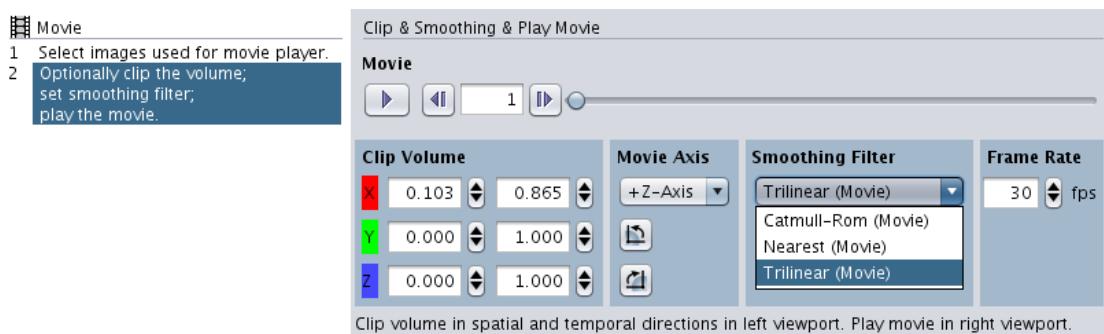


Figure 1.128: Clip, Smooth and Play a Movie

Notice:

In the Movie panel (see Figure [Clip, Smooth and Play a Movie \[149\]](#), right), the movie frame number can be entered to navigate to a certain position in the movie. However, note that the movie frame number is not necessarily equal to the linear frame number of acquired images included in the movie, because the total number of movie frames also depends on the frame rate.

Notice:

To export the movie from the Movie Player to a file in (uncompressed) AVI or QuickTime format, see Chapter [Creating Movies \[▶ 163\]](#).

1.4.5 Analysis Tools

1.4.5.1 Overview

The following Analysis Tools are available on the Palette:

Symbol	Function
	Read off pixel values and display line profiles (see Chapter Accessing Pixel Values and Profiles [▶ 156])
	Define Regions of Interest and display image statistics (see Chapter Add a Region of Interest [▶ 150])
	Measure distances and angles on images (see Chapter Performing Measurements on an Image [▶ 159])
	Create a snapshot of the selected viewport (see Chapter Creating Snapshots [▶ 162])
	Create a movie (see Chapter Creating Movies [▶ 163])

Notice:

The smoothing filter selected in the View Tools (see Chapter [Changing the Color Map and Image Smoothing \[▶ 145\]](#)) has no effect on the quantitative Analysis Tools (pixel values, profiles, ROIs). For these tools, the raw image values are used without interpolation, and ROI borders do not cut across the pixels. However, for snapshots the currently selected smoothing filter is applied as displayed on the viewport. Also, in distance and angle measurements the vertices are not restricted to the acquisition resolution. They can be placed at arbitrary positions, even finer than the initial viewport resolution when using the Zoom Tool.

1.4.5.2 Add a Region of Interest

Goal:

Add a Region of Interest (ROI) to an image and obtain statistical information about the image values in the ROI.

1. Select the viewport with the image of interest by left-clicking it.
2. Use the Palette to access the Analysis Tools, then select the tab with the symbol.
 - The Regions of Interest Tool opens (see Figure [The Region Of Interest Tool \[▶ 151\]](#)).
3. Click the button and choose the type of ROI from the list of shapes, e.g. an Ellipse .
4. Click into the image to place the new ROI. An elliptical ROI appears on the selected image (see Figure [Initial Elliptical ROI \[▶ 151\]](#)).
 - The sizes and area of the ROI are displayed as a legend directly on the image.
 - On the Palette, the minimum, maximum, mean, standard deviation and a histogram of values inside the ROI are displayed (see Figure [The Region Of Interest Tool \[▶ 151\]](#)).

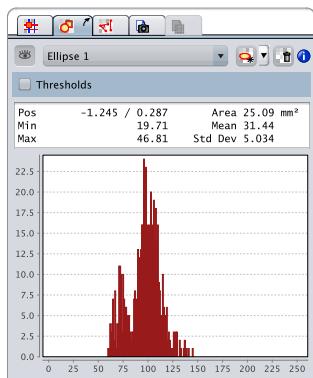


Figure 1.129: The Region Of Interest Tool

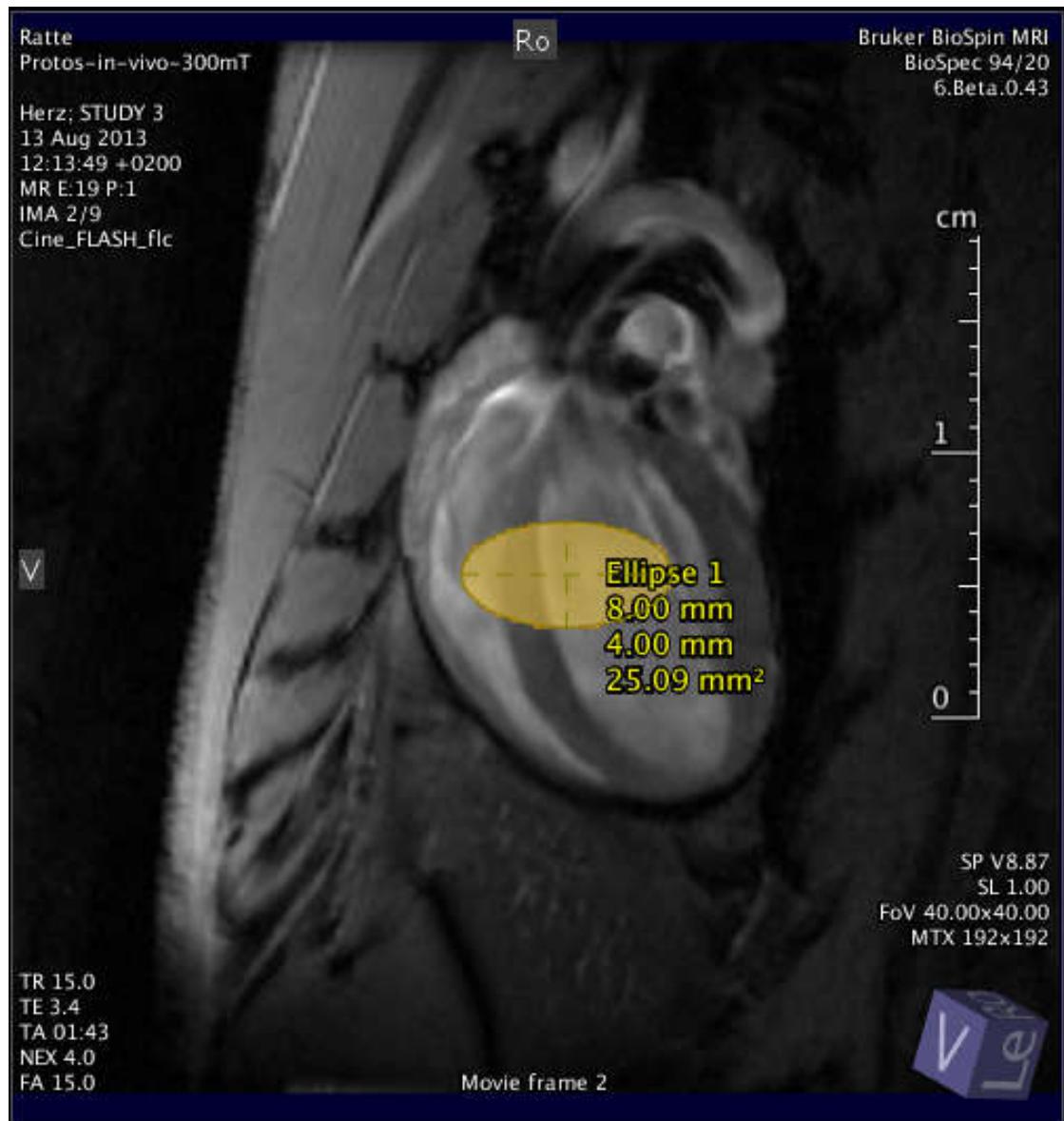


Figure 1.130: Initial Elliptical ROI

Notice:

Multiple ROIs can be added to an image. To display the statistics for a specific ROI, select it from the drop-down menu on the Regions of Interest Tool.

Notice:

ROIs are saved automatically with the image.

1.4.5.3 Modify a Region of Interest

Goal:

Move, resize and rotate a ROI.

1. Make sure the viewport is not in interactive mode (mouse pointer representing a View Tool, see Chapter [Using View Tools Interactively on a Viewport \[▶ 141\]](#))
2. To activate a ROI, click into the center, onto the border or onto the legend of the desired ROI.
 - The ROI legend changes to dark red.

Symbol	Function
	To move the active ROI, point the mouse to the center of the ROI. The mouse pointer changes to  and the ROI center is highlighted (see Figure Move a ROI [▶ 153]). Click and drag the ROI center to the desired location.
	To rotate the active ROI, point the mouse over an area of the ROI that is not occupied by the ROI legend. The mouse pointer changes to  and the whole ROI is highlighted (see Figure Rotate a ROI [▶ 154]). Click and drag the ROI to the desired orientation.
	To resize the active ROI, point the mouse to the border of the ROI you would like to move. The mouse pointer changes to  and the ROI border is highlighted (see Figure Resize a ROI [▶ 155]). Click and drag the border until the desired ROI size is reached.

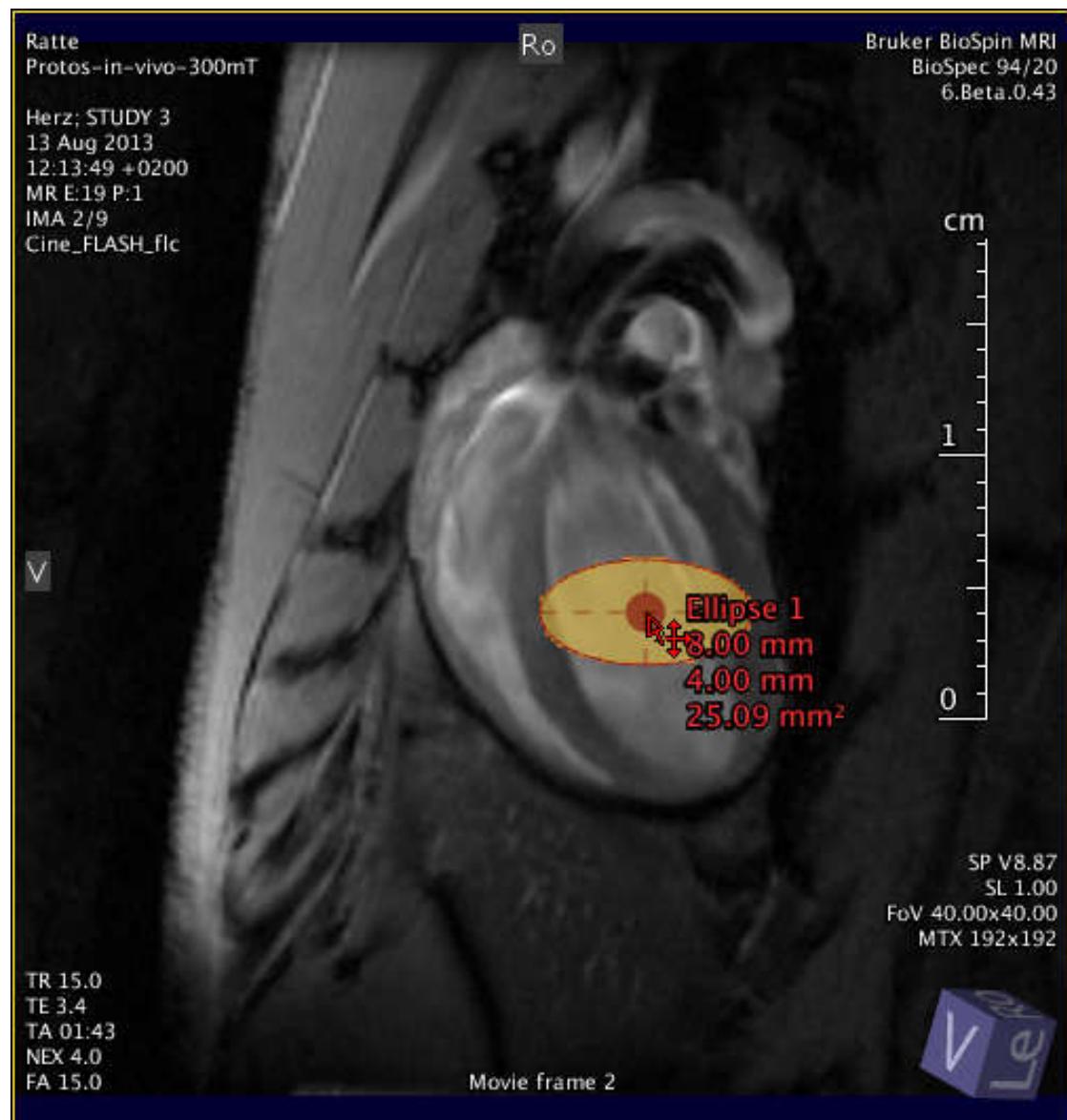


Figure 1.131: Move a ROI

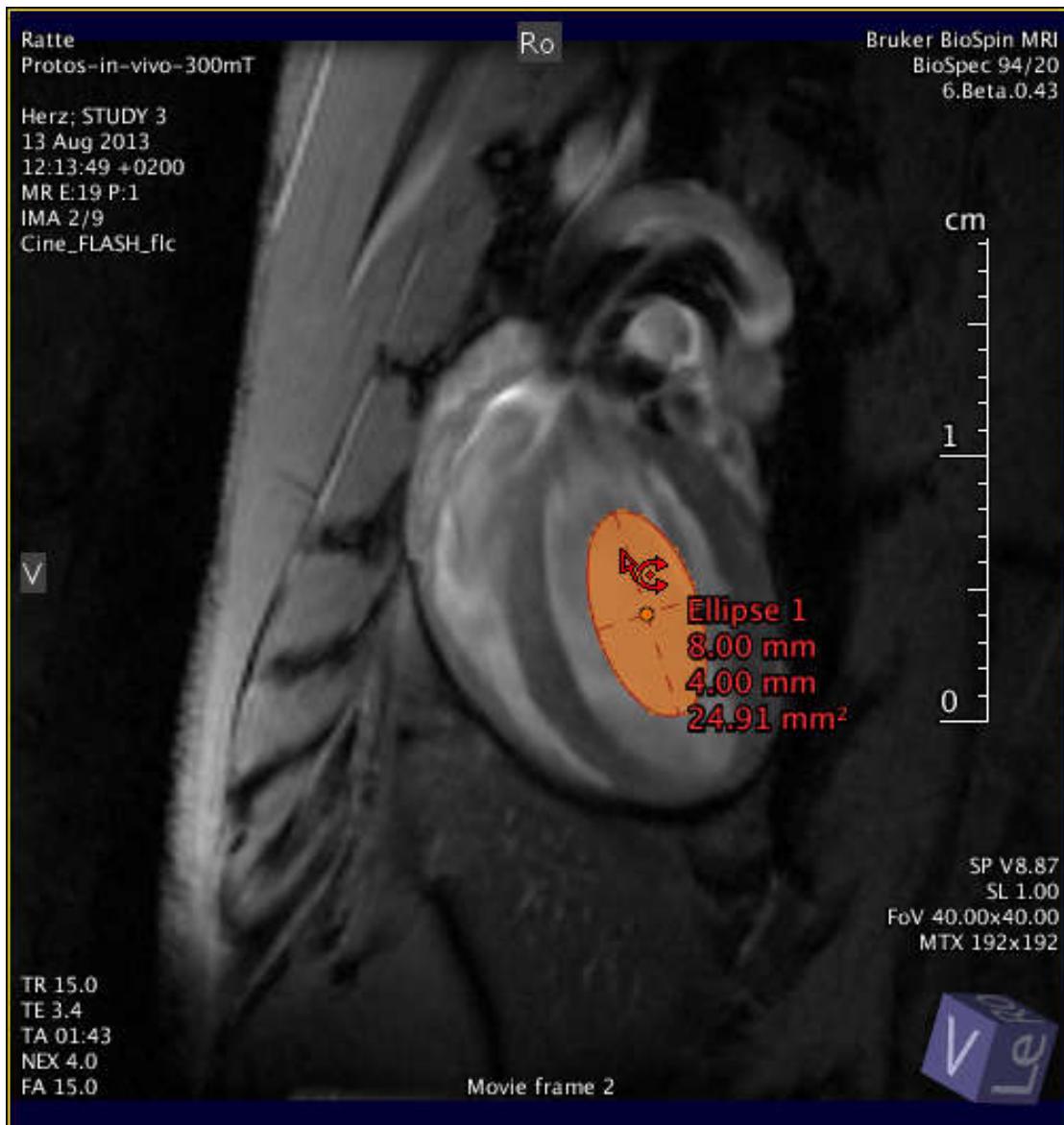


Figure 1.132: Rotate a ROI

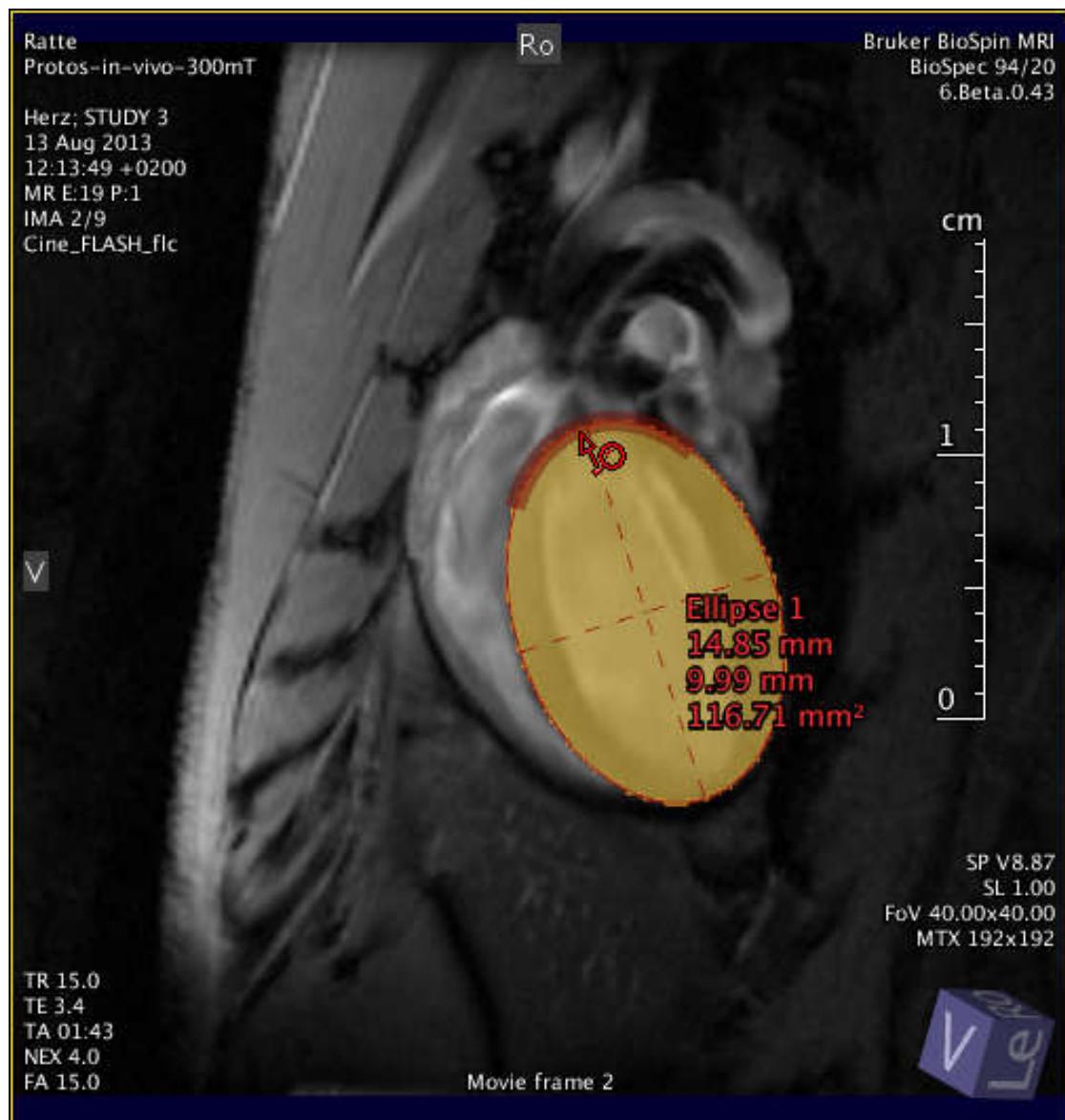


Figure 1.133: Resize a ROI

Notice:

If several ROIs in a viewport overlap, it may become difficult to activate a desired ROI. In this case use the drop-down list of ROIs on the Regions of Interest Tool to select a ROI.

Notice:

The active ROI can also be manipulated using the keyboard: The arrow keys shift the active ROI, **<Shift>-arrow** changes the ROI size, and the **<PageUp>** and **<PageDown>** keys rotate the active ROI. To rotate the ROI in the original orientation, press the **<Home>** key, to align the ROI perpendicular to the original orientation press the **<End>** key. Click **?** for detailed information about the key-bindings.

1.4.5.4 Specify Thresholds in a ROI

Goal:

Specify a signal range for the ROI statistics.

When a ROI contains regions with very low signal, like air cavities or areas outside the object, one would often like to exclude that signal and noise from the ROI statistics. Also, in some cases, regions with high signal need to be excluded, e.g. to mask out blood. To specify thresholds for the ROI:

1. In the Regions of Interest Tool, select the desired ROI from the drop-down menu or activate the ROI by clicking into its center or border.
2. In the Regions of Interest Tool, check the box "Thresholds".
 - Fields for lower and upper threshold appear, containing the minimum and maximum signal value, respectively.
3. Specify the desired signal range by typing into the fields or use the arrow buttons to adjust these values interactively.
 - The ROI changes its shape as you move the thresholds (see Figure [ROI with Thresholding \[▶ 156\]](#)) and the ROI legend and statistics are updated.

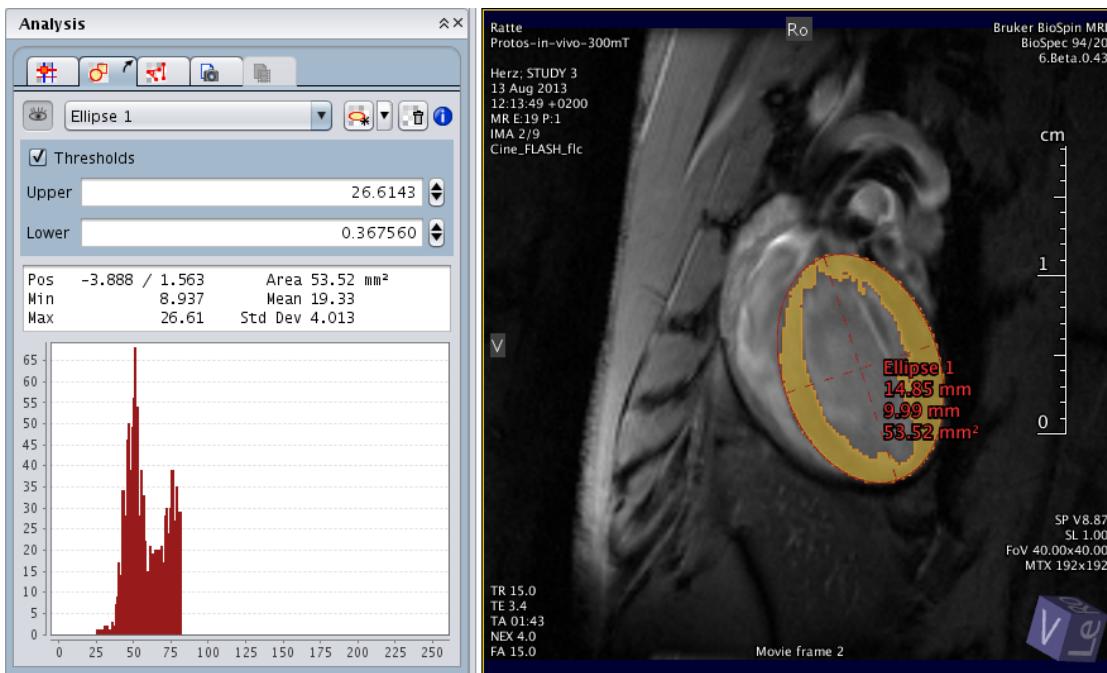


Figure 1.134: ROI with Thresholding

1.4.5.5 Accessing Pixel Values and Profiles

Goal:

Read off values of single pixels and display line profiles across an image.

1. Select the viewport with the image of interest by left-clicking it.
2. Use the Palette to access the Analysis Tools, then select the tab with the symbol.
 - The Scans and Profiles Tool opens (see Figure [The Scans and Profiles Tool \[▶ 157\]](#)).
3. Click the button and select to read off a single pixel, or select to add a line profile.
 - Pixel scan cross-hairs / two crossed line profiles appear centered on the image.
4. To move the Scan or Profile, move the mouse to the center of the Scan or Profile.
 - The mouse pointer changes to and the center is highlighted (see Figure [Move a Profile \[▶ 158\]](#)).

5. Drag the center to the desired location.

- The Scans and Profiles Tool displays the pixel value, coordinate and position in magnet coordinates (pixel scan) or the pixel value, coordinate and line profiles in a chart (line profile).

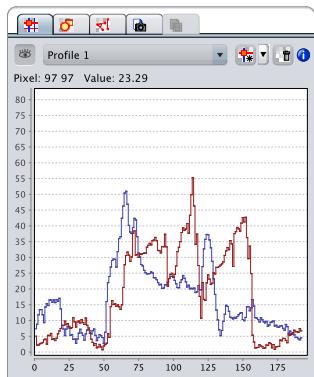


Figure 1.135: The Scans and Profiles Tool

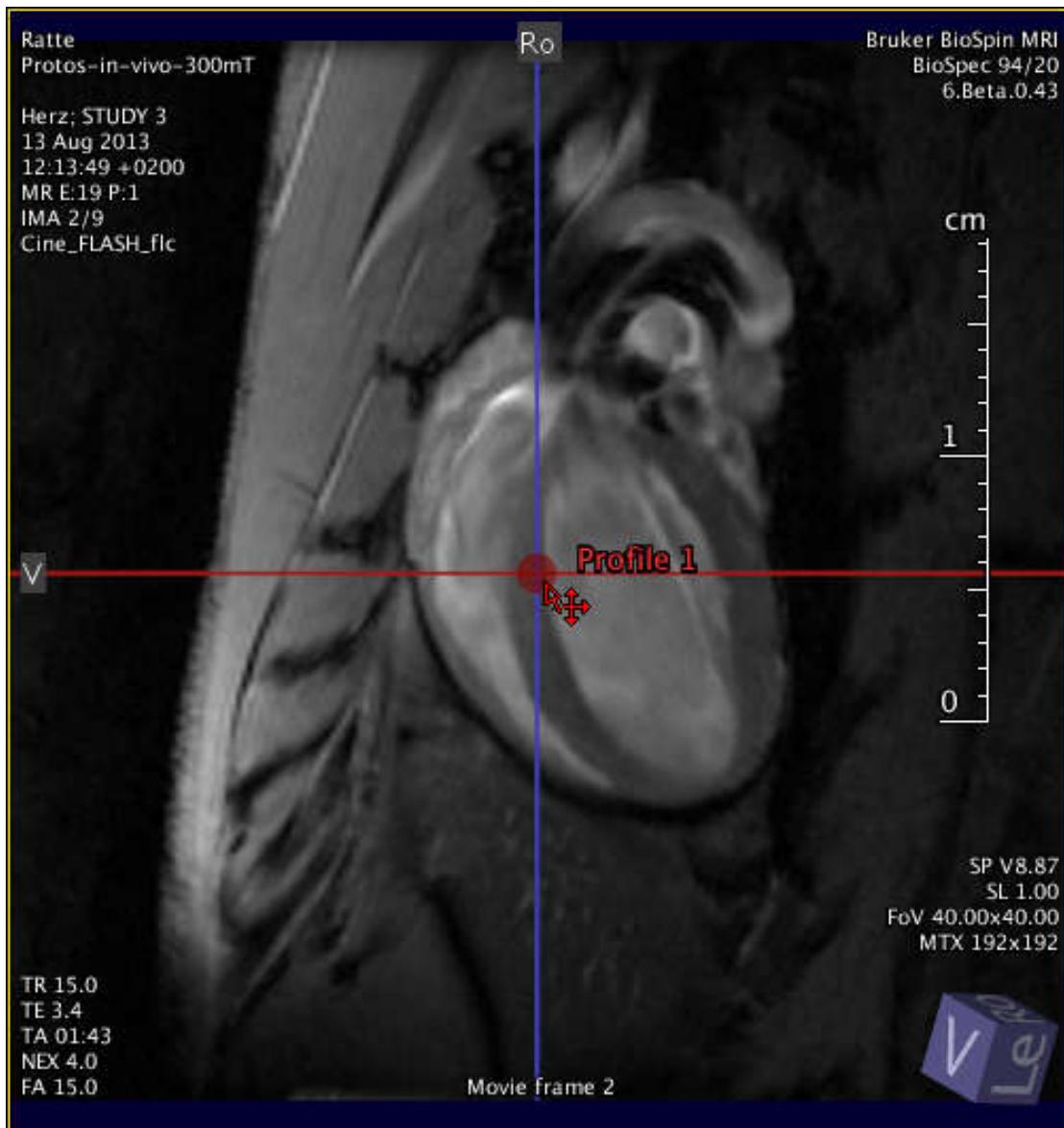


Figure 1.136: Move a Profile

Notice:

Currently, only horizontal and vertical line profiles are supported.

Notice:

The pixel scan and line profile cross-hairs can also be manipulated using the keyboard. Click **i** for detailed information about the key-bindings.

1.4.5.6 Exporting and Printing Analysis Results

The results of the ROI analysis and the line profiles can be exported as a list of numerical values or as graphical charts. The charts can also be printed directly on the printers available on the system.

Goal:

Export analysis results numerically.

1. Right-click the chart or statistics panel.

2. Choose "Export" or "Export->Data" from the context menu.
 - An export dialog appears (see Figure [Export Chart Data \[▶ 159\]](#).)
3. Choose target location, file name and format (available formats are: CSV, HTML, LaTeX) and click "Save".

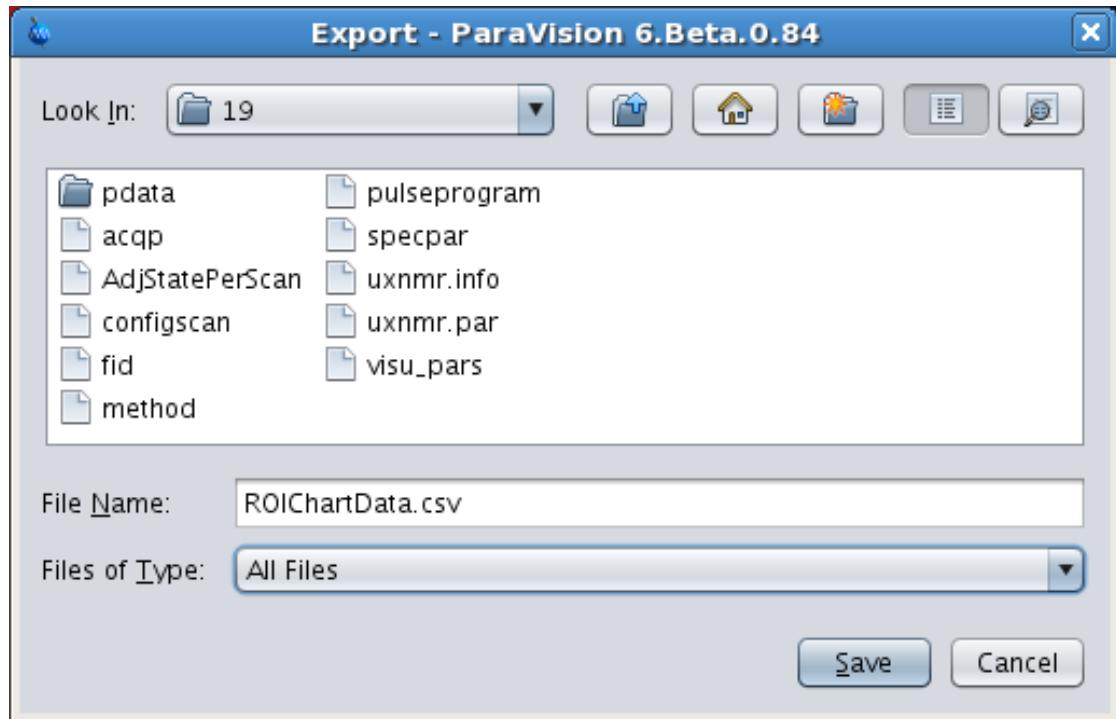


Figure 1.137: Export Chart Data

Goal:

Export analysis charts as graphics file.

1. Right-click the chart and choose "Export->Chart" from the context menu.
 - An export dialog appears.
2. Choose target location, file name and format (available formats are: SVG, PDF, and a number of bitmap formats, e.g. PNG, TIFF, JPEG, GIF, ..) and click "Save".

1.4.5.7 Performing Measurements on an Image

Goal:

Measure the distance between two features or length of an object.

1. Select the viewport with the image of interest by left-clicking it.
2. Use the Palette to access the Analysis Tools, then select the tab with the  symbol.
 - The Measurement Tool opens (see Figure [The Measurement Tool \[▶ 160\]](#)).
3. Click the button 
 - A red line appears centered on the selected image, with markers in the center and at each end.
 - ⇒ To place the ends of the line, point the mouse to a marker at the end, and drag it to the desired position (see Figure [The Distance Measurement \[▶ 160\]](#)).
 - ⇒ To move the line as a whole, point the mouse to the marker in the middle, and drag it to the desired position.

On the legend next to the line, the distance of the end markers is displayed .



Figure 1.138: The Measurement Tool

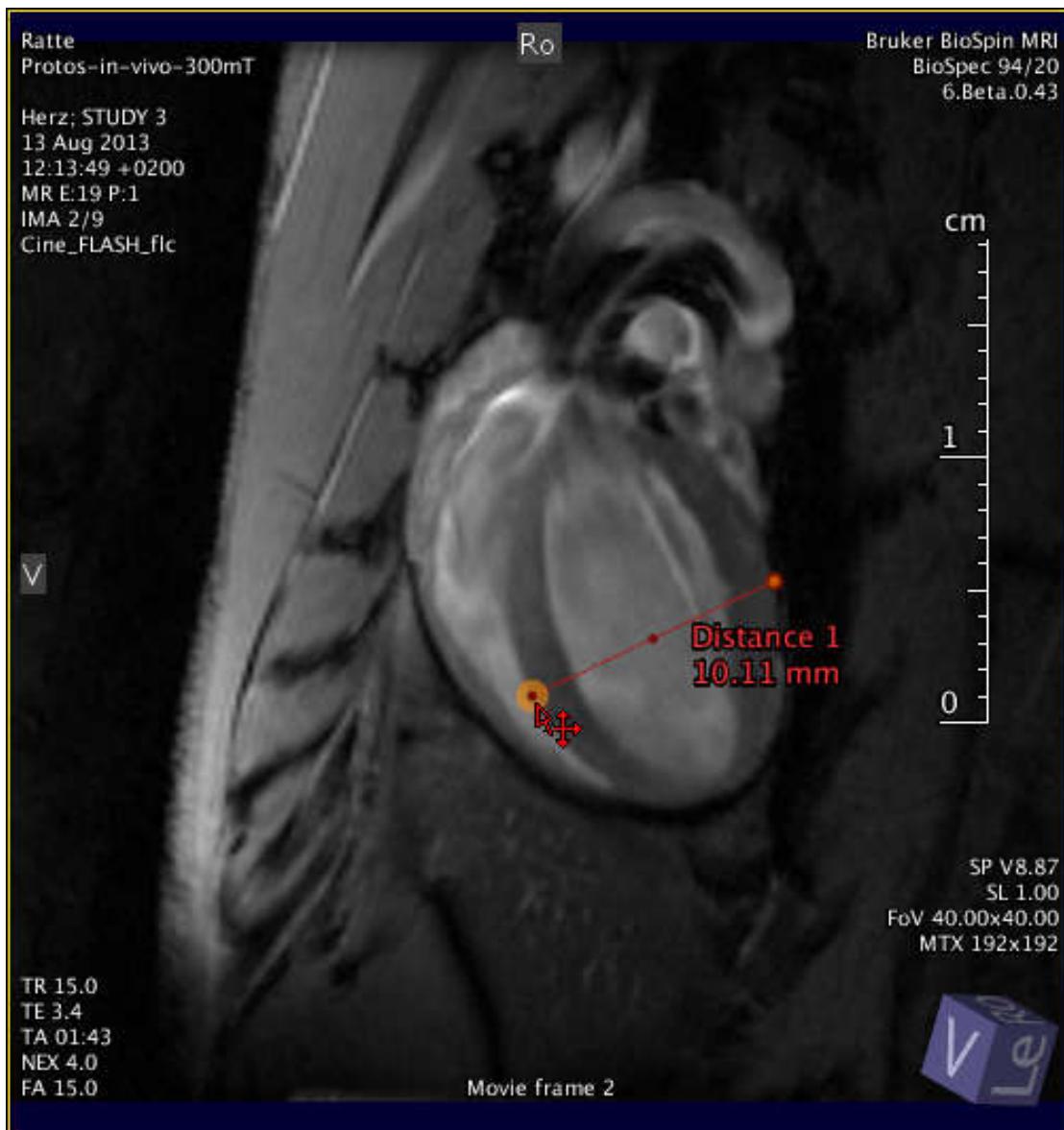


Figure 1.139: The Distance Measurement

Goal:

Measure an angle on the image.

1. Access the Measurement Tool, then click the button and select .
- Two red lines appear centered on the selected image, forming an initial angle, with markers in the center and at the end of each line.
2. To change the angle, point the mouse to a marker at any end, and drag it to the desired position with the mouse (see Figure [The Angle Measurement \[▶ 161\]](#)).

3. To move the angle as a whole, point the mouse to one of the markers in the middle of the lines, and drag it to the desired position.
 - On the legend next to the angle, the angle's value is displayed.

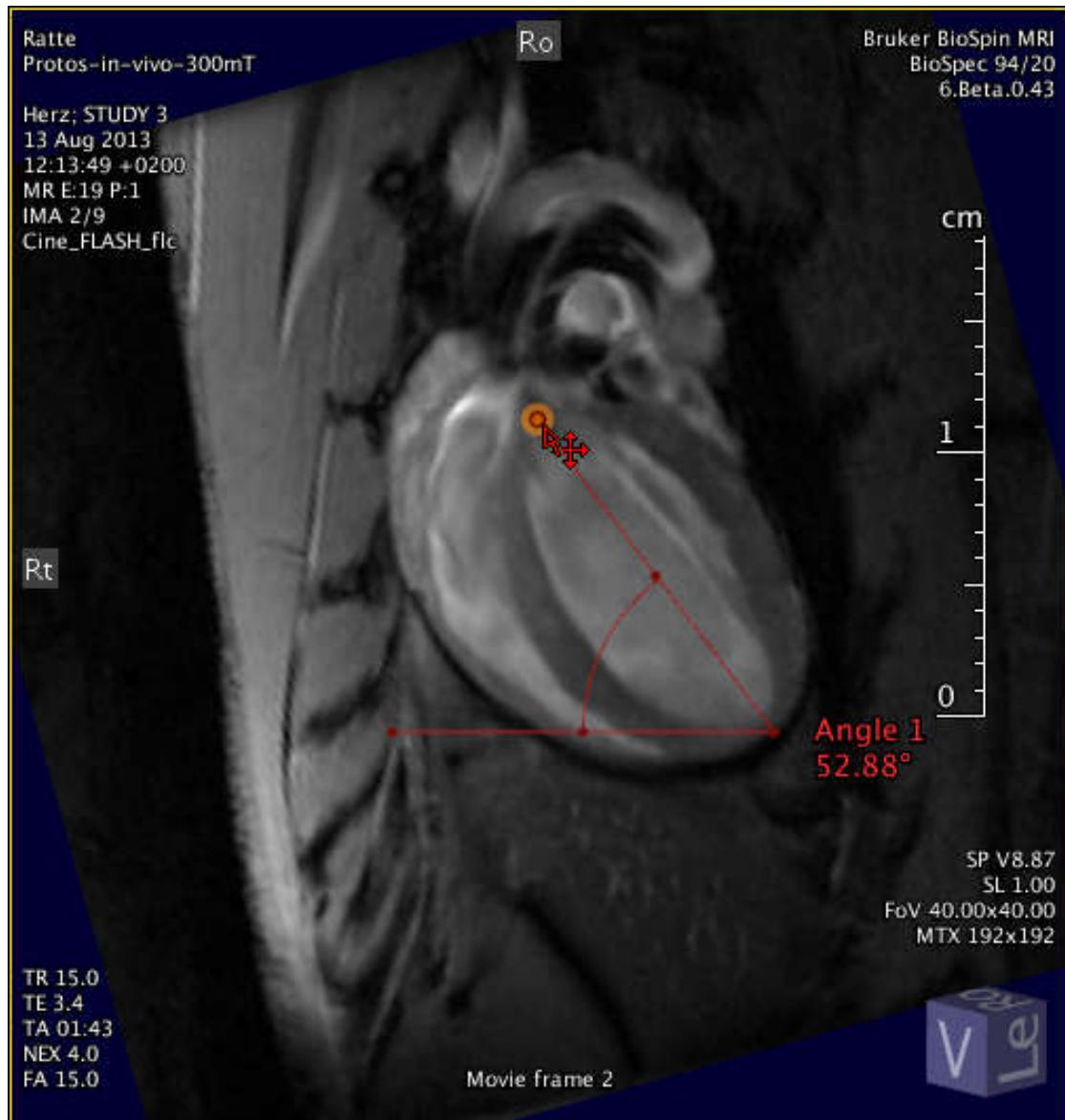


Figure 1.140: The Angle Measurement

Notice:

The measurement tools can also be manipulated using the keyboard. Click ⓘ for detailed information about the key-bindings.

1.4.5.8 Hiding and Deleting Analysis Tools on the Image

Goal:

Hide ROIs, line profiles and measurement overlays on an image, while keeping the analysis results and charts.

1. Access the Scans and Profiles Tool, Regions of Interest Tool, or Measurement Tool.
2. Click the button .

- The respective overlay on the image disappears. However, the Analysis Tools are not deleted, and the analysis results remain visible.

Goal:

Delete ROIs, line profiles and measurement overlays, results and charts.

1. Access the Scans and Profiles Tool, Regions of Interest Tool, or Measurement Tool.

2. In the drop-down menu, select the desired object to delete.



3. Click the button.

- The selected Analysis Tool is deleted permanently. The image overlay, analysis results and charts are removed.

1.4.5.9 Creating Snapshots

You can create snapshots of single viewport displays as well as of the whole Viewing Card without the need for an external screenshot application.

Goal:

Save a snapshot of a single viewport, including parameter overlay and Analysis Tool overlay.

1. Select the viewport of interest by left-clicking it.

2. Use the Palette to access the Analysis Tools, then select the tab with the symbol.

- The Create Snapshot Tool opens (see Figure [The Create Snapshot Tool \[162\]](#)).

3. Enter the desired target image size

4. Click "Capture"

- An export dialog appears

5. Choose target location, file name and format and click "Save"



Figure 1.141: The Create Snapshot Tool

Notice:

The ratio width:height for the snapshot is fixed to the viewport aspect ratio. To change the aspect ratio, resize the viewport by changing the size of the ParaVision main window.

Notice:

The following image formats are available:

Format	File extension	Details
BMP	*.bmp	Compression types: BITFIELDS, JPEG, PNG, RGB, RLE4, RLE8
GIF	*.gif	Dithering may be needed
JPEG	*.jpg, *.jpeg, *.jfif, *.jls	Compression types: lossy (DCT) or lossless
JPEG 2000	*.jp2	
PNG	*.png	Compression types: DEFAULT, FILTERED, HUFFMAN_ONLY
PNM	*.ppm, *.pgm, *.pbm	
RAW	*	
TIFF	*.tif, *.tiff	Compression types: Deflate, JPEG, LZW, PackBits, ZLib
WBMP	*.wbmp	

Goal:

Save a snapshot of a whole Viewing Card.

1. On the top of the Viewing Card, right-click the Tab “ Viewing”
2. In the context menu select "Export Tab ..."
 ▶ An export dialog appears
3. Choose target location, file name and format and click "Save"

1.4.5.10 Creating Movies

Movies displayed in the ParaVision Movie Player can be exported to a file in (uncompressed) AVI or QuickTime format to be viewed independently of ParaVision. For instructions how to open the Movie Player and display images as a movie, see [Displaying Images As A Movie](#) [146].

Goal:

Export a movie from the Movie Player to a file.

1. In the Movie Player, click the right-hand viewport.
 ▶ The viewport border changes to yellow.
2. On the Palette, in the Analysis Panel, select the tab with the  symbol.
 ▶ The Create Movie Tool opens (see Figure [The Create Movies Tool](#) [164]).

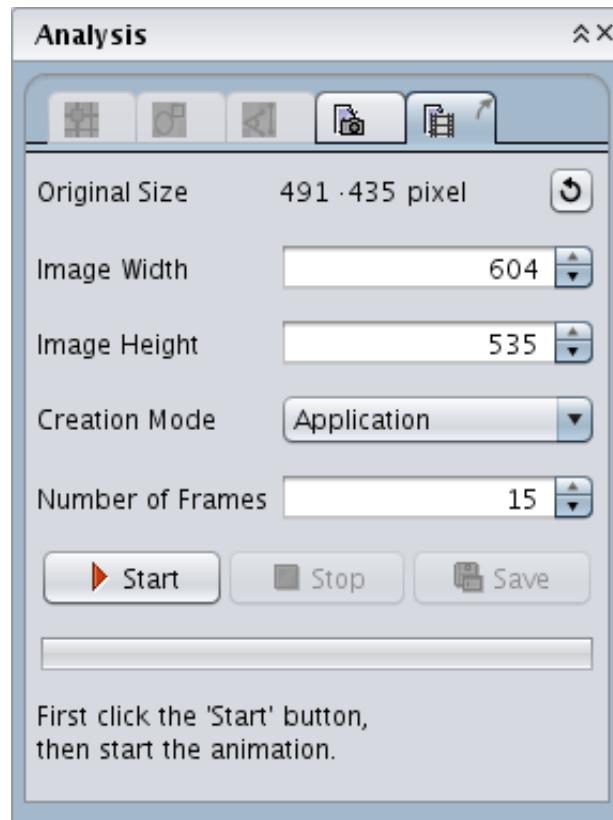
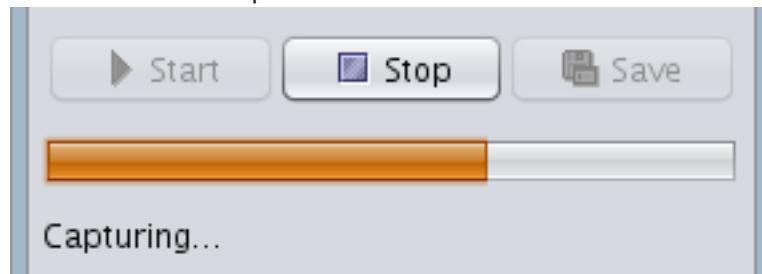


Figure 1.142: The Create Movies Tool

1. Specify the desired width or height (in pixels) of the movie to export.
2. Specify the number of frames to export to the movie. The default number is one complete movie cycle. By increasing the number of frames, multiple movie cycles will be exported.
3. Click the button "Start", then start the movie playback in the Movie Player. (To capture a complete cycle, make sure the Movie Player is reset to the first frame before starting the playback, by dragging the slider to the left or by entering "1" into the frame field).
 - The movie will be captured



4. Wait until the movie capture has finished, then click "Save" to save the captured movie to the desired location.

Notice:

The ratio width:height for the movie export is fixed to the viewport aspect ratio. To change the aspect ratio, resize the viewport by changing the size of the ParaVision main window.

Notice:

The number of frames in a movie cycle is not necessarily equal to the number of frames in the image categories included into the movie (e.g. the number of slices acquired in the experiment). It also depends on the frame rate selected in the Movie Player and thus a movie cycle usually also contains frames that are the result of temporal interpolation between acquired images. To switch off interpolation, in the Movie Player use “Nearest (Movie)” as the Smoothing Filter.

Notice:

The following movie formats are available:

Format	File extension	Details
QuickTime	*.mov	QuickTime container with M-JPEG content; compression size/quality trade-off currently fixed. Reasonable file size.
AVI	*.avi	AVI container with uncompressed content; huge files will result. Use QuickTime instead, if possible.

Notice:

Uncompressed AVI movies can require a lot of disk space. Please use third-party software to compress the AVI output to the desired compressed target format, or save movies in QuickTime format if supported by the application used for playback.

Goal:

Export the rotating 3D volume as a movie.

1. In the Movie Player, click the left-hand viewport (3D viewport).
2. On the Palette, in the Analysis Panel, select the tab with the  symbol.
 - The Create Movie Tool opens (see Figure [The Create Movies Tool ▶ 164](#), with Creation Mode “Camera”).
3. Specify the desired width or height (in pixels) of the movie to export.
4. Use interactive Rotate Mode to spin the 3D volume around the desired axis.
5. Specify the number of frames to export to the movie. One complete rotation of the volume will be divided into the specified number of steps.
 - The rotation speed will adapt according to the number of frames specified.
6. Click the button “Start”.
 - The movie will be captured.
7. Wait until the movie capture has finished, then click “Save” to save the captured movie to the desired location.

Notice:

To make the scene spin in interactive Rotate Mode, press the left mouse button in the viewport center and drag the mouse in the direction of the desired rotation. Release the mouse button while still moving the mouse. For in-plane rotation, drag the mouse along a viewport edge. This might need a moderate amount of practice.

Notice:

If you click into the 3D viewport during capture, the capture will be interrupted. You can set the volume spinning around a different axis with the interactive Rotate Tool. The capture will then continue, resulting in a movie with the volume spinning around both specified axes.

1.5 Dataset Browser

1.5.1 Introduction

The **Dataset Browser** is a navigation tool to search, review and manage datasets and protocols or scan programs in the ParaVision database and perform actions on selected dataset entities. Below the overview, describing the GUI, the most commonly used workflows are listed. It is shown how to adjust the GUI to the personal needs and biases.

1.5.2 Overview

The central table view of the **Dataset Browser** shows the datasets or protocols stored in the ParaVision database.

Datasets are arranged in a hierarchical structure, a subject entity represents an animal that is examined with the spectrometer. For each subject several studies can be created. Several examinations build a study and an examination may have several image series.

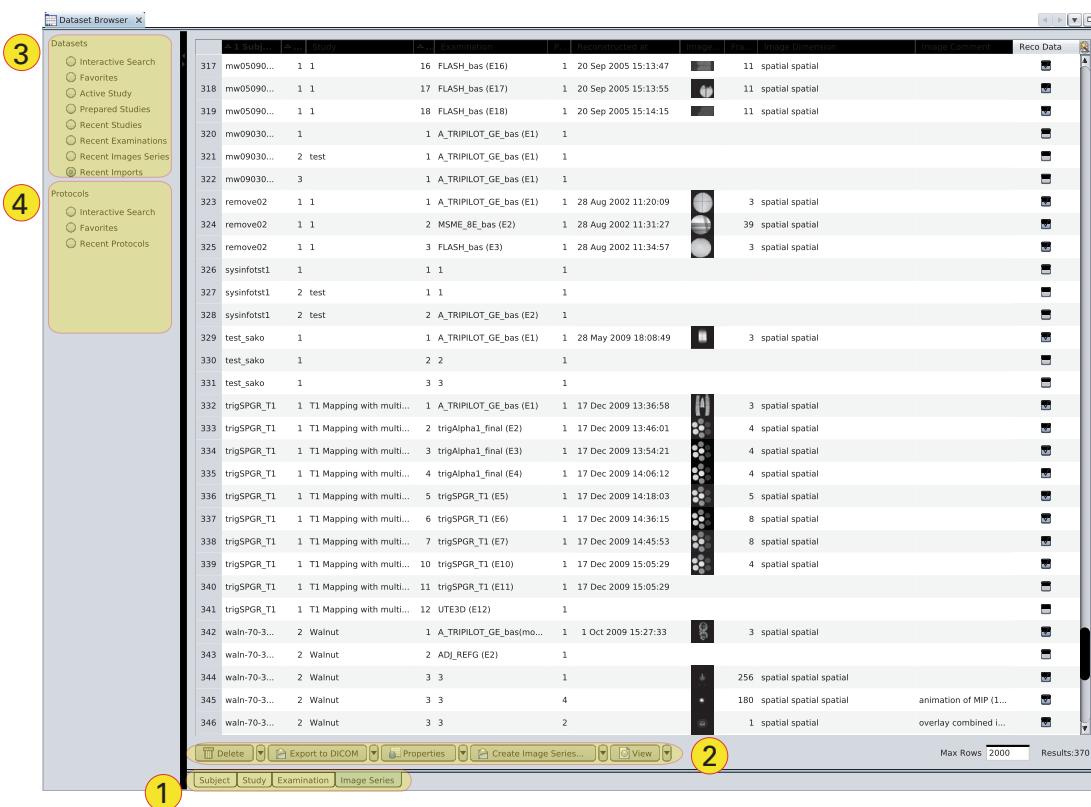


Figure 1.143: Dataset Browser

Therefore the user can switch through four different tables to browse datasets (1):

Subject	Study	Examination	Image Series
---------	-------	-------------	--------------

- The **subject** table shows subject properties only.
- The **study** table shows study and subject properties.
- The **examination** table shows examination, study and subject properties

- The **image series** table shows image series, examination, study and subject properties.

Below the browser table, a row of **ComboButtons** offers actions on selected datasets (2).



If no datasets are selected, this buttons may be invisible or disabled. Similar to a the GUI element ComboBox, a **ComboButton** is a combination of a drop-down list and a button providing actions of a particular category. Clicking the button element of the **ComboButton** performs the default category action while clicking the triangle icon of the **ComboButton** opens the a popup menu where the additional actions can be selected and performed.

The number and content of **ComboButtons** depends on the number, type, state and context of the selected dataset entities. Even if the button of the **ComboButton** is disabled, meaning the default action can not be performed for the selected dataset entities, additional actions may be available.

Left of the browser tables, a column of **Presets** offers predefined queries to search and sort the database.

The **Presets** for the datasets are (3):



- **Interactive Search**

Shows all datasets. The center area of the browser window is split and above the dataset tables an area with three selection lists and a search field is added. These lists allow to select subject IDs, studies and/or examinations to filter the datasets, displayed in the dataset tables.

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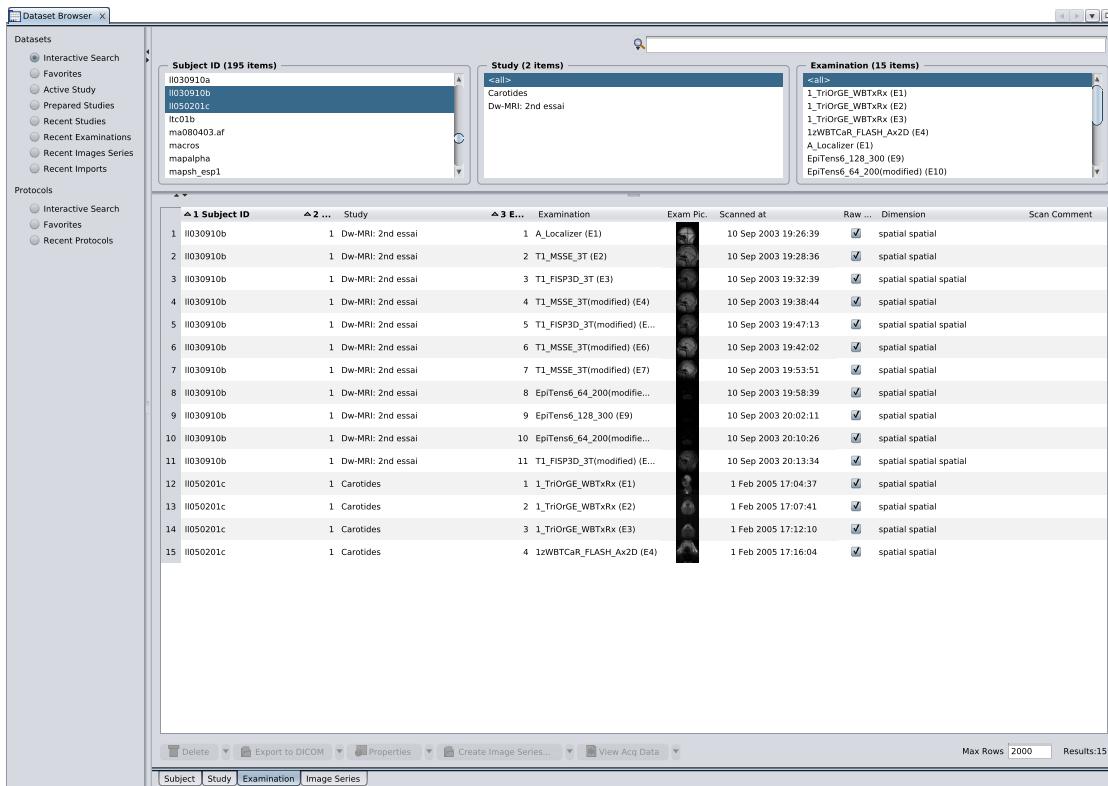


Figure 1.144: Browsing Datasets

- **Favorites**

Shows all datasets that are marked as favorites. Each dataset entity can be a favorite - see the actions “Favorite” and “No Favorite” on dataset entries. Note that the browser table shows not only the favorite dataset entities but also dataset entities that are related to favorite dataset entities. For instance, if you choose the **Preset** “Favorite” and switch to the examination table, you see all examinations that are marked as favorites but also all examinations that belong to studies or subjects that are favorites. The examinations that have favorite image series are also added.

- **Active Study**

Shows the “Active Study”. There is always one or none “Active Study” in the database. This is the study that is currently edited in the **Examination Card** or the latest study edited but still not completed.

- **Prepared Studies**

Shows the studies that are prepared for examination. This are all studies that are not completed.

- **Recent Studies**

Shows the studies created the last 12 month but not more then 20. They are sorted by their creation date with the newest studies first.

- **Recent Examinations**

Shows the 20 last recently acquired examinations with the newest examinations first.

- **Recent Image Series**

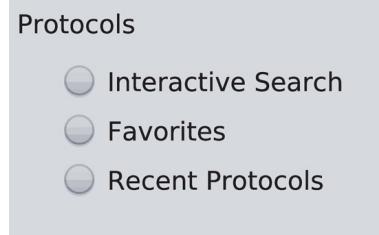
Shows the 20 last recently viewed image series of the last 30 days. They are sorted by their viewing date, with the last viewed image series first.

- **Recent Imports**

Shows all imported image series sorted by their import date with the last imported image series first.

Beneath the datasets, protocols and scan programs are also stored in the ParaVision database. Initially all protocols and scan programs that are delivered by Bruker are in this database. It can be enriched by user protocols and user scan programs stored from inside the **Examination Card**. The protocols and scan programs are categorized in a hierarchical structure with the **Object** as the highest level category (e.g. "Mouse"). Next is the **Region** category (e.g. "Head") followed by the **Application** category (e.g. "Angiography").

The protocol repository can be viewed by using the protocol type **Presets (4)**:



- **Interactive Search**

Shows all repository protocols. The center area of the browser window is split and above the protocol table an area with selection lists and a search field is added. Search the displayed protocols by selecting from the lists a gradient (if multiple gradients are registered at your system) and location properties (object, region, application). The 5th list allows to specify a repository scan program to search protocols that are embedded in a repository scan program.

Frequency	▲ 1 Gradient	▲ 2 Object	▲ 3 Region	▲ 4 Application	▲ 5 Protocol Name	Duration	Protocol Description	Prot...	Scan Mode	In...	Scan...
22	400	BGA125	Mouse	Head	Angiography	TOF_2D_FLASH_fic	665600	2D inflow angiography:Flow comp...	<input type="checkbox"/>	AUTOMATIC,...	0
23	400	BGA125	Mouse	Head	Angiography	TOF_3D_FLASH	407296	3D inflow angiography:Gradient e...	<input type="checkbox"/>	AUTOMATIC,...	0
24	400	BGA125	Mouse	Head	Angiography	Velocity_map	32768	Triggered velocity map1 slice/sec...	<input type="checkbox"/>	AUTOMATIC,...	0
25	400	BGA125	Mouse	Head	Diffusion	1_Localizer	12800	Overview scan3 orthogonal slices...	<input type="checkbox"/>	AUTOMATIC,...	0
26	400	BGA125	Mouse	Head	Diffusion	1_Localizer_multi_slice	129600	3 orthogonal slice packages5 slic...	<input type="checkbox"/>	AUTOMATIC,...	0
27	400	BGA125	Mouse	Head	Diffusion	DTI_EPI_30dir_sat	105000	Evaluation diffusion tensorSingle ...	<input type="checkbox"/>	AUTOMATIC,...	0
28	400	BGA125	Mouse	Head	Diffusion	DTI_EPI_seg_30dir_sat	280000	Evaluation diffusion tensorSegment...	<input type="checkbox"/>	AUTOMATIC,...	0
29	400	BGA125	Mouse	Head	Diffusion	D_Trace_EPI_sat	12000	Evaluation diffusion tensorSingle ...	<input type="checkbox"/>	AUTOMATIC,...	0
30	400	BGA125	Mouse	Head	Diffusion	Diffusion_map_EPI_sat	22400	Evaluation of diffusion mapSingle ...	<input type="checkbox"/>	AUTOMATIC,...	0
31	400	BGA125	Mouse	Head	Diffusion	Diffusion_weight_EPI_sat	6000	Diffusion weightedSingle shot EPI...	<input type="checkbox"/>	AUTOMATIC,...	0
32	400	BGA125	Mouse	Head	Diffusion	Diffusion_weight_SE_sat	480000	Diffusion weightedSpin Echo5 slice...	<input type="checkbox"/>	AUTOMATIC,...	0
33	400	BGA125	Mouse	Head	Diffusion	T2_TurboARE	160000	T2 contrastFast spin echo9 slices...	<input type="checkbox"/>	AUTOMATIC,...	0
34	400	BGA125	Mouse	Head	Perfusion	1_Localizer	12800	Overview scan3 orthogonal slices...	<input type="checkbox"/>	AUTOMATIC,...	0
35	400	BGA125	Mouse	Head	Perfusion	1_Localizer_multi_slice	129600	3 orthogonal slice packages5 slic...	<input type="checkbox"/>	AUTOMATIC,...	0
36	400	BGA125	Mouse	Head	Perfusion	DCE_FLASH	2400	Dynamic contrast enhancementG...	<input type="checkbox"/>	AUTOMATIC,...	0
37	400	BGA125	Mouse	Head	Perfusion	Perfusion_FAIR_EPI	345099	Perfusion measurementFAIR EPI1...	<input type="checkbox"/>	AUTOMATIC,...	0
38	400	BGA125	Mouse	Head	Perfusion	Perfusion_FAIR_RARE	700272	Perfusion measurementFAIR RARE...	<input type="checkbox"/>	AUTOMATIC,...	0
39	400	BGA125	Mouse	Head	Perfusion	T2_TurboRARE	160000	T2 contrastFast spin echo9 slices...	<input type="checkbox"/>	AUTOMATIC,...	0
40	400	BGA125	Mouse	Head	Perfusion	T2star_FID_EPI	1500	Single shot FID EP15 slicesMtx. 12...	<input type="checkbox"/>	AUTOMATIC,...	0
41	400	BGA125	Mouse	Head	Relaxometry	1_Localizer	12800	Overview scan3 orthogonal slices...	<input type="checkbox"/>	AUTOMATIC,...	0
42	400	BGA125	Mouse	Head	Relaxometry	1_Localizer_multi_slice	129600	3 orthogonal slice packages5 slic...	<input type="checkbox"/>	AUTOMATIC,...	0
43	400	BGA125	Mouse	Head	Relaxometry	T1_T2map_RARE	1094400	T1 and T2 evaluationSaturation r...	<input type="checkbox"/>	AUTOMATIC,...	0
44	400	BGA125	Mouse	Head	Relaxometry	T1_T2map_TrueFISP	576000	T1 and T2 evaluationTrue FISP1 s...	<input type="checkbox"/>	AUTOMATIC,...	0

Figure 1.145: Browsing Protocols

- **Favorites**

Shows all repository protocols that are marked as favorites or protocols that belong to a repository scan program that is a favorite.

- **Recent Protocols**

Shows all repository protocols stored or imported by the user, sorted by the creation or import date with the newest protocol first.

1.5.3 Selections in the Browser Tables

Pre-Selections

Selections made in a browser table are continued during **Preset change** and table change. For instance when you select the single study from the **Preset** "Active Study" and switch to the **Preset** "Interactive Search" where you can see all existing studies, the single selected study stays selected in the visible scroll area. When you switch now to the examination table, all examinations, that belong to the selected study are pre-selected. That means, they are high-lighted by a blue background color, slightly brighter than the dark blue selection background color. When you switch to the subject table, the subject of the selected study is pre-selected.

Selection Propagation

You can propagate selections to the **Dataset Explorer** or **Palette Explorer**. Submit the action "Select in Explorer" from the context menu after you made your selections in a dataset or protocols browser table. If the **Workspace Explorer** or **Palette Explorer** are open, the matching dataset or protocols nodes are expanded and selected there.

The Dataset Browser also receives selections, propagated from other tools, that provide the "Select in Explorer" action, like the **Examination Card** or **Picture Viewer**.

Drag & Drop

You can drag dataset entities or protocols from the dataset or protocols tables and drop them on any tools that can handle these (**Examination Card**, **Study Registration**, **Image Viewer**, etc.).

1.5.4 Common Workflows

1.5.4.1 Searching datasets

Goal:

Search the database for datasets using any character sequence.

1. Switch to the Dataset Browser. If it is not open currently, start it by activating the menu item "Window ▶ Dataset Browser" from the main menu.
2. Select the Preset "Datasets ▶ Interactive Search".
 - The extended Dataset Browser window with the search field and the three selection list on top becomes visible. The table shows all datasets in the database.
3. Use the search field to enter a search string.
 - Any 2 or more characters entered in the search field are used as a search string. This will be used for a case insensitive text search during typing on all string properties of the datasets.

Example: The sequence "pin" will find studies with the position "HEAD_SUPINE", studies with the name "T1-Mapping" or examinations with name "spin-echo".

If the search string matches the name of a boolean property of a dataset that is visualized in the browser table as a check box, all datasets are found where this property is set. If you put a '!' or a '\' character or a "not" string before the property name, all datasets are found where this property is cleared.

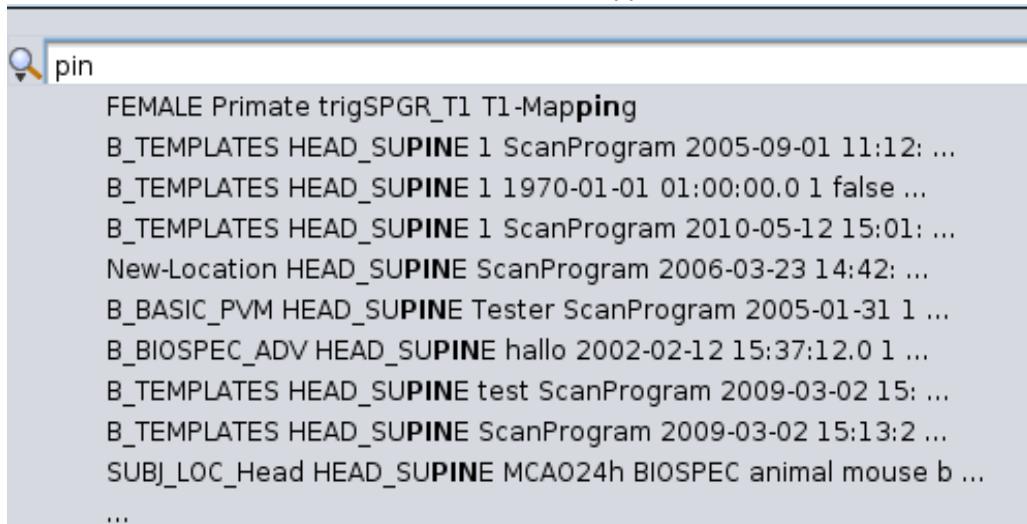
Example: The sequence "raw data" finds all examinations with acquired data, "! reco data" finds the image series without reconstructed data.

If the search string has number format it will be used for a numerical search.

Example: Entering “13” finds animals with a weight of 13 gr., examinations with index 13 and image series with index 13. Also all subjects, studies, etc. that are created, archived, acquired, etc. in the year 13 (AD) will be found.

-> A more detailed date format can also be used for a date search. Accepted formats are “03/28/2006”, “Mar 28, 2006” or “March 28, 2006”.

-> If a search has some hits, a list with the results appears:



4. Select a single entry in this result list to fill the browser table with the datasets belonging to that entry or press <Enter> to select all hits. Press <Esc> to clear the search field.

1.5.4.2 Open a study in the Examination Card

Goal:

Find a prepared study and load it into the Examination Card.

1. Switch to the Dataset Browser. If it is not open currently, start it by activating the menu item “Window ▶ Dataset Browser” from the main menu.
2. Select the Preset “Datasets ▶ Active Study”.
 - The study table is switched on. It shows the “Active Study” if it exists. Alternatively you can select the Preset “Datasets ▶ Prepared Studies”, the table shows all studies that are not completed yet.
3. In the study table select the study that you want to open.
 - Below the study table a row of ComboButtons becomes visible, providing all actions that are available on the selected study.
4. Locate the ComboButton named “Exam” and click it.
 - The Examination Card is opened and the selected study is loaded and can be edited.

Notice:

Instead of clicking the “Exam” button, this action can also be performed by double-clicking the respective study table row. Avoid here the field for the “Study Comment” property because double-clicking comment properties activates an editor where these comments can be changed.

1.5.4.3 View a dataset

Goal:

Open a dataset with an appropriate viewing tool.

1. Switch to the **Dataset Browser**. If it is not open currently, start it by activating the menu item “Window ▶ Dataset Browser” from the main menu.
2. Find your dataset by using one of the dataset **Presets**.
3. In the examination or image series table select the row in the browser table that represents your desired dataset.
 - Below the browser table a row of ComboButtons becomes visible, providing all actions that are available on the selected dataset.
4. Locate the **ComboButton** named “View Acq Data” for examinations or “View” for image series and click it. If a dataset does not have acquired or reconstructed data, these buttons may be absent or disabled.
 - An appropriate viewing tool is opened and shows the selected data. For examinations the acquired data will be rendered in a 1D data viewer normally. The reconstructed image of a spatial image series will be rendered in an image viewer and spectroscopic image series data will be rendered in the 1D data viewer.

Notice:

Instead of clicking the “View” button, the default viewing action can also be performed by double-clicking the respective browser table row. Avoid again the table cells of a comment property (“Image Comment” or “Scan Comment”) not to open the comment editor.

1.5.4.4 Export Browser Table Content

Goal:

Write the content of a dataset or protocol table to a file.

1. Open the context menu with the mouse anywhere in a browser table, normally by pressing the right mouse button. Select the action “Export Table...” from the context menu.
 - A dialog is shown that allows you to specify an output file (see Figure [Export \[▶ 173\]](#)). By the extension of the output file you can determine the format of the file:
 - csv: A “comma separated value” file is written.
 - html: An HTML file is written.
 - tex: A Latex file is written.
2. Enter or select an output file and press the OK button.
 - The browser content is written to the specified file.

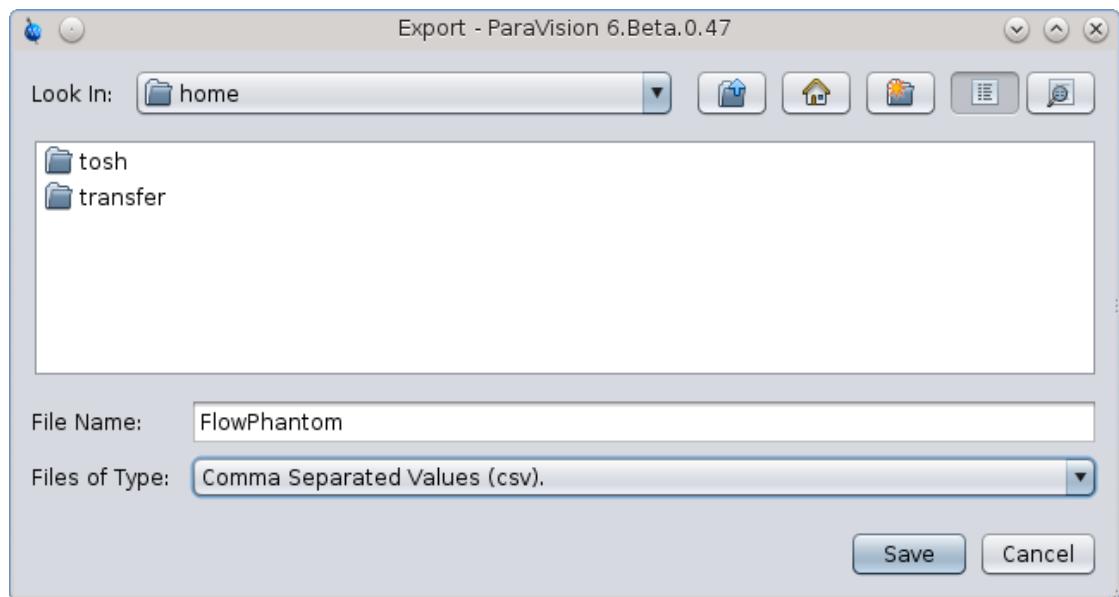


Figure 1.146: Export

1.5.4.5 Print Browser Table Content

Goal:

Print the content of a dataset or protocol table.

1. Open the context menu with the mouse anywhere in a browser table, normally by pressing the right mouse button. Select the action “Print Table...” from the context menu. A dialog is shown that allows you to send the table data to an available printer or to a postscript file (see Figure [Print \[▶ 174\]](#)).
2. Select a printer and press the OK button.
 - The table content is printed.

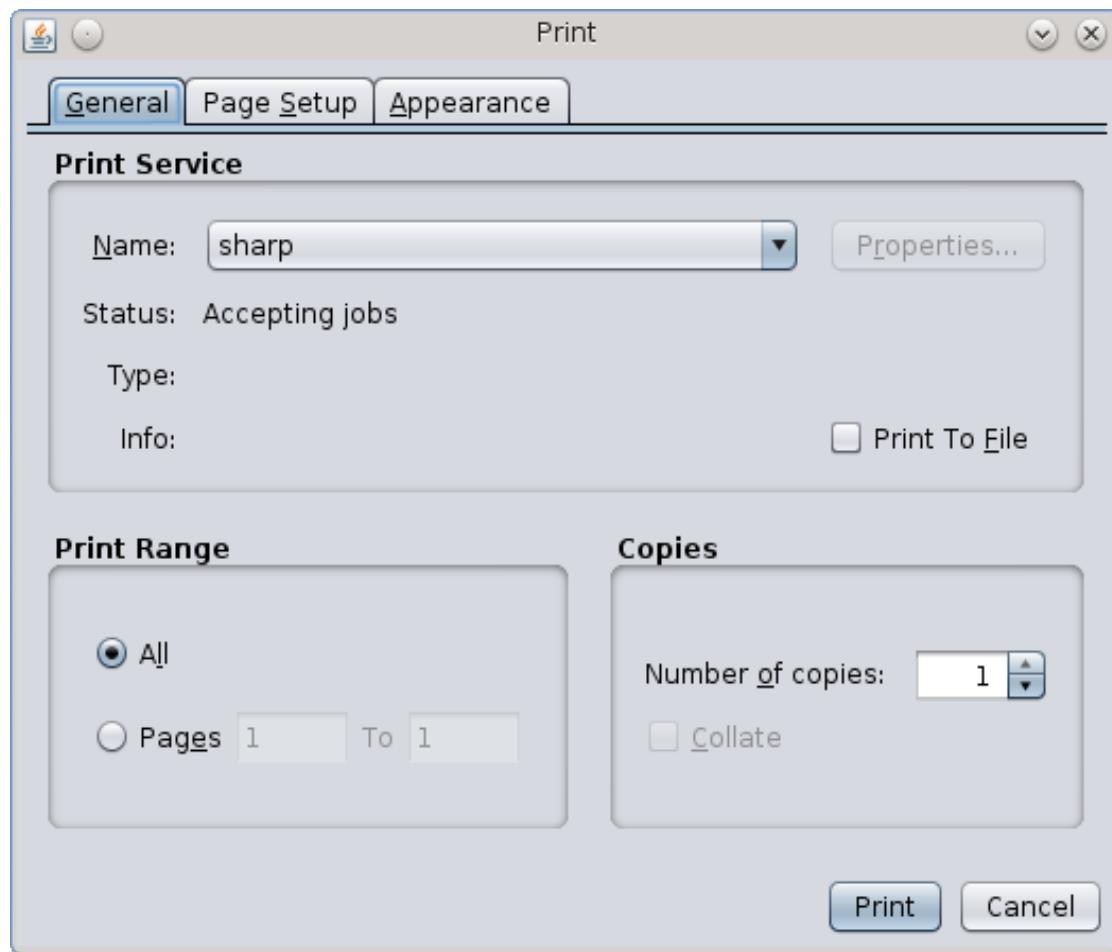


Figure 1.147: Print

1.5.4.6 Select Visible Properties

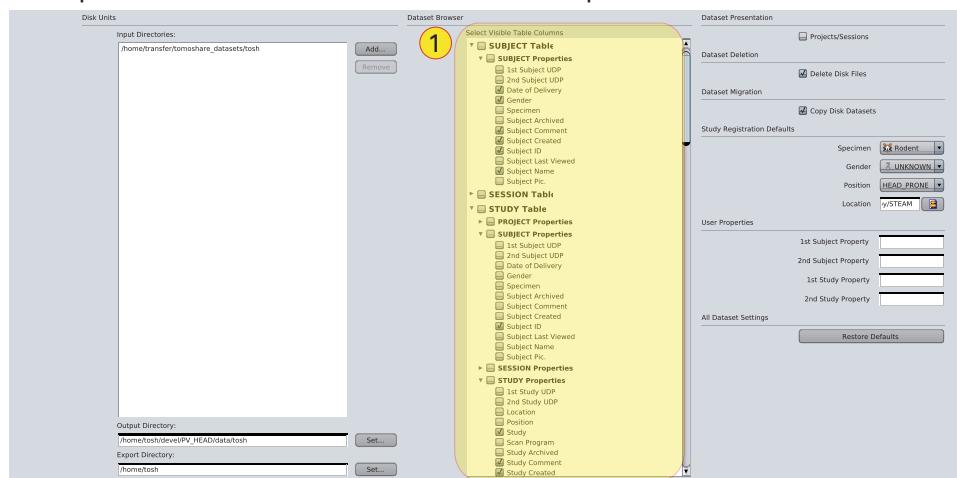
Datasets, especially at image series level, are described by dozens of properties. These are way to many properties to visualize in a single table row. Initially the set of visible properties is defined to meet the most needs but each user can define, which properties he wants to see in his dataset and protocol browser tables.

Goal:

Adjust the amount of visible browser table columns to personal needs.

1. Select the menu item "Window ▶ Options" from the main menu.
 - The Options Window appears.
2. Locate the "Dataset" icon on the icon bar on top of the Options Window and click it.

- The Options Window shows the dataset related options.



The tree view in the middle of the window with the title "Select Visible Table Columns" (1) offers check box elements for all available dataset and protocol properties to adjust the visibility in the different tables. Each browser table has its own sub-tree (ignore the project and session tables for now). In a sub-tree you can find the properties ordered by their category:

- The study table combines study and subject properties (ignore the project and session properties).
- The examination table adds examination properties to the study and subject properties.
- The image series table shows everything: image series, examination, study and subject properties.
- The protocol table ("INSTRUCTION Table" here) shows protocol, instructions and scan program properties.

3. Select the properties you want to see in the respective tables and close the Options Window by pressing the OK button.

- The browser tables will be refreshed immediately without having to be re-opened. These adjustments are stored persistently for each user.

1.5.4.7 Adjust Browser Table Columns

Adjust Browser Table Columns

Once you have selected which properties you'd like to see in the different tables, you may want to arrange the position and size of the columns of the browser tables. You can also sort the tables by different criteria.

Goal:

Arrange the browser table columns and sort the content.

1. Press the mouse button on a column title (e.g. "Subject ID") and drag it horizontally. Release the mouse button when the column reaches the desired position. Repeat this with the other columns.
 - The table columns are arranged in your preferred order.
2. Press the mouse button exactly on the separator between two columns titles and drag it horizontally to resize the column widths. Release the mouse button if the column left to the mouse cursor has the preferred size. Repeat this with the other columns.
 - The table columns get the preferred width sizes.

3. Use mouse clicks on a columns title to switch on and off table sorting.

- ▶ A first click selects the property of the particular column for sorting the table in ascending order. Another click switches to descending order and a third one cancels the sorting. A triangle icon beneath the property name pointing upwards or downwards indicates the sorting order.
- ▶ Holding the <Shift> key during mouse click on different column titles allows to specify multiple properties for a sorting cascade. A number at the triangle icon indicates this sorting cascade.

1.5.4.8 Enable the visibility of Projects and Sessions

Goal:

Make project and session levels of datasets visible in **Workspace Explorer**, **Dataset Browser** and **Study Registration** dialog.

1. Select the menu item **Window ▶ Options** from the main menu.
 - ▶ The **Options Window** appears.
2. Locate the “Dataset” icon on the icon bar on top of the **Options Window** and click it.
 - ▶ The **Options Window** shows the dataset related options.
3. Locate the check button “Projects/Sessions” in the “Dataset Presentation” segment in the most right column of the **Options Window**.
4. Enable it and close the **Options Window** by clicking the “OK” button on the bottom.
5. Close and restart ParaVision.

The Dataset Browser shows now the Project and Session dataset levels in additional selection lists and tables.

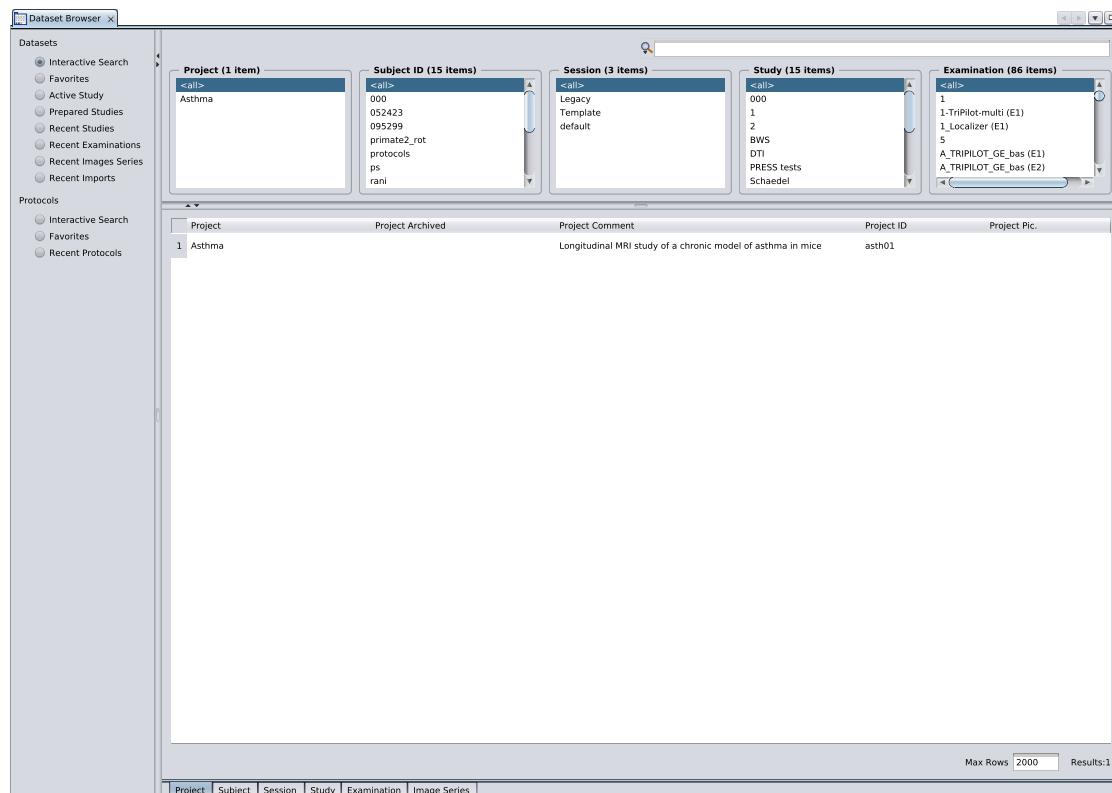


Figure 1.148: Dataset Browser P&S

1.6 3D Image Viewing

1.6.1 Overview

ParaVision contains a variety of possibilities to visualize 3D image data. The following list provides a brief overview:

- Display of slices or slabs in a 3D-viewport (see Chapter [Loading and 3D-Displaying Task \[▶ 187\]](#)).
If an Image Series contains spatial slabs (3D-cubes) or 2D-slices that form a cube it is possible to display this cube in a 3D-viewport. If other categories exist (e.g. echos, repetitions) the fixed category element (e.g. the 2nd echo and 3rd repetition) can be selected and the corresponding spatial slice (slab) cube is displayed, e.g. all slices of the 2nd echo and 3rd repetition as cube.
If the spatial slices do not form a cube (e.g. a Localizer), the slices can be shown in the 3D space in their correct spatial relationship. For example, a localizer often contains 3 orthogonal slices. In the 3D-viewport these slices are displayed in the correct spatial relation (orientation, extent).
- Multi-planar reformatting (MPR) of an Image Series (see Chapter [Simple Slices \(MPR\) Task \[▶ 189\]](#))
An Image Series of equidistant coplanar images with the same arbitrary orientation forming a 3D-cube can be created from a 3D Image Series or a 2D-image series where the slices create a 3D-cube. The newly created Image Series is stored as a 3D-Image Series.
In addition, it allows easy re-sampling of the image data along its principal axes.
- DTI visualization (see Chapter [DTI Visualization Task \[▶ 198\]](#))
Direction Encoded Color (DEC) visualizations of volumes of Diffusion Tensor Imaging (DTI) reconstructed Image Series can be displayed in a 3D-viewport. Tensor eigenvector components are color-coded and optionally mapped onto morphology data. The eigenvector components are stored in the DTI reconstructed Image Series.
- Dataset converter (see Chapter [Dataset Conversion Task \[▶ 204\]](#))
Stores the selected slab of the current Image Series as a simple 3D Image Series.

1.6.2 Loading Image Series for 3D Image Viewing

To start the 3D-Image Viewers on an Image Series:

1. Select an Image series
 - ▶ in the **Workspace Explorer** below the **Datasets** node by expanding the Image Series node
 - ▶ in the **Palette Explorer**
 - ▶ in the **Dataset Browser** in the **Image Series** dataset view
2. Open the general 3D-viewer and load the selected Image Series by
 - ▶ clicking the **Advanced Viewing** menu entry in the context menu of the **2D/3D Image Data** node below the Image Series node in the **Workspace Explorer**
 - ▶ clicking the **Advanced Viewing** menu entry in the context menu of the selected Image Series in the **Palette Explorer**
 - ▶ clicking **Advanced Viewing** in a sub-menu of the buttons below the **Image Series** view in the **Dataset Browser**. The **Advanced Viewing** entry can be found in the sub-menu of the **View** button (click on the triangular button)

- ▶ drag and drop an Image Series onto the tab of an already opened 3D Image Viewer
- 3. The general 3D-Viewer graphical user interfaces opens. It loads the slices of the first frame categories. For example, if the dataset contains an echo and repetition category all slices of the first echo and first repetition are loaded.

The tasks briefly described in Chapter [Overview \[▶ 177\]](#) have different start buttons which are covered by the chapters corresponding to the tasks.

1.6.3 Anatomy of the User Interface

The main tab can be divided into the following areas (see Figure [3D Viewing Tab with Loaded Image Series \[▶ 179\]](#))

- The left viewport shows a 3D viewer displaying the current slice of an Image Series. If the Images Series is 3D the center slice of the 3D-cube is shown per default. It is possible to navigate through the different slices in the scene.
- The right viewport is a 2D Plane Viewer. It shows the selected slice (rotated or translated in the 3D scene) in the different applications.

The usage of these viewers is described in Chapter [Using the Viewers \[▶ 179\]](#).

In the bottom left a tool panel is located. The tool panel includes the color mapper, the controls for the three orthogonal slice planes, and the oblique plane transformation panel. The tool panels are described in Chapter [The Tool Panels \[▶ 183\]](#).

In the bottom right the task panel is located. It launches the wizards that guide through the different applications:

- **Primary Dataset** and **Secondary Dataset** task (see Chapter [Loading and 3D-Displaying Task \[▶ 187\]](#))
Load Image Series directly by using the path. Two different Image Series can be loaded and it is possible to switch between them (Click **Select** button right of the Image Series path).
- **Simple Slices** task (see Chapter [Simple Slices \(MPR\) Task \[▶ 189\]](#))
Starts a tool for multi-planar reformatting.
- **DTI Visualization** task (see Chapter [DTI Visualization Task \[▶ 198\]](#))
Color coded visualization of DTI reconstructed Image Series.
- **Dataset Converter** task (see Chapter [Dataset Conversion Task \[▶ 204\]](#))
Convert loaded 3D-cube into a new Image Series.

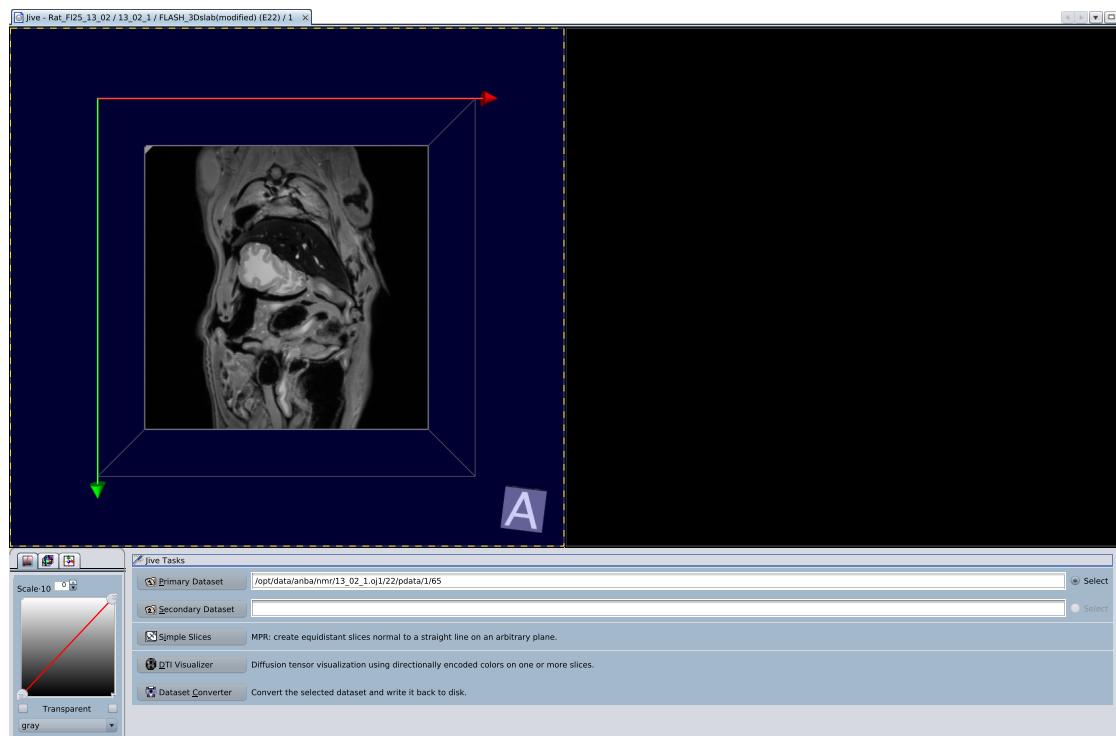


Figure 1.149: 3D Viewing Tab with Loaded Image Series

1.6.4 Using the Viewers

Each viewer has an orientation cube in the lower right corner. This cube represents the current view of the shown object in the subject coordinate system. The different coordinate systems and the corresponding cubes are described in Chapter [Subject Coordinate Systems ▶ 127](#).

The viewports are best understood using the concept of a virtual camera through which the objects in the scene are shown. Camera operations do not change anything within the objects. They only affect the spectator's point of view. The Hybrid 3D-Viewer (left) uses a perspective camera and the 2D Plane Viewer (right) uses an orthographic camera.

Both viewers can operate in two different modes:

- Pick Mode
The Pick Mode is used to select and manipulate the objects within the scene.
- View Modes
The View Modes are used to navigate through the scene without changing any object. All operations only adjust the camera position or color settings. The following View Modes exist:
 - Zoom changes the distance of the camera to the object.
 - Rotate rotates the camera around the objects.
 - Pan shifts the camera without changing distance or zoom.
 - Map changes the color lookup table for the camera.

These modes can be switched using the Interactive Tool Selection Bar as described in Chapter [Overview ▶ 140](#) and Chapter [Using View Tools Interactively on a Viewport ▶ 141](#) on a Viewport.

Clicking with the right mouse button into one of the viewers opens the context menu:

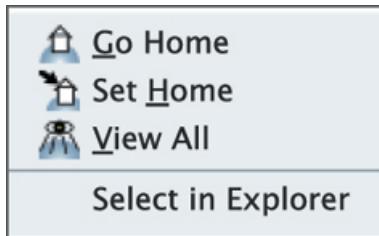


Figure 1.150: Viewport Context Menu

- **Go Home**
Revert the camera to the initial or current home position.
- **Set Home**
Define the current camera position as new home.
- **View All**
Changes the camera, so that the whole scene is visible. This is quite useful if you got lost in space. Also sets bounding box center of the current scene as new center of camera rotation.
- **Select in Explorer**
Selects the Image Series loaded into the viewport in the Explorer or the Dataset Browser.

1.6.4.1 Viewing in the Hybrid 3D-Viewer

The Hybrid 3D-Viewer contains arrows in the middle of the viewport and outside of the displayed object. These arrows have different colors:

- The red arrows show the direction of the local x-axis.
- The green arrows show the direction of the local y-axis.
- The blue arrows show the direction of the local z-axis.

Depending on the setting of the camera it is possible that some of the axis arrows are not or only partly visible.

Clicking into a selected object in the viewport in Pick mode creates plane manipulators to the scene. Oblique Plane, Transformer, Trackball, and Transform Box manipulators are available depending on the task. In some tasks the user can select appropriate manipulators.

The Oblique Plane manipulator is the default and available in all tasks (see Figure [Oblique Plane Manipulators \[181 \]](#)).

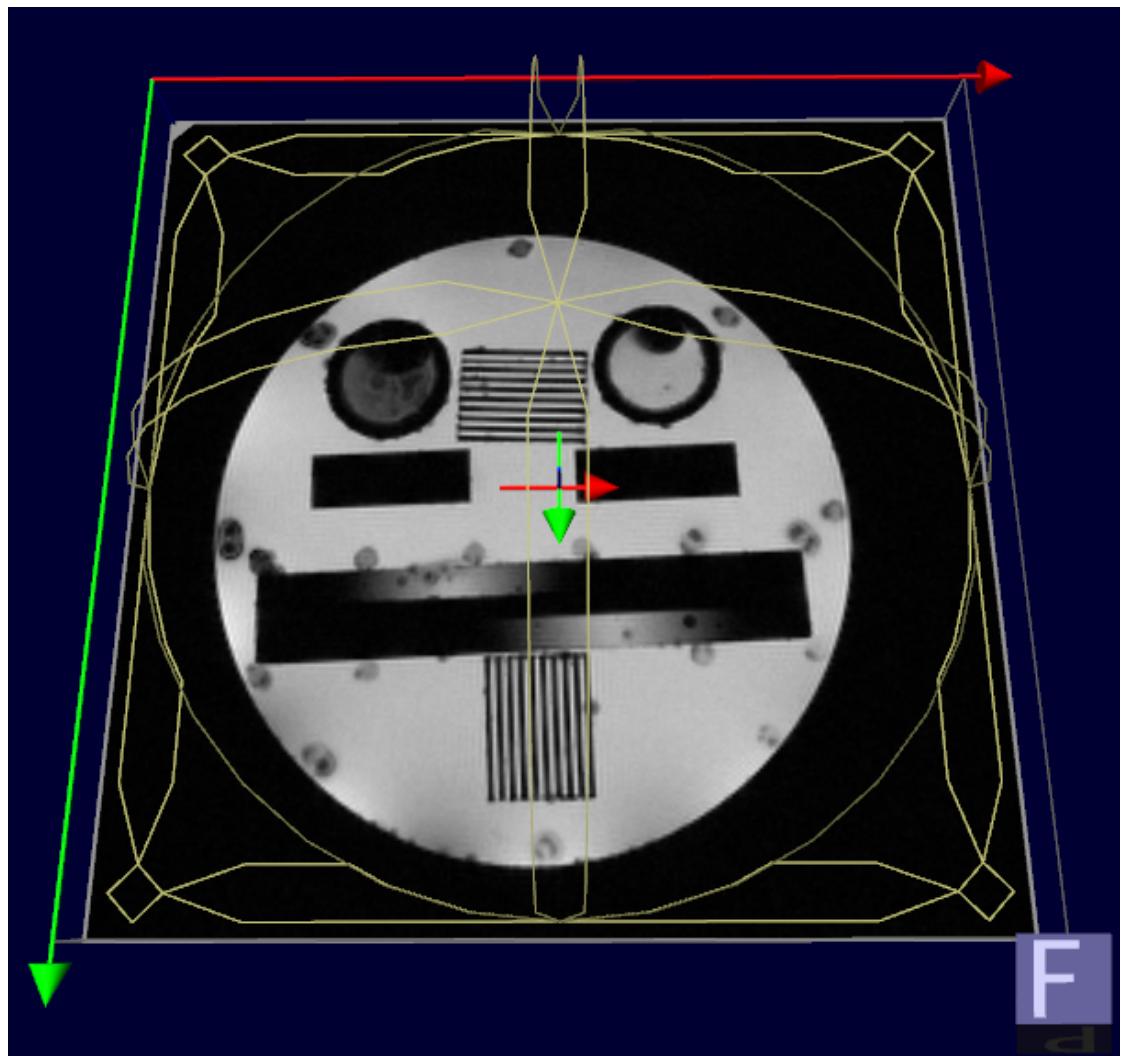
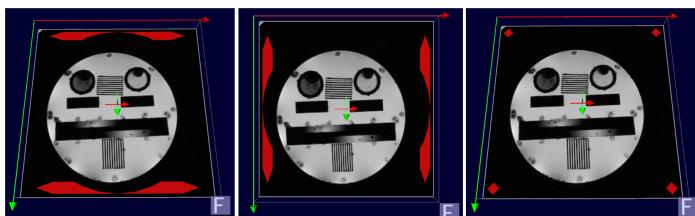
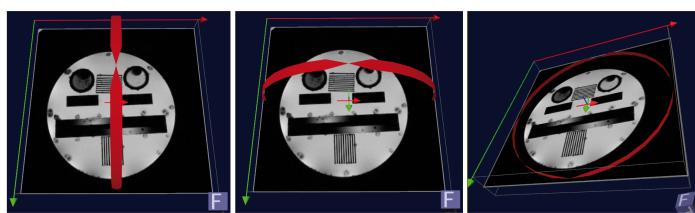


Figure 1.151: Oblique Plane Manipulators

The Oblique Plane manipulator appears as shown in Figure [Oblique Plane Manipulators 181](#) as golden wire-frame sphere and in-plane polygons that allow to rotate and translate the object. The manipulator lines get an orange highlight on mouse-over and the active areas get filled in solid red while dragging. Supported operations are:



Constrained translation along one axis by dragging after clicking into the polygons shown within the plane. There is no free translation mode.



Constrained rotation about one axis by dragging after clicking into the narrow space between two golden lines on the sphere, as shown.

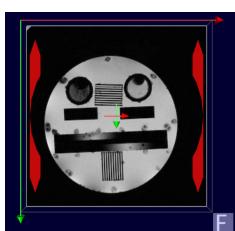


Free rotation by clicking and dragging anywhere else on the sphere.

In detail



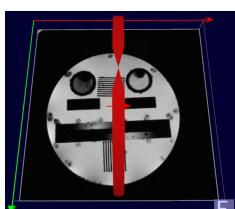
drag the solid red areas to shift the object in the local in-plane x-axis (red).



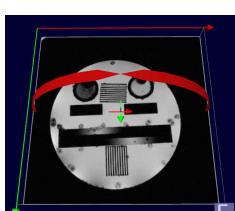
drag the solid red areas to shift the object in the local in-plane y-axis (green).



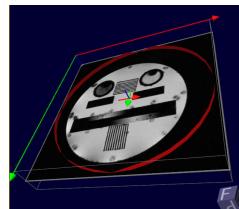
drag the solid red areas to shift the object in the local z-axis perpendicular to the plane (blue).



drag the solid red to rotate the object around the local x-axis (red).



drag the solid red to rotate the object around the local y-axis (green).



drag the solid red areas to rotate the object in-plane around the local z-axis (blue).



drag the sphere outside of any red area to rotate freely in any direction.

1.6.4.2 The Tool Panels

The lower left corner of the main 3D window is used by a stack of tool panels:

- Color Mapper panel (see Chapter [Color Mapper Panel \[▶ 183\]](#)).
The Color Mapper panel is used for basic windowing and lookup table selection.
- Orthogonal Slices panel (see Chapter [Orthogonal Slices Panel \[▶ 184\]](#)).
The panel controls 3 mutually perpendicular slice planes aligned with the object coordinate system.
- Transformation panel (see Chapter [Transformation Panel \[▶ 185\]](#)).
The panel can transform the oblique plane and is an alternative to the Oblique Plane Manipulators described in Chapter [Viewing in the Hybrid 3D-Viewer \[▶ 180\]](#). The Transformation panel is not available in some of the wizards (e.g. Simple Slices Wizard).

1.6.4.2.1 Color Mapper Panel

The Color Mapper tool panel is used for basic windowing and lookup table selection (see Figure [Color Mapper Panel \[▶ 184\]](#)). The panel consists of the following parts (from top to bottom):

- **Scale factor and Color Mapper with riders**

Set scale and bias by moving the color mapper's two riders. The data domain goes from left (minimum) to right (maximum), the mapping range from bottom to top.

The scale exponent can be set with the spinner.

Clicking with the right mouse button into the Color Mapper opens a context menu with the following entries:

- **Reset Scale/Bias** sets the color scaling to the original values (full range of image intensities).
- **Scale * 10** and **Scale / 10** are self explaining.

- **Transparency**

The transparency check boxes apply only to generated slices in the Simple Slices task. They have no effect on any other images. Regions below and/or above the mapping range are made transparent to allow a better view through a whole stack of slices.

- **Color Maps**

Color Maps are selected by means of the drop-down box at the bottom. The same standard color maps as in **Image Display & Processing** are available (see Chapter [Classic Image Display & Processing \[▶ 440\]](#)). Changing the color map is not possible within the DTI Visualization task.

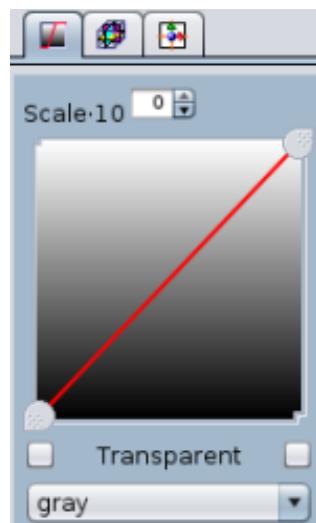


Figure 1.152: Color Mapper Panel

1.6.4.2.2 Orthogonal Slices Panel

The Orthogonal Slices panel is shown in Figure [Orthogonal Slices Planes \[▶ 184\]](#).

It controls three mutually perpendicular slice planes aligned with the dataset coordinate system. The buttons to the left are used to show or hide the planes, the sliders in the center translate them along their normal, and the buttons to the right reset a plane to the center position. The plane properties are summarized in the following table:

Plane	Border Color	Controls	Slider direction
XY	Magenta	Top row	Z-axis
XZ	Yellow	Middle row	Y-axis
YZ	Cyan	Bottom row	X-Axis

Table 1.1: Properties of the Orthogonal Slices Panel

The manipulators associated with the orthogonal planes are restricted to translations only.

For example, in Figure [Example: Three Centered Slice Planes \[▶ 185\]](#) all three slice planes are enabled and centered.

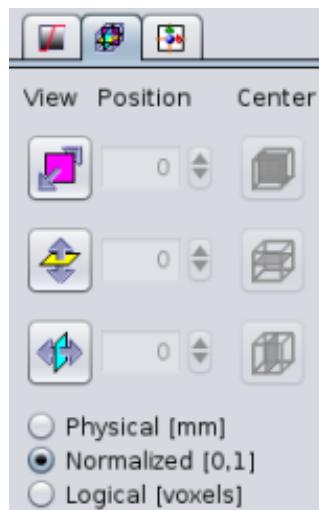


Figure 1.153: Orthogonal Slices Planes

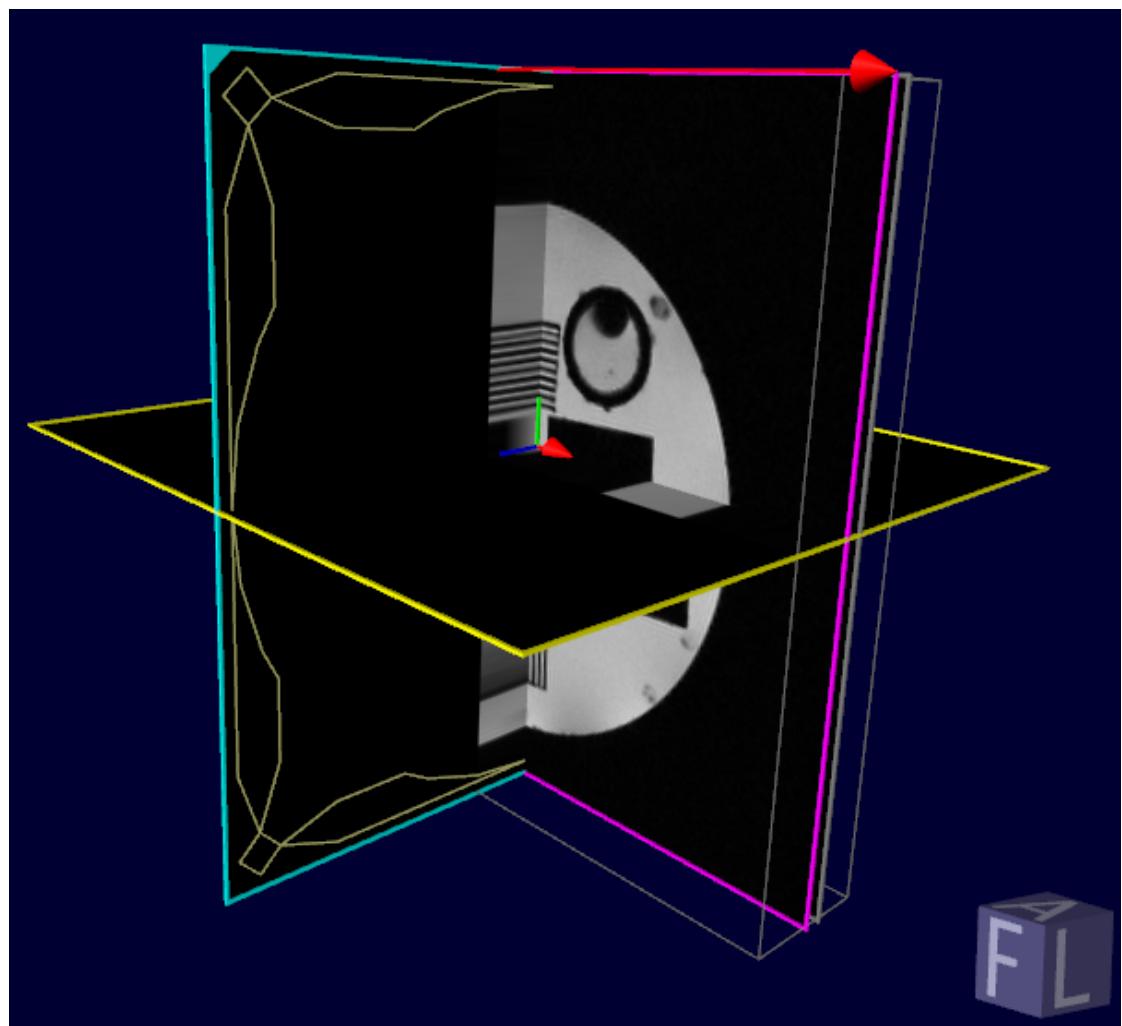


Figure 1.154: Example: Three Centered Slice Planes

1.6.4.2.3 Transformation Panel

The Transformation Panel is shown in Figure [Transformation Panel \[▶ 185\]](#). It is an alternative to using a manipulator to transform the Oblique Plane Manipulators (see Chapter [Viewing in the Hybrid 3D-Viewer \[▶ 180\]](#)).

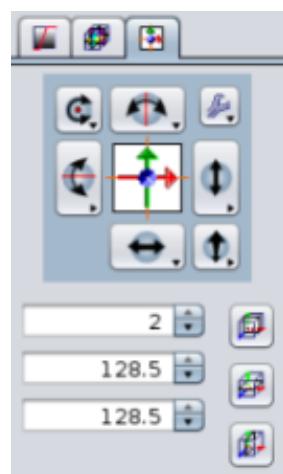
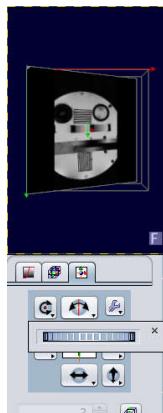


Figure 1.155: Transformation Panel

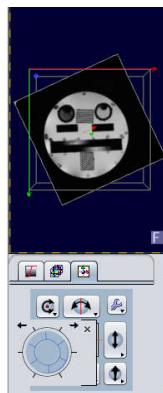
The following operations are supported:



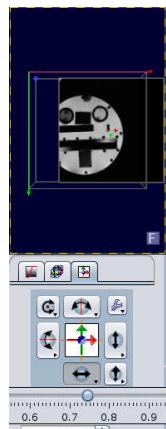
Rotate the object plane around the local x-axis (red).



Rotate the object plane around the local y-axis (green).



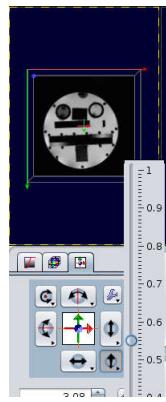
Rotate the object plane around the local z-axis (blue).



Translate the object plane along the local x-axis (red).



Translate the object plane along the local y-axis (green).



Translate the object plane along the local z-axis (blue).

All transformations occur with respect to the plane's local coordinate system, visualized with three orthogonal color coded arrows located at the plane center.

The three spinners at the bottom of the panel move the plane slice-by-slice along the local x-, y-, or z-axis, as long as it stays perpendicular to the respective axis. Spinners are disabled otherwise.

The three center buttons to the right of the spinners reset the plane's position and orientation to the center of one of the axes.

1.6.5 Loading and 3D-Displaying Task

This task loads suitable Image Series to display them in 3D. For some Image Series, such as Localizer or single slice Image Series only visualization but no processing is possible. For other Image Series (e.g. MSME) a subset of data can be selected (e.g. all slices of the third echo).

Almost all kinds of Image Series created by ParaVision can be read. Image Series without spatial dimensions (e.g. Spectroscopic Image Series) as well as Image Series created with the post-processing tools of releases preceding ParaVision 4 are not supported.

To start the Image Series loading task start the 3D-Viewer as described in Chapter [Loading Image Series for 3D Image Viewing \[▶ 177\]](#).

- Click the **Primary Dataset** or the **Secondary Dataset** button on the Task panel. The respective wizard opens (see Figure [Load Dataset Task: Select a ParaVision Dataset \[▶ 188\]](#)). The following description uses the primary dataset reader; the functionality of the secondary dataset reader is identical.
- Use the directory selection box by clicking the **Browse...** button to select a PROCNO (or Image Series) directory on disk. The format of the PROCNO directory is described in the PDF documentation [ParaVision File Formats](#) Chapter 1.1 (Dataset Paths). The ten most recently loaded datasets can be accessed using a shortcut: Click the triangular button right of the **Browse...** button and select one of the datasets. After selecting a correct PROCNO path the Image Series is loaded and the wizard changes to the next step.
- If an Image Series is already loaded and only the dataset categories (e.g. echo or repetition number) to specify the cube to be loaded should be changed click the right arrow button to skip over this task.
- The second step allows to choose the dataset categories (see Figure [Load Dataset Task: Set dataset reader parameters \[▶ 189\]](#)).
- Most operations in Jive require a 3D volume of consecutive slices. Simple 2D multi-slice or 3D single slab datasets are read in directly. An according subset of a dataset with a complex structure is defined by setting dataset categories in this step; as shown in Figure [Load Dataset Task: Set dataset reader parameters \[▶ 189\]](#). The shown dataset contains slice and echo categories. In the 3D viewer all slices can be displayed as a 3D-cube for a selected echo (e.g. the 4th echo). To change the echo number select the **Value** field in the **Echo** row. A popup menu opens where the new echo number can be selected. It is possible that the value is not a number but text describing the image. For example, in DTI reconstructed Image Series the DTI quantities (like FA Image, 1st Eigenvalue, etc.) can be chosen from the DTI row values.
- Click the right arrow at the bottom of the task panel to switch to the final wizard step. This step loads the slices of the selected category (dataset) into the 3D-Viewer (e.g. all slices of the 4th echo). Loading the pixel data may take some time, the respective panel shows a progress bar and by default closes automatically after successful completion. If it does not close automatically click the **Accept** button.

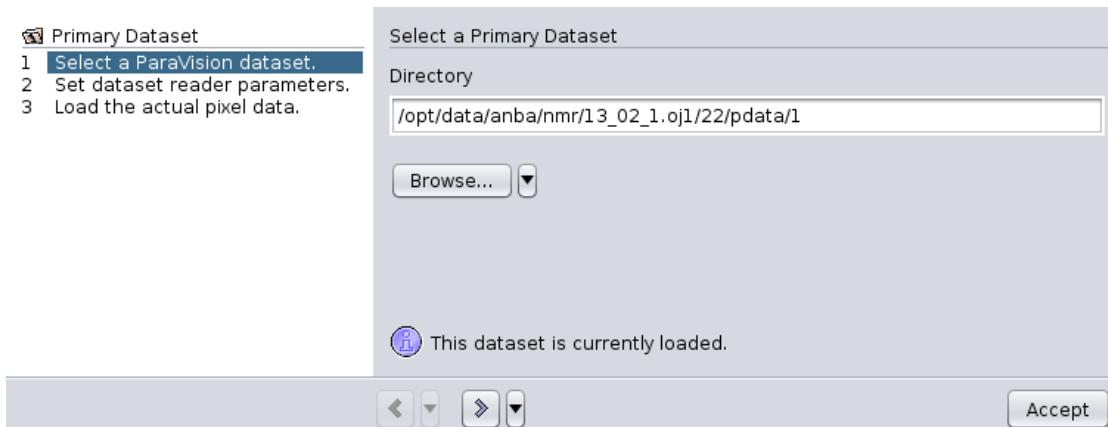


Figure 1.156: Load Dataset Task: Select a ParaVision Dataset

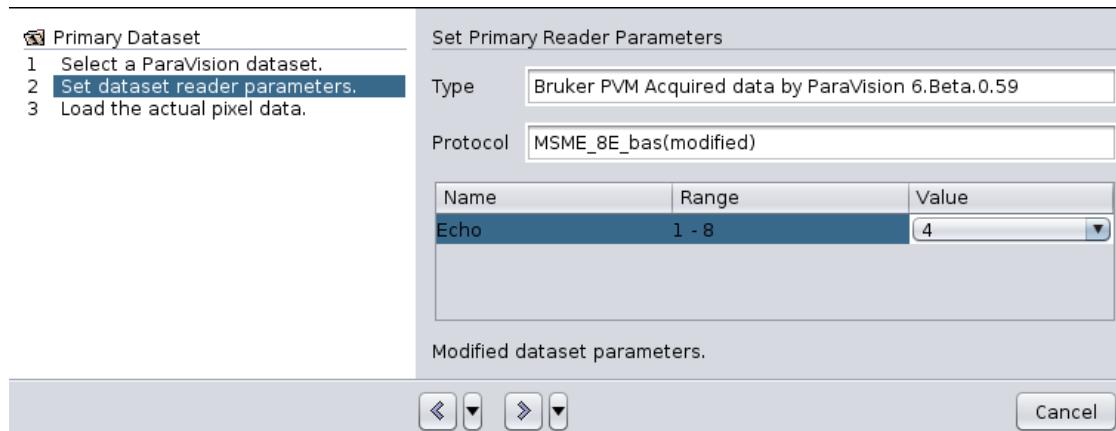


Figure 1.157: Load Dataset Task: Set dataset reader parameters

As soon as loading has completed the center slice is shown in the hybrid viewer. The **Select** radio buttons right to the **Primary Dataset** or the **Secondary Dataset** buttons allow to switch Image Series if two are present at the same time.

For Image Series where a 3D-volume cannot be created from the existing slices (e.g. Localizer or Image with only one slice) only viewing is possible. For other datasets the other tasks can be started if the Image Series fulfills the conditions, e.g. for the DTI Visualization a DTI secondary reconstructed Image Series must be selected.

1.6.6 Simple Slices (MPR) Task

The Simple Slices task does multi-planar reformatting of a dataset. It allows to generate a stack of equidistant coplanar sections with arbitrary matching orientations. The slice centers must all lie on a straight line perpendicular to the slice planes.

1.6.6.1 Start the Simple Slices (MPR) Task

Image Series suitable for the Simple Slices (MPR) task have at least two slices, arranged parallel to each other and equidistant within a rectangular box. Multiple echoes, repetitions, movies, etc. are no problem because an appropriate subset of all frames is selected during data loading.

To start the Simple Slices Task on an Image Series:

1. Select an Image series
 - in the **Workspace Explorer** below the **Datasets** node by opening the **Image Series node**,
 - in the **Palette Explorer**,
 - or in the **Dataset Browser** in the **Image Series** dataset view.
2. Open the general 3D-viewer and load the selected Image Series by
 - double clicking the **MPR Image Data** node below the **Image Series** node in the **Workspace Explorer**.
 - clicking the **MPR Image Data** menu entry in the context menu of the selected **Image Series** in the **Palette Explorer**,
 - or clicking **MPR Image Data** in a sub-menu of the buttons below the **Image Series views** in the **Dataset Browser**. The **MPR Image Data** entry can be found in the sub-menu of the View button (click the triangular button).

3. The Simple Slices wizard starts and shows the slices or slab where all other categories are set to the first value, e.g. for an 2D-image series with 3 echoes, 4 repetitions and 5 slices the 5 slices of the 1st echo and 1st repetition are loaded into the Simple Slices wizard.

4. Click the right arrow button to advance to the next step.

If the default categories should not be processed click the **Cancel** button in the task and use the **Primary Dataset** or the **Secondary Dataset** button to change the category elements as described in Chapter [Loading and 3D-Displaying Task \[▶ 187\]](#). Then restart the wizard by clicking on the **Simple Slices** button.

1.6.6.2 The Simple Slices Wizard: Select the Reference Plane

Browse through the Image Series and select an arbitrarily oriented plane as reference for further steps. Generated slices will be perpendicular to this plane.

The goal of this step is to transform the oblique slice plane so that it may be used as reference for the trajectory defining the slices. Two strategies are possible, see Figure [Browse through dataset and select reference plane \[▶ 191\]](#):

- In pick mode use the Oblique Plane Manipulator (see Chapter [Viewing in the Hybrid 3D-Viewer \[▶ 180\]](#)) to translate and rotate the plane.
- Use the **Transformation** controls of the reference plane panel to manipulate the plane. The functionality of these controls is similar to the controls discussed in Chapter [Transformation Panel \[▶ 185\]](#). The **Center On** buttons reset the plane to a center position in one of the three axis directions.

Both approaches can be mixed without any restrictions.

Depending on the desired orientation of the reference plane it might be necessary to adjust the camera. Switch to one of the view modes for doing so (see Chapter [Using the Viewers \[▶ 179\]](#)).

Click the right arrow button to advance to the next step.

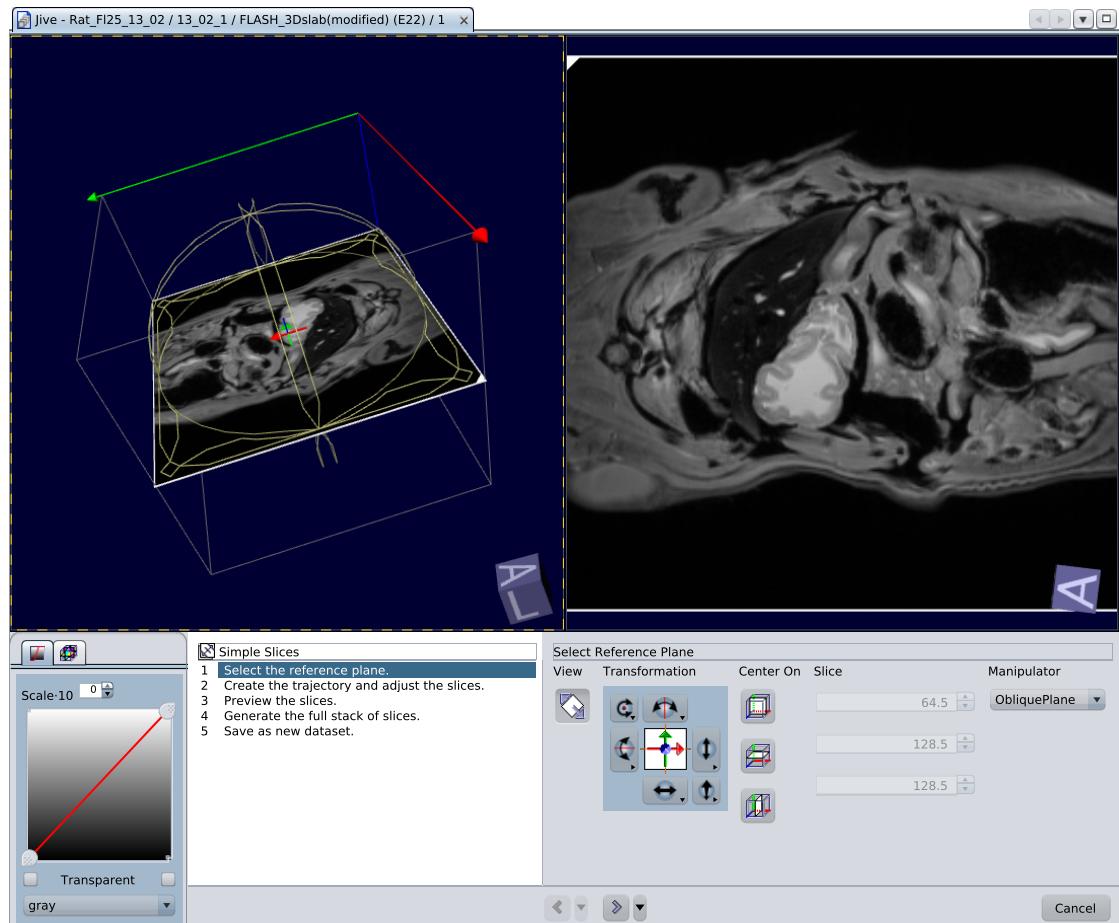


Figure 1.158: Browse through dataset and select reference plane

1.6.6.3 The Simple Slices Wizard: Create the Trajectory

In this step the trajectory (yellow line) defining the slice centers is created. This is done by drawing the trajectory in the plane viewer, maybe adapting slice parameters by means of the controls on the trajectory panel shown in Figure [Create a trajectory on the reference plane](#) [▶ [192](#)]. The hybrid viewer visualizes the resulting slices.

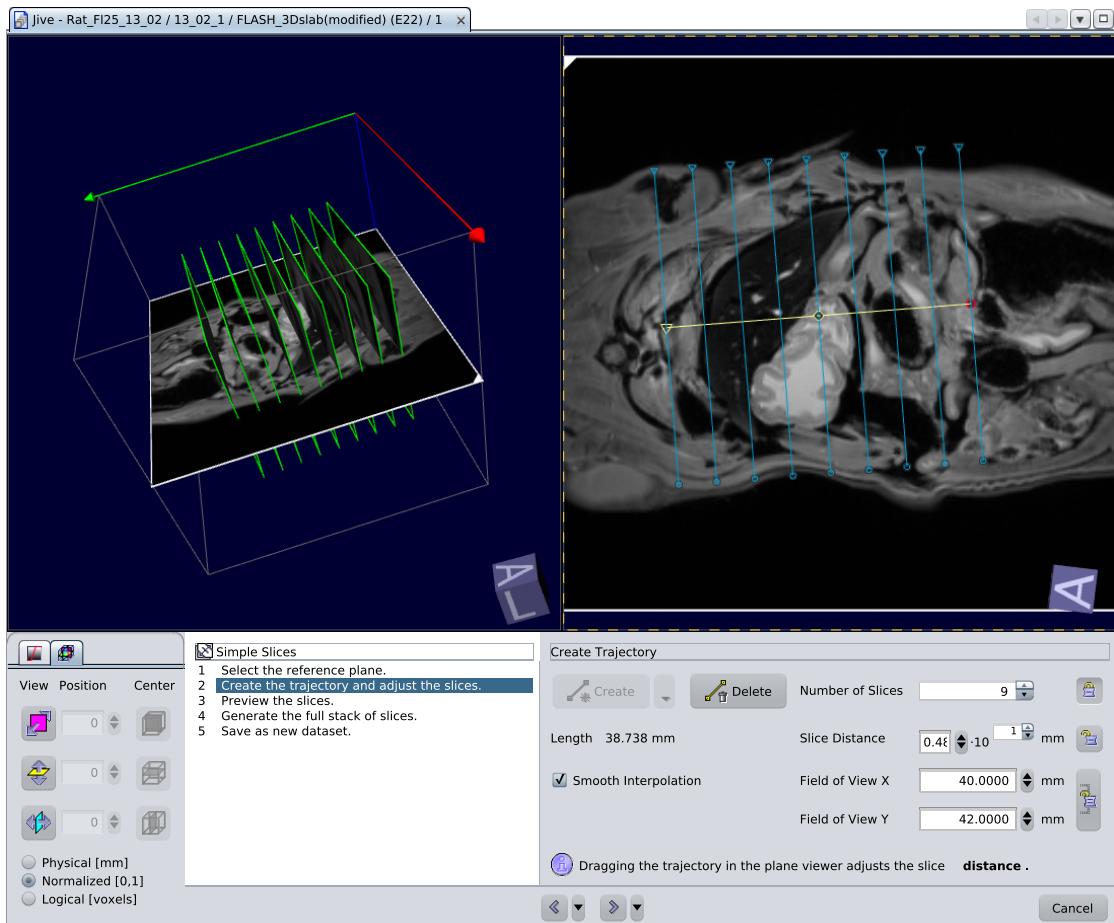


Figure 1.159: Create a trajectory on the reference plane

The trajectory can be modified:

- Move the trajectory by dragging the middle circle.
- Change the length, position, and orientation of the trajectory by dragging the triangle or circle at the end of the trajectory:
 - Dragging either end changes the position of this end. The other end is fixed and is used as rotation center.
 - Holding the **Ctrl** key while dragging rotates and resizes the trajectory relative to its center.
 - Holding **Ctrl** and **Shift** while dragging the trajectory only rotates but does not resize.

Dragging the ends of the trajectory leads to different behavior for the creation of the slices (blue lines) depending on the current mode. Use the two lock buttons next right to **Number of Slices** and **Slice Distance** to switch modes:

- In adjust-distance-mode (upper lock right to **Number of Slices** closed) the number of slices is fixed and the slice distance is adapted to the trajectory length.
- In adjust-number-of-slices-mode (lower lock right to **Slice Distance** closed) the distance stays the same and the number of slices varies with the trajectory length.
- In adjust-none-mode (both locks closed) only position and orientation but not the trajectory length may change. Thus, the number of slices as well as their distance cannot change.

The field of view of the created slices is square (may be changed later). The created slices are shown as blue lines perpendicular to the trajectory. If the slice count exceeds a given threshold then they are displayed as translucent rectangle (in both viewers). The first slice is created at or near the start of the trajectory (triangle) and the last slice created at or near the end of the trajectory (circle).

A trajectory can also be created using the **Create** button and its associated drop-down menu (click on triangle) offering the following variations:

- Diagonal (default)
Create a trajectory leading from upper left to the lower right on the plane viewer image, using the current number of slices, slice distance, extents, and matrix dimensions.
- Top to Bottom
Create a trajectory leading from top to bottom, using current values.
- Bottom to Top
Create a trajectory leading from bottom to top, using current values.
- Left to Right
Create a trajectory leading from left to right, using current values.
- Right to Left
Create a trajectory leading from right to left, using current values.
- Span Top to Bottom
Create a trajectory leading from top to bottom, spanning the extent of the dataset and with number of slices, slice distance, extent and matrix dimensions, so that a cube that maps the whole dataset is created.
- Span Bottom to Top
Create a spanning trajectory leading from bottom to top.
- Span Left to Right
Create a spanning trajectory leading from left to right.
- Span Right to Left
Create a spanning trajectory leading from right to left.

Clicking the **Delete** button removes the current trajectory.

Click the right arrow button to advance to the next step.

1.6.6.4 The Simple Slices Wizard: Preview the Slices

The preview step (see Figure [Preview the slices \[▶ 194\]](#)) allows a quick preview by stepping through the generated slices, either one-by-one or as an animation computed on-the-fly.

The current frame selected by means of the slider (see Figure [Preview the slices \[▶ 194\]](#)) is shown in the plane viewer and marked with a red frame in the hybrid viewer.

The main purposes of the preview step are adjusting the Field of View and the selection of new matrix dimensions for the generated data. If the lock between the **Field of View X** and **Field of View Y** editors is closed then the Field of View is identical for X and Y direction. This also applies to **Dimension X** and **Dimension Y** if the corresponding lock is closed.

Click the right arrow button to advance to the next step.

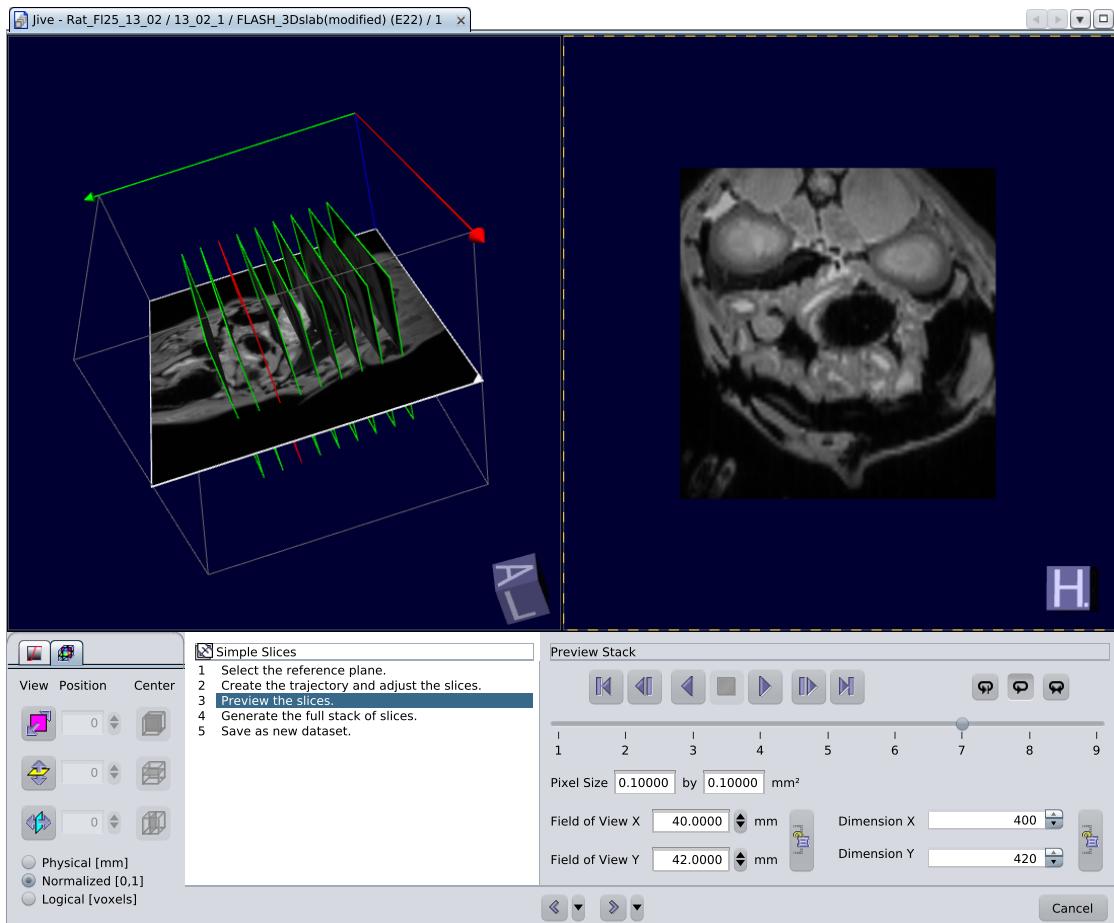


Figure 1.160: Preview the slices

1.6.6.5 The Simple Slices Wizard: Generate the Slices

In this step, the full stack of slices is generated. This may take a while, so a progress bar is shown, and the operation may be canceled by the user at any time. After the slices are generated it automatically advances to the next step.

1.6.6.6 The Simple Slices Wizard: Save the new Image Series

This step, shown in Figure [Save Stack of Slices as Image Series \[195\]](#), writes the Image Series created from the stack of slices back to disk:

1. Select a free processing (Image Series) number (PROCNO).
2. Select a pixel data type. If Floating point data is stored the pixel values are normalized with offset and slope parameters being set accordingly. If the real values are to be written out (such as a T2 map in milliseconds) then check the box **Apply offset/slope**. The offset parameter will then be 1 and the slope 0. This makes the data interpretation simpler during further processing.
3. Click **Write** to save the data.

Dragging the newly created Image series from the **Dataset Path** text field to an opened tab of the Viewing Card loads the Image Series images immediately into the Viewing Card.

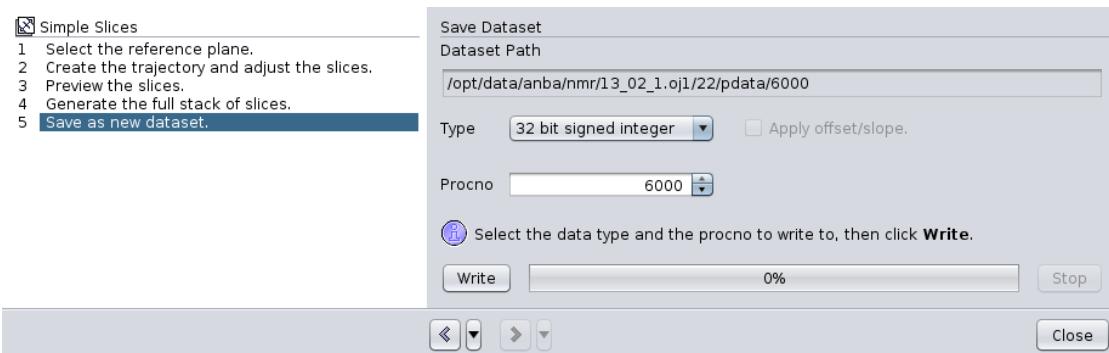


Figure 1.161: Save Stack of Slices as Image Series

1.6.6.7 Transformation between Standard Views

These are step-by-step instructions on how to use the Simple Slices wizard introduced in Chapters [The Simple Slices Wizard: Select the Reference Plane \[▶ 190\]](#) - [The Simple Slices Wizard: Save the new Image Series \[▶ 194\]](#) to transform datasets between three standard views. It is important that the user does not confuse the front and back faces of the image planes. The front face is marked with a tiny triangle (see Figure [Front Face marked with triangle top left \[▶ 196\]](#)) in one of its corners. It also marks the origin of the local coordinate system for the image. The following transformations are only shown in the primate coordinate system. They can be done in a similar manner in the material and rodent coordinate systems. The following mapping applies:

Primate	Rodent	Material
L (left)	Le (left)	-X
R (right)	Ri (right)	+X
A (anterior)	V (ventral)	-Y
P (posterior)	D (dorsal)	+Y
F (feet)	Cd (caudal)	-Z
H (head)	Ro (rostral)	+Z

Table 1.2: Overview Coordinate Systems

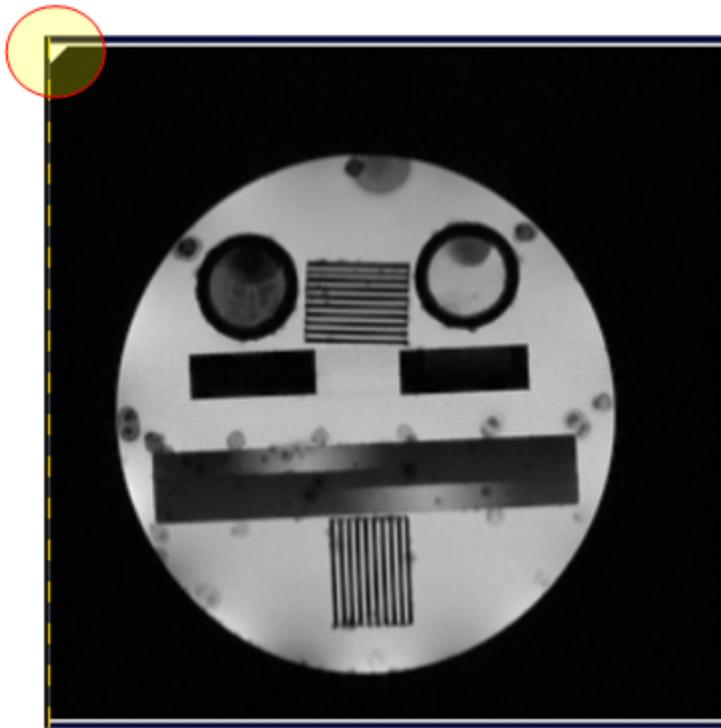


Figure 1.162: Front Face marked with triangle top left

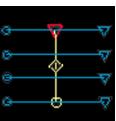
1.6.6.7.1 Transform from Axial to Sagittal

Initial View	Axial	
Step 1	Rotate by 180° about the local y-axis.	
Step 2	Draw a trajectory from left to right on the screen or use the Create button pop up menu entry Left to Right or Span Left to Right option.	
Result	Sagittal slices	

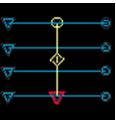
1.6.6.7.2 Transform from Axial to Coronal

Initial View	Axial	
Step 1	Rotate by 180° about the local y-axis.	
Step 2	Draw a trajectory from top to bottom on the screen or use the Create button pop up menu entry Top to Bottom or Span Top to Bottom option.	
Result	Coronal slices	

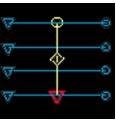
1.6.6.7.3 Transform from Sagittal to Coronal

Initial View	Sagittal	
Step 1	Rotate by 90° about the local x-axis.	
Step 2	Rotate by 90° about the local z-axis.	
Step 3	Draw a trajectory from top to bottom on the screen or use the Create button pop up menu entry Top to Bottom or Span Top to Bottom option.	
Result	Coronal slices	

1.6.6.7.4 Transform from Sagittal to Axial

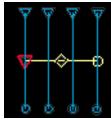
Initial View	Sagittal	
Step 1	Rotate by -90° about the local y-axis.	
Step 2	Draw a trajectory from bottom to top on the screen or use the Create button pop-up menu entry Bottom to Top or Span Bottom to Top option.	
Result	Axial Slices	

1.6.6.7.5 Transform from Coronal to Axial

Initial View	Coronal	
Step 1	Draw a trajectory from bottom to top on the screen or use the Create button pop-up menu entry Bottom to Top or Span Bottom to Top option.	
Result	Axial Slices	

1.6.6.7.6 Transform from Coronal to Sagittal

Initial View	Coronal	
Step 1	Rotate by 90° about the local x-axis.	
Step 2	Rotate by 180° about the local y-axis.	

Step 2	Draw a trajectory from left to right on the screen or use the Create button pop up menu entry Left to Right or Span Left to Right option.	
Result	Sagittal Slices	

1.6.7 DTI Visualization Task

This task performs a DEC (Directional Encoded Color) visualization of DTI (Diffusion Tensor Imaging) Image Series. Tensor eigenvector components are color-coded and optionally mapped onto morphology data.

DTI Images may have single or multiple slices and must be reconstructed by the macro **DTI_PROC_TENSOR** or **DTI_PROC_TENSOR_ASK**.

A dataset usable for the DTI Visualization must have at least:

- a DTI category in the description of the frames.
- in the DTI category a fractional anisotropy quantity must exist.
- in the DTI category all three components of the first eigenvector must exist.

1.6.7.1 Secondary Reconstruction of Image Series for DTI Visualization

A scan created from the DtiEpi, DtiSpiral, and DtiStandard methods can be used to create an Image Series for DTI visualization. Information about setup and acquisition of DTI images can be found in Chapter [Diffusion Tensor Imaging \(DTI\) \[▶ 527\]](#). The primary standard reconstruction of DTI scans creates Image Series that cannot be used for DTI visualization. A special secondary DTI reconstruction must be performed using the primary reconstructed Image Series as input. This can be done in several ways:

- The secondary DTI reconstruction can be performed automatically after the acquisition.
- The secondary DTI reconstruction can be done manually using the macros **DTI_PROC_TENSOR** or **DTI_PROC_TENSOR_ASK**.
- The secondary DTI reconstruction can be executed manually in the Classic Image Display & Processing program.

1.6.7.1.1 Automatic Secondary DTI Reconstruction after Acquisition

DTI scans must be specially reconstructed to be used in the DTI Visualization. The standard primary reconstruction is used as source for the special secondary reconstruction.

To perform the secondary reconstruction automatically after acquisition:

1. Edit the Scan Instruction in the Examination card (see Chapter [Editing a Scan Instruction \[▶ 551\]](#)).
2. Open the Processing Platform for the edited Scan Instruction (see Chapter [Opening the Processing Platform \[▶ 731\]](#)).
3. Edit the first **Data Reconstruction** instruction (see Chapter [Editing a Processing \[▶ 761\]](#)).
4. In the opened editor on the right there is a list of **Post Image Series Activities** (see Figure [Reco Processing Editor \[▶ 199\]](#)). In this editor mark **Execute Macro**.
5. The **Execute Macros** dialog opens where all available macros can be selected. Select the BRUKER category and the macro **DTI_PROC_TENSOR** as shown in Figure [Execute Macro DTI PROC TENSOR \[▶ 199\]](#) and click **OK**.

6. Click the **Apply** button above the instruction list to close the **Data Reconstruction** editor.
7. Click **Back** to change back to the Scan Instruction.

After acquisition and primary reconstruction the secondary reconstruction for DTI Visualization is performed.

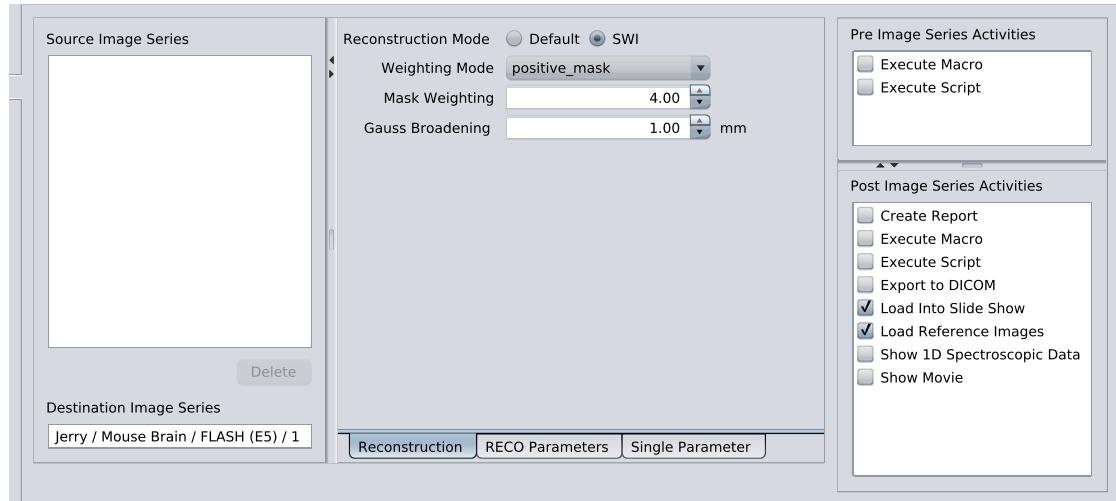


Figure 1.163: Reco Processing Editor



Figure 1.164: Execute Macro DTI_PROC_TENSOR

1.6.7.1.2 Manual Secondary DTI Reconstruction using Macros

DTI scans must be specially reconstructed to be used in the DTI Visualization. The standard primary reconstruction is used as source for the special secondary reconstruction.

1. Select a primary reconstructed DTI Image series
 - in the **Workspace Explorer** below the **Datasets** node by selecting the **Image Series** node,
 - in the **Palette Explorer**,
 - or in the **Dataset Browser** in the **Image Series** dataset view.
2. Open the macro selection dialog by
 - clicking the **Execute Macros...** context menu entry of the selected Image Series in the **Palette Explorer** or **Workspace Explorer**,
 - or clicking **Execute Macros...** in a sub-menu of the buttons below the **Image Series** views in the **Dataset Browser**. The **Execute Macros...** entry can be found in the sub-menu of the **Properties** button (click on the triangular button).
3. The **Execute Macros** dialog opens where all available macros can be selected. Select the **BRUKER** category and the macro **DTI_PROC_TENSOR** or **DTI_PROC_TENSOR_ASK** as shown in Figure [Execute Macro DTI PROC TENSOR \[199\]](#) and click **OK**.

The **Image Display & Processing** program is started in the background (if not already running) and the secondary DTI reconstruction for all slices starts. A new Image Series is created in the same Examination as the primary reconstructed Image Series.

The **DTI_PROC_TENSOR** macro selects the new processing (Image Series) number automatically without user interactions whereas the macro **DTI_PROC_TENSOR_ASK** asks the user to specify the processing number.

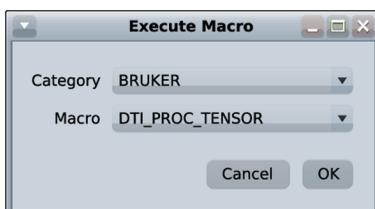


Figure 1.165: Execute Macro DTI_PROC_TENSOR

1.6.7.1.3 Manual Secondary DTI Reconstruction in Image Display & Processing

DTI scans must be specially reconstructed to be used in the DTI Visualization. The standard primary reconstruction is used as source for the special secondary reconstruction.

If the **Image Display & Processing** program is started and a primary reconstructed DTI Image Series is loaded into the current viewport (see Chapter [Classic Image Display & Processing \[▶ 440\]](#)) then the secondary DTI reconstruction can be started by

- **Processing > DTI Reconstruction All Slices.** This reconstructs all slices of the Image Series.
- **Processing > DTI Reconstruction Current Slice.** This reconstructs the slice shown in the currently active viewport.

1.6.7.2 Start of the DTI Visualization Task

Secondary reconstructed DTI Image Series for the DTI Visualization task have at least a DTI frame category and this category contains a fractional anisotropy quantity and three component quantities of the first eigenvector.

To start the DTI Visualization on an Image Series:

1. Select a secondary reconstructed DTI Image series
 - ▶ in the **Workspace Explorer** below the **Datasets** node by opening the **Image Series node**,
 - ▶ in the **Palette Explorer**,
 - ▶ or in the **Dataset Browser** in the **Image Series** dataset view.
2. Open the DTI Visualization and load the selected Image Series by
 - ▶ double clicking the **DTI Image Data** node below the Image Series node in the **Workspace Explorer**.
 - ▶ clicking the **DTI Image Data** menu entry in the context menu of the selected Image Series in the Palette Explorer,
 - ▶ or clicking **DTI Image Data** in a sub-menu of the buttons below the Image Series views in the **Dataset Browser**. The **DTI Image Data** entry can be found in the sub-menu of the **View** button (click the triangular button).
3. The Visualization wizard starts.

It is also possible to use the Advanced Viewing action in the **Workspace Explorer**, **Palette Explorer**, or **Dataset Browser** and then click the **Primary Dataset** or the **Secondary Dataset** button to load the Image Series as described in Chapter [Loading and 3D-Displaying Task \[▶ 181\]](#).

1.6.7.3 DTI Visualization Wizard: Select Map and Mask Images

This step is used to

- select a morphology image where the wizard will map color coded tensor data onto, see **Map Images** section in Figure [Select Map and Mask Images \[▶ 201\]](#). By default the intensity image is used as base to map tensor data onto.
- select a mask quantity in the **Mask Images** section. A rough mask is required to segment the region of interest where the actual DEC mapping is to be performed. The tensor eigenvector components are first filtered by this mask and then weighted with the local fractional anisotropy value to compute the final image. Thus, the segmentation does not have to be very accurate since it is just used as a preprocessing step. Any quantity image within the Image Series may be used to create the mask: The trace weighted image, intensity image, or first eigenvalue images usually are good candidates.

This task can be performed using the primary or secondary dataset. If a geometrically compatible dataset is available it is possible to use it as a morphology. Load the dataset as secondary dataset.

After defining the morphology and mask image advance to the next step by clicking the right arrow button.

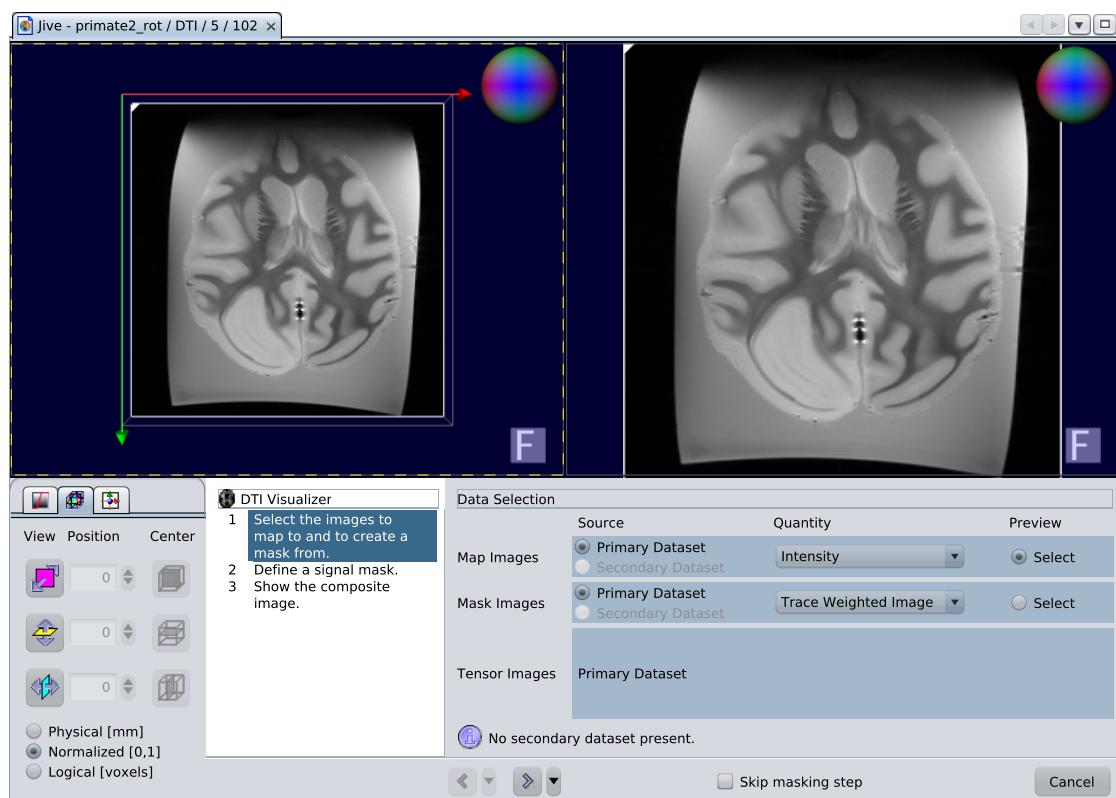


Figure 1.166: Select Map and Mask Images

1.6.7.4 DTI Visualization Wizard: Define a Signal Mask

A mask must be defined to specify the region of interest for the DTI Visualization (see Figure [Define a Signal Mask \[▶ 202\]](#)).

To define the mask:

- Set a seed point, shown as blinking diamond, by clicking into the plane viewer. The mask is shown in red with a yellow outline in the plane viewer.
- Move the seed point by dragging the left mouse button. Region growing thresholds are adapted automatically by computing pixel statistics in a local neighborhood around the seed point.
- Change **Upper** and **Lower** values in the **Thresholds** section to adapt the upper and lower threshold values manually.
- Optionally use the **Morphology** controls to quickly fix up the mask.
- Click **Lock Seed Plane** to lock down the seed plane, the mask now appears inside the hybrid viewer in an examination plane decoupled from the seed. Use the manipulators or the transformation panel to examine the mask.
- Click **Return to Seed** to bring the examination plane back to the seed plane.
- Optionally use the **Show Mask Surface** button to visualize a surface rendering of the current mask.
- Use the **Invert** button to invert the mask if segmenting the background is easier.

After defining the signal mask advance to the next step by clicking the right arrow button.

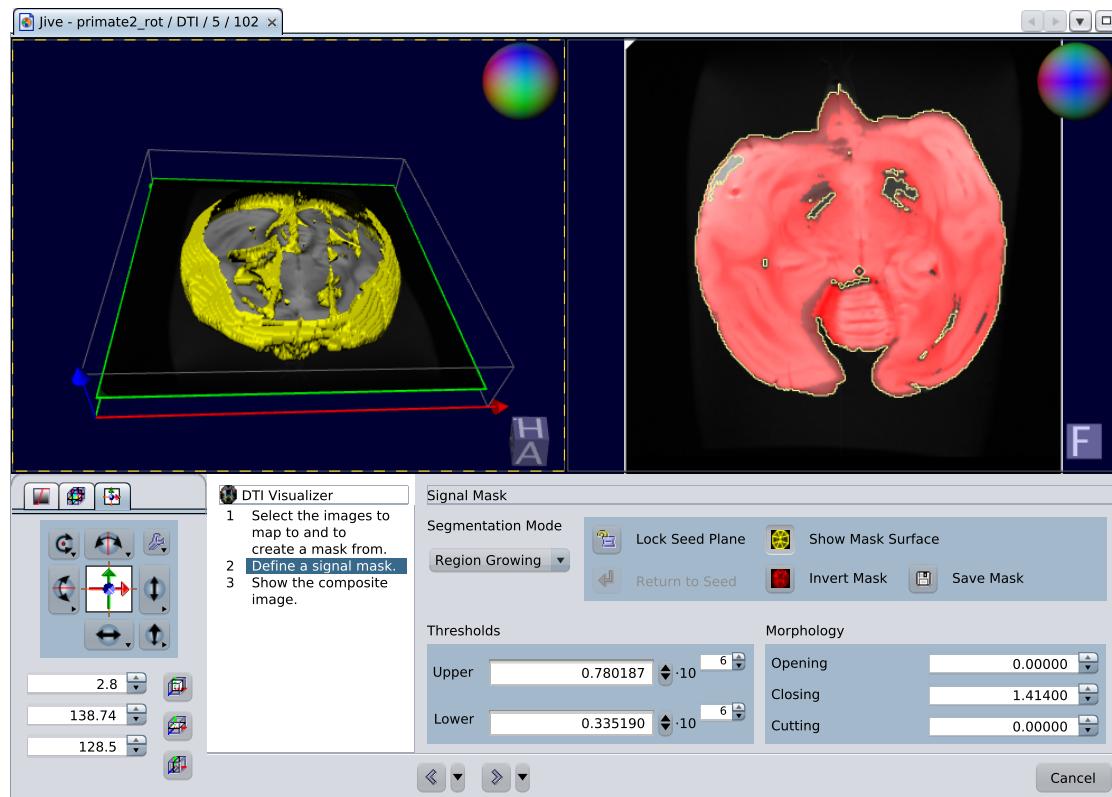


Figure 1.167: Define a Signal Mask

1.6.7.5 DTI Visualization Wizard: Show the Composite Image

In this task the three components of the selected tensor eigenvector are masked and then color-coded using an absolute value mapping. With this approach, we avoid color discontinuity artifacts at the expense of some orientation ambiguity. The graphical user interface is shown in Figure [DEC mapped DTI images \[▶ 203\]](#).

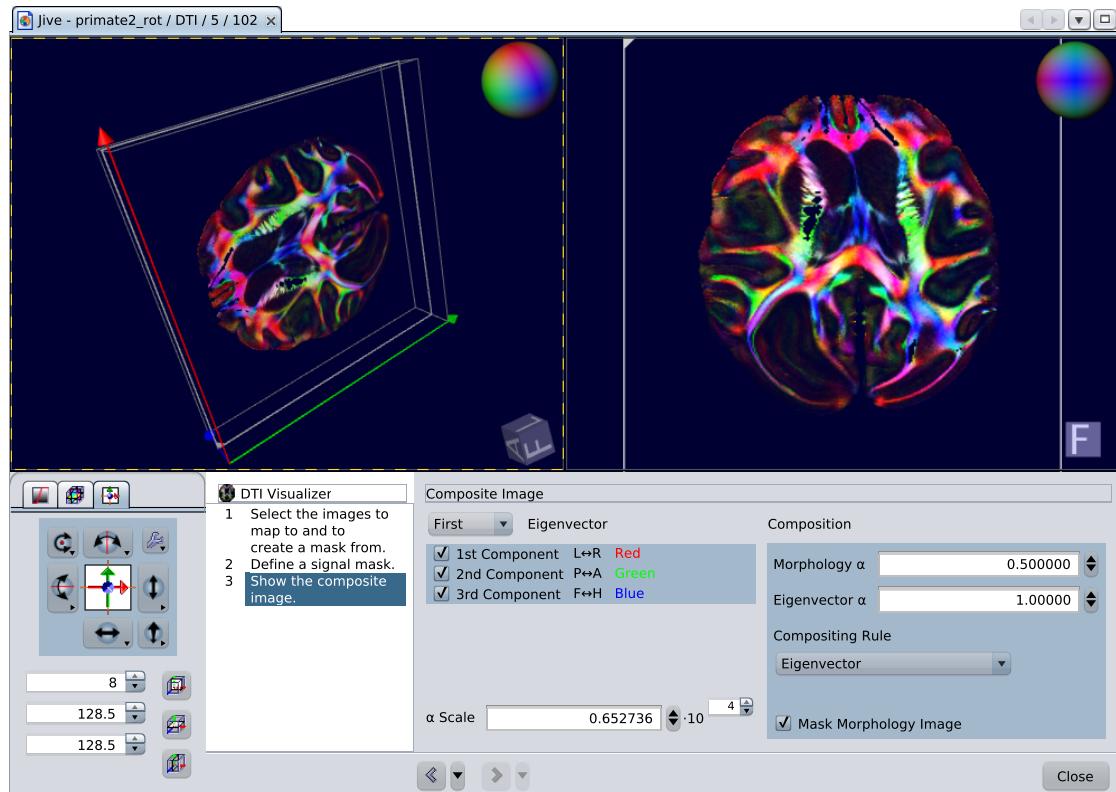


Figure 1.168: DEC mapped DTI images

The three eigenvector components are transformed to the subject coordinate system and then mapped as follows to the color channels:

- The first component, left <-> right, maps to red.
- The second component, posterior <-> anterior, dorsal <-> ventral, maps to green
- The third component, foot <-> head, caudal <-> rostral, maps to blue.

The resulting color is assigned a transparency based on fractional anisotropy and gets finally mapped onto the map image, according to the composition rule.

It might be necessary to adjust the overall scale factor of the fractional anisotropy to transparency mapping (α Scale).

The first eigenvector of the tensor is shown, directions are expressed as colors. The color sphere at the top right indicates the mapping of the colors to the directions.

It is possible to select the eigenvectors or eigenvector components for the visualization:

- Click on the combo box left to the **Eigenvector** label to change the eigenvector. As the eigenvectors are oriented perpendicularly to each other overall colors change accordingly.
- Change the 3 check boxes (1st Component, 2nd Component, 3rd Component) to enable or disable components of the current eigenvector.

The process of compositing two color images with transparency information has been formalized by Porter and Duff (see [References \[▶ 692\]](#)). The transparency factors (Morphology Alpha, Eigenvector Alpha) and the image compositing rule may be adjusted to achieve any desired effect.

To browse through the composite image use the transformation panel in the lower left corner to slice through the data in any direction:

- Turn the hybrid viewer camera with direct manipulation in view mode.
- Click the Center buttons in the right bottom of the transformation panel to switch plane orientations.
- Use the lower right pop-up slider of the transformation panel to slice perpendicularly to the current plane orientation.

To store the resulting color coded images:

- Use the **Create Snapshot** tab of the **Analysis** section of the **Viewing Palette** to create a stored image of the 2D plane viewer.
- Use the **Create Movie** tab of the **Analysis** section of the **Viewing Palette** to create a stored movie of the 3D-image viewer. Spin the camera in Rotate mode or spin the manipulator and record the rotation animation in the 3D-Hybrid viewer.

1.6.8 Dataset Conversion Task

This task stores a currently loaded slice cube as a simple 3D dataset in a new Image Series. The other categories (e.g. echoes, repetitions, DTI) are fixed for the stored 3D-cube. For example, for an Image Series with 8 echoes, 5 slices and 3 repetitions it is possible to store all slices of the 4th echo and 2nd repetition into a new Image Series. Only slices that form a spatial 3D-cube are allowed (same as for the Simple Slices task, see Chapter [Start the Simple Slices \(MPR\) Task \[▶ 189\]](#)).

1. Load an Image Series using the Advanced Imaging action (see Chapter [Loading Image Series for 3D Image Viewing \[▶ 177\]](#))
2. Launch the conversion task by clicking the **Dataset Converter** button.

The Dataset Converter wizard opens, see Figure [The Dataset Converter Wizard \[▶ 205\]](#).

The converter will work on the single slice or 3D volume defined through the settings on the respective Reader Parameters panel. This means for a MSME dataset, for instance, that all slices of the current echo will be used to create a new 3D-dataset.

The converter allows to select another pixel data type (if desired) and an empty processing (Image Series) number (**PROCNO**).

Refer to Chapter [The Simple Slices Wizard: Save the new Image Series \[▶ 194\]](#) for further details, as the last step of the MPR wizard uses the same interface.

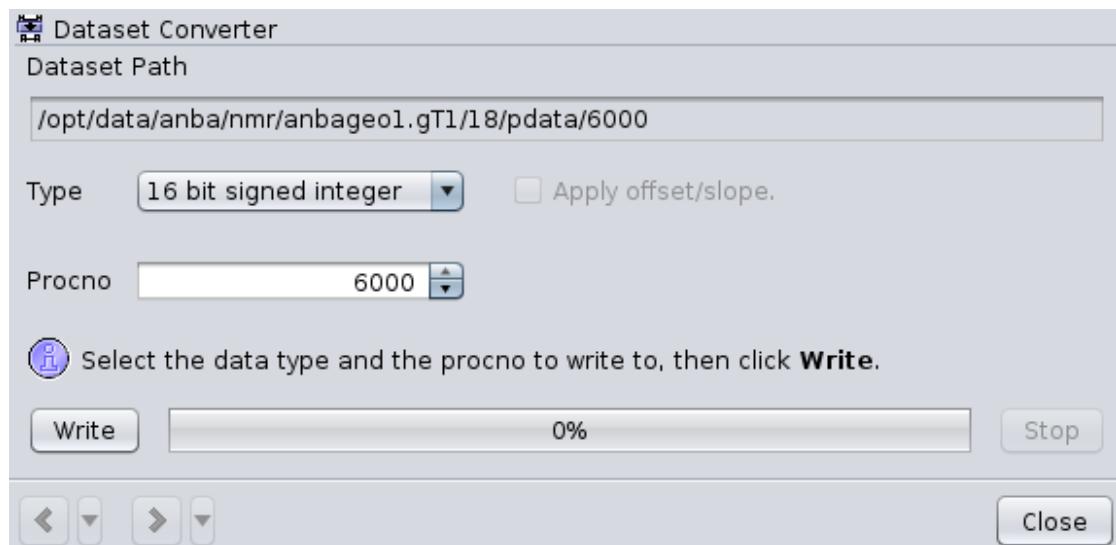


Figure 1.169: The Dataset Converter Wizard

1.7 Study Registration

1.7.1 Introduction

The **Study Registration** dialog allows to create new subjects and new studies. Below the Overview, describing the GUI, the most commonly used workflows are enlisted:

- Create a new subject with a new study.
- Create a study for an already existing subject.
- Change the default values for the **Study Registration** window.
- Define additional subject and study properties.
- Create a new subject without a study.
- Change study properties.

Finally, the additional dataset levels Project and Session are explained and the workflows to create longitudinal studies are described.

1.7.2 Overview

In the left area of the **Study Registration** window the subject parameters are located and the right area provides the study parameters.

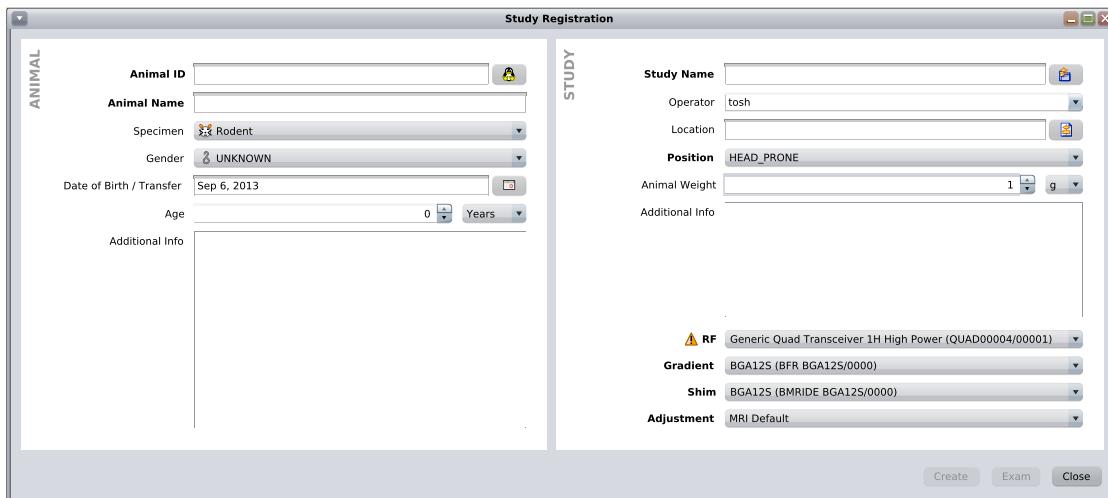


Figure 1.170: Study Registration

The names of mandatory parameters are printed in bold face.

Three action buttons are located in the bottom row:

- **Create button**

This button is enabled if at least the mandatory input fields contain valid values.

Clicking it a new study will be created and assigned to the subject, specified in the subject input elements. If this subject is not already existing it will be created also.

- **Exam button**

This button is enabled if the study input elements specify an existing, valid study.

Clicking it will open this study into the **Examination Card**. If the **Examination Card** is already opened, an error dialog will be shown.

- **Close button**

Clicking this button will close the **Study Registration** window.

Input elements for the subject parameters are:

- **Animal ID / Material ID (Mandatory Parameter)**

Enter the unique identifier of the subject here. During keyboard activities in this field the database is continuously queried and if a subject is found for the entered ID value, the subject parameters are filled with the matching values and disabled to prohibit changing parameters of that existing subject.

Notice: Though the “Animal ID” has to be unique for new studies, imported legacy datasets from older ParaVision versions are allowed to offend this requirement. Therefore an entered “Animal ID” may fit for different subjects. In that case a table with these matching subjects is shown that allows the selection of a single one.

Clicking the button on the right of the input field will submit a scan for existing subjects. If the input field contains some characters, all subjects with a subject name or a registration ID string beginning with these characters are found. If the input field is empty, all subjects are found. A table appears showing the result of the database search and a subject row can be selected.

Subject ID	Subject Name	Sp...	Date of Birth / ...	Creation Date	Additional Info
100111sako	100111sako				
josh	josh				
mw080312.a	117/16 Shim				
mw080312.b	117/16 Shim Calib				
mw080318.a	dtensor repeated				
mw080327.a	repeated dtensor				
mw080403.a	117/16 Calibratio...				
mw080415.af	new shim calibrati...				
mw080904.a	70-20 Pharmascan				
mw090213.af	DtiDse				400 MHz 94-20
mw090216.a	DTI 70-30				
mw090227.a	DtiDse 47/60				
mw7016-9-09-28.a	DtiDse Alphatest				
pv6geo1	Geometry PV6				Geometry test
rani	Nicole				

Figure 1.171: Subject Selection

- **Animal Name / Material Name (Mandatory Parameter)**

Enter the name of the subject here. Any characters are allowed.

- **Specimen**

Select the type of the subject here. Options are:

- Rodent – Use this one for four-legged animals.
- Primate – Use this one for two-legged animals.
- Other – Use this one for all other kinds of animals.
- Material – Use this one for none animal subjects.

Notice: If “Material“ is selected, the top two elements are named “Material ID” and “Material Name” and the input elements “Gender”, “Date of Birth / Transfer” and “Age” disappear from the subject area and the inputs elements “Animal Weight” and “Position” disappear from the study area.

- **Gender**

Select the gender of the subject here. Options are:

- Female
- Male
- Unknown
- Other

- **Date of Birth / Transfer**

Enter the birth-date or transfer-date of the subject here. You can enter the date using the keyboard directly or select a date from a calendar GUI element. To open this calendar GUI element, click the button right of the date input field.

- **Age**

Instead of entering a date value you can also enter a age value directly by using this input element.

- **Additional Info**

You can enter any text here to describe the subject.

Input elements for the study parameters are:

- **Study Name (Mandatory Parameter)**

Enter a name for the study you want to create. A newly created study name has to be unique for a subject but like like the Animal IDs of legacy datasets, a new study may exist beneath an imported study with the same name.

If an existing subject is loaded in the subject area of the **Study Registration** window, clicking the button on the right of the study name input field will submit a scan for the studies of that subject. If the input field contains some characters, only studies with a name beginning with these characters are found. If the input field is empty, all studies are found. A table appears, showing the result of the database search.

St...	Study Name	Creation Date	Opera...	Additi...
1	Geo Phantom	Thu Sep 19 08:39:35 CEST 2013		
1	Dti Dse 9420 SpecPhant	Thu Sep 19 08:41:20 CEST 2013		
2	Sphere Phantom 6cm in Probehead	Thu Sep 19 08:41:21 CEST 2013		

Figure 1.172: Study Selection

If you select one of these, the study input elements are filled with the properties of the loaded study.

- **Operator**

Enter or select the operator for the study here. You can enter any name or select from the list of operators already known to the system. To make this list visible click on the triangle on the right of the input field. At least your linux login name will be in this list.

- **Location**

The “Location” can be used to classify the study relating to the protocol locations. Any path of the “Protocol” or “Scan Program” tree can be used. If a full path to a protocol is selected (e.g. “Mouse/Abdomen/Anatomy/1_Localizer”) this protocol is already inserted as the first scan in the scan program of the created study. When the study is opened in the **Examination Card** the “Location” path is selected in the **Palette Protocol Explorer**, that is shown beneath the **Examination Card**.

Click the button on the right of the location text field to open the tree view of the protocol repository. A click on the triangle icon in front of a tree node or a double-click on the node itself expands or collapses it. A single-click on a node selects it as the “Location” value and closes the tree view.

- **Position**

You can select the position of the animal in the magnet here. The list of available values is determined by the selected subject specimen in the subject parameter area. If “Material” is selected here, the “Position” input element is not shown.

- **Animal Weight**

Enter the weight of the animal here. If “Material” subject specimen is selected, the “Animal Weight” input element is not shown.

- **Additional Info**

You can enter any text here to describe the study.

Each study references coil and adjustment configurations. Select these in the area below the study input element “Additional Info”:

- **RF (Mandatory Parameter)**

Select the RF Coil Configuration for the study.

- **Gradient (Mandatory Parameter)**

Select the Gradient Coil for the study.

- **Shim (Mandatory Parameter)**

Select the Shim Coil for the study.

- **Adjustment (Mandatory Parameter)**

Select the Adjustment Configuration for the study.

If these parameters already have valid data they are not visible unless you click the “More...” button. Initially they are visible if:

- The **Study Registration** window is opened the first time after **ParaVision** start.

- Some of the Coil or Adjustment configurations have no value.
- Another RF configuration or Gradient or Shim Coil has been **activated** since the last time, the **Study Registration** window has been open.

If some of these coil and adjustment configuration elements have no selectable data, your spectrometer is not configured properly.

1.7.3 Common Workflows

1.7.3.1 Create a new Animal Subject and a New Study

Goal:

Register a new subject with a first study, that is prepared for examination. Optionally open this study in the **Examination Card**.

1. Select the menu item File ▶ New ▶ Study... from the main menu.
► The **Study Registration** window appears.
2. Enter a new ID string into the text field named "Animal ID".
► If the other subject parameter fields are filled with data and become disabled, this indicates that a subject with the entered ID already exists in the database. Enter a different ID until the input fields become enabled again.
3. Enter the name of your animal subject into the text field named "Animal Name". Also enter the "Age" or "Date of Birth / Transfer" data and ensure that the gender and specimen fields show the correct values. You can add a description for your animal in the "Additional Info" field.
4. Enter or select correct values for "Study Name", "Operator", "Position", "Animal Weight". Additionally you can select a "Location" path and enter "Additional Info" for the study.
5. If the "More..." button is shown below the study "Additional Info" field, click it.
6. Select an "RF", "Gradient", "Shim" coil and an "Adjustment" configuration for your study. This four elements must offer selectable data, otherwise your spectrometer is not configured properly.
7. Click the "Create" button that became enabled as soon as all mandatory parameters got valid data.
► Your specified subject and study is created. The subject input becomes disabled, because a subject matching the entered "Animal ID" can be found in the database now. The "Exam" button becomes enabled.
8. If you want to plan or perform examinations with the new study, click the "Exam" button.
► The **Examination Card** is opened with the created study. If it can not be opened (e. g. it is already open for another study) an error dialog is shown.

1.7.3.2 Create a Study for an already Existing Subject

Goal:

Search the subjects in the database, select one and create a new study for it. Optionally open this study in the **Examination Card**.

1. Select the menu item File ▶ New ▶ Study... from the main menu.
► The **Study Registration** window appears.
2. If the input field "Animal ID" contains some text, delete it by using the keyboard's <Backspace> or keys. Click the button on the right of the input field.

- A table appears showing an overview of all subjects in your database. If you typed in some characters into the “Animal ID” input field, before clicking the button, only subjects with a name or a subject id beginning with these characters are shown.
3. Click a table row.
- The subject shown in that row is selected and the subject input elements are loaded with the particular subject properties. The studies that are created now, will be assigned to that subject.
- Notice:** You can also drag a subject or study object from the **Dataset Browser** or **Workspace Explorer** and drop it anywhere on the **Study Registration** window to load the properties of that subject or study.
4. Enter the name of your animal subject into the text field named “Animal Name”. Also enter the “Age” or “Date of Birth / Transfer” data and ensure that the gender and specimen fields show the correct values. You can add a description for your animal in the “Additional Info” field.
 5. Enter or select correct values for “Study Name”, “Operator”, “Position”, “Animal Weight”. Additionally you can select a “Location” path and enter “Additional Info” for the study.
 6. If the “More...” button is shown below the study “Additional Info” field, click it.
 7. Select an “RF”, “Gradient”, “Shim” coil and an “Adjustment” configuration for your study. This four elements must offer selectable data, otherwise your spectrometer is not configured properly.
 8. Click the “Create” button that became enabled as soon as all mandatory parameters got valid data.
 - Your specified study is created and assigned to the selected subject. The “Exam” button becomes enabled.
 9. Click the “Exam” button, if you want to plan or perform examinations with the new study.

The “Examination Card” is opened with the created study. If it can not be opened (e. g. it's already open for another study) an error dialog is shown.

1.7.3.3 Change the default Values for the Study Registration Window

For the first time the **Study Registration** window is opened after the start of ParaVision, some of the subject and study input elements are preset with default values. For the following times, the values from the previous run are taken.

Goal:

Change the default values for the first launch of the **Study Registration Window**.

1. Select the menu item Window ▶ Options from the main menu.
 - The **Options Window** appears.
2. Locate the “Dataset” icon on the icon bar on top of the **Options Window** and click it.
 - The **Options Window** shows the dataset related options.

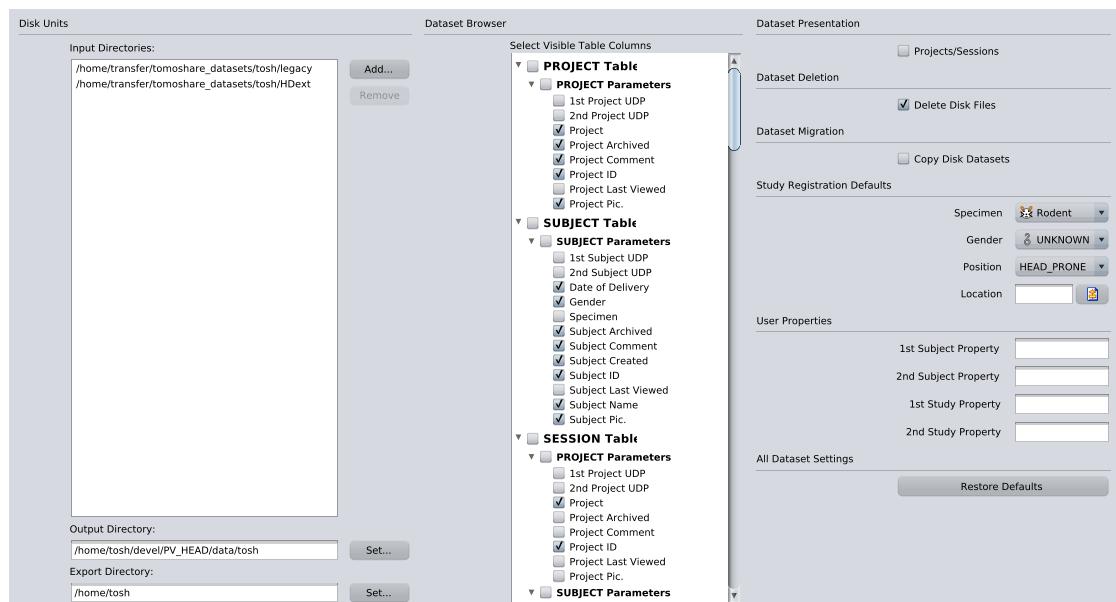


Figure 1.173: Dataset Options

- Locate the "Study Registration Defaults" segment in the most right column of the **Options Window**. You can find and change here the default values for:
 - Specimen
 - Gender
 - Position
 - Location
- After you made your changes, click the "OK" button on the bottom of the **Options Window** to save the changes or the "Cancel" button to discard the changes.
 - The new values are saved or discarded and the **Options Window** is closed.

1.7.3.4 Define additional Subject and Study Properties

You can add two subject and two study properties to describe your datasets more detailed. These properties can help you to specify, find and arrange your data.

Goal:

Define Subject and Study User Properties.

- Select the menu item Window ▶ Options from the main menu.
 - The **Options Window** appears.
- Locate the "Dataset" icon on the icon bar on top of the **Options Window** and click it.
 - The **Options Window** shows the dataset related options.
- Locate the "User Properties" segment in the most right column of the **Options Window**. You can find and enter values here for:
 - 1st Subject Property
 - 2nd Subject Property
 - 1st Study Property
 - 2nd Study Property
 - Enter names for the User Properties you want to add.

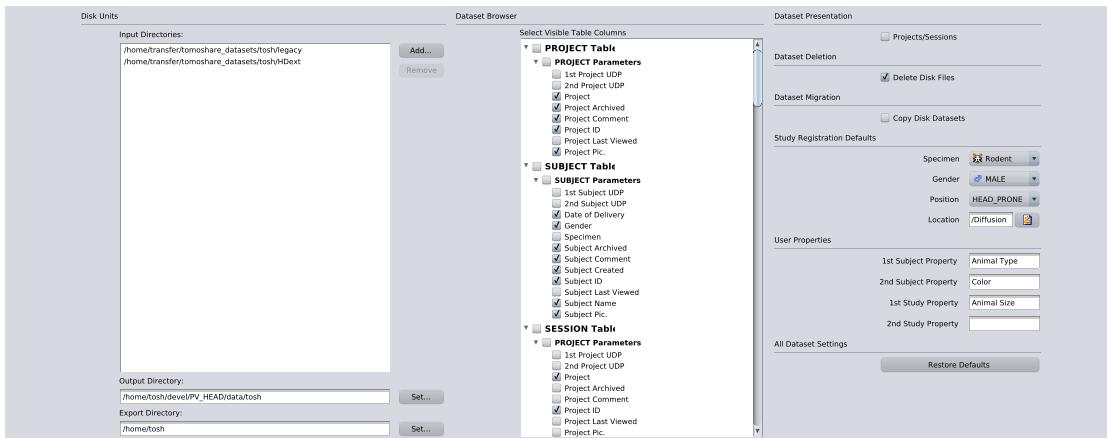


Figure 1.174: Dataset Options: User Properties

To delete a User Property, just clear its input field.

1. After you made your changes, click the “OK” button on the bottom of the **Options Window** to save the changes or the “Cancel” button to discard the changes.
 - The names for the User Properties are saved or discarded and the **Options Window** is closed.
 - Now, the **Registration Dialog** window will contain additional elements to enter values for the defined User Properties.

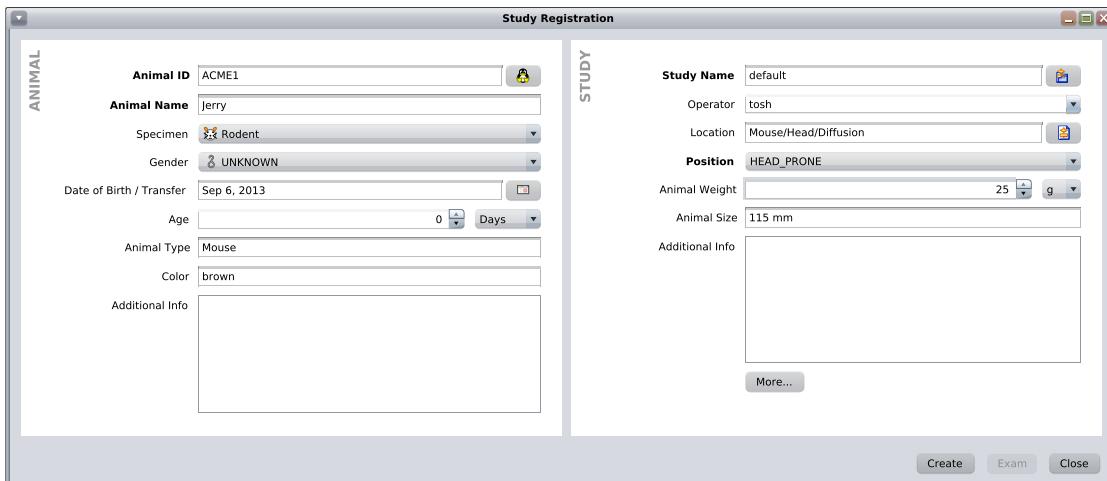


Figure 1.175: Study Registration: User Properties

1.7.3.5 Create new Subject without Creating a Study

You can create subjects without any studies. For instance if some new animals have been delivered to your site and you want to register them to the system.

Goal:

Register a new subject without creating a study.

1. Select the menu item File ▶ New ▶ Subject... from the main menu.
 - The **Create Subject** dialog appears. It is a subset of the **Registration Dialog** window, containing only input elements for the subject parameters.

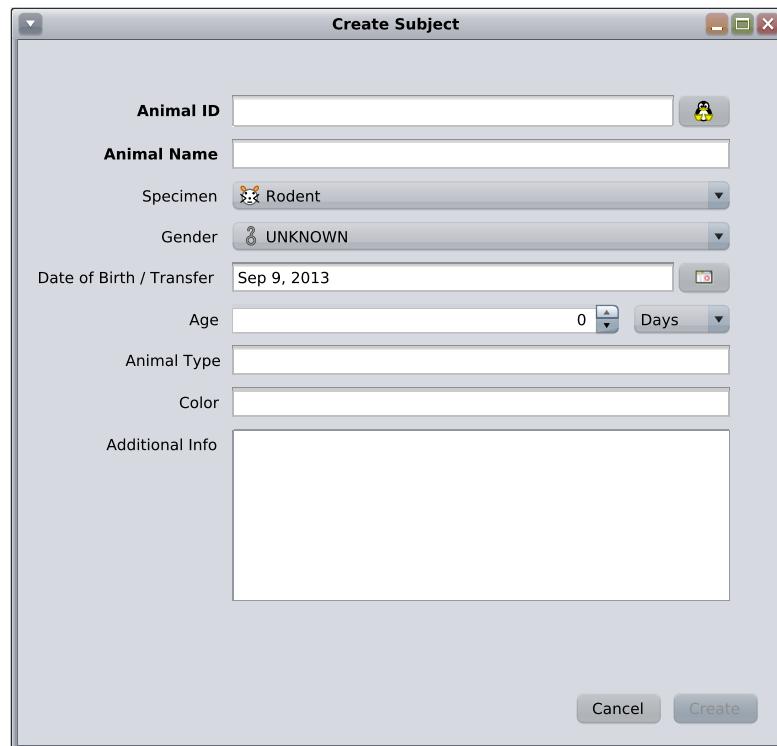


Figure 1.176: Subject Registration

2. Enter a new ID string into the text field named “Animal ID”.
 - If the other subject parameter fields are filled with data and become disabled, this indicates that a subject with the entered ID already exists in the database. Enter a different ID until the input fields become enabled again.
3. Enter the name of your animal subject into the text field named “Animal Name”. Also enter the “Age” or “Date of Birth / Transfer” data and ensure that the gender and specimen fields show the correct values. You can add a description for your animal in the “Additional Info” field.
4. Click the “Create” button that became enabled as soon as all mandatory parameters got valid data.
 - The **Create Subject** dialog is closed and the specified subject is created.

1.7.3.6 Change Study Properties

You can edit study properties as long as no scans of this study have been performed.

Goal:

Change properties of an existing study and save them.

1. Select a study with no scans at all or at least not without performed scans in the **Dataset Browser** or **Workspace Explorer** and initiate the action “Edit Study”.
 - The **Registration Dialog** window appears. The subject and study input elements are filled with the respected values where the subject parameters on the left are disabled but the study parameters in the right area can be overwritten.

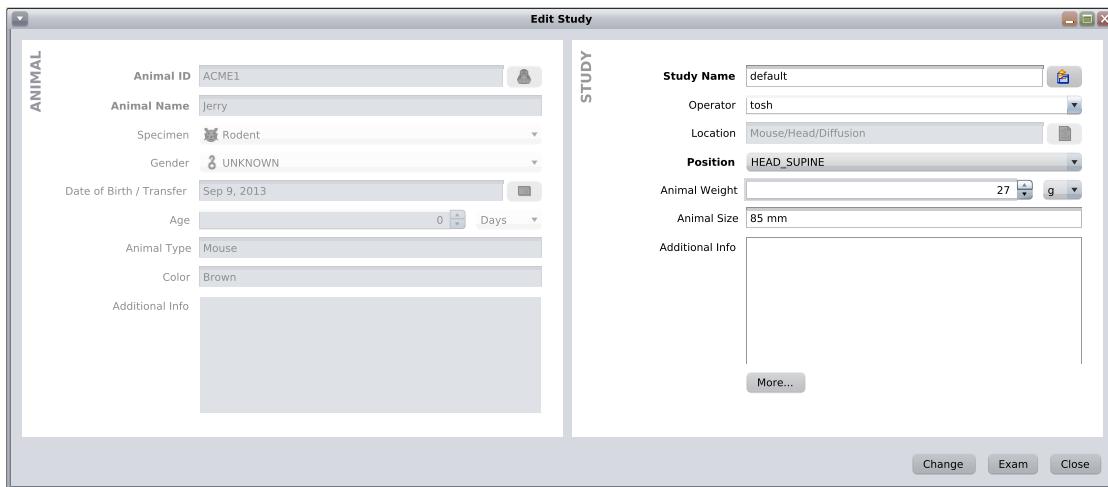


Figure 1.177: Edit Study

2. Make your changes and click the “Change” button to save the new values.
3. If you want to plan or perform examinations with this study, click the “Exam” button.

The **Examination Card** is opened with the particular study. If it can not be opened (e. g. it is already open for another study) an error dialog is shown.

1.7.4 Projects and Sessions

Datasets are arranged in a hierarchical structure:

Basically, a subject entity represents an animal that is examined with the spectrometer. For each subject several studies can be created. Several examinations build a study and an examination may have several image series.

In ParaVision 6 these dataset levels are extended by projects and sessions: Several subjects may be assigned to a project and an additional session level is inserted between subject and study level. Projects and Sessions are invisible by default until the option “Projects/Sessions” is enabled in the **Options Window**.

If the “Projects/Sessions” option is enabled (see Chapter [Enable the Visibility of Projects and Sessions \[▶ 215\]](#)) the **Study Registration** dialog contains additional areas with the project and sessions properties.

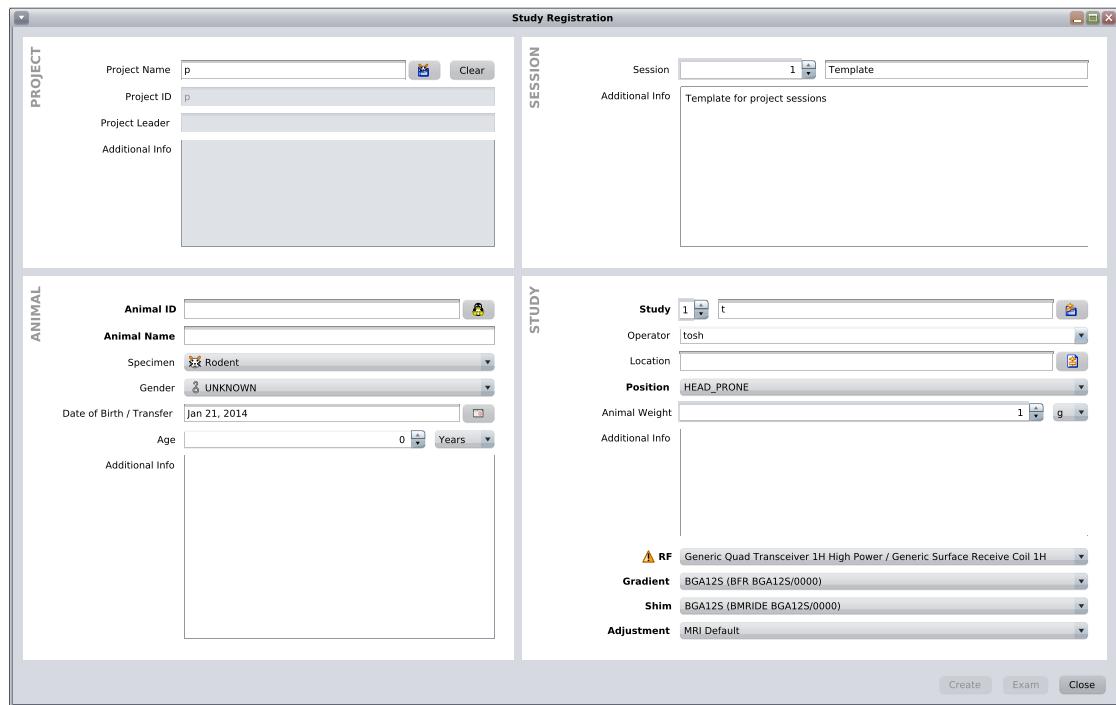


Figure 1.178: Study Registration Project

In this dialog an existing project can be selected but not edited or created.

If no project is selected any value for session name and session comment can be entered and an arbitrary study will be created. If no session name is specified the “Default” session is used. This “Default” session is also used if the visibility flag of projects and sessions is disabled.

If a project is selected additional number spinner elements appear in front of the session and study name inputs allowing to cycle through sessions and study templates for the selected project and subject.

Before a longitudinal study can be created a study has to be assigned to an existing project as a study template (see Chapter [Create a study template for a project \[▶ 216\]](#)).

1.7.4.1 Enable the Visibility of Projects and Sessions

Goal:

Make project and session levels of datasets visible in **Workspace Explorer**, **Dataset Browser** and **Study Registration** dialog.

1. Select the menu item Window ▶ Options from the main menu.
► The **Options Window** appears.
2. Locate the “Dataset” icon on the icon bar on top of the **Options Window** and click it.
► The **Options Window** shows the dataset related options.
3. Locate the check button “Projects/Sessions” in the “Dataset Presentation” segment in the most right column of the **Options Window**.
4. Enable it and close the **Options Window** by clicking the “OK” button on the bottom.
5. Close and restart ParaVision.

1.7.4.2 Create a project

Goal:

Create a project that can be used to arrange a collection of subjects that are examined in comparable, longitudinal studies.

1. Select the menu item File ▶ New ▶ Project... from the main menu.
 - The **Create Project** dialog appears. It is a subset of the **Registration Dialog** window, containing only input elements for the project parameters (see Figure [Project Registration \[▶ 216\]](#)).
2. Enter a unique name and a unique id for your new project. Additionally, you can enter a project leader and a description for your project in the “Additional Info” field.
3. Click the “Create” button that became enabled as soon as all mandatory parameters got valid and unique data.
 - The **Create Project** dialog is closed and the specified project is created.

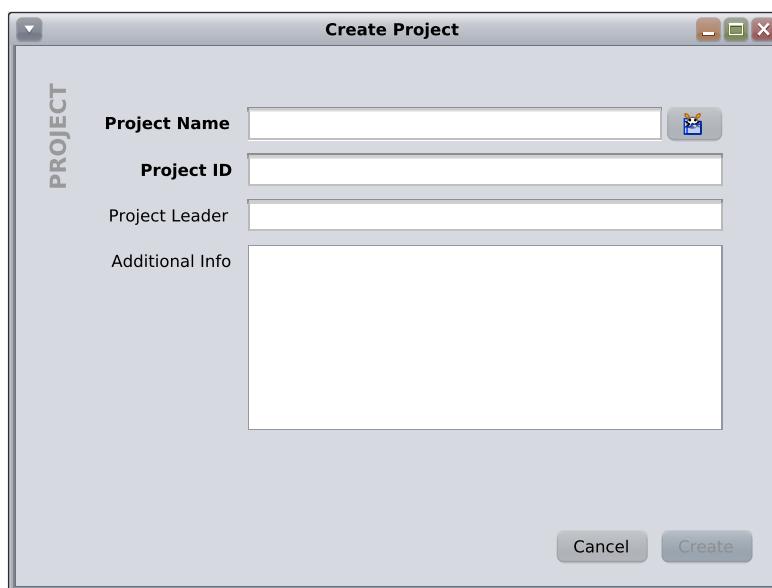


Figure 1.179: Project Registration

1.7.4.3 Create a study template for a project

Goal:

Assign an existing study to a project as a study template.

1. Select a study in the **Dataset Browser** or **Workspace Explorer** and initiate the action “Save as Study Template...”. Using this **Dataset Browser** you can find this action inside the 3rd combo button “Properties” or in the context menu if you use the **Workspace Explorer**.
 - The **Create Study Template** dialog appears (see Figure [Create Study Template \[▶ 217\]](#)).
2. Select your project and enter a name and description for the study template. You can assign several study templates to each project. Just use the number spinner element to find an empty slot for your new template.
3. Click the “Create” button that became enabled as soon as a project is selected, an empty study template slot was selected and a valid study name was entered.
 - The **Create Study Template** dialog is closed and the study template was created and assigned to the project.

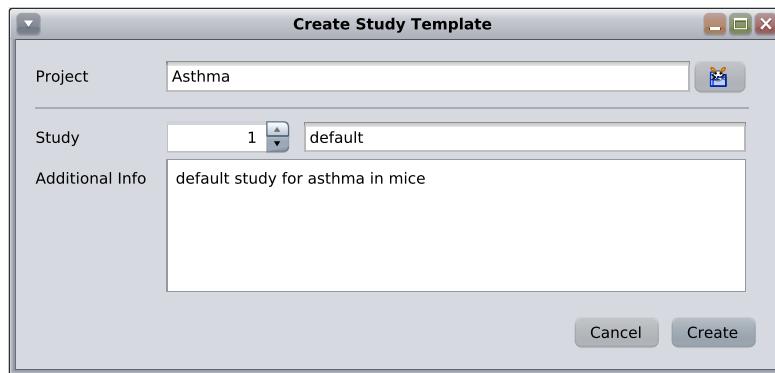


Figure 1.180: Create Study Template

1.7.4.4 Create a new longitudinal study for a project

Goal:

Create a new instance of a longitudinal study for an existing project.

1. Select a project in the **Dataset Browser** or **Workspace Explorer** and initiate the action “Add Study...” from the browser’s action buttons or the explorer’s context menu.
 - The **Study Registration** dialog appears. The project parameter fields are filled with the values of the selected project. Selecting another project is disabled.
2. Specify a new subject or select an already existing subject in the subject area below the project parameters.
 - The first session with empty study slots is loaded into the session area.
3. Use the session number spinner to select a new session or an already existing session with empty study slots. If needed change the name and description of the session.
 - The study template is loaded into the study area (see Figure [Study Registration Longitudinal Study \[218\]](#)).
4. Select the study template using the study number spinner. Change the study properties if needed.
 - The **Study Registration** dialog is closed and the study (and potentially the specified subject and session) was created.

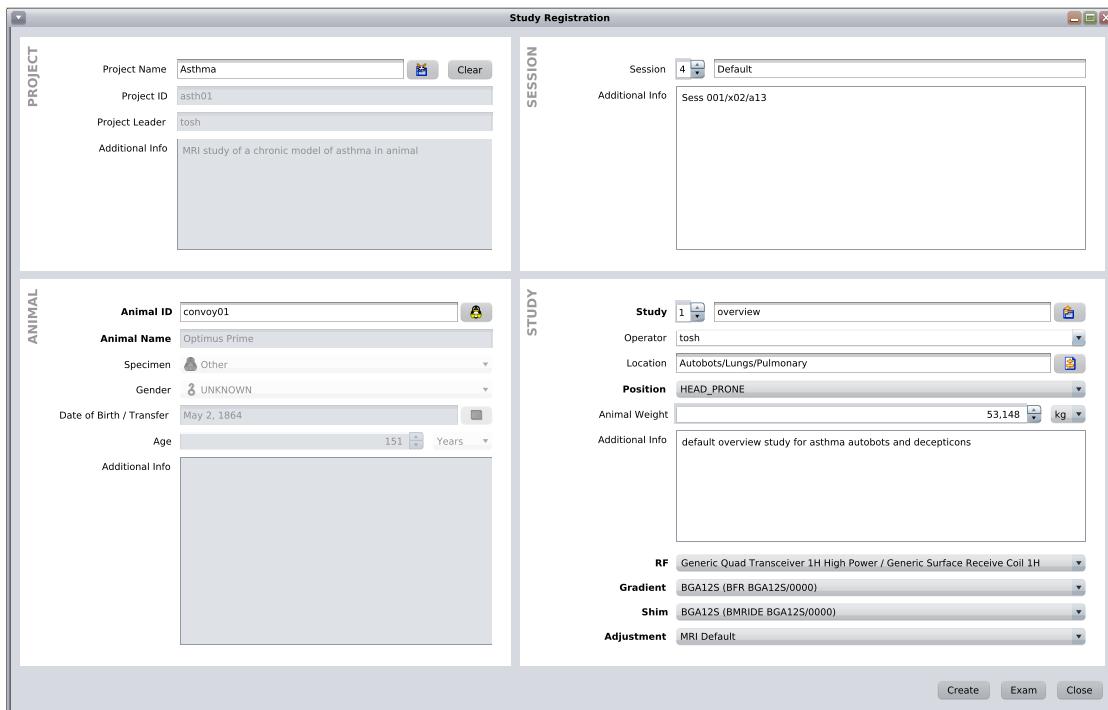


Figure 1.181: Study Registration Longitudinal Study

1.8 Adjustments

1.8.1 Adjustment Methods

1.8.1.1 Principles

The quality of MRI data strongly depends on a proper setting of several parameters such as the resonance frequency, RF power or shims. These parameters are automatically measured and set in a series of experiments called Adjustments. Some adjustments are carried out only once at the beginning of the study, others are running before every scan, or only when explicitly demanded by the user. The sequence of per-study, per-scan and on-demand adjustments can be specified in the Configuration Card.

Adjustments are controlled by special methods and their parameters are saved in adjustment protocols. The Configuration Card allows attributing a protocol to each adjustment.

The sequence of adjustments together with the choice of adjustment protocols can be saved as an adjustment configuration. An adjustment configuration can be individually selected for each study (in the field **Adjustment** on the Study Registration Card). Adjustment configurations provided with the system (MRI_default, ICON, MRI_PT, MRI_TxSUC) cover all typical requirements. Further configurations can be added by the users when necessary.

On top of the configured adjustments, some measurement methods add their individual, specific adjustments, e.g. UTE adjusts the k-space trajectory, EPI the ghost correction, etc. These adjustments do not have special protocols – they rely on parameters set for particular scans.

The Adjustment Platform (see Chapter [Using the Adjustment Platform \[▶ 65\]](#)) allows inspecting all adjustments involved in the currently selected scan, viewing their status, re-running selected adjustments with modified parameters, and “manual” tweaking of the adjustment results.

1.8.1.2 Typical Adjustments

The following table lists adjustments implemented in ParaVision 6.0 and their features. Details of methods controlling these adjustments can be found in dedicated chapters.

Name	Protocol	Method	Purpose
Wobble Adj.	ADJ_WOBBLE	Wobble	Allows wobbling the RF coil (measuring its absorption spectrum) for manual tuning/matching (in Setup mode). Automatic tuning/matching on special coils.
Study Shim	ADJ_SHIM	AdjShim	Iterative adjustment of global linear shims based on non-localized FID integral. Runs at the beginning of each study.
Scan Shim	none	AdjShim	Calculation of map-based shims (option), localized iterative linear shim correction (option), and localized frequency re-adjustment. Runs for each scan.
Basic Frequency	ADJ_SF	AdjSf	Finds the resonance frequency
Reference Power	ADJ_REFG, ADJ_REFG_Tx Suc	AdjRefG	Calibrates the RF pulse power
Receiver Gain	none	none	Sets the optimal receiver gain for the current scan
B0 Map	ADJ_B0MAP	FieldMap	Measures the B0 map in the object for shimming

1.8.1.3 Repeating Adjustments

Adjustments can be repeated when they have failed or when experiment conditions have changed (e.g. the animal has moved). For that purpose, the adjustment should be opened in the Adjustment Platform and its parameters adapted if necessary. This could be, e.g. changing the frequency range in Basic Frequency adjustment if it has failed due to particularly wrong starting value, or changing the position of the selected slice (with Geometry Editor) in the Reference Power Adjustment to better match to the geometry of a surface transmission coil. To run an adjustment after these modifications, press the **Start** button.

1.8.1.4 Adjustment Results

Each adjustment has a Result parameter card showing what it has adjusted. Adjustment results can be edited by the user. This is possible when the adjustment was successful but the user knows better what is correct, or when the adjustment has failed, and the user knows the target values from other sources. After a modification, the new result must be saved using one of the options of the context menu (right mouse button):

- **Save Adjustment Results:** The result will be used in all remaining scans of this study. This option is used in most situations.
- **Save Adjustment Result for Other Studies:** The result will be used per default in all other studies (and objects) created by the same user. This option can be used, e.g. to set a reference power for an X-nucleus coil, for which the automatic adjustment is impossible.
- **Save Adjustment Results Globally:** The result will be used per default by all users in all studies. This option is active only for some system calibration procedures.

1.8.2 Wobble (Impedance Matching)

1.8.2.1 Principles

Starting the wobble adjustment shows a wobble curve of a selected coil element inside the Acq/Reco Display. The adjustment normally has to be performed only once per study and uses the protocol Wobble. It can be repeated manually within the Adjustment Platform.

The curve itself represents a measure for the reflected power at the connection point between the spectrometer and an attached RF coil. To guarantee an optimal power transmission at a given frequency, both their impedances have to be matched. Therefore the coils' resonance circuits are typically equipped with two mechanically (or in some cases voltage ("Varicaps")) controlled capacitors. Altering their capacitance is called "tuning" and "matching".

A wobble curve is plotted over a given bandwidth around the nucleus frequency, see [Example of a wobble curve \[▶ 220\]](#). During wobble the user has to tune and match until the dip reaches the centre and its minimum is close to the zero line.

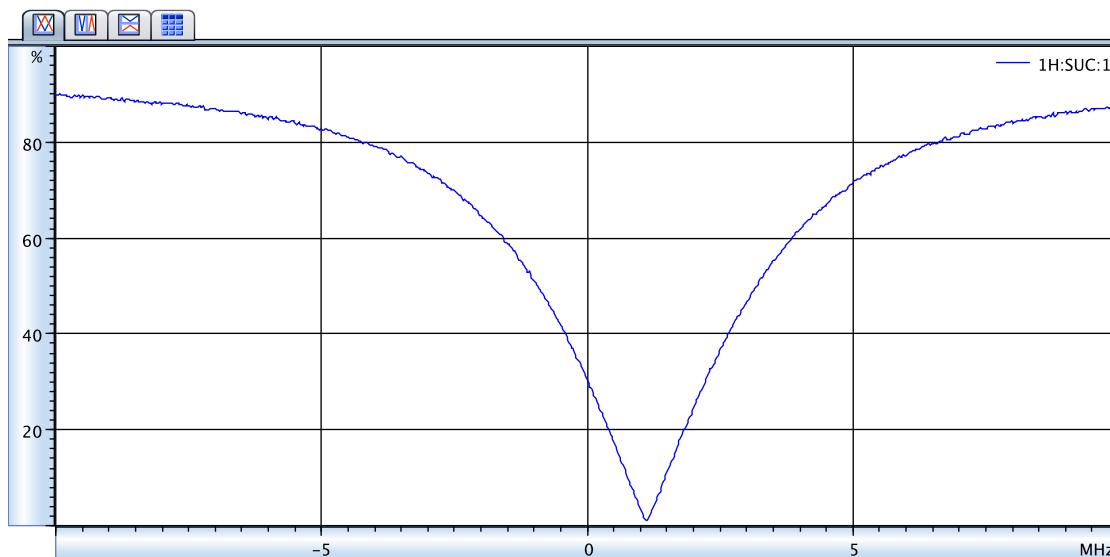


Figure 1.182: Example of a wobble curve

1.8.2.2 Starting wobble using "Setup" (Standard Wobble)

In "Setup"-Mode, wobble curves are continuously recorded and shown inside the Acq/Reco Display. The user can then tune and match the selected coil element either by turning the knobs on the back of a coil or applying different tune/match values from within the ParaVision GUI (Varicap coils only).

The adjusted values for varicap coils have to be saved manually, either within the context of the current study, or all studies created for the identical coil configuration.

1.8.2.3 Starting wobble using “Start” (Automatic Adjustment)

For coil elements using varicaps, wobble can be started as automatic adjustment. An underlying algorithm performs the otherwise manual steps of tuning and matching automatically. Its performance can be supervised in the “Acq/Reco Display”.

The resulting tune and match values are stored within the context of the current study. They can also be manually stored for all studies which use the identical coil configuration.

Storing the wobble curve:

When performing wobble as auto-adjustment the parameter **Store Wobbleresult** on the **Result** card can be set to save the wobble curve itself as an adjustment result. The curve can be stored, no matter if the coil can actually be wobbled automatically or not.

The following table summarizes the performed actions when pressing “Start”:

Coil	Stored Wobbleresult disabled	Stored Wobbleresult enabled
No varicaps	- Nothing is done. The adjustment immediately finishes successfully.	- A single wobble curve is recorded and stored.
Varicaps	- The coil element is wobbled automatically. - The resulting tune/match values are stored.	- The coil element is wobbled automatically. - The final wobble curve is stored along with the resulting tune/match values.

1.8.2.4 Applications

- Manual or automated impedance matching of a connected coil.

1.8.2.5 Specific Parameters

The adjustment is based on a protocol **ADJ_WOBBLE** in **Scan Programs & Protocols** in the region **Adjustments**.

Routine Card

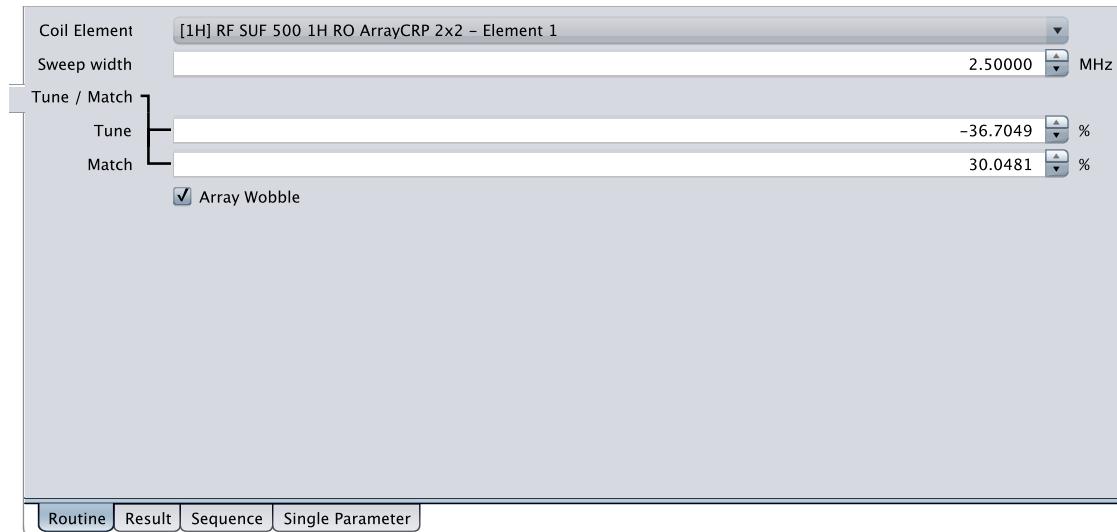


Figure 1.183: Wobble Routine Card

Coil Element (WobbleCoilElement) – Allows selecting the coil element for which the wobble curve should be recorded.

Sweep Width (WobbleSweepWidth) – Bandwidth of the excitation sweep. Defines the frequency range around the nucleus frequency.

Tune/Match (PVM_WobbleShownTmValue) (Varicap coils only) – Tune and match value for the selected coil element.

Array Wobble (WobbleArrayWobEnable) (Bruker Array-CRP only) – Activates the interleaved wobble mode via the ADM-CRP module. Wobble curves of all Array-CRP elements are recorded within a single scan.

Result Card

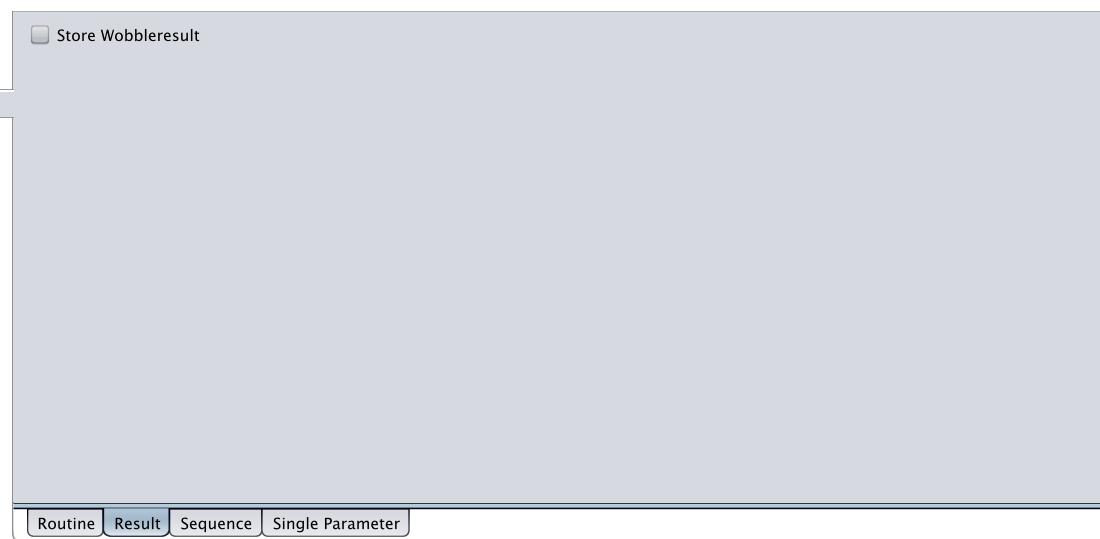


Figure 1.184: Wobble Result Card

Store Wobbleresult (StoreWobbleRes) – When activated, the wobble-curve is stored as the result of an auto-adjustment.

1.8.3 AdjSf (Frequency adjustment)

1.8.3.1 Principles

AdjSf is a frequency auto-adjustment procedure. It searches the frequency of the dominating resonance (typically water) to set the spectrometer reference frequency. A number of non-volume-selective FID signals are acquired with a certain acquisition bandwidth, but each with a shifted frequency centre to cover a contiguous frequency range of appropriate size. A user-defined chemical shift of the reference line (per default, 4.7 ppm for water) is stored along with the frequency value to allow correct frequency setting for different chemical shifts in the study. The values of **Reference Frequency** (PVM_FrqRef) and **Reference Chemical Shift** (PVM_FrqRef) visible in all scans on the Sequence Card, Subcard Frequency Ch.1 are derived from the result of this adjustment.

The adjustment is normally performed only once per study and uses the protocol ADJ_SF. It can be repeated manually within the Adjustment Platform. As long as no valid adjustment has been stored, the configuration frequency for water (CONFIG_basic_frequency) and its standard chemical shift value of 4.7 ppm are used.

1.8.3.2 Applications

- Automated non-localized frequency search and setting of the reference frequency

1.8.3.3 Specific Parameters

The adjustment is based on a protocol ADJ_SF in **Scan Programs & Protocols** in the region **Adjustments**.

Routine Card

Main

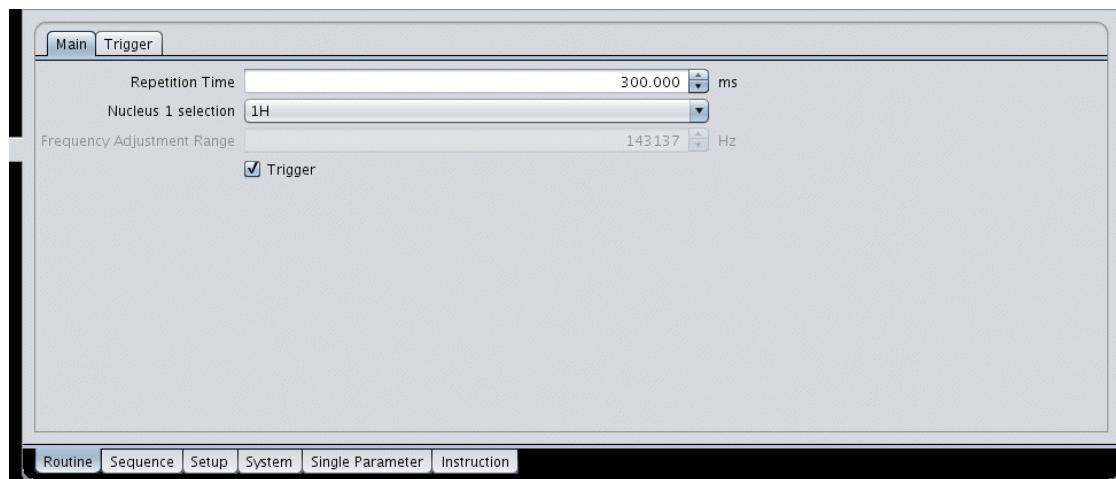


Figure 1.185: AdjSf Routine Card Main

Nucleus 1 Selection (PVM_Nucleus1Enum) – Allows selecting the nucleus for channel 1 from a list of nuclei available in current operation mode

Frequency Adjustment Range (FreqAdjRange) – Non-editable. This parameter shows the complete frequency range within which the MR resonance is searched. It is derived from the parameters **Resolution** and **Number of Excitations** specified on the Sequence Card.

Trigger (PVM_TriggerModule) – Activates the trigger module. Note: The state of this parameter is not stored in protocols of the method AdjSf, its state is inherited from the state of the scan in the Examination Card.

Trigger

See Chapter [Trigger \[▶ 256\]](#)

Sequence Card

Main

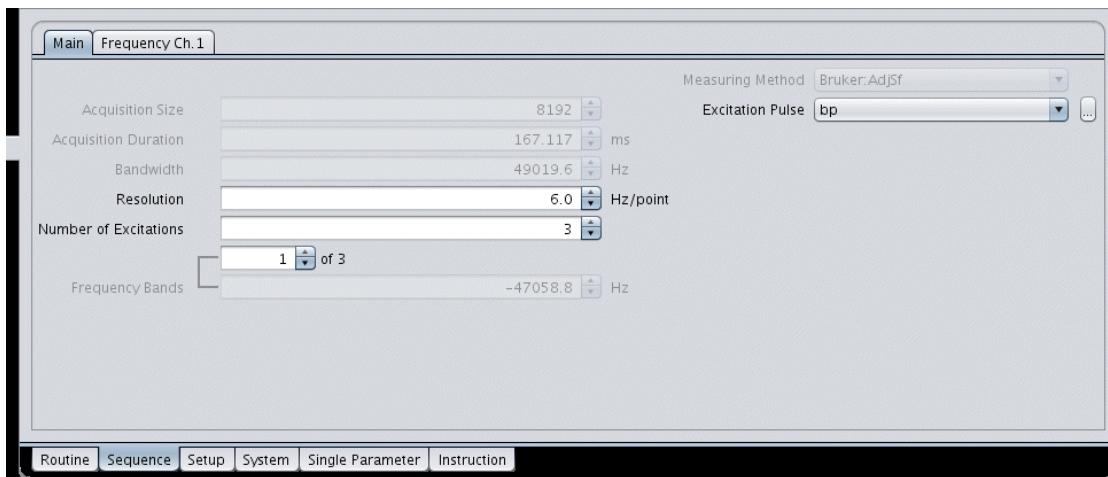


Figure 1.186: AdjSf Sequence Card Main

Acquisition Size (AcqSize) – Number of complex data points acquired

Resolution (FreqRes) – Spectral resolution of the acquired data points in Hz/point

Number of Excitations (Nexc) – Number of data sets (FIDs) acquired with different receiver frequencies. This is the recommended parameter to change if the **Frequency Adjustment Range** needs to be adapted.

Frequency Bands (FreqOffsList) – Non-editable. This parameter shows the mid-frequency for the selected Nexc. The frequency bands are slightly overlapping to cover the complete range contiguously.

Frequency Ch. 1

See Chapter [Frequency \[▶ 280\]](#)

Result Card

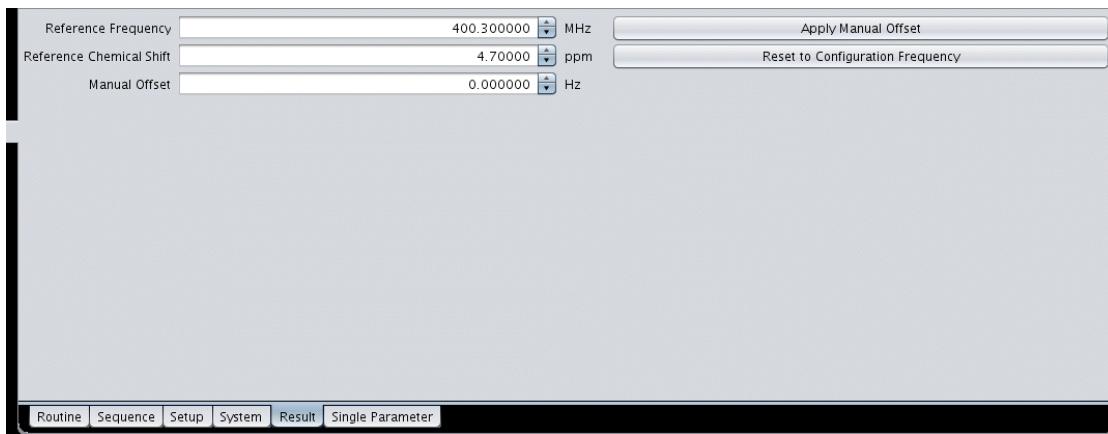


Figure 1.187: AdjSf Result Card

Reference Frequency (FrqRef) – Automatically determined reference frequency. For water it is equal to PVM_FrqAdj1H. For X-nuclei it is non-editable as it is derived by multiplying the 1H-0ppm frequency with the gamma ratio.

Reference Chemical Shift (FrqRefPpm) – Chemical shift for which the reference frequency is automatically adjusted, typically 4.7 ppm for ^1H , meaning that the dominating signal comes from water. If the signal is dominated by other substances (e.g. fat), then the reference chemical shift may be adapted (e.g. to 1.2 ppm for lipids). For X-nuclei the default value is 0.0 ppm. However, it can be changed if a user-convention of ppm labelling is required.

Manual Offset (O1) – This parameter shows the current value of the transmitter offset frequency O1 which can be found on the Setup Card in some methods.

Apply Manual Offset (ApplyManAdjOffset) – For the ^1H nucleus this button adds the O1-value to the reference frequency FreqRef. For other nuclei it adds the O1-value scaled in ppm to the reference chemical shift FrqRefPpm. In both cases O1 is reset to zero, and the line which was previously on resonance with the O1 offset remains on-resonance without it.

Reset to Configuration Frequency (FrqResetCfg) – Pressing this button restores default frequency parameters. The reference frequency for ^1H is reset to CONFIG_basic_frequency, and reference chemical shifts are reset to 4.7 ppm for ^1H and 0 ppm for other nuclei. This action may be needed when a wrong frequency result has been stored by mistake.

1.8.3.4 Caveat

AdjSf is the typically first measurement of a study. Therefore, it is usually this adjustment step that reveals hardware or measuring object setup insufficiencies. Some common reasons for a failure of the resonance search are listed below:

Reason	Solution
The object to be measured is not centered	Reposition the object
The difference between the working and the current MR signal frequency is too large	Increase Nexc in the basic frequency protocol within the Adjustment Platform and start the measurement of this protocol manually
Receive path or coil itself is not ok	Use another coil for test purposes only
No signal	For non-HD electronics RF-transmitter may not be switched on (HD electronics is equipped with an auto-recognition and a status control).
Incorrect, large shim values	Check the shim setting on the Setup Card, Sub-card Shim

1.8.4 AdjShim

1.8.4.1 Principles

This adjustment method fulfills various tasks related to shimming (homogenizing of the static magnetic field):

- Iterative shimming without signal localization (e.g. to find the initial study shims)
- Calculation of shims from a measured map (as a part of the MAPSHIM utility)

- Iterative shimming with signal localization (as an optional correction after MAPSHIM calculation)
- Correction of system frequency after shim changes (in each scan)

Non localized shimming mode

The FID signal is generated by a non-selective RF pulse with different shim settings. The shim adjustment is based on the iterative Tune Shim algorithm, see [Optimization Card ▶ 267](#).

Per default, a 50us, 10mW block RF pulse is used. For very small RF coils power is reduced to the coil limit. At the end of the shimming procedure, the basic frequency is adjusted using the position of the maximum peak of the Fourier transformed signal.

Localized shimming mode

The Tune Shim algorithm is used to find linear shims for a voxel selected with a stimulated echo sequence (similar to STEAM). This mode is used as an additional correction after the MAPSHIM calculation with the voxel defined by the shimming volume, see [Setup Card ▶ 283](#). Frequency is adjusted at the end.

Study Shim Adjustment

Method AdjShim is used in the standard configuration to adjust the linear shims based on a non localized signal once per study (further referred as study shim). This is done based on the adjustment protocol ADJ_SHIM (AnyObject/AnyRegion/Adjustments) for the study protocol based adjustment study shim visible in the Adjustment Platform.

Scan Shim Adjustment

The standard adjustment configuration defines also a shim adjustment based on method AdjShim that establishes special shim conditions as defined by the MAPSHIM parameter group (see Chapter [MAPSHIM ▶ 238](#)). This adjustment may be selected and executed in the Adjustment Platform as Scan Protocol based adjustment Scan Shim. It is executed automatically in each scan preceding specific adjustments to assure an appropriate resonance and shim condition.

1.8.4.2 Applications

-
- Automated non localized/localized iterative shimming
 - FieldMap based shim setting
 - Non localized/localized frequency adjustment in combination with changes of the shim condition

1.8.4.3 Specific Parameters

Routine Card

Main

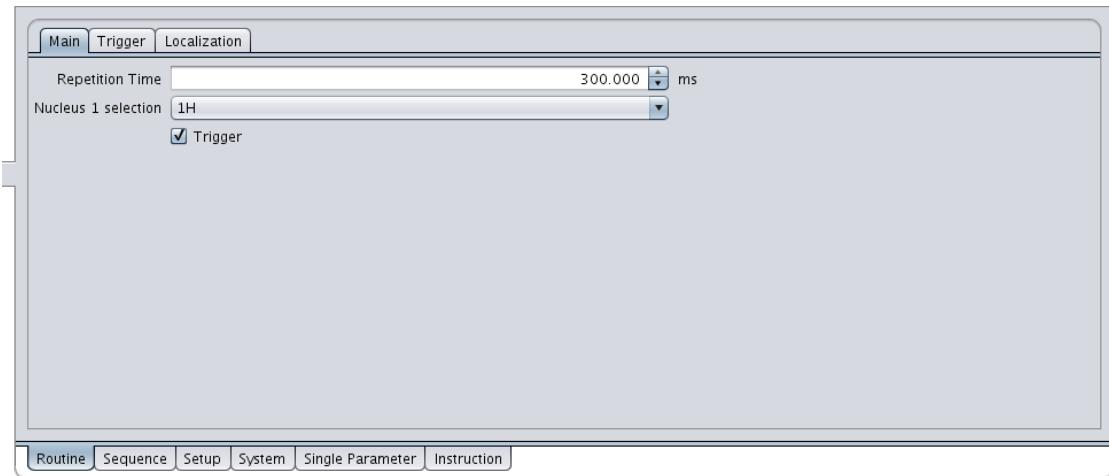


Figure 1.188: AdjShim Routine Card Main

Nucleus 1 Selection (PVM_Nucleus1Enum) – Allows to select the nucleus for channel 1 from a list of nuclei available in current operation mode that is defined on the System Card

Trigger (PVM_TriggerModule) – Activates the trigger module. Note: The state of this parameter is not stored in protocols of method AdjShim, its state is inherited from the state of the scan in the Examination Card.

Trigger

See Chapter [Trigger \[▶ 256\]](#)

Localization

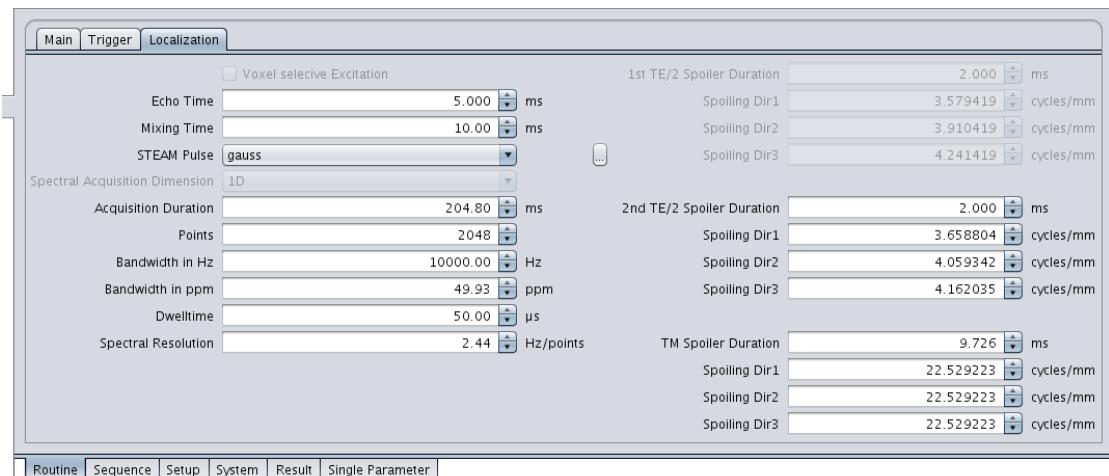


Figure 1.189: AdjShim Routine Card Localization

This parameter group controls the STEAM localization for localized iterative shimming and/or localized frequency adjustments. The localization depends on the desired shim condition as defined by the MAPSHIM parameter group (see Chapter [MAPSHIM \[238\]](#)). A localization is done in case a FieldMap shim is required and all conditions for its calculation are prepared (Status field in Auto Shim Card shows Mapshim Ready).

Voxel Selective Excitation (VoxelExc) – Flag (not editable). If activated a STEAM localization of the signal is performed inside the shim volume (as shown in the Geometry Editor for cuboid shape).

Echo Time (PVM_EchoTime) - Sum of delays between the effective center of the 1st and 2nd excitation pulse (the 2nd pulse is used as backrotation pulse) in the first TE/2 period and between the effective center of the 3rd excitation pulse and the center of the stimulated echo in the second TE/2 period. The effective center of the RF pulses depends on the pulse rephrasing properties.

Mixing Time (StTM, abbreviation TM) – Delay between the effective center of the 2nd and 3rd RF pulse. The minimum TM depends on the duration and rephrasing properties of the RF pulses and the duration of the spoiling gradient switched in the TM period.

STEAM Pulse (VoxPul1Enum) – Enumeration parameter to use one of the excitation pulses installed on the system. Pulse details define length, bandwidth and other properties of the excitation pulse used in STEAM. For volume selection the same pulse is applied in the slice selective parts of the STEAM localization. To prevent shifted excitation because of frequency caused by calculated shims a high bandwidth (10000 Hz) should be chosen.

Spectral Acquisition Dimension (PVM_SpecDimEnum) – Dimensionality of the spectroscopic experiment (constrained to 1D, not editable in this method)

Acquisition Duration (PVM_SpecAcquisitionTime) – Duration of the acquisition time as calculated from **Points** and **Dwelltime**

Points (PVM_SpecMatrix) – Number of sampling points for each spectroscopic dimension

Bandwidth in Hz (PVM_SpecSWH) – Maximum spectral width fulfilling the Nyquist condition expressed in absolute units [Hz]

Bandwidth in ppm (PVM_SpecSW) – Maximum spectral width fulfilling the Nyquist condition expressed in units of the resonance frequency of the nucleus under investigation [ppm]

Dwelltime (PVM_SpecDwellTime) – Time between two successive sampling points of the digitizer

Spectral Resolution (PVM_SpecNomRes) – Best possible nominal spectral resolution of the time domain data assuming twofold zero filling before spectral reconstruction

During the STEAM localization sequence, the following three kinds of spoilers are applied:

1st TE/2 Spoiler (StSpTE1) – Defines the spoiler gradient in the first TE/2 period of the STEAM localization. Its parameters appear non editable. Since the TE spoiler gradients have to be balanced to assure the refocusing of the stimulated echo signal, the duration and amplitudes of the spoiler are derived from values specified for the 2nd TE/2 spoiler.

2nd TE/2 Spoiler (StSpTE2) – Defines the spoiler gradient in the second TE/2 period of the STEAM localization. Increasing its duration will increase the minimum TE of the sequence, the duration of the 1st TE/2 spoiler is increased to the same value. In order to balance the gradient area with respect to a refocused stimulated echo (STE), the spoiling gradient amplitudes of the TE/2 spoilers in a given direction are different to refocus the dephasing effect of the slice selection gradients used in the STEAM sequence.

TM Spoiler (StSpTM) – Defines the spoiler gradient in the mixing interval TM of the STEAM localization. Increasing its duration will increase the minimum TM of the sequence. The duration of the spoiler is also controlled by the desired duration of the TM period. To prevent refocusing of unwanted signal the duration as well as the spoiling capacity in of the TM spoiler in each direction is at least 3 times longer than the duration of the TE spoilers.

Each of these spoilers can be customized by the following fields:

Duration (.dur) – Duration of the spoiler gradient

Spoiling Dir1 (.spoil_dir1), Spoiling Dir2 (.spoil_dir2), Spoiling Dir3 (.spoil_dir3) – Amplitude of the spoiling gradients along the direction of the 1st, 2nd and 3rd slice excited in the STEAM voxel selection sequence. The values can be specified as spoiling efficiency in cycles of the transverse magnetization per mm.

Sequence Card

Main

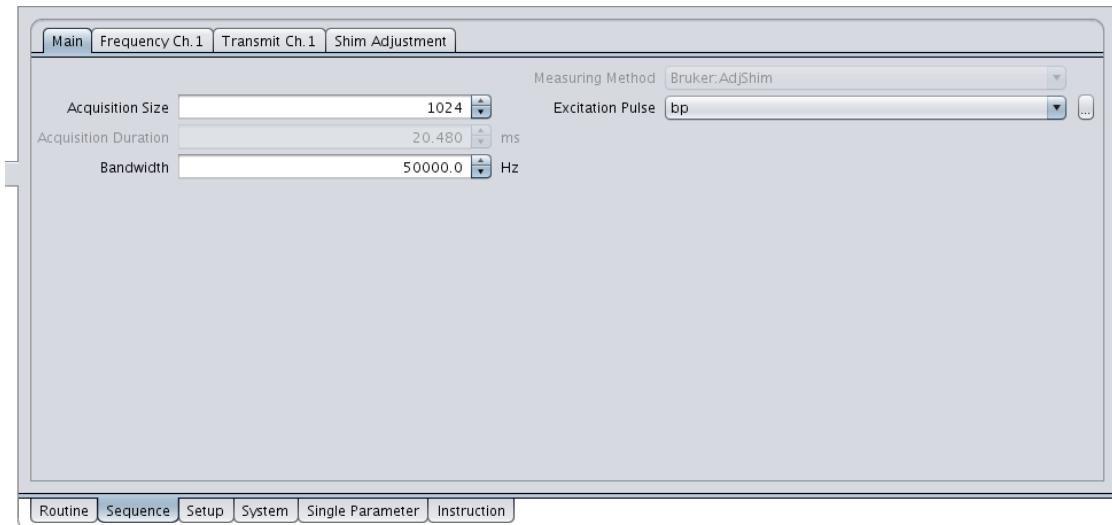


Figure 1.190: AdjShim Sequence Card Main

In this card details of the non-selective excitation and data acquisition are specified.

Acquisition Size (AcqSize) – Number of complex data points acquired

Acquisition Duration (PVM_Acquisition) – Duration of the data acquisition period [ms] (appears not editable). It depends on the acquisition size and the sampling bandwidth.

Bandwidth (PVM_EffSwh) – Bandwidth of data sampling [Hz]

Excitation Pulse (ExcPulse1Enum) – Nonselective excitation pulse of the sequence

Result Card

CalcMapshim (CalcMapshim) – If pressed a shim is calculated within the specified shim volume.

Shim Calc. Status (PVM_MapShimCalcStat) – Shows the status of the shim calculation

1.8.5 AdjRefG

1.8.5.1 Principles

Method AdjRefG adjusts the reference power – the peak power of a 1ms 90° blockpulse. This value is used to calculate the pulse angle of (shaped) RF pulses in PVM methods.

The adjustment algorithm is based on a 3-pulse sequence:

$$\alpha - \frac{TE}{2} - 2\alpha - SE - TM - \alpha - \frac{TE}{2} - STE$$

where α denotes the pulse angle of an RF pulse (to be calibrated), TE is the echo time, TM denotes a filling period (the mixing period for a stimulated echo generation), SE (STE) is the spinecho (stimulated echo respectively). During the entire sequence a constant gradient is applied that serves a slice selection, spoiling and frequency encoding gradient. The timing of the sequence ensures a SE and STE signal centered in 2 acquisition periods. The Fourier transformed signal shows the projection of the RF pulse profile along the direction of the gradient. The RF waveform used for the calibration may be chosen in the Sequence Card. The adjustment algorithm varies pulse amplitudes for both pulses and minimizes the signal amplitude at the center of the STE slice profile (phase sensitive). In case of multi-channel acquisition (if demanded by the active scan), the individually phased profile of each channel is added to get a (signal weighted) average profile used to optimize the reference power. The duration of the second RF pulse is twice the duration of the first one. The default protocol sets a 0.5 ms blockpulse for the first and third excitation.

After successful adjustment, the reference power for the selected nucleus and RF coil hardware is calibrated in the examined object. The adjustment result is visible in the Sequence Card, Subcard Transmit Ch. X together with a status that shows the method name and adjustment protocol used for the calibration (X denotes the transmit channel, mostly the 1st channel).

1.8.5.2 Preconditions

A successful frequency adjustment is mandatory, a fairly good shim is desirable but not mandatory because the adjustment algorithm is working on RF refocused signal. The adjustment result depends strongly on the coil load and therefore on the measurement object. Before running the Reference Power Adjustment a tuning-matching adjustment must be performed. The adjustment volume (i.e. the place of the selected slice) must be set to an appropriate position of the measurement object. The standard adjustment configuration protocol sets up an axial slice selection at $z = 0$ position and a slice thickness of 5 mm. The appropriate position of the slice is mandatory for a successful adjustment result. If the resonator is placed in the center of the magnet, the measurement object should be placed inside the sensitivity center of the coil, in this case position and orientation of the adjustment slice needs not to be changed. A good preemphasis setting is mandatory since the adjustment algorithm is working on the phased signal in frequency domain to achieve a fast convergence. If long time eddy current and B0 effects of the gradient switching distort the phase distribution of the SE and STE differently incorrect adjustment results or adjustment failures may occur.



The standard adjustment behavior depends on the chosen adjustment configuration (during study) setup and is performed for the first scan started in the Automatic Setup + Acquisition of the Instruction Card.

1.8.5.3 Specific Parameters

Routine Card

Main

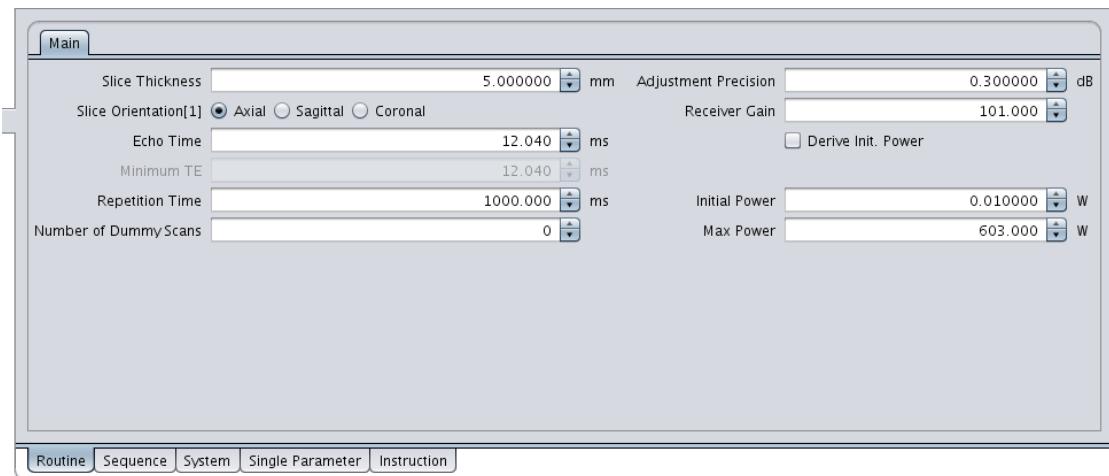


Figure 1.191: AdjRefG Routine Card Main

Slice Thickness (SliceThick) – Thickness of the selected slice [mm]

Slice Orientation[1] (PVM_SPackArrSliceOrient) – Allows to change the major slice orientation (Axial/Sagittal/Coronal). Angulations of the slice selective excitation may be specified in the Geometry Editor.

Echo Time (PVM_EchoTime) – Controls the echo time periods (center of 1st RF pulse to center of spin echo)

Minimum TE (PVM_MinEchoTime) – Displays the minimum echotime, depends on duration of acquisition periods and pulse duration, non editable

Repetition Time (PVM_RepetitionTime) – Time between consecutive repetition of the pulse sequence [ms]

Number of Dummy Scans (NDummies) – Number of excitations without data acquisition to establish a steady state condition of the signal

Trigger (PVM_TriggerModule) – If activated the sequence is synchronized with trigger events. The state of this parameter is inherited from the active method in the scanlist.

Adjustment Precision (AdjPrec) – Controls the convergence criterium of the adjustment algorithm. It stops in case the difference in the estimated RF pulse amplitude differs less or equal to the value specified as adjustment precision (in units of dB). Increase this value in case of unstable signal due to motion of the object.

Receiver Gain (RecGain) – Controls the receiver gain (RG) when the adjustment is started. The RG is readjusted if an overflow occurs during acquisition.

Derive Init. Power (DeriveInitPow) – Flag. If selected the initial power of the RF pulse is derived from **Nominal Init. Flip Angle** before the adjustment is started.

Nominal Init. Flip Angle (InitFa) – Initial flipangle of the excitation pulse. If **Derive Init. Power** is activated **Initial Power** is derived from the desired flip angle as specified by this parameter. This parameter is range-checked to lie within [1°,60°]. The derivation is either done using the result of a previous Reference Power Adjustment (if succeeded in the study or stored for this coil for other studies) or from basic information stored together with the configuration of the coil used for excitation. The reference power that is used to derive the

pulseangle may be inspected in the Result Card of the method if opened in the Adjustment Platform. Note: The adjustment should start with a pulse power that corresponds to a pulse angle less than 90° a value of 10° is recommended.

Initial Power (InitPow) – The initial pulse power controls the pulse amplitude (peak power) at the start of the adjustment. If **Derive Init. Power** is activated, the **Initial Power** is always derived from the **Nominal Init. Flip Angle**. If a reference power is available see Result Card of the method (accessible if the method is opened in the Adjustment Platform).

Max Power (MaxPow) – The maximum peak power of the RF pulse that can be set during adjustment. The value may not be changed, it depends on the maximum power of the RF amplifier, the power limitation of the RF coil that is chosen and the RF amplifier capabilities.

Sequence Card

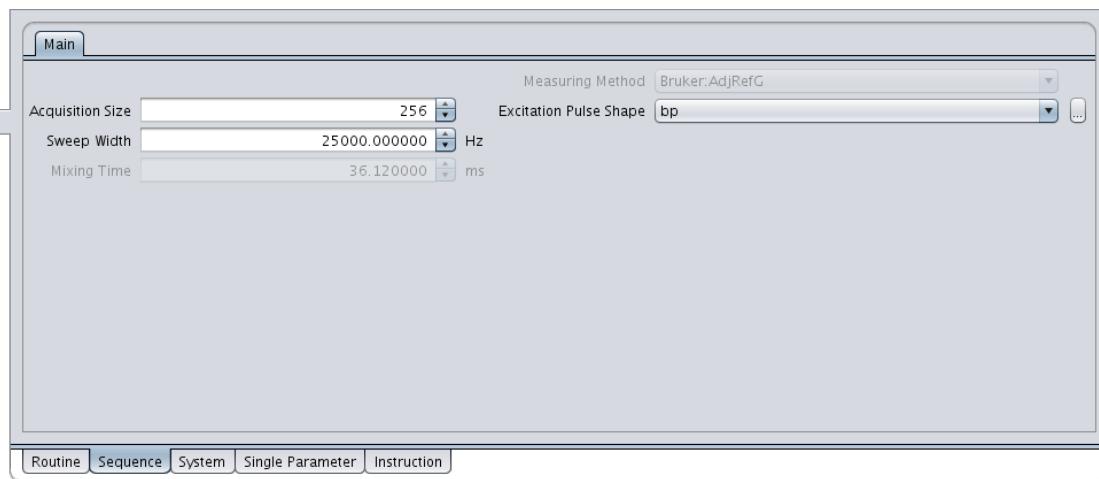


Figure 1.192: AdjRefG Sequence Card Main

Acquisition Size (AcqSize) – Number of complex datapoints acquired for the spin echo (SE) and the stimulated echo (STE). The acquisition size and the **Sweep Width** determine the duration of the acquisition periods and therefore the minimum echo and mixing time.

Sweep Width (SweepWidth) – Sampling bandwidth of the data acquisition

Mixing Time (MixingTime) – Mixing time (period between center of 2nd and 3rd RF pulse) of the sequence. Parameter is not editable and is automatically derived from the TE of the sequence ($TM = 3 \cdot TE$).

Excitation Pulse Shape (ExcPulse1Enum) – Enumeration parameter to use one of the excitation pulses installed on the system. Pulse details define length, bandwidth and other properties of the excitation pulse used in the sequence.

Result Card

The Result Card is only visible if method AdjRefG is selected inside the Adjustment Platform.

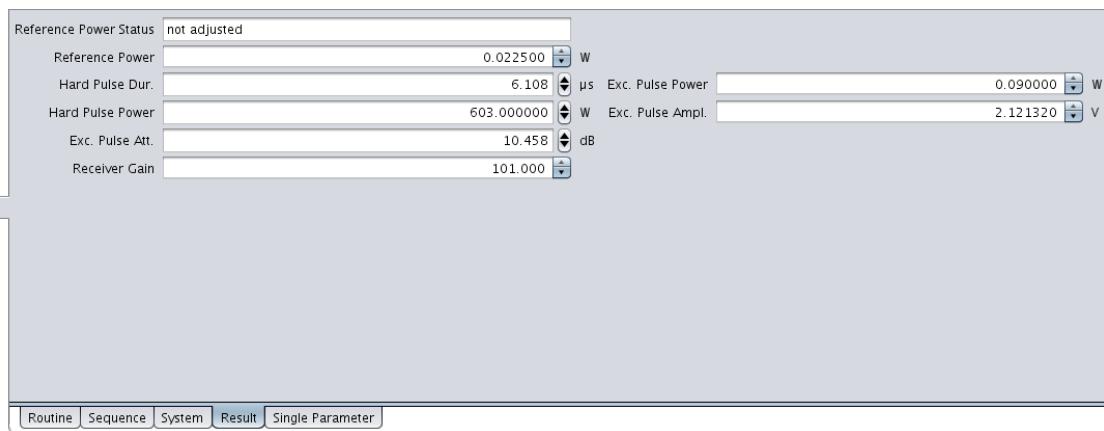


Figure 1.193: AdjRefG Result Card

Reference Power Status (PVM_StudyRefPow.Stat) – Shows the status of the reference power. It may either show information about the protocol and measurement method used to calibrate the reference power. In case values are changed in the Result Card the status shows Manually adjusted. Dependent on previous adjustments or coil configurations different information is shown:

- not adjusted: The reference power has not been adjusted in the study and neither coil information nor calibration results for this coil adjusted in previous studies are available. For this status the derivation of initial pulse angles is initially deactivated.
- System (coil): A typical value of the reference power for a low load condition is available in the configuration of the coil that is used. Its value is visible in the coil editor (see Chapter [Coil Configurations](#) [676]).
- Adj by AdjRefG (protocol ADJ_REFG): The reference power for this coil has been adjusted either in the current study or in previous studies.
- Manually adjusted within method AdjRefG: The user provided a value for the reference power in the Result Card of method AdjRefG.

The status of the adjustment is also visible in the examination cards (Sequence Card/Transmit Ch. X, see Chapter [Transmit](#) [281]). Here X denotes the transmit channel that is used in the experiment (mostly channel 1).

Reference Power (PVM_StudyRefPow.RefPow) – Reference power (power of a 1ms 90° blockpulse) in [W]

Hard Pulse Dur. (HPDur) – Hard pulse duration in [μ s]. The hard pulse is defined as the duration of a blockpulse with a peak power defined by **Hard Pulse Power** for a 90° pulse angle. The hard pulse duration in combination with the hard pulse power may be adjusted in TopSpin (by procedure paropt).

Hard Pulse Power (HPPow) – Peak power of a hard pulse that results together with the **Hard Pulse Dur.** in a 90° excitation pulse angle (see above)

The following parameters control the amplitude of the excitation pulse used in the sequence.

Exc. Pulse Att. (ExcPulse1Ampl.patt) – Pulse attenuation of the excitation pulse in [dB]. Note: The dB scale is normalized with the convention 0 dB = 1W

Exc. Pulse Power. (ExcPulse1Ampl.ppow) – Peak power of the excitation pulse in W

Exc. Pulse Ampl. (ExcPulse1Ampl.pampl) – Amplitude of the excitation pulse in [V] assuming a coil impedance of 50 Ω

i Reference Power, Hard Pulse Dur., Exc. Pulse Att., Exc. Pulse Power and Exc. Pulse Ampl. are bound together by key equations thus changing one of the parameters will change the others. This assures a consistant state between these parameters and the signal as a function of RF pulse amplitude in case the reference power is adjusted manually within the Adjustment Platform.

1.8.5.4 Possible Error Conditions

The Reference Power Adjustment by AdjRefG is typically the third adjustment in a new study. Before execution the coil impedance should have been adapted to the sample load (tuning/matching) and the frequency and shim adjustment should have been executed to establish a reasonable resonance condition of the signal. The adjustment algorithm may fail in some situations with error messages mentioned below.

Signal Intensity too low

During adjustment the digitizer filling of the time domain signal is below 0.1%. Possible reasons are:

Reason	Solution
The object to be measured is not centered	Reposition the object
Weak object signal	If a hardware failure may be excluded the signal of the sample may be too weak for this adjustment. In case of X-nucleus acquisition the reference power may be adjusted in TopSpin and the corresponding value of hard pulse duration may be set in the Result Card. A weak proton signal is measured for objects with extremely short T2 relaxation times. In this case a typical value of the reference power may be set in the Result Card and stored for this study.

Power Range exceeded <X> W (Max <Y> W)

The algorithm stops because the required RF pulse power is above the allowed limits for the RF-coil. Possible reasons are:

Reason	Solution
Bad tuning/matching of the coil	Tune/match the coil and repeat the adjustment

Initial pulse amplitude is too high	<p>This may happen if the adjustment has been successfully performed without tuning/matching in a study and has been repeated afterwards. In this case the initial power is derived based on the nominal pulse angle and the result of the first adjustment.</p> <p>Solution 1:</p> <ul style="list-style-type: none"> • Open the Adjustment Platform • Select the Reference Power Adjustment • If activated deactivate Derive Init. Power (Routine Card) and set Initial Power to a lower value (see how to adjust the initial pulse amplitude below) • Start the adjustment <p>Solution 2:</p> <p>In case the start amplitude has been derived from coil information, the adjustment should be repeated in the Adjustment Platform with a lower value of Nominal Init. Flip Angle. For coils without hardware detection the reference power entry of the selected coil configuration should be decreased.</p>
Strong variation of the B1 field across the adjustment slice	<p>In case surface coils are used for excitation the orientation of the adjustment volume should be aligned parallel to the coil based on reference images. In this case it is recommended to use adjustment configuration MRI_TxSuc (see Chapter Principles [▶ 218])</p>

1.8.5.5 Manual Adjustments

Manual adjustment of the initial pulse power

Adjustment protocol ADJ_REFG is used in the standard adjustment configuration delivered with the software. It provides fairly good starting values for most hardware configurations. For some special conditions a faster convergence is achieved or an adjustment failure may be prevented adjusting **Initial Power** by the following steps:

- Assure a centered position of the measurement object
- If not done perform a frequency and shim adjustment
- Enter the Adjustment Platform and select Reference Power Adjustment
- If activated deactivate **Derive Init. Power**
- Start **Setup** and inspect the profiles in the reconstructed data display
- Adjust the RF pulse amplitude (use **Exc. Pulse Att.**, **Exc. Pulse Power** or **Exc. Pulse Ampl.** in the Result Card). Begin the adjustment with low RF pulse amplitudes (high dB values, low power/amplitude values)
- Increase the RF pulse amplitude until the stimulated echo profile (right profile in the reconstructed data display) begins to dent in the center
- Adjust the receiver gain (in the Result Card) to get a digitizer filling of > 1% and < 20% (inspect values shown in time domain data display)
- Stop the setup
- Transfer the value of **Exc. Pulse Power** (Result Card) into **Initial Power** (Routine Card)
- Start the adjustment with this setting

Manual adjustment of the reference power

If the adjustment fails (e.g. because of instable signal due to object motion) the reference power used in the study may be adjusted manually as follows:

- Assure a centered position of the measurement object
- If not done perform a frequency and shim adjustment
- Enter the Adjustment Platform and select Reference Power Adjustment
- Start **Setup** and inspect the profiles in the reconstructed data display
- Adjust the RF pulse amplitude (use **Exc. Pulse Att.**, **Exc. Pulse Power** or **Exc. Pulse Ampl.** in the Result Card). Begin the adjustment with low RF pulse amplitudes (high dB values, low power/amplitude values)
- Increase the RF pulse amplitude until the stimulated echo profile (right profile in the reconstructed data display) begins to dent. Try to minimize the center of stimulated echo profile by carefully increasing/decreasing the RF pulse amplitude
- Press the **Stop** button
- Press the right mouse button and select **Save Adjustment Results** in the context menu



If the adjustment fails due to object motion the convergence criterium of the algorithm may be weakened by increasing the parameter **Adjustment Precision** (Routine Card), see above.

1.8.6 AdjDrift (Frequency Drift Correction)

1.8.6.1 Principles

AdjDrift is a frequency auto-adjustment procedure. It repeatedly records FID signals over a period of time and co-registers the acquisition time of each FID. The offsets between spectrometer and resonance frequency as a function of time are used to estimate a drift of the main magnetic field. It is determined by a least-squares-fit assuming a linear frequency evolution. The result of the adjustment is the rate of the field change (PVM_FreqDriftVal).

The scan for which the adjustment was started uses the frequency drift value to regularly update its working frequency during scan time. The update is done in the acquisition pipeline filter FreqDriftCorr each time when data are acquired and handed to the reconstruction process.

While the drift correction is not required for most systems it may be helpful for systems based on permanent magnets. For the latter a check-box **Frequency Drift Correction** is available on the Sequence Card and the method AdjDrift is configured into the adjustments as a **Per Scan** adjustment. Only a few methods use this adjustment procedure. Other methods have intrinsic corrections based on navigator techniques.

As permanent magnets may also retain spurious residual magnetizations due to preceding measurements (ferromagnetic memory effects, hysteresis) it is this adjustment step that provides an additional demagnetization module that sweeps the remaining magnetization to zero – superconducting magnets do not exhibit this memory effect.

1.8.6.2 Applications

- Automated non-localized frequency drift estimation

1.8.6.3 Specific Parameters

The adjustment is based on a protocol ADJ_DRIFT in **Scan Programs & Protocols** in the region Adjustments.

Routine Card

Main

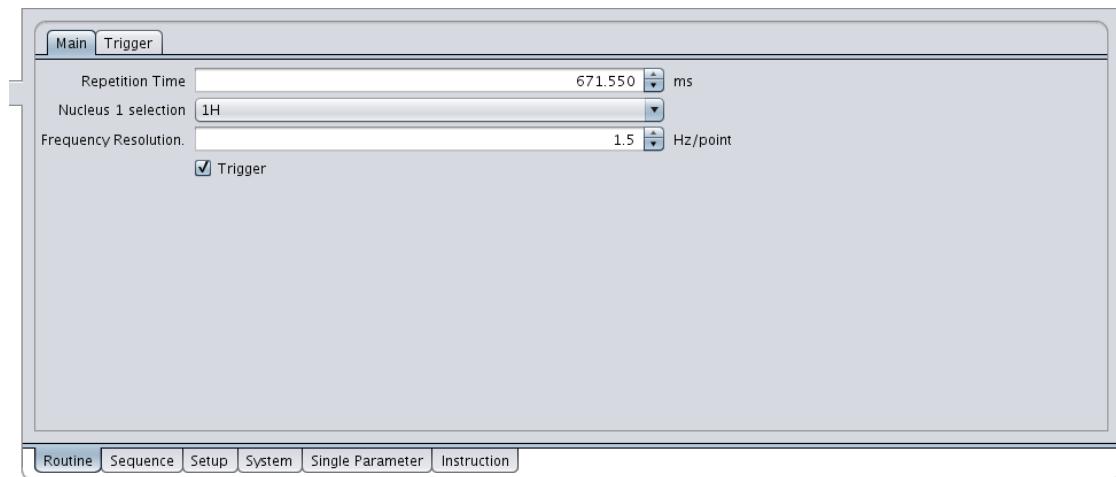


Figure 1.194: AdjDrift Routine Card Main

Nucleus 1 Selection (PVM_Nucleus1Enum) – Allows to select the nucleus for channel 1 from a list of nuclei available in current operation mode that is defined on the System Card

Frequency Resolution (FreqRes) – Spectral resolution of the acquired data points [Hz/point]

Trigger (PVM_TriggerModule) – Activates the trigger module. Note: The state of this parameter is not stored in protocols of method AdjDrift, its state is inherited from the state of the scan in the Examination Card.

Trigger

See Chapter [Trigger \[▶ 256\]](#)

Sequence Card

Main

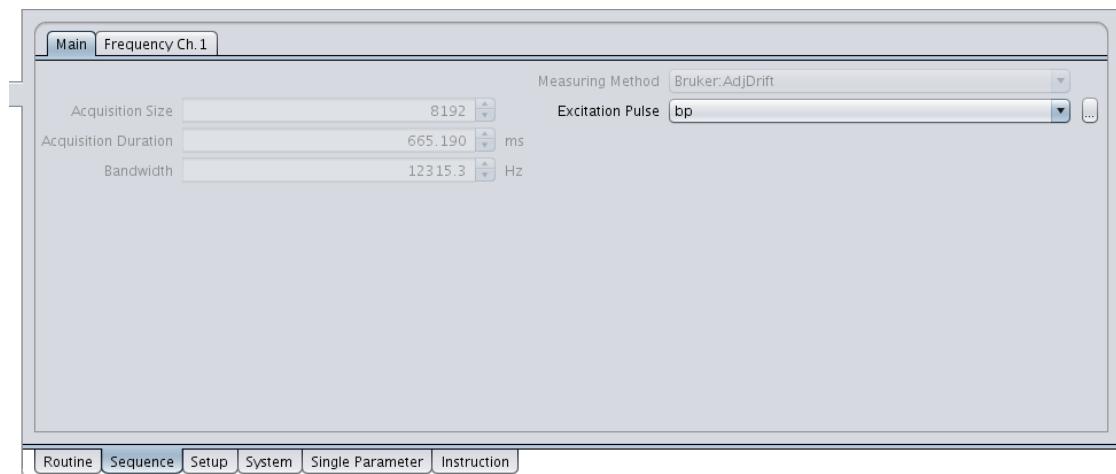


Figure 1.195: AdjDrift Sequence Card Main

Bandwidth (PVM_EffSWh) – Non-editable, informs about the effective acquisition bandwidth

Frequency Ch. 1

See Chapter [Frequency \[▶ 280\]](#)

Result Card



Figure 1.196: AdjDrift Result Card

Adjusted 1H Frequency (PVM_FrqAdj1H) – Intercept of the least-squares fit result. Used to set the new working frequency after the adjustment.

Frequency Drift (PVM_FreqDriftVal) – Slope of the least-squares fit result. Rate of frequency (or main magnetic field) change [Hz/s]. Used to update the working frequency in the calling scan.

1.8.6.4 Caveat

While for superconducting magnets a frequency drift is no issue on a time-scale of a study it may be observable within a single scan for permanent magnets.

The correction procedure AdjDrift assumes the drift to be linear. This assumption is a useful approximation for a reasonable short period of time. However, the duration is difficult to specify for permanent magnets as the drift depends on the device's heating history before the adjustment and the heating future during the scan in preparation. Not only can temperature changes be induced by the environment (e.g. room temperature) but also by the measurement itself due to exposure of changing RF- and gradient fields.

Configuring AdjDrift as a Per Scan adjustment helps to a certain degree but cannot prevent an insufficient correction within a scan itself when the scan time is too long, e.g. due to a larger number of averages. Thus, the period of validity is limited to only several minutes.

1.8.7 MAPSHIM

1.8.7.1 Principles

The MAPSHIM utility calculates the optimum shim values based on a measured map of the B0 field in the object. It requires a calibration of the shim system, which is performed by the service during the installation. After positioning the object and running the first pilot scan the user has to acquire the field map by starting a special on-demand adjustment. For each scan that follows, the shims will be automatically calculated for a graphically selected volume if

specified so in the protocol. It is also possible to run scans with previously established shims, and to return to the default shims adjusted automatically at the beginning of the study. The system will automatically adjust the RF frequency after all shim changes.

1.8.7.2 Workflow

General

- Acquire the first scan (typically, a pilot image). The system will run a series of adjustments, among them – the iterative adjustment of the default “study shim”.
- In a new scan, open the Adjustment Platform, open the **B0 Map** adjustment, adapt the field of view if needed, press Start. When finished, leave the adjustment platform.
- Select the scan for which the shims should be calculated. Open Setup/Auto Shim card. The parameter Requested Shim controls the shim behavior. Its possible values are
 - **Current_Shim**: the shims will remain as set for the previous scan
 - **Study_Shim**: the shims will return to the result of the initial adjustment.
 - **Map_Shim**: the shims will be calculated to optimize the field homogeneity in the selected Shim Volume.
- Select **Map_Shim** and define the shim volume. Select the **Shape** of the shim volume (Cuboid, Cylinder, Ellipsoid) as it best suits your object. The volume can be shifted, resized and rotated in the geometry editor. When you select Automatic Shim Volume, the volume will be adapted to your voxel or the first slice package with a specified margin (Shim Volume Margin).
- You can reduce the order of calculated shims using the “**Shim up to**” option. This is needed in rare cases (mostly on micro-MRI systems) when the calculated shims exceed allowed power limits. The default value **AllShims** should be kept on BioSpec systems
- For localized spectroscopy, select **Iterative Correction**. This adds an optimization sequence for the linear shims that further improves the spectral resolution.
- Verify the **Status** on the Auto Shim card. “Mapshim ready” means all conditions for the shim calculation (calibration, map measurement) are fulfilled. Otherwise, a comment explaining the problem (e.g. “No map acquired”) will be visible

Simplified workflow with prepared protocols

You can save the preferred options described above, including the selection of Automatic shim Volume in a protocol. This makes the workflow much easier:

- Acquire the pilot scan
- In a new scan, acquire the B0 map in the adjustment platform
- Load your protocol, adapt the geometry of the method’s voxel or slice package, and start.

Workflow with X-nuclei

MAPSHIM is not active with nuclei other than 1H because their signal is generally too weak for the adjustment of frequency after the shim calculation. You have to acquire one scan using the 1H nucleus for the purpose of shim calculation with the required shim volume. You can then switch to the X nucleus in another scan and run it with the Current shim option.

1.8.7.3 Hints

- The field map measured on the adjustment platform can be viewed on Palette/Explorer/ Datasets.

- The intensity threshold for the map calculation can be set with the parameter **Map S/N** in the reconstruction card. If the threshold requires change, the B0 Map adjustment has to be repeated with the adapted threshold.
- Maps can also be measured by loading the FieldMap method to the scan list, which can be useful for setting up a good protocol. However, results obtained in this way cannot be used for shimming.
- The protocol for the B0 Map adjustment can be selected on the Adjustments tab of the configuration card.
- If the initial shim conditions are poor, the B0 map may be not quite reliable. In such case, one can provisionally shim the entire object with the first map, and acquire a new, more reliable one afterwards. It is always the last map acquired in the adjustment platform that is used for the shim calculation.
- When you select the shim volume, it is preferable to exclude regions of particularly strong field deviations (neighborhood air filled cavities, bigger bones, fat tissue). The B0 field in such locations will not improve much after shimming, but it will unnecessarily affect the shim fit in the majority of the shim volume.

1.9 Method Description

1.9.1 Common Parameters

Parameters controlling the measurement methods can be edited on one of the Parameter Cards in the right bottom of the Examination Card. The cards available for most methods are:

- **Routine** – Opens first and contains most often used parameters, such as the repetition time and image matrix size
- **Contrast** – Contains parameters relevant for image contrast, such as the flip angle and preparation modules in imaging methods
- **Preparation** – Water suppression and other preparation elements in spectroscopy methods
- **Spectroscopy** – Acquisition size, bandwidth and resolution in spectroscopy methods
- **Resolution** – Parameters controlling image resolution, acquisition matrix size and acceleration in imaging methods
- **Geometry** – Parameters controlling image geometry, including field of view, orientation, slice thickness
- **Sequence** – Bandwidth, RF pulses, spoilers, frequency offsets, and other “technical” parameters
- **Setup** – Parameters for manual sequence setup, such as receiver gain and shims
- **Reconstruction** – Parameters controlling the image reconstruction

Parameters appearing on these cards in most measurement methods are described in this chapter. Further, method-specific parameters and cards can be found in chapters describing each method.

1.9.1.1 Routine Card

Echo Time (typically, PVM_EchoTime) – Time between the center of the excitation pulse and the center of the echo, usually denoted TE in MRI literature, determining the T2 contrast of the sequence. In segmented sequences based on several echoes (e.g. RARE) this parameter describes the effective TE, i.e. the time of the echo which samples the center of k-space.

Repetition Time (PVM_RepetitionTime) – Time between consecutive excitation pulses of the same slice, usually denoted TR in MRI literature. In sequences where the excitation is repeated in segments, like FISP, this parameter describes the repetition time within a segment; a different parameter is usually available to control the repetition time of the whole segments. In most methods minimum TR depends on the number of slices.

Averages (PVM_NAverages) – Number of times the signal is accumulated prior to the storage on disk and the reconstruction, sometimes referred to as NEX in MRI jargon. The signal-to-noise ratio of images/spectra increases as the square root of the number of accumulations.

Repetitions (PVM_NRepetitions) – Number of repetitions (executions) of the experiment

Scan Time (PVM_ScanTimeStr) – Total duration of the experiment

Slice Package (PVM_NSpacks) – See [Geometry Card \[▶ 271\]](#)

Slices (PVM_SPackArrNSlices) – See [Geometry Card \[▶ 271\]](#)

Slice Orientation (PVM_SPackArrSliceOrient) – See [Geometry Card \[▶ 271\]](#)

Read Orientation (PVM_SPackArrReadOrient) – See [Geometry Card \[▶ 271\]](#)

Slice Thickness (PVM_SliceThick) – See [Geometry Card \[▶ 271\]](#)

Image Size (PVM_Matrix) – See [Resolution Card \[▶ 269\]](#)

Field of View (PVM_Fov) – See [Resolution Card \[▶ 269\]](#)

1.9.1.2 Diffusion Card

This card is present in methods using the diffusion module, in the current version – DtStandard, DtEpi and DtSpiral. Parameters on this card allow setting up different diffusion sensitizing schemes and defining directions and strength of diffusion gradients. The module allows, among others, the following types of experiments:

- Diffusion Weighted Imaging (DWI) with one value/direction of diffusion gradients
- Apparent diffusion constant (ADC) measurements with several (at least two) values of diffusion gradients
- Diffusion Tensor Imaging (DTI) experiments with several (at least six) directions of the diffusion gradient allowing the calculation of tensor components, main diffusion axis and diffusion anisotropy
- Diffusion tensor trace measurement with at least four gradient directions



Experiments with more than one direction of diffusion-sensitizing gradients require the PVMDTI license.

Principles

Diffusion is the process by which matter is transported from one part of a system to another as result of irregular Brownian motion. For this reason an additional transverse relaxation process causes irreversible signal loss due to translational diffusion in a static magnetic field gradient.

Using strong magnetic field gradient pulses during preparation periods in which the magnetization which generates the NMR signal is transversal, the signal attenuation due to a gaussian diffusion process follows an exponential decay $S_b = S_0 \cdot \exp(-b \cdot D)$.

The scalar diffusion coefficient D is usually expressed in units of mm^2/s . The diffusion weighting factor b is always a quadratic function of the diffusion gradient strength g and timing constants (i.e. $b = \gamma^2 \delta^2 g^2 (\Delta - \delta/3)$).

Detecting the signal S at different values of b allows the calculation of the diffusion constant.

Generally all gradient switching events during transverse magnetization periods have to be considered in order to calculate the correct b -values. Therefore not only gradient pulses used for diffusion sensitization but also imaging gradients as well as static field gradients (caused by bad shimming conditions or susceptibility variations) contribute to the b -value. However, appropriate gradient switching schemes of diffusion imaging sequences reduce the sensitivity to poor shims or susceptibility variations and simplify the calculation of b -values.

The DTI module described in this section offers variants of a Stejskal–Tanner diffusion preparation (see Reference [\[17\] ▶ \[69\]](#)) in which the b -value variation is established by alteration of the diffusion gradient strength and -direction. It should be always located during periods of completely refocused transverse magnetization as shown above. Subject to these conditions, the diffusion attenuation is separated into a constant part (caused by imaging gradients) and a variable part caused by gradients under control of the DTI module.

Since the brownian motion of spins in biological tissues is hindered or even restricted by obstacles (e.g. cellular borders), the average diffusion properties in an imaging voxel is generally direction dependent and reflects the microstructure of the imaged tissue. The direction dependent signal attenuation might be approximated by an extension of the diffusion equation leading to the following formula

$$S_b = S_0 \cdot \exp\left(-\sum_{i,j} b_{ij} \cdot D_{ij}\right) \quad i, j = r, p, s$$

The direction dependency of the diffusion constant might be described for uncharged matter by a symmetric (3x3) matrix expressed in the imaging coordinate system. Since a single gradient may only detect the projection of the brownian motion along the applied gradient direction, the direction dependency can be detected by variations of gradient-amplitudes as well as -directions. The direction dependency of the diffusion experiment can be described by the b -matrix b_{ij} . The DTI module offers the possibility to setup two dimensional diffusion experiments in which an arbitrary number of diffusion gradient directions as well as different diffusion gradient amplitudes (for each direction) may be specified.

Main

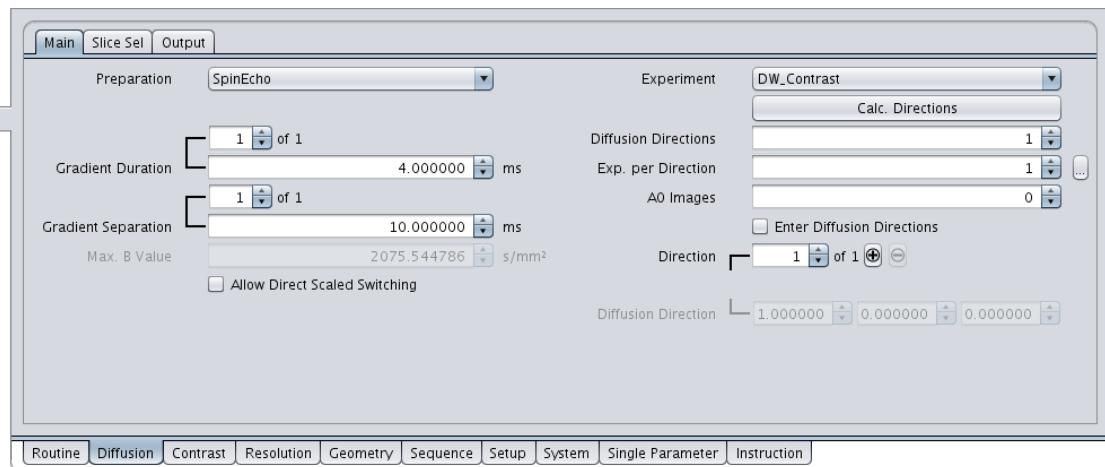


Figure 1.197: Diffusion Card Main

Preparation (PVM_DiffPrepMode) – The DTI module provides three preparation modes: SpinEcho, StimulatedEcho, and DoubleSpinEcho.

The SpinEcho mode sets up a slice selective refocusing 180 deg pulse surrounded by the diffusion gradients. In this mode the total duration of the diffusion module contributes to the minimum possible echo time (TE).

The StimulatedEcho mode sets up a mixing period surrounded by two slice selective 90 deg pulses. In this mode, the **Gradient Separation** might be modified without an effect to the minimum echo time, since it controls the mixing period. Only the **Gradient Duration** affects the minimum echo time. This mode should be chosen in any case where the T2 relaxation time is critical and/or longer diffusion times are desired.

The DoubleSpinEcho mode sets up a twice refocused double spin echo with diffusion weighting intervals that are effective also between the 180 deg pulses since the magnetization is always in the transverse plane. The duration and separation as well as the amplitude of the diffusion gradients are controlled in a special way that guarantees a total antisymmetric diffusion gradient switching scheme with respect to the module center. Furthermore the generation of a twice refocused echo requires a separation of the 180 deg pulses to be TE/2. This mode may be used to minimize distortions due to eddy current effects (if existant) and to cancel out the crossterm contribution between diffusion gradients and unknown background gradients in area of strong susceptibility induced inhomogenous area of the sample (e.g. close to the nose or ears of the animal).

Gradient Duration (PVM_DwGradDur) – Provides access to the δ of the diffusion experiment. This parameter is implemented as a 1-element array. Future versions (with different gradient switching schemes) may have more than one value.

Gradient Separation (PVM_DwGradSep) – Provides access to the Δ of the diffusion experiment. This parameter is implemented as a 1-element array. Future versions (with different gradient switching schemes) may have more than one value.

Max. B Value (PVM_DwMaxBval) – Non-editable parameter showing the maximum possible b-value. It depends for direct scaled switching not only on the timing parameters but also on the norm of the diffusion directions. The maximum b-value as well as the b-values per direction are calculated with respect to the diffusion gradients only. However, the effect of crossterms to slice and spoiler gradients is calculated for the b-matrix as well as their trace (both parameters are located in the **DiffOutput** class).

Allow Direct Scaled Switching (PVM_DwDirectScale) – Determines the coordinate system in which diffusion gradients are switched.

If selected, the diffusion gradients are not effected by gradient rotations performed to establish oblique slices. For this reason the norm (i.e. amount) of the diffusion direction vector is not limited to 1.0 which allows stronger b-values at given gradient durations.

If not selected (default), the norm of the diffusion gradient direction is limited to 1.0 at the expense of the efficiency of diffusion weighting for a given echo time.



⚠ CAUTION

- ▶ Direct Scaled Switching carries a potential risk of overheating the gradient coils.
- ▶ The DTI module does not constrain the method timing to prevent duty cycle violations in the case of Direct Scaled Switching. To make sure that the existing Protocol does not cause a duty cycle violation of the gradient system it should be tested with the simulation platform.
- ▶ Direct Scaled Switching can only be used at the customer's own risk.

Experiment (PVM_DwMeasMode) – Currently three different measurement modes are provided:

- DW_Contrast - In this mode there is no constraint on **Diffusion Directions** and **A0 Images**.

This mode is intended to setup diffusion experiments for mono exponential fitting. It is still possible to setup different diffusion directions to get a direction averaging effect in the mono exponential fitting as a function of the effective b-values (trace of b-matrix, see below).

- DW_MultishotTrace - In this mode the **Diffusion Directions** is fixed to 3 and the **A0 Images** must be at least 1.

A default initialization of diffusion directions is performed:
(1|1|-0.5), (1|-0.5|1), (-0.5|1|1).

This mode is intended to estimate the trace of the diffusion tensor. For this purpose the diffusion directions must be perpendicular to each other (this is not checked for!).

- DW_Tensor - The **Diffusion Directions** must be greater or equal to 6, the **A0 Images** must be at least 1. A default initialization of diffusion directions is performed: cyclic permutation of (1|+/-0.5|0).

This mode is intended to set up complete tensor measurements. For this purpose the diffusion directions must be non-collinear (this is not checked for!).

Calc. Directions (PVM_DwCalcDirs) – Press this button to set up a diffusion gradient direction scheme (stored in PVM_DwDir, see below) automatically for the current number of directions. The generated scheme assures an isotropic distribution of directions mini-mizing the directional dependency of the experimental error. The algorithm is based on electrostatic repulsion of charged pairs. Details about directional schemes may be found in [References ▶ 692](#).



Since the charged pair algorithm is time consuming, the diffusion direction scheme is calculated only when the button **Calc. Directions** is pressed. To prevent inappropriate diffusion direction sets, any time the number of directions (**Diffusion Directions**) is changed, **Calc. Directions** should be pressed to re-calculate the direction scheme.

Diffusion Directions (PVM_DwNDiffDir) – Number of different directions of the diffusion gradients

Exp. per Direction (PVM_DwNDiffExpEach) – Number of experiments with different diffusion weighting sequentially performed in each specified direction. The following group of vector parameters specifies the weighting for each experiment.

Diffusion Weighting (pop-up card):

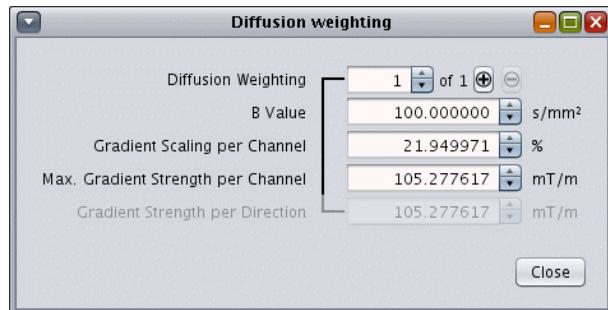


Figure 1.198: Diffusion Card Main Diffusion Weighting

Diffusion Weighting (PVM_DwNDiffExpEach) – Index of the experiment (running from 1 to Exp. per Direction)

B Value (PVM_DwBvalEach) – Diffusion weighting strength. Depends on the amplitude, duration and separation of diffusion gradient pulses. When changed, it leads to a change of the gradient amplitude.

Gradient Scaling per Channel (PVM_DwGradAmp) – Diffusion gradient amplitude in % of maximum. A modification of this parameter will affect the b-value

Max. Gradient Strength per Channel (PVM_DwGradStr) – Diffusion gradient amplitude in mT/m

Gradient Strength per Direction (PVM_DwEffGradStr) – This parameter is always visible but non-editable. In case of non direct scaled switching it is identical to PVM_DwGradStr. In case of direct scaled switching the effect of the norm (which might be > 1.0) is converted to an effective gradient strength.

A0 Images (PVM_DwAoImages) – Number of images acquired without diffusion gradients. In experiments with a large number of high b-values (e.g. high number of diffusion directions and 1 b-value per direction) the A0 reference point might be underestimated if set to 1.

Enter Diffusion Directions (PVM_DwEnterDiffDir) – If selected the parameter **Diffusion Direction Input** is visible (and editable).

Direction (PVM_DwNDiffDir) – Number of different directions of the diffusion gradients

Diffusion Direction Input (PVM_DwDirInput) – Array of 3-component vectors to set up diffusion directions. This array is only visible if **Enter Diffusion Directions** (PVM_DwEnterDiffDir) is selected. Each vector represents one direction. At least one component has to be greater than 0. Each component is constrained to lie in the interval [-1,1]. In the default case (i.e. **Allow Direct Scaled Switching** is not selected) the directions are specified in the r,p,s- coordinate system. Otherwise (i.e. when **Allow Direct Scaled Switching** is selected) the directions are specified in the x,y,z-coordinate system. For example, (1|0|0) corresponds to the read direction if direct scaled switching is not selected, and to the x- direction if direct scaled switching is selected. Each input of that array will be immediately transferred to the 3-component vector array PVM_DwDir (see below). This transfer is combined with a scaling procedure to get the final diffusion direction vectors PVM_DwDir with a unified norm.

Diffusion Direction (PVM_DwDir) – Non-editable array of 3-component vectors defining the diffusion gradient directions entered in PVM_DwDirInput. Each component is constrained to lie in the interval [-1,1]. Compared with PVM_DwDirInput all vectors are scaled to have the same norm. The result of this scaling procedure depends on the setting of the parameter PVM_DwDirectScale:

- In the default case (PVM_DwDirectScale is not selected) the norm for all direction vectors becomes 1.0 (PVM_DwEffGradStr = PVM_DwGradStr, see later).
- In the exceptional case (PVM_DwDirectScale is selected) the norm lies between $\sqrt{1.0} = 1.0$ and $\sqrt{3.0} = 1.57$ depending on the chosen directions. The maximum diffusion gradient strength (norm = 1.57) is achieved when the following directions are chosen (or a selection of it):
 - (+1.0|+1.0|+1.0), (-1.0|+1.0|+1.0), (-1.0|-1.0|+1.0),
 - (+1.0|-1.0|+1.0),
 - (+1.0|+1.0|-1.0), (-1.0|+1.0|-1.0), (-1.0|-1.0|-1.0), (+1.0|-1.0|-1.0).

Choosing such directions, the Max. B Value is 3 times stronger than in the non direct scaled case (see PVM_DwEffGradStr \geq PVM_DwGradStr, see later). When setting one of the components to zero (e.g. (+0.0|+1.0|+1.0) instead (+1.0|+1.0|+1.0)) the Max. B Value is 2 times stronger than in the non direct scaled case. When setting PVM_DwEnterDiffDir from selected to not selected the current values of PVM_DwDir will be transferred back to PVM_DwDirInput (without any scaling). The result can be checked after the next selecting of PVM_DwEnterDiffDir.

Slice Selection (Slice Sel)

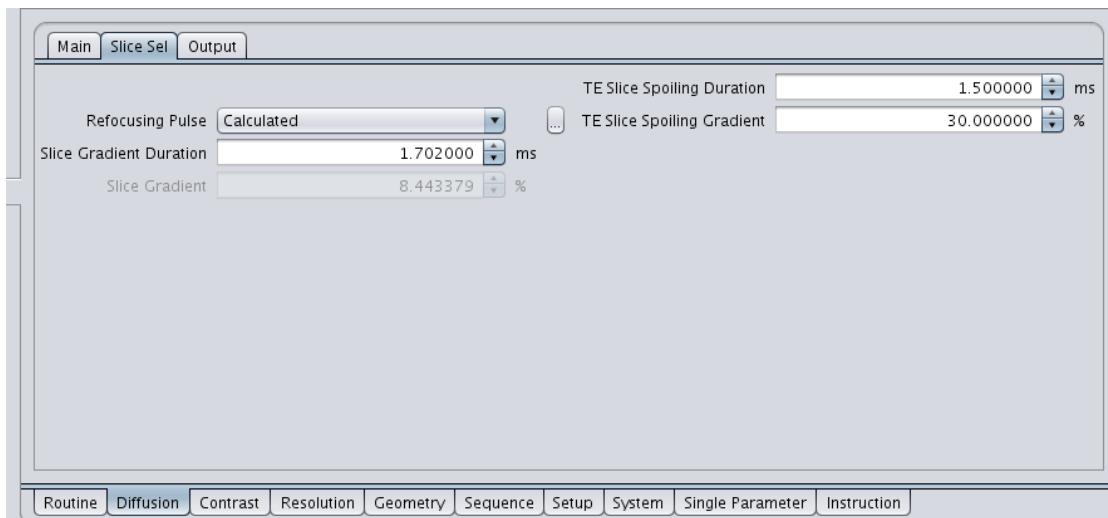


Figure 1.199: Diffusion Card Slice Sel

Refocusing Pulse (PVM_DwRfcPulse1Enum) – Enumeration parameter to choose one of the refocusing pulses installed on the system, applicable in the spin-echo and double-spin echo preparation

Excitation Pulse (PVM_DwExcPulse1Enum) – Enumeration parameter to choose one of the excitation pulses installed on the system, applicable in the stimulated echo preparation

Slice Gradient Duration (PVM_DwSliceGradDur) – Duration of the slice selection gradient applied during the RF pulses. It is possible to modify this duration within the limits of [min,min +4*rise time]. The minimum is defined by the actual duration of the RF pulse. With the help of this parameter a certain duration of the slice gradient plateau between the gradient switching event of the slice gradient and the start of the RF pulse can be specified. By default, the minimum duration is set.

Slice Gradient (PVM_DwSliceGrad) – Amplitude of the slice selection gradient

TE Slice Spoiling Duration (PVM_TeDwSliceSpoilGradDur) – Duration of the slice spoiler gradients around the refocusing pulse in the spin-echo mode, or during the echo periods in the stimulated echo mode

TE Slice Spoiling Gradient (PVM_TeDwSliceSpoilGrad) – Amplitude of the slice spoiler gradients (expressed in% of maximum)

Output

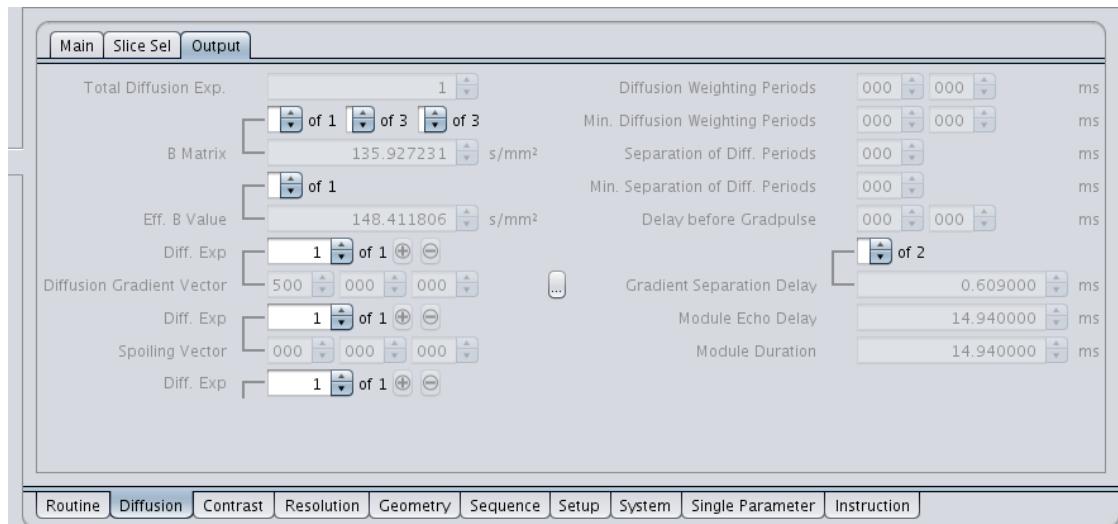


Figure 1.200: Diffusion Card Output

Total Diffusion Exp. (PVM_DwNDiffExp) – Is calculated as

$$N_D = N_{A0} + N_{Dir} \cdot N_{Dea}$$

where N_D is the total number of diffusion experiments, N_{A0} is the number of A0 images, N_{Dir} is the number of diffusion directions and N_{Dea} is the number of diffusion experiments in each diffusion direction.

B Matrix (PVM_DwBMat) – B-matrix for each diffusion experiment

$$[B_k] = \begin{bmatrix} b_{rrk} & b_{rpk} & b_{rsk} \\ b_{prk} & b_{ppk} & b_{psk} \\ b_{srk} & b_{spk} & b_{ssk} \end{bmatrix} \quad (k = 1, 2, \dots, N_D)$$

This B-Matrix (implemented as symmetric 3x3 matrix array of size N_D) is calculated for each diffusion experiment in the imaging coordinate system (r,p,s). The gradient ramps as well as crossterms to the amplitude of the slice and slice spoiler gradients are considered in this calculation. In case of direct scaled switching the x,y,z coordinates of the diffusion gradient direction are transformed to the r,p,s coordinate system before the calculation is done. Please note that since the spoiler and slice selection gradients also contribute to the diffusion attenuation, not all entries of the b-matrix associated with the A0 experiments are 0. However, their contribution is usually small (except for large spoiler gradients or microimaging systems).

Eff. B Value (PVM_DwEffBval) – The trace of the b-matrix (is implemented as an array of size N_D):

$$b_k = \sum_{i=r,p,s} b_{iik} \quad (k = 1, 2, \dots, N_D)$$

In homogenous isotropic media, this parameter may be used for a mono exponential fit of the signal as a function of the b-value. There are slight differences between the b-values as specified in PVM_DwBvalEach (see above) and the values of this parameter since the effect of the imaging gradients is now considered.

Diffusion Gradient Vector (PVM_DwGradVec) – Parameter of dimension $N_D \times 3$ specifying the diffusion gradient amplitudes in the x,y,z coordinate system. This parameter is used in the pulse-program part of the DTI module in the case of direct scaled switching.

Diffusion Vector

Diffusion Read/Phase/Slice Gradient (PVM_DwGradRead / PVM_DwGradPhase / PVM_DwGradSlice) – Parameters of dimension N_D specifying the diffusion gradient amplitudes in read/phase and slice direction in the case of non direct scaled switching. In this case these parameters are used in the pulse-program part of the DTI module.

Spoiling Vector (PVM_DwSpDir) – Array of spoiling vectors used to suppress unwanted signals. The array size is the total number of diffusion experiments, the direction and amplitude of the spoiling vector components are calculated automatically considering the direction and amplitude of the diffusion gradients to prevent suboptimal spoiling due to possible compensation of gradient areas for some directions and amplitudes of the diffusion gradients. The calculation of the spoiling vector guarantees the same or even more spoiling capacity that has been optimized for the A0 images (i.e. for zero diffusion gradient amplitude). The contribution to the diffusion weighting of the spoiling gradients including crossterms to the diffusion gradients are considered in the calculation of the b-matrix.

Module Echo Delay (PVM_DwModEchDel) – Contribution of the DTI module to the echo time. For spin echo preparation it is identical to the total module duration.

Module Duration (PVM_DwModDur) – Total duration of the DTI module

1.9.1.3 Contrast/Preparation Card

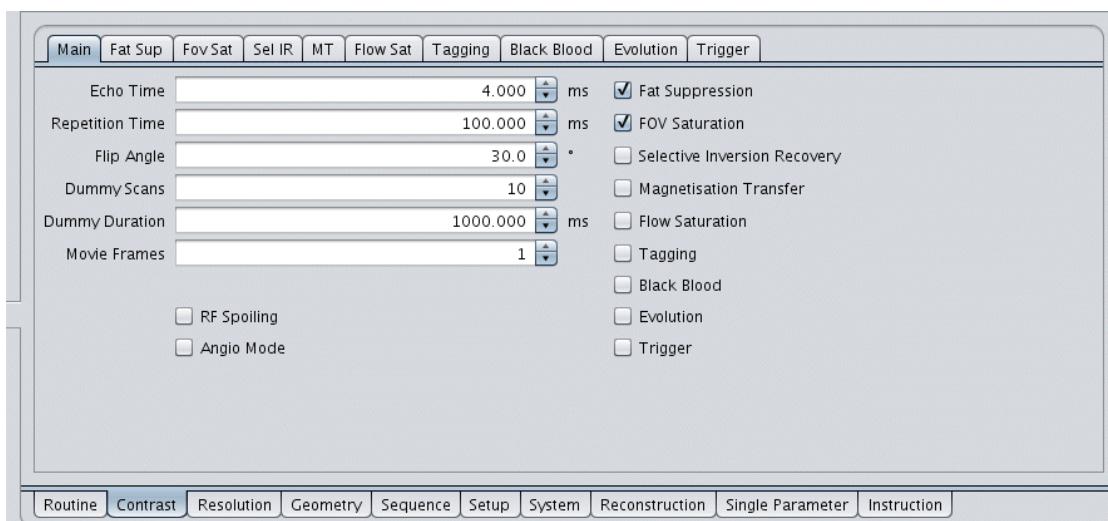


Figure 1.201: Contrast Card Main

Echo Time (PVM_EchoTime) – See [Routine Card ▶ 241](#)

Repetition Time (PVM_RepetitionTime) – See [Routine Card ▶ 241](#)

Dummy Scans (PVM_DummyScans) – Number of repetitions of the sequence without signal acquisition used to establish a steady state, which is particularly important in segmented methods, such as [RARE \(Rapid Acquisition with Relaxation Enhancement\) ▶ 309](#).

Dummy Duration (PVM_DummyScansDur) – Duration of the dummy scan loop. Should be set to at least T1 to guarantee a steady signal.

The buttons on the right-hand side activate the correspondent contrast modules. Parameters of each module can be found on one of the following subcards:

- **Fat Suppression** (PVM_FatSupOnOff)
- **FOV Saturation** (PVM_FovSatOnOff)

- **Selective Inversion Recovery** (PVM_SellrOnOff)
- **Magnetization Transfer** (PVM_MagTransOnOff)
- **Tagging** (PVM_TaggingOnOff)
- **Black Blood** (PVM_BIBloodOnOff)
- **Flow Saturation** (PVM_InFlowSatOnOff)
- **Evolution** (PVM_EvolutionOnOff)
- **Trigger** (PVM_TriggerModule)
- **Trigger Out** (PVM_TriggerOutOnOff)
- **Water Suppression (PVM_WsMode)**
- **Outer Volume Suppression** (PVM_OvsOnOff)
- **Decoupling** (PVM_DecOnOff)
- **NOE** (PVM_NoeOnOff)

1.9.1.3.1 Fat Suppression (Fat Sup)

Principles

A frequency-selective 90 degree pulse is applied to a frequency offset of -3.5 ppm relative to water. If the bandwidth of the pulse exceeds 7 ppm, the frequency offset will be increased to avoid saturation of water. Transverse magnetization produced by the pulse is suppressed with a gradient spoiler.

Applications

Reduction of chemical shift artifacts (EPI, FISP), suppression of fat appearing bright in T1 weighted images (especially at higher fields)



Because of the fixed ppm-offset this module is intended to be used only for protons (1H nuclei).

Parameters

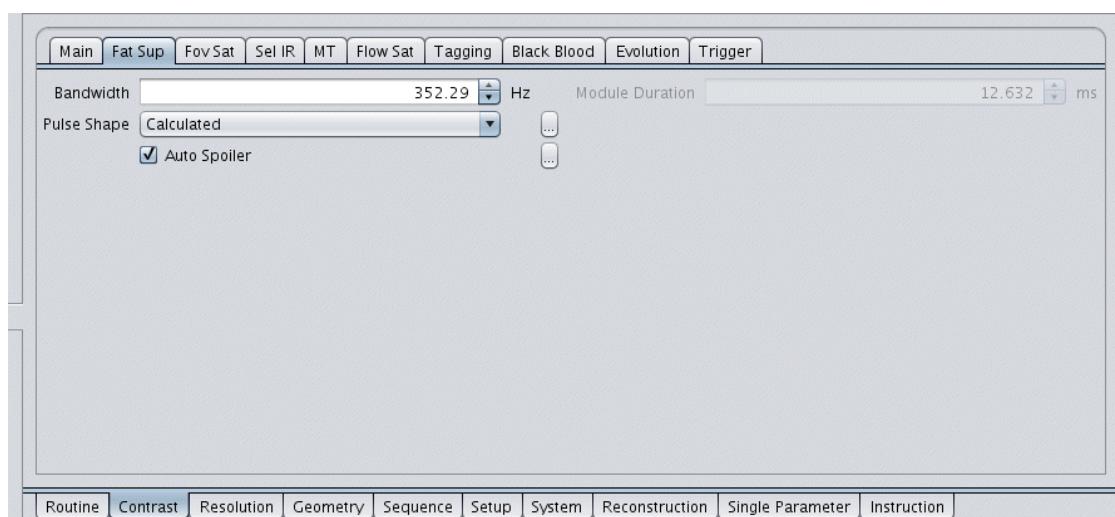


Figure 1.202: Contrast Card Fat Sup

Bandwidth (PVM_FatSupBandWidth) – Bandwidth of the RF excitation

Pulse Shape (PVM_FatSupPulEnum) – Shape of RF pulse. Properties of the pulse may be edited with a pop-up menu. See [RF Pulses \[▶ 273\]](#) for details of RF pulse parameters.

Auto Spoiler (PVM_FatSupSpoil.automatic) – If selected, the strength and duration of the spoiler is automatically calculated. Otherwise, the user may edit spoiler details using the associated pop-up menu. See [Spoilers \[▶ 275\]](#).

Module Duration (PVM_FatSupModuleTime) – Duration of the fat suppression sequence, non-editable.

1.9.1.3.2 Field-of-View Saturation (Fov Sat)

Principles

Slice selective 90 deg pulses are applied to selected slices. Transverse magnetization is dephased using a spoiler gradient of variable duration and amplitude. The saturation slice orientations may be set using the Geometry Editor in case the saturation slices parameter PVM_FovSatOnOff is set to `On`. However, similar to the slice geometry, the principal directions of the saturation slices may also be specified in the `Sat_Slice_Parameter` class.

Applications

Outer Volume suppression in CSI, free saturation

Since thick slices are usually excited, it is recommended to use a sech or sinc10H.exc pulse (large bandwidth, sharp profile, low chemical shift artifacts)

Parameters

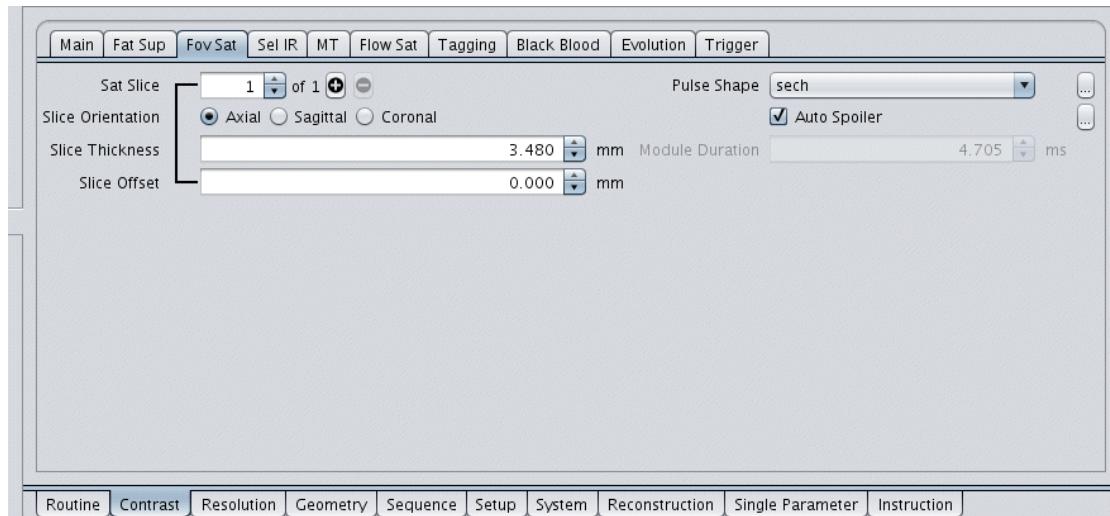


Figure 1.203: Contrast Card Fov Sat

Slice Orientation (PVM_FovSatSliceOri) – Main orientation of the saturation slices



Oblique orientation of saturation slices can be set up only in the Geometry Editor (in the saturation slices mode).

Slice Thickness (PVM_FovSatThick) – Thickness of saturation slices

Slice Offset (PVM_FovSatOffset) – Distance of the saturation slice [mm] to the isocenter of the patient coordinate system. Although this parameter is editable, the slice distances should be set up in the **Geometry Editor**.

Pulse Shape (PVM_FovSatPulEnum) – Shape of RF pulse. Properties of the pulse may be edited with a pop-up menu. See [RF Pulses ▶ 273](#) for details of RF pulse parameters.

Auto Spoiler (PVM_FovSatSpoil.automatic) – If selected, the strength and duration of the spoiler is automatically calculated. Otherwise, the user may edit spoiler details using the associated pop-up menu. See [Spoilers ▶ 275](#).

Module Duration (PVM_FovSatModuleTime) – Duration of the FOV saturation sequence, non-editable

1.9.1.3.3 Slice-selective Inversion Recovery (Sel IR)

Principles

The module provides a train of selective inversion RF pulses followed by a recovery delay. The module is used in methods in which all slices are first inverted and then acquired whereby each slice has the same inversion time and the same recovery time.

Applications

T1 contrast enhancement (FLAIR)

Parameters

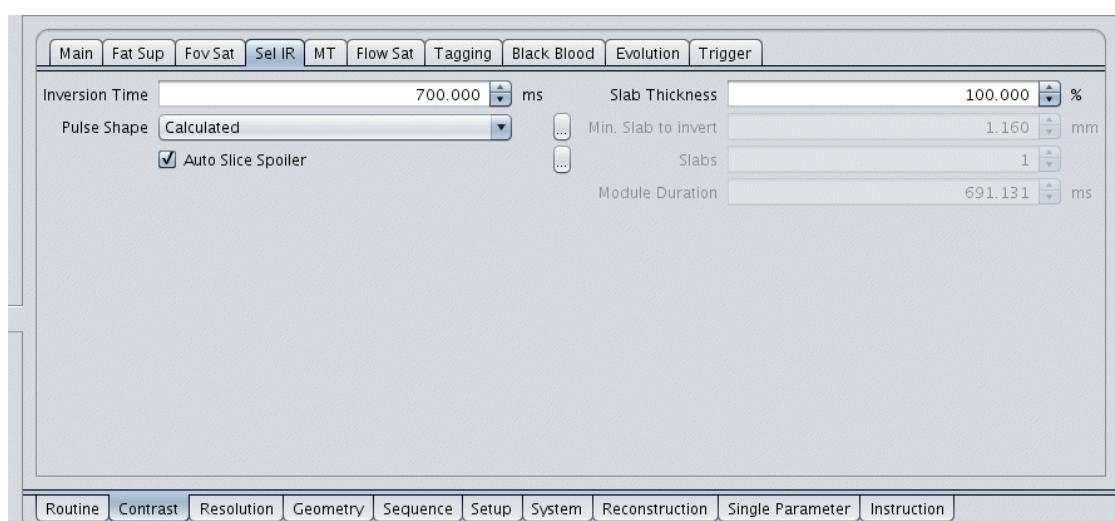


Figure 1.204: Contrast Card Sel IR

Inversion Time (PVM_SellrInvTime) – Inversion delay. The inversion delay is the same for each slice.

Pulse Shape (PVM_SellrPulEnum) – Shape of RF pulse. Properties of the pulse may be edited with a pop-up menu. See [RF Pulses ▶ 273](#) for details of RF pulse parameters.

Auto Slice Spoiler (PVM_SellrSpoiler.automatic) – If selected, the strength and duration of the spoiler is automatically calculated. Otherwise, the user may edit spoiler details using the associated pop-up menu. See [Spoilers ▶ 275](#).

Slab Thickness (PVM_SellrSlabThick) – Thickness of each slab. The parameter is set in percent of the minimum thickness of the slab.

Min. Slab to invert (PVM_SellrMinThick) – Minimum thickness of the slabs. Defined by the method (input of the module updater).

Slabs (PVM_SellrNSlabs) – Number of different inverted slabs. The parameter is set by the method in which the module is inserted (input of the module updater) and is not editable. The name slab is used having the possibility to invert selectively a slice or a package of slices with one inversion pulse.

Module Duration (PVM_SellrModuleTime) – Duration of the selective inversion module, non-editable

1.9.1.3.4 Magnetization Transfer (MT)

Principles

An off resonance shaped pulse or series of pulses are used to saturate short T2 components (e.g. bound water).

The pulse gain is calculated from the RF power parameter [μT] calibrated by the **MTC ref pulse gain** parameter. This parameter has a default value of 30 dB or the amplitude of a 1 ms 90 deg rectangular pulse (if calibrated).



This module is intended to be used for protons (1H nuclei) only.

Applications

Contrast enhancement in angiography sequences to saturate water signal from bound tissue.

Parameters

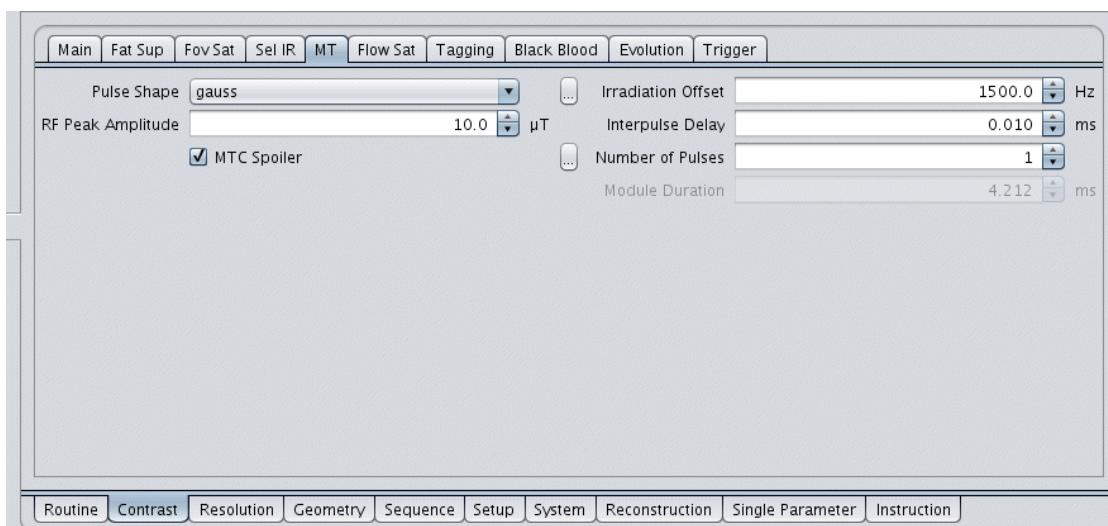


Figure 1.205: Contrast Card MT

Pulse Shape (PVM_MagTransPulse1Enum) – Shape of RF pulse. Properties of the pulse may be edited with a pop-up menu. See [RF Pulses \[273 \]](#) for details of RF pulse parameters.

RF Peak Amplitude (PVM_MagTransPower) – Peak RF power in units of the B1 field. This value will be used to set the attenuation field of the MTC pulse (since the flip angle field is not of interest for this specific application).

MTC Spoiler (PVM_MagTransSpoil.automatic) – If selected, the strength and duration of the spoiler is automatically calculated. Otherwise, the user may edit spoiler details using the associated pop-up menu. See [Spoilers \[▶ 275\]](#).

Irradiation Offset (PVM_MagTransOffset) – Frequency offset (relative to the adjusted center frequency) of the magnetization transfer pulses.

Interpulse Delay (PVM_MagTransInterDelay) – Time delay between preparation pulses

Number of Pulses (PVM_MagTransPulsNumb) – Number of preparation pulses

Module Duration (PVM_MagTransModuleTime) – Duration of the magnetization transfer module, non-editable

1.9.1.3.5 Flow Saturation (Flow Sat)

Principles

One or two saturation slices parallel to the imaging slices are excited using spatial selective 90° pulses. Transverse magnetization is dephased using a spoiler gradient of variable duration and amplitude. The position of saturation slices may be specified as the gap between the saturation slice and the imaging slice. In a time-of-flight angiography sequence this module allows selective enhancement of vessels depending on the flow direction.

Parameters

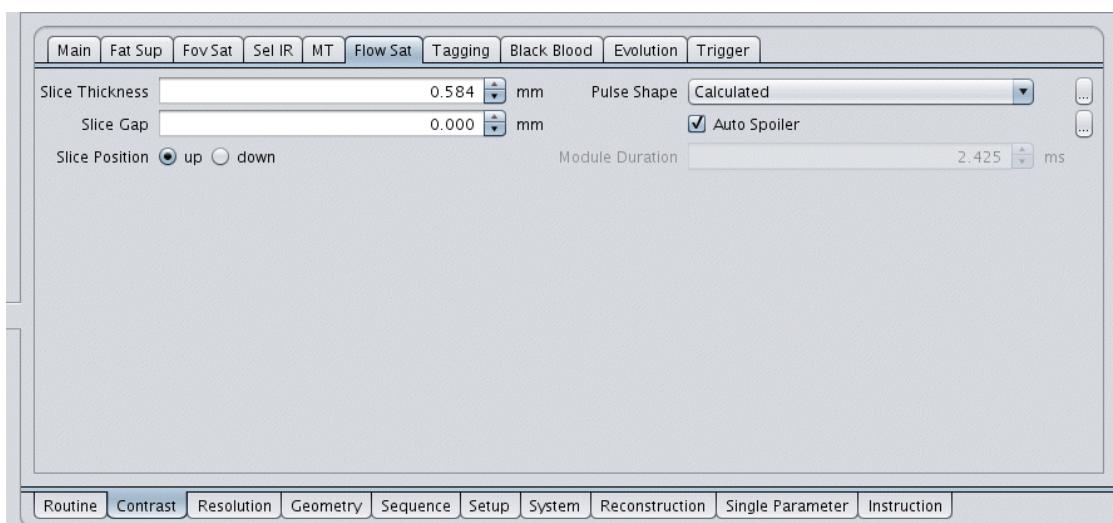


Figure 1.206: Contrast Card Flow Sat

Slice Thickness (PVM_InFlowSatThick) – Thickness of the saturation slice

Slice Gap (PVM_InFlowSatSliceGap) – Distance between the center of the imaging slice and the center of the corresponding inflow saturation slice

Slice Position (PVM_InFlowSatPos) – Choice between Up and Down to decide on which side of the imaging slice the saturation is positioned

Pulse Shape (PVM_FlowSatPulEnum) – RF Pulse shape for saturation

Auto Spoiler (PVM_InFlowSatSpoil.automatic) – If selected, the strength and duration of the spoiler is automatically calculated. Otherwise, the user may edit spoiler details using the associated pop-up menu. See [Spoilers \[▶ 275\]](#).

Module Duration (PVM_InFlowSatModuleTime) – Duration of the flow saturation module, non-editable

1.9.1.3.6 Tagging

Principles

A pulse train combined with a gradient pulse is applied to create saturated stripes in the image plane. The stripes are distorted in the presence of motion or field variations.

Applications

Tagging allows

- to follow the motion of the heart wall in cardiology
- to shim in 2D mode in methods like EPI

Parameters

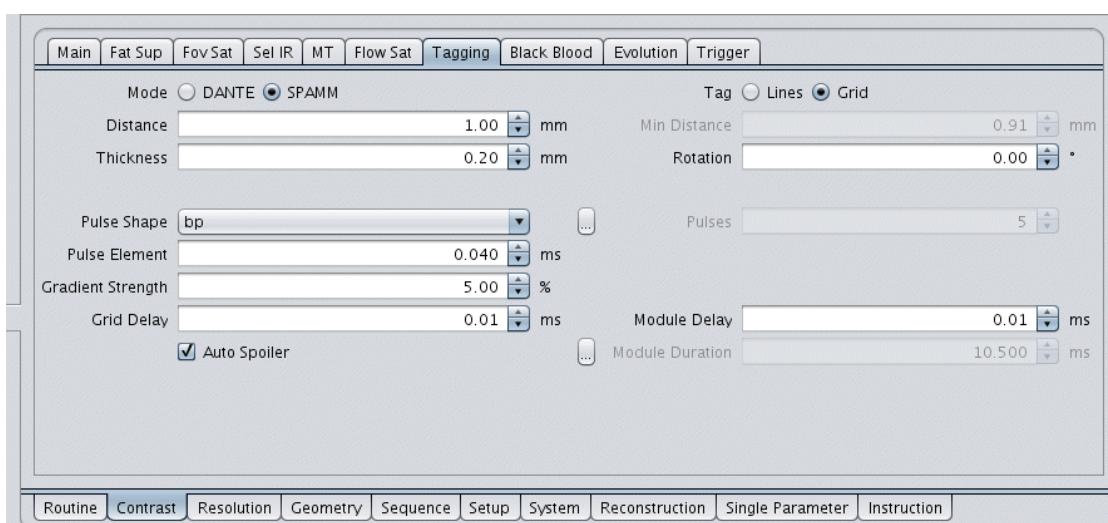


Figure 1.207: Contrast Card Tagging

Mode (PVM_TaggingMode) – Two tagging modes are available: SPAMM and DANTE.

Distance (PVM_TaggingDistance) – Distance between two tagging lines

Thickness (PVM_TaggingThick) – Defines the thickness of the tagging lines (at least two image pixels)

Offset 1 (PVM_TaggingOffset1) – Shift of the tagging pattern in the readout direction

Pulse Shape (PVM_TaggingPulEnum) – Choice of RF pulses usable for Tagging

Pulse Element (PVM_TaggingPulseElement) – Duration of an element of the pulse train. See [RF Pulses](#) [▶ 273] for pulse details.

Gradient Strength (PVM_TaggingGradientStrength) – Amplitude of the tagging gradient in % of the maximum value

Grid Delay (PVM_TaggingGridDelay) – Delay between the two pulse trains in Tagging_grid mode

Auto Spoiler (PVM_TaggingSpoiler.automatic) – If selected, the strength and duration of the spoiler is automatically calculated. Otherwise, the user may edit spoiler details using the associated pop-up menu. See [Spoilers](#) [▶ 275].

Tag (PVM_TaggingDir) – Defines which directions are tagged (Lines or Grid)

Min Distance (PVM_TaggingMinDistance) – Minimum distance between two lines depending on the tagging thickness

- Rotation** (PVM_TaggingAngle) – Defines the orientation of the lines or the grid in the image plane
- Offset 2** (PVM_TaggingOffset2) – Shift of the saturation pattern in the phase direction
- Pulses** (PVM_TaggingPulseNumber) – Number of the elements of the tagging pulse train
- Module Delay** (PVM_TaggingDelay) – Delay between the end of the tagging pulses and the first excitation pulse of the imaging method
- Module Duration** (PVM_TaggingModuleTime) – Duration of the tagging module

1.9.1.3.7 Black Blood

Principles

A double inversion (selective - non selective) preparation module used to enhance the tissue signal compared to the blood signal. Due to the flow blood experiences only one of the pulses and gets nulled by inversion recovery.

Applications

Cardiac imaging

Parameters

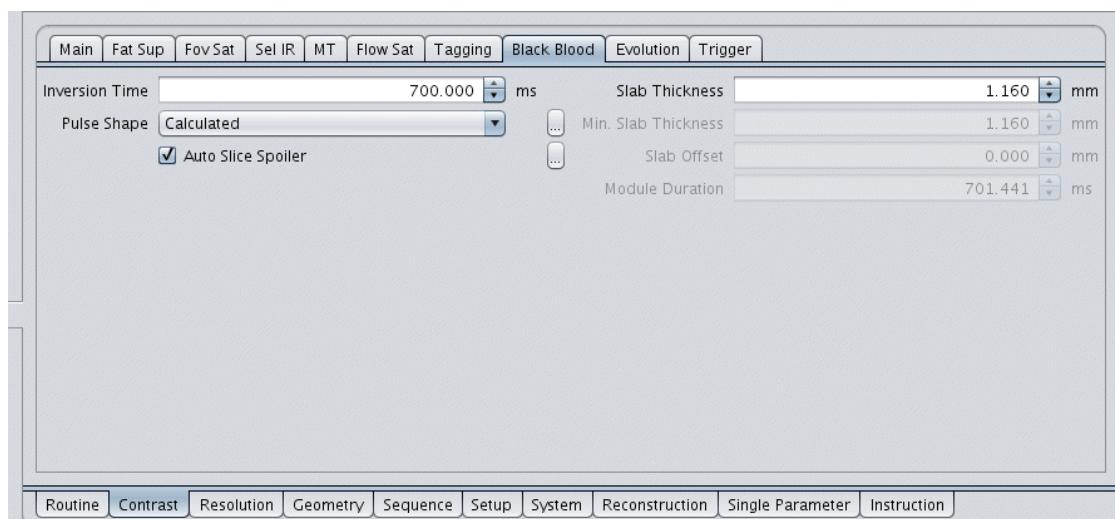


Figure 1.208: Contrast Card Black Blood

Inversion Time (PVM_BIBloodInvTime) – Time between the second inversion pulse and the first excitation pulse. It is typically set to the zero crossing time of the blood.

Pulse Shape (PVM_BIBloodPulEnum) – Shape of the inversion RF pulse

Auto Slice Spoiler (PVM_BIBloodSpoiler.automatic) – If selected, the strength and duration of the spoiler is automatically calculated. Otherwise, the user may edit spoiler details using the associated pop-up menu. See [Spoilers ▶ 275](#).

Slab Thickness (PVM_BIBloodSlabThick) – Thickness of the inverted slabs. The slab can be thicker than the slices to invert.

Min. Slab Thickness (PVM_BIBloodMinThick) – The minimum slab thickness is fixed by the method depending on the slices to invert.

Slab Offset (PVM_BIBloodSlabOffset) – Defines the position of the center of the slab [mm]. It corresponds to the offset of the slice or the slice package to invert.

Module Duration (PVM_BIBLoodModuleTime) – Duration of the black blood module

1.9.1.3.8 Evolution

Principles

The module is used to insert an additional repetition loop in the method with a delay between the experiments.

Applications

Dynamic studies

Parameters

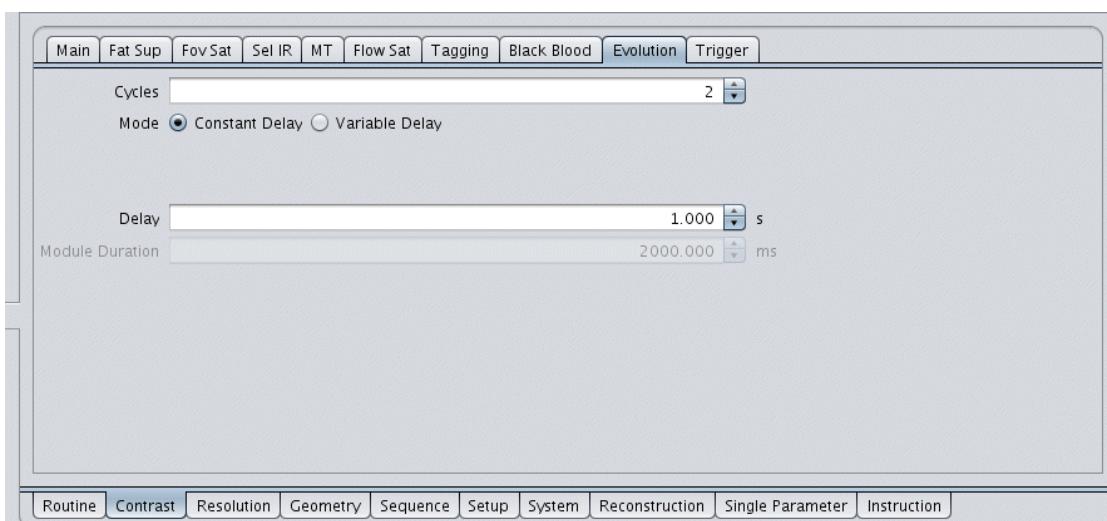


Figure 1.209: Contrast Card Evolution

Cycles (PVM_NEvolutionCycles) – Defines the number of repetitive executions of the experiment.

Mode (PVM_EvolutionMode) – Two modes are available to set the delays between experiments: Constant_Delay mode and Variable_Delay mode.

Delay (PVM_EvolutionDelay or PVM_EvolutionTime) – Parameter corresponding to the list of delays in seconds between the experiment repetitions. In Constant_Delay mode, the parameter is a single number; in Variable_Delay mode, the parameter is an array.

Module Duration (PVM_EvolutionModuleTime) – Sum of all delays

1.9.1.3.9 Trigger

Principles

The module is used to synchronize the sequence with external events. These events are provided as external TTL signals to the BNC connector labelled “ECG TRIG” at the spectrometer panel. Active-low logic is used (low voltage triggers the sequence).

Parameters

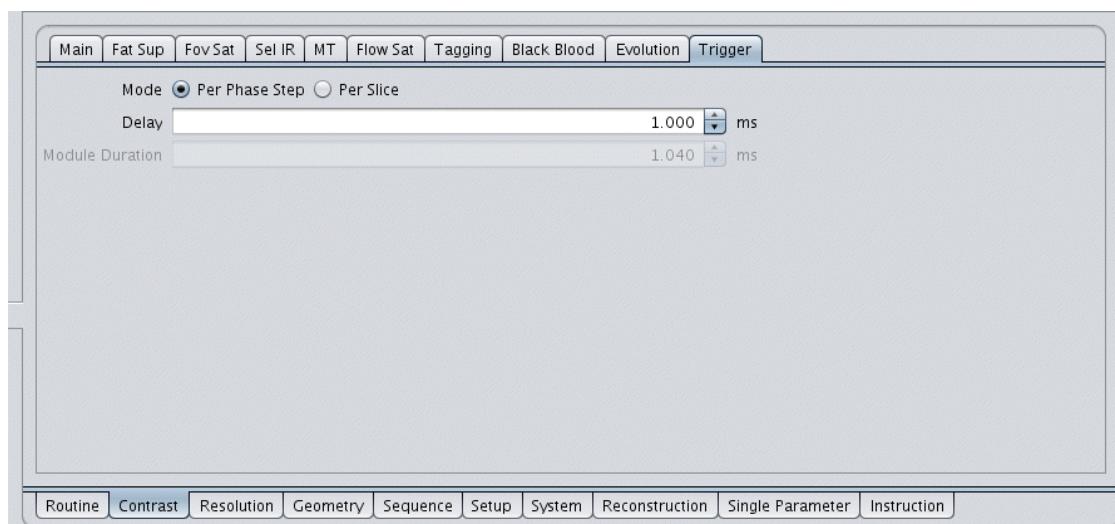


Figure 1.210: Contrast Card Trigger

Mode (PVM_TriggerMode) – The operator may decide which of two loops of the experiment may be synchronized with the TTL trigger signal (Per Phase Step or Per Slice).

Delay (PVM_TriggerDelay) – Delay in the pulse program after the trigger event

Module Duration (PVM_TriggerModuleTime) – Duration of the trigger module



If the trigger module is activated in the absence of an external triggering signal, the sequence does not start.

1.9.1.3.10 Trigger Out

Principles

The module is used to generate TTL pulses to synchronize external devices with the pulse program (e.g. for visual stimulation in fMRI). The pulse is generated in active-low TTL logic (on = 0 Volts) at the output TTL1.

Parameters

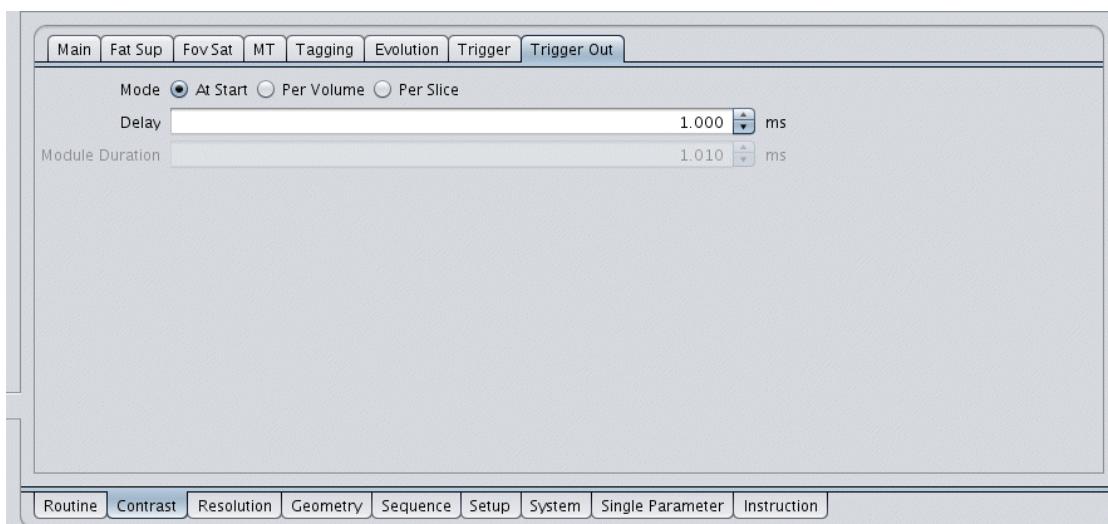


Figure 1.211: Contrast Card Trigger Out

Mode (PVM_TriggerOutMode) – Controls the TTL pulse generation frequency. Possible values are:

- At Start – A single TTL pulse will be generated at the beginning of the pulse program (precisely, at the line where TrigOutStart.mod occurs).
- Per Volume – A single TTL pulse will be generated for each volume (where TrigOutVolume.mod occurs in the pulse program).
- Per Slice – TTL pulses will be generated for each slice acquisition (where TrigOutSlice.mod occurs in pulse program).

Delay (PVM_TriggerOutDelay) - Duration of the trigger output pulse [ms]. This delay is also part of the pulse sequence.

Module Duration (PVM_TriggerOutModuleTime) – Duration of the trigger out module

1.9.1.3.11 Water Suppression (Water Sup)

Principles

Frequency selective pulses combined with spoiler gradient are applied to suppress the signal of the solution solvent (typically water). Two modes are available:

CHESS and VAPOR

Applications

Solvent (water) suppression in the spectroscopy methods PRESS, CSI, NSPECT

Parameters

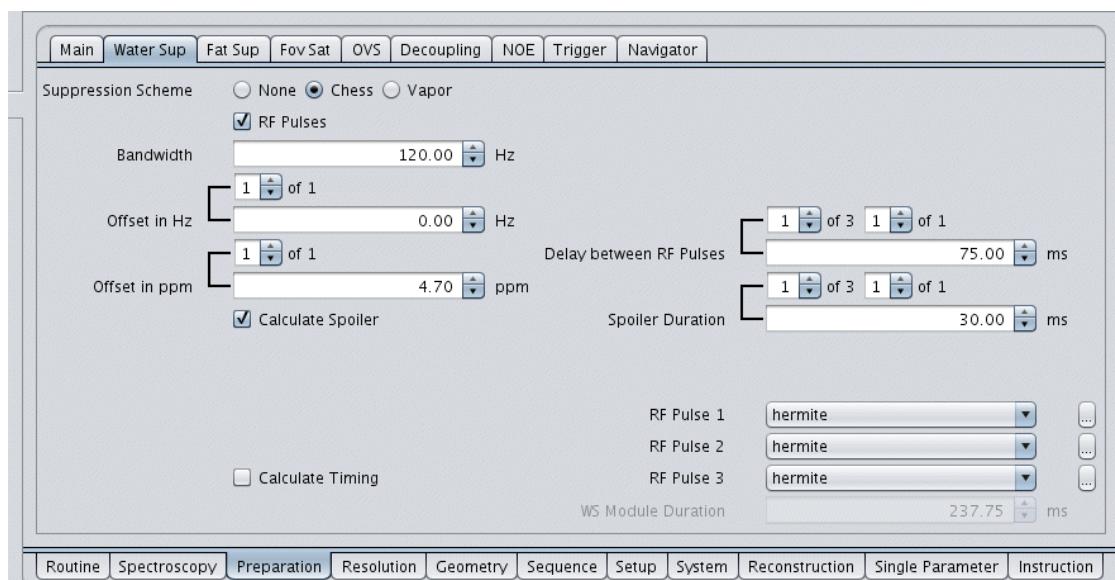


Figure 1.212: Preparation Card Water Sup (Chess Mode)

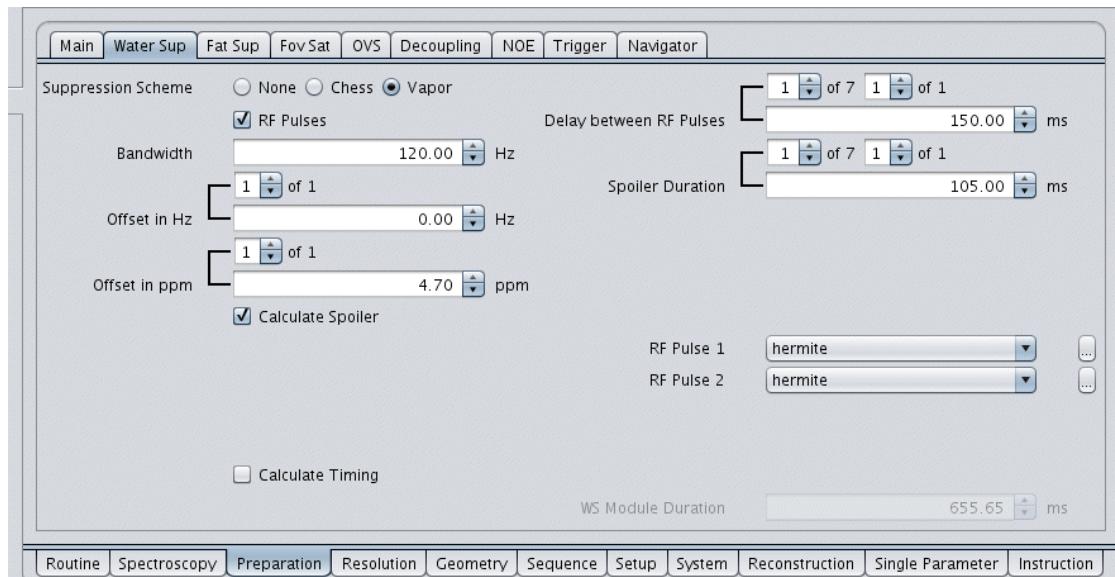


Figure 1.213: Preparation Card Water Sup (Vapor Mode)

Suppression Scheme (PVM_WsMode) – Selection of the water suppression scheme. One might choose between `None`, a general three pulse scheme `Chess` or a seven pulse `Vapor` scheme.

RF Pulses (PVM_WsOnOff) – The RF pulse of the water suppression scheme can be switched off while keeping the timing and the gradient scheme active. This is a useful setting for the acquisition of navigator scans.

Bandwidth (PVM_WsBandwidth) – Changing the **Bandwidth** parameter is a quick way to change the bandwidths of all RF pulses involved in the water suppression scheme. The value represents the full width at half maximum of each pulse.

Offset in Hz/ppm (PVM_WsOffsetHz, PVM_WsOffsetPPM) – The frequency offset of the suppression pulses can be selected. This allows you to suppress resonance lines other than the water resonance in a ¹H spectroscopic experiment.

Calculate Spoiler (PVM_WsCalcSpoiler) – On/Off parameter controlling the calculation mode of the parameter **Spoiler Strength** (see next parameter). The spoiler gradients strengths are calculated based on the permitted maximum strengths to minimize refocusing of unwanted coherency.

Spoiler Strength (PVM_ChSpoilerStrength) – If PVM_WsCalcSpoiler is not selected a single input value can be specified in the first element of the array as starting point for the calculation of all spoilers.

Spoiler Strength (PVM_VpSpoilerStrength) – If PVM_WsCalcSpoiler is not selected an array of spoiler gradient values can be specified between 0% and a maximum value.

Calculate Timing (PVM_WsCalcTiming) – If selected, the timing of the suppression spoiler gradients is optimized to suit the timing of the suppression pulse sequence.

Average T1 (PVM_WsMeanT1) – Estimation of T1 used for the calculation of timing

Delay between RF Pulses (PVM_ChInterPulseDelay, PVM_VpInterPulseDelay) – The intervals between the various RF pulses of the water suppression scheme have a strong effect on the quality of the water suppression and can be selected with an array of seven (Vapor) or three (Chess) entries. The RF pulse duration and the use of interleaved outer volume suppression influences the minimum possible delay between the RF pulses.

Spoiler Duration (PVM_ChSpoilerOnDuration, PVM_VpSpoilerOnDuration) – Duration of gradient spoilers

RF Pulse 1/2/3 (PVM_ChPul1Enum, PVM_ChPul2Enum, PVM_ChPul3Enum, PVM_VpPul1Enum, PVM_VpPul2Enum) – Selection of the first/second/third pulse shape of the water suppression scheme

WS Module Duration (PVM_WsModuleDuration) – Duration of the suppression module

1.9.1.3.12 Outer Volume Suppression (OVS)

Principles

Outer volume suppression (OVS) consists of three repetitions of six suppression slices placed parallel to the surfaces of the voxel. The use of outer volume suppression allows a reduction of gradient spoilers inside the PRESS and STEAM sequences and therefore decreases the minimum echo time. When water suppression is used, OVS is interleaved within its free periods and does not require additional time.

Applications

Localized spectroscopy

Parameters

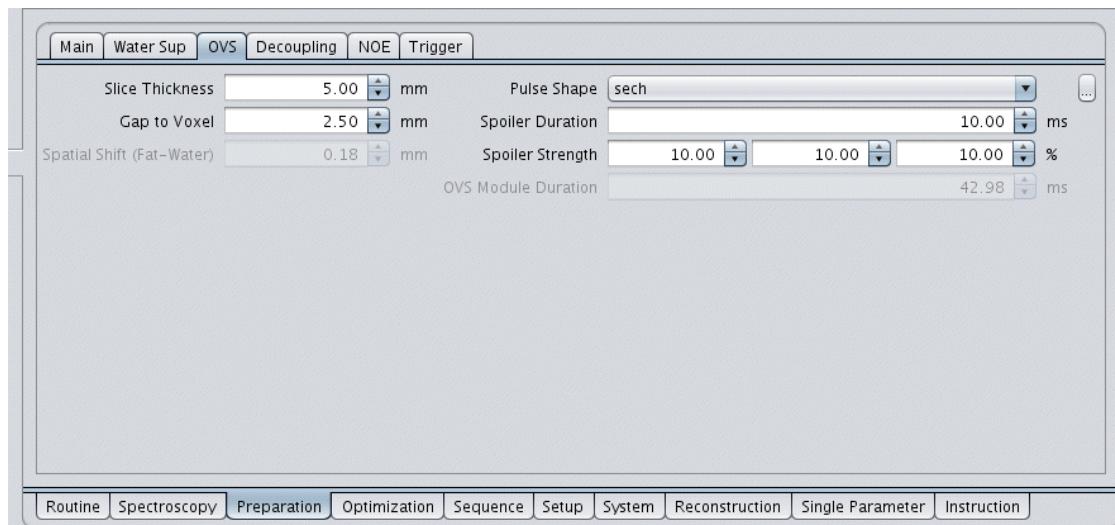


Figure 1.214: Preparation Card OVS

Slice Thickness (PVM_OvsSliceThickness) – Slice thickness of one outer volume suppression slice

Gap to Voxel (PVM_OvsGapToVoxel) – Distance between the (inner) edge of the outer volume suppression slice and the (outer) surface of the voxel. The minimum value is zero, which results in a partial overlap between the voxel excitation profile and the suppression slice profile.

Spatial Shift (Fat-Water) (PVM_OvsChemShiftDisplacement) – The exact position of the saturation slices (and the voxel itself) depends on the chemical shift of the component under investigation. This chemical shift displacement (in mm) of the positions is calculated for fat and water. It depends on the field strength, the pulse shape, the pulse duration, and the slice thickness.

Pulse Shape (PVM_OvsPulse1Enum) – Pulse shape of the outer volume suppression pulse

Spoiler Duration (PVM_OvsSpoilerDuration) – Within a set of six RF pulses of one outer volume suppression cycle, every second RF pulse is followed by a gradient spoiler pulse. Their duration and strength is specified in the arrays which each posses three entries, one for every gradient spoiler pulse. The three repetitions of the outer volume suppression scheme are executed with the same gradient strengths and duration as defined above.

Spoiler Strength (PVM_OvsSpoilerStrength) – See [Spoiler Duration \[▶ 261\]](#)

OVS Module Duration (PVM_OvsModuleDuration) – Duration of the outer volume suppression module included in the solvent suppression module use to calculate the repetition time of the method

1.9.1.3.13 Decoupling

Principles

RF power is applied at the decoupling frequency using continuous wave or composite pulse during the spectrum acquisition or a part of the spectrum acquisition.

Applications

Spectroscopy (e.g. ^{13}C spectroscopy)

Parameters

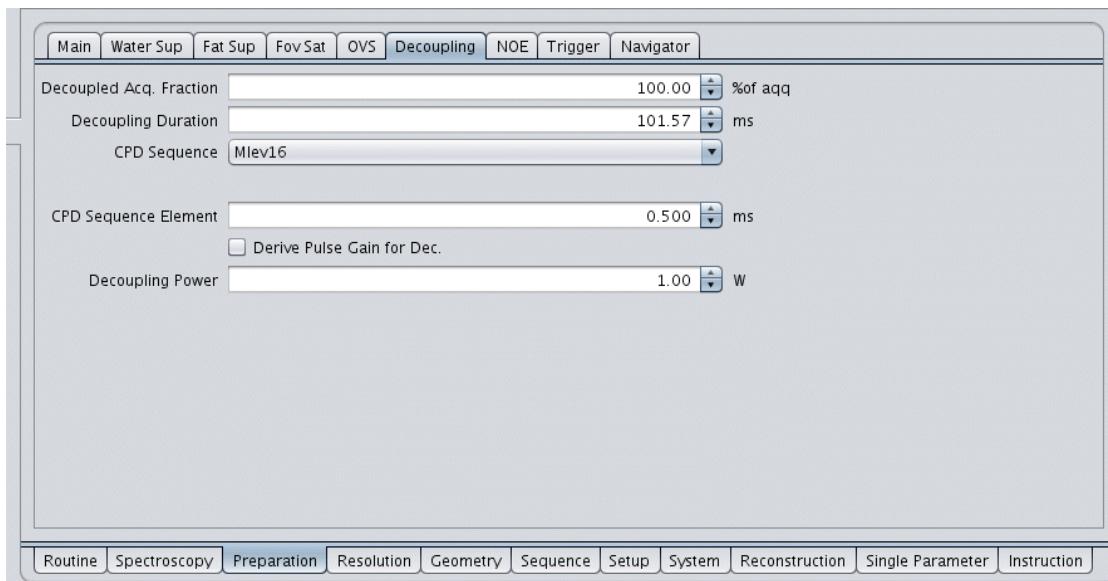


Figure 1.215: Preparation Card Decoupling

Decoupled Acq. Fraction (PVM_DecDuration) – Duration of the decoupling wave in percent of the acquisition duration

Decoupling Duration (PVM_DecTime) – Duration of the decoupling wave [ms]

CPD Sequence (PVM_DecPulseEnum) – List of the composite pulses

CPD User Pulse Name (PVM_DecUserPulse) – User composite pulse name (relevant when the previous parameter is set to User_Pulse)

CPD Sequence Element (PVM_DecPulseElementDuration) – Duration of the composite pulse element [μ s]

Derive Pulse Gain for Dec. (PVM_DeriveDecPowerYesNo) – Enables the derivation of the gain of the composite pulse element from the reference gain of the corresponding nucleus (corresponding to a flip angle of 90 degree for the composite pulse element duration)

Decoupling Power (PVM_DecPower) – Amplitude of the decoupling wave [dB]

1.9.1.3.14 NOE

Principles

RF power is applied at the decoupling frequency using continuous wave or composite pulse during the repetition time of the sequence.

Applications

Spectroscopy (e.g. ^{13}C signal enhancement)

Parameters

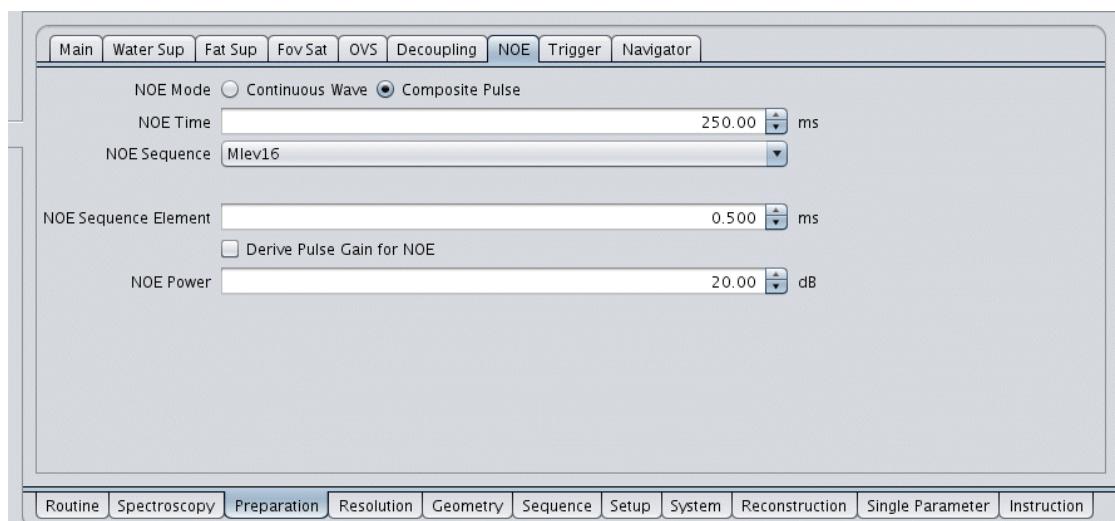


Figure 1.216: Preparation Card NOE

NOE Mode (PVM_NoMode) – Two modes of NOE are available:

Composite Pulse using cpd pulses and Continuous Wave

NOE Time (PVM_NoTime) – Defines the duration of the irradiation for NOE

NOE Sequence (PVM_NoPulseEnum) – List of the composite pulse

NOE User Pulse Name (PVM_NoUserPulse) – User composite pulse name (relevant when the previous parameter is set to User_Pulse)

NOE Sequence Element (PVM_NoPulseElementDuration) – Duration of the composite pulse element [ms]

Derive Pulse Gain for NOE (PVM_DeriveNoePowerYesNo) – Enables the derivation of the gain of the composite pulse element from the reference gain of the corresponding nucleus (corresponding to a flip angle of 90 degree for the composite pulse element duration)

NOE Power (PVM_NoPower) – Amplitude of the irradiation wave [dB]

1.9.1.4 Spectroscopy Card

1D Spectroscopy

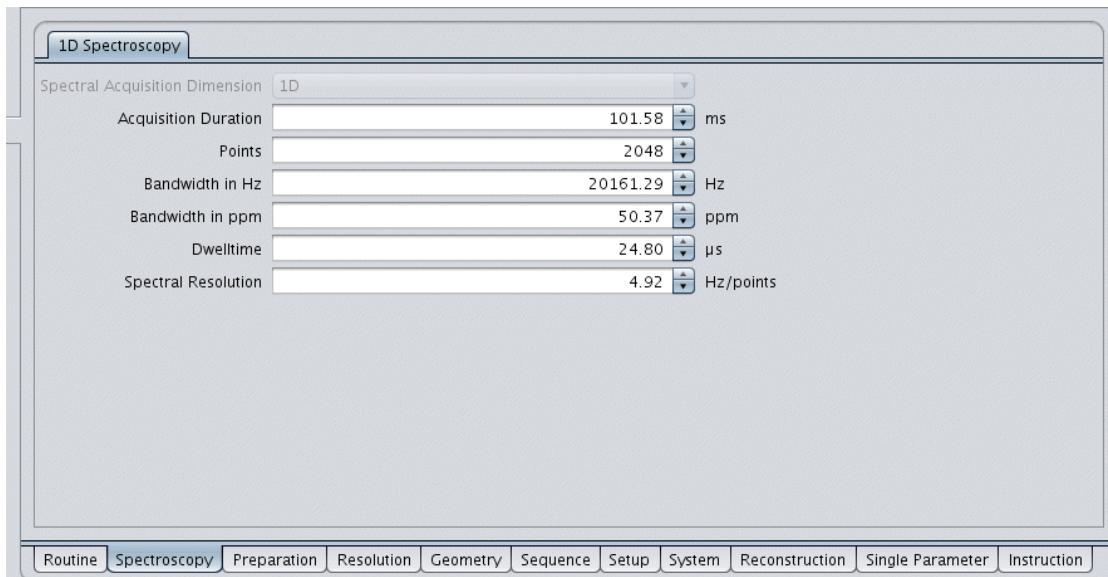


Figure 1.217: 1D Spectroscopy Card

Spectral Acquisition Dimension (PVM_SpecDimEnum) – Dimensionality of the spectroscopic experiment. Changing the dimensionality of the experiment changes the value of PVM_SpecDim and modifies all spectroscopic arrays (PVM_SpecOffsetHz, PVM_SpecOffsetppm, PVM_SpecMatrix, PVM_SpecSWH, PVM_SpecSW, PVM_SpecDwellTime, PVM_SpecNomRes).

Acquisition Duration (PVM_SpecAcquisitionTime) – Duration of the acquisition time as calculated from the **Points** and the **Dwelltime**

Points (PVM_SpecMatrix) – Number of sampling points for each spectroscopic dimension

Bandwidth in Hz (PVM_SpecSWH) – Maximum spectral width fulfilling the Nyquist condition expressed in absolute units [Hz]

Bandwidth in ppm (PVM_SpecSW) – Maximum spectral width fulfilling the Nyquist condition expressed in units of the resonance frequency of the nucleus under investigation [ppm]

Dwelltime (PVM_SpecDwellTime) – Time between two successive (real-valued) sampling points of the digitizer, which is the half of the dwelltime of the acquired complex-valued points

Spectral Resolution (PVM_SpecNomRes) – Best possible nominal spectral resolution of the time domain data assuming twofold zero filling before spectral reconstruction

1.9.1.5 Optimization Card

This card is present in spectroscopic methods and provides access to various optimization tools such as navigators, drift correction, etc.

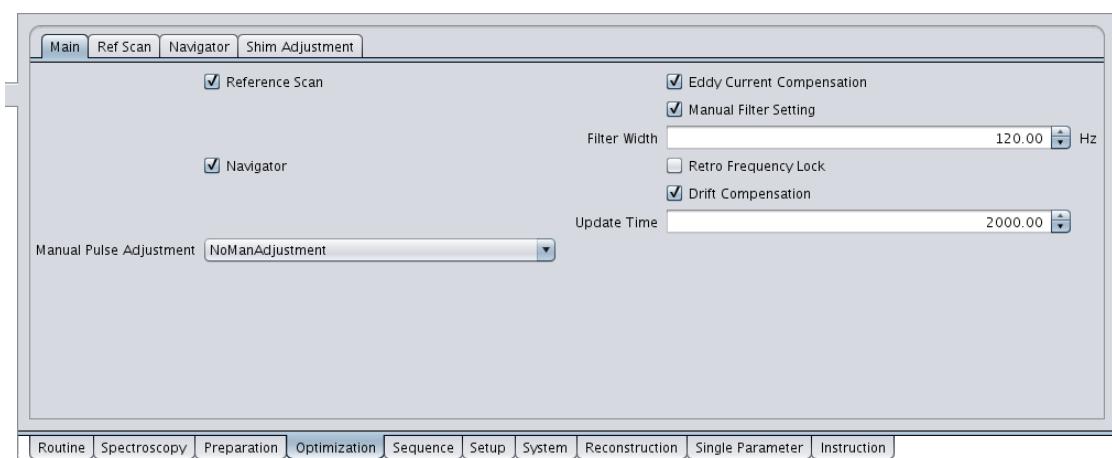
Main

Figure 1.218: Optimization Card Main

Reference Scan (PVM_RefScanYN) – If selected, this parameter causes the acquisition of a reference scan without water suppression before the actual scan. This reference is required for the eddy current compensation. The accumulated reference signal is stored in the parameter PVM_RefScan and in the data file fid.refscan (see Chapter [Data Files ▶ 380](#)).

Navigator (PVM_NavOnOff) – If selected, this parameter causes the acquisition of navigator scans. For each navigator scan an additional non-selective excitation pulse is applied immediately after the end of each acquisition. The resulting FID signal is acquired and serially stored in the file rawdata.job1. Low flip angles and no water suppression are used. The navigator signal is displayed in a second frame of the acquisition window. Note that manual adjustment of the RF pulse gains is deactivated when the navigator is switched on.

Manual Pulse Adjustment (OPT_ManAdjustment) – Switches the sequence to a manual pulse power correction mode. One of the excitation pulses can be chosen and its selection profile can be observed in the setup mode. The profile is displayed within a field of view specified with the FOV parameter.

Eddy Current Compensation (Edc_OnOff) – Activates an optional reconstruction step reducing the line shape distortion caused by eddy currents. It is based on the accumulated signal from the reference scan. Therefore, this option can only be activated if the parameter **Reference Scan** is selected. If this condition is fulfilled, the eddy current compensation can be switched on/off also for subsequent reconstructions of a completed scan in the processing platform.

The result of an eddy current compensated experiment is a signal whose temporal phase evolution has been demodulated by the temporal phase evolution of the strongest spectral component of the reference scan.

Manual Filter Setting (EdcManualFilter) – Deactivates the automatic determination of the width of a Gaussian filter that is applied for extraction of the strongest spectral component during Eddy Current Compensation

Filter Width (EdcFilterWidthHz) – Specifies the width of the Gaussian filter for Eddy Current Compensation, if the parameter **Manual Filter Setting** is activated

Retro Frequency Lock (RetroFrequencyLock_OnOff) – Compensates field drifts during a long accumulation of scans. Based on navigator data, a reconstruction algorithm corrects frequency drifts retrospectively at the end of the experiment. Therefore, this retro frequency lock can only be activated if the parameter **Navigator** is selected. If this condition is fulfilled, the retro frequency lock can be switched on/off also for subsequent processings of completed scans in the processing platform.

The result of a retro frequency locked experiment is a frequency corrected and accumulated single FID for each repetition.

Drift Compensation (PVM_DriftCompYesNo) – Activation of field drift compensation during the experiment based on a navigator signal and a reload mechanism of the B0 field. Therefore, the drift compensation can only be activated if the parameter **Navigator** is selected.

Update Time (PVM_DriftCompUpdateTime) – Time period of B0 reload events. The minimum update time depends on the repetition time and the system architecture.

FOV (OPT_FOV) – Field of view used for the manual pulse adjustment

Reference Scan

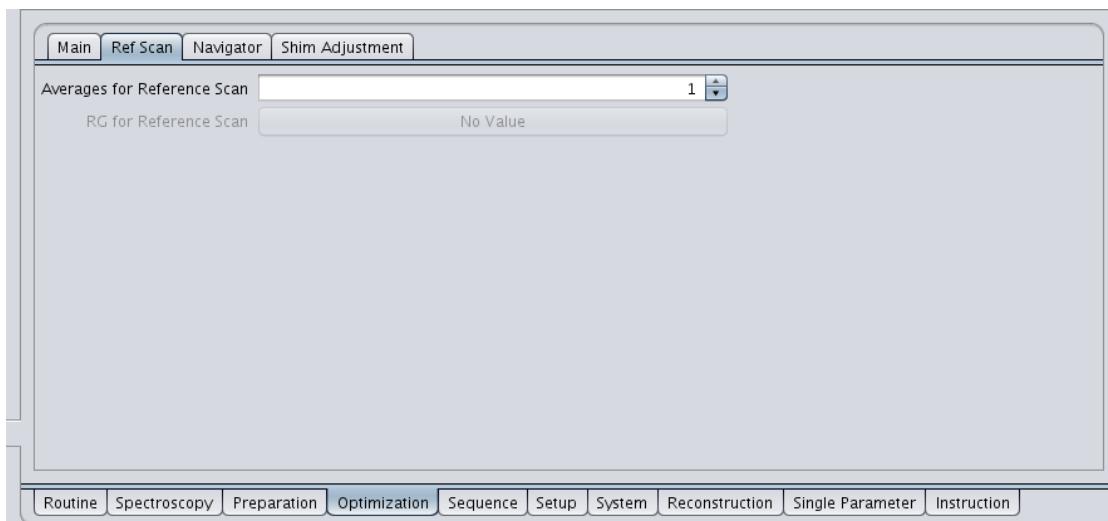


Figure 1.219: Optimization Card Reference Scan

Averages for Reference Scan (PVM_RefScanNA) – Number of averages of the reference scan (typically set to a lower number than the number of accumulations of the actual scan)

RG for Reference Scan (PVM_RefScanRG) – Value of the receiver gain adjusted for the reference scan. The parameter is set by the auto-adjustment and remains non-editable. It may be used for the absolute quantification of metabolites.

Navigator

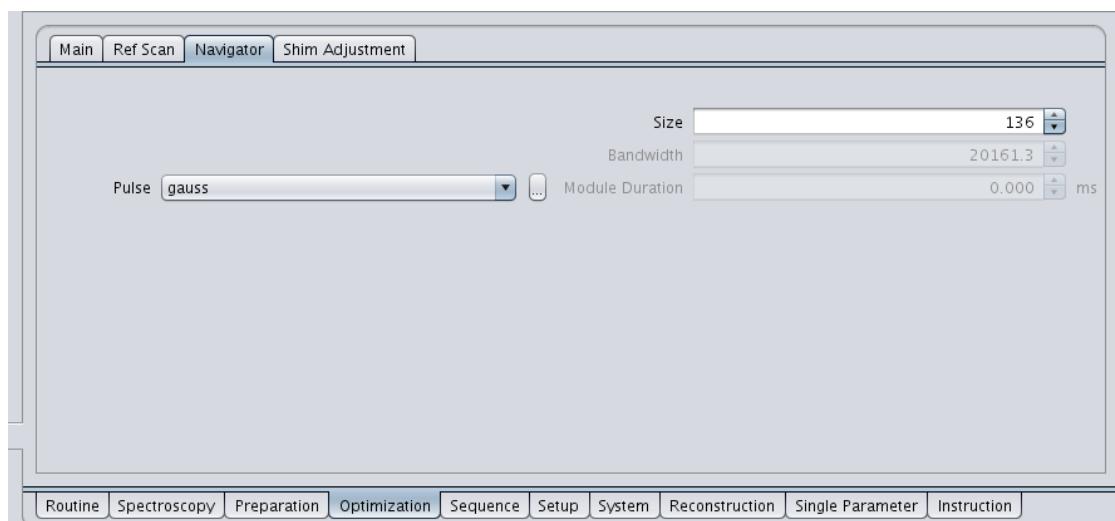


Figure 1.220: Optimization Card Navigator

Pulse (PVM_NavPulseEnum) – Choice of excitation pulse for navigator signal

Size (PVM_NavPoints) – Controls the acquisition size of the navigator scan

Bandwidth (PVM_NavSWh) – Acquisition bandwidth of navigator scan

Module Duration (PVM_NavigatorModuleTime) – Duration of the navigator module

Shim Adjustment

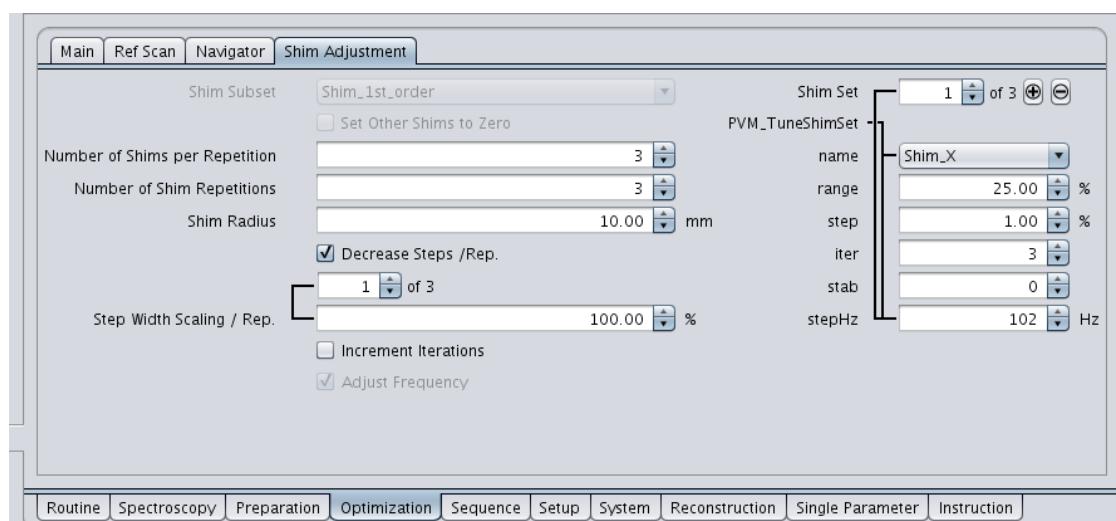


Figure 1.221: Optimization Card Shim Adjustment

This card is present in localized spectroscopy methods (PRESS / STEAM) and in the adjustment method AdjShim. Parameters on this card control the iterative shimming procedure based on the Tune-Shim algorithm. A user-defined group of shims is examined in an iterative cycle. Each shim in succession is adjusted individually to maximize a quality parameter (the area of the FID/Echo signal in dime domain, visible as GS_normalized area). Each shim that is optimized will be varied using a increment specified by the protocol, the variation of the quality parameter as a function of shim strength is fitted to a Gaussian function and the optimized value of the shim is set to the center of the Gaussian curve. The amount of values used to estimate the Gaussian curve may be controlled by protocol

parameters for each shim. Shims are classified according to the B0-field distribution they generate. If expressed in terms of spherical harmonic functions the following types are distinguished by the algorithm:

- **First order shims:** 3 shims: Shim_X, Shim_Y, Shim_Z (also referred as linear shims)
- **Second order shims:** 5 shims: Shim_Z2, Shim_XZ, Shim_YZ, Shim_2XY and Shim_X2_Y2
- **Higher order shims** (all remaining shims)

In case of multichannel acquisition (if demanded by the active scan), the signal weighted sum of signal areas is used to optimize the shim settings. High order shims require a readjustment of lower order shim sets in general. Since these mutual dependencies (interactions) between various shims and high order effects will generally not be considered by the adjustment algorithm itself, special care must be taken if high order shimming protocols are optimized. A detailed information about shimming using Bruker hardware is given in a spin report article (see Reference [References \[▶ 692\]](#)).



Dependent on different methods, some parameters of this card may be not editable to prevent improper settings with respect to the signal generation.

Shim Subset (PVM_TuneShimSubset) – Acts as a filter for selectable shim channels in PVM_TuneShimSet (see below). Note: In addition to this filter only shims that are available on the scanner may be selected. The following values are implemented:

- Shim_1st_order: Only linear shims may be selected.
- Shim_1st_order_z2: Only linear shims and Z2 channel may be selected.
- Shim_1st_2nd_order: Only linear and 2nd order shims may be selected.
- Shim_all: No constrain, all shims may be selected.

Set Other Shims to Zero (PVM_TuneShimForceSubset) – If activated all shims that are not selected in PVM_TuneShimSet (see below) are set to 0 before the adjustment starts

Number of Shims per Repetition (PVM_TuneShimNShimRep) – Number of shims that are adjusted in one repetition. It defines the number of entries in array PVM_TuneShimSet.

Number of Shim Repetitions (PVM_TuneShimRep) – Defines how often the sequence of shim adjustments (as defined by PVM_TuneShimSet) is repeated

Shim Radius (PVM_TuneShimRadius) – The field effect of different shim channels may be described by the maximum field deviation inside a centered sphere. The shim radius defines the size of this sphere and is considered for the .stepHz-field of PVM_TuneShimSet (see below).

Decrease Steps / Rep. (PVM_TuneShimActStw) – If activated the stepwidth of shim variations during the adjustment is decreased in different repetitions of the shim sequence. The scaling may be specified by Step Width Scaling / Rep. (see below).

Step Width Scaling / Rep. (PVM_TuneShimStepWidth) – Is visible if **Decrease Steps / Rep.** is activated. The number of entries of this array is defined by the **Number of Shim Repetitions** (see above). During the adjustment the step width of shim variations as defined in the .step-field of PVM_TuneShimSet (see below) is scaled down by a factor defined by this array. The first entry is always constrained to 100%, following entries are sorted to assure a decreasing stepwidth for consecutive shim repetitions. The scaling factors are initialized to reduce the stepwidth by 50% compared to the previous repetition.

Increment Iterations (PVM_TuneShimInclter) – If activated the number of points for the Gaussian estimation as defined by the .iter-field in PVM_TuneShimSet (see below) is incremented for each repetition of the shim sequence.

Adjust Frequency (PVM_TuneShimAdjFreq) – If activated the basic frequency is readjusted based on the peak position of the signal in frequency domain at the end of the adjustment

Shim Set (PVM_TuneShimSet) – Used to control the algorithm in detail. It defines the sequence of different shims that are optimized in one iterative cycle, the number of sequence elements is defined by **Number of Shims per Repetition**. For each shim in the sequence the following fields may be specified:

- **name** – Name of the shim that is optimized. Only those shims that belong to the selected shim subset (see **Shim Subset** above) and that are available on the system may be chosen.
- **range** – Allowed range of shim variations during adjustment. This field is constrained to 100% and shown only because of backward compatibility to previous versions.
- **step** – Allows to control the stepsize (% of maximum current) that is used in the first iteration. Since the shim field depends on the sensitivity of the shims and the maximum current through the shim coils, the step width may be changed individually for each shim.
- **iter** – Controls the number of points used to perform a Gaussian fit of the quality parameter as a function of shimstrength
- **stab** – Controls the number of dummy acquisitions before the quality parameter for a given shimstrength is estimated. Set this to a nonzero value for shims that need a certain settling time before their field is stable.
- **stepHz** – Controls the step width of shim variations in a unit that is independent on the sensitivity and maximum current of the shim system. Based on the **Shim Radius** the shim increment is calculated from the desired maximum field effect in a sphere as specified by this field taking hardware information into account.

1.9.1.6 Resolution Card

This card contains parameters controlling the dimensions of the image and the way this image is “encoded” in the acquisition matrix, including various acceleration schemes.

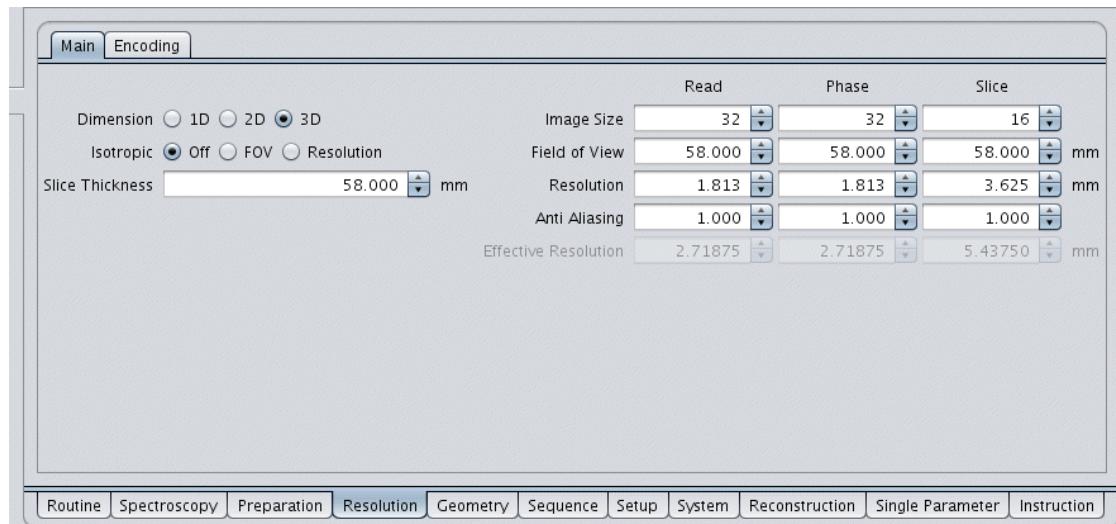


Figure 1.222: Resolution Card Main

Dimension (PVM_SpatDimEnum) – Dependent on the method, a selection between 1D, 2D and 3D acquisition mode can be made with this parameter.

Isotropic (PVM_IsotropicFovRes) – Allows switching between no restrictions (`Off`), an isotropic `FOV`, and isotropic `Resolution`. This choice affects the way the Image Size, Field of View and Resolution react when their elements are edited.

Slice Thickness (PVM_SliceThick) – See [Geometry Card ▶ 271](#)

Image Size (PVM_Matrix) – Number of pixels along each dimension of the reconstructed image

Field of View (PVM_Fov) – Extents covered by the image

Resolution (PVM_SpatResol) – Size of image pixels

Anti Aliasing (PVM_AntiAlias) – Factors controlling the aliasing effect in each dimension. With Anti Aliasing set to 1.0, signal sources placed outside the FOV are folded (aliased) into the image. Higher anti-aliasing values scale the folding limit up. Anti-aliasing in phase-encoding directions increases the measurement time.

1.9.1.6.1 Encoding

This card contains parameters controlling the phase encoding scheme, i.e the number of the phase encoding steps, their corresponding positions in the k-space, and their order. Encoding parameters allow a reduction of the experiment time by means of various acceleration mechanisms, such as zero-filling or parallel imaging (PPI, see [Parallel EPI ▶ 342](#)).

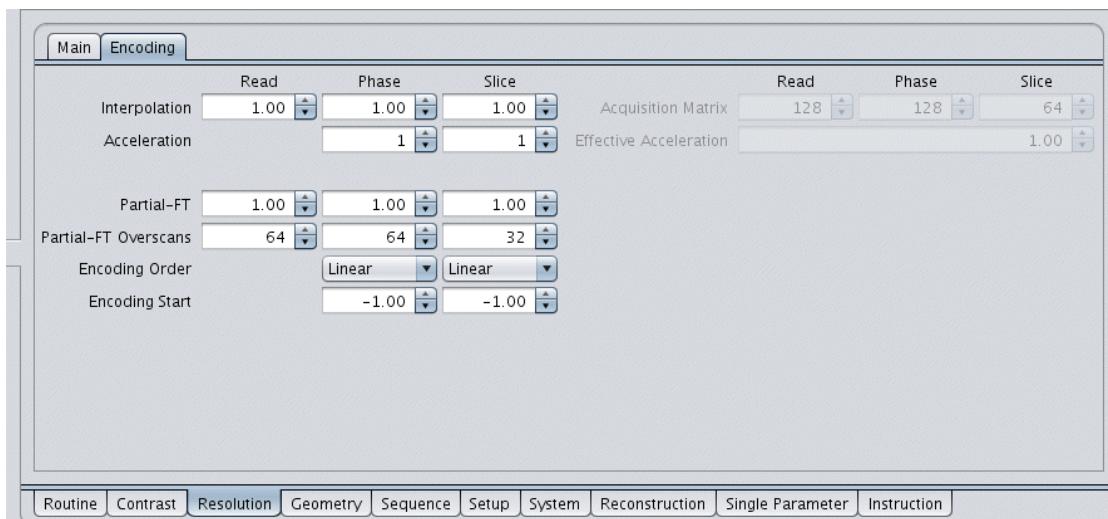


Figure 1.223: Resolution Card Encoding

Interpolation (PVM_EncZf) – Fourier interpolation by zero-filling. Zero-filling should be used with caution since it reduces the effective resolution of the image.

Acceleration (PVM_EncPpi) – Parallel imaging acceleration, available only with array coils. With **Acceleration = n** (n being at most equal to the number of active array elements) only every n'th k-space line is acquired while the remaining ones are skipped, except for the **Reference Lines** in the center (see below).

Reference Lines (PVM_EncPpiRefLines) – Number of k-space lines in the center sampled with full density used to calibrate the “reconstruction” of skipped lines in accelerated acquisition. Higher numbers allow more reliable reconstruction but reduce the effective acceleration. The parameter is visible only when Acceleration is higher than one.

Partial-FT (PVM_EncPft) – Partial Fourier factor defining the reduction of the data by a one-sided truncation (2.0 means only one half of k-space is acquired)

Partial-FT Overscans (PVM_EncPftOverscans) – Integer representing the number of lines sampled on the “negative” k-space half in a partial-FT experiment. It is linked to the Partial-FT factor. Increasing this parameter reduces artefacts caused by the partial-FT scheme in gradient-echo methods. Due to the partial-FT reconstruction strategy this parameter should not be set below 4. Partial FT can be selected only in one dimension. When used in the read

direction, it allows an asymmetric positioning of the echo and a reduction of the echo time. Partial FT in the phase direction typically reduces the acquisition time, except for EPI where it also reduces the echo time.

Encoding Order (PVM_EncOrder) – Symbol taking values LINEAR or CENTRIC and determining the order of acquisition of k-space lines (from edge to edge, or from center outwards, respectively). The centric order allows achieving minimum effective echo times in multiple spin-echo methods such as RARE. It can also increase the signal-to-noise ratio in fast gradient echo methods (e.g. FISP) by effectively using the approach to the steady state. However, the centric scheme usually introduces a blurring effect.

Encoding Start (PVM_EncStart) – Number indicating the starting value of the phase encoding, ranging from -1 (lower edge of k-space) to +1 (upper edge). When the encoding start is higher than -1, the k-space is sampled cyclically. This parameter may be used to shorten the effective echo time in segmented experiments, such as RARE. This parameter is not available with the centric encoding and with partial-FT.

Acquisition Matrix (PVM_EncMatrix) – Effective size of the acquisition matrix taking into account the geometry parameters and all acceleration methods. Non-editable. When all acceleration parameters are set to 1.0 (no acceleration), the acquisition matrix size is a product of the image size (PVM_Matrix, [Resolution Card ▶ 2701](#)) and the anti-aliasing factor (PVM_AntiAlias). Selecting one or more acceleration schemes (parallel, partial-FT, zero-filling) causes the acquisition matrix size to be reduced.

Effective Acceleration (PVM_EncTotalAccel) – Number indicating the total acceleration of the acquisition obtained with parallel, partial-FT and zero-filling factors.

1.9.1.7 Geometry Card

This class is present in all imaging methods and contains parameters controlling the slice positioning. The slice geometry parameters can also be graphically manipulated with the Geometry Editor.

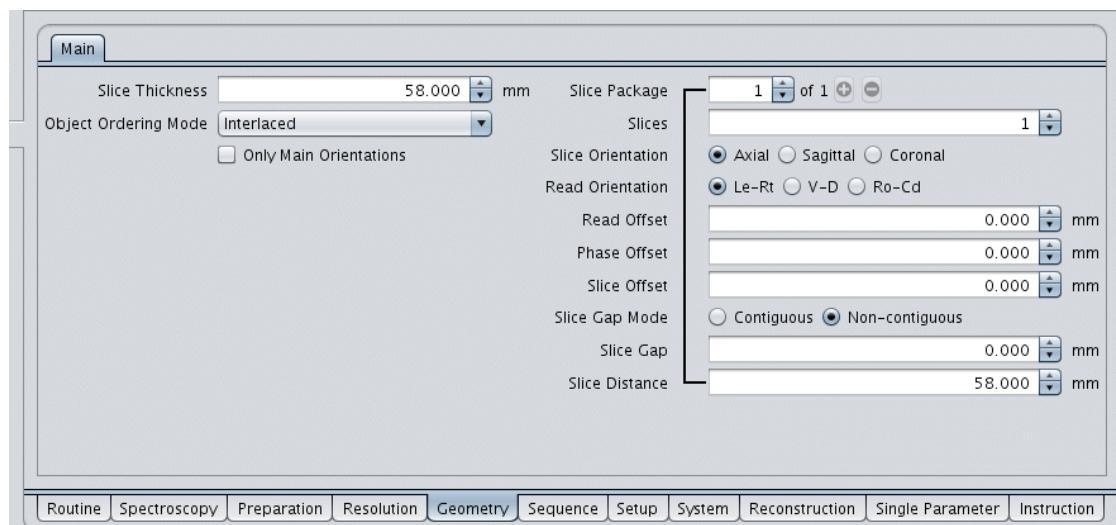


Figure 1.224: Geometry Card Main

Slice Thickness (PVM_SliceThick) – Assigns the thickness of the slice. The actual slice selection profiles depend on the selected RF pulses. This parameter specifies the profile thickness at half maximum.

Object Ordering Mode (PVM_ObjOrderScheme) – Selects the order in which the slices are excited in a multislice experiment. Interlaced ordering (default) reduces the cross-talk with neighboring slices. Other schemes are possible for special purposes.

Only Main Orientations (PVM_MajSliceOri) – If selected, this parameter will disable rotations of the packages in the Geometry Editor; only pure axial, sagittal, and coronal orientations will be allowed. This option allows using higher gradient amplitudes and reaching a higher resolution in some methods.

Slice Package (PVM_NSPacks) – Slices can be grouped in packages. Within a package all slices have the same orientation and spacing; packages may differ in orientation and spacing.

Slices (PVM_SPackArrNSlices) – Number of slices in each package

Slice Orientation (PVM_SPackArrSliceOrient) – General orientation of each slice package (axial, sagittal, coronal). The precise orientation can be set up using the angle sliders in the Geometry Editor.

Read Orientation (PVM_SPackArrReadOrient) – Direction of the readout gradient. Since this is the only direction in which out-of-FOV elements do not get aliased, it should be chosen along the long axis of the object (e.g head-feet for sagittal or coronal images).

Read Offset (PVM_SPackArrReadOffset) – Offset of the FOV for each package along the read direction.

Phase Offset (PVM_SPackArrPhase1Offset) – Offset of the FOV for each package along the first phase encoding direction.

Slice Offset (PVM_SPackArrSliceOffset) – Distance of the center of each slice package from the center of the gradient system. For a package containing an odd number of slices this is the offset of the central slice; for even numbers, this is the position of the midpoint between central slices.

Slice Gap Mode (PVM_SPackArrSliceGapMode) – To be set to Contiguous or Non-contiguous depending if one allows putting a gap between slices

Slice Gap (PVM_SPackArrSliceGap) – Distance between slice edges (zero for contiguous slices)

Slice Distance (PVM_SPackArrSliceDistance) – Distance between slice centers

Note that most methods allow setting up a multi-slab 3D experiment. In such case, the Spatial Acquisition Dimension is set to 3D in the Resolution Card, and each "slice" specified in the Geometry actually means a 3D slab. For this reason, the slice thickness is linked to the FOV in the third direction.

1.9.1.8 Sequence Card

This card groups parameters directly related to the pulse sequence, such as the band-width, RF pulses and spoilers. Its content is different for different methods. On the Frequency and Transmit Subcards, an expert user may select the frequency offset for the experiment (e.g. to bring a required chemical shift on-resonance), change the nucleus for a multi-band RF coil, manipulate the reference power, and select parallel transmission channels. Some methods have additional subcards here, e.g. EPI.

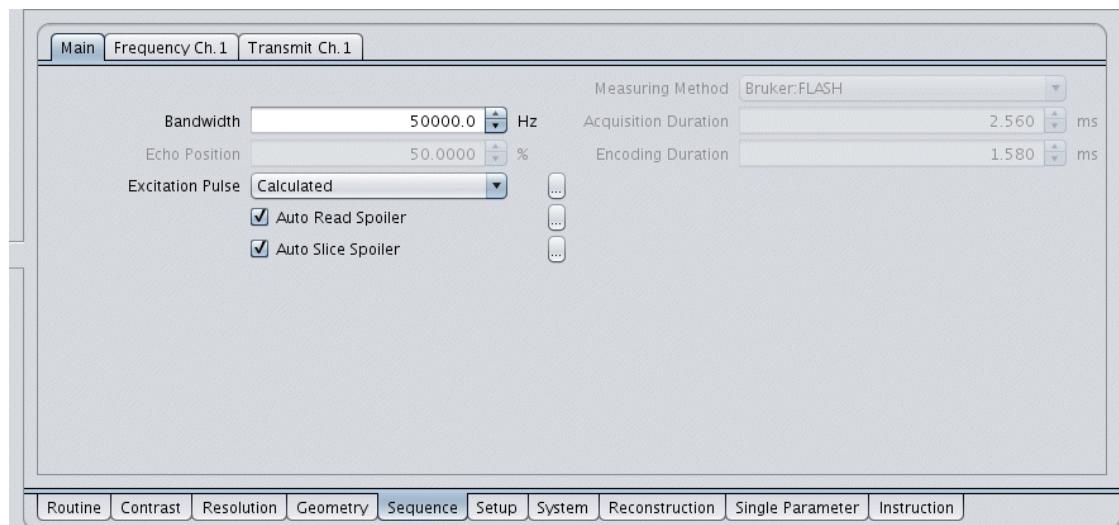


Figure 1.225: Sequence Card Main

Bandwidth (PVM_EffSWh) – Effective bandwidth of the image in the frequency encoding (readout) dimension. A higher bandwidth reduces chemical shift artifacts (fat-water displacement) and allows reaching shorter echo times at the price of a lower signal-to-noise ratio of the image (the SNR is inverse-proportional to the square root of the effective bandwidth).

Acquisition Duration (PVM_AcquisitionTime) – Total time of the measurement excluding dummy scans

Measuring Method (Method) – Name of the method used for the experiment

1.9.1.8.1 RF Pulses

Pulse Shape

Each radiofrequency pulse used by the method is represented by an enumeration parameter (called e.g., **Excitation Pulse**, **Refocusing Pulse**, etc.) which gives access to the pulse shapes installed on the system (bp, gauss, sinc3, etc.). A shape can also be set to Calculated in which case the system produces an appropriate pulse shape automatically. Further details of the pulse are gathered in a structure parameter accessible by the associated “...” button.

Pulse Details

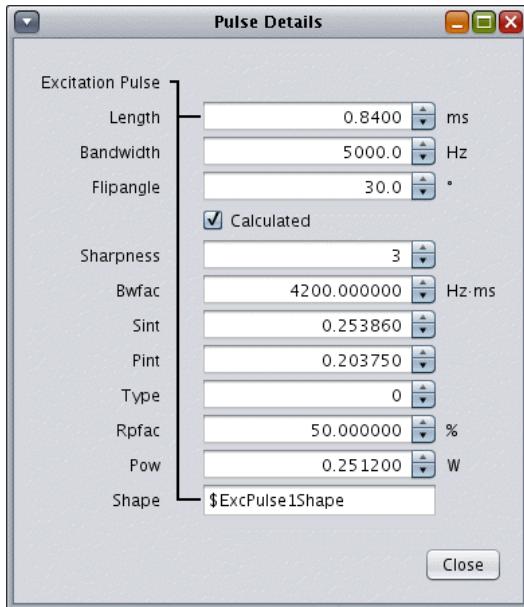


Figure 1.226: Pulse Details

Length – Length (duration) of the pulse

Bandwidth – Bandwidth (full width at half maximum in the frequency domain)

Flipangle – Flip angle produced by the pulse, when the reference RF power adjustment has run (otherwise, meaningless)

Calculated – When selected, the pulse shape is calculated automatically by the software to reach the given bandwidth, flip angle and sharpness. Equivalent to the selection of Calculated in the associated enumeration parameter.

Sharpness – Integer ranging from 1 to 10 related to the sharpness of the profile (meaningful only for Calculated pulses). Pulses of high sharpness (5-10) give a broader flat top and shorter flanks of the selection profile, making them useful for 3D slab- or voxel selection, but need more length at a given bandwidth.

Bwfac – Bandwidth factor of the pulse (product of length [ms] and bandwidth [Hz]), dependent on sharpness, non-editable

Sint – Normalized shape integral, non-editable

Pint – Normalized power integral, non-editable

Type – Integer dependent on the physical action of the pulse (1-excitation, 2-refocusing, 3-inversion), non-editable

Rpfac – Rephasing factor of the pulse (50% for symmetric pulses)

Pow – Derived power of the pulse [Watts]

Shape – Name of the pulse shape, or Calculated

RF pulses can also be found on other cards, in particular those of each module on the Contrast Card. For the purpose of manual adjustments, the power/amplitude of each pulse can also be accessed on the [Setup Card](#) [283].

1.9.1.8.2 Spoilers

Most sequences contain so called spoilers, or spoiling gradient pulses, whose purpose is to dephase the unwanted signals, e.g. those remaining from the previous repetition. Each spoiler used by a method can be found on the Sequence Card in the form of an On/Off button, which, when selected, sets the duration and amplitude of the spoiler automatically. Experts can modify these details, by pressing the associated “...” button.

Spoiler Details



Figure 1.227: *Spoiler Details*

AutoSetting – When selected, remaining parameters are automatically filled according to a pre-programmed procedure and remain non-editable.

Spoiling – Spoiling efficiency in cycles of the transverse magnetization per image element (e.g. per pixel or per slice thickness for spoilers on read or slice gradient channels, respectively).

Duration – Duration of the spoiler gradient

Amplitude – Amplitude of the spoiler gradient

1.9.1.8.3 Echo Planar Imaging (EPI)

The class **EPI_Parameters** appears in all methods in which the signal is acquired using the principles of Echo-Planar Imaging. Its parameters control the module `epi.mod` which is included in the pulse program of these methods and represents the EPI signal acquisition.

Navigator (PVM_EpiPrefixNavYes) – Activates the acquisition of a navigator signal (non-encoded FID section before the echo train). The navigator is used by the reconstruction to improve signal stability in segmented EPI. It is particularly useful in diffusion-weighted experiments where tiny movements of the object lead to phase fluctuations. Optionally, the navigator can be used for a frequency drift correction (see [Drift Correction \[▶ 276\]](#)).

Navigator Parameters

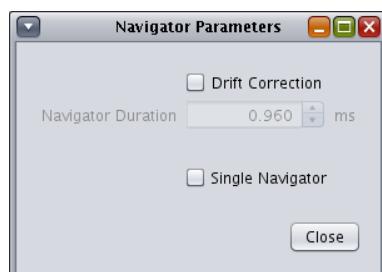


Figure 1.228: *Navigator Parameters*

Drift Correction (PVM_EpiDriftCorr) – May be selected when the navigator is selected (see [Navigator \[▶ 275\]](#)) to produce a correction of the frequency drift during the reconstruction. In this case the duration of the navigator can be freely selected. Increased duration gives a better frequency precision at the price of a longer echo time.

Navigator Duration (PVM_EpiPrefixNavDur) – Duration of the navigator

Single Navigator (PVM_EpiSingleNav) – Relevant for multi-echo EPI; when selected, only the navigator of the first echo data will be used for correction.

Automatic Ghost Correction (PVM_EpiAutoGhost) – When selected (default), phase correction parameters for the Nyquist ghost suppression will be automatically measured during the receiver gain adjustment.

Ghost Correction Order (PVM_EpiMaxOrder) – For the phase correction a polynomial function is fitted to reference scan data. The degree of the polynomial is given by this parameter, which is limited to the range between 0 and 10. The default value is 1 (linear phase correction). If ghosts remain that show an oscillating intensity in read direction one should try to increase the parameter value.

Dynamic Ghost Correction (PVM_EpiDynCorr) – In rare cases of a time-dependent ghost modulation (e.g. due to gradient coil heating) this option will give a better ghost suppression. Dynamic correction requires additional navigator echoes and may increase TE. It should therefore be used only if necessary.

Double Sampling (PVM_EpiCombine) – Activates a modus in which each k-space line is sampled twice to produce images free of the Nyquist ghost (see Reference [\[14\] \[▶ 691\]](#)). The data from both sampling directions are reconstructed as separate magnitude images, which are added in the end. The reconstruction can therefore leave out the ghost correction for a mismatch between odd and even echoes. The doubling of the data acquisition time leads to a doubling of the echo time. This, however, can be avoided by doubling the acquisition bandwidth if the limits of the gradients are not reached. The increased bandwidth leads to a reduction in signal-to-noise ratio, but it is largely compensated by the summation of the magnitude images.

Grappa Multishot Adj. (PVM_EpiGrappaSegAdj) – If selected (default), the Epi Grappa adjustment will increase the number of segments by the Grappa acceleration factor to achieve identical image distortion level as in the actual measurement. In case of signal instabilities, a single shot adjustment may give better results (parameter not selected).

Grappa SVD Threshold (PVM_EpiGrappaThresh) – Singular value truncation threshold applied during the GRAPPA reconstruction. A higher value reduces the noise but increases the aliasing artifacts. The recommended value range for this parameter is 0.01 - 0.1.

Regridding based on Trajectory (PVM_EpiTrajAdjYesNo) – When selected, the regridding will be based on the measured trajectory if it is available. Otherwise the shape of the read gradient is assumed to be ideal (with linear or sinusoidal ramps) and the further parameters are invisible in the parameter editor.

Automatic Trajectory Adjustment (PVM_EpiTrajAdjAutomatic) – If selected, the trajectory adjustment will start automatically when no valid trajectory is available. If not selected, the adjustment will not start automatically, but may be started manually (Adjustment Platform).

Trajectory measured (PVM_EpiTrajAdjMeasured) – This non-editable parameter indicates whether the stored trajectory is valid or not. A valid trajectory becomes invalid when parameters are changed that influence the shape of the read gradient. A successful trajectory measurement will select this parameter. In some cases, e.g. for a very high resolution, the trajectory adjustment may fail due to insufficient SNR. The parameter PVM_EpiTrajAdjMeasured will then remain unselected, and the theoretical trajectory will be used for regridding. A solution might be to use a higher number of averages for the adjustment.

Gradient Synchronization (PVM_EpiGradSync) – Turn on a synchronization of the sequence with the clock of the preemphasis filter

Ramp Mode (PVM_EpiRampMode) – Enumeration parameter allowing the user to choose the ramp mode. It can take 3 different values: SystemRamp, UserRamp, UserSlope.

SystemRamp

- The associated gradient shape is the system default gradient shape, namely a trapezoidal gradient.
- The corresponding ramp time duration is system dependent (the default value depends on the PREEMP_ramp_time parameter).
- In case of SystemRamp the gradient slope value (see below) is automatically derived from the read gradient amplitude.

UserRamp

- The possible gradient ramp shapes are those accessible through the ramp form parameter (PVM_EpiRampForm).
- The corresponding ramp time duration is editable. For a given read gradient amplitude, the ramp time duration is obviously limited by the system capabilities (proportional to the PREEMP_ramp_time parameter).
- In that case, the gradient slope value is a derived value according to the parameter definition (see below). Its value is the same for both read and blip gradients.

UserSlope

- The possible gradient ramp shapes are those accessible through the ramp form parameter (PVM_EpiRampForm).
- The corresponding gradient slope value is editable. The gradient slope value has the range [1%,100%].
- The gradient slope together with the resolution and bandwidth determine the ramp time (inversely proportional to the gradient slope value) and blip duration.

Gradient Parameters:

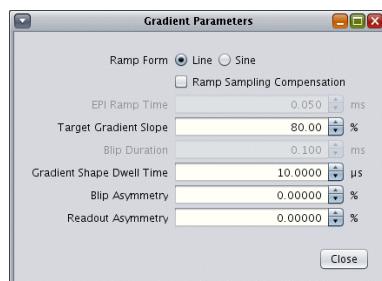


Figure 1.229: Gradient Parameters

Ramp Form (PVM_EpiRampForm) – Enumeration parameter allowing the user to choose the gradient ramp shape. It can take two different values:

- Line: calculated linear gradient ramp
- Sine: sinusoidal read gradient ramp calculated using the formula $y = \sin(px / 2.0)$

The blip gradient shape is calculated from the formula $y = 0.5(1.0 - \cos(px))$.

Ramp Sampling Compensation (PVM_EpiRampComp) – Turns on an oversampling mechanism that compensates the resolution loss caused by the sampling of the signal during the readout gradient ramps.

EPI Ramp Time (PVM_EpiRampTime) – Determines the ramp time duration when PVM_EpiRampMode is set to UserRamp. As previously seen (description of the ramp mode parameter), this parameter is non-editable when PVM_EpiRampMode is set to SystemRamp or to UserSlope.

Target Gradient Slope (PVM_EpiSlope) – Required slope of the readout gradient ramps in percent of maximum. The system calculates the actual slope (Gradient Slope, PVM_EpiEffSlope) as close as possible to the target slope under several constraints (echo spacing, gradient dwell time, etc.).

Blip Duration (PVM_EpiBlipTime) – Determines the blip time duration when the PVM_EpiRampMode is set to UserRamp. The maximum allowed value is proportional to the ramp time duration. In all other cases, this parameter is derived from other parameters with the above specified limitation.

Gradient Shape Dwell Time (PVM_EpiGradDwellTime) – Determines the dwell time used by the gradient controller (GCU) in order to generate the gradient ramp shape. The total number of points of the calculated shape depends on this parameter. In most of the current BRUKER configurations, dwell times of eight micro seconds (8 μ s) are required to obtain well-defined gradient shapes at the output of the gradient amplifier.

Blip Asymmetry (PVM_EpiBlipAsym) – Correction of blip amplitudes which can be used for reducing the so-called oblique ghosts. Possible causes are different response delays of gradient channels in double-oblique slice geometry or eddycurrent cross-terms. Rarely necessary.

Readout Asymmetry (PVM_EpiReadAsym) – Amplitude correction for the calculated read gradient shapes in the case of a non-linear response of the gradient system. This results in a wrong positioning of the echoes in the k-space inducing some geometric distortions. Rarely necessary.

Echo Spacing (PVM_EpiEchoSpacing) – Time between centers of consecutive gradient echoes of the EPI sequence. Shorter echo spacing leads to lower image distortions. Increasing the signal bandwidth and reducing the readout matrix size reduces the echo spacing.

Eff Image Bandwidth (PVM_EpiEffBandwidth) – Effective bandwidth of the EPI image in the phase encoding (blip) direction. Higher bandwidth means lower distortions and blurring. The bandwidth increases with the number of segments and GRAPPA acceleration.

1.9.1.8.4 Trajectory

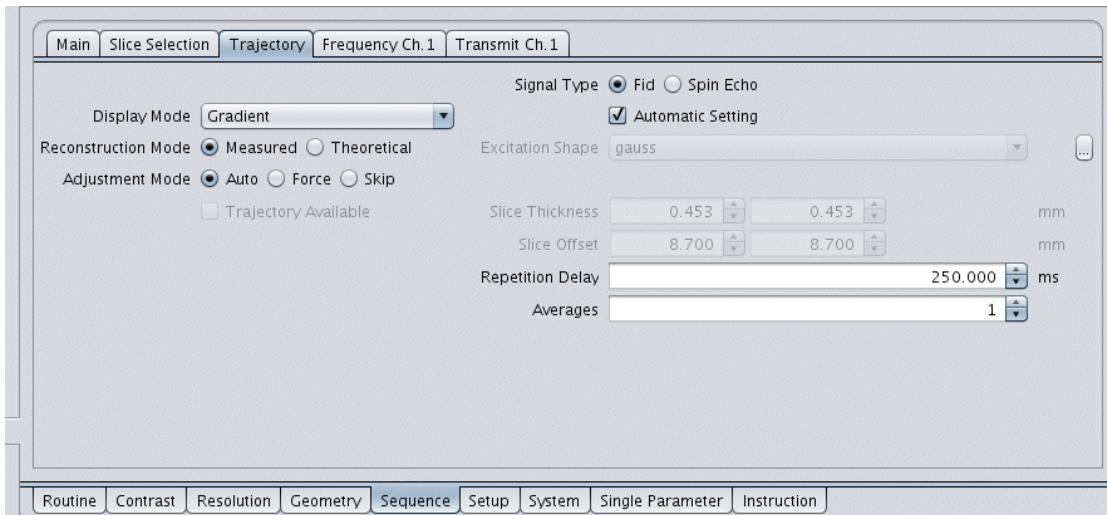


Figure 1.230: Sequence Card Trajectory

This card is present in non-cartesian imaging methods like UTE or SPIRAL which need the k-space trajectory for data reconstruction. It contains parameters of an automatic adjustment which measures k-space trajectories created by gradient shapes before the actual scan.

Principles

The signal from off-centered spins is acquired while playing out the gradient shape in the investigated dimension. From the phase difference of the measured signals the k-space trajectory can be calculated (see References [\[01\]](#) [\[691\]](#), [\[15\]](#) [\[691\]](#), [\[16\]](#) [\[691\]](#)).

Although the gradients are described - as usual - in the RPS coordinate system, the actual measurement is executed separately for all involved physical gradients directly in the XYZ object coordinate system. Thus, the effects of different gradient delays can be detected.

Parameters

Display Mode (PVM_TrajDisplayStyle) – Choice of data which will be displayed in the Acq/Reco Display during the adjustment. Available Settings : Trajectory, Gradient, Spectrum

Reconstruction Mode (PVM_TrajRecoMode) – Determines if the measured or the theoretical trajectory will be used for reconstruction

Adjustment Mode (PVM_TrajAdjMode) – Defines in which cases the trajectory adjustment will be performed:

- Auto: The trajectory adjustment will start automatically if no measured trajectory is available.
- Force: The trajectory adjustment will always start before the actual scan.
- Skip: The trajectory adjustment will be skipped.

Trajectory Available (PVM_TrajUpToDate) – Indicates if a measured trajectory is available

Signal Type (PVM_TrajSignalType) – Defines the type of the observed signal: Fid or Spin Echo

Automatic Setting (PVM_TrajAuto) – The following parameters will automatically be derived from method settings:

- **Excitation Shape** (PVM_TrajExcPulseEnum) – Slice selective excitation pulse
- **Refocusing Shape** (PVM_TrajRfcPulseEnum) – Refocusing pulse in the spin-echo mode
- **Slice Thickness** (PVM_TrajSliceThick) – Defines the slice thickness of the trajectory measurement
- **Slice Offset** (PVM_TrajOffset) – Defines the offset position of the trajectory measurement. This offset position is displayed in the Geometry Editor thus the user can check if the trajectory slice is located inside the object. If this is not the case, the automatic settings can be switched off and the slice offset can be adapted accordingly.

Repetition Delay (PVM_TrajRepDelay) – Additional relaxation delay before the next RF excitation is performed

Averages (PVM_TrajAvgs) – To improve SNR averages can be carried out.

Workflow

Most samples contain components with short as well as long T₂. In such a case the automatic trajectory measurement can be used. However, if only short T₂ components are available the trajectory measurement should be carried out on a homogenous phantom with longer T₂ components. For this purpose, create the required protocol, open the Adjustment Platform and start the Trajectory Measurement. After successful completion of the adjustment, the trajectory can be saved with right mouse click Save Adjustment Result for other Studies.

1.9.1.8.5 Frequency

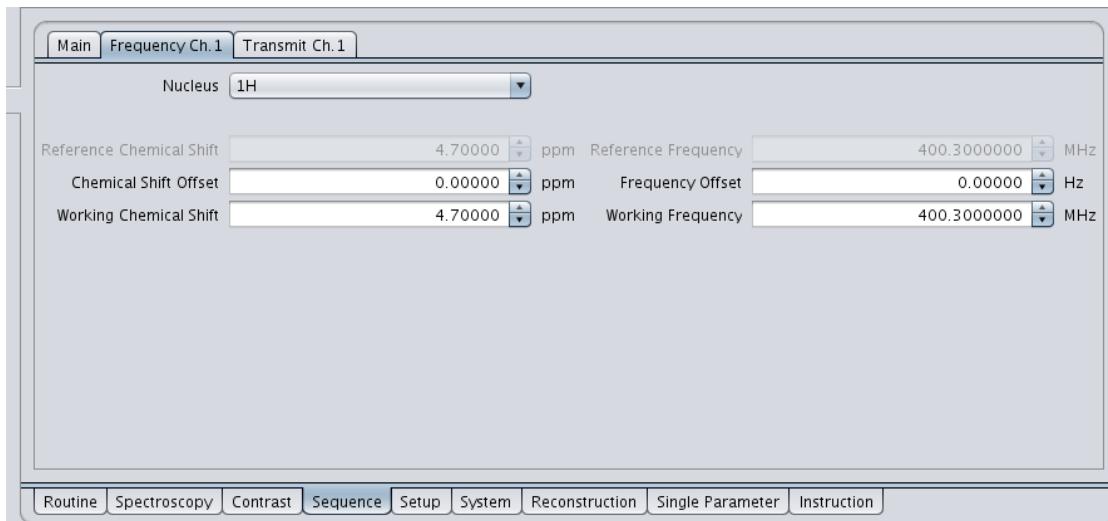


Figure 1.231: Sequence Card Frequency Ch 1

Nucleus (PVM_Nucleus1Enum) – Allows to select the nucleus for channel 1 from a list of nuclei available in current operation mode

Reference Chemical Shift (PVM_FrqRefPpm) – Chemical shift for which the reference frequency has been automatically adjusted, typically 4.7 ppm, meaning that the dominating signal comes from water. This parameter is not editable. If its change is necessary, for example when fat signal is dominating and the reference frequency represents lipids (1.2 ppm), the modification has to be made in the Adjustment Platform.

Chemical Shift Offset (PVM_FrqWorkOffsetPpm) – Difference between working and reference chemical shifts (typically zero, when working on water signal and water frequency is reference)

Working Chemical Shift (PVM_FrqWorkPpm) – Central chemical shift of the experiment (by default, 4.7 meaning the experiment is centered on water line). This signal component will be represented at the correct position in the image, and will be excited at the nominal slice (voxel) location. Other components may be shifted proportionally to their deviation from the working chemical shift. For example, in a localized 1H MRS study, one can set this parameter to 2.0 to make sure the NAA signal originates from the exact voxel position.

Reference Frequency (PVM_FrqRef) – Automatically adjusted frequency, non-editable; a change is possible in the Adjustment Platform.

Frequency Offset (PVM_FrqWorkOffset) – Difference between working and reference frequencies

Working Frequency (PVM_FrqWork) – Central frequency of the experiment. Slice-selective pulses will have this frequency plus a position-dependent offset.

1.9.1.8.6 Transmit



Figure 1.232: Sequence Card Transmit Ch 1

Nucleus (PVM_Nucleus1Enum) – Selection of the nucleus for channel 1 from a list of nuclei

Reference Power Mode (PVM_RefPowMod1) – When set to **Auto**, the reference power is derived from the previously run adjustment. When set to **User**, **Reference Power** can be edited. Changes made in this way will only be effective for the current scan. It is possible to change the reference power for the entire study in the Adjustment Platform.

Reference Power (PVM_RefPowCh1) – Power needed for a 1 millisecond, rectangular 90 degree pulse, used to calculate power for other pulse shapes and flip angles

Reference Power Status (PVM_RefPowStat1) – String describing the status of the reference RF power (manually/automatically adjusted, etc.)

1.9.1.9 FAIR Card

This card is present in perfusion MRI methods using the flow-sensitive alternating inversion recovery (FAIR) module for arterial spin labeling. This module alternatively inverts the spins in a selected slab and in the entire RF coil volume, and controls the following recovery delay. Its parameters describe the details of the inversion, order of selective/non-selective experiments and the table of recovery delays.

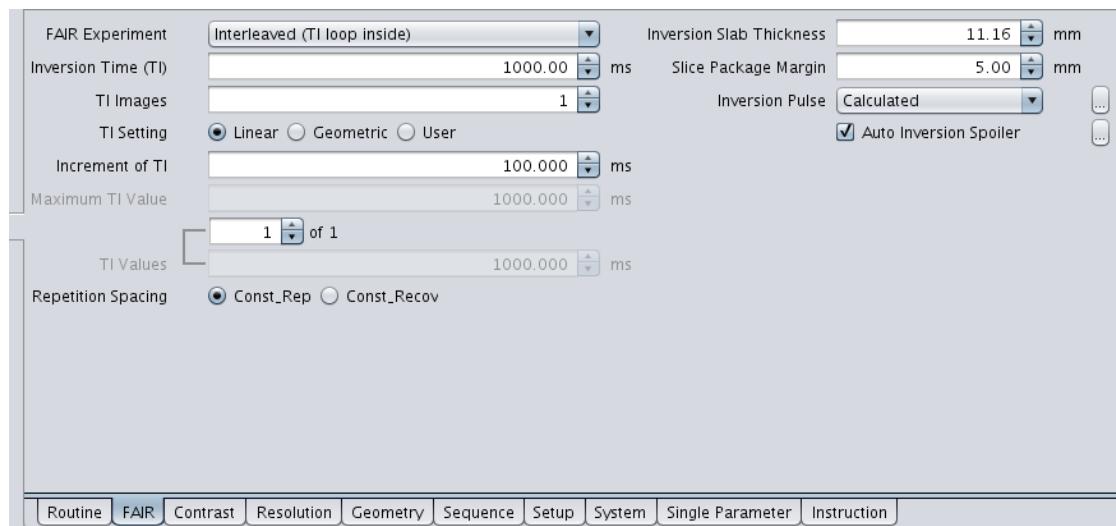


Figure 1.233: Fair Card

FAIR Experiment (FairMode) – Possible values are:

- Selective – Only slice-selective inversions will be performed (for example for a perfusion-sensitive dynamic study, such as fMRI).
- Non-selective – Only non-selective inversions will be performed (a perfusion-insensitive study).
- Interleaved (TI loop inside) – Selective and non-selective inversions will be interleaved in consecutive repetitions (the classic mode of FAIR, for example for a quantitative, dynamic perfusion study). The selective inversion comes first. When more than one inversion recovery time (TI) is measured, all TI values are acquired with a selective inversion, and then with a non-selective inversion.
- Interleaved (TI loop outside) – Identical to previous option for a single TI; for multiple TI's each TI value is acquired with a selective and with a non-selective inversion before moving to the next.

Inversion Time (TI) (FairTIR) – First inversion recovery time. The time between the inversion pulse and the excitation pulse of the first slice. Consecutive slices have slightly different TIR values. For this reason, the method should not be used with more than 3-5 slices.

TI Images (FairTIR_NExp) – Number of different TI values repeated with each inversion mode (selective and non-selective). More than one TI value is needed when a T1-based perfusion evaluation is to be applied.

TI Setting (FairTIR_Mode) – Controls the setting of multiple inversion recovery times. Possible values are:

- Linear – A linear sequence of TI values is calculated starting from FairTIR and incrementing by FairTIR_inc (see below).
- Geometric – A geometric sequence of TI values is calculated starting from FairTIR and ending with MaxTIR (see below).
- User – The sequence of TIR values is freely editable.

Increment of TI (FairTIR_Inc) – Difference between consecutive TIR values when FairTIR_NExp > 1, visible when FairTIR_Mode = Linear

Maximum TI value (MaxTIR) – Last (and highest) TIR value, visible when FairTIR_Mode = Geometric

TI Values (FairTIR_Arr) – Array of TIR values, editable when FairTIR_Mode = User

Repetition Spacing (RepetitionSpacing) – Controls the timing of dynamic experiments. Possible values are:

- Const_Rep – Providing a constant repetition time (given by PVM_RepetitionTime)
- Const_Recov – Giving a constant recovery time (given by RecoveryTime). In experiments with short and long TIR-times (see below), the constant recovery mode is more time-efficient.

Inversion Slab Thickness (InvSlabThick) – Thickness of the inversion slab in the selective mode. Can not be set to less than the extent of the package.

Slice Package Margin (InvSlabMargin) – Extent of the selective inversion slab beyond the imaging slice package

Inversion Pulse (InvPulse1Enum) – Inversion pulse. When set to Calculated, the system automatically generates an adiabatic full passage pulse shape, which guarantees a 180 degree flip and gives an excellent selection profile.

Auto Inversion Spoiler (FairSpoiler.automatic) – Gradient spoiler applied after the inversion pulse to dephase residual transverse magnetization.

1.9.1.10 Setup Card

This card contains parameters which may be manually adjusted during a setup experiment.

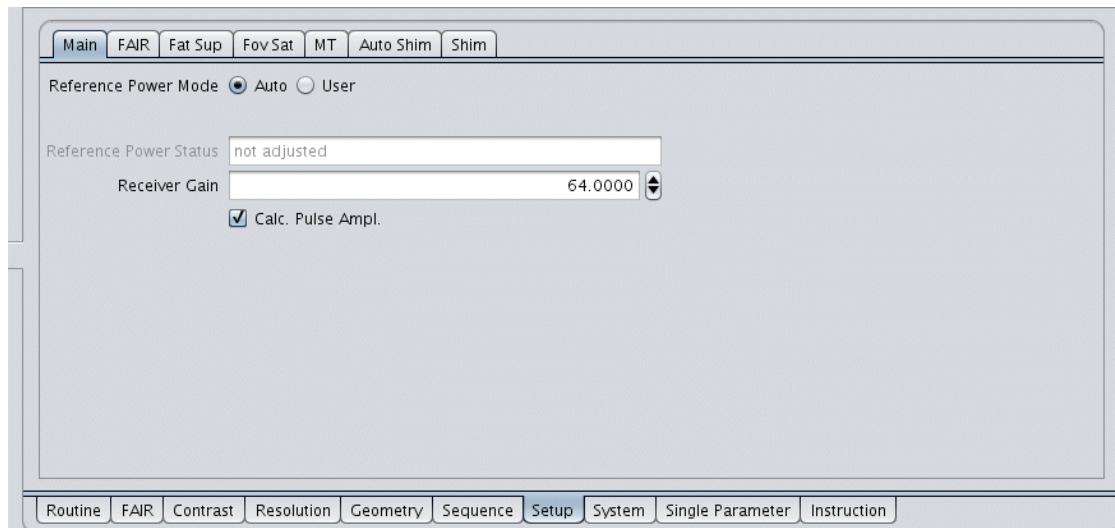


Figure 1.234: Setup Card

Reference Power parameters – See [Transmit \[▶ 281\]](#)

Calc. Pulse Ampl. (PVM_DeriveGains) – Determines if the system should automatically calculate the RF pulse gains to obtain the specified flip angles. Not selecting this parameter allows a manual gain adjustment (not recommended for standard use).

Typically, this card also contains parameters controlling the power and amplitude of the RF pulses used by the sequence (e.g. Exc. Pulse Attenuation) when the calculation of pulse amplitude is switched off (see above). Further subcards may be present providing similar access to RF pulses used by contrast modules.

Auto Shim

This card controls the strategy of automatic shimming (magnetic field homogeneity correction) before the scan. In particular, shimming based on a measured field map (MapShim) can be activated here. Tools for manual shimming can be found on a different card (Shim). Note that any change of the shims (automatic or manual) will force an additional frequency adjustment before the scan. When MapShim is selected, this frequency adjustment will be localized to the shim volume.

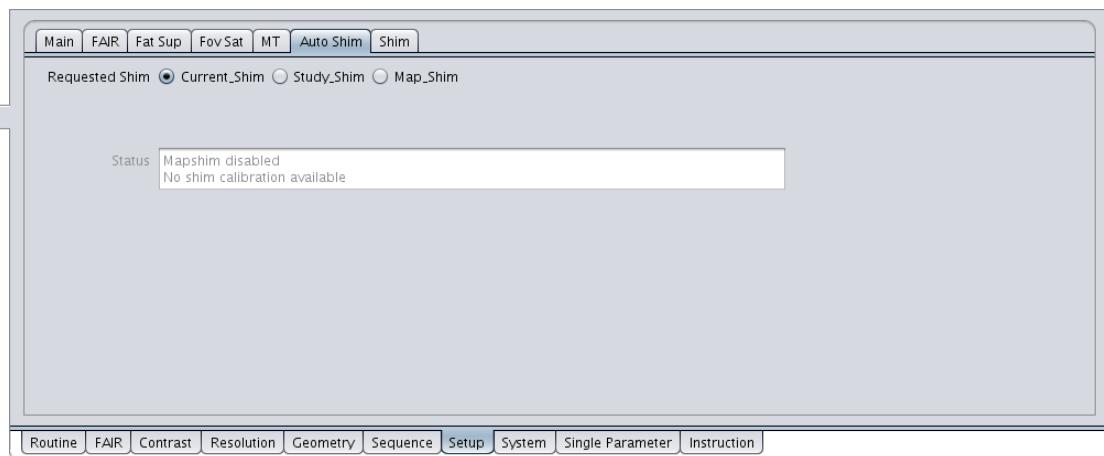


Figure 1.235: Setup Card Auto Shim

Requested Shim (PVM_ReqShimEnum) – Defines the way the shims will be set for the present scan. Three modes are implemented:

- **Current_Shim**: The shim remains unchanged. This option should be used in case the shim optimized in previous scans should be also used for the current scan.
- **Study_Shim**: The global shim adjusted in the first scan of a study should be used for the current scan.
- **Map_Shim**: The shim will be calculated based on a previously measured B0-field map to optimize the field homogeneity within the Shim Volume, which appears as an additional object in the Geometry Editor. This volume can be directly manipulated (shifted, resized, rotated) in the editor, or it can be automatically linked to the image/voxel geometry. The B0 map necessary for MapShim has to be acquired in the Adjustment Platform. The calculation takes place during a special adjustment before the scan. In this mode additional parameters controlling the algorithm appear editable on the card.

Shim up to (PVM_MapShimUseShims) – Defines which shims should be fitted by the MapShim algorithm. Per default, all calibrated shims are used. In case of small shim volumes an attempt to calculate high order shims may lead to excessive shim power on some systems and cause the experiment to stop with an error message; in that case a reduction of the shim order is necessary. The choice is:

- **AllShims**: All calibrated shims are calculated by the shimming algorithm.
- **ThirdOrder**: Shims up to the 3rd order are calculated by the shimming algorithm.
- **SecondOrder**: Shims up to the 2nd order are calculated by the shimming algorithm.
- **FirstOrder**: Only linear shims are calculated by the shimming algorithm.

Iterative Correction (PVM_MapShimLocShim) – When activated, an iterative correction of the linear shims is performed after the map shim calculation based on a signal localized within the cuboid shim volume. This option provides narrowest lines in voxel spectroscopy.

Status (PVM_MapShimStatus) – A non-editable text parameter informing if the MapShim calculation is possible and what to do if it is not (Map not acquired, shims not calibrated etc.)

Automatic Shim Volume (PVM_MapShimVolDerive) – This parameter is only visible in imaging or localized spectroscopy methods in which slices or voxels are visualized in the Geometry Editor. If activated, the shim volume is bound to the dimension, orientation and position of the master geometry object (first slice package or voxel).

Shim Volume Margin (PVM_MapShimVolMargin) – This parameter is visible if **Automatic Shim Volume** is activated. The extent of the shim volume is defined by the master geometry object (1st slice package or voxel) and each extent of the shim volume may be increased by an additional margin as defined by this parameter. For localized spectroscopy, extending the area of the shim calculation may improve linewidth and water suppression performance.

Shape of shim volume (PVM_MapShimVolShape) – Defines the shape of the shim volume. The following shapes are defined:

- **Cuboid**: a box-like shim volume
- **Cylinder**: a cylindrical shim volume
- **Ellipsoid**: an elliptical shim volume (extents are main axes)

1.9.1.11 Reconstruction Card

In addition to the RECO parameters controlling the image word size and mapping (available in all methods) this subclass contains parameters that allow the selection of special reconstruction features (e.g of FLASH), in particular those needed for Susceptibility-Weighted Imaging (SWI). Parameters of this subclass can be modified after the experiment completion to produce various reconstructions from the same raw data.

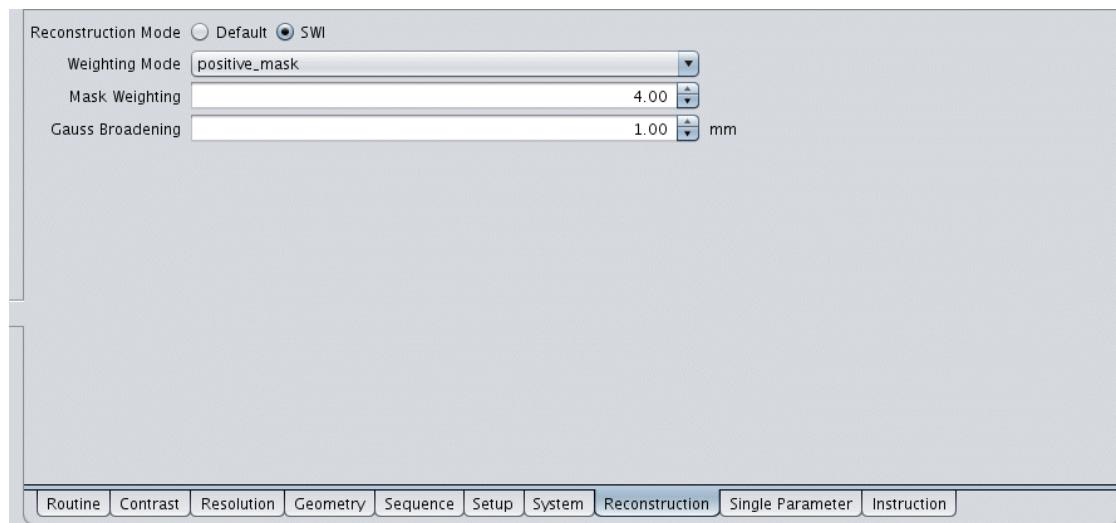


Figure 1.236: Reconstruction Card

Reconstruction Mode (RecoMethMode) – Switches between the standard magnitude reconstruction (`Default`) and the Susceptibility Weighted Imaging mode (`SWI`). The latter allows combining of the phase information with the magnitude value of the image to enhance the contrast depending on local susceptibility variations of the tissue. The way this combination takes place is determined by the following parameters, which appear only when the `SWI` mode is selected.

Weighting Mode (WeightingMode) – Allows the selection of one of the `SWI` weighting modes, i.e., the way the phase information influences the image intensity:

- `positive_mask`: Positive phase will reduce the image intensity.
- `negative_mask`: Negative phase will reduce the image intensity.
- `magnitude_mask`: Negative and positive phase will reduce the image intensity.
- `phase_image`: The phase value is directly reconstructed (magnitude information is ignored)

The three mask options produce an enhancement of the natural $T2^*$ contrast of the image. Areas of local susceptibility variations that appear dark at long echo times due to short $T2^*$ (e.g. veins) will be additionally attenuated due to phase changes caused by local frequency offsets. The last option (`phase_image`) allows a visualization of such areas based solely on the frequency offset, disregarding $T2^*$.

Mask Weighting (MaskWeighting) – Controls the strength of the weighting in one of the mask modes (ignored in the `phase_image` mode). The phase-based mask function will be taken to the power given by this parameter before being multiplied by the magnitude image.

Gauss Broadening (GaussBroadening) – Defines the broadening (smoothing) effect [mm] of the Gauss filter that is used to create a low-resolution reference image. This operation is needed to separate smooth phase variations that are due to shim imperfections from the local phase effects which are of interest in the experiment. The phase value used for the image weighting mentioned above is actually a deviation of the true image phase from the phase of the Gaussian-filtered reference image. Only the phase variations that are of a shorter spatial range than the value of **Gauss Broadening** will lead to a contrast enhancement.

1.9.2 FLASH

1.9.2.1 Principles

FLASH (Fast Low Angle Shot) is a general purpose 2D/3D MRI method based on a gradient echo generated with a single slice-selective RF pulse. Compensated (rewound) phase encoding and constant spoiling gradients allow running the sequence with short TR. The contrast is relatively independent of T1 and T2 with short TE and TR because of the steady-state character of the signal. T1-dependent contrast can be obtained with the RF spoiling option, which removes the echo contributions to the signal. With longer echo times, T2* contrast becomes dominant. A special reconstruction option is available that mixes the phase and magnitude information to produce susceptibility-weighted images. The method allows cine acquisitions (a series of movie frames following a trigger event) to visualize periodic motion such as the cardiac cycle. With activated Angio Mode the method can be used for time-of-flight (TOF) angiography.

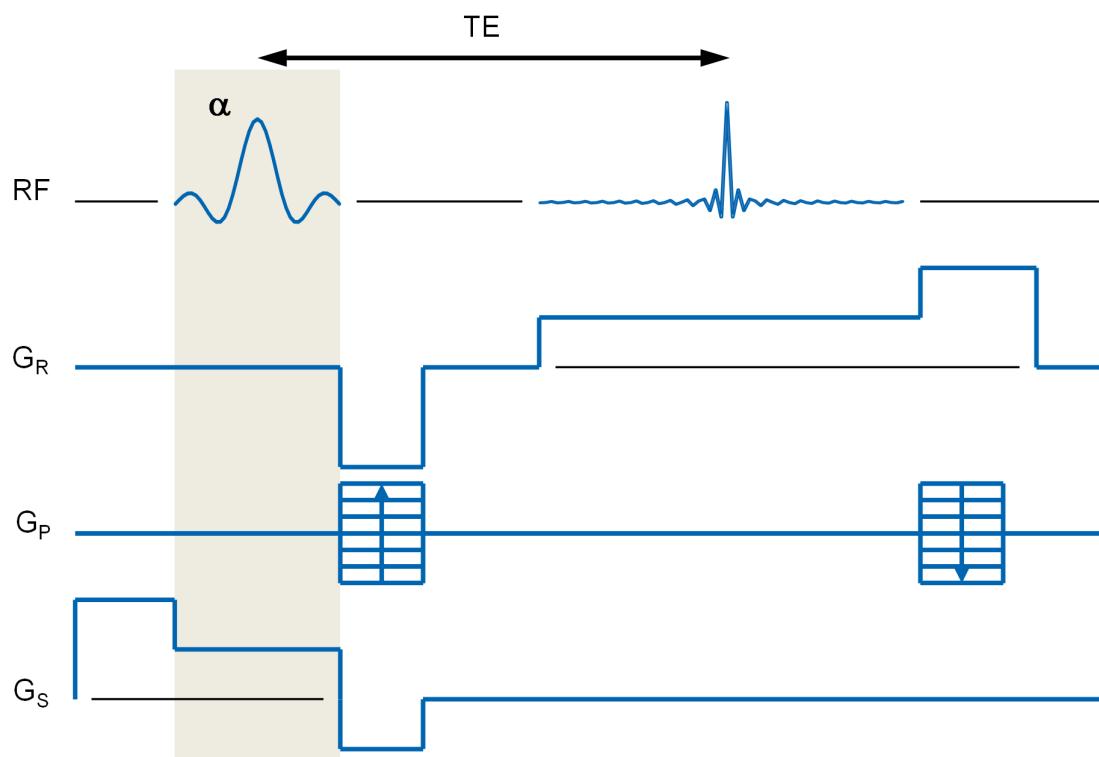


Figure 1.237: Pulse sequence of FLASH

1.9.2.2 Applications

- Rapid pilot images
- High-resolution BOLD contrast imaging (fMRI) with $TE = T2^*$
- T1-weighted MRI with short TE and $T1 > TR > T2$, or with short TR and RF spoiling
- Susceptibility-weighted imaging
- Cardiac cine imaging

1.9.2.3 Loop Structure

Two different acquisition loop structures are available depending on the value of Angio Mode.

From inner to outer loops:

- **Angio Mode off:** slices, movie frames (special option), accumulation, phase-encoding, repetitions
- **Angio Mode on:** phase-encoding, slices, accumulation (NA), repetitions (movies not possible)
- Image order in 2dseq file: slices, movie frames, repetitions

1.9.2.4 Specific Parameters

Routine Card

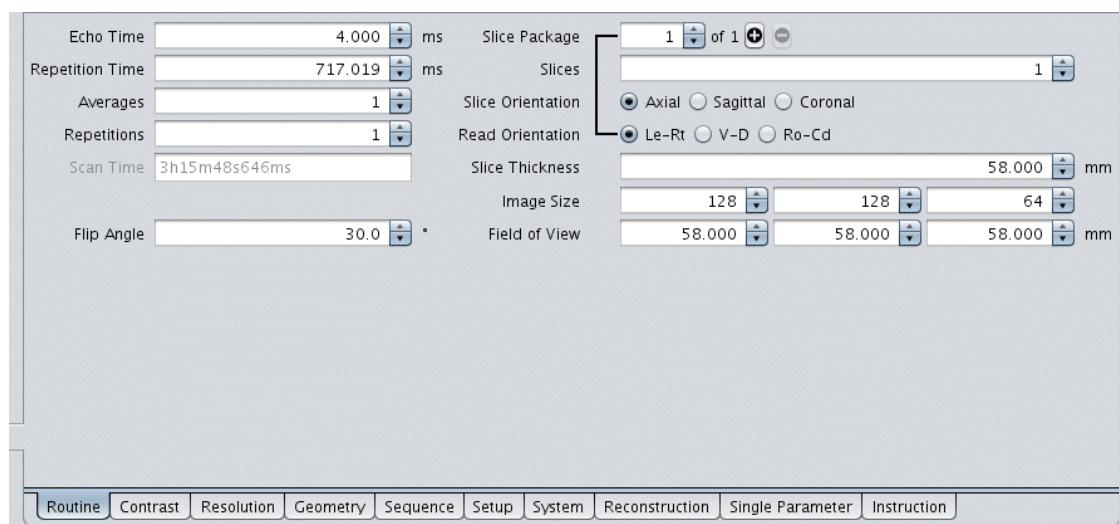


Figure 1.238: FLASH Routine Card

Echo Time (PVM_EchoTime) – Time between the center of the excitation RF pulse and the center of the gradient echo. This parameter determines the T2* contrast of the image.

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse. Determines both T1 and T2 contrast of the image. In particular, with short TR and RF spoiling, increasing the flip angle enhances the T1 contrast of the image (long T1 components appear darker).

Contrast Card

Main

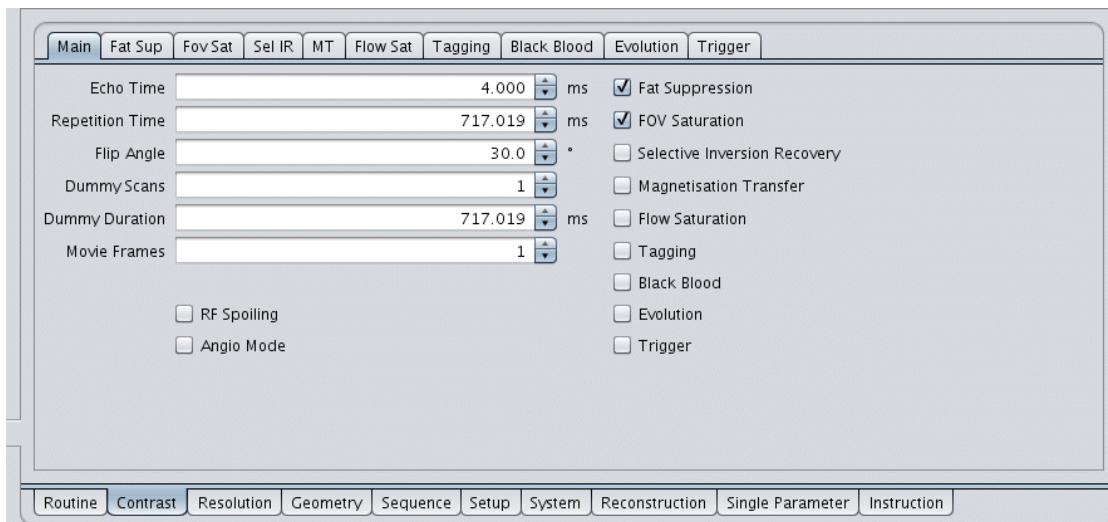


Figure 1.239: FLASH Contrast Card Main

Flip Angle (ExcPulse1.Flipangle) – See [Routine Card \[▶ 287\]](#)

Movie Frames (PVM_NMovieFrames) – Each phase encoding step (for all slices) will be repeated the number of times given by this parameter to produce a series of images showing different phases of a periodical motion (i.e. of the heart), as shown in Figure [FLASH Contrast Card Main \[▶ 288\]](#). The time from frame to frame is given by TR. Movies are typically acquired with the triggering (e.g. by ECG), in which case the frames represent different delays after the trigger event.

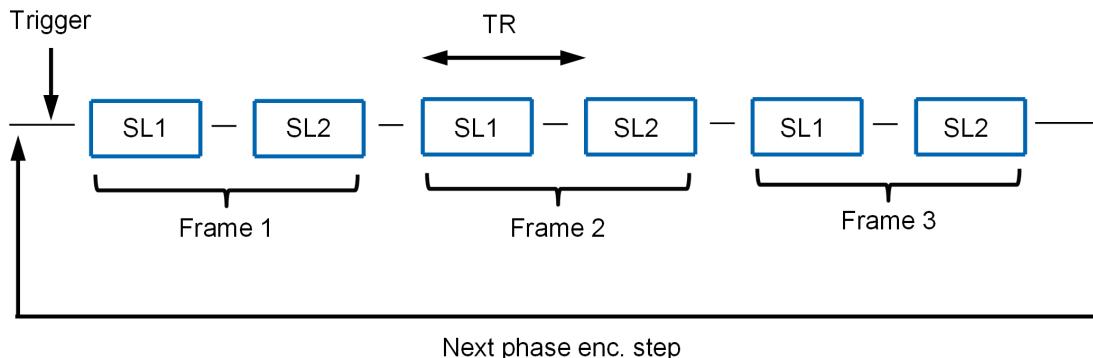


Figure 1.240: Diagram FLASH after contrast



Movies of consecutive slices are phase-shifted; the movie option should be used with low numbers of slices.



It is possible to select the parallel acceleration option (see [Encoding \[▶ 270\]](#)) to reduce measurement time and artefacts, if necessary.

RF Spoiling (RFSpoiling) – Turns on an RF phase cycle that removes echo components from the steady state signal. With short TR and TE and high flip angles this option produces T1-dependent contrast.

Angio Mode (AngioMode) – Changes the loop structure to the time-of-flight angiography mode. All phase encoding steps are completed for a given slice before moving to another one. This gives a saturation of the static spins, while the blood flowing into the slice produces a strong signal. The effect is enhanced by short TR, high flip angles and RF spoiling.

Sequence Card

Main

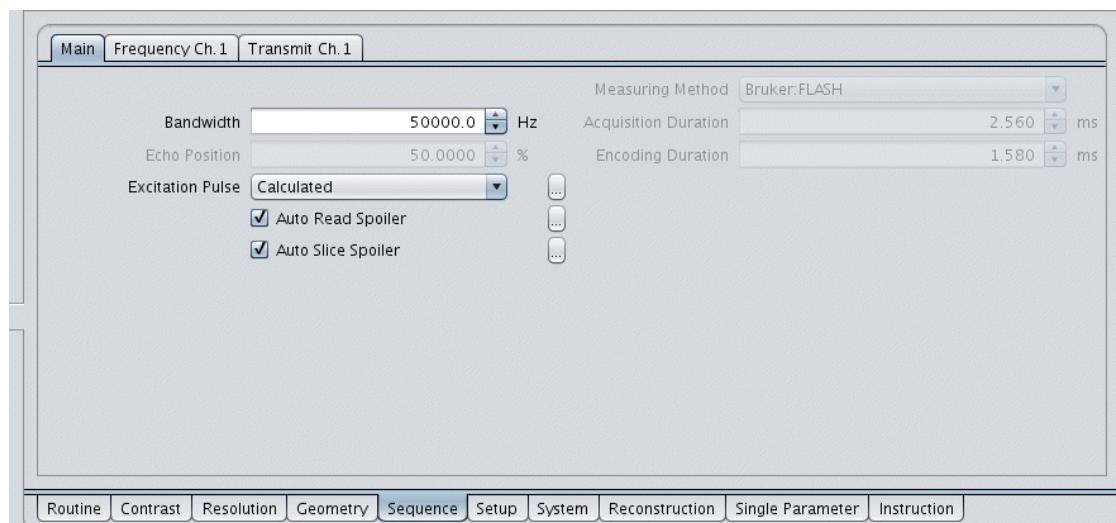


Figure 1.241: FLASH Sequence Card Main

Echo Position (PVM_EchoPosition) – Determines the position of the echo in the acquisition window. Values below 50% allow lower TE. Depends on the Partial FT setting for the read direction on the Resolution Card.

Excitation Pulse (ExcPulse1Enum) – The slice selective excitation pulse. When the method works in the 3D mode (selection in the Resolution Card) this pulse selects the slab that is reconstructed as 3D volume. In this case it is important to select a high sharpness factor for this pulse (7 or higher) avoid aliasing of out-of-slab signals.

Auto Read Spoiler (ReadSpoiler.automatic) – A constant gradient pulse applied on the read channel after the echo acquisition.

Auto Slice Spoiler (SliceSpoiler.automatic) – A constant gradient pulse applied on the slice channel after the echo acquisition.

1.9.3 FcFLASH (FcFast Low Angle Shot)

1.9.3.1 Principles

This method is identical with FLASH except for the flow compensation of all gradient channels. Flow compensation removes unwanted phase shifts of the signal caused by the flow and thus reduces signal dephasing within vessels and ghosting artefacts related to pulsation. Its trade-off is a longer echo time. The method is advantageous compared to FLASH mainly in angiography and cardiac applications.

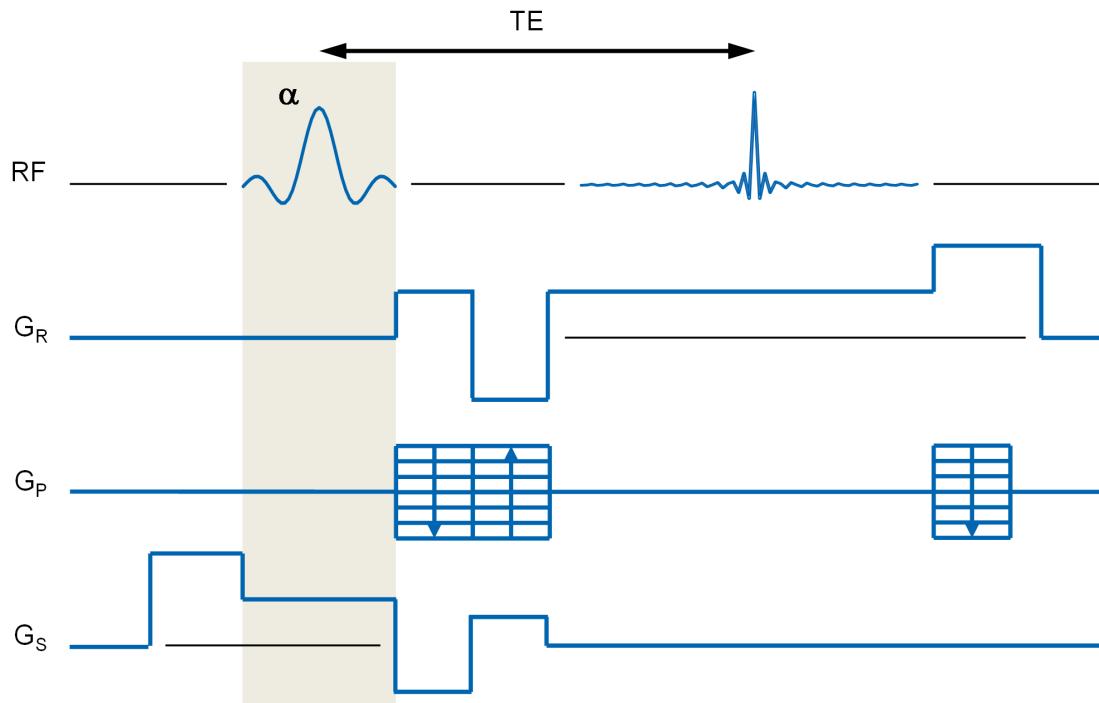


Figure 1.242: Pulse sequence of FcFLASH

1.9.3.2 Applications

- All applications in which the standard gradient echo method suffers from signal loss caused by flow or motion
- Signal enhancement in heart imaging
- TOF Angiography (3D and 2D multislice; the latter in Angio Mode)

1.9.3.3 Loop Structure

Two different acquisition loop structures are available depending on the value of Angio Mode.

From inner to outer loops:

- **Angio Mode off:** slices, movie frames (special option), accumulation (NA), phase-encoding, repetitions
- **Angio Mode on:** phase-encoding, slices, accumulation (NA), repetitions (movies not possible)
- Image order in `2dseq` file: slices, repetitions

1.9.3.4 Specific Parameters

Parameters are the same as in Chapter [FLASH \[▶ 286\]](#).

1.9.4 IgFLASH

1.9.4.1 Principles

IgFLASH is a variant of the FLASH method featuring IntraGate – Bruker Biospin's proprietary implementation of the navigator-based self-gated cine MRI. It produces movies of cardiac and respiratory cycles without the need of physiologic signals. Prior to the gradient echo imaging segment, a navigator signal is acquired from a slab which can be graphically prescribed by the operator. The reconstruction uses the navigator to detect the phase of cardiac and respiratory cycles and correspondingly assign the following MRI signal. Once the experiment is completed, the user can select various reconstruction options including the choice of the targeted motion (cardiac or respiratory), the number of reconstructed movie frames, and the degree of time interpolation. During the setup phase the detected motion signal is displayed in real time allowing a verification of the navigator slab positioning before the start of acquisition.

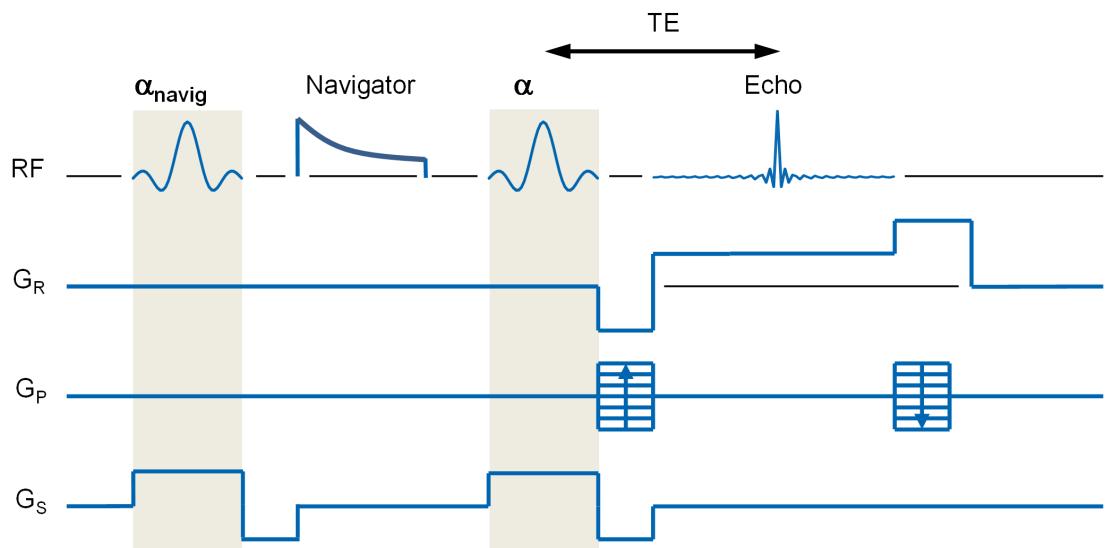


Figure 1.243: Pulse sequence of IgFLASH

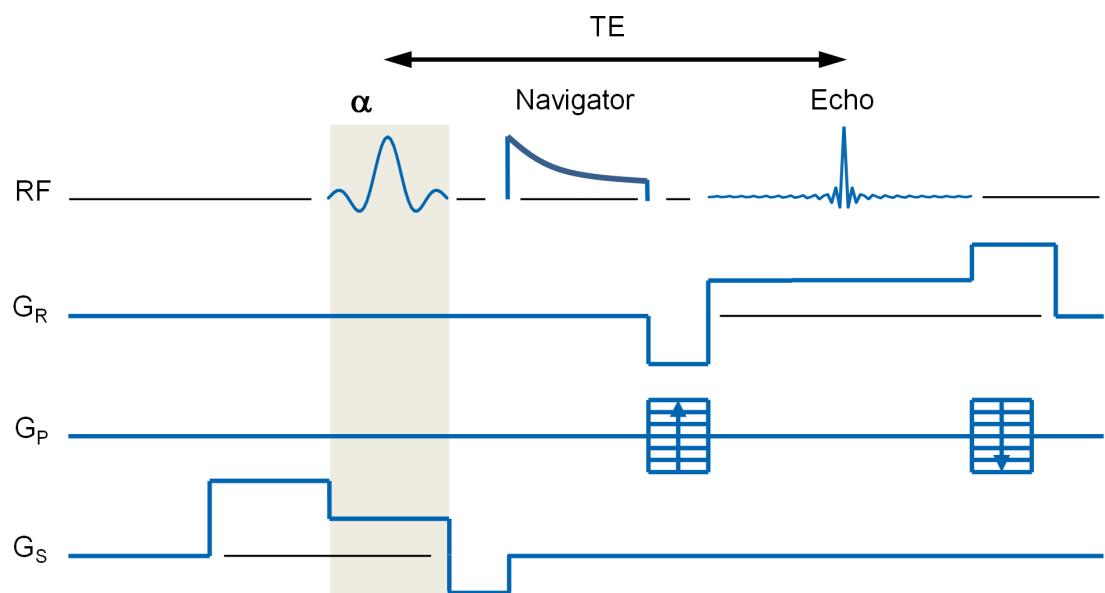


Figure 1.244: Pulse sequence of IgFLASH (In-slice navigator)

1.9.4.2 Applications

- Cardiac cine imaging without ECG signals
- Abdominal images free of motion artefacts
- Time course cines
- Respiratory cine imaging without respiratory monitoring

1.9.4.3 Loop Structure

From inner to outer loops:

- Acquisition order: slices, phase encoding inside segment, oversampling, next segment, repetitions
- Image order in `2dseq` file: slices, cardiac and respiratory phases, time course

1.9.4.4 Specific Parameters

Routine Card

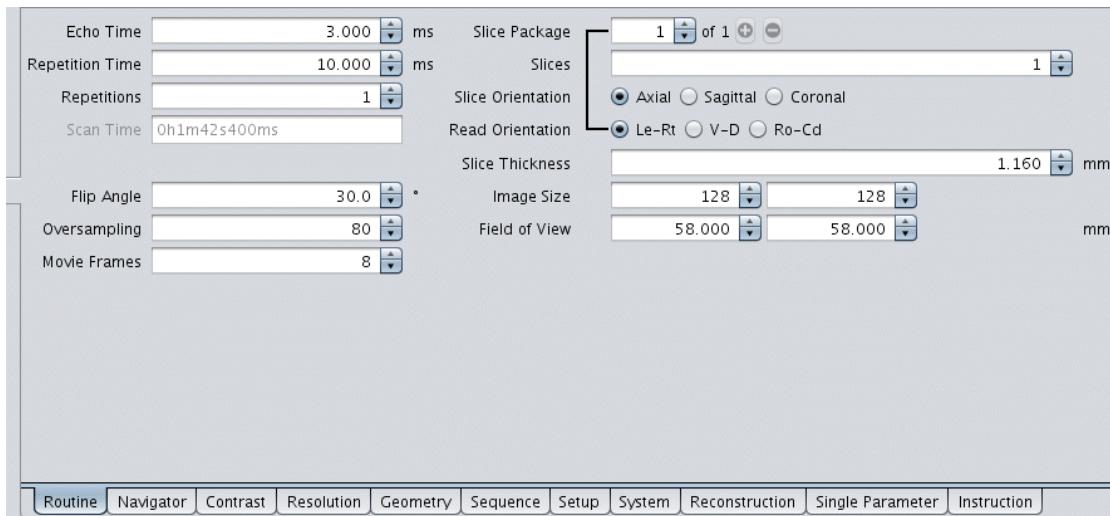


Figure 1.245: IgFLASH Routine Card

Echo Time (PVM_EchoTime) – Time between the center of the excitation RF pulse and the center of the gradient echo. This parameter determines the T2* contrast of the image.

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse. Determines both T1 and T2 contrast of the image. In particular, with short TR and RF spoiling, increasing the flip angle enhances the T1 contrast of the image (long T1 components appear darker).

Oversampling (Oversampling) – Number of times each phase encoding step is repeated. It should be set high enough to sufficiently sample cardiac and respiratory cycles, e.g., to 100 for a cardiac movie with 10 frames. Experiment duration is proportional to this parameter.

Movie Frames (PVM_NMovieFrames) – Number of frames of the reconstructed movie. Further parameters defining the movie can be found on the [Reconstruction Card \[▶ 295\]](#).

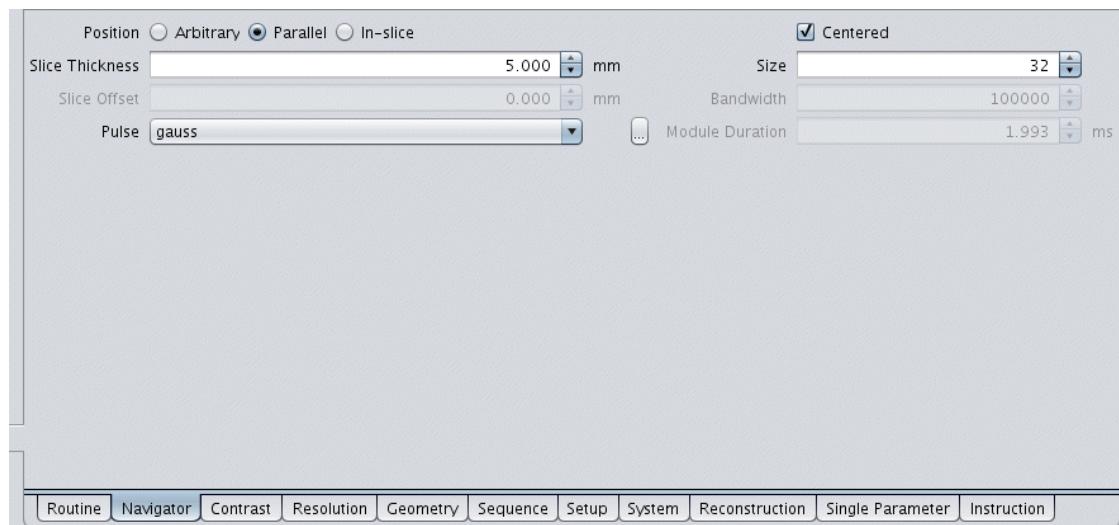


Figure 1.246: IgFLASH Navigator Card

Position (PVM_NavPosMode) – Controls the navigator slice position: without any restrictions (Arbitrary), parallel to imaging slice (Parallel) or derived from imaging slice (In-slice). For Arbitrary and Parallel orientation the navigator slice is visualized in the Geometry Editor. The In-slice option limits the number of imaging slices to one.

Slice Thickness (PVM_NavSliceThickness) – Defines the thickness of the navigator slice

Slice Offset (PVM_NavSliceOffset) – Offset position of the navigator slice

Pulse (PVM_NavPulseEnum) – Choice of excitation pulse for navigator signal

Centered (PVM_NavPosCentered) – In case of Parallel position the navigator slice can be centered around the imaging slice package

Size (PVM_NavPoints) – Controls the acquisition size of the navigator scan

Bandwidth (PVM_NavSWh) – Acquisition bandwidth of the navigator scan

Module Duration (PVM_NavigatorModuleTime) – Duration of the navigator module

Contrast Card

Main

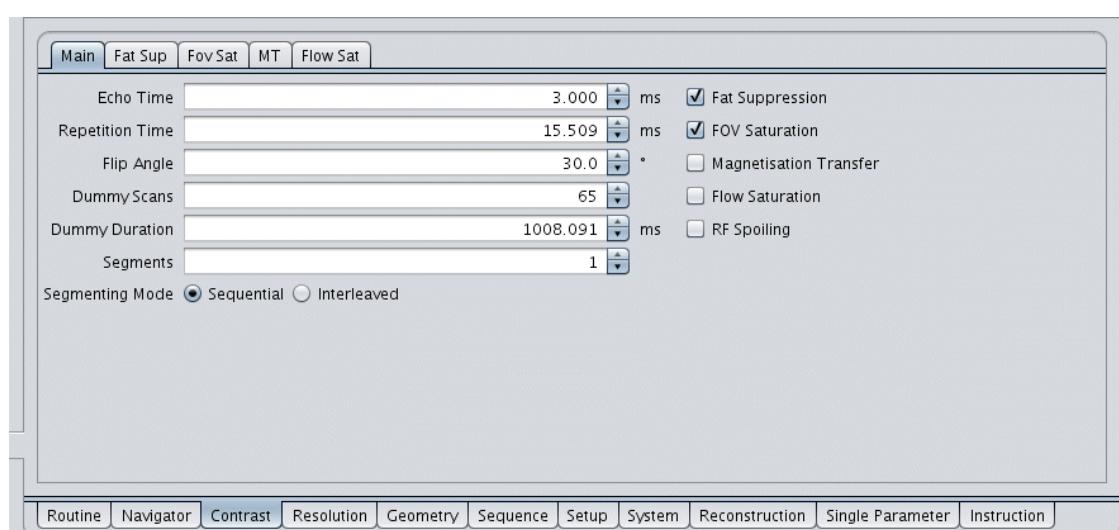


Figure 1.247: IgFLASH Contrast Card Main

Flip Angle (ExcPulse1.Flipangle) – See [Routine Card \[▶ 292\]](#).

Segments (Nsegments) – If segmentation is used (Nsegments>1), only a part of k-space is acquired inside the oversampling loop before moving to the next segment.

Segmenting Mode (Seg_mode) – Determines the way the phase encoding is performed in case of segmentation. Possible values: Interleaved or Sequential

RF Spoiling (RFSpoiling) – Turns on an RF phase cycle that removes echo components from the steady state signal. With short TR and TE and high flip angles this option produces T1-dependent contrast.

Sequence Card

Main

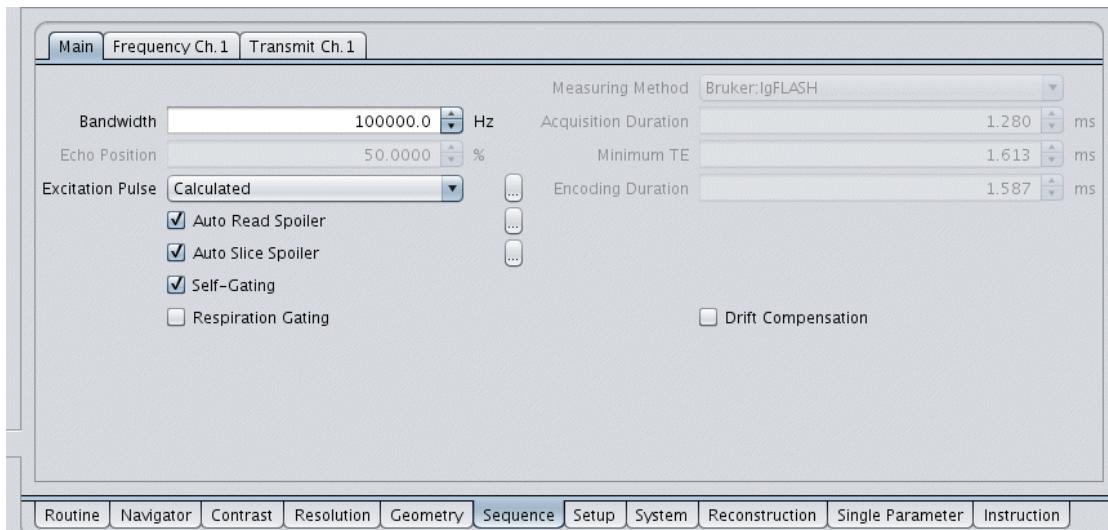


Figure 1.248: IgFLASH Sequence Card Main

Echo Position (PVM_EchoPosition) – Determines the position of the echo in the acquisition window. Values below 50% allow lower TE. Depends on the Partial FT setting for the read direction on the [Resolution Card \[▶ 269\]](#).

Excitation Pulse (ExcPulse1Enum) – The slice selective excitation pulse. When the method works in the 3D mode (selection in the [Resolution Card \[▶ 269\]](#)) this pulse selects the slab that is reconstructed as 3D volume. In this case it is important to select a high sharpness factor for this pulse (7 or higher) to avoid aliasing of out-of-slab signals.

Auto Read Spoiler (ReadSpoiler.automatic) – A constant gradient pulse applied on the read channel after the echo acquisition

Auto Slice Spoiler (SliceSpoiler.automatic) – A constant gradient pulse applied on the slice channel after the echo acquisition

Self-Gating (SelfGating) – Turns on the self-gating (IntraGate) reconstruction. When deselected, only a default reconstruction without data sorting will be carried out.

Respiration Gating (RespGate) – Activates the standard physical respiratory gating (the respiration trigger must be connected). The self-gating reconstruction will only be applied for cardiac phases allowing a faster acquisition with lower oversampling. The sequence performs dummy scans while waiting for the respiratory trigger to preserve steady-state signal.

Minimum TE (PVM_MinEchoTime) – Indicates the minimum echo time

Drift Compensation (PVM_DriftCompYesNo) – Activation of field drift compensation based on a navigator signal and a reload mechanism of the B0 field

Update Time (PVM_DriftCompUpdateTime) – Time period of B0 reload events

Reconstruction Card

These parameters can be set individually for different reconstructions in the Processing Platform to produce different types of movies from the same data.

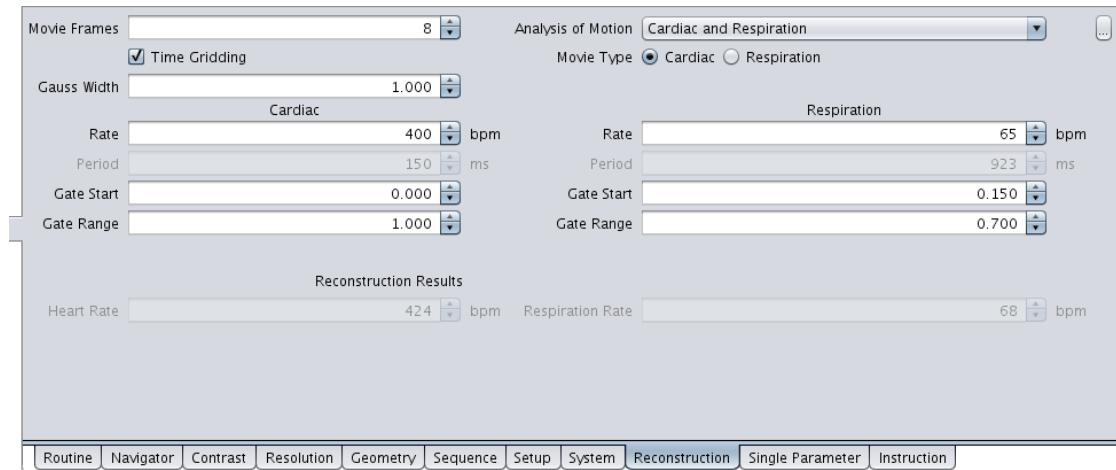


Figure 1.249: IgFLASH Reconstruction Card

Movie Frames (OutputMovieFrames) – Number of movie frames to be reconstructed from the data. Excessive numbers of frames (for which the selected oversampling did not produce sufficient data) may lead to artefacts on some frames. These, in turn, can be reduced by stronger filtering (see [Gauss Width](#) [▶ 295] below).

Time Gridding (TimeGridding) – Turns on time interpolation of movie frames with a Gaussian kernel

Gauss Width (GaussWidth) – Width of the Gaussian kernel used for time interpolation. Higher widths improve SNR at the price of a stronger filtering (time-smoothing) effect.

Cardiac Rate (HeartRate) – Expected heart rate of the animal under investigation in beats per minute. Precision of $\pm 50\%$ is required for a successful self-gating reconstruction.

Cardiac Period (CardiacPeriod) – Describes cardiac period [ms] derived from **Heart Rate**

Cardiac Gate Start (FreezePhase0) – Cardiac Gate Start and Cardiac Gate Range define which portion of data of the heart period is used for reconstruction. Gate Start describes the starting point of the data window as a fraction of its period. Typically for generating a cardiac movie, Gate Start is set to 0.0 and Gate Range to 1.0 to visualize the whole cardiac cycle.

Cardiac Gate Range (FreezePhaseRange0) – Range of data window used for reconstruction

Reconstruction Results / Heart Rate (HeartRateRecoResult) – Shows the Heart Rate calculated by the reconstruction. This could be useful in the Setup Mode (**Online Navigator Signal** must be activated on the Setup Card) to check if the Heart Rate derived by the reconstruction is in the range of the expected Heart Rate. If this is not the case, the navigator position can be changed online to improve the result.

Analysis of Motion (AnalysisOfMotion) – Defines which kind of motion is considered during reconstruction: Cardiac and Respiration, Only Cardiac, Only Respiration

Navigator Analysis (NavigatorAnalysis) – Defines if the navigator analysis is based on magnitude or phase data. Auto mode chooses the result with the best SNR.

Movie Type (MovieType) – Selection between the reconstruction of a cardiac or respiratory movie

Respiration Rate (RespRate) – Expected respiration rate of the animal under investigation in beats per minute. Precision of $\pm 50\%$ is required for a successful self-gating reconstruction.

Respiration Period (RespPeriod) – Describes respiration period [ms] derived from **Respiration Rate**

Respiration Gate Start (FreezePhase) – Respiration Gate Start and Respiration Gate Range define which portion of data of the respiration period is used for reconstruction. **Gate Start** describes the starting point of the data window as a fraction of its period. For example, when **Movie Type** is set to **Cardiac**, **Respiration Gate Start** to 0.25 and **Respiration Gate Range** to 0.5, the cardiac movie represents the average animal positions in the central 50% of the respiration cycle. The broader the gate, the more data is used for the movie reconstruction resulting in a higher SNR. On the other hand, phases of fast motion should not be included to avoid artefacts. It is helpful to reconstruct a respiratory movie first to select the proper gate position where the animal moves least.

Respiration Gate Range (FreezePhaseRange0) – Range of data window as a fraction of its period

Reconstruction Results / Respiration Rate (RespirationRateRecoResult) – Shows the Respiration Rate calculated by the reconstruction. This could be useful in the Setup Mode (**Online Navigator Signal** must be activated on the Setup Card) to check if the Respiration Rate derived by the reconstruction is in the range of the expected Respiration Rate. If this is not the case, the navigator position can be changed online to improve the result.

1.9.5 SegFLASH

1.9.5.1 Principles

SegFLASH is a 2D-derivative of the FLASH method which offers segmentation for multi-slice acquisition. The segment slice order can be chosen to be either interleaved or sequential: The latter is advantageous in angiographic or fast cardiac imaging. Alternatively, the segmentation can be replaced by movie acquisition allowing multi-slice cine imaging.

T1-weighted contrast can be created by inversion recovery. The inversion can be chosen to be effective either globally or slice selectively. In addition to a trigger for the image acquisition, the inversion can also be triggered (double trigger). This helps to ensure that inversion and acquisition pulses affect the same slice and to reduce a scatter of inversion times in heart imaging.

SegFLASH offers an optional flow compensation on all axes which removes unwanted phase shifts of the signal caused by flow and thus reduces signal dephasing within vessels and ghosting artefacts related to pulsation.

Also available is a prospective drift compensation for the main magnetic field. While this compensation is not required for most systems it may be helpful for systems based on permanent magnets.

1.9.5.2 Applications

- High resolution snapshot imaging
- Fast cardiac imaging with segmentation
- T1-weighting by inversion recovery
- TOF Angiography (2D multi-slice)
- Cardiac movies

1.9.5.3 Loop Structure

Two different acquisition loop structures are available depending on the value of **Segment Slice Order**.

From inner to outer loops (see Figure [Order of segments and slices \[▶ 300\]](#)):

- **Segment Slice Order Alternate:** phase-encoding (in-segment), movie frames, slices, phase encoding (segments), accumulation, repetitions
- **Segment Slice Order Serial:** phase-encoding (in-segment), movie frames, phase encoding (segments), slices, accumulation, repetitions
- Image order in `2dseq` file: movie frames, slices, repetitions

1.9.5.4 Specific Parameters

Most parameters are identical to those in the FLASH method (see Chapter [FLASH ▶ 286](#)). Their description will be omitted here.

Routine Card

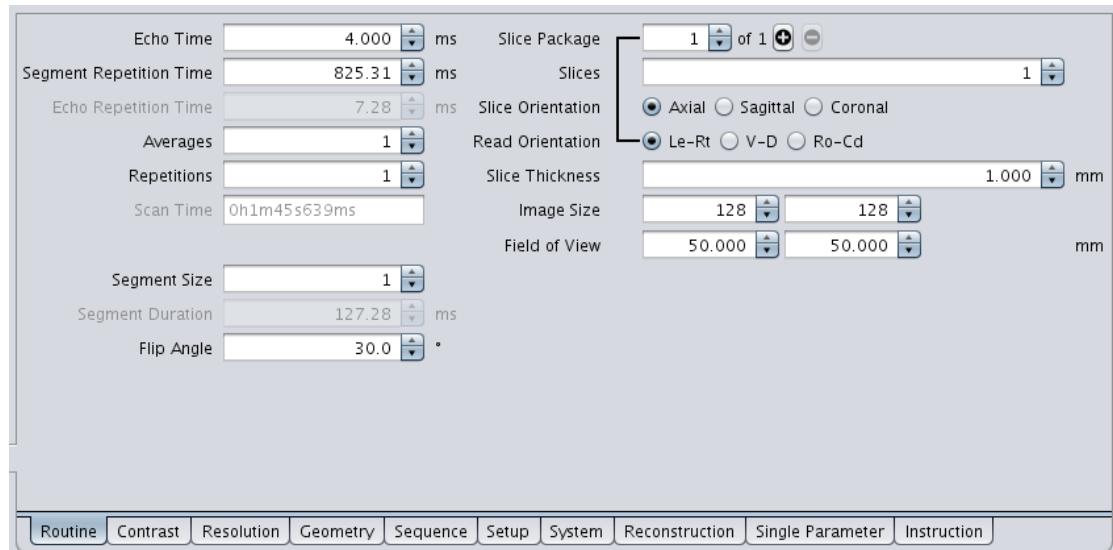


Figure 1.250: SegFLASH Routine Card

Segment Repetition Time (SegmentRepTime) – Time between two segments of the same slice (see Figures [Position of the slice selective inversion pulses ▶ 299](#), [Order of segments and slices ▶ 300](#)). Note the dependence of the minimum repetition time on **Segment Slice Order**.

Echo Repetition Time (EchoRepTime) – Non-editable; always the shortest possible

Averages (PVM_NAverages) – Only Motion Averaging is possible (NAE loop)

Segment Size (SegmentSize) – Number of echoes per segment

Segment Duration (SegmentDuration) – Non-editable; time needed for the whole segment consisting of the specified number of movie frames and segment size



Segment Size instead of the usual number of Segments was chosen as an input parameter. With Segment Duration and Echo Repetition Time it simplifies filling an RR interval.

Contrast Card

Main

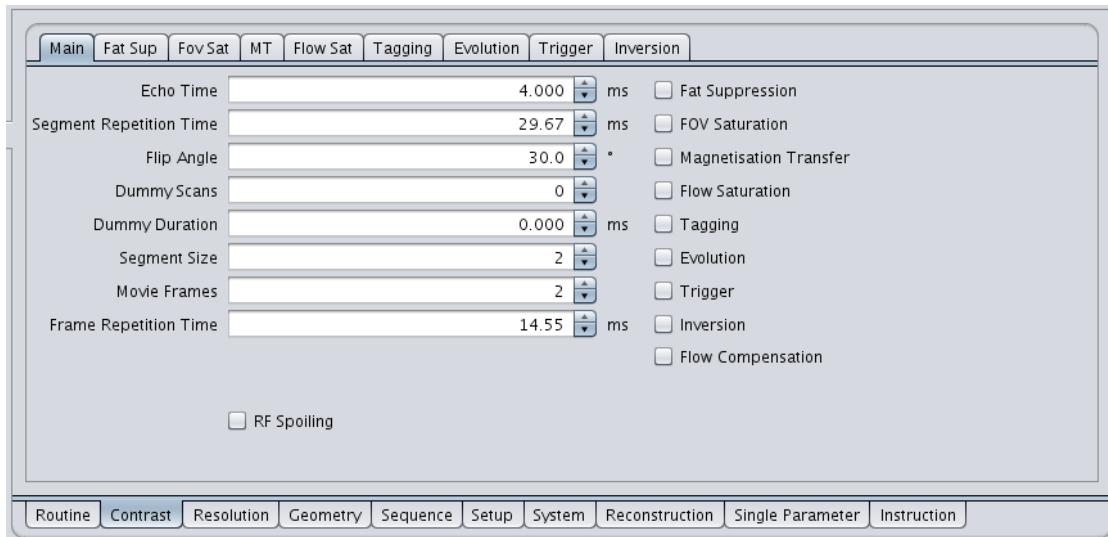


Figure 1.251: SegFLASH Contrast Card Main

Segment Size – Number of k-space lines (echoes) per segment

Movie Frames (PVM_NMovieFrames) – The measurement of SegmentSize echoes is repeated PVM_NMovieFrames times in a temporal interval of FrameRepetitionTime. Both, segment size and movie frames belong to the same segment.

Frame Repetition Time (FrameRepetitionTime) – Delay between movie frames. It becomes visible for PVM_NMovieFrames > 1.

Trigger

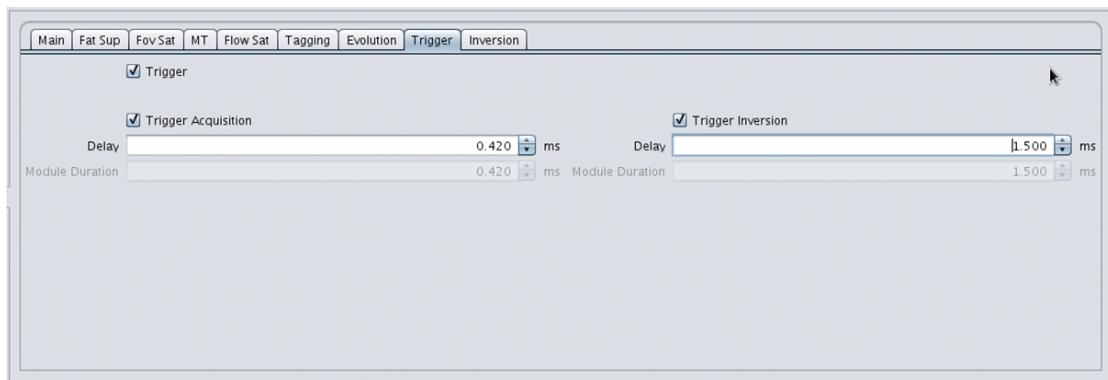


Figure 1.252: SegFLASH Contrast Card Trigger

A trigger synchronizes data acquisition with external events such as heart beats or respiration. SegFLASH offers two trigger points. Unlike with FLASH both triggers can be activated simultaneously, each with its own delay.

Trigger Inversion – Triggers the inversion pulse. It is visible only for inversion recovery experiments (InversionOnOff switched on). Triggering the inversion pulse helps to ensure that the inversion and the acquisition pulses affect the same slice. It may also be used to reduce the scatter in TI.

Trigger Acquisition – Triggers the acquisition and all the modules other than the Inversion and the Evolution module

Delay – Delay in the pulse program after the trigger event



For triggered acquisition unsteady external signals as may occur from cardiac arrhythmia or gasping respiration can result in imprecise repetition time and/or inversion time.

Inversion

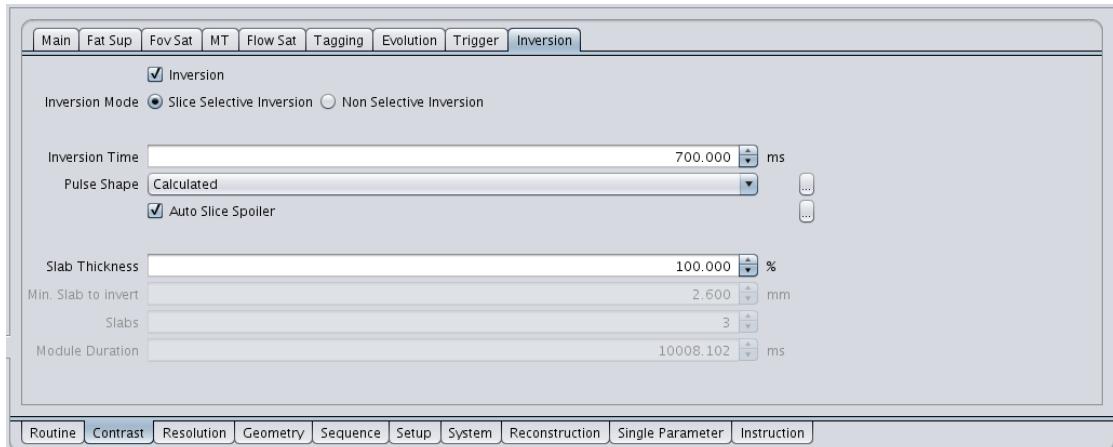


Figure 1.253: SegFLASH Contrast Card Inversion

The inversion module implemented in most methods usually consists of a number of consecutive RF pulses – each of them selecting a different slice (see Chapter [Common Parameters \[▶ 240\]](#)). This arrangement may lead to limitations, e.g. when combining multi-slice inversion experiments with segmentation or CINE-imaging: It is not possible to fill an RR interval with movie frames. In SegFLASH each segment has its own preceding inversion pulse (see Figure [Position of the slice selective inversion pulses \[▶ 299\]](#)).

Slice Selective Inversion – Choosing this mode will open further parameters (see Chapter [Slice-selective Inversion Recovery \(Sel IR\) \[▶ 251\]](#))

Non Selective Inversion – This mode requires **Segment Slice Order Serial**. Otherwise the slices would experience more than one inversion pulse during a repetition time.

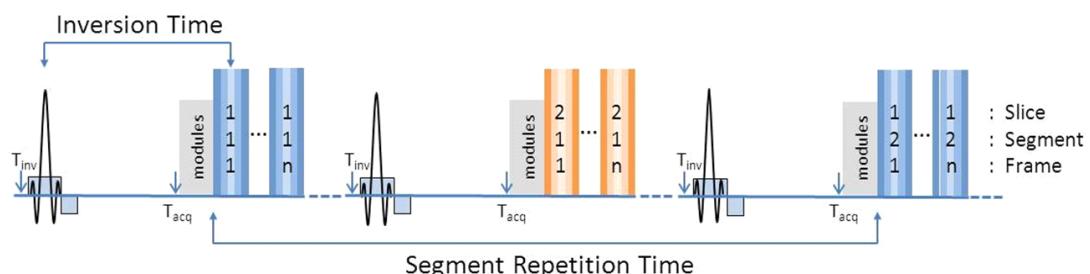


Figure 1.254: Position of the slice selective inversion pulses in SegFLASH shown for 2 slices, 5 segments (indicated by slightly different shadings) and n movie frames for Segment Slice Mode Alternate. The blue arrows mark the positions of Trigger Acquisition T_{acq} and Trigger Inversion T_{inv} . The diagram also illustrates why non-selective inversion is restricted to Segment Slice Order Serial.



The inversion time is exact for one echo of a segment only. With an increasing number of segment size the image contrast suffers increasingly from deviations of the specified inversion time. The inversion time is defined as the temporal distance between the center of the inversion pulse and the acquisition of the central k-space line within a segment.



It is possible to sample several points of a T1 decay curve by setting movie frames > 1. The first frame is measured at the specified inversion time. Each subsequent frame has an inversion time offset of Frame Separation. These are the times shown in the images as TI.

Flow Compensation - Flow compensation of all gradient channels



Despite its drawback of a longer echo time flow compensation can be advantageous in angiography and cardiac applications.

Geometry Card

Segment Slice Order – Defines the order of slices and segments if more than one slice is acquired (see Figure [Order of segments and slices \[▶ 300\]](#)):

For **Segment Slice Order** Alternate the minimum repetition time scales with the number of slices. Vice versa for Serial the measurement time increases by the slice number for a given repetition time.

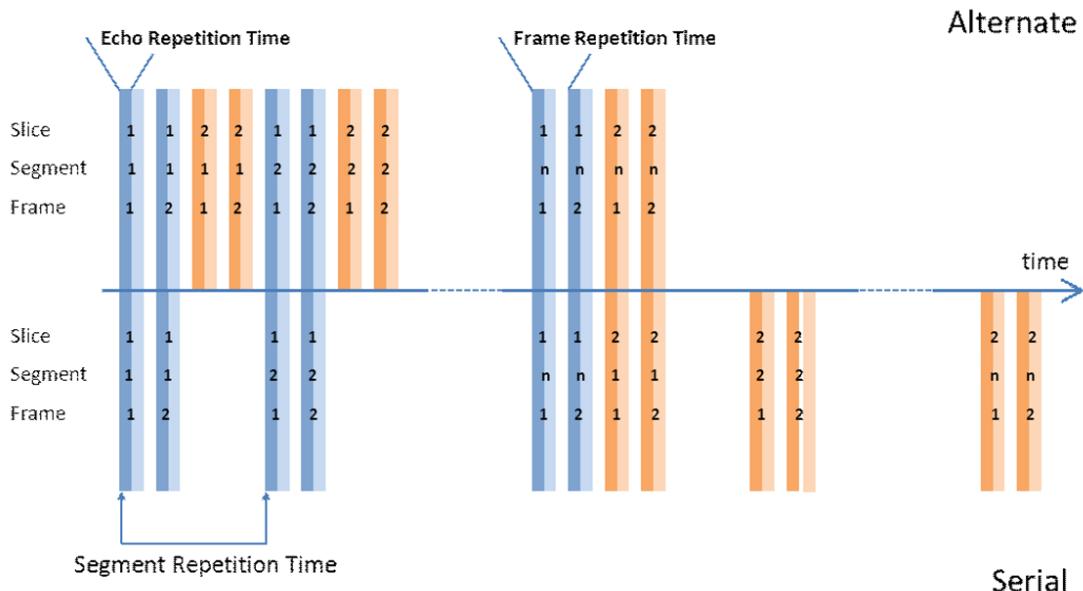


Figure 1.255: Order of segments and slices for Segment Slice Order Alternate and Serial. Here, 2 slices are acquired with a Segment Size of 2 (indicated by slightly different shadings), and 2 Movie Frames. The number of segments per slice, n , is the number of phase encoding steps / Segment Size. The Frame Repetition Time is the time between two consecutive frames in a segment.

Sequence Card

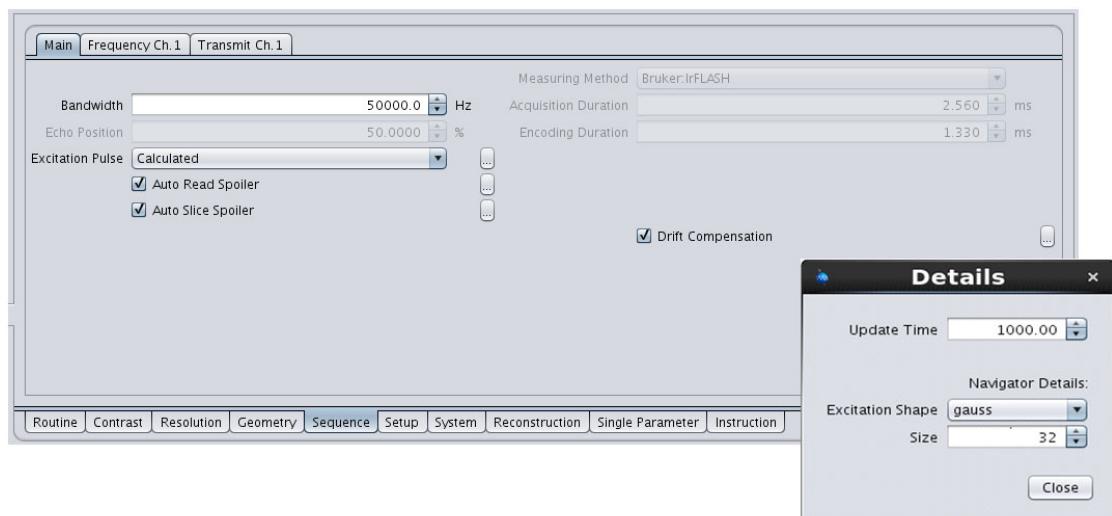


Figure 1.256: SegFLASH Sequence Card with Drift Compensation and its details

Drift compensation is implemented as an additional navigator resulting in two different types of acquired data within a scan - navigator and image data, respectively. Job acquisition technique is used to control and administer the data stream. The navigator is spatially non-selective. The user can change the RF pulse type and the acquisition data size. The acquired data size of the navigator should be large enough to obtain a sufficiently accurate frequency.

Drift Compensation (PVM_DriftCompYesNo) – Activation of field drift compensation during the experiment based on a navigator signal and a reload mechanism of the B0 field

Update Time (PVM_DriftCompUpdateTime) – Time period of B0 reload events. The minimum update time depends on the repetition time and the system architecture.



While for superconducting magnets a frequency drift is no issue on a time-scale of a study it may be observable within a single scan for permanent magnets.

1.9.6 IgUTE

1.9.6.1 Principles

IgUTE is a variant of the UTE method (2D radial scan with Ultra-short TE) featuring IntraGate – Bruker Biospin's proprietary implementation of the navigator-based self-gated cine MRI. It produces movies of cardiac and respiratory cycles without the need of physiologic signals. The required navigator information can be derived either from the first point of the FID signal (In-slice Position) or from a separate slab which can be graphically positioned (Arbitrary/Parallel Position).

The advantage of IgUTE compared to its Cartesian counterpart IgFLASH is the shorter achievable TE which helps to reduce flow artefacts. Furthermore, the radial imaging technique is less prone to motion artefacts in general. It is also more tolerant to missing samples, which allows faster protocols with a reduced oversampling factor.

The reconstruction uses the navigator to detect the phase of cardiac and respiratory cycles and correspondingly assigns the following MRI signal. Once the experiment is completed, the user can select various reconstruction options including the choice of the targeted motion (cardiac or respiratory), the number of reconstructed movie frames, and the degree of time interpolation.

1.9.6.2 Applications

- Cardiac cine imaging without ECG signals
- Abdominal images free of motion artefacts
- Time course cines
- Respiratory cine imaging without respiratory monitoring

1.9.6.3 Loop Structure

From inner to outer loops:

- Acquisition order: slices, oversampling, projections, repetitions
- Image order in `2dseq` file: slices, cardiac and respiratory phases, time course

1.9.6.4 Specific Parameters

IgUTE is a variant of the UTE method with the embedded IntraGate feature. Therefore the description of specific parameters can be found in the corresponding Chapter [UTE \(Ultra-short TE\) ▶ 360](#) or [IgFLASH ▶ 291](#).

1.9.6.5 Workflow

Trajectory Measurement

As described in Chapter [Trajectory ▶ 278](#) the k-space trajectory can be measured in a previous study on a homogenous object and saved for the in-vivo study. If it is necessary to measure the trajectory during the in-vivo session, triggering (if ECG electrodes are connected) and/or averaging can be activated on the Trajectory parameter card in order to improve accuracy of the measurement.

1.9.7 MGE (Multiple Gradient Echo)

1.9.7.1 Principles

MGE consists of a slice selective excitation followed by a train of gradient echoes produced by reversals of the readout gradient. All echoes are identically phase encoded. The first echo time and the echo spacing are editable. Two acquisition modes are available. In the `allEchoes` mode, echoes created by both polarities of the read gradient are acquired. In the `positiveReadOutEchoes` mode only the echoes created with the positive polarity are acquired.

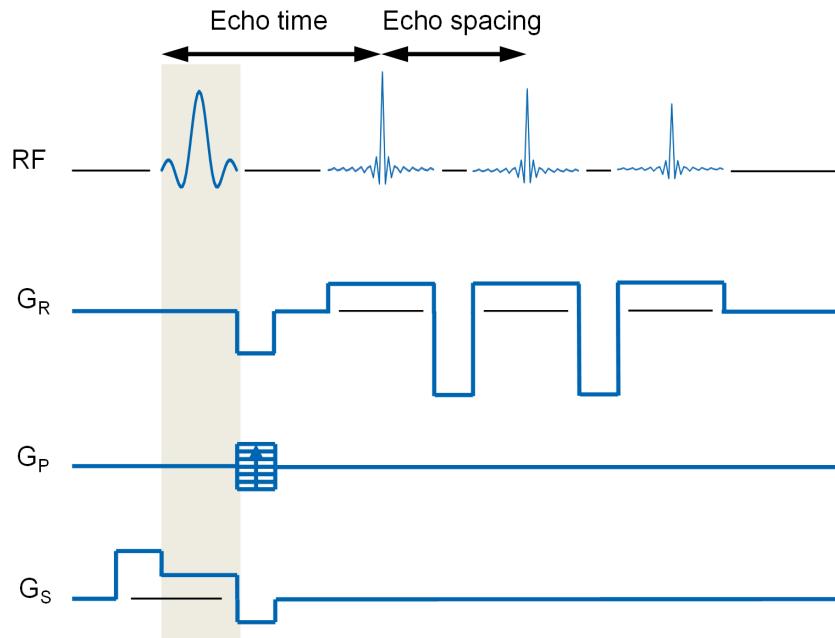


Figure 1.257: Pulse sequence of MGE

1.9.7.2 Applications

The method can be used to calculate maps of the apparent transverse relaxation time, T_2^* or to generate a series of differently T_2^* weighted images. The maps of T_2^* find applications in tissue susceptibility measurements, quantification of iron concentration and in the optimization of BOLD fMRI protocols (for the selection of the echo time, which is typically set equal to T_2^*).

1.9.7.3 Loop Structure

From inner to outer loops:

- Acquisition order: echo loop, slice loop, accumulation (NA), phase-encoding, repetitions
- Image order: echoes, slices, repetitions

Available Preparation Modules

- Trigger module
- Fat Suppression module
- Saturation Slices module

1.9.7.4 Specific Parameters

Routine Card

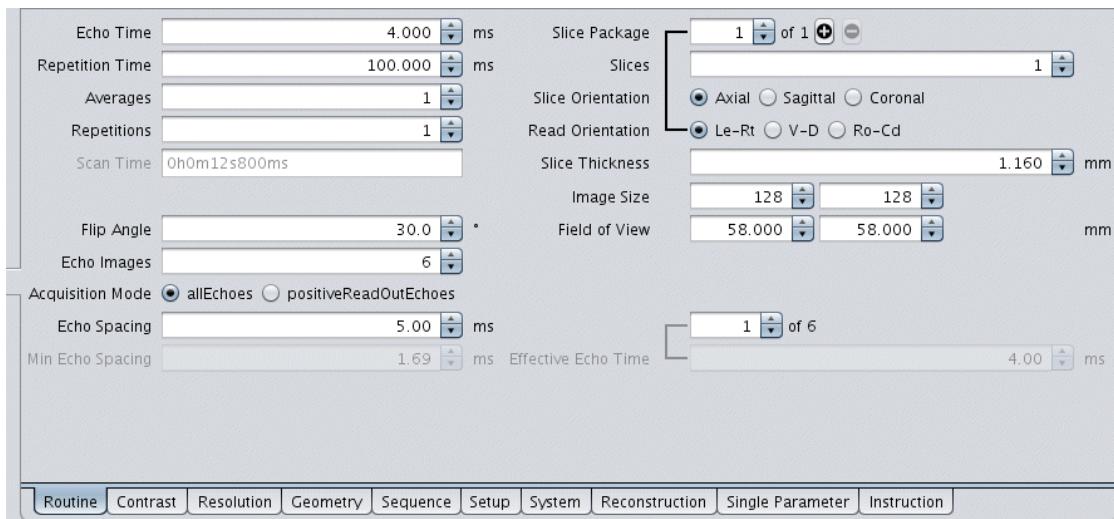


Figure 1.258: MGE Routine Card

Echo Time (PVM_EchoTime) – Time of the first echo of the sequence

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse

Echo Images (PVM_NEchoImages) – Number of images with different echo times generated for each slice

Acquisition Mode (EchoAcqMode) – Allows to acquire all echoes (allEchoes) or only the ones generated with positive gradient (positiveReadOutEchoes). The latter option assures identical distortion on all images, but requires higher echo spacing.

Echo Spacing (EchoSpacing) – Delay between two following acquired echoes in multiple echo mode

Min Echo Spacing (MinEchoSpacing) – Minimum delay between two gradient echoes. It depends on the matrix size and the acquisition bandwidth.

Effective Echo Time (EffectiveTE) – Effective echo times of all echo images. Non-editable and determined by the first echo time and the echo spacing.

Contrast Card

Main

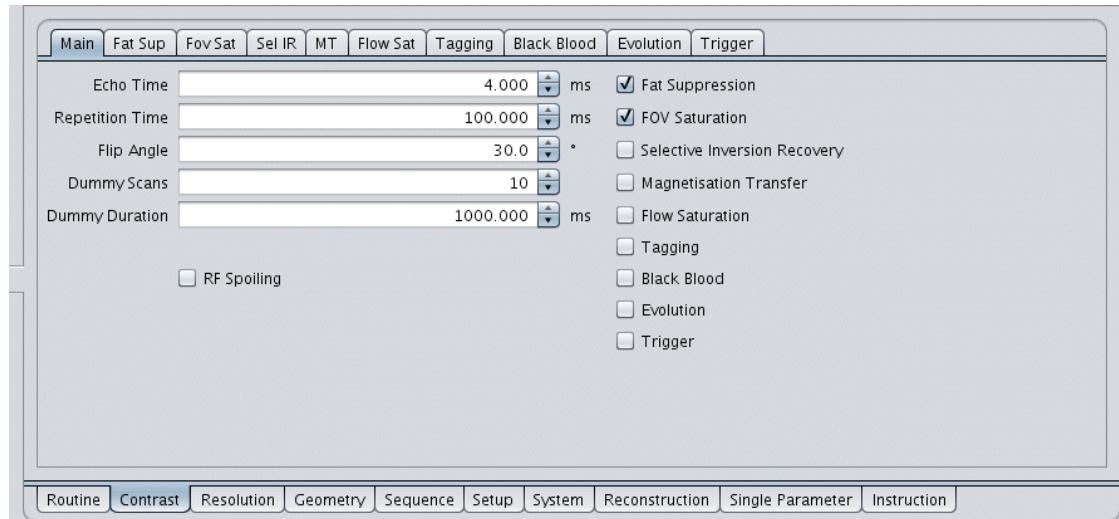


Figure 1.259: MGE Contrast Card Main

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse

RF Spoiling (RFSpoiling) – Turns on an RF phase cycle that removes echo components from the steady state signal. With short TR and TE and high flip angles this option produces T1-dependent contrast.

Sequence Card

Main

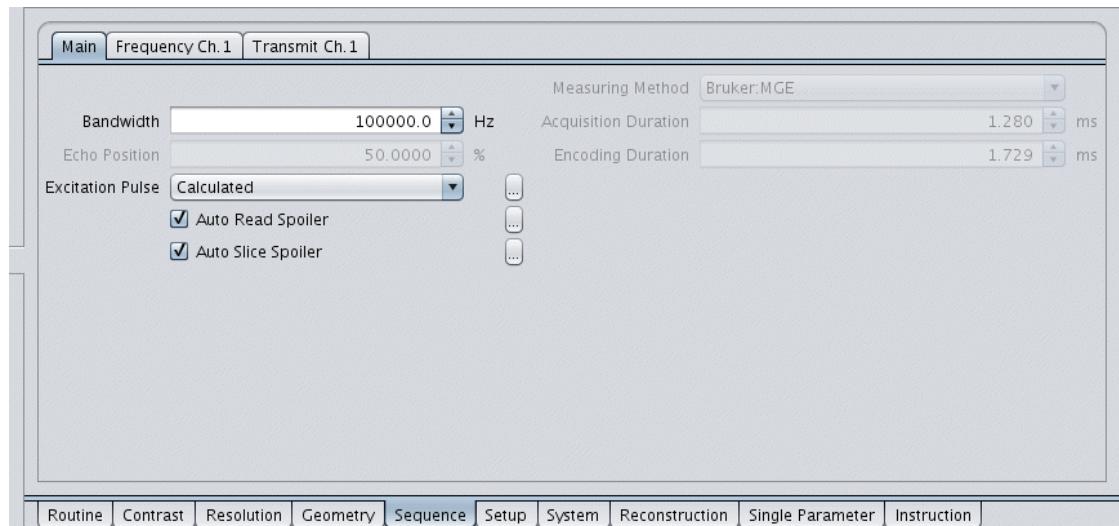


Figure 1.260: MGE Sequence Card Main

Echo Position (PVM_EchoPosition) – Determines the position of the echo in the acquisition window. Values below 50% allow lower TE. Depends on the Partial FT setting for the read direction in Chapter [Encoding](#) ▶ 270].

Excitation Pulse (ExcPulse1Enum) – The slice selective excitation pulse. When the method works in the 3D mode (selection in the [Resolution Card](#) ▶ 269]) this pulse selects the slab that is reconstructed as 3D volume. In this case it is important to select a high sharpness factor for this pulse (7 or higher) avoid aliasing of out-of-slab signals.

Auto Read Spoiler (ReadSpoiler.automatic) – Constant gradient pulse applied on the read channel after the echo acquisition

Auto Slice Spoiler (SliceSpoiler.automatic) – Constant gradient pulse applied on the slice channel after the echo acquisition

1.9.8 MSME (Multi Slice Multi Echo)

1.9.8.1 Principles

Multiple spin echoes are generated using the CPMG sequence with slice selective RF pulses, whereby each echo is used to obtain an image with a different echo time (TE). Each echo is separately phase-encoded and rewound to obtain a coherent superposition of all signal components even with non-180 deg. refocusing pulses. Groups of consecutive echoes can be accumulated to give an image with an average effective TE.

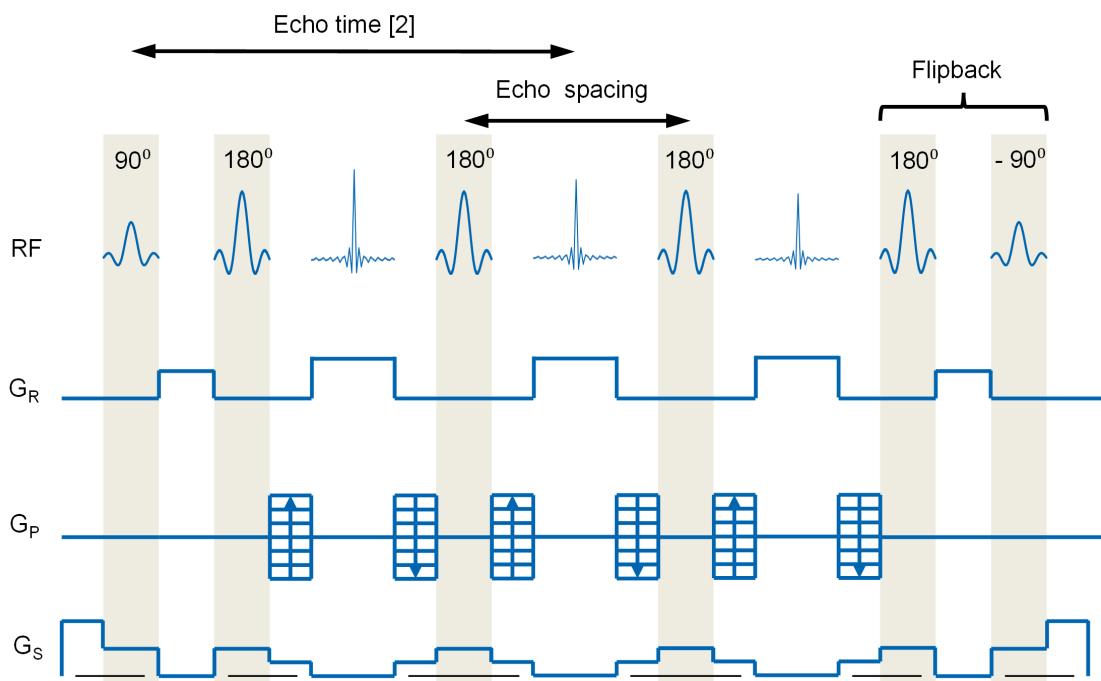


Figure 1.261: Pulse sequence of MSME

1.9.8.2 Applications

- T2 weighted MRI (TE = T2, TR>T1), T2 mapping
- Double contrast MRI (first echo group for T1, second with T2 contrast; reduced TR)

1.9.8.3 Loop Structure

From inner to outer loops:

- Acquisition order: echo-accumulation, echoes, slices, accumulation (NA), phase-encoding, repetitions
- Image order in `2dseq`: echoes, slices, repetitions

1.9.8.4 Specific Parameters

Routine Card

The Routine Card interface shows the following settings:

- Echo Spacing:** 20.000 ms
- Repetition Time:** 1000.000 ms
- Averages:** 1
- Repetitions:** 1
- Scan Time:** 0h8m34s0ms
- Echo Images:** 1
- Echo Images:** 1 of 1
- Echo Time:** 20.00 ms
- Echo Averages:** 1
- Equal Averaging:**
- Slice Package:** 1 of 1
- Slices:** 1
- Slice Orientation:** Axial (selected)
- Read Orientation:** Le-Rt (selected)
- Slice Thickness:** 1.160 mm
- Image Size:** 256 x 256
- Field of View:** 58.000 x 58.000 mm

Figure 1.262: MSME Routine Card

Echo Spacing (PVM_EchoTime) – Time between the centers of consecutive echoes. Lower spacing allows shorter effective echo times.

Echo Images (PVM_NEcholImages) – Number of images with different effective echo times. Not necessarily equal to number of echoes (see [NEchoesPerEcholImage \[▶ 307\]](#)).

Echo Time (EffectiveTE) – Effective echo times of all echo-images

Echo Averages (NEchoesPerEcholImage) – Number of consecutive echoes that will be averaged to give the echo image

Equal Averaging (ConstNEchoes) – If Yes, each successive echo image will use the same value for [NEchoesPerEcholImage \[▶ 307\]](#).

Contrast Card

Main

The Main tab of the Contrast Card shows the following parameters:

- Echo Spacing:** 20.000 ms
- Echo Images:** 1
- Echo Images:** 1 of 1
- Echo Time:** 20.00 ms
- Echo Averages:** 1
- Repetition Time:** 1000.000 ms
- Excitation Angle:** 90.0 °
- Refocusing Angle:** 180.0 °
- Dummy Scans:** 1
- Dummy Duration:** 1000.000 ms

Checkboxes on the right side:

- Fat Suppression
- FOV Saturation
- Selective Inversion Recovery
- Magnetisation Transfer
- Flow Saturation
- Evolution
- Trigger

Flip Back

Figure 1.263: MSME Contrast Card Main

Echo Spacing (PVM_EchoTime) – See [Routine Card \[▶ 307\]](#)

Echo Images (PVM_NEcholmages) – See [Routine Card \[▶ 307\]](#)

Echo Time (EffectiveTE) – See [Routine Card \[▶ 307\]](#)

Echo Averages (NEchoesPerEcholImage) – See [NEchoesPerEcholImage \[▶ 307\]](#)

Excitation Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse, typically set to 90 degrees

Refocusing Angle (RefPulse1.Flipangle) – Flip angle of the refocusing pulse, typically set to 180 degrees. When the method is used for qualitative T2-weighted images rather than for quantitative T2 mapping, this flip angle can be reduced to limit the RF power of the sequence.

Flip Back (PVM_FlipBackOnOff) – When selected, an additional 90 degree pulse is appended to flip the transverse magnetization forming the last echo back to the z axis. When T2 is longer than the echo train, the flip-back limits the saturation and maintains the T2 contrast despite short repetition times.

Sequence Card

Main

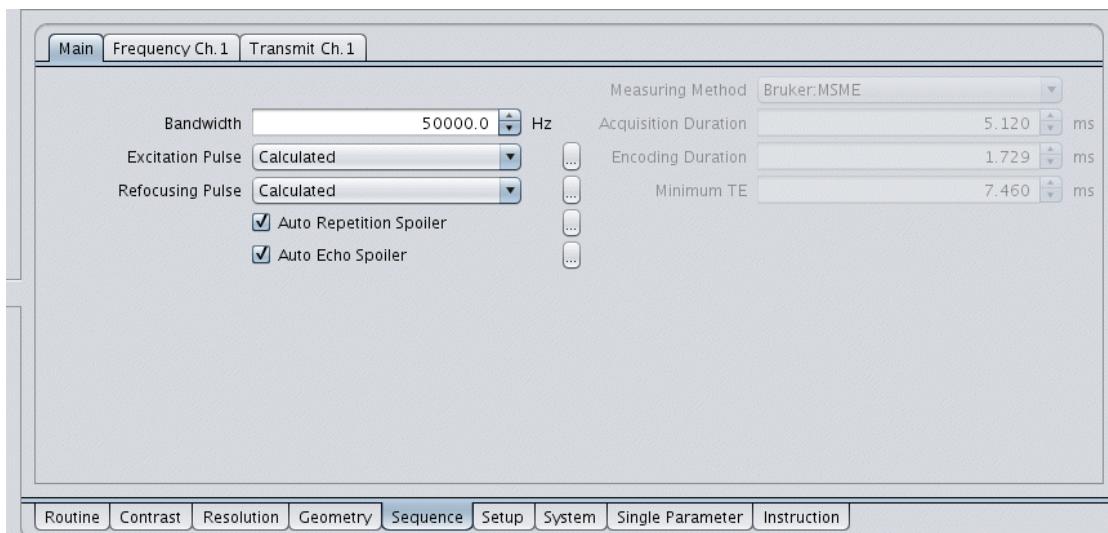


Figure 1.264: MSME Sequence Card Main

Excitation Pulse (ExcPulse1Enum) – Excitation pulse of the sequence. For the 3D mode, sharpness of 5 or higher is recommended to limit the out-of-slab aliasing.

Refocusing Pulse (RefPulse1Enum) – Refocusing pulse of the sequence. The sharpness of this pulse may be set lower than the excitation when a short echo spacing is required. For multi-slice acquisitions the refocusing bandwidth should be set to the same value as the excitation to limit the saturation of adjacent slices. However, for quantitative T2 mapping a broader bandwidth should be selected to make sure that only the flat part of the pulse profile (where the flip angle is precisely 180 degrees) contributes to the signal.

Auto Repetition Spoiler (RepetitionSpoiler.automatic) – Gradient spoiler applied before the excitation to remove interference with previous signals

Auto Echo Spoiler (EchoSpoilingAuto) – Gradient spoiler on both sides of the refocusing RF pulses

Minimum TE (PVM_MinEchoTime) – Minimum echo spacing, non-editable, depends on bandwidth, matrix size, resolution and RF pulse lengths

1.9.9 RARE (Rapid Acquisition with Relaxation Enhancement)

1.9.9.1 Principles

Multiple spin echoes are generated using the CPMG sequence with slice selective RF pulses. Each echo is separately phase-encoded, and the phase encoding is incremented within one echo train to accelerate the acquisition. It is possible to obtain two or more echo-images with different effective TEs.

The sequence diagram is identical to [MSME \(Multi Slice Multi Echo\) \[▶ 306\]](#).

1.9.9.2 Applications

- Accelerated T2 weighted MRI (TE = T2, TR>T1)
- Preferred technique for ultra-high resolution (2048x2048 is feasible)
- Myelography (CSF imaging) with very long echo trains
- Snapshot imaging without susceptibility artifacts

1.9.9.3 Loop Structure

From inner to outer loops:

- Acquisition order: phase-encoding 1, echoes, slices, accumulation (NA), phase-encoding 2, repetitions
- Image order in 2dseq: echoes, slices, repetitions

1.9.9.4 Specific Parameters

Routine Card

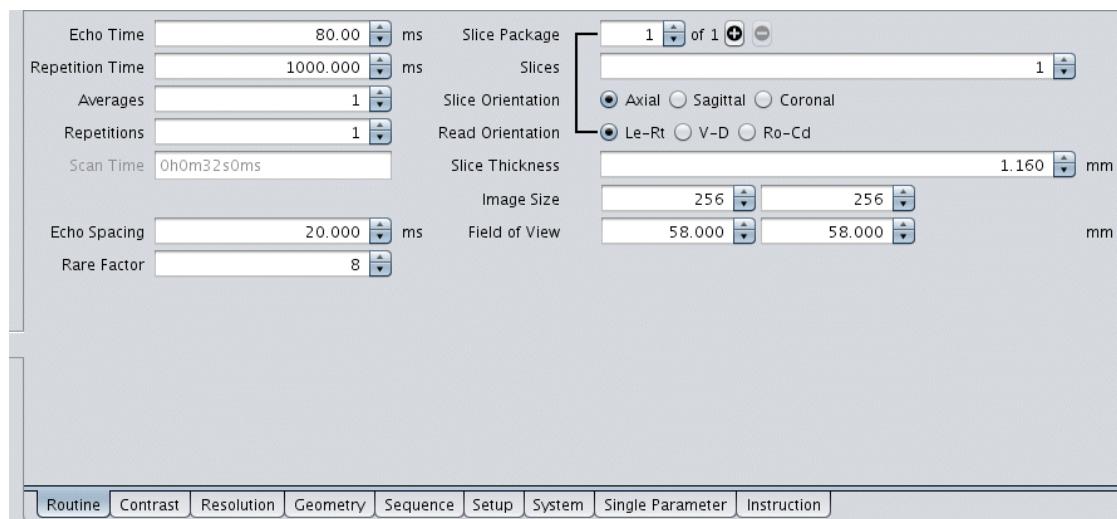


Figure 1.265: RARE Routine Card

Echo Time (EffectiveTE) – Delay between the excitation pulse and the central phase-encoding step. This parameter determines the T2 contrast and depends on the echo spacing, the RARE factor and the phase encoding start.

Echo Spacing (PVM_EchoTime) – Time between the centers of consecutive echoes. Lower spacing allows shorter effective echo times.

Rare Factor (PVM_RareFactor) – Number of differently phase encoded echoes. Increasing the RARE factor reduces the scan time but typically increases the effective TE and the blurring caused by T2 relaxation.

Contrast Card

Main

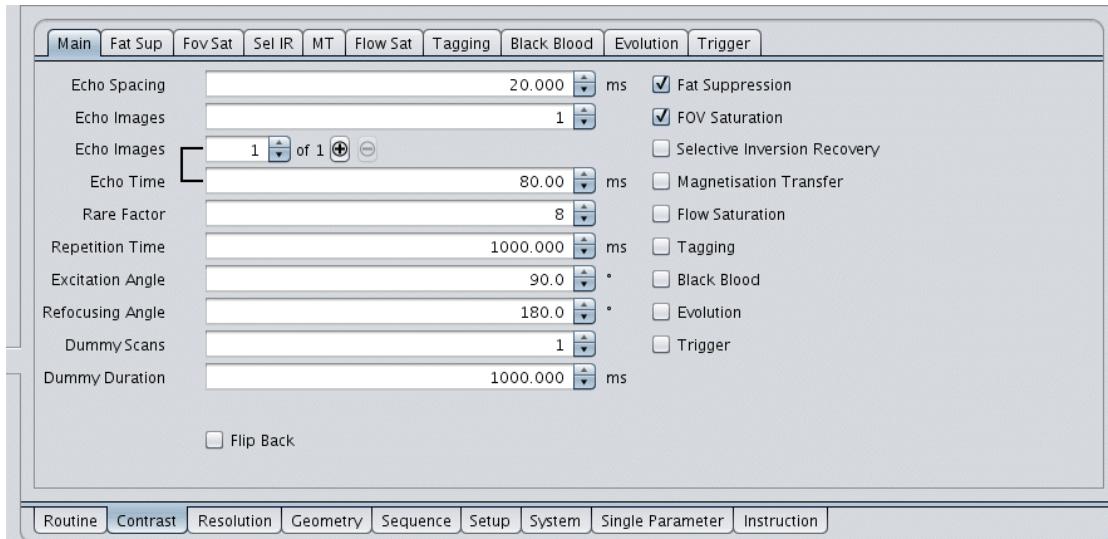


Figure 1.266: RARE Contrast Card Main

Echo Spacing (PVM_EchoTime) – See [Routine Card ▶ 309](#)

Echo Images (PVM_NEcholImages) – Number of images with different effective echo times. Not necessarily equal to number of echoes, see below.

Echo Time (EffectiveTE) – See [Routine Card ▶ 309](#)

Rare Factor (PVM_RareFactor) – See [Routine Card ▶ 309](#)

Repetition Time (PVM_RepetitionTime) – See [Routine Card ▶ 241](#)

Excitation Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse, typically set to 90 degrees

Refocusing Angle (RefPulse1.Flipangle) – Flip angle of the refocusing pulse, typically set to 180 degrees, however, it can be reduced without big SNR penalty to limit the RF power of the sequence.

Flip Back (PVM_FlipBackOnOff) – When selected, an additional 90 degree pulse is appended to flip the transverse magnetization forming the last echo back to the z axis. When T2 is longer than the echo train, the flip-back limits the saturation and maintains the T2 contrast despite short repetition times.

Sequence Card

Main

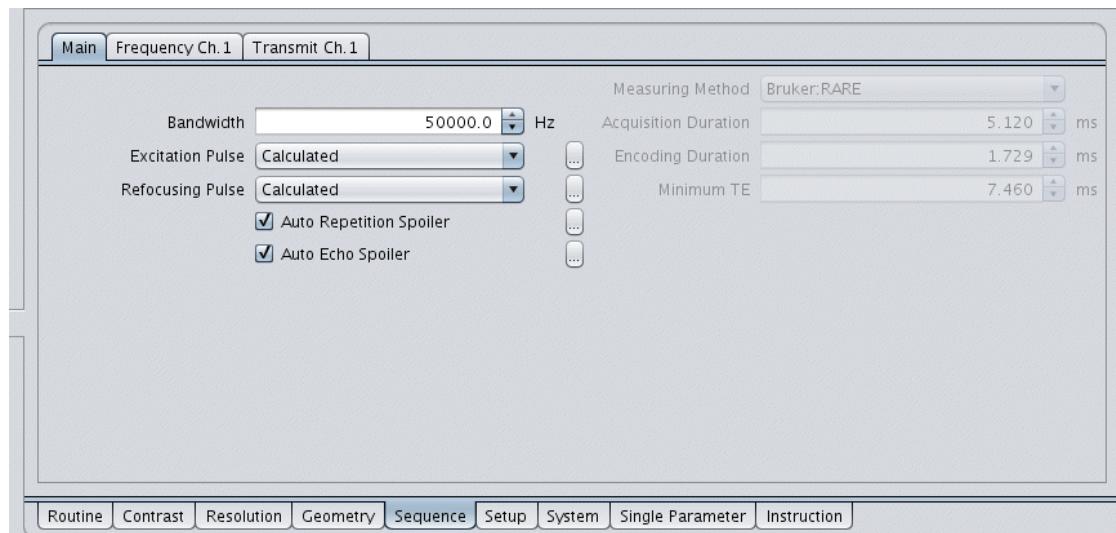


Figure 1.267: RARE Sequence Card Main

Excitation Pulse (ExcPulse1Enum) – Excitation pulse of the sequence. For the 3D mode, sharpness of 5 or higher is recommended to limit the out-of-slab aliasing.

Refocusing Pulse (RefPulse1Enum) – Refocusing pulse of the sequence. The sharpness of this pulse may be set lower than the excitation when a short echo spacing is required. For multi-slice acquisitions the refocusing bandwidth should be set to the same value as the excitation to limit the saturation of adjacent slices.

Auto Repetition Spoiler (RepetitionSpoiler.automatic) – Gradient spoiler applied before the excitation to remove interference with previous signals

Auto Echo Spoiler (EchoSpoilingAuto) – Gradient spoiler on both sides of the refocusing RF pulses

Minimum TE (PVM_MinEchoTime) – Minimum echo spacing, non-editable, depends on bandwidth, matrix size, resolution and RF pulse lengths

1.9.10 FAIR_RARE (Flow-sensitive Alternating IR RARE)

1.9.10.1 Principles

Perfusion measurement based on pulsed spin labeling using the principles of Chapter [FAIR_EPI \(Flow-sensitive Alternating IR EPI\) \[342\]](#) with the echo-planar readout replaced by a fast spin echo sequence. The advantage of the method compared to FAIR_EPI is the lack of image distortions caused by resonance offsets. The method can therefore be used for areas which are not accessible for the EPI acquisition due to strong susceptibility variations, especially at high magnetic fields. On the other side, the readout of FAIR_RARE is longer than that of FAIR_EPI for the same matrix size, which may lead to stronger differences in the inversion-recovery time between the slices. The method should preferably be used for single-slice experiments.

Single shot acquisitions are possible with a limited matrix size (128x128 or lower), short echo spacing and partial FT encoding.

1.9.10.2 Applications

- Perfusion-sensitive dynamic studies (with selective inversion)

- Perfusion quantification (with interleaved selective/non-selective inversions)
- Mapping of T1 (with a series of non-selective inversions with different recovery times)

1.9.10.3 Loop Structure

Abbreviation: TIR = starting value for incremented inversion recovery delays

From inner to outer loops:

- Acquisition: RARE echoes, slices, RARE segments, inversion recovery increments, selective/non selective inversion. The two outermost loops can be exchanged depending on the value of FairMode (see [Specific Parameters \[▶ 342\]](#)).
- Image file: same order as the acquisition

1.9.10.4 Specific Parameters

Routine Card

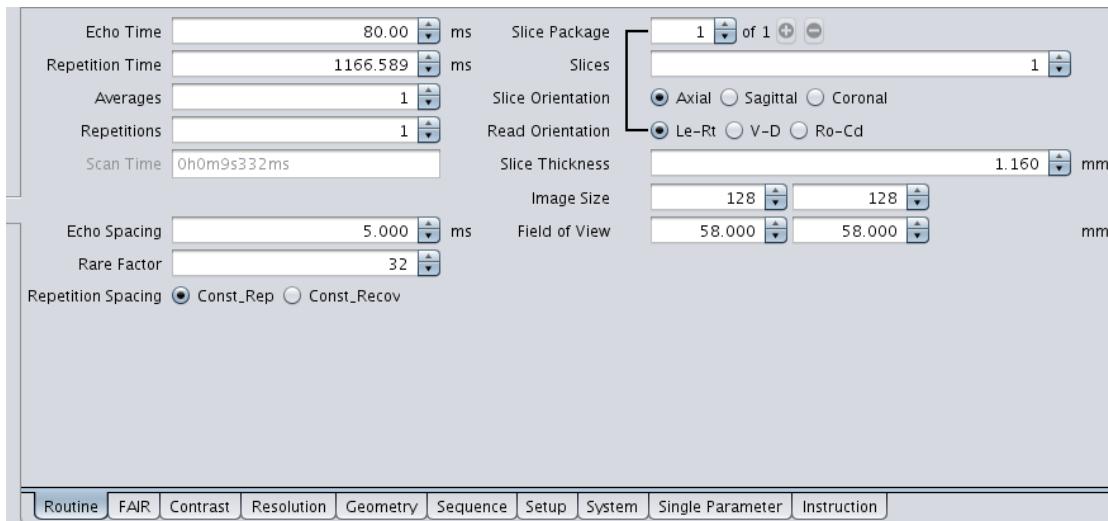


Figure 1.268: FAIR_RARE Routine Card

Echo Time (EffectiveTE) – Delay between the excitation pulse and the central phase-encoding step. This parameter determines the T2 contrast and depends on the echo spacing, the RARE factor and the phase encoding start.

Echo Spacing (PVM_EchoTime) – Time between centers of consecutive echoes

Rare Factor (PVM_RareFactor) – Number of differently phase encoded echoes

Repetition Spacing (RepetitionSpacing) – Controls the timing of dynamic experiments. Possible values are:

- Const_Rep – Providing a constant repetition time (given by PVM_RepetitionTime)
- Const_Recov – Giving a constant recovery time (given by RecoveryTime). In experiments with short and long TIR-times (see below), the constant recovery mode is more time-efficient.

FAIR Card

This card contains all parameters controlling the spin labelling with the FAIR module. See Chapter [FAIR Card \[▶ 281\]](#) for details.

Contrast Card

Main

Parameter	Value	Unit	Status
Echo Spacing	5.000	ms	<input checked="" type="checkbox"/> Fat Suppression
Echo Time	80.00	ms	<input checked="" type="checkbox"/> FOV Saturation
Rare Factor	32		<input type="checkbox"/> Magnetisation Transfer
Repetition Time	1166.589	ms	<input type="checkbox"/> Trigger
Excitation Angle	90.0	°	
Refocusing Angle	180.0	°	
Dummy Scans	1		
Dummy Duration	1166.589	ms	

Figure 1.269: FAIR_RARE Contrast Card Main

Echo Spacing (PVM_EchoTime) – See [Routine Card \[▶ 312\]](#)

Echo Time (EffectiveTE) – See [Routine Card \[▶ 312\]](#)

Rare Factor (PVM_RareFactor) – See [Routine Card \[▶ 312\]](#)

Excitation Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse, typically set to 90 degrees

Refocusing Angle (RefPulse1.Flipangle) – Flip angle of the refocusing pulse, typically set to 180 degrees, however, it can be reduced without big SNR penalty to limit the RF power of the sequence.

Sequence Card

Main

Parameter	Value	Unit	Status
Bandwidth	100000.0	Hz	
Excitation Pulse	Calculated		
Refocusing Pulse	Calculated		
Measuring Method	Bruker:FAIR_RARE		
Acquisition Duration	1.280	ms	
RampForm	<input checked="" type="radio"/> LinearRamp <input type="radio"/> SinusoidalRamp		
Usable Slew Rate	75.00	%	
Gradient Stabilization Time	0.050	ms	
Automatic spoiler setting	<input checked="" type="checkbox"/>		
Auto Repetition Spoiler	<input checked="" type="checkbox"/>		
CPMG read-spoiling	0.70	cycles/Pixel	
CPMG slice-spoiling	3.51	cycles/SI	

Figure 1.270: FAIR_RARE Sequence Card Main

Excitation Pulse (ExcPulse1Enum) – Excitation pulse of the sequence

Refocusing Pulse (RefPulse1Enum) – Refocusing pulse of the sequence. The sharpness of this pulse may be set lower than the excitation when a short echo spacing is required. For multi-slice acquisitions the refocusing bandwidth should be set to the same value as the excitation to limit the saturation of adjacent slices.

RampForm (RampForm) – Allows switching between the linear gradient ramp shape (LinearRamp, default) and the sinusoidal ramp (SinusoidalRamp). Linear ramps are more time efficient while the sinusoidal ones generally quieter.

Usable Slew Rate (SlewRatePerCent) – Specifies the gradient slew rate for the sequence in % of the system maximum. Higher slew rate gives shorter echo spacing but makes the sequence more sensitive to eddy currents and louder.

Gradient Stabilization Time (GradStab) – An additional delay used after the gradient ramps to avoid eddy current-related artifacts

Automatic Spoiler Setting (AutoSpoil) – When selected, this parameter causes an automatic calculation of the spoiling gradient pulses.

Auto Repetition Spoiler (RepetitionSpoiler.automatic) – Gradient spoiler applied before the excitation to remove interference with previous signals

CPMG Read-Spoiling (SpoilingReadPx) – The efficiency of the spoiling pulse of the read gradient used to remove the interference with FID-signals of the refocusing pulses in the CPMG sequence. It is expressed in terms of magnetization de-phasing across one pixel.

CPMG Slice-Spoiling (SpoilingSliceSI) – The efficiency of the spoiling pulse of the slice selection gradient in the CPMG sequence. It is expressed in terms of magnetization de-phasing across the slice thickness.

1.9.11 RAREVTR (RARE with variable repetition time TR)

1.9.11.1 Principles

Multiple spin echoes are generated using the CPMG sequence with slice selective RF pulses. Each echo is separately phase-encoded, and the phase encoding is incremented within one echo train to accelerate the acquisition.

It is possible to obtain two or more echo-images with different effective TEs. Multiple acquisitions may be made with the repetition time (TR) varied for a saturation recovery series.

1.9.11.2 Applications

Simultaneous measurement of T1 and T2

1.9.11.3 Loop Structure

From inner to outer loops:

- Acquisition order: phase encoding 1, echoes, slices, accumulation (NA), phase encoding 2, variable repetition time, repetitions
- Image order in `2dseq`: echoes, slices, repetition times, repetitions

1.9.11.4 Specific Parameters

Routine Card

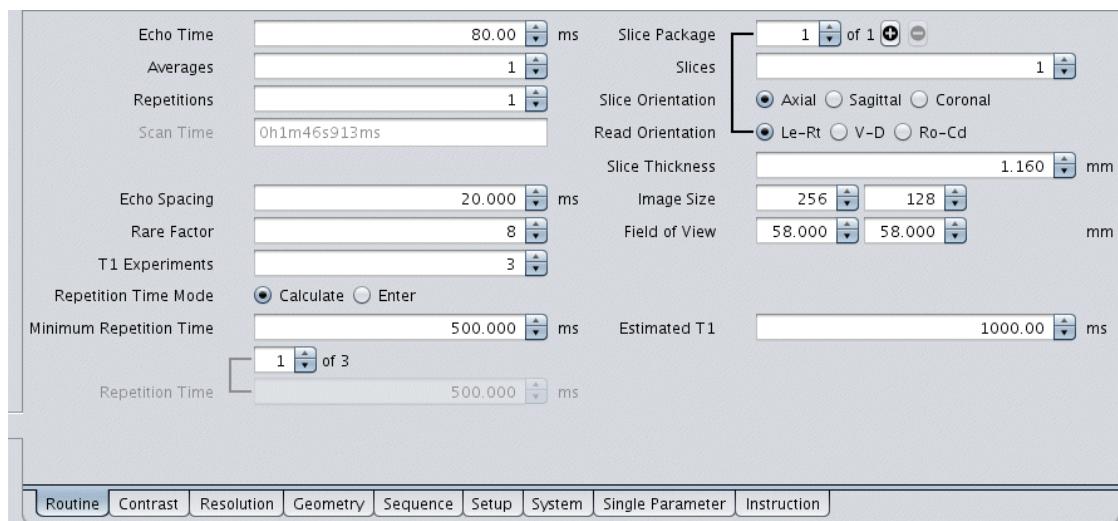


Figure 1.271: RAREVTR Routine Card

Echo Time (EffectiveTE) – Delay between the excitation pulse and the central phase-encoding step. This parameter determines the T2 contrast and depends on the echo spacing, RARE factor and the phase encoding start.

Echo Spacing (PVM_EchoTime) – Time between the centers of consecutive echoes. Lower spacing allows shorter effective echo times.

Rare Factor (PVM_RareFactor) – Number of differently phase encoded echoes. Increasing the RARE factor reduces the scan time but typically increases the effective TE and the blurring caused by T2 relaxation.

T1 Experiments (T1Exp) – Number of experiments with different repetition times

Repetition Time Mode (RepTimeMode) – The values Calculate or Enter define whether the repetition time(s) will be either entered into the array or calculated from a specified estimated T1 value.

Minimum Repetition Time (MinT1RepTime) – Is shown when RepTimeMode is set to Calculate and defines the minimum repetition time to be used for the series of images

Repetition Time (MultiRepTime) – An array of delays between consecutive excitations of the same slice. The minimum value depends on the number of slices and number of echoes.

Estimated T1 (EstT1Value) – Is shown when RepTimeMode is set to Calculate and is used to estimate the T1 value for the sample; the estimated value is used to calculate the best repetition times sampling for the experiment.

Contrast Card

Main

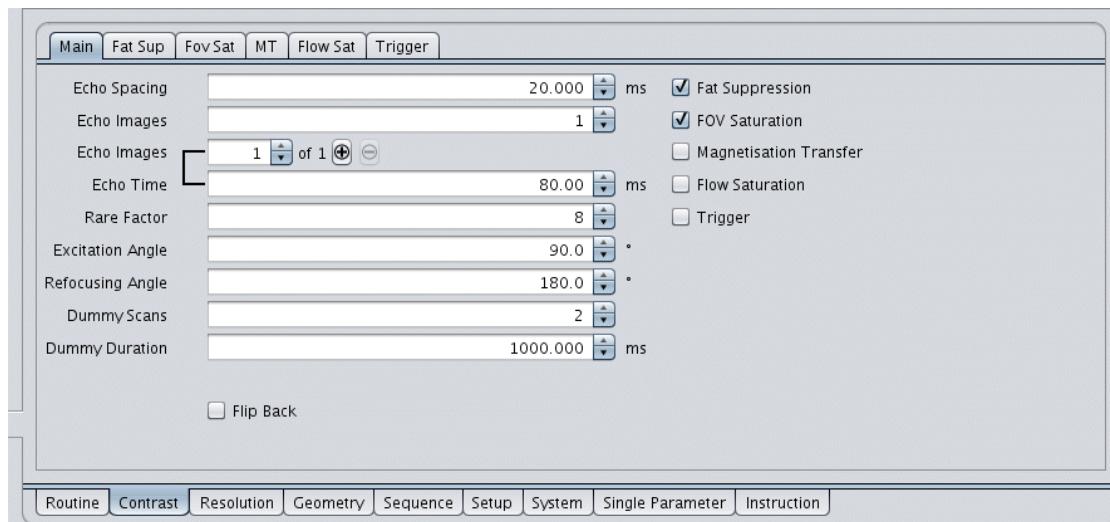


Figure 1.272: RAREVTR Contrast Card Main

Echo Spacing (PVM_EchoTime) – See [Routine Card ▶ 315](#)

Echo Images (PVM_NEchoImages) – Number of images with different effective echo times

Echo Time (EffectiveTE) – See [Routine Card ▶ 315](#)

Rare Factor (PVM_RareFactor) – See [Routine Card ▶ 315](#)

Excitation Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse, typically set to 90 degrees

Refocusing Angle (RefPulse1.Flipangle) – Flip angle of the refocusing pulse, typically 180 degrees. When the method is used for qualitative T2-weighted images rather than for quantitative T2 mapping, this flip angle can be reduced to limit the RF power of the sequence.

Flip Back (PVM_FlipBackOnOff) – When selected, an additional 90 degree pulse is appended to flip the transverse magnetization forming the last echo back to the z axis. When T2 is longer than the echo train, the flip-back limits the saturation and maintains the T2 contrast despite short repetition times.

Sequence Card

Main

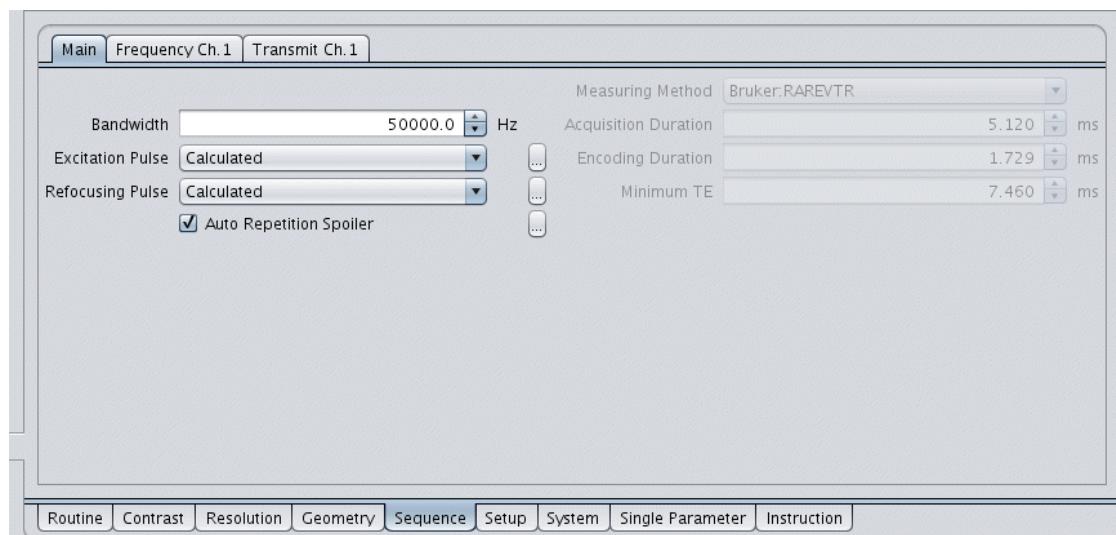


Figure 1.273: RAREVTR Sequence Card Main

Excitation Pulse (ExcPulse1Enum) – Excitation pulse of the sequence. For the 3D mode, sharpness of 5 or higher is recommended to limit the out-of-slab aliasing.

Refocusing Pulse (RefPulse1Enum) – Refocusing pulse of the sequence. The sharpness of this pulse may be set lower than the excitation when a short echo spacing is required. For multi-slice acquisitions the refocusing bandwidth should be set to the same value as the excitation to limit the saturation of adjacent slices. However, for quantitative T2 mapping a broader bandwidth should be selected to make sure that only the flat part of the pulse profile (where the flip angle is precisely 180 degrees) contributes to the signal.

Auto Repetition Spoiler (RepetitionSpoiler.automatic) – Gradient spoiler applied before the excitation to remove interference with previous signals.

Minimum TE (PVM_MinEchoTime) – Minimum echo spacing, non-editable, depends on bandwidth, matrix size, resolution and RF pulse lengths.

1.9.12 RAREst (RARE with short echo time)

1.9.12.1 Principles

The sequence performs a rapid scan based on the CPMG spin echo train, just like the standard RARE (see [RARE \(Rapid Acquisition with Relaxation Enhancement\) \[▶ 309\]](#)). It is programmed to achieve the shortest echo spacing and thus the shortest effective echo time within the limits imposed by the gradient system. The gradient pulses are calculated in a slew rate-oriented manner and the number of gradient ramps is reduced to minimum. The spoiling gradient pulses are automatically optimized. The RAREst method should be selected for the applications where the echo spacing is critical, in particular in single shot acquisitions with partial Fourier encoding (sequence known as HASTE). With the echo spacing above 10 ms the standard RARE method is recommended.

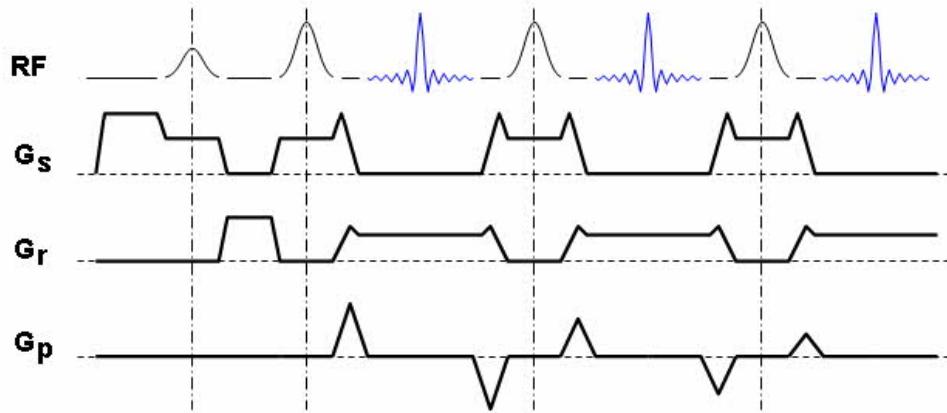


Figure 1.274: Pulse sequence of RAREst

1.9.12.2 Applications

Fast (in particular, single-shot) T2-weighted imaging without susceptibility artefacts

1.9.12.3 Loop Structure

From inner to outer loops:

- Acquisition order: phase encoding 1, slices, accumulations, phase encoding 2 (interleaving), repetitions
- Image order in 2dseq file: slices, repetitions

1.9.12.4 Specific Parameters

Routine Card

A screenshot of a software interface titled 'Routine Card'. The card contains various input fields and controls for MRI parameters. On the left, there are fields for Echo Time (40.00 ms), Repetition Time (3000.000 ms), Averages (1), Repetitions (1), Scan Time (0h0m3s0ms), Echo Spacing (5.000 ms), and Rare Factor (71). On the right, there are sections for Slice Package (1 of 1), Slices (1), Slice Orientation (Axial selected), Read Orientation (Le-Rt selected), Slice Thickness (1.160 mm), Image Size (128 x 128), and Field of View (58.000 mm x 58.000 mm). At the bottom, there are tabs for Routine, Contrast, Resolution, Geometry, Sequence, Setup, System, Single Parameter, and Instruction, with 'Routine' being the active tab.

Figure 1.275: RAREst Routine Card

Echo Time (EffectiveTE) – Delay between the excitation pulse and the central phase-encoding step. This parameter determines the T2 contrast and depends on the echo spacing, RARE factor and the phase encoding start.

Echo Spacing (PVM_EchoTime) – Time between the centers of consecutive echoes. Lower spacing allows shorter effective echo times.

Rare Factor (PVM_RareFactor) – Length of the spin echo train. Increasing the RARE factor reduces the scan time but typically increases the effective TE and the blurring caused by T2 relaxation.

Contrast Card

Main

Figure 1.276: RAREst Contrast Card Main

Echo Spacing (PVM_EchoTime) – See [Routine Card \[▶ 318\]](#)

Echo Images (PVM_NEcholmages) – Number of images with different effective echo times. Not necessarily equal to number of echoes, see below.

Echo Time (EffectiveTE) – See [Routine Card \[▶ 318\]](#)

Rare Factor (PVM_RareFactor) – See [Routine Card \[▶ 318\]](#)

Repetition Time (PVM_RepetitionTime) – See [Routine Card \[▶ 241\]](#)

Excitation Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse, typically set to 90 degrees

Refocusing Angle (RefPulse1.Flipangle) – Flip angle of the refocusing pulse, typically 180 degrees, however, it can be reduced without big SNR penalty to limit the RF power of the sequence.

Sequence Card

Main

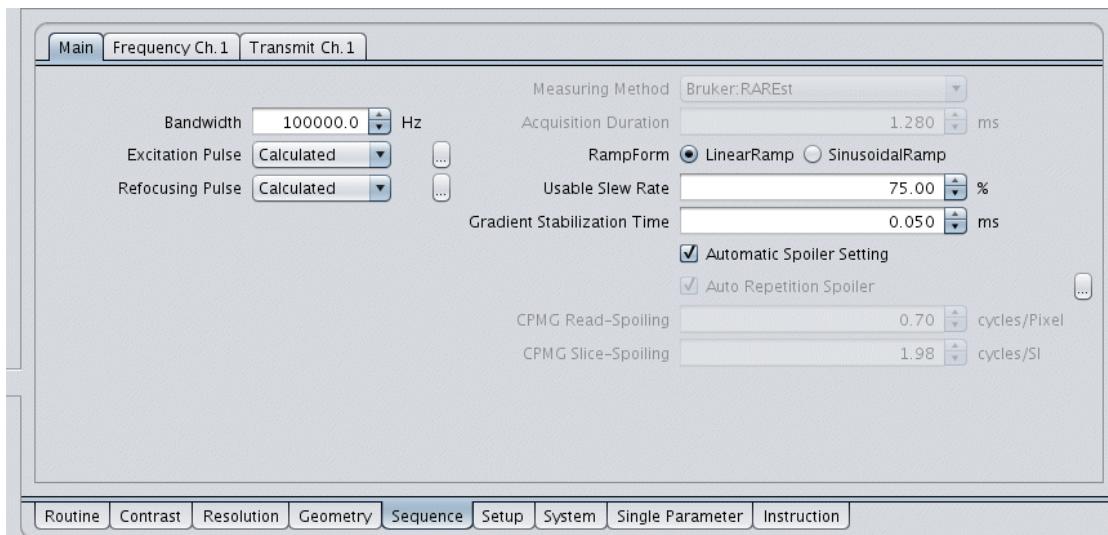


Figure 1.277: RAREst Sequence Card Main

Excitation Pulse (ExcPulse1Enum) – Excitation pulse of the sequence

Refocusing Pulse (RefPulse1Enum) – Refocusing pulse of the sequence. The sharpness of this pulse may be set lower than the excitation when a short echo spacing is required. For multi-slice acquisitions the refocusing bandwidth should be set to the same value as the excitation to limit the saturation of adjacent slices.

RampForm (RampForm) – Allows switching between the linear gradient ramp shape (LinearRamp, default) and the sinusoidal ramp (SinusoidalRamp). Linear ramps are more time efficient while the sinusoidal ones generally quieter.

Usable Slew Rate (SlewRatePerCent) – Specifies the gradient slew rate for the sequence in % of the system maximum. Higher slew rate gives shorter echo spacing but makes the sequence more sensitive to eddy currents and louder.

Gradient Stabilization Time (GradStab) – An additional delay used after the gradient ramps to avoid eddy current-related artifacts

Automatic Spoiler Setting (AutoSpoil) – When selected, this parameter causes an automatic calculation of the spoiling gradient pulses.

Auto Repetition Spoiler (RepetitionSpoiler.automatic) – Gradient spoiler placed before the exitation to remove interferences with previous signals

CPMG Read-Spoiling (SpoilingReadPx) – The efficiency of the spoiling pulse of the read gradient used to remove the interference with FID-signals of the refocusing pulses in the CPMG sequence. It is expressed in terms of magnetization de-phasing across one pixel.

CPMG Slice-Spoiling (SpoilingSliceSI) – The efficiency of the spoiling pulse of the slice selection gradient in the CPMG sequence. It is expressed in terms of magnetization de-phasing across the slice thickness.

1.9.13 MDEFT (Modified Driven-Equilibrium FT)

1.9.13.1 Principles

The purpose of MDEFT is high resolution 3D imaging with T1 contrast. The sequence is based on a segmented 3D gradient echo acquisition with each segment optionally prepared by a non-selective inversion-recovery. The method allows different T1-weighting schemes, such as the classical MDEFT, IR-prepared FLASH (also known as MP-RAGE), or a simple RF-spoiled gradient echo (known as SPGR).

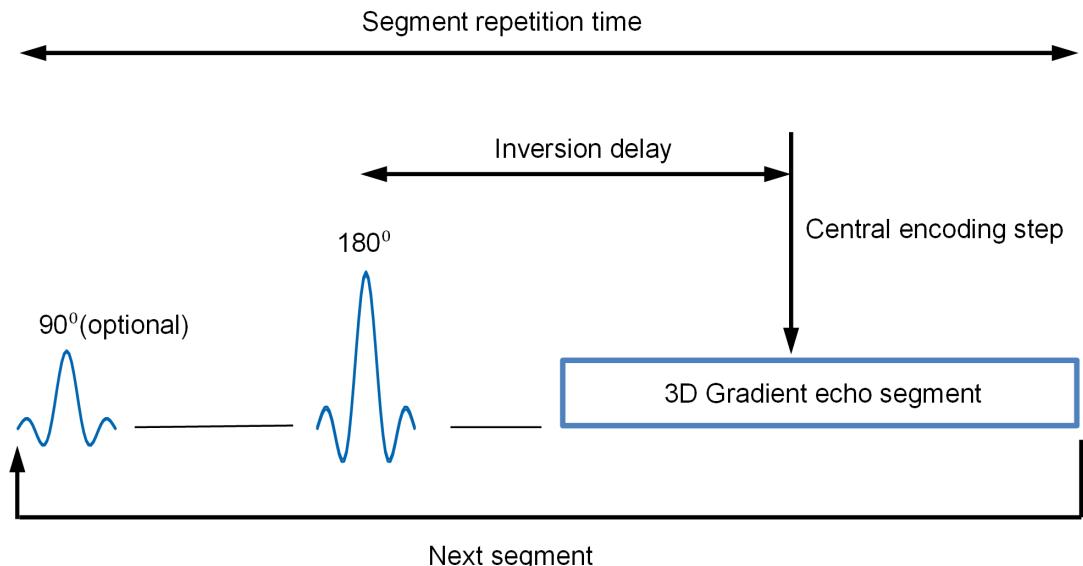


Figure 1.278: Pulse sequence of MDEFT

1.9.13.2 Applications

- High resolution T1-weighted imaging with high numbers of contiguous slices (16 or more)
- Anatomical reference for fMRI

1.9.13.3 Loop Structure

From inner to outer loops:

- Acquisition order: preparation followed by the inner 2D encoding loop, outer 2D loop (segments), 3D encoding loop
- Image order in the `2dseq` file: slices, repetitions

1.9.13.4 Specific Parameters

Routine Card

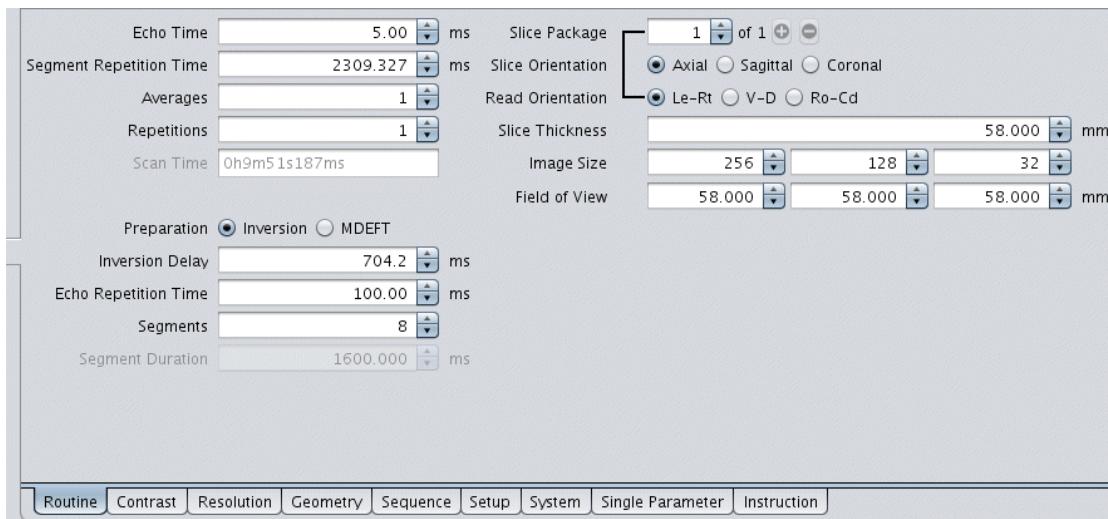


Figure 1.279: MDEFT Routine Card

Echo Time (EchoTime) – Time from the excitation pulse center to the gradient echo center. In Scan Editor represented by **TE effective 1**.

Segment Repetition Time (SegmRepTime) – Repetition time of the entire segment, or the time from one inversion RF pulse to the next. Together with the **Inversion Delay** it determines the image contrast. When **Preparation** is set to **MDEFT** (see below) this parameter is automatically derived from the **Inversion Delay** and remains non-editable.

Preparation (PreparationMode) – Determines the kind of preparation for each acquisition segment. Possible values are:

- **Inversion** – A non-selective inversion pulse (parameters described in the `Mdeft_preparation_parameters` group) is applied in front of each segment. The inversion delay and segment repetition time can be freely chosen. This mode can be used with either centric or linear encoding mode (see below), and with one or more segments. With the encoding mode set to linear and with one segment the sequence corresponds to what is known as MP-RAGE.
- **MDEFT** – The classical **MDEFT** mode differs from **Inversion** by an additional 90 degree RF pulse applied after each segment to destroy the remaining longitudinal magnetization, and by restricting the segment repetition time so that the delay between the 90 and 180 deg pulses is equal to the inversion delay. This mode is typically used with the centric encoding.

Inversion Delay (PVM_InversionTime) – Time from the middle of the inversion RF pulse to the point in the acquisition segment when the central k-space line is sampled. Minimum Inversion Delay depends on the segment duration and Phase Encoding modes selected on the Sequence-Encoding Card.

Echo Repetition Time (EchoRepTime) – Time from one gradient echo to the next (or from one excitation RF pulse to the next) within one segment

Segments (SegmNumber) – Number of segments used to cover one 2D plane in k-space. Each segment is separately prepared by an inversion RF pulse. A higher number of segments gives shorter segments and thus a more precise T1-weighting of the k-space data, but prolongs the total experiment time.

Segment Duration (SegmDuration) – Duration of one acquisition segment

Contrast Card

Main

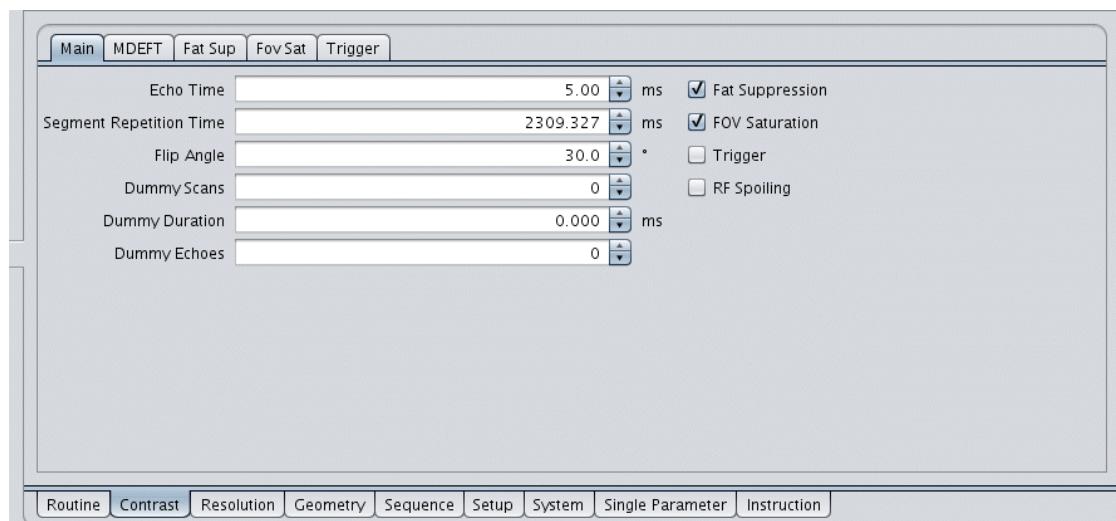


Figure 1.280: MDEFT Contrast Card Main

Echo Time (EchoTime) – See [Routine Card \[▶ 322\]](#)

Segment Repetition Time (SegmRepTime) – See [Routine Card \[▶ 322\]](#)

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse, typically between 10 and 30 degrees

Dummy Echoes (NDummyEchoes) – Number of echoes skipped at the beginning of each segment to stabilize the signal within segments

RF Spoiling (RFSpoiling) – Allows switching the **RF Spoiling** on or off. RF spoiling enhances the T1 contrast.

MDEFT

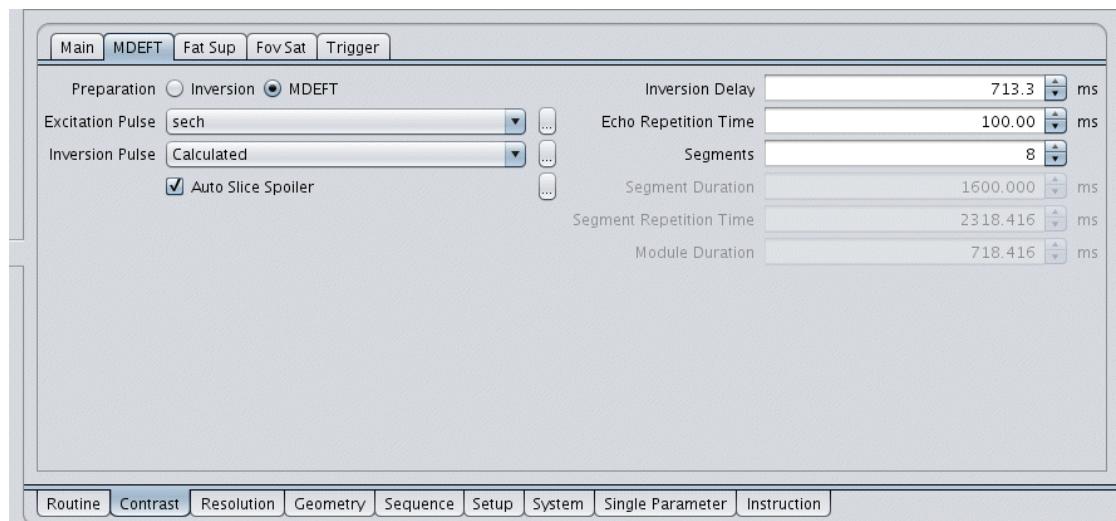


Figure 1.281: MDEFT Contrast Card MDEFT

Preparation (PreparationMode) – See [Routine Card \[▶ 322\]](#)

Excitation Pulse (Mdeft_ExcPulse1Enum) – Non-selective saturation applied at the beginning of the MDEFT preparation

Inversion Pulse (Mdeft_InvPulse1Enum) – Non-selective inversion pulse used in both MDEFT and Inversion preparations. When set to Calculated, the system creates an adiabatic shape that guarantees a 180-degree flip.

Auto Slice Spoiler (Mdeft_SliceSpoiler.automatic) – Gradient spoiler after the inversion pulse
Inversion Delay (PVM_InversionTime) – See [Routine Card \[▶ 322\]](#)
Echo Repetition Time (EchoRepTime) – See [Routine Card \[▶ 322\]](#)
Segments (SegmNumber) – See [Routine Card \[▶ 322\]](#)
Segment Duration (SegmDuration) – See [Routine Card \[▶ 322\]](#)
Segment Repetition Time (SegmRepTime) – See [Routine Card \[▶ 322\]](#)
Module Duration (Mdeft_PrepModuleTime) – Duration of the preparatory part of the sequence, non-editable

Sequence Card

Main

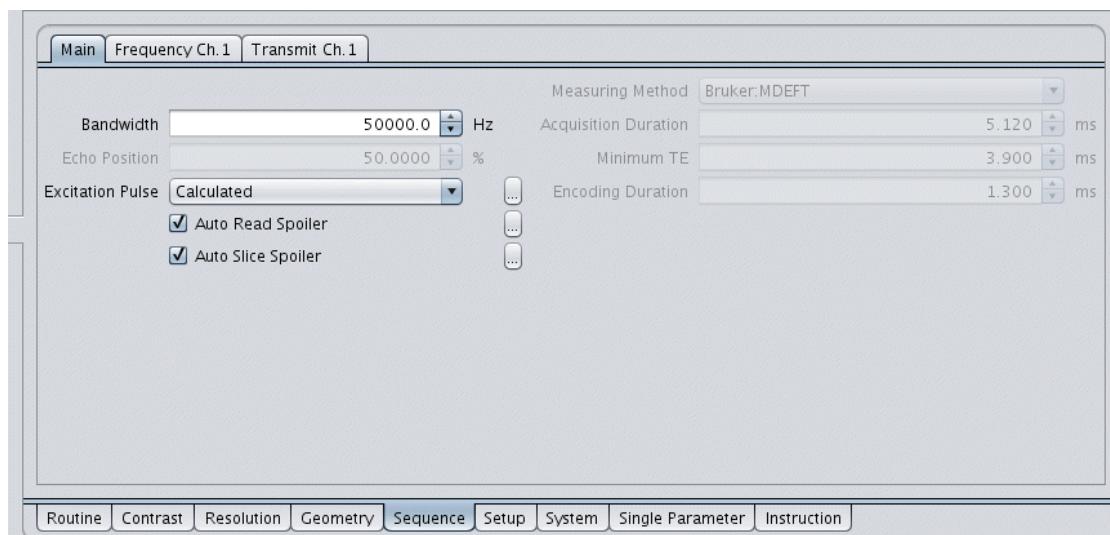


Figure 1.282: MDEFT Sequence Card Main

Echo Position (PVM_EchoPosition) – Determines the position of the echo in the acquisition window. Values below 50% allow lower TE. Depends on the Partial FT setting for the read direction on the Resolution Card.

Excitation Pulse (ExcPulse1Enum) – The slab-selective excitation pulse. It is important to select a high sharpness factor for this pulse (7 or higher) to avoid aliasing of out-of-slab signals.

Auto Read Spoiler (ReadSpoiler.automatic) – Gradient spoiler on the readout channel

Auto Slice Spoiler (SliceSpoiler.automatic) – Gradient spoiler on the slice channel

Minimum TE (PVM_MinEchoTime) – Minimum echo time. Depends on bandwidth, resolution, RF pulse duration and echo position; non-editable.

1.9.14 FISP (Fast Imaging with Steady State Precession)

1.9.14.1 Principles

Gradient echoes are generated by slice-selective RF pulses with $TE=TR/2$ and a complete refocusing of all gradient channels (TrueFISP mode). Consecutive RF pulses are phase coherent, and follow the cycle $x, -x, x, -x, \dots$ in the on-resonance frame. The signal is built up by all components of SSFP, provided the object is on-resonance and very well shimmed.

In this case, the sequence gives the maximum possible signal-to-noise ratio per unit time. If the shim is poor, black bands appear in the image at frequencies $(n+1/2)/TR$. These bands can be removed by running the sequence in FID or ECHO modes, but at the cost of about 30% reduction in overall signal.

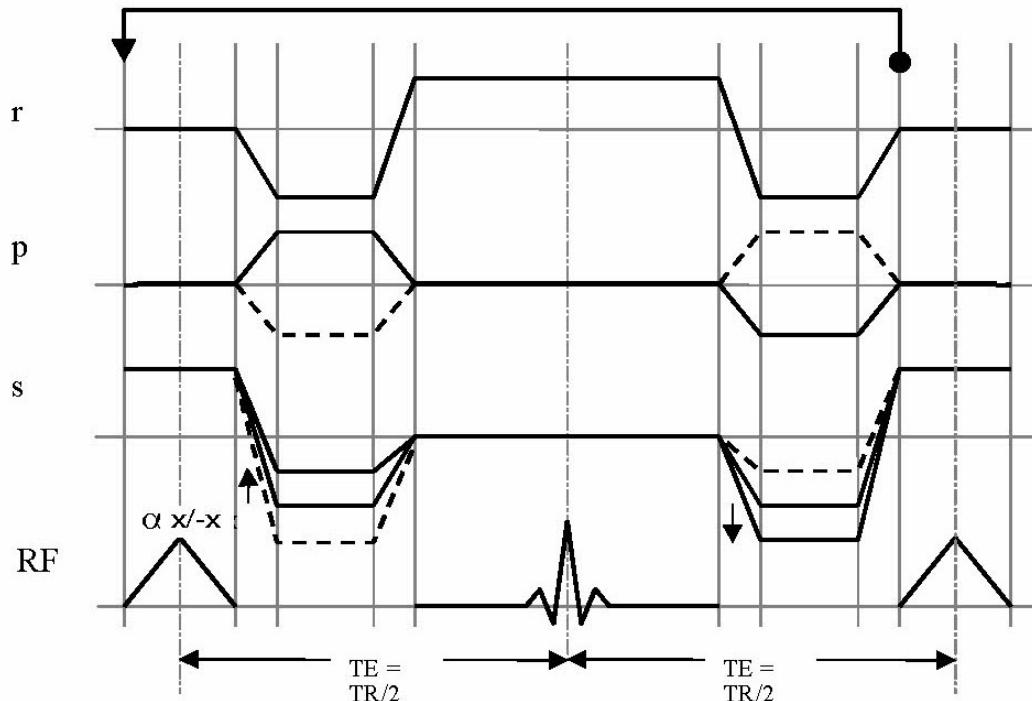


Figure 1.283: Pulse sequence of FISP

1.9.14.2 Applications

- High-resolution snapshot images
- Cardiac movies
- Rapid T1 measurements (in IR mode)

1.9.14.3 Loop Structure

From inner to outer loops:

- Acquisition order: phase-encoding (in-segment), movie frames, slices, phase-encoding (segments), accumulation (NAE), repetitions
- Image order in 2dseq: movie frames, slices, repetitions

1.9.14.4 Specific Parameters

Routine Card

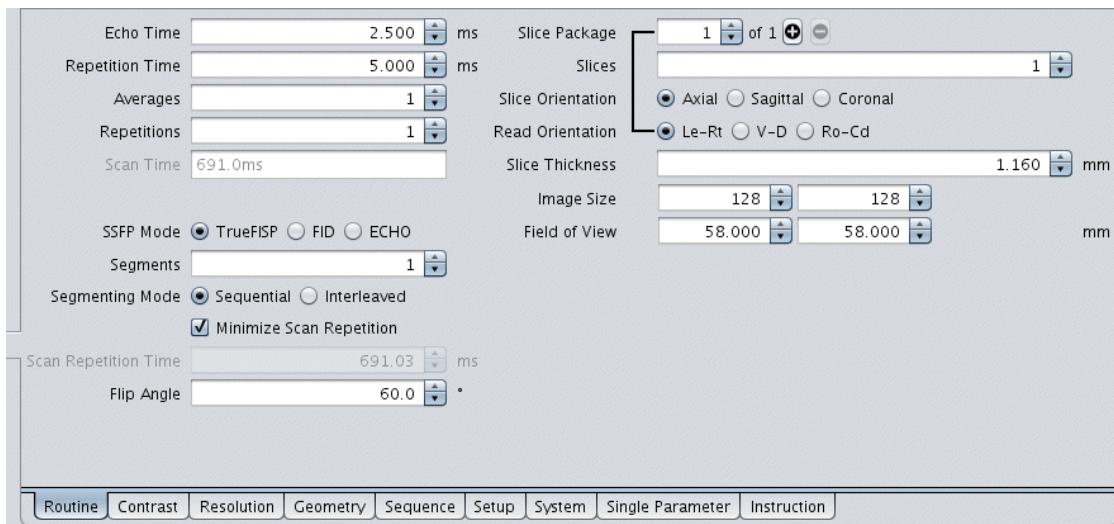


Figure 1.284: FISP Routine Card

SSFP Mode (Ssfp) – Selection of the component of the steady-state free precession (SSFP) :

- **TrueFISP:** Coherent superposition of all components is achieved by balancing all gradient pulses (mode also known as Balanced SSFP). Black stripes may appear in poorly shimmed regions. In this mode TR is always equal to 2*TE.
- **FID:** The component coherent with the FID of the last RF pulse is selected, which makes the sequence equivalent to FLASH. TR may be set longer than 2*TE.
- **ECHO:** The component coherent with the echo of the preceding FID is selected (mode also known as CE-FAST or PSIF).

Segments (Nsegments) – To increase the time resolution of movies, k-space can be segmented (only one k-space segment in one movie frame).

Segmenting Mode (Seg_mode) – Possible values are **Interleaved** or **Sequential**. The former is better for IR experiments, the latter for cardiac movies.

Minimize Scan Repetition (YesNoMinScanRepTime) – When selected, **Scan Repetition Time** is kept at its minimum.

Scan Repetition Time (Scan_RepetitionTime) – Time between the starts of consecutive acquisition segments. One segment may contain several movie frames, if selected in Preparation.

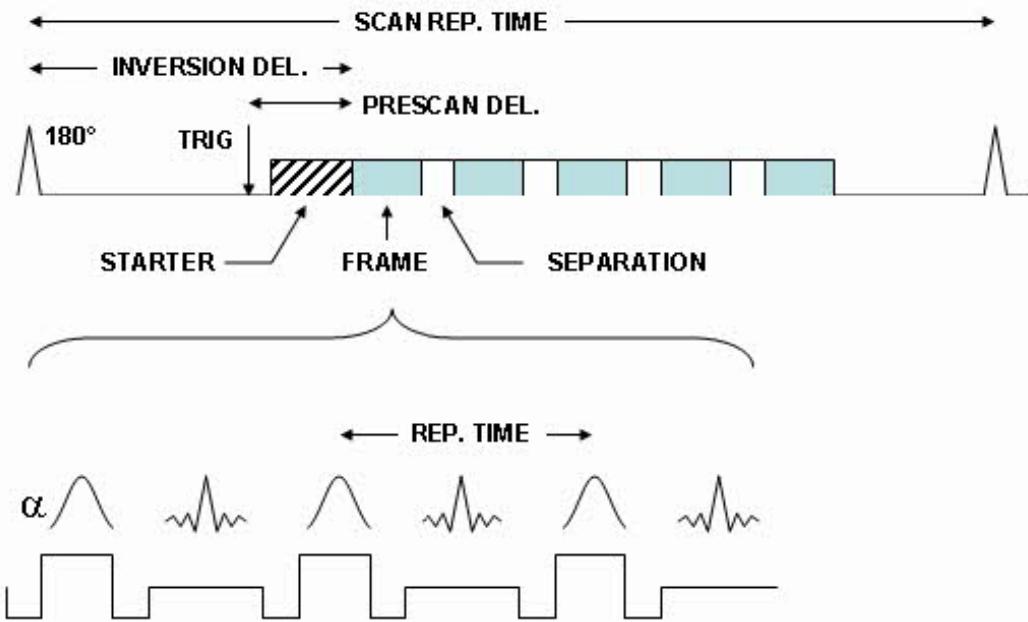


Figure 1.285: Timing parameters of FISP

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse. Should be kept low in the FID mode, and around 40-60 degrees in the TruFISP and ECHO modes.

Contrast Card

Main

Main	Inversion	Evolution	Trigger		
Echo Time	2.500	ms	<input checked="" type="checkbox"/> Inversion		
Repetition Time	5.000	ms	<input checked="" type="checkbox"/> Evolution		
Flip Angle	60.0	°	<input type="checkbox"/> Trigger		
RF Phase Advance	180.00	°			
SSFP Mode	<input checked="" type="radio"/> TrueFISP	<input type="radio"/> FID	<input type="radio"/> ECHO		
SSFP Preparation	<input type="radio"/> Alpha/2	<input checked="" type="radio"/> Starter Sequence	<input type="radio"/> None		
Flip Angle for Mz	30.00	°	Preparation Duration	45.93	ms
Segments	1		Preparations for Mxy	8	
Movie Frames	1		Segment Time	640.00	ms
<input type="button" value="Routine"/> <input type="button" value="Contrast"/> <input type="button" value="Resolution"/> <input type="button" value="Geometry"/> <input type="button" value="Sequence"/> <input type="button" value="Setup"/> <input type="button" value="System"/> <input type="button" value="Single Parameter"/> <input type="button" value="Instruction"/>					

Figure 1.286: FISP Contrast Card Main

Flip Angle (ExcPulse1.Flipangle) – See [Routine Card I ▶ 326](#)

RF Phase Advance (PhaseAdvance) – Difference in phase of consecutive RF pulses as seen in the on-resonance frame. The value of 180 is default and gives best signal on-resonance with good shims. However, if black stripes appear, by changing this value one can shift them away from a crucial element of the image (e.g. heart). This parameter is relevant only in the TrueFISP mode.

SSFP Mode (Ssfp) – See [Routine Card \[▶ 326\]](#)

SSFP Preparation (Ssfp_preparation) – Allows selection of a preparation sequence to stabilize the steady state signal in each segment. Possible choices are

- Alpha/2 – A single pulse with half the flip angle
- Starter Sequence – A longer but more efficient sequence of pulses comprising a Mz preparation with a programmable flip angle and a Mxy preparation with a specified number of pulses
- None – In this case a specified number of echoes can be skipped at the beginning of each segment.

Flip Angle for Mz (FlipAngMz) – Flip angle used in the starter sequence

Segments (Nsegments) – See [Routine Card \[▶ 326\]](#)

Movie Frames (PVM_NMovieFrames) – Number of images acquired after a single trigger (cardiac movie) or after a single inversion (T1 experiments)

Inversion (FISP_inversion_enable) – Activates the inversion recovery preparation of each segment (further details on the Inversion Subcard)

Trigger (PVM_TriggerModule) – Activates the trigger option (further details on the Trigger Subcard)

Preparation Duration (PreScan_Delay) – Time between the onset of a segment and the acquisition of the first echo, depends on the preparation mode

Preparations for Mxy (NumPrep) – Number of preparatory excitations in the starter sequence

Segment Time (Seg_time) – Acquisition time of one movie frame

Inversion

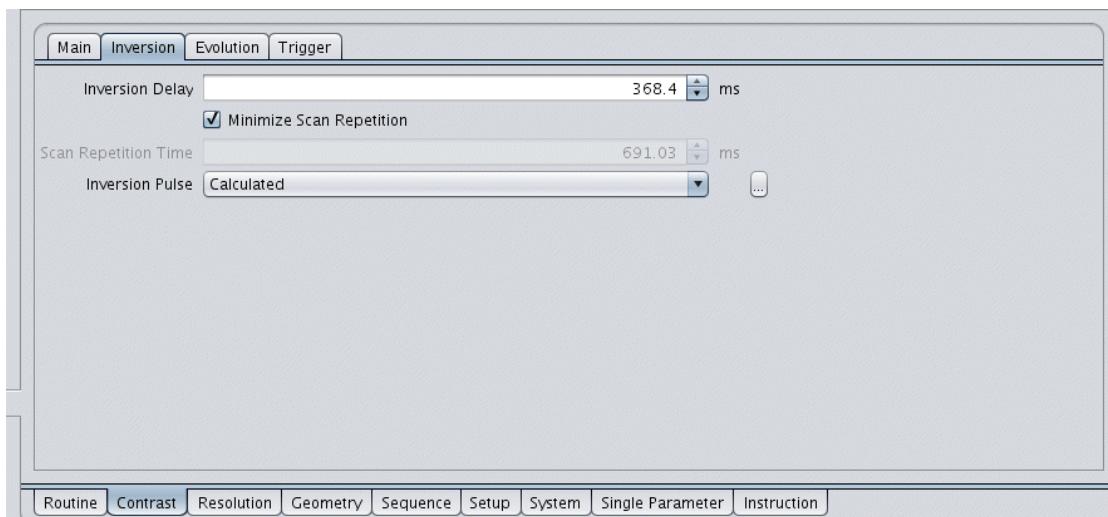


Figure 1.287: FISP Contrast Card Inversion

Inversion Delay (PVM_InversionTime) – Recovery delay for the first movie frame (if Inversion is selected)

Minimize Scan Repetition (YesNoMinScanRepTime) – See [Routine Card \[▶ 326\]](#)

Scan Repetition Time (Inv_Rep_time) – See [Routine Card \[▶ 326\]](#)

Inversion Pulse (InvPulse1Enum) – Pulse used for the non-selective inversion. When set to Calculated, the system generates an adiabatic full passage shape that guarantees a 180-degree flip.

Trigger

Mode (PVM_TriggerMode) – This parameter, belonging to the Trigger Parameters class, has a special meaning in FISP. See following Figure for details.

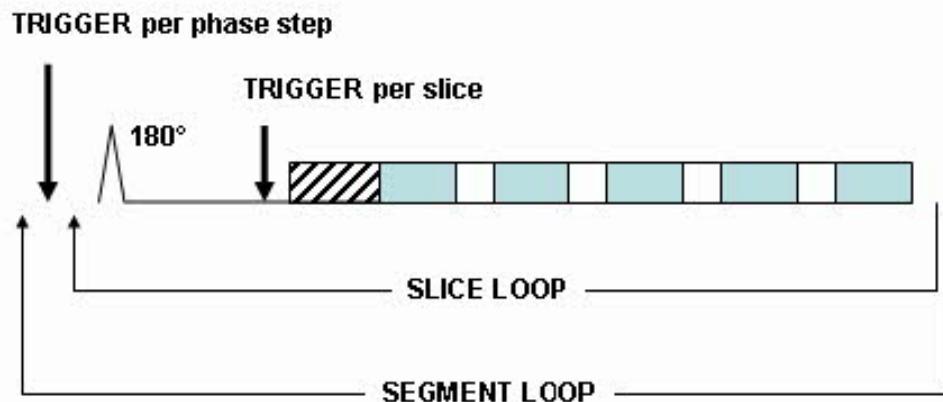


Figure 1.288: Triggering in FISP



It is possible to select the parallel acceleration option (see [Encoding \[▶ 270\]](#)) to reduce measurement time and artefacts, if necessary.

Sequence Card

Main

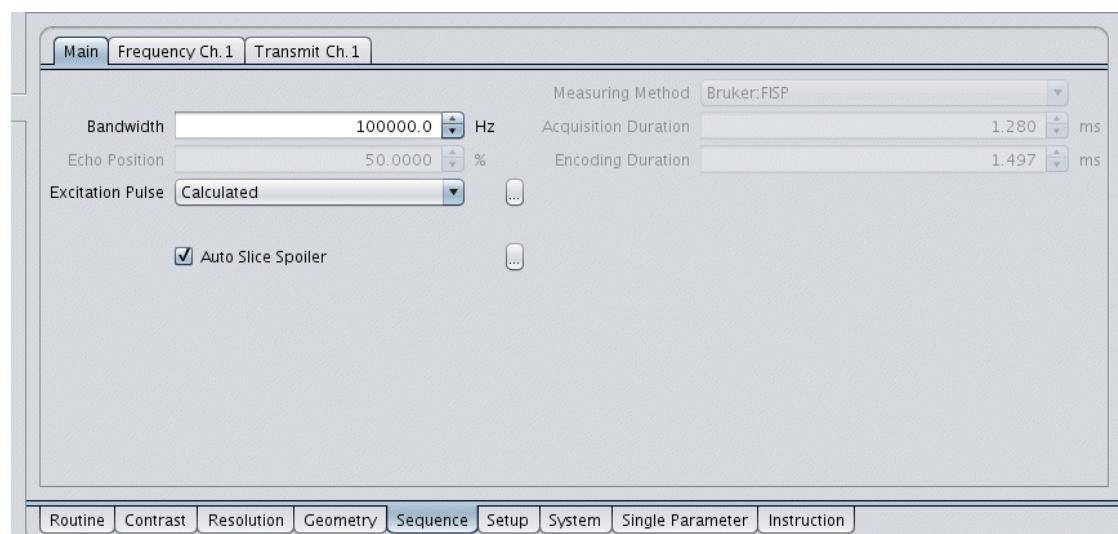


Figure 1.289: FISP Sequence Card Main

Echo Position (PVM_EchoPosition) – In TrueFISP mode non editable. In FID or ECHO mode this parameter value can be decreased in order to shorten the echo time.

Excitation Pulse (ExcPulse1Enum) – Slice selective excitation pulse. When the method works in the 3D mode (selection in [Routine Card ▶ 326](#)) this pulse selects the slab that is reconstructed as 3D volume. In this case it is important to select a high sharpness factor for this pulse (7 or higher) to avoid aliasing of out-of-slab signals.

Inversion Pulse (InvPulse1Enum) – See [Contrast Card Inversion ▶ 328](#).

Auto Slice Spoiler (SliceSpoiler.automatic) – Gradient spoiler applied after the inversion pulse

1.9.15 FLOWMAP

1.9.15.1 Principles

FLOWMAP is a flow-compensated gradient echo method (similar to [FcFLASH \(FcFast Low Angle Shot\) ▶ 289](#)) in which bipolar gradient pulses are added during the encoding period to produce a flow-dependent signal phase. The method can work in three modes which differ by the number of flow encoding steps and by the reconstruction procedure:

- **Phase contrast angiography:** The resulting image intensity indicates the presence of flow.
- **Velocity mapping:** The resulting images are scaled in cm/s and represent the maps of flow velocity components.
- **Fourier flow imaging:** An additional dimension is added to the experiment to produce the spectrum of velocities within each pixel.

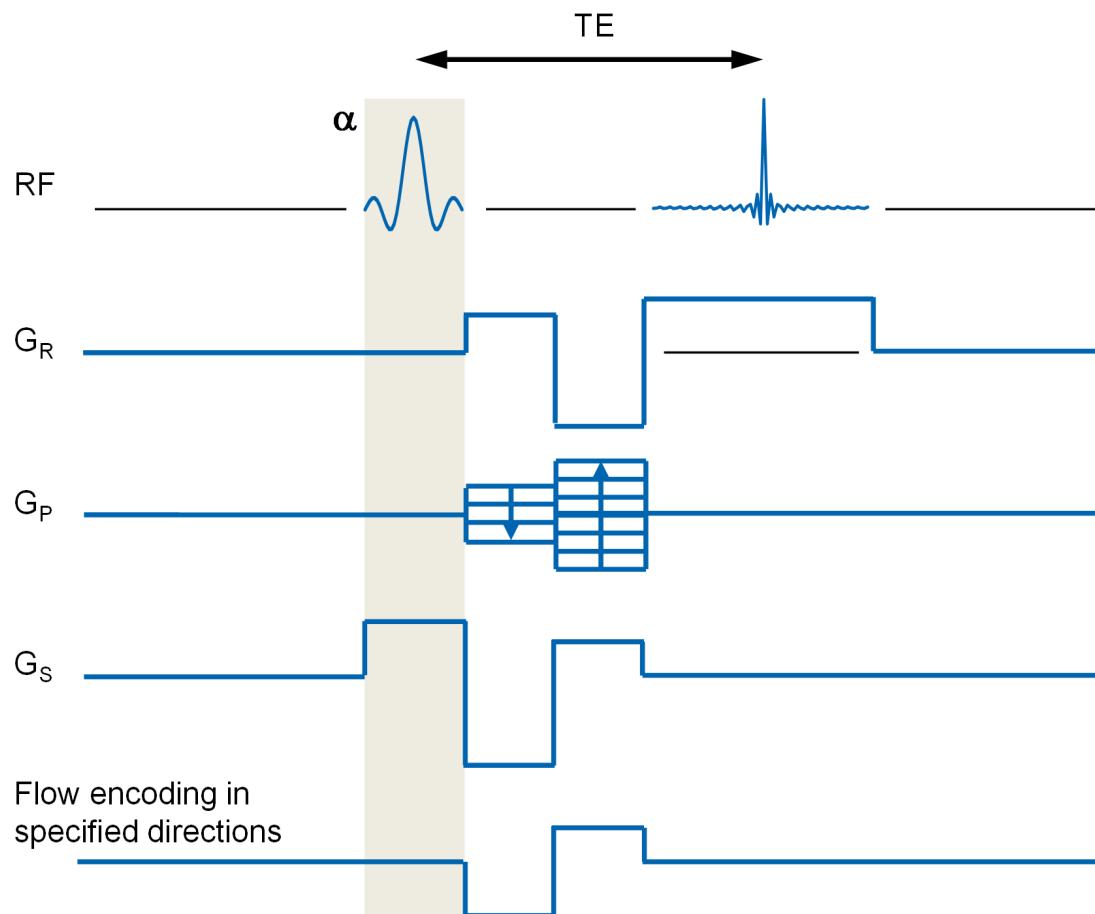


Figure 1.290: Pulse sequence of FLOWMAP

1.9.15.2 Applications

- Angiography, in particular in 3D mode
- Quantitative mapping of blood velocity in heart and large vessels
- Measurement of intra-voxel velocity distributions

1.9.15.3 Loop Structure

From inner to outer loops:

- Acquisition order: flow encoding, slices, spatial encoding, repetitions

1.9.15.4 Specific Parameters

Routine Card

Figure 1.291: FLOWMAP Routine Card Mode PhaseContrastAngiography

Figure 1.292: FLOWMAP Routine Card Mode FourierFlowImaging

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse

Mode (FlowMode) – This parameter defines the type of experiment. It can take one of the following values:

PhaseContrastAngiography: Two acquisitions are done with opposite polarity of the flow encoding gradient. The reconstruction delivers an amplitude angiogram calculated as the magnitude of the complex image difference. One can choose between one selected flow direction and all directions. In the latter case, the Hadamard flow encoding is used with 4 combinations of the three main directions (see following table) to obtain an angiogram sensitive to flow magnitude. 2D and 3D acquisition modes are available.

	r-gradient	p-gradient	s-gradient
Scan A	-	-	-
B	+	+	-
C	+	-	+
D	-	+	+

Table 1.3: Hadamard flow encoding scheme

VelocityMapping: The sequence is identical with the one used for PCA, but the processing is different. With a single flow direction an image of the corresponding velocity component is calculated from the phase difference between the opposite-encoded images. With all directions selected three velocity component images are calculated from the Hadamard scheme. This mode allows acquiring multiple movie frames (cine mode).

FourierFlowImaging: A 3D Fourier transform image is acquired. The first two directions are the read and phase directions of a standard imaging acquisition. The third direction represents the distribution of velocities within a pixel. In this experiment a specified number of increments of the bipolar flow gradient is produced to obtain a given flow resolution within a specified velocity range.

Direction (FlowEncodingDirection) – Defines the flow encoding direction in image coordinates. Possible values are: Slice, Phase, Read, and All. In case of All, the three directions are encoded using the Hadamard scheme.

Velocity Range (FlowRange) – The parameter gives the velocity for which the encoded phase is π . Only velocities between -Venc and +Venc can be measured unambiguously; higher velocities will be aliased. Reducing this parameter increases the precision of flow measurement.

Flow Encoding Steps (FlowEncSteps) – Number of flow encoding steps used in the FourierFlowImaging mode

Flow Zero-Fill Factor (FlowZeroFillFactor) – Interpolation factor in the flow encoding direction used in the FourierFlowImaging mode. The effectively reconstructed matrix size is the product of this factor and the **Flow Encoding Steps**.

Velocity Resolution (FlowResolution) – Resolution in the velocity spectrum in the FourierFlowImaging mode. This parameter is non editable and depends on **Velocity Range** and **Flow Encoding Steps**.

Contrast Card

Main

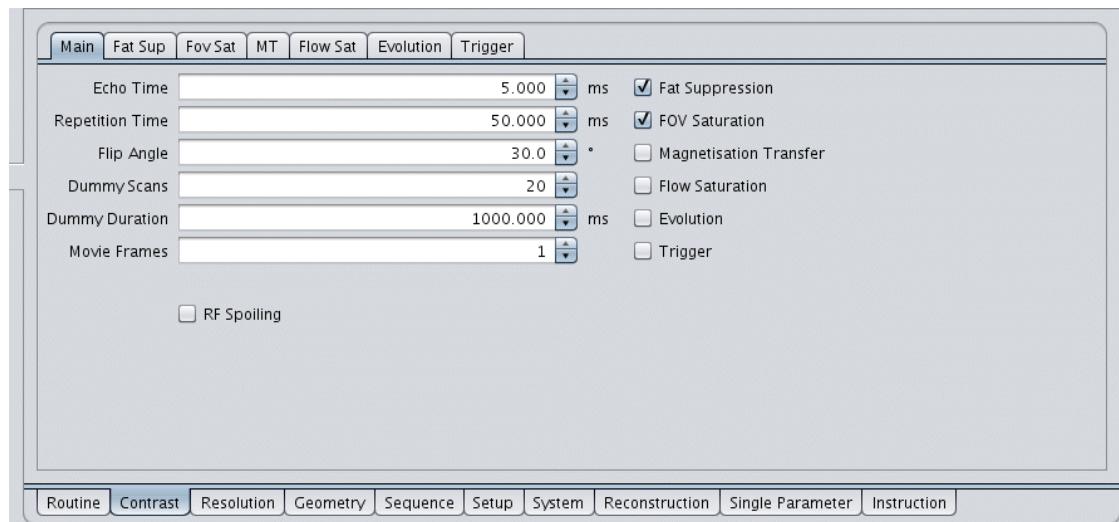


Figure 1.293: FLOWMAP Contrast Card Main

Flip Angle (ExcPulse1.Flipangle) – See [Routine Card ↗ 331](#)

Movie Frames (PVM_NMovieFrames) – Number of cycles (frames) of a movie. This option is typically used together with ECG triggering to produce heart movies (cine acquisition). The trigger should be set to Per Phase Step mode. Following the trigger, every phase encoding step is repeated for all slices the number of times given by this parameter (see following Figure). The time resolution of the movie is given by the repetition time.

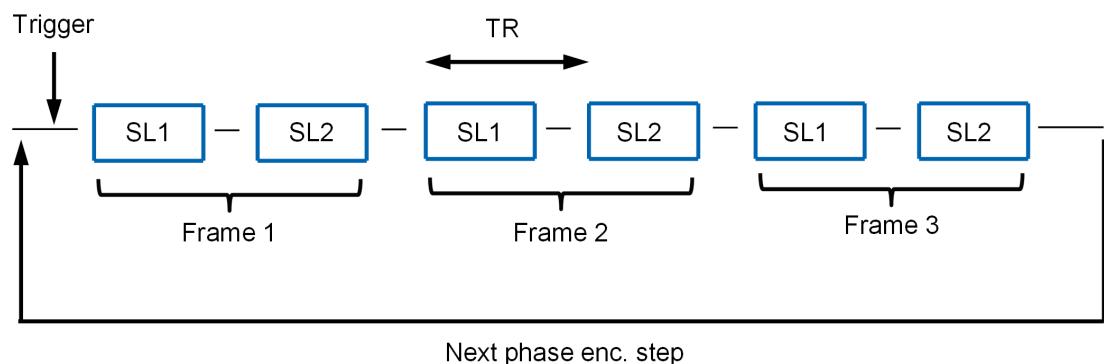


Figure 1.294: Diagram FLASH after contrast



Movies of consecutive slices are phase-shifted; the movie option should be used with low numbers of slices.



It is possible to select the parallel acceleration option (see [Encoding ↗ 270](#)) to reduce measurement time and artefacts, if necessary.

RF Spoiling (RFSpoiling) – Allows switching the RF spoiling on or off. RF spoiling provides T1 contrast by reduced SNR

Sequence Card

Main

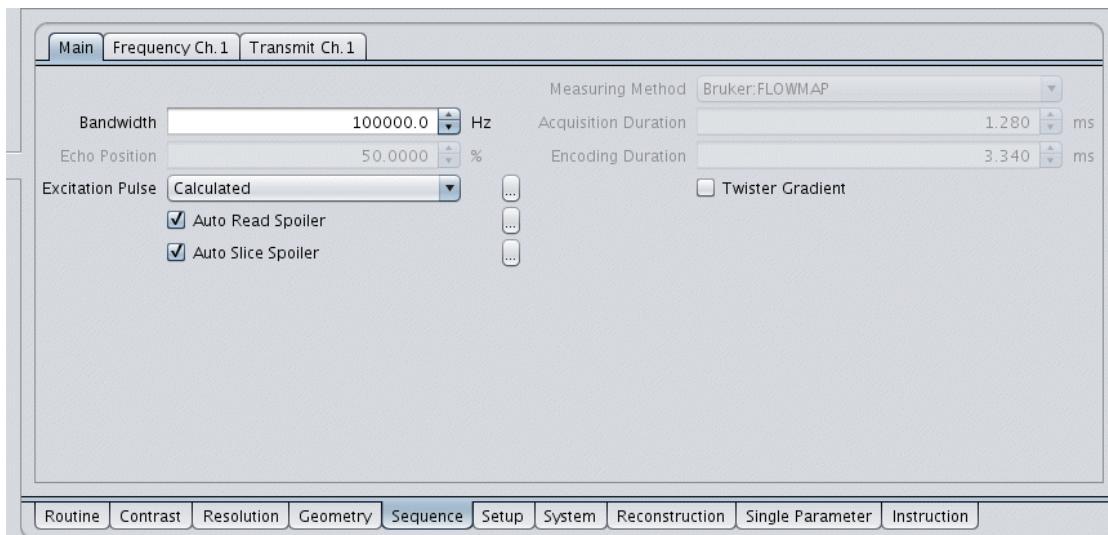


Figure 1.295: FLOWMAP Sequence Card Main

Echo Position (PVM_EchoPosition) – Determines the position of the echo in the acquisition window. Values below 50% allow lower TE. Depends on the Partial FT setting for the read direction on the Resolution Card.

Excitation Pulse (ExcPulse1Enum) – The slice selective excitation pulse. When the method works in the 3D mode (selection in Resolution Card) this pulse selects the slab that is reconstructed as 3D volume. In this case it is important to select a high sharpness factor for this pulse (7 or higher) to avoid aliasing of out-of-slab signals.

Auto Read Spoiler (ReadSpoiler.automatic) – A constant gradient pulse applied on the read channel after the echo acquisition

Auto Slice Spoiler (SliceSpoiler.automatic) – A constant gradient pulse applied on the slice channel after the echo acquisition

Twister Gradient (FlowTwister) – In 2D **PhaseContrastAngiography** and **VelocityMapping** modes a small gradient can be used in the slice direction to dephase the magnetization of the static spins. This improves the contrast between the static tissue and blood. The twister gradient is activated using this On/Off parameter.

Twister Effect (FlowTwisterGradient) – The parameter is shown if the parameter **Twister Gradient** is selected. Its value (in mm) corresponds to the slab thickness on which a dephasing effect of 360 degree is produced by the twister gradient.

Reconstruction Card

Signal Mask Threshold (SignalMask) – Defines an image threshold for the reconstruction. The output is set to zero for data points whose magnitude is below this threshold. This parameter is visible only for Flow Encoding Mode **VelocityMapping**.

Flow Zero-Fill Factor (FlowZeroFillFactor) – Interpolation factor in the flow encoding direction used in the **FourierFlowImaging** mode. The effectively reconstructed matrix size is the product of this factor and the **Flow Encoding Steps**.

1.9.16 DtiStandard (Diffusion Tensor Imaging Standard)

1.9.16.1 Principles

This method combines the Diffusion module ([Diffusion Card ▶ 336](#)) with the standard “spin-warp” imaging scheme. It allows an acquisition of simple diffusion-weighted images as well as measurements of the full diffusion tensor, from which further parameters, such as the fractional isotropy, isotropic diffusion constant (tensor trace) or main diffusion axis (basis for brain tractography) can be calculated. Since each k-space line is acquired with a separate excitation, the experiment takes a considerable time (in 3D mode even hours), and is extremely sensitive to the object’s motion. For that reason, DtiStandard is mainly used for post-mortem investigations and material science. For in-vivo studies fast counterparts of this method, [DtiEpi \(Diffusion tensor imaging with EPI\) ▶ 345](#) and [DtiSpiral \(Diffusion Tensor Imaging with Spiral scan\) ▶ 359](#) are mostly used. However, the great advantage of DtiStandard over these sequences is the complete lack of distortions caused by inhomogeneous magnetic field.

Like all methods using the Diffusion module DtiStandard allows the acquisition of Stejskal-Tanner pulsed gradient spin-echo (PGSE), stimulated echo, and double spin echo. The choice of the refocusing scheme and other parameters of the Diffusion module allow finding the best compromise between the weighting strength, signal losses caused by T2 relaxation and the sensitivity to susceptibility gradients.

1.9.16.2 Applications

- Standard (direction dependent) diffusion weighted imaging
- Measurement of ADC maps
- Measurement of ADC trace maps
- Measurement of diffusion tensors in anisotropic samples (brain, etc.)
- Q-space imaging

Due to a high sensitivity to motion the method should be used, in case of in vivo applications, with activated trigger module. To prevent severe saturation effects which cause signal loss and slice profile deformations the method should be used with repetition times adapted to the T1 of the sample at the given field strength.

1.9.16.3 Loop Structure

From inner to outer loops:

- Acquisition order: slice selection, diffusion, averages, 2d phase encoding, (plus dummy scans), 3d phase encoding, repetitions
- Image order in 2dseq: slices, diffusion images, repetitions

1.9.16.4 Specific Parameters

Routine Card

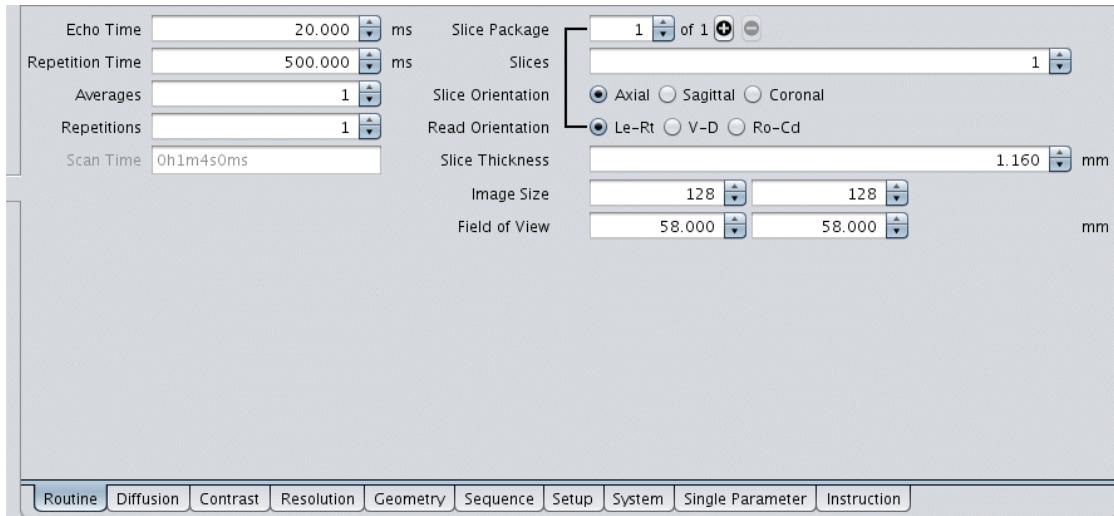


Figure 1.296: Dtistandard Routine Card

Repetition Time (PVM_RepetitionTime) – Time between consecutive excitations of the same slice (TR). Since the diffusion gradients contribute significantly to gradient duty cycle, protocols with TR close to minimum may lead to excessive gradient heating. Such protocols should be tested with the simulation platform before starting.

Repetitions (PVM_NRepetitions) – Number of repetitions of the entire set of experiments as defined on the [Diffusion Card \[▶ 241\]](#).

Diffusion Card

Parameters describing the diffusion weighting, number of diffusion experiments, etc. see [Diffusion Card \[▶ 241\]](#).

Contrast Card

Main

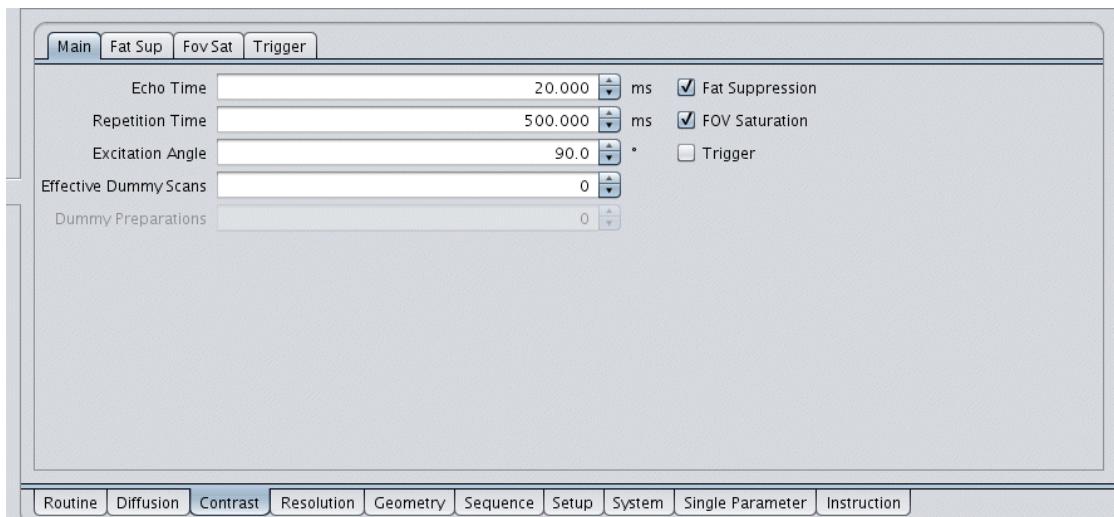


Figure 1.297: Dtistandard Contrast Card Main

Excitation Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse, typically 90 degrees

Effective Dummy Scans (EffDummyScans) – Number of dummy scans performed on each slice to establish a steady state. A time of at least $5 \cdot T_1$ should be spent on dummy scans to prevent incorrect determination of diffusion coefficients. Since the excitation of each slice is repeated for each diffusion preparation period ND times, the effective number of dummy scans is limited to be the closest multiple of ND (where ND = total number of diffusion experiments).

Dummy Preparations (NDummyScans) – Non-editable parameter. It displays the number of diffusion periods performed to establish the **Effective Dummy Scans**.

Sequence Card

Main

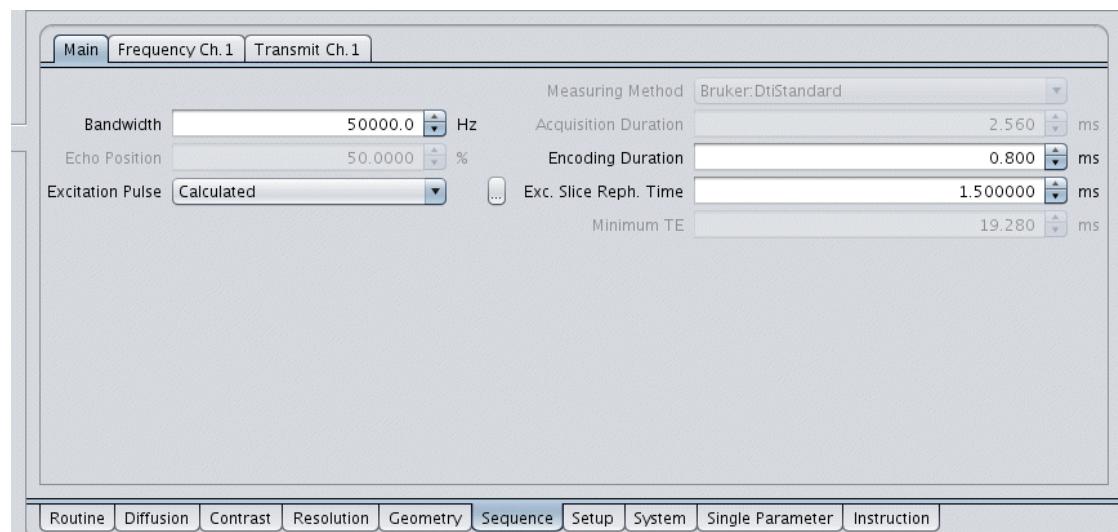


Figure 1.298: DtiStandard Sequence Card Main

Bandwidth (PVM_EffSWh) – The effective bandwidth of data sampling during the frequency encoding period. The optimal bandwidth choice is a trade-off between the field strength (to decrease chemical shift artifacts, increase bandwidth), the S/N ratio (decrease bandwidth) and the minimum possible TE (increase bandwidth).

Echo Position (PVM_EchoPosition) – Determines the position of the echo in the acquisition window. Values below 50% allow lower TE. Depends on the Partial FT setting for the read direction on the [Resolution Card ▶ 269\]](#).

Excitation Pulse (ExcPulse1Enum) – The slice selective excitation pulse. When the method works in the 3D mode (selection in [Resolution Card ▶ 269\]](#)) this pulse selects the slab that is reconstructed as 3D volume. In this case it is important to select a high sharpness factor for this pulse (7 or higher) to avoid aliasing of out-of-slab signals.

Encoding Duration (EncGradDur) – Duration of encoding gradient

Exc. Slice Reph. Time (ExcSliceRephTime) – Duration of the slice refocusing gradient. It should be increased if the minimum slice thickness should be reduced. The minimum TE will be increased by the same amount.

Minimum TE (PVM_MinEchoTime) – The minimum echo time is limited by the timing requirements of the DTI module. For echo times longer than these requirements, delays surrounding the DTI module of appropriate duration will be filled to satisfy this request. Although the TE is always a critical parameter, slightly larger echo time values (of the order of one ramp time) could be advantageous to separate the strong diffusion gradients from imaging events (phase and frequency-encoding).

1.9.17 EPI (Echo-Planar Imaging)

1.9.17.1 Principles

A train of differently phase-encoded gradient echoes is generated after an FID or spin-echo excitation using periodic reversals of the readout gradient accompanied by short phase encoding gradient blips. The entire k-space matrix can be covered in one scan, or in several interleaved segments. Depending on the excitation mode, the sequence has gradient echo or spin-echo contrast properties. The minimum effective echo time in the typical setting (symmetric k-space sampling) is rather long; the sequence is thus inherently strongly T2*/T2 weighted with a moderate T1 weighting depending on the repetition time and flip angle. In the spin echo mode the echo time can be significantly reduced by partial FT encoding. Due to the delays between consecutive k-space line scans (echoes), magnetic field inhomogeneity and chemical shifts lead to pixel displacements (image distortions). Image distortions can be reduced by interleaving and parallel acceleration.

1.9.17.2 Special Features

The method allows changing the duration and slew rate of the gradient ramp and switching its shape between linear and sinusoidal. A special auto-adjustment is provided to measure the k-space trajectory corresponding to the readout gradient, which is then used in the reconstruction (regridding) to reduce artifacts. Another adjustment measures the phase correction coefficients for an automatic removal of the “N/2 ghost”. A navigator option improves signal stability in segmented acquisitions in the presence of object motion and frequency drifts.

1.9.17.3 Applications

- Ultra-fast T2* weighted imaging for functional brain MRI and perfusion studies. More generally, for all ultra-fast MRI applications provided that the magnetic field is sufficiently homogeneous.
- In multi-shot mode and with long sinusoidal ramps the sequence produces a much lower acoustic noise than the standard EPI. This has interesting applications in fMRI.

1.9.17.4 Loop Structure

From inner to outer loops:

- Acquisition order: slices, accumulation (NA), segments (PVM_EpiNShots), repetitions (NR)
- Image order in `2dseq`: slices, repetitions

1.9.17.5 Specific Parameters

Routine Card

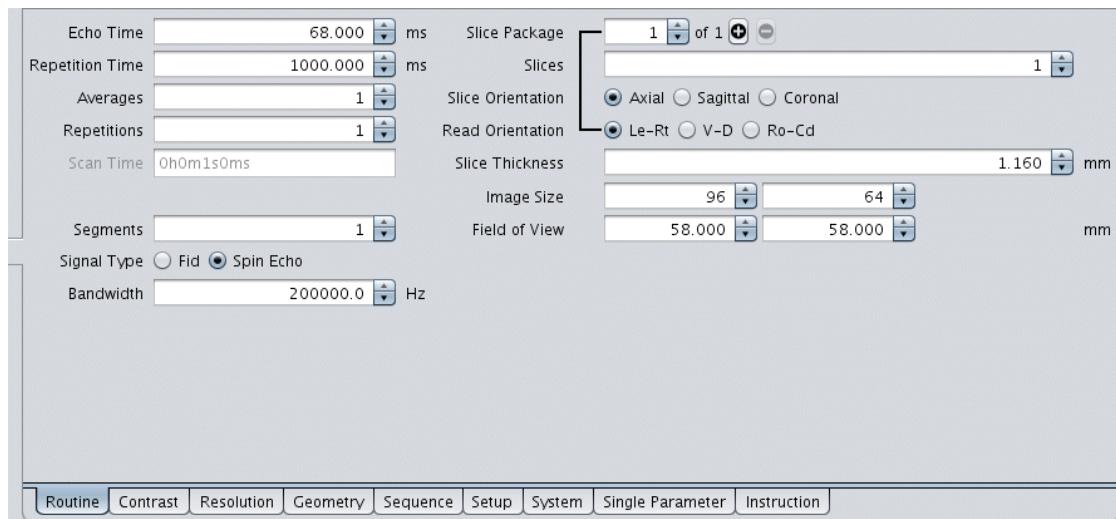


Figure 1.299: EPI Routine Card

Echo Time (EchoTime) – Delay between the effective center of the excitation pulse (depends on pulse rephasing properties) and the acquisition of the kspace center (depends on PVM_EpiEchoPosition parameter defined in the EPI parameter class). Determines the T2* contrast of the sequence.

Repetition Time (PVM_RepetitionTime) – Delay between corresponding slices in consecutive volumes. Its minimum depends on the number of slices and on the volume related delay (PackDel parameter defined on the [Contrast Card/Main \[▶ 340\]](#)).

Segments (NSegments) – Allows running the sequence in a number of interleaved shots to reduce image distortions caused by magnetic field inhomogeneity

Signal Type (PVM_SignalType) – Allows the user to select the type of observed signal. Possible values are:

- Fid – A single RF pulse is used to generate the FID. The image has a gradient-echo nature and is T2* weighted.
- Spin Echo – Two RF pulses generate a spin echo. The center of the k-space is automatically located in the spin echo center. The image is T2 weighted.

Bandwidth (PVM_EffSWh) – Effective bandwidth of the image in the frequency encoding (readout) dimension. A higher bandwidth reduces chemical shift artifacts (fat-water displacement) and allows reaching shorter echo times at the price of a lower signal-to-noise ratio of the image (the SNR is inverse-proportional to the square root of the effective bandwidth).

Software Manual

Contrast Card

Main

Main

Repetition Time: 1000.000 ms Fat Suppression

Inter-Volume Delay: 0.00 ms Magnetisation Transfer

Echo Time: 37.760 ms FOV Saturation

Flip Angle: 90.0 ° Tagging

Dummy Scans: 1 Trigger

Dummy Duration: 1000.000 ms Trigger Out

Routine Contrast Resolution Geometry Sequence Setup System Single Parameter Instruction

Figure 1.300: EPI Contrast Card Main

Repetition Time (PVM_RepetitionTime) – See [Routine Card](#) [▶ 339]

Inter-Volume Delay (PackDel) – An additional delay after each complete acquisition of all slices. It can be used to group slice excitations closer to each other in a dynamic experiment, or to offer a quiet break for the presentation of auditory stimuli in fMRI.

Echo Time (EchoTime) – See [Routine Card](#) [▶ 339]

Flip Angle (ExcPul.Flipangle) – Flip angle of the excitation pulse, typically 90 degrees

Sequence Card

Main

Main

Bandwidth: 200000.0 Hz Measuring Method: Bruker:EPI

Signal Type: Fid Spin Echo Minimum TE: 37.760 ms

Segments: 1

Excitation Pulse: Calculated

Refocusing Pulse: Calculated

Auto Slice Spoiler

Routine Contrast Resolution Geometry Sequence Setup System Single Parameter Instruction

Figure 1.301: EPI Sequence Card Main

Signal Type (PVM_SignalType) – See [Routine Card](#) [▶ 339]

Segments (PVM_NSegments) – See [Routine Card](#) [▶ 339]

Excitation Pulse (ExcPulseEnum) – The slice selective excitation pulse. When the method works in the 3D mode (selection in [Resolution Card ▶ 269](#)) this pulse selects the slab that is reconstructed as 3D volume. In this case it is important to select a high sharpness factor for this pulse (7 or higher) to avoid aliasing of out-of-slab signals.

Refocusing Pulse (RefPulseEnum) – Refocusing pulse in the spin-echo mode. Should be set to the same bandwidth as the excitation to avoid saturations of adjacent slices.

Auto Slice Spoiler (SliceSpoiler.automatic) – Gradient spoiler placed on each side of the refocusing pulse to avoid interference with this pulse's FID

Minimum TE (PVM_MinEchoTime) – The minimum echo time depends on bandwidth, matrix size, number of segments and the Partial FT factor; non-editable.

EPI

This subcard contains parameters controlling the EPI signal readout including navigator options (see [Echo Planar Imaging \(EPI\) ▶ 275](#)).

1.9.17.6 Ghost Correction

EPI is prone to a particular artifact called N/2 or Nyquist ghost due to its displacement by FOV/2 with respect to the original image in the single shot mode. This artifact is related to the oscillation of the readout gradient and has several causes such as:

- time lag of the readout gradient,
- time lag of the signal filters,
- uncompensated eddy currents.

The ghost artifact is automatically suppressed by the reconstruction based on the information acquired during the receiver gain adjustment. This adjustment will not take place when the sequence is started with the GOP instruction.

1.9.17.7 Multi-shot interleaved EPI

The EPI sequence can be applied in the multi-shot (interleaved) mode to reduce the susceptibility-related image distortions and blurring. This option is particularly useful at very high magnetic fields where the susceptibility effects are strong. The multi-shot mode is activated by setting the parameter **Segments** more than one. As this parameter is increased, the minimum effective echo time gets shorter (for a given bandwidth and matrix size) and the image becomes less distorted.

In addition to the even-odd echo mismatch, ghosting can also be caused by signal instability from shot to shot. For this reason it is recommended to use a sufficient number of dummy scans to achieve the steady state. Ghosting caused by other instability sources (e.g. uncontrolled object movement) cannot be reduced.

1.9.17.8 Partial-Fourier EPI

The Partial-Fourier Acceleration option available on the Resolution-Encoding Card (refer to [Encoding ▶ 270](#)) is particularly advantageous in EPI since it reduces the minimum effective echo time. Setting the Partial-FT Acceleration in the phase direction to a number higher than one reduces the matrix size and shifts the position of the central echo towards the beginning of the echo train. The Partial-FT option behaves best with the spin-echo mode. With FID the quality of the image depends on the echo time and on the number of Partial-FT overscans (more overscans allow longer TEs).

1.9.17.9 Parallel EPI

Like all standard methods EPI can work with coil arrays in which case the reconstruction produces sum-of-squares-combined images. It is also possible to select the parallel acceleration option in the Encoding parameter class (see [Encoding ↗ 2701](#)), which, in the case of EPI leads not only to a reduced measurement time, but also to reduced distortions and to a lower minimum echo time. Parallel and partial-FT accelerations can be combined allowing high resolution images to be acquired in a single shot. Parallel acceleration may also be activated in the segmented mode for a further reduction of artefacts.

Parallel EPI is reconstructed using the reference information acquired in a special adjustment. Therefore, it is not recommended to start a parallel EPI scan with the GOP instruction. The quality of the GRAPPA reconstruction can be improved by increasing the number of PPI reference lines, but it must be taken into account that this will decrease the effective acceleration (PVM_EncTotalAccel).

The resulting SNR of an accelerated parallel acquisition is reduced at least by the square root of the effective acceleration, since the number of phase encoding steps is reduced by this factor.

1.9.18 FAIR_EPI (Flow-sensitive Alternating IR EPI)

1.9.18.1 Principles

The method allows perfusion measurement or perfusion-weighted imaging based on the Flow-sensitive Alternating Inversion-Recovery (see Reference [\[18\] ↗ 691](#)). A package of slices is acquired using a spin-echo or gradient-echo EPI after either a selective or a non-selective adiabatic inversion. The selective inversion is applied to a slab covering the slice package with a user-defined margin. By subtraction of selectively-prepared and non-selectively prepared images blood flowing into the imaging package can be visualized. A quantitative perfusion measurement is possible by acquiring images with different inversion recovery times.

1.9.18.2 Applications

- Perfusion quantification in the brain, single slice
- Dynamic perfusion-weighted MRI
- T1-mapping

1.9.18.3 Loop Structure

Abbreviation: TIR = starting value for incremented inversion recovery delays

From inner to outer loops:

- Acquisition: slices, slice selective TIR loop followed by non-selective TIR loop, repetition loop
- Image file: same order as the acquisition

1.9.18.4 Specific Parameters

FAIR_EPI is a variant of EPI. Most parameters have the same meaning and can be found in the corresponding Chapter [EPI \(Echo-Planar Imaging\) ↗ 3381](#). This chapter includes only parameters that have a different meaning or that are not described in the EPI paragraph.

Routine Card

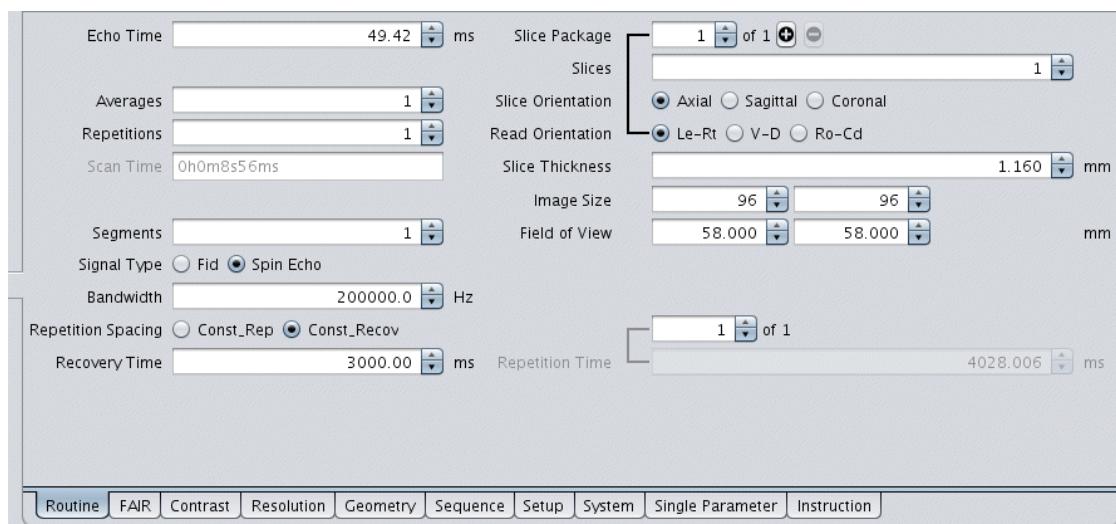


Figure 1.302: FAIR_EPI Routine Card

Repetition Spacing (PVM_FairRepSpacing) – This parameter is part of the FAIR module, see [FAIR Card ▶ 281](#) for details. It has been placed on the Routine Card as well because the repetition time depends on it.

Recovery Time (RecoveryTime) – Time between the last excitation pulse and the next inversion pulse, visible for **Repetition Spacing = Const_Recov**.

Repetition Time (MultiRepTime) – For **Repetition Spacing = Const_Rep** the repetition time is given by the usual repetition time (PVM_RepetitionTime).

For **Const_Recov** however, this repetition time is replaced by an array of repetition times (MultiRepTime) of size **TI Images**.

FAIR Card

This card contains all parameters controlling the spin labelling with the FAIR module. See [FAIR Card ▶ 281](#) for details.

1.9.19 CASL_EPI

1.9.19.1 Principles

CASL_EPI consists of a continuous arterial spin labeling (CASL) preparation combined with the EPI readout. Continuous inversion of arterial spins is realized by flow-driven adiabatic fast passage: A constant RF pulse is applied off-resonance in the presence of a constant gradient along the direction of flow in the arteries being labeled. The frequency offset of the RF pulse is determined by the labeling gradient strength and by the desired distance from the plane of inversion to the magnet's isocenter. Flowing along the labeling gradient, the arterial spins experience a frequency sweep. When they pass the labeling plane they undergo an adiabatic inversion which is maintained as they continue to flow away from the labeling plane.

A typical CASL experiment consists of two acquired images per slice: a `Label` and a `Control` image. During control a frequency offset of `-flabel` relative to the imaging plane is used which moves the tagging plane to the opposite side in order to compensate magnetization transfer effects. When using a separate labeling coil, magnetization transfer effects are negligible and the labeling power can be switched off during control.

1.9.19.2 Applications

- Perfusion quantification, especially quantification of cerebral blood flow

1.9.19.3 Loop Structure

From inner to outer loops:

- Acquisition order: slices, accumulation, phase-encoding, label, control, repetitions
- Image order in `2dseq` file: slices, label, control, repetitions

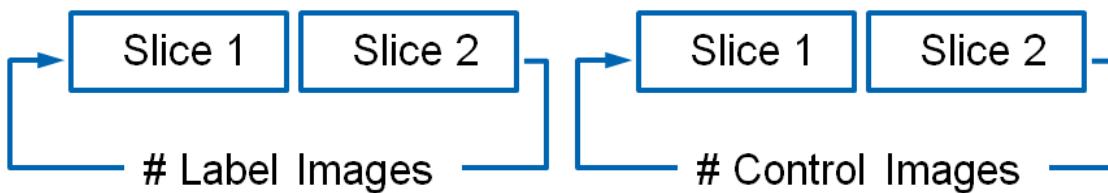


Figure 1.303: Acquisition order of Label and Control images

1.9.19.4 Specific Parameters

CASL_EPI is a variant of EPI. Most parameters can be found in the corresponding paragraph of [EPI \(Echo-Planar Imaging\) \[338\]](#). Here, only parameters controlling the CASL preparation are described.

CASL Card

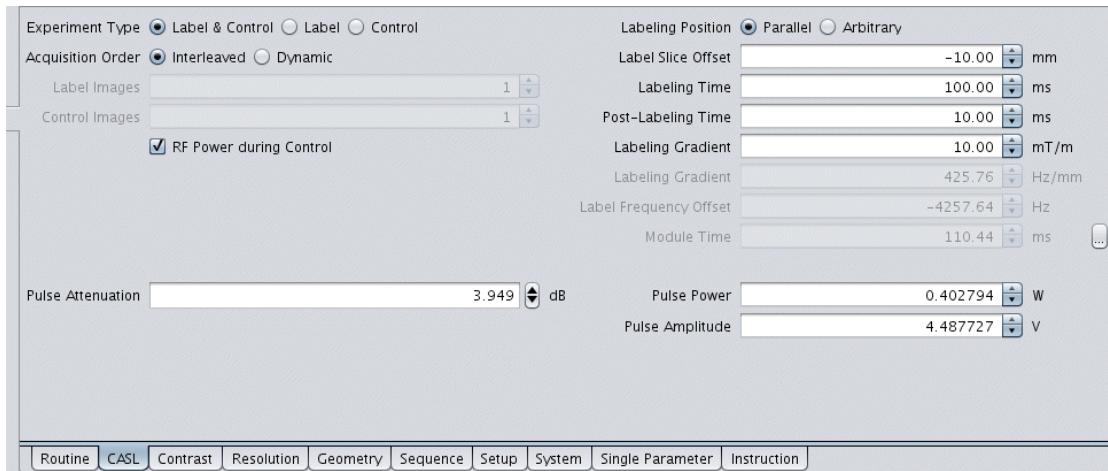


Figure 1.304: CASL_EPI CASL Card

Experiment Type (CASL_Exptype) – The user can select if Label & Control, only Label or only Control images should be acquired.

Acquisition Order (CASL_AcqOrder) – The Label & Control images can be acquired interleaved or in a dynamic way:

- In Interleaved mode just one label and one control image per slice will be acquired.
- For Dynamic acquisition the number of label and control images per slice can be separately specified by the following parameters:

Label Images (CASL_LabelImages) – Defines the number of labeled images

Control Images (CASL_ControlImages) – Defines the number of control images

RF Power during Control (CASL_RFPowerYesNo) – Switches the labeling RF pulse power during control experiment on or off

Pulse Attenuation, Pulse Power, Pulse Amplitude (CASL_RFPulAmpl) – Controls the labeling pulse power. The required pulse power for adiabatic inversion can be manually adjusted in the Setup mode.

Labeling Position (CASL_LabelPos) – Controls the labeling slice orientation: parallel to imaging slice (**Parallel**) or without any restrictions (**Arbitrary**)

Label Slice Offset (CASL_LabelSliceOffset) – Defines the offset position of the labeling slice

Labeling Time (CASL_LabelTime) – Duration of labeling period

Post-Labeling Time (CASL_PostLabelTime) – Time delay between labeling and imaging part of the sequence

Labeling Gradient (CASL_LabelGradient) – Controls the strength of the labeling gradient

Label Frequency Offset (CASL_Frequency) – The frequency offset of the labeling pulse is defined by the **Labeling Gradient** and the **Label Slice Offset**.

Module Time (CASL_ModuleTime) – Time duration of CASL preparation

Details

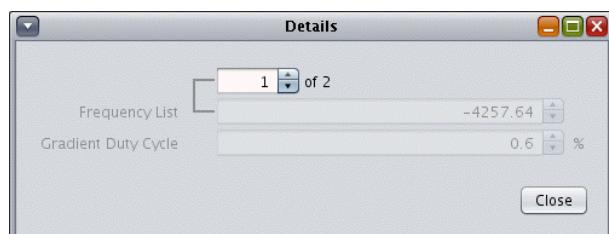


Figure 1.305: CASL_EPI CASL Card Module Time Details

Frequency List (CASL_FrequencyList) – Frequency offset list used for CASL preparation

Gradient Duty Cycle (CASL_GradientDutyCycle) – Gradient duty cycle of CASL module

1.9.20 DtiEpi (Diffusion tensor imaging with EPI)

1.9.20.1 Principles

This method combines the Diffusion Module (see [Diffusion Card ▶ 241](#)) with Echo Planar Imaging (see [Echo Planar Imaging \(EPI\) ▶ 275](#)) to allow fast acquisition of diffusion weighted images or quantitative diffusion data, including diffusion tensor imaging. The main advantage of DtiEpi compared to standard diffusion MRI (see [DtI Standard \(Diffusion Tensor Imaging Standard\) ▶ 335](#)) is the possibility of taking entire images with a single shot. This not only reduces the scan time, but, most importantly, eliminates the sensitivity of the experiment to microscopic motion of the animal.

Like all methods using the Diffusion module, DtiEpi can acquire spin echo, stimulated echo or double spin echo signals, and allows setting of arbitrary strengths and directions of diffusion-sensitizing gradient pulses. Due to intense use of gradients during both diffusion preparation and signal readout, the method can reach high values of the gradient duty cycle, especially with many slices. It is recommended to verify the duty cycle on the Simulation Platform before starting the scan.

All special features of EPI apply to DtiEpi as well. These include distortions caused by magnetic susceptibility of the object, enhanced fat-water shift, and relatively long minimum echo time, all problems growing with the image matrix size. For best results it is essential to

shim the imaging region, preferably using MAPSHIM. Similar to EPI, distortions, chemical shift and echo time can be reduced by segmenting. This option, however, should be used with care for in-vivo diffusion experiments since it re-introduces the sensitivity to animal motion. Triggering and the navigator option should be used to reduce the motion sensitivity. To reduce TE, partial FT acceleration can be selected in the phase encoding direction.

1.9.20.2 Applications

- Ultrafast diffusion weighted imaging
- Ultrafast measurement of ADC maps
- Ultrafast measurement of diffusion tensor images

1.9.20.3 Loop Structure

From inner to outer loops:

- Acquisition order: slices, accumulation (NA), dummy scans (if specified), 2d phase encoding (if segmented acquisition is selected, PVM_EpiNShots), diffusion loop, number of repetitions (NR)
- Data in `fid`: slices, diffusion loop, repetitions
- Image order in `2dseq`: slices, diffusion experiments, repetitions

1.9.20.4 Specific Parameters

DtiEpi is a variant of EPI. Most parameters have the same meaning and can be found in the corresponding chapter [EPI \(Echo-Planar Imaging\) \[▶ 338\]](#). The parameters of the Diffusion Card are described in detail in chapter [Diffusion Card \[▶ 241\]](#).

1.9.21 T1_EPI for rapid measurement of the effective relaxation time T1

1.9.21.1 Principles

The method T1_EPI (Echo Planar Imaging) allows rapid measurements of the effective longitudinal relaxation time T1. It is a variant of Echo Planar Imaging, similar to reference (see References [\[071\] \[▶ 691\]](#), [\[081\] \[▶ 691\]](#), [\[091\] \[▶ 691\]](#)). After a non-selective inversion pulse, the longitudinal magnetization is sampled by multiple application of the EPI sequence. In this way the entire T1 recovery curve is measured using a single inversion (or a few inversions for a larger number of slices). The experiment can be run in several shots using the standard EPI segmenting to reduce the susceptibility-related image distortions. The methods includes all EPI features, like ghost correction, partial Fourier reconstruction and parallel acceleration. Imaging geometry is restricted to one slice package. A special T1 fit function (`t1epic`) is implemented in the ISA tool for the purpose of this method.

The method allows various strategies for multi-slice acquisition. The inversion recovery can be sampled separately for each slice with a low flip angle pulse (a classical Look-Locker sequence, see Reference [\[081\] \[▶ 691\]](#)). Alternatively, small slice groups can be sampled during a single recovery to save the measurement time. It is also possible to rotate the positions of slices in consecutive scans to improve the IR sampling resolution and maximize the signal (see Reference [\[071\] \[▶ 691\]](#)).

1.9.21.2 Applications

Ultra-fast T1 mapping

1.9.21.3 Loop Structure

From inner to outer loops:

- Acquisition order: slices (internal loop), inversion recovery points, slices (external loop), accumulation (NA), segments (PVM_EpiNShots), repetitions (NR)
- Image order in 2dseq: inversion time, slices, repetitions

1.9.21.4 Specific Parameters

T1_EPI is a variant of EPI. Most parameters have the same meaning and can be found in the corresponding Chapter [EPI \(Echo-Planar Imaging\) \[338\]](#). This chapter includes only parameters that have a particular meaning or that are not described in the EPI paragraph.

Routine Card

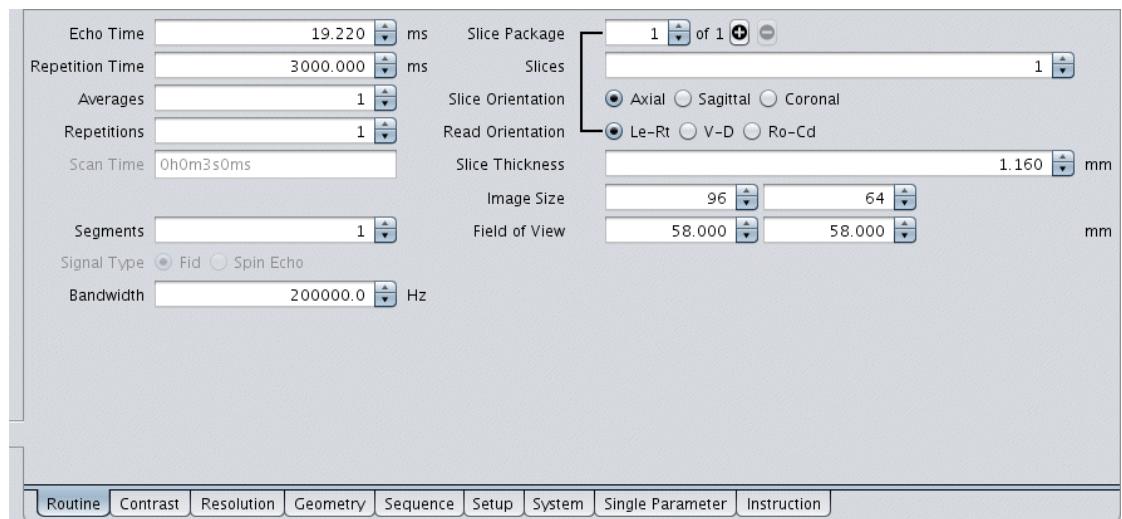


Figure 1.306: T1_EPI Routine Card

Signal Type (PVM_SignalType) – This parameter is set to FID and remains non-editable. The Spin Echo option is disabled since it is not compatible with the Look-Locker sampling method.

Contrast Card

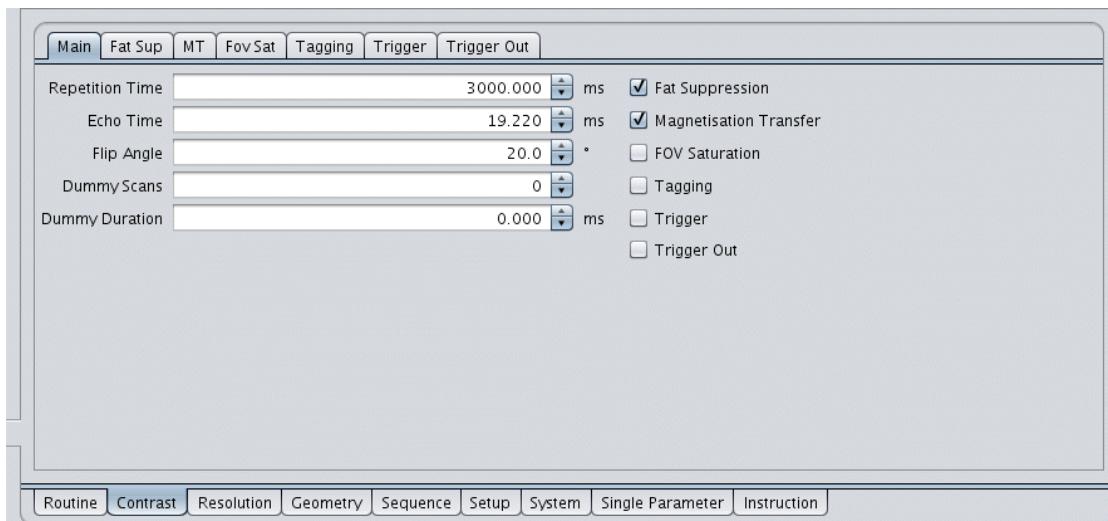


Figure 1.307: T1_EPI Contrast Card Main

Flip Angle (ExcPul.Flipangle) – Flip angle of the excitation pulse. It is recommended to use low flip angles (below 20 degrees) in experiments with several excitations of the same slice during one inversion recovery. Higher flip angles cannot be correctly taken into account by the T1 fitting function.

Sequence Card

Main

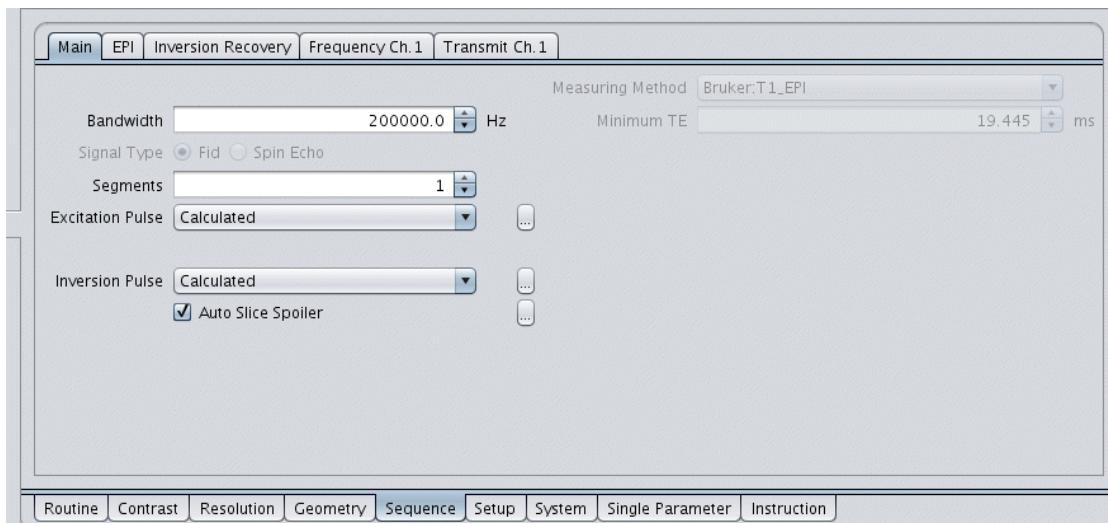


Figure 1.308: T1_EPI Sequence Card Main

Signal Type (PVM_SignalType) – See [Routine Card ▶ 347](#)

Excitation Pulse (ExcPulseEnum) – Slice-selective excitation pulse repeating with each EPI readout module

Inversion Pulse (InvPulseEnum) – Non-selective inversion pulse applied at the beginning of the sequence. When set to Calculated, the system generates an adiabatic full passage pulse assuring a perfect 180-degree inversion.

Inversion Recovery

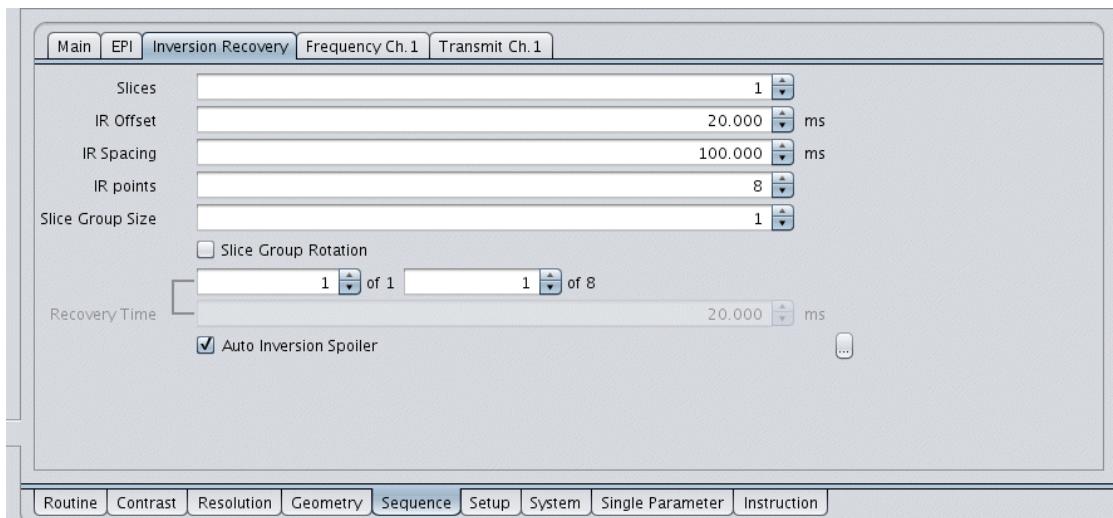


Figure 1.309: T1_EPI Sequence Card Inversion Recovery

Slices (InpSlices) – Mirrored parameter from the Geometry Card. It can only take values that are multiples of **Slice Group Size** (see below). If a smaller value is entered it will be rounded up to the next possible one.

IR Offset (IROffset) – Time offset of the inversion-recovery samples (delay between the inversion and the first excitation)

IR Spacing (IRSpacing) – Time between consecutive samples of the inversion recovery for the same slice. It is possible to acquire more than one slice within IR Spacing, see **Slice Group Size**.

IR Points (NIRPoints) – Number of inversion recovery samples. With **Slice Group Rotation**, **IR Points** can only take values that are multiples of **Slice Group Size** (see below).

Slice Group Size (SliceGroupSize) – Number of slices measured during one inversion recovery. Increasing this parameter (with **Slice Group Rotation** off) typically reduces the measurement time and increases the minimum IR spacing (to accommodate all slice excitations). It is even possible to carry out the entire multi-slice IR experiment in a single shot by setting **Slice Group Size** to the total number of slices. Note, that slices are sampled with different time offsets in this case, however, this does not influence the T1 fit.

Slice Group Rotation (SliceGroupRotation) – If selected, more measurements are performed with cyclical permutations of slice order, so that all slices are sampled at the same recovery times. This option allows keeping **IR Spacing** short with high **Slice Group Sizes**, but requires a longer total time (precisely, the same time as an experiment with **Slice Group Size** set to one). The advantage of the rotation is that slices are excited less often during one inversion recovery, which allows using higher excitation flip angles and results in a better SNR. In particular, when

$$\text{IR Points} = \text{Slice Group Size} = \text{total number of slices},$$

each slice will be excited only once per inversion so that a 90° flip angle can be used.

Recovery Time (IRTime) – Effective inversion recovery times of all slices

Auto Inversion Spoiler (InvSliceSpoiler.automatic) – Spoiling gradient pulse applied after the inversion

1.9.21.5 Postprocessing

Data produced by T1_EPI can be analyzed with the **Image Sequence Analysis (ISA) Tool**. The recommended function for fitting is t1epic. It is automatically pre-selected.

1.9.22 T2_EPI for rapid measurement of the relaxation time T2

1.9.22.1 Principles

Standard spin echo EPI acquires data at only one echo time after an excitation. T2_EPI allows to sample the data at several echo times by refocussing the signal after the data readout. This variant is a fast alternative to standard spin echo EPI to collect data for an estimation of the transverse relaxation time T2. (In a similar manner, T2* can be mapped with T2S_EPI, see [T2S_EPI Fast measurement of T2* with EPI \[▶ 352\]](#)).

The refocussing RF pulse satisfies the CPMG phase condition. Similar approaches have been described in References [\[10\] \[▶ 691\]](#), [\[11\] \[▶ 691\]](#). The T2 parameters maps have the advantage over single echo images that they are less affected by variation of the initial magnetization for example due to blood flow changes in larger blood vessels.

Optionally the sequence can be run in several shots using the standard EPI interleaving. The acquisition also supports other EPI features, like ghost correction, partial fourier reconstruction and parallel imaging.

1.9.22.2 Applications

Ultra-fast T2 mapping

1.9.22.3 Loop Structure

From inner to outer loops:

- Acquisition order: echoes, slices, accumulation (NA), segments (PVM_EpiNShots), repetitions (NR)
- Image order in `2dseq`: echoes, slices, repetitions

1.9.22.4 Specific Parameters

T2_EPI is a variant of EPI. Most parameters have the same meaning and can be found in the corresponding chapter [EPI \(Echo-Planar Imaging\) \[▶ 338\]](#). Here, only parameters are described that have a different meaning or that are not described in the EPI paragraph.

Routine Card

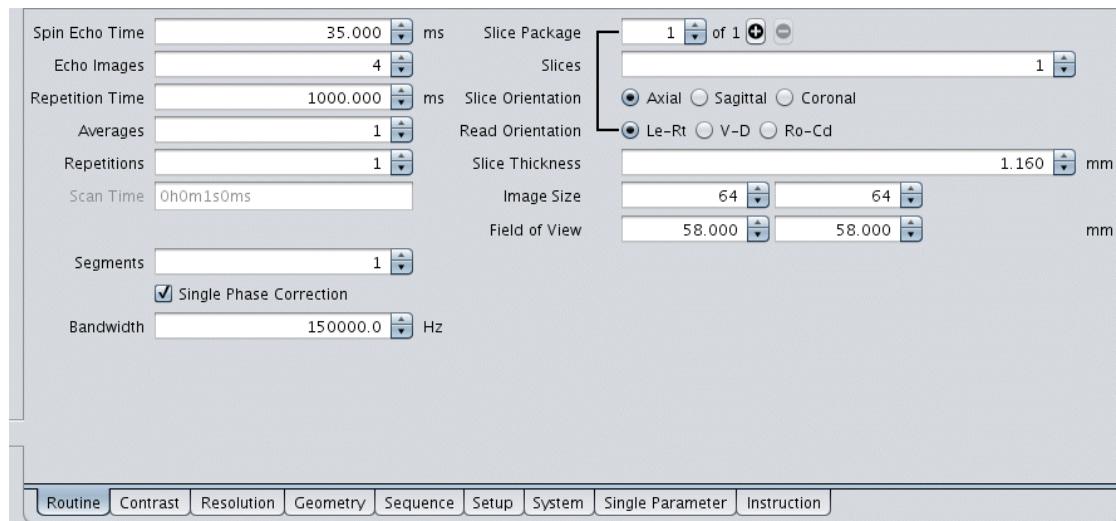


Figure 1.310: T2_EPI Routine Card

Spin Echo Time (SpinEchoTime) – Delay between the center of the excitation pulse and the k-space center of the first EPI readout. Alternatively, the delay between the centers of two successive EPI readouts.

Echo Images (PVM_NEcholImages) – Number of images with different effective echo times

Single Phase Correction (SinglePhaseCorrection) – By default this parameter is selected, which is the recommended choice. In this case the phase correction values of the first echo acquisition (necessary to reduce the EPI ghost) will be used for the phase correction of the latter ones. Otherwise the correction will be performed with values determined individually for each echo acquisition.

Contrast Card

Main

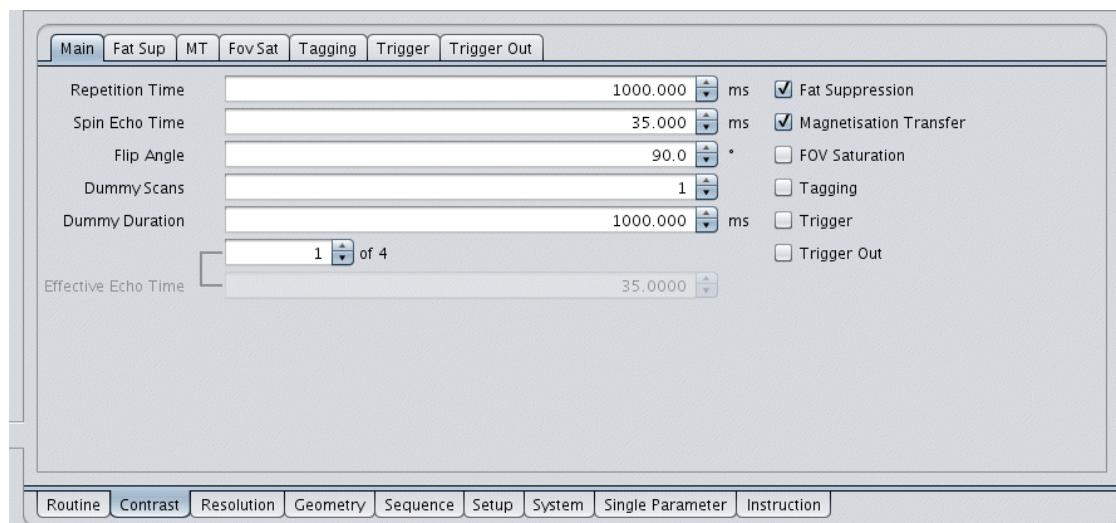


Figure 1.311: T2_EPI Contrast Card Main

Spin Echo Time (SpinEchoTime) – See [Routine Card \[▶ 351\]](#)

Effective Echo Time (EffectiveEchoTime) – Array of lengths PVM_NEcholImages giving the delay for each echo acquisition. The delays are multiples of **Spin Echo Time**.

1.9.23 T2S_EPI Fast measurement of T2* with EPI

1.9.23.1 Principles

Standard EPI in Fid mode acquires data at only one gradient echo time. In T2S_EPI data is sampled repeatedly after an excitation pulse, i.e. multiple echo times are sampled in a single shot (see references [\[12\] ▶ 691](#), [\[13\] ▶ 691](#)). This variant is a fast alternative to MGE for an estimation of the effective transverse relaxation time T2*. For functional MR studies, T2* parameter maps have the advantage over single echo images that they are less affected by variation of the initial magnetization due to blood flow changes in larger blood vessels.

The method offers a Fid- and Spin Echo mode like the conventional EPI. The latter allows accessing the “time origin” of the T2* relaxation by taking the first image in the center of the spin echo.

Optionally, the sequence can be run in several shots using the standard EPI interleaving. The method also supports other EPI features, like automatic ghost correction, partial Fourier reconstruction and parallel imaging.

1.9.23.2 Applications

- Ultra-fast T2* mapping
- Quantitative BOLD fMRI of the brain

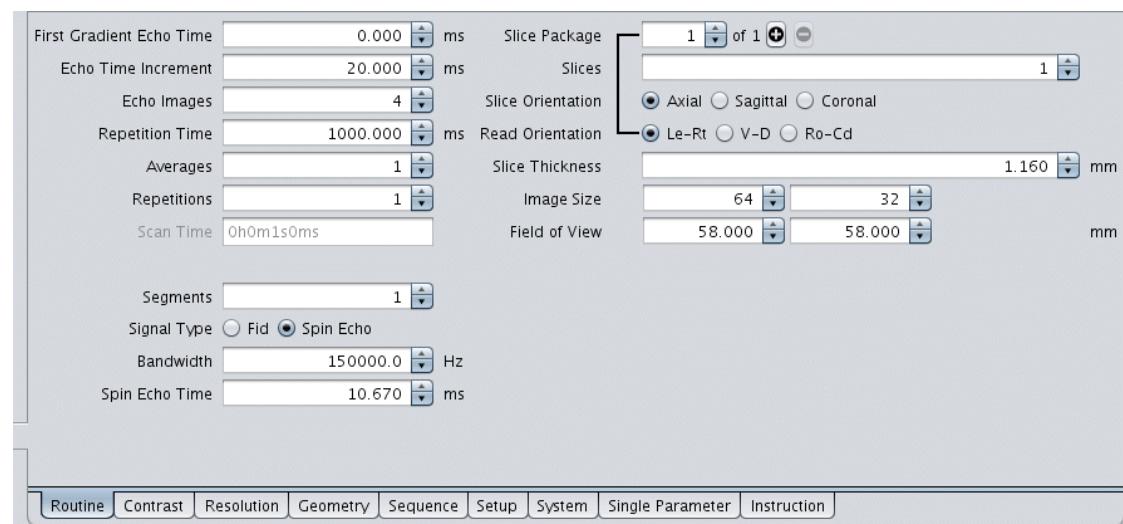
1.9.23.3 Loop Structure

From inner to outer loops:

- Acquisition order: echoes, slices, accumulation (NA), segments (PVM_EpiNShots), repetitions (NR)
- Image order in 2dseq: echoes, slices, repetitions

1.9.23.4 Specific Parameters

T2S_EPI is a variant of EPI. Most parameters have the same meaning and can be found in the corresponding chapter [EPI \(Echo-Planar Imaging\) ▶ 338](#). Here, only parameters are described that have a different meaning or that are not described in the EPI paragraph.

Routine Card*Figure 1.312: T2S_EPI Routine Card*

First Gradient Echo Time (FirstGradientEchoTime) – Delay between the center of the excitation pulse (in FID mode) or the center of the spin echo (in Spin Echo mode) and the acquisition of the k-space center of the first image

Echo Time Increment (EchoTimeIncrement) – Spacing between consecutive echo images

Echo Images (PVM_NEcholImages) – Number of images with different echo times

Spin Echo Time (SpinEchoTime) – (Only in Spin Echo mode) Delay between the centers of the excitation pulse and the spin echo

Contrast Card

Main

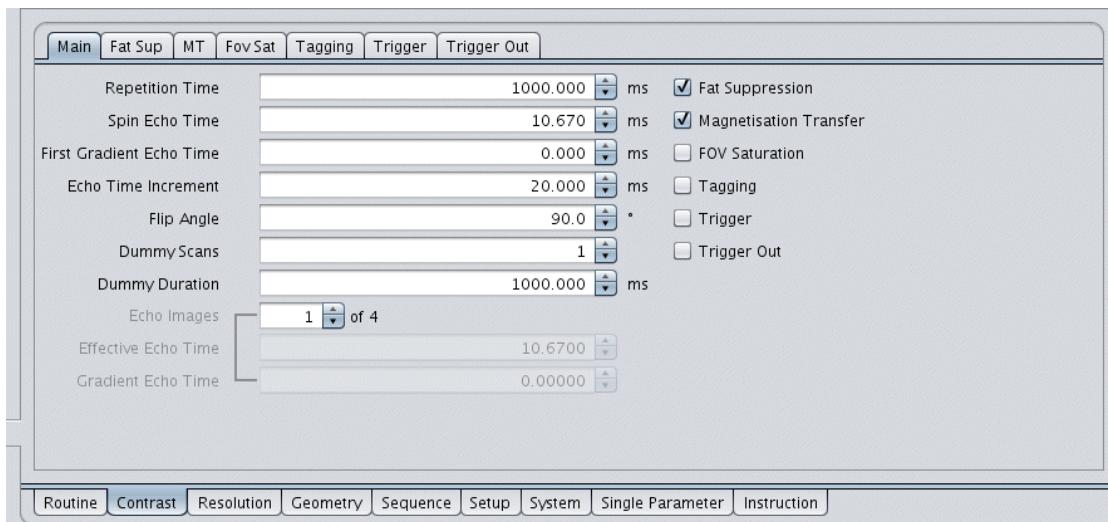


Figure 1.313: T2S_EPI Contrast Card Main

Spin Echo Time (SpinEchoTime) – See [Routine Card \[▶ 353\]](#)

First Gradient Echo Time (FirstGradientEchoTime) – See [Routine Card \[▶ 353\]](#)

Echo Time Increment (EchoTimeIncrement) – See [Routine Card \[▶ 353\]](#)

Effective Echo Time (EffectiveEchoTime) – Echo times for all echo images. In the Spin Echo mode, it is the sum of the spin echo time and the gradient echo time.

Gradient Echo Time (GradientEchoTime) – Gradient echo time of each image. In the Spin Echo mode this value counts from the center of the spin echo.

1.9.24 SPIRAL

1.9.24.1 Principles

The SPIRAL method allows ultrafast image acquisition using a single signal (or a few signals) in a way similar to EPI. The particular feature of SPIRAL is that the signal domain (k-space) is sampled on a spiral trajectory (or a set of interleaved spiral trajectories) rather than on a zigzag line. Compared to EPI this strategy has a few advantages:

- Potentially higher speed due to a more effective use of gradients (two gradient channels are used simultaneously)
- Very short minimum echo time since the trajectory may start from the k-space center
- Reduced sensitivity to motion and flow due to gradient first moment nulling

What SPIRAL and EPI have in common is the sensitivity to chemical shift and field inhomogeneity. In the SPIRAL method these effects lead to isotropic blurring rather than to pixel shifts and blurring in the phase-encoding direction, which may also be regarded as an advantage. These effects can be reduced by increasing the number of interleaved shots, just like in EPI.

Depending on the selected signal type, SPIRAL images may have gradient echo or spin echo properties. One can choose between opposite spiral scanning directions (In/Out) to optimally use the available signal depending on the required echo time. The In-mode allows shortest TE values, comparable to 2d-UTE.

1.9.24.2 Special Features

- Optimal use of the gradients by the original three-domains spiral design. This feature allows minimum echo and scan times and minimum blurring at given frequency slew rate and amplitude limits of the gradient system.
- Automatic measurement of k-space trajectory in a pre-scan adjustment. This allows a standard usage of SPIRAL just as any other MRI method. In a situation where a very low signal or very short T2* precludes the trajectory measurement, the method automatically re-uses trajectories measured with previous studies (e.g. with a phantom) with identical geometry.
- Imbedded navigator provides reduction of motion and drift-related artefacts in segmented acquisitions.
- 2D and 3D acquisition modes. In the latter, an additional encoding gradient pulse is applied on the slice selection channel to produce a stack of spirals in the k-space.
- The method has a circular FOV, which may be displayed graphically in the Geometry Editor. Signal originating anywhere outside the FOV circle leads to artefacts. Unlike EPI, there is no aliasing-free “readout” direction.

1.9.24.3 Applications

- Ultra-fast dynamic studies, e.g. fMRI
- Imaging in the presence of motion and flow, e.g. cardiac cine-MRI
- Diffusion MRI with short echo times. A dedicated variant of the method is provided for this purpose, see [DtSpiral \(Diffusion Tensor Imaging with Spiral scan\) ▶ 359](#).

1.9.24.4 Loop Structure

From inner to outer loops:

- Acquisition order in `fid` file: slices, segments (PVM_SpiralNbOfInterleaves), 3D encoding (if applicable), repetitions
- Image order in `2dseq`: slices, repetitions

1.9.24.5 Specific Parameters

Routine Card

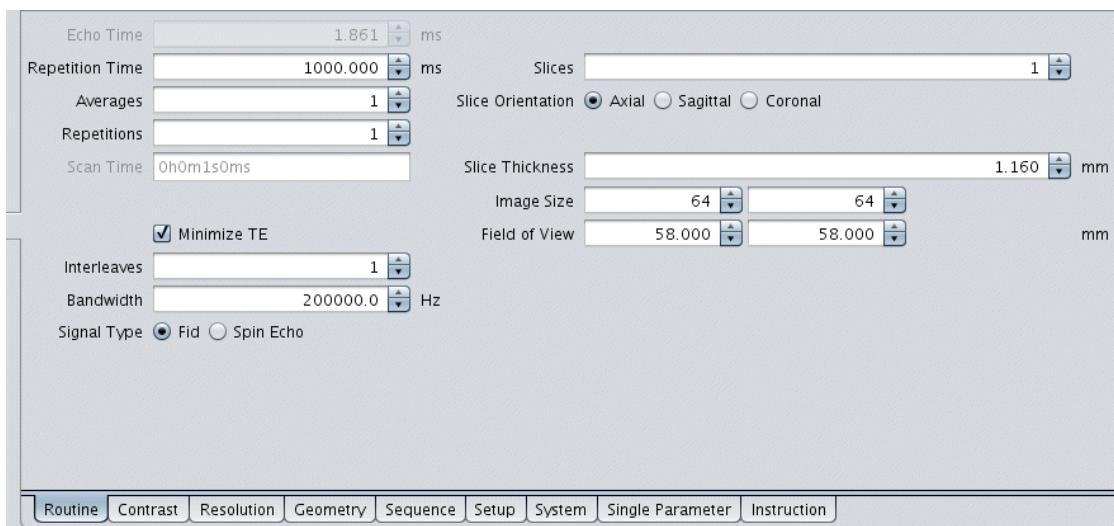


Figure 1.314: SPIRAL Routine Card

Echo Time (PVM_EchoTime) – Delay between the effective center of the excitation pulse (depends on pulse rephasing properties) and the acquisition of the kspace center. Its minimum depends on PVM_SpiralMode parameter selectable on the Sequence Card, Subcard Spiral. **Echo Time** determines the T2* contrast of the sequence in the Fid mode or T2 contrast in the Spin Echo mode (see below).

Minimize TE (MinimiseTE) – Minimizes the echo time

Interleaves (PVM_SpiralNbOfInterleaves) – Number of scans used to collect the data. Each scan covers a different spiral interleaf in the k-space. Interleaving shortens the data sampling period and reduces the sensitivity of the method to resonance offsets and short T2*. The trade-off is a longer measurement time per image and higher sensitivity to object motion.

Bandwidth (PVM_EffSWh) – Signal bandwidth (sampling rate) – Increasing the bandwidth shortens the data sampling period and reduces the sensitivity of the method to resonance offsets and short T2*. On the other hand, high bandwidths may limit the resolution and lead to an excessive gradient duty cycle.

Signal Type (PVM_SignalType) – Allows selecting the type of observed signal. Possible values are:

- **Fid** – A single RF pulse is used to generate the FID. Combined with the spiral mode In (see [Sequence Card Spiral \[▶ 357\]](#)) this mode allows a very short echo time and maximum signal.
- **Spin Echo** – Two RF pulses generate a spin echo. The center of the k-space corresponds to the spin echo center.

Sequence Card

Main

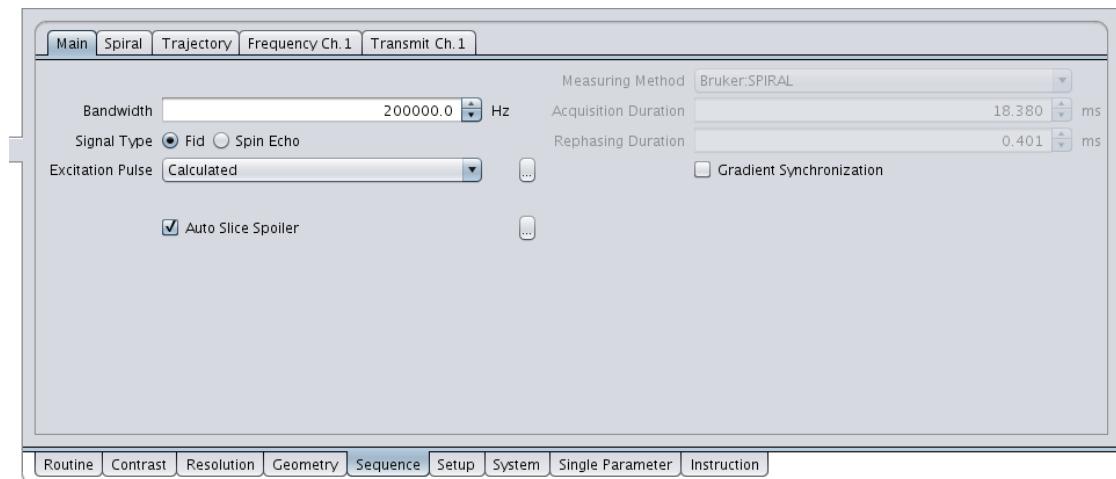


Figure 1.315: SPIRAL Sequence Card Main

Rephasing Duration (RepGradDur) – Duration of the slice rephrasing gradient pulse, non-editable.

Gradient Synchronization (GradSync) – When selected, the pulse sequence is synchronised with the clock of the digital preemphasis, which improves signal stability on some systems.

Spiral

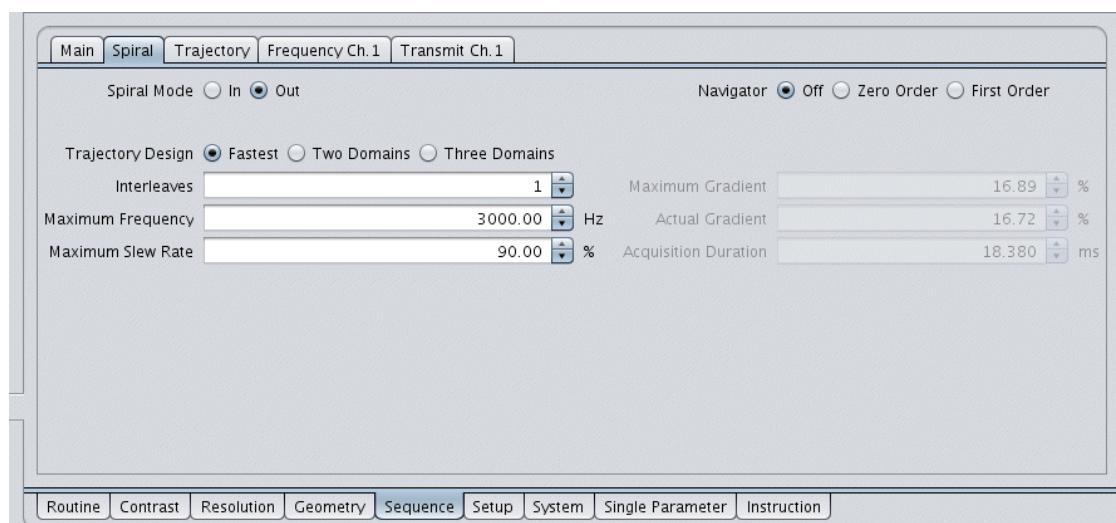


Figure 1.316: SPIRAL Sequence Card SPIRAL

Spiral Mode (PVM_SpiralMode) – Determines the direction of the spiral. It can take two different values:

- Out (default) – The spiral trajectory starts at the origin of the kspace and evolves outwards. This mode allows very short echo times (TE).
- In – The spiral trajectory starts at the edge of the sampling region and ends at the k-space origin. This mode gives the optimum sampling efficiency with long echo times (more slices per second can be acquired) but increases the minimum TE.

Flow Compensation (PVM_SpiralFlowComp) – **Spiral Mode** = In activates an additional lobe at the beginning of the gradient waveform to zero its first moment and thus to reduce the sensitivity of the sequence to flow.

Trajectory Design (PVM_SpiralDesign) – Imposes manually adjustable restrictions on the gradient waveform:

- Fastest (default) – Automatic choice of one of the following modes
- Two Domains – Gradient waveform is designed under constraint of a maximum slew rate (PVM_SpiralSlewRate) and an amplitude limit (PVM_SpiralGradientLimit).
- Three Domains – Gradient waveform is designed under the additional constraint of a frequency limit (PVM_SpiralFrequencyLimit).

Interleaves (PVM_SpiralNbOfInterleaves) – See [Routine Card \[356\]](#)

Maximum Frequency (PVM_SpiralFrequencyLimit) – Frequency limit of the gradient system. Used as a constraint in the design of spiral gradients.

Maximum Slew Rate (PVM_SpiralSlewRateLimit) – Slew rate constraint of the spiral gradient design, in percentage of the maximum slew rate of the gradient system

Navigator (PVM_SpiralNavMode) – Controls the use of the navigator. An unencoded portion of the signal measured before the spiral readout to correct phase and frequency fluctuations caused e.g. by motion and respiration of the animal. Possible values are:

- Off (default) – No navigator, shortest TE possible
- Zero Order – A short navigator allowing the zero order phase correction. Minimum TE is slightly higher.
- First Order – A long navigator allowing the first order phase correction, i.e., the correction of phase and frequency changes. Significantly increases minimum TE.

Maximum Gradient (PVM_SpiralGradientLimit) – Maximum gradient amplitude allowed for the spiral readout gradients

Actual Gradient (PVM_SpiralEffectiveGradient) – Effectively reached amplitude of the gradient waveform. May be smaller than the maximum when the slew rate constraint is dominating, typically with low matrices.

Acquisition Duration (PVM_SpiralAcquisitionTime) – Duration of the acquisition (including the navigator)

Trajectory

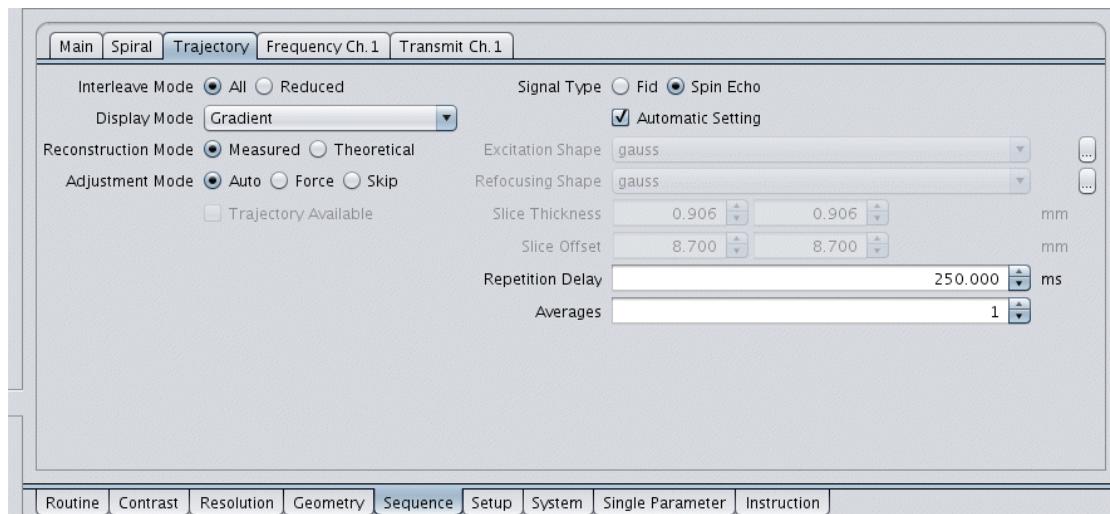


Figure 1.317: SPIRAL Sequence Card Trajectory

Parameters controlling the automatic adjustment of k-space trajectory, which is essential for the quality of SPIRAL images. See [Trajectory \[▶ 278\]](#).

Interleave Mode (PVM_TrajIntMode) – Determines how many interleaves are measured:

- All – Trajectory is measured individually for all interleaves.
- Reduced – Trajectory is measured for one interleaf and estimated for the rest.

1.9.24.6 Multi-shot interleaved SPIRAL

The SPIRAL sequence can be applied in the interleaved multi-shot mode to reduce the susceptibility related image blurring. This option is particularly useful at very high magnetic fields where the susceptibility effects are enhanced. The multi-shot mode is activated by setting the parameter **Interleaves** to more than one. As this parameter is increased, the duration of per shot acquisition gets shorter leading to reduced blurring effects.

Ghosting can be caused by signal instability between shots. For that reason it is recommended to use a sufficient number of dummy scans to achieve a steady state and to use the navigator option. Ghosting caused by physiologic fluctuations (respiration, cardiac cycle) can additionally be reduced by triggering.

1.9.25 DtiSpiral (Diffusion Tensor Imaging with Spiral scan)

1.9.25.1 Principles

This method combines the DTI module (see [Diffusion Card \[▶ 241\]](#)) with the SPIRAL readout module (see [SPIRAL \[▶ 354\]](#)) to allow fast acquisition of diffusion weighted images or quantitative diffusion data, including diffusion tensor imaging. Similar to [DtiEpi \(Diffusion tensor imaging with EPI\) \[▶ 345\]](#) it can take entire images with a single shot, which not only reduces the scan time, but, most importantly, eliminates the sensitivity of the experiment to microscopic motion of the animal. DtiSpiral can reach shorter echo times than DtiEpi because the spiral data sampling starts in the k-space origin.

Like all methods using the Diffusion module, DtiSpiral can acquire spin echo, stimulated echo or double spin echo signals, and allows setting of arbitrary strengths and directions of diffusion-sensitizing gradient pulses. Due to intense use of gradients during both diffusion preparation and signal readout, the method can reach high values of the gradient duty cycle, especially with many slices. It is recommended to verify the duty cycle on the Simulation Platform before starting the scan.

All special features of SPIRAL apply to DtiSpiral as well. These include blurring caused by magnetic susceptibility of the object and short T2*, a problem growing with the image matrix size. For best results it is essential to shim the imaging region, preferably using MAPSHIM. Similar to SPIRAL, blurring can be reduced by segmenting. This option, however, should be used with care for in vivo diffusion experiments since it reintroduces the sensitivity to animal motion. Triggering and the navigator option should be used to reduce the motion sensitivity.

1.9.25.2 Applications

- Ultrafast diffusion weighted imaging
- Ultrafast measurement of ADC maps
- Ultrafast measurement of diffusion tensor images

Remarks

Spiral images may suffer from blurring artefacts (degradation of the resolution) caused by magnetic field inhomogeneity or chemical shifts. Blurring and 'halo' effects can also be caused by signals origination outside the field of view. In order to avoid these effects:

- Shim the imaging region with MAPSHIM.
- Use high signal bandwidth (at least 200 kHz).
- Carefully plan the image geometry. The object should not extend beyond the field of view, which is circular in spiral methods. (The FOV-circle can be made visible in the Geometry Editor.)
- Use the navigator and triggering for segmented experiments in-vivo.

1.9.25.3 Loop Structure

From inner to outer loops:

- Acquisition order: slices, accumulation (NA), dummy scans (if specified), number of shots (PVM_SpiralNbOfInterleaves), diffusion loop, repetitions (NR)
- Data regredded in `fid`: slices, diffusion loop, repetitions
- Image order in `2dseq`: slices, diffusion experiments, repetitions

1.9.25.4 Specific Parameters

DtiSpiral is a variant of the method SPIRAL. Parameters controlling the spiral readout have the same meaning and can be found in the corresponding section of [SPIRAL \[▶ 354\]](#). The parameters of the Diffusion Card are described in detail in Chapter [Diffusion Card \[▶ 241\]](#).

1.9.26 UTE (Ultra-short TE)

1.9.26.1 Principles

Ultra-short echo time (UTE) is a 2D imaging sequence based on a ramp-sampled 2D radial acquisition combined optionally with a half-pulse RF excitation. It allows visualization of objects having very short transverse relaxation times with various degrees of T2-contrast.

Radial Acquisition

Radial acquisition, also called projection acquisition (PA), fills in k-space data with radial spokes. If we assume that a 2D PA is performed in the physical XY plane, the physical readout gradient waveform amplitudes for 2D PA are:

$$G_x = G_0 * \cos\phi, G_y = G_0 * \sin\phi$$

where G_0 is the readout waveform amplitude.

2D PA k-space trajectories usually collect data either with $0 \leq \phi \leq 2\pi$ (FID or half-echo sampling) or $0 \leq \phi \leq \pi$ (full-echo sampling). In case of FID sampling the radial spokes always start from the center of k-space.

When compared to Cartesian acquisition, the number of spokes NS is larger than the number of phase encoding lines NP in order to achieve the same FOV and resolution:

- full-echo sampling: $NS = \pi/2 * NP$,
- half-echo sampling: $NS = \pi * NP$.

Half-Pulse Excitation

This optional excitation scheme allows an additional reduction of TE. It consists of two excitations, each one scanning one-half of the excitation k-space. The first excitation is played out in the presence of a positive slice-select gradient and traverses excitation k-space from the minimum k_{\min} to the origin. For the second half-excitation, the polarity of the slice-select gradient is reversed, which implies a linear trajectory beginning at k-space maximum k_{\max} and again ending at the origin. Data acquisition occurs after each half-excitation. The same readout gradients are applied for each pair of half-excitations, and the two individual measurements are summed. In the absence of irregularities (such as field inhomogeneities or eddy currents), the resultant signal is the same as that generated by the corresponding conventional excitation.

1.9.26.2 Special features

The UTE method can handle conventional and half-pulse excitation as well as full-echo or half-echo sampling.

Acquisition Mode: ECHO

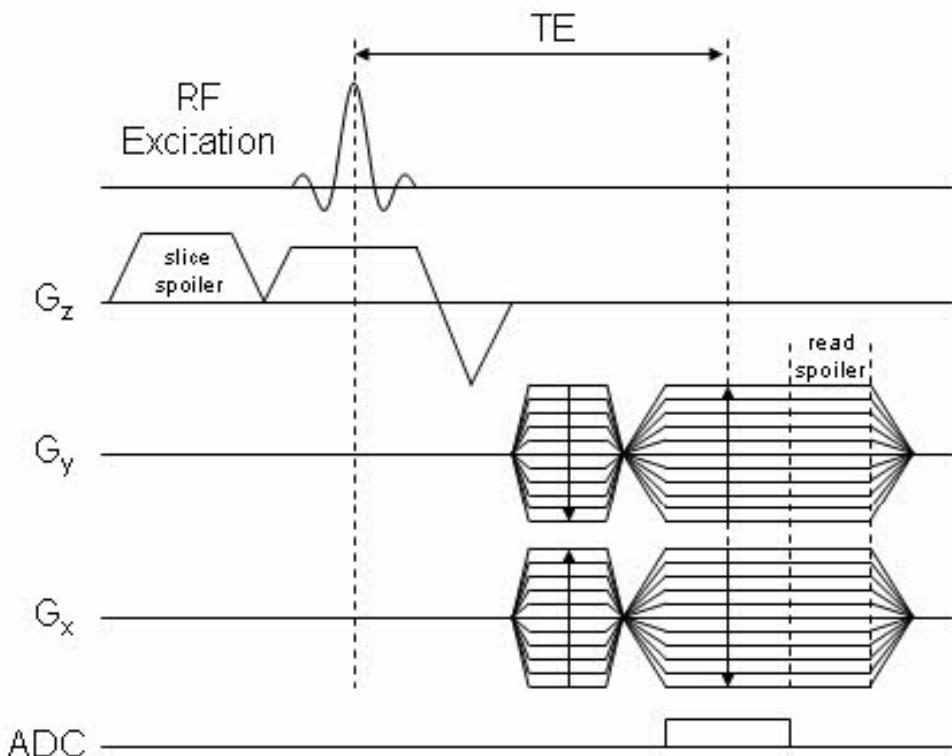


Figure 1.318: Diagram of the UTE sequence in the ECHO mode

The achievable TE for a radial echo acquisition is the same as in conventional Cartesian gradient echo imaging.

Acquisition Mode: FID

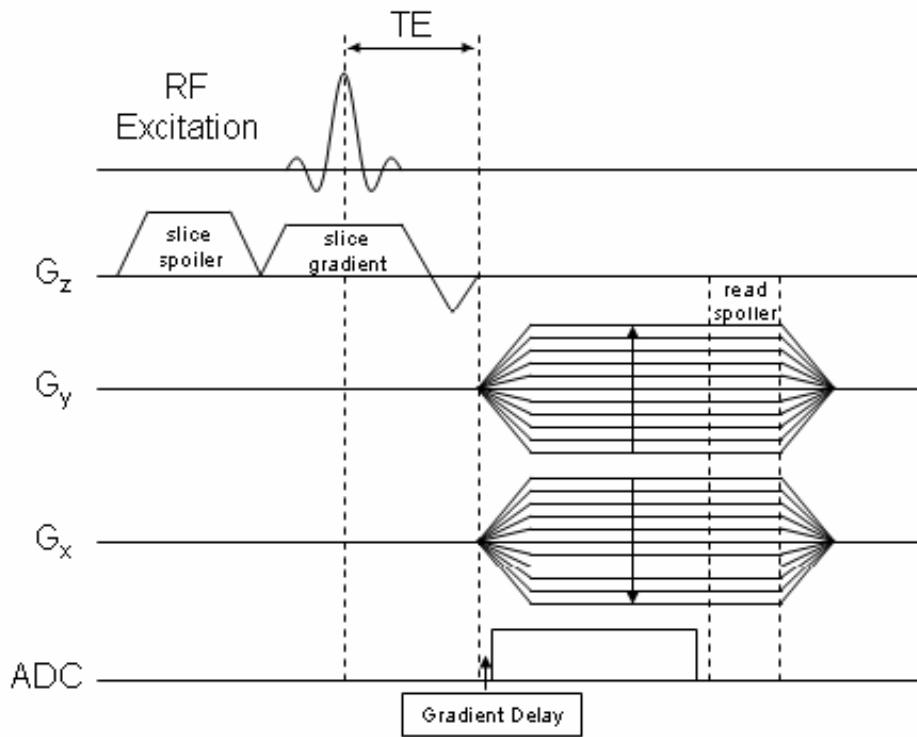


Figure 1.319: Diagram of the UTE sequence in the FID mode

In this acquisition mode echo times of 300 - 400 μ s can be achieved due to slice refocusing with maximum slew rate of the gradient system and ramp-sampled FID acquisition.

Half-Pulse Excitation and FID Acquisition Mode

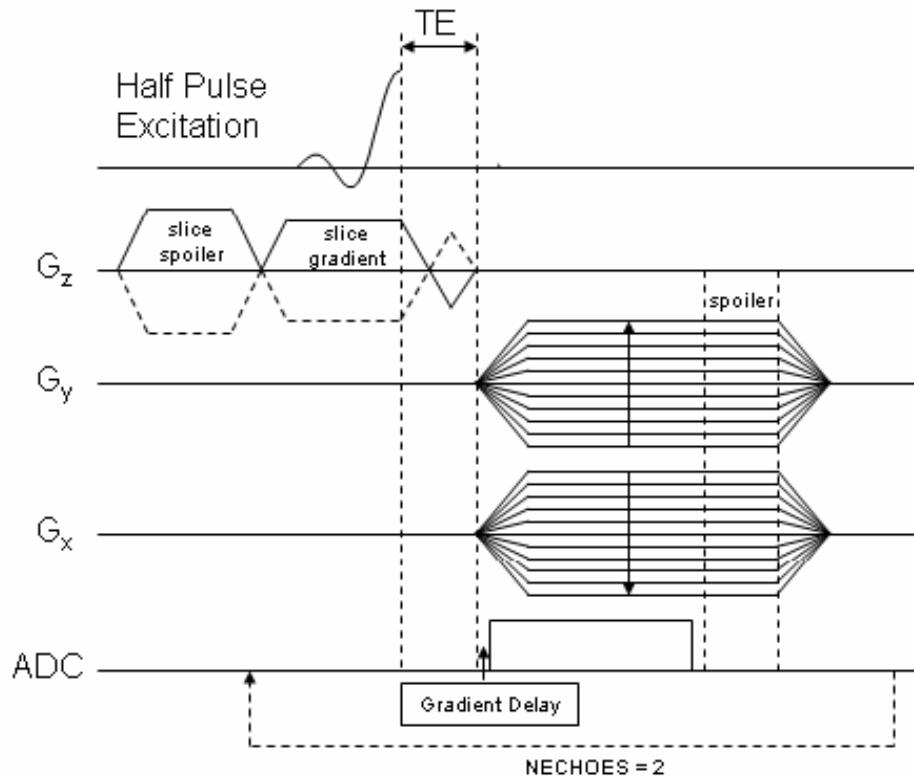


Figure 1.320: Diagram of the UTE sequence with Half-Pulse Excitation and FID acquisition

Echo times below 300 µs can be achieved using a half pulse excitation combined with a radial FID acquisition.

REMARKS:

- The half-pulse principle doubles the total scan time, because two excitations (one with a positive and the other with a negative slice selection gradient) are required for each radial line.
- The half excitation approach is very sensitive to gradient imperfections which can have influence on the resultant slice excitation profile.

1.9.26.3 Applications

Ultrashort echo time imaging allows the detection of

- short T2 nuclei (23Na, 31P),
- musculoskeletal tissue with short T2 like tendons, ligaments, and periosteum,
- tissue with short T2* such as liver and lung parenchyma,
- superparamagnetic contrast agents in molecular imaging.

1.9.26.4 Loop Structure

From inner to outer loops:

- Acquisition order: movie frames, slices, slice alternation (special option), accumulation (NA), repetitions

- Image order in `2dseq` file: movie frames, slices, repetitions

1.9.26.5 Specific Parameters

Routine Card

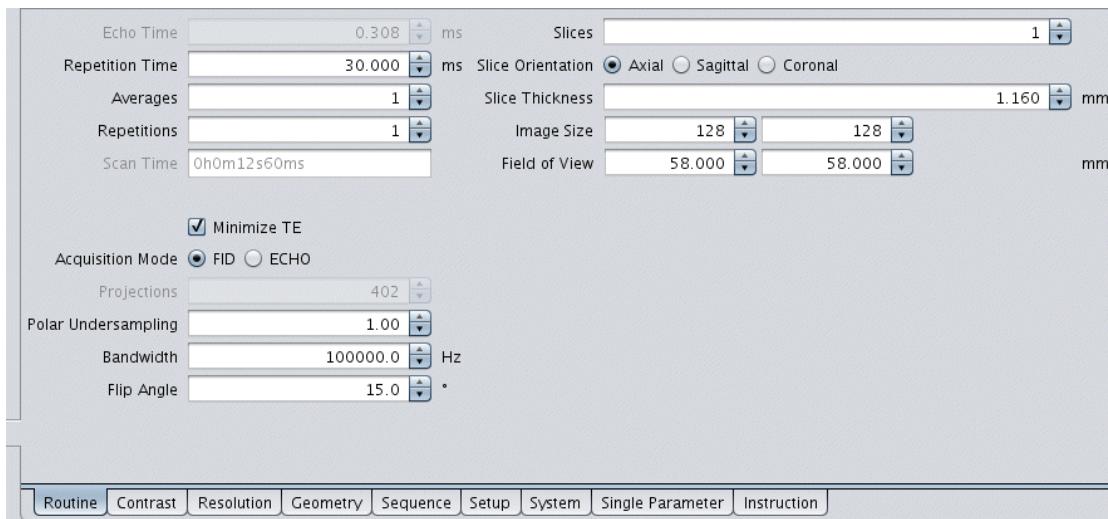


Figure 1.321: UTE Routine Card

Minimize TE (YesNoMinEchoTime) – Uses always the minimum possible echo time

Acquisition Mode (AcqMode) – Allows the user to select between FID and ECHO signal

Projections (NPro) – Non-editable parameter describing the total number of radial scans. It depends on the polar undersampling and the image matrix size. The default value (**Polar Undersampling** = 1) is calculated to obtain the nominal density (Nyquist criterion) in the entire k-space and to avoid intra-FOV aliasing (streaks).

Polar Undersampling (ProUndersampling) – Allows reducing the imaging time by lowering the number of projections below the nominal value. This option should be used carefully since it leads to streaking artifacts.

Bandwidth (PVM_EffSWh) – Effective acquisition bandwidth

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse

Contrast Card

Main

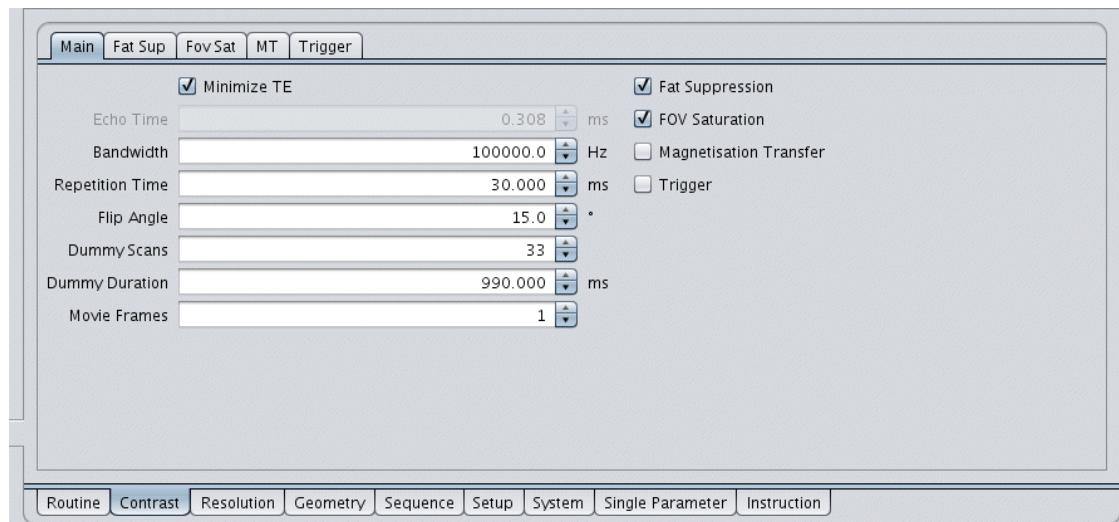


Figure 1.322: UTE Contrast Card Main

Minimize TE (YesNoMinEchoTime) – See [Routine Card \[▶ 364\]](#)

Bandwidth (PVM_EffSWh) – See [Routine Card \[▶ 364\]](#)

Flip Angle (ExcPulse1.Flipangle) – See [Routine Card \[▶ 364\]](#)

Movie Frames (PVM_NMovieFrames) – Defines the number of acquired and reconstructed movie frames

Sequence Card

Main

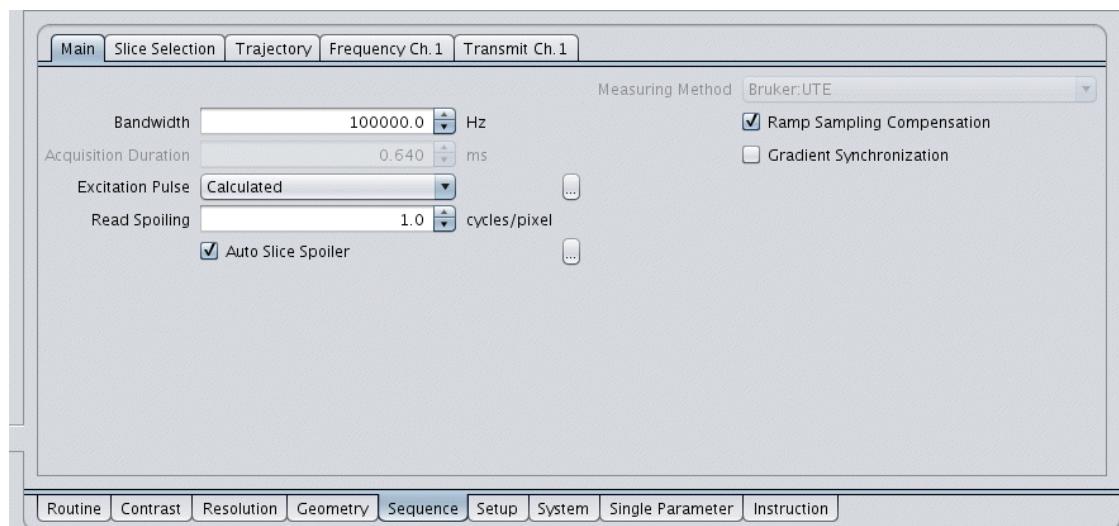


Figure 1.323: UTE Sequence Card Main

Excitation Pulse (ExcPulse1Enum) – Slice selective excitation pulse

Read Spoiling (ReadSpoiling) – Gradient pulse applied to the two readout channels after data acquisition

Auto Slice Spoiler (SliceSpoiler.automatic) – Constant gradient pulse applied to the slice channel just before slice excitation

Ramp Sampling Compensation (RampCompYN) – Turns on an oversampling mechanism that compensates the resolution loss caused by the sampling of the signal during the readout gradient ramps

Gradient Synchronization (GradSync) – Turns on a synchronization of the sequence with the clock of the preemphasis filter

Slice Selection

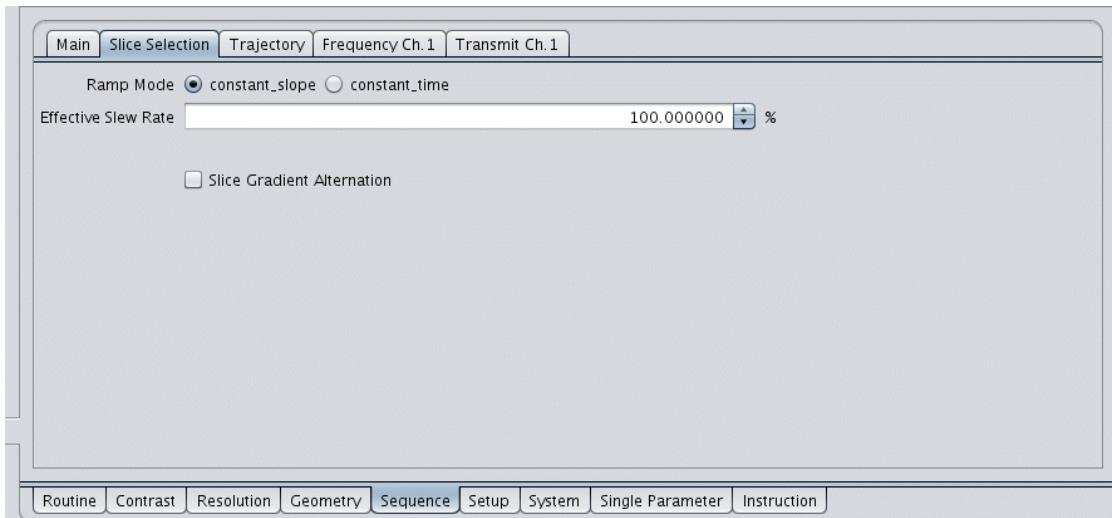


Figure 1.324: UTE Sequence Card Slice Selection

Ramp Mode (RampMode) – Allows the user to select the ramp mode for the slice refocusing gradient. Possible values are `constant_slope` or `constant_time`. In case of `constant_slope`, the effective slew rate is editable, otherwise the ramp time can be defined.

Effective Slew Rate (EffSlewRate) – Used slew rate for slice refocusing gradient in percentage of the maximum allowed slew rate

Ramp Time (Ramptime) – Used ramp time for slice refocusing gradient

Slice Gradient Alteration (SliceAlter) – Parameter in order to switch on alternation of the slice gradient, which is necessary for half-pulse excitation

Trajectory

See [Trajectory \[▶ 278\]](#)

1.9.27 UTE3D (Ultrashort TE 3D)

1.9.27.1 Principles

The 3D implementation of the ultra-short TE technique (UTE3D) allows shorter echo times than the 2D implementation (UTE) because of the use of a non-selective RF excitation. The minimum TE is limited only by the duration of the RF pulse and the time needed to switch between the RF excitation and the data acquisition. Sampling is performed already on the rising gradient ramp and therefore starts always from the k-space center and continues to the surface of a sphere. The number of scans and directions of the readout gradient for each scan are calculated to achieve an even distribution of the "end points" at the sphere with a density that is required by the field of view.

The sensitivity of UTE to signals of very short T2 makes the method prone to artefacts caused by materials of the RF coils or animal bed. Ways to avoid these problems, which are common also to the ZTE method, are described in [Special Features \[▶ 370\]](#).

1.9.27.2 Applications

Ultra-short echo time imaging allows the detection of

- short T2 nuclei (²³Na, ³¹P),
- musculoskeletal tissue with short T2 like tendons, ligaments, and periosteum,
- tissue with short T2* such as liver and lung parenchyma,
- superparamagnetic contrast agents in molecular imaging.

1.9.27.3 Loop Structure

From inner to outer loops:

- Acquisition order: projections, accumulations (NAE), repetitions
- Image order in `2dseq` file: slices, repetitions

1.9.27.4 Specific Parameters

Routine Card

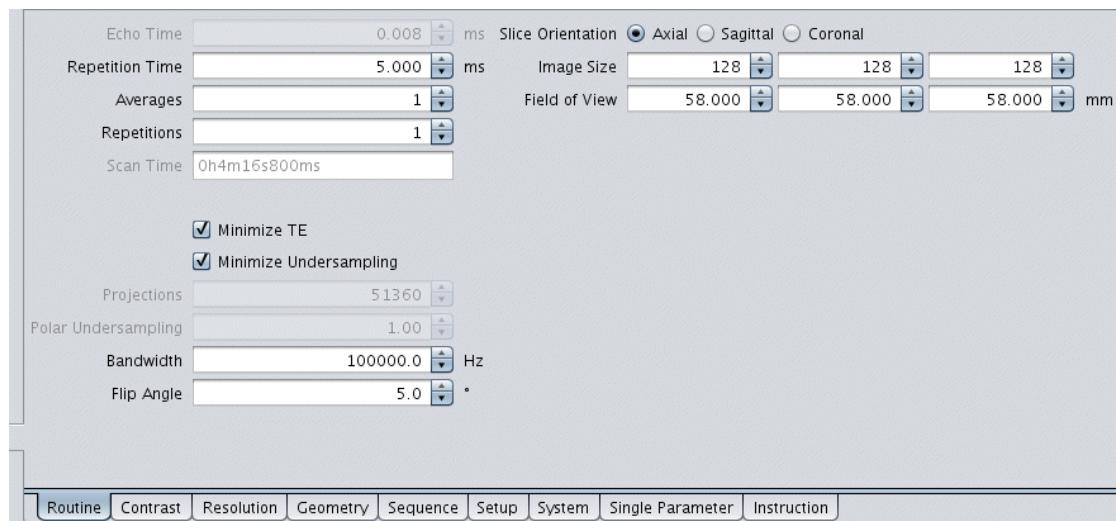


Figure 1.325: UTE3D Routine Card

Echo Time (PVM_EchoTime) – Time between the excitation and the first signal sample. Although the sequence does actually not produce echoes, this parameter affects the T2 contrast in a similar manner as the ‘TE’ in gradient echo methods.

Minimize TE (YesNoMinEchoTime) – When selected, **Echo Time** is automatically set to minimum and remains non-editable.

Minimize Undersampling (MinimumUnderSampling) – If switched on always the minimum possible [Polar Undersampling \[▶ 368\]](#) factor is realized.

Projections (NPro) – Non-editable parameter describing the total number of radial scans. It depends on the polar undersampling and the image matrix size. For **Polar Undersampling** = 1, the number of projections are calculated to obtain the nominal density (Nyquist criterion) in the entire k-space and to avoid intra-FOV aliasing (streaks).

Polar Undersampling (ProUndersampling) – Allows reducing the imaging time by lowering the number of projections below the nominal value. This option should be used carefully since it leads to streaking artifacts. With big matrices and/or phased array coils the undersampling is automatically adapted to the memory demands of the reconstruction.

Bandwidth (PVM_EffSWh) – Effective acquisition bandwidth

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse

Contrast Card

Main

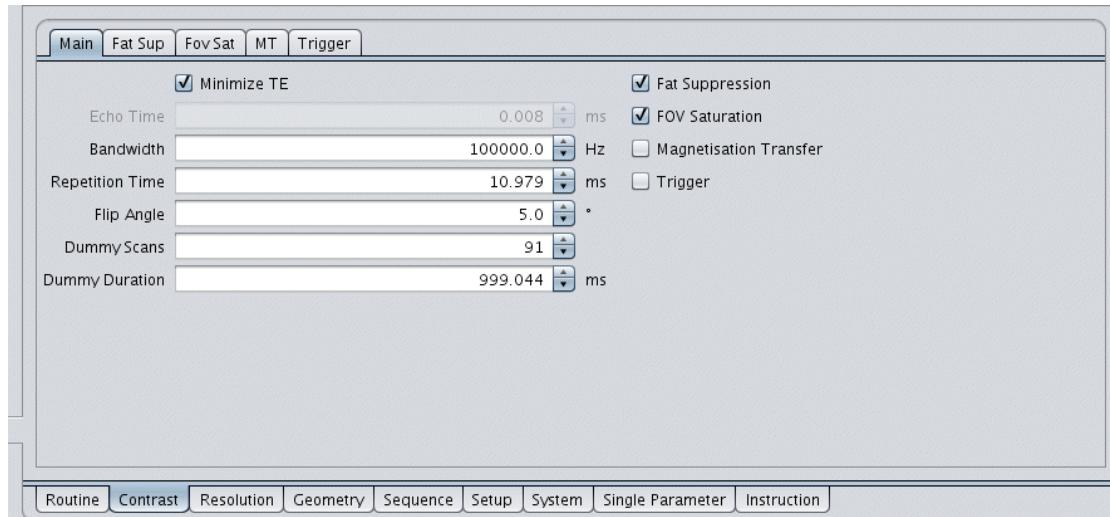


Figure 1.326: UTE3D Contrast Card Main

Minimize TE (YesNoMinEchoTime) – See [Routine Card \[▶ 367\]](#)

Bandwidth (PVM_EffSWh) – See [Routine Card \[▶ 367\]](#)

Flip Angle (ExcPulse1.Flipangle) – See [Routine Card \[▶ 367\]](#)

Sequence Card

Main

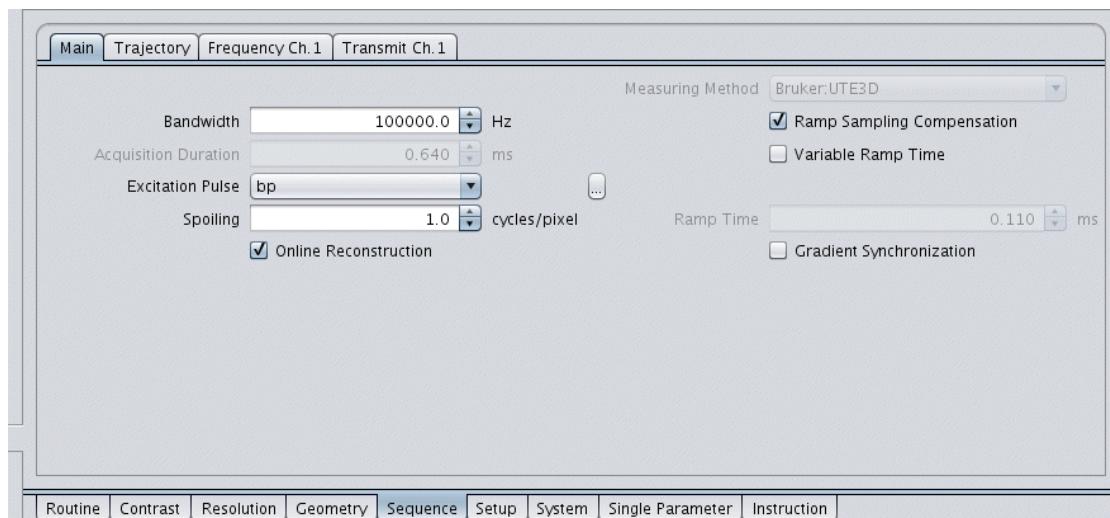


Figure 1.327: UTE3D Sequence Card Main

Excitation Pulse (ExcPulse1Enum) – Slice selective excitation pulse

Spoiling (Spoiling) – Gradient spoiling applied to the three readout channels after data acquisition

Online Reconstruction (RecoOnline) – Image reconstruction using regridding is more time-consuming and memory demanding than conventional Fourier transform reconstruction. This leads to a limitation of the maximum allowed matrix size. To enable the acquisition of larger matrices the online reconstruction can be switched off.

Ramp Sampling Compensation (RampCompYN) – Turns on an oversampling mechanism that compensates the resolution loss caused by the sampling of the signal during the readout gradient ramps

Variable Ramp Time (VarRampTimeYN) – Allows changing the gradient ramp-up time for the three readout gradients based on the slew rate of the gradients

Effective Slew Rate (EffSlewRate) – Used slew rate for the ramp of the readout gradients in percentage of the maximum allowed slew rate

Ramp Time (RampTime) – Used ramp time for the three readout gradients

Gradient Synchronization (GradSync) – Turns on a synchronization of the sequence with the clock of the preemphasis filter

Trajectory

See [Trajectory \[▶ 278\]](#)

1.9.28 ZTE (Zero TE)

1.9.28.1 Principles

The method ZTE is based on a non-selective excitation and a signal acquisition in the presence of a constant gradient. It offers some particular features such as zero echo time, sensitivity to extremely short T2 values, robustness against off-resonance, and a silent and fast operation (see References [\[2\] \[▶ 691\]](#) - [\[6\] \[▶ 691\]](#), [\[19\] \[▶ 691\]](#), [\[20\] \[▶ 691\]](#), [\[21\] \[▶ 692\]](#))

3D Radial Acquisition

ZTE is a 3D radial acquisition method, performing center-out readouts according to the schemes as shown in Figure [Acquisition of a ZTE center-out readout \[▶ 370\]](#). A total number of approximately $\pi \times (\text{matrix size})^2$ readouts with regularly spaced directions is required to fulfill the Nyquist criterion and to avoid aliasing artifacts in the reconstructed 3D image.

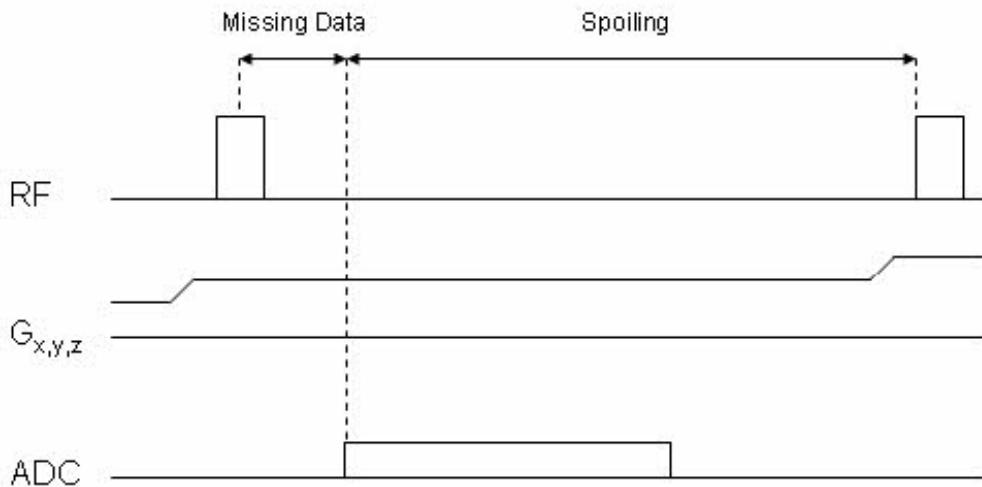
Geometry

As a 3D radial method, ZTE allows only isotropic matrix size. Furthermore, it is particularly prone to aliasing artifacts. Therefore the user must carefully avoid the imaged object to exceed the inscribed ellipsoid of the FOV shown in the Geometry Editor.

Steady State

ZTE operates in a steady state of the magnetization. For efficient scanning usually a short TR of a few milliseconds is used with a small flip angle of a few degrees. In order to avoid artifacts sufficient spoiling as well as dummy scans are required.

a) Stepped gradients



b) Switched gradients

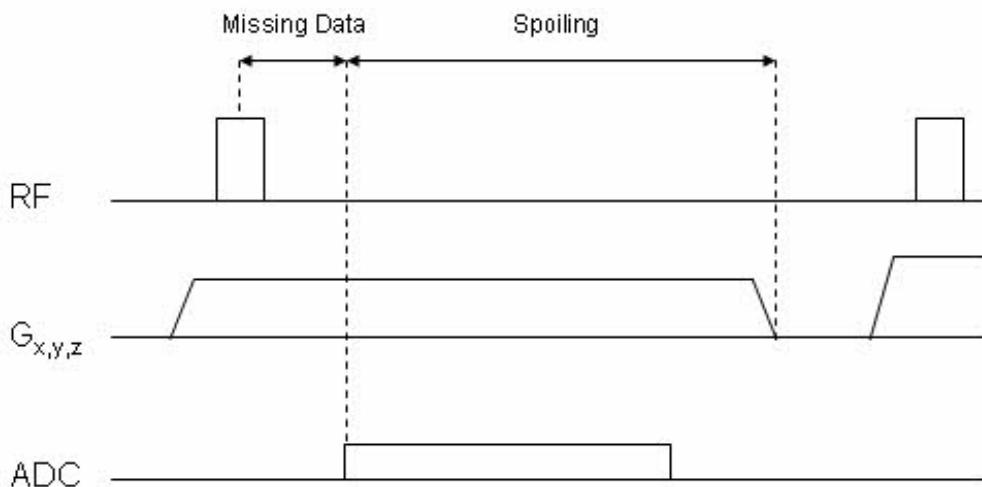


Figure 1.328: Acquisition of a ZTE center-out readout with different gradient operation modes: a) GradOff = No, b) GradOff = Yes

1.9.28.2 Special Features

Hardware Requirements

For optimum results, RF coils made from proton-free materials are most suitable but not necessarily required (see [Background Signal \[▶ 371\]](#) below).

Matrix Limitation

The increased memory requirements of the non-standard image reconstruction of ZTE can lead to a limitation of the matrix size and an automatic adaption of radial undersampling depending on the working memory in the spectrometer PC. To enable the acquisition of larger matrix sizes the online reconstruction can be switched off (see [Online Reconstruction ▶ 376](#)).

Coil Arrays

In principle, using RF coil arrays is possible. However, they increase the data amount and thus the acquisition and memory requirements. Therefore acquisition of data with multiple receive coils can require an increased TR. Furthermore, reconstruction can require reduction of matrix size and/or increased undersampling.

Large Bandwidth Excitation

As the RF excitation occurs while the gradient is on, the RF pulse must provide a sufficiently large bandwidth to excite the complete object. Therefore, very short hard pulses are used which may limit the possible flip angle depending on the used RF equipment. Appropriate pulse bandwidth is ensured via the parameter **Excitation Pulse Auto**.

Silent Acquisition

As shown in Figure [Acquisition of a ZTE center-out readout ▶ 370](#) two different gradient operation modes are available. As a particular feature of ZTE, gradients can be stepped between consecutive directions which makes the sequence very silent. Alternatively, gradients can be switched off between excitations which is noisier but reduces the gradient duty cycle. The gradient modes are controlled via the parameter **Switch Gradient**.

Missing Data

For technical reasons the FID signal cannot be acquired right after it has been created. Half the pulse duration, transmit-receive switching, and the group delay of the digital filter lead to some data missing at the beginning. Depending on the size of this gap, noise enhancement occurs, resulting in a reduced SNR. In order to keep the gap small, the RF pulse should be as short as possible.

Algebraic and Regridding Reconstruction

To reconstruct data with an initial gap without artifacts, an algebraic reconstruction is employed, references [\[61 ▶ 691\]](#), [\[201 ▶ 691\]](#), [\[211 ▶ 692\]](#). In this way, 1D projections are obtained which are combined to provide a 3D image by means of 3D regridding followed by Fourier transform.

Background Signal

With zero TE even signals with extremely short T2 (below 100 µs) are captured, which often originate from materials of the MRI equipment (predominantly the RF coil) rather than the sample itself. In the reconstructed images such signal appears as a blurred background and can also manifest as a central spike accompanied by extended ringing, as e.g. shown in [Spike artifact in a ZTE image of a walnut ▶ 372](#). Therefore, ideally, RF coils and animal support elements made of proton-free materials should be used.

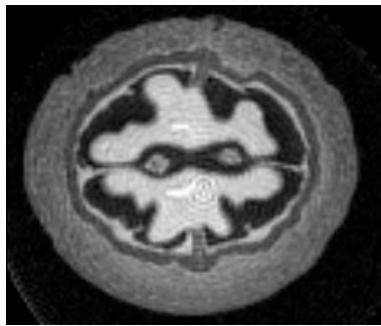


Figure 1.329: Spike artifact in a ZTE image of a walnut due to background signal

Segmented Preparation

Image contrast and other features can be influenced by means of magnetization preparation. Currently, two preparation modules are implemented, fat suppression and FOV saturation using saturation slices. The latter option can help to reduce the necessary FOV in certain cases. Preparation in ZTE is implemented in a segmented fashion where a preparation block is followed by a series of acquisition shots (see Figure [Preparation and segmentation scheme in ZTE \[▶ 372\]](#)). The actual acquisition may be preceded by a series of dummy shots to recover the steady-state that was disturbed by the preparation.

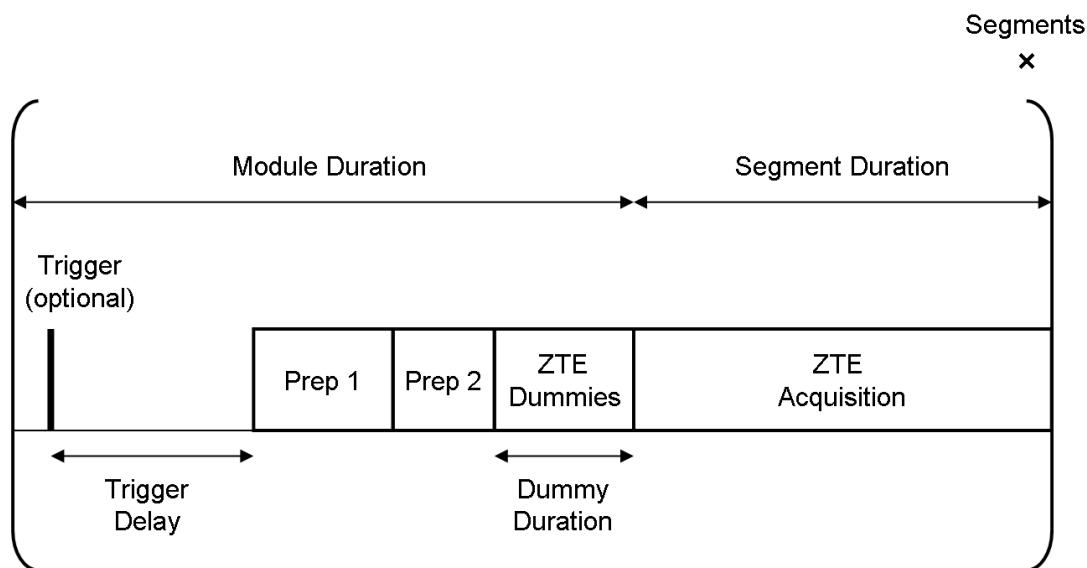


Figure 1.330: Preparation and segmentation scheme in ZTE

Optionally, a segment can be triggered by an external device. Here, two strategies are possible:

1. Level triggering: a relatively short segment duration is chosen and segments are acquired as long as the required trigger level is available.
2. Edge triggering: the segment duration is set to the desired acquisition window and after a level change the segment is fully executed.

1.9.28.3 Applications

Zero TE imaging allows the detection of

- short T2 nuclei (^{23}Na , ^{31}P),
- musculoskeletal tissue with short T2 like tendons, ligaments, and periosteum,

- tissue with short T2* such as liver and lung parenchyma,
- superparamagnetic contrast agents in molecular imaging.

1.9.28.4 Loop Structure

From inner to outer loops:

- Acquisition order: projections, accumulations (NAE), repetitions
- Image order in 2dseq file: slices, repetitions

1.9.28.5 Specific Parameters

Routine Card

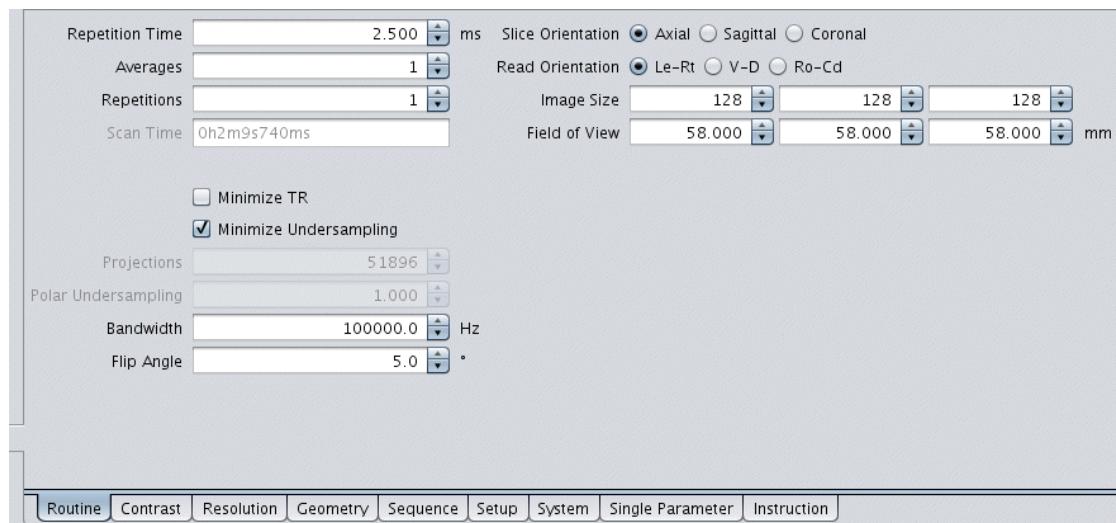


Figure 1.331: ZTE Routine Card

Minimize TR (MinimumTR) – Determines if the minimum possible TR should always be realized. Avoids unnecessary long TR after, e.g. reducing the spoiling.

Minimize Undersampling (MinimumUnderSampling) – If switched on always the minimum possible [Polar Undersampling](#) [373] factor is realized.

Projections (NPro) – Non-editable parameter describing the total number of radial scans. It depends on the polar undersampling and the image matrix size. The default value (**Polar Undersampling** = 1) is calculated to obtain the nominal density (Nyquist criterion) in the entire k-space and to avoid intra-FOV aliasing (streaks).

Polar Undersampling (ProUnderSampling) – Enables to increase the angular distance between readout directions leading to a smaller number of projections and hence a reduced scan time. Moderate undersampling up to about 3 results only in minor high-frequency aliasing. High matrices and/or phased array coils can lead to an automatic adapted undersampling factor in order to optimize memory demands for the reconstruction.

Bandwidth (PVM_EffSWh) – Nominal signal bandwidth spanned by the gradient over the FOV. The actual acquisition bandwidth is higher as oversampling is performed. Changing the bandwidth has an effect on the acquisition duration and thus on the T2* contrast. Typical values are 50 – 200 kHz.

Flip Angle (ExcPul.Flipangle) – Flip angle of the excitation pulse

Contrast Card

Main

Repetition Time	1.920	ms	<input checked="" type="checkbox"/> Fat Suppression
Flip Angle	5.0	°	<input checked="" type="checkbox"/> FOV Saturation
Dummy Scans	521		<input type="checkbox"/> Trigger
Dummy Duration	1000.320	ms	<input checked="" type="checkbox"/> Segmented Preparation
			<input type="checkbox"/> Evolution

Figure 1.332: ZTE Contrast Card Main

Flip Angle (ExcPul.Flipangle) – See [Routine Card ▶ 373\]](#)

Segmented Preparation (PVM_SegmentationOnOff) – Enables segmented preparation. It is always switched on in case a preparation module is activated.

Segmentation

Segment Duration	100.000	ms	<input checked="" type="checkbox"/> Minimum Duration		
Shots	52		Module Duration	8.613	ms
Segments	998.00		Total Duration	8596.010	ms
Dummy Duration	0.000	ms			
Dummies	0				

Figure 1.333: ZTE Contrast Card Segmentation

Segment Duration (PVM_SegmentationDur) – Duration of one ZTE acquisition segment. Should be on the order of T1 of the sample.

Shots (PVM_SegmentationShots) – Number of acquisition shots (TRs) per segment

Segments (PVM_SegmentationSegments) – Total number of segments (may be non-integer)

Dummy Duration (PVM_SegmentationDummyDur) – Duration of dummies after preparation

Dummies (PVM_SegmentationDummies) – Number of dummies after preparation

Minimum Duration (PVM_SegmentationMinDur) – On/Off parameter determining if the minimum possible module duration should be used. If switched off, an extra delay can be added, e.g. for testing purposes.

Module Duration (PVM_SegmentationModuleTime) – Duration of preparation module per segment (excluding the acquisition part)

Total Duration (PVM_SegmentationTotalTime) – Accumulated duration of segmented preparation

Sequence Card

Main

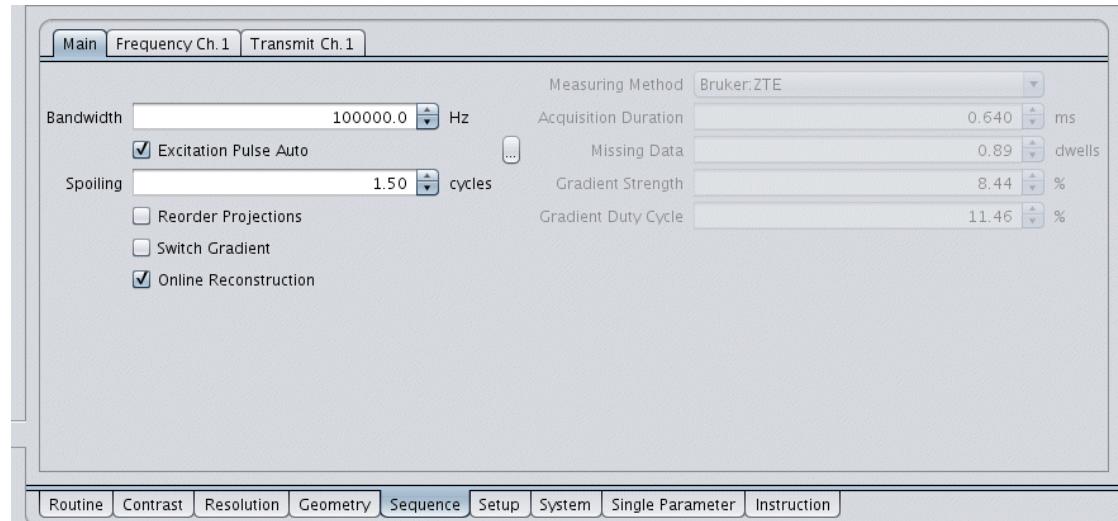


Figure 1.334: ZTE Sequence Card Main

Excitation Pulse Auto (ExcPulseAuto) – On/Off parameter to force the excitation pulse length being set short enough to provide a sufficiently large bandwidth corresponding to the selected signal bandwidth

Spoiling (Spoiling) – Minimum spoiling realised by the readout gradient during and after acquisition (see Figure [Acquisition of a ZTE center-out readout \[▶ 370\]](#)). Should be 1.5 to avoid artifacts from unwanted coherences without reordering projections (see Figure [Insufficient spoiling creates stripe artifacts \[▶ 376\]](#)). However, large spoiling increases the minimum possible TR.

Reorder Projections (Reorder) – On/Off parameter for reordering gradient directions for improved spoiling at small values of **Spoiling**. Slightly increases acoustical noise (see Figure [Insufficient spoiling creates stripe artifacts \[▶ 376\]](#)).

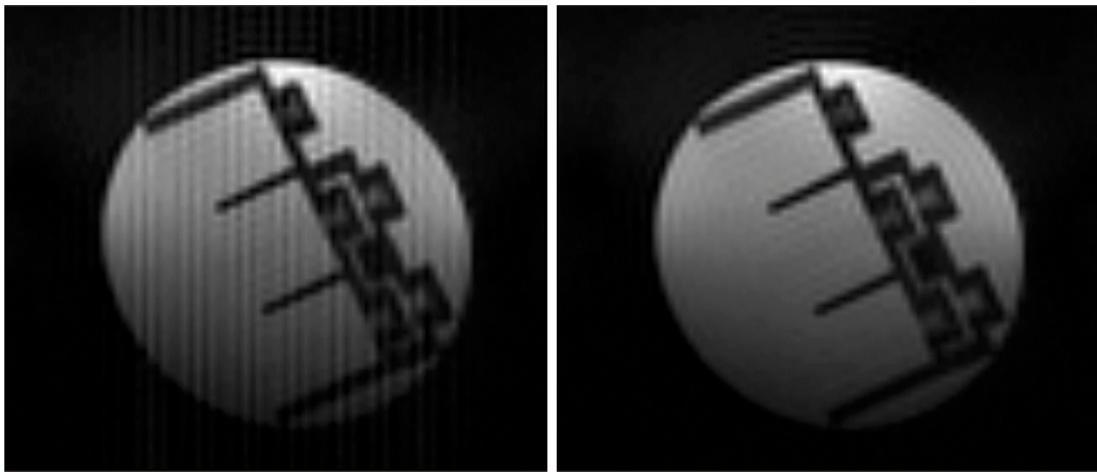


Figure 1.335: Insufficient spoiling creates stripe artifacts (*left*) which can be removed by reordering the gradient directions (*right*).

Switch Gradient (GradOff) – On/Off parameter for setting the gradient operation mode. Gradient switching reduces the gradient duty cycle (for non-minimum TR) but increases acoustical noise.

Online Reconstruction (RecoOnline) – Switches online reconstruction on or off. For the online case, it also ensures that the acquired data can be reconstructed by setting the acquisition parameter ProUnderSampling and the regridding parameters depending on the current matrix size. In the offline case, no memory checks are made and the images can be reconstructed offline afterwards. This mode enables also the acquisition of larger matrix sizes.

Missing Data (MissingData) – Amount of data missing at the beginning of the FID. Should not exceed 2.0 to enable sufficient image quality.

Acquisition Delay (AcqDelay) – Inserts an additional delay between the pulse and the start of data acquisition

Gradient Strength (ReadGrad) – Relative strength of the readout gradient

Gradient Duty Cycle (GradDutyCycle) – Estimation of the gradient duty cycle employed with respect to the maximum possible value. Should not exceed 100%. Can be reduced by changing the gradient operation mode with **Switch Gradient** and increasing TR. In the case when the estimated duty cycle approaches 100%, it is recommended to check its precise value with the DutyCycle macro. The duty cycle calculation requires a correct configuration of the gradient system.

Special Reconstruction Parameters Card

Special reconstruction parameters are accessible via the Processing Platform (see Chapter [Using the Processing Platform \[72\]](#)).

Skip Initial Data (RecoSkip) – Number of samples skipped additionally from the initial part of the FID data for reconstruction

Use Origin for Reco (RecoUseOrigin) – Determines if the data value acquired for the k -space origin is used for reconstruction

Scaling of Origin (RecoScaleOrigin) – Correction of background signal

T2* Estimate (T2Estimate) – Estimate of T_2^* automatically derived from the data acquired for the k -space origin. Only representative if the signal is dominated by short T_2 contributions

T2* Filter (RecoT2Filter) – Value of an exponential filter applied during reconstruction to compensate the signal decay for a specific T_2^* . Improves the resolution but reduces the SNR. Can be taken from T2Estimate.

B0 Estimate (B0Estimate) – Estimate of B0 off-resonance automatically derived from the data acquired for the k -space origin.

Off-resonance (RecoOffResonance) – Value for a B0 off-resonance correction by demodulation of the data during reconstruction.

1.9.28.6 Workflow

Most samples contain components with short as well as long T2. In such a case sample positioning and adjustments work as usual. However, if only short T2 components are available some specific handling is required, as described below.

Reference Pulse Gain

For samples containing short T2 components only, the adjustment of the reference pulse gain may fail. In this case, the RF pulse has to be set manually in the method or approximate reference values could be set.

Positioning

In the Setup mode 1D projections of the sample are obtained. The three main directions are available as projections perpendicular to the plane selected by the **Slice Orientation** parameter (see [Geometry Card \[▶ 271\]](#)). Note that short TR usually does not result in projections of good quality due to insufficient spoiling. Therefore a TR of a few hundred milliseconds should be chosen. Also note that due to repeated gradient switching the Setup mode is not silent. Finally, apparently distorted projections do not necessarily indicate insufficient 3D image quality.

1.9.28.7 Troubleshooting

Acquisition aborts

The receiver gain adjustment aborts with an acquisition error, which may occur with TR below 1 ms. In this case perform the RG adjustment separately or set RG manually, and run the actual scan without the adjustment.

The scan aborts with a receiver error. There may be a data throughput problem in the receiver. Slightly increase TR.

1.9.29 SINGLEPULSE

1.9.29.1 Principles

Free Induction decay generated with a (low angle) RF pulse, variable repetition time (TR)

1.9.29.2 Applications

- Manual shimming
- Acquisition of non-localized spectra
- Optimization of fat suppression for imaging

1.9.29.3 Loop Structure

From inner to outer loops:

- Acquisition order: accumulation (NA), repetitions

1.9.29.4 Specific Parameters

Routine Card

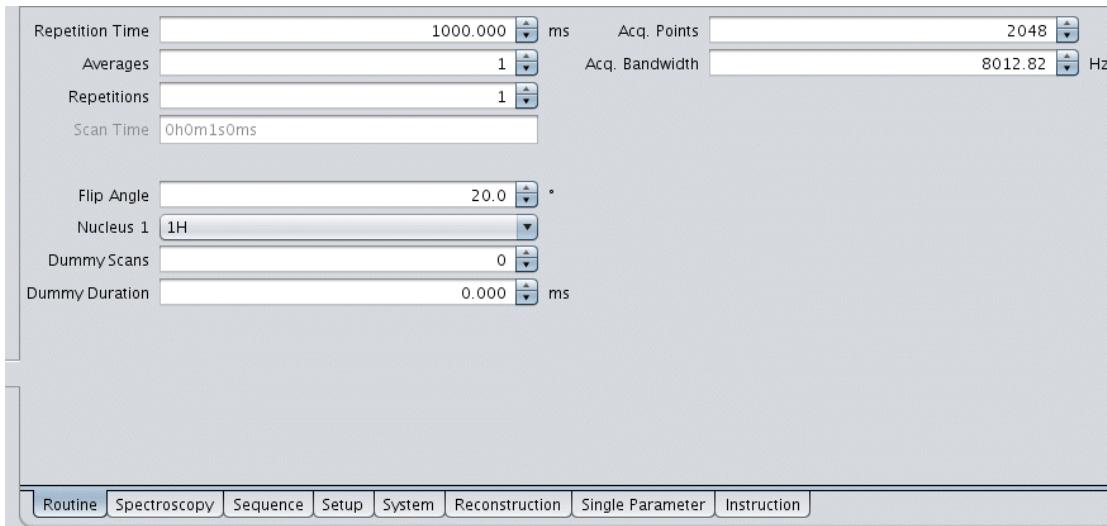


Figure 1.336: SINGLEPULSE Routine Card

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse

Nucleus 1 (PVM_Nucleus1Enum) – Allows to select the nucleus for channel 1 from a list of nuclei available for the active operation mode

Dummy Scans (PVM_DummyScans) – See [Contrast/Preparation Card \[▶ 248\]](#)

Dummy Duration (PVM_DummyScansDur) – See [Contrast/Preparation Card \[▶ 248\]](#)

Acq. Points (PVM_SpecMatrix) – Number of sampling points

Acq. Bandwidth (PVM_SpecSWh) – Maximum spectral width fulfilling the Nyquist condition expressed in absolute units [Hz]

Sequence Card

Main

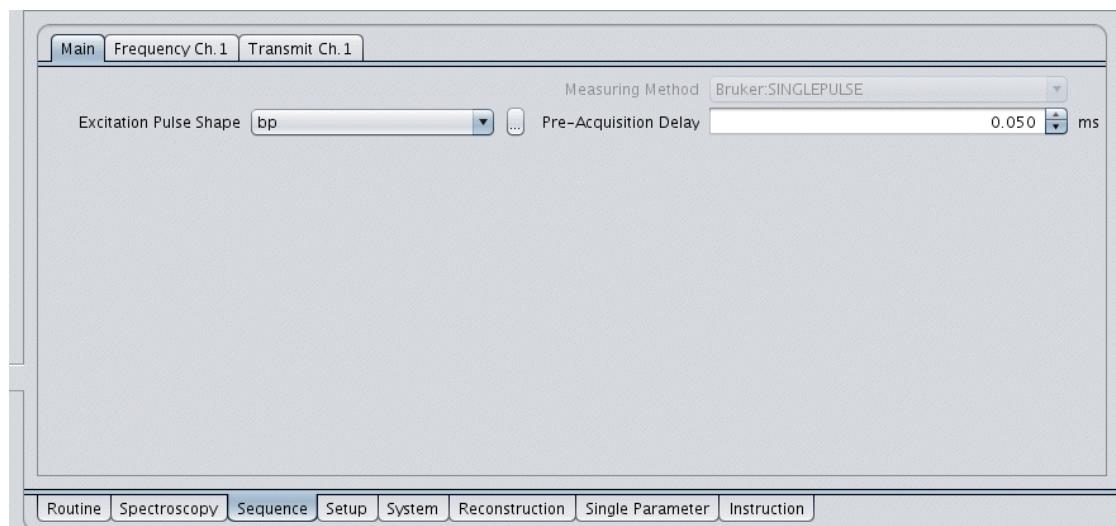


Figure 1.337: SINGLEPULSE Sequence Card Main

Excitation Pulse Shape (ExcPulse1Enum) – Nonselective excitation pulse of the sequence

Pre-Acquisition Delay (DeadTime) – Time gap between pulse and acquisition (<= 5 ms)

1.9.30 NSPECT (Non-localized Spectroscopy)

1.9.30.1 Principles

This is a variant of the SINGLEPULSE method in which several additional modules and optimization features are included, namely:

- Fat Suppression (see [Fat Suppression \(Fat Sup\) ▶ 249](#))
- Field-of-View Saturation (see [Flow Saturation \(Flow Sat\) ▶ 253](#))
- Solvent Suppression (see [Water Suppression \(Water Sup\) ▶ 258](#))
- Decoupling (see [Decoupling ▶ 261](#))
- Nuclear Overhauser Enhancement (NOE) (see [NOE ▶ 262](#))
- Trigger (see [Trigger ▶ 256](#))
- Navigator for drift compensation (see [Optimization Card ▶ 264](#))
- Reference scan for eddy current compensation (see [Optimization Card ▶ 264](#))

Multiple receive channels are combined by complex summation of phase-corrected channel data. The phase correction coefficients are determined in an automatic adjustment prior to the scan.

1.9.30.2 Applications

- Acquisition of non-localized spectra of ^1H and other nuclei. A simple localization can be achieved with the FOV-saturation module.
- Manual shimming
- Optimization of fat suppression for imaging

1.9.30.3 Loop Structure

From inner to outer loops:

- Acquisition order: accumulation (NA), repetitions (NR)

1.9.30.4 Data Files

NSPECT uses the `job` acquisition mode and stores the data in the following files:

rawdata.job0: Contains non-combined, non-accumulated, serially stored FIDs of each individual scan. File size = scan size x number of RX channels x NA x NR.

rawdata.job1: Contains serially stored FIDs of each navigator scan. File size = scan size x number of RX channels x NA x NR. File exists if navigator acquisition is selected (see [Optimization Card \[▶ 264\]](#)).



Spectroscopy methods using the job acquisition mode, apply receiver gain values specifically for each job number `n`. These values are stored in the baselevel parameter `ACQ_jobs[n].receiverGain`. (The conventional parameter RG is not applicable in this case.)

fid: Created during data reconstruction on the basis of the data in the `rawdata.job0` file. Contains combined, accumulated and corrected FIDs. The data from multiple receive channels is combined, averages are accumulated and the optional corrections for eddy current compensation and retro frequency lock are applied (see [Optimization Card \[▶ 264\]](#)). File size = scan size x NR.

fid.refscan: Contains the data of the reference scan, if activated (see [Optimization Card \[▶ 264\]](#)). The file is created during the setup of the reconstruction network and multiple receive channels are combined by complex summation of phase-corrected channel data. File size = scan size.



Each data reconstruction rewrites the `fid` and `fid.refscan` files in the scan directory, irrespectively of the processing number. Consequently, previously generated files will be overwritten.

ser: Copy of the `fid` file, which is generated when a multidimensional data set is exported to/loaded in TopSpin (for NSPECT, this is the case when NR > 1). File size = scan size x NR.



Each export to/load in TopSpin rewrites the `ser` file in the scan directory from an existing `fid` file, irrespectively of the processing number. Consequently, previously generated `ser` files will be overwritten.

1.9.30.5 Specific Parameters

Routine Card

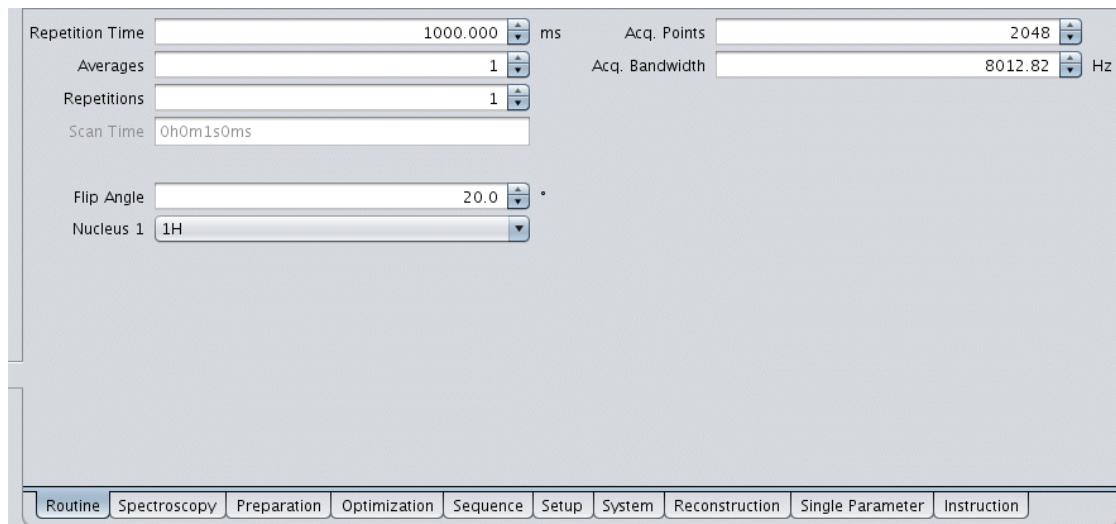


Figure 1.338: NSPECT Routine Card

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse

Nucleus 1 (PVM_Nucleus1Enum) – Allows selecting the nucleus for channel 1 from a list of nuclei that are available for the active operation mode

Acq. Points (PVM_SpecMatrix) – Number of sampling points

Acq. Bandwidth (PVM_SpecSWh) – Maximum spectral width fulfilling the Nyquist condition expressed in absolute units [Hz]

Sequence Card

Main

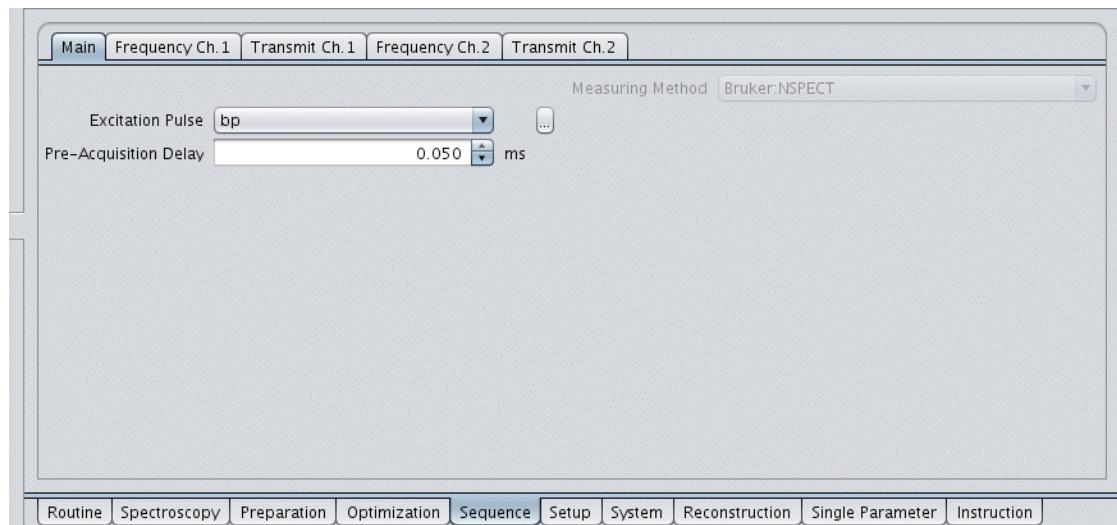


Figure 1.339: NSPECT Sequence Card Main

Excitation Pulse (ExcPulse1Enum) – Non-selective excitation pulse of the sequence

Pre-Acquisition Delay (DeadTime) – Time gap between pulse and acquisition (<= 5 ms)

Reconstruction Card

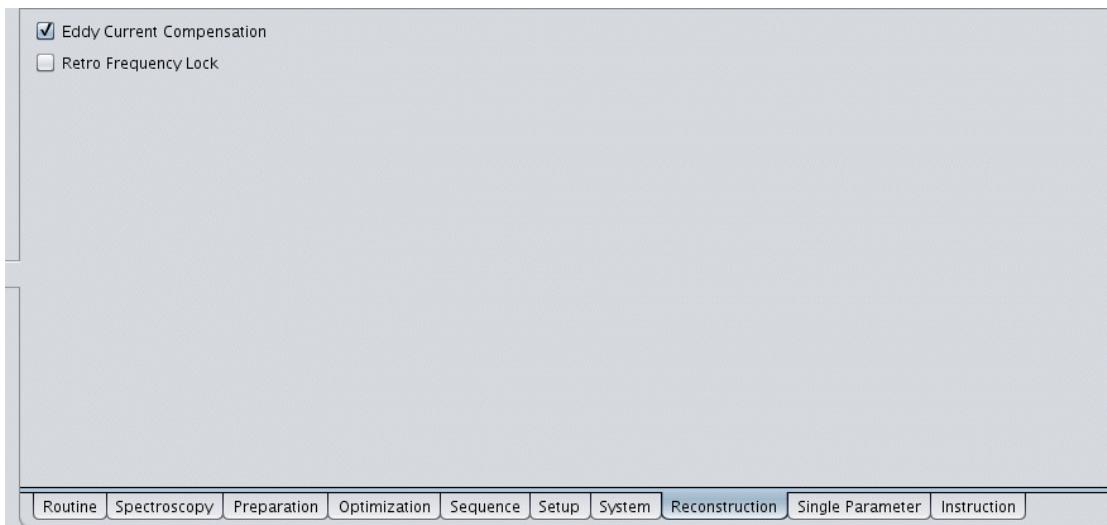


Figure 1.340: NSPECT Reconstruction Card

Eddy Current Compensation (Edc_OnOff) – See [Optimization Card \[▶ 264\]](#)

Retro Frequency Lock (RetroFrequencyLock_OnOff) – See [Optimization Card \[▶ 264\]](#)

1.9.31 CSI (Chemical Shift Imaging)

1.9.31.1 Principles

Chemical Shift Imaging, also called spectroscopic MRI provides localized NMR spectra in all pixels of the image. A single slice selective RF pulse, a spin echo sequence or the PRESS scheme is used to excite the imaging slice or a rectangular voxel within the slice. After the excitation, phase encoding gradients are applied in all spatial dimensions. The signal is then recorded with all gradients off. For proton CSI, fat-, water-, and outer volume suppression modules can be added. Additionally, navigator signal can be acquired to compensate field drifts. The measurement is restricted to one slice or voxel per scan.

During the reconstruction the Fourier transformation is applied to all dimensions (spatial and spectroscopic) to provide pixel spectra, which can be scanned with the CSI Visualization tool (see Chapter [Chemical Shift Imaging Visualization \[▶ 441\]](#)). Additionally, only spatially transformed data, containing time domain signals of all pixels are produced for the spectroscopic processing in TopSpin.

Since all spatial dimensions are phase encoded (with one excitation per encoding step), CSI requires much longer scan times than MRI. For that reason, and due to the low concentration of metabolites observed in in-vivo spectra, CSI is typically used with small matrix sizes, such as 16×16, or 8×8×8. To assure uncontaminated spectra despite small matrix sizes, a spatial filter is used during the reconstruction. A special “k-space weighted” averaging scheme, matched to the spatial filter is used to optimize the signal-to-noise ratio.

The method can be used with array receive coils in which case a global phase correction is automatically adjusted and applied before the combination of complex signals from array elements.

1.9.31.2 Applications

- Simultaneous acquisition of spectra from different locations
- Measurement of spectra from arbitrary regions of interest

- Measurement of maps of metabolite concentrations
- Localized spectroscopy with a single RF pulse (in the `Slice_FID` mode), particularly advantageous with short-T2 nuclei such as ³¹P

1.9.31.3 Loop Structure and Data Storage

From inner to outer loops:

- Acquisition order: accumulation (variable, according to k-space position), phase encoding, repetitions

CSI uses the job acquisition mode and stores the data in the files `rawdata.job0`, `rawdata.job1`, `fid` and `ser` as described in Chapter [Data Files ↗ 3801](#). The `fid` and `ser` files contain data which is Fourier transformed along spatial directions and represents time domain signals from each pixel. After loading to TopSpin, these signals can be selected with the `rser` command. For example, in an experiment with a 16x16 matrix, the signal of the pixel in the 3rd row, 4th column can be read by `rser 36`.

1.9.31.4 Specific Parameters

Routine Card

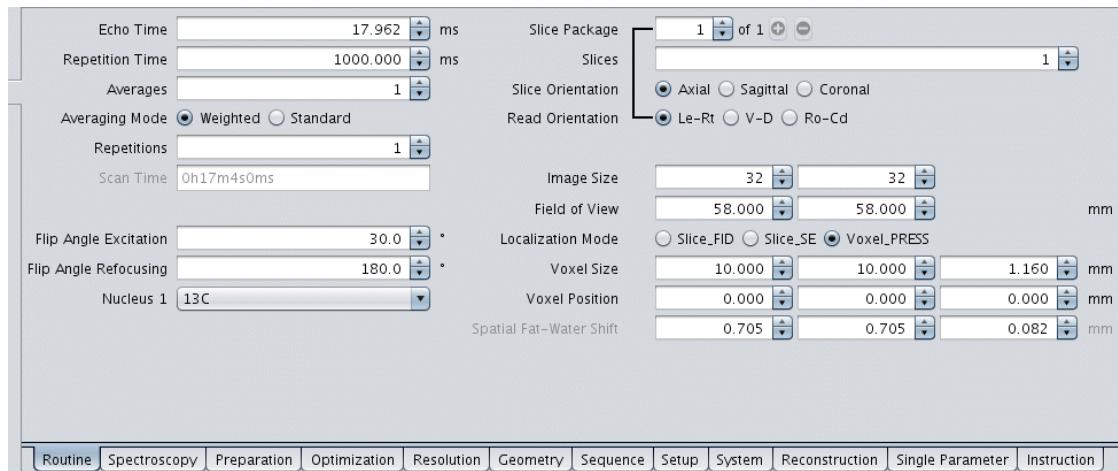


Figure 1.341: CSI Routine Card

Averages (PVM_NAverages) – Number of averages of the signal representing the center of the k-space. Remaining k-space positions may be averaged a lower number of times dependent on **Averaging Mode**. In both cases, doubling the number of averages doubles the measurement time and increases SNR by square root of 2.

Averaging Mode (AverageMode) – Selects the way in which the averaging is distributed:

- **Weighted** – Number of averages depends on the k-space position and corresponds to the weight given to this position by the spatial Hamming filter. In this mode the best SNR is achieved in a given measurement time.
- **Standard** – All k-space positions are averaged the same number of times. This mode is kept for compatibility with earlier implementations.

Flip Angle Excitation (ExcPulse1.Flipangle) – Flip angle of the excitation pulse

Flip Angle Refocusing (RefPulse1.Flipangle) – Flip angle of the refocusing pulse in the `Slice_SE` and `Voxel_PRESS` Localization Mode

Nucleus 1 (PVM_Nucleus1Enum) – Allows selecting the nucleus for channel 1 from a list of nuclei that are available for the active operation mode

Localization Mode (LocalizationMode) – Selects the way the signal is excited and localized:

- Slice_FID: The FID signal is acquired after slice selective excitation. In 3D experiments, the FOV size in slice direction is determined by the slice thickness.
- Slice_SE: Spin echo signal is acquired after slice selective excitation and refocusing. In 3D experiments, the FOV size in slice direction is determined by the slice thickness.
- Voxel_PRESS: The signal is acquired from a voxel localized using the PRESS scheme (double spin echo). This mode allows eliminating the signal from unwanted parts of the field of view, for example the subcutaneous fat. In this mode voxel parameters become visible. Voxel and imaging geometry parameters are correlated: The voxel has the same orientation as the imaging FOV and its position is restricted within the imaging FOV.

Voxel Size (PVM_VoxArrSize) – Voxel size in PRESS mode

Voxel Position (PVM_VoxArrPosition) – Voxel position in the coordinate system of the reference image

Spatial Fat-Water Shift (PVM_VoxArrCSDisplacement) – Information on the spatial displacement of different chemical shifts for the water and fat resonance. Non-editable.

Resolution Card

This card controls the size and resolution in spatial dimensions. Spectral size and resolution can be found in Chapter [Spectroscopy Card ▶ 2641](#).

Main

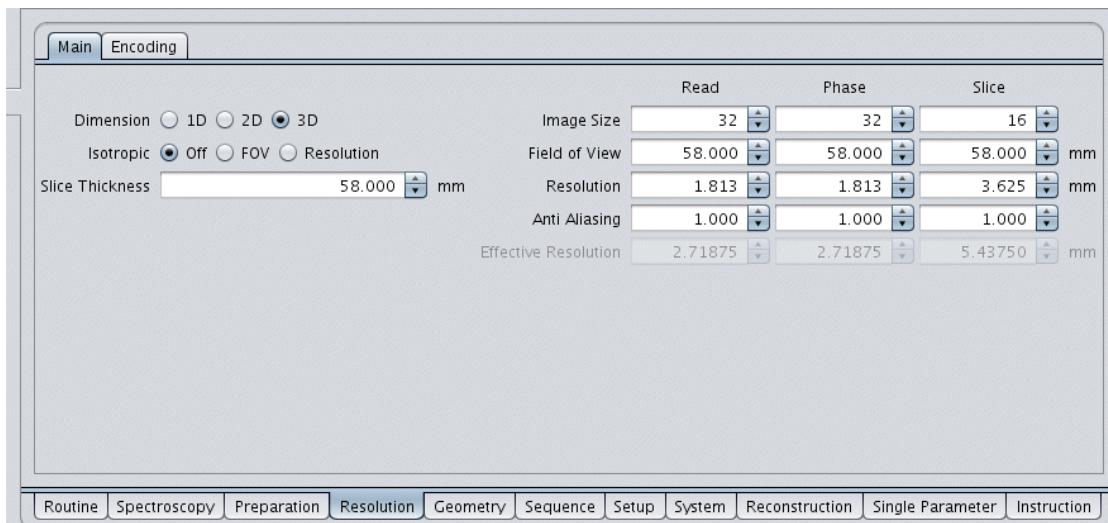


Figure 1.342: CSI Resolution Card Main

Dimension (PVM_SpatDimEnum) – Number of spatial dimensions

Image Size (PVM_Matrix) – Number of pixels along each spatial dimension of the reconstructed image. It does not include the spectral size, which can be set on the **Spectroscopy Card** (see Chapter [Spectroscopy Card ▶ 2641](#)). The acquisition matrix size is smaller than the **Image Size** when interpolation (zero-filling) is used (see Chapter [Encoding ▶ 2701](#)).

Field of View (PVM_Fov) – Extents covered by the image. Note that in CSI aliasing of out-of-FOV signals takes place in all dimensions. The FOV has always to be selected higher than the object size within the reception range of the coil.

Resolution (PVM_SpatResol) – Spatial size of image pixels [mm]

Effective Resolution (EffResolution) – Displays the effective resolution (width of the point-spread function). It is higher than the nominal resolution because of the spatial filter and, if applied, zero-filling.

Encoding

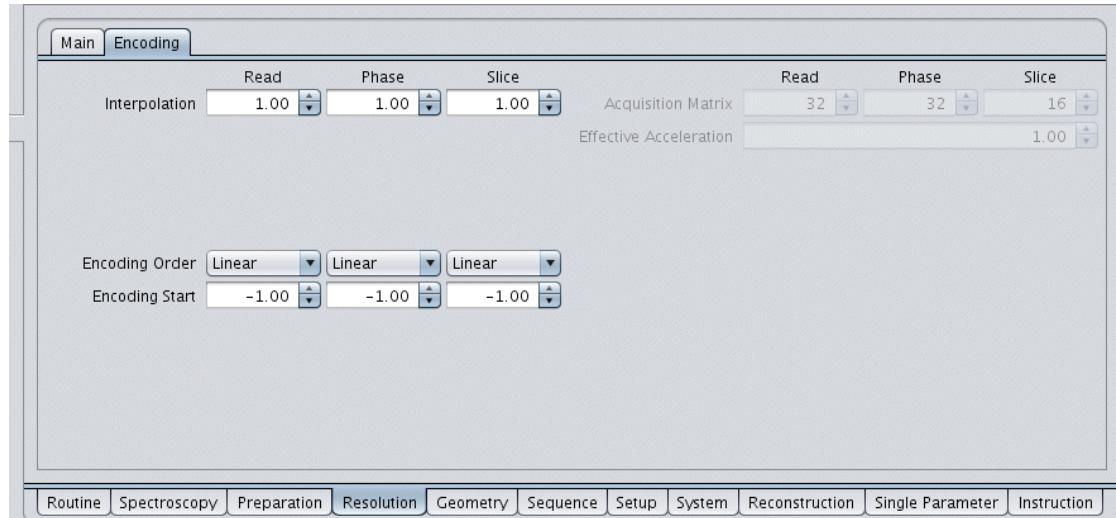


Figure 1.343: CSI Resolution Card Encoding

Interpolation (PVM_EncZf) – Fourier interpolation by zero-filling in spatial dimensions. Interpolation reduces the measurement time and the effective resolution.

Acquisition Matrix (PVM_EncMatrix) – Size of the acquisition matrix in the spatial dimensions

Sequence Card

Main

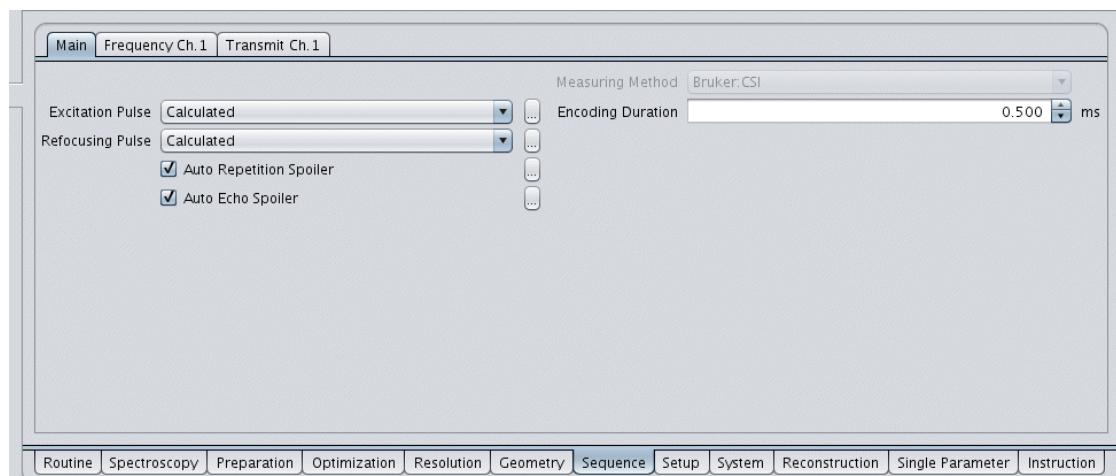


Figure 1.344: CSI Sequence Card Main

Excitation Pulse (ExcPulse1Enum) – Excitation pulse of the sequence

Refocusing Pulse (RefPulse1Enum) – Refocusing pulse of the sequence if the **Localization Mode** is Slice_SE or Voxel_PRESS

Auto Repetition Spoiler (Spoiler.automatic) – Gradient spoiler applied to the slice channel before the excitation to remove interference with previous signals

Auto Echo Spoiler (RefSpoiler.automatic) – Gradient spoiler on both sides of the refocusing RF pulses if the **Localization Mode** is Slice_SE or Voxel_PRESS

Reconstruction Card

Retro Frequency Lock (RetroFrequencyLock_OnOff) – See Chapter [Optimization Card \[264\]](#)

1.9.32 EPSI

1.9.32.1 Principles

Echo-Planar Spectroscopic Imaging (EPSI) (see [References \[691\]](#)) is a fast variant of CSI in which a combined spatial-spectral read-out allows speeding up the acquisition. Each k-space line is measured repeatedly during the signal decay using reversals of the readout gradient similar to EPI. The spectral width is therefore determined by the length of one gradient echo. This strongly limits achievable spectral widths compared to CSI. However, the spectral width can be increased by segmentation: The sampling of the gradient echoes is distributed over a certain number of interleaved acquisitions (segments) with an incrementing delay after the excitation.

1.9.32.2 Applications

Since a reduction of the measurement time always reduces the signal-to-noise ratio (SNR), EPSI should only be applied in situations where the SNR of a single-average CSI is high enough to be traded off. Typical examples include the spectroscopy of the water line (quantitative analysis of T2*), water-fat separation, and the separation of other chemical components in material science. An emerging application is the spectroscopic imaging of hyperpolarized nuclei where the main advantage of EPSI is a reduced number of excitations.

1.9.32.3 Loop Structure

From inner to outer loops:

- Acquisition order: echoes, segments, phase encoding
- Order in 2dseq: The dimensions have different order than in CSI, starting from the first spatial dimension (readout), followed by the spectral dimension and the second spatial dimension. This order is not compatible with the current version of the CSI display tool.

1.9.32.4 Specific Parameters

Routine Card

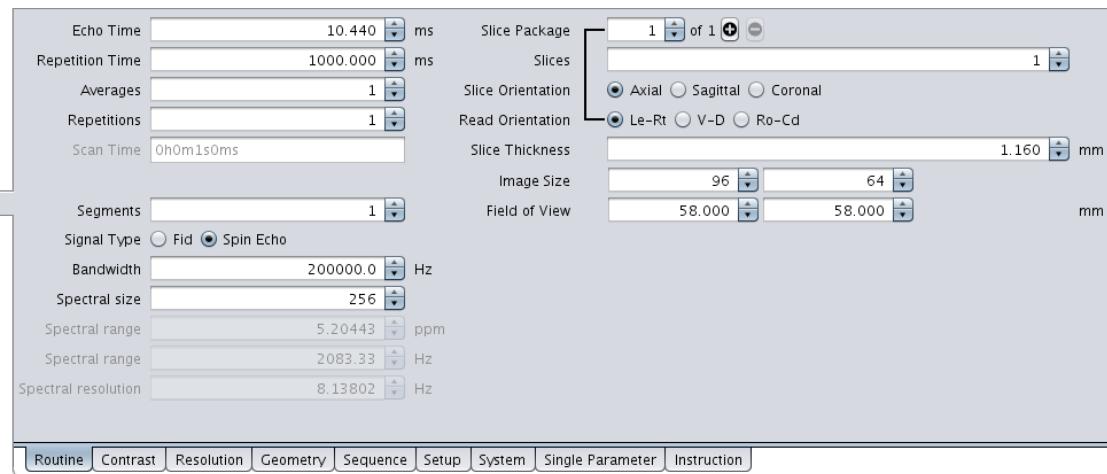


Figure 1.345: EPSI Routine Card

Echo Time (EchoTime) – Time from the excitation to the first gradient echo. In the **Fid** mode this corresponds to the non-sampled “dead time”. In the **Spin Echo** mode this parameter describes the time of the spin echo (the first gradient echo coincides with the spin echo, there is no “dead time”).

Segments (NSegments) – Number of scans with time-interleaved echoes. Increases the spectral range.

Signal Type (PVM_SignalType) – Selection between **Fid** and **Spin Echo** modes

Bandwidth (PVM_EffSWh) – Sampling bandwidth. Not to be confused with **Spectral Range**, which depends on this and other parameters. High bandwidth increases the spectral range at the price of a higher gradient duty cycle and acoustic noise level.

Spectral Size (SpecSize) – Data matrix size in the spectral dimension. The number of gradient echoes is given by **Spectral Size** divided by the number of segments. **Spectral Size** should not be set higher than necessary for the practically achievable spectral resolution to avoid excessive gradient duty cycle.

Spectral Range (SpecBandPpm, SpecBand) – Frequency range (spectral bandwidth) covered by the acquisition without aliasing, displayed twice in ppm and Hz units. Unlike CSI, frequencies exceeding this range will be folded in (aliased). **Spectral Range** depends on the sampling bandwidth, matrix size in the readout direction and on the number of segments.

Spectral Resolution (SpecResol) – Nominal resolution in the spectral dimension

1.9.33 PRESS (Point-Resolved Spectroscopy)

1.9.33.1 Principles

PRESS provides localized spectra from rectangular voxels selected with a sequence of 90° - 180° - 180° RF pulses producing a double spin echo. Due to a relatively long minimum echo time and the sensitivity of 180° pulses to transmission RF homogeneity, it is mainly used for ${}^1\text{H}$ spectroscopy with volume transmission coils, where it gives highest SNR among localized spectroscopy methods. For short-TE spectra, non- ${}^1\text{H}$ nuclei and surface transmission coils, STEAM or ISIS methods are more appropriate.

The method supports arbitrary sizes, orientations and positions of the voxel, which can be graphically prescribed in the Geometry Editor.

Water suppression with VAPOR and CHESS sequences is available, as well as the outer volume suppression (OVS) for an improved voxel definition. When both options are used simultaneously, the OVS sequence is interleaved with the water suppression for a better efficiency.

In the case of array coil acquisition multiple receive channels are combined by complex summation of phase corrected channel data. The phase corrections are determined in an automatic adjustment prior to the scan.

The method allows localized shimming and frequency adjustments based on the voxel signal. These adjustments can be performed on demand in the Adjustment Platform.

1.9.33.2 Applications

Localized in vivo proton spectroscopy

1.9.33.3 Loop Structure and Data Storage

From inner to outer loops:

- Acquisition order: accumulation (NA), repetitions (NR)

PRESS uses the job acquisition mode and stores the data in the files `rawdata.job0`, `rawdata.job1`, `fid` and `ser` as described in [Data Files ▶ 380\].](#)

1.9.33.4 Specific Parameters

Routine Card

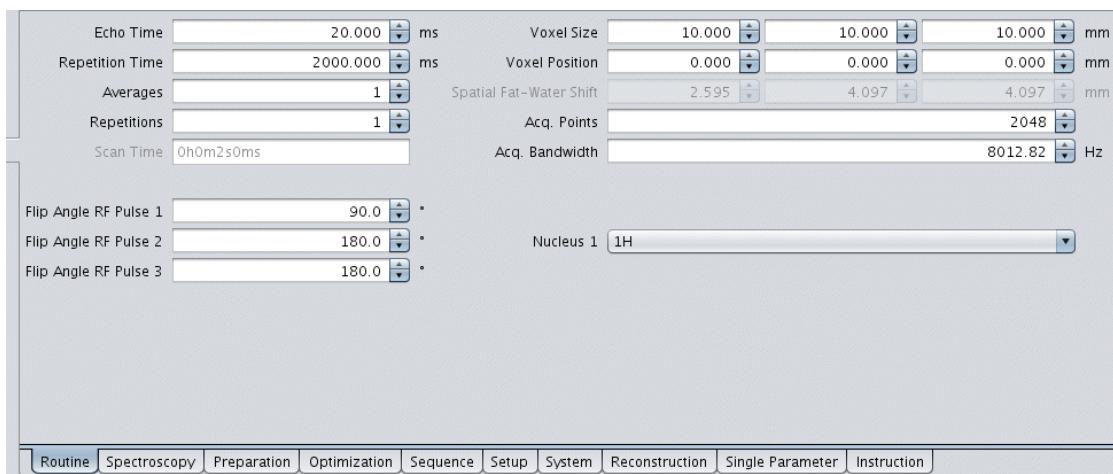


Figure 1.346: PRESS Routine Card

Echo Time (PVM_EchoTime) – Time between the center of the excitation pulse and the center of the second spin echo, usually denoted TE in MRI literature, determining the T2 weighting of the spectra.

Repetition Time (PVM_RepetitionTime) – Time between consecutive excitations of the voxel, usually denoted TR in MRI literature

Flip Angle RF Pulse 1 (VoxPul1.Flipangle) – Flip angle of the excitation pulse

Flip Angle RF Pulse 2 (VoxPul2.Flipangle) – Flip angle of the first refocusing pulse

Flip Angle RF Pulse 3 (VoxPul3.Flipangle) – Flip angle of the second refocusing pulse

Voxel Size (PVM_VoxArrSize) – Definition of the voxel size [mm]

Voxel Position (PVM_VoxArrPosition) – Definition of the voxel position in the coordinate system of the reference image [mm]

Spatial Fat-Water Shift (PVM_VoxArrCSDisplacement) – Information on the spatial displacement of different chemical shifts for the water and fat resonance. Non-editable parameter.

Acq. Points (PVM_SpecMatrix) – Number of sampling points

Acq. Bandwidth (PVM_SpecSWh) – Maximum spectral width fulfilling the Nyquist condition expressed in absolute units [Hz]

Nucleus 1 (PVM_Nucleus1Enum) – Allows to select the nucleus for channel 1 from a list of nuclei that are available for the active operation mode

Optimization Card

Main

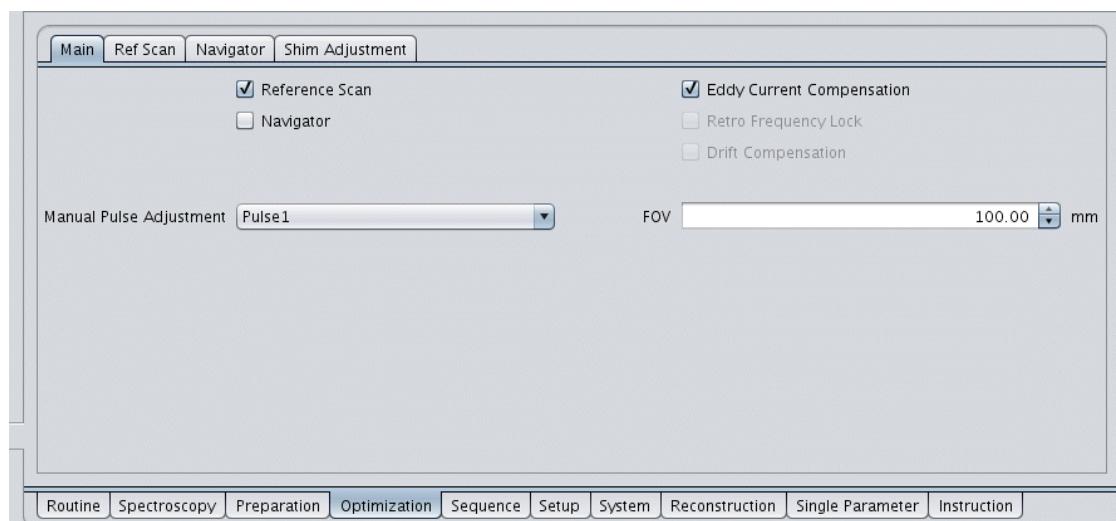


Figure 1.347: PRESS Optimization Card Main

Manual Pulse Adjustment (OPT_ManAdjustment) – Manual adjustments of RF gains can be performed on the basis of RF profiles for the pulses. To change the power levels of the RF pulses manually, deactivate **Calc. Pulse Ampl.** and use the corresponding parameters on the Setup Card while the scan is running in setup mode.

FOV (OPT_Fov) – Extents covered by the profile acquired during Manual Pulse Adjustment

Shim Adjustment

This card contains parameters controlling an iterative voxel shim adjustment, which works in the same way as in the AdjShim method, and can be started on the Adjustment Platform as Local Shim. See Chapter [AdjShim \[▶ 225\]](#) for details.

Sequence Card

Main

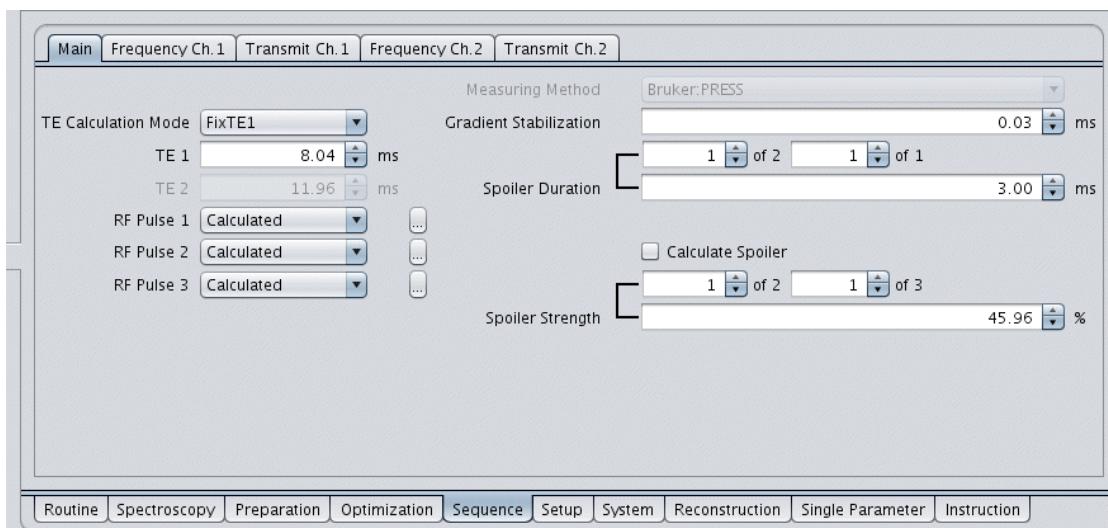


Figure 1.348: PRESS Sequence Card Main

TE Calculation Mode (EchoTimeMode) – Selects the behavior of TE1 and TE2 whenever TE is changed: MinTE (min.TE), Equalize (TE1 = TE2 = TE/2), FixTE1 (TE1 and TE are editable, TE1 with higher priority), FixTE2 (TE2 and TE are editable, TE2 with higher priority)

TE 1 (TE1) – Time for the formation of the first spin echo

TE 2 (TE2) – Time between the first and the second spin echo. TE = TE1 + TE2

RF Pulse 1/2/3 (VoxPul1Enum, VoxPul2Enum, VoxPul3Enum) – Excitation Pulse, first refocusing pulse and second refocusing pulse in the PRESS localization sequence

Gradient Stabilization (GradStabDelay) – Gradient stabilization delay between the end of a slice selection gradient ramp and the start of the RF pulse to assure a certain plateau duration of slice selection gradients before RF pulses are switched. Increasing this parameter may reduce distortions of the volume selection caused by eddy current effects at the expense of an increased minimum TE. The maximum stabilization delay is constrained to be less or equal to 3 times the duration of a gradient ramp.

Spoiler Duration (SpoilerDuration) – A spoiler is used to enhance the volume selectivity by suppressing signals from outside the voxel. SpoilerDuration is an array to set the durations of spoiler gradient pulses surrounding the refocusing pulses. SpoilerDuration[0] specifies the duration for the spoiler gradients surrounding the second pulse. SpoilerDuration[1] specifies the duration for the spoiler gradients surrounding the third pulse.

Spoiler Strength (SpoilerStrength) – If **Calculate Spoiler** is selected a single input value can be specified between 0% and a max. value as starting point for calculated strengths of spoiler gradients surrounding the both refocusing pulses (inspect these values by deactivating **Calculate Spoiler**).

Spoiler Strength (SpoilerStrengthArr) – If **Calculate Spoiler** is not selected all values of a two dimensional array can be specified for strengths of spoiler gradients surrounding both refocusing pulses.

SpoilerStrengthArr[1][i], i = 1,2,3 specify the read, phase, slice spoiler gradient strengths for the gradients surrounding the first refocusing pulse

SpoilerStrengthArr[i][2], i = 1,2,3 specify the read, phase, slice spoiler gradient strengths for the gradients surrounding the second refocusing pulse

Calculate Spoiler (CalcSpoiler) – On/Off parameter controlling the calculation mode of the parameter **Spoiler Strength**

Reconstruction Card

Eddy Current Compensation (Edc_OnOff) – See Chapter [Optimization Card \[▶ 264\]](#)

Retro Frequency Lock (RetroFrequencyLock_OnOff) – See Chapter [Optimization Card \[▶ 264\]](#)

1.9.34 STEAM (Stimulated Echo Acquisition Mode)

1.9.34.1 Principles

STEAM provides localized spectra from rectangular voxels selected with a sequence of three 90° RF pulses producing a stimulated echo. Although this signal is twice lower than the double spin echo used in PRESS, there are several situations where STEAM is advantageous. These include spectroscopy at short echo times (STEAM can reach much shorter TE than PRESS, because the time between 2nd and 3rd RF pulse does not count to TE), experiments with surface transmission coils (the stimulated echo is less sensitive to RF field variations) and with non-¹H-nuclei (which typically have shorter T₂ and for which surface transmission coils are often used).

The method supports arbitrary sizes, orientations and positions of the voxel, which can be graphically prescribed in the Geometry Editor.

Water suppression with VAPOR and CHESS sequences is available, as well as the outer volume suppression (OVS) for an improved voxel definition. When both options are used simultaneously, the OVS sequence is interleaved with the water suppression for a better efficiency. Decoupling and NOE signal enhancement can be used for X-nuclei with double-tuned RF coils.

In the case of array coil acquisition multiple receive channels are combined by complex summation of phase corrected channel data. The phase corrections are determined in an automatic adjustment prior to the scan.

The method allows localized shimming and frequency adjustments based on the voxel signal. These adjustments can be performed on demand in the Adjustment Platform.

1.9.34.2 Applications

Localized in vivo proton or X-nuclei spectroscopy at medium and short echo times

1.9.34.3 Loop Structure

From inner to outer loops:

- Acquisition order: accumulation (NA), repetitions (NR)

STEAM uses the job acquisition mode and stores the data in the files `rawdata.job0`, `rawdata.job1`, `fid` and `ser` as described in [Data Files \[▶ 380\]](#).

1.9.34.4 Specific Parameters

Routine Card

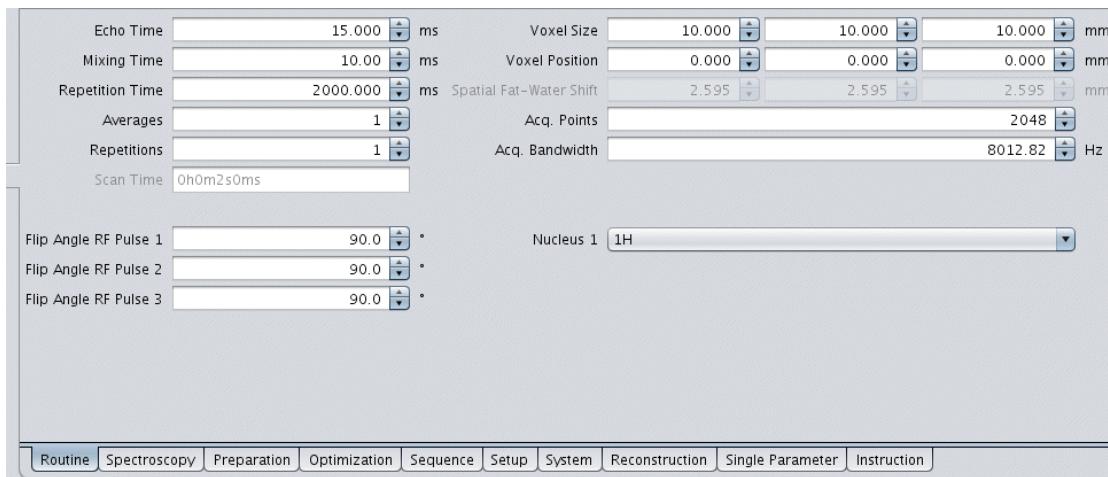


Figure 1.349: STEAM Routine Card

Echo Time (PVM_EchoTime) – Sum of delays between the effective center of the 1st and 2nd excitation pulse (the 2nd pulse is used as backrotation pulse) in the first TE/2 period and between the effective center of the 3rd excitation pulse and the center of the stimulated echo in the second TE/2 period. The effective centers of the RF pulses depend on the pulse rephrasing properties.

Mixing Time (StTM, abbreviation TM) – Delay between the effective center of the 2nd and 3rd RF pulse. The minimum TM depends on the duration and rephrasing properties of the RF pulses and the duration of the spoiling gradient switched in the TM period.

Repetition Time (PVM_RepetitionTime) – Time between consecutive excitations of the voxel, usually denoted TR in MRI literature

Flip Angle RF Pulse 1 (VoxPul1.Flipangle) - Flip angle of the first RF pulse

Flip Angle RF Pulse 2 (VoxPul1.Flipangle) - Flip angle of the second RF pulse

Flip Angle RF Pulse 3 (VoxPul1.Flipangle) - Flip angle of the third RF pulse

Voxel Size (PVM_VoxArrSize) – Definition of the voxel size [mm]

Voxel Position (PVM_VoxArrPosition) – Definition of the voxel position in the coordinate system of the reference image [mm]

Spatial Fat-Water Shift (PVM_VoxArrCSDisplacement) – Information on the spatial displacement of different chemical shifts for the water and fat resonance. Non-editable parameter.

Acq. Points (PVM_SpecMatrix) – Number of sampling points

Acq. Bandwidth (PVM_SpecSWh) – Maximum spectral width fulfilling the Nyquist condition expressed in absolute units [Hz]

Nucleus 1 (PVM_Nucleus1Enum) – Allows to select the nucleus for channel 1 from a list of nuclei that are available for the active operation mode

Optimization Card

Main

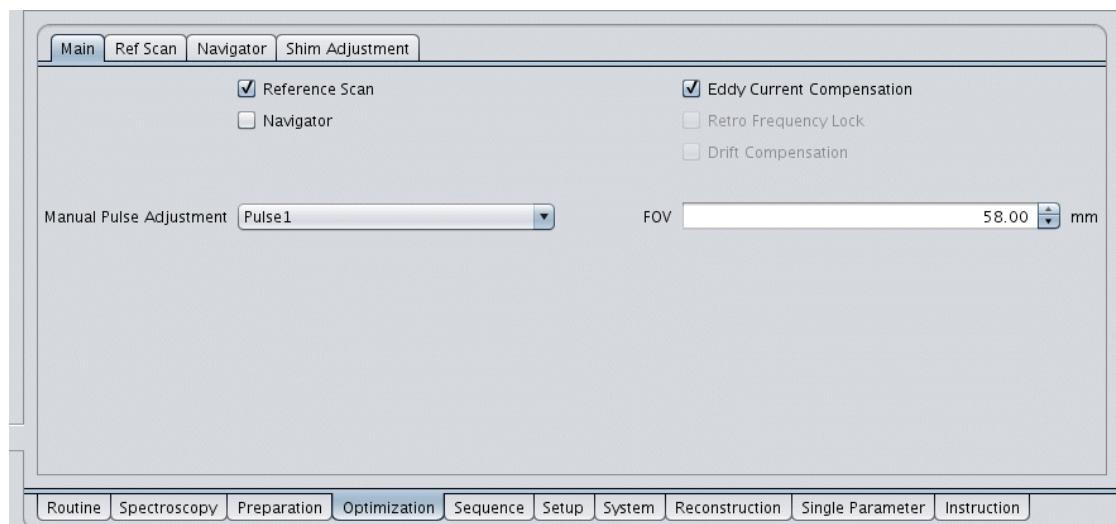


Figure 1.350: STEAM Optimization Card Main

Manual Pulse Adjustment (OPT_ManAdjustment) – Manual adjustments of RF gains can be performed on the basis of RF profiles for the pulses. To change the power levels of the RF pulses manually, deactivate **Calc. Pulse Ampl.** and use the corresponding parameters on the Setup Card while the scan is running in setup mode.

FOV (OPT_Fov) – Extents covered by the profile acquired during Manual Pulse Adjustment

Shim Adjustment

This card contains parameters controlling an iterative voxel shim adjustment, which works in the same way as in the AdjShim method, and can be started on the Adjustment Platform as Local Shim. See Chapter [AdjShim \[▶ 225\]](#) for details.

Sequence Card

Main

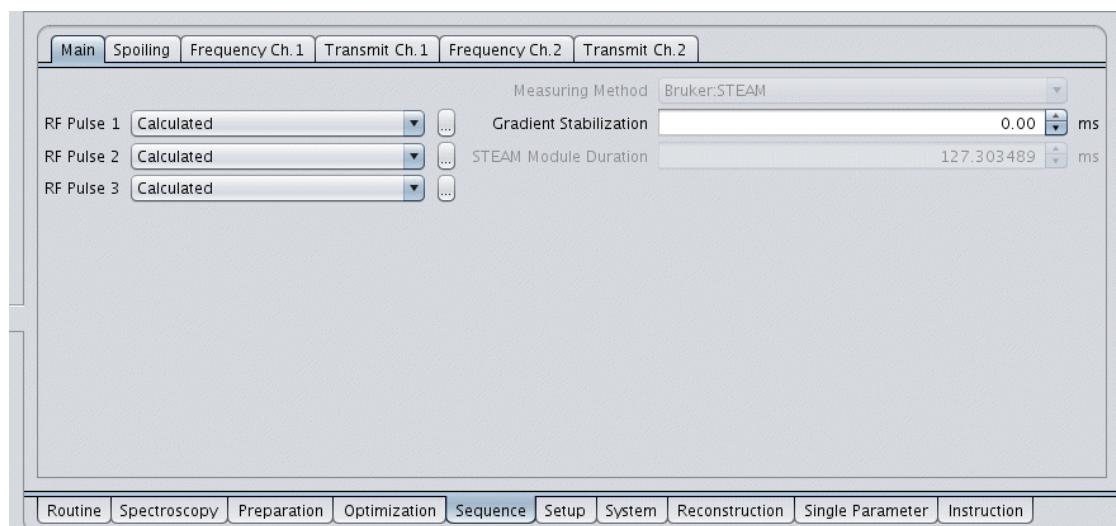


Figure 1.351: STEAM Sequence Card Main

RF Pulse 1/2/3 (VoxPul1Enum, VoxPul2Enum, VoxPul3Enum) – 1st, 2nd or 3rd RF pulse in the STEAM localization sequence

Gradient Stabilization (StGStabD) – Gradient stabilization delay between the end of a slice selection gradient ramp and the start of the RF pulse to assure a certain plateau duration of slice selection gradients before RF pulses are switched. Increasing this parameter may reduce distortions of the volume selection caused by eddy current effects at the expense of an increased minimum TE. The maximum stabilization delay is constrained to be less or equal to 3 times the duration of a gradient ramp.

STEAM Module Duration (StDur) – Duration of the STEAM localization period (including data acquisition)

Spoiling

Main				Spoiling		Frequency Ch. 1		Transmit Ch. 1		Frequency Ch. 2		Transmit Ch. 2	
1st TE/2 Spoiler Duration				2.000 ms									
Strength Dir1		54.099110 %				Strength Dir1		5.000000 cycles/mm					
Strength Dir2		54.099110 %				Strength Dir2		5.000000 cycles/mm					
Strength Dir3		54.099110 %				Strength Dir3		5.000000 cycles/mm					
2nd TE/2 Spoiler Duration				2.000 ms									
Strength Dir1		56.955543 %				Strength Dir1		5.264000 cycles/mm					
Strength Dir2		56.955543 %				Strength Dir2		5.264000 cycles/mm					
Strength Dir3		51.242677 %				Strength Dir3		4.736000 cycles/mm					
TM Spoiler Duration				9.222 ms									
Strength Dir1		57.000000 %				Strength Dir1		26.405583 cycles/mm					
Strength Dir2		57.000000 %				Strength Dir2		26.405583 cycles/mm					
Strength Dir3		57.000000 %				Strength Dir3		26.405583 cycles/mm					
Routine Spectroscopy Preparation Optimization Sequence Setup System Reconstruction Single Parameter Instruction													

Figure 1.352: STEAM Sequence Card Spoiling

During the STEAM localization sequence, the following three kinds of spoilers are applied:

1st TE/2 Spoiler (StSpTE1) – Defines the spoiler gradient in the first TE/2 period of the STEAM localization. Its parameters appear non editable. Since the TE spoiler gradients have to be balanced to assure the refocusing of the stimulated echo signal, the duration and amplitudes of the spoiler are derived from values specified for the 2nd TE/2 spoiler.

2nd TE/2 Spoiler (StSpTE2) – Defines the spoiler gradient in the second TE/2 period of the STEAM localization. Increasing its duration will increase the minimum TE of the sequence, the duration of the 1st TE/2 spoiler is increased to the same value. In order to balance the gradient area with respect to a refocused stimulated echo (STE), the spoiling gradient amplitudes of the TE/2 spoilers in a given direction are different to refocus the dephasing effect of the slice selection gradients used in the STEAM sequence.

TM Spoiler (StSpTM) – Defines the spoiler gradient in the mixing interval TM of the STEAM localization. Increasing its duration will increase the minimum TM of the sequence. The duration of the spoiler is also controlled by the desired duration of the TM period. To prevent refocusing of unwanted signal the duration as well as the spoiling capacity in of the TM spoiler in each direction is at least 3 times longer than the duration of the TE spoilers.

Each of these spoilers can be customized by the following fields:

Duration (.dur) – Duration of the spoiler gradient

Strength Dir1 (.grad_dir1/spoil_dir1), **Strength Dir2** (.grad_dir2/spoil_dir2), **Strength Dir3** (.grad_dir3/spoil_dir3) – Amplitude of the spoiling gradients along the direction of the 1st, 2nd and 3rd slice excited in the STEAM voxel selection sequence. The values can be specified as percentage (constrained to 57%) of the maximum amplitude or as spoiling efficiency in cycles of the transverse magnetization per mm.

Reconstruction Card

Eddy Current Compensation (Edc_OnOff) – See [Optimization Card ▶ 265](#)

Retro Frequency Lock (RetroFrequencyLock_OnOff) – See [Optimization Card ▶ 265](#)

1.9.35 ISIS

1.9.35.1 Principles

ISIS is a localized spectroscopy method using an 8-step averaging cycle with various combinations of selective inversion pulses to define the voxel. The acquisition of the FID signal instead of echoes (that are used in PRESS and STEAM) makes ISIS advantageous for experiments with short-T2 nuclei. Additionally, since efficient inversions can be produced with adiabatic RF pulses even in strongly inhomogeneous B1 fields, ISIS is a method of choice for transmit surface coils. The method supports arbitrary oblique voxel orientation and sizes and a selectable voxel excitation order within the Geometry Editor. In addition, outer volume suppression (OVS) is supported in a multiple loop mode improving the localization performance and reducing the demands for spoiler gradients.

Multiple receive channels are combined by complex summation of phase corrected channel data. The phase corrections are determined in an automatic adjustment prior to the scan.

1.9.35.2 Applications

Localized spectroscopy with short-T2 nuclei and/or transmit surface coils

1.9.35.3 Loop Structure

From inner to outer loops:

- Acquisition order: 8 ISIS inversion accumulations, accumulation (NA), repetitions (NR)

ISIS uses the job acquisition mode and stores the data in the files rawdata.job0, fid and ser as described in [Data Files ▶ 380](#).

1.9.35.4 Specific Parameters

Routine Card

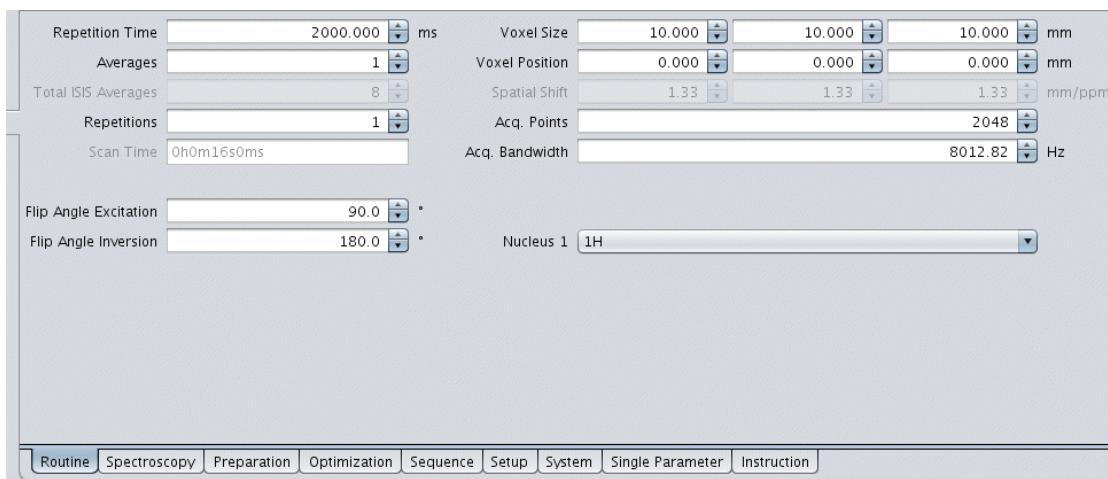


Figure 1.353: ISIS Routine Card

Repetition Time (PVM_RepetitionTime) – Time between consecutive excitations. Due to the use of inversion pulses, a long TR is recommended, e.g. equal to 5 times T1.

Averages (PVM_NAverages) – Number of groups of 8 accumulations that are added together to increase the signal-to-noise ratio of the spectrum

Total ISIS Averages (IsisNAverages) – Total number of accumulations that are averaged together to isolate the voxel signal (by each group of 8 consecutive accumulations) and to increase the signal-to-noise ratio of the spectrum (IsisNAverages=8 x PVM_NAverages)

Flip Angle Excitation (ExcPul1.Flipangle) - Flip angle of the excitation pulse

Flip Angle Inversion (InvPul1.Flipangle) - Flip angle of the inversion pulses

Voxel Size (PVM_VoxArrSize) – Definition of the voxel size

Voxel Position (PVM_VoxArrPosition) – Definition of the voxel position in the coordinate system of the reference image

Spatial Shift (IsisSpatialDispl) – Information on the spatial displacement of different chemical shifts [mm] per ppm. Non-editable.

Acq. Points (PVM_SpecMatrix) – Number of sampling points

Acq. Bandwidth (PVM_SpecSWh) – Maximum spectral width fulfilling the Nyquist condition expressed in absolute units [Hz]

Nucleus 1/2 (PVM_Nucleus1Enum, PVM_Nucleus2Enum) – Allows to select the nucleus for channel 1/2 from a list of nuclei that are available for the active operation mode

Optimization Card

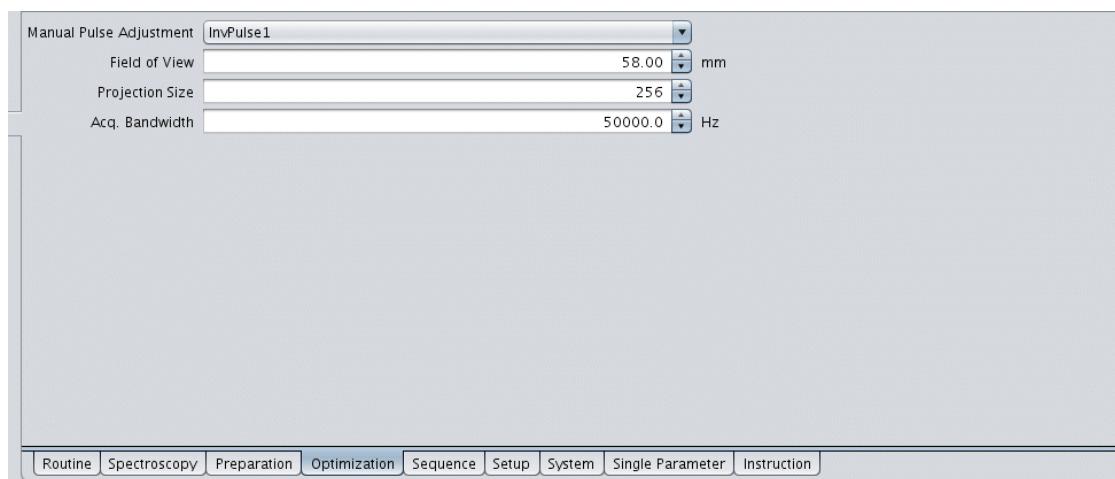


Figure 1.354: ISIS Optimization Card

Manual Pulse Adjustment (OPT_ManAdjustment) – Manual adjustments of RF gains can be performed on the basis of RF profiles for the pulses. To change the power levels of the RF pulses manually, deactivate **Calc. Pulse Ampl.** and use the corresponding parameters on the Setup Card while the scan is running in setup mode. The timing of the sequence remains the same as if a spectroscopic acquisition was made.

Field of View (IsisFov) – Extents covered by the profile acquired during Manual Pulse Adjustment

Projection Size (IsisProjSize) – Specifies the number of data points in the acquisition window along the read axis as with any imaging sequence

Acq. Bandwidth (PVM_EffSWh) – Bandwidth to acquire the profile

Sequence Card

Main

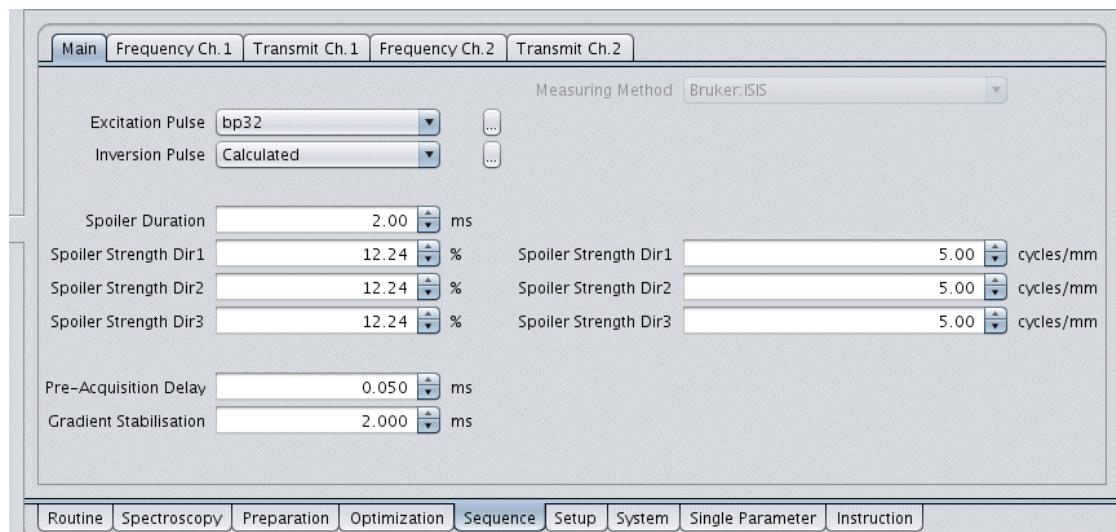


Figure 1.355: ISIS Sequence Card

Excitation Pulse (ExcPul1Enum) – Excitation pulse of the sequence

Inversion Pulse (InvPul1Enum) – Inversion pulse for voxel selection. When set to Calculated, the system generates an adiabatic full passage pulse.

Spoiler Duration (IsisSpoilDur) – Duration of the spoiler gradient that is applied immediately after each inversion pulse

Spoiler Strength Dir1/2/3 (IsisSpoilPerc1/2/3 and IsisSpoilCyMm1/2/3)) – Amplitude of the spoiling gradients along the direction of the 1st, 2nd and 3rd voxel dimension. The values can be specified as percentage (constrained to 57%) of the maximum amplitude or as spoiling efficiency in cycles of the transverse magnetization per mm.

Pre-Acquisition Delay (DeadTime) – Time gap between excitation pulse and acquisition (<= 5 ms). Its value may be increased to avoid potential probehead ringing during acquisition.

Gradient Stabilization (IsisStabDur) – Gradient stabilization delay between the end of the inversion spoiler gradient ramp and excitation pulse to allow gradient settling

1.9.36 FieldMap

1.9.36.1 Principles

FieldMap provides quantitative maps of the static magnetic field B_0 scaled in resonance frequency units. Following the acquisition of a 3D double gradient echo dataset (with a sequence similar to MGE), the reconstruction performs a phase difference calculation, a noise-robust phase unwrapping and a conversion to a frequency map. Optionally, it is possible to reconstruct separate magnitude images of both echoes as in MGE, e.g., to verify the effect of T_2^* dephasing. Map sensitivity can be controlled by changing the echo spacing. Thereby, artefacts caused by the presence of fat can be eliminated by an automatic rounding up of the echo spacing so as to keep fat signal in phase with water. To reduce the sensitivity of mapping to eddy currents, the excitation pulse can be made non-selective. Regions of low signal-to-noise ratio can be excluded from the evaluation by setting a proper SNR threshold.

1.9.36.2 Applications

- Acquisition of the field map for shimming with MAPSHIM. For this purpose, it is not necessary to load a FieldMap protocol to the scan program; the experiment has to be started in the Adjustment Platform (as the adjustment Bo Map).
- Calibration of the shim coils for MAPSHIM (required once during system installation). This also works via the Adjustment Platform, and requires the service mode.
- Direct acquisition of field maps for inspection of field homogeneity or for a quantitative imaging of magnetic susceptibility (processing not provided). This requires loading a protocol based on the FieldMap method to the scan program.

1.9.36.3 Protocol optimization strategies

An appropriate FieldMap protocol is available for field mapping in vivo in the location

AnyObject/AnyRegion/Adjustments/ADJ_BOMAP, as well as in

AnyObject/AnyRegion/Service/SvShimCalMap (service mode activated) for shim field mapping.

Several aspects of the protocol can be optimized for a particular application:

Map Sensitivity

Sensitivity of the map increases with the echo spacing. On the other hand, high spacing means long TE of the second echo and a signal loss due to T_2^* , especially in regions of strong field inhomogeneity. In living objects at 9.4 Tesla echo spacing of about 4ms is a good

trade-off between map sensitivity and T2* losses. It should be decreased at higher fields and increased in lower fields. In homogenous samples (used e.g. during map calibration) the echo spacing may be increased to 8 ms.

Resolution

Theoretically, a very low-resolved (and thus rapidly acquired) field map is sufficient to calculate the shims, since the shim coils produce smoothly varying fields. However, decreasing the resolution bears the risk of a stronger T2* dephasing of the second image (de-phasing is faster when pixels are bigger) and of unwrapping errors (phase gradients of more than π per pixel cannot be unwrapped). Too high, a resolution, on the other hand, leads to errors caused by the overall reduced SNR and unnecessarily prolongs the study. A good compromise for most in vivo studies is a 64x64x64 image matrix.

Noise threshold

Pixels of low SNR do not allow reliable phase difference calculation and cause errors in the field map. This applies above all to the exterior of the object and to regions where the T2* is short. When the map is acquired for the purpose of shimming, such pixels may deteriorate the result if they are included in the shim volume. The parameter **Map SNR** can be used to set a threshold below which the map will not be calculated.

Reduction of eddy current effects

The non-selective excitation option eliminates the switching of slice selection gradient and reduces the influence of the eddy currents on the measured map. However, this option requires that the object entirely fits the FOV in the phase encoding direction. In most cases this is most easily achieved when the readout direction is along the axis of the magnet (z/caudal-rostral/head-feet).

Reduction of chemical shift phase evolution

Fat can cause phase differences between the two gradient echoes that can be misinterpreted as field deviations. This can be avoided by choosing an echo spacing equal to the inverse of fat-water chemical shift or its multiple. When **Fat/Water Inphase Condition** is selected, the echo spacing will be automatically rounded up to a nearest value of this kind.

1.9.36.4 Specific Parameters

Routine Card

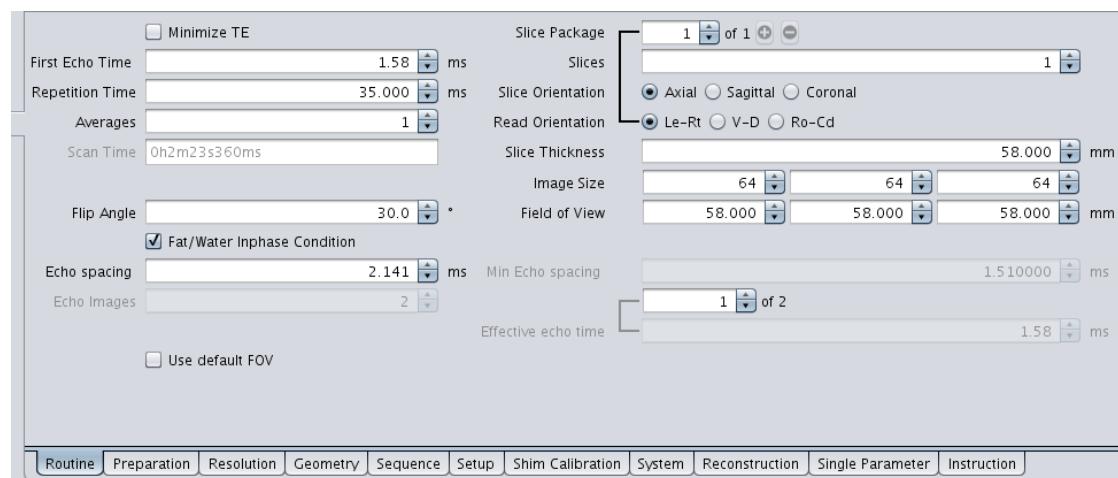


Figure 1.356: FieldMap Routine Card

Minimize TE (YesNoMinEchoTime) – If activated, the first echo time will be set to the minimum possible value according to the current state of the protocol and the parameter **First Echo Time** appears not editable.

First Echo Time (FirstEchoTime) – Delay between the effective center of the excitation pulse and the center of the first echo. Determines the T2* contrast of the sequence. The minimum echo time depends on bandwidth, matrix size, and the 2D phase encoding period of the sequence. For field mapping a small first echo time is required to keep the signal loss due to T2* relaxation as small as possible.

Fat/Water Inphase Condition (FWInphase) – When selected, the echo spacing will be automatically rounded up to the closest value which assures that fat accrues the same phase shift between the gradient echoes than water, and thus does not cause map artefacts.

Echo Spacing (EchoSpacing) – Delay between the two gradient echoes. Increasing the echo spacing increases the map sensitivity, provided the second echo image is still free of dephasing losses.

Echo Images (PVM_NEcholImages) – Number of echo images; fixed to 2 in this method

Use default FOV (DefaultFov) – If activated, the FOV is derived automatically from the system information. The corresponding parameter appears not editable. To change the FOV this parameter has to be set to No (deactivated).

Min Echo Spacing (MinEchoSpacing) – Minimum delay between the two gradient echoes

Effective Echo Time (EffectiveTE) – Effective echo time of the two gradient echoes. Non-editable and determined by the first echo time and the echo spacing.

Preparation Card

Main

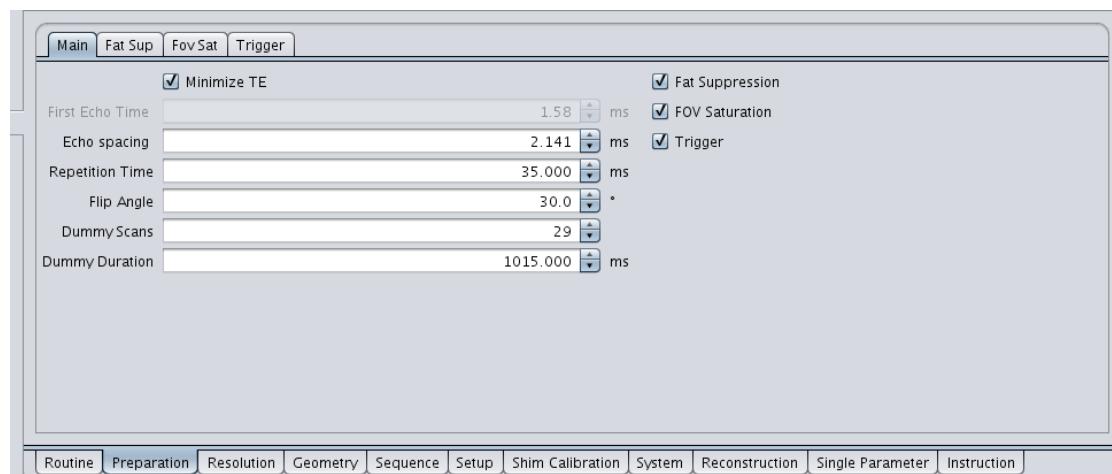


Figure 1.357: FieldMap Preparation Card Main

Minimize TE (YesNoMinEchoTime) – See [Routine Card \[▶ 399\]](#)

First Echo Time (FirstEchoTime) – See [Routine Card \[▶ 399\]](#)

Echo Spacing (EchoSpacing) – See [Routine Card \[▶ 399\]](#)

Sequence Card

Main

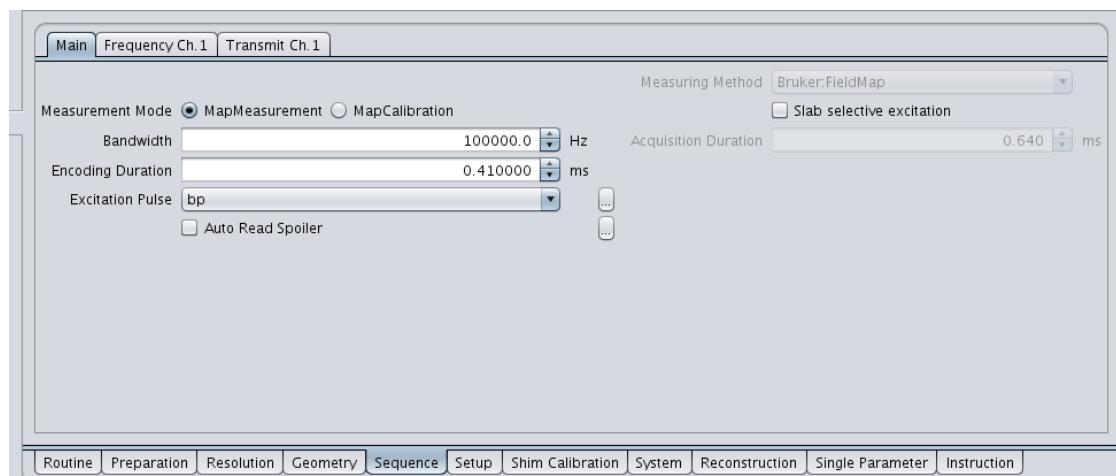


Figure 1.358: FieldMap Sequence Card Main

Measurement Mode (MeasMode) – Measurement Mode = MapMeasurement is used to acquire B0 field maps. In this mode a method-based on-demand adjustment (adjustment name B0 Map) is shown in the Adjustment Platform for this purpose. Measurement Mode = MapCalibration is used to calibrate the shim system. In this mode an On Demand adjustment (adjustment name Shim Calib.) is shown in the Adjustment Platform. It is neither necessary nor recommended to change the measurement mode to MapCalibration within a routine study. This mode is only used for service purposes.

Bandwidth (PVM_EffSWh) – Bandwidth (BW) of the data acquisition. A high bandwidth (100-150 kHz) is recommended for field mapping to avoid errors caused by frequency offset-related pixel shifts.

Excitation Pulse (ExcPulse1Enum) – Slice selective excitation pulse. This pulse selects the slab that is reconstructed as 3D volume. In the case **Slab Selective Excitation** (see below) is activated, it is important to select a high sharpness factor for this pulse (7 or higher) to avoid aliasing of out-of-slab signals.

Auto Read Spoiler (ReadSpoiler.automatic) – Constant gradient pulse applied on the read channel after the echo acquisition

Slab Selective Excitation (SlabSel) – Switches between a slice selective and a non-selective excitation. If deactivated, it is recommended to choose a non-selective pulse such as bp with a high bandwidth (>25000 Hz) to excite the whole imaging object even in the presence of resonance offsets.

Shim Calibration Card

The shim calibration card provides control about the shim calibration procedure in measurement mode MapCalibration. (It is empty for measurement mode MapMeasurement).

Main

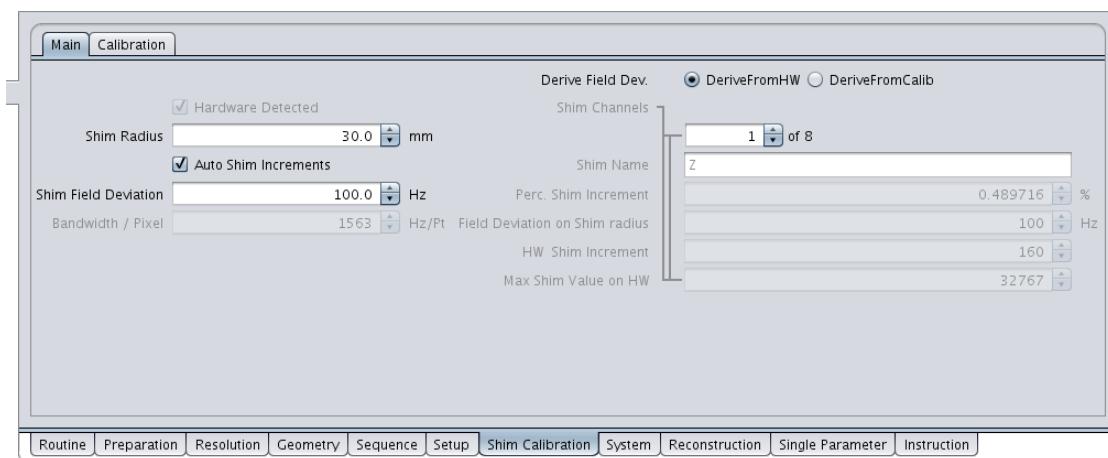


Figure 1.359: FieldMap Shim Calibration Card Main

Hardware Detected (ShimHwInfoAvail) – Shows whether all information about the actual shim hardware is available on software level. It should always appear activated and this parameter is not editable.

Shim Radius (ShimRadius) – Defines the radius of the sphere (displayed in the Geometry Editor) that is used to examine the shim fields during shim calibration. It is not editable in case **Use default FOV** (see [Routine Card \[▶ 399\]](#)) is activated. Thus, modification of the shim radius requires **Use default FOV** to be deactivated. Note: It is not possible to change the spherical shim volume in the Geometry Editor. It will always be a centered sphere.

Auto Shim Increments (ShimIncAuto) – If activated shim increments for different shim coils are calculated according to the desired field deviation (see [Shim Field Deviation \[▶ 402\]](#)) using sensitivity information from previous calibrations (**Derive Field Dev.** = `DeriveFromCalib`) or based on hardware specifications (**Derive Field Dev.** = `DeriveFromHW` (see [Derive Field Dev. \[▶ 402\]](#))). If deactivated the parameter [Shim Channels \[▶ 402\]](#) becomes editable and shim increments may be specified manually.

Shim Field Deviation (ShimFieldDev) – Specifies the maximum field deviation within the specified sphere (as shown in the Geometry Editor) caused by shims during the calibration procedure. This parameter is shown if [Auto Shim Increments \[▶ 402\]](#) is activated. For the standard protocols a value of 100 Hz is sufficient for shim field mapping without distortions of the map due to high values of shim increments.

Bandwidth / Pixel (PixelBW) – Displays the imaging bandwidth divided by the number of data points acquired in readout direction. Shim field deviations should be one order of magnitude lower than the pixel bandwidth to prevent shifts of the imaging pixels in readout direction. To minimize the effect of spatial distortions of the field maps due to the additional shim fields it is recommended to use a value of about 10-20% of the **Bandwidth / Pixel** value.

Derive Field Dev. (ShimFieldDevMode) – Derives the source of sensitivity information for shims to be calibrated (see [Auto Shim Increments \[▶ 402\]](#)).

Shim Channels (ShimChannels) – Parameter array used to specify the shim coils that should be calibrated and the increment of the shim during the calibration procedure. The size of this array depends on the number of available shims for the given scanner hardware. This parameter is editable only in case [Auto Shim Increments \[▶ 402\]](#) is deactivated. For each shim channel the following set of entries are available:

.Shim Name (.name) – Unique name of the shim coil that is controlled by this shim channel. This field cannot be modified by the user.

.Perc Shim Increment (.incr) – Defines the percentage of the maximum shim strength. The shim is increased during the calibration process. Setting this field to 0 % will deactivate the calibration of this shim. Shim X,Y,Z and Z2 cannot be deactivated. Any input will be constrained to be positive and below or equal to 50 %. The input will be set to the closest value that can be realized by the hardware. Since shims differ in the sensitivity it is recommended to set the increment by the [.Field Deviation on Shim radius \[▶ 403\]](#).

.Field Deviation on Shim radius (.incrHz) – Defines the maximal value of the shim field inside a sphere centered in the shim system with a radius defined by [Shim Radius \[▶ 402\]](#) for the shim increased by a value defined by [.Perc Shim Increment \[▶ 403\]](#). In order to assure a similar sensitivity of the shim calibration procedure it is recommended to use the same value for all shims (automatically done if [Auto Shim Increments \[▶ 402\]](#)) is activated. Only values ≥ 0.0 Hz are accepted, a zero value will disable the calibration of the corresponding shim (not possible for linear shims and Z2).

.HW Shim Increment (.incrAbs) – Defines the shim increment in hardware units. These values are always derived from the specified [.Perc Shim Increment \[▶ 403\]](#) and the [.Max Shim Value on HW \[▶ 403\]](#).

.Max Shim Value on HW (.maxAbs) – Defines the maximum shim value in hardware units. This value is always updated according to hardware specific information.

Calibration

Parameters of this card are not editable and provide information only if a calibration of the actual shim hardware has been done previously.

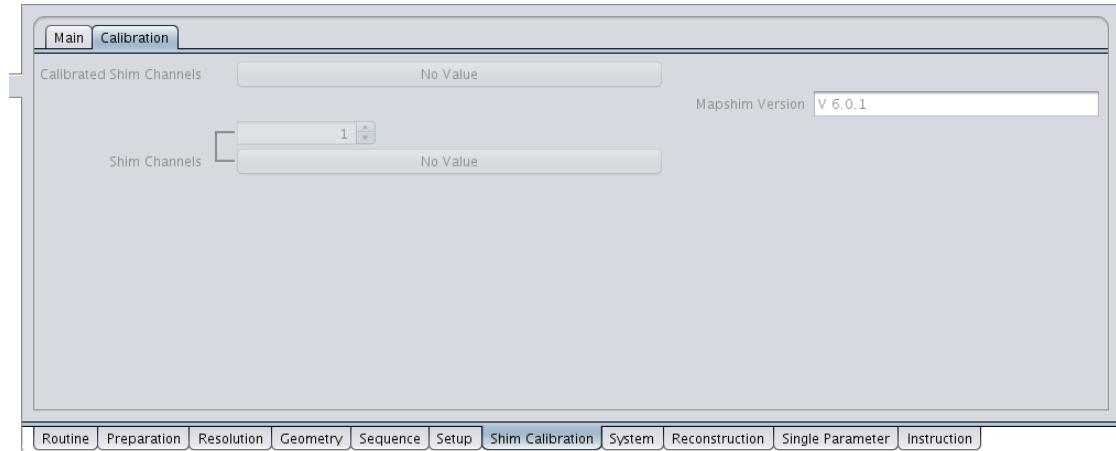


Figure 1.360: FieldMap Shim Calibration Card Calibration

Calibrated Shim Channels (PVM_ShimCoeffNcal) – Number of shim channels that can be used for shim calculations

Shim Channels (PVM_ShimCoeffChan) – Table of the calibrated shims. The table size is the value of [Calibrated Shim Channels \[▶ 403\]](#).

Mapshim Version (PVM_ShimCoeffCalVersion) – String parameter that shows the actual version of the FieldMap shim calibration

Reconstruction Card



Figure 1.361: FieldMap Reconstruction Card

Reconstruction Mode (RecoMethMode) – Defines how the data are reconstructed.

- **FieldMap:** A B0 map in units of Hz is reconstructed.
- **Magnitude:** Magnitude images reconstructed for the first and second echo are reconstructed.

Map S/N (MapSnr) – Signal-to-noise threshold for B0 fieldmap reconstruction: Only the pixels which reach the given signal-to-noise threshold are taken into account for the reconstruction process.

Result Card

The Result parameter card is only visible in the Adjustment Platform. Dependent on the application it is visible for the On Demand protocol based adjustment B0 Map which is used to measure a fieldmap of the object that is used in a study to calculate shims or it is visible for the On Demand method based adjustment Shim Calib if a protocol of FieldMap with measurement mode MapCalibration was selected in the Examination Card before the Adjustment Platform was opened. The result card consists of two cards: **Map** which is currently empty and **Shim Calibration**.

Calibration Info Card

This sub-card of the Result Card is divided in two columns: **Progress** and **Results**. The results column provides a summary of information about the calibrated coils and the leading spherical harmonic coefficients (last one after a successful calibration). The progress column shows information during the calibration procedure.

Current Adj (CurrentAdjName) – String parameter that shows the current adjustment process during the shim calibration

Calibration of Shim (CurrCalibShim) – Data structure providing information about the coil that is calibrated. It provides information only during the calibration procedure. See [Calibrated Coil](#) [405] for detailed description about the different fields of this data structure.

Report Information (CalibReportInfo) – String parameter informing which dataset needs to be selected to create a calibration report file

Calibrated Coil (CalibShims) – Parameter array providing information about the coils that are calibrated. The array size is the number of shims with nonzero shim increments as specified in the [Shim Calibration Card \[▶ 401\]](#). For each calibrated coil the following information is available:

Coil Name (.name) – Unique name of the shim coil that is calibrated

Max Current (.lmax) – Maximum current that can be applied on this shim coil in units of A.

Inc Current (.linc) – Current increment during calibration in units of A

Identifies (.ld) – Unique hardware identifier of this shim coil

Coefficients (CalibShimCoeff) – Leading spherical harmonic coefficients in units of Hz/cm^{Order} for the maximum shim. The spherical harmonic norming convention is according to the definition of Romeo and Hoult (see [References \[▶ 692\]](#)). These values are displayed after a successful calibration.

1.9.37 POSITION

1.9.37.1 Principles

A simple spin-echo sequence is applied to produce a one-dimensional projection of the object on a selected gradient direction.

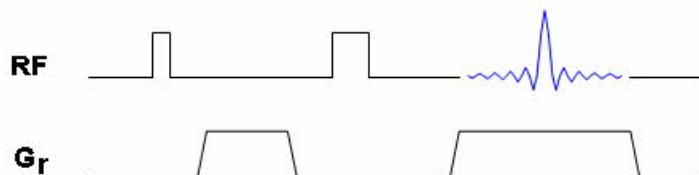


Figure 1.362: Pulse Sequence of Position

1.9.37.2 Applications

The method is intended for a rapid positioning of the animal in the magnet. It usually runs in the setup mode and the projection is visualized in the Acq/Reco Display. The positioning usually takes place before the automatic scanner adjustments are performed. Therefore the basic frequency adjustment should be started manually using the Adjustment Platform. Also the RF pulse power needs to be optimized manually using the sliders on the Setup Card (for this purpose deactivate the automatic calculation of Pulse Amplitudes).

1.9.37.3 Specific Parameters

Routine Card

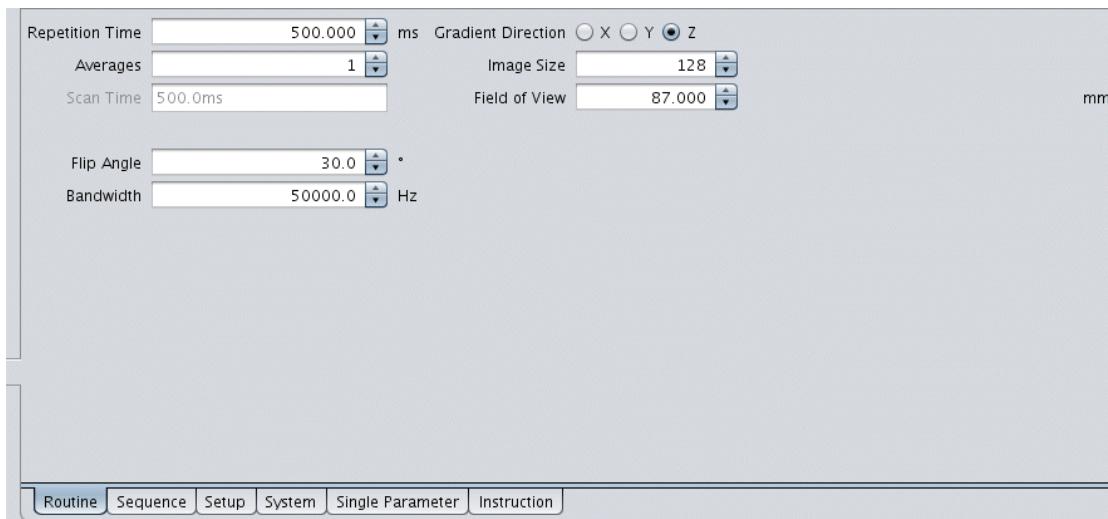


Figure 1.363: Position Routine Card

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse

Bandwidth (PVM_EffSWh) – Acquisition bandwidth

Gradient Direction (GradientDirection) – Selects the direction of the readout gradient. The default value is Z giving the projection of the object along the magnet axis.

Field of View (PVM_Fov) – Parameter of the Geometry class defining the field of view along the selected gradient axis

Sequence Card

Main

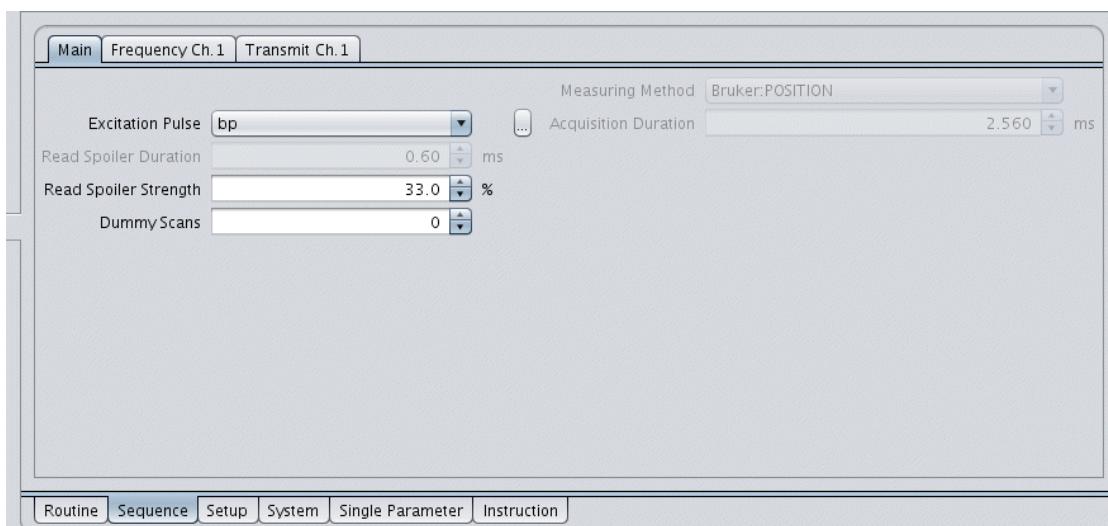


Figure 1.364: Position Sequence Card Main

Excitation Pulse (ExcPulse1Enum) – Describes the non-selective excitation pulse

Read Spoiler Duration (ReadSpoilerDuration) – Duration of the gradient spoiler

Read Spoiler Strength (ReadSpoilerStrength) – Strength of the gradient spoiler

Dummy Scans (NDummyScans) – Number of dummy scans

1.9.38 CPMG

1.9.38.1 Principles

The sequence consists of a non-selective 90° RF pulse followed by a train of orthogonal non-selective 180° RF pulses, according to the CPMG sequence, with optional gradient spoilers.

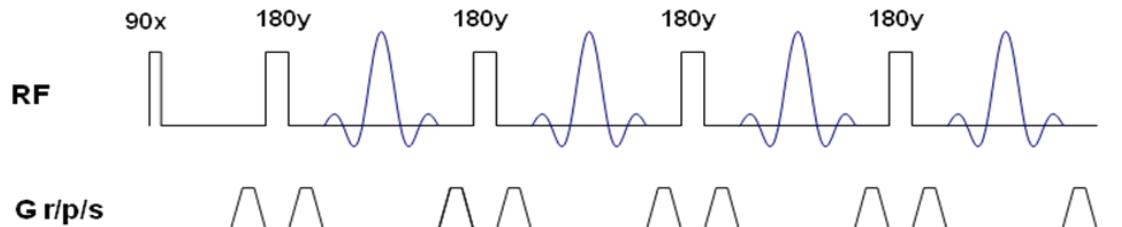


Figure 1.365: Pulse Sequence of CPMG

1.9.38.2 Applications

Non localized measurement of T2

1.9.38.3 Specific Parameters

Routine Card

Echo Spacing	20.00	ms	Echoes	12	
Repetition Time	1000.000	ms	<input checked="" type="checkbox"/> Spoiler		
Averages	1		Spoiler Duration	1.00	ms
Scan Time	0h0m1s0ms		Spoiler Strength	10.0	%

[Routine](#) [Spectroscopy](#) [Contrast](#) [Sequence](#) [Setup](#) [System](#) [Reconstruction](#) [Single Parameter](#) [Instruction](#)

Figure 1.366: CPMG Routine Card

Echo Spacing (EchoSpacing) – Time between the centers of consecutive echoes

Echoes (NEchoes) – Defines how many echoes are acquired

Spoiler (SpoilerOnOff) – Switches on gradient spoiler around the refocusing RF pulses

Spoiler Duration (Spoiler_duration) – Duration of the gradient spoiler

Spoiler Strength (Spoiler_strength) – Strength of the gradient spoiler

Software Manual

Contrast Card

Main

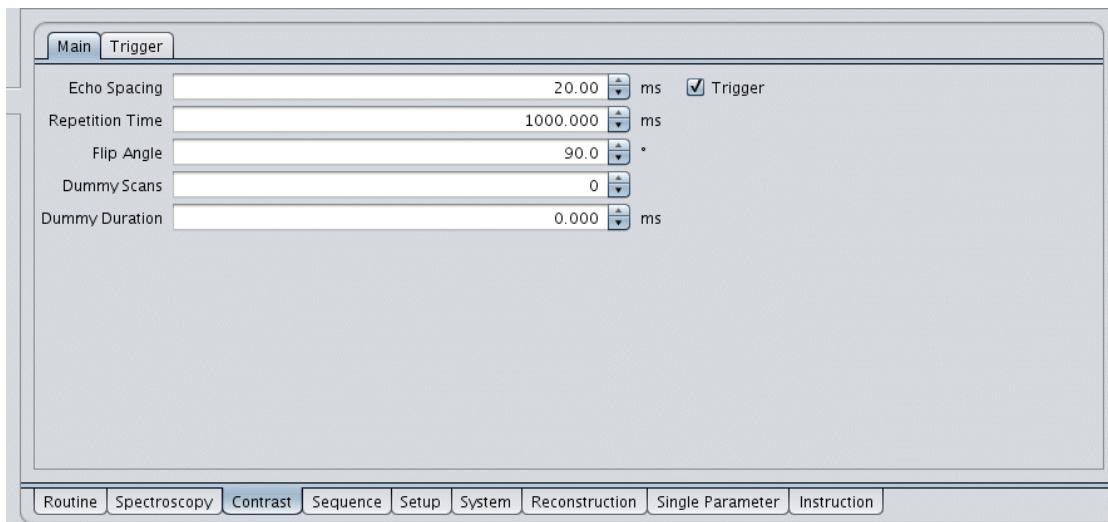


Figure 1.367: CPMG Contrast Card Main

Echo Spacing (EchoSpacing) – See [Routine Card \[▶ 407\]](#)

Flip Angle (ExcPulse1.Flipangle) – Flip angle of the excitation pulse, typically set to 90 degrees

Sequence Card

Main

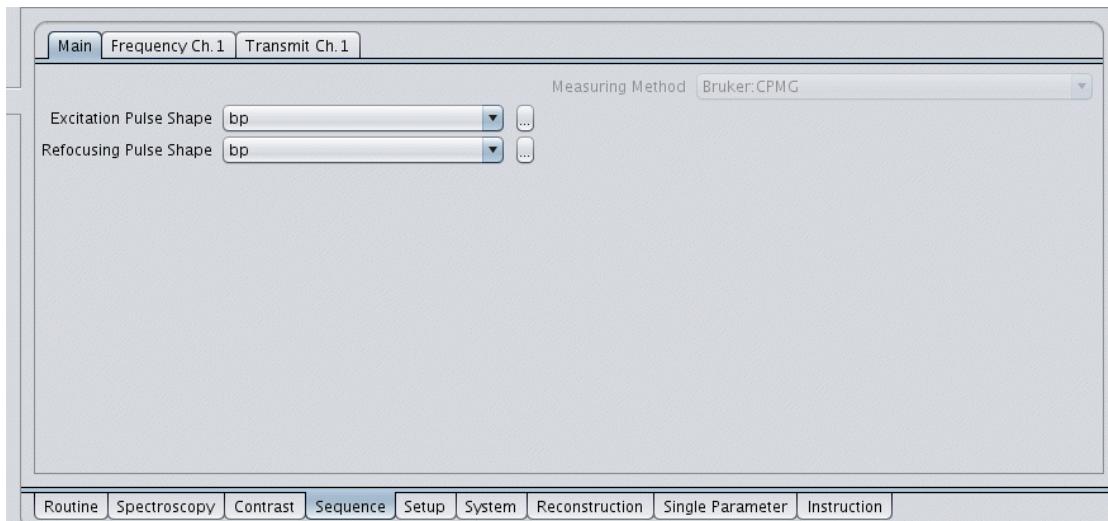


Figure 1.368: CPMG Sequence Card Main

Excitation Pulse Shape (ExcPulse1Enum) – Pulse shape used for excitation

Refocusing Pulse Shape (RefPulse1Enum) – Pulse shape used for refocusing

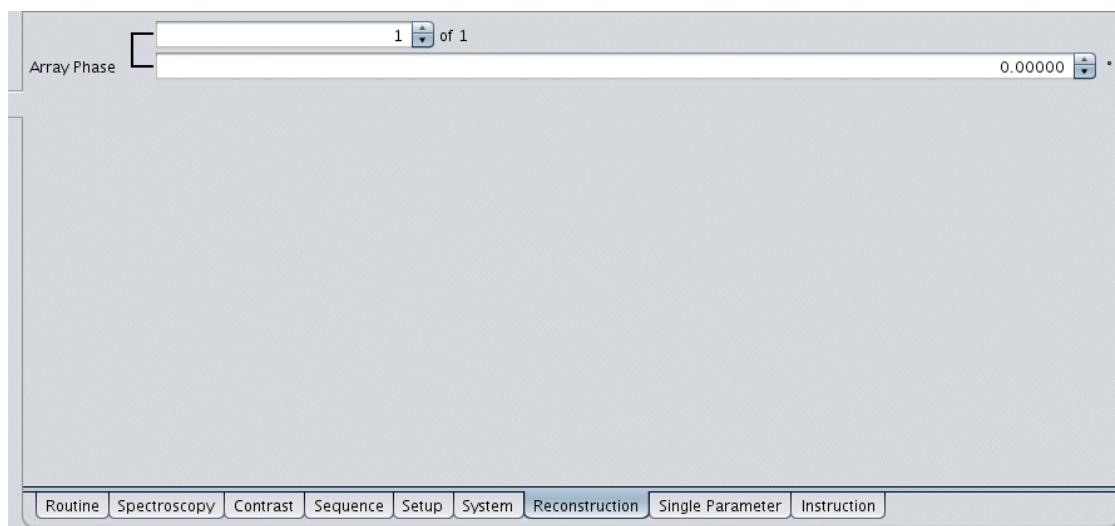
Reconstruction Card

Figure 1.369: CPMG Reconstruction Card

Array Phase (ArrayPhase) – Phase correction values for array coil combination

1.9.39 RfProfile (Method to measure RF Profiles)

1.9.39.1 Principles

The sequence consists of a slice-selective spin-echo with an optional inversion/saturation-recovery preparation. One of the three RF pulses is the selective pulse under investigation, while the remaining ones are hard pulses. The echo is read out in the presence of the same gradient as the one used for the slice selection. This gives a direct one-to-one mapping of the pulse profiles into the frequency domain detected under the read gradient.

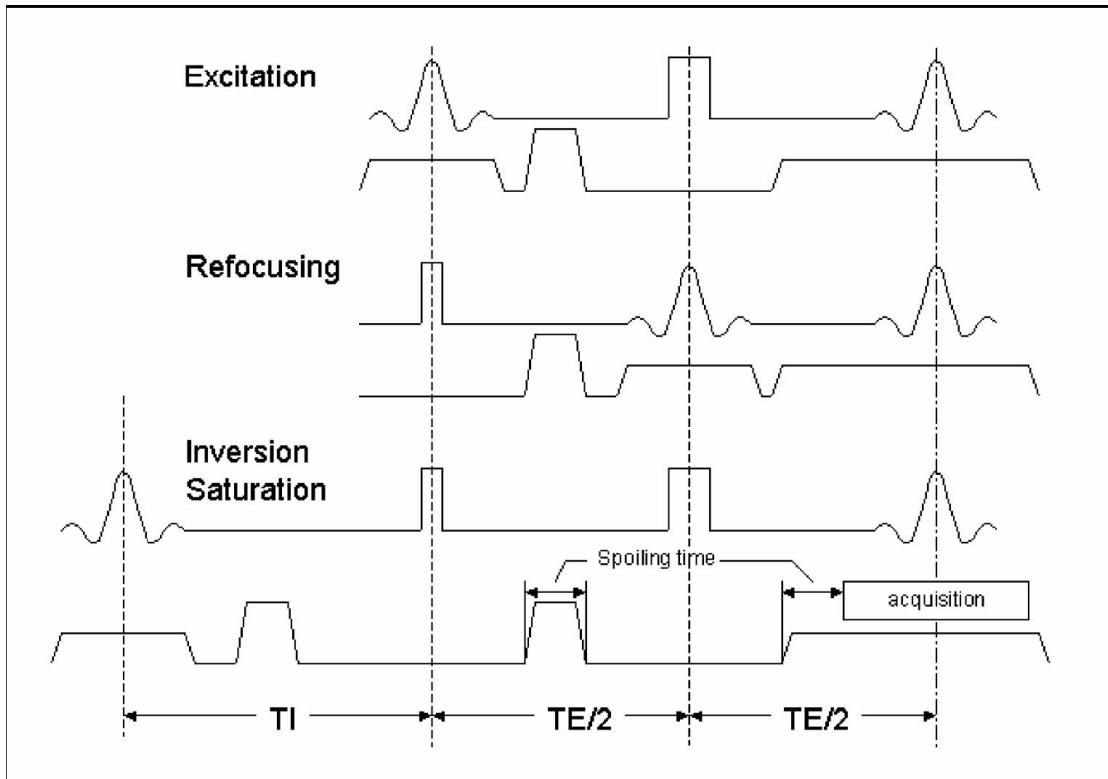


Figure 1.370: Pulse sequence of RfProfile

1.9.39.2 Applications

Investigation of excitation, refocusing, inversion or saturation pulse profiles

1.9.39.3 Specific Parameters

Routine Card

Echo Time	14.004 ms	Gradient Direction	<input type="radio"/> X_dir <input type="radio"/> Y_dir <input checked="" type="radio"/> Z_dir
Repetition Time	500.000 ms	Profile Mode	Excitation_Profile
Averages	1	Image Size	256
Repetitions	1	Field of View	50.000 mm
Scan Time	500.0ms		
Examined Exc. Pulse	gauss	<input type="checkbox"/> Derive Examined Pulse Ampl	
Examined Rfc. Pulse	gauss	<input type="checkbox"/> Derive Hard Pulse Ampl	
Examined Inv. Pulse	gauss	If calculated, then:	
Duration of Hardpulse	0.0640 ms	Conventional	

Figure 1.371: RfProfile Routine Card

Depending on the Profile Mode the corresponding RF pulse under investigation can be specified with the following parameters:

- **Examined Exc. Pulse** (SPExamExcEnum)
- **Examined Rfc. Pulse** (SPExamRfcEnum)
- **Examined Inv. Pulse** (SPExamInvEnum)

Duration of Hardpulse (HardPulse.Length) – Determines the duration of the used hard pulses

Gradient Direction (GradientDirection) – Selection of the gradient direction (X, Y, Z)

Profile Mode (ProfileMode) – The user can select four different operation modes:

- Excitation_Profile
- Refocusing_Profile
- Inversion_Profile
- Saturation_Profile

Inversion / Saturation Delay (InversionTime) – Relaxation delay after inversion/saturation pulse

Field of View (PVM_Fov) – One-dimensional FOV can be defined and should have a meaningful size with regard to the phantom size.

Derive Examined Pulse Ampl (DeriveExaminedPulseGain) – Automatic derivation of the pulse amplitude of the examined pulse

Derive Hard Pulse Ampl (DeriveHardPulseGain) – Automatic derivation of the pulse amplitude of the hard pulse

If calculated, then (PulseAlg) – If calculated RF pulses are used the algorithm can be specified.

Sequence Card

Main

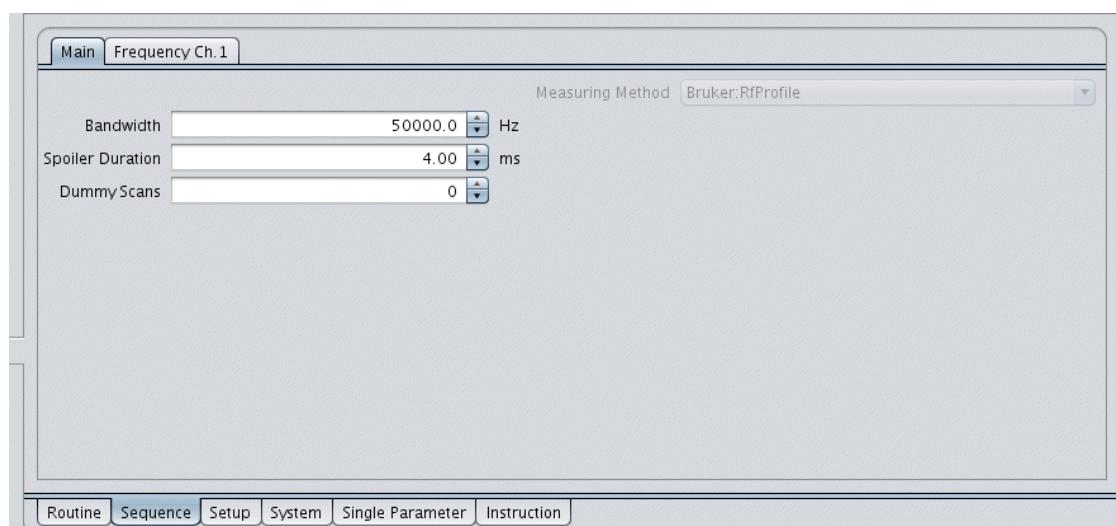


Figure 1.372: RfProfile Sequence Card Main

Spoiler Duration (Spoiler_duration) – Duration of the spoiler between excitation and refocusing pulses, equal to the duration of the readout pulse before the start of the acquisition

Dummy Scans (Ndummy) – Number of dummy scans

1.9.39.4 Handling

The method is intended for expert users. A proper initialized protocol for measuring an excitation profile can be found in the BrukerMethods location. The user can select a different mode (excitation, refocusing, inversion, saturation) and a different pulse shape and length, as well as the spectral parameters (bandwidth, size), field of view and selection gradient direction. The amplitude of the RF pulses should be set manually. For that purpose the sliders on the Setup Card can be used. The profiles are shown in the Acq/Reco Display window and can be transferred to Topspin for processing.

1.10 Import / Export

1.10.1 Overview

ParaVision contains an import / export framework that allows to export

- protocols and scan programs
- user defined source and binary PVM methods
- user defined pulse programs
- coil configurations
- adjustment configurations
- datasets (subjects, studies, examinations, image series)

The Import / Export framework creates a file in a format that ParaVision can import.

In ParaVision this information is user specific. For example, if a user acquires several images or creates Protocols and Scan Programs these cannot be seen or used by other users. To share this information with other users the information must be exported and then imported by the other user.

Additionally, ParaVision can

- transfer and archive datasets to files, FTP servers, SFTP servers, and DVDs
- send Datasets and Subject information to other (remote) ParaVision versions
- export datasets to DICOM objects (files or DICOM servers)
- import DICOM files from different modalities (e.g. CT, MR, CR)
- import legacy datasets (created with previous ParaVision versions)

In general:

- Export means that all selected items are exported into a single local file.
- Transfer does only work for datasets and means that each selected item (e.g. study) is exported into a separate file. The files can be stored in a directory, transferred to an FTP/SFTP server, or written on a DVD.
- Archive is similar to Transfer but the destination is memorized (registered) in ParaVision. This allows a semi-automatic retrieve of the archived datasets.

1.10.2 The Import / Export Framework

The framework allows import and export in a common way. This chapter describes the import / export of

- protocols and scan programs
- user defined source and binary PVM methods

- user defined pulse programs
- coil configurations
- adjustment configurations

The Export / Archive / Transfer of datasets is described in detail in Chapter [Export / Transfer / Archive of Datasets \[420\]](#).

1.10.2.1 Public and Private Export Locations

Two special export locations are defined:

- Public or Share
The exported files can be seen and imported by all users of this ParaVision version.
- Private
The exported files can only be seen and imported by the user who performed the export.

1.10.2.2 Common Import / Export Dialogs

The Import / Export framework provides common dialogs that are described in this section.

1.10.2.2.1 Export To Public Location Dialog

The Export To Public Location dialog is used for the export of

- user defined source and binary PVM methods
- user defined pulse programs
- coil configurations
- adjustment configurations

As an example in Figure [Dialog: Export to Public \(example\) \[413\]](#) the dialog for the export of PVM source methods is shown.

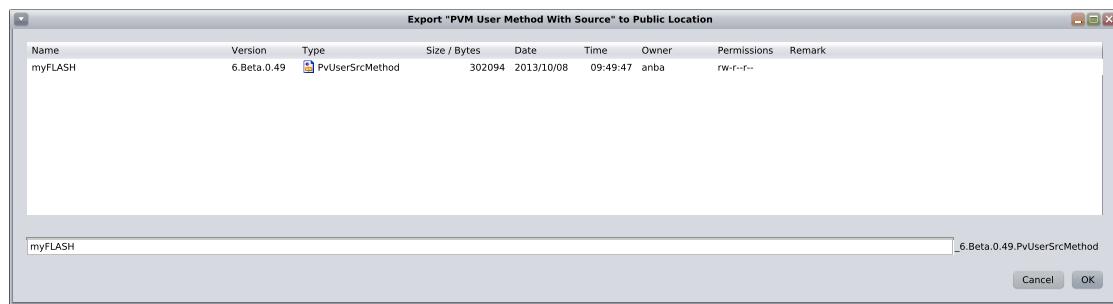


Figure 1.373: Dialog: Export to Public (example)

The dialog contains a table that shows all exported files of the same type (e.g. source methods).

- The **Name** column shows the name of the exported files.
- The **Version** column shows the ParaVision version from which the files were exported.
- The **Type** column shows the type of the exported objects:
 - **PvUserSrcMethod** for user defined PVM methods with source code
 - **PvUserBinMethod** for user defined PVM binary methods
 - **PvUserPulseProgram** for user defined pulse programs
 - **PvAdjConf** for adjustment configurations
 - **PvCoilConfig** for coil configurations

- **PvProtocols** for protocols and scan programs
- **PvDatasets** for datasets
- The **Size / Bytes** column shows the size of the exported files in bytes.
- The **Date** column shows the creation date of the exported files.
- The **Time** column shows the creation time of the exported files.
- The **Permission** column shows the file permissions of the exported files.
- The **Remark** column shows remarks that have been stored with the exported files.

In the dialog a unique export file name must be specified. Clicking the **OK** button performs the actual export.

1.10.2.2.2 Export To Custom Location Dialog

The Export To Custom Location is used for datasets (Projects, Sessions, Subjects, Studies, Examinations, Image Series), Protocols, and Scan Programs. For example, figure [Dialog: Export to Custom Location \(example\) \[414\]](#) shows the dialog for datasets.

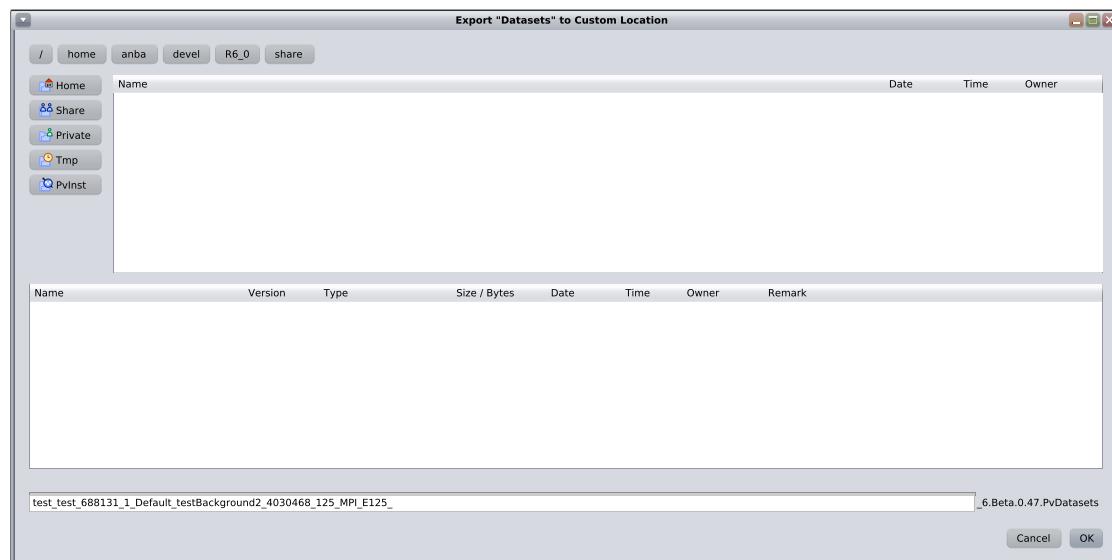


Figure 1.374: Dialog: Export to Custom Location (example)

The user can select

- destination directory presets with the button column on the left side
 - **Home**
HOME directory of the current user
 - **Share**
Public directory for all users of this ParaVision version where exported files can be shared between users (<PvInstDir>/share)
 - **Private**
Private directory in the current ParaVision version where the user can save information (<PvInstDir>/prog/curdirc/<User>/ParaVision/private)
 - **Tmp**
Standard temporary directory of the operating system
 - **PvInst**
Installation directory of the used ParaVision version

- the destination sub-directory in the directory selection list or via the button row above the table
- the name of the export file. A default name is given. The default name is constructed from the selected objects to export. For example, a Study export file name includes the subject name, the Subject identification, and the Study identification. The version number of the current ParaVision version and a suffix identifying the type of export (e.g. for dataset export it is **PvDatasets**) is automatically added.

The dialog also shows a table that contains the exported files of the given type in the selected directory. This table has the same structure as the table of the Export To Public Location dialogs described in Chapter [Export To Public Location Dialog \[413\]](#).

1.10.2.2.3 Import From Public / Private Location Dialog

The Import from Public / Private Location dialog is used for all exported entities.

For example, for datasets this dialog is shown in Figure [Dialog: Import from Public/Private Location \(example\) \[415\]](#).

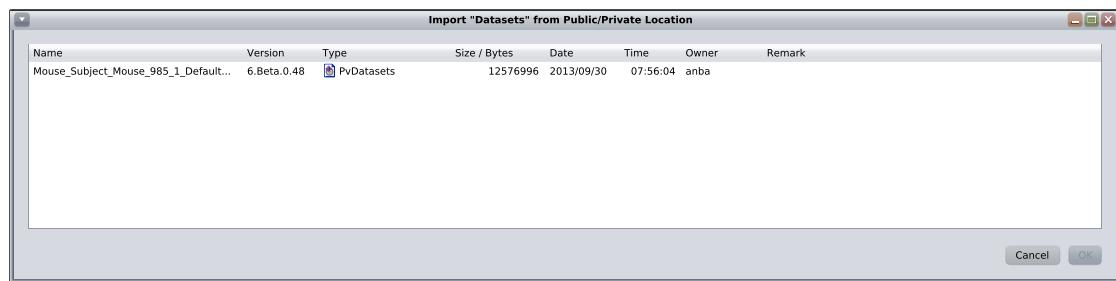


Figure 1.375: Dialog: Import from Public/Private Location (example)

The dialog contains a table that shows exported files in Public and/or Private Locations in the rows. The table has a similar format than the table in the Export To Public Location dialog described in Chapter [Export To Public Location Dialog \[413\]](#).

Select a row in the table and Click **OK** to import the given file.

In the dialog the datasets can be removed from Public / Private Location by clicking **Delete** in the context menu of a selected line in the table.

1.10.2.2.4 Import From Custom Location Dialog

The Import From Custom Location dialog is mainly used for the import of datasets, Protocols and Scan Programs. An example of such a dialog is shown in Figure [Dialog: Import "Protocols and Scan Programs" from Custom Location \[416\]](#).

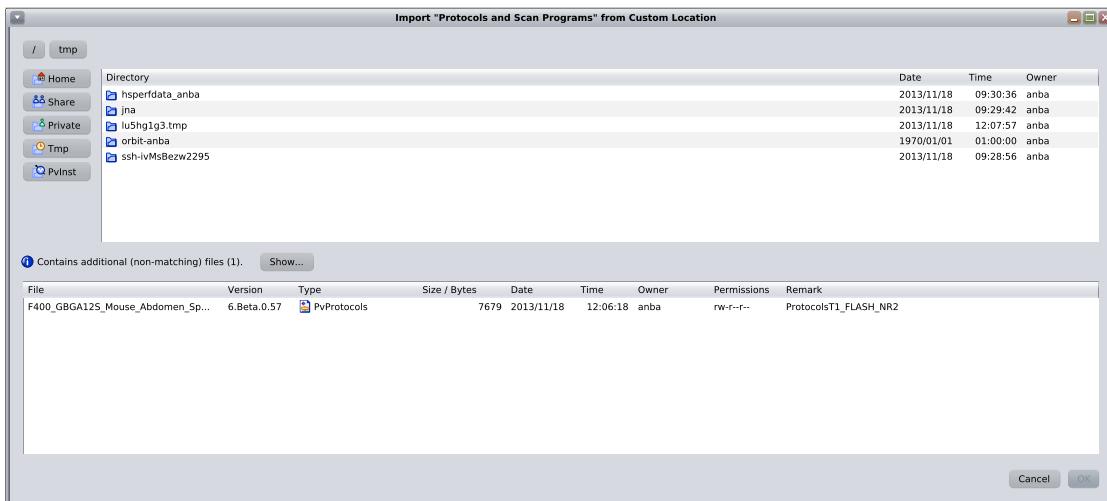


Figure 1.376: Dialog: Import “Protocols and Scan Programs” from Custom Location

The dialog has a similar format than the Export To Custom Location dialog described in Chapter [Export To Custom Location Dialog \[414\]](#).

Select an exported file in the table and click **OK** to import the file. The complete content of the file is imported, e.g. if it contains several studies all of them are imported.

Between the directory selection and the file selection part of the dialog a line **Contains additional (non-matching) files** may appear if the selected directory contains files that have the correct type extension but do not have a correct specification for the exported version. The name of these files can be seen by clicking the **Show...** button. To import these files they need to be manually renamed to match the syntax for exported files:

<name>_<version>.<type>, e.g. MySubject_60.PvDatasets

1.10.2.3 Export of Protocols

User defined Protocols are user specific and can be exported to be exchanged between ParaVision users and installations or to create backups. Bruker defined Protocols and Protocols contained in Scan Programs cannot be exported.

1. Select a Protocol
 - ▶ in the **Workspace Explorer** below the **Scan Program & Protocols** node
 - ▶ in the **Palette Explorer** of the Examination Card in the **Protocols & Scan Program** section
 - ▶ or in the **Dataset Browser**
2. Perform the export by
 - ▶ clicking **Export to File...** in the context menu of the selected Protocols or Scan Programs in the **Workspace Explorer** or **Palette Explorer**
 - ▶ or clicking the button **Export to File...** in the action row below the Protocols and Scan Programs table

An Export To Custom Location dialog (see Chapter [Export To Custom Location Dialog \[414\]](#)) opens. Select the directory and specify the name of the export file. After Clicking **OK** the Protocols are exported into a file.

1.10.2.4 Export of Scan Programs

User defined Scan Programs are user specific and can be exported to be exchanged between ParaVision users and installations or to create backups. Bruker defined Scan Programs cannot be exported.

1. Select a
 - ▶ Scan Program in the **Workspace Explorer** below the **Scan Program & Protocols** node
 - ▶ Scan Program in the **Palette Explorer** of the Examination Card in the **Protocols & Scan Program** section
 - ▶ Protocol belonging to a Scan Protocol in the **Dataset Browser**. A protocol belongs to a Scan Program if the **Scan Program** column table entry contains the name of a Scan Program.
2. Perform the export by
 - ▶ clicking **Export to File...** in the context menu of the selected Scan Programs in the **Workspace Explorer** or **Palette Explorer**
 - ▶ or clicking the button **Export Scan Program to File...** in the action row below the Protocols and Scan Programs table

An Export To Custom Location dialog (see Chapter [Export To Custom Location Dialog \[▶ 414\]](#)) opens. Select the directory and specify the name of the export file. After Clicking **OK** the Scan Programs are exported into a file.

1.10.2.5 Import of Protocols and Scan Programs

Exported Protocols and Scan Programs from any ParaVision instance can be imported into the current ParaVision version. This can be used to

- exchange Protocols and Scan Programs
- add Protocols and Scan Programs created for another gradient system to be used with the current gradient system. Protocols and Scan Programs are gradient specific. Imported Protocols and Scan Programs are assigned to the currently active gradient system independent of the gradient system stored in the exported file.

1. Use **File > Import > Protocols...** or **File > Import > Received Protocols...** to import Protocols and Scan Program.
 - ▶ **File > Import > Protocols...** allows to import from any directory on the disk.
 - ▶ **File > Import > Received Protocols...** allows to import from the Public or Private location.
2. The Import From Custom Location (see Chapter [Import From Custom Location Dialog \[▶ 415\]](#)) or Import From Public / Private Location (see Chapter [Import From Public / Private Location Dialog \[▶ 415\]](#)) dialog opens. In the Import from Custom Location dialog choose the directory where the file to import is located. In the file table choose the file containing the Protocols or Scan Programs.
3. Clicking **OK** starts the actual import which is shown in a progress bar. The imported Protocols or Scan Programs are assigned to the currently active gradient system which is shown in bold below the **Scan Program & Protocols** node of the Workspace Explorer.

1.10.2.6 Export of User Defined PVM Source or Binary Methods

User defined PVM source and binary methods are user specific and can be exported to share them between different users of a ParaVision installation. An exported binary method contains the method binary, the method editor layout file, and the pulse program of the method. An exported source method contains the complete method source code.

1. Open the Workspace Explorer using **Window > Workspace Explorer**.
2. In the Workspace Explorer open the node **Method Development > User Methods (USER)**. All user created methods are shown.
3. Select one of the methods to be exported and click **Share > As Source...** or **Share > As Binary...** in the context menu.
4. An Export To Public Location dialog opens (see Chapter [Export To Public Location Dialog \[▶ 413\]](#)) where the exported file can be stored.

1.10.2.7 Import of User Defined PVM Source or Binary Methods

The user can import source or binary methods exported from any ParaVision 6 user. This allows the exchange of methods between different ParaVision users.

1. Choose the menu entry **File > Import > Source Method...** or **File > Import > Binary Method...** or click **Import** in the context menu of **Method Development > User Methods (USER)** in the Workspace Explorer.
2. An Import From Public / Private Location Dialog opens (see Chapter [Import From Public / Private Location Dialog \[▶ 415\]](#)). Select the method file to import. After the import is finished a new item in the **Method Development > User Methods (USER)** node of the Workspace Explorer is created with the name of the new method.

1.10.2.8 Export of User Defined Pulse Programs

User defined pulse programs are user specific and can be exported to share them between different users of a ParaVision installation.

1. Open the Workspace Explorer using **Window > Workspace Explorer**.
2. Below the node **Pulse Program > User (USER)** the user created pulse programs are shown. Select the pulse program to be exported and click **Share** in the context menu.
3. An Export To Public Location dialog opens (see Chapter [Export To Public Location Dialog \[▶ 413\]](#)) where the exported file can be stored.

1.10.2.9 Import of User Defined Pulse Programs

Exported pulse programs from any ParaVision 6 user can be imported. This allows the exchange of user defined pulse programs between users.

1. Open the Workspace Explorer using **Window > Workspace Explorer**.
2. Click **Import...** in the context menu of the **Pulse Program > User (USER)** node.
3. An Import From Public / Private Location Dialog opens (see Chapter [Import From Public / Private Location Dialog \[▶ 415\]](#)). Select the pulse program file to be imported. After the import is finished a new node below the **Pulse Program > User (USER)** node of the Workspace Explorer is created.

1.10.2.10 Export of Adjustment Configurations

Adjustment configurations are user specific and can be exported to share them with other users of a ParaVision installation. The default adjustment configurations delivered by Bruker are identical and, therefore, need not to be shared. Only user defined adjustment configurations should be shared between users or spectrometers.

1. Click **Window > Configuration** and select the **Adjustments** tab in the Configuration card.
2. Select an adjustment configuration in the **Adjustments** tab.
3. Click the **Share** button. An Export To Public Location dialog opens (see Chapter [Export To Public Location Dialog \[▶ 413\]](#)) where the exported adjustment configuration can be stored.

1.10.2.11 Import of Adjustment Configurations

The goal of the import of adjustment configurations is to create a identical adjustment environment for different users or spectrometers.

1. Click **Window > Configuration** and select the **Adjustments** tab in the Configuration card.
2. Click the **Import** button in the **Adjustments** tab in the Configuration card.
3. An Import From Custom Location dialog opens (see Chapter [Import From Custom Location Dialog \[▶ 415\]](#)). Select the adjustment configuration file to import. The imported adjustment configuration is included into the list of adjustment configurations. It is not possible to import adjustment configurations with an already existing name.

1.10.2.12 Export of Coil Configurations

Coil configurations are user specific and can be exported to share them between different users or different ParaVision installations for the same spectrometer. For example, they are needed on a preparation workplace if a scan program should be prepared that should later be executed on the acquisition workspace from which the coil configuration has been exported (see Chapter [Exchange Between ParaVision Instances \[▶ 427\]](#)).

1. Click **Window > Configuration** and select the **Coil** tab.
2. In the coil configuration tree select a coil configuration to be exported and click **Share** in the context menu.
3. An Export To Public Location dialog opens (see Chapter [Export To Public Location Dialog \[▶ 413\]](#)) to store the selected coil configurations.

1.10.2.13 Import of Coil Configurations

Coil configurations are user specific. They need to be imported on a processing workplace if scan programs should be prepared that should later be performed on the acquisition workplace.

1. Click **Window > Configuration** and select the **Coil** tab.
2. Click **Import Coil Configuration...** in the context menu of the **Coil Configurations** node.
3. An Import From Public / Private Location Dialog opens (see Chapter [Import From Public / Private Location Dialog \[▶ 415\]](#)). Select the file to import. The imported coil configurations are included into the of coil configuration tree.

1.10.3 Export / Transfer / Archive of Datasets

To Export / Transfer / Archive select the desired dataset entities (Projects, Sessions, Subjects, Studies, Examinations, Image Series) and start the corresponding action.

The actions are

- **Export To File...**

All datasets belonging to the selected entities are exported into one local file. The Export To Custom Location dialog (see Chapter [Export To Custom Location Dialog \[414\]](#)) opens. Select the export directory, set a new file name or use the proposed file name and click **OK**. The entities are exported into the given file. When this file is imported all stored dataset entities are imported. It is not possible to import only a selection of the stored dataset entities.

- **Transfer...**

Each selected entity is exported into a separate file. For example, if the user selects a Study, a Subject, and an Examination then 3 different files are created. The first file contains all datasets and accompanying information from the Study, the next file from the Subject, and the last file from the Examination. The export destination must be configured in **Window > Options > Archive / Transfer** (see Chapter [Archive / Transfer \[421\]](#)). The export destinations can be a directory, a DVD, an SFTP server, or an FTP server. Depending on the configuration a selection list of transfer destinations may appear (see Figure [Select an Archive / Transfer destination \[420\]](#)).

The transfer destination is not stored in the ParaVision database. This action is mainly meant for exchange in a “fire and forget” manner.



Figure 1.377: Select an Archive / Transfer destination

- **Archive...**

Archive is an extension to Transfer where the export destination is memorized (stored) in the ParaVision database. Therefore, archive can be used for backup. The user can display the export destinations using the **Show Archive Locations...** action (see Chapter [Show Archive Locations for Datasets \[▶ 427\]](#)).

Archive and Transfer can only be used if they have been configured previously.

1.10.3.1 Export of Datasets

Datasets (Projects, Sessions, Subjects, Studies, Examinations, Image Series) are user specific. They can be exported to share them between different users of the same ParaVision installation or for backup purposes.

1. Select datasets (Projects, Sessions, Subjects, Studies, Examinations, Image Series) to be exported
 - ▶ in the **Workspace Explorer** below the **Datasets** node
 - ▶ in the **Palette Explorer** (only Image Series)
 - ▶ or in the **Dataset Browser** in the different dataset views
2. Perform the export by
 - ▶ clicking **Export to File...** in the context menu of the selected datasets in the **Workspace Explorer** or **Palette Explorer**
 - ▶ or clicking **Export to File...** in a sub-menu of the buttons below the dataset views in the **Dataset Browser**. The **Export to File...** entry can be found in the sub-menu of the second button (click on the triangular button).
3. The Export to Custom Location dialog (see section [Export To Custom Location Dialog \[▶ 414\]](#)) opens. Select the export destination directory and provide a file name or use the default file name. If the user wants to share the datasets with other ParaVision users the **Share** destination directory should be selected. After clicking **OK** the export starts. A progress bar is shown next to the main menu bar. Depending on the number and size of the selected datasets the operation may be very time consuming.

The exported datasets are registered in ParaVision (see Chapter [Show Archive Locations for Datasets \[▶ 427\]](#)).

1.10.3.2 Archive / Transfer

Datasets (Subjects, Studies, Examinations, Image Series) can be archived or transferred to files, to an FTP/SFTP server, or on a DVD. Archive and transfer are essentially the same operations but for Archive the destination (file name, FTP/SFTP server location, DVD label and location) is registered in ParaVision for retrieval purposes (see Chapter [Detach and Attach of Datasets \[▶ 430\]](#)). This means, that Transfer is meant for exchange and Archive for backup purposes.

Datasets can only be selected if image series exist that contain image data.

1. Select datasets (Subjects, Studies, Examinations, Image Series) to be exported
 - ▶ in the **Workspace Explorer** below the **Datasets** node
 - ▶ in the **Palette Explorer** (only Image Series)
 - ▶ or in the **Dataset Browser** in the different dataset views.
Datasets can only be selected if image series exist that contain image data.
2. Perform the Archive or Transfer operation by
 - ▶ clicking **Archive** or **Transfer** in the context menu of the selected datasets in the **Workspace Explorer** or **Palette Explorer**

- or clicking the **Archive** or **Transfer** button in a sub-menu of the action row below one of the dataset views. The **Archive** or **Transfer** entries can be found in the sub-menu of the second button (click on the triangular button).
3. If a default Archive or Transfer destination (see Chapter [Default Archive / Transfer Destination \[▶ 426\]](#)) is not configured a dialog requesting the Archive or Transfer destination opens (see Figure [Select Archive / Transfer Destination \[▶ 422\]](#)).
 - Select a destination and click **OK**.
 4. Depending on the destination more information may be requested:
For the FTP/SFTP destination a password may be requested (see Chapter [FTP Destination \[▶ 425\]](#)).
 - For the DISK destination the directory selection dialog where the destination directory must be specified may appear (see Chapter [DISK Destination \[▶ 423\]](#)).
 - For the DVD destination a label is requested if an Archiving operation was started. The label is used to identify the DVD. If the size of the files to archive or transfer is greater than the capacity of the DVD a dialog appears where the user can limit the datasets to be archived or transferred on this DVD (see Chapter [DVD Destination \[▶ 424\]](#)).
 5. The Archive / Transfer operation starts. A progress bar is shown next to the main menu bar. Depending on the number and size of the selected datasets the operation may be very time consuming.



Figure 1.378: Select Archive / Transfer Destination

1.10.3.2.1 General Archive / Transfer Configuration

Before using the Archive / Transfer actions these actions must be configured using **Window > Options > Archive / Transfer**.

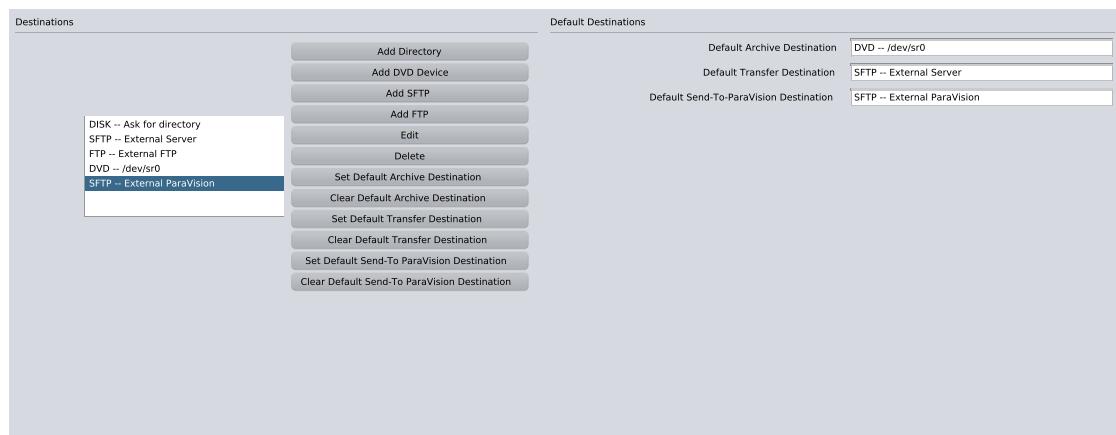


Figure 1.379: Archive / Transfer configuration options

The dialog consists of

- a list of configured Archive / Transfer destinations. The destinations are named using the destination type, 2 dashes, and the transfer destination name (e.g. **SFTP – External Server**). Supported destination types are
 - DISK: directory on a mounted file system (see Chapter [DISK Destination \[▶ 423\]](#))
 - DVD: recordable DVD (see Chapter [DVD Destination \[▶ 424\]](#))
 - SFTP: SFTP server (see Chapter [SFTP Destination \[▶ 425\]](#))
 - FTP: FTP server (see Chapter [FTP Destination \[▶ 425\]](#))
- a button column where destinations can be added, removed, and edited. It is also possible to make a specific destination the default for Transfer or Archiving.
- some text fields displaying the default destinations for Archive / Transfer and Send-To (see Chapter [Exchange Between ParaVision Instances \[▶ 427\]](#))

1.10.3.2.2 DISK Destination

ParaVision can archive or transfer to a directory. For example, the destination directory can be mounted from a network server (e.g. a NAS) or from an USB disk, etc. The destination directory must be writable by the current user.

To configure the DISK destination:

1. Open the **Window > Options > Archive / Transfer** dialog.
2. Click the **Add Directory** button to configure a DISK destination.
3. A dialog opens in which the user can choose:
 - ▶ **Ask User for Destination Directory**
The user is asked to choose a destination directory every time an archive or transfer with this destination is performed.
 - ▶ **Choose Default Destination Directory**
A new directory selection dialog appears where the user can select the default destination directory. If the user starts an archive / transfer operation using this destination the configured directory is used to store the exported files.
4. Confirm the DISK destination using the **OK** button in the **Add Destination Directory** dialog. A directory destination line in the list of destinations is added displaying the absolute directory path if a directory is configured or **Ask for directory**.

1.10.3.2.3 DVD Destination

ParaVision can transfer or archive to a DVD. All selected datasets are recorded to one DVD. Then the DVD is finalized. It is not possible to record further datasets on the DVD. The type of supported DVDs depends on the used DVD recorder.

To configure a DVD destination:

1. Open the **Window > Options > Archive / Transfer** dialog.
2. Click the **Add DVD Device** button.
3. A dialog opens where the following information must be specified:
 - The **DVD Device**. If it is possible to detect a DVD device automatically the text field contains the detected device. Otherwise the text field is empty and the user must specify a valid device.
 - The **Recording Speed**. The recording speed depends on the DVD medium and the recorder. A recording speed of 2.0 is predefined but this is a very conservative speed. Most recorders and newer DVD media support higher recording speeds. But for some no-name media the speed should be 1.0. Using a speed too high may result in a corrupt DVD. The problem on the DVD may not be detected by the writer during recording.
4. After clicking **OK** a DVD entry is added to the list of destinations. The DVD line contains the device file of the DVD device.

It is possible to edit the DVD configuration in by selecting the DVD entry in the destination list and clicking the **Edit** button.

If an archive operation starts ParaVision asks to specify a label for the disk to record. This label is stored on the DVD together with the current time. It is used to identify the DVD medium and this information can be used in the semi-automatic retrieve (Attach operation, see Chapter [Attach Datasets \[▶ 431\]](#)).

After the start of the Archive and Transfer operation ParaVision checks if a recordable DVD is present in the DVD device. If this is not the case an error dialog is shown and the operation is aborted.

If the size of the archived datasets is greater than the capacity of the DVD medium a dialog (Figure [Dialog: DVD Capacity Exceeded \[▶ 424\]](#)) is shown where all files are shown and the user can choose those that should be written to the DVD. The size of the chosen files and the available space on the DVD are shown in this dialog.

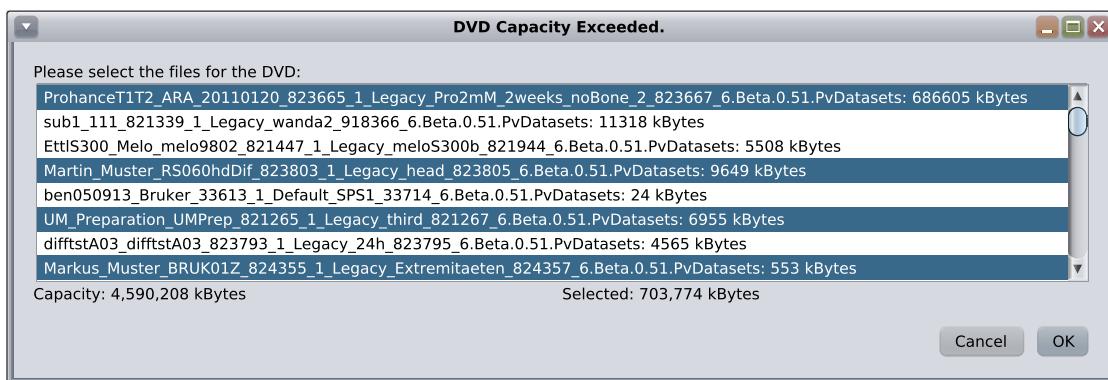


Figure 1.380: Dialog: DVD Capacity Exceeded

After the recording the DVD may be ejected from the device.

1.10.3.2.4 SFTP Destination

ParaVision can archive or transfer to an SFTP server. All selected datasets are converted into archive files and then transferred via SFTP to a remote server.

To configure an SFTP destination:

1. Open the **Window > Options > Archive / Transfer** dialog.
 2. Click the **Add SFTP** button. An **Add SFTP Destination** dialog appears (see Figure [Add SFTP Destination dialog \[▶ 425\]](#)).
- The dialog provides the following information:
- **Destination Name** is a user defined unique name which identifies this destination.
 - **Remote User** is a user name on the remote machine. The password for this user must be available to the user of this ParaVision instance.
 - **Remote Host** is the host name or IP address of the remote host.
 - **Remote Directory** is an existing directory on the remote host where the remote user can write.
3. Confirm the dialog with **OK**. An SFTP line containing the defined Destination Name is added to the list of destinations. The destination can be corrected using the Edit button.



Figure 1.381: Add SFTP Destination dialog

If an SFTP destination is used for archiving or transfer the user may be asked for the password of the remote user on the remote host. If the user provides the correct password the archive files are transferred using SFTP to the given directory on the remote host.

The password is not requested if

- the password was requested in a previous Archive, Transfer, or Send-To (see Chapter [Exchange Between ParaVision Instances \[▶ 427\]](#)) operation in the same ParaVision run
- a password-less SSH connection is configured between the local and remote computer and user

1.10.3.2.5 FTP Destination

ParaVision can archive or transfer to an FTP server. All selected datasets are converted into archive files and transferred via FTP to a remote server.

To configure an FTP destination:

1. Open the **Window > Options > Archive / Transfer** dialog.
2. Click the **Add FTP** button. An **Add FTP Destination** dialog appears that is similar to the **Add SFTP Destination** dialog from Chapter [SFTP Destination \[▶ 425\]](#) step 2. The elements have the same meaning.
3. Confirm the dialog with **OK**. An FTP line containing the defined Destination Name is added to the list of destinations. The destination can be corrected using the Edit button.

If an FTP destination is used for archiving or transfer the user may be asked for the FTP password of the remote user on the remote host. If the user provides the correct password the archive files are transferred using FTP to the given directory on the remote host.

The password is not requested if a .netrc file exists in the users home directory containing an entry for a remote host, user and password, see Linux manual page for netrc.

1.10.3.2.6 Default Archive / Transfer Destination

If the user chooses an Archive or Transfer action ParaVision opens a dialog to select an archive or transfer destination (see Figure [Select an Archive / Transfer destination \[▶ 420\]](#)). If a default destination is defined this dialog will not be shown.

Set the default destination:

1. Open the **Window > Options > Archive / Transfer** dialog.
2. Select a destination from the destination list and click the
 - ▶ **Set Default Archive Destination** button to set the default Archive destination
 - ▶ or **Set Default Transfer Destination** button to set the default Transfer destination
3. The selected default destinations are displayed in the text fields labeled with **Default Archive Destination** or **Default Transfer Destination**.

Clear the default destination:

1. Open the **Window > Options > Archive / Transfer** dialog.
2. Clear a default destination by clicking the
 - ▶ **Clear Default Archive Destination** button to clear the default Archive destination
 - ▶ or the **Clear Default Transfer Destination** button to set the default Transfer destination
3. **Default Archive Destination** or **Default Transfer Destination** are empty.

1.10.3 Import of Datasets

Datasets are user specific in ParaVision. If a different user needs to work with a dataset of another user it must be exported by the original user and imported by the user who want to work with the dataset.

Exported, archived or transferred datasets can only be imported if they are not available in the Dataset Browser or the Workspace Explorer. If they exist in the Dataset Browser or Workspace Explorer they must be removed previously to import them.

To import:

1. Choose **File > Import > Datasets...**.
2. The Import From Custom Location Dialog opens (see Chapter [Import From Custom Location Dialog \[▶ 415\]](#)) where the user can navigate through directories and choose the dataset archive file to be imported. After clicking **OK** the selected file with all included datasets is imported.

or

1. Choose **File > Import > Received Datasets...**.
2. The Import From Public / Private Location opens (see Chapter [Import From Public / Private Location Dialog \[▶ 415\]](#)) and the import file can be chosen from the list of dataset files. The list includes all dataset files that are shared by other users. After clicking **OK** the selected file with all included datasets is imported.

The imported datasets (Projects, Sessions, Subjects, Studies, Examinations, Image Series) can easily be found in the **Recent Imports** presets of the Data Browser. The displayed table can be sorted by the **Imported At** column to find the latest imports.

1.10.3.4 Show Archive Locations for Datasets

Archive and Export register the destination locations in ParaVision. This information can be used to

- semi-automatic retrieve the dataset using the Attach operation (see Chapter [Attach Datasets \[▶ 431\]](#))
- find exported or archived dataset files

To show the destination locations of archived or exported datasets:

1. Select an exported or archived dataset (Subject, Study, Examination, Image Series)
 - ▶ in the **Workspace Explorer** below the **Datasets** node
 - ▶ in the **Palette Explorer** (only Image Series)
 - ▶ or in the **Dataset Browser** in the different dataset views
2. Open a dialog containing a list of export or archive locations by
 - ▶ clicking **Show Archive Locations...** in the context menu of the selected dataset in the **Workspace Explorer**
 - ▶ or clicking the **Show Archive Locations...** button in a sub-menu of the action row below one of the dataset views. The **Show Archive Locations...** entry can be found in the sub-menu of the second button (click on the triangular button).

1.10.4 Exchange Between ParaVision Instances

ParaVision supports the exchange of datasets and subject information between users and ParaVision installations on different workstations. Datasets can be subjects (containing all studies, examinations, etc), studies, or examinations.

For example, a study can be prepared on a secondary datastation computer and then be sent to the spectrometer workstation where it will be measured. In this case the datastation ParaVision installation must be configured similar to the acquisition ParaVision installation. To achieve this the spectrometer configuration, the used coil configuration and the used adjustment configuration (if user defined) must be exported from the acquisition ParaVision installation and manually transferred to the preparation workstation. On the preparation workstation the exported spectrometer configuration must be imported as datastation into the preparation ParaVision version (see Migration document). Additionally, the exported coil configuration and adjustment configuration must be imported by the user of the acquisition ParaVision installation (see Chapter [Export of Coil Configurations \[▶ 419\]](#) and [Export of Adjustment Configurations \[▶ 419\]](#)).

The exchange of datasets can also be used to process acquired images on a secondary processing workstation. In this case all acquired images can be sent to a user of a ParaVision installation on the processing workstation.

Subject information are attributes of the subject (like subject name, id, etc). These subject only attributes can also be exchanged between users of different ParaVision installations. For example, it is possible to create a subject on a spectrometer workstation and distribute it to another spectrometer workstation where the subject should be examined. It is not necessary to provide the information on every workstation manually.

1.10.4.1 Configuration

The exchange destinations are configured as special Archive / Transfer destinations (**Window > Options > Archive / Transfer** dialog, see Chapter [General Archive / Transfer Configuration \[▶ 422\]](#)). Only destinations of type SFTP and DISK can be used as Send-To

(exchange) destinations. The exchange destination directory is the Import/Export Private Location (see Chapter [Public and Private Export Locations \[▶ 413\]](#)) of the user of the (remote) ParaVision installation.

- For SFTP the **Remote Directory** (see Chapter [SFTP Destination \[▶ 425\]](#) and Figure [Add SFTP Destination dialog \[▶ 425\]](#)) must be configured as the Private Location of a remote ParaVision user and installation. The Private Location of a user is defined as

```
<PvInstDir>/prog/curdir/<USER>/ParaVision/private
```

where

- <PvInstDir> is the ParaVision installation directory on the remote computer.
- <USER> is a valid user of the ParaVision installation on the remote computer.

The **Remote User** must be configured as a user of the ParaVision installation on the remote computer and must be the same as the <USER> in the **Remote Directory**.

- For DISK (see Chapter [DISK Destination \[▶ 423\]](#)) the Private Location of a user of a remote ParaVision installation must be configured. For example, the ParaVision installation directory of the remote computer may be mounted read-writable via NFS to /mnt/RemoteHost. In this case the DISK destination must be configured to /mnt/RemoteHost/prog/curdir/<USER>/ParaVision/private. <USER> must be the same user on the local and remote machine. This user must have the same Linux user identification (UID) on both systems. Otherwise the operating system prevents the sent datasets to be written into the Private Location because of permission problems.

To set the exchange (Send-To) destination:

1. Open the **Window > Options > Archive / Transfer** dialog.
2. Select a valid SFTP or DISK destination from the destination list.
3. Click the **Set Default Send-To ParaVision Destination** button.
4. The new default destination is displayed in the **Default Send-To ParaVision Destination** text field.

To clear the exchange (Send-To) destination:

1. Open the **Window > Options > Archive / Transfer** dialog.
2. Click the **Clear Default Send-To ParaVision Destination** button.
3. The **Default Send-To ParaVision Destination** text field is cleared.

1.10.4.2 Send Datasets to ParaVision

Datasets (Studies, Examinations, or Image Series) can be exchanged between ParaVision installations on different computers

- to prepare studies (scan programs) on a preparation station and acquiring (performing) them on the spectrometer station
 - to send acquired Image Series to a remote processing station to view and process them
1. Select datasets (Studies, Examinations, Image Series) to be exported
 - ▶ in the **Workspace Explorer** below the **Datasets** node
 - ▶ in the **Palette Explorer** (only Image Series)
 - ▶ or in the **Dataset Browser** in the different dataset views
 2. Send Datasets to a remote ParaVision installation by
 - ▶ clicking **Send Datasets to ParaVision...** in the context menu of the selected datasets in the **Workspace Explorer** or **Palette Explorer**

- ▶ or clicking the **Send Datasets to ParaVision...** button in a sub-menu of the action row below one of the dataset views. The **Send Datasets to ParaVision...** entries can be found in the sub-menu of the second button (click on the triangular button).
The operation can only start if a valid default Send-To destination has been configured (see Chapter [Configuration \[427\]](#)).
3. If the default Send-To destination is an SFTP server a password may be requested (see Chapter [FTP Destination \[425\]](#)).
 4. The operation is performed in the same way as the corresponding transfer operation (see Chapter [Export / Transfer / Archive of Datasets \[420\]](#)). The entire selected subjects, studies, or examination are transferred to the Private Location of a user of the remote ParaVision installation.

1.10.4.3 Import Received Datasets

After datasets are sent to a user of a remote ParaVision installation, they can be received. For example, this allows to import prepared studies which should be acquired on a spectrometer station or acquired images that should be processed on a processing station.

To import sent datasets:

1. Choose **File > Import > Received Datasets...** .
2. The Import From Public / Private Location opens (see Chapter [Import From Public / Private Location Dialog \[415\]](#)). Select the sent file from the list of dataset files. This list includes all dataset files from the Private Location of the current user. After clicking **OK** the selected file with all included datasets is imported.
3. After the successful import the datasets can be deleted from the Private Location by clicking the context menu entry **Delete** on a selected entry in the table of dataset files.

Received datasets can easily be found in the **Recent Imports** presets in one of the dataset views in the Data Browser. The displayed table can be sorted by the **Imported At** column to find the latest imports.

1.10.4.4 Send Subject Information to ParaVision

Subject identifying information can be provided once in a spectrometer station and then distributed to another spectrometer stations. Different studies can be set up and acquired on the two spectrometers which are assigned to the same subject.

The Send Subject Information to ParaVision operation can only start if a valid default Send-To destination is configured (see Chapter [Configuration \[427\]](#)).

To distribute subject information to a user of a remote ParaVision installation:

1. Select Subject information to be exported
 - ▶ in the **Workspace Explorer** below the **Subject Datasets** node
 - ▶ or in the **Dataset Browser** in the **Subject** views
2. Send Subject information to a user of a remote ParaVision installation by
 - ▶ clicking **Send Subject to ParaVision...** in the context menu of the selected Subject in the **Workspace Explorer**
 - ▶ or clicking the **Send Subject to ParaVision...** button in a sub-menu of the action row below the **Subject** view. The **Send Subject to ParaVision...** entry can be found in the sub-menu of the second button (click on the triangular button).

If the default Send-To destination is an SFTP server the remote user password may be requested (see Chapter [SFTP Destination \[425\]](#)).

3. The operation is performed in the same way as the corresponding transfer operation (see Chapter [Export / Transfer / Archive of Datasets \[▶ 420\]](#)). The selected Subject information is transferred to the Private Location of the user of the remote ParaVision installation.

1.10.4.5 Import Received Subjects

Subject identifying information can be entered once on a spectrometer station and then distributed to another spectrometer station. Different studies can then be set up and acquired on the two spectrometers referring both to the same subject.

To import Subjects sent from another station

1. choose **File > Import > Received Subjects...**
2. The Import From Public / Private Location opens (see Chapter [Import From Public / Private Location Dialog \[▶ 415\]](#)). Select the sent subject information file from the list of files and click **OK**.
3. After the successful import the subject file can be deleted from the Private Location by clicking **Delete** in the context menu of the selected entry.

Received datasets can easily be found in the **Recent Imports** presets of the **Subject** view in the Data Browser. The displayed table can be sorted by the **Imported At** column to find the latest imports.

1.10.5 Detach and Attach of Datasets

To free disk space Studies, Examinations, or Image Series can be detached. This means that the data files are deleted from the hard disk while the dataset attributes remain in the ParaVision database. Detaching a dataset is only possible if the dataset has previously been archived or exported. The dataset goes offline.

Offline datasets can be identified in the Dataset Browser with the Offline flag:

- In the Study view the Study Offline column is checked.
- In the Examination view the Exam Offline column is checked.
- In the Image Series view the Image Offline column is checked.

Offline datasets cannot be acquired, viewed, etc. They can be searched and it is possible to view the archive locations (see Chapter [Show Archive Locations for Datasets \[▶ 427\]](#)).

Attaching offline datasets will restore the data files from the last exported or archived destination. After an Attach the Studies, Examinations, or Image Series can again be viewed or processed.

1.10.5.1 Detach Datasets

Detaching a dataset removes its data files and frees disk space (e.g. for further acquisitions). Only previously archived or exported datasets that have not been changed since then may be detached.

To Detach Studies, Examinations, or Image Series:

1. Select the Studies, Examinations, Image Series to be detached.
 - ▶ in the **Workspace Explorer** below the **Datasets** node
 - ▶ in the **Palette Explorer** (only Image Series)
 - ▶ or in the **Dataset Browser** in the different dataset views
2. Detach by

- ▶ clicking **Detach** in the context menu of the selected datasets in the **Workspace Explorer** or **Palette Explorer**
- ▶ or clicking the **Detach** button in a sub-menu of the action row below one of the dataset views. The **Detach** entry can be found in the sub-menu of the first button (click on the triangular button).
- ▶ The data files of the Studies, Examinations, or Image Series are removed and they are marked as offline.

1.10.5.2 Attach Datasets

Offline Studies, Examinations, or Image series can be made online again in a semi-automatic way using the Attach action. Attach can be seen as a Retrieve operation of previously archived data. This makes the Study, Examination, or Image Series available for further processing.

To Attach a Study, Examination, or Image series:

1. Select the Study, Examination, Image Series to be attached in the **Dataset Browser** in the different dataset views
2. Click the **Attach** button in a sub-menu of the action row below one of the dataset views. The **Attach** entry can be found in the sub-menu of the first button (click on the triangular button).
3. The last exported or archived file for the corresponding study, examination, or Image Series is retrieved:
 - ▶ If the datasets were exported or archived on disk the file is automatically retrieved and unpacked into the writable data directory.
 - ▶ If the datasets were archived on an SFTP or FTP server the user may be asked for the password of the SFTP or FTP server. The archived file is received from the server and the corresponding datasets are unpacked into the writable data directory. The password is only requested once in a ParaVision run for a specific server and user.
 - ▶ If the datasets were archived on a DVD, the user is asked to insert the DVD identified by a given label and the archiving date. Insert the DVD and mount it into the operating system. Then confirm the dialog. ParaVision tries to find the mount point of the DVD. If this does not work the user is asked for the DVD mount point using a directory selection dialog. For example, if the DVD is mounted to /media/dvd the user must specify this directory in the dialog. Then the corresponding datasets are unpacked from the archive file on DVD into the writable disk unit.

1.10.6 DICOM Export and Import

ParaVision can export datasets (Subject, Studies, Examinations, Image Series) as DICOM information objects (see on *Homepage from the 'The Association of Electrical Equipment and Medical Imaging Manufacturers'*: <http://www.nema.org/pages/default.aspx>):

- MRI dataset can be exported as Enhanced MR Information Objects. These are multi-frame objects, i.e all 2D-frames of the dataset are exported into one object. ParaVision supports only the export of imaging datasets into these objects. The export of spectroscopic objects is not supported.
- MRI datasets can be exported as Magnetic Resonance Image Information Objects. These are single frame objects, i.e each 2D frame of the dataset is exported into a separate object (and therefore also in a separate file). ParaVision supports only the export of imaging datasets into these objects. The export of spectroscopic objects is not supported (even though an information object is created but it is an imaging object).

The Conformance Statement (see chapter DICOM conformance statement) specifies the DICOM export in technical detail.

The export is possible to files or a DICOM server (DICOM Service Class Provider).

ParaVision can in principle import all DICOM image information objects. They are converted into ParaVision datasets.

1.10.6.1 DICOM Export

DICOM Export can be used to exchange dataset information with third party products. These can be

- PACS servers used to archive images
- DICOM viewers and processing programs to view and process images

DICOM export is only possible for Subjects, Studies, Examinations, or Image Series. Each image series contained in the selected subjects, studies, examinations is exported separately. All exported image series must be succeeded, i.e. image data must exist.

To export ParaVision datasets to DICOM:

1. Select Subjects, Studies, Examinations, Image Series to be exported to DICOM
 - ▶ in the **Workspace Explorer** below the **Datasets** node
 - ▶ in the **Palette Explorer** (only Image Series)
 - ▶ or in the **Dataset Browser** in the different dataset views
2. Export the datasets to DICOM by
 - ▶ clicking **Export to DICOM...** in the context menu of the selected datasets in the **Workspace Explorer** or **Palette Explorer**
 - ▶ or clicking the **Export to DICOM...** button in the action row below one of the dataset views
3. If the DICOM export is done to a directory a directory selection dialog appears that requests the base directory to store the DICOM files.
4. The actual export operation starts. A progress may appear. Depending on the number of exported datasets and their size the export may be very time consuming.
5. After the export is finished a dialog is displayed which shows in its details which image series have been correctly converted to DICOM files and which have not been.

1.10.6.1.1 Configuration

The DICOM export can be configured to meet the requirements of third-party DICOM software, e.g. a third-party software may only support the Magnetic Resonance Image Information Object but none of the others objects ParaVision supports.

To configure the DICOM export:

1. Open the Window > Options > DICOM dialog.
2. The dialog in Figure [DICOM configuration dialog ▶ 433](#) opens.
3. After changing the export configuration options click **OK** to confirm the changes.

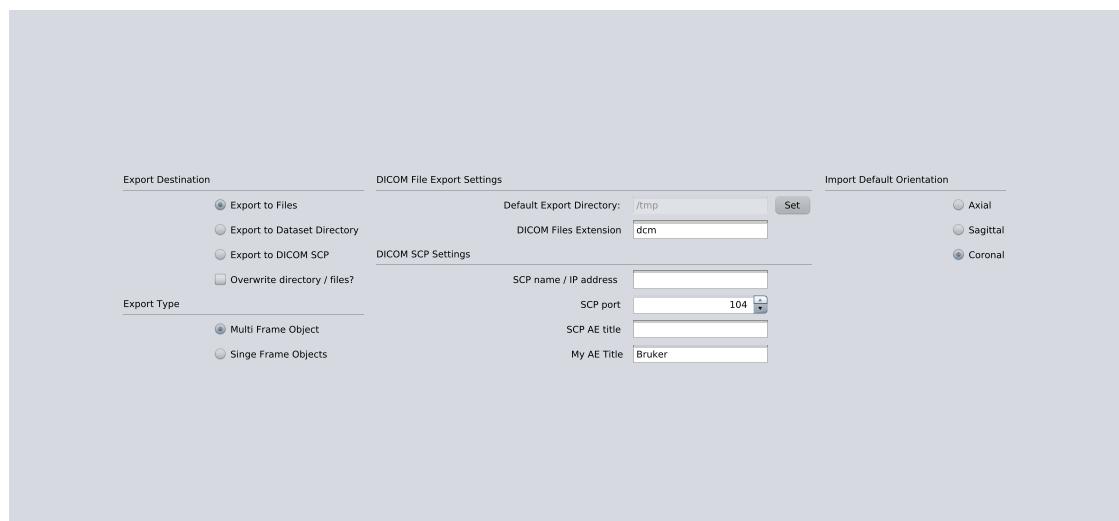


Figure 1.382: DICOM configuration dialog

The export configuration options are

- **Export Destination**

ParaVision can export to files or a DICOM server

- **Export to Files**

ParaVision exports datasets into DICOM files. The base export directory is requested with a directory selection dialog. For each image series a new directory is created in the specified base export directory. The names of the created directories have the following format:

<Subject Id>_<Subject Name>_<Study Id>_E<EXPNO>_P<PROCNO>

An additional number may be added to make the directory name unique.

- **Export to Dataset Directory**

The DICOM files are stored in the `dicom` sub-directory of the Image Series. The image series directory can be determined in the **Properties** dialog of an image series. Open the properties dialog by selecting an Image Series in the Dataset Browser and click on the **Properties** button. It can also be opened in the Workspace Explorer by clicking on **Properties** in the context menu of an Image Series node. In this dialog the **Storage Location** row shows the path of the Image Series. To read the path completely it may be necessary to click on the ... button in the third column of the **Storage Location** row.

This is the default Export Destination.

- **Export to DICOM SCP**

The DICOM objects are sent to a DICOM server (e.g. PACS system). The special configuration of the DICOM server is located in the **DICOM SCP Settings** section described later in this section.

- **Overwrite Directories / Files?**

This check box is only enabled if the **Export to Files** destination is used. If checked an export of a previously exported dataset will be overwritten. Otherwise a new directory is created.

- **Export Type**

- **Multi Frame Object**

Each image series is exported into a multi-frame DICOM object (Enhanced MR Information Object).

– Single Frame Objects

Each image series is exported into several single-frame DICOM objects (Magnetic Resonance Image Information Objects).

This is the default export type.

• DICOM File Export Settings

These options are only valid if the **Export Destination** setting is either **Export to Files** or **Export to Dataset Directory**.

– Default Export Directory

The default export directory is used for the **Export to Files** destination as a default in the directory selection box. It can be selected using the **Browse...** button.

– DICOM Files Extension

The default extension (part of the file name after the last dot) of the exported DICOM files is specified here. The extension is `dcm` (supported by most DICOM programs).

This is also the default configuration.

• DICOM SCP Settings

These options describe the communication settings to the DICOM storage server.

– SCP name / IP address

The DNS name or IP address of the host where the DICOM storage server runs.

– SCP port

The TCP/IP port of the DICOM SCP. Please consult the documentation of your DICOM server.

– SCP AE title

The DICOM name of the DICOM server. Please consult the documentation of your DICOM server.

– My AE title

The DICOM name of this ParaVision instance. The default is Bruker.

1.10.6.2 DICOM Import

DICOM image objects from different vendors can be imported into ParaVision. They are converted into ParaVision datasets and can be viewed and processed like ParaVision MR datasets.

To import DICOM files:

1. Choose **File > Import > DICOM...** .
2. A file selection dialog opens where the DICOM files can be selected. Multiple selection is supported. This allows to select all images of an image series. The file selection box supports DICOM files with `dcm` extension and a DICOM directory file (`DICOMDIR`). It is also possible to select all file types (if DICOM files have different extensions). A `DICOMDIR` is a file that contains references to and information about DICOM files (e.g. to which Patient, Study, Series the file belongs).
3. If more than one image series is included in the selected DICOM files, a **Choose Subject / Study / Series to Import** dialog opens (see Figure [Choose a DICOM Series for Import \[▶ 435\]](#)).

In Figure [Choose a DICOM Series for Import \[▶ 435\]](#) the subjects of the CAR '97 DICOM Demonstration CD are shown. The dialog displays the DICOM hierarchy Subject / Study / Series. Arbitrary nodes on every level can be selected. All image series of the selected items (e.g. Subjects, Studies, Series) are imported after **OK** is clicked. For each DICOM series a new Image Series is created in ParaVision containing all imported images of the series. The corresponding subjects and studies are created from the imported DICOM

information.

If a DICOM file is imported several times a new series is created for each import operation.

- After the import operation is finished an error or completion dialog is displayed. Potential errors are logged in the log service.

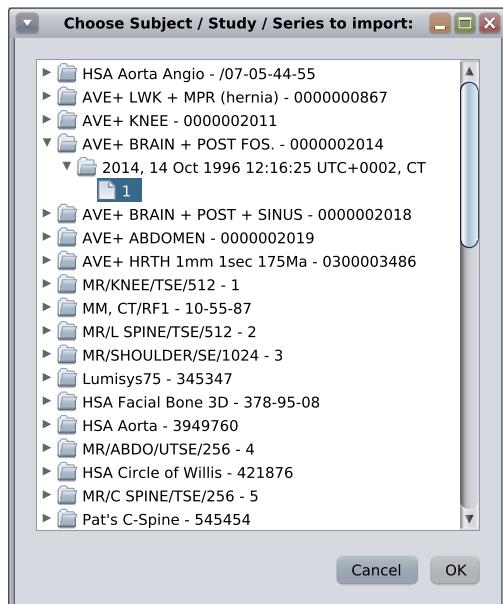


Figure 1.383: Choose a DICOM Series for Import

DICOM import can only be successful if the geometry of a DICOM series is defined conforming to the ParaVision parameter model. Problems may occur with DICOM Series where pixel spacing and matrix sizes (rows, columns) are not identical for all images.

The imported DICOM datasets can easily be found in the **Recent Imports** presets of the Data Browser. The displayed table can be sorted by the **Imported At** column to find the latest imports.

1.10.6.2.1 Configuration

ParaVision needs a defined orientation for viewing and processing of images. Some DICOM image information objects only contain optional orientation information. To allow the import of DICOM images without orientation information a default orientation can be configured.

Configure the default orientation for DICOM objects without orientation information by:

- Open the **Window > Options > DICOM** dialog.
- The dialog in Figure [DICOM configuration dialog \[433\]](#) opens. Choose one of the **Import Default Orientation** settings:
 - **Axial** means that the geometry is defined for a standard axial image where all angles are zero.
 - **Sagittal** means that the geometry is defined for a standard sagittal image where all angles are zero.
 - **Coronal** means that the geometry is defined for a standard coronal image where all angles are zero. This is the default since the geometry is most often not available in secondary capture images. These are often coronal.
- Confirm the setting by clicking **OK** on the **Option** dialog.

1.10.7 Import Legacy Datasets

Legacy datasets are datasets that are created by previous ParaVision versions. These datasets cannot be seen by default. They must be imported if they should be viewed or processed. Only the import of completed datasets is possible. It is not possible to work with ready datasets.

To import legacy datasets:

1. Choose **File > Import > Legacy Datasets...**.
2. A dialog (see Figure [Import Legacy Datasets Dialog \[436\]](#)) opens.
On the left side a list of directories (**Input Directories**) is shown from which datasets should be imported.
3. To add directories click the **Add...** button. This opens a directory selection dialog where another base directory for the import can be selected. A selected directory can be removed from the **Input Directories** list by using the **Remove** button. For example, in Figure [Import Legacy Datasets Dialog \[436\]](#) an entire ParaVision 5.1 data directory is defined. All subjects, studies, examinations and image series stored in the data directory are imported. It is also possible to import only parts of the data directory of a previous version. If only some studies should be imported add the corresponding study directories to the list of input directories.
4. Check **Copy Disk Datasets** if the datasets should be copied into the data director of the user in the current ParaVision installation. Otherwise a reference is created. If the legacy datasets are referenced by this ParaVision version they should not be changed from other ParaVision instalations or users. If they are changed by the legacy ParaVision installation the dataset description in ParaVision 6 may be inconsistent.
Copy Disk Datasets must be checked if some of the input directories are on a read-only directory (e.g. a CDROM, DVD archived with a previous ParaVision version).
5. After clicking **OK** in the dialog all datasets in the **Import Directories** are imported. It is done in the background and a progress bar is shown. At the end of the import the number of successful imported Images Series is reported. It is possible that some Image Series from ParaVision 1 – 3 cannot be imported.

The imported legacy datasets can easily be found in the **Recent Imports** presets of the Data Browser. The displayed table can be sorted by the **Imported At** column to find the latest imports.



Figure 1.384: Import Legacy Datasets Dialog

1.11 Image Sequence Analysis

1.11.1 Overview

Many imaging experiments produce Image Series where the image intensities are related to an independent variable that is varied during acquisition of the series. For example, the echo time in a multi-echo train or the b-value in a diffusion weighting series. These image sequences may form a subset of the total number of images in an Image Series, sequences being present for e.g. several slices.

The Image Sequence Analysis tool (ISA Tool) is a sub-package of the Classic ParaVision **Image Display & Processing** program (see Chapter [Classic Image Display & Processing ▶ 440](#)) and provides a general and flexible framework for the visualization and statistical analysis of such sequences of images.



The Image Sequence Analysis tool is described in the PDF manual chapter [Image Sequence Analysis](#).



The PDF manual contains information that has not or only little changed between ParaVision versions. In addition it contains

- the table of contents for the PDF manual: [Table of Contents](#).
- an index for the PDF manual: [Index](#).
- a parameter index for all parameters described in the PDF manual: [Parameter Index](#).

Note: In future versions the functionality of the Image Sequence Analysis tool will be integrated into the main graphical user interface.

1.11.2 Start of the Image Sequence Analysis Tool

The Image Sequence Analysis tool (ISA Tool) provides a general and flexible framework for the visualization and statistical analysis of image sequences where the image intensities are related to an independent variable that is varied during acquisition.

The Image Sequence Analysis tool can be started in the **Image Display & Processing** program. The start of the **Image Display & Processing** program is described in Chapter [Start of the Image Display & Processing program ▶ 440](#) and Chapter [Start of the Image Display & Processing program with an Image Series ▶ 440](#).



The start of the Image Sequence Analysis is described in the in the PDF manual chapter [Image Sequence Analysis](#).

1.11.3 Automatic Fitting of an Image Series

The Image Sequence Analysis tool (ISA Tool) provides a general and flexible framework for the visualization and statistical analysis of image sequences where the image intensities are related to an independent variable that is varied during acquisition. It is possible to automatically fit an image series and create parameter images for all slices.

1. Select an Image series

- in the **Workspace Explorer** below the **Datasets** node by selecting the **Image Series** node,
 - in the **Palette Explorer**,
 - or in the **Dataset Browser** in the **Image Series** dataset views.
2. Open the macro selection dialog by
- clicking on the Execute Macros.. context menu entry of the selected Image Series in the **Palette Explorer** or **Workspace Explorer**,
 - or clicking **Execute Macros...** in a sub-menu of the buttons below the **Image Series** views in the **Dataset Browser**. The **Execute Macros...** entry can be found in the sub-menu of the **Properties** button (click on the triangular button).
3. The **Execute Macros** dialog opens where all available macros can be selected. Select the **BRUKER** category and the macro **Fitinlsa** as shown in Figure [Dialog: Execute Macro ▶ 438](#) and click **OK**.



Figure 1.385: Dialog: Execute Macro

The **Image Display & Processing** program is started in the background (if not already running) and the Image Sequence Analysis tool is used to fit and create an Image Series containing the fitted parameter images for all slices. If an error appears dialogs from the Image Display & Processing tool may appear. Otherwise the operation runs in the background. The created parameter image is shown in an additional Image Series to the Examination in which the original series is located.

If the **Image Display & Processing** graphical user interface is brought into the foreground the first viewport shows an image of the original Image Series and the second viewport shows an image of the created fitted Image Series.

It is also possible to use the macro **FitinlsalInteractive** which does not work completely in the background and allows the user to see the actual fit.

1.11.4 Automatic Fitting after Reconstruction

The Image Sequence Analysis tool (ISA Tool) provides a general and flexible framework for the visualization and statistical analysis of image sequences where the image intensities are related to an independent variable that is varied during acquisition. It is possible to fit an image series and create parameter images for all slices automatically after reconstruction. In this case the scan instruction in the examination card (see Chapter [Using the Scan Program Table ▶ 25](#)) creates two Images Series:

- the Image Series reconstructed from the acquisition
- and the fitted images series where for each slice a set of parameter images is calculated by the Image Sequence Analysis tool.

To define the automatic fitting after reconstruction

1. Edit the Scan Instruction in the Examination card (see Chapter [Editing a Scan Instruction \[▶ 55\]](#)).
2. Open the Processing Platform for the edited Scan Instruction (see Chapter [Opening the Processing Platform \[▶ 73\]](#)).
3. Edit the first **Data Reconstruction** instruction (see Chapter [Editing a Processing \[▶ 76\]](#)).
4. In the opened editor on the right there is a list of **Post Image Series Activities** (see Figure [Reco Processing Editor \[▶ 439\]](#)). In this editor mark **Execute Macro**.
5. The **Execute Macros** dialog opens where all available macros can be selected. Select the **BRUKER** category and the macro **Fitinlsa** as shown in Figure [Dialog: Execute Macro \[▶ 439\]](#) and click OK.
6. Click the **Apply** button in top of the the instruction list to close the **Data Reconstruction** editor.
7. Click **Back** to change back to the Scan Instruction.

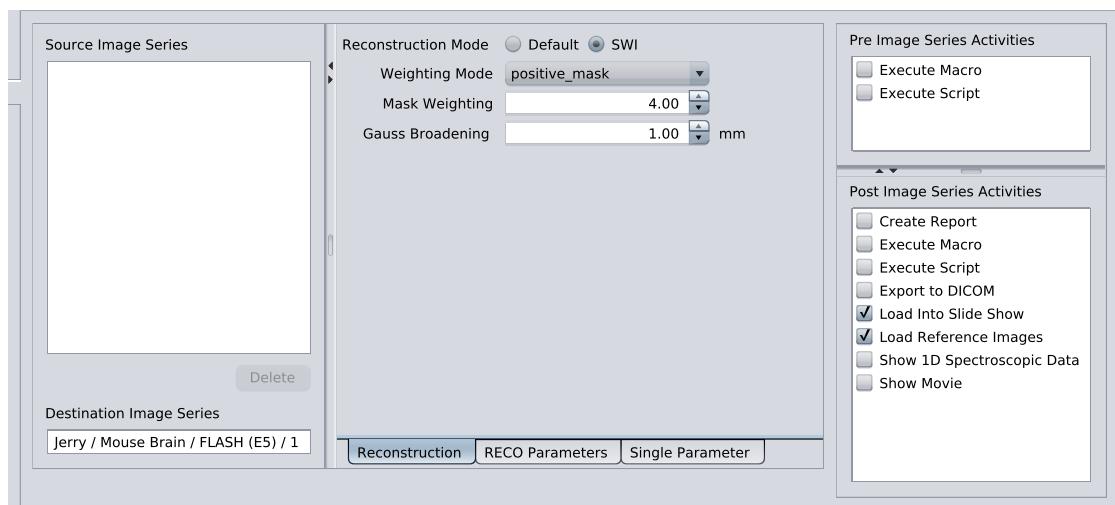


Figure 1.386: Reco Processing Editor



Figure 1.387: Dialog: Execute Macro

1.12 Classic Image Display & Processing

1.12.1 Overview

ParaVision 6 contains the **Image Display & Processing** program known from previous ParaVision versions. It provides

- basic and advanced viewing functionality,
- enhanced region of interest functionality (region growing, morphology, etc),
- image sequence analysis functionality (see Chapter [Image Sequence Analysis ▶ 437](#)),
- functional imaging processing (see Chapter [Functional Imaging Processing ▶ 441](#)),
- CSI visualization functionality (see Chapter [Chemical Shift Imaging Visualization ▶ 441](#)),

Note: In future versions the functionality of the Image Display & Processing program will be integrated into the main graphical user interface.



The Image Display & Processing program is described in the PDF manual Chapter [Image Display & Processing](#)



The PDF manual contains information that has not or only little changed between ParaVision versions. In addition it contains

- ▶ the table of contents for the PDF manual: [Table of Contents](#).
- ▶ an index for the PDF manual: [Index](#).
- ▶ a parameter index for all parameters described in the PDF manual: [Parameter Index](#).

1.12.2 Start of the Image Display & Processing program

To perform enhanced image processing or to use image processing macros from previous ParaVision versions the classic **Image Display & Processing** program can be used.

- Start the **Image Display & Processing** program by clicking the **Programs > Image Display & Processing** menu entry.

If the **Image Display & Processing** program is in the background or iconified it will be shown in the foreground displaying the viewports with the previously shown image frames.

If the **Image Display & Processing** program is not running it is started and shows in the first viewport the image frame of the currently selected viewport at the time of the last completion.



Further information about how to use the Image Display & Processing Program can be found in the manual chapter [Image Display & Processing](#).

1.12.3 Start of the Image Display & Processing program with an Image Series

To perform enhanced image processing or to use image processing macros from previous ParaVision versions on a selected Image series the classic **Image Display & Processing** program can be started with an Image series.

1. Select an Image series
 - ▶ in the **Workspace Explorer** below the Datasets node by opening the Image Series node,

- ▶ in the **Palette Explorer**,
 - ▶ or in the **Dataset Browser** in the **Image Series** dataset views.
2. Open the **Image Display & Processing** program and load the selected dataset by
- ▶ clicking on the **View in Image Display** menu entry in the context menu of the 2D/3D Image Data node below the Image Series node in the **Workspace Explorer**,
 - ▶ clicking on the **View in Image Display** menu entry in the context menu of the selected Image Series in the **Palette Explorer**,
 - ▶ or clicking **View in Image Display** in a sub-menu of the buttons below the **Image Series** views in the **Dataset Browser**. The **View in Image Display** entry can be found in the sub-menu of the **View** button (click on the triangular button).
3. The **Image Display & Processing** program opens or comes into the foreground (if it was iconified or in the background). The middle frame of the selected Image Series is loaded into the first viewport.



Further information about how to use the Image Display & Processing Program can be found in the manual chapter [Image Display & Processing](#).

1.12.4 Functional Imaging Processing

The Functional Imaging Tool (FUN Tool) is part of the **Image Display & Processing** program (see Chapter [Classic Image Display & Processing \[▶ 440\]](#)). It is a processing tool to support the evaluation and analysis of appropriate fMRI Image Series.



The tool is described in the PDF manual Chapter [Functional Imaging Tool \(FUN Tool\)](#).

1.12.5 Chemical Shift Imaging Visualization

The Chemical Shift Imaging Visualization is part of the **Image Display & Processing** program (see Chapter [Classic Image Display & Processing \[▶ 440\]](#)). The CSI Visualization Tool is a tool for displaying, analyzing, and manipulating the acquired CSI Image Series.



The tool is described in the in the PDF manual Chapter [CSI Visualization Tool](#).

2 Application Manual

2.1 Getting Started

Introduction

Intended Readers

The present chapter of the Application Manual is intended to provide the beginner with basic knowledge of ParaVision and is a guide through the acquisition of the first images.

This is a brief description of the conditions which have to be complied with and the steps which have to be taken to obtain an image.

Prerequisite

- Basic knowledge of MR imaging.
- Knowledge of the safety requirements for a MR installation.



For the safety requirements of your system please see the ParaVision System Manual.

Initial Situation

The system is up and ready for measurements, a transmit/receive coil is connected and tuned/matched, and a sample is placed at the center of the coil. *Instructions on coil connection can be found in the System Manual.*

You should be logged in as a user and ParaVision should be started from the icon on the desktop.

2.1.1 Registering a Subject for an Examination

Figure 2.1: Study Registration window



Figure 2.2: Set the Location

To start an examination, create a new dataset first. Click on the **New** and **Study** option of the File menu. The **Study Registration** window appears. The following entries: **Animal ID**, **Animal Name**, **Study**, and **Position** must be filled in. For the **Location** select the **Object** (e.g. Rat), **Region** (e.g. Head), **Application** (e.g. Anatomy), and the first protocol 1_Localizer. Click on **Create** to store the study. Click on **Exam** to open the study in the **Examination Card**. The interface will change to the **Examination Card**.

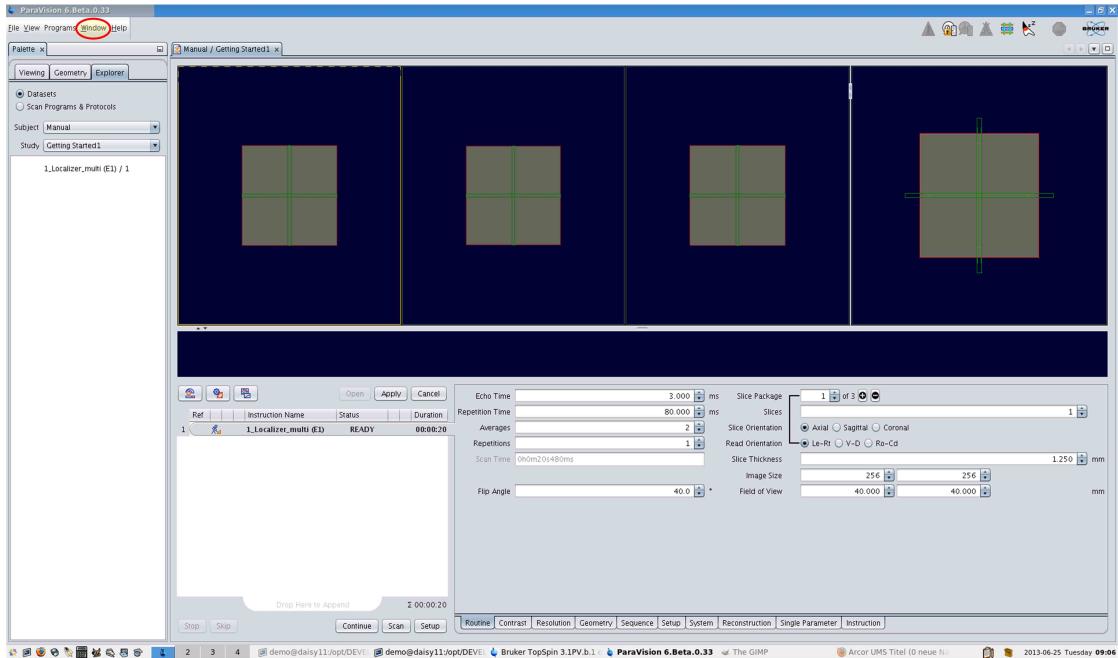


Figure 2.3: Examination Card



MORE INFORMATION about the functionalities of the interface please see the Chapter [Study Registration \[▶ 205\]](#).

2.1.2 Starting the Scan

The **Palette Explorer** gives you context sensitive access to the **Scan Programs** and Protocols and to the **Datasets** of your study. Click on the **Palette** menu item of the **Window** menu to open the palette explorer in case it is not already opened.

The Subject Name, Study and the selected protocol appear under Dataset. The selected protocol appears in the **Instruction List** as well. The first scan is now ready to be acquired.

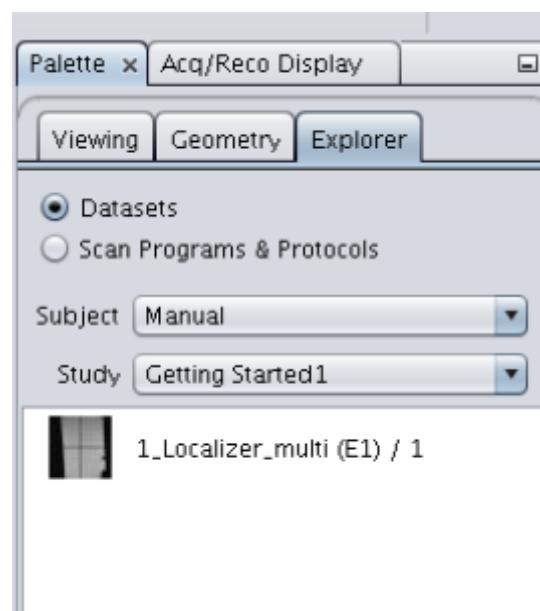


Figure 2.4: Datasets in the Palette Explorer



Figure 2.5: Instruction List

Click onto **Continue** to run the first scan. The scan status goes through several states: **READY**, **ADJUST**, **SCANNING**, and ends with **SUCCEEDED**. The green bar shows the scan progress. The 1_LOCALIZER records three slices, an axial, a sagittal, and a coronal slice.



MORE INFORMATION in Chapter [Examination Card \[23 \]](#)

2.1.3 Viewing the Completed Scan in the Examination Card

The images of the succeeded scan appear in the viewports of the Geometry Editor. The left viewport shows the axial, the middle the sagittal, and the right viewport shows the coronal image. In the fourth viewport, a 3-dimensional representation of all three orientations shows the location of the slices with respect to the reference image. It is intended only for visualization providing a better view of the selected geometry.

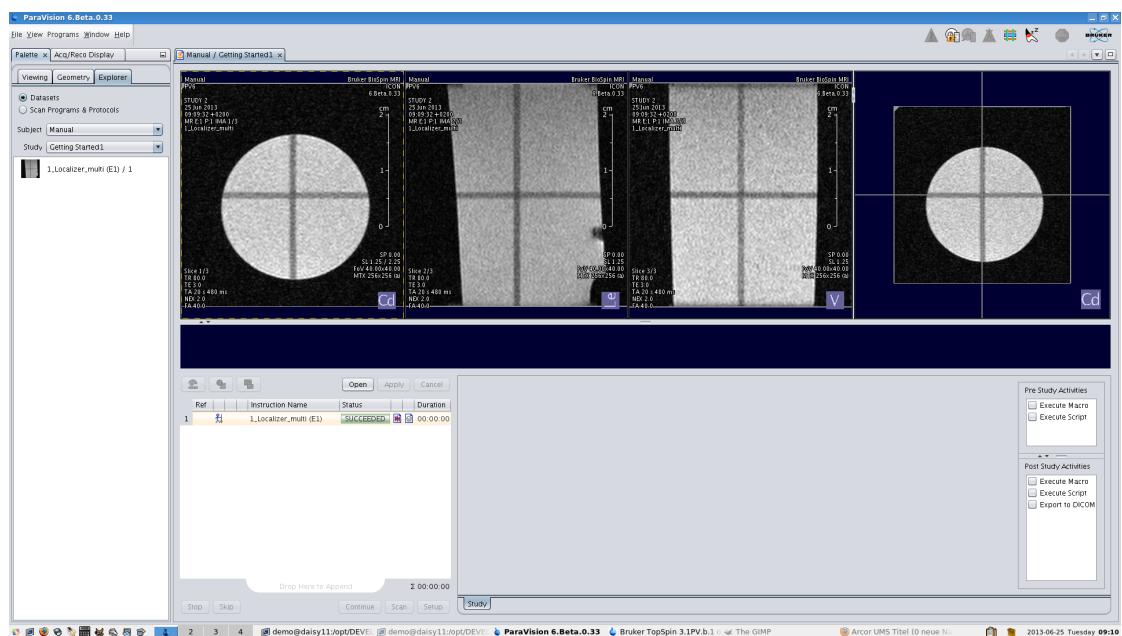


Figure 2.6: Geometry Editor

The images can be processed via the **Viewport Toolbar**, where options such as zoom, pan, roll, and navigate are available. To activate the **Viewport Toolbar** select an image by clicking in the viewport, and move the cursor to the right edge of the active viewport. The **Viewport Toolbar** will appear. Click first in the desired tool and a tooltip will be visible explaining the function of the mode. Then click in the image and process by moving the cursor. Use the **Navigation Mode** to scroll through the images. By clicking the cursor in the 3D image and using the **Viewport Toolbar** the volume can be rotated and shows where the slices are located.

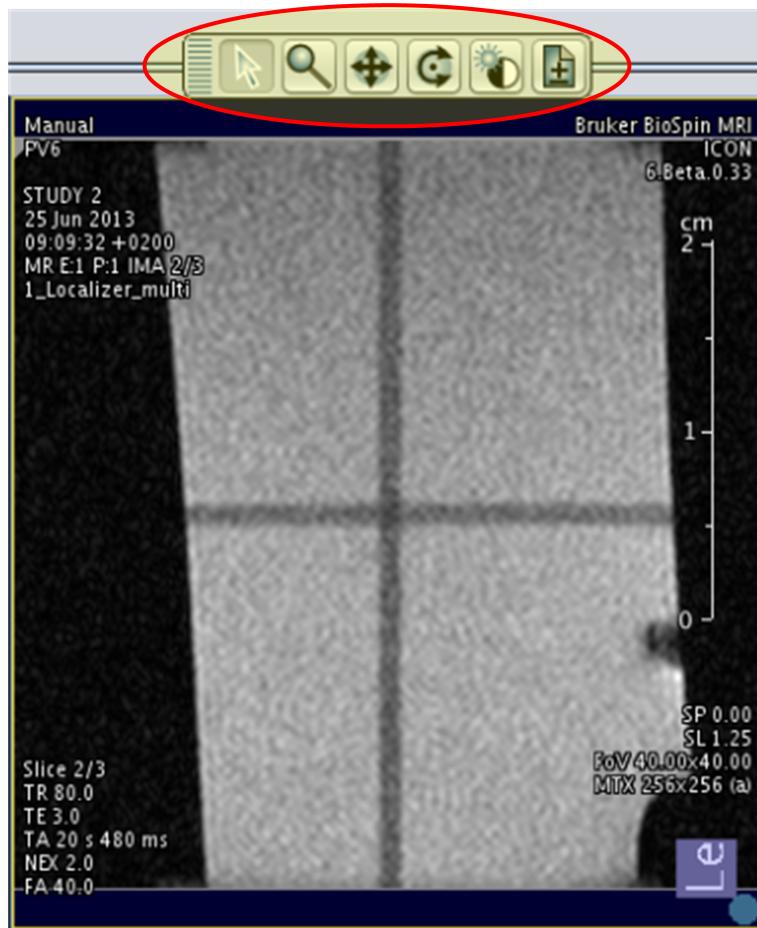


Figure 2.7: Viewport Toolbar

2.1.4 Acquiring the next Scans

To acquire the next scan change from **Dataset** to **Scan Programs & Protocols** where all appropriate protocols for the created study are listed. Select the scan T2_(Turbo)RARE and drag and drop it in the **Instruction list**. The slice geometry of the selected scan is overlaid onto the displayed reference images in the Geometry Editor. Click onto **Continue** to run the second scan. Under **Duration** in the **Instruction list** a countdown shows the progress of the running scan. The T2_(Turbo)RARE records an odd number of axial slices. Drag the succeeded scan from the instruction list and drop it in the left viewport of the Geometry Editor. The three middle images will be displayed in the viewports. To show all images of this scan drag and drop it in the **Slide Show** which is located below the Geometry Editor window or change to the **Image Viewer**.

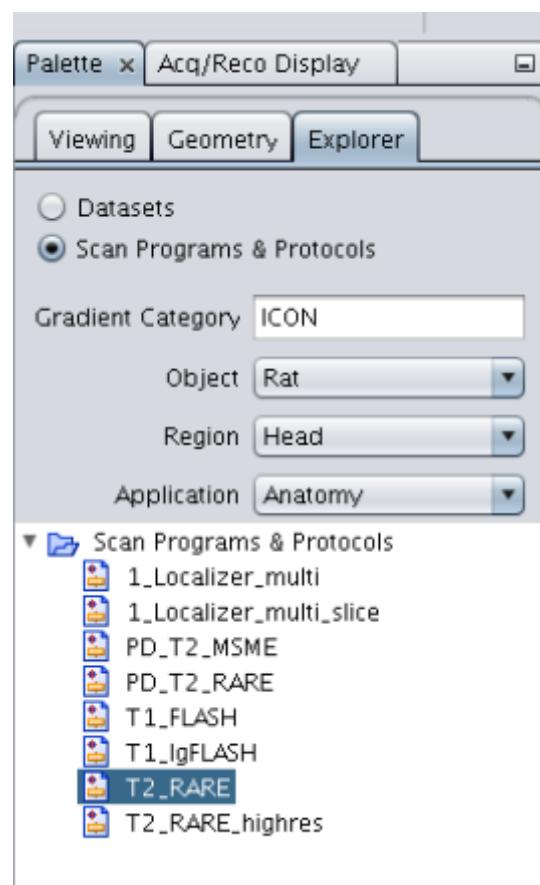


Figure 2.8: Scan Programs & Protocols

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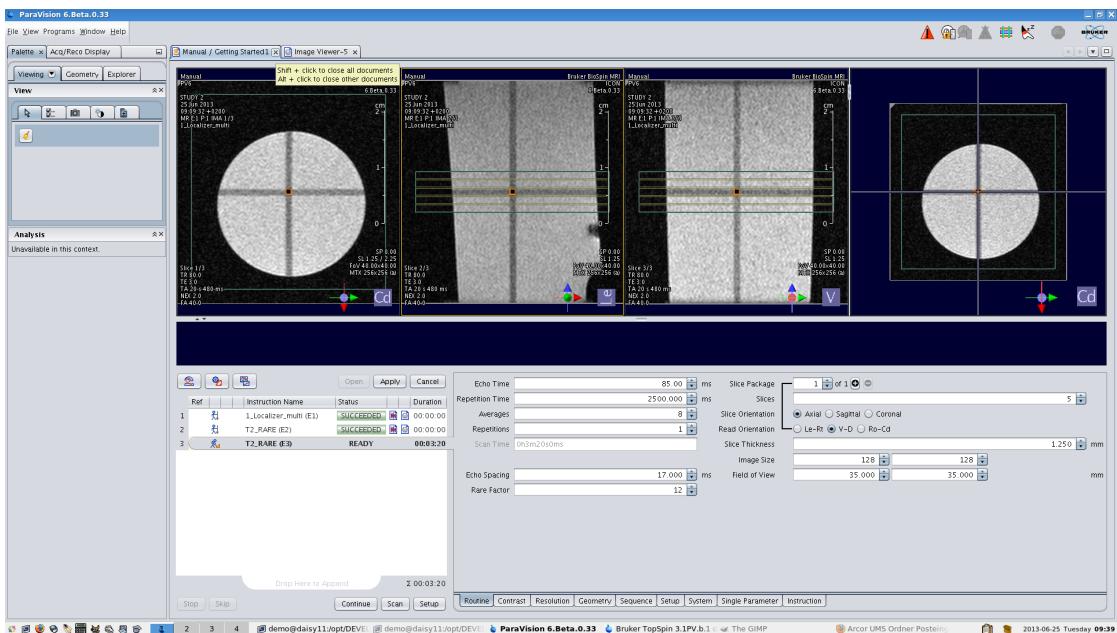


Figure 2.9: Geometry of the Second Scan

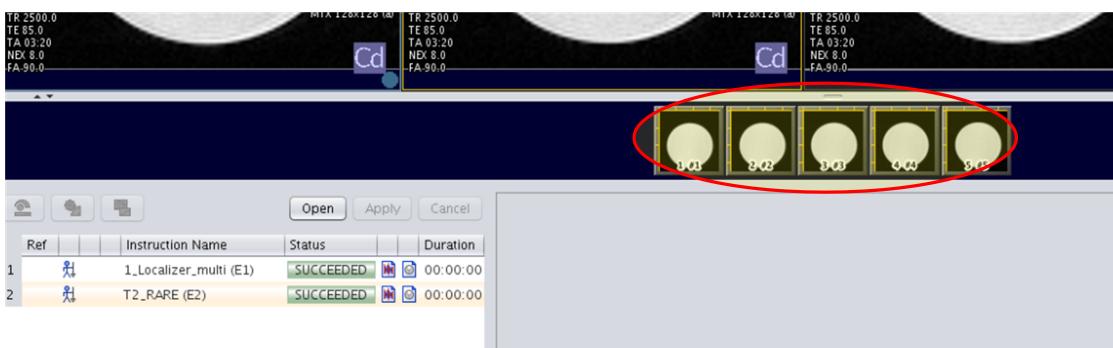


Figure 2.10: Slide Show



For further scans it is possible to use completed scans of the same study as references for positioning.

2.1.5 Viewing the Data in the Image Viewer

To have more access for processing completed scans, open the **Image Viewer**. Click on **Datasets** in the **Palette Explorer** and double click the scan which should be visualized. The interface will change to the **Image Viewer** and the selected scan will be visualized in the viewports. Every double click will open a new window of the Image Viewer. It is also possible to drag and drop a scan into an open window of the Image Viewer.

To activate the **Viewport Toolbar** of the **Image Viewer** see Chapter A-1-4 [Viewing the Completed Scan in the Exam Card \[446\]](#).

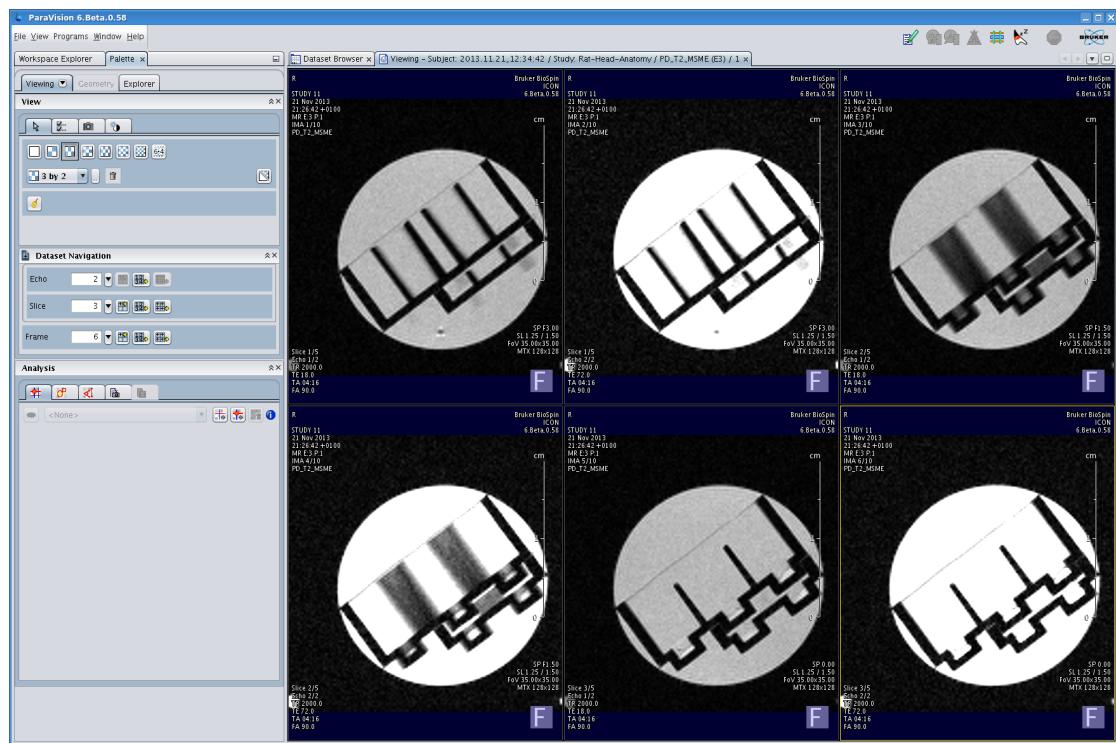


Figure 2.11: Image Viewer

The **View** tab is activated and the subtabs **Viewport Layout** and **Dataset Navigation** are open as default. Select a viewport layout by clicking on the layout icons or by using the pulldown menu to visualize the acquired data in a viewport layout with appropriate number of viewports. To page through all images of a completed dataset in the Image Viewer click in the **Dataset Navigation** on **Navigation with viewport advance will fill all remaining viewports** followed by **show next slice image with viewport advance**. This feature is also available to navigate through different echoes and through all frames. More details explaining the function of this mode are visible on the corresponding tooltips. With the **Dataset Navigation** you can scroll through the images. The processing state of the loaded image (e.g. zoom/pan, windowing) will be automatically inherited during dataset navigation.

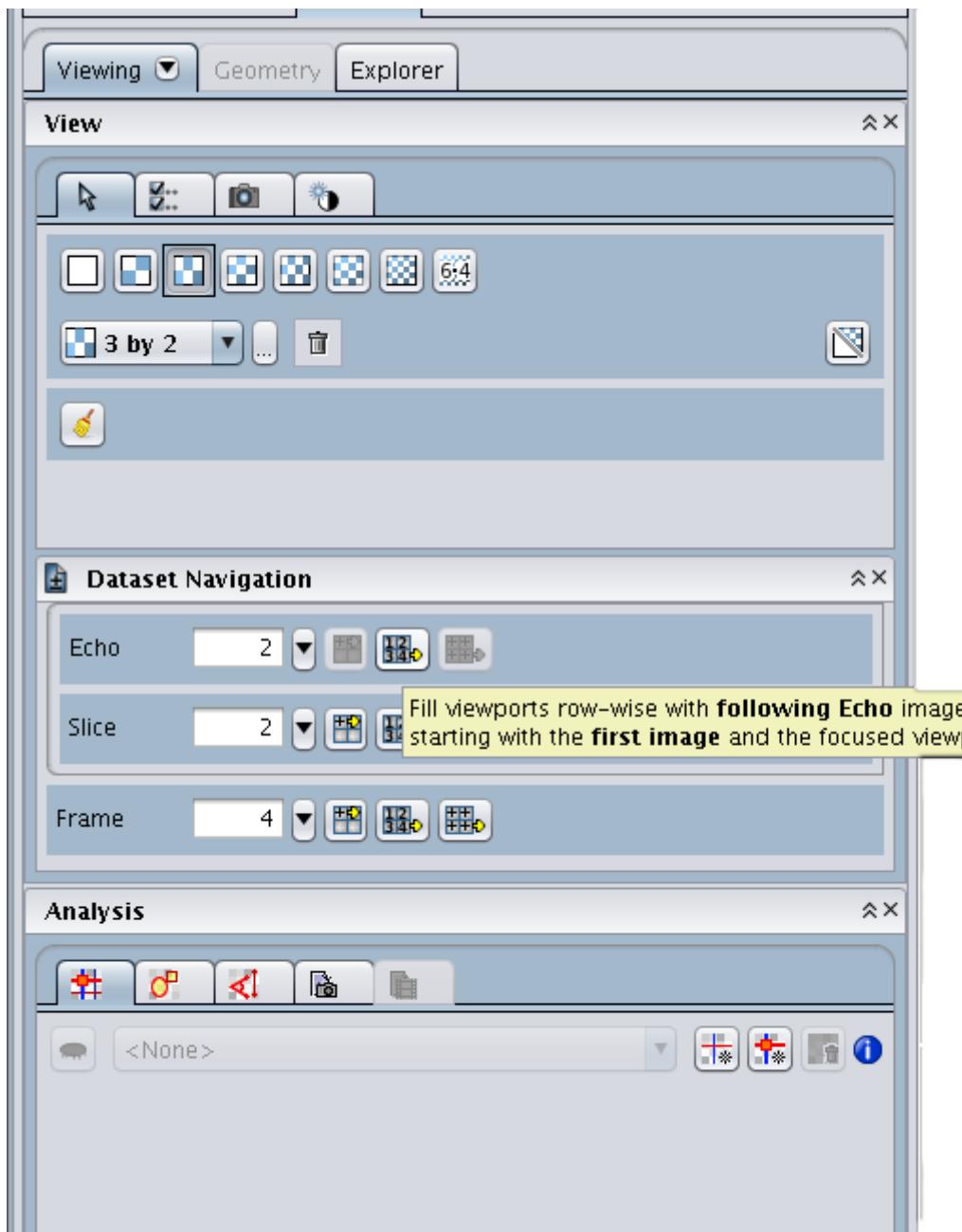


Figure 2.12: Navigation Viewport

To plan and perform more examinations go back to the **Examination Card** by clicking on the Examination tab.

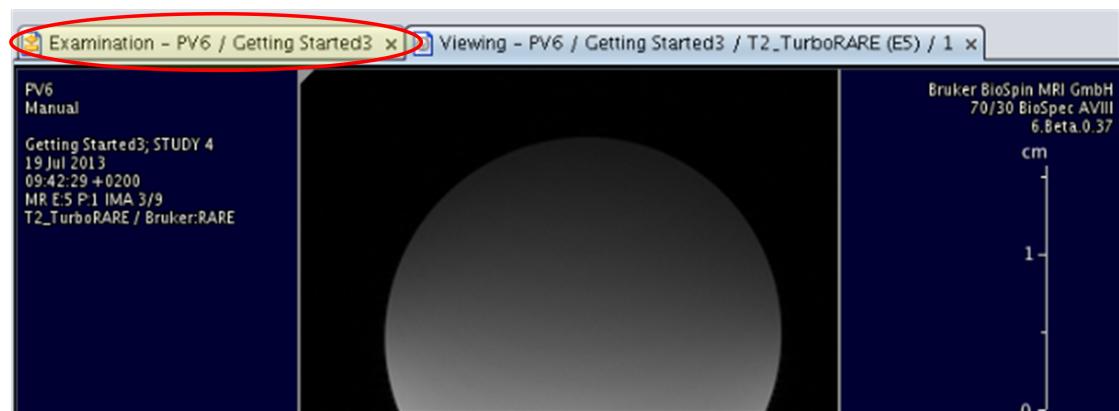


Figure 2.13: Examination tab

2.1.6 Planning the Geometry

To repeat the second scan click the right mouse onto the succeeded T2-(Turbo) RARE in the instruction list. Select the option **Duplicate Instruction** in the context menu.

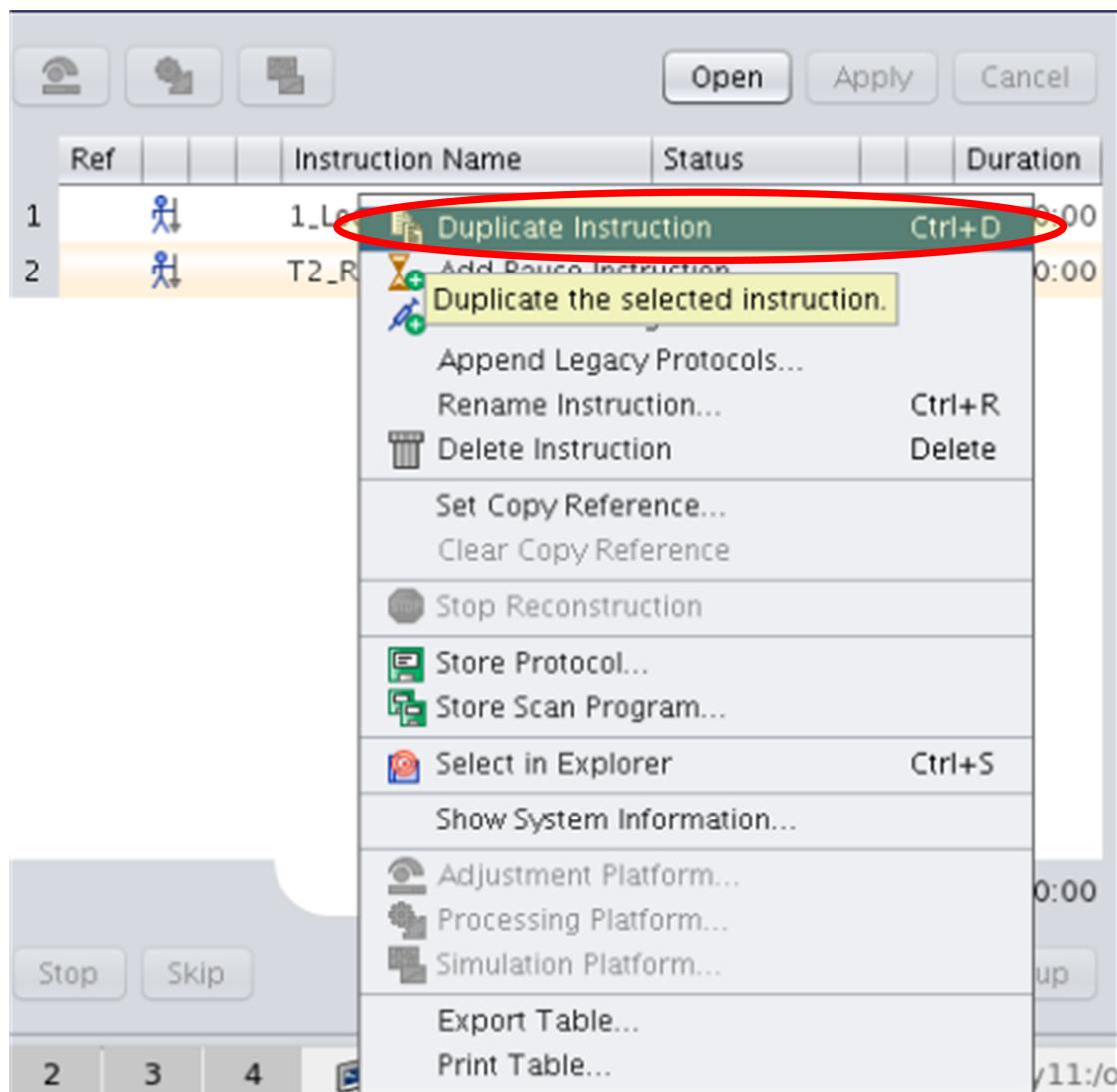


Figure 2.14: Duplicate instruction

The scan, parameters and positioning will be duplicated. For planning the scan on a reference image drag and drop the first scan 1_Localizer in the viewport of the Geometry Editor.

To change slice position, field of view, or angle of the scan, click now on the slices in the active viewport. From there on, a number of interactive control features are available which are intuitive. Click onto **Continue** to run the scan.

To delete the scan, click the right mouse onto the scan in the instruction list and select the option **Delete Instruction** in the context menu. The scan will be completely erased.

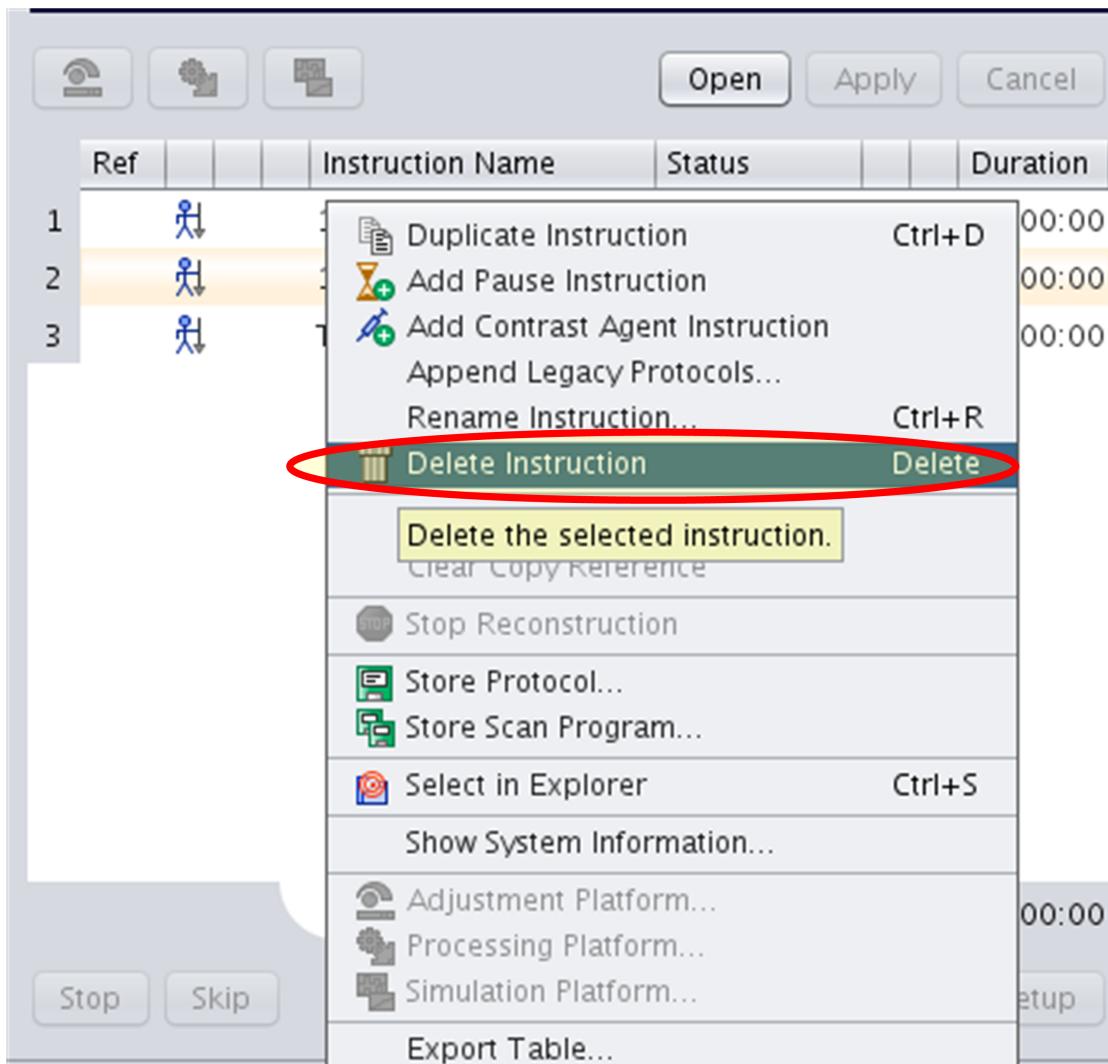


Figure 2.15: Delete Instruction

2.1.7 Editing Parameters

To acquire the next scan, duplicate the succeeded scan or change to the **Explorer** in **Palette** to **Scan Programs & Protocols** and drag and drop a protocol in the instruction list. In the **Instruction Editor** different cards are available. The **Routine** card is selected by default. This card provides you the most important parameters of the sequence.

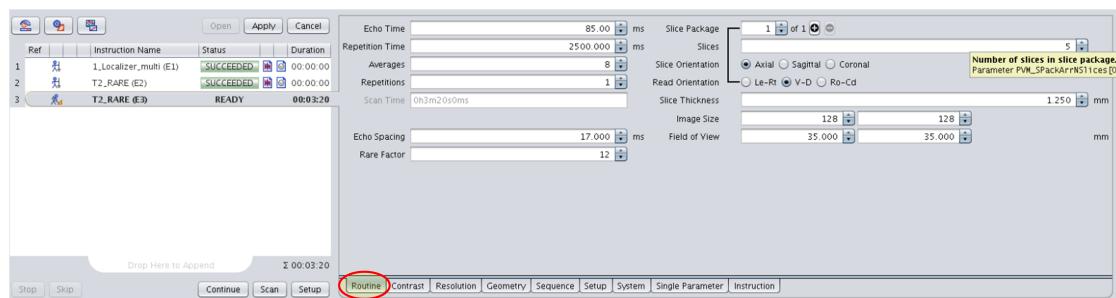


Figure 2.16: Instruction Editor

To change the number of slices, setup this in the **Routine** card by typing in a value or click on the arrows.

Click **Apply** to confirm parameter modifications and click **Continue** to run the scan.

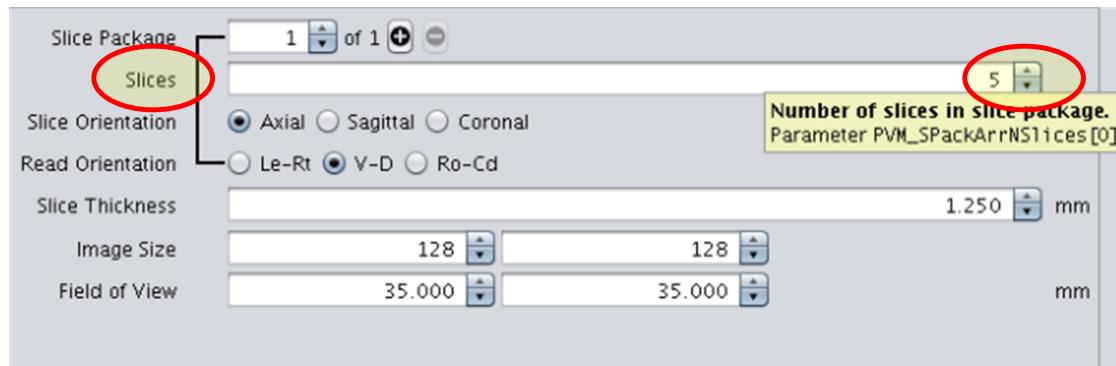


Figure 2.17: Modification Slice Thickness

2.1.8 Archiving and Transfer of Data

This is a brief step-by-step description of how to archive and transmit your data.

Export to Dicom

Click on the **Dataset Browser** of the **Window** menu. The interface switches to the **Dataset Browser** window.

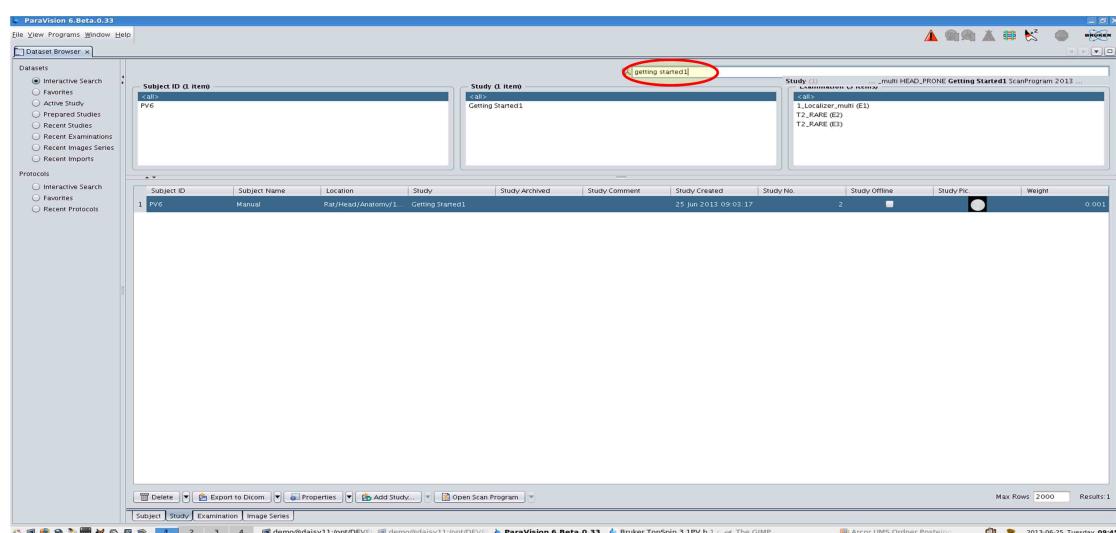


Figure 2.18: Databrowser

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The study which shall be archived or transferred must not be opened in the exam card. Close the **Exam** by clicking on the cross of the **Examination tab**. Confirm the appearing dialog window with **YES**. Select now **Interactive Search** in **Dataset** in the **Dataset Browser** window. Type in the search window a keyword of the subject or study which shall be processed. All subjects or studies containing the keyword are listed.



Figure 2.19: Searching with a keyword

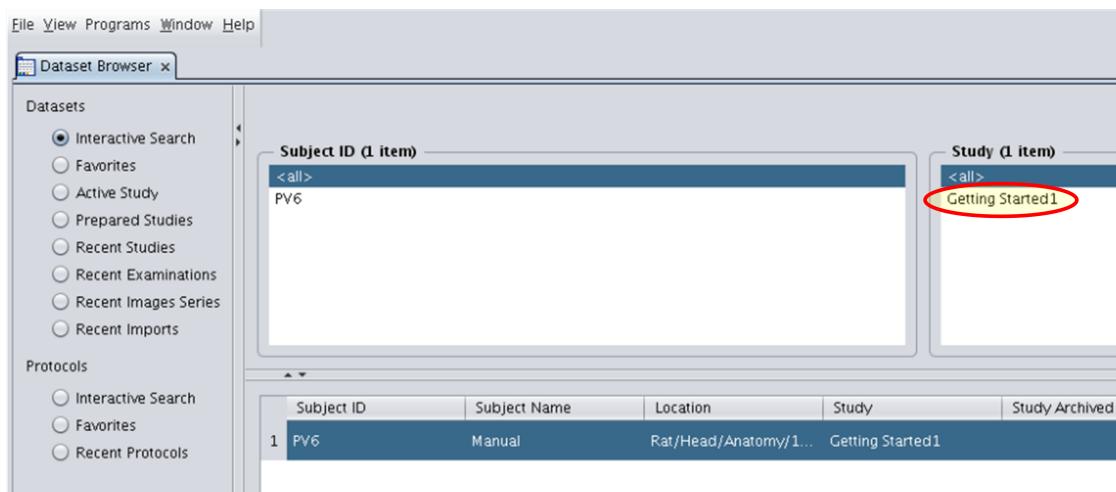


Figure 2.20: Finding the study corresponding to the selected keyword

Click on the selected study and on the button **Export to Dicom**. The Dicom dataset will be stored in the ParaVision dataset directory.



MORE INFORMATION: see Chapter [DICOM Export \[432 \]](#)



Figure 2.21: Export to Dicom

Archive to DVD

Put a DVD in the disk drive of your computer. Expand the button **Export to Dicom**. Click on the option **Archive**. A dialog window pops up and requests to name the DVD. Type in a name and confirm with **OK**. The selected dataset will be archived on the DVD. See the recording status line on the ParaVision screen.



MORE INFORMATION: see Chapter [DVD Destination \[424 \]](#)



Figure 2.22: Dialog window DVD

2.2 Creating and Saving Protocols and Scan Programs

2.2.1 Introduction

2.2.1.1 Intended Readers

This portion of the Application Manual is intended to provide information on how to adapt Bruker protocols and methods for individual use, how to create scan programs, and how to save these individual protocols and scan programs for future use. The creation of individual protocols and scan programs should be performed by users with more in-depth MRI and ParaVision knowledge. They can then be applied by this user or stored for routine use by users with less MRI insight.

For a better understanding of the discussed topics, it is recommended to have ParaVision running. An appropriate coil/coils (¹H) should be connected and wobbled. Instructions on coil connection can be found in the System Manual.

2.2.1.2 Prerequisites

This manual must be used in the greater context of other manuals, particularly the respective System Manual and the safety instructions located therein. It is assumed that the reader has advanced knowledge of MR and understands the effects of changing parameters in various methods.

2.2.2 Bruker Protocols and Methods

2.2.2.1 Bruker Protocols and Locations

Bruker provides prepared protocols that provide excellent image quality when used for their foreseen applications. These protocols are found in the many Bruker animal locations. Locations are groups of protocols that are common to a certain goal. All of the Bruker locations can be accessed in the Location field of the Study Registration dialog, which is used to create datasets.

It is strongly recommended to choose an appropriate Bruker location in the Study Registration dialog when creating a new datasets.

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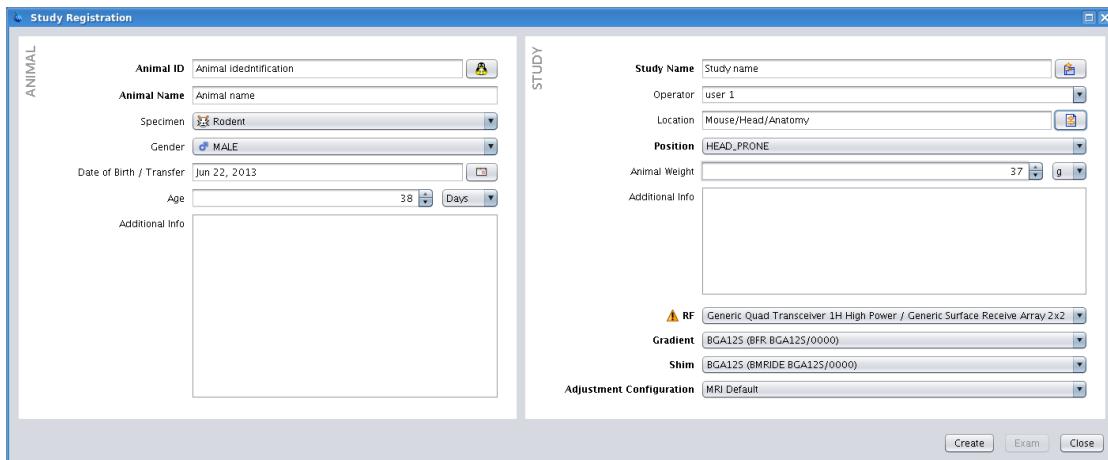


Figure 2.23: The Study Registration dialog. The Location Mouse/Head/Anatomy has been selected.

When a location has been selected in the Study Registration dialog, it will appear in the Scan Programs and Protocols list on the Explorer tab of the Palette on the Exam Card.

The user can then run the scans from this location or if necessary, switch to another location by clicking in the Object, Region, and/or Application fields.

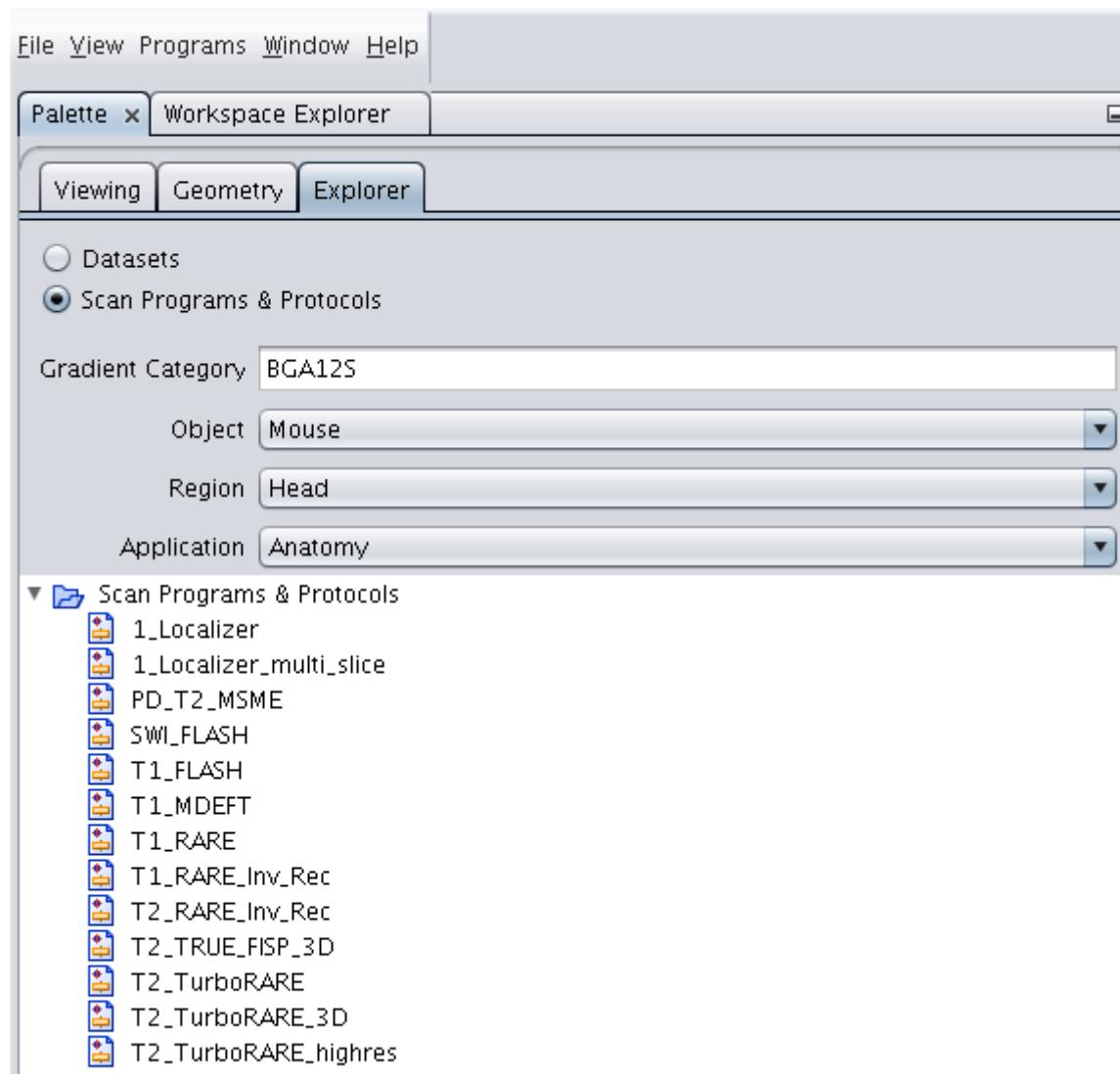


Figure 2.24: Scan Programs and Protocols in the Explorer tab of the Palette. The location Mouse/Head/Anatomy is shown.

All Bruker locations can be accessed here. Since the majority of users work with mice and rats, all systems capable of mice and rat measurements contain Bruker locations found in these two variations, which mainly differ in the size of the field of view.

For a full list of Bruker protocols and locations, please see Protocols.

2.2.2.2 Bruker Protocols versus Methods

Additionally, all of the Bruker methods are available here under the location AnyObject/AnyRegion. Bruker methods are pulse programs and associated programs that perform such tasks as parameter cross-checks, reconstruction, etc.. The parameters of methods have not been optimized for use on animals. For example, the non-optimized method RARE is found under AnyObject/AnyRegion. Six variants of RARE are stored as the protocols T1_RARE, T1_RARE_INV_REC, T2_RARE_INV_REC, T2_TurboRARE, T2_TurboRARE_3D, and T2_TurboRARE_highres in the location Mouse/Head/Anatomy. All six of these protocols are based on the RARE method, but differ in protocol parameters such as inversion time, repetition time, RARE factor, resolution, etc.

For a detailed description of Bruker methods, please see [Method Description \[▶ 240\]](#).

2.2.3 Editing Protocols

In some cases, such as when objects other than mice or rats are being scanned, or when the user's study goal is not covered by the locations Bruker provides, the user may need to or choose to adapt Bruker protocols.

Changes can be made to the protocols on the various tabs of the Parameter Editor of the Exam Card.

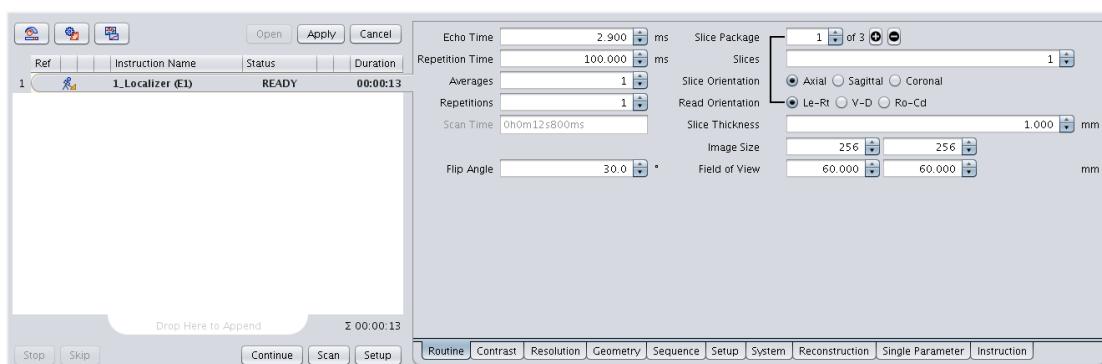


Figure 2.25: A 1_Localizer has been loaded to the instruction list. It is opened and changes can be made in the tabs of the Parameter Editor on the right. The Routine tab is open here.

Once changes have been made to a protocol, save them by clicking on Apply.

Generally, it is best to use one of the Bruker protocols as a starting point for creation of individual protocols since these have been optimized to provide excellent image quality. In many cases, the user will only have to make minor changes to these protocols, such as adapting the field of view or slice thickness to obtain a protocol that meets his individual needs. Bruker, however, does not currently provide optimized protocols for all of the methods available. Some examples of methods for which optimized Bruker protocols do not currently exist are CSI, SPIRAL, UTE, and ZTE. If it is desired to work with these methods, they must be opened from AnyObject/AnyRegion for a starting point.

Be aware that in some cases, not all changes that have been stored to protocols will be retained if the coil combination with which the protocol was stored is changed. For example, if a protocol is edited when a phased array coil is connected and the protocol is stored with an acceleration factor, this acceleration factor will not be active if the protocol is loaded in the future without having a phased array coil connected.

2.2.4 Creating Scan Programs

Users may also choose to create scan protocols using Bruker protocols or their own optimized protocols. A scan program is an entire list of protocols and/or instructions such as pauses, application of contrast agent, etc. that are stored together. Loading a scan program will cause all instructions (protocols, pauses, etc.) to load into the instruction list. As long as there are no user interactions necessary, clicking on continue on the first instruction will start the entire scan program running and no further user interaction is necessary.



WARNING

Do not leave animals unattended. Scan programs are designed to be run without supervision on material subjects only.

Although not designed to run on animals without supervision, scan programs are useful in longitudinal studies. In this case scan programs ensure that the same protocols are run each time. Scan programs can also be used to test a series of new user protocols on phantoms or to create an extensive set of trajectories for later use in, e. g., UTE studies.

Bruker does not offer any scan programs. Instead Bruker provides an extensive number of optimized protocols, which cover numerous applications. The user must decide which of these protocols are most tailored to his needs and select these individual protocols to save to a personalized scan program.

To create a scan program, load all of the desired instructions into the instruction list and save them with the Store Scan Program dialog. See [Saving Protocols and Scan Programs \[▶ 461\]](#)

2.2.5 Saving Protocols and Scan Programs

Once changes have been made to protocols, it is possible to store these new protocols to a user location so as to have access to them in the future. The protocols in the Bruker locations, as well as the locations themselves, are write protected. Protocols that users have created must be stored to user created locations. In addition to storing single protocols, the user may choose to store an entire scan program.

- Right click on the protocol to be stored or by using the Control key and right clicking, highlight the protocols to be stored.
- Select **Store Scan Protocol** or **Store Scan Program**.
- In the Store Scan dialog that appears, enter a name for the protocol or program.
- Select the location to which the protocol or program should be stored. If an appropriate user location does not exist, create a new location by typing new names in the Object, Region, and Application fields.
- Click on **Store**.

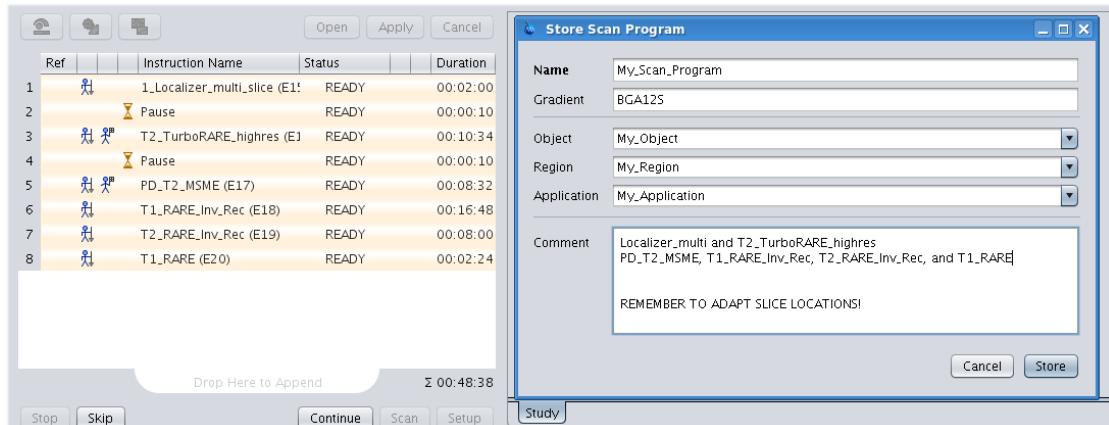


Figure 2.26: The Store Scan Program window. All six of the scans and the two pauses in the instruction list will be stored as the scan program “My_Scan_Program” under the location My_Object/My_Region/My_Application.

The scan protocol or scan program will be stored in the specified location. In the Scan Programs & Protocols list of the Explorer of the Palette, scan protocols are indicated with a file icon and scan programs with a file folder icon.

2.2.6 Running Scan Programs

Scan programs that have been saved can be run by the user who created them, or they can be stored in a common location or in multiple users' locations so that, for example, all users run identical protocols when more than one user is responsible for running scans within a study, or so that more advanced users can create scan programs for inexperienced users.

To run an entire scan program, drag and drop the scan program into the instruction list. All of the scans in the scan program will automatically be loaded.

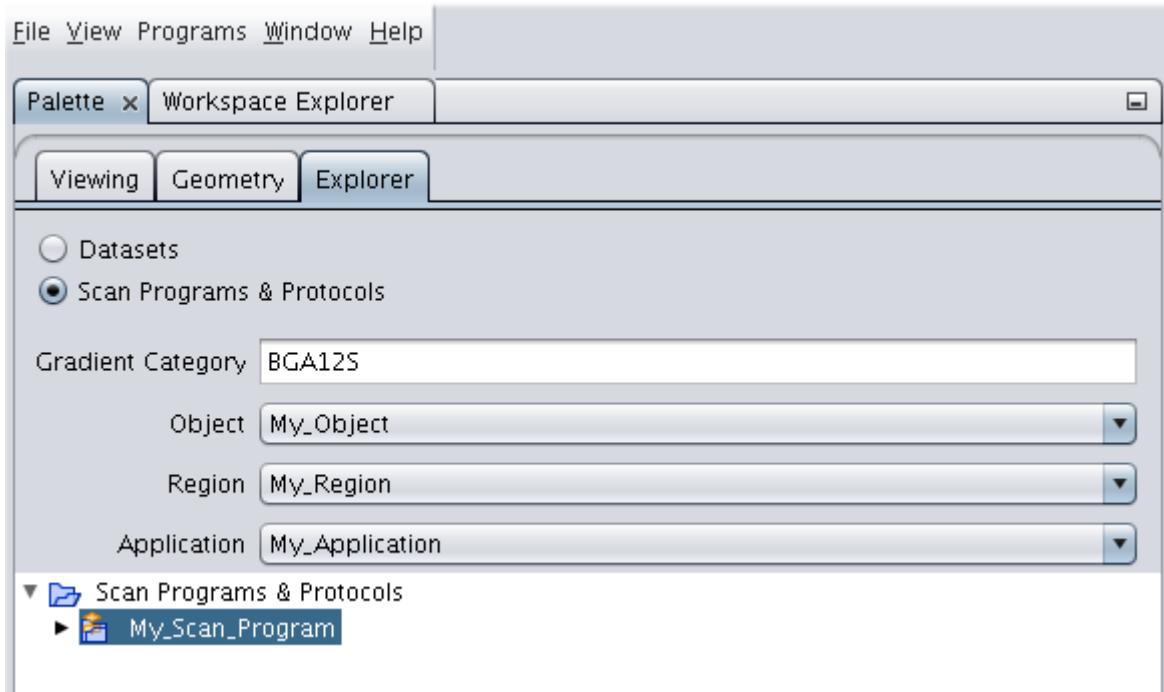


Figure 2.27: The scan program My_Scan_Program can be dragged into the instruction list.

Start the first scan by clicking on "Continue".

If the user now does not interact with the scanner, all of the following scans in the scan program will be started automatically. An exception to this is if a scan specifically requires user interaction. In this case a working man holding a flag will appear to the left of the scan in the instruction list.

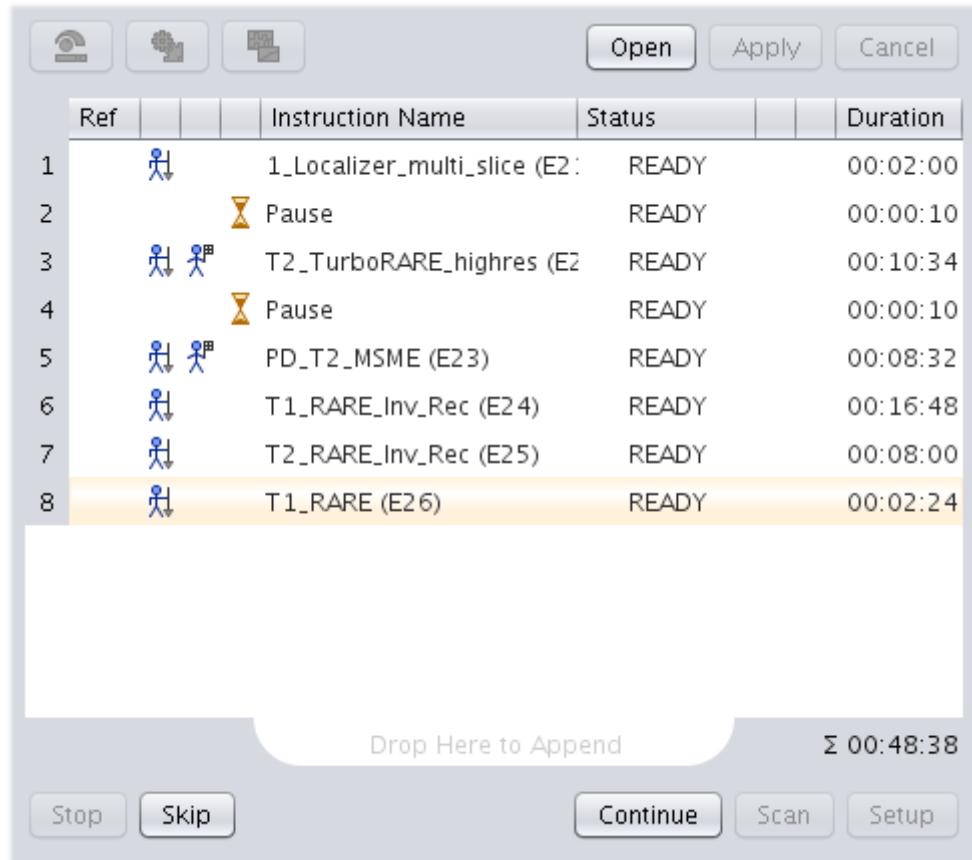


Figure 2.28: The loaded “My_Scan_Program”. When the 1_LOCALIZER_MULTI_SLICE is opened, the user can click on Continue to start scanning. A pause has then been inserted to remind the user to adjust the slice position of the T2_TurboRARE_highres before running it. The T2_TurboRARE_highres will not start until the user specifically starts it by clicking on Continue. This is indicated by the man holding the flag to the left of the instruction name. A second pause has been added after the T2_TurboRARE_highres to remind the user to apply the slice position adjustment to all of the following scans. After starting the PD_T2_MSME with Continue, all following scans will run automatically.

2.2.7 Copying Parameters to Other Protocols

The protocols of scan programs can each be started individually. However, it is more convenient to let the scan program run on its own. Most situations, though, will require the user to adjust the scan geometry. After an initial 1_LOCALIZER or similar image for positioning is run, adjust the slice location. This position can then be easily copied to all other scans in the scan program.

- Open the protocol in the instruction list from which the parameters should be copied.
- Drag the protocol onto the protocol or one of the protocols to which the parameters should be copied.
- When the protocol to which the parameters should be copied appears blue, release the mouse button.
- Select the protocols to which the parameters should be copied under Destination Instructions on the left side of the pop-up window Select Parameter Group.
- Select the parameters to be copied under Parameter Groups on the right side of the pop-up window Select Parameter Group.
- Click on **Okay**.

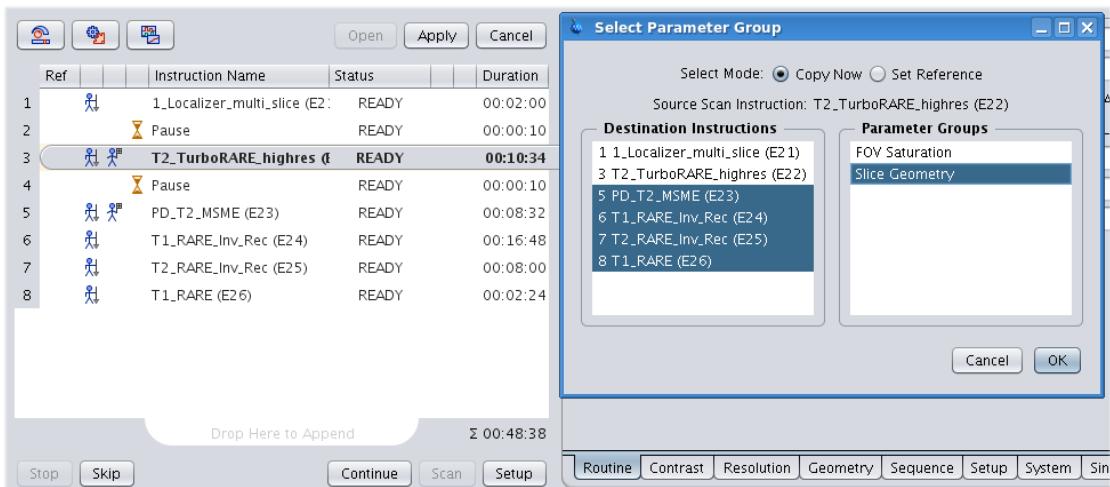


Figure 2.29: The Select Parameter Group window. The slice geometry of the T2_TurboRARE_highres will be copied to all of the following scans in the instruction list.

2.3 Detailed Workflow Description

Introduction

Intended Readers

This portion of the Application Manual is intended to provide advanced users with more in-depth knowledge on usage of ParaVision than provided in Chapter Getting Started, which covers beginning topics for users who are not familiar with ParaVision or users who only make limited use of ParaVision's functions. As opposed to standard users, advanced users make use of possibilities such as changing protocol parameters, using the adjustment, processing, and simulation platforms, or performing additional shimming. It is assumed that readers of this chapter have a firm command of the information provided in Chapter Getting Started. For a better understanding of the discussed topics, it is recommended to have the system switched on and have ParaVision running. An appropriate coil/coils (1H) should be connected and wobbled. Instructions on coil connection can be found in the System Manual.

Prerequisites

This manual must be used in the greater context of other manuals, particularly the respective Advanced User Manual and the safety instructions located therein. It is assumed that the reader has advanced knowledge of MR and understands the effects of changing parameters in various methods. Many topics within the present Application Manual are discussed only in the context of application, for complete coverage refer to the System Manual and the Advanced User Manual.

2.3.1 Registering a Patient/Subject for an Examination

Creating a New Dataset for an Examination

To start an examination, create a new dataset.

- In the **File** menu, click on **New** and then on **Study**.
- The **Study Registration dialog** appears.
- Register the data about the animal on the left side and information about the study on the right side.

The fields **Animal Name**, **Animal ID**, **Study**, and **Position** must be filled.

As the animal ID, it is recommended to enter text describing the overall goal of the entire project, which may only run for one day, but may run over the course of many years. It is later possible to search for the Animal IDs under the category “Subject ID” in the Dataset Browser. For the Study, it is recommended to enter text describing the main goal of the current data to be measured in one session. It is later possible to search for the Study under the category “Study” in the Dataset Browser.

Be sure that the setting for RF corresponds to the current coil configuration. This setting cannot be changed afterwards within an existing study.



It is useful to select a mouse or rat location, for example, Rat/Head/Relaxometry in the location field. Locations are groups of protocols that are common to a certain goal, such as relaxometry, cardiac, or perfusion measurements in a certain region, for example the head, of a certain object, such as a rat. Protocols, which are methods prepared for data acquisition, are found in the mouse and rat locations as well as the special location AnyObject/AnyRegion/BrukerMethods. The location AnyObject/AnyRegion/BrukerMethods contains basic protocols for every measurement method. For example, the RARE method is found here, but the protocols T2_TURBORARE and T1_RARE, which are two different optimizations of the RARE method used to obtain two different types of contrast can be found under Rat/Head/Relaxometry. Therefore, when working with animals, it is highly recommended to work from the Mouse or Rat locations.

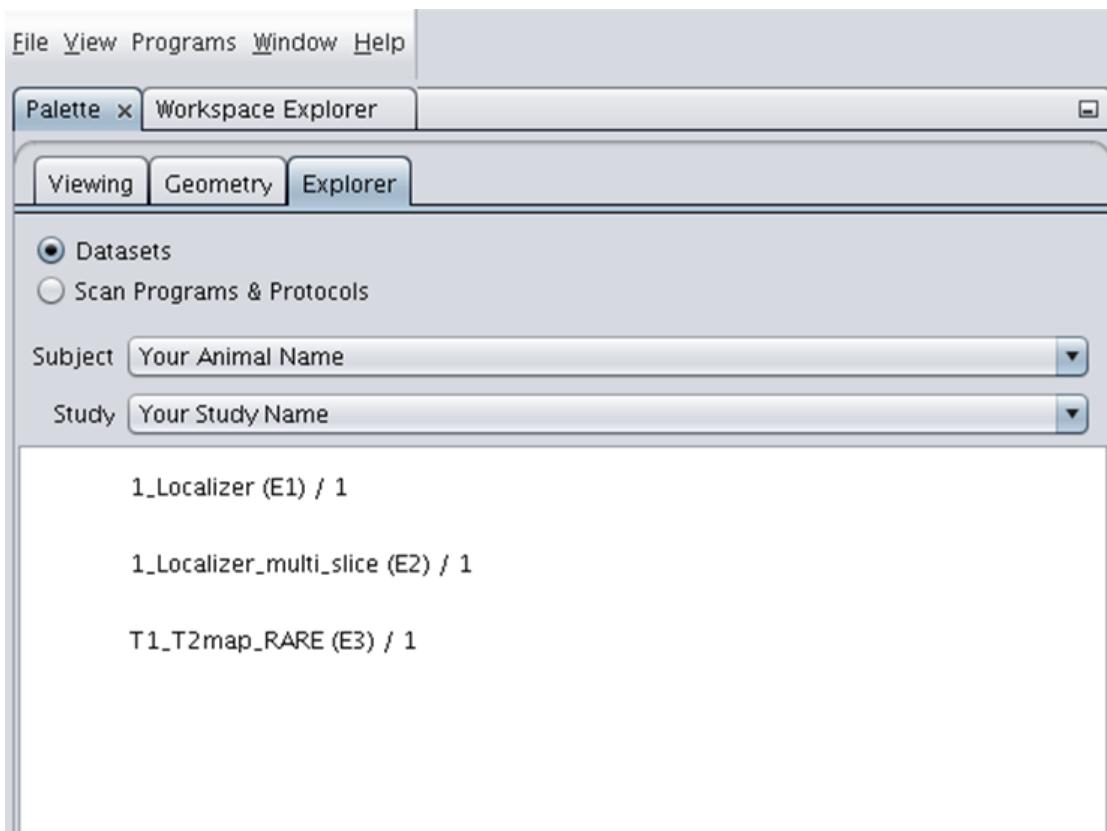
Click on Create to set up a study to run at a later time, or on Exam to automatically create the study and open up the Exam Card for the study.

2.3.2 Loading Protocols

Clicking on Exam will cause the **Exam Card** to open on the right side of the screen with a **tab** at the top with the Animal Name and Study name.

The Animal Name and Study name are shown in the Palette window under Explorer under Datasets.

The white field on the bottom left is empty at first. Scans that have been loaded into the instruction list are listed here.



Datasets under Palette and Explorer is open. A 1_LOCALIZER, a 1_LOCALIZER_MULTI_SLICE; and a T1_T2MAP_RARE have been loaded into the instruction list.

- Click onto **Scan Programs & Protocols** to see the list of protocols in your Study.
- Generally a 1_LOCALIZER (Tripilot) or 1_LOCALIZER_MULTI_SLICE (Multi_Tripilot) are run as the first scans of a study. Tripilot protocols are found in all rat and mouse locations.
- Drag and drop the 1_LOCALIZER into the instruction list. Below it drag and drop other protocols to be run.

A protocol that is open (gray background which continues to the protocol parameters to the right) can be moved further down the scan list by dragging and dropping. The lines to which it can be dropped will appear blue and orange.

2.3.3 Editing Protocols

The Parameter Editor Tabs

Changes can be made to the protocol on the various tabs of the Parameter Editor of the Exam Card.

Some of the most important scan parameters, such as Echo Time and Repetition Time, are found on the **Routine tab**.

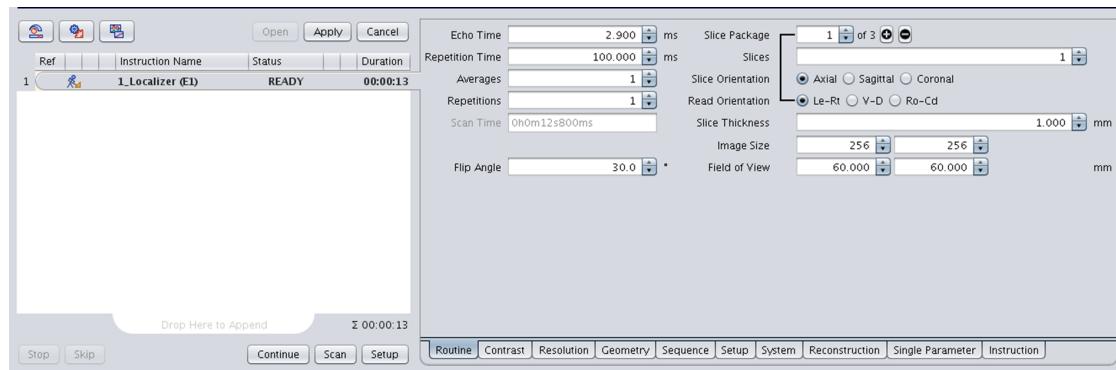


Figure 2.30: The Routine tab of the Parameter Editor is open for the 1_LOCALIZER

The **Contrast** tab contains ten subtabs at the top, which can be used to improve scan quality or increase contrast. The Main subtab is opened as the default. The other nine tabs only display setup options if the subtab itself has been selected on the Main subtab. The options can be selected by clicking in the box to the left of the option, or anywhere along the text line.

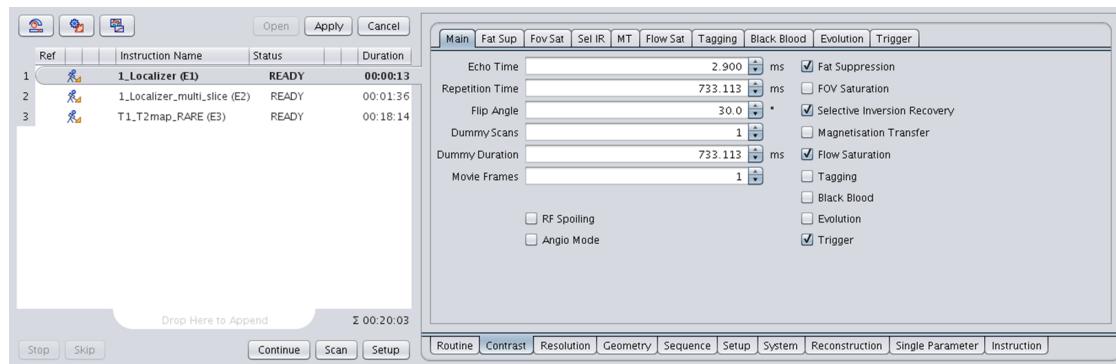


Figure 2.31: The Contrast tab of the Parameter Editor. The Fat Suppression, Selective Inversion Recovery, Flow Saturation, and Trigger subtabs are activated. Black Blood cannot be activated when Selective Inversion Recovery is active, and vice versa.

Information about the resolution of a scan and which parameters influence this is found on the **Resolution** tab.

The **Geometry** tab provides information about the slices and their orientation to one another. The Slice Gap is the distance between the edges of two adjacent slices.

The **Sequence** tab contains information about the frequencies involved in the scan. The bandwidth found on the Main subtab is the bandwidth around the working frequency that will be recorded. On the Frequency Ch. 1 subtab the nucleus being used and its working frequency in MHz are found. Attention should be paid when working with dual X-nuclei/proton coils that the desired nucleus is selected. On the Transmit Ch. 1 subtab, the power used as a reference for the coil is found.

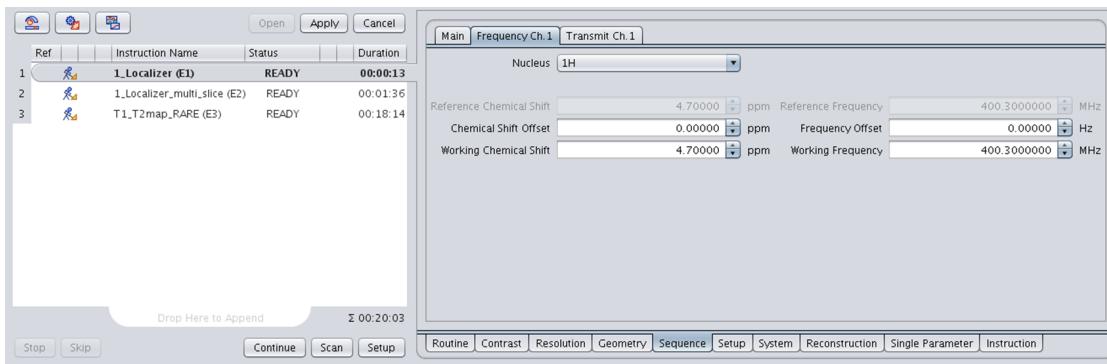


Figure 2.32: The Sequence tab of the Parameter Editor. The Nucleus 1H is selected as the receiving frequency.

The Main tab of the **Setup tab** shows the setting of the receiver gain, which has a maximum of 203. This value is set during the auto-adjustments, but can be changed by either typing a value in the line or holding down on the arrows and sliding the mouse along the slider which appears. The other subtabs contain parameters such as shim which can be adjusted manually with the help of feedback from the scanner. To work interactively with the scanner, click on the **Setup** button below the instruction list. This will start the scanner running in an endless loop mode which is displayed in the Acq/Reco Display window. The status of the scan will read GSP. To stop the endless scanning, click on the **Stop** button.

The **System tab** shows the configuration of the coils in use. Attention should be paid when working with dual X-nuclei/proton coils that the desired nucleus is selected in the operation mode.

Reconstruction options are found on the **Reconstruction tab**.

The **Single Parameter tab** can be useful for users with advanced programming knowledge. It is possible to search for parameters based on their nomenclature in the PVM code and then adjust them directly.

The list of adjustments that take place before the actual scan runs can be found on the **Instruction tab**. A user-defined individual setup/acquisition can be created by dragging and dropping options such as study shim or receiver gain into the field on the left. Pre- and Post Examination Activities, such as the execution of user written scripts, execution of Bruker or user written macros, exportation to DICOM, or the automatic loading of the acquired data in a new image viewer card can be selected here. If one or more of the options here are selected and applied, a magician's hat will appear to the left of the scan name in the instruction list.

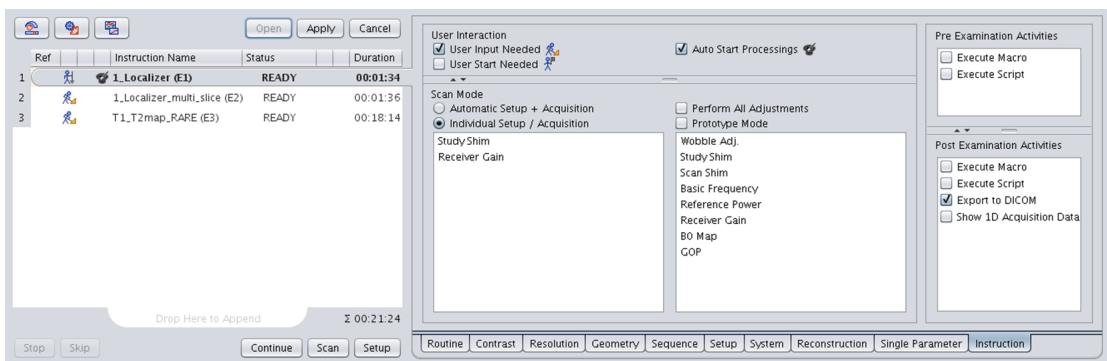


Figure 2.33: The Instruction tab of the Parameter Editor. An individual setup has been selected in which only the study shim and receiver gain adjustments will be performed. As a post examination activity, exportation to DICOM has been selected. This causes a magician's hat to appear to the left of the 1_LOCALIZER scan in the instruction list.

Critical Parameters

Changes of parameters that the user makes on any of the cards can have an effect on critical parameters. If critical parameters are affected, a pop-up message will appear informing the user of this effect. The user may then choose to accept this change or not. Critical parameters are TR, TE, FOV, and slice thickness.

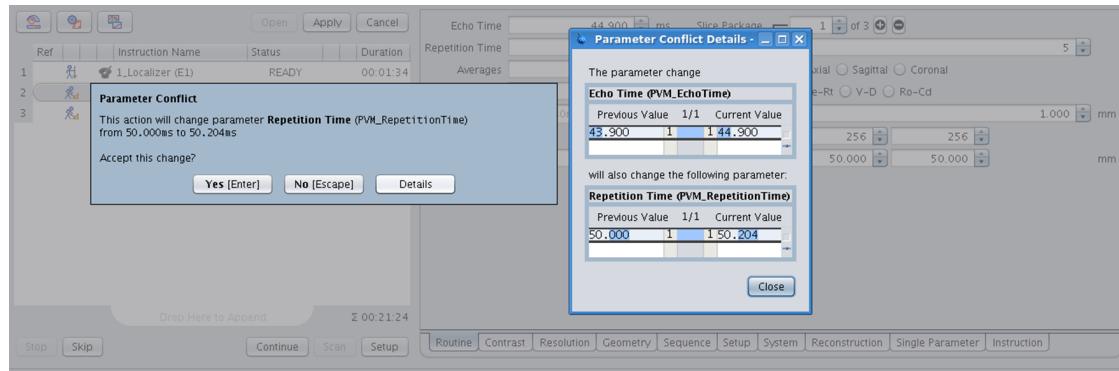
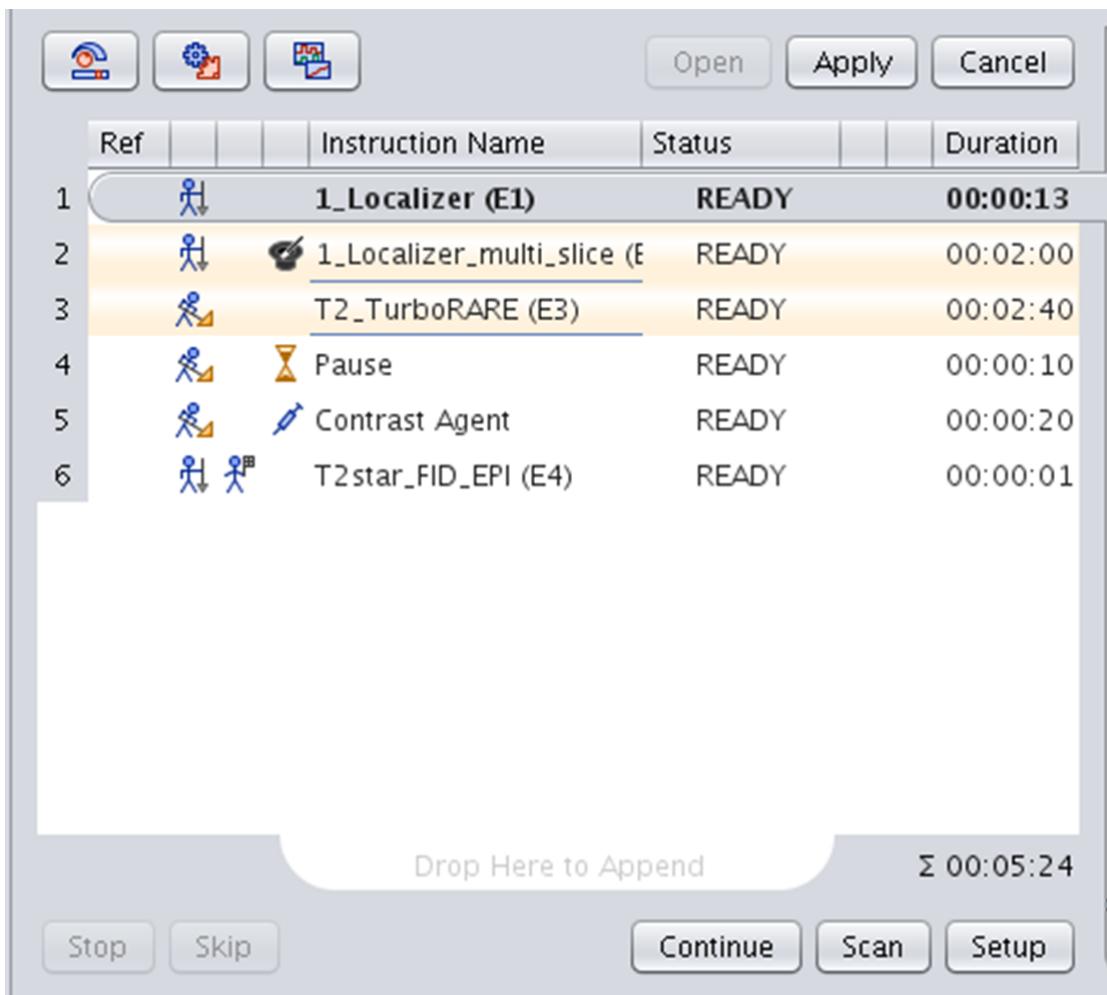


Figure 2.34: A pop-up message informing of a parameter conflict. The TE value has been changed from 43.900 ms to 44.900 ms, which causes the TR to increase from 50.000 ms to 50.204 ms. The user is asked to accept this change. The Parameter Conflict Details window on the right is opened by clicking on the Details button in the Parameter Conflict window on the left.

Status of the scans on the instruction list

The status of the scans can be seen in the instruction list. If changes to a scan must be applied, a working man with a downward yellow arrow is located to the left of the scan name in the instruction list. If changes have been confirmed, a gray arrow will point down. If the user must specifically start the scan (as opposed to the confirmed scan which will run automatically), a working man with a checkered flag is shown.



Instruction list with four scans. The 1_LOCALIZER (E1) and 1_LOCALIZER_MULTI_SLICE (E2) are ready to be run. A magician's hat beside the 1_LOCALIZER_MULTI_SLICE (E2) is seen because, for example, a Post Examination Activity is activated. Changes to the T2_TURBORARE (E3) must be confirmed. The changes made to T2STAR_FID_EPI (E4) have been confirmed, but the scan will not run until the user specifically starts it. The 1_LOCALIZER (E1) is gray because it is open. The 1_LOCALIZER_MULTI_SLICE (E2) and the T2_TURBORARE (E3) are in orange because they are currently activated with the mouse allowing, for example, both be deleted at once by selecting the delete option with the right mouse button.

2.3.4 Geometry Planning

2.3.4.1 Viewing the Reference Image

Generally there will be no reference image available for geometry planning for the first scan in a study. The first scan is usually a Tripilot or Multi_Tripilot. Once a Tripilot or Multi_Tripilot is recorded, it can be dragged and dropped into the Geometry Editor viewports of the Exam Card and used for further geometry planning. If another scan within the study has been recorded, this may also be used for geometrical planning.

2.3.4.2 Navigating Through the Images

If the reference scan has more than three images the central three images will be displayed in the Geometry Editor. If the scan has more than one slice package (such as in the case of the 1_LOCALIZER_MULTI_SLICE), the middle slice of each slice package will be displayed.

To scroll through the slices:

- Move the cursor to the right edge of the active viewport.
- Select the bottom icon of the toolbar that appears
- Use the arrows that appear to scroll through slice packages, slices, frames, etc.

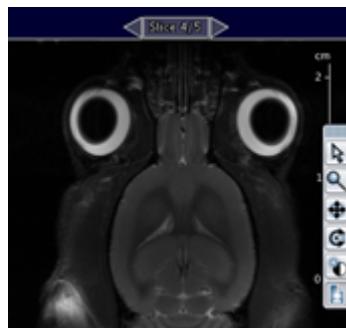
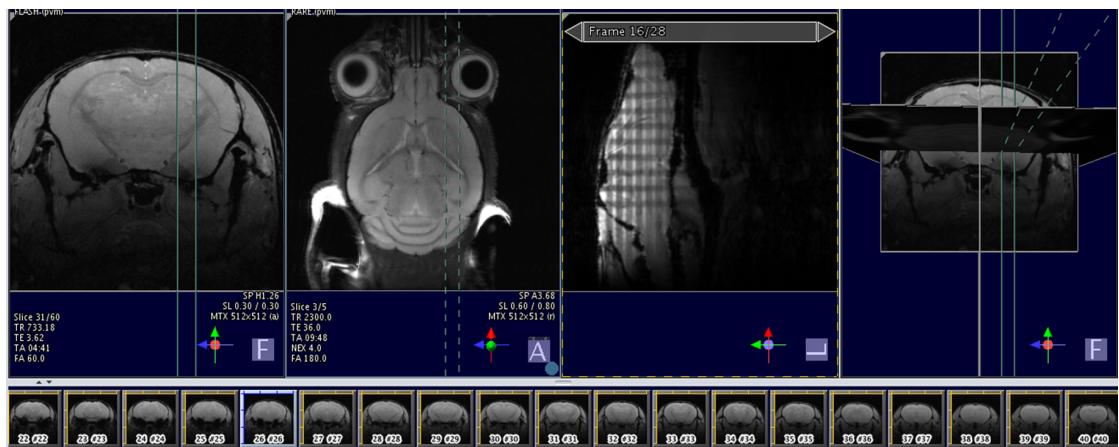


Figure 2.35: Viewport Toolbar

or

- Drag and drop images from the slide show bar into the main viewports.



Images can be dragged from the slide show bar at the bottom of the Geometry Editor into the viewports.

or

- Use the tab or shift and tab keys to page through slice packages..

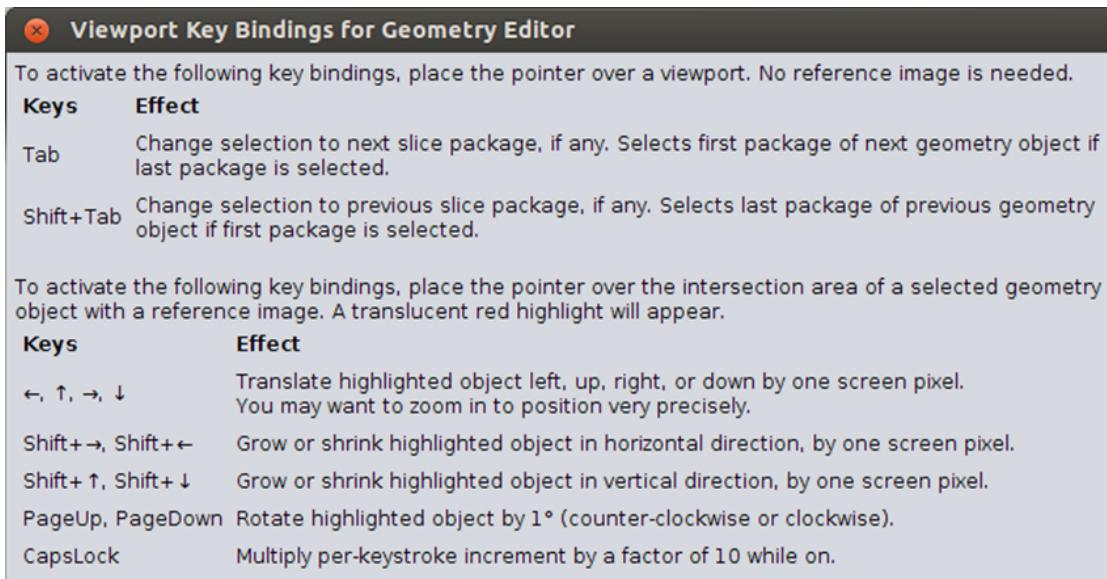


Figure 2.36: Key Bindings of the Geometry Editor

For adaption of image scaling, zooming, etc, see Chapter [Viewing completed scans in the Image Viewer \[▶ 480\]](#).

2.3.4.3 Adjusting Slice Position

- Click on the slice in the active viewport. Slices that are double oblique to the reference image are dashed.

If the **Geometry** tab of the **Palette** window is open, it is possible to switch between slices by clicking on the slice index in the Slice Package List of the Selection field.

- Move the cursor to the center of the slice to cause a cross or circular arrow to appear.
- Clicking on the orange arrow at the bottom right of the Selection field gives priority to either the cross for shifting or circular arrow for rotation. See Figure [Selection field \[▶ 474\]](#).

Shifting Slices

- Shift the slices when the cross appears.

or

- Enter the shift values manually on the **Geometry** tab of the scan.

or

- Use the arrow keys of the keyboard. See Figure [Key Bindings \[▶ 475\]](#).



- Use the sliders in the **Geometry** tab of the **Palette**.



or

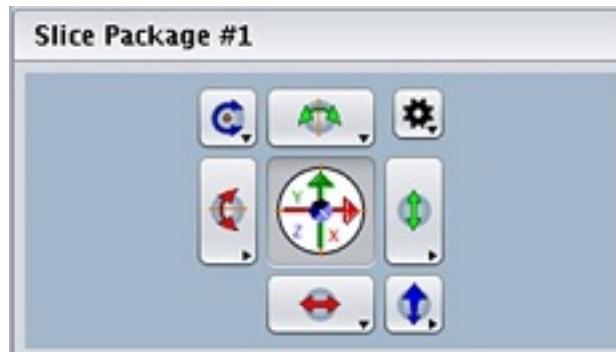
- Enter the value in the **Translate** field of the **Geometry** card of the **Palette**.



By clicking on the center icon of the Slice Package field, it is possible to switch between read, phase, and slice and the x,y, and z axes of the magnet.

Using the Align field, the slices can be aligned with the reference image

Geometry tab of the Palette with slice sliders and rotation wheels. By clicking on the center icon, it is possible to switch between read, phase, and slice and x,y, and z.



Geometry tab of the Palette with slice sliders and rotation wheels. By clicking on the center icon, it is possible to switch between read, phase, and slice and x,y, and z.

Rotating Slices

- Rotate the slices when the circular arrow appears.

or

- Use the rotation wheels in the Geometry tab of the Palette.



or

- Enter the value in the Rotate field of the Geometry tab of the Palette.

or

- Use the page up and page down keys of the keyboard. See Figure [Key Bindings \[▶ 475\]](#).

Adaption of Slice Properties

Move the cursor to the edge of the slice to cause an arrow to appear.

The arrow at the edge of the slice package can be used to increase the slice thickness, increase the slice gap, increase the number of slices, or adapt the slice thickness to the gap ratio depending on the slice mode that is selected in the Geometry tab of the Palette.

The read, phase, and slice directions of the slice can be set to be perpendicular to the reference image by clicking on the corresponding **Align** buttons.

Slice packages can be grouped by selecting the individual groups on the Selection tab of the Geometry tab. The grouped slice packages can then be moved by adjusting the lead slice package.

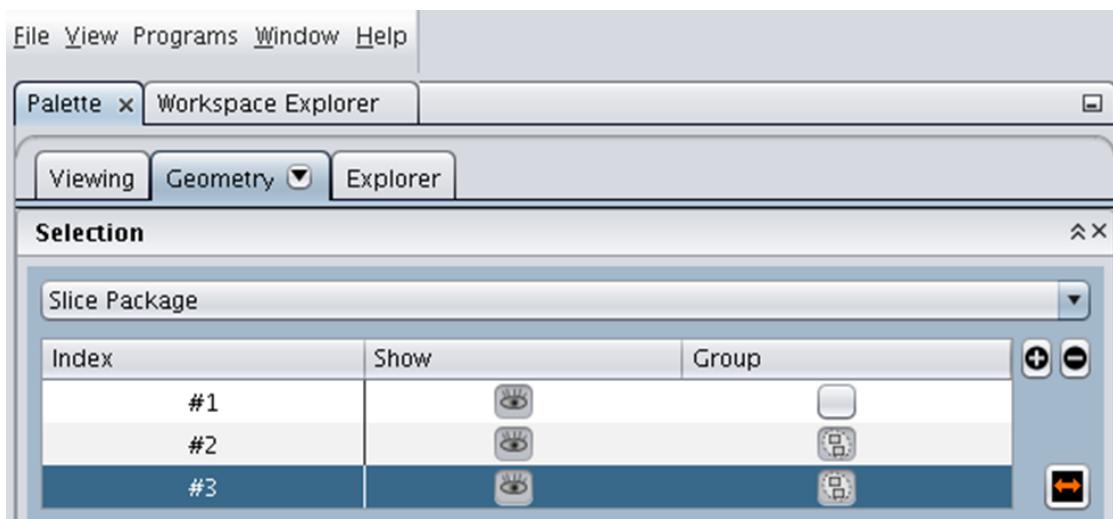


Figure 2.37: The Selection field. Slice packages 2 and 3 are grouped. The orange arrow at the bottom right sets the shifting/rotating priority to shifting.

Key Bindings

Viewport Key Bindings for Geometry Editor	
To activate the following key bindings, place the pointer over a viewport. No reference image is needed.	
Keys	Effect
Tab	Change selection to next slice package, if any. Selects first package of next geometry object if last package is selected.
Shift+Tab	Change selection to previous slice package, if any. Selects last package of previous geometry object if first package is selected.
To activate the following key bindings, place the pointer over the intersection area of a selected geometry object with a reference image. A translucent red highlight will appear.	
Keys	Effect
←, ↑, →, ↓	Translate highlighted object left, up, right, or down by one screen pixel. You may want to zoom in to position very precisely.
Shift+→, Shift+←	Grow or shrink highlighted object in horizontal direction, by one screen pixel.
Shift+↑, Shift+↓	Grow or shrink highlighted object in vertical direction, by one screen pixel.
PageUp, PageDown	Rotate highlighted object by 1° (counter-clockwise or clockwise).
CapsLock	Multiply per-keystroke increment by a factor of 10 while on.

Figure 2.38: Key Bindings of the Geometry Editor

2.3.5 The Processing Platform

In addition to the pre- and post-scanning options found on the instruction card, it is also possible to activate further options that can be run before or after the scan. These options are found in the Processing Platform.



The Processing Platform can be opened by clicking on the middle icon of the three icons located above the instruction list.

Some very useful options are found in the list of Post Image Series Activities on the right. These include **Load Reference Image**, which automatically loads the scan into the Geometry Editor, and **Create Report**, which generates a PDF document with many of the most important scan parameters and some representative images. A report can also be created from the “1” level of the data tree in the workspace explorer.

Depending on the scan protocol, the tabs of the Processing Platform contain options such as Reconstruction, RECO Parameters, and Single Parameter. Reconstruction allows the user to reconstruct the data as, for example, an SWI, or to adjust regridding parameters. Parameters such as the Reconstruction size, Output Word Size, Output Image Type, and Filters can be found on the RECO Parameters tab.

Reconstructed data can be re-reconstructed in a different manner.

Additional reconstruction possibilities are explained in Chapter [Reconstructing Recorded Data](#) [\[479\]](#)

2.3.6 The Simulation Platform

Changes that a user makes to a Bruker protocol may potentially cause the protocol to not be executable because the demand on the gradients is more than that which is achievable by the system. It is possible to simulate a scan before it is started to ensure that the gradient duty cycle can be run by the system.



- To do this, open the simulation platform (right icon of the three to the top left of the instruction list) with the scan open and click on **Start**.
- The gradient duty cycle simulation will start and at completion will read either “Gradient Duty Cycle: OK”, “Gradient Duty Cycle: Critical”, or “Gradient Duty Cycle: Violated”.

To decrease a gradient duty cycle:

- ▶ increase the FOV
- ▶ increase slice thickness
- ▶ decrease the number of slices
- ▶ decrease matrix size
and/or
- ▶ decrease the number of averages

i The gradient duty cycle simulation is in real time. Therefore it is not recommended to test long scans on animals. If a gradient duty cycle is critical or violated, this will most likely become apparent within the first minutes of simulation. To have absolute assurance that the gradient duty cycle will be OK, it is recommended to simulate long scans on phantoms before applying them to animals.

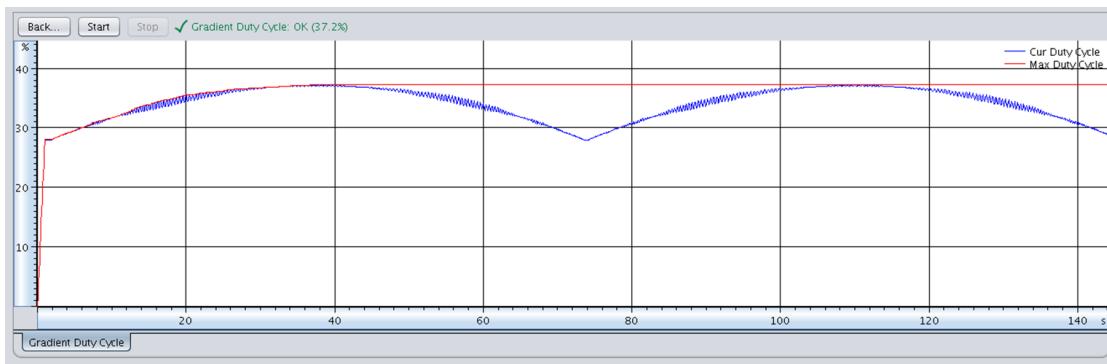


Figure 2.39: Gradient duty cycle simulation. The maximum duty cycle (red) is reached within the first minutes of the scan.

2.3.7 Starting the Scan

- If no changes to a protocol have been made, start the scan by clicking on **Continue**.
- If changes have been made, apply these by clicking on **Apply** and start the scan with **Continue**.
- Clicking on **Scan** will start the scan and create a duplicate of it in the scan list that will be recorded next.

The time remaining until the scan is completed can be read under “Duration”.

A man with a yellow arrow to the left of the protocol name means that the user must accept the changes that have been made before a scan can be run. A man with a gray arrow indicates that changes have been accepted. Unless user input is necessary, when one scan is finished, the next will start automatically. See also Section [Status of the scans on the instruction list. \[▶ 469\]](#)

2.3.8 Auto-adjustments and Adjustment Platform

Standard Auto-adjustments

If no changes to the auto-adjustments have been made, the default adjustments will be run. These are wobbling, adjustment of the basic frequency, adjustment of the study shim, adjustment of the reference power, and adjustment of the receiver gain. The actual scanning will then start and the status will read “scanning” or “reco”.

These adjustments will be run for the first scan of a study. Further scans will only be preceded by adjustment of the receiver gain, as the other adjustments are valid for all scans in the study. An exception to this can be if specific shimming is performed for a certain scan.

Scanning without Auto-adjustments

To run a scan without any auto-adjustments, drag the **GOP** option into the left field on the Instruction tab.

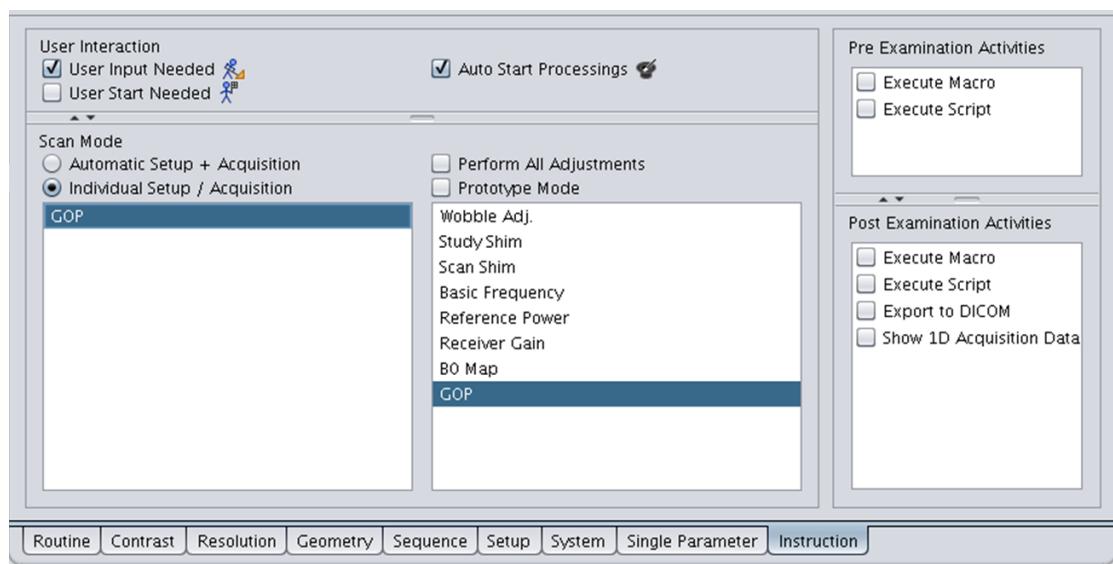


Figure 2.40: The **GOP** option has been dragged into the left field on the **Instruction** tab of the Parameter Editor. When the scan is started, no auto-adjustments will be run.

Rerunning Auto-adjustments



⚠ CAUTION

If the position of the animal or sample is moved within the scanner, it is necessary to rerun the auto-adjustments.

If it is necessary to rerun the adjustments, for example if the object being scanned has been moved within the scanner, **Perform All Adjustments** on the Instruction tab should be selected before rerunning the scan.

If an adjustment is not run successfully, (status line will read “FAILED”), the user may change the way the adjustment is run in order to obtain successful adjustments. This may, for example, be the case with the reference power when using transmit/receive surface coils. The reference power can generally not be adjusted with these coils using the standard reference power adjustment method, since the standard adjustment runs using an axial slice.



- To run this adjustment successfully, open the Adjustment Platform by clicking on the adjustment platform icon. The adjustment platform icon is the left icon of the three to the top left of the instruction list.
- Open the reference power adjustment.
- Change the slice orientation to coronal.
- Click on **Apply** and **Start**. After the adjustment has run successfully, a green check will appear under “Status”.
- Right click on the adjustment and select **Save Adjustment Result**.
- Click on **Back** to return to the Parameter Editor.

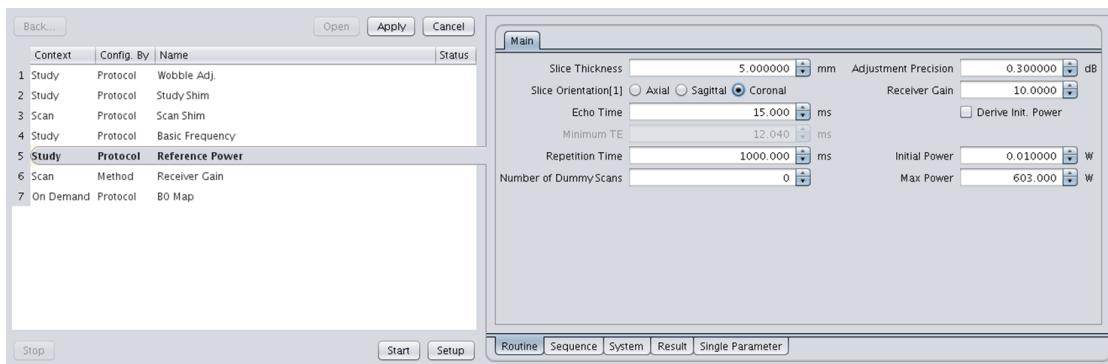


Figure 2.41: The reference power adjustment has been changed from the default axial to coronal on the adjustment platform.

2.3.8.1 Shimming

When a scan of a study is started with the Scan Mode set to Automatic Setup + Acquisition, a Study Shim is recorded. This Study Shim will only be performed once for the first scan in a study where the Scan Mode is set this way and will be valid for the rest of the study if no other shimming is performed by the user.

The Study Shim method of shimming is based on the narrowing of the Full Width at Half Maximum of the 1D reconstruction of the signal.

The Study Shim method is ParaVision's standard method for shimming, since it provides shims that lead to excellent image quality in almost all cases. In a few exceptional situations, the user may choose to perform further shimming within a study, for example with the MAPSHIM utility. This is, however, generally not necessary. For more information on MAPSHIM, please see Chapter FASTMRI and for localized spectroscopy please see Chapter [Spectroscopy \[▶ 556\]](#).

2.3.9 Viewing Completed Scans in Examination card

Once the scanning and reconstruction are completed, the images can be dragged and dropped into the Geometry Editor.

In the case of a Tripilot or Tripilot_multi, axial, sagittal, and coronal images will appear in the three left viewports, as well as an axial interactive 3D image in the right viewport.



Figure 2.42: Geometry Editor with Interactive 3D viewport on right. The fifth image in the slideshow (with the blue boarder) is ready to be dragged into one of the viewports.

The completed scan can also be loaded into the slide show at the bottom of the Geometry Editor via dragging and dropping. This is useful when a large number of slices have been recorded, since it is then possible to drag and drop a slice from the slide show bar into the main viewports at the top.

For adaption of **image scaling**, **zooming**, etc, see Chapter [Viewing completed scans in the Image Viewer \[▶ 480\]](#).

2.3.10 Reconstructing Recorded Data

It is sometimes desirable to have multiple reconstructions of one dataset. For example, a FLASH may be reconstructed as a magnitude or a susceptibility weighted image. Re-reconstructions of data can be performed in the Dataset Browser.

- Open the **Dataset Browser** by selecting it in the Window menu.
- Open the **Examination** or **Image Series** tab.
- Select the dataset to be re-reconstructed by clicking on it once in the list in the middle of the screen.
- Click on **Create Image Series**.
- Click on **Data Reconstruction** in the Select Processing pop-up window.
- Edit the reconstruction as desired in the Data Reconstruction tab that appears.

- Click on **Save**.
- Click on **Execute**.

A new procno will be created on the Image Series tab. It will additionally appear in the Workspace Explorer tree under the protocol name and 1D Acquisition Data.

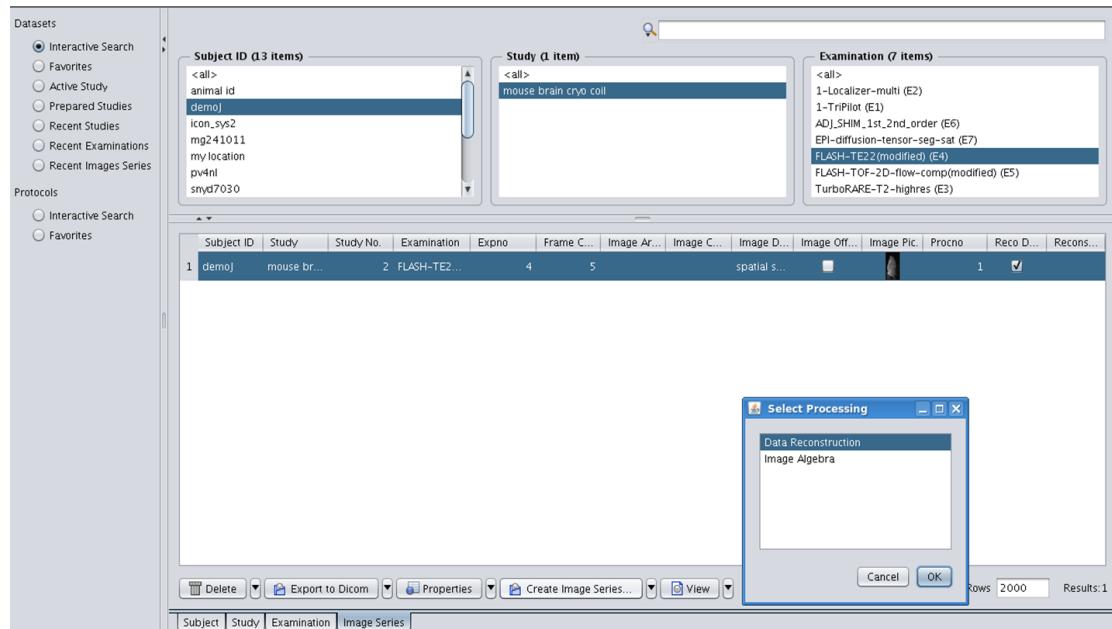


Figure 2.43: Reconstructing data in the Dataset Browser. The dataset (demoj/mousebr.../2/FLASH-TE2.../4/5/spatial s...) to be re-reconstructed is selected in the middle field.

2.3.11 Viewing completed scans in the Image Viewer

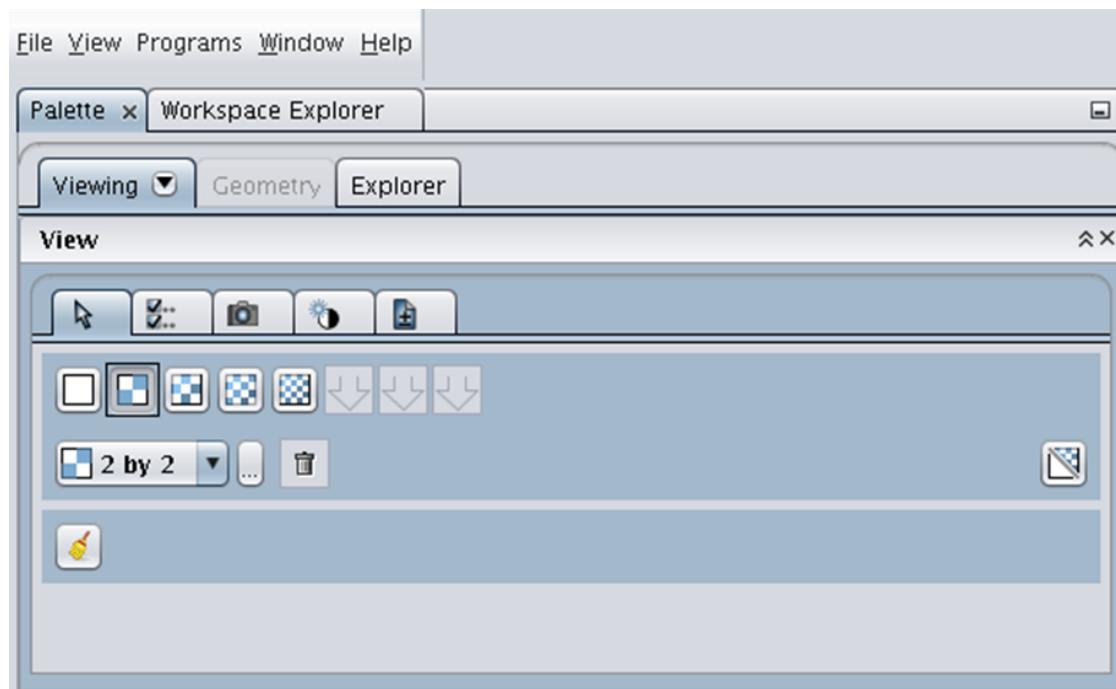
Chapter [Viewing Completed Scans in Examination card \[479\]](#) covered how to view images within the Geometry Editor of the Exam Card. Viewing images here is useful during scanning itself, since the user can view the images without losing sight of the parameter cards and instruction list. Additionally, the slide show bar, which can be accessed here, is useful when handling a large number of images.

Whereas the main function of the Exam Card is geometry planning, the Image Viewer, with its extended viewing options, is used for detailed examination and analysis of completed scans.

- To view completed scans in the Image Viewer, double click on the scan in the instruction list.

The viewing options in the Image Viewer can be accessed from the Viewing tab of the Palette. The View and Analysis tabs are open as default. They contain additional options as subtabs, which can be displayed individually by clicking on the arrow on the top right of the individual subtabs.

The View tab contains the Viewport Layout, Viewport State, Camera Tool, Lookup Table and Smoothing, and Navigation options as subtabs.



Viewing tab of the Palette with tabs for Viewport Layout, Viewport State, Camera Tool, Lookup Table and Smoothing, and Navigation. The Viewport Layout tab is open.

Additionally, many of the functions can be evoked by moving the cursor to the right edge of the active viewport. See Chapter [Navigating Through the Images](#) [▶ 471].

2.3.11.1 Layout Options

The viewport Layout option allows the user to change the number of rows and columns in the Image Viewer.



- Click on one of the layout icons in the pull-down list to change the number of viewports.

It is possible to create viewport layouts that are not offered as a default.



- Click on the icon with the three dots to the left of the trash can icon.
- Enter the number of columns and rows desired.
- Click on **Add Layout** and if desired, **Set as Default**.



Eight layouts can be saved as icons in the top of the layout tab. To add or delete a layout, drag and drop it either from the list of layouts into the free arrow space or from the saved icons list onto the trash can icon, respectively. For better viewing of an image in one of the Image Viewer viewports, it is possible to switch back and forth between a single viewport and the previous viewport layout.



With the desired viewport active (dashed yellow border), click on the viewport layout icon with a diagonal stripe to the right of the trash can.

For better viewing of an image in one of the Image Viewer viewports, it is possible to switch back and forth between a single viewport and the previous viewport layout.

It is also possible to clear all of the viewports by clicking on the broom icon.



2.3.11.2 Camera Tool

Images can be shifted, rotated, and zoomed using the options on the left side of the Camera Tool.

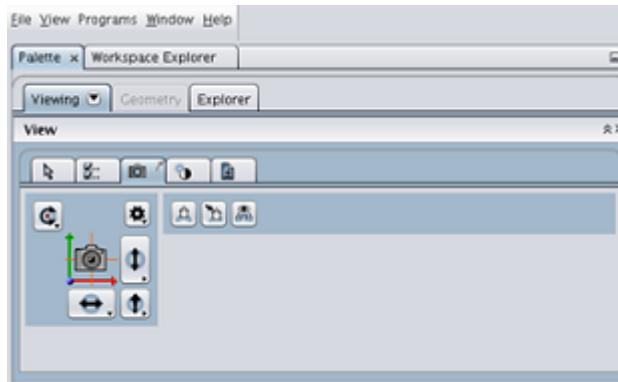


Figure 2.44: The Camera Tool

Shift images using the arrows to the right of and below the camera symbol.



Rotate images with the curved arrow to the top left of the camera symbol.



Zoom images with the arrow to the bottom right of the camera symbol.



Rotate images 90 degrees with the rotation wheel to the top right of the camera symbol.

The options on the top right side of the Camera Tool allow a position of the image to be set to which it is easy to return.



To set this “home”, click on the middle icon (house with arrow).



To return to this position after changes in shifting, rotating, or zooming have been made, click on the left icon (house without arrow).

2.3.11.3 Lookup Table and Smoothing

On the Lookup Table and Smoothing card, the red scale can be used to adjust the scaling of the image.

Colors of the image can be changed in the pull-down list in which gray is the default.

Smoothing options are included at the bottom of the tab.

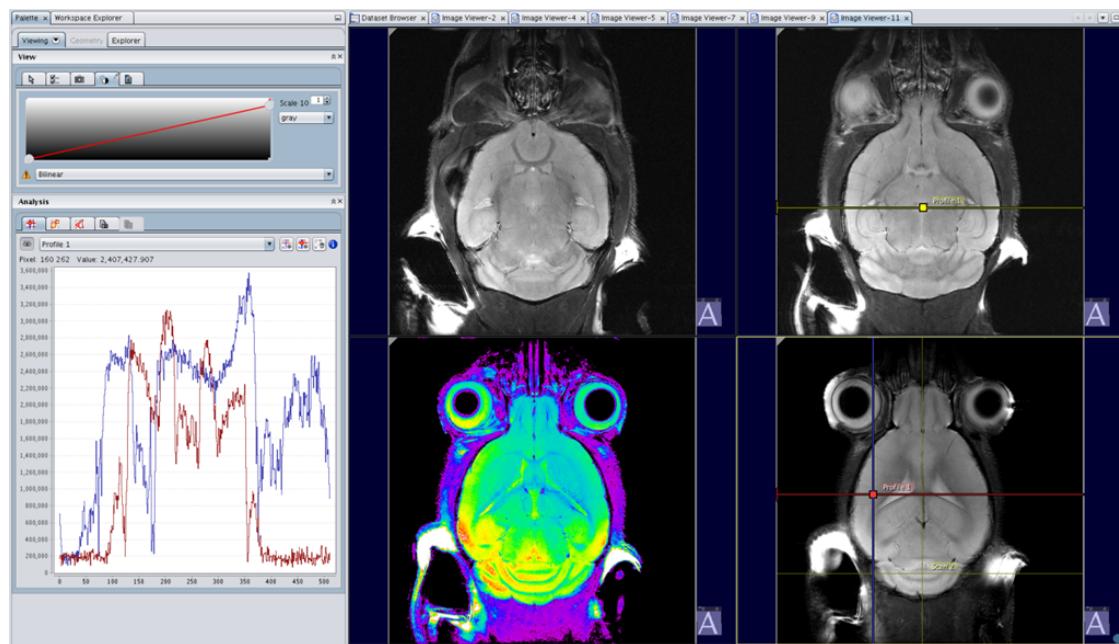


Figure 2.45: The Smoothing tab. The bottom right viewport is active with gray as the selected color. The viewport on the bottom left has the color nmr2.

2.3.11.4 Dataset Navigation

Using the Dataset Navigation, it is possible to navigate through the slices and frames of a dataset. By using the drop-down list on the left, it is possible to change the active viewport to a specific slice number or position. The two icons to the right of the drop-down list display the next or previous slice relative to the active viewport in the next viewport and advance the active viewport by one viewport throughout the viewport layout. When the last viewport in the layout is active, clicking on one of the icons will activate the first viewport in the layout. To page through slices within one viewport, see Chapter [Navigating Through the Images](#) [471].

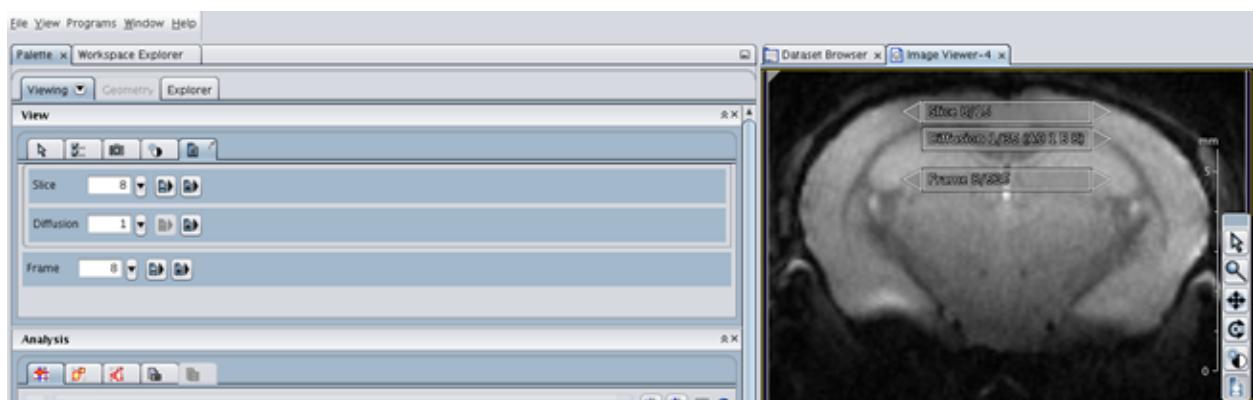


Figure 2.46: Navigating through slices can be done with either the Dataset Navigation tab of the View tab or with the toolbar that appears when the cursor is placed at the edge of the viewport. Here the 8th slice of 15 is selected and the first diffusion direction of 35. This is frame number 8.

2.3.11.5 Viewport State

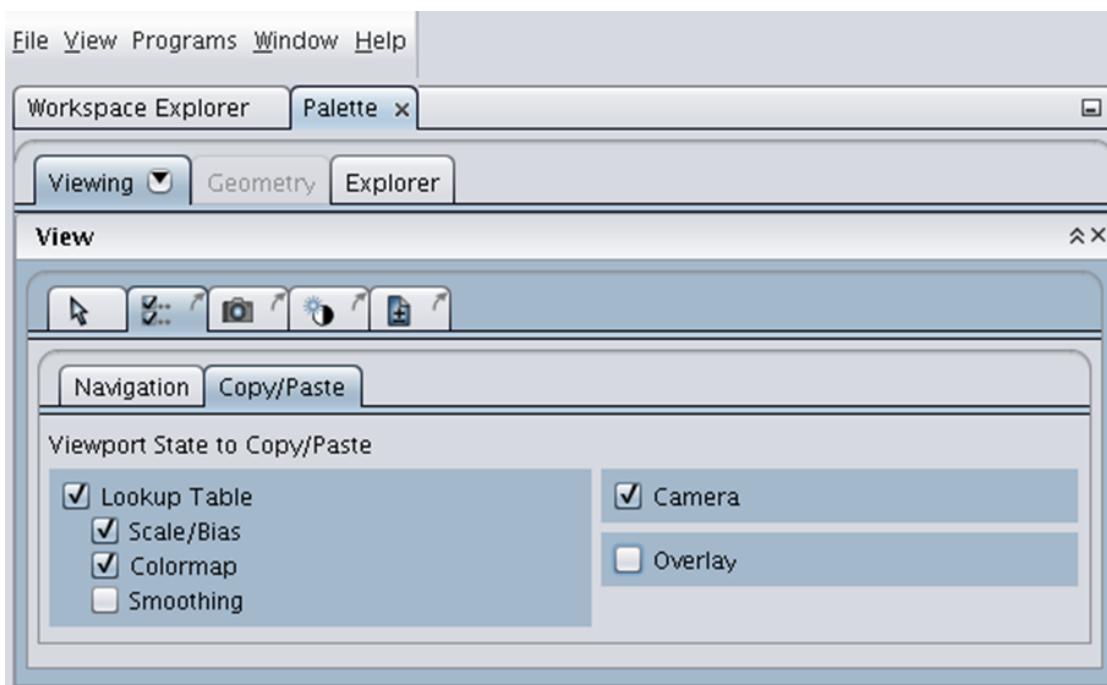
Changes made with the Camera Tool and with the Lookup Table and Smoothing option can be retained when navigating through slices and frames within one viewport as well as transferred to other viewports.

To retain the changes when navigating within a viewport

- Select the checkboxes of the changes to be retained on the Navigation tab of the Viewport State tab.

To copy changes to another viewport

- Select the checkboxes of the changes to be retained on the Copy/Paste tab of the Viewport State tab.
- Activate the viewport with the changes to be copied.
- Right click.
- Select **Copy State**.
- Activate the viewport to which the changes should be copied.
- Right click.
- Select **Paste State**.



The Copy/Paste tab of the Viewport State tab. The Scale/Bias, Colormap, and Camera functions will be copied to other viewports.

To copy all changes to other viewports, it is also possible to use the copy and paste options found when right clicking in the viewport frames.

2.3.11.6 Displaying Scan Information Text

- To remove the text that is overlaid onto the image, right click on the active viewport and deselect the option Parameter Overlay.

2.3.11.7 Analysis

The Analysis Tab contains subtabs for scans and profiles, regions of interest, measurements, creating snapshots, and creating movies.

Scans and Profiles

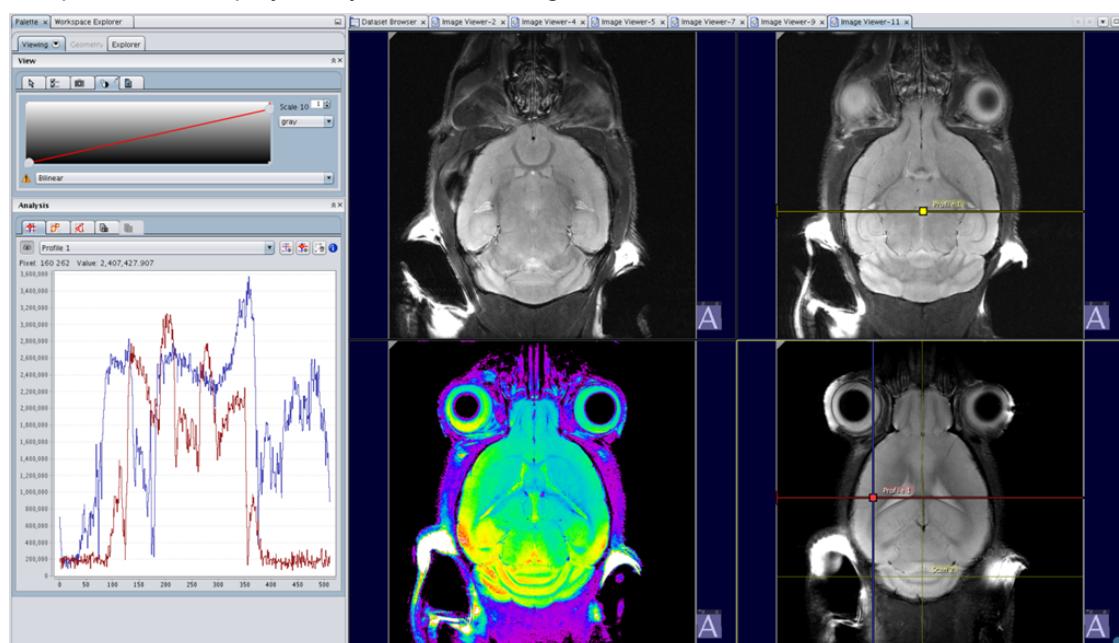
The left tab of the Analysis tab is used for Scans and Profiles.

The first icon to the right of the pull-down list is used to create scans. Scans show values for a specific position/pixel location.

The second icon to the right of the pull-down list is used to create profiles. Profiles show values along one or two lines through the image.

Scans and profiles can be shifted by placing the cursor at their position (for scans) or intersection (for profiles) and then moving with the mouse or by activating them and using the keyboard arrows. Placing the cursor along one of the lines in a profile will evoke a curved arrow. This can be used to remove one of the two lines of a profile, so that only a single profile line is shown.

The values of the scans and profiles are found in the pull-down list. The scan or profile that is currently active in the pull-down list is displayed in blue and red in the image. All other scan and profiles are displayed in yellow in the image.



The Scans and Profiles tab. The bottom right viewport is active and contains a profile, which is active (blue and red) and displayed in the Analysis tab on the left. It also contains a scan, which is inactive (in yellow). The top right viewport contains an inactive profile (in yellow) in which one of the two lines has been removed.

All scans and profiles can be hidden and redisplayed using the eye icon on the left or deleted using the trashcan icon on the right.

All scans and profiles are saved with the image. If the image is reloaded into the Image Viewer at a later time, the scans and profiles will appear with the image.

Regions of Interest

The right tab of the Analysis tab is used for Regions of Interest (RIO). Use the icon to the right of the pull-down list to create ROIs.

ROIs can be shifted or rotated by placing the cursor at their center and then moving with the mouse when the cross or curved arrow appears, respectively. The size of the ROI can be changed by using the arrow that appears when the cursor is placed at the edge of the ROI.

The histogram of the values of the pixels of the ROI is found in the pull-down list. The ROI that is currently active in the pull-down list is displayed in solid yellow in the image. All other ROIs have only yellow boarders.

By activating the Thresholds checkboxes on the ROI tab, thresholds can be set so that only pixels containing values within the threshold values within the ROI are displayed.

Additional changes to the ROI can be made by using the ROI key bindings.

Viewport Key Bindings for ROIs	
Keys	Effect
Tab	Change selection to next ROI.
Shift+Tab	Change selection to previous ROI.
←, ↑, →, ↓	Translate selected ROI left, up, right, or down by one image pixel.
Shift+→, Shift+←	Grow or shrink selected ROI in horizontal direction, by one image pixel.
Shift+↑, Shift+↓	Grow or shrink selected ROI in vertical direction, by one image pixel.
PageUp, PageDown	Rotate selected ROI by 1° (counter-clockwise or clockwise).
Home	Set rotation angle of selected ROI to 0°.
End	Set rotation angle of selected ROI to 90°.
CapsLock	Multiply per-keystroke increment by a factor of 10 while on.

Note: key bindings are only active while a viewport has focus (shown as continuous yellow border).

Figure 2.47: ROI Key Bindings

All ROIs can be hidden and redisplayed using the eye icon on the left or deleted using the trashcan icon on the right.

All ROIs are saved with the image. If the image is reloaded into the Image Viewer at a later time, the ROIs will appear with the image.

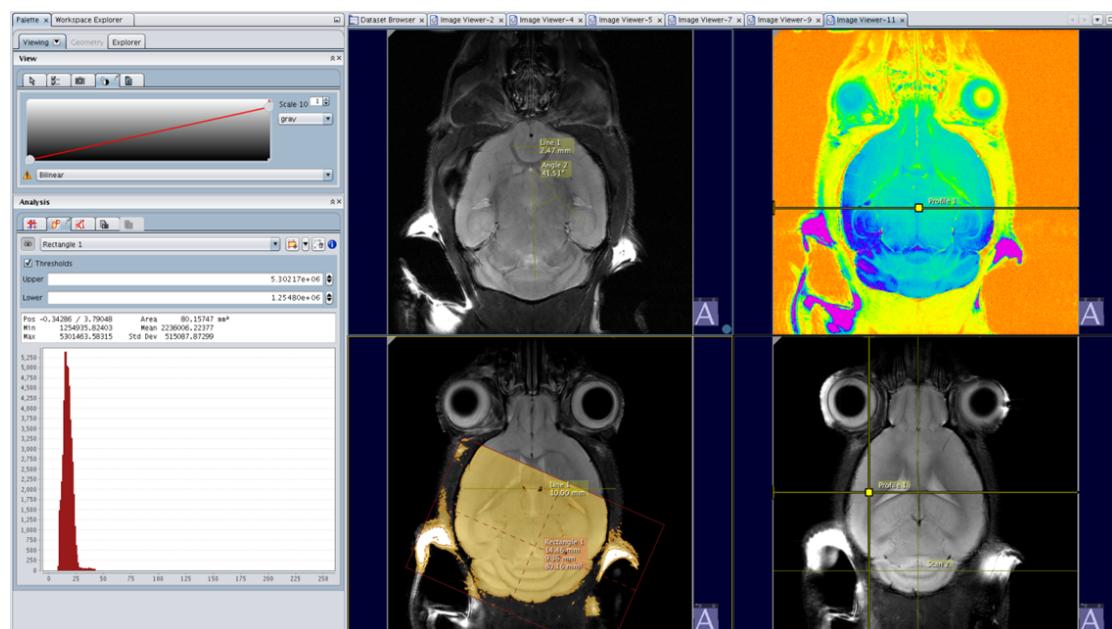


Figure 2.48: ROI subtab of the Analysis tab. The ROI in the bottom left viewport is active. Thresholds for the ROI have been set.

Measurements

The center tab of Analysis tab is used for measurements. Use the icon to the right of the pull-down list to create distance measurements.

Lines can be shifted by dragging the mouse at the center of the line. Lines can be shortened or lengthened by dragging the mouse at one of the ends of the line. To rotate the line, drag the mouse at one of the lines ends.

The length of the lines is displayed in the viewport.

Use the second icon to the right of the pull-down list to create angular measurements.

Angles can be shifted by dragging the mouse at the center of one of the two lines. Angles can be increased or decreased by dragging the mouse at the end of one of the two lines. The angles starting point can be adjusted by dragging the mouse at the tip of the angle.

The angle's value is displayed in the viewport.

Key bindings can also be used to make changes to the lines and angles.

Viewport Key Bindings for Measurements	
Keys	Effect
Tab	Change selection to next line or angle.
Shift+Tab	Change selection to previous line or angle.
Ctrl+↑, Ctrl+→	Activate next vertex on current line or angle.
Ctrl+←, Ctrl+↓	Activate previous vertex on current line or angle.
←, ↑, →, ↓	Translate selected vertex left, up, right, or down by one image pixel.
CapsLock	Multiply per-keystroke increment by a factor of 10 while on.

Note: key bindings are only active while a viewport has focus (shown as continuous yellow border).

Figure 2.49: Measurement Key Bindings

The active line or angle is displayed in red. All other lines and angles are displayed in yellow.

The top left viewport in Figure [The Camera Tool ▶ 482](#) is active and contains an inactive line and an active angle measurement. Their values are shown in the viewport.

All lines and angles can be hidden and redisplayed using the eye icon on the left or deleted using the trashcan icon on the right.

All lines and angles are saved with the image. If the image is reloaded into the Image Viewer at a later time, the lines and angles will appear with the image.

i For further analysis options specific to certain methods (for example relaxation value mapping), see the corresponding application chapters.

Create Snapshot

- Activate the viewport.
- Click on the subtab Create Snapshot.
- Click on **Capture**.
- Select the file type and the location to which the file should be saved in the pop-up window Save Snapshot.
- Click on **Save**.

The viewport will be saved as the desired type of file along with a table of the individual pixel values of the scan.

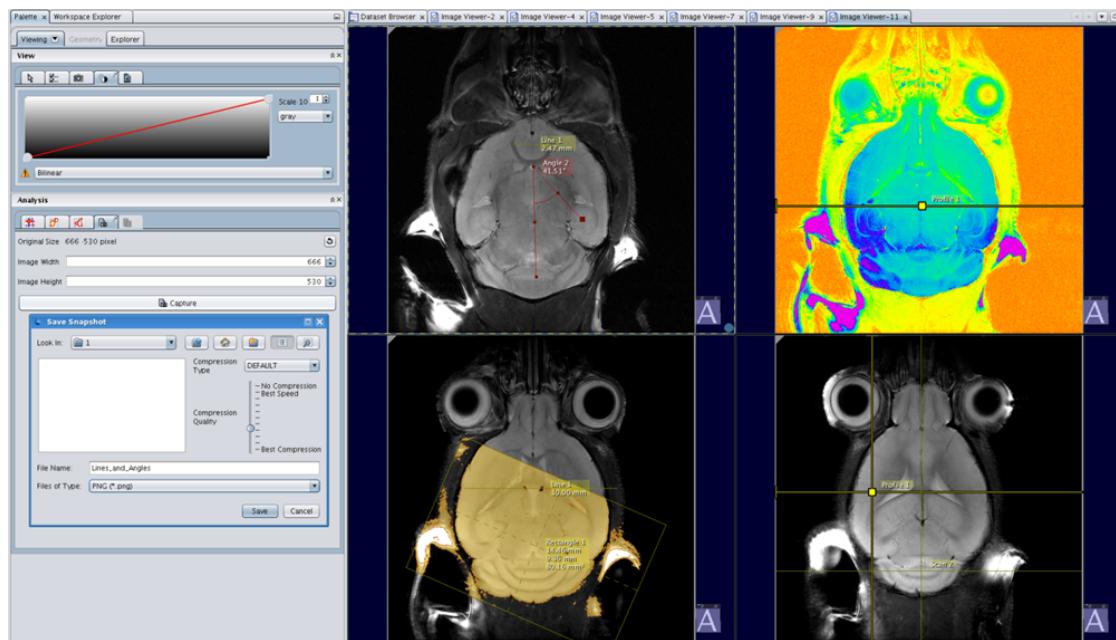


Figure 2.50: A snapshot of the active top left viewport will be saved as a png named “Lines_and_Angles” to the location “1”.

2.3.12 Copying Parameters to Other Protocols

It is sometimes useful to have the exact same parameters in more than one scan. For example, one often wants to have the same slice position in different scans. Parameters can easily be copied from one protocol to another.

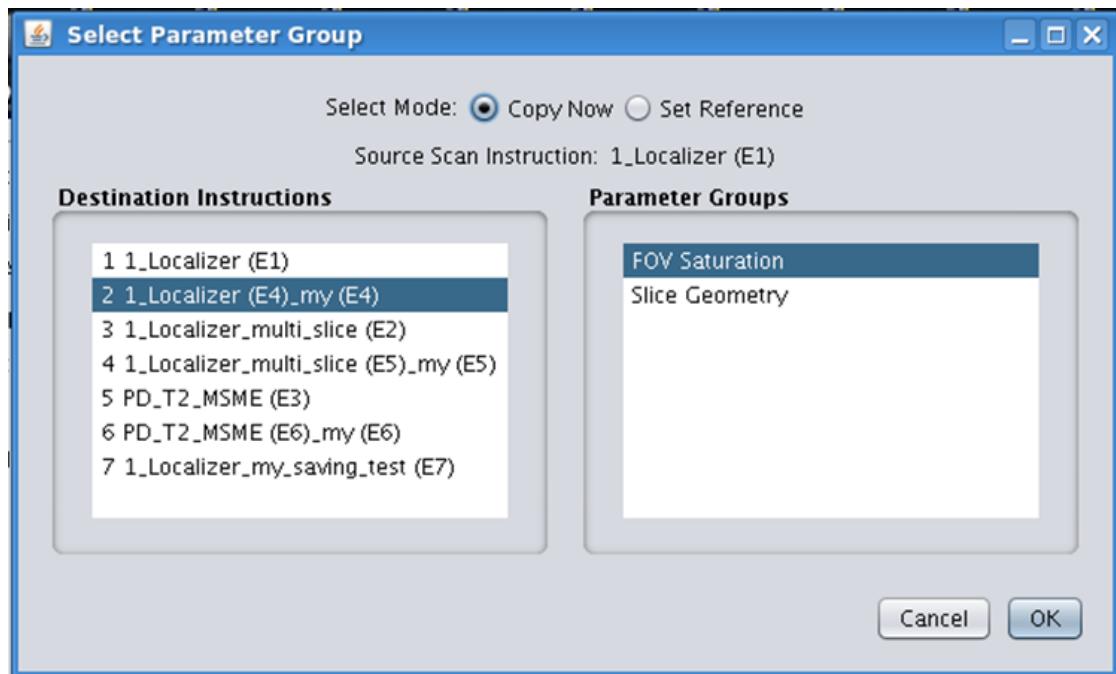


Figure 2.51: Select Parameter Group window

- Open the protocol protocol in the instruction list from which the parameters should be copied.
- Drag the protocol onto the protocol to which the parameters should be copied.
- When the protocol to which the parameters should be copied appears blue, release the mouse button.
- Select the parameters to be copied under Parameter Groups in the pop-up window Select Parameter Group.
- Click on **Okay**.

2.3.13 Saving Protocols and Studies

It is possible to store changes that have been made to a protocol or protocols so that it is possible to run the same protocol(s) in the future without having to apply the changes again.

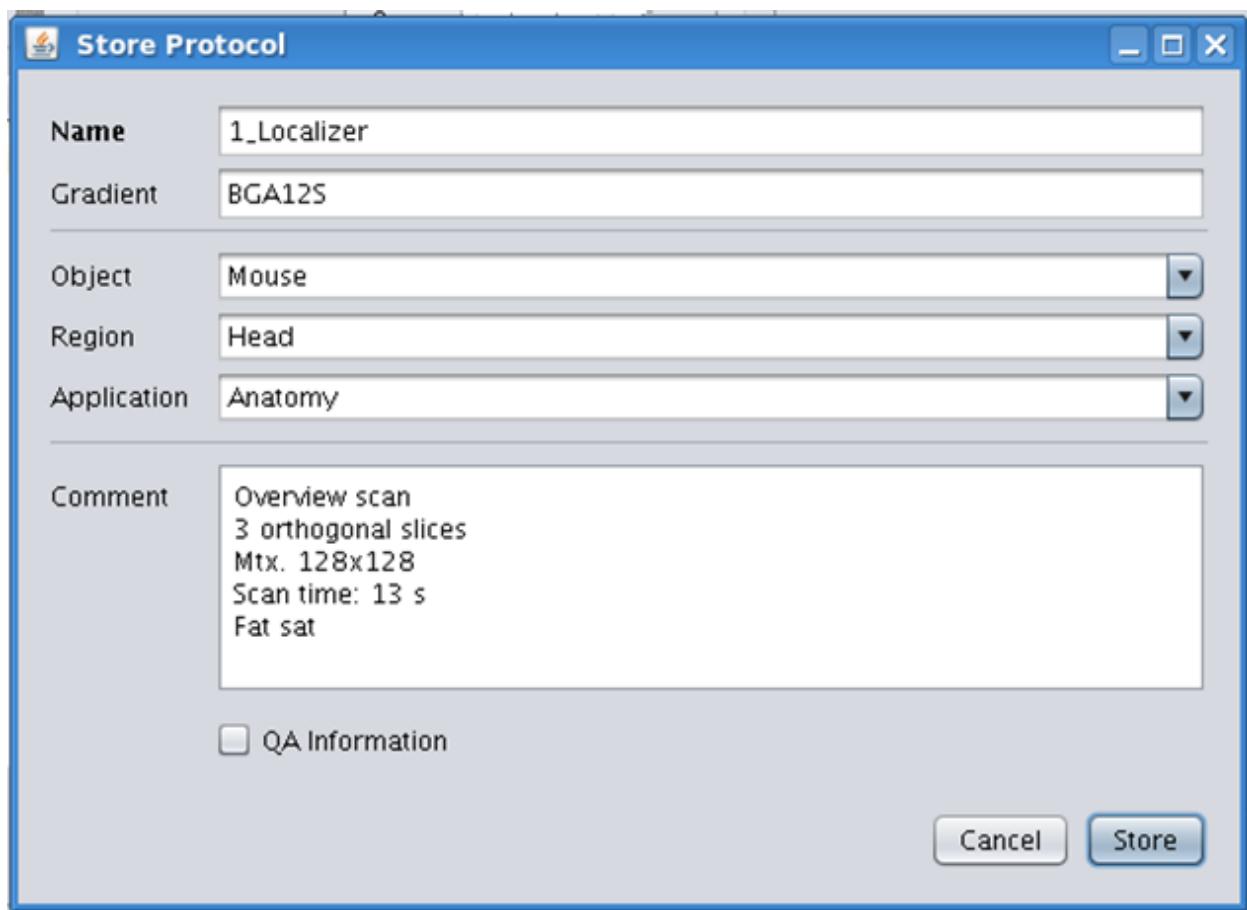


Figure 2.52: Store Protocol window

- Make the desired changes to the protocol(s).
- Right click on the protocol to be stored or using the Control key and right clicking, highlight the protocols to be stored.
- Select **Store Scan Protocol** or **Store Scan Program**.
- In the Store Protocol window that appears, enter a name for the protocol or program.

- Select the location to which the protocol or program should be stored. Create a new location by typing in new names in the Object, Region, and Application fields.
- Click on **Store**.

It is now possible to load an entire scan program, for example, directly from the Explorer tab of the Palette without having to load each protocol individually.

2.4 RF Coil Selection and Usage

2.4.1 Introduction

2.4.1.1 Intended Readers

This portion of the Application Manual is intended to provide the user with a brief overview of the advantages of the various rf coils, so that the best coil for a certain application can be chosen when setting up an experiment, and so that the user knows how to switch between coils within an experiment when more than one coil is in the system. For a better understanding of the discussed topics, it is recommended to have the system switched on and have ParaVision running. An appropriate coil combination should be connected and wobbled. Instructions on coil connection can be found in the System Manual.

2.4.1.2 Prerequisites

This manual must be used in the greater context of other manuals, particularly the respective System Manual and the safety instructions located therein.

2.4.2 Coil Selection

2.4.2.1 Type of Coils

There are six main types of Bruker rf coils: 1H transmit/receive volume coils, 1H transmit only volume coils, 1H surface receive coils, 1H surface array receive coils, dual resonance X-nuclei/1H coils, and cyroprobes. Bruker offers additional coil types for specialized applications. The majority of all experiments, however, will be performed with one of these six main coil types or a combination of two of them.



Figure 2.53: Examples of coil types. On the top left (1) a volume resonator. On the top right (2) a surface array receive coil. The four individual elements of the 2x2 array are seen. On the bottom left (3) a dual resonance coil. On the bottom right (4) a cyro coil.

Each coil has a label which is specific to the coil. The Item line of the label provides the user with important information about the coil. The line starts with the abbreviation RF RES, which indicates that the coil is a radio frequency resonator. This is followed by the frequency at which the coil is used, the nuclei for which it is used, its outer and inner dimensions in mm, whether it is a transmit/receive (TX/RX), transmit only (TO), receive only (RO), etc., and usually ends with the abbreviation AD, which means that the coil is actively decoupled.

Bruker BioSpin MRI GmbH
Rudolf-Plank-Strasse 23, D-76275 Ettlingen/Germany
ITEM: RF RES 200 1H/31P 112/072 L/L TR AD
MODEL NO.: 1P T20100V3
SERIAL NO.: S 0010
REV/EC: 2P XY
peak power 1H: 1000 Watt, 5 ms
mean power 1H: 22 Watt
peak power 31P: 1000 Watt, 5 ms
mean power 31P: 22 Watt



Figure 2.54: A coil label. The line "Item" informs the user that this is a 1H/31P transmit/receive (TR) coil, which is to be used at 200 MHz.

2.4.2.2 Choice of Coils

In order to perform an MRI experiment, both a transmit and a receive coil must be active. These can be two separate coils or one coil, such as a transmit/receive volume resonator, that performs both functions.

Ideally, both the transmit coil and the receive coil are located as close to the object to be measured as possible, as this provides the greatest signal to noise ratio. Therefore, it is recommended to use a transmit volume resonator in combination with a receive surface coil for most applications which focus on a specific area of the object. Volume transmit/receive resonators should be chosen only when no surface coil is available that covers the entire area to be examined. If a surface receive coil which has specifically been designed for a certain object region exists, such as the mouse brain coils, these should be chosen, since these are shaped to fit best to the specific region and therefore yield the highest signal to noise ratio. Whereas acceleration factors can be enabled when surface array coils are used, simple surface receive coils provide more homogeneous images. Cyroprobes provide an excellent signal to noise ratio and nuclei other than ^1H can be measured with dual resonance coils.

2.4.3 Coil Recognition

Coils must be given a descriptive name the first time that they are connected. This is normally done by Bruker's service department during installation. It can occur, however, that the user connects two coils in a combination that has not been connected before. In this case, a descriptive name must be given. It is suggested to use the abbreviations in the item line on the coil label for the name, as this contains the most relevant coil information.

A new study must be started each time that coils (whether previously named or not) are connected to the system. When the Study Registration dialog is opened, the connected coils are listed under RF when the button "More" is opened. On systems with AVII+ or higher, coils that are properly connected are automatically recognized by ParaVision.

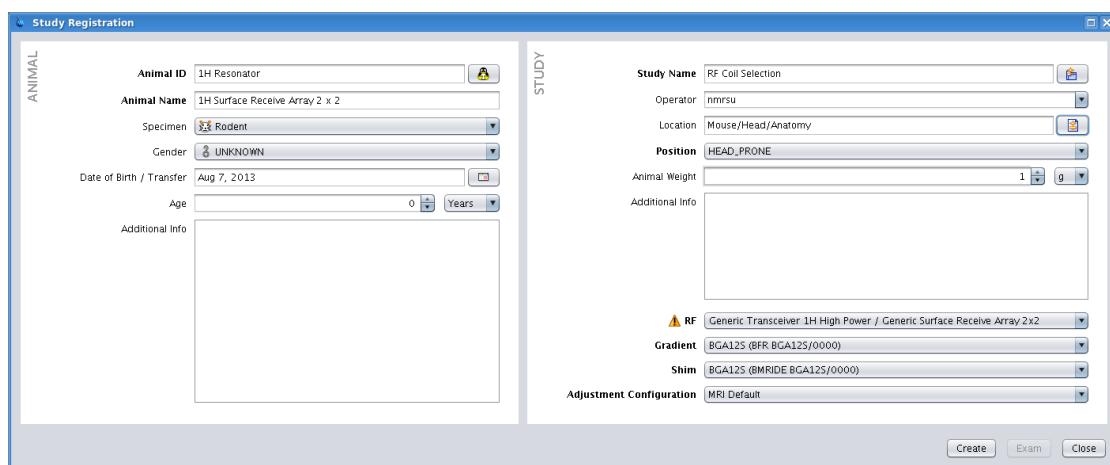


Figure 2.55: The Study Registration dialog with the "More" button opened. A transmit/receive resonator is connected along with a four element surface array receive coil.

The coils can then also be seen on the System tab of the Parameter Editor. For dual resonance coils, the active nucleus is seen on the Sequence tab of the Parameter Editor.

2.4.4 Switching between Coils

2.4.4.1 Operation Mode

In some cases it can be useful to switch between connected coils within a study. If, for example, an animal is in a transmit/receive volume resonator and a brain surface array receive coil is connected, a brain study can be run in the brain using the brain surface array coil as the receive coil and then a quick check of a new user protocol that includes triggering can be run in the abdomen using the transmit/receive resonator as the receive coil.

To switch between coils:

- Open the **System** tab of the Parameter Editor.
- Select the desired coil in the field **Operation Mode**.
- Click on **Apply**.

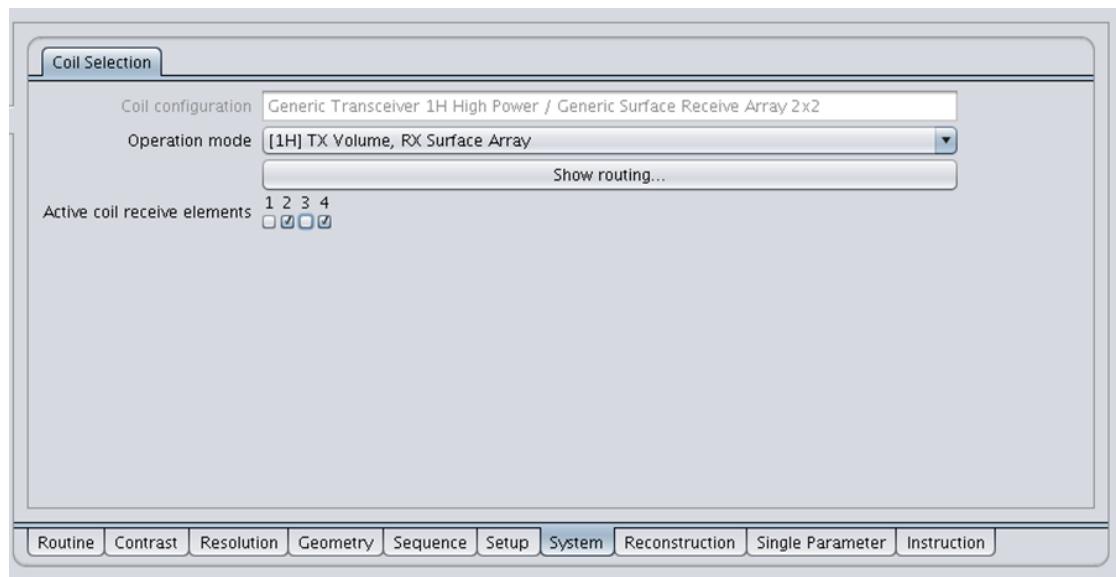


Figure 2.56: The System tab of the Parameter Editor. The 1H volume resonator is used as the transmit coil and the 1H surface array is used as the receive coil. Receive elements 1 and 3 have been deactivated.

2.4.4.2 Double resonance Coils

When running X nuclei experiments, it is recommended to start the experiment with the 1H active in order to perform the auto-adjustments and acquire a reference image before switching to the X-nuclei part of the experiment.

To active the desired nucleus:

- Open the **System** tab of the Parameter Editor
- Select the **Operation Mode** for the desired nucleus
- Open the **Sequence** tab of the Parameter Editor.
- Open the **Frequency Ch 1.** subtab.

- Select the desired nucleus in the field **Nucleus**. (if the Operation Mode allows more than one nucleus)
- Select the desired **Working Chemical Shift**
- Click on **Apply**.

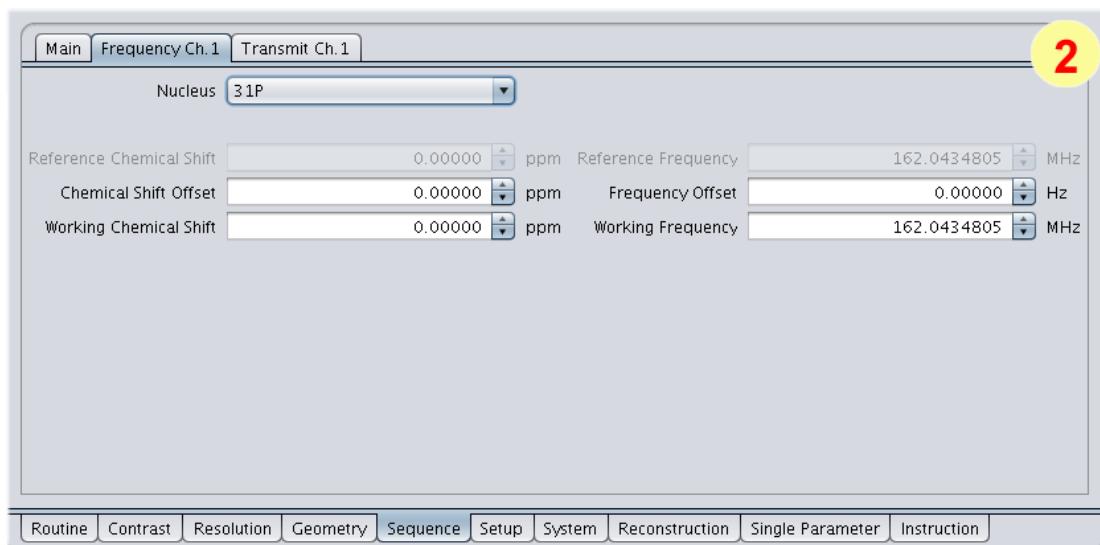
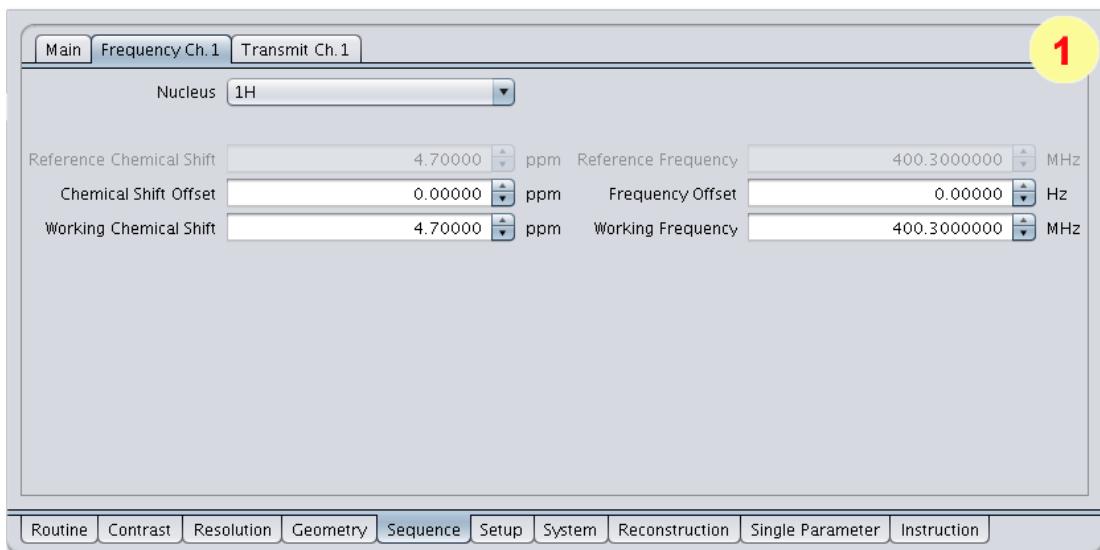


Figure 2.57: The Sequence tab of the Parameter Editor. 1H is selected on the top (1) with the working chemical shift set to 4.7 ppm (that of water). 31P is selected on the bottom (2). The working frequencies correspond to a 9.4 Tesla system.

2.4.5 Working with Transmit/Receive Surface Coils

Many dual resonance coils as well as cyroprobes among others are transmit/receive surface coils. These coils require special attention in terms of the reference gain adjustment, which is used to determine the necessary power for calculating flip angles. The reference gain varies with distance to the coil when surface coils are used as the transmit coil. By default, the reference gain auto-adjustment is run in an axial (vertical) slice. A reference gain cannot be properly adjusted with transmit surface coils, since axial slices are perpendicular to the coil

itself. It is therefore necessary to run the reference gain auto-adjustment in a coronal (horizontal) slice. See Chapter [Auto-adjustments and Adjustment Platform \[▶ 478\]](#). The position of the coronal slice should be placed according to the desired application. For imaging, it is recommended to place the slice at as close to the coil as possible, remaining within the object. This not only provides the most signal for the adjustment, but also minimizes the probability that flip angles deeper within the object will be run higher than those calculated within the protocol. For localized spectroscopy, place the coronal slice at the depth of the desired voxel. If localized spectroscopy and imaging are performed within one study, it is best to re-perform the reference gain adjustment when switching between the two.

2.5 Anatomy

2.5.1 Introduction

Abbreviations

- FISP - Fast Imaging with Steady Precession
- FLASH - Fast Low Angle Shot
- GE - Gradient Echo
- IR - Inversion Recovery
- MDEFT - Modified Driven Equilibrium Fourier Transform
- MSME - Multi-Slice Multi Echo
- PD - Proton Density
- RARE - Rapid Acquisition with Refocused Echoes
- SE - Spin Echo
- SWI - Susceptibility Weighted Imaging
- T1 - Spin-Lattice Relaxation Time
- T2 - Spin-Spin Relaxation Time
- T_SATRIG - Tomography Small Animal Triggering
- TE - Echo Time
- TR - Repetition Time

Purpose

Protocols in the Anatomy location are primarily used to scan the anatomy of rats and mice. Different techniques to generate images with a variety of contrasts are available. Typical pathologies for protocols with T1 or T2 contrast are:

- Cancer (most cancers): Dark on T1 weighted images, bright on T2 weighted images.
- Defect integrity of the blood-brain barrier: Bright on T1 weighted images using Gadolinium containing contrast agents
- Lesion containing fat (e.g. intracranial dermoids): Bright on T1 weighted images, less bright on T2 weighted images.

2.5.2 Hardware Setup

No special requirements.

2.5.3 Object Setup

No special requirements for brain imaging. For abdominal imaging, use the triggering and gating in the Chapter [Cardio \[507\]](#).

2.5.4 Protocol Setup

For brain imaging

T1_RARE_InvRec and T1_MDEFT are designed for an optimized T1 contrast between grey and white matter (see Chapters [RARE \(Rapid Acquisition with Relaxation Enhancement\) \[309\]](#), [MDEFT \(Modified Driven-Equilibrium FT\) \[321\]](#)). T1_FLASH and T1_RARE have a smaller scan time compared to T1_RARE_InvRec and T1_MDEFT, but the T1 contrast is lower (see Chapter [FLASH \[286\]](#)). Keep in mind, that the higher the magnetic field strength is the smaller the contrast between grey and white brain matter. An overview of the correlation between signal intensity and contrast is given in Table 1. To avoid the hyperintense representation of fatty tissue, fat suppression is active for most of the protocols in the Location ANATOMY.

The TurboRARE protocols are relatively fast protocols to generate images with T2-contrast. They are available in 2D and in 3D mode. The T2_TRUE_FISP_3D protocol is a fast 3D imaging sequence to achieve T2 contrast (see Chapter [FISP \(Fast Imaging with Steady State Precession\) \[324\]](#)). T2_RARE_InvRec generates T2 weighted images but due to the inversion preparation tissue or liquids with very long T2 relaxation times will be suppressed. This technique is very often used in research for multiple sclerosis. In order to locate plaques that are usually next to CSF filled ventricles the timing is setup to suppress the CSF but tissue with intermediate T2 values will show a T2 contrast.

PD_T2_MSME is used to acquire a proton density weighted image together with a T2-weighted image in one scan (see Chapter [MSME \(Multi Slice Multi Echo\) \[306\]](#)). The first two echoes are summed up to display proton density and the subsequent echoes (3 to 12) are added for a T2 weighted image.

Suppression of tissue in a certain range of T1 values can be achieved with the protocols T1_RARE_Inv_Rec and T2_RARE_Inv_Rec by choosing the appropriate inversion time.

SWI_FLASH uses a fully flow compensated, long echo, gradient recalled echo pulse sequence to acquire images (see Chapter [FLASH \[286\]](#)). This method exploits the susceptibility differences between tissues and uses the phase image to detect these differences. The magnitude and phase data are combined to produce an enhanced contrast magnitude image which is exquisitely sensitive to venous blood, hemorrhage and iron storage.

A good shim is needed for SWI_FLASH. It is recommended to use MAPSHIM to shim on the brain. To improve the shims proceed as follows: load the scan in the instruction list, enable Map_Shim in the Auto Shim Sub-card of the Setup Card. The shim volume is now visible in the Examination card. Adapt its geometry to cover only the brain, without tissue/bone/air interfaces (e.g. skull, air cavities). Open the Adjustment Platform, select and open the On Demand Protocol B0 Map. Acquire the B0 map by pressing Start and leave the Adjustment Platform once the map is acquired (Green tick mark appears) by clicking Apply and Back. Once acquired, the B0 map will be displayed in the Palette tab under Explorer, Datasets. Start the acquisition with Continue. The shims will be calculated in an automatic adjustment in the preselected shim volume prior to the start of the diffusion acquisition itself.



If Map_Shim was previously performed and you want to keep the shim values, keep the option Current_Shim in the Auto Shim Sub-card of the Setup Card.

For abdominal imaging

There are 5 Protocols especially adapted for abdominal imaging. In 3 protocols (T1_FISP_3D, T1-FLASH, T2_TurboRARE, FLASH_3D) the trigger is activated and an external triggering-device is needed. The 4th protocol (T1_IG-FLASH) works with retrospective gating (see Chapter IntraGate) and so no external triggering is needed.

The FLASH_3D protocol is especially adapted for whole-body imaging of mice (the gradient-system and the volume-resonator need to have a linear region of about 8 cm; see manual of the gradient-system and manual of the volume-coil).

In case you would like to adapt other protocols to image the whole animal, keep the following points in mind:

- Read out direction rostral-caudal (head-feet), to avoid infolding in phase direction
- The image can be distorted at the outer parts of the image in z-direction of the magnet, if the field of view is to large (depending on your gradient-system and coil-setup)

Weighting	Signal intensity	Tissue
T1	Low	Air, bones, fast flowing blood
	Intermediate	Free water tissue (CSF, bladder, edema, kidneys, ...), bound water tissue (liver, pancreas, muscle, ...), ligaments, tendons
	High	Fat, fatty bone marrow, paramagnetic contrast agents, slow flowing blood
T2	Low	Air, bones, fast flowing blood
	Intermediate	Bound water tissue (liver, pancreas, muscle, ...), fat, fatty bone marrow, ligaments, tendons
	High	Free water tissue (CSF, bladder, edema, kidneys, ...), blood products (oxyhemoglobin, extracellular methemoglobin)

Table 2.1: Signal intensity of various tissues at T1- and T2-weighted imaging, Ref. 1.

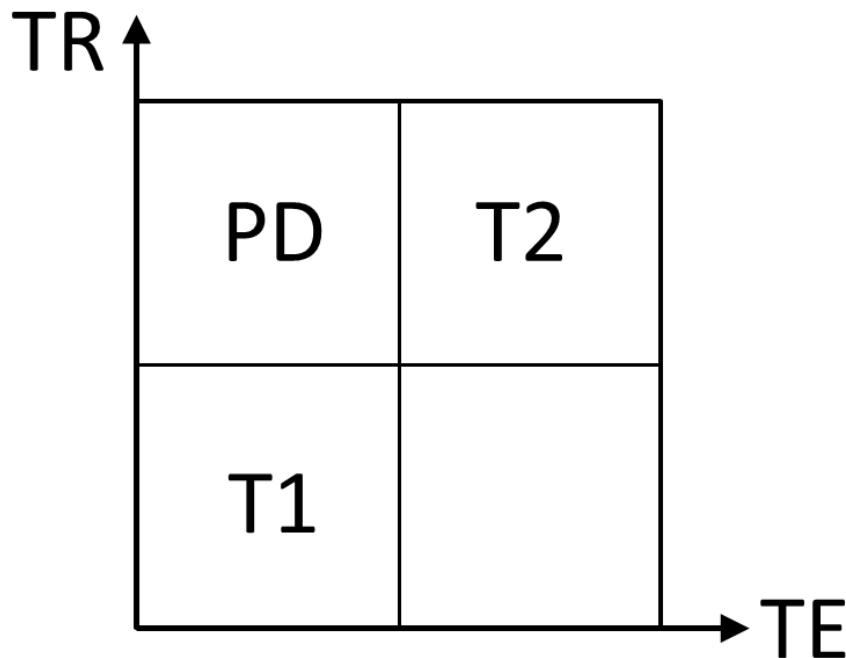


Figure 2.58: Image contrast weighting by varying TR and TE in spin echo sequences.

Parameter recommendations for T1 contrast

(see Fig. [Image contrast weighting by varying TR and TE in spin echo sequences. \[▶ 498\]](#), Ref. [2]):

- For SE, TE << T2
- For GE, TE << T2*
- TR ~ T1
- Flip angle ~ 90°
- Inversion can be used, but this will increase the repetition time TR and therefore results in a longer scan time and as it attenuates the signal of a range of tissue the signal/noise ratio in the image will be reduced.

Parameter recommendations for T2 contrast

(see Fig. [Image contrast weighting by varying TR and TE in spin echo sequences. \[▶ 498\]](#), Ref. [2]):

- TE ~ T2
- For SE TR ~ T1
- For GE TR < T1

Parameter recommendations for proton density contrast

(see Fig. [Image contrast weighting by varying TR and TE in spin echo sequences. \[▶ 498\]](#), Ref. [2]):

- TE<< T2
- For SE TR ~ T1
- For GE TR < T1

Use the magnetization transfer module to saturate bound water. Magnetization transfer imaging measures the exchange of magnetization between bound (macromolecular) protons and free (mobile) protons in tissues. If an off-resonance radio frequency pulse is used to selectively saturate the bound proton fraction, the signal intensity of the images is reduced because of the transfer reaction between the two proton pools. This technique is used in e.g. multiple sclerosis.



Magnetization transfer imaging can result in a high specific absorption rate (SAR), this means heating up the animal.

2.5.5 Data Analysis

Load the image data either to the Viewing Card or to the Image Data Analysis & Processing Tool for data analysis.

2.5.6 References

- [1] Bitar R. et al. MR Pulse Sequences: What Every Radiologist Wants to Know but Is Afraid to Ask. *RadioGraphics* 26, 2006; 513–537
- [2] Schröder L. Faber C. In Vivo NMR Imaging. Methods and Protocols. *Methods in Molecular Biology* 771. 2011, Humana Press, New York

2.6 Protocols

2.6.1 Introduction

This chapter is intended to provide an overview of the Bruker protocol concept and the protocols delivered with ParaVision 6.0.

2.6.1.1 The Protocol Concept

A scan protocol is a combination of a measuring method combined with a set of suitable parameter values stored as a file in a Protocol Location on disk. All method parameters are visible in the Parameter Editor of the **Exam Card**.

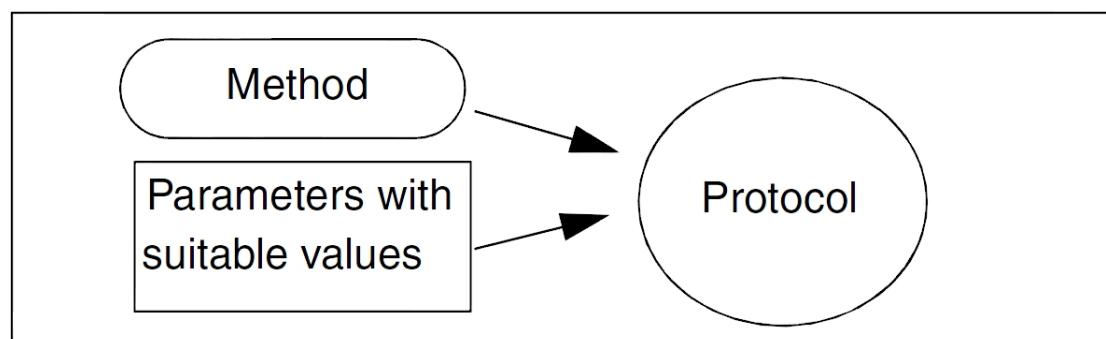


Figure 2.59: Protocol = Method plus suitable parameter values

Example:

T2_TurboRARE_highres is a protocol based on the method RARE with timing parameters to generate a T2 contrast with a high spatial resolution.

2.6.1.1.1 Organisation and Scheme

The protocols are adapted to different magnetic field and gradient strengths, objects (rats and mice), anatomical regions, and applications. For a given field strength and a given gradient system the protocols are structured as follows:

Object (e. g. animal)

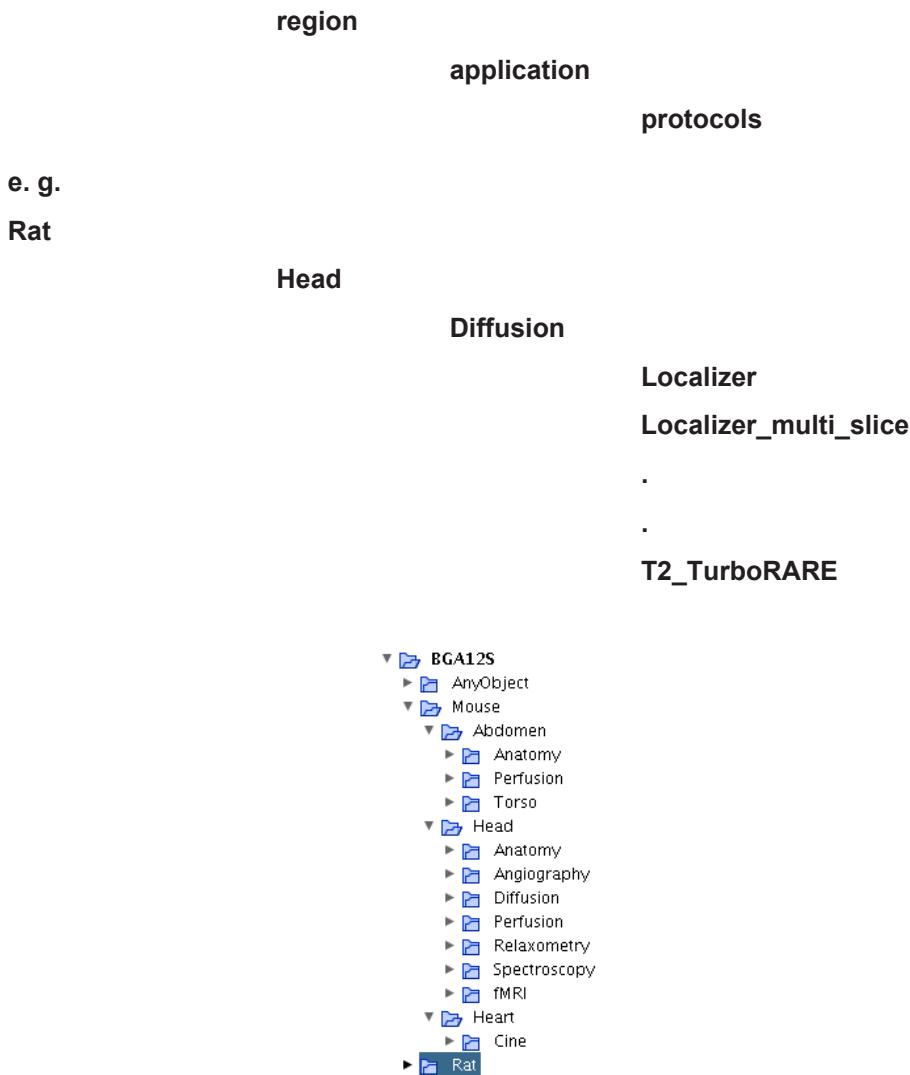


Figure 2.60: Protocol structure in Workspace Explorer

The location **AnyObject** contains one protocol of each method available on the system.

The protocols in the **Mouse** and **Rat** locations are all application oriented and have been tested in vivo. This means, if such a protocol is used with the same hardware (coil setup) the resulting image should have a good quality from the outset.

The protocols have been developed using the typical coil/coil combination used for this application. However, if not specifically mentioned, the protocols have no restrictions with respect to a specific coil setup. Therefore a protocol that has been developed with e. g. a

surface brain coil can be used with a head volume coil. One just has to take into account the reduced signal to noise performance with this coil and change the corresponding parameters, e. g. increase the number of averages.

2.6.1.1.2 Conventions

Aside from a few exceptions the naming of protocols follows the following conventions:

Contrast/mode_Method_option_option_option

Abbreviations:

Blackblood -> parameters are set for blackblood contrast. In FLASH based protocols the blackblood module is active.

dir	directions in diffusion weighted protocols
flic	flow compensation
Inv-Rec	Inversion recovery module active
PCA	Phase contrast angiography
sat	saturation slice(s) active
seg	segmented
SWI	Susceptibility weighted imaging
TOF	Time-of-flight
Turbo	flip back is active

2.6.2 Bruker Protocols

Bruker application oriented protocols are available for 1 T, 7 T, 9.4 T, 11.7 T and 15 T and, with exemption of 15 T, for **Rat** and **Mouse**. If available for a given field strength the protocols are delivered for gradient strengths of 300 mT/m, 600 mT/m and 1000 mT/m, reflecting different gradient coils.

With exception of 1 T, the protocols names are the same for all field strengths and the protocols themselves differ only in terms of adaption to field strength or gradient strength dependent factors.

ParaVision 6 automatically loads the correct protocols for the active field and gradient system configuration.



Bruker protocols are write protected

User Protocols:

Any user can create a user-dependent protocol location.



All users are able to store and modify protocols in their own protocol locations.

To store a protocol after having defined all parameters in the **Exam Card**, activate it in the **Instruction List**. Open the **Context Menu** with a right click and select **Store Protocol**. Specify Name, Object, Region, and Application. Text information can also be entered. This will be shown as a tool tip when the cursor is over this protocol in the (Workspace) Explorer.

2.6.2.1 Bruker Applications Protocols

Some basic protocols are common to all applications.

1_Localizer:

A fast reference scan acquiring 3 orthogonal slices at the iso-center of the magnet. Each slice produces a saturation line in the two orthogonal slices. This allows a quick check of which part of the object is at the magnet's center.

1_Localizer_multi_slice:

A fast reference scan acquiring 3 orthogonal slice packages. Each slice package consists of several slices. Usually each package is shifted with respect to the iso-center in order to cover the area of interest. This protocol has a higher spatial resolution than 1_Localizer and in order to reduce the saturation effects from the orthogonal slices it is acquired in **Angio Mode**.

T1_TurboRARE:

A T1-weighted RARE protocol as a quick anatomical reference is available in several applications

T2_TurboRARE:

A T2-weighted RARE protocol as a quick anatomical reference is available in each application.

Gating and trigger:

The **Trigger** is active in all protocols in the **Abdomen** and **Heart locations** except for **IgFLASH** based protocols. Please read the tool tip information of the protocol carefully. Usually the protocols are stored with a very short TR. To generate a specific effective TR set **Trigger Mode** to **Trigger_per_slice** and set the length of the gate to a fraction of the minimum TR on the triggering unit.



Protocols in which Trigger is activated will not start until a trigger is received from the animal monitoring unit. It is therefore important to set up the triggering on the monitoring unit properly.

Abdomen - Anatomy

This location contains protocols for acquiring images for anatomical information in 2D and 3D mode and in different contrasts: T1 and T2. Protocols are based on gradient echo (FISP, FLASH) and fast spin echo techniques (RARE).

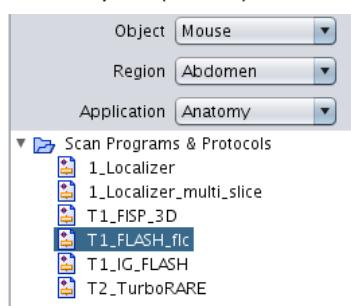


Figure 2.61: Protocols in Abdomen - Anatomy

Except for T1_IG_FLASH, **Trigger** is active in all protocols. The TR in the triggered protocols is very short. Carefully plan trigger parameters (e. g. start and length of respiration gate). If used without **Trigger** the resulting image quality and contrast will most likely not be as intended.

Abdomen - Perfusion

Besides protocols for anatomical information this location contains the protocol DCE_FLASH to acquire a time course, e. g. after administration of contrast agent. It is a gradient echo protocol based on FLASH.

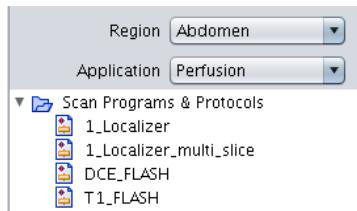


Figure 2.62: Protocols in Abdomen - Perfusion

Except for DCE_FLASH, **Trigger** is active in all protocols. The TR in the triggered protocols is very short. Carefully plan trigger parameters (e. g. start and length of respiration gate). If used without **Trigger** the resulting image quality and contrast will most likely not be as intended.

Abdomen - Torso

Protocols in this location are similar to the protocols in Abdomen - Anatomy. The field of view is larger to cover a larger area of the subject.

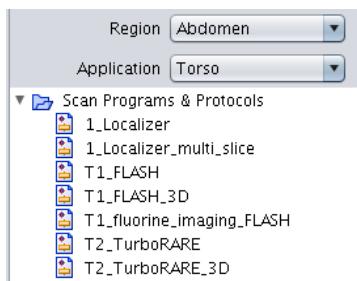


Figure 2.63: Protocols in Abdomen - Torso

Parameters in T1_fluorine_imaging_FLASH are setup to create a fluorine image. It needs a coil for both nuclei, protons and fluorine and fluorine has to be in the subject.

Trigger is active in all protocols. The TR in the triggered protocols is very short. Carefully plan trigger parameters (e. g. start and length of respiration gate). If used without **Trigger** the resulting image quality and contrast will most likely not be as intended.

Head - Anatomy

This location contains protocols for acquiring images for anatomical information in 2D and 3D techniques and in different contrasts: PD, T1, T2, and susceptibility weighted. Protocols are based on gradient echo (FISP, FLASH) and spin echo techniques (MSME, RARE).

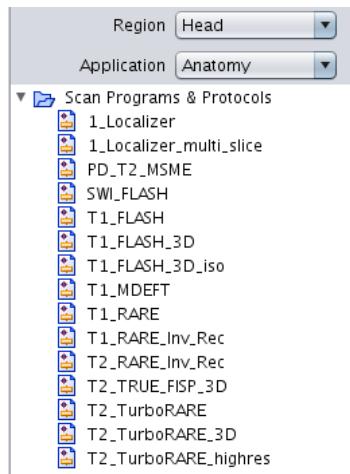


Figure 2.64: Protocols in Head - Anatomy

At high magnetic field strengths it is a challenge to generate mr images with a good contrast between gray and white brain matter. T1_RARE_InvRec and T1_MDEFT are designed for an optimized T1 contrast between gray and white matter.

T2_RARE_InvRec generates T2 weighted images, but tissue or liquids with very long T2 relaxation times will be suppressed due to the inversion preparation. This technique is very often used in research for multiple sclerosis. Plaques that are usually found next to CSF filled ventricles can be located since the timing is setup to suppress the CSF but to show a T2 contrast from tissue with intermediate T2 values.

Head - Angiography

Besides protocols for anatomical information this location contains the protocols for angiographic examinations.

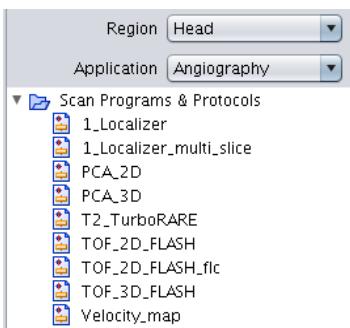


Figure 2.65: Protocols in Head - Angiography

Two techniques are used for this purpose: time of flight (TOF) technique for flow direction mainly orthogonal to the slice orientation and phase contrast angiography (PCA) for flow directions mainly within the slice.

Head - Diffusion

These protocols allow the acquisition of diffusion weighted images in EPI or Spin Echo techniques as well as data to evaluate the diffusion constant and to generate diffusion maps.

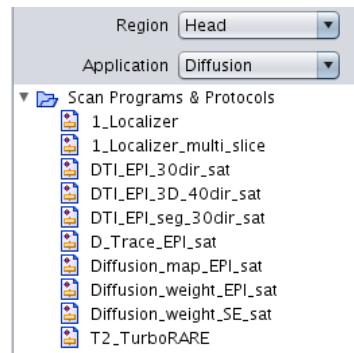


Figure 2.66: Protocols in Head - Diffusion

In addition there are protocols to acquire diffusion tensor data with a different number of diffusion directions and to evaluate the diffusion tensor trace.

Head - Perfusion

These protocols can be used to get information on the perfusion of the subject.

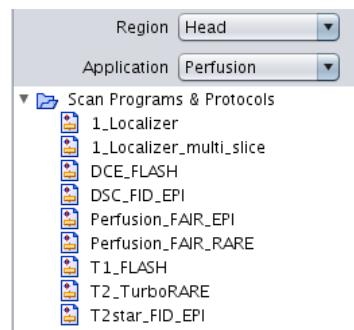


Figure 2.67: Protocols in Head - Perfusion

FAIR protocols are used to quantitatively evaluate the CBF. DCE_FLASH is used to acquire a time course, e. g. after administration of contrast agent. It is a gradient echo protocol based on FLASH.

Head - Relaxometry

Two protocols, based on RARE or FISP, allow the simultaneous acquisition of data to evaluate T1 and T2.

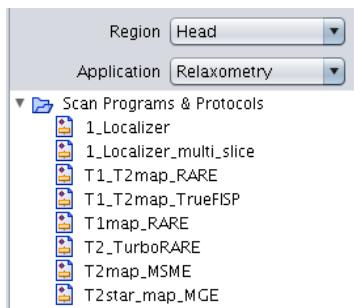


Figure 2.68: Protocols in Head - Relaxometry

Multi echo techniques, based on **MSME** and **MGE** are used to calculate T2, resp. T2*.

Head - Spectroscopy

Localized spectra can be acquired with **PRESS** and **STEAM** techniques, and a non-localized spectrum with **Singlepulse_1H**.

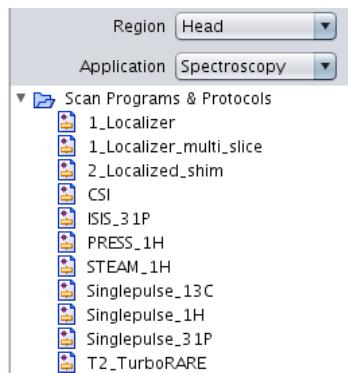


Figure 2.69: Protocols in Head - Spectroscopy

To investigate **31P Singlepulse_31P** and **ISIS_31_P**, for **13C Singlepulse_13C** can be used.

Head - fMRI

A time series can be acquired with single shot EPI protocols in FID or SE modes by simply specifying the number of repetitions.

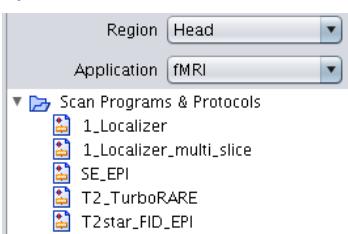


Figure 2.70: Protocols in Head - fMRI

Heart - Cine

With the exception of IntraGateFLASH based protocols (*IG*), localizer and planning scans all protocols are triggered. Protocols for anatomical reference are **T1_FLASH** and the flow compensated **T1_FLASH_flc**.

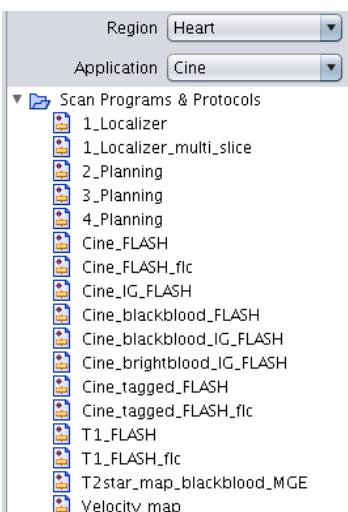


Figure 2.71: Protocols in Heart - Cine

Cine* protocols acquire a series of images within one cardiac cycle thus allowing studies of the dynamics of the heart. Additional contrast modules, like blackblood or tagging, can be selected.

T2star_map_MGE_blackblood allows the evaluation of T2* of the myocardium.

2.7 Cardio

2.7.1 Introduction

Abbreviations, Terms and Definitions

- **Cine** - Acquisition technique that allows to create heart movies showing the dynamic motion of the heart
- **ecg** - electrocardiogram
- **FOV** - Field of view
- **IG** - IntraGate
- **Prospective** - acquisition technique, where an external signal is used to start a scan
- **R-wave** - biggest signal in the ecg
- **Retrospective** - acquisition technique, where an additional signal is acquired prior to each echo and its assignment to the image data is done after the scan is finished
- **RR-interval** - time between 2 R-waves
- **RESP** - Respiration
- **T-SATRIG** - Tomography Small Animal Triggering

Purpose

The purpose of cardiac MR imaging is to determine the anatomy and the dynamics of heart structures (e.g. walls and cavities). The motion of the heart during the acquisition of MR signals can create strong motion artifacts. As small rodents have a very high heart rate cardiac imaging is a challenging task.

There are two major groups of imaging techniques: cine protocols show the motion of the heart dynamically protocols which freeze the heart motion at a given point in time within the RR-interval.

This workflow describes the acquisition of cardiac images in the case of a rat which has approximately a heart rate of 300 - 400 beats per minute.

Physiological background

The ECG is a cumulative electrical signal of the depolarization and repolarization of the myocardial cell membranes during heart activity (see Figure [Scheme of ECG signal \[▶ 508\]](#)). The biggest signal, the so-called R-wave is detected by the monitoring and triggering system. The temporal distance of R-waves has to be considered in planning the image sequence. A selectable delay time allows to measure different phases of the cardiac cycle. This trigger delay can be used to synchronize the data acquisition with a specific time point in the cardiac cycle. The first part of the cardiac cycle (about 30%) represents the systole and the remaining two-thirds represent the diastole. Therefore short trigger delays are used to image the heart in systole.

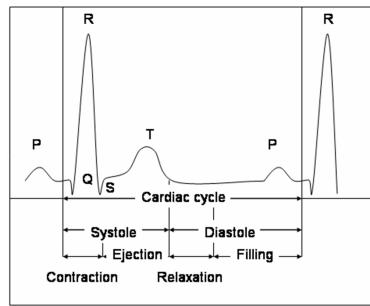


Figure 2.72: Scheme of ECG signal

Requirements

Use a standard animal imaging setup and an appropriate animal bed.

2.7.2 Hardware Setup

For monitoring and triggering use the T-SATRIG equipment. Connect the BNC connector "Gate" of the Control Gating Module with the "Ecg Trig" of your spectrometer electronics. For details see the System manual and Figure [Inter connections of monitoring system \[▶ 508\]](#).

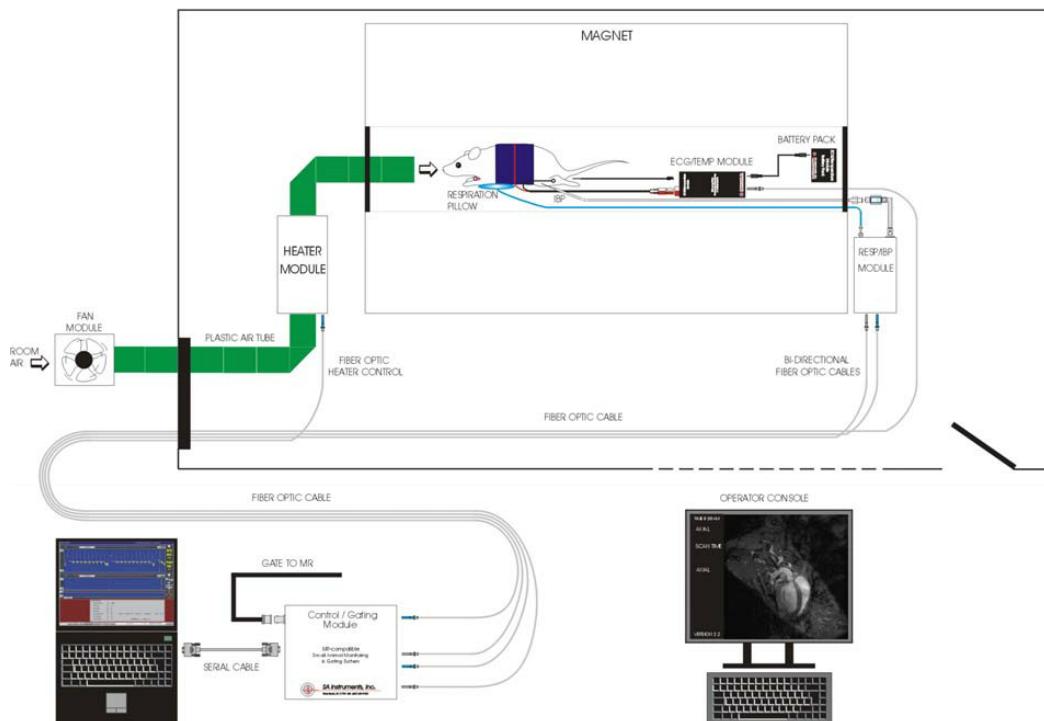


Figure 2.73: Inter connections of monitoring system

Coils

A body coil in quadrature mode or an appropriate surface coil is suitable for cardiac applications.

2.7.3 Object Setup

Preparation

A rat/mouse should be appropriately anesthetized prior to the preparation of the fore paws and skin for the ecg electrode application. This area should be cleaned by wiping with isopropyl alcohol (using similar products as Alco wipe® or Medi-Swab®). It is important to clean the skin from dead skin cells, dirt, and grease in order to get a good electrical contact with very low impedance. Apply electrode gel or cream to the paws before attaching the electrodes. Surgical tape will assist in maintaining good contact between the electrode and the animal.

The carbon fiber electrodes used in the experiment should be plaited or twisted to achieve opti-mum noise rejection. Excess cable length should be tightly fixed to the animal bed, not to the animal. Figure [Anesthetized rat in preparation for triggering on ECG and RESP \(front view\)](#). ▶ 509] depicts the above application of two electrodes on a rat. To move the animal into the magnet the forepaws have to be placed into the animal bed and secured with tape. Take care not to hurt the animal when the animal bed is moved into the resonator. Ideally, the electrodes should be positioned towards the head inside the animal bed to reduce respiratory artifacts in the ecg signal.

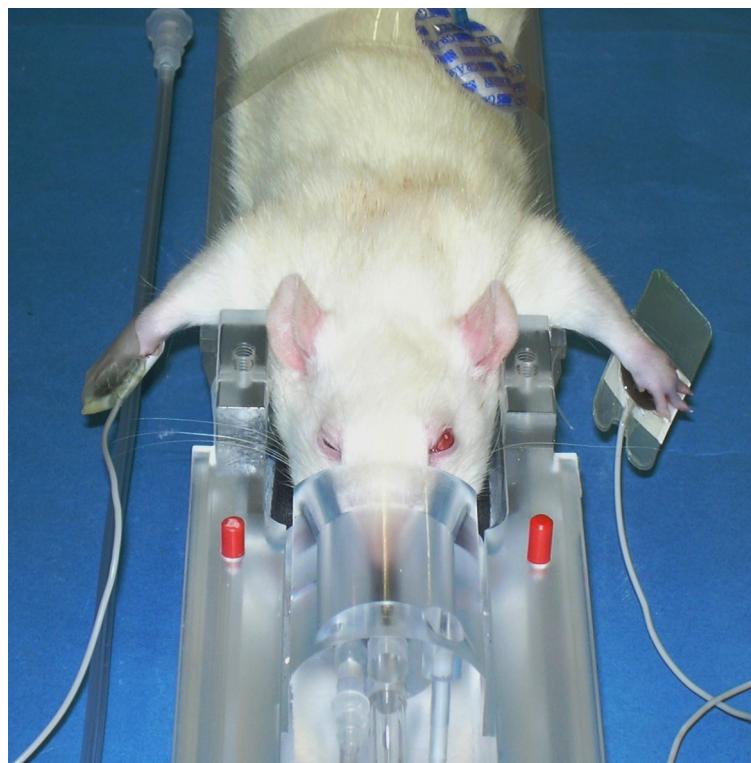


Figure 2.74: Anesthetized rat in preparation for triggering on ECG and RESP (front view).



Figure 2.75: Anesthetized rat prepared for triggering on ECG and RESP (side view).

In Figure [Anesthetized rat in preparation for triggering on ECG and RESP \(front view\). \[▶ 509\]](#) two electrodes are attached to the front paws, the paws are positioned towards the ears, one lead is conducted over the animal's neck to the second lead, where both are twisted and attached to the animal bed with tape.

It is often desirable to combine the ecg trigger with a respiration signal. Position the respiration sensor as shown in Figure [Anesthetized rat prepared for triggering on ECG and RESP \(side view\). \[▶ 510\]](#). For optimal MR image quality use a combination of respiration gate and ecg trigger (Figure).

Standard Gating Setup

The gating system can be used to gate on a single physiological signal or a combination of two or more signals. Single triggering means that a physiological event is recognized by the monitoring system, a trigger pulse is generated and sent to the spectrometer electronics. If combined gating of respiration and ecg is desired, the monitoring system detects the respiration, opens a gating window and generates trigger pulses if ecg events occur within this gating window.

A red line above the physiological signal indicate the detection of the corresponding signal indicates the detection and a white dot indicates the signal send to the scanner.

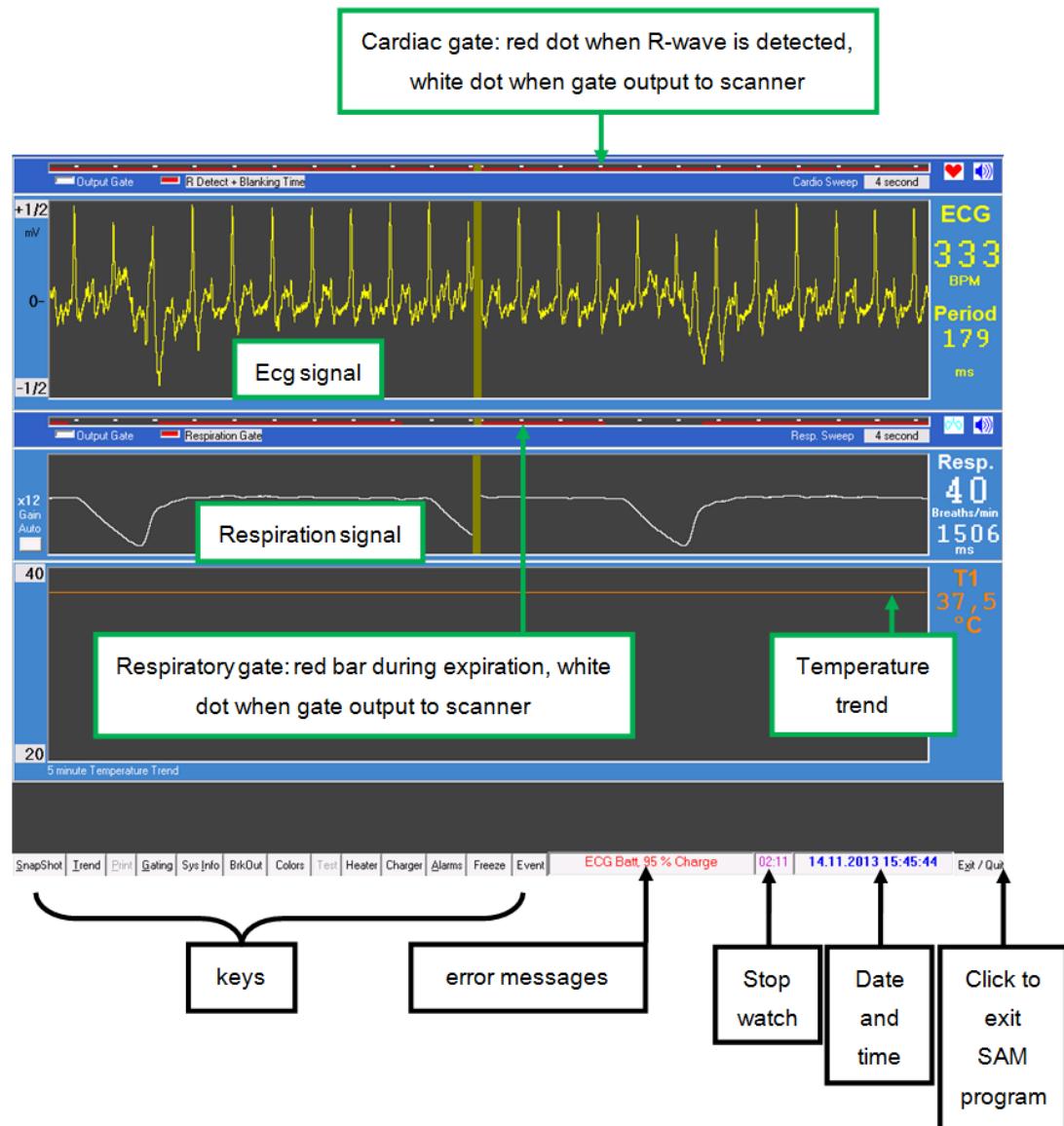


Figure 2.76: Ecg signal and respiration signal shown on the monitoring system T-SATRIG

Click the Gating key ([Figure Ecg signal and respiration signal shown on the monitoring system T-SATRIG \[▶ 511\]](#)) to open the Gating Setup window ([Figure Gating Setup Form provides the possibility to choose the channel for gating \[▶ 512\]](#))

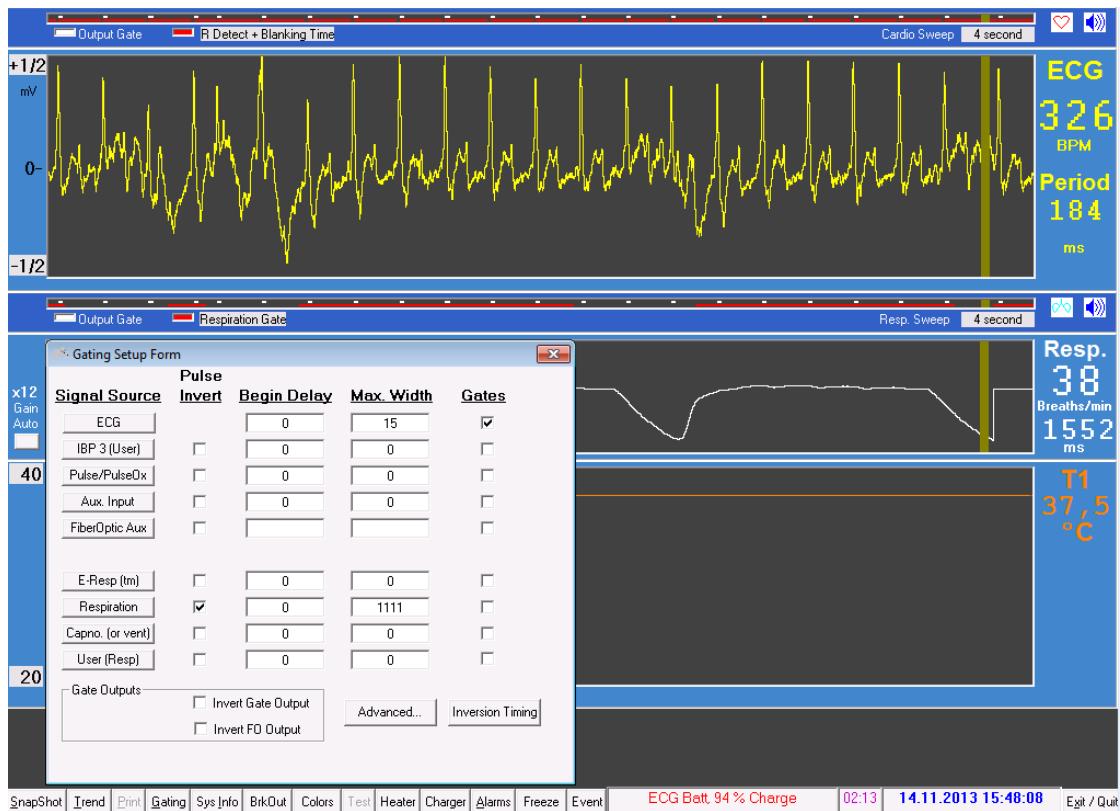


Figure 2.77: Gating Setup Form provides the possibility to choose the channel for gating

This window provides the possibility to gate on different signals. For cardiac imaging **ecg** and **Respiration** should be selected. A check in the **Pulse Invert** box inverts the detection logic, e.g. if the respiration is top-down, bottom-up the pulse invert has to be checked.

Customized Gating Setup

Working with animal models with diseases that modify the ecg or respiration signals the standard setup for signal detection can result in unstable trigger signals. In such a case modifying the parameters for signal detection can improve the situation.

For details on how the software does the analysis of the ecg signal to derive the trigger condition click the **ECG** button in the **Gating Setup Form** or right click in the ecg wave form display to view the R-detect setup window (Figure [Ecg wave form display to view the R-detect setup window \[▶ 513\]](#))

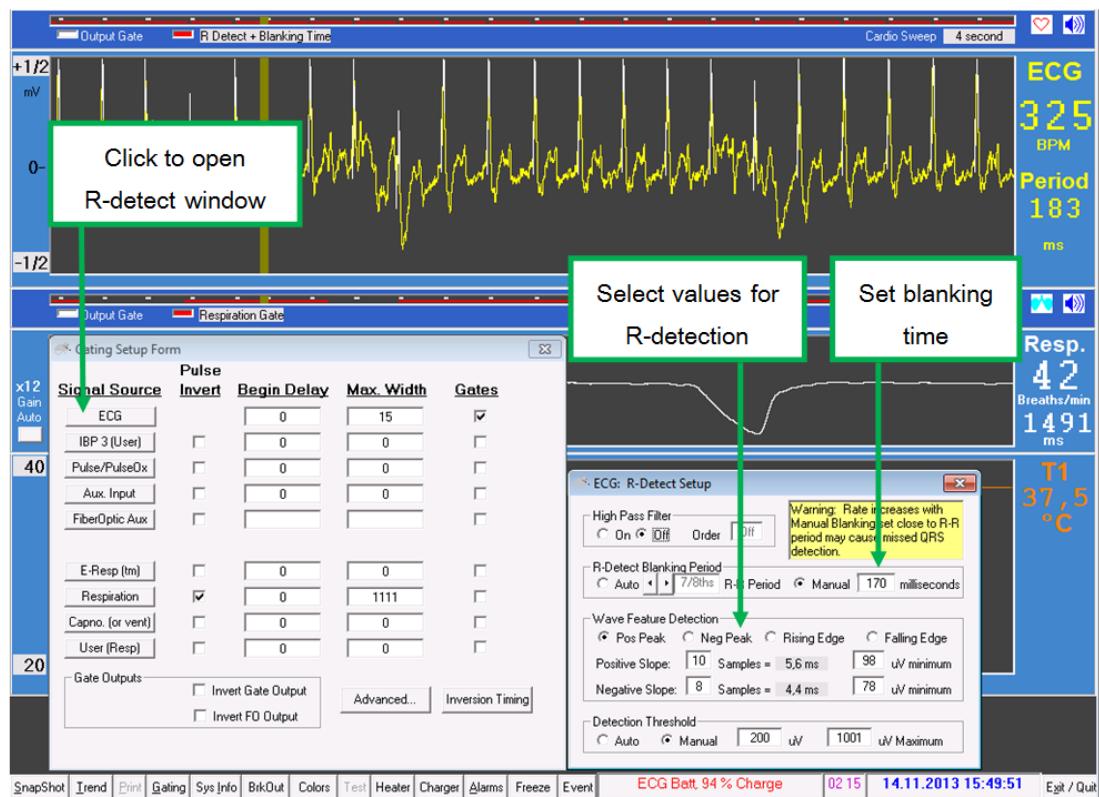


Figure 2.78: Ecg wave form display to view the R-detect setup window

The R-detect blanking period or blanking time can be used to eliminate false triggers, e.g. from gradient vibrations detection. Once an R-wave has been detected, the software inhibits R-wave gate generation for the blanking time.

Usually the blanking time is about 10 ms to 20 ms shorter than the RR-interval at start of data acquisition. With this during the scan the heart rate can decrease to some extent without causing false triggers.

To avoid false triggers due to gradient interference the blanking time in the R-Detect Setup window should be set to "Manual" with a length 5 ms to 10 ms longer than the TR of the sequence if only one cine frame is acquired or TR multiplied by the number of movie frames in case of a cine protocol.

The R-detect algorithm is based on 2 or 3 points and their positive and/or negative slew rates or slopes (amplitude/time). The waveform shown in Figure [R-wave gate generation](#) [▶ 514] shows R-wave gate generation for factory defaults: Positive peak with positive slope of 200 mV/6.7 ms and a negative slope of 98 V/4.4 ms. The gate is generated at the end of the negative slope. In this example the R-wave is about 200 μ V in amplitude. The positive slope requirement is easily exceeded and the gate is generated as soon as the negative slope requirement is satisfied. Note that the mid point that satisfies the gate requirement is earlier in time than the R-wave peak. Thus the delay of the scanner gate is less than the negative slope time (e.g. less than 4.4 ms).

Proper selection of parameter for R-wave detection is important in obtaining reliable results. This is especially true when the ecg waveform contains large distortions from blood flow, vibration or respiration.



Figure 2.79: R-wave gate generation

Four R-wave detection mechanisms are possible:

- 1) the positive peak,
- 2) the rising edge,
- 3) the negative peak,
- 4) the falling edge.

For a R-wave "bottom up" the positive peak detection and the rising edge detection can be used.

Perform the following steps to determine optimum setting for ECG detection (the software works in a similar way for a negative R-wave):

- **Select a feature to detect:** Usually the R-wave is a positive peak. Selecting **Pos. peak** will give more reliable detection than **Rising Edge**. The only reason to select **Rising Edge** would be to obtain a gate occurring before the R-wave peak in time.
- **Pick the times for the slopes:** There are a maximum of 31 sample points or about 17 ms. Different animals have different rise times for the R-wave. Select the largest time appropriate for the animal's rise time. For mice the rise time is about 7.5 ms. As the gate is generated at the end of the fall time, the fall time is usually set to be less than the rise time.
- **Select the amplitudes:** Determine the peak amplitude of the R-wave, usually 500 mV - 1000 μ V. In the case of mice with a rise and fall time selected of 6.7 and 4.4 ms respectively, we select rise and fall amplitudes of less than $6.7/7.5 = 90\%$ and $4.4/7.5 = 60\%$ of the peak amplitude. The software can be used to determine the amplitudes: Set the amplitude smaller than you expect, but large enough not to get false gates, then slowly increase one of the amplitudes until R-waves will not be detected and the corresponding gates will not be generated.

2.7.4 Protocols for Cardiac Imaging

General

There are two basically different imaging techniques: retrospectively triggered and prospectively triggered.

Prospective triggered protocols

Prospective triggered protocols need an ecg signal to start data acquisition.

For ecg triggered scans some precautions have to be considered: radio frequency pulses and gradient switching can induce interferences in the ecg signal and creating false triggers. To avoid this the animal preparation has to be done very carefully (see Chapter [Object Setup](#) [▶ 509]) and in the setup of the animal monitoring system the blanking time should be a few ms longer than the data acquisition time within one RR-interval. In the example shown in Figure [Ecg wave form display to view the R-detect setup window](#) [▶ 513] blanking time should

be longer than the repetition time multiplied with the number of movie frame. As the heart rate can change during the examination it's recommended to set blanking time about 10 ms to 20 ms shorter the the RR-intervall just prior to the start of the scan.

The prospective triggered protocols delivered with ParaVision are adjusted to work for typical heart cycles for anaesthetized rodents, eg 180 ms for rats and 120 ms for mice. If animals have faster heart cycles the number of cine frames must be reduced, for longer heart cycles more frames can be acquired.

Protocols for heart movies

The schematic of a typical imaging sequence is shown in Figure [Ecg wave form display to view the R-detect setup window \[▶ 513\]](#). The ecg signal starts the acquisition of a given number of signals or frames. An example with 8 frames of one slice is shown in Figure [Triggered imaging sequence \[▶ 515\]](#). The phase encoding for each of the 8 frames is identical (K-space line). This shows the acquisition of a heart movie consisting of 8 images at different points in time within one heart cycle.

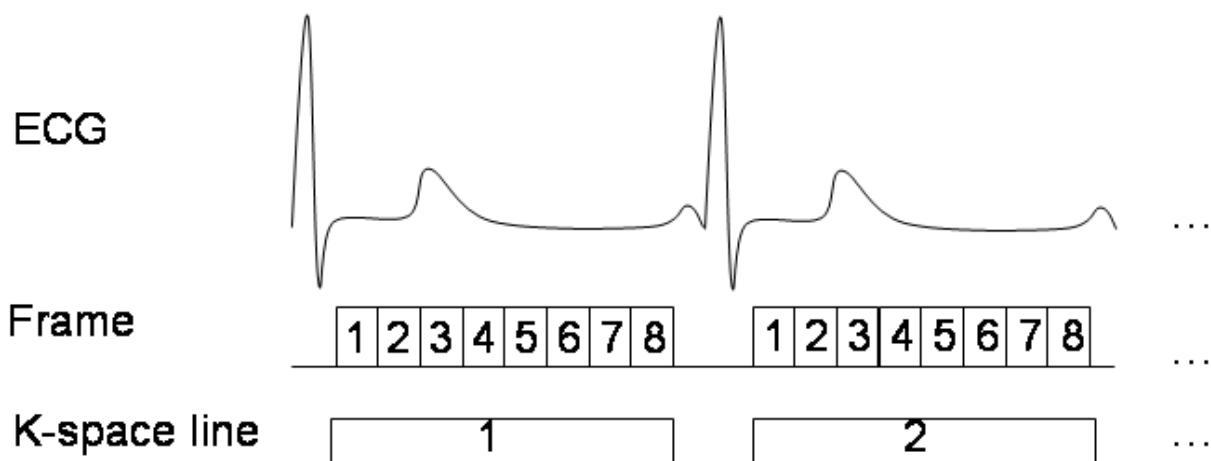


Figure 2.80: Triggered imaging sequence

The total scan time of such a protocol, e. g. **Cine_FLASH**, will be the product of the repetition time, number of phase encoding steps (K-space lines) and averages. If a respiration gate is active then the part of the respiration cycle with the strongest motion will be blocked for data acquisition and consequently the total acquisition time will be longer. In the context menu of a protocol, when the mouse pointer points to this protocol, information on the scan time is given.

Protocols with tagging

Tagging is technique that allows visualizing the relative motion of different parts of the heart. To achieve this, at the beginning of data acquisition of each cycle, areas in the heart are saturated in a regular geometrical pattern with special radio frequency and gradient pulses. These areas are, line or grid. As during a cardiac cycle the tissue moves, the originally saturated areas will move and the structure will be distorted.

The tagging pattern is imposed right after the trigger, before the subsequent data acquisition, e. g. a cine sequence. For the calculation of the number of movie frames one has to take into account that the tagging part needs about 10 ms to 15 ms and therefore less movie frames than in a standard cine sequence, e. g. **Cine_tagged_FLASH**, can be acquired in the cine part.

Protocols for blackblood contrast

If not enough data have been acquired to reconstruct the requested number of slices and/or cine frames the reconstructed images can be off bad quality or can be completely black. In this case a new reconstruction with less cine frames can help.

If the physiological rates specified in the scan protocol differ too much from the actual values the reconstructed images can be off bad quality or can be completely black. In this case a new reconstruction with different rates can help.

When working without ecg electrode the heart rate of the animal can be checked in the setup mode. For this, on the **Examination Card --> Setup** the option **Online Navigator Signal** has to be activated. The actual heart rate will be shown on the reconstruction tab as **Reconstruction Results** and can be corrected before starting the scan.

In order to suppress the signal from flowing blood triggered protocols use a double inversion technique. With the first trigger a global inversion pulse followed by a slice selective inversion pulse are applied. The first trigger signal after the inversion time starts the data acquisition. The inversion time in the triggered blackblood protocols is shorter than a cardiac period, thus the acquisition of the data read out will start with the trigger generated from the next R-wave. A complete phase encoding under these conditions will take 2 cardiac periods and the effective repetition time TR will be $2 * RR\text{-interval}$.

The protocols **Cine_brightblood_IG_FLASH** and **Cine_blackblood_IG_FLASH** are already prepared for multi-slice acquisition.

Measures against external perturbances:

Usually for cardio MRI at high magnetic fields a combination of respiration gate and ecg trigger is selected. If a blackblood protocol with double inversion preparation and combined respiratory and cardio trigger is used, it can happen that the R-wave following the inversion preparation occurs while no respiration gate is active. In such a case the readout will be started not with the first R-wave after inversion but with a later R-wave. Thus the effective inversion time TI will be longer. If the setup is only for ecg trigger and no respiratory gate is used then the TI will be always one RR-interval at the risk of being more sensitive to respiration artifacts.

Usually the interference of the radio frequency and gradient pulses are visible in the ecg signal on the animal monitoring system. Blackblood protocols show a very short signal with high amplitude from the inversion preparation and a longer interference with lower amplitude for the following read out in the next RR-interval. Without respiratory gate the signal from the inversion pulses should be observable every second R-wave if TI in the protocol is shorter than the RR-interval. If a longer interval is observed it can be due to an activated respiratory gate or an overload of the ecg detection unit of the animal monitoring unit. At the bottom line in the R-Detect-Setup of the SA-Instruments there is an option to set the trigger threshold to automatic or manual. Both options can be tried to avoid such an overload.

Checklist for triggered scans

Before starting the scan:

- Check the RR-interval to define the number of cine frames to be acquired
- Check blanking time. It should be longer than $(TR * Number\ of\ movie\ frames)$ and shorter than RR-interval
- Check the respiration gate (if respiration trigger is active)

Retrospective triggered protocols

Retrospectively triggered protocols don't use a physiological signal to start data acquisition and therefore no ecg electrodes are required. Additionally they acquire a signal, a so called navigator, prior to each echo. After the scan this navigator signal is analyzed and used to assign each echo to its correct position in the image. For this analysis, estimates for the respiration rate and heart rate have to be specified in the protocol.

Protocols using this feature are based upon the method **IG_FLASH (IntraGate_FLASH)**.

IG_FLASH protocols, e. g. **Cine_IG_FLASH**, can detect the respiration and heart motion and thus allowing the creation of respiration and heart movies. In the protocol the type of movie and the number of cine frames is specified. For additional reconstructions the number of cine frames can be changed after the data have been acquired.

As phase encoding steps acquired during periods of motion are not used in reconstruction it is necessary to acquire more data than just specified by the matrix size in phase direction. The amount of total data to be acquired is controlled with the parameter **Oversampling**. In addition to compensate for data not being used due to motion this parameter controls as well the quality (signal/noise ratio) of the image and it has to be adapted as well to the max. number of cine frames that might be reconstructed later. The more time frames needed the higher should be the number for **Oversampling**. This is an important difference to prospectively triggered protocols: in ecg-triggered protocols the temporal resolution is fixed and is defined by the repetition time TR. In IG-based protocols the time resolution is the RR-interval divided by the number of frames being calculated. This number can be changed after data acquisition to achieve a better time resolution.

Protocols for heart movies

These protocols, e. g. **Cine_IG_FLASH**, create several images within one RR-interval. Displayed in a movie loop they show the dynamics of a heart. The temporal resolution is the RR-interval divided by the number of cine frames. If a higher temporal resolution is desired more frames have to be calculated and for the same image quality a higher number for **Oversampling** has to be specified in the protocol before the scan.

Protocols for blackblood contrast

Most of the imaging techniques in cardio mri show the blood with bright intensity. If this is not desired, special techniques have to be used to suppress the signal from flowing blood. In **IG_FLASH** based blackblood protocols, e. g. **Cine_blackblood_IG_FLASH**, the suppression of flowing blood is done by saturating blood that flows into the heart. This is achieved by positioning the navigator slice over the vessels delivering blood to the heart and to use the navigator slice as a saturation slice with a high flip angle for the navigator pulse. To enhance the saturation effect the excitation scheme of the slices is reversed. This means the first slice to be excited by the rf pulses is the slice next to the saturation resp. navigator area.

Cardio applications

There are two major applications in cardiac MRI: anatomical information and quantitative evaluation.

For stationary (one image per heart phase) anatomical information the recommended protocols are **T1_FLASH**, **T1_FLASH_flc** and **Cine_IG_FLASH**. For dynamic anatomical information any "Cine_..." protocol can be used.

For quantitative evaluation to measure parameters like Ejection Fraction, End Diastolic or Systolic Volume, Stroke Volume etc. usually a multi-slice cine dataset in short axis view is needed. "Cine_..." protocols have to be used. Triggered "Cine_..." protocols acquire only one slice. Therefore a triggered protocol has to be started as many times as slices are needed with a new position for each slice. The protocols **Cine_brightblood_FLASH** and **Cine_blackblood_FLASH** are already prepared for multi-slice acquisition.

For the subsequent quantitative evaluation, the acquired data have to be transferred to a third party software. If this software cannot use the original Bruker data format the images have to be exported into DICOM format.

Modifying protocols

All delivered rat and mouse protocols have been tested in-vivo. The parameters have been setup with healthy mice and rats. If they are used with a similar setup, especially coil configuration, the resulting images should have good quality. However, as the protocols have to run on systems that can differ slightly with respect to gradient performance, the protocols are not pushed to the limits.

Especially in cardiac MRI the image quality is sensitive to flow effects which decrease with shorter echo time TE. Therefore it is recommended to use a very short TE and to check if the TE can be decreased (Exam Card → Parameter Editor → Routine Card).

If TE is already set to its minimum value cannot then to further reduce it a higher bandwidth (Exam Card → Parameter Editor → Sequence) can be selected. This allows for shorter TE and for shorter repetition time TR. In cine protocols a shorter TR allows to measure more frames within one RR interval. However, a higher bandwidth will result in an image with lower to signal-to-noise ratio (SNR). To compensate for this it might be necessary to increase the number of averages (Exam Card → Parameter Editor → Routine).

The **Localizer** and **Planning** scans are stored without trigger. This allows to use them in both setups, for prospective (ecg leads) and retrospective (IntraGate) triggered examinations. If trigger is needed and activated in these protocols the number of averages can be reduced to about 2 to 4 averages. As the repetition time will be controlled by the animals heart rate TR can be reduced as well. Activating the trigger option in the **Localizer** and **Planning** scans will activate in some of these protocols a short **Trigger Delay** to acquire the data in late diastole.

2.7.5 Localization

The heart of the rat should be in the center of the RF coil and of the magnet.

Note: All protocols, except for localizer, planning scans and IG_FLASH based protocols, are triggered and the data acquisition will not start if the BNC cable for triggering is not connected.

Start with protocols from location **Rat-Heart-Cine** or **Mouse_Heart_Cine**. Perform overview images e.g. with a **1_Localizer** protocol, location **Heart_Cine**. This protocol acquires 3 orthogonal slice packages. Check for correct position of the heart in the center of the magnet with respect to rostral-caudal (head – feet) orientation, indicated by the intersection of the orthogonal slices (black lines) in each image. If necessary correct the position of the animal.

Note: If the position of the animal has to be corrected the following scan has to be started with “All Setup + Acquisition” (Exam Card → Parameter Editor → Instruction) including coil tuning (wobble).

1_Localizer is a fast reference scan, mainly used for a quick check of the position of the animal. If more slices per orientation are needed **1_Localizer_multi_slice** from **Heart_Cine** location can be used in addition. This acquires 3 orthogonal slice packages with multiple slices per package and a better resolution. Plan this scan with reference to the first localizer and shift each slice package to cover the heart.

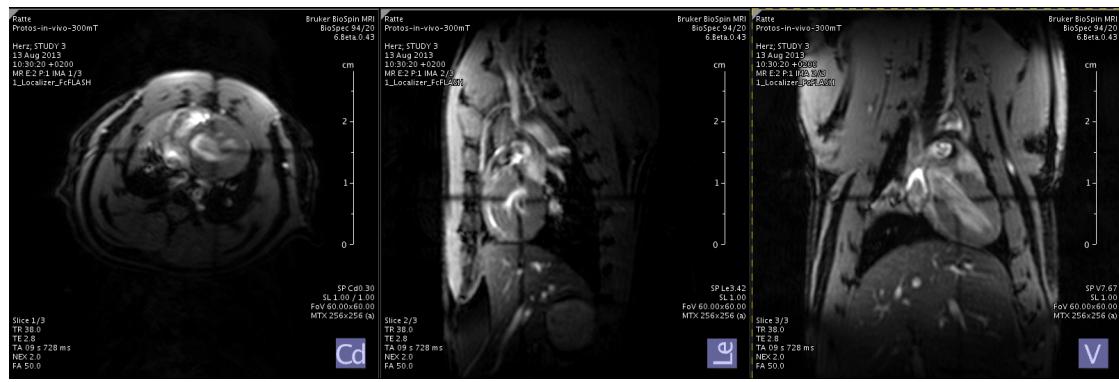


Figure 2.81: Triggered 1_Localizer for localization of the heart

Based on these overview scans any other views can be planned.

Standard views in cardio vascular research

In the assessment of cardiovascular function standard views have been established. In the following section the steps to obtain these views are described in [Reference \[521 \]](#).

In this context 3 additional reference scans are acquired and they will serve as a reference to setup short axis or 4 chamber views.

First load the protocol **2_Planning**, define 4 axial slices with a gap of 0.2 mm to 2 mm through the heart and start the scan (see Figure [Planning four axial slices \(1\) and resulting images \(2\) \[519 \]](#)).

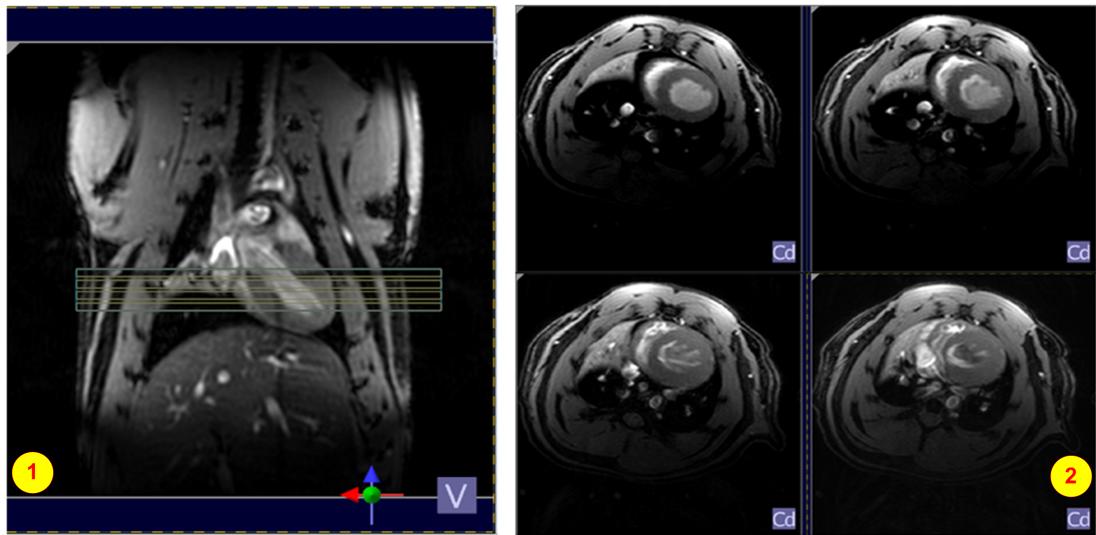


Figure 2.82: Planning four axial slices (1) and resulting images (2)

Next, load the protocol **3_Planning**, main slice orientation coronal, define 1 slice perpendicular to the previous (**2_Planning**) scan and through the left and right ventricle (see Figure [Setup for protocol 3 Planning and resulting image \[520 \]](#)).

Note: To avoid fold back artefacts ensure that the read-out direction is set to rostral-caudal (head - feet). If necessary increase the FOV in phase direction.

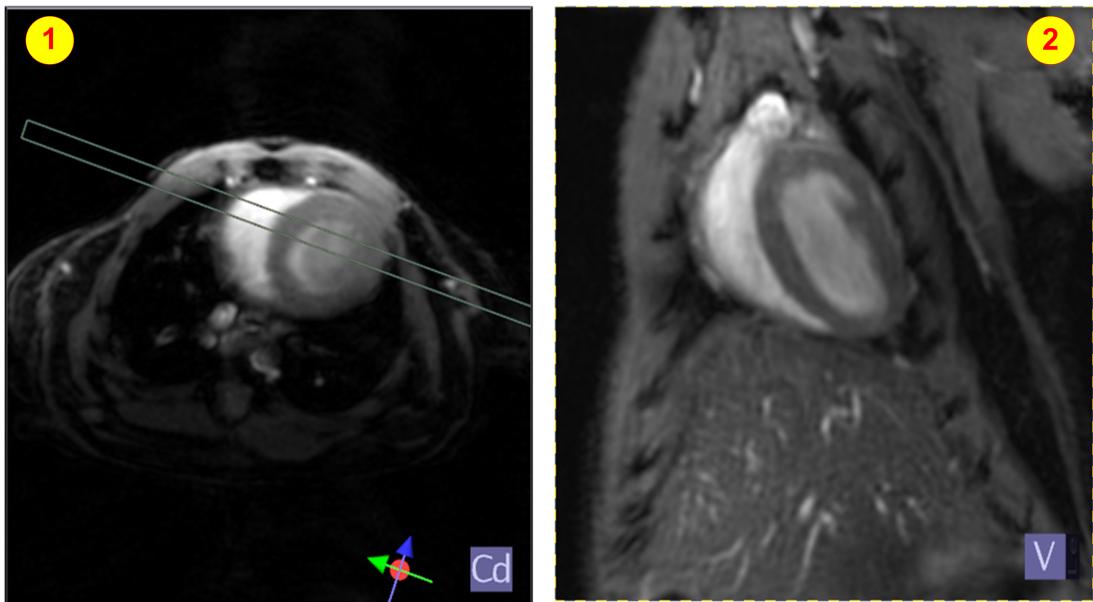


Figure 2.83: Setup for protocol 3_Planning (1) and resulting image (2)

Then, load the protocol **4_Planning**, main slice orientation sagittal, define 1 slice orthogonal to the previous (**3_Planning**) scan through the outflow tract of the left ventricle and the apex (see Figure [Setup for protocol 4_Planning and resulting image \[▶ 520\]](#)).

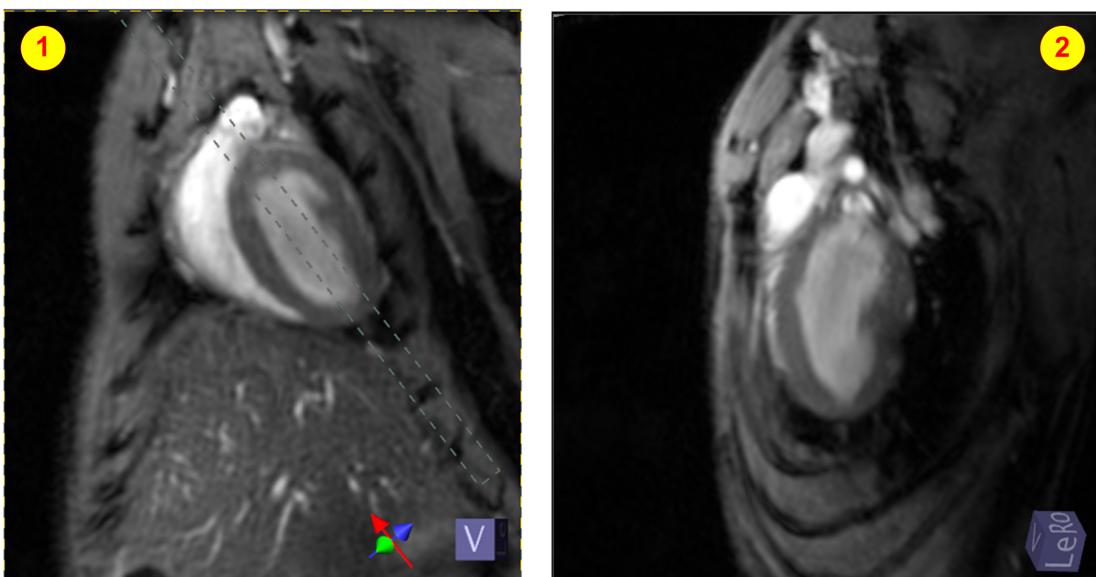


Figure 2.84: Setup for protocol 4_Planning (1) and resulting image (2)

Short axis view

Load the desired protocol from **Heart_Cine**. As a first reference load the image from **3_Planning**, rotate the imaging slice such that it orthogonally intersects the septum. As another reference image load the image from **4_Planning**; with reference to this scan rotate the slice to be oriented orthogonal to the long axis. Usually the resulting slice orientation will be axial, ensure readout direction is left – right (see Figure [Planning a short axis view with reference to 3_Planning, 4_Planning and resulting short axis view \[▶ 521\]](#)).

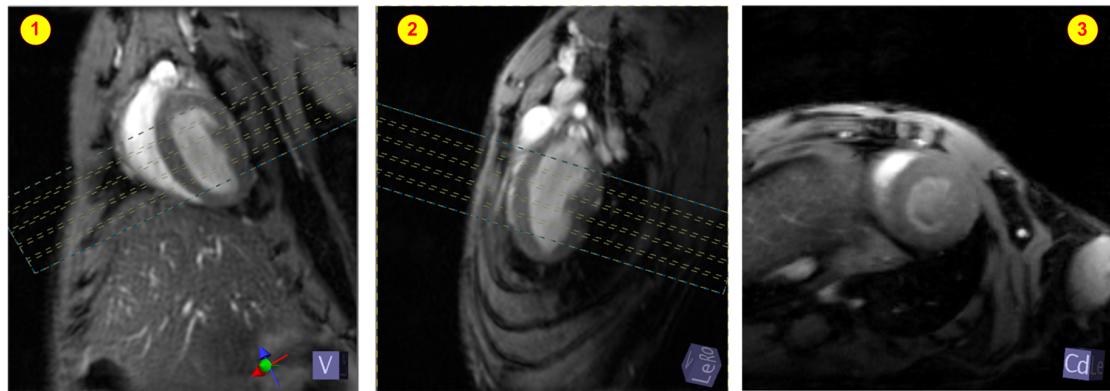


Figure 2.85: Planning a short axis view with reference to 3_Planning (1), 4_Planning (2) and resulting short axis view (3)

Four chamber view

Load the desired protocol from **Heart_Cine**, set the main slice orientation coronal and orthogonal to an image from **4_Planning**. Position the slice through the apex and base of the heart. With reference to the short axis images the slice should go through the left and right ventricle (see Figure [Planning a four chamber view and resulting image \[▶ 521\]](#)). Ensure that the readout direction is rostral – caudal (head – feet).

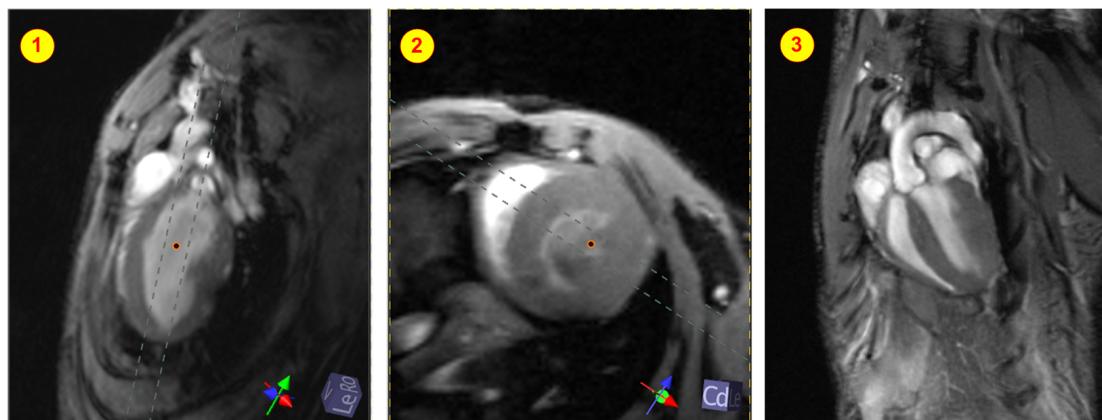


Figure 2.86: Planning a four chamber view (1, 2) and resulting image (3)

Additional scans

After acquisition of a short axis and/or a four chamber view for the following scans it is only necessary to import the slice geometry and specify protocol specific parameters.

2.7.6 Reference

[1] Assessment of Global Cardiac Function; Jürgen E. Schneider; "In Vivo NMR Imaging - Methods and Protocols";
Editors: Leif Schröder, Cornelius Faber

2.8 Diffusion

2.8.1 DWI

2.8.1.1 Introduction

Diffusion reflects the mobility (i.e. Brownian motion) of water molecules within tissue. Diffusion Weighted Imaging makes use of magnetic field gradients to detect the phase dispersion of the transverse magnetization caused by diffusion. This results in the attenuation of the MR signal, the degree of which depends on tissue type, structure, and microenvironment. The diffusion contrast is a measure of diffusion strength and not of its orientation. It is quantified via the apparent diffusion coefficient (ADC). In diffusion weighted (DW) images, structures with high diffusion (strong water mobility) appear hypo-intense compared to the surrounding tissue (strong diffusion coefficient, hyper-intense ADC maps). Conversely, areas of reduced diffusion show hyper-intensity signal (weak diffusion coefficient, hypo-intense ADC maps).

Abbreviations

- ADC - Apparent Diffusion Coefficient
- DTI - Diffusion Tensor Imaging
- DWI - Diffusion Weighted Imaging
- EPI - Echo Planar Imaging
- ISA - Image Sequence Analysis
- RF - Radio Frequency
- ROI - Region of Interest
- T1 - Spin-Lattice Relaxation Time
- T2 - Spin-Spin Relaxation Time
- TE - Echo Time
- TR - Repetition Time

Purpose

DWI typically employs a single B value along one single direction to produce an image. The B value controls the degree of the diffusion weighting in the image. The diffusion constant can be measured by acquiring a series of diffusion-weighted images, each with a different level of diffusion labeling (different B values). From this image series, a pixel-by-pixel quantitative diffusion coefficient map, also called ADC mapping can be calculated. To remove the patient-orientation dependence, the diffusion trace protocol with ADC values measured along three orthogonal directions is also available.

The present chapter describes how to perform routine diffusion based measurements in ParaVision 6 using the following three techniques: Diffusion weighted imaging (DWI), Quantitative mapping of diffusion coefficients (ADC mapping) and Diffusion Trace. Options for data evaluation are briefly overviewed in the second part of the chapter.

2.8.1.2 Hardware Setup



To ensure that the DTI Protocols do not demand stronger gradients than what it is achievable by the system, it is possible to simulate a scan before it is started to ensure that the gradient duty cycle can be run by the system. To do this, open the simulation platform (right icon of the three to the top left of the instruction list) with the scan open and click on Start. The gradient duty cycle simulation will start and at completion will read either “Gradient Duty Cycle: OK”, “Gradient Duty Cycle: Critical”, or “Gradient Duty Cycle: Violated”. See Chapter [Using the Simulation Platform \[▶ 78\]](#)

Limitations and Troubleshooting

Gradient instabilities can occur when gradient amplifiers are operated with short switching times or with very high gradient intensities. These instabilities can cause ghost artifacts. In diffusion experiments, it is recommended to run the Duty Cycle simulation via the Simulation Platform to ensure the gradients are not used at critical strength values. Such extreme conditions can generate eddy currents that will vary with the diffusion gradient strength and diffusion direction. The measured diffusion constants are very dependent on the ambient temperature, and can be influenced by air conditioning, temperature of the gradient cooling, duty cycle of the RF-pulses etc.

2.8.1.3 Object Setup

Positioning

Diffusion experiments are intrinsically sensitive to macroscopic motion. To avoid vibrations the animal should be well restrained.

2.8.1.4 Protocol Setup

Protocol and Method

The most common pulse sequence used for DW-MRI is single shot Echo Planar Imaging due to its high acquisition speed and motion insensitivity.

To measure the ADC coefficient along one single direction (a typical DW-contrast image) select the protocol **Diffusion_weight_EPI** from the **Palette tab** under **Explorer, Scan Programs & Protocols**, location **Rat** (or **Mouse**) **Head / Diffusion**. The protocol has an assigned B value of 650 s/mm². The standard spin echo based diffusion protocol (**Diffusion_weight_SE**) is available and can also be used to provide DW-contrast images. It is recommended to run this protocol with respiratory triggering due to its high sensitivity to motion. Its acquisition time can be, however, very long (~10 min) which inhibits its widespread acceptance for pre-clinical applications.

To perform a quantitative mapping of the diffusion coefficients (ADC mapping) select the protocol **Diffusion_map_EPI** from the **Palette tab** under **Explorer, Scan Programs & Protocols**, location **Rat** (or **Mouse**) **Head / Diffusion**. This protocol is already optimized for the rat (or mouse) brain investigations but still offers the flexibility for a smaller FOV or thinner slice thickness. A detailed pulse sequence description is given in Chapter [DtiEpi \(Diffusion tensor imaging with EPI\) \[▶ 345\]](#).

The **Diffusion_map_EPI** protocol provides diffusion maps of the apparent diffusion coefficient by using a series of 6 diffusion experiments with the diffusion weighting factors (**B values**) 100, 200, 400, 600, 800, and 1000 s/mm². This range of B values is sufficient to access weak diffusion coefficients such as those found in brain white matter. One A₀ image is also measured. The diffusion-encoding gradient direction is applied along the readout gradient. All mentioned parameters can be changed so that they match the requirements of each specific experiment.

The contrast of the resultant DW-contrast image is specific to the gradient direction and can change with patient orientation, affecting the ADC results. To measure the diffusion coefficients independent of anisotropy one can average diffusion images measured at different directions and calculate the trace of the diffusion tensor. The protocol **D_Trace_EPI** is designed for this purpose. Three diffusion directions perpendicular to each other and one A₀ image are measured. The Trace image is of interest primarily in longitudinal studies when slightly different subject positioning may cause a displacement of diffusion orientation with respect to the diffusion axes.

Parameter Selection

Diffusion specific parameter optimization is performed via the **Parameter Editor**, by accessing the **Diffusion Card** where parameters such as **Gradient duration** (small delta, δ), **Gradient separation** (big delta, Δ), **B value**, type of **Diffusion Experiment** (DW_contrast, DW_MultiShotTrace) are available on the **Main sub-card**. The number of B Values can be modified in the Exp. Per Direction entry and their value on the corresponding pop-up card.

A post-processing macro **Fitinlsa**, which automatically starts the ADC (or the Tensor Trace) parameter map calculation, is preselected in the default protocol. To disable the automatic calculation open the **Processing Platform** (left icon of the three top left of the instruction list) followed by the **Data Reconstruction** card and unselect **Execute Macro Fitinlsa** in the **Post Image Series Activities** field.

Adjustments

B₀ field homogeneity: A good shim is essential for DWI because of EPI sensitivity to B₀ field inhomogeneity. It is recommended to use the **Map_Shim** utility to optimize the field homogeneity in the region of interest. For brain applications, a shim volume covering the entire brain is already active in the protocol.

To improve the shims proceed as follows: load the scan in the instruction list, enable **Map_Shim** in the Auto Shim Sub-card of the Setup Card. The shim volume is now visible in the Examination card. Adapt its geometry to cover only the brain, without tissue/bone/air interfaces (e.g. skull, air cavities). Open the **Adjustment Platform**, select and open the **On Demand Protocol B₀ Map**. Acquire the B₀ map by pressing **Start** and leave the **Adjustment Platform** once the map is acquired (Green tick mark appears) by clicking **Apply** and **Back**. Once acquired, the B₀ map will be displayed in the Palette tab under Explorer, Datasets. Start the acquisition with **Continue**. The shims will be calculated in an automatic adjustment prior to the start of the diffusion acquisition itself.

Note: If **Map_Shim** was previously performed and you want to keep the calculated shim values, keep the by default option **Current_Shim** in the Auto Shim Sub-card of the Setup Card.

Standard Protocol Execution

All Diffusion Weighted-based protocols described here are ready to be run in standard routine mode and deliver the following images:

- The **Diffusion_weight_EPI** and the **Diffusion_weight_SE** deliver a DW-contrast image per slice.

- The **Diffusion_map_EPI** delivers one diffusion weighted image for each B value and each slice. From this image series, the diffusion constant for one or more regions of interest (ROI) and the diffusion constant map (ADC map) are calculated.
- The **D_Trace_EPI** acquires one diffusion weighted image for each of the three selected diffusion directions. From this image series, the Tensor trace (also called Mean Diffusivity) image is computed.



[**The Simulation Platform** \[▶ 476\]](#)



[**DtiEpi \(Diffusion tensor imaging with EPI\)** \[▶ 345\]](#)

2.8.1.5 Data Analysis

Tools and Analysis

Based on the post-processing macro **Fitinlsa**, the data analysis will automatically provide an ADC (or Tensor Trace) map. The ADC-fit is performed using the ISA-Tool and the ROI Tool available in the Image Display & Processing Tool. [Knoten]

The diffusion constant is calculated using the dtraceb ISA function. The **fit function dtraceb** is defined in the macro **and** uses the B value list calculated from the protocol parameters. The fit is based on the magnitude images of the reconstructed dataset.

Displaying the results

After the automatic **Fitinlsa** macro processing, the result is stored under the same experiment number (Expno) with a new processing number (Procno). Both acquired and post-processed images are automatically loaded in the **Palette Tab** under **Explorer, Datasets**. At the same time, they are also displayed in the first two viewports of the **Image Display & Processing Tool**. This last option is intended for manually performing the ADC-fit. To display the ADC values from the generated ADC maps open the **ISA Tool** and place a new ROI in the region of interest. The ISA-Tool can be started via **Image Display & Processing > Processing > Image Sequence Analysis**.

By changing the position or the size of the ROI, the display of the fit curve and the fit result is updated in real time. To change the shape of the ROI, use **Define ROI** (**File > more buttons**).

To compare the ADC (or Tensor Trace) values from different regions, create a **New ISA ROI**. A new table with the data is added to the display.

The fit provides five parametric images in the new Procno, namely:

The signal intensity image

- Standard deviation image of the signal intensity
- The diffusion constant image (or the Tensor trace image)
- Standard deviation image of the ADC (or Tensor Trace) values
- Standard deviation image of the whole fit.
- To manually process the DW data use the recommended workflow described below:

The Diffusion Constant (ADC) Values

To calculate the diffusion constant out of one (or more) ROIs:

Load a **Diffusion_weight_EPI**(or **Diffusion_weight_SE**) dataset into the **Image Display and Processing Tool** and open the **ISA Tool**.

Select and position a New ISA ROI in the Image Display & Processing Tool viewport. In ISA-Tool change into mode Points & Curves and Refresh Cur ROI.

The data points and the fit curve are displayed. The numerical results will be added to the statistics table. Use **Modify Cur ROI** to move the ROI. The display of the fit curve and the fit result is updated in real time when changing the position or the size of the ROI.

To change the type of the ROI, use Define ROI (File > More buttons).

To compare the ADC values from different regions, create a New ISA ROI. A new statistic table with the data is added to the display.

Note: With lower diffusion sensitization there is significant T_2 weighting, also known as " T_2 shine through". Diffusion images are also affected, to a smaller extent, by T_1 relaxation and proton density, depending on the sequence parameters. MRI fails to differentiate between diffusion-related motion from blood flow, perfusion, bulk tissue, and tissue pulsation-related motion. Thus, the diffusion value obtained is not an actual but an apparent diffusion coefficient (ADC). ADC maps have contrast proportional only to diffusivity and they are independent of B_0 .

Computing the ADC and the Tensor Trace Maps

To generate the ADC maps:

After running the **Diffusion_map_EPI** protocol, load the acquired dataset into the **Image Display and Processing Tool** and open the **ISA Tool**. Select **Images > Calculate Parameter Images-All Slices** and store the result under the same examination number but with a new processing number (Procno) in the Processed Image Editor pop-up window.

The same procedure is used to generate the **Tensor Trace image derived from the D_Trace_EPI** protocol.

In order to avoid areas with noise in the ADC map create an All-ROI with a lower threshold of 10% in the active viewport and Cut Away the low intensities. This cuts off the noise level of the calculated ADC image. Select **Images > Calculate Parameter Images** and store the result under the same examination number but with a new processing number (Procno). Load it into the **Image Display and Processing Tool**.

Limitations

Errors in ADC measurements include systematic errors, which arise from temperature variations and gradients, incorrect gradient scaling adjustments as well as low SNR.

Practical Considerations for Specific Diffusion Experiments

All above mentioned diffusion-based protocols can be customized so that they match the requirements of specific experiments in which the user is interested. Several suggestions for optimization of the DW protocol, involve scan time, SNR, resolution, and reduction of geometric distortions.

Scan time and SNR: DWI generally suffers from low SNR due to strong diffusion gradient dephasing and long TE values. In multi-compartmental analysis experiments, both high diffusion sensitization and high SNR are required (e.g. in order to distinguish between the intra/extracellular environment behavior). In this case, optimal SNR is achieved with a TR larger than $5 \times T_1$, to ensure complete recovery of magnetization to equilibrium, at the expense of a longer scan time. To achieve faster acquisitions, a tradeoff between the level of diffusion sensitization and the experiment duration must be considered. When a maximum B

value is chosen, the diffusion gradient durations are typically minimized to reduce T_2 signal loss and overall scan time. An element always to be considered is the maximum available gradient power. High gradient power enables high B values to be achieved without increasing the duration of the experiment.

Resolution: In case of low SNR images and very long echo train, reducing phase encoded resolution may improve SNR more significantly than reducing the frequency encoded resolution does. Reducing the frequency encoded resolution can additionally reduce geometric distortions which typically arise when using a EPI readout.

The relative values of small delta, big delta and B values should be determined from the type of diffusion one wishes to detect. For the slow diffusion component one needs large small delta and large big delta values. By selecting Stimulated Echo as Diffusion Experiment, longer diffusion times can be achieved without increasing TE and without affecting the corresponding SNR (due to T_2 relaxation).



Image Sequence Analysis Tool (ISA Tool)



Region of Interest Tool (ROI)

2.8.1.6 References

- [1] Brockstedt S. Diffusion Imaging. Syllabus ESMRMB, 2000; 89-102.
- [2] Le Bihan D. Molecular diffusion Nuclear Magnetic Resonance Imaging. Magnetic Resonance Quarterly 7,1, 1999; 1-30.
- [3] Stejskal EO and Tanner JE. J. Chem. Physics 42, 1965; 288-292.

2.8.2 Diffusion Tensor Imaging (DTI)

2.8.2.1 Introduction

When measuring diffusion in the presence of tissue boundaries, the behavior of the water molecules can no longer be characterized adequately with a single apparent diffusion coefficient (ADC) as ADC will strongly depend on the direction in which it is measured. Therefore, in tissues with highly oriented barriers (i.e. white matter tracts in the brain or in the spinal cord) Diffusion Tensor Imaging (DTI) is extensively used to track fiber pathways [1, 2].

The present chapter explains how to perform routine DTI examinations and overviews the data evaluation possibilities. It is assumed that the reader has basic knowledge about the fundamentals of diffusion MRI.

Abbreviations

- ADC - Apparent Diffusion Coefficient
- DTI - Diffusion Tensor Imaging
- DWI - Diffusion Weighted Imaging
- EPI - Echo Planar Imaging
- ISA - Image Sequence Analysis
- MPR - Multi Planar Reformatting

- ROI - Region of Interest
- T1 - Spin-Lattice Relaxation Time
- T2 - Spin-Spin Relaxation Time
- T-SATRIG - Tomography Small Animal Triggering
- TE - Echo Time

Purpose

Diffusion Tensor Imaging requires a set of diffusion-weighted images acquired with the same diffusion gradient strength and different diffusion gradient directions. At least 6 non-collinear directions are mandatory for preserving uniform space sampling. One image acquired without diffusion sensitivity (called A_0 image) is necessary for the absolute scaling of the diffusion tensor [3]. Whereas ADC maps and Trace images show the diffusion strength (see Chapter [DWI \[522\]](#)), DTI provides information about the orientation of the anisotropic diffusion.

Coordinate systems

Beside the acquisition coordinate system read (**r**), phase (**p**), and slice (**s**), an image display coordinate system Left-Right, Dorsal-Ventral, Caudal-Rostral is used for the data evaluation in the DTI Image. In the image display coordinate system, the Left-Right coordinate can either correspond to the **r** or to the **p** coordinate of the **r**, **p**, **s** system, depending on the selected readout direction.



Chapter [DWI \[522\]](#)

2.8.2.2 Hardware Setup

Gradients

To ensure that the DTI Protocols do not demand stronger gradients than what it is achievable by the system, it is possible to simulate a scan before starting it to ensure that the gradient duty cycle can be run by the system.



To do this, open the simulation platform (third icon of the top left of the instruction list) with the scan open and click on Start. The gradient duty cycle simulation will start and at completion will read either “Gradient Duty Cycle: OK”, “Gradient Duty Cycle: Critical”, or “Gradient Duty Cycle: Violated”. See Chapter [The Simulation Platform \[476\]](#).

Limitations and Troubleshooting

Gradient instabilities can occur when gradient amplifiers are operated with short switching times or with very high gradient intensities. These instabilities can cause ghost artifacts. In diffusion experiments, it is recommended to run the duty cycle simulation via the Simulation Platform to ensure the gradients are not used at critical strength values. Such extreme conditions can generate eddy currents that will vary with the diffusion gradient strength and

diffusion direction. The measured diffusion constants are very dependent on the ambient temperature, and can be influenced by air conditioning, temperature of the gradient cooling, duty cycle of the RF-pulses etc.



Chapter [The Simulation Platform \[▶ 476\]](#)

2.8.2.3 Object Setup

Preparation

Diffusion experiments are intrinsically sensitive to macroscopic motion. To avoid vibrations, the animal should be well restrained.

In case of physiological motion, respiratory (and rarely cardiac triggering) might be necessary. This can be achieved by using an appropriate physiological monitoring system, e.g.: T-SATRIG.

For this, open the **Contrast Card** in the instruction editor and activate triggering (per slice). Specific parameters should be adjusted as described in the Chapter Cardio.



Chapter [Trigger \[▶ 256\]](#)



Chapter Cardio

2.8.2.4 Protocol Setup

Protocol and Method

The most common pulse sequence used for diffusion tensor MRI is single shot Echo Planar Imaging due to its high acquisition speed and motion insensitivity.

To perform a complete tensor measurement, select the **DTI_EPI_30dir** protocol from the **Palette tab** under **Explorer, Scan Programs & Protocols**, location **Rat (or Mouse) / Head / Diffusion**. The method is based on a spin echo EPI pulse sequence with a pair of identical diffusion-weighted gradient lobes placed on either side of the 180° refocusing pulse. It has been demonstrated that 30 diffusion directions (with three to five non-diffusion weighted scans) will provide DTI measures that are statistically rotationally invariant [4]. The **DTI_EPI_30dir** protocol is designed for this purpose. It acquires 5 A₀ images and 30 diffusion images distributed based on the Jones gradient scheme [4].

The protocol is already optimized for rat (or mouse) brain investigations but still offers flexibility for a smaller FOV or a thinner slice thickness.

Parameter Selection

Diffusion specific parameter optimization is performed via the **Parameter editor**, by accessing the **Diffusion Card** where parameters such as **Gradient duration** (small delta), **Gradient separation** (big delta), **B value**, and type of **Diffusion Experiment** (DW_Tensor) are available on the **Main sub-card**. The B Value can be modified on the corresponding pop-up card of the Exp. Per Direction entry.

A post-processing macro **DTI_PROC_TENSOR**, which automatically starts the **DTI Tensor Reconstruction** is preselected in the default protocol. To disable the automatic DTI Tensor Reconstruction open the **Processing Platform** followed by the **Data Reconstruction** card and unselect **Execute Macro DTI_PROC_TENSOR** in the **Post Image Series Activities** field.

Adjustments

B_0 field homogeneity: A good shim is essential for DTI because of EPI sensitivity to B_0 field inhomogeneity. It is recommended to use the **Map_Shim** utility to optimize the field homogeneity in the region of interest. For brain applications, a shim volume covering the entire brain is already active in the protocol.

To improve the shims proceed as follows: load the scan in the instruction list, enable **Map_Shim** in the Auto Shim Sub-card of the Setup Card. The shim volume is now visible in the Examination card. Adapt its geometry to cover only the brain, without tissue/bone/air interfaces (e.g. skull, air cavities). Open the **Adjustment Platform**, select and open the **On Demand Protocol B_0 Map**. Acquire the B_0 map by pressing **Start** and leave the **Adjustment Platform** once the map is acquired (Green tick mark appears) by clicking **Apply** and **Back**. Once acquired, the B_0 map will be displayed in the Palette tab under Explorer, Datasets. Start the acquisition with **Continue**. The shims will be calculated in an automatic adjustment in the preselected shim volume prior to the start of the diffusion acquisition itself.

Note: If **Map_Shim** was previously performed and you want to keep the calculated shim values, keep the option **Current_Shim** in the Auto Shim Sub-card of the Setup Card.

Standard Protocol Execution

The DTI protocol described here is ready to be run in the standard routine mode and delivers the following parametric images:

- **Fractional Anisotropy (FA)** map that measures the degree of anisotropy. Takes values from zero (dark contrast, referring to isotropic diffusion) to one (bright contrast, referring to the diffusion constrained along one axis only).
- **Tensor Trace** map measuring the diffusion coefficients (ADC) independent of anisotropy (is equivalent to the mean diffusivity)
- **Eigenvalue maps (λ_1 , λ_2 and λ_3)** corresponding to the three diffusivities along the principal axes of the diffusion tensor (each representing one direction of anisotropy), where:
 - λ_1 represents the ADC of water along the length of the fiber
 - λ_2 , λ_3 represent the ADC of water perpendicular to the fiber

Practical Considerations for Specific Diffusion Experiments

The above mentioned diffusion-based protocol can be customized so that it matches the requirements of specific experiments in which the user is interested. Suggestions for optimization of the DTI protocol, involve scan time, SNR, diffusion sensitivity, anisotropy and motion sensitivity.

Diffusion sensitivity and SNR: Higher diffusion sensitivity can be obtained through the combination of high amplitude gradients and long diffusion times. This increases TE which leads to a loss of signal due to the T₂ tissue relaxation, especially at high field strength. In this context, TE must be minimized at a given B value while TR should be maximized within the total scan time constraint. The stronger the gradient strength (shorter δ), the shorter the minimum TE. However, it is recommended not to exceed 85% of the diffusion gradient scaling per channel. Use more gradient directions instead of more averages. It has been demonstrated that a larger number of directions allows for smaller B Values without compromising image quality [5].

Anisotropy and number of diffusion directions: It has been shown that a better contrast between tissues with high anisotropy (e.g. white matter) and the surrounding regions can be obtained primarily on the FA maps by increasing the number of diffusion directions. The use of a large number of directions which are uniformly distributed in space is available in all DTI protocols. For this, select the desired number of **Diffusion Directions** (up to 1024) into the Diffusion card and click on **Calc. Directions**. The directions will be automatically calculated based on the charged pair model described in [6].

It is also possible to set up, in the diffusion module, diffusion weighting gradients directions with values written in a text file. This is done using the macro **DTI_SET_DIRECTIONS**. The desired number of directions as well as the direction scheme has to be written in an ASCII file of special format, easy to implement in output routines of dedicated external software. To use this macro, the following steps are required:

1. Create a text (ASCII) file containing information about the number and the scheme of the diffusion directions (see example below).
2. Select the dataset in the **Pallette/Explorer** with right mouse button, choose the “Execute Macro” from the context menu and press OK.
3. Select the **DTI_SET_DIRECTIONS** macro in Category BRUKER and select the filename in the file selection dialogue.

The following example shows how to setup 3 unit vectors as diffusion gradient direction scheme:

```
[directions=3]
CoordinateSystem = xyz
Normalisation = unity
Vector[0] = ( 0.59807082, 0.74043916, -0.30669391 )
Vector[1] = ( 0.97327271, 0.20794208, -0.09746961 )
Vector[2] = ( 0.03594130, 0.23557830, -0.97119055 )
```

For tractography applications, it is recommended, if the signal to noise allows it, to use isotropic imaging voxels to remove any preferential averaging of fiber orientation along one axis.

Motion sensitivity: Although diffusion protocols based on single shot EPI are considered rather insensitive to motion, motion among different diffusion images or multiple segments can still degrade the diffusion image quality, especially when using segmented DTI-EPI. One solution is to reduce the B Value (keeping the same diffusion gradient duration). The respiratory trigger can also be used to reduce motion artifacts with the expense of a longer effective scan time.

Practical considerations to overcome EPI-related artifacts under which DTI-EPI based sequences may suffer are given in chapter Fast MRI.



Chapter [Bruker Applications Protocols \[▶ 502\]](#) Location Rat (or Mouse) / Head / Diffusion



Chapter DtiEpi (Diffusion tensor imaging Epi)



Chapter Fast MRI

2.8.2.5 Data Analysis

Tools and Analysis

Based on the post-processing macro **DTI_PROC_TENSOR**, the data analysis will automatically provide parametric images such as: Fractional Anisotropy, Trace [mm²/s], Intensity, Trace Weighted Image. The analysis is performed using the DTI Image Viewer within Jive.

Displaying the results

After the automatic **DTI_PROC_TENSOR** macro processing, the result is stored under the same experiment number (Expno) with a new processing number (Procno) and will be automatically displayed in the **Palette tab** under **Explorer/Datasets**.

The new DTI procno can be loaded and post-processed within the DTI Image Viewer. For this, right mouse click and select **DTI Image Data** from the context menu. The DTI Visualizer will open and guide you through the steps required to reconstruct a DTI composite image, namely:

- **Step 1:** Select the images to map and from which a signal mask should be created (see Figure [DTI Visualizer: DTI data selection for mapping and masking the images \[▶ 533\]](#)).

Typically the A₀ image is used as the morphological image onto which the tensor data is overlaid. Any image from the Diffusion Tensor images can be used to create the mask. Specifically, the trace weighted image, the A₀ image, or first eigenvalue images provide good masking capabilities.

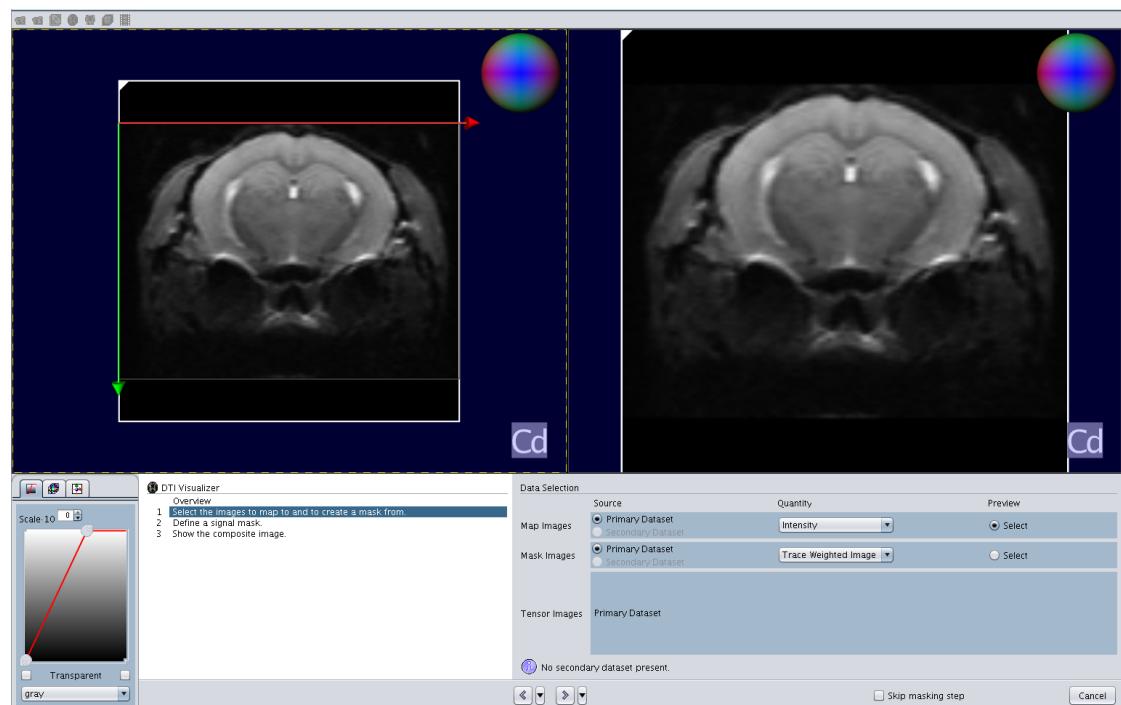


Figure 2.87: DTI Visualizer: DTI data selection for mapping and masking the images

- **Step 2:** Define a signal mask.

All steps to follow for defining a signal mask are described in the Chapter “MPR and DTI 3D-Visualization”. One representative image (see Figure [DTI Visualizer: Creating a signal mask. \[▶ 534\]](#)) is illustrated below.

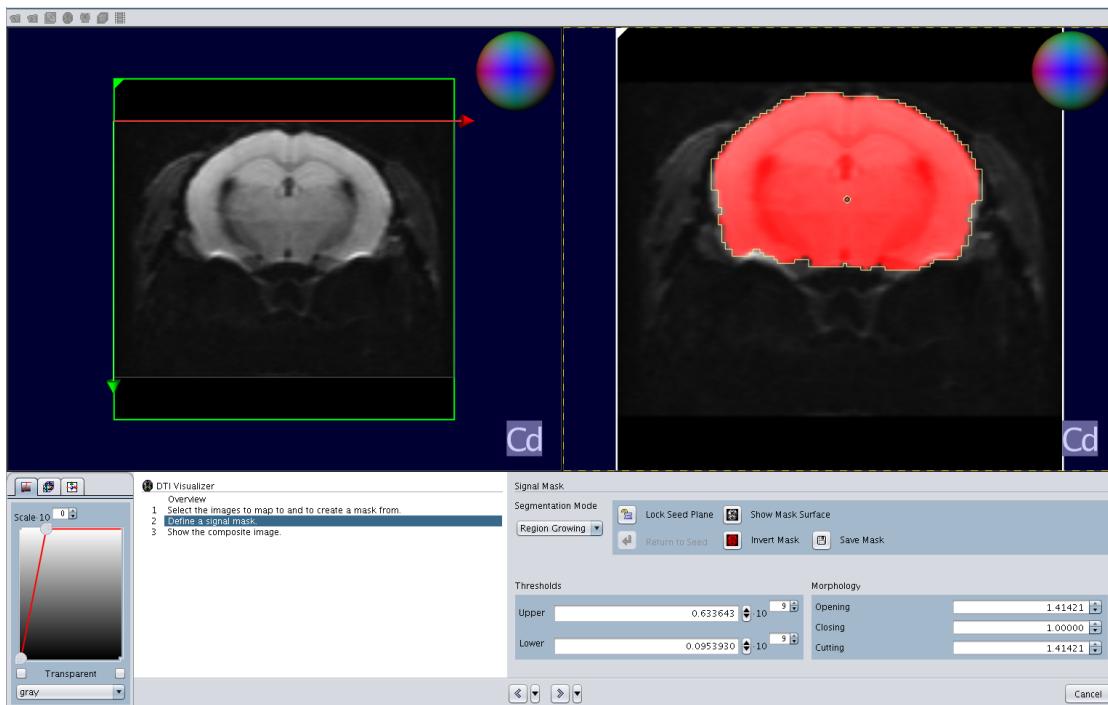


Figure 2.88: DTI Visualizer: Creating a signal mask.

- **Step 3:** Visualize the composite images. The three components of the three eigenvectors are marked as follows:
 - 1st component **Le-Rt** in Red,
 - 2nd component **D-V** in Green,
 - 3rd component **Cd-Ro** in Blue.

Options such as selection of eigenvalues and components, mapping of the eigenvectors to the A_0 image, browsing through the composite image and storing the results are available within the DTI Visualizer and they are all described in detail in the Chapter MPR and DTI 3D-Visualization.

A representative DTI composite image is shown in Figure [DTI visualizer of a DTI-EPI dataset acquired on a rat brain. \[▶ 535\]](#).

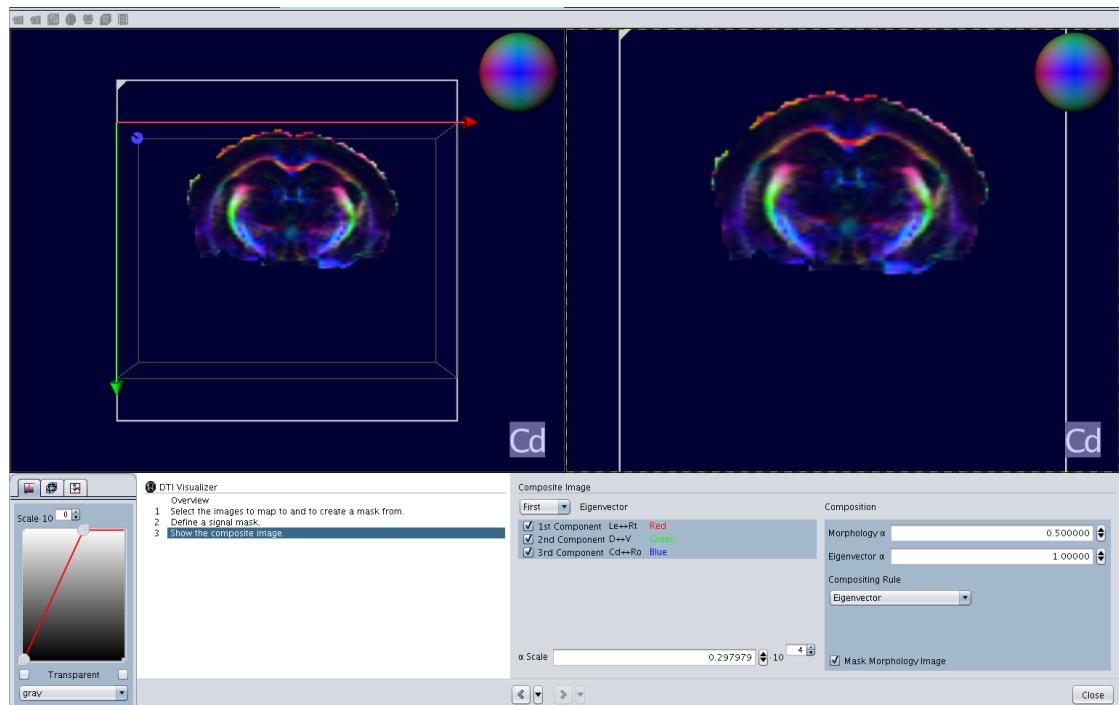


Figure 2.89: DTI visualizer of a DTI-EPI dataset acquired on a rat brain.

The Fractional Anisotropy (FA), the Tensor Trace or the eigenvalues (λ_1 , λ_2 , λ_3) can be calculated in different regions of interest (ROI) using the Analysis tab of the Image Viewer.

To create ROIs, use the ROI subtab of the Analysis tab from Palette/Viewing. The workflow of working with ROIs is described in the Chapter [Add a Region of Interest \[▶ 150\]](#).

2.8.2.6 References

- [1] Beaulieu C. The basis of anisotropic water diffusion in the nervous system – a technical review. *NMR Biomed.* 2002;15:435-455.
- [2] Harsan LA et al. In vivo diffusion tensor magnetic resonance imaging and fiber tracking of the mouse brain. *NMR Biomed.* 2010;23:884-96.
- [3] Le Bihan D. Molecular diffusion Nuclear Magnetic Resonance Imaging. *Magnetic Resonance Quarterly* 7,1, 1999; 1-30.
- [4] Jones DK. The effect of gradient sampling schemes on measures derived from diffusion tensor MRI: a Monte Carlo study. *Magn Reson Med.* 2004 Apr;51(4):807-15.
- [5] Poonawalla AH et al. Optimization of b-value and gradient orientation for diffusion tensor MRI. *Proc of 8th ISMRM* 2000.
- [6] Jones DK, Horsfield MA, Simmons A. Optimal strategies for measuring diffusion in anisotropic systems by magnetic resonance imaging. *Magn Reson Med.* 1999; 42:515-525.
- [7] Wick M, Salnikow G, Werner C. *Diffusion Tensor Imaging*. BRUKER Spin Report, 2004; 154-155.

2.9 Angiography

2.9.1 Introduction

Abbreviations

- **FLASH** - Fast Low Angle Shot
- **FcFLASH** - Gradient Echo Flow Compensated
- **MIP** - Maximum Intensity Projection
- **MRA** - Magnetic Resonance Angiography
- **MRI** - Magnetic Resonance Imaging
- **PCA** - Phase Contrast Angiography
- **RECO** - Reconstruction
- **TOF** - Time Of Flight

Purpose

Magnetic Resonance Angiography (MRA) is used for the direct visualization of the vascular structure. A quantitative measurement of flow in the vessels can be obtained using the velocity mapping methods (Velocity Mapping – Fourier Flow Imaging). Vascular malformations are easily demonstrated with MRA and or blood flow measurements.

With angiography, the blood vessels can be displayed with and without the injection of a contrast agent. MRA techniques allow the acquisition of a 2D or 3D data set from which the projections and surfaces can be calculated. Various physical effects of flowing blood can be used for contrasting the vessels and for measuring the blood flow.

This chapter describes to measure and process the angiography data. Two techniques of Angiography are demonstrated, the Time Of Flight (TOF) method based on the different saturation state between flowing and non-flowing spins[1,2] and the Phase Contrast Angiography (PCA) based of the effect of flow on the phase of the signal [3]. With Velocity Mapping, the images are directly contrasted in velocity and flow profiles in the vessels can be extracted from the images [5].

2.9.2 Hardware Setup

Gradients

No special requirements.

Coils

There is no special requirements for TOF Angiography. For PCA and Velocity Mapping, use preferably an adapted Transmit -Receive Resonator.

2.9.3 Object Setup

See that your imaged volume is well centered in the coil.

2.9.4 Protocol Setup for Time of Flight (TOF) Angiography

Protocol and Method for 2D TOF

The 2D Time Of Flight method (TOF) is used to image the veins and arteries from all parts of the body of a rodent (Head , Abdomen, legs).

To acquire a 2D TOF angiography of the head of a rodent, select one of the two protocols:

TOF_2D_FLASH or TOF_2D_FLASH_flc

in the location Rat(Mouse)-Head-Angiography.

The 2D TOF protocols are based on a series of 2D gradient echo images that cover the volume containing the vessels to be imaged. The **TOF_2D_FLASH_flc** protocol is less sensible to pulsatile flow artifacts than the **TOF_2D_FLASH** protocol.

The same protocols are used for the other part of the body.

Parameter Selection

- Choose your Field of View (FOV), Slice Orientation and Slice Number to cover the volume to be imaged. The slice must be oriented perpendicular to the main direction of the flowing blood.
- The volume can be extended by increasing the slice number, with the result of an increased acquisition time.
- Vein or arteries can be selectively imaged using different placement of saturation slices (see Figure [Setup of Flow Saturation Slices to image only the arteries of the rat brain. \[▶ 538\]](#)). To set a flow saturation slice, activate the FlowSat module in the Contrast Card. The saturation slice is positioned using the Geometry tool.
- To image the arteries the saturation slice is positioned on the rostral side of the image volume and for veins on the caudal side.

Motion artifacts can be minimized using averaging.

Adjustments

No manual adjustments are required.

Acquisition

Start acquisition with **Continue** or **Scan**.

Reconstruction

No special considerations

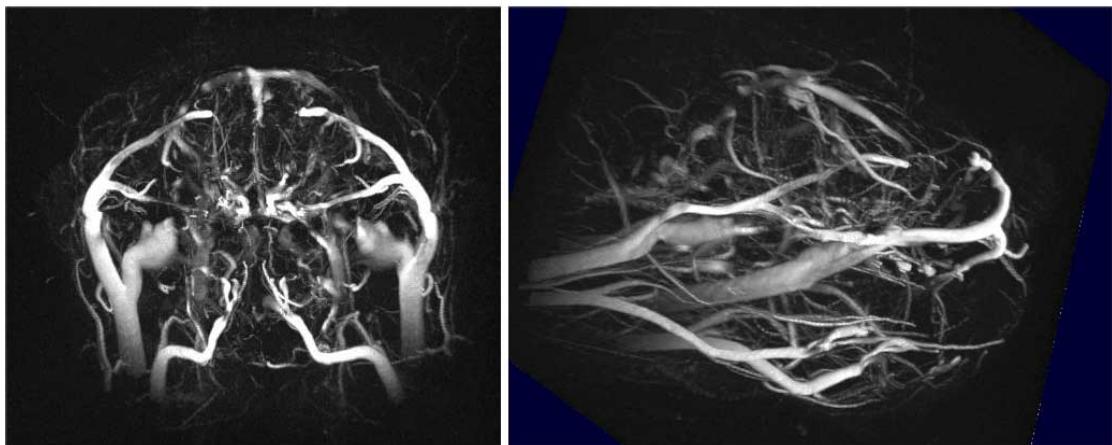


Figure 2.90: Representatives 2D TOF Angiograms of the rat head

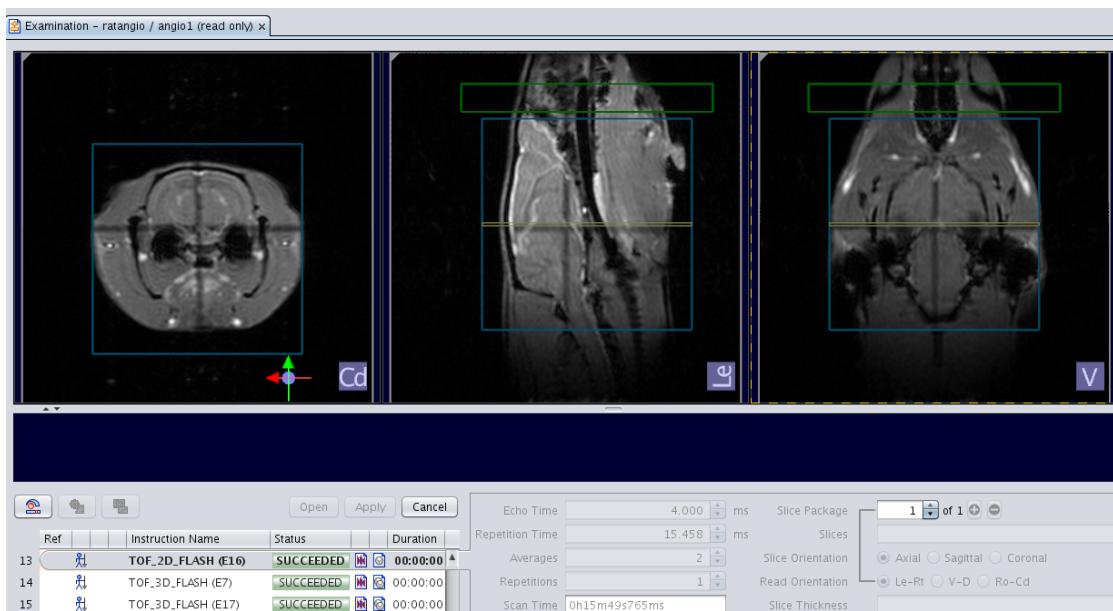


Figure 2.91: Setup of Flow Saturation Slices to image only the arteries of the rat brain.

To image the veins, the saturation slices should be placed on the lower (caudal) side of the brain.

Protocol and Method for 3D TOF

The 3D Time Of Flight method (TOF) is used to image arteries especially in the head of a rodent (see Figure [Representatives 3D TOF Angiograms of the rat head \[▶ 539\]](#)).

To acquire a 3D TOF angiography select the protocol:

TOF_3D_FLASH

in the location Rat(Mouse)-Head-Angiography

The 3D TOF protocol is based on a 3D gradient echo image that cover the volume containing the vessels to be imaged. The method parameters are choose to enhance the contrast of vessels compared to the surrounding tissues.

Parameter Selection

Choose your Field of View (FOV), the Slab orientation and thickness to cover the volume to be imaged. The slab should be oriented perpendicular to the main direction of the flowing blood.

Adjustments

No manual Adjustments are required

Acquisition

Start acquisition with **Continue** or **Scan**.

Reconstruction

No special considerations



Figure 2.92: Representatives 3D TOF Angiograms of the rat head

2.9.5 Protocol Setup for Flow Measurements Velocity Mapping

Protocol and Method For Velocity Mapping

Velocity Mapping [5] allows to measure quantitative flow maps (in units of cm/s), in different regions of a rodent (head, heart, abdomen, legs...).

To acquire a velocity map of the head to visualize vessels such as carotids, select the protocol:

Velocity_map

In the location Rat(Mouse)-Head-Angiography.

Similar to the PCA angiography methods , Velocity mapping is an option of the FLOWMAP method. The contrast issued from the phase image is directly quantified in velocity (cm/sec).

Parameter Selection

- Choose your Field of View (FOV), Slab Orientation and thickness to cover the volume to be imaged. Typically, the slice is oriented perpendicular to the main direction of the vessels to measure the main velocity direction. However, it is possible (like in PCA) to encode the three directions of flow by setting the parameter Direction in the Routine Card. One velocity map image will be delivered for each encoding direction. The Velocity Range parameter is set to 60 cm/sec which is adapted to visualize the carotid arteries of a rodent.
- In case of heart imaging, it is recommended to set the Range parameter superieur to 200cm/sec to measure the velocity without aliasing.

- When the velocity map protocol is acquired without ECG triggering, the mean velocity during the heart cycle will be measured. To follow the flow variations in the vessels during the heart cycle, the acquisition should be made in movie mode using ECG triggering. The movie mode and the ECG trigger can be enabled from the Contrast Card. Set ECG trigger on in mode Per Slice. Set the Movie Frames number as performed when acquiring a cine protocol. More details are given in the Chapter [Cardio ↗ 507](#).

Adjustments

No manual Adjustments are required

Acquisition

Start acquisition with **Continue** or **Scan**.

Reconstruction

No special considerations

2.9.6 Data Analysis for Velocity Mapping

Tools

The phase images calibrated in Velocity(cm/sec) can be displayed in the Viewer or in Movie mode in case of multi-frame triggered acquisition.

The velocity variations during the heart cycle can be calculated in a ROI and displayed in the ISA tool using the evolution fit function.

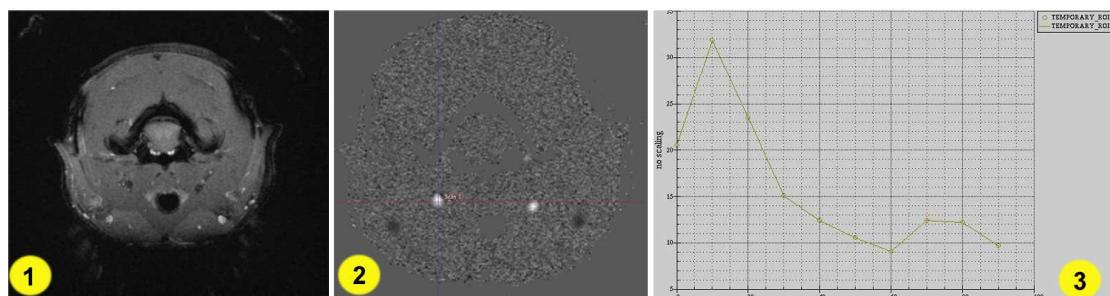


Figure 2.93: (1) magnitude-image, (2) Velocity Image Phase Contrast, (3)Velocity variation in a carotid artery

Fourier flow imaging (Advanced Protocol)

Fourier flow mapping encodes two spatial dimensions (read and phase direction) and one flow dimension. The application of a 3D Fourier transform results in a two dimensional spatial image with a quantitative flow velocity distribution in the third dimension [6].

BRUKER does not offer currently pre-optimized Fourier Flow imaging Protocols. To create your own Fourier flow imaging Protocol, select the **Velocity_map** protocol from the location Rat(Mouse)-Head-Angiography. Open the Routine Card and change the following parameters :

- Set Mode to FourierFlowImaging
- Set Direction to slice
- Set Flow Encoding Steps to 32
- Set Flow Zero Fill Factor to 8

Adjustments

No manual Adjustments are required

Acquisition

Start acquisition with **Continue** or **Scan**.

Reconstruction

No special considerations

2.9.7 References

- [1] Reese T, et al. Magnetic Resonance Angiography of the Rat Cerebrovascular System without the Use of Contrast Agents. NMR Biomed. 12, 1999; 189-196.
- [2] Beckmann N. High Resolution Magnetic Resonance Angiography Non-invasively Reveals Mouse Strain Differences in the Cerebrovascular Anatomy in Vivo. MRM 44, 2000; 252-258.
- [3] Dumoulin CL, Turski PA. Phase Contrast MR. Methods in Biomedical Magnetic Resonance Imaging and Spectroscopy, Ian R. Young, 2000.
- [4] Dumoulin CL, et al. Simultaneous Acquisition of Phase Contrast Angiograms and Stationary Tissue Images with Hadamard Encoding Flow-induced Phase Shifts in JMRI 1,1991;399-404
- [5] Underwood SR et al. MagneticResonance Velocity Mapping: Clinical Application of a new Technique in British Heart Journal. 57,1987;404-412
- [6] Bittoun J et al. High-Precision MR velocity mapping by 3D-fourier phase encoding with a small number of encoding steps. Magnetic Resonance in Medicine 29(5),1993;674-680

2.10 Arterial Spin Labeling (ASL)**2.10.1 Introduction****Abbreviations**

- ASL - Arterial Spin Labeling
- CBF - Cerebral Blood Flow: rate at which blood flows through the microvasculature (in ml of blood per 100g of tissue per minute)
- EPI - Echo Planar Imaging
- FAIR - Flow-sensitive Alternating Inversion Recovery
- RARE - Rapid Acquisition with Relaxation Enhancement
- ROI - Region of Interest
- T1 - Longitudinal Relaxation Time (T1 - Spin-Lattice Relaxation Time)
- TIR - Inversion Recovery Time

Purpose

Arterial Spin Labeling (ASL) techniques are used for the quantification of tissue perfusion (Cerebral Blood Flow – CBF, Cerebral Blood Volume – CBV, Mean Transit Time - MTT...) without external tracers or contrast agent injection. Bruker delivers protocols for perfusion in small rodent brain.

In ASL, the blood in the arteries upstream from the imaging volume is magnetically "labeled". As a consequence, image intensity changes will occur depending on the blood supply to the tissue in the imaged slice: the labeled water molecules flow into the slice of interest where it

exchanges with tissue water altering the tissue magnetization and therefore the image intensity. Upon subtraction of an image acquired without labeling, the background signal from static spins is removed and the difference image can be used to quantify Cerebral Blood Flow for instance.

A simple approach to ASL is Pulsed-ASL or PASL. Here, the inflowing blood is labeled by a spatially selective inversion of the equilibrium magnetization (see reference [1]). This chapter describes a PASL variant known as FAIR (Flow-sensitive Alternating Inversion-Recovery). Figure [FAIR labeling principle \[▶ 542\]](#) illustrates the basic principle of FAIR (see reference [2]): alternate images are acquired after a slice selective inversion followed by a global inversion of the volume seen by the excitation RF coil therefore including (part of) the heart if possible as well as all slice surrounding tissues containing the supplying arteries. The CBF can be quantified indirectly by the apparent T1 of the brain tissue that will be affected by the effect of the inflowing spins following the spatially selective inversion.

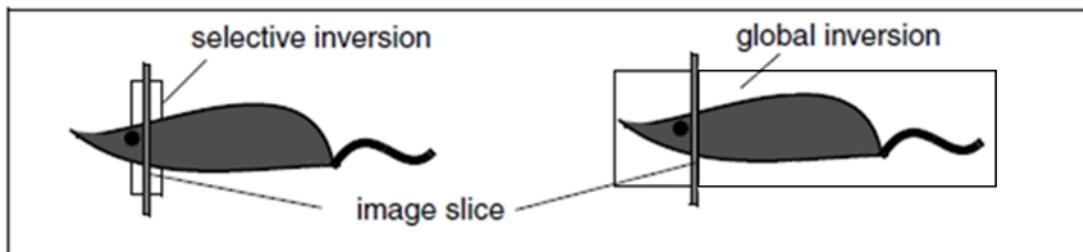


Figure 2.94: FAIR labeling principle: A non-selective inversion scheme (right) follows up a slice selective inversion scheme (left). The selective inversion slice coincides with the measured slice but is slightly thicker. The non-selective inversion volume is determined by the active volume of the RF resonator and the inversion pulse profile.

2.10.2 Hardware Setup

A volume resonator combined with a brain surface coil should be used in order to:

- cover in the best possible way the heart region where the blood supplying the brain comes from
- allow an optimal SNR in the brain, therefore improving the quantification of CBF

2.10.3 Object Setup

Perfusion experiments are intrinsically sensitive to motion: the animal head should be well immobilized by the use of an appropriate stereotaxic system.

2.10.4 Protocol Setup

Protocol and Method

Select the protocol **Perfusion_FAIR_EPI** (see Chapter [FAIR EPI \(Flow-sensitive Alternating IR EPI\) \[▶ 342\]](#)) from the location **Rat** or Mouse Head/Perfusion. This protocol based on EPI readout allows measurement of CBF-map of the animal brain.

The protocol **Perfusion_FAIR_RARE** (see Chapter [FAIR RARE \(Flow-sensitive Alternating IR RARE\) \[▶ 311\]](#)) found in the same location and based on RARE does the same.

The main advantage of RARE over EPI is its less sensitivity to magnetic susceptibility artifacts, however RARE has one major drawback that compromise the CBF-values: strong T2 weighting because of its long effective Echo Time (TE).



Non-brain ASL applications (e.g. perfusion on heart, abdomen...) are subject of ongoing research and are not covered by the protocols described in this chapter.

Running the Experiment

Load one of the previous protocols and adapt the geometry as wished: Field of View (FOV), Slice Orientation...

A good shim is important for FAIR-EPI because of EPI sensitivity to the field inhomogeneity. In order to improve your shims, proceed as follow:

- After loading the scan, activate **Map_Shim** in **Setup** card, **AutoShim**
- Define your shim volume: an ellipsoidal shape is recommended since it better covers the tissue in-vivo
- Position your shim volume, use the **Geometry** card of the **Palette** and select the item **Shim Volume**: you can now place your shim volume
- Open the **Adjustment Platform** and select the **B₀ Map** protocol, **Open** and **Start**. The B₀ map will be measured and displayed in the **Palette** card under **Explorer, Datasets**
- Click **Apply** and **Back** to come back to the **Instruction list**
- Start the scan with **Continue**.

When starting the scan the shims will be first automatically calculated in the pre-selected shim volume and then the acquisition will start.

A series of inversion-recovery images (one image for each inversion time) is generated. In order to achieve CBF maps, those images require further processing with manual interactions (refer to the Data Analysis part of this chapter).

Adjustments

No manual adjustments are required.

Changing Parameters

In case you would like to optimize these protocols for your own purposes, please refer to the [FAIR Card \[▶ 281\]](#) in order to access a more detailed list of protocol parameters.

2.10.5 Data Analysis

Analysis and evaluation of the CBF from the acquired FAIR images is done with the **ASL_Perfusion_Processing** macro.

Open the **Processing Platform** (see Chapter [The Processing Platform \[▶ 475\]](#)) and select **Execute Macro ASL_Perfusion_processing** in the **Post Image Series Activities** field, then click **Start**. This macro (see Figure [Perfusion quantification tool \(macro Perfusion ASL\) \[▶ 544\]](#)) opens in the **Image Display & Processing** Tool. The processing steps are described below:

- Load your ASL data by clicking on **Load ASL Data** (prerequisite: the appropriate FAIR scan must have been selected in the scan list prior to the macro execution)
- Start the calculation of T1 maps by clicking on **Calculate Selective/Global T1 Map** and follow the instructions for defining the image mask (described in more details in
- Prior to calculation of the CBF value, specify a T1 value of blood appropriate to the magnetic field strength (see information note below), and then click on **Calculate Perfusion Map**. The resulting CBF map is calculated according to equations mentioned in the references [3] and [4]. It is displayed in the large viewport in the lower right hand corner of the Image Display & Processing Tool.

Blood T1 values depending on magnetic fields:

At 4.7T: around 1700 +/- 100ms measured on rat/bovine blood (Kober et al. in MRM 2004;51(1), Williams et al. in PNAS 1992;89(1), Dobre et al. in MRI 2007;25(5))

AT 7T: around 2300 +/- 100ms measured on rat/bovine blood (Barbier et al. in MRM 2002;47(6), Exp. Neurol. 2008 Mar;210(1))

At 9.4T: 2429 +/- 49ms measured on bovine blood (Dobre et al. in MRI 2007; 25(5))

At 11.7T: 2813 +/- 56ms measured on rat blood (Lin et al. in MAGMA 2012;25(3))

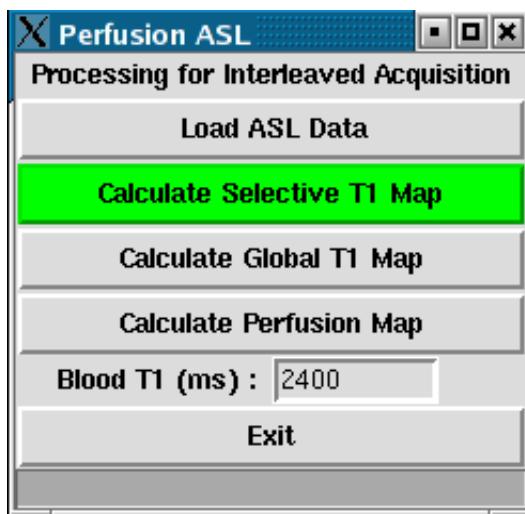


Figure 2.95: Perfusion quantification tool (macro Perfusion ASL)

Once obtained, the CBF map can be visualized and analyzed from the **Palette** card under **Explorer, Datasets**. Double click on it to load it into the **Image Viewer**.

In order to evaluate the CBF values, you can place a Region Of Interest – ROI (**Palette/Viewing/Analysis/Regions of Interest**) on the map image in the anatomical region under investigation. You will thus obtain the mean value expressed in ml of blood per 100 g of tissue per minute (its standard deviation is also available).

2.10.6 References

- [1] Detre JA, et al. Perfusion Imaging. MRM 23, 1992; 37-45.
- [2] Kim SG. Quantification of relative cerebral blood flow change by flow-sensitive alternating inversion recovery (FAIR) technique: Application to functional mapping. MRM 34, 1995; 293-301.
- [3] Herscovitch P an Raichle ME. What is the correct value for the Brain-Blood Partition Coefficient for water? Jour. Cereb. Blood Flow Metab 5, 1985; 65-69.

[4] Kober et al. MRM 51, 2004, 62-67.

2.11 Short TE

2.11.1 Introduction

Abbreviations

FOV	- Field of View
PD	-Proton Density
T1	- Spin-Lattice Relaxation Time
T2	- Spin-Spin Relaxation Time
TE	- Echo Time
UTE	- Ultra-Short Echo Time
ZTE	-Zero Echo Time

Purpose

Short echo time imaging is used to display

- short T2 nuclei (²³Na, ³¹P),
- musculoskeletal tissue with short T2 like tendons, ligaments, and periosteum,
- tissue with short T2*, such as liver and lung parenchyma,
- superparamagnetic contrast agents in molecular imaging.

2.11.2 Hardware Setup

No special requirements for **UTE**.

For **ZTE** it is recommended to use a coil and animal bed which have itself no proton signal.

2.11.3 Object Setup

For **UTE3D** and **ZTE** the **FOV** must be larger than the Object size or the sensitivity of coil to avoid artifacts.

2.11.4 Protocol Setup

The Protocols for **UTE**, **UTE3D** and **ZTE** are stored as templates in the Location: **AnyObject – AnyRegion – BrukerMethods** (see Chapters [UTE \(Ultra-short TE\) \[▶ 360\]](#), [UTE3D \(Ultrashort TE 3D\) \[▶ 366\]](#), [ZTE \(Zero TE\) \[▶ 369\]](#)). The protocols can be used as a starting point for imaging mice and rats.

For **UTE** and **UTE3D** a trajectory must be measured. Open the **Adjustment Platform**, select and open the **On Demand Protocol Trajectory**. Acquire the trajectory by pressing **Start** and leave the **Adjustment Platform** once the trajectory is acquired (Green tick mark appears) by clicking **Apply** and **Back**. If you want to keep the trajectory you can store the trajectory by rightclick on **Trajectory** in the **Adjustment Platform**: **Save Adjustment Result** or **Save Adjustment Result for other Studies**.

In cases where the trajectory cannot be measured on the object, e.g. during an in-vivo lung experiment because of the short T2* relaxation, the trajectory should be measured on a homogenous phantom of the size of the object to be measured and the trajectory must be stored.

Remark: The trajectory is only valid for a given acquisition bandwidth, matrix size, FOV and orientation. When one of these parameters is changed, the measured trajectory becomes invalid and the tick in the **Setup Card - Trajectory** for **TrajectoryAvailable** will automatically disappear. In such a case the trajectory measurement will start automatically, but the result is not stored!

Remark: If the achieved image quality is not sufficient, the trajectory measurement should be optimized under the following aspects:

- Modify the flip angle of the trajectory excitation pulse and the **Repetition Delay** in order to get the maximum signal for the trajectory measurement.
- The slice thickness should be small enough to avoid in-slice dephasing effects, but big enough to get enough SNR for the trajectory calculation.

Half Pulse Excitation:

- Load **HalfGauss** as **Excitation Pulse Shape** (**Setup Card – Sequence – Main**).
- In the **Setup Card – Sequence – SliceSliceSelection** set **Slice Gradient Alternation** to **Yes**. This is necessary for the half pulse acquisition (reverses the slice gradient).
- Check the excited slice thickness with a resolution phantom.

Hint: For a Matrix size of 512 x 512 x 512 (**Polar Undersampling** of 1) a working memory of 18 GB is necessary per acquisition channel! Since the reconstruction of such a big dataset takes very long, the dataset can be reconstructed later on. For this, unselect **Online Reconstruction** in the **Setup Card -Sequence – MainMain** and unselect **Auto Start Processings** in the **Setup Card – Instruction**. The reconstruction can be started later on in the **Processing Platform**!

2.11.5 Data Analysis

Load the image data either to the **Viewing Card** or to the **Image Data Analysis & Processing Tool** (**View in Image Display**) for data analysis.

2.12 Relaxation

2.12.1 T1-mapping

2.12.1.1 Introduction

Abbreviations

- T_1 - Spin-Lattice Relaxation Time
- T_2 - Spin-Spin Relaxation Time
- ISA - Image Sequence Analysis
- TR - Repetition time

Overview

The measurement of the relaxation times *in vivo* is important for characterizing tissue properties, e.g. to differentiate between normal and cancerous tissue or to diagnose brain injuries. Quantitative knowledge of T_1 and T_2 is a prerequisite for optimizing contrast in imaging methods such as functional MRI and perfusion imaging.

T_1 is strongly dependent on the magnetic field strength. Although it may be extrapolated to other field strengths based on theoretical predictions, such results will have significant uncertainty. Typical *in vivo* T_1 values lie in the range 1-2 s.

Especially the water content of a tissue can be accessed due to the essentially linear relation of $1/T_1$ on $1/W$ where W is the weight percent of water in a tissue.

2.12.1.2 Hardware Setup

Preferably use a **transmit-receive volume coil** or a combination of a **transmit only volume resonator** with a **receive only quadrature coil**.

2.12.1.3 Object Setup

See that your imaged area is well centered in the coil.

2.12.1.4 Protocol Setup

Protocol and Method

Select the Location **Rat (or Mouse) /Head/ Relaxometry** and load the Protocol **T1_map_RARE**. This protocol is based on a RARE-sequence with one **Echo Image**, **Rare Factor** of two and six **T1 Experiments** (see **Routine** card). Each experiment has a different TR producing one image. By default a T_1 -map is generated automatically for a single slice. Typically a T_1 -map can be used in the study of brain ischemia. An example for an abdominal application is the study of liver fibrosis. The workflow remains the same in the abdomen except that the reference image protocols should be taken from the **Abdomen** directory. Generally, it is best to set up own reference measurements for control. Literature values for a certain tissue could deviate up to 20 % from what one finds locally.

A detailed sequence description is given in Chapter [RAREVTR \(RARE with variable repetition time TR\) \[▶ 314\]](#)

Parameter Selection

Choose your Field of View (FOV), Slice Orientation, etc. It is recommended to use only one **Echo Image** (see **Contrast** card) to avoid interference between the T_1 and T_2 decays. Adapt your number of images so that they cover a time up to five times the T_1 . Typical values for T_1 for rat brain can be found in Table [Longitudinal relaxation times for rat brain measured with RAREVTR and FAIR_RARE \[▶ 548\]](#) and in some of the references. The distribution of the time points may either be calculated or entered manually changing the **Repetition Time Mode** on the **Routine** card.

A post-processing macro **Fitinlsa**, which automatically starts the T_1 parameter map calculation, is preselected in the default protocol. To deactivate automatic T_1 -calculation open the **Processing Platform** followed by the **Data Reconstruction** card and deselect **Execute Macro Fitinlsa** in the **Post Image Series Activities** field. The evaluation can also be done manually (see section on Chapter [T2-mapping \[▶ 549\]](#))

	11.7 T		9.4 T		7.0 T	
cortex	1945	± 24	1842	± 32	1515	± 12
caudate putamen	1706	± 36	1715	± 20	1491	± 12
hippocampus	2023	± 22	1867	± 23	1615	± 25
olfactory bulb	2184	± 7	1862	± 27	1466	± 20
corpus callosum	1710	± 11	1642	± 35	1303	± 12
cerebellar white	1693	± 41	1552	± 41	1382	± 42
cerebellar grey	1806	± 30	1846	± 42	1439	± 25

Table 2.2: Longitudinal relaxation times for rat brain measured with RAREVTR and FAIR_RARE

Adjustments

No manual adjustments are required.

Acquisition

Start acquisition with **Continue** or **Scan**.

Reconstruction

No special considerations.

2.12.1.5 Data Analysis

Triggered by the post-processing macro **Fitinlsa**, the data analysis will provide you automatically with a T_1 -fit and a T_1 -map. The **fit function** `t1sat` is defined in the macro.

Tools

The results can be viewed with the ISA Tool. For more details see [ISA Tool](#).

Analysis

T_1 is calculated from the **ISA function** `t1sat`:

$$Y = A + C \times \left(1 - \exp\left(-\frac{t}{T_1}\right) \right)$$

The parameters are defined in the following way:

- A - absolute bias,
- C - signal intensity,
- T_1 - spin-lattice relaxation time.

This function supplied by BRUKER uses a **Repetition Time** list calculated from the Protocol parameters to generate the t-axis (i.e. time-axis = x-axis). The fit is based on magnitude images of the reconstructed dataset.

Display the results

Please refer to the section on Chapter [T2-mapping \[▶ 549\]](#).

2.12.1.6 References

-
- [1] Guilfoyle DN, Dyakin VV, O'Shea J, Pell GS, Helpern JA. Quantitative Measurement of Proton Spin-Lattice (T_1) and Spin-Spin (T_2) Relaxation Times in the Mouse Brain at 7.0T. Magnetic Resonance in Medicine 49, 2003; 576-580.
- [2] de Graaf RA, Brown PB, McIntyre S, Nixon TW, Behar KL, Rothman DL. High Magnetic Field Water and Metabolite Proton T_1 and T_2 Relaxation in Rat Brain In Vivo. Magnetic Resonance in Medicine 56, 2006; 386-394.
- [3] Chow AM, Gao DS, Fan SJ, Qiao Z, Lee FY, Yang J, Man K, Wu EX. Measurement of Liver T_1 and T_2 Relaxation Times in an Experimental Mouse Model of Liver Fibrosis. Journal of Magnetic Resonance Imaging 36, 2012; 152-158.
- [4] Barbier EL, Liu L, Grillon E, Payen JF, Lebas JF, Segebarth C, Rémy C. Focal brain ischemia in rat: acute changes in brain tissue T_1 reflect acute increase in brain tissue water content. NMR in Biomedicine 18, 2005; 499-506.
- [5] Lin W, Venkatesan R, Gurleyik K, He YY, Powers WJ, Hsu CY. An Absolute Measurement of Brain Water Content Using Magnetic Resonance Imaging in Two Focal Cerebral Ischemic Rat Models. Journal of Cerebral Blood Flow & Metabolism 20, 2000; 37-44.

2.12.2 T2-mapping

2.12.2.1 Introduction

Abbreviations

- T_2 - Spin-Spin Relaxation Time
- ROI - Region of Interest
- ISA - Image Sequence Analysis

- MSME - Multi Slice Multi Echo
- TR - Repetition time
- TE - Echo time

Overview

The Spin-Spin Relaxation Time T_2 is a specific attribute of spins which depends on their surrounding (i.e. tissue, solution). T_2 measurements are helpful in detecting pathological tissues due to their changed T_2 relaxation time (e.g. degenerative changes of cartilage, muscular atrophy, ischemia and high signal intensity in tumors). Typical T_2 values in vivo are in the range of tens of milliseconds, though values from microseconds to hundreds of milliseconds are possible.

The workflow describes a fully automatic acquisition of a T_2 series, followed by a semi-automatic image analysis resulting in a T_2 -map.

This example for a T_2 measurement is carried out using an MSME-sequence:
A series of images with the same TR and slice position but different echo times is acquired.

2.12.2.2 Hardware Setup

Preferably use a transmit-receive volume coil or a combination of a transmit only volume resonator with a receive only quadrature coil.

2.12.2.3 Object Setup

See that your imaged area is well centered in the coil.

2.12.2.4 Protocol Setup

Protocol and Method

Select the Location **Rat (or Mouse) /Head/ Relaxometry** and load the Protocol **T2map_MSME**.

This Protocol is based on an MSME-sequence with a series of 25 echo-images. For each echo time one image is generated. By default a T_2 -map is generated automatically for five slices. Typically a T_2 -map can be used in the study of brain ischemia. Other applications and targets in small animal MRI are scarcer and include tumors or the influence of contrast agents. Generally, it is best to set up own reference measurements for control. Literature values for a certain tissue could deviate up to 20 % from what one finds locally.

A detailed sequence description is given in Chapter [MSME \(Multi Slice Multi Echo\) \[▶ 306\]](#).

Parameter Selection

Choose your Field of View (FOV), Slice Orientation, etc.

With the predicted T_2 relaxation period of the object in mind the **Echo Spacing** (TE) and the **number of Echo Images** (see **Routine card**) should be adapted. Typical values for T_2 can be found in Table [Transverse relaxation times for rat brain measured with MSME \[▶ 551\]](#) as well in some of the references below. Adapt your number of images so that they cover a time up to five times the T_2 . For samples with long T_2 relaxation times, it is better to choose a larger **number of Echo Images** per train with shorter TE, to avoid diffusion and flow effects. Too high resolution may give artificially low T_2 values due to diffusion. For this reason always compare your result with a measurement with the default resolution.

A post-processing macro **Fitinlsa**, which automatically starts the T_2 parameter map calculation, is preselected in the default protocol. To deactivate automatic T_2 -calculation open the **Processing Platform** followed by the **Data Reconstruction** card and deselect **Execute Macro Fitinlsa** in the **Post Image Series Activities** field. The evaluation can also be done manually (see below).

	11.7 T		9.4 T		7.0 T	
cortex	34,2	$\pm 0,2$	38,6	$\pm 0,3$	46,7	$\pm 0,3$
caudate putamen	34,2	$\pm 0,1$	37,4	$\pm 0,3$	46,5	$\pm 0,3$
hippocampus	37,1	$\pm 0,2$	39,5	$\pm 0,3$	49,6	$\pm 0,3$
olfactory bulb	36,5	$\pm 0,5$	41,3	$\pm 0,4$	50,7	$\pm 0,5$
corpus callosum	31,2	$\pm 0,2$	32,8	$\pm 0,6$	41,5	$\pm 0,3$
cerebellar white	31,7	$\pm 0,3$	36,6	$\pm 0,6$	48,5	$\pm 0,4$
cerebellar grey	36,2	$\pm 1,0$	39,7	$\pm 0,5$	46,7	$\pm 0,3$

Table 2.3: Transverse relaxation times for rat brain measured with MSME

Adjustments

No manual adjustments are required.

Acquisition

Start acquisition with **Continue** or **Scan**.

Reconstruction

No special considerations.

2.12.2.5 Data Analysis

Triggered by the post-processing macro **Fitinlsa**, the data analysis will provide you automatically with T_2 -maps. The **fit function** t2vtr is defined in the macro.

Tools

The results can be viewed with the **ISA Tool**. For more details see [ISA Tool](#).

Analysis

T_2 is calculated from the **ISA function** t2vtr:

$$Y = A + C \times \exp\left(-\frac{t}{T_2}\right)$$

The parameters are defined in the following way:

- A - absolute bias,
- C - signal intensity,

- T_2 - spin-spin relaxation time.

This function supplied by BRUKER uses an **Echo Time** list calculated from the protocol parameters to generate the t-axis (i.e. time-axis = x-axis). The fit is based on magnitude images of the reconstructed dataset.

Display the results

For a T_2 -map an **All-ROI** with a lower threshold of 10% is automatically defined in the active viewport. This generates a cut off of the noise level for the T_2 calculation of the image. The result is stored under the same experiment number (EXPNO) but with a new processing number (PROCNO), which can be seen in the **Image Display & Processing Tool**. The T_2 map is displayed automatically in the next viewport in the **Image Display & Processing Tool**.

To see all calculated results select **frame** on the pull-down menu at the bottom of the **Image Display & Processing Tool** window. Apply the button **All** to the left of the drop down menu.

The T_2 fit creates five parameter images for each slice:

- signal-intensity-image,
- standard deviation image of the signal intensity,
- T_2 image,
- standard deviation image of the T_2 values,
- standard deviation image of the whole fit.

The order of images is identical to the order of the variable parameters, each parameter's standard deviation following the parameter itself. The standard deviation of the whole fit is the last image in the sequence. To find out which parameter map that is displayed go to the pull-down menu at the bottom of the **Image Display & Processing Tool** window and select **T2 Relaxation**. Click on the image of interest and the corresponding label will be shown to the right of the pull-down menu.

To start the fit manually (e.g. with your own ISA function):

- Go to the **Explorer** and on the **Palette** select the scan and **View in Image Display** by a right mouse click
- open the **ISA Tool** (click **Processing > Image Sequence Analysis...**),
- select your desired **ISA function**,
- select and position a **New ISA ROI** in the **Image Display & Processing Tool** viewport.

Change mode into **Pnts & Curves** and press **Refresh Cur. ROI**.

The data points and the fit curve are displayed. The numerical results will be added to the table.

A detailed description about all ISA functionalities is given in chapter [ISA Tool](#).

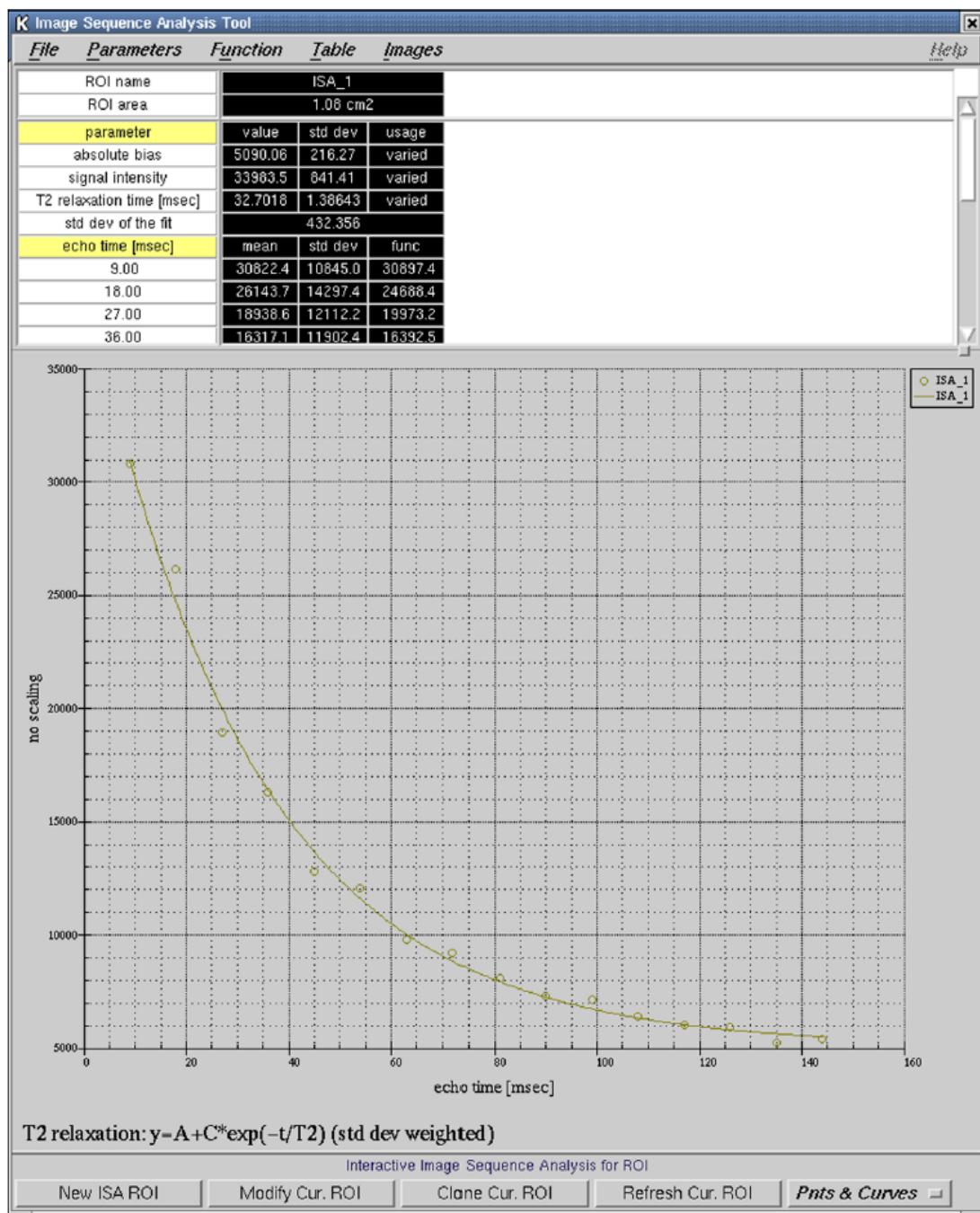


Figure 2.96: ISA Tool: The envelope of the spin-echo peaks decays exponentially with T2

2.12.2.6 References

- [1] Crémillieux Y, Ding S, Dunn JF. High-Resolution In Vivo Measurements of Transverse Relaxation Times in Rats at 7 Tesla. Magnetic Resonance in Medicine 39, 1998; 285-290.
- [2] Guilfoyle DN, Dyakin VV, O'Shea J, Pell GS, Helpern JA. Quantitative Measurement of Proton Spin-Lattice (T_1) and Spin-Spin (T_2) Relaxation Times in the Mouse Brain at 7.0T. Magnetic Resonance in Medicine 49, 2003; 576-580.

- [3] de Graaf RA, Brown PB, McIntyre S, Nixon TW, Behar KL, Rothman DL. High Magnetic Field Water and Metabolite Proton T_1 and T_2 Relaxation in Rat Brain In Vivo. *Magnetic Resonance in Medicine* 56, 2006; 386-394.
- [4] Weber R, Ramos-Cabrer P, Hoehn M. Present status of magnetic resonance imaging and spectroscopy in animal stroke models. *Journal of Cerebral Blood Flow & Metabolism* 26, 2006; 591-604.
- [5] Tuor UI, Meng S, Qiao M, Webster NB, Crowley SM, Dyck RH, Tomanek B. Differential progression of magnetization transfer imaging changes depending on severity of cerebral hypoxic-ischemic injury. *Journal of Cerebral Blood Flow & Metabolism* 28, 2008; 1613-1623.
- [6] Dortch RD, Yankeelov TE, Yue Z, Quarles CC, Gore JC, Does MD. Evidence of multiexponential T_2 in rat glioblastoma. *NMR in Biomedicine* 22, 2009; 609-618.
- [7] Oostendorp M, Douma K, Hackeng TM, Post MJ, van Zandvoort MAMJ, Backes WH. Gadolinium-Labeled Quantum Dots for Molecular Magnetic Resonance Imaging: R_1 Versus R_2 Mapping. *Magnetic Resonance in Medicine* 64, 2010; 291-298.

2.12.3 T₂*-mapping

2.12.3.1 Introduction

Abbreviations

- T_2^* - T_2 star relaxation time
- ISA - Image Sequence Analysis
- MGE - Multi Gradient Echo
- TR - Repetition time
- TE - Echo time

Purpose

T_2^* is the transverse relaxation T_2 time plus the contribution R'_2 to the signal. The contribution R'_2 can be caused by macroscopic field inhomogeneities due to magnet imperfections or imperfect shimming. Other reasons for signal loss are local fields due to the object structure, air-tissue interfaces or motion producing phase differences, susceptibility effects, or the presence of paramagnetic agents (e.g. deoxygenated haemoglobin).

An important application of T_2^* contrast is based on the BOLD effect used in functional imaging. The paramagnetic state of deoxygenated haemoglobin compared to the oxygenated haemoglobin creates a magnetically inhomogeneous environment, leading to a local signal decrease and decrease of T_2^* .

2.12.3.2 Hardware Setup

No special considerations.

2.12.3.3 Object Setup

See that your imaged area is well centred in the coil and that the object is centred in the magnet. The latter facilitates shimming.

2.12.3.4 Protocol Setup

Protocol and Method

Select the Location **Rat (or Mouse) /Head/ Relaxometry** and load the Protocol **T2star_map_MGE**. This protocol is based on an MGE-sequence with a series of 9 **Echo Images** (see **Routine card**). For each echo time one image is generated. By default a T_2^* -map is generated automatically for a single slice.

Typically knowledge of T_2^* is needed for experiments like functional MRI and MR oximetry where one sets TE close to T_2^* . The measure of T_2^* is also used for the determination vessel size particularly in the brain region. Abdominal applications are scarcer. Generally, it is advisable to set up own reference measurements to obtain standard values for control.

A detailed sequence description is given in [MGE \(Multiple Gradient Echo\) \[▶ 302\]](#).

Parameter Selection

Choose your Field of View (FOV), Slice Orientation, etc.

With the predicted T_2^* relaxation period of the object in mind the **Echo Spacing (TE)** and the **number of Echo Images** (see **Routine card**) should be adapted. Adapt your number of images so that they cover until the signal has decayed, i.e. 3-5 times T_2^* . An initial guess for T_2^* is that it is shorter than T_2 (see the Chapter on T_2 -mapping). The T_2^* relaxation process depends on the local field homogeneities. It is therefore recommended to use high resolution images. Especially images with low resolution may give too short T_2^* values.

The protocol allows two **Acquisition Modes** for the Echoes (see **Routine card**). The option **allEchoes** allows a smaller spacing of the Echoes, and thus higher time resolution, but may produce displacements in subsequent images. The default option is therefore **positiveReadOutEchoes** which is insensitive to shifts.

A post-processing macro **Fitinlsa**, which automatically starts the T_2^* parameter map calculation, is selected by default. To deactivate automatic T_2^* -calculation open the **Processing Platform** followed by the **Data Reconstruction** card and deselect **Execute Macro Fitinlsa** in the **Post Image Series Activities** field. The data analysis can also be done manually (see Chapter [T2-mapping \[▶ 549\]](#)).

Adjustments

It is very important to have a good shim before the measurement of the T_2^* relaxation. The option **Map_Shim** in the **Auto Shim Sub-card** of the **Setup Card** is selected by default. Define a shim volume in the Geometry Editor that covers the region that you would like to study. Avoid any air cavities or bones. These are typically located in regions giving no signal in the reference images, thereby appearing black. Go to the **Adjustment Platform** and open the **On Demand Protocol B0 Map**. Acquire the B0 map by pressing **Start** and leave the **Adjustment Platform** by clicking **Apply** and **Back**.

Acquisition

Start acquisition with **Continue** or **Scan**.

Reconstruction

No special considerations.

2.12.3.5 Data Analysis

Triggered by the post-processing macro **FitinIsa**, the data analysis will provide you automatically with a T_2^* -fit and a T_2^* -map. The **fit function** t2vtr is defined in the macro.

Tools

The results can be viewed with the **ISA Tool**. For more details see [ISA Tool](#).

Analysis

The fitting function is defined in the section on Chapter [T2-mapping \[▶ 549\]](#).

Display the results

Please refer to the section on Chapter [T2-mapping \[▶ 549\]](#).

2.12.3.6 References

- [1] Schröder L, Faber C editors. In Vivo NMR Imaging, Methods and Protocols. Humana Press 2011.
- [2] Lemasson B, Valable S, Farion R, Krainik A, Rémy C, Barbier EL. In Vivo Imaging of Vessel Diameter, Size and Density: A comparative Study Between MRI and Histology. Magnetic Resonance in Medicine 69, 2013; 18-26.

2.13 Spectroscopy

2.13.1 Proton Magnetic Resonance Spectroscopy

2.13.1.1 Introduction

Abbreviations

- PRESS - Point Resolved Spectroscopy
- STEAM - Stimulated Echo Acquisition Mode Spectroscopy
- VAPOR - Variable Pulse power and Optimized Relaxation delays
- OVS - Outer Volume Suppression
- WS - Water Suppression
- TE - Echo Time
- RMB - Right Mouse Button
- LMB - Left Mouse Button

Purpose

Single voxel spectroscopy allows the study of metabolite molecules by detecting their individual signals and thereby their concentrations *in vivo*. Disease can thus be identified directly from its molecular profile. Single voxel spectroscopy can be measured with the methods [PRESS \[▶ 387\]](#) and [STEAM \[▶ 391\]](#). Both methods allow arbitrary oblique voxel

orientation and size. Good water suppression with the VAPOR scheme assures a flat baseline under the metabolic peaks and allows accurate quantification of the metabolite concentrations.

Requirements

A good homogeneity of the main magnetic field within the selected volume is the most important requirement to obtain good quality spectra. It increases the signal level and allows a better discrimination of nearby resonance lines (signals).

2.13.1.2 Hardware Setup

Coils

Generally, transmit-receive (volume) **Resonators** offer the best opportunity for localization, since they provide higher power for the pulses. The pulse bandwidth can thus be made higher which gives better localization due to a reduction of the chemical shift displacement error. PRESS requires a homogeneous radio frequency excitation and therefore it does not work properly with **Surface Transmit-receive Coils**. STEAM can be used also with **Surface Transmit-receive Coils**. In many cases **Receive-only Surface Coils** can be used in combination with **Transmit-only Resonators**. The **Receive-only Surface Coils** give a better signal to noise with the drawback of less accurate localization in spectroscopy.

2.13.1.3 Object Setup

Preparation

In all cases, position the sample in such a way, that the desired voxel position is as close as possible to the center of the gradient system. If **Surface Coils** are used, place their sensitive volume as close as possible to the desired voxel position. Position the **Resonators** such that the voxel position is centered in its homogeneous region.

Voxel Positioning

The voxel size, position, and orientation can be defined in the **Geometry Tab** of the **Palette** window or by directly rotating, translating and changing the size of the voxel in reference images in the Geometry Editor. Any type of image can serve as reference image. Under *in vivo* conditions, accurate voxel position definitions are possible on anatomical multi-slice spin-echo based images with a high contrast, i.e. RARE images.

Shimming

A good shim is necessary before performing the protocol setup. To start shimming first open the **Location Rat (or Mouse)/Head/Spectroscopy** and load the protocol **2_Localised_shim**. In this protocol **MapShim** and

Iterative Correction are preselected. These options assure that the best possible shim is calculated and iteratively adjusted for the selected volume. Open the **Auto Shim Sub-card** of the **Setup Card**. The shim volume can be defined as **Cuboid**, **Cylinder** or **Ellipsoid** and one also has the option **Automatic Shim Volume** which allows having the shim volume locked to the voxel with the possibility to expand it further with the **Shim Volume Margin**. The usual tools can be used to modify the shim volume in the Geometry Editor. Now open the **Adjustment Platform** and select the **On Demand Protocol B0 Map**. Measure the **B0 Map**

by applying **Start**. Once the map is acquired return to the **Instruction Editor**. Start the measurement with **Continue**. The shim has now been established and one can continue with further setup.



Note that the selected voxel geometry can be copied into further scans. Select the scan with the LMB and drag it onto the new experiment. A dialog window opens. With the LMB select **Voxel Geometry** and click **OK**.

2.13.1.4 Protocol Setup

Protocol & Method

Select the **Location Rat (or Mouse)/Head/Spectroscopy** and load the Protocol **PRESS** or **STEAM**. This protocol is adapted to give a localized short echo time spectrum in the brain. Short TE spectra permit to see a wider range of metabolites, lipids and macromolecules. Especially glutamine and glutamate detection is easier at short TE such as set in the default protocols for **STEAM** and **PRESS**. Longer TE can be selected to reduce the signal from macromolecules and lipids and to focus on particular metabolites. Typical candidates for long TE measurements ($TE > 30$ ms) are N-acetyl asparate, choline and creatine.

Brain spectroscopy can be used in the study of many different diseases, for instance cancer and ischemia.

Outside the head localized spectroscopy can be applied for instance on liver and spinal cord. Also tumor xenografts represent an interesting target. When working outside the brain respiratory triggering becomes important everywhere where the respiration results in motion. It can be set on the **Main Sub-card** of the **Preparation Card** by selecting **Trigger**. When loading a protocol one must make sure that the flip angles are correct. That is 90° - 180° - 180° for **PRESS** and 90° - 90° - 90° for **STEAM**. To do this open the **Instruction Editor**. Access the **Pulse Details** field next to the **RF Pulses** on the **Main Sub-card** of the **Sequence Card**. Increase the **RF Pulse Length** if you are not able to adjust the **Flipangles**.

The Advanced sections at the end of this chapter can be omitted for routine operation.

Parameter Selection

Select the **Echo Time** on the **Routine Card**. The default echo time is selected to make the protocol work with a variety of different coil combinations. It can easily be set longer to suppress macromolecule and lipid signals or to refocus a particular resonance. Shorter echo times are discussed in the Advanced Parameters Settings below. Set an appropriate number of **Averages**. For a typical *in vivo* voxel size of $3 \times 3 \times 3$ mm 3 128 **Averages** are suitable for **PRESS** and 256 or more for **STEAM**.

The **Repetition Time** in the **Routine card** should be selected with the longitudinal relaxation times of the metabolites in mind, which are in the range 1-2 s. Too fast repetition may reduce the metabolite signal significantly. On the **Auto Shim Sub-card** of the **Setup Card** select **Current_Shim**. This will keep the shim as set according to the Shimming section in Object Setup.

Adjustments

Good water suppression is very important in *in vivo* spectroscopy. The preselected **Vapor** scheme assures good starting conditions for the water suppression. To reduce the water signal further select the **Water Sup Sub-card** of the **Setup Card**. Deselect **Calc Pulse Ampl**. Start the scan in **Setup** mode by selecting the corresponding icon underneath the **Instruction List**. Adjust using the sliders selected by applying the **LMB** on the double arrows or simply type in the values manually. Note that manual adjustment can only be done when

the **Navigator** on the **Main Sub-card** of the **Optimization Card** is temporarily turned off. Finish the adjustment with **Stop**. Do not reactivate **Calc Pulse Ampl.** since this will overwrite your optimized values.

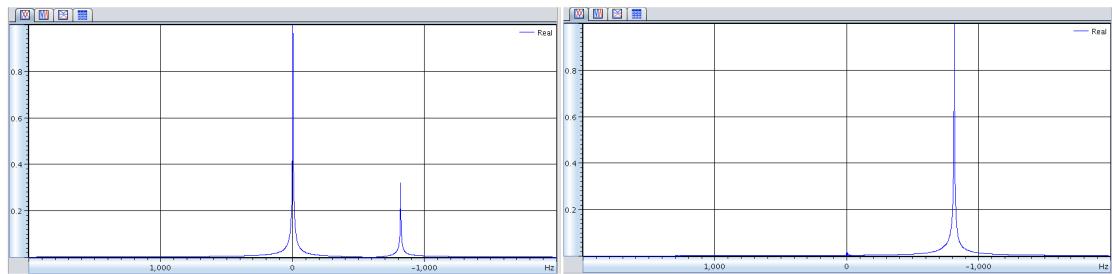


Figure 2.97: The water suppression should reduce the height of the water peak to an amplitude similar or below that of the metabolite peaks. This can be seen when comparing the spectrum left with no WS and right with WS.

2.13.1.5 Data Analysis

Processing of spectra for qualitative evaluation can be done in **TopSpin**, which is the Bruker software for spectroscopy. For metabolite quantification we recommend the use of external software like jMRUI or LCModel. To view the acquired data export the dataset into the **TopSpin** window. Do this by opening the **Explorer** tab of the **Palette window**. Select your scan and use the **RMB** to activate the pop-up menu. In this select **Load in TopSpin**. Set the size (**si**) and the line broadening (**lb**) and Fourier transform the data (**ef**) by typing the commands in the **TopSpin** command line. Typical values for **si** and **lb** are 4k and 2, respectively. Type **.ph** to enter the phase correction and phase by selecting the **0** and **1** buttons in the upper menu and moving the mouse. Save and return using the same upper menu. For further and detailed information see the **TopSpin** software manual.

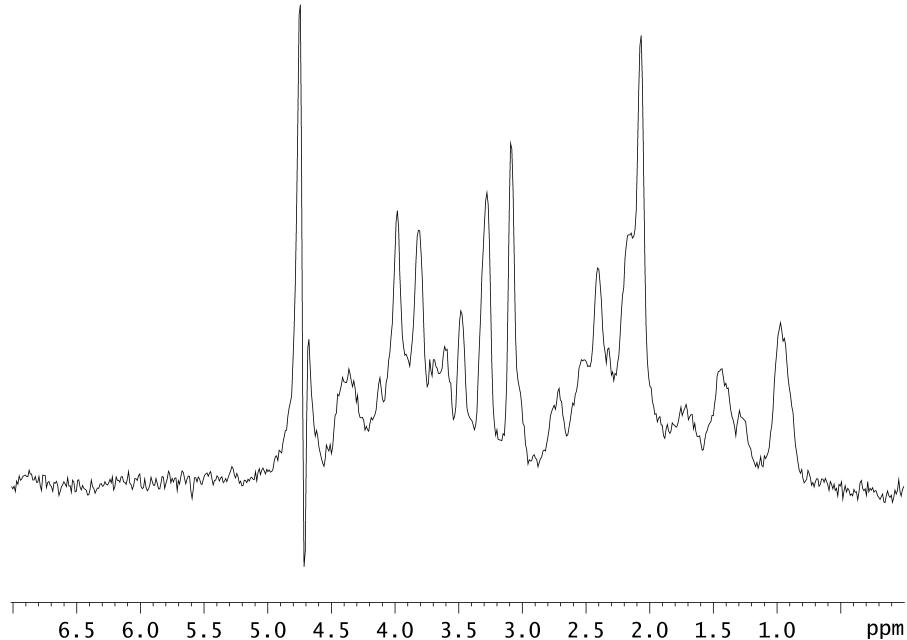


Figure 2.98: PRESS spectrum at 7.0 T of a $3 \times 3 \times 3 \text{ mm}^3$ voxel in the right hemisphere of rat brain. The number of Averages was 256, Echo Time 16 ms, Repetition Time 2.5 s and Scan Time 10 min 40 s. The water suppression is sufficient for accurate metabolite quantification as can be seen from the size of the residual water signal at 4.7 ppm. A line broadening of 2 Hz has been applied to the spectrum.

2.13.1.6 Advanced Paramter Selection

For short echo time spectroscopy it is advisable to work at **Echo Times** close to 10 ms for **PRESS** and 3 ms for **STEAM**. To minimize the echo time one can modify the **RF Pulse Length** and the **Spoiler Duration** on the **Main Sub-card** of the **Sequence Card** to values below those in the default protocol. Have in mind that it is the area under the spoiler gradient that is important. Shorter **Spoiler Duration** requires more **Spoiler Strength**. To change the **Spoiler Strength** you must deselect **Calculate Spoiler**.

An important issue is to try to reduce the chemical shift displacement error. The default protocols have relatively low pulse **Bandwidths** to make them work with a variety of different coil setups. This means that you can improve your localization by decreasing your chemical shift displacement error. This can be done by increasing the pulse **Bandwidth**, which can be accessed over the **Pulse Details** field next to the **RF Pulses** on the **Main Sub-card** of the **Sequence Card**. On the **Routine Card** one can see the **Spatial Fat-Water Shift**, which should be as small as possible in relation to the **Voxel Size**.

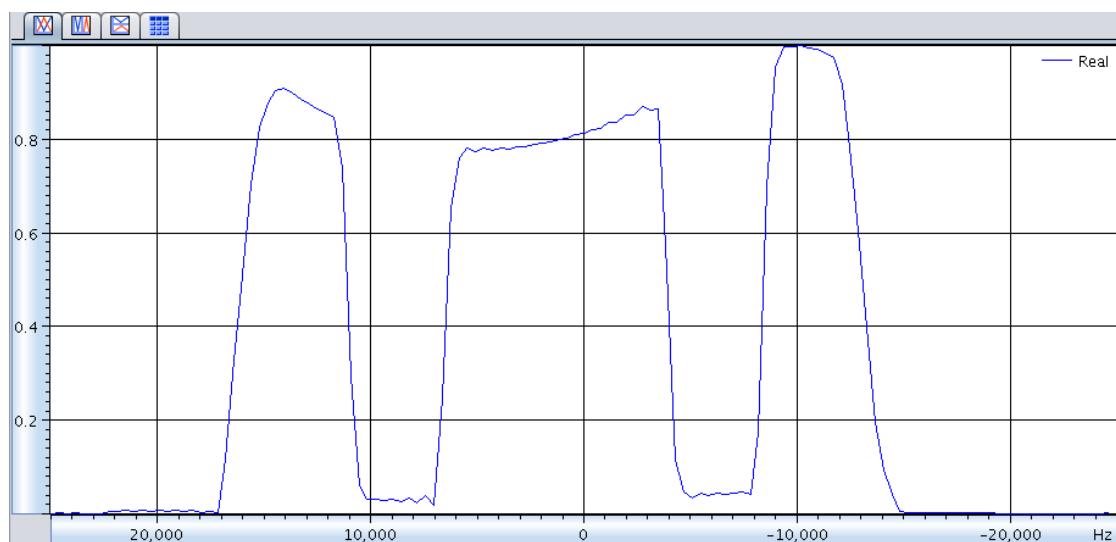
When adjusting the **Bandwidth** or **RF Pulse Length** make sure that the pulses stay 90° - 180° - 180° for **PRESS** and 90° - 90° - 90° for **STEAM**, otherwise the localization is not accurate.

In order to compensate for small frequency drifts one can chose to activate **Navigator** and **Drift Compensation** on the **Main Sub-card** of the **Optimization Card**.

2.13.1.7 Advanced Adjustments

Advanced Adjustments

The profile of the suppressed and unsuppressed areas due to OVS can be visualized in the three orthogonal directions. Use this to fine tune the **Slice Thickness** and the **Gap to Voxel** found in the **OVS Sub-card** of the **Preparation Card**. A too small gap may lead to loss in signal from the voxel and a too small thickness may cause contamination of the voxel with signal from the surroundings. To check select **OVS Pulse1-3** in the **Manual Pulse Adjustment** field of the **Main Optimization Card**. Start the scan in **Setup** mode by selecting the corresponding icon underneath the **Instruction List**. Adjust gap and thickness. Finish the adjustment with **Stop**.



The OVS pulse profile. The middle region contains the voxel and is unsuppressed. It is surrounded by suppressed and then unsuppressed regions.

2.13.1.8 References

- [1] jMRUI: <http://www.mrui.uab.es/mrui/>
- [2] LCModel: <http://s-provencher.com/pages/lcmodel.shtml>
- [3] Michaelis T, Boretius S, Frahm J. Localised proton MRS of animal brain in vivo: Models of human disorders. *Progress in Nuclear Magnetic Resonance Spectroscopy* 55, 2009; 1-34.
- [4] Lee Y, Jee HJ, Noh H, Kang GH, Park J, Cho J, Cho JH, Ahn S, Lee C, Kim OH, Oh BC, Kim H. In Vivo ¹H-MRS Hepatic Lipid Profiling in Nonalcoholic Fatty Liver Disease: an Animal Study 9.4 T. *Magnetic Resonance in Medicine* 70, 2013; 620-629.
- [5] Tachroud M, Duhamel G, Laurin J, Marqueste T, Maues de Paula A, Decherchi P, Cozzzone PJ, Callot V. In Vivo Short TE Localized ¹H MR Spectroscopy of Mouse Cervical Spinal Cord at Very High Magnetic Field (11.75 T) *Magnetic Resonance in Medicine* 69, 2013; 1226-1232.
- [6] Zhu M, Fischl AS, Trowbridge MA, Shannon HE. Reproducibility of Total Choline/Water Ratios in Mouse U87MG Xenograft Tumours by ¹H-MRS. *Journal of Magnetic Resonance Imaging* 36, 2012; 459-467.

2.13.2 Chemical Shift Imaging

2.13.2.1 Introduction

Abbreviations

CSI - Chemical Shift Imaging
FOV - Field of View
OVS - Outer Volume Suppression
WS – Water Suppression
VAPOR - Variable pulse power and optimized relaxation delays

Purpose

In living tissue, the MRI signal is largely made up of ^1H in water, and the effects coming from other hydrogen nuclei are small. Therefore, the chemical shift effect is typically ignored in MRI. The Chemical Shift Imaging is a combination of imaging and spectroscopy methods allowing to measure metabolites maps (see Figure [CSI Visualization Tool](#) ▶ 567).

Different resonance frequencies of different component and metabolites (such as water, fat, choline, n-acetyl aspartate, lactate) lead to an additional dimension for imaging. CSI techniques are multi-dimensional imaging sequences without a readout gradient. The spatial directions are encoded by phase encoding gradients which are varied as the experiment is repeated. In order to evaluate the CSI data, Fourier Transformations (FT) are performed over the spatial axis in addition to the FT for the spectrum dimension (reference).

The metabolite maps should be displayed together with an anatomical image. This is done in the **CSI Visualization Tool**. The spectrum of each pixel map should be processed in **TopSpin**.

Requirements

A good homogeneity of the magnetic field in the selected volume is needed. The [CSI method](#) ▶ 382 is available for all gradient systems.

2.13.2.2 Hardware Setup

Receive-only Surface Coils (quadrature or array coils) can be used in combination with Transmit-only Resonators. In case of high field systems($\geq 9.4\text{T}$), Transmit-receive resonators of small diameter (40mm) provide best performance. They provide enough power for the short pulses having the pulse bandwidth necessary to avoid chemical shift displacement error.

2.13.2.3 Object Setup

Preparation

Position the sample with the volume of interest as close as possible to the center of the gradient system. If Surface Coils are used, place their sensitive volume as close as possible to the volume of interest. When resonators are used, the volume of interest should be centered in the homogeneous region of the resonator.

2.13.2.4 Protocol Setup

Protocol and Method

Select the **Location Rat (or Mouse)/Head/Spectroscopy** and load the protocol **CSI**. The protocol is based on the CSI Bruker method with 2 spatial dimensions and one spectroscopy dimension (see reference 1,5). The acquisition parameters are:

- Field of View: 40 mm for rat head
- Slice thickness 2 mm
- Matrix in spatial directions 16x16
- Echo Time 20 ms and Repetition Time 1800 ms.
- Spectral bandwidth 6000 Hz.

Only the signal issued from a voxel of 10x10x2mm is acquired using a PRESS scheme (see Chapter [Data Analysis \[▶ 566\]](#)).

The typical parameters are defined in the Routine Card of the CSI method (see Figure [Routine Card of the CSI method \[▶ 563\]](#)).

To acquire the anatomical image, go in the **Location Rat (or Mouse)/Head/Spectroscopy** and load the protocol **T2_TurboRARE**. This is necessary to display the metabolite maps.

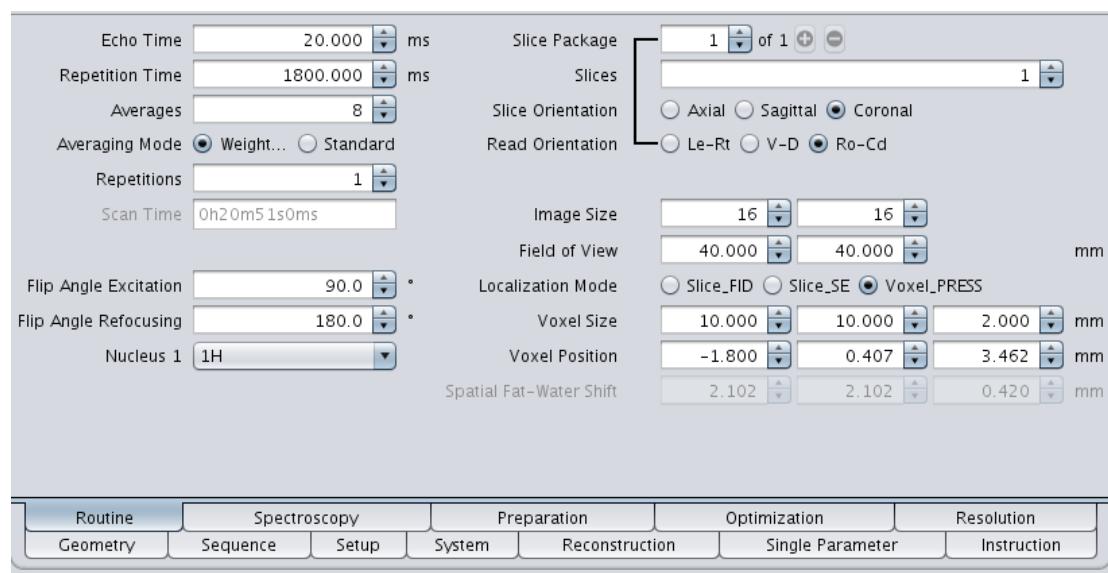


Figure 2.99: Routine Card of the CSI method

Positioning

The slice position of the Chemical shift image and the measured voxel position are defined in the **Geometry Tab** of the **Palette** window. You can also define the geometry and the positioning of the slice/voxel by rotating, translating and changing their size on the reference images using the **Examination** window (see Figure [Positioning of the Chemical shift imaging \[▶ 564\]](#)). To switch between Slice and Voxel use the **Selection** window of the **Geometry Tab**.

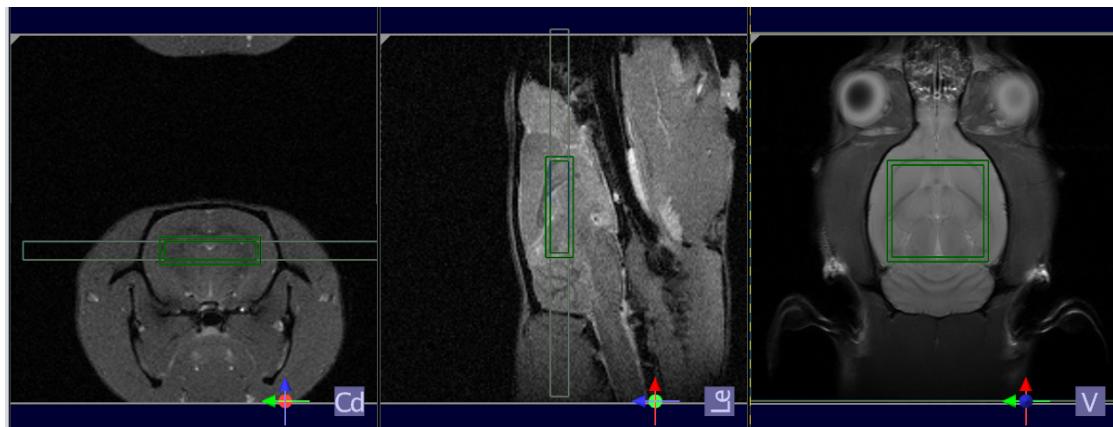


Figure 2.100: Positioning of the Chemical shift imaging

Import the slice geometry of the Chemical shift imaging in the **T2_TurboRARE** reference protocol as illustrated in Figure [Import geometry of the CSI image in the Reference Image ▶ 564](#). Select the **CSI** protocol. With **RMB** open the **pop-up menu** and select **Copy Parameter Group**. In the left window select the **T2_TurboRare** protocol and the Slice Geometry in the right window and then click **OK**.

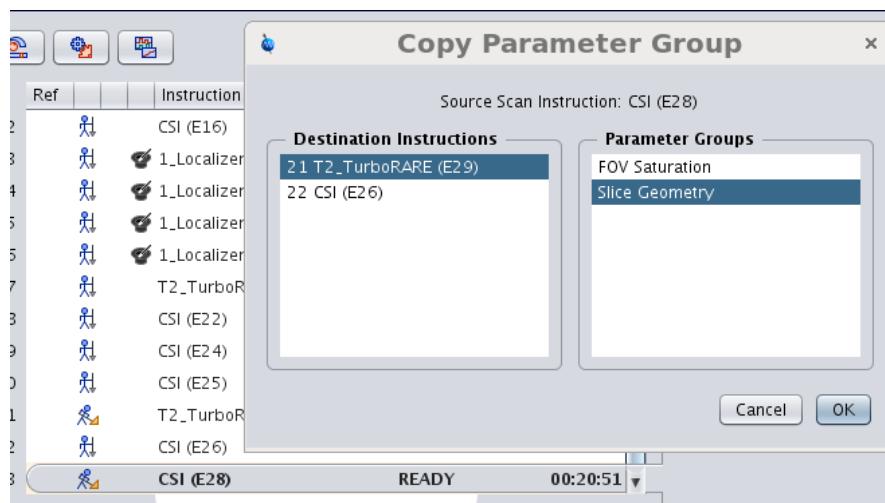


Figure 2.101: Import geometry of the CSI image in the Reference Image

Shimming

A localized shim is necessary to be done in the voxel defined in the brain. To do this, open the **Auto Shim Sub-Card** of the **Setup Card**. Select **MapShim**. Select the shim volume as **Cuboid**. Select **Automatic Shim Volume** to link the shim volume to the voxel and set the **Shim Volume Margin** to 1 mm. Select **Iterative Correction** to automatically adjust the local linear shims after MapShim (see Figure [Auto Shim Setup SubCard ▶ 565](#)).

Now open the **Adjustment Platform** and select the **On Demand Protocol B0 Map**. Measure the **B0 Map** with **Start**. Once the map is acquired return to the **Instruction List**.

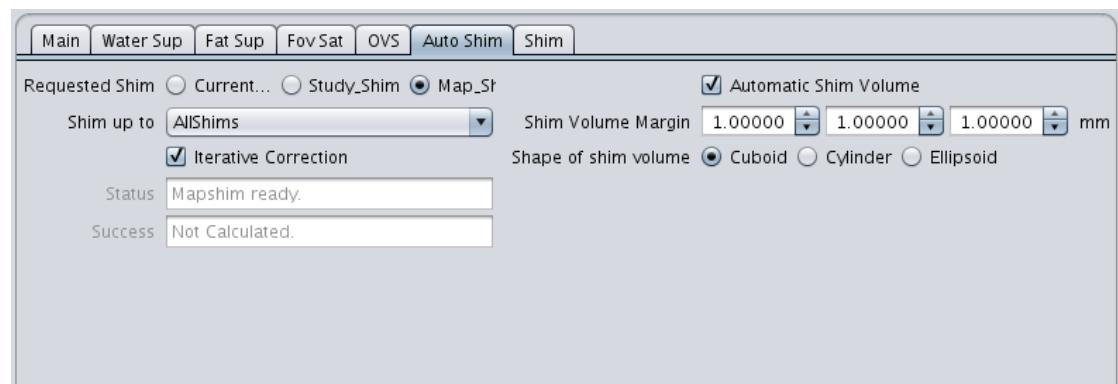


Figure 2.102: Auto Shim Setup SubCard

Further Adjustments

Good water suppression is very important for in vivo spectroscopy. The preselected **Vapor** scheme assures good starting conditions for the water suppression. To further reduce the water signal go in the **Water Sup Sub-card** of the **Setup Card** (see Figure [Water Suppression Setup Card \[▶ 565\]](#)). Unselect **Calc Sup Pulse Ampl.**. Start the scan in **Setup** mode by clicking the corresponding icon below the **Instruction List**. Adjust the pulse attenuation by using the sliders selected with LMB on the double arrows or simply type in the values manually. Finish the adjustment with **Stop**. Do not reactivate **Calc Sup Pulse Ampl.** since this will overwrite your optimized values. The water suppression should reduce the height of the water peak to amplitude similar or below that of the metabolite peaks. The area of time signal is minimized.

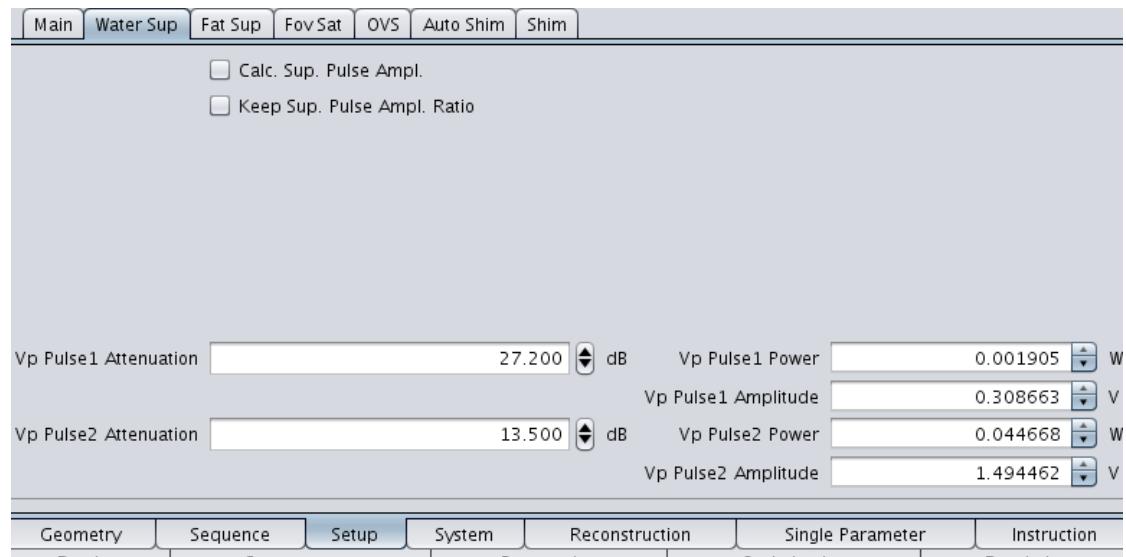


Figure 2.103: Water Suppression Setup Card

Acquisition of the CSI and the Reference Images

Once the water suppression adjustment is finished, set the **Averages** value to 8, enable the **Navigator** and **Drift Compensation** in the **Optimization Card** to compensate for potential frequency shifts occurring during long acquisition time (see Figure [Navigator Card \[▶ 566\]](#)).

Start the **CSI** and the **T2_TurboRARE** protocols with **Continue**.

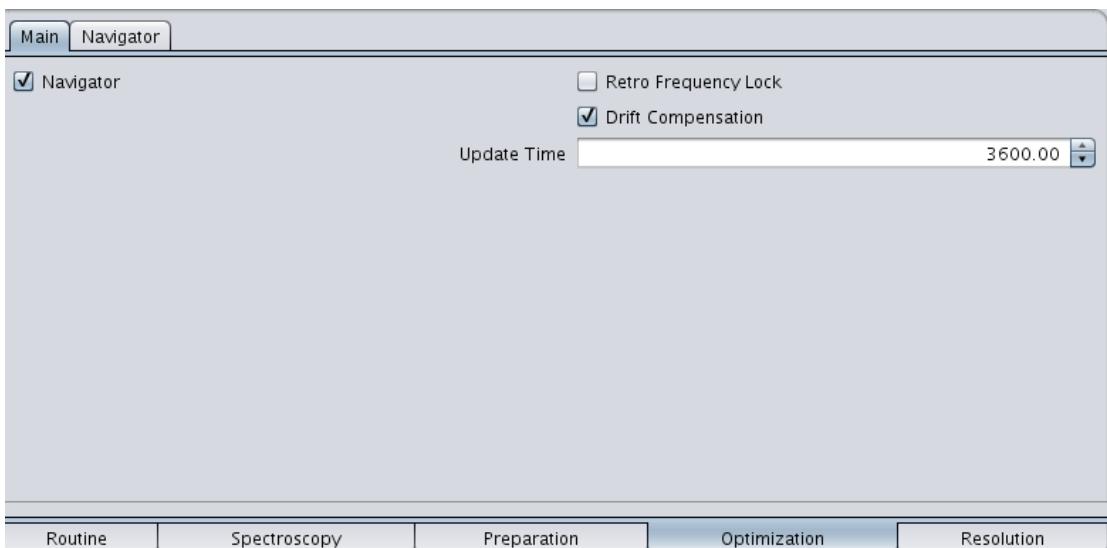


Figure 2.104: Navigator Card

Protocol Modifications for Specific Applications

The Chemical Shift Imaging method can be used for applications investigating other body regions. The Trigger mode must be activated for abdomen (liver) and heart applications.

For X Nuclei applications, the **Slice_FID** mode is selected (see Figure [Routine Card of the CSI method \[▶ 563\]](#)) for nuclei with short T2.

The acquisition is made in the entire slice and the shim volume must be adapted respectively.

2.13.2.5 Data Analysis

Visualization of the Metabolite Images

The metabolite images can be viewed in the **CSI Visualization Tool**. To visualize the metabolite images, load the reference Image and the CSI data in the **Image Display & Processing Tool**. Go in the **Explorer** tab of the **Palette** window. Select each scan and use the **RMB** to activate the **context menu**. In this select **View in Image Display**. For a detailed description of all features of this tool see **Chemical Shift Imaging Visualization** in the **Classic Image Display & Processing** chapter of the documentation. The Visualization Tool in mode pixel scan is shown in following Figure (LEFT) with the spectrum corresponding to one CSI pixel. The map corresponding to the NAA metabolite is displayed in following Figure (RIGHT).

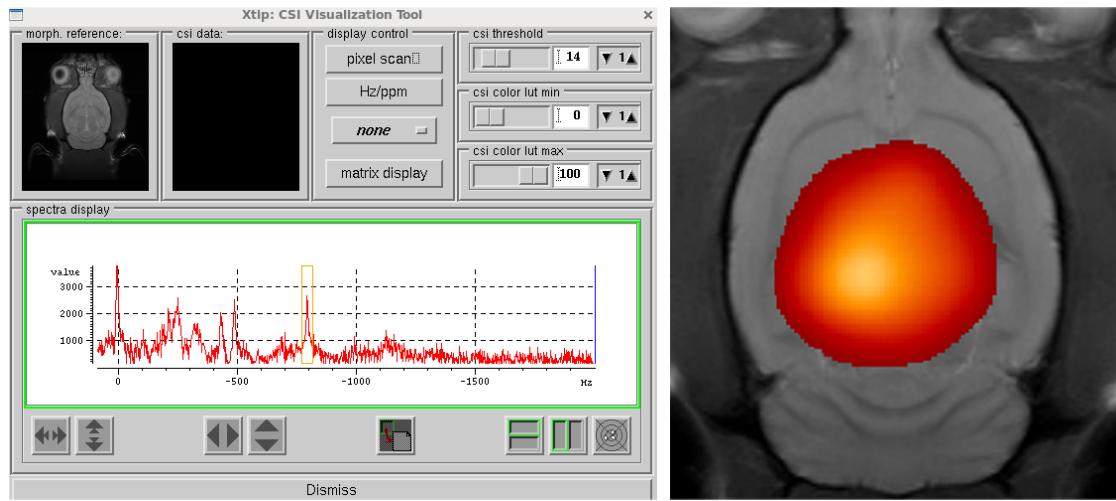


Figure 2.105: **LEFT:** CSI Visualization Tool in pixel scan mode **RIGHT:** NAA map

Processing of the spectra

The processing of the spectra can be done in **TopSpin**, which is the Bruker software for spectroscopy. To view the acquired data export the dataset into the **TopSpin** window. For this, select the scan and use the **RMB** to activate the **context menu**. In this menu, select **Load in TopSpin**. The data are exported as 3D dataset in **TopSpin** containing the FID of each CSI voxel. Open the **ProcPars** parameter class and set the sizes of F2 and F1 to the spatial dimensions of the CSI protocol (16 in default protocol). Fourier Transform the data in the first direction by typing the command **tf3**.

To process the spectrum of each CSI voxel, type the **rser** command following by the number of the selected voxel in the command line of **TopSpin**. **TopSpin** will move in 1D processing mode (see following Figure). Set the size (**si**), the line broadening (**lb**) and Fourier Transform the data (**efp**) by typing the commands in the **TopSpin** command line. For further and detailed information see the **TopSpin** software manual.

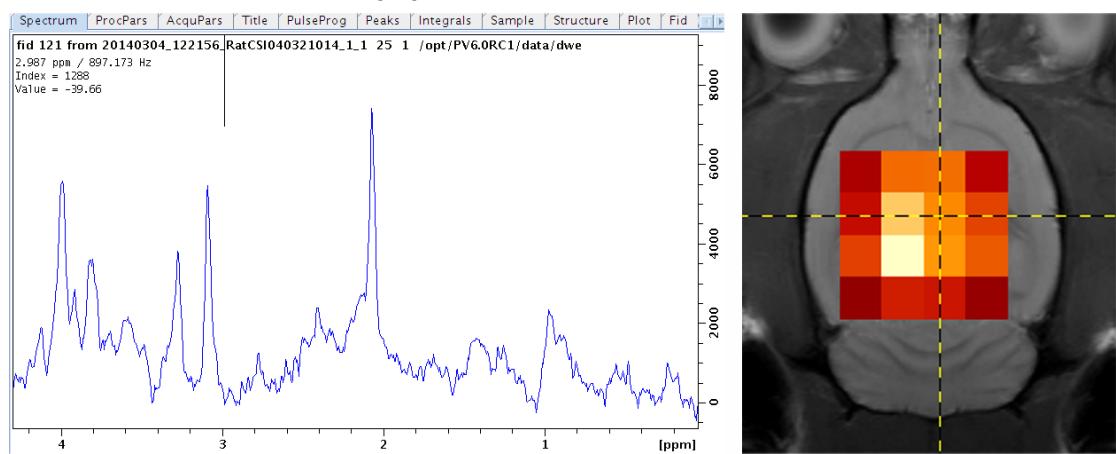


Figure 2.106: **LEFT:** 1D spectrum the Csi pixel **RIGHT:** Position of the pixel in the brain

The following figure shows the matrix of the spectrum in the voxel measured in the rat brain.

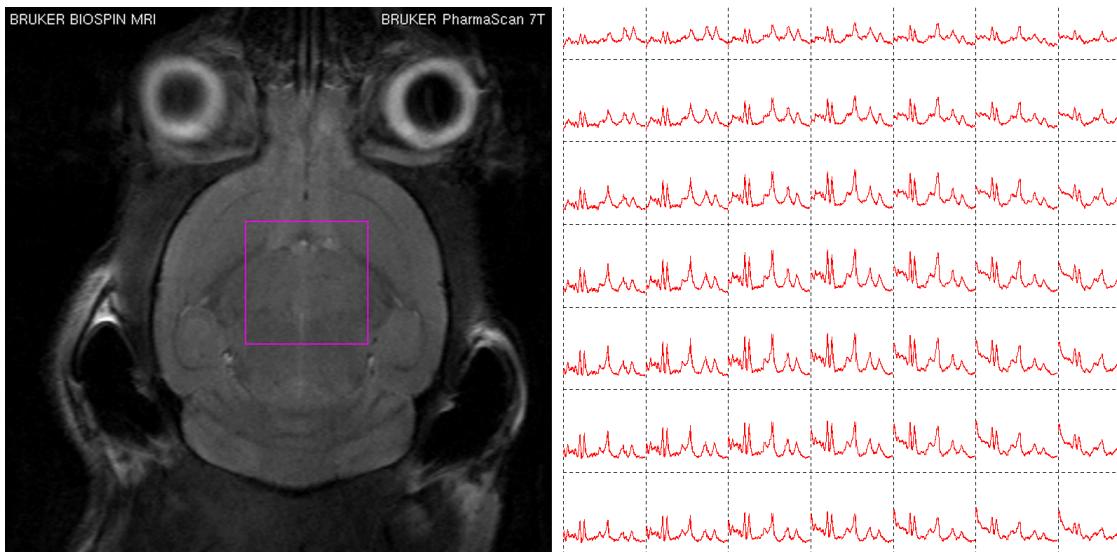


Figure 2.107: CSI of the mouse brain, 16 x 16 CSI matrix, 7 x 7 visible within the volume of interest; in the left corner the reference image with the volume of interest (zoomed as background)

2.13.2.6 References

- [1] Decors M, Dupeyre R, Remy C, LeFur Y, Devoulon P, Bourgeois D. Spectroscopic Imaging. Chapter 6 in Magnetic Resonance Spectroscopy in Biology and Medicine, Pergamon Press, 1992.
- [2] Brown TR, Kincaid BM, Ugurbil K. NMR Chemical Shift Imaging in three Dimensions. Proceedings of the National Academy of Sciences of the United States of America 79 (11), 1982; 3523-3526.
- [3] Brateman L. Chemical Shift Imaging: A Review AJR 146, 1986,971-980.
- [4] De Graaf R. A. In vivo NMR Spectroscopy, John Wiley ,Chichester 1998.
- [5] Klomp D.W.J. and Klaas W. Spectroscopic Imaging of the Mouse Brain Chapter 18 In Vivo NMR Imaging Methods in Molecular Biology 771, Springer Science 2011.

2.13.3 X-nuclei Spectroscopy and Imaging

2.13.3.1 Introduction

Abbreviations

- T1 - Spin-Lattice Relaxation Time
- T2 - Spin-Spin Relaxation Time
- TE - Echo Time
- TR - Repetition Time
- LMB - Left Mouse Button
- RMB - Right Mouse Button

Purpose

X-nuclei spectroscopy provides a technique to obtain signals of other nuclei than protons, the nuclei most commonly used in imaging and spectroscopy. The general advantage in comparison to proton spectroscopy is the greater dispersion of the MR-signals. The disadvantage is the generally lower signal strength, due to lower gyromagnetic ratio (γ) and the lower abundance in tissue in comparison with protons. The concentration of protons is always higher than for other naturally occurring nuclei like ^{13}C , ^{23}Na and ^{31}P . While ^{13}C and ^{31}P are mainly used in X-nuclei spectroscopy, ^{23}Na is essentially used in X-nuclei imaging. Also ^{19}F is a good candidate for imaging due to its high γ . In ^{19}F spectroscopy and imaging fluorine containing molecules have to be supplied. ^{13}C chemical shift imaging is of interest when working with hyperpolarized substances.

The main characteristics of the most popular X-nuclei are given in Table [Comparison of the main characteristics of the most popular X-nuclei and protons \[▶ 569\]](#).

Nucleus	In vivo chemical shift dispersion [ppm]	Natural abundance [%]	Receptivity Molar rel. ^1H	Spin	Remarks	γ (MHz/T)
^1H	10	99.989	1	$1/2$		42.58
^{13}C	200	1.07	0.016	$1/2$	long T1	10.71
^{19}F	200	100	0.832	$1/2$		40.08
^{23}Na	70	100	0.093	$3/2$	short T1 and T2	11.27
^{31}P	40	100	0.067	$1/2$		17.25

Table 2.4: Comparison of the main characteristics of the most popular X-nuclei and protons

Requirements

A BioSpec equipped with hardware, capable of dealing with X-nuclei, and the corresponding RF coils. X-nuclei spectroscopy is less sensitive to good shimming conditions than ^1H spectroscopy because of the greater signal separation between the individual signals and the inherently broader peaks.

2.13.3.2 Hardware Setup

Double tuned **X-nuclei/ ^1H** coils are recommended. **Transmit-receive Surface Coils**, **Transmit-receive (volume) Resonators** or a **Transmit-only Resonator** in combination with a **Receive-only Surface Coil** may be used for acquisition.

Note that when working with **Transmit-receive** or **Receive-only Surface Coils** one may use the fact that a limited spatial region is covered by the coil for the purpose of volume selection. Voxel sizes for localized X-nuclei spectroscopy are normally of such size that this is not a major drawback.

Wobble both channels by switching between the **Coil Element(s)** in the **On Demand Protocol Wobble Adj** in the **Adjustment Platform**.

2.13.3.3 Object Setup

Preparation

X-nuclei spectroscopy generally suffers of the drawback of poor signal to noise. For instance the measurement of a localized ³¹P spectrum on mouse liver can take two hours. It is therefore a good idea to check protocols initially on phantom solutions. Table [Suggested filling solutions for test objects. Please read handling instructions and data sheets \[▶ 570\]](#) shows a number of suggested test object filling solutions, that can be used as imaging phantoms for different X-nuclei experiments. In case of aqueous solutions with ions, note possibly the high conductivity and loading effects, which gives rise to the need of increased pulse amplitudes. On the other hand non-conductive samples would have less loading than the body of animals.

Nucleus	Suggested filling solutions for test object
²³ Na	NaCl aqueous solution, e.g. common saline solution (0.9%)
³¹ P	H ₃ PO ₄ (Phosphoric Acid)
¹⁹ F	CF ₃ CH ₂ OH (Trifluoroethanol)
¹³ C	Vegetable oil, DMSO (Dimethylsulfoxide)

Table 2.5: Suggested filling solutions for test objects. Please read handling instructions and data sheets

Voxel Positioning

The voxel size, position, and orientation can be defined in the **Geometry Tab** of the **Palette** window or by directly rotating, translating and changing the size of the voxel in reference images in the Geometry Editor. Any type of image can serve as reference image. Under in vivo conditions, accurate voxel position definitions are possible on anatomical multi-slice spin or gradient echo based images i.e. RARE and FLASH images.

2.13.3.4 Protocol Setup

Protocol and Method

Select the **Location Rat (or Mouse)/Head/Spectroscopy** and load the protocol [Singlepulse \[▶ 377\]](#) for the particular X-nuclei. This protocol serves as a good starting point for X-nuclei spectroscopy. Once the basic setup steps described below have been done, one can continue with localized spectroscopy with the corresponding [ISIS \[▶ 395\]](#) protocol. For imaging purposes the protocol **T1_Fluorine_imaging_flash** can be used.

Even though ¹³C natural abundance spectroscopy can be done on entire organs, especially in rat, the signal to noise is rather poor. For this reason one normally works with ¹³C enriched metabolites. As the major source of ¹³C signal will come from these metabolites originating from the injected ¹³C enriched substrate one can also study metabolic flux this way. Possible targets are brain, liver and tumors. An increasingly used signal enhancement technique is ¹³C hyperpolarization. The signal is thereby increased several orders of magnitude.

The ¹⁹F nucleus has found several applications as active group in tracer molecules. Possible applications are assessment of tumor hypoxia, monitoring of cell migration or heart infarction. In most applications imaging yields the relevant information.

³¹P spectroscopy benefits from the 100 % natural abundance. Even though the dispersion and variety of the signals is less important than for the case ¹³C, localized spectra of the whole brain or liver can easily be obtained on rat. The spectroscopic study of muscle activity is another potential target. Also the physiological pH can be determined with help of phosphorus signals.

²³Na is mainly used for imaging, for instance for the determination of the sodium concentration in vivo. Possible targets are prostate or brain ischemia.

Adjustments and Basic Spectroscopy

Shimming has to be done using the proton signal before one starts with X-nuclei experiments. The appropriate workflow is described in the Chapter [Proton Magnetic Resonance Spectroscopy \[▶ 556\]](#).

With the appropriate **Singlepulse** protocol go to the **System Card** and set the **Operation mode** to the X-nuclei of interest. Acquire a spectrum with **Scan**. Select your experiment in the **Explorer Sub-tab** of the **Palette** and use the **RMB** to activate the pop-up menu. In this select **Load in TopSpin**.

Processing of spectra for qualitative evaluation can be done in **TopSpin**, which is the Bruker software for spectroscopy. Set the line broadening (**lb**) and Fourier transform the data (**ef**) by typing the commands in the **TopSpin** command line at the bottom of the window. A typical value for **lb** is 10. Type **apk** to apply automatic phase correction. If additional phasing is needed type **.ph** to enter the phase correction and phase by selecting the **0** and **1** buttons in the upper menu and moving the mouse. Save and return using the same upper menu. For further information on processing see the **TopSpin User Manual**. Use the **LMB** to measure the difference (offset) in ppm or Hz from the middle of the spectrum to the signal region of interest. Return to the **Exam Card** in **ParaVision**.

Go to the **Frequency Ch.1. Sub-card** of the **Sequence Card** and put your measured offset. The offset should be negative if the peaks were to the right in **TopSpin** and positive if they were to the left. Adapt the number of **Averages** on the **Routine Card** and acquire the spectrum. Postprocessing can be done as described above.

Alternatively, the frequency offset can be saved permanently for further experiments. In this case **Frequency Offset** should be set to zero on the **Frequency Ch.1. Sub-card**. Open the **Adjustment Platform**. Select the **Protocol Basic Frequency**. Got to the **Result Sub-card** and type your offset into **Manual Offset**. Apply the button **Apply Manual Offset**. Right click on the **Basic Frequency** protocol field and select **Save Adjustment Result**. Finish with **Apply** and **Back**.

Setting the Reference Power for the Pulses

This adjustment has to be run at least once on a phantom for a particular nucleus. Start with setting up a **Singlepulse** experiment to find the X-nuclei signal and to set up reasonable parameters. Duplicate this scan with **Duplicate Instruction**. Open the scan and select the **Main Sub-card** of the **Setup card**. Deselect **Calc. Pulse Ampl.** and set **Exc. Pulse Power** to a large value eg. 1000 W. Make sure that this is the maximum power, i.e. if the power does not change set a higher value than 1000 W. Write down the value of **Exc. Pulse Attenuation** in dB, this is the maximum power available for this coil. Select **Calc. Pulse Ampl.** again.

Go to the **Explorer Sub-card** of the **Palette** window. Select your experiment. Right click and select **Load in TopSpin**. Close the **Exam card**. In **TopSpin** go to **File** on the upper menu tab or to the yellow disks (depending on how your **TopSpin** was configured) and select **NEW (or New)**. Select a **NAME** for your experiment other than the one given and reset **EXPNO** to 1. **Use current parameters** should be selected otherwise you will not import the parameters into topspin. Finish by clicking **OK**. Type **eda** on the topspin command line (at the bottom of the **Topspin** window). Alternatively, select the **AcquPars** card in **TopSpin**. Set **PULPROG** to **zg** by selecting the three dots next to the field. Apply **Set PULPROG** and then **Close**.

If you do not find any **zg** pulse program it must be created first. To do this type **expinstall** in the topspin command line. The only thing that has to be changed is to select **High Resolution Systems** on the third page. Do not change any other parameter. Just click your way through.

Set **NS** to between 2 and 16, and **RG** to 203. Scroll down and check that **Nucleus 1** is your selected X-nucleus. Continue and set **P[1]** to 200 μ s (40 μ s if a **Resonator** is used), **D[1]** long in relation to the expected T1 of the X-nuclei and **PLdB[1]** to the maximum power attenuation obtained from ParaVision. If you do not know the T1 try values for **D[1]** in the range 5-20s. If the position of the maximum does not change the repetition time **D[1]** is correct. Start a scan with **zg**.

Once the scan is finished process your spectrum as described above. Zoom in your peak of interest with the **LMB** and type **dpl1**. This chooses the selected region for the optimisation. Type **PH_mod** and set this to **pk**. This assures automatical phase correction during the optimisation procedure. Check that your **PULPROG** is **zg**.

Type **popt** in the command line. Set the **PARAMETER** to vary to **p1**. Typically set **STARTVAL** to 25 and **ENDVAL** to 300 (5 and 75 μ s if a **Resonator** is used). Finally select **NEXP** to between 10-20. Start by selecting **Start Optimize** in the bottom row. Once the optimisation is finished write down the value of **POSMAX** this is the duration of the calibrated 90 degree block pulse for the X-nuclei.

To see the curve corresponding to **Figure 1** go to the **Spectrum Sub-card** in **TopSpin** and magnify the display by clicking the ***2** button in the upper menu with **LMB**. Check that a maximum is clearly seen, otherwise repeat the experiment with a different distribution of **p1**.

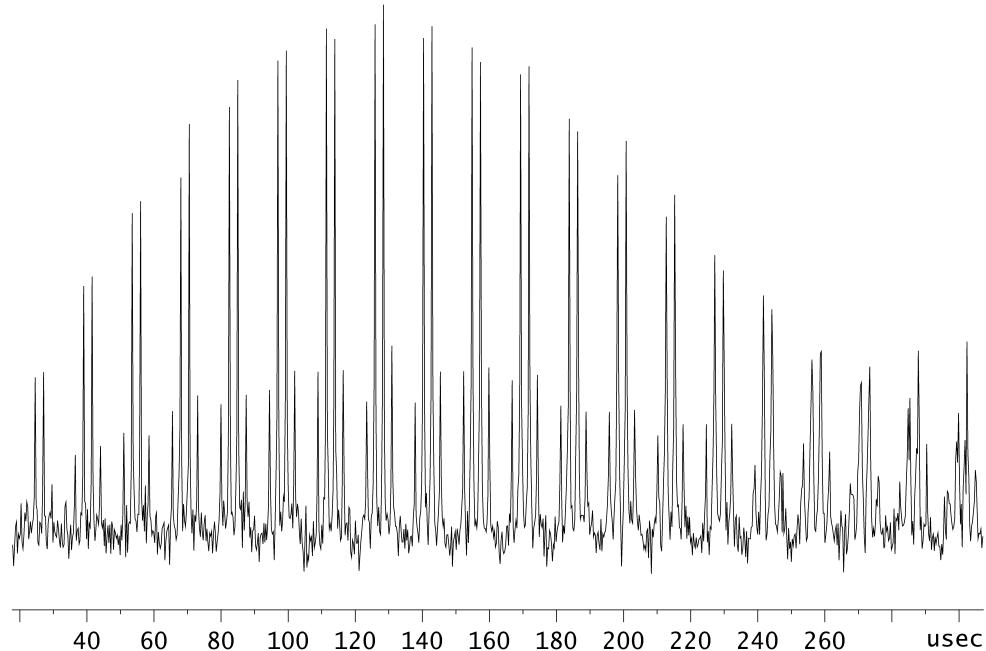


Figure 2.108: The result from running **popt**. A maximum is clearly seen.

Go back to the **Workspace Explorer** in **ParaVision**. Select the dataset and open the **Exam Card**. Open the X-nuclei experiment. Enter the **Adjustment Platform** and **Open the Reference Power** adjustment. Verify that the right nuclei is selected under **Operation Mode** on the **System Card**. Select the **Result Card** and put in the determined **Hard Pulse Dur.**. Apply the **RMB** on the adjustment and save by selecting **Save Adjustment Result**.

Decoupling

Select **Decoupling** on the **Main Sub-card** of the **Preparation Card**. Switch to the **Decoupling Sub-card**. By default **Mlev16** is selected as **CPD Sequence**. An alternative is **Waltz16**. To limit the power deposition during decoupling it is only recommended to have decoupling on when signal remains. To find out one can inspect the time domain signal in the **Acq/Reco Display**. Visually estimate how much of the acquisition window that contains signal and edit **Decoupled Acq. Fraction** on the **Decoupling Sub-card** accordingly.

Advanced Parameter Selection

One can optimize the signal intensity by varying either the parameters **Flip Angle** or **Repetition Time** in the **Routine Card**. The **Flip Angle** can be varied from 5 - 90°. Repetition times are typically in the range 1-40 s for 13C, 31P and 19F and 40-200 ms for 23Na.

Adapt the **Bandwidth in Hz** to cover the metabolite signal of interest by modifying this parameter in the **Spectroscopy Card**. Also increase the number of **Points** if you wish a higher resolution. Before performing the final parameter selection make sure that you have a determined **Reference Power** for the pulses as described above. Go to **Main Sub-card** of the **Sequence Card** and select the **Pulse Details** field next to the **Excitation Pulse** and increase the **Bandwidth** to the same value as set in the **Spectroscopy Card**. Note that there is a limit how high the **Bandwidth** can be set. At some stage the **Flipangle** will start to decrease because there is not enough power available. The frequency range needed to be covered can easily be determined from the spectrum in **TopSpin** using the same approach as for determining the offset.

2.13.3.5 Localized Spectroscopy and X-nuclei Imaging

Localized Spectroscopy and X-nuclei Imaging

Once one has done the basic setup steps as described above one can continue with localized spectroscopy and imaging.

For localized spectroscopy select the **Location Rat (or Mouse)/Head/Spectroscopy** and load the appropriate **ISIS** protocol. Set the voxel size and place the voxel. On the **Routine Card** verify that the **Flip Angle Excitation** is 90°. If not go to the **Main Sub-card** of the **Sequence Card** and select the **Pulse Details** field next to the **Excitation Pulse**, decrease the **Bandwidth** and correct the **Flipangle**. Proceed in the same way for the **Flip Angle Inversion** which should be 180°. Set the **Frequency Ch.1** and **Averages** and possibly **Bandwidths** and **Points** as described above. Postprocess as described previously.

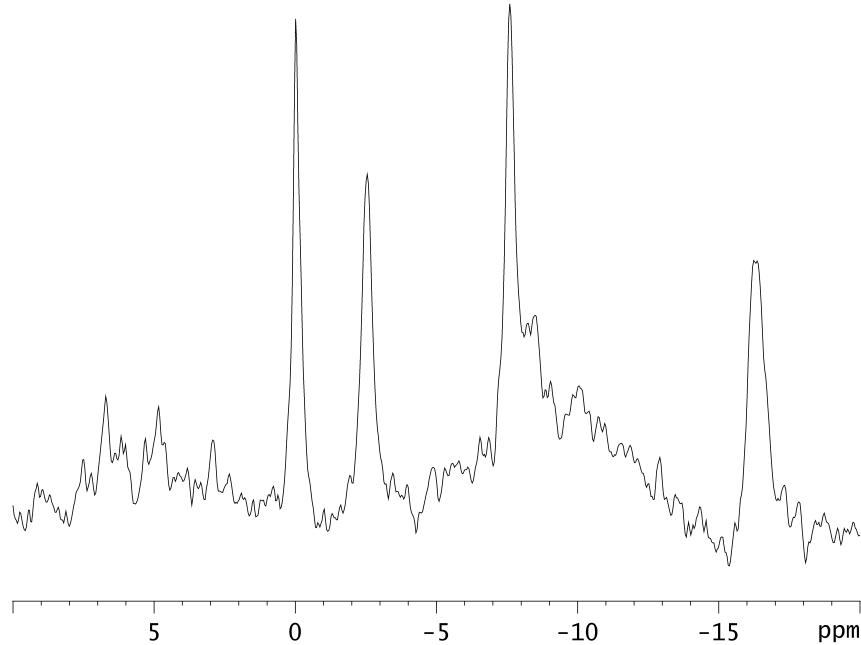


Figure 2.109: Isis spectrum acquired on rat brain with a voxel size of $10 \times 6 \times 12 \text{ mm}^3$. An acquisition time of 21 min was used with 80 ISIS averages. A line broadening of 20 Hz has been applied as well as 0 and 1 order phasing.

For X-nuclei Imaging select the Location **Rat (or Mouse)/Abdomen/Torso** and load the protocol **T1_Fluorine_imaging_flash**. Set the **Frequency Ch.1** and **Averages** and acquire. In the default protocol a big FOV and thick slices are selected. It is recommended to start with these settings. Acquire images and adjust the number of **Averages** until you clearly see the signal in the center of your image. Then adapt your FOV to match the object and increase the resolution. Note that you will also have to increase the number of **Averages**.

2.13.3.6 References

- [1] de Graaf RA. In vivo NMR Spectroscopy - 2nd Edition, Principles and Techniques, John Wiley & Sons Ltd, 2007.
- [2] Künnecke B, Küstermann E, Seelig J. Simultaneous In Vivo Monitoring of Hepatic Glucose and Glucose-6-Phosphate by ^{13}C -NMR Spectroscopy. Magnetic Resonance in Medicine 44, 2000; 556-562.
- [3] Brindle KM, Bohndiek SE, Gallagher FA, Kettunen MI. Tumour Imaging Using Hyperpolarized ^{13}C Magnetic Resonance Spectroscopy. Magnetic Resonance in Medicine 66, 2011; 505-519.
- [4] Hurd RE, Yen Y-F, Chen A, Ardenkjær-Larsen JH. Hyperpolarized ^{13}C Metabolic Imaging Using Dissolution Dynamic Nuclear Polarization. Journal of Magnetic Resonance Imaging 36, 2012; 1314-1328.
- [5] in 't Zandt HJA, Renema WKJ, Streijger F, Jost C, Klomp DWJ, Oerlemans F, Van der Zee CEEM, Wieringa B, Heerschap A. Cerebral creatine kinase deficiency influences metabolite levels and morphology in the mouse brain: a quantitative in vivo ^1H and ^{31}P magnetic resonance study. Journal of Neurochemistry 90, 2004; 1321-1330.
- [6] Giannesini B, Cozzone PJ, Bendahan D. In vivo MR investigation of skeletal muscle function in small animals. MAGMA 17, 2004; 210-218.

- [7] Penet M-F, Viola A, Confort-Gouny S, Le Fur Y, Duhamel G, Kober F, Ibarrola D, Izquierdo M, Coltel N, Gharib B, Grau GE Cozzone PJ. Imaging Experimental Cerebral Malaria In Vivo: Significant Role of Ischemic Brain Edema. *The Journal of Neuroscience* 25, 2005; 7352-7358.
- [8] Robinson SP, Griffiths JR. Current issues in the utility of ¹⁹F nuclear magnetic resonance methodologies for the assessment of tumour hypoxia. *Philosophical transactions of the Royal Society B* 359, 2004; 987-996.
- [9] Ruiz-Cabello J, Barnett BP, Bottomley PA, Bulte JWM. Fluorine (¹⁹F) MRS and MRI in biomedicine. *NMR in Biomedicine* 24, 2011; 114-129.
- [10] Near J, Bartha R. Quantitative Sodium MRI of the Mouse Prostate. *Magnetic Resonance in Medicine* 63, 2010; 822-827.
- [11] Yushmanov VE, Yanovski B, Kharlamov A, LaVerde G, Boada FE, Jones SC. Sodium Mapping in Focal Cerebral Ischemia in the Rat by Quantitative ²³Na MRI. *Journal of Magnetic Resonance Imaging* 29, 2009; 962-966.

2.14 Contrast Agent DCE DSC

2.14.1 Introduction

Intravenously injected contrast agents are changing the MR signal intensity course due to relaxation effects (T_1 , T_2 or T_2^*). They are used to depict physiological modifications issued from pathological regions (i.e. leakage in brain tumors with disrupted blood brain barrier) or from the vessels when using blood pool MR tracers. Repeated *in vivo* fast MR imaging during a bolus of contrast agent (i.e. Gd-DTPA) enables to monitor dynamic changes as the agent passes through the tissue. Two techniques are typically employed: DCE-MRI (Dynamic Contrast Enhanced MRI) and DSC-MRI (Dynamic Susceptibility Contrast MRI).

Gd-based contrast agents (Gd-DTPA) are typically used in DCE-MRI investigations as they decrease the relaxation times T_1 during their distribution in the tissue resulting in a positive contrast on T_1 weighted images.

Iron-based contrast agents and Gd-DTPA at high concentrations are used in perfusion MR studies (DSC-MRI or bolus tracking) as the presence of these contrast agents in the tissue of interest will decrease the T_2 and T_2^* relaxation time values and will provide a negative contrast on the retrieved images.

This chapter explains how to perform routine dynamic MR examinations (DCE-MRI, DSC-MRI) and overviews the current data evaluation possibilities.

Abbreviations

- DCE-MRI – Dynamic Contrast Enhanced MRI
- DSC-MRI – Dynamic Susceptibility Contrast MRI
- FOV - Field of View
- Gd-DTPA - Gadopentetate-Diethylenetriamine Pentaacetic Acid
- SPIO – Superparamagnetic Iron Oxides
- USPIO – Ultrasmall Superparamagnetic Iron Oxides

Purpose

Dynamic contrast agent MRI is a well-established technique that uses exogenous agents as tracers for examining physiological parameters, such as: tumor perfusion (intra-cranial, in thoracic or abdominal organs), capillary leakage, cerebral ischemia (cerebral infarcts), stenosis in vessels, flow rates, or quantitative/qualitative heart analysis. It uses a series of images acquired before (baseline), (often during) and following the intravenous injection of a contrast agent. It measures the changes in the relaxation rate of water and provides physiological information about contrast agent distribution and tissue perfusion. Among many exogenous tracers used in dynamic MR investigations, gadolinium chelates, manganese or iron (named positive contrast agents, typically used in DCE-MRI) and superparamagnetic iron oxides (SPIO, USPIO – named negative contrast agents, typically used in DSC-MRI) are most prevalent.

This following section describes the workflow of routine DCE-MRI and DSC-MRI investigations. The delivered protocols can be used for brain and body (i.e. liver, or kidney) applications.



Cardiac DCE/DSC applications are subject of ongoing research and are not covered by the protocols described in this chapter.

Requirements

Use a standard animal imaging setup and an appropriate animal bed (see System Manual).

2.14.2 Hardware Setup

Respiratory triggering is not recommended for brain and body (liver, kidney) DCE/DSC investigations as the respiration rate could significantly change during the contrast agent administration and the trigger signal is often lost. This will decrease the temporal resolution and eventually reduce the designed timeline for following dynamic processes after contrast agent administration.

Gradient

No special requirements.

2.14.3 Object Setup

Preparation

The animal should be appropriately anesthetized and positioned in the animal bed. For brain imaging, fix the head with the stereotactic devices provided by the animal bed or tape the head to avoid movements due to respiration. During the experiments, the respiration rate and the temperature should be monitored. For injection of the contrast agent, insert a cannula with a long tube i.e. into the tail vein of a rat/mouse.

2.14.4 Protocol Setup

Protocol and Method

The acquisition of DCE/DSC experiments requires the continuous acquisition of more dynamics (multiple **Repetitions**) including: 10 to 15 baseline images (to cover 10 to 15 seconds acquisition) followed by the contrast agent injection and the acquisition of the first pass of the bolus (to cover approximately 2 to 3 minutes acquisition after contrast agent administration – depending on the contrast agent). The protocols are delivered with the **Repetitions** set to 10. The recommendation is to run these protocols prior to the administration of the contrast agent to first evaluate the signal quality after reaching a steady state condition. For the experiment with contrast agent, the user is advised to select the number of Repetitions to reach the required scan time based on the recommendations given above.

Dynamic Susceptibility Contrast MRI

The most common protocols are based on T_2^* weighted images, mainly EPI due to its superior temporal and spatial resolution compared to other pulse sequences. It can benefit of the use of parallel acceleration to improve spatial resolution and to reduce susceptibility artifacts (especially in single-shot EPI). The typical acquisition workflow of a DSC experiment is schematically illustrated in Figure [Typical workflow of a DSC experiment \[▶ 577\]](#)

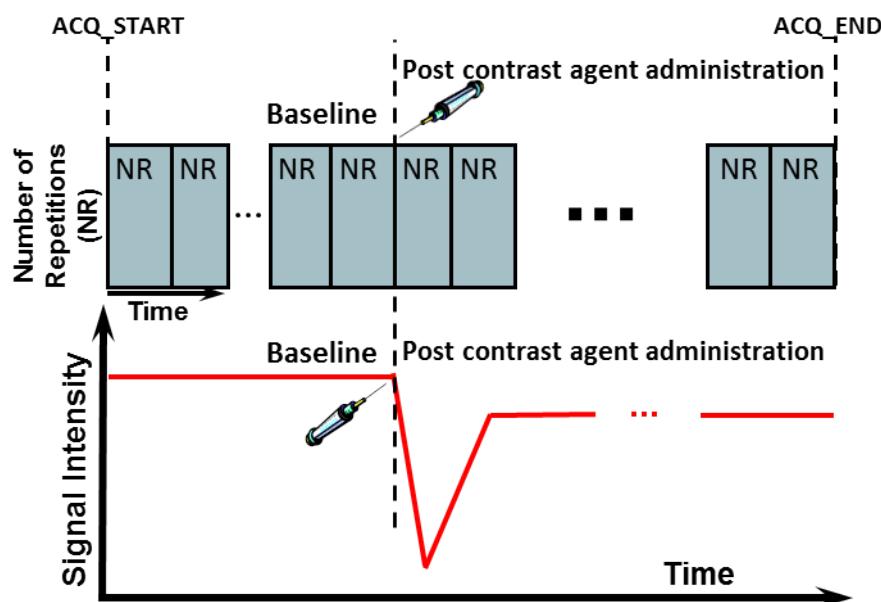


Figure 2.110: Typical workflow of a DSC experiment, with ACQ_START representing the beginning of the DSC acquisition and ACQ-END the end of the acquisition. NR denotes the number of Repetitions (often referred as dynamics).

To run a dynamic DSC-MRI experiment, load the **DSC_T2star_FID_EPI** protocol from the **Rat (or Mouse) /Head / Perfusion** location (for brain) or **Rat (or Mouse) /Abdomen / Perfusion**(for body), respectively. For the contrast agent experiment, define the number of **Repetitions** from the **Routine** card according to the desired scan time. Afterwards, the protocols are ready to be run.

Dynamic Contrast Enhanced MRI

Before the administration of the contrast agent, a T₁-weighted image is generally acquired as a reference. The protocol **T1_FLASH** is intended for this purpose. To run a complete dynamic DCE-MRI experiment, load the **DCE_FLASH** protocol from the location **Rat (Mouse)Rat (Mouse) /Head / Perfusion** (for brain), or **Rat (or Mouse) /Abdomen / Perfusion**(for body), respectively. Define the number of **Repetitions** from the **Routine card** according to the desired scan time. Afterwards, the protocols are ready to be run.

Parameter Selection

The here described protocols can be used as templates but still offer the flexibility for a smaller Field Of View, thinner slice thickness, or different spatial and temporal resolution. The FOV, or the Slice Thickness/Orientation can be adapted from the **Routine card**. Additional information about the slices and their orientation to one another is provided in the **Geometry card**.

In case this is not needed, the protocols can be modified to achieve a shorter echo time (typically required in DCE experiments) for example. This can be performed in the **Geometry** and the **Resolution card** of the **Parameter editor**.

Adjustments

For EPI-based protocols (for brain investigations), it is recommended to use the **Map_Shim** utility to optimize the field homogeneity in the region of interest. For brain applications, a shim volume covering the entire brain is already active in the protocol.

To improve the shims proceed as follows:

- load the scan in the instruction list, enable **Map_Shim** in the Auto Shim Sub-card of the Setup Card. The shim volume is now visible in the Examination card. Adapt its geometry to cover only the brain, without tissue/bone/air interfaces (e.g. skull, air cavities).
- Open the **Adjustment Platform**, select and open the **On Demand Protocol B₀ Map**. Acquire the B₀ map by pressing **Start** and leave the **Adjustment Platform** once the map is acquired (after the Green tick mark appears) by clicking **Apply** and **Back**. Once acquired, the B₀ map will be displayed in the Palette tab under Explorer, Datasets.
- Start the acquisition with **Continue**. The shims will be calculated in an automatic adjustment in the shim volume prior to the start of the acquisition itself.

Note: If **Map_Shim** was previously performed and you want to keep the calculated shim values, keep the option **Current_Shim** in the Auto Shim Sub-card of the Setup Card. For body applications, the shim adjustment using **Map_shim** is not necessary.

Acquisition

The EPI based protocols must be started with the **Continue**.

Reconstruction

The standard RECO is automatically invoked.

Practical considerations

Specific considerations for DCE and DSC protocols are given below.

Include enough reference images for the baseline acquisition. Inject quickly for a more significant signal drop in the DSC experiments.

To keep the same receiver gain in case of multiple DCE datasets (acquired separately before and after contrast agent injection) do the following: load the **T1_FLASH** protocol (this is the pre-contrast scan), right mouse click and select Duplicate Instruction from the context menu. The duplicated scan represents the post-contrast scan. To run the later with the same receiver gain, go into the **Instruction card**, drag and drop GOP into the Scan Mode/Individual Setup/Acquisition. Click on **Apply**. Right mouse click on the duplicated **T1_FLASH** protocol and select **Contrast Administration** from the context menu. An instruction named **Contrast Administration** will be loaded in between the two selected **T1_FLASH** images. Open it and specify the time to wait before/after contrast agent administration. By default a value of 10 seconds is selected in both cases. Press **Continue**. The loaded examinations will run in a queued acquisition mode. At the end of the pre-contrast **T1_FLASH** acquisition, the following popup window message will appear:



Inject the contrast agent and click **Close**. The second scan will start running after the time specified in the **Contrast Administration** Instruction.

2.14.5 Data Analysis

Tools and Analysis

ParaVision offers the possibility to observe the signal intensity profile interactively through multiple dynamics. This is performed using the **Functional Imaging Tool** from the **Image Display and Processing Tool**. The subtraction of two datasets (i.e. prior and after contrast agent administration) is performed using the **Algebra** functionality in the **Image Display and Processing Tool**.

Displaying the results

Timeprofile in dynamic datasets

Load the acquired DSC/DCE dataset into the Image Display and Processing Tool, select the data from the **Palette tab** under **Explorer, Datasets**. Right mouse click and select **View in Image Display** from the context menu. The data will be automatically loaded into the first viewport of the Image Display.

- Open the FUN Tool via Processing ->Functional Imaging. In the FUNctional Controller (or FUN Tool) click on More Utilities -> Time Profile -> Default. Choose MultiSlice from Frame Selection.
- Select the slice you want to analyze in the Image Display & Processing.
- In the FUN Tool select ROI Scan. A ROI named TimeProfile will be automatically created in the ROI Tool. Click on Cut Away -> OK -> Overlay. In the FUN Tool click on ROI Scan. The time course is interactively displayed in the FUN Tool corresponding to the selected ROI position.

Subtraction of individual datasets

Load both datasets (i.e. acquired prior and after contrast agent administration) into two different viewports of the **Image Display & Processing Tool**.

- Select **Processing > Algebra > Edit**, and edit the formula for the subtraction of two images.
- Select **Processing > Algebra > Execute** and click on the loaded images corresponding to both scans. The result is displayed in a third viewport chosen during execution of the formula.

Troubleshooting

If you cannot recognize a difference between both scans (i.e. no signal in the difference image) the administration of contrast material may have failed.

2.14.6 References

[1] J-V Gaustad, KG Brurberg, TG Simonsen, CS Mollatt, EK Rofstad. Tumor Vascularity Assessed By Magnetic Resonance Imaging and Intravital Microscopy Imaging. *Neoplasia* 10(4); 2008:354-362.

2.15 Tips & Tricks

2.15.1 Detecting and avoiding Image Artifacts

Image artifacts are structures in the image that do not correspond to the spatial distribution of tissue, they are not present in the real object and may lead to misinterpretations.

It is recommended to learn how to detect, allocate, and avoid these artifacts.

2.15.1.1 Artifacts originating from Technical Aspects

Aliasing

Aliasing (wrap around, fold in) occurs when the FOV is smaller than the object.

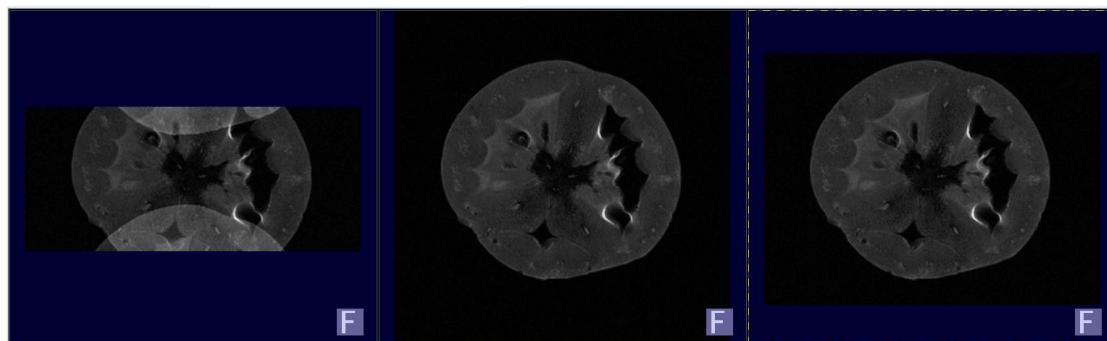


Figure 2.111: **Cherry tomato.** **Left:** Aliasing leads to misregistration and overlay of structures. **Middle:** FOV and Image Size is increased in phase encoding direction and is now larger than the object size (isotropic resolution). This leads to an increase in Scan Time. **Right:** FOV and Image Size is reduced to the extension of the object and the amount of phase encoding steps is also reduced, correspondingly. This leads to the same resolution at a reduced Scan Time.

 Tips

- Use Anti Aliasing in readout direction (this leads to no increase in Scan Time).
- Use FOV in phase encoding direction larger than object size.
- Reduce FOV and Image Size correspondingly (mark Isotropic Resolution) to obtain the same resolution at a shorter Scan Time.

Magnetic Field Inhomogeneity

Magnetic field inhomogeneities may result in deformed structures and incorrect dimensions seen in the image.

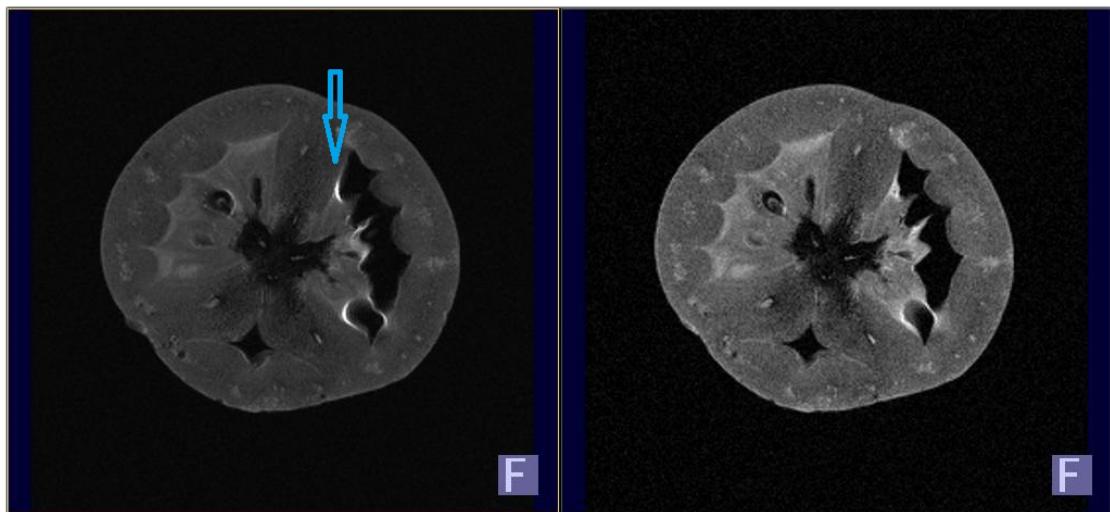


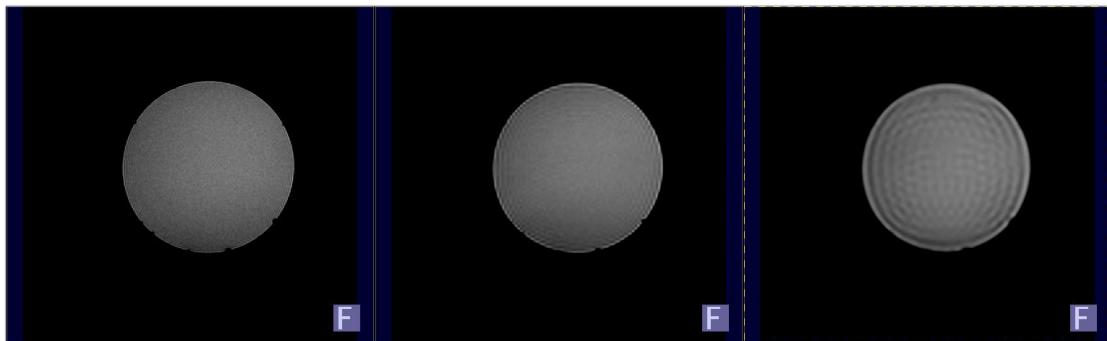
Figure 2.112: **Cherry tomato:** the structure (for example at the arrow) is deformed due to the magnetic susceptibility difference between different tissues. **Left:** Image taken at 33 kHz bandwidth. **Right:** The increased bandwidth of 100 kHz reduces the artifact at the drawback of a reduced SNR.

 Tips

- Increase the bandwidth

Gibbs ringing or Truncation Artifacts

Bright and dark lines alternating parallel and adjacent to borders of strong intensity change or called edge oscillations or Gibbs ringing. The artifact is related to the finite number of encoding steps used by the Fourier transform to reconstruct the image.



*Figure 2.113: Alternating bright and dark lines adjacent to edges with high contrast (edge oscillation). **Left:** Image Size 256. **Middle:** Image Size 128 with artifact visible. **Right:** Interpolation 2 of Image Size reduces the Image Size to 64. The artifact becomes more prominent.*

Tips

- At increased Image Size, the artifacts get less intense and narrower.
- Do not use interpolation since the measured Image Size is reduced and thus artifacts become more pronounced.
- Apply in Data Reconstruction, RECO Parameters, a Filter in all directions (currently not for FLASH and MGE).

RF Interference(s)

RF sources radiating at corresponding frequencies (for example radio stations or electronic equipment in the proximity) will lead to disturbances seen as single or multiple dotted lines (bands) in phase encoding direction.

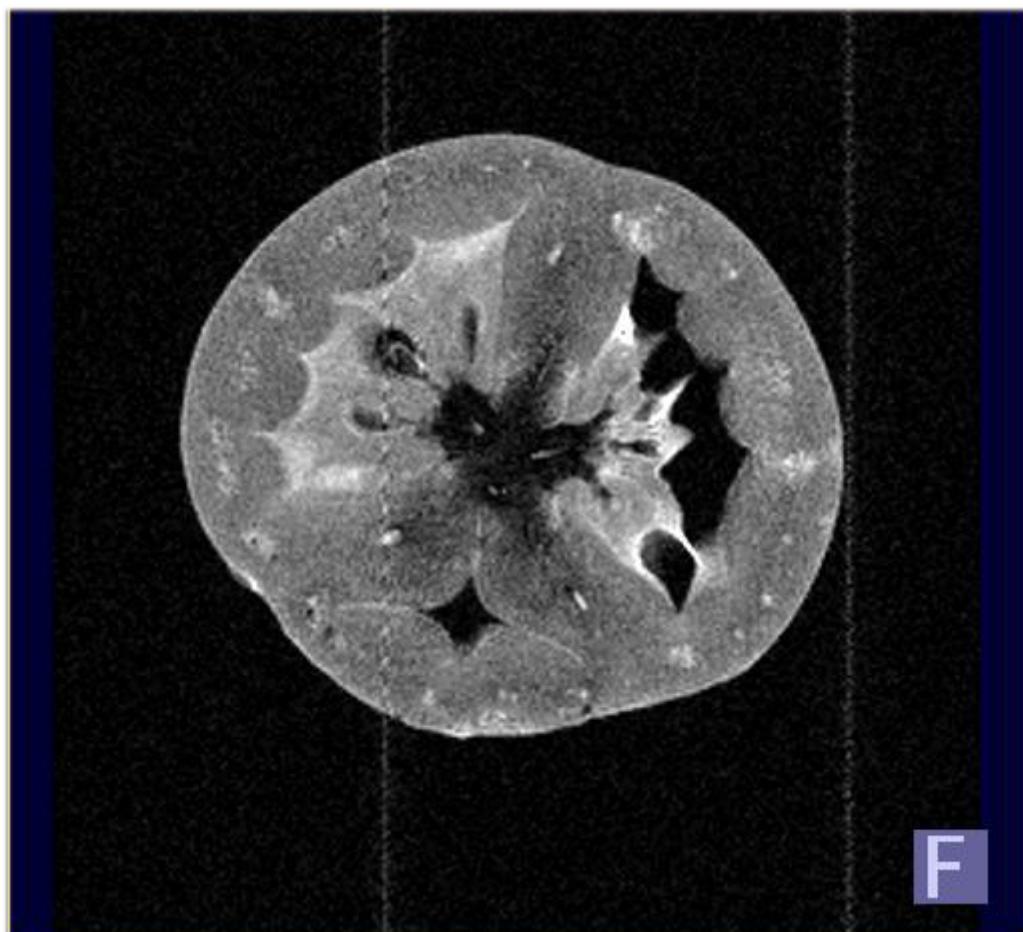


Figure 2.114: **Cherry tomato.** Dotted line artifact in phase encoding direction by RF interferences.

Tips

- Close the door of the magnet room if a Faraday cage is installed.
- Close the door of the CCM and use cover of the AutoPac table if no Faraday cage is installed.
- Check RF screening of the magnet room or CCM door.
- Switch off electronic equipment used within the RF shielded environment.
- Avoid conducting wires laid into the magnet that serve as antennas for RF (for example ECG electrodes).
- Do not penetrate the RF shielded room with unfiltered conducting wires.

Parallel Imaging

Parallel imaging is based on deconvolution of folded images. If too high acceleration factors are selected, fold in artifacts arise.

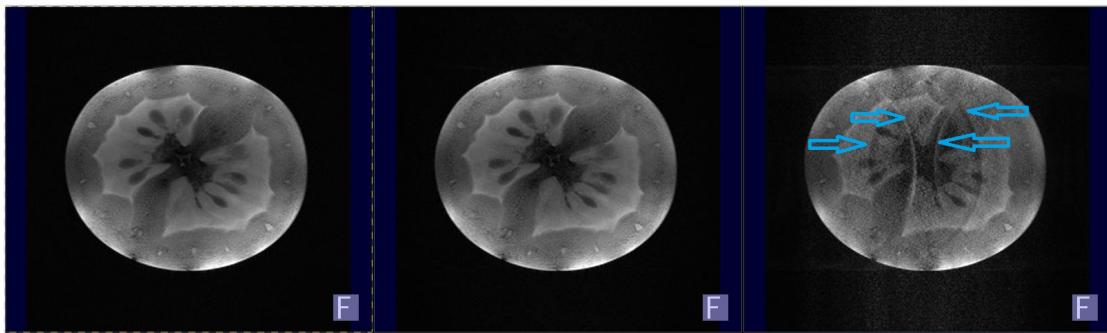


Figure 2.115: **Cherry tomato**, 8-channel array coil. **Left:** Parallel imaging with encoding acceleration factor 2 in left right direction. **Middle:** Encoding acceleration factor 3. **Right:** Encoding acceleration factor 5. At factor 5, fold in artifacts and noise become prominent.

Tips

- Reduce the acceleration factor of the encoding in phase direction
- Use the phase encoding direction along array elements (try swapping for a change)

Gradient Linearity

Dimensions of objects are not shown correctly in areas where the magnetic field gradients become non-linear.

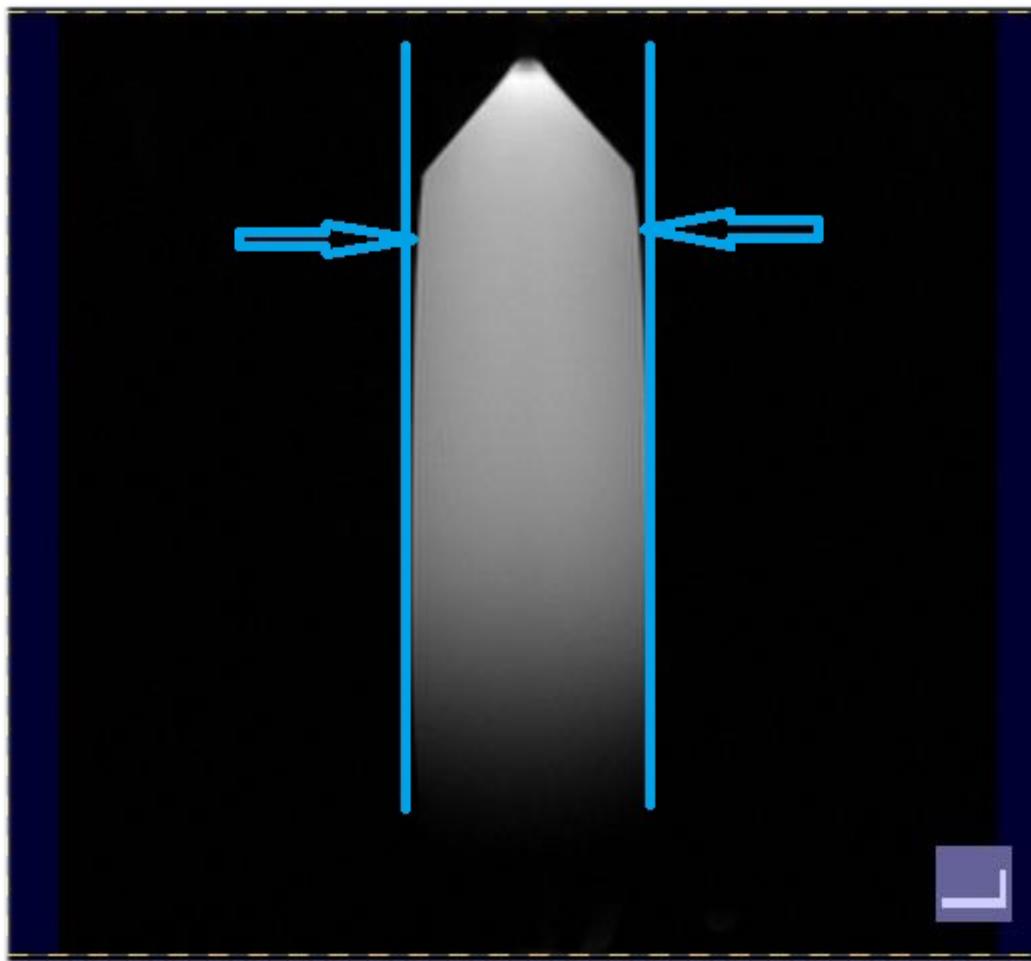


Figure 2.116: The straight phantom is not shown correctly in the non-linear gradient field.

Tips

- Always measure in the magnet and gradient center
- Check gradient linearity specification in the Technical Documentation
- Do not use RF coils that detect signals from areas where the magnetic field gradients are not correctly present any more (fold in artifacts arise that are sometimes referred to as "third arm artifact").

Halo Artifact

Intensity is seen as bright area (Halo) circularly around the object due to a too high Receiver Gain. Typically, a smeared and cloudy looking overlay on the object and the noise regions is seen in both, readout and phase encoding direction.

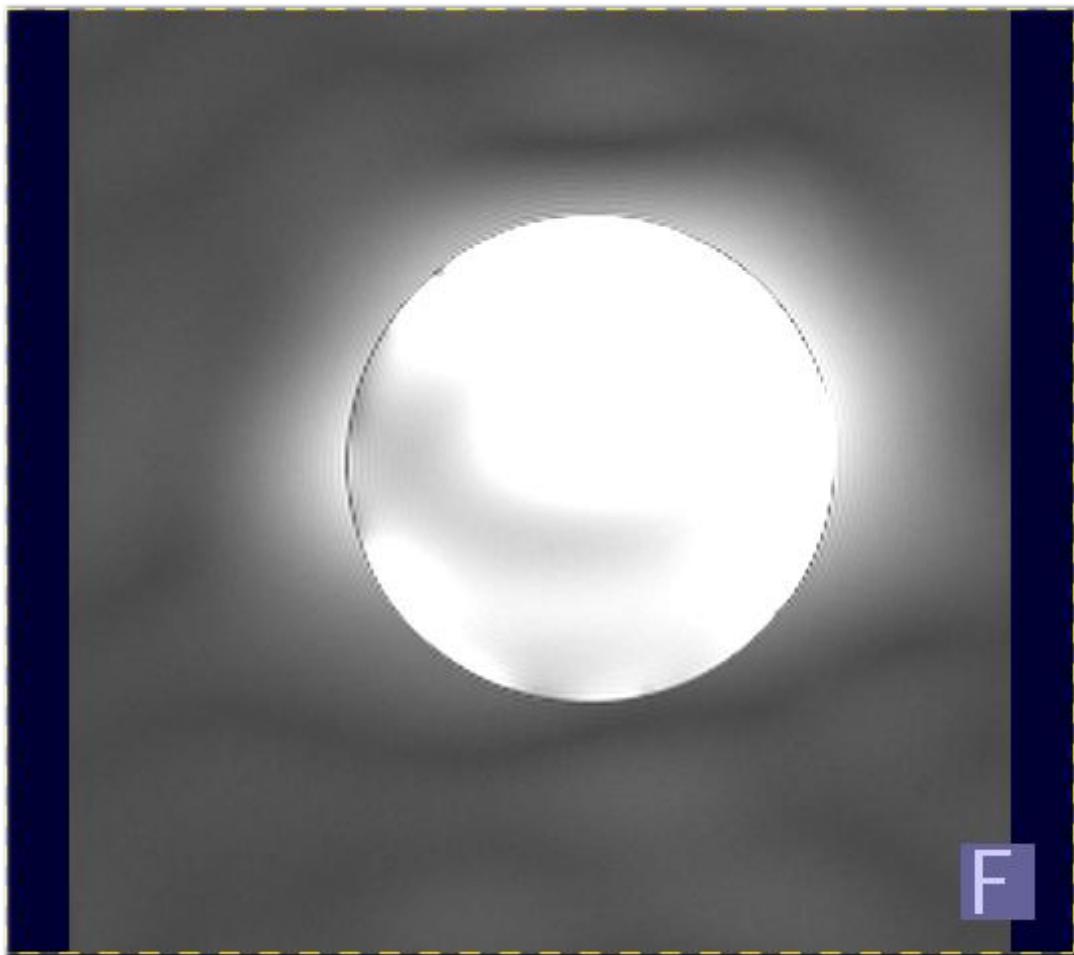


Figure 2.117: Halo artifact



- Reduce the Receiver Gain

3 Programming & Administration Manual

3.1 Method Programming

3.1.1 ParaVision Methods (PVM)

Methods are programmable components of ParaVision providing a user-friendly interface to acquisition and reconstruction processes. As described in previous chapters, acquisition and reconstruction are controlled by a pulse program and by numerous “base-level” parameters belonging mainly to ACQP and RECO groups. In principle, it is possible to set up an experiment by editing these parameters directly. On the other hand, one usually prefers to specify the measurement in terms of “high level” parameters which may not have direct representation in ACQP or RECO. For example, it is more convenient to specify the Repetition Time than to set delays used in the pulse program. The mechanism linking the high-level requests with the base-level parameters is provided by the methods. When you enter Repetition Time = 50 ms in the Scan Editor, it is the currently active method which checks if this value is allowed and calculates the corresponding delays. Similarly, when you graphically manipulate the field of view in the Geometry Editor, the active method ensures you do not go below the minimum and calculates the required gradient amplitudes. In general, the role of a method is to:

- provide high-level parameters for experiment description,
- give parameters initial values,
- decide which parameters should be visible, editable and saved in protocol files,
- respond to loading a protocol,
- respond to changes of parameters made in the Scan or Geometry Editor,
- check if the new parameter values are allowed, and if all parameters are compatible with each other,
- notify the user about implicit parameter changes,
- derive base-level parameters from high-level parameters.

Several methods developed by BRUKER-BioSpin MRI come with the ParaVision release. Users may easily program, import or export their own methods.

3.1.1.1 Binary Files

Methods available on the system can be found in one of the special protocol locations for AnyObject/AnyRegion:

BrukerMethods – methods provided with the system

UserMethods – methods added by the user. Note that each user (login) has his/her set of added methods. Making a method available to other users requires sharing (see Chapter [Sharing and Exporting \[▶ 589\]](#)).

“Protocols” found in these locations have the same names as the underlying methods. When one of such protocols is loaded to the scan list, parameters are not read from a file, as it happens with ordinary protocols. Instead, the method is loaded and initialized as programmed (see Chapter [Initialization \[▶ 594\]](#)).

Each method has its binary file with extension `.so`, created during compilation. Bruker method binaries can be found on disk in the `prog/parx/methods/` directory. User method binaries are saved in `prog/curd़ir/<user>/ParaVision/methods/`. Additionally, each method contains an xml file placed in the same directory, and a pulse program file placed in `exp/stan/nmr/lists/pp` (for `BrukerMethods`) or `prog/curd़ir/<user>/ParaVision/exp/lists/pp` (for `UserMethods`).

3.1.1.2 Source Code

PVM are programmed in C language. Most Bruker methods are distributed with the source code, which can be found in the **Workspace Explorer** under the **Method Development/Bruker Methods** node. Source code of user methods appears under **User Methods (<user>)**. Only methods of the currently logged user can be accessed. On the disk, each method's code is saved in a separate directory, named as the method itself, placed in `prog/parx/src` for Bruker methods, or in `prog/curd़ir/<user>/ParaVision/methods/src` for user methods.

3.1.1.3 Copying a Method

A method can be copied by RMB-clicking on the source-method name in the **Workspace Explorer** and selecting the **Copy** entry of the appearing menu. The name of the new method has to be entered in a subsequent dialog window followed by a list of the compilation options. When these options are left as proposed, the new user method will be compiled and installed automatically. User methods names must start with a lowercase letter to avoid conflicts with Bruker methods.

3.1.1.4 Editing

The **Workspace Explorer** allows “expanding” each method's directory to see all its files. Double-clicking on a file opens it in an embedded editor. Of course, it is possible to use any text editor directly in the method directory; however, it is important to save all modified files before compiling. The embedded editor saves files automatically when the compilation is started.

3.1.1.5 Compiling

A method is compiled (its binary file is generated from the source code) by RMB-clicking on its name in the **Workspace Explorer** and selecting **Build/Install**. In a dialog window that follows, one can select necessary compilation options. Leaving all options active is correct in all cases. To save time (several seconds) when the code modification did not involve function interfaces and no new files were added, the options **clean**, **cproto**, **depend** can be deselected.

Compiler messages, including the list of errors with corresponding file names and line numbers appear in a dedicated tab of the **Output** window. After successful compilation the method is immediately available for use. However, if a scan containing this method is already open in the Scan Editor, it has to be closed and opened again before parameter editing or scanning.

Users who prefer editing source files with an editor of their choice may find it practical to compile the method by the following shell command in the method's directory:

```
make clean cproto depend install installppg
```

or with some options omitted. Method compilation requires the PVM Development License.

3.1.1.6 Sharing and Exporting

Per default, methods are available only for the user who has programmed them. To make a method available for others, one has to **Share** it (RMB click on the method name in the **Workspace Explorer**). This creates an archive file of the method and places it in the share directory. Depending on the selected option the archive will or will not contain the source code. The user willing to use or edit the method has to **Import** it from the share directory (RMB click on **User Methods** in the **Workspace Explorer**).

To export a method to a different system (or a different ParaVision installation), the archive file has to be transferred between the corresponding share directories. On the new system, the method has to be imported as described above.

3.1.2 Programming Basics

The following sections explain basic elements of method programming such as parameter definitions, relations, and the group handling. It is recommended to try them on a copy of the BRUKER method `gre`, which is a simplified version of gradient echo MRI developed specially for training purpose.

3.1.2.1 Organization of the Code

The method source code is written in the C language with a few extensions (e.g. the syntax of parameter definition) and is divided into several files, all contained in one directory. Their role is explained here based on the example of `gre`.

File	Purpose
Makefile	Recipes for the compilation
<code>gre.c</code>	A glue file, always bearing the method's name, needs no modification
<code>gre.xml</code>	Description of the Editor Cards
<code>method.h</code>	Link to necessary header files. Identical for all methods, needs no modification.
<code>relProtos.h</code>	Link to function prototypes. Identical for all methods, needs no modification.
<code>parsTypes.h</code>	User defined parameter types (e.g. enumerations)
<code>parsDefintion.h</code>	Definitions of parameters
<code>parsLayout.h</code>	Definition of the MethodClass: defines the contents of a protocol, MethodRecoGroup: list of method-specific reconstruction parameters, and conflict parameters.
<code>callbackDefs.h</code>	Redirection of global (predefined) parameter relations
<code>initMeth.c</code>	Code of the <code>initMeth</code> function (required)
<code>loadMeth.c</code>	Code of the <code>loadMeth</code> function (required)
<code>parsRelations.c</code>	Parameter relations
<code>backbone.c</code>	backbone (function controlling interdependencies of parameters) and auxiliary functions

BaseLevelRelations.c	Functions for setting ACQP parameters
RecoRelations.c	Functions for setting RECO parameters

An experienced user may change the organization of source code. In particular, it is possible to add more C files if necessary.

3.1.2.2 Adapting the Makefile

The `Makefile` contains several important method specific definitions which are automatically adapted when the method is created by copying in the **Workspace Explorer**. A change of the `Makefile` is thus needed only in rare cases, e.g., when a new C file is added. The relevant definitions are:

DISKUNIT = <PvInstDir>	ParaVision directory
OVERLAY = gre	Name of the method; must agree with the name of the <code><method>.c</code> file
METHODS_DIR = prog/curdir/ <user>/ParaVision/methods/	Target directory for the binary method file
SRCDIR = ./	Source directory of this method
RELOBJS = \ initMeth\$(OBJEXT) \ loadMeth\$(OBJEXT) \ (...)	List of all .c files with the extensions replaced by <code>\$(OBJEXT)</code> , printed in one line, or separated by <code>\<new-line></code> followed by <code><tab></code>
PULPROG = none	Standard setting (<code>none</code>) for methods with a separate pulse program (see Chapter Embedding the Pulse Program in the Method [▶ 590]). In case the pulse program should be included into the method binary, the pulse program name (e.g. <code>gre.ppg</code>) should be specified after the '=' character. In this case the pulse program must be present in the method source directory.
PULPROG_INC =	Standard setting (empty) for methods with a separate pulse program. In case the pulse program should be included into the method binary, the path to all include files of the pulse program should be specified. In most cases this is the path specified by the following setting: <code>PULPROG_INC = \$(PARX_PP_STD_INCL)</code> to make use of the modules.
PARCOMP_DEBUG =	Standard setting (empty) does not allow debugging. The macro <code>DB_MSG</code> does not produce any output and it is not possible to use a debugger. Setting <code>PARCOMP_DEBUG = -g</code> switches on debugging and activates <code>DB_MSG</code> .

3.1.2.3 Embedding the Pulse Program in the Method

By default, each user method has a pulse program placed in the `prog/curdir/<user>/ParaVision/exp/lists/pp` directory and one of the method's actions is to set the `PULPROG` parameter of the `ACQP` class to the name of the pulse program (this usually

happens in `BaseLevelRelations.c`). However, it is also possible to incorporate the pulse program in the binary file of the method. This has the advantage of the method being represented by a single file. As a result, the method's functionality cannot be changed without access to the source code. To embed the pulse program in the method's binary file, two additional definitions are necessary in the `Makefile` as shown in the table above. Additionally, the method should set the parameter `PULPROG` to `ParaVision.ppg`.

3.1.2.4 Defining New Parameters

Parameters can be defined in the `parsDefinition.h` file. All parameters defined in the method code are local which means they exist only while the given method is active. By contrast, the parameters predefined in the internal PVM code are global, i.e. visible for all PVM methods. A typical parameter definition is:

```
double parameter
{
    display_name "Gradient value";
    format "%.2f";
    units "mT/m";
    relations GradValRelations;
} GradVal;
```

The first word (here: `double`) determines the parameter's type. Allowed types are `int`, `double`, `char`, `YesNo`, `void` and predefined types based on `struct` or `enum`. The `void` allows generation of push-buttons in the Scan Editor tabs (corresponding parameter do not have value). The last word (`GradVal`) is the parameter identifier, which can be used in the method code just like a C variable. Identifiers can be shown in the Scan Editor instead of the display names by holding the mouse pointer over the parameter value. Entries listed within `{ }` are optional and define parameter attributes. The word in the `relations` entry (here, `GradValRelations`) specifies a function which must be written somewhere in the method code (typically in `parsRelations.c`). This function is bound to the parameter and will be called its "relations". It will be executed by ParaVision every time the user changes the value of this parameter in the editor. Parameter relations are the basic building block of ParaVision methods. The full list of parameter attributes is:

<code>display_name "string";</code>	Name displayed on the Editor Card
<code>short_description "string";</code>	Text displayed in the "tool tip"
<code>format "%.3f";</code>	Format string as in <code>printf</code> function
<code>minimum <value>;</code> <code>minimum <value></code> <code> outofrange origval;</code>	Minimum value. When a lower value is entered, the editor returns to the original value.
<code>minimum <value></code> <code> outofrange nearestval;</code>	Minimum value. When a lower value is entered, the editor sets it to minimum.
<code>maximum <value>;</code> <code>maximum <value></code> <code> outofrange origval;</code>	Maximum value. When a higher value is entered, the editor returns to the original value.
<code>maximum <value></code> <code> outofrange nearestval;</code>	Maximum value. When a higher value is entered, the editor sets it to maximum.

widget slider;	A slider is available to modify the parameter value
units "string";	Definition of units presented in the editor
store true/false;	Parameter will (not) be stored in the method file
visible true/false;	Parameter will (not) be visible in the editor
editable true/false;	Parameter will (not) be editable
relations <function>;	Name of the relations function
style inline_array;	Elements displayed in one line
maxdim once <max_size>	Size limit for dynamic arrays

A parameter can be declared as an array by adding [<size>] after its identifier. The following is a definition of a 16-element character array:

```
char parameter
{
    display name "Number of iterations";
} Iterations[16];
```

Arrays of type `char` are used for string parameters. Multi-dimensional arrays can be declared by specifying more than one pair of [] brackets. Array parameters for which the [] brackets are empty can be re-dimensioned (re-allocated) in the method code using the `PARX_change_dims` function (see Chapter [Parx Library \[▶ 595\]](#)). The following shows a definition of a 2-dimensional integer array and the way how it can be allocated for 16 x 8 elements:

```
int parameter
{
    display name "Correction matrix";
} Corrections[][];

/* somewhere in the method code: */
PARX_change_dims("Corrections", 16, 8);
Corrections[15][0] = 77;
```

Please note: The maximum array size is 1e6 per dimension.

3.1.2.5 Defining a New Type

In addition to standard C types (`double`, `int`, `char`) parameters may be of user-defined type. It is possible to define structure types and enumerations. Such definitions are made in the file `parsTypes.h`.

Examples:

```
/* ----- parsTypes.h -----*/
typedef enum
{
    Wait,
    Ignore,
    Repeat
} DECISION;

typedef struct
```

```

{
    double duration;
    double amplitude;
} SPOILER;

/* ----- parsDefinition.h -----*/
DECISION parameter
{
    display_name "Your choice";
    relations UserChoice;
} UserDecision;

SPOILER parameter
{
    display_name "Spoiler on read channel";
    relations ReadSpoilRels;
} ReadSpoiler;

```

Formats and units for user defined struct parameter types may be specified for each struct member separately. This should be done in `parsDefinition.h` after the struct parameter definition:

```

format SPOILER
{
    duration "%.3f";
    amplitude "%.3f";
};

units SPOILER
{
    duration "ms";
    amplitude "mT/m";
};

```

3.1.2.6 Parameter Layout and Storage

Parameters declared in `parsDefinitions.h` are not automatically visible in the Scan Editor, although one can access them in the Single Parameter Editor. To make parameters visible the file `<method name>.xml` has to be modified. This file contains definitions of Editor Cards and parameter layout on each card.

Per default, new parameters will also not be written to disk, which means their values will be lost when a scan is closed, or when a protocol is saved and restored. To be taken into account in the disk storage, parameter names must be included in the definition of the parclass `MethodClass`, in the file `parsLayout.h` (a parclass is simply a group of parameters). For historical reasons, in many methods `MethodClass` has a multi-level structure (with parclasses included in each other). With the new Scan Editor introduced with ParaVision 6.0 ordering of parameters in `MethodClass` has no importance, except for the parameter `Method`, which must be listed first.

Visibility and storage of parameters can further be controlled by library functions (see Chapter [Parx Library \[595\]](#)) or by parameter attributes during parameter definition (see Chapter [Defining New Parameters \[591\]](#)).

The `MethodClass` should also include all global PVM parameter and parclasses used by the method. You can find the list of all global PVM parameters in

`<PvInstDir>/prog/include/proto/pvm_extern.h`.

3.1.2.7 Initialization

Every method must contain two functions, `initMeth()` and `loadMeth()` which are called by ParaVision when a scan is selected or created, or when a protocol is loaded. These functions are defined in files `initMeth.c` and `loadMeth.c`, respectively. Their role is to assure that every new scan has valid initial parameter values and that values loaded from protocols are also valid. The recommended sequence of these functions is as follows:

- `loadMeth` calls `initMeth`.
- `initMeth` checks whether all parameters used by the method have values (see below). If not, initial values are assigned.
- `initMeth` calls initialization functions for all parameter groups used by the method (see Chapter [Using Parameter Groups \[▶ 596\]](#)).
- `initMeth` calls the method's `backbone` function (see below).

3.1.2.8 Version Requirement

A very important duty of the `initMeth` function is to require a proper version of PVM toolbox libraries. This assures a correct functioning of the method with later versions of the software. The version requirement lets old methods ask PVM to "behave in the old way". All methods included in ParaVision 6.0 make the following requirement:

```
PTB_VersionRequirement( Yes, 20100101, "" );
```

3.1.2.9 Parameter Relations

As mentioned above, all functions declared in the parameter definitions as "relations" must be defined in the method code (e.g. in `parsRelations.c`). The relations must be `void` functions with no arguments. The recommended action of relations is to

- check if the new parameter value is allowed,
- call the method's `backbone()`.

The `backbone` function (this name is not obligatory) is thus called by all parameters used by the method. Such converging arrangement of relations guarantees that whichever parameter is edited by the user, all parameters are set to a consistent state. The `backbone` must be written in the method code, typically in `backbone.c`. Its action consists of:

- solving inter-dependencies of all parameters,
- constraining all parameters to their allowed limits,
- updating all parameter groups (see Chapter [Using Parameter Groups \[▶ 596\]](#)),
- deriving base-level parameters (ACQP, RECO) from local and global PVM parameters. This is typically done by calling `SetBaseLevelParam` and `SetRecoParam`, functions defined in `BaseLevelRelations.c` and `RecoRelations.c`, respectively.

3.1.2.10 Toolbox Functions

ParaVision is delivered with a rich function toolbox contained in the following libraries:

library	Prefix	Applications
PvCfgTools	CFG_	Deriving information about system configuration
PvMrTools	MRT_	Utilities related to MR physics
PvPvmTools	PTB_	Communication with internal PVM mechanisms

PvSeqTools	STB_	“Sequence tools” – all group Initializers and Updaters (see below) belong to this library
PvGeoTools	GTB_	Geometry tools
PvAcqTools	ATB_	Functions for setting ACQP parameters
PvUtilTools	UT_	General utilities, not related to PVM or MR physics, e.g. for matrix manipulation

Documentation of the toolbox functions is available in the html format. Using a web browser, open the file [Method Programming](#) and follow the links.

3.1.2.11 Parx Library

In addition to the PVM toolbox, several functions from the PARX library may be used in methods for testing and setting of parameter attributes. These are:

- `void PARX_change_dims(const char *name, int size1, ...)`

This function re-dimensions the array parameter `name` to new sizes given in the `size1, ...` argument list. The list size must match the number of parameter's dimensions and none of its elements may be smaller than 1. The first element of the size list affects the dimension represented by the first bracket pair in the parameter definition, and so on. The re-dimensioning preserves the existing array values within the new size. When the size increases, the missing values are zero-filled.

- `unsigned int PARX_get_dim(const char *name, int dim)`

Returns the current size of the dimension `dim` in the array parameter `name`. Value `dim=1` means the first bracket pair in the parameter definition, value 2 the second, and so on.

- `void PARX_sprintf(const char *format, ...)`

Prints a string in the message log window. The argument list is identical to that of `printf`.

- `void ParxRelsParRelations(const char *name,`

`YesNo ForceDefault)`

causes execution of the relations of parameter `name`. If `ForceDefault` is `Yes`, the default relations (those declared in the parameter definition) will be called disregarding a possible redirection (see Chapter [Using Global Parameters ▶ 596](#)). This function is essentially only used with base level parameters. Using it with most PVM parameters may lead to an endless recursion.

- `int ParxRelsParHasValue(const char *name)`

returns `0` if the parameter `name` has not yet been assigned a value, or `1` otherwise. Used mainly in method initialization.

- `void ParxRelsMakeEditable (const char *name)`

`void ParxRelsMakeNonEditable (const char *name)`

With the call of these functions one decides if the value of parameter `name` may be changed in the Scan Editor.

- `void ParxRelsShowInEditor(const char * name)`

`void ParxRelsHideInEditor(const char * name)`

These functions control the visibility of parameters in the editor. By default, all new parameters are visible in the editor if they are included in the layout (see Chapter [Parameter Layout and Storage ▶ 593](#)).

- `void ParxRelsShowInFile(const char * name)`

```
void ParxRelsHideInFile(const char * name)
```

These functions decide if the parameter `name` should be stored in the `method` file and in a protocol. By default, all new parameters are visible in files if they are members of `MethodClass` (see Chapter [Parameter Layout and Storage \[▶ 593\]](#)).

- `int ParxRelsParIsEditable(const char * name)`
- `int ParxRelsVisibleForEdit(const char * name)`
- `int ParxRelsVisibleInFile(const char * name)`

These functions return 1 if the respective attributes (editability, visibility in editor, visibility in file) of the named parameter are set, or zero otherwise.

3.1.2.12 Using Global Parameters

As mentioned in Chapter [Parameter Layout and Storage \[▶ 593\]](#), a method can include pre-defined, global PVM parameters in its layout. One can also assign local relations to such parameters. The local relations will replace the default relations of the global parameters; therefore, we call these assignments “redirections”. Redirections are programmed in the file `callbackDefs.h` by statements such as:

```
relations PVM_NAverages LocalNArelations;
```

where the last word is the name of a function defined in the method’s code.

Global parameters may be used to avoid re-defining typical MRI features such as the echo time (`PVM_EchoTime`) or number of repetitions (`PVM_NRepetitions`), and to link global parameter groups with the method (see Chapter [Using Parameter Groups \[▶ 596\]](#)).

Additionally, redirections allow a method to react to various events taking place in ParaVision, such as the start of a scan, end of an adjustment etc. Such events call default relations of special “function” parameters, which may be redirected to local functions.

Event	Function parameter
Change on the System Card (e.g. different coil operation mode)	<code>PVM_SysConfigHandler</code>
Start of the scan	<code>PVM_AcqScanHandler</code>
Start of the reconstruction	<code>RecoUserUpdate</code>
End of reconstruction (deriving Visu parameters)	<code>VisuDerivePars</code>
Start of an adjustment	<code>PVM_AdjHandler</code>
End of an adjustment	<code>PVM_AdjResultHandler</code>

3.1.2.13 Using Parameter Groups

There are quite a lot of global parameters one might want to link with the method code, for example all those used by the Geometry Editor. Redirecting them one by one would not be practical. To make the task easier, global parameters have been gathered in groups of common functionality. It is possible to link a whole group to a method by a single redirection. In addition, toolbox functions are provided for easy handling of entire groups. The key element of the group handling mechanism is the possibility to build chains of relations: the relations of parameter A can make a call of the relations of B (using a `Parx` function, as we have seen above). The mechanism of group handling is as follows:

ParaVision code:

- All members of a group have simple default relations consisting of
 - a trivial range checking (independent of other parameters),
 - setting a request (telling the PVM “I’ve been edited”; full description of request handling is given further),
 - a call of the relations of the Group Handler.
- The Group Handler is a dummy parameter with no value and empty relations. It serves as a link with the method code.

Method code:

- The relations of the Group Handler are redirected to local code (e.g. the backbone).
- In the backbone, a toolbox function `Group Updater` is called to resolve dependencies within the group. If some information is needed for that, it is passed via function arguments. The updater knows which member was last edited (thanks to the request set in default relations) and adjusts its action accordingly.
- In `initMeth`, a toolbox function `Group Initializer` is called to assure that all group members have allowed initial values.

Note that the global parameters remain completely independent of each other until the group redirection is done to the `backbone` and the updater is called there. In this way, the internal code has been reduced to the very minimum. Everything that happens with the global parameters is under the method’s control.

The following global parameter groups are defined:

Group (parclass)	ImageGeometry
Members	Parameters describing image FOV, slice thickness, resolution and orientation of slice packages, numbers of slices etc. Most of them can be set graphically in the Geometry Editor.
Handler	<code>PVM_ImageGeometryHandler</code>
Initializer	<code>STB_InitImageGeometry</code>
Updater	<code>STB_UpdateImageGeometry</code>

Group (parclass)	Nuclei
Members	Nuclei names and enumerations, gradient calibration constant, frequency parameters
Handler	<code>PVM_NucleiHandler</code>
Initializer	<code>STB_InitNuclei</code>
Updater	<code>STB_UpdateNuclei</code>

Group (parclass)	Spectroscopy
Members	Parameters describing spectral dimensionality, resolution, and matrix size.
Handler	PVM_SpecHandler
Initializer	STB_InitSpectroscopy
Updater	STB_UpdateSpectroscopy

Group (parclass)	Voxel_Geometry
Members	Parameters describing voxel geometry in localised spectroscopy: number of voxels, sizes, positions and angles.
Handler	PVM_VoxCallBack
Initializer	STB_InitVoxelGeometry
Updater	STB_UpdateVoxelGeometry

Parameters controlling the preparation modules, EPI acquisition, diffusion weighting and other functionalities are also implemented as PVM groups. They are described in the online documentation.

Parameter groups (parclasses) are defined in the file `prog/include/methodClassDefs.h`. Inspecting this file allows finding out which parameters belong to each group. Do not change this file, since modifications will affect all Bruker and User methods.

3.1.2.14 Recommended Method Structure

A method is composed of two parts: one defined in the internal ParaVision code and one defined in the user code. As explained earlier, the internal part is reduced to a minimum. It consists of definitions of global parameters and their very simple default relations. At this level all parameters remain independent. In the method part, it is first decided which of the global parameters should have their relations redirected to some local code. Such redirections can be made for single parameters and for group handlers. Additionally, local parameters and their relations are defined in the method code, as well as the `loadMeth` and the `initMeth` functions. All local relations as well as `initMeth` call the `backbone` routine, in which all dependencies between parameters are programmed. Toolbox functions may be used for this purpose, in particular the group updaters. Finally, at the end of `backbone`, local functions are called to set the ACQP and RECO parameters (`SetBaseLevelParam()` and `SetRecoParam()`). Figure [Method structure \[▶ 599\]](#) shows this arrangement together with corresponding file names.

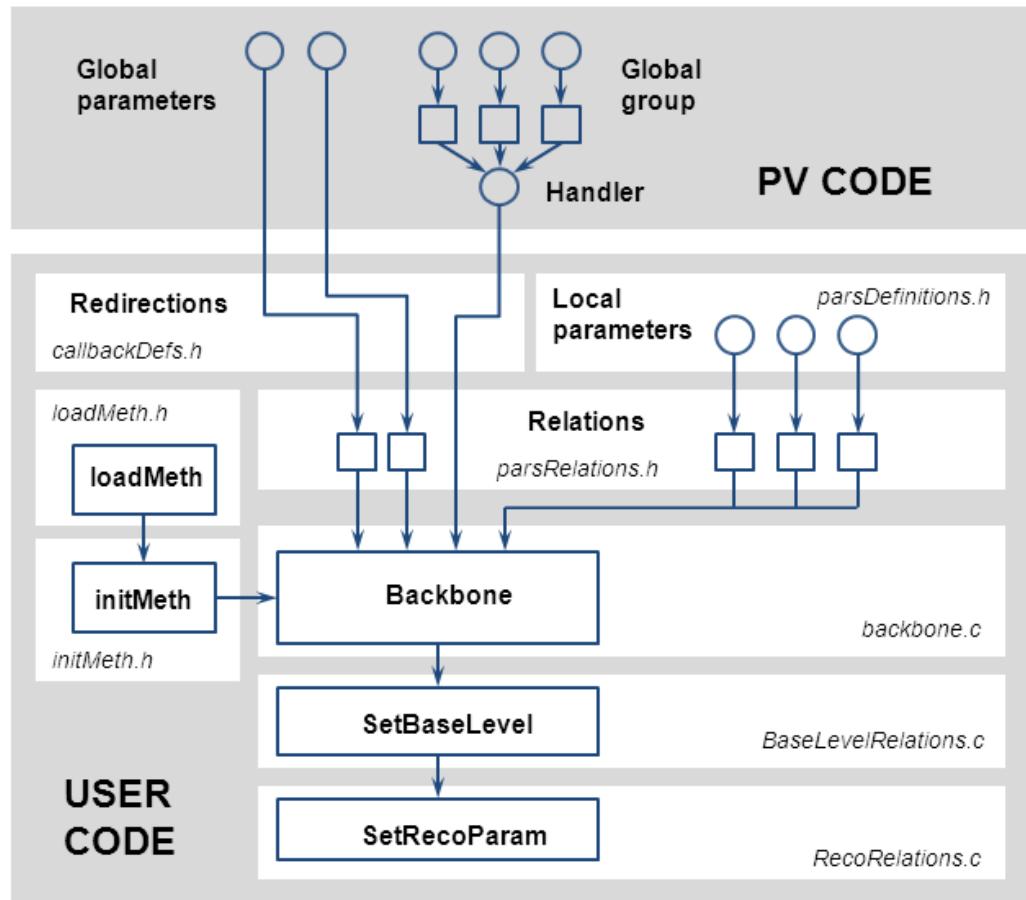


Figure 3.1: Method structure

3.1.3 Selected Tasks

This chapter presents ways to implement typical tasks of a method using parameter groups and toolboxes provided in ParaVision.

3.1.3.1 Nuclei and Basic Frequency

Depending on the connected RF coil configuration and the selected operation mode the method should set the proper nuclei for all transmission channels and calculate the corresponding basic frequencies (allowing a user-defined offset). This functionality is provided by the **Nuclei** group, which contains parameters for the nuclei names, frequencies and offsets (in Hz and ppm) for all channels. In addition to including this group into `MethodClass`, redirecting `PVM_NucleiHandler` to the `backbone` routine, calling `STB_InitNuclei()` in `initMeth()` and `STB_UpdateNuclei()` in the `backbone()`, the method should propagate the value of the calculated working frequencies `PVM_FrqWork[0/1]` to the base level frequency parameters `BF1` and `BF2`. In order to allow the group updater to react to changes of the operation mode, `PVM_SysConfigHandler` must be redirected to `backbone`. The frequency selection mechanism based on `ACQ_BF` used in previous software versions should no longer be used (starting from PV 6.0).

3.1.3.2 Bandwidth

Methods must constrain the signal bandwidth depending on the hardware version and on several system parameters such as the quadrature detection mode or the digital filter selection. This quite complex dependency is easily solved using the **DigitizerPars** parameter group, which includes all parameters affecting the bandwidth as well as a switch deciding whether the bandwidth-related parameters should be selected automatically. Including this group in a method requires

- adding `DigitizerPars` to `MethodClass` in `parsLayout.h`,
- calling `STB_InitDigPars()` in `initMeth()`,
- redirecting the `PVM_DigHandler` to `backbone()`,
- updating the group in the backbone by calling `STB_UpdateDigPars()`,
- and setting the base-level parameters controlling the bandwidth and digitizer (`SW_h`, `DIGMOD`, `DSPFIRM` and `AQ_mod`) by calling `ATB_SetDigPars()` in `BaseLevelRelations()`.

Two of the members of the `DigitizerPars` group may be used to calculate pulse program delays. These are:

`PVM_DigEndDelMin` – Minimum delay between the end of scan and the `ADC_END` command in the pulse program [ms]

`PVM_DigEndDelOpt` – Optimum delay between the end of scan and the `ADC_END` delay in the pulse program. Using this delay guarantees that the group delay of the digital filters is correctly compensated (which may not be the case if only `PVM_DigEndDelMin` is used).

3.1.3.3 RF Pulses

The PVM toolbox contains a mechanism for a convenient description of RF pulses in a method. It covers all important features of an RF pulse, like bandwidth, duration and flip angle, handles their interdependence and allows automatic calculation of optimized pulse shapes. The necessary programming steps for each pulse are:

- Defining a parameter of the type `PVM_RF_PULSE` to hold the structure describing an RF pulse
- Optionally, defining a `double[]` parameter to hold the calculated pulse shape
- Optionally, defining a parameter of the type `PVM_PULSE_LIST`, which let the user choose between existing pulse shapes (without it, shape names have to be typed in the field name of the pulse structure)
- Optionally, defining a parameter of the type `PVM_RF_PULSE_AMP_TYPE`, which is a structure allowing manual adjustments of pulse power on the Setup Card.
- Initializing all defined parameters with a single call of `STB_InitRfPulse`. This function requires the names of involved parameters in its arguments list.
- Updating the pulse structure with `STB_UpdateRfpulse`. This function “knows” that the pulse is linked to its optional auxiliary parameters (list choice, shape array, amplitude correction) and keeps consistency between them depending on which parameter (or struct field) has last been edited. It also calculates automatic shapes when the user selects this option and the shape array is defined.
- Transferring the pulse structure to the base level arrays `P[]` and `ACQ_RfShape[]`, which is used in the pulse program `pN:spN` command, with a call of `ACQ_SetRfPulse`. On a system with parallel transmission capability this function sets phase- and amplitude corrections for all TX channels based on the result of a dedicated adjustment.

3.1.3.4 Phase Encoding

PVM provide a mechanism for controlling the phase encoding steps in MRI methods. It can handle all common encoding schemes including parallel imaging with or without reference lines, linear and centric k-space sampling, block-wise and interleaved segmentation, partial Fourier encoding and zero filling. The mechanism is implemented with a dedicated parameter group called `Encoding`. It lets the user specify the required encoding scheme and calculates the corresponding acquisition matrix size as well as the table of the phase encoding steps.

Like any other parameter group, `Encoding` must be included in the definition of `MethodClass` in the file `parsLayout.h` to become part of the protocol. In the `callbackDefs.h` file the group handler `PVM_EncodingHandler` must be directed to the method's backbone. The group must be initialized with `STB_InitEncoding` and updated with `STB_UpdateEncoding`. After the update, parameters belonging to the group may be used for calculating further method features, e.g. the effective matrix size can be used to derive the total scan time, and the phase encoding order can be transferred to gradient tables.

3.1.3.5 Imaging Geometry

One of the most complex tasks of each MRI method is to derive gradient amplitudes and orientation, frequency offsets and other base-level parameters from the geometry of the scan (field of view, slice thickness and orientation, etc.) as defined in the Geometry Editor. In PVM this task can be easily realized using the `ImageGeometry` group, its handler (`PVM_ImageGeometryHandler`) and toolbox functions: `STB_InitImageGeometry` and `STB_UpdateImageGeometry`.

When the handler is redirected to the backbone, each action in the Geometry Editor (e.g. displacement or rotation of a slice package) and each change of a geometry parameter in the Scan Editor will result in a call of this function. Inside the backbone the call of the group updater guarantees that all geometry parameters are consistent: FOV agrees with image pixel size and resolution, slice spacing with the thickness and gap, and so on. Further, parameters controlling the slice offsets (`PVM_SPackArrSliceOffsets`) and orientation (`PVM_SPackArrSliceOrient`) agree with the graphical prescription in the Geometry Editor. These parameters can then be used to derive frequency lists and gradient amplitudes in the remaining backbone code.

3.1.3.6 Preparation Modules

A module is a section of a pulse program which can be included in any method's *.ppg-file to modify the image contrast or add a new functionality. Each module is accompanied by a group of PVM parameters and a couple of supporting toolbox functions. This arrangement makes it very easy to use modules in PVM programming.

Each module consists of

- a piece of pulse program which must be included in the method's *.ppg-file. This is achieved by either `#include <module-name>.mod` or by call of the corresponding subroutine `subr module-name()` (see Base Level Acquisition/Subroutines). An additional `#include<PrepModulesHead.mod>` is necessary at the beginning of the pulse program to introduce all definitions needed for the preparation modules.
- a parclass called `<module-name>_Parameters` which contains all parameters controlling the module. This parclass should be included by the method programmer in the `MethodClass` (in file `parsLayout.h`).

- a parameter called `PVM_<module-name>OnOff`, which should also be included in the `MethodClass`, and which allows the module to be switched on or off. This parameter together with the parclass members constitutes a group in the sense described in Chapter [Using Parameter Groups \[▶ 596\]](#).
- layout specifications for the Scan Editor, which should be included in the `<method>.xml` (together with the OnOff-Parameter) file. Typically, include files `<module short description>.xml` and `<module short description>Setup.xml` are provided in order to access certain module parameters via the Scan Editor.
- a group handler parameter called `PVM_<module-name>Handler` whose relations should be redirected to the method's backbone in `callbackDefs.h`. As with any PVM parameter group, the relations of this handler are called by the default relations of all group members.
- a toolbox function `STB_Init<module-name>Module()` which initializes the module parameters. It should be called in the `initMeth()` function of a method (file `initMeth.c`).
- a toolbox function `STB_Update<module-name>Module()` which makes an update of the module parameters. It should be used in method's backbone.
- a toolbox function `ATB_Set<module-name>Baselevel()` which sets all ACQP parameters used in `<module-name>.mod`. This function should be called at the end of `backbone()`, when all other ACQP parameters have been set.

Modules are independent of the rest of the method in which they are included. If an interaction with the method is necessary, all information is passed to the module via the arguments of its `Update` function. Therefore, the call of the `Update` can only be made when this information is ready. Each module contains a non-editable parameter specifying its duration. This parameter is calculated by the `Update` function and can be used in the method code for the repetition time calculation.

3.1.3.7 Diffusion Weighting

A special module is provided for the programming of diffusion-weighted imaging methods. The module allows experiments with freely programmable diffusion weighting strengths and directions and can be used e.g. for diffusion tensor measurements. The module incorporates a diffusion sensitizing gradient pulse pair separated by slice selective RF refocusing. The RF refocusing mode can be switched between spin echo, stimulated echo and double spin echo (in the latter, four diffusion gradient pulses are applied). The module parameters allow the user to specify a series of different diffusion experiments in terms of gradient strengths (or corresponding b-values) and directions. The module handling mechanism automatically calculates the effective b-matrices for each diffusion experiment. The effect of the refocusing slice selection gradient, spoilers (including ramps) and the cross-terms between them and the diffusion gradient pulses is taken into account in this calculation. For the validity of this calculation it is required that the method's own gradient pulses will be re-focused before the start of the module.

The use of all features of the diffusion module needs a special license represented by the feature `PVMDTI` in the license file. This applies to both Bruker methods and user methods containing this module.

From the application point of view, the module is described in Chapter [Diffusion Card \[▶ 241\]](#). Building the module into a user method requires following steps:

Pulse program

- The file `DwiHead.mod` has to be included before `INIT_DEVICES`. This introduces all definitions necessary for the module.
- A label, e.g. `DiffL` has to be given to the line in which the diffusion weighting loop begins.
- The subroutine `DwiInit()` has to be called before the start of the sequence.
- The subroutine `DwiPrep(ph1)` has to be called at the right position, typically between the excitation and the acquisition segments. This file contains the main part of the module (diffusion gradients and RF refocusing). The argument is the phase list used for the refocusing RF pulses.
- The slice selection frequency list used by the module (`DwF10`) has to be incremented at the same time as the frequency list for excitation.
- The subroutine `DwiLoop(DiffL)` has to be called at the point where the diffusion loop ends. This file contains diffusion gradient increments and a jump to the label given in the argument.

Method code

- The relations of the group handler parameter `PVM_DiffusionHandler` should be redirected to a local function in which the group is updated, typically to the backbone.
- The parclass `Diffusion` has to be included in the method layout (`parsLayout.h`).
- In method's xml file the include of `Diffusion.xml` should be used to make module parameters accessible in the Scan Editor.
- The diffusion group should be initialized in the `initMeth` function by calling `STB_InitDiffusionPreparation`.
- The group should be updated in the backbone by a call of `STB_UpdateDiffusionPreparation`.

3.1.3.8 VISU Parameter Handling

A reconstructed dataset is described by the VISU parameters (see Chapter [ParaVision Parameters](#), section D-2.4.11 VISU Parameter Group).

At the end of the reconstruction process the VISU parameters are automatically derived from the acquisition parameters. This default derivation may not be fully adapted to specific properties of a method. Therefore, it is possible to change the default derivation of VISU parameters in the method.

The calculation of VISU parameters is implemented as a relation of the parameter `VisuDerivePars`, which is called by the reconstruction process. It is possible to redirect this relation to a local function in `callbackDefs.h`:

```
relations VisuDerivePars deriveVisu;
```

Since this relation is called after the acquisition, the programmer must fulfill the following requirements in the implementation:

- The relations (`deriveVisu`) should not change any acquisition or method parameters. In particular, `backbone` should not be called.
- One should first call the default relation creating VISU parameters and then adapt them to the needs of the method.

For example, in FLASH the default derivation of the VISU parameters identifies the movie frame group as echo frame group. This can be modified with the following code:

```
#include "method.h"
#include "generated/VisuIds.h"

void deriveVisu(void)
{
    DB_MSG (( "Entered deriveVisu() "));

    /* Standard Visu Derivation */
    ParxRelsParRelations("VisuDerivePars", Yes);

    if (On == PVM_MovieOnOff)
        /* Change id of Echo loop to movie loop */
        PTB_VisuSetEchoLoopId(PV_IDL_CONSTANT(visuid_framegroup_MOVIE))
;

    DB_MSG (( "Leave deriveVisu() "));
}
```

The function `PTB_VisuSetEchoLoopId` changes the identifier of the echo loop to the identifier of the movie loop. All valid identifiers can be found in the file `<PvInstDir>/prog/include/generated/VisuIds.h`. The macro `PV_IDL_CONSTANT` adds the prefix `de_bruker_mri_generated_` to the name, e.g. `PV_IDL_CONSTANT(visuid_framegroup_MOVIE)` becomes `de_bruker_mri_generated_visuid_framegroup_MOVIE`. The available frame group identifiers have the prefix `de_bruker_mri_generated_visuid_framegroup` in the `VisuIds.h` file.

Further PVM toolbox functions exist for particular VISU-related tasks:

`PTB_VisuSetLoopId` - Changes the identifier of an arbitrary frame group/loop

`PTB_VisuSetEchoLoopId` - Changes the identifier of the echo frame group/loop

`PTB_VisuSetMovieLoopId` - Changes the identifier of the movie frame group/loop

`PTB_VisuSetLoopName` - Changes the name/comment of an arbitrary frame group/loop

`PTB_VisuSetEchoLoopName` - Changes the name/comment of the echo frame group/loop

`PTB_VisuSetMovieLoopName` - Changes the name/comment of the movie frame group/loop

`PTB_VisuSetLoopDependantParameter` - Sets a dependant parameter for a frame group

`PTB_VisuRemoveLoopDependantParameter` - Removes a dependant parameter for a frame group

`PTB_VisuInsertLoop` - Inserts a new frame group

`PTB_VisuDecreaseFGLen` - Decreases the length of a frame group, i.e. the group has lower elements

`PTB_VisuSetFGElementComment` - Sets the comment array for all elements of a frame group

3.1.4 Adjustment programming

Adjustments are special experiments that start automatically before the actual scan to optimize selected parameters. A mechanism exists that controls the order of necessary adjustments for each scan and keeps track of their results. Chapter [Adjustments \[▶ 218\]](#) describes how to configure the default list of adjustments for every study and every scan. Chapter [Using the Adjustment Platform \[▶ 65\]](#) describes the Adjustment Platform where single

adjustments can be started or repeated on demand and where the adjustment results can be viewed or edited. Additionally, every measuring method may request its specific adjustments and provide algorithms for that purpose.

3.1.4.1 Requesting Adjustments

A method can request an adjustment by calling `PTB_AppendAdjustment()`. The requested adjustment will be added to the end of the so far specified list of per-scan adjustments. If one prefers to set the entire list, the function `PTB_ClearAdjustments()` should be called first, and then all adjustments should be appended in the required order of execution. Note, that this call also removes all default per-scan adjustments set in the Adjustment configuration. If these are needed, one should use `PTB_AppendConfiguredAdjustment()` to put them back on the list. These functions are typically called in the backbone.

3.1.4.2 Preparing for Adjustment Start

Before the start of every adjustment the relation of the parameter `PVM_AdjHandler` is called by ParaVision. A method requesting adjustments should redirect this relation to a local function, typically called `HandleAdjustmentRequests`, in which the following actions take place:

- Checking the name of the starting adjustment with `PTB_GetAdjName()`. (One can also test its category with `PTB_GetAdjCategory()` and the fact that the adjustment is method-specific with `PTB_AdjMethSpec()`). If it differs from the previous declaration with `PTB_AppendAdjustment`, one calls the default relations of `PVM_AdjHandler` (allowing “foreign” adjustment to set up) and exits. Otherwise, one continues with:
- Preparing the experiment parameters for the adjustment. For example, water suppression may be deactivated for the frequency adjustment, etc. All these changes are temporary because they take place in a copy of the parameter space. After the adjustment the original parameter space will be restored, and only the adjusted parameters will be taken over (see next point).
- Setting the list of adjusted parameters which should keep their values after the adjustment by calling `PvAdjManSetAdjParameterList()` and optionally `PvAdjManAppendAdjParameterList()`. This is sufficient if the adjusted parameters are used in the scan where the adjustment was started. Additionally, if the parameters should be made available for other scans, a call of `PvAdjManStorePar()` will tell the Adjustment mechanism to store the adjusted list as a result after adjustment completion. These results can be later obtained with `PvAdjManRestorePar()` and `PvAdjManRestoreParFromHwContext()`.
- Setting the `GS_auto_name` parameter to define the adjustment algorithm, as described below (see Chapter [Adjustment Algorithm \[606\]](#)). If the adjustment is based on the standard RG adjustment, this point and the next one can be replaced by the call of `ATB_RgAdjSetGsPars`.
- Setting other GS parameters to obtain access to the signal, digitizer filling, etc., see Chapter [Access to Data \[607\]](#). Alternatively, this can take place in the initialization phase of the adjustment algorithm.
- Optionally, setting up a sequence of sub-adjustments using `STB_InitSubProcess()` and `STB_CheckSubprocess()`.
- Optionally, it is possible to declare that the adjustment should run in the GOP mode, in which the `GS_auto_name` mechanism is not used and the data is saved in an experiment directory as in an ordinary scan. This is done by calling `PvSysManRequestNewExpno()`. To obtain the path to these data, a parameter of the type `AdjProcnoResultType` has to

be defined in the method and included in the adjusted list; the path will be coded in this parameter upon successful completion of the adjustment and can be recovered as a string with `PvAdjManProcnoResultPath()`.

- To prevent an adjustment from starting a scan, the parameter `AdjPerformState` can be set to `adj_successful`. This can be used for adjustments that calculate parameters without the need of an acquisition.

3.1.4.3 Validity of Adjustment Results

When the adjustment results are saved, they can be additionally “tagged” to allow checking their validity when they are restored. A tag consists of three elements: the name of the adjusting method, the “method context” - a string optionally provided in the argument `methodContext` of `PTB_AppendAdjustment`, and the so called hardware scope, which is a list of hardware “chains” critical for the result (`HW_SCOPE_ENUM: TRANS_CHAIN, REC_CHAIN, GRAD_CHAIN, SHIM_CHAIN`) along with channel numbers. The latter are relevant only for the `TRANS_CHAIN` and `REC_CHAIN`, and mean the physical transmitter/receiver channels (negative integers) or logical ones (positive integers). The hardware scope can be defined by calling `PvAdjManSetHwScope()` in the relations of `PVM_AdjHandler`. Separate calls are needed for every chain involved. When adjustment results are recovered with `PvAdjManRestorePar`, the state of the hardware scope present during the adjustment will be compared with the current state. (If a result has been stored several times with different hardware states, all stored versions will be compared). The result will only be restored if the state of the relevant hardware has not changed. For example, if a result is tagged with the scope of `TRANS_CHAIN` and channel -1, it will not be returned after the change of the RF coil connected to the first physical transmitter channel. However, if the adjustment is repeated with the new coil, one can switch between the two coils and `AdjManRestorePar` will give the proper result each time.

Additionally one can filter the possible results by specifying the method that has stored them and the method context used upon storing with the optional arguments of `PvAdjManRestorePar`.

The function `PvAdjManRestoreParFromHwContext` allows retrieving results for a particular hardware state (not necessarily for the current one).

3.1.4.4 Adjustment Algorithm

When an adjustment is started, the acquisition is controlled by the so called GS Auto pipeline, which, similarly to the Setup pipeline, lets the sequence run in an endless loop and uploads selected scan parameters to the hardware when these parameters are modified. Additionally, the GS Auto pipeline calls relations of a special parameter (called Auto Counter) each time the signal measured the uploaded parameter is available. This allows implementing the adjustment algorithm in the relations of the Auto Counter.

A typical definition of the Auto Counter is:

```
int parameter
{
    display_name "Auto Counter";
    relations AutoCounterRel;
} AutoCounter;
```

With this definition `AutoCounter` becomes just an ordinary local method parameter. To designate this parameter the Auto Parameter, the adjustment method must copy its name to the string parameter `GS_auto_name`:

```
strcpy(GS_auto_name, "AutoCounter");
```

Now, the function `AutoCounterRel`, which has to be defined inside the method's code, will carry out the adjustment algorithm while the auto pipeline is running and eventually stop the adjustment by giving the Auto Counter appropriate values.

The interaction between the pipeline (data acquisition) and the method code is as follows:

- **Initialization of the adjustment pipeline.** This should not be confused with the method initialization (which is done by the routine `initMeth()`). When the adjustment pipeline is initialized, ParaVision sets the Auto Counter to zero and calls its relations (`AutoCounterRel`). The function reacts by initializing the algorithm (if necessary) and setting the Auto Counter to one as a sign of “correct behavior”. Setting the counter to any other value at this point will result in an error condition!
- **During the adjustment pipeline.** After each data acquisition the adjustment pipeline increments the Auto Counter by one and calls its relations again. This allows the adjustment algorithm to calculate new values of parameter(s) being optimized from the measured data. Access to the data is possible via the GS parameter class (see [Access to Data \[▶ 607\]](#)).
- **Successful completion.** The Auto Counter Relation tells the pipeline that the adjustment is completed by setting the counter to zero. The pipeline will then terminate and the system will move to the next adjustment or start the actual experiment.
- **Adjustment failure.** The Auto Relation may inform the pipeline that the adjustment has failed by setting the Auto Parameter to -1. The pipeline will then terminate. The Auto Relation can also define an error message that will appear in the GUI (see below).

Note, that the value of the Auto Counter (-1, 0, 1, >1) exclusively specifies the status of the adjustment as described above. In particular, it may not count the actual number of acquisitions correctly and cannot be decreased or increased by the method code (except of the status indicating values -1,0,1).

3.1.4.5 Access to Data

The GS parameters are used to control the actions of the setup- and auto-adjustment pipelines and to let these pipelines return values derived from the sampled signal or its spectrum. A detailed description of these parameters may be found in Chapter [ParaVision Parameters](#), section Subclass GS Parameters. Since GS parameters are affected by the relations of the baselevel reconstruction and acquisition parameters, they should be set at a point of the method code where the ACQP and RECO parameters have been set to their final values.

Example: Provided that the adjustment method acquires two objects per repetition (`NI = 2`) and a number of `AcqSize` complex data point per call of the ADC command, the following setting of the GS parameter class ensures that all raw data points are stored in the parameter `GS_points`:

```
void SetGS(void)
{
    int i, np;
    np = 4*AcqSize;

    strcpy(GS_auto_name, "AutoCounter");
```

```
GS_dim = 1;
GS_disp_update = Each_Accum;
GS_online_reco = Yes;
GS_reco_display = Yes;
GS_image_type = MAGNITUDE_IMAGE;
GS_typ = Spectrometer_Parameters;
GS_info_dig_filling = Yes;
GS_info_normalized_area = Of_raw_data;
GS_info_max_point = No_info;
GS_info_max_point = Of_raw_data;
GS_get_info_points = Of_raw_data;
GS_info_points = np;
ParxReIsParRelations("GS_info_points",Yes);
PARX_change_dims("GS_info_offset", GS_info_points);
for (i=0; i<np; i++)
    GS_info_offset[i]=i;
}
```

3.1.4.6 Using Adjustment Results

After a successful adjustment the relations of `PVM_AdjResultHandler` are called. Redirecting this parameter to a local function (typically `backbone`) assures that the method effectively uses the adjustment results. This call takes place in the original parameter space, so all changes made at this point will stay.

A similar mechanism for the GOP adjustments uses a different parameter: `PVM_GopAdjResultHandler`. In contrast to ordinary adjustments, its relations are called in the adjustment parameter space. In these relations the method can call `PTB_RegisterGopAdj()` to register the created dataset in the database, which makes it available for viewing like any other data.

3.1.5 Reconstruction

Methods take on important tasks related to image (or spectrum) reconstruction. As mentioned in Chapter [Recommended Method Structure \[▶ 598\]](#), a method has to set several parameters controlling the reconstruction. Optionally, a method can modify the default reconstruction procedure, which consists of networks of “reconstruction filters” realizing various processing steps. A method can change connections between these filters, or include additional ones. It can also provide the processing code for filters of a particular type, called “method filter”, and insert them at any position in the network.

3.1.5.1 Parameters

At the end of `backbone`, when all PVM and ACQP parameters have their ultimate values, the function `SetRecoParam` sets all parameters controlling the reconstruction. Most of it is done with a call of `ATB_InitUserModeReco`, which takes care of dimensionality, sizes, sorting, and parallel reconstruction (GRAPPA) parameters. (It also sets `RECO_mode = USER_MODE`, which turns on the network-based reconstruction). Further reconstruction parameters, e.g. `RECO_rotate`, `RECO_transposition` are set explicitly or by means of special ATB tools after this function call. Note that this only prepares the information needed to build the filter network; the network itself will be created later, when the actual reconstruction starts. See Chapter [ParaVision Parameters](#), section RECO Parameters for a description of most important reconstruction parameters.

3.1.5.2 Network

The reconstruction is designed as a network of processing units called “stages” connected with each other. The data flows from stage to stage along the connections. Depending on how they can be connected, stages are of three kinds: sources (which have outputs only), filters (with inputs and outputs) and sinks (inputs only). Most steps of MRI reconstruction are implemented as filters, e.g., data sorting (`RecoSortFilter`), Fourier transform (`RecoFTFilter`), magnitude calculation (`RecoMagnitudeFilter`). The action of each stage can be influenced by arguments provided in its interface string. For details on the most important reconstruction stages, open the html documentation [Method Programming](#) and follow the link Method Programming -> Topics -> Reconstruction Stages. The network is typically divided to a few “passes”. Data of one experiment repetition is processed in one pass before it goes to another.

The architecture of the network (passes, involved stages with their interface strings, and their connections) is contained in parameters `RecoStageNodes` and `RecoStageEdges`. When the reconstruction is starting, the system calls relations of a special parameter `RecoUserUpdate` to create the network architecture. This parameter has predefined relations which fill `RecoStageNodes` and `RecoStageEdges` according to reconstruction parameters set beforehand by the method. This is sufficient for most situations in MRI.

Methods requiring special reconstruction may redirect the relations of `RecoUserUpdate` to a local function. Currently implemented examples include susceptibility weighted reconstruction in FLASH, phase difference reconstruction in FieldMap and FlowMap and navigator processing in NSPECT. The local relations of `RecoUserUpdate` typically call its default relations first (to establish the standard network) and then insert additional filters using toolbox functions for manipulating the reco network, e.g. `RecoComputeAppendStage`. For details open the html documentation [Method Programming](#) and follow the link Method Programming -> Topics -> Reconstruction Tools..

To visualize the reconstruction architecture set by the method (in a more practical way than inspecting `RecoStageNodes` and `-Edges`), one should find the parameter `RecoUserUpdate` in the Single Parameter Editor, set it to `No` and back to `Yes` (to execute its relations). Then, another parameter – `RecoDebug` – should be found and “pressed”. This generates a text in the Parx Server tab of the Output window which lists all filters with their interface strings and describes their connections. Below is an excerpt from the reconstruction printout of FLASH (with some lengthy interface strings truncated):

```

FIRSTPASS{
    RecoQueueSource Q0{initFromACQP=true;initOnce=true;};
    RecoBufferSink S0{procDim=1;frameDim=2;bufferId="FIRSTPASS0"...
    RecoCastFilter CAST0{dataRep=FLOAT;wordSize=8;};
    RecoFTShiftFilter FTS0{frameDim=2;winDirection=0;...
    RecoFTFilter FT0{direction=0;exponent=1};
    RecoSortFilter REORD0{sortDim=<RecoSortDim>;...
    Q0->CAST0;
    CAST0->FTS0;
    FTS0->FT0;
    FT0->REORD0;
    REORD0->S0;
}

```

3.1.5.3 Method Filter

The special reconstruction filter type `RecoMethodFilter` allows programming of a processing task in the method code. This filter takes two arguments in its interface, which are names of two `int` parameters defined in the method, the “counter” and the “buffer”. When

the filter has received a portion of data at its input, it copies it to the output, sets the counter to the size of this portion in bytes, sets the buffer to the address of the output, and calls the relations of the buffer. In these relations, which are programmed in the method code, one can convert the buffer to a pointer to the data portion, and, knowing its size from the counter, perform any processing one wants. However, it is not possible to change the size of the data portion in the same step. To achieve this, one has to insert dedicated reconstruction filters like `RecoZfillFilter` and `RecoCutoffFilter` before or after the method filter.

The size of data provided to the method filter depends on the position in the network where it is inserted. In the first pass, where data is processed along the first dimension, the size is always a multiple of one echo. At later passes, the size may be a multiple of one 2D or 3D image.

The method filter can be inserted many times at different places, each time with a different pair of counter/buffer to handle different processing tasks.

Here is an example of a filter negating the imaginary part of each sample. It is inserted before the first Fourier transform in the network printed in previous chapter.

```
// callbackDefs.h:  
relations RecoUserUpdate DeriveReco;  
  
// parsDefinition.h  
int parameter Count;  
int parameter {relations BuffRels;} Buff;  
  
// RecoRelations.c  
void DeriveReco(void)  
{  
    // create standard network  
    ParxRelsParRelations("RecoUserUpdate", Yes);  
    // insert method filter  
    RecoComputeAppendStage(RECOFIRSTPASS, 0, "FTS", "RecoMethodFilter",  
        "MF", "cntParameter=<Count>;bufParameter=<Buff>;");  
}  
  
void BuffRels(void)  
{  
    RecoGlobalMemory M(Buff);  
    double *data = (double*) M.getAddress();  
    int sizeComplex = Count/(2*sizeof(double));  
    for(int i=0; i<sizeComplex; i++)  
        data[2*i+1] *= -1;  
}
```

3.2 Base Level Acquisition

3.2.1 Chapter Objectives

Base Level Acquisition means the generation of data using a pulse sequence followed by a subsequent data processing. Base Level means: the terms, parameters, commands, programs, and tools used to describe and to control the acquisition are in rather close contact to the hardware (i.e. without PVM support).

Typically it is not necessary for the user to set the base level parameters manually. The routine user interface which includes the PVM mechanisms will automatically set them.

Note: If base level parameters are set manually these new settings are usually not kept when the instruction is executed with continue/scan, as base level parameters will be rederived by method code at the start of an acquisition. Furthermore, this PVM mechanisms will reset the manually set values at least at the end of the automatic adjustment procedures.

To keep manually set parameter values you have to start the data acquisition either by the **SETUP** command or the **GOP** command instruction with selecting prototype mode in the instruction card.

Items of the Present Chapter

Chapter [Special Terms \[▶ 611\]](#): At the beginning terms will be defined which are basically of interest in the context of Base Level Acquisition.

Chapter [Pipeline Acquisition \[▶ 613\]](#): Pipeline Acquisition means the data flow and the data management in ParaVision.

Chapter [Parameters Controlling the Acquisition \[▶ 621\]](#): In contrast to terms described in Chapter [Special Terms \[▶ 611\]](#) this section describes parameters.

Chapter [Pulse Programming \[▶ 627\]](#): Creation of pulse programs and the handling of gradient commands as base level tools.

Chapter [GOP Simulation Tool \(HPDISP\) \[▶ 666\]](#): Simulated acquisition is treated in this section.

3.2.2 Special Terms

3.2.2.1 Arrangements

The following definitions will introduce some special terms used to relate the base level ACQP parameters described in Chapter [Parameters Controlling the Acquisition \[▶ 621\]](#). Terms should not be confused with Parameters, e.g. terms cannot be checked or changed via any parameter editor.

Parameters mentioned in the present section will be written in a normal style. **Examples:** NS, NI, NA, ACQ_dim.

Terms will be written in an emphasized style. **Example:** **coding** during the definition, **coding** within the text.

Note: The following definitions will be given with respect to capital or small letters. In some cases this is important. **Example:** **Experiment** is defined here, experiment can be used in the normal sense.

3.2.2.2 Definitions

coding

Means the procedure in which parameters are changed following a certain algorithm to prepare N-dimensional information. During reconstruction the dataset is decoded. The **coding** may have spectral, spatial, and/or time dependent information.

During an AVSCAN the **coding** is constant in most **Experiments** (exception: **RARE**).

phase encoding step

A coding step in a 2D-FT-imaging Experiment

projection step

A coding step in a radial **Experiment**

Experiment

An **Experiment** refers to the execution of all **coding** events for all **Objects** including all repetitions for inner loop averaging.

An **Experiment** can be averaged as a whole with NAE > 1. In this case all **coding** events for all **Objects** including all repetitions for inner loop averaging will be repeated NAE times in an outer loop (writing data in place). An **Experiment** averaged with NAE > 1 will **not** have more **Objects** than with NAE=1.

An **Experiment** (averaged or not averaged) can be repeated NR times with NR > 1 (e.g. in order to achieve a dynamic study). In case of **Experiment** repetitions with NR > 1 the number of **Objects** becomes NI x NR.

Parallel Experiment

Several **Experiments** performed within a parallel acquisition pipeline.

Object

Each spectrum and each image as well as the corresponding raw data is defined as an **Object**. The number of raw data **Objects** created during data acquisition is specified by the parameters NI and NR (NI = number of **Objects** per **Experiment**, NR = number of repetitions of the **Experiment**).

scan

The digitalization of a time domain signal (e.g. fid or echo) during the execution of an acquisition command in the pulse program is referred to as a **scan**. The ADC_START pulse program command starts the digitizer for sampling of TD (real, not complex) data points (TD = time domain size = ACQ_size[0]). Do not confuse the term **scan** with the lowest level of the **Patient**, **Study**, **Scan** dataset hierarchy.

NSCAN

An **NSCAN** is the result of the accumulation of n subsequent **scans**. In case ACQ_ns_list_size = 1, an integer ACQ_ns specifies the number of **scans** to be accumulated. In case ACQ_ns_list_size > 1, different **NSCANs** will be performed according to the current ACQ_ns_list[] (an array). Subsequent elements of that array lead to subsequent **NSCANs**. The number of all echoes included in all **NSCANs** is summarized and expressed as **NECHOES** to be used within the pulse program as loop counter. **NECHOES** is not an ACQP parameter (only an info parameter). Further accumulations are controlled by the parameters NA and NAE.

Example: Consider a multi-slice / multi-echo Experiment with 5 slices and 6 echoes per slice. The user wants to acquire 2 images per slice (= 10 Objects) with accumulation of the first 2 and the other 4 echoes per slice. With ACQ_ns_list [0] = 2, ACQ_ns_list [1] = 4 two **NSCANs** will be acquired for each slice.

The number of echoes to be acquired per slice is **NECHOES** = 6, the number of all **NSCANs** performed for each phase encoding step (all slices) is therefore 10.

2 scans	4 scans	1st slice
1st NSCAN	2nd NSCAN	
		...
2 scans	4 scans	5th slice
9th NSCAN	10th NSCAN	

multiplex step

In a multi **Object Experiment**, the **Objects** may be acquired sequentially and/ or interleaved. In case of interleaved acquisition, one or a subset of **coding steps** are repeated for each **Object** before the next **coding** takes place. One **multiplex step** is the acquisition of all **NSCANs** with the current **coding** and before the next **coding** takes place. The size needed for one **multiplex step** (e.g. memory size for a **dummy scan**) is often termed size for one phase encoding step.

Example: In a common multi-slice **Experiment**, there are e.g. 5 slices (= 5 **Objects**) to be imaged in an interleaved manner, whereby e.g. 256 different **phase encoding steps** are required to get the final 5 images. In this example, one **multiplex step** consists therefore of 5 times **NSCANs**.

AVSCAN

The Pipeline Acquisition offers a special accumulation mode, whereby one multiplex step is repeated NA times for accumulation.

NREC

The number of independent receiving channels (e.g. when working with an array coil system).

PSCAN

A **PSCAN** is the result of **NREC scans** during a parallel acquisition pipeline. The size of a **PSCAN** is **NREC** times the size for one scan.

3.2.3 Pipeline Acquisition

3.2.3.1 Acquisition Pipeline

The Acquisition Pipeline is a mechanism used in *ParaVision* to acquire data and to process different stages of data in parallel in order to minimize the time between the end of the **Experiment** and the time until all images/spectra are reconstructed. As soon as a **scan** (or **NSCAN/PSCAN**) is acquired, it will be passed through several processes of the pipeline. The number of processes in a Pipeline Acquisition are determined by the acquisition command (GOP or Setup or GS Auto) and the values of the parameters in the parameter classes GO and GS.

3.2.3.1.1 Dummy Scans

Before the first **scan** becomes valid after typing a **GOP** command or a **GS Auto** command (not after **Setup**), the user can force the execution of some so called **initial dummy scans** to achieve a steady state of the spin system. While the spectrometer performs **dummy scans**, the acquired data will be discarded and the coding step will be maintained.

Note: The pulse sequence is responsible for the generation of **dummy scans** - the acquisition framework will only ensure, that the correct **scans** will be discarded.

The number of initial **dummy scans** depends on the parameters **DS** and **ACQ_dim_desc[0]** as described in the following table:

ACQ_dim_desc[0]	Number of initial dummy scans
Spectroscopic	DS
Spatial	$DS * NS * NI * NA * ACQ_phase_factor = DS * AVSCANS$

Table 3.1: Initial dummy scans

Technical Background on Data Accumulation

Data Accumulation is used to increase the signal to noise ratio S/N, to reduce baseline artifacts and motion artifacts, or to achieve special weightings (e.g. T1/T2 weighting of a multi-echo **Experiment**).

CPU Accumulation: The entire data is transferred before accumulation to the workstation.

Depending on the requirements for the Acquisition Pipeline, the raw data will pass through several memory buffers. If the accumulation of the entire **Experiment** is requested (selected by the parameter **NAE**), an additional raw data buffer is required which has to accommodate the data for a complete **Experiment**. In case of an on-line reconstruction, another data buffer is used to keep the reconstructed data.

3.2.3.1.2 Final Destination of Data

The final destination of the raw- and reconstructed data is the screen and/or the following file names on the hard disk:

<PvInstDir>/data/USER/NAME/EXPNO/fid for the raw data,

<PvInstDir>/data/USER/NAME/EXPNO/pdata/PROCNO/2dseq for the processed data.

When acquisition jobs described by the parameter **ACQ_jobs** are used, raw data is stored in

<PvInstDir>/data/USER/NAME/EXPNO/rawdata.job<x>

where <x> is the job index.

3.2.3.2 How to Start a Pipeline Acquisition

Currently, three pipeline commands for data acquisition have been implemented: GSP, GOP, GS Auto. Pressing the Setup button in the Exam Card will start a GSP pipeline. Continue/Scan will execute normally a GS Auto pipeline executing all adjustments necessary for a scan and finally a GOP pipeline to acquire the experiment data. In the instruction card, the subset of adjustments can be changed. In the adjustment card, adjustments can be run individually in the GS Auto pipeline.

3.2.3.2.1 Commands Controlling Data Flow

The Pipeline Acquisition supports a circular buffer management for data acquisition instead of double buffering. Whenever data are collected with an **ADC_START/ADC_END** command combination - (suitable combinations of **adc/eosc** low level commands depending on the spectrometer hardware), the digitized data are transferred to the controlling workstation for averaging and joining parallel channels.

Storage and transfer is controlled implicitly by the acquisition parameters, which control accumulation and **scan** sizes:

ACQ_size, ACQ_ns_list_size, ACQ_ns_list, ACQ_phase_factor, NI, NA, NAE and NR (see also the first sections of the present chapter).

Alternatively, acquisition can be described by the ACQ_jobs parameter, allowing in an easier way to parameterize non Cartesian acquisition schemes.

The end of the acquisition is determined by the end of the pulse program. The acquisition pipeline will remain stuck, if the expected number of scans was not acquired during the pulse program.

Note: The pulse program commands ze, zd, st, wr #, if # as described in the *TOPSPIN* pulse program reference manual should not be used in pipeline acquisition as they may interfere with the buffering mechanism described above.

3.2.3.2.2 Workflow for Acquiring Data: GOP

GOP starts the pipeline for data acquisition (see Figure [Schematic workflow during GOP](#)  [\[616\]](#)). The various processes in the pipeline are determined by the parameters of the parameter class GO.

After GOP has been started, all acquisition parameters are valid: the pulse program, defined by the parameter PULPROG will be compiled and the acquisition starts after all spectrometer devices are loaded.

Dummy scans will be performed according to the parameters DS and ACQ_dim_desc (see above).

Termination

The pulse program must ensure, that it will be terminated (exit command) after the entire **Experiment** is finished. The number of anticipated **scans (NTOTAL)** is:

$$NTOTAL = \prod_{i=1}^{ACQ_dim-1} ACQ_size[i] * NI * NR * NA \left(\sum_{k=0}^{ACQ_ns_list_size-1} ACQ_ns_list[k] \right)$$

When the ACQ_jobs parameter is used to describe the experiment, exactly ACQ_jobs[].nrTotalScans must be acquired for each job.

It may also be aborted at any time by clicking the **STOP** button. When an experiment is aborted by the user, the collected data will remain stored on the workstation. Depending on the experiment settings, it may however not be possible to reconstruct partially acquired data in a reasonable way.

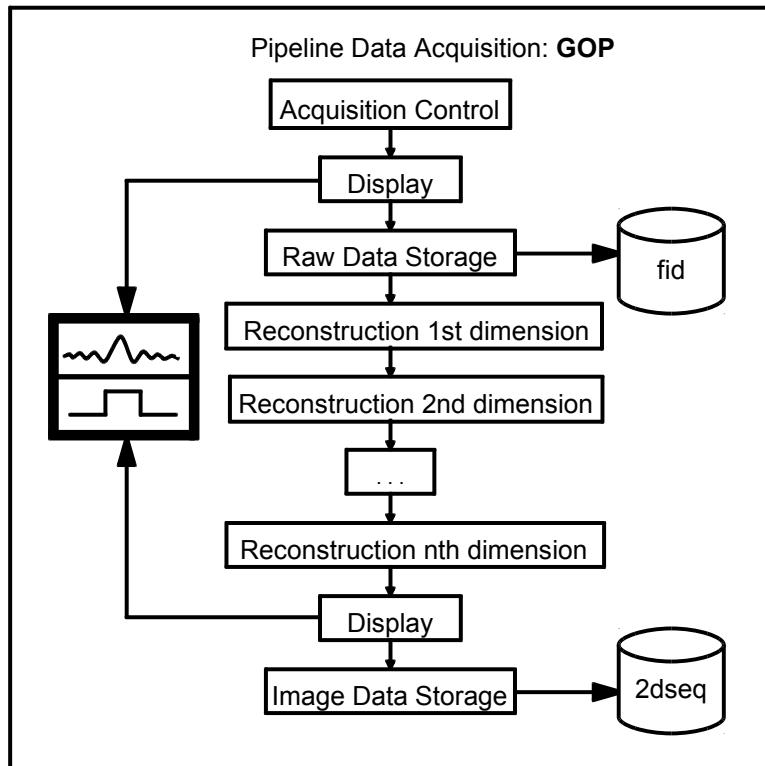


Figure 3.2: Schematic workflow during GOP

3.2.3.2.3 Workflow for Manual Adjustment: Setup (GSP)

GSP starts a pipeline which allows the manual adjustment of the acquisition parameters (see Figure [Schematic workflow during GSP \[▶ 617\]](#)). The processes in the pipeline and the functionality of **GSP** are determined by the parameters of the parameter class GS. After starting **GSP**, all acquisition parameters are valid with the following exceptions: **GS_dim** is used instead of **ACQ_dim**, the current settings of the parameters **DS**, **NAE** and **NR** are ignored, instead **DS** = 0, **NAE** = 1 and **NR** = 1 is assumed. The pulse program, defined by the acquisition parameter **PULPROG** will be compiled and executed.

Note: No dummy scans during GSP - Pipeline!

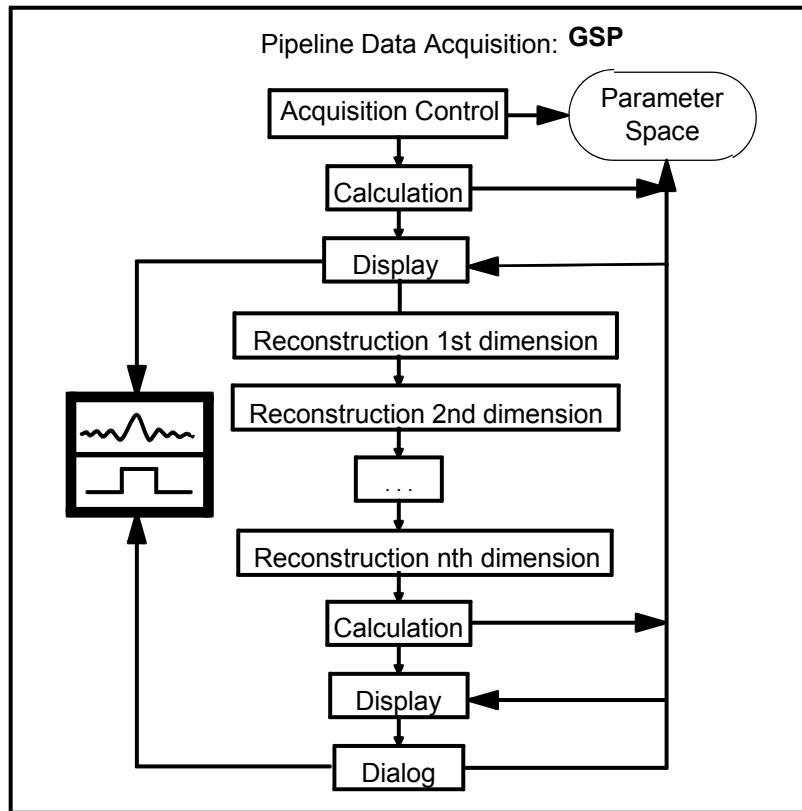


Figure 3.3: Schematic workflow during GSP

Update Mechanisms during GSP-Pipeline

1. The parameter `GS_typ` (possible settings are `Spectrometer_Parameters`, `Gradients`, `Preemphasis`, `Shim`) is set depending on whether the operator wants to adjust spectrometer-, gradient-, preemphasis- or shim-parameters.
2. Some parameters require the recompilation of the pulse program because the acquisition time changes after modification of the parameter `SW_h` (Sweep Width in Hertz). In this case the relation-functions of the parameter `SW_h` will set the parameter `GS_restart = Recompile` to prepare a later recompilation of the pulse program. The recompilation of the pulse program will cause the acquisition to stop and resume automatically after a few seconds.
3. Some parameters require the restart of the GSP-pipeline because the memory requirements have been changed after modification of the parameter `NI`. In this case, the relation-functions of the parameter `NI` will set the parameter `GS_restart = Restart` to prepare a subsequent restart of the GSP.
4. After acquisition of each scan the parameter `GS_restart` is evaluated and according to its setting, either the parameter group selected by `GS_typ` will be reloaded (`No_Restart`) or the acquisition will be interrupted and restarted with a recompiled pulse (`Recompile`) program or the pipeline may be restarted completely (`Restart`).

Termination

The GSP-pipeline must be aborted by clicking the STOP button.

Note: If the timing generated by the current pulse program has to be evaluated the parameter `GS_steady_state` has to be set to `Yes`. Otherwise the measured time intervals may be incorrect.

3.2.3.2.4 Workflow for Automatic Adjustment: GS Auto

GS Auto starts a pipeline for an automatic adjustment of the acquisition parameters (see Figure [Schematic workflow during GS Auto ▶ 619](#)). The processes in the pipeline and the functionality of GS Auto are also determined by the parameters of the parameter class GS. The GS Auto-pipeline works as follows:

1. The parameter `GS_auto_name` contains the name of an integer parameter whose relation-functions are used to perform the automatic adjustment.
2. This parameter value will be set to zero before the pipeline is started. Any acquisition parameter may now be set by the relation-functions of this integer parameter (e.g. parameters of the parameter class GS, name of the pulse program etc.).
3. After the relation-functions of the integer parameter are executed, the acquisition parameters become valid and the pulse program specified by the acquisition parameter `PULPROG` will be compiled and the **Experiment** will be executed.

Note: **Dummy scans** according DS and `ACQ_dim_desc` will be performed after each GS Auto-start or restart of the pulse program. Also, changes in certain parameters such as frequency or pulse power during a GS Auto will cause a few dummy scans to be performed to allow a new steady-state to be reached.

4. The integer parameter defined in `GS_auto_name` will be incremented by one after each **Experiment** and the acquisition parameters can be optimized by the relation-functions of this integer parameter.
5. The **Experiment** will be repeated as long as the value of this integer parameter remains greater than zero.
6. The relation-functions of the integer parameter may set the value of it to zero to indicate a successful termination of the auto adjustment pipeline. A negative value of this integer parameter will indicate an error during the adjustment.
7. A subsequent GS Auto pipeline can be initiated by setting the parameter `GS_continue = Repeat_gsauto`.
8. The start of the final **Experiment** can also be automatically initiated by setting the parameter `GS_continue = Start_gop`.

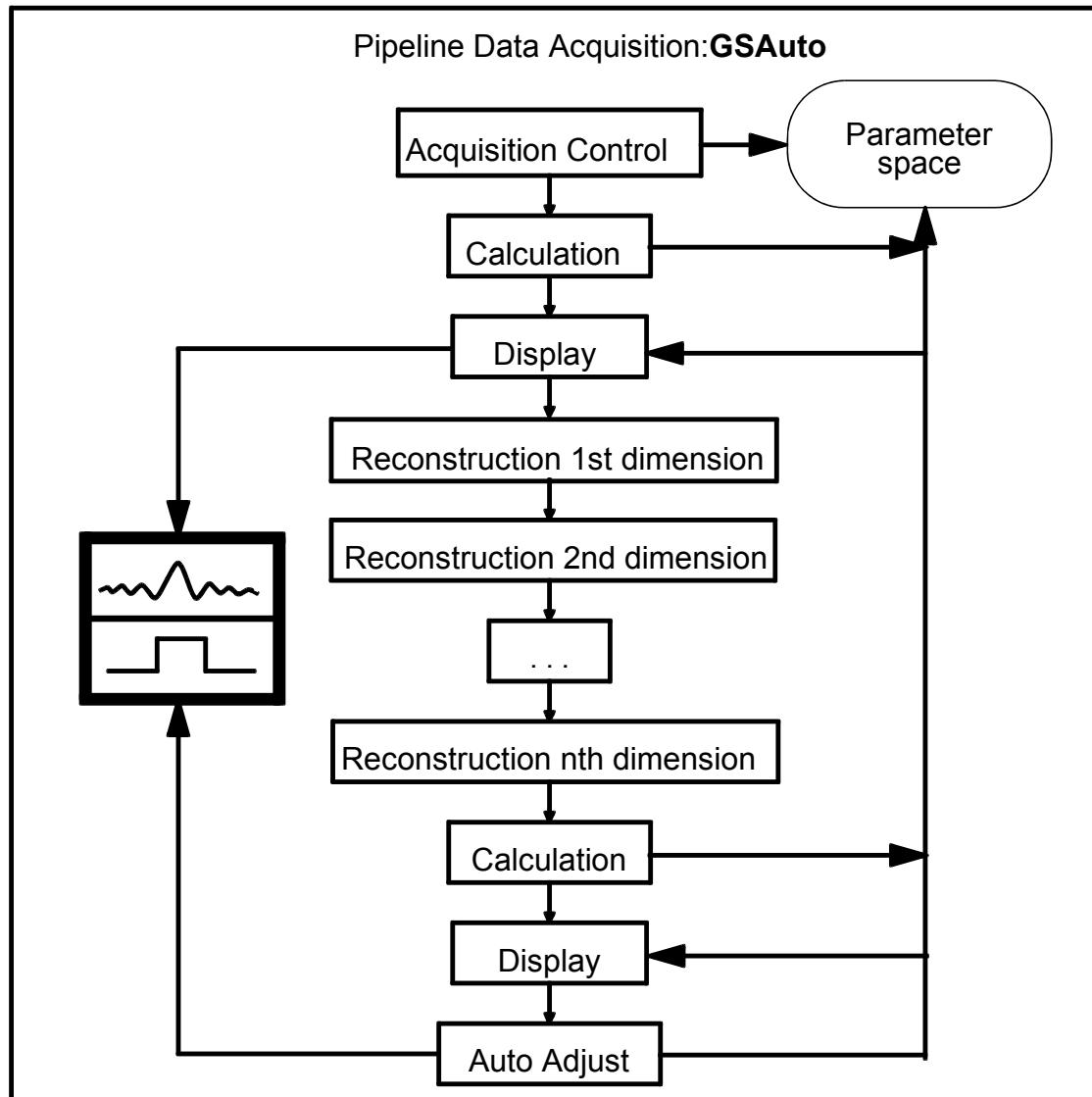


Figure 3.4: Schematic workflow during GS Auto

Termination

The GS Auto pipeline will **automatically stop** after the integer parameter, defined by `GS_auto_name`, becomes zero or negative. The GS Auto pipeline may be **aborted** at any time by the STOP button.

3.2.3.2.5 Pipeline Filter

In *ParaVision*, it is possible to add an additional filter process into the acquisition pipeline between the raw data acquisition and raw data storage as illustrated in Figure [Schematic workflow with user pipeline filter \[620\]](#). The filter process is in fact a special automation (AU) program following certain conventions. The coding of such an automation program is described in detail in [Automation Programming](#), Chapter AU filters for Pipelined Acquisition.

Note:

With ParaVision 6, using acquisition jobs, non Cartesian sampling patterns can be acquired and stored without any regridding on the stored data. All the necessary reconstruction steps can be done in a user accessible way in the reconstruction pipeline. For this reason, the usage of pipeline filters is discouraged, whenever the same functionality can be achieved using job acquisition and reco filters. Pipeline filters cannot be used for jobs.

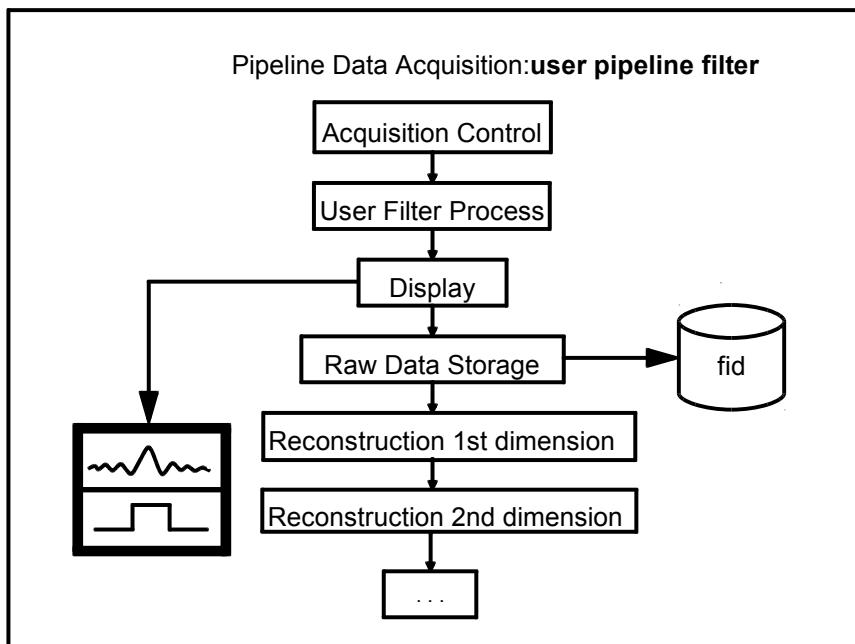


Figure 3.5: Schematic workflow with user pipeline filter

To use such a pipeline filter, one has to set

```

ACQ_user_filter = Yes
ACQ_user_filter_name = <au_program>
ACQ_user_filter_memory = <size_of_databuffer>
ACQ_user_filter_mode = Standard or Special.
  
```

`ACQ_user_filter_name = <au_program>` must contain the name of the AU program to execute. The AU program will act like a regular process of the pipeline. It will get a pointer to the input data and it will get a memory partition assigned for data processing. The size of this data buffer must be specified by the enumeration parameter `ACQ_user_filter_memory = <size_of_databuffer>`.

The AU program may operate in two different modes, specified by the parameter `ACQ_user_filter_mode = Standard or Special`.

- `ACQ_user_filter_mode = Standard`

All basic ACQP parameters are valid for all processes of the pipeline as well as for the AU program itself. Therefore, the number of input points of the AU program equals the number of its output points. No data reduction or extension occurs. In this case, it is usually efficient enough to set

```

ACQ_user_filter_memory = For_one_scan or
ACQ_user_filter_memory = For_one_PE_step or
ACQ_user_filter_memory = For_one_experiment.
  
```

- `ACQ_user_filter_mode = Special`

The AU program will receive ACQ_user_filter_size[1] scans of the size ACQ_user_filter_size[0] per **Experiment**. The regular processes of the pipeline need to receive the raw data according to the basic ACQP parameters. The main use of this mode is to perform data reduction (e.g. k-space weighted averaging) or data extension (e.g. key-hole imaging).

ACQ_user_filter_size[2] has the following meaning: In ACQ_experiment_mode = ParallelExperiment (see later), the number of effective channels can be changed by a pipeline filter. If ACQ_user_filter_size[2] > 0, then data will be acquired on the ACQ_user_filter_size[2] first channels of the spectrometer and the filter must transform this data to create **NREC** scans.

Sometimes it is convenient to use different filter processes during setup, when usually only a subset of the data is generated. To handle this case the parameter ACQ_user_filter_setup_name[] can specify different pipeline filter for any setup dimension. In this case, the size in **Special** mode will be taken from the parameter ACQ_user_filter_setup_size[].

Note: In case of ACQ_user_filter_mode = **Special**, short-cuts have been implemented in order to make user-defined filters independent of the type of acquisition (either setup **Experiments** during GSP, GS Auto or scan **Experiments** during GOP, see ACQ_scan_type in [ParaVision Parameters](#), Chapter ACQ_INFO Parameters). These short-cuts are:

ACQ_user_filter_size[0] = 0 will be replaced by ACQ_size[0].

ACQ_user_filter_size[1] = 0 will be replaced by the total number of scans anticipated/required by the current setup/scan **Experiment** (=NTOTAL). If ACQ_user_filter_size[1] < 0, then the AU program will receive (-1) * ACQ_user_filter_size[1] * NTOTAL scans instead.

ACQ_user_filter_size[2] = 0 indicates that the AU program does not intend to change the number of effective channels in the pipeline.

3.2.4 Parameters Controlling the Acquisition

3.2.4.1 Basic ACQP Parameters

3.2.4.1.1 Base Level ACQP Parameters

This section covers base level parameters defining the sizes and the chronological order for the acquisition of raw data. The following list is a grouped overview of the parameter names, which will be explained in detail below.

- ACQ_dim = 1, 2,...,10
- ACQ_size[]
- ACQ_ns_list_size, ACQ_ns = ACQ_ns_list[0], ACQ_ns_list[]
- NS = ACQ_ns, NI, NA, NSLICES, NAE, NR
- ACQ_phase_factor
- ACQ_jobs_size, ACQ_jobs

ACQP class

These parameters belong to the ACQP class of parameters and may be examined and changed in the single parameter editor.

3.2.4.1.2 Parameter Descriptions

ACQ_dim - Defines the dimensionality of an **Experiment**. In the case of a two dimensional acquisition, ACQ_dim is set to 2. In the case of a three dimensional acquisition, ACQ_dim is set to 3 and so on. Dimensions may describe spatial or spectroscopic coding. The maximum number of independent dimensions supported by *ParaVision* is 10.

ACQ_size[] - Defines the size of an **Experiment** in each dimension. It defines the number of data points acquired in each dimension. ACQ_size is a one dimensional array containing ACQ_dim elements. ACQ_size[0] is the number of raw data points (as real, not complex numbers) acquired during each scan.

For parallel experiments ACQ_size[0] points are acquired simultaneously on **NREC** receiver channels and concatenated into one parallel scan (**PSCAN**).

In case of a 2D-FT image acquisition ACQ_size[1] equals the number of phase encoding steps. ACQ_size[1] must be a multiple of ACQ_phase_factor.

Example: In a 2D image acquisition method a matrix size of 256x256 points is selected, then the following settings for the size parameters are derived. ACQ_size[0] = 512 and ACQ_size[1] = 256, if no anti-aliasing is specified.

In a 3D image acquisition, ACQ_size[1] contains the number of fast phase encoding steps while ACQ_size[2] is the number of slow phase encoding steps. If the image matrix is 128 x 128 x 64, then ACQ_size[0] = 256, ACQ_size[1] = 128, and ACQ_size[2] = 64.

ACQ_ns_list_size - Defines the number of elements within the array ACQ_ns_list []. ACQ_ns_list_size > 1 is accepted if NI > 1 (= number of Objects). In this case NI must be a multiple of ACQ_ns_list_size. ACQ_ns_list[] is a one-dimensional array having ACQ_ns_list_size elements.

Example: Consider a multi-echo **Experiment** with 6 echoes. A T1-weighted image can be achieved by adding up the first and the second echo image. A T2- weighted image can be achieved by adding up the echoes 3 - 6. To do this in time domain one can set ACQ_ns_list_size = 2, ACQ_ns_list[0] = 2 and ACQ_ns_list[1] = 4.

ACQ_phase_factor - Defines the number of phase encoding steps per Object during a multiplex acquisition. ACQ_phase_factor is used together with NI to sort the scans in a multi-Object acquisition. Typically, this parameter is set to 1 which will keep the coding constant within a multiplex step. If ACQ_phase_factor > 1, this parameter will give the number of consecutively acquired phase encoding steps that belong to a single Object.

Example: The simplest example is an MSME **Experiment** in which a single scan is acquired from every slice before the phase encoding is changed. In this case, ACQ_phase_factor = 1. It is also possible to acquire two phase encoding steps from one slice, then go to the next slice and acquire two phase encoding steps, etc. In this case, ACQ_phase_factor = 2. A typical application of the ACQ_phase_factor is the RARE **Experiment** in which each echo of a multi echo **Experiment** gets a different coding to reduce the total acquisition time. Suppose 256 phase encoding steps are desired and the ACQ_rare_factor = 8. The corresponding ACQP parameters (ACQ_size[1] = 256 and ACQ_phase_factor = 8) require 32 multiplex steps to be acquired. In this **Experiment**, each multiplex step consists of 8 **NSCANs** with each **NSCAN** having a different phase encoded echo.

NI - Defines the number of multiplex acquired Objects produced by a single **Experiment**. The software allows NI to be a multiple of ACQ_ns_list_size (for multi-slice **Experiments**). If NI is not a multiple, a conflict message will be displayed. In a multi-slice multi-echo **Experiment**, NI equals the number of slices times the number of echo images. To acquire a single 3D image, NI is set to 1.

NA - Defines the number of accumulations. A multiplex step including NI * ACQ_phase_factor NSCANs will be repeated NA times and accumulated before the coding parameter of an n-dimensional **Experiment** is incremented to the next step. NA leads to a superposition of corresponding multiplex steps.

NAE - Refers to the number of accumulated **Experiments**. After an entire **Experiment** is acquired, it will be repeated NAE times for accumulation. All **Experiments** are added together. One application of using NAE instead of NA is to reduce artifacts due to motions which are slow compared to the NA repetition time and not correlated with the NAE cycle.

NR - Refers to the number of repetitions of an **Experiment** including all accumulations with NA and NAE. For each repetition, a new set of NI Objects will be created. This parameter is used to acquire similar datasets as a function of time for the purpose of generating movies.

Example: A single slice, single echo-2D **Experiment** (NI = 1) might be repeated 8 times (NR = 8) to produce 8 Objects. A two slice double echo **Experiment** (NI = 4) might be repeated 8 times (NR = 8) to produce 32 Objects.

ACQ_jobs_size - This parameter is used to select the number of jobs to be used within the current experiment.

ACQ_jobs[] - This parameter allows to describe the acquisition jobs used within the experiment. Each job has the following members:

.**scanSize** - Number of (real valued) points (TD) to be acquired with a single job scan

.**transactionBlocks** - Number of scans to be acquired in a single setup step

.**dummyScans** - Number of scans to be discarded at the beginning of the experiment

.**nTotalScans** - Total number of scans to be acquired within the experiment before averaging

.**receiverGain** - Receiver Gain to be used for the job

.**swh** - Detection bandwidth for the job. Currently, selecting different swh values for different jobs will not work in all situations and thus is classified experimental.

.**scanshift** - Group delay compensation to be applied for the digital filter

.**nStoredScans** - Number of scans to be stored for the job

Digital filter settings currently cannot be selected independently for the different jobs but will be taken from the ACQ filter description parameters DIGMOD, DSPFIRM.

There is no default averaging available for job acquired data though the parameter nStoredScans is prepared to distinguish averaged from acquired data. Currently, averaging must be done as part of the image reconstruction pipeline.

Example: A single slice radial experiment acquiring 31 spokes of size 198 complex to be reconstructed into a 128x128 grid is averaged twice and repeated 10 times. Then ACQ_jobs[0].scanSize = 396, ACQ_jobs[0].nTotalScans = ACQ_jobs[0].nStoredScans = 620.

To make it easier to add jobs e.g. for navigators in Cartesian experiments, a hybrid mode is also possible. When ACQ_jobs_size > 0 and ACQ_jobs[0].scanSize = 0, the parameters for the first acquisition job will be taken from ACQ_dim/_size as before. A second job will then use the description in ACQ_jobs[1].

3.2.4.2 Parameters Controlling the Data Flow

Hierarchy of Parameters

Figure [Parameters Controlling Data Flow in Pipeline Acquisition \[624\]](#) illustrates the loop structure of a general pulse sequence in Pipeline Acquisition, i.e. the order in which the acquisition, accumulation and coding steps are repeated within an **Experiment**. The digitizer generates scans of the size ACQ_size[0]. These scans are added together (accumulated) according ACQ_ns to form an **NSCAN**. ACQ_phase_factor NSCANs will be differently coded in k-space for one Object (or image). This procedure will be repeated for all Objects (NI times) to form a multiplex step. NA multiplex steps will be accumulated to form one AVSCAN. There will be $N_{AVSCANS}$ AVSCANS acquired to have a complete **Experiment**.

$$N_{AVSCANS} = \left(\prod_{i=1}^{ACQ_dim-1} ACQ_size[i] \right) / (ACQ_phase_factor)$$

There will be NAE Objects accumulated before the first NI Objects are completely acquired. This procedure is now repeated NR times.

Note: It is not necessary to implement this general loop structure in every pulse sequence. If you ensure that certain parameters have constant values, you can restrict yourself to a subset of these parameters. Most imaging **Experiments** will e.g. support only a 2D or 3D mode. You might for example start to implement a method for a single slice **Experiment** only. You must however keep in mind that the number of scans to be acquired by the scanner is described by these parameters and the acquisition will run, until the anticipated amount of data has been acquired.

The following section gives an overview of typical settings of the parameters described above for common measuring methods provided with *ParaVision*.

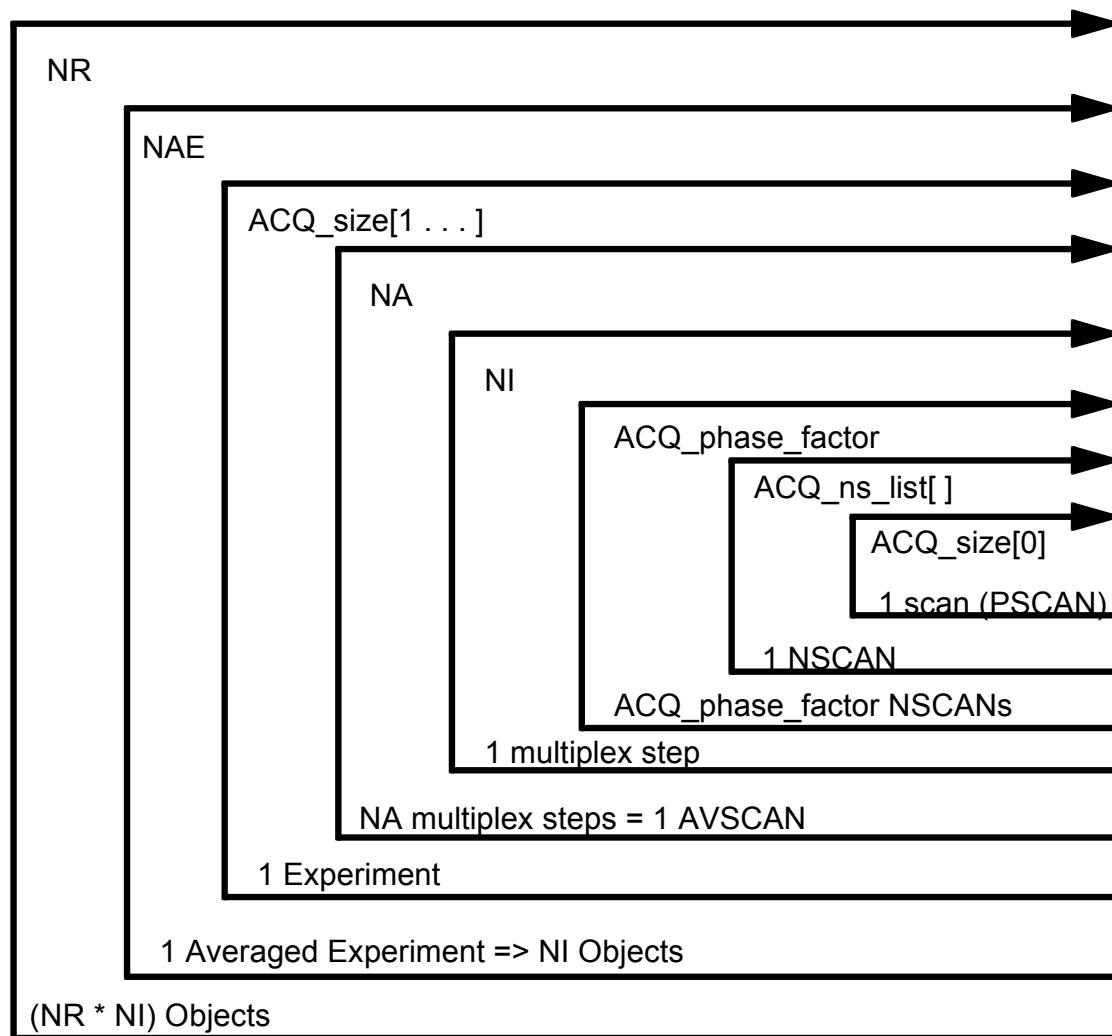


Figure 3.6: Parameters Controlling Data Flow in Pipeline Acquisition

Typical Settings of ACQP Parameters

Parameters	FLASH	FLASH motion suppression	FLASH time series (16 im.)	MSME 6 echoes	MSME 15 echo coll. 1:1, 2:2, 3:4, 4:8	RARE RareF. = 8
ACQ_dim	2	2	2	2	2	2
ACQ_size	512x128	512x128	512x128	512x128	512x128	512x128
ACQ_ns_list_size	1	1	1	1	4	1
ACQ_ns_list	-	-	-	-	1, 2, 4, 8	-
ACQ_ns (NS)	1	1	1	1	1	1
ACQ_phase_factor	1	1	1	1	1	8
NI ; NA	5 ; 4	5 ; 1	5 ; 4	30 ; 4	20 ; 4	5 ; 4
NAE ; NR	1 ; 1	4 ; 1	1 ; 16	1 ; 1	1 ; 1	1 ; 1

Table 3.2: Typical settings of ACQP parameters (5 slices)

Note: Bold entries represent default settings.

Parameters	RARE 128	3 D FLASH one slab (256 x 128 x 64)	DtiStandard - 7 weightings	EPI (128 x 128) single shot	EPI segmented (2 x 64)
ACQ_dim	2	3	2	2	2
ACQ_size	512x128	512x128x64	512x128	32768x1	16384x2
ACQ_ns_list_size	1	1	1	1	1
ACQ_ns_list	-	-	-	-	-
ACQ_ns (NS)	1	1	1	1	1
ACQ_phase_factor	128	1	1	1	1
NI ; NA	5 ; 4	1 ; 4	35 ; 4	5 ; 4	5 ; 4
NAE ; NR	1 ; 1	1 ; 1	1 ; 1	1 ; 1	1 ; 1

Table 3.3: Typical settings of ACQP parameters (5 slices)

Note: Bold entries represent default settings.

Parameters	CSI (2+1D) – (32x16x2048)	PRESS 2K single voxel	SINGLEPULSE 2K	SPIRAL 4 interleaves
ACQ_dim	3	1	1	2
ACQ_size	4096x32x16	4096	4096	2166x4
ACQ_ns_list_size	1	1	1	1
ACQ_ns_list	-	-	-	-
ACQ_ns (NS)	4	4	4	1
NI ; NA	5 ; 1	1 ; 1	1 ; 1	5 ; 1
NAE ; NR	1 ; 1	1 ; 1	1 ; 1	1 ; 1

Table 3.4: Typical settings of ACQP parameters

An **Experiment** is established by the parameters listed below.

Type of Experiments

ACQ_experiment_mode - Controls the data flow depending on the type of **Experiment**.
ACQ_experiment_mode is an enumeration parameter which may have the values:

- **SingleExperiment** - To define a regular **Experiment** (default)
- **ParallelExperiment** - To define a **Parallel Experiment**

3.2.5 Parameters Controlling Parallel Experiments

Parallel acquisition is typically activated within the Encoding class of a measurement method. Parallel Experiments can be selected only when more than one receiver channel is available ($NRCU > 1$). On base level, parallel acquisition can be selected by setting ACQ_experiment_mode = ParallelExperiment. Then specific receive channels can be activated by the array parameter ACQ_ReceiverSelect[NRCU].

This array of YesNo parameters allows to switch on receivers for data acquisition individually for the available receive channels during a GOP / setup pipeline.

Note: In order to reconstruct data acquired with parallel acquisition, the RECO_mode = USER_mode must be selected and appropriate RECO parameters must be set. For methods which support multiple receivers in their Encoding class, this is handled automatically.

Data flow for a Parallel Experiment

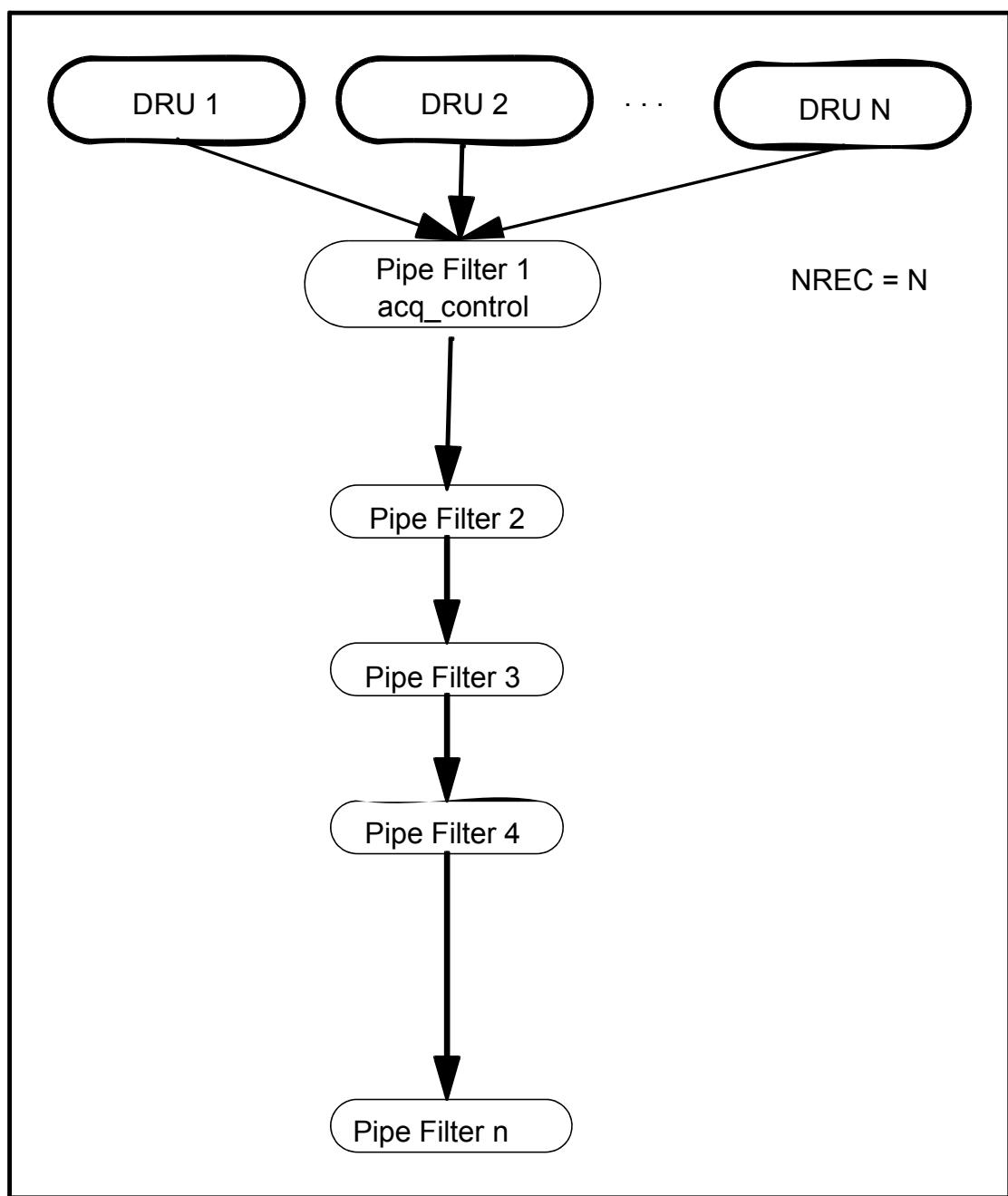


Figure 3.7: Data flow for a Parallel Experiment

3.2.6 Pulse Programming

3.2.6.1 Introduction

The pulse programming section is intended as a reference for pulse program development. *ParaVision 6.0* has been released for AVANCE II, III and IIIHD systems.

Pulse Programming for AVANCE Systems may be different for

- Standard Acquisition means acquisition in *TOPSPIN*

- Pipeline Acquisition means acquisition in *ParaVision*

The present manual deals mainly with **Pipeline Acquisition**.



For detailed information about writing pulse programs for Standard Acquisition please refer to the **NMR-SUITE Pulse program Reference Manual** (Help menu of TOPSPIN > Help > Programming > Pulse Programming).

The most important differences between Standard Acquisition and Pipeline Acquisition concern

- access to *ParaVision* parameters is only possible in Pipeline Acquisition,
- storage of acquired data is controlled by different commands,
- enhanced gradient controller commands are available in Pipeline Acquisition.

Control of the **gradient controller** plays an essential role for imaging sequences.

3.2.6.2 Editing and Execution of a Pulse Program

A **pulse sequence** in *ParaVision* is set up in the form of a pulse program, i.e. as a sequence of appropriate pulse program commands (as described later). Like programs in higher programming languages a pulse program is set up using a text editor and stored as a text file. By convention, filenames containing pulse programs usually have a suffix `.ppg`.

3.2.6.2.1 The Current Pulse Program

The pulse program specified within the ACQP class by the parameter PULPROG (e.g. `PULPROG = SINGLEPULSE.ppg`) is called the **current pulse program**. When the current dataset is READY this current pulse program will be started for the next **Experiment**. The current pulse program file itself must be located within the directory `<PvInstDir>/exp/stan/nmr/lists/pp/` for Bruker library methods or `<PvInstDir>/prog/curdir/<user>/ParaVision/exp/lists/pp/` for user Methods. Otherwise an error message occurs when trying to start GOP, GSP or GS Auto: File not found..."

Attention: Special hints for COMPLETED datasets:



The current pulse program of a COMPLETED dataset may be not the pulse program used during data acquisition. For reference, the expanded text of the pulse program used for acquisition is stored in the file `pulse program` within the data set.

3.2.6.2.2 Start of a Pulse Program

A pulse program can only be started as current pulse program. The execution is started by one of the three Pipeline Acquisition commands implicitly associated with a scan instruction.

- **GOP**
- **GSP**
- **GS Auto**

Individual pipeline acquisition commands can be selected in the Instruction Card in the parameter editor in the examination card.

3.2.6.2.3 Termination of Pulse Program Execution

A running pulse program may be terminated any time by clicking the **STOP** button. In case of interrupting a **GOP** “pipeline” only a part of the acquired data is stored (and a message about this is displayed).

3.2.6.3 General Pulse Program Features

Pulse program statements can be classified into several groups:

- pulse sequence timing
- RF-Pulse generation
- data acquisition
- controlling data flow
- expressions
- controlling further hardware units

As mentioned before, gradient control is an essential aspect of pulse sequences.

Sometimes it is useful to have a little background knowledge of the pulse program compiler in order to understand the effect of certain actions.

C-Preprocessor

Before the text of the pulse program is evaluated in *ParaVision*, it is passed through a C-preprocessor `cpp`. The preprocessor will process include statements to combine the pulse program text from various files. Macros will be substituted and conditions can be evaluated. You can find further information on these concepts in the operating system man-pages for the preprocessor (`man cpp`) or in standard literature on the C programming language.

Include Files

Any pulse program for an MR imaging system must include the header file `MRI.include` in the beginning with the statement

```
#include "MRI.include"
```

This provides necessary definitions for operating the *AVANCE* system. Preparations and further definitions for certain spectrometer platforms are made in the macro `INIT_DEVICES`, which must be executed after parameter definitions immediately before the first delay in any *BRUKER* pulse program.

Comments

The text following a semicolon (;) until the end of a line will be ignored.

User Defined Names

User defined names may have arbitrary length, but only the first 15 characters are significant. This is true for pulse and delay names and user defined lists. The names of *ParaVision* parameters in a pulse program may have arbitrary length and all of the name will be significant.

Commands and Parameters

Many pulse program commands are closely related to *ParaVision* parameters.

Pulse Program Command	Related Parameters
d0-d63	D[0]-D[63]
p0-p63	P[0]-P[63]
l0-l63	L[0]-L[63]
fq1-fq3	ACQ_O1_list-ACQ_O3_list/ACQ_O1_list_size-ACQ_O3_list_size
sp0-sp63	ACQ_RfShapes[0]-ACQ_RfShapes[63]
aqq	SW_h ACQ_size[0]
ADC_INIT	DE

The table shows a list of parameters related to pulse program commands.

3.2.6.4 Pulse Sequence Timing

A pulse program is used to control the exact timing of an **MR-Experiment**. So the first aspect of a pulse program is to specify the starting point and duration of each action. For this reason, a pulse program is built out of a sequence of consecutive time intervals, so called delays. Any action specified will typically start at the beginning of such a time interval. Only special complex actions may have an offset, to become active or will imply preparations to be executed in advance.

3.2.6.4.1 Delay Commands

To specify a certain time amount, a delay command is used within a pulse sequence. No action is caused by a delay command. In most cases, the duration of a delay command is linked to a delay parameter. For this reason, instead of a delay command or delay parameter, we often refer to either simply as a delay, when the meaning should be clear from the context. There are several different groups of delay commands:

Fixed Delay Commands

Fixed delays specify the absolute time for a duration. They are built out of a nonnegative fixed point number and a time unit. Valid time units are **s** for seconds, **m** for milliseconds and **u** for microseconds. The time unit must be added to the length without a blank.

Examples are:

```
1u      ;1 microsecond
17.3m   ;17.3 milliseconds
0.2s    ;0.2 seconds
```

General Purpose Parameter Delay Commands

There are 64 predefined parameter delays available. They are called **d0...d63** and they are initialized from the contents of the ACQP parameters **D[0]-D[63]** evaluated as seconds. Because of the limited number of these delays, usually certain conventions are observed for their use, which make it easier to understand pulse sequences.

Examples are:

```
d0; wait for time defined in D[0] - typically repetition time
d4; wait for time defined in D[4] - typically ramp delay
```

Predefined Delay List Commands

In addition to the predefined parameter delays, a built in list of delays of arbitrary length exists. The length of the list is defined by the parameter ACQ_vd_listsize, the list entries are initialized from the values of the parameter array ACQ_vd_list. The command for executing the built in delay is `vd` (variable delay).

Example:

```
vd ; duration according to a list entry depending on pointer
    ; position
```

The list pointer can be incremented by one by the command `ivd` given within an arbitrary delay. The list index can also be addressed directly in an expression as `vdidx`. The following example illustrates the use of index manipulation commands:

```
vd          ; current delay
0.1u ivd   ; move to next list entry
vd          ; next delay
"vdidx=0"  ; move to first list entry.
vd          ; first delay
```

User defined delay lists can be manipulated easier than the predefined delay list. For this reason, the use of a user defined delay list is recommended.

User Defined Delay Commands

In the same way as predefined parameter delays, further delay commands can be defined. These delays can be initialized from a (double valued) parameter, if the parameter name is given in its definition.

The syntax is:

```
define delay <delayname> [ = { $<parameternname> } ]
```

with the initialization part optional. If no initialisation parameter is given, the value is set to 0. In this case, the delay must be assigned a value in an expression.

Examples are:

```
define delay risetime = { $PREEMP_ramp_time }
"risetime = abs(risetime) * 1E-6" ; rescaling may be necessary
define delay aqq
"aqq = td * dw" ; delay initialized from dw and scansize
...
risetime      ;
aqq          ; typical acquisition time
```

User Defined Delay List Commands

In a similar way as user defined delay commands, delay lists can be defined and initialized from a parameter.

The syntax is:

```
define list<delay> <delayname> = { $<parameternname> }
```

or

```
define list<delay> <delayname> = { <list of double numbers> }
```

Delay lists must be initialized during the definition either from a parameter (an array of double precision numbers) or directly from a list of floating point numbers (which are interpreted as the lengths of the delays in seconds).

Examples:

```
define list<delay> reldel = { 0.1 10 30.0 }
define list<delay> pulses = { $P } ; pulses in seconds
...
pulses ; wait P[0] interpreted as seconds
reldel ; wait 0.1 second
```

A collection of commands exists to switch between different positions in user defined delay lists. These commands are described in Chapter [Navigating in User Defined Lists \[▶ 649\]](#).

Special Delay Commands

In addition to the freely accessible delay commands d0–d63, a few built in delay commands exist with special meanings. Their values depend on configuration parameters or different acquisition parameters. In pipeline acquisition these parameters are usually not used. These delay commands are dw, aq, de, derx, deadc, depa, dwov. These built-in commands are used for the fine tuning of the start of acquisition and acquisition time and are usually hidden from the user. They are closely linked to hardware properties and for this reason may change their meaning or disappear in future. For this reason, their use is not recommended in *ParaVision* pulse programs. The interested user can find a precise description in the Help menu of TOPSPIN: *NMR-SUITE Pulse program Manual*, chapter 3.1, “Special Purpose Delays”, p.40 and in the *TOPSPIN Acquisition Commands and Parameters*, chapter 2.4, “Acquisition (eda) Parameters”, p. A-11.

Delay Commands with Constant Factor

Any of the delay commands described above may be combined with a constant factor, to be scaled.

Example: `d0*0.5 ; delay of d0/2`

Implicit Delay Commands

Many actions can be executed without explicitly specifying a delay for their execution. In this case a default duration is used for the command. If you want to be sure about the duration of a command, you should specify the command with an explicit delay.

Additional Remarks

Durations may be specified with arbitrary (double) precision. Any calculations will again be performed with this precision. You must note however, that hardware units work with a fixed clock frequency. Typically the timing resolution is 12.5 nanoseconds, i.e. any duration will be rounded to a multiple of 1.25E-8s. You should have this in mind when fine tuning your pulse sequence. Certain hardware units may have a coarser resolution however.

The following section of a pulse program summarizes the use of delays. The resulting timing for a given parameter context is illustrated in Figure [Delays in pulse sequences \[▶ 633\]](#).

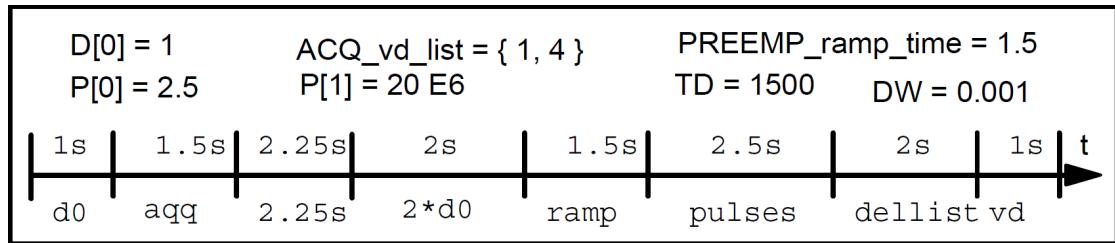


Figure 3.8: Delays in pulse sequences

```

define delay ramp = { $PREEMP_ramp_time }

define delay aqq
    "aqq = td*dw"

define list <delay> pulses = { $P }

define list <delay> dellist= { 2 }

d0
aqq
2.25s
2*d0
ramp
pulses
dellist
vd

```

3.2.6.4.2 Pulse Duration Commands

In addition to the delay commands described in the previous sections, a similar set of commands exists to describe the timing of transmitter pulses. The general philosophy is to replace the term delay by pulse wherever it occurs and the letter `d` by `p`. These pulse delays will generate a transmitter pulse, whose properties are controlled by several parameters and commands. These will be described in detail in Chapter [RF-Pulse Generation \[▶ 635\]](#). Below we describe the different types of pulse delay commands as for delay commands. The same ambiguity between pulse delay commands and pulse delay parameters exists as for simple delays. Sometimes pulse delays are simply referred to as pulses, though the complete description of a pulse involves further description. You should be aware of the fact, that **pulse delay parameters** describe durations in **microseconds** in general, where delay parameters are in seconds.

Fixed Pulse Delay Commands

Fixed pulse delays give the absolute time for a pulse duration. They consist of a fixed point number, a time unit and the letter `p`. Valid time units are `s` for seconds, `m` for milliseconds and `u` for microseconds. The time unit must append the length without a blank.

Examples:

```

12up      ;12 microseconds
2.3mp     ;2.3 milliseconds
1.2sp     ;1.2 seconds

```

General Purpose Parameter Delay Commands

There are 64 predefined parameter pulse delay commands available. They are called p0...p63 and they are initialized from the contents of the ACQP parameters P[0] - P[63] interpreted as microseconds. Because of the limited number of these delays, usually certain conventions are observed for their usage, which make it easier to understand pulse sequences. Examples are:

```
p1; pulse of length defined in P[1]
; - typically excitation pulse
p2; pulse of length defined in P[2]
; - typically refocusing pulse
```

Predefined Pulse Delay List Command

In addition to the predefined parameter pulse delays, a built in list of delays of arbitrary length exists. The length of the list is defined by the parameter ACQ_vp_listsize. The list entries are initialized from the values of the parameter array ACQ_vp_list[]. The command for executing the built in delay is vp (variable pulse).

Example:

```
vp ; pulse duration according to a list entry depending on
; pointer position
```

The list pointer can be incremented by one by the command ivp given within an arbitrary delay. The list index can also be addressed directly with an expression vpidx. The following example illustrates the use of index manipulation commands:

```
vp ; current delay
0.1u ivp ; move to next list entry
vp ; next delay
"vpidx=0" ; move to first list entry.
vp ; first delay
```

User defined pulse delay lists can be manipulated more easily than the predefined pulse delay list. For this reason, the use of a user defined pulse delay list is recommended.

User Defined Pulse Delay Commands

In the same way as predefined parameter pulse delays, further pulse delay commands can be defined. These pulse delays can be initialized from a (double precision valued) parameter, if the parameter name is given in its definition. Its value is interpreted as pulse length in microseconds. The syntax is

```
define pulse <pulsename> [ = { $<parameternname> } ]
```

with the initialization part optional. If no initialisation parameter is given, the value is set to 0. In this case, the pulse delay must be assigned a value in an expression. Examples are:

```
define pulse trigpul = { $PVM_trig_time }
define pulse px
"px = 10u"      ; pulse delay initialized in expression
...
trigpul         ; pulse duration depends on PVM_trig_time
px              ; 10 microsecond pulse
```

User Pulse Delay List Commands

In a similar way as user defined pulse delay commands, pulse delay lists can be defined and initialized from a parameter. The syntax is

```
define list<pulse> <pulsename> = { $<parametername> }
```

or

```
define list<pulse> <pulsename> = {<list of float numbers>}
```

Pulse delay lists must be initialized during the definition either from a parameter (an array of double precision numbers) or directly from a list of floating point numbers (which are interpreted as the lengths of the pulses in microseconds).

Examples are:

```
define list<pulse> relpul = { 10 0.5 20.0 }
define list<pulse> delays = { $D } ;delays in microseconds
...
delays ; pulse D[0] interpreted as microseconds
relpul ; pulselength 10 microseconds
```

A collection of commands exists, to switch between different positions in user defined pulse delay lists. These commands are described in Chapter [Navigating in User Defined Lists \[649\]](#).

3.2.6.4.3 Simultaneous Durations

Sometimes it is necessary to describe actions, which take place simultaneously. Within a pulse program, sequences of independent actions can be defined in parentheses within the same line and then will be evaluated in parallel:

(<first duration sequence>) (<second duration sequence >)

The overall length of multiple parallel duration sequences is the length of the longest sequence. E.g. the sequence

(10m ... 5m ...) (5m ... 1m ...)

will last 15 milliseconds with actions possibly taking place after 5,6,10 and 15 milliseconds. You can find further information on parallel timing in the *NMRSUITE Pulse program Reference Manual*, chapter 1.7, Simultaneous Pulses and Delays, p.41.

3.2.6.5 RF-Pulse Generation

A general RF-Pulse can be described by a number of properties:

- duration (pulse length)
- amplitude (pulse strength)
- carrier frequency + offset
- carrier phase
- shape

The following sections describe how arbitrary pulses can be generated in a pulse program.

Pulse Duration

The pulse duration is defined by a pulse delay command `p0,...,p63`. If no further arguments are given to the pulse delay command, a rectangular shaped pulse will be transmitted on channel F1 with the phase, frequency and amplitude currently selected for this transmitter channel. This default behavior is sufficient for basic spectroscopy **Experiments** and allows the user to write very compact pulse programs.

Pulse Shape and Amplitude

The pulse shape and pulse amplitude are defined by a shape postfix specifier `sp0,...,sp63` separated by a colon. The shape commands select a shape description defined in the parameter **ACQ_RfShapes**. The parameter also specifies the powerWatt (in Watt) of the individual pulse. A frequency offset (implemented by pointwise phase increment) and phase alignment may also be given – these features are not used in ParaVision pulsprograms. See section for detailed description of the **ACQ_RfShapes** parameter.

Carrier Frequency

Each transmitter pulse is bound to a transmitter channel. By default this is channel F1. A different channel can be selected by a postfix command `f1,...,f8` separated by a colon. The basic frequency of each transmitter channel is determined by the nucleus which has been selected on that channel. Offset frequencies can be selected by executing a frequency list command `fq1,...,fq8` for the channel according to parameters **ACQ_O1_list**. See Chapter [Frequency Setting Lists \[▶ 651\]](#) below for details.

Carrier Phase

The phase of the carrier signal can be set by phase list commands `ph0,...,ph31`. If the transmitter phase is set within the pulse delay, the actual switching of the carrier frequency will be advanced, to make sure that the carrier signal will be stable when the transmitter pulse is generated. See Chapter [Phase Lists \[▶ 652\]](#) for the handling of phase lists.

Summary

In summary the example below illustrates how to generate an arbitrary pulse, select the correct frequency of the transmitter channel, then specify a pulse delay command with the desired shape and phase.

Example:

```
1m      fq1:f1      ; prepare carrier frequency
        (p1:sp0 ph0):f1    ; pulse delay p1 with shape sp0 (defined
                            ; in ACQ_RfShapes[0]) on channel f1 with
                            ; phase ph0
```

Figure [Composition of an RF-Pulse \[▶ 637\]](#) illustrates the different commands and parameters making up a complete RF-pulse.

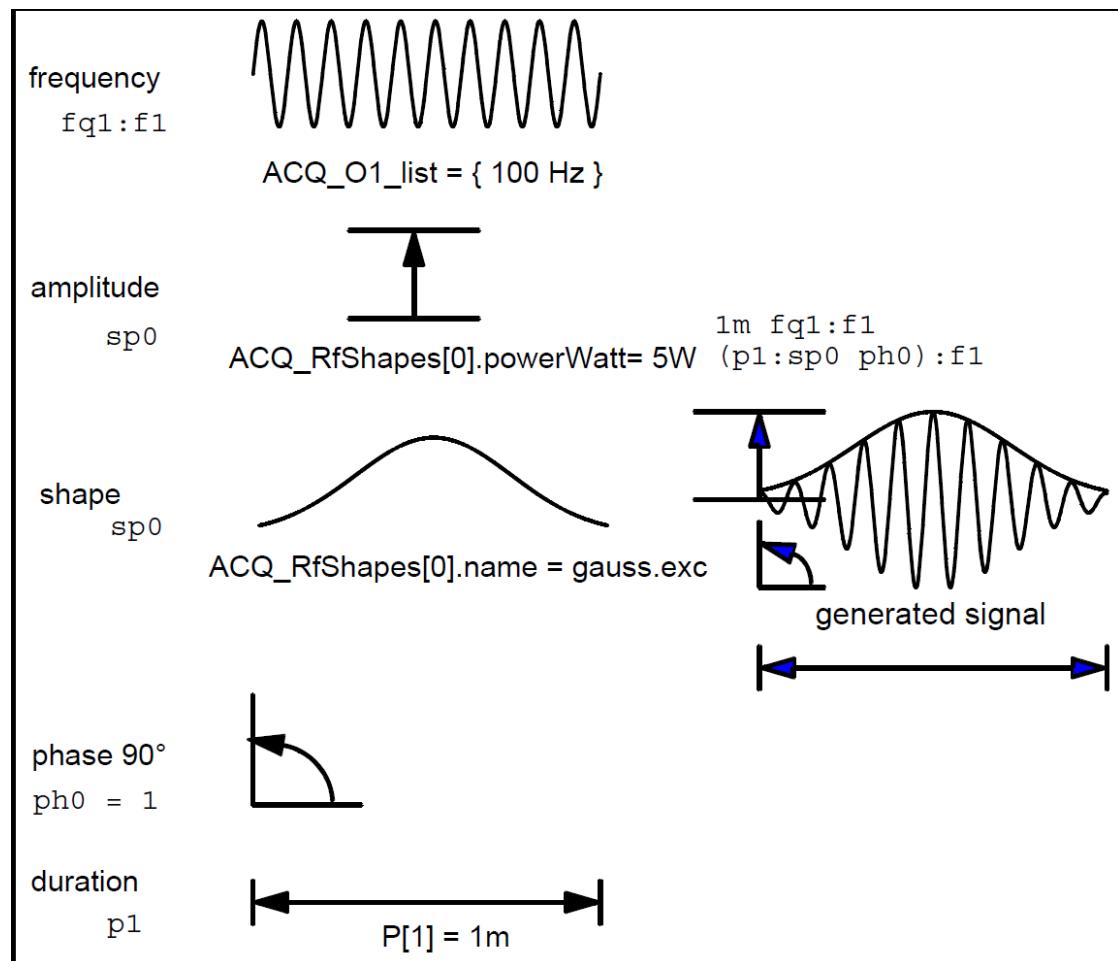


Figure 3.9: Composition of an RF-Pulse

3.2.6.5.1 Technical Details of Pulse Generation

The exact actions taking place during pulse generation depend on the spectrometer configuration and hardware. In any case, the different units, which compose the signal must be triggered. Typical actions are transmitter gating and receiver blanking. When your **Experiment** is sensitive to timing less than microseconds you probably will be interested in the details of the timing. You can find an overview of the impact of setup parameters in the *TOPSPIN Acquisition Commands and Parameters Reference Guide*, chapter 3, Spectrometer configuration commands: edscon, p. A-99.

At this point, we want to give some hints for **troubleshooting**.

To create a pulse, a sequencer unit (F-Controllers) must create rapidly the desired RFshape. This digital device takes as input a discrete function (the shape file) and will switch at predefined time intervals to the next point. The length of the time intervals is determined by the number of points in the shape file and the length of the pulse. Obviously, for a given pulse shape, a minimum delay exists, which is needed to synthesize the desired shape. This delay is typically $100\text{ns} \times \# \text{points}$. If the pulse shape is too short, an error message will be generated, when the **Experiment** is started.

Because calculating shape tables involves complex calculations, it must be done before the start of the **Experiment**. This implies that the amplitude and length of a given pulse are fixed at the beginning of the **Experiment**. Within certain limitations, two parameters can be changed however:

Changing the Power Level

Instead of the predefined power level (ACQ_RfShapes[].powerWatt), the power level currently selected for the pulse channel can be used. This is done by adding the argument currentpower in parentheses to the shape command

```
p0:sp0(currentpower) :f1
```

The power level of a channel must be set by suitable p1 commands prior to the pulse execution, as will be described in Chapter [Power Lists ↗ 655](#). You must note however, that this will not cause a complete recalculation of the shape but just cause a linear modulation of the multiplier unit. I.e. no compensation for nonlinearity of amplifiers is done. If you are using the transmitter at its power limit, you may obtain poorly defined shapes.

Changing the Pulse Delay

Most pulse delays may change their value during the execution of an **Experiment**, e.g. when pulse delay lists are used. Again, the new sequencer table cannot be adapted to the new delay on the fly. By changing registers of the sequencer, the timing of a shape can be modified within a certain resolution, which is a multiple of the number of sampling points of the shape. Error messages will be displayed, when the timing is changed without observing the resolution. In general, you should avoid changing the pulse delay of a shaped pulse, because the result usually will not be, what you intended.

For simple rectangular pulses, i.e. without a shape command, these limitations do not apply.

Gating Pulses

Usually transmitter gating pulses - also called blanking pulses - are generated implicitly by the timing controlled unit at appropriate times (controlled by SCON parameters). Transmitter gating pulses can however also be generated explicitly by the gatepulse command. As parameter the gatepulse command has a list of channels separated by a vertical bar. The gatepulse command must be specified within a delay. Typically, the delay d8 is initialized with an appropriate value. The complete syntax is

```
<delay> gatepulse 1 [ | 2 ...]
```

The explicit generation of gating pulses may be necessary for fast imaging **Experiments**, when the implicit generation of the blanking exceeds the capacity of the timing control unit. The command preset off at the beginning of a pulse program will pass responsibility of generation of gating pulses to the pulse program. The use is illustrated in the following example:

```
preset off  
...  
3u gatepulse 1      ;generate blanking pulse for f1  
p1:f1              ;generate pulse on channel 1  
d1  
2u gatepulse 1|2    ;generate blanking pulses for f1 and f2  
(p1):f1 (p2):f2   ;parallel pulses on channel 1 and 2
```

3.2.6.6 Data Acquisition

From one point of view, the data acquisition process simply consists of triggering a digitizer to start data collection at a predefined rate for a given number of points. In practice several different hardware units are involved in data acquisition and must be controlled: coils, preamplifiers, receivers, digitizer, DRU units. A collection of macros built of more basic

commands is used in imaging pulse programs to trigger and synchronize these actions. These macros divide the complete acquisition process into three different steps, which are necessary to prepare acquisition, start it and mark its end. This approach is necessary to make sure, that hardware units will not interfere at unexpected points. The basic commands, which in fact depend on the installed hardware components are explained in detail in the *NMR-SUITE Pulse program Reference Manual*, chapter 9.1, Start data acquisition, p.98. It is strongly advised, to use the proposed macros for acquisition in order to write pulse programs, which are portable to different spectrometer configurations. The macros are defined in the `MRI.include` header file which must be inserted into the pulse program.

Preparation of Acquisition

The macro `ADC_INIT` is used to prepare the scanner for acquisition. It includes a delay of `length = de`: this is in fact the minimum admissible time between the end of a pulse and the beginning of acquisition. The `ADC_INIT` macro has two parameters: the receiver phase and the synthesizer phase (reference phase):

```
ADC_INIT(receiver phase, reference phase)
```

A phase list must be used for both parameters. The receiver phase may be omitted by specifying `NOPH` instead. The main task of this macro is, to open gates in advance, switch the RF-chain to generate the correct input frequency for the receiver. For multi slice **Experiments**, phase coherence is necessary. This is usually achieved by using a second internal synthesizer channel, which can provide phase coherent frequency switching. This assumes of course, that the correct frequency values are set. Details on frequency switching can be found in Chapter [Frequency Setting Lists \[▶ 651\]](#).

Start of Acquisition

The generation of dwell pulses and thus the operation of the digitizer is started with the `ADC_START` macro. It must occur within a delay - typically `aqq`. The number of points acquired is `ACQ_size[0]` accessible also as constant `td` (time domain) in the pulse program.

For special imaging **Experiments**, subsequent lines in k-spaces sometimes must be acquired with or without a very short delay between the lines. Setting the parameter `ACQ_scan_size` to `ACQ_phase_factor_scans` assures, that `ACQ_phase_factor_scans` will be acquired at once by a single `ADC_START` command. This features is deprecated. Instead, the scan size should be set to the length of the combined scan. In single shot methods like EPI, the complete acquired scan may have to be regridded or partially mapped out. For this reason there is no direct association between the number of acquired points and the final image grid.

End of Acquisition

The end of acquisition must be marked in the pulse program with an `ADC_END` macro. The `ADC_END` can be used within a delay, otherwise a delay of 3 milliseconds (3 ms) will be automatically inserted. The minimum duration which can be used depends on the hardware, but is typically 8 microseconds (8 us). The `ADC_END` macro will ensure, that the correct internal synthesizer channel is reselected and correct frequencies are set. No phase increment is performed at this point.

The time between the start and the end of scan must be sufficient for the digitizer to collect all the points taking into account also implicit delays at the beginning of the scan and a possible scanshift for group delay compensation. This time is always longer than the theoretical acquisition time `aqq=dw*td`. A delay parameter `DEOSC` is however available, which contains the minimum necessary time between start and end of acquisition (in microseconds) depending on bandwidth and digitizer settings. To use this parameter in your pulse program as a delay, you should add the definition in the beginning of your pulse program:

```
define delay deosc = { $DEOSC }
"deosc = 1.0E-6*abs(deosc)"
```

The redefinition of the value in the second line is necessary, because the value of the parameter DEOSC is specified in microseconds in analogy to the value of the delay DE internally. The two lines above may become part of a default header file in future.

It does not cause any problems, to wait longer than this time between the start and end of acquisition and so the ADC_END macro may be executed at a point together with another action e.g. a gradient command.

Special Requirements

No frequency setting commands may occur between ADC_START and ADC_END.

The minimum delay between ADC_END and ADC_INIT commands is approximately 0.7ms. If the timing is shorter, runtime errors may occur or scans may be ignored leading to incorrect images.

For special purposes (e.g. single point imaging) the digitizer can be used in a mode where the dwell pulses for the digitizer are generated individually for each single data point.

Basic Commands

The macros described above make use of basic commands for frequency switching, adc triggering etc. A detailed description of these commands can be found in the *NMR-SUITE Pulse program Reference Manual*, chapter 4.1, Start data acquisition, p.69. Use of these basic commands will in general produce pulse programs, which will not run on every AVANCE spectrometer without modification. You can however still execute pulse programs developed for your spectrometer in earlier versions of *ParaVision*.

The use of pulse program macros, hardware units and parameters is illustrated in Figure [Data Acquisition \[640\]](#).

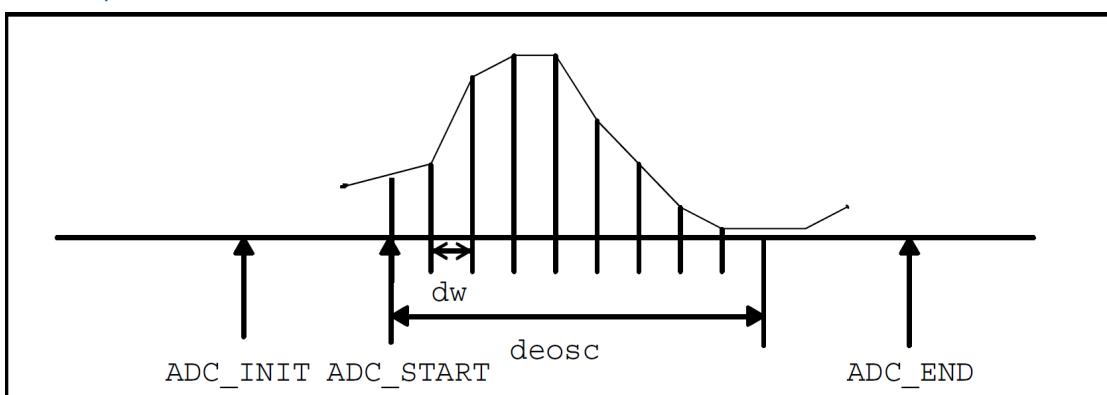


Figure 3.10: Data Acquisition

The following example shows minimum timing for a pulse program created with the acquisition macros described above.

```
#include <MRI.include>
define delay deosc = { $DEOSC }
"deosc = 1.0e-6 * abs(deosc)"
INIT_DEVICES
p1
ADC_INIT(NOPH,ph0)
deosc ADC_START
```

```

8u ADC_END
exit
ph0 = 0

```

External Dwell Pulses

For certain applications such as single point imaging, it is necessary to acquire each point separately. For that purpose, the dwell clock for the digitizer can be generated separately for each single point. The mechanism and syntax used here is essentially different for systems with AQX and AQS racks and thus must be handled separately. The `ADC_INIT` and `ADC_START` macros cannot be used in these cases.

For AQS rack systems, the dwell signal is generated by the FCU/SGU. In standard **Experiments**, a decoupling sequence will fulfill this purpose (as you can see inspecting the definition of the `ACQ_START` macro). This is the reason, why this macro cannot be used in this case. The preparation must be done explicitly instead. The macros `DWL_CLK_ON` and `DWL_CLK_OFF` will generate a single dwell pulse in this case. The following example illustrates the generation of external dwell pulses for AVANCE AQS systems:

```

deparx      RGP_PA_ON
derxadc    RGP_RX_ON
rdeadc     RGP_ADC_ON
1u DW_CLK_ON
dw*2 DW_CLK_OFF
10u ADC_END

```

Acquisition of the pair of data points will start at the beginning of the dwell clock pulse, the length of this pulse itself is not relevant.

On Avance II/III spectrometers (with DRU) the digitizer is running continuously at a sampling rate of 20MHz. This grid for data acquisition cannot be changed but the points to form a scan from the stream of sampled data can be selected individually by switching a dwell pulse on and off with the `DWL_CLK_ON` and `DWL_CLK_OFF` macros in analog mode. A simple averaging filter will be applied when the parameter `anavpt` is set in a relation at the beginning of the pulse program, e.g. `anavpt = 4`

Its value must be a power of two and is one by default. Each dwell pulse will then sample `anavpt` points which are averaged.

For special hardware / digitizer combinations, further actions may be necessary.

The pulse program `wobble.ppg` may serve as a reference for an application using external address advance.

The macros described above are linked to basic acquisition parameters `ACQ_size`, `SW_h`, `RG` which were designed for description of a single dataset acquired with cartesian trajectories.

Job Based Acquisition

A further parameter `ACQ_jobs` may be used to overwrite these settings and use more than one sets of digitizer settings within a single experiment together with specific commands to select the different parameter sets. Jobs may differ in acquisition size and receiver gain. The setting of different sweepwidths is experimental and will not work for arbitrary combination of dwelltimes.

A maximum of 8 individual acquisition jobs could be used within a single pulse program. Current ParaVision library pulse programs make only use of two independent jobs. For this application convenience macros are defined to allow straightforward access to acquisition jobs. Further jobs could be addressed by extension of those macros (defined in the MRI.include file) in an analogue way.

Job based acquisition has the following parts:

- Different macro for initialization
- Preparation of an acquisition job
- Job specific adapted acquisition macros

When jobs are used, the INIT_DEVICES macro must be preplaced by the INIT_DEVICES_JOBS macro.

The actual sequence of acquisition macros (ADC_INIT/START/END) for a single job must be replaced by the corresponding job specific version (ADC_INIT/START/END_JOB0/1). Mixing the commands for a single job will result in runtime errors.

To prepare a job, the command SWITCH_JOB0/1 must be executed before the corresponding ADC_INIT_JOB0/1 command. A minimum time of about 50u must be respected. Each job can make use of an individual receiver gain. The job specific receiver gain can be selected with macros RG_JOB0/1. The job can be incremented by a NEXT_RG command. These receiver gain selection macros have built in delays of 10u resp 200u. Please be aware, that the settling time of the actual receiver hardware may be considerably longer. For this reason it is advised, to select the receiver gain for the next job as early as possible after terminating data sampling of the previous one.

The following table summarizes Job macros with the corresponding timing constraints.

Command	Duration	Timing Constraints
INIT_DEVICES_JOBS		wait at least 200u until next RG command
RG_JOB0	10u	wait at least 200u until next RG command
RG_JOB1	200u	wait at least 200u until next RG command
NEXT_RG	10u	wait at least 200u until next RG command
ADC_INIT_JOB0	de	
ADC_INIT_JOB1	de	
ADC_START_JOB0		needs delay scanSize * sweepwidth
ADC_START_JOB1		needs delay scanSize * sweepwidth
ADC_END_JOB0		minimum 10u
ADC_END_JOB1		minimum 10u
SWITCH_JOB0		minimum 10u needs 40u until ADC_INIT
SWITCH_JOB1		minimum 10u needs 30u until ADC_INIT

The order of acquisition of the different jobs is deliberate.

Example

```
INIT_DEVICES_JOBS

start, RG_JOB1 ;200u
...
10u SWITCH_JOB1; needs delay
```

```

...
; wait at least 50u
ADC_INIT_JOB1(ph0,ph1)
aqjob1 ADC_START_JOB1 ; delay must be long enough
10u ADC_END_JOB1
100u
...
NEXT_RG ; wraparound to job 0 - first select receiver gain
10u SWITCH_JOB0 ;
...
ADC_INIT_JOB0(ph0,ph1)
aqjob1 ADC_START_JOB0
10u ADC_END_JOB0
100u
lo to start times 11

```

Attention: Using job based macros without correct setting of the **ACQ_jobs** parameter will lead to runtime errors.

The number of scans acquired in the pulse program must match the parameter **ACQ_jobs[].dummyScans** + **nTotalScans** for a GOP experiment. In setup mode, the number of scans making up one setup step is given by the parameter **ACQ_jobs[].transactionBlocks**.

3.2.6.7 Flow Control - Dynamic Aspects of Pulse Programs

This section deals with commands and structures which describe dynamic aspects of pulse programs. This includes changing values of variables in expressions during runtime, decisions, repetition of code segments and navigation within lists.

3.2.6.7.1 Expressions

During a pulse sequence, various arbitrary calculations can be done forming expressions with pulse program parameters such as delays, loop counters, etc. *ParaVision* parameters cannot occur in expressions. The *TOPSPIN* parameters **ds**, **td**, **dw** are allowed in expressions written before the first delay (see later).

An expression must be a part of an assignment, unless it is used as a condition in an **if**-statement (see Chapter [Statements if and else \[▶ 645\]](#)).

An assignment is enclosed in double quotes and has a syntax close to the C-programming language. In addition, timing units will be converted correctly, when this makes sense. For this reason, we will not describe each operation in detail but give a short list of operators and functions available in expressions, closing with a comprehensive example.

Operators:

assignment (with operation)	=, *=, /=, +=, -=
logical tests	==, !=, &&,

arithmetic operators	* , /, +, -
function calls	abs, acos, asin, atan, cos, exp, sin, log, nextpow, pow, sin, sqrt, tan, trunc

Table 3.5: Assignment operators

Examples:

```
"10 += 1" ; increment 10 by one
"d1 = log(d1)" ; assign to d1 its natural logarithm
"d2 /= (3 * pow(d2,3))" ; divide d2 by 3 times its 3rd power
"10 < 23*11-2" ; test for 10
```

An important remark must be made on the position of assignments within the pulse program. We have to distinguish two different cases:

- A) When an assignment is made before the first pulse program delay, the calculated parameter values will be the initial values for the time course of the pulse program. The result of the calculation can be seen in the pulse program display.
- B) When an assignment is made after the first pulse program delay, the calculated parameter values will be evaluated only during runtime. At the beginning of the time course these parameters have no value. Therefore the result of such runtime assignments cannot be seen in the pulse program display even when they work as expected.
- C) *TOPSPIN* parameters `ds`, `td`, `dw` in expressions **before** the first delay will have the current values; in expressions **after** the first delay the starting values are undefined. It is therefore mandatory to place assignments using these *TOPSPIN* parameters before the first delay is executed.

Note: A lot of pulse program commands (e.g. `r2d.inc`, `r2d.dec`, `r2d.res`, used without specification of a duration, generate internal delays and have to be respected as described above. Also the `INIT_DEVICES` macro contains durations which have to be considered with respect to the mentioned rules A), B) and C). `INIT_DEVICES` must be placed after the initial assignments.

3.2.6.7.2 exit, jump and loop - labels

This subsection deals with commands causing the thread of execution to be continued at a different place.

exit command

The `exit` command within a pulse program stops the execution of the pulse sequence immediately. Note, that acquisition started with `GOP` will stop in any case on spectrometers using RCU boards for data acquisition, as soon as the anticipated amount of data has been acquired. The number of scans to be acquired is described by acquisition parameters, see Chapter [Basic ACQP Parameters \[▶ 621\]](#). It is common sense however to finish a pulse program with an `exit` command, even if it will never be reached, in order to mark the end of the duration list.

goto command

The `goto` command can be used to continue the execution of a pulse program at a different position. The argument of the `goto` command is a label, defining the line, where execution is continued.

A label is either a text string followed by a comma or an integer number. Labels must be unique within the pulse program.

Example:

```

        goto 1      ; continue in line labelled 1
start, d1      ; define label start
1      d2      ; define label 1
        goto start ; return to start
    
```

The `goto` command is usually used to repeat the same action endlessly or to branch the flow of control, e.g. in combination with an `if` statement.

lo to command

The `lo to` command is in fact the combination of a decision with a jump statement. It must be specified with a jump label and a counter:

```
lo to <label> times <counter>[*|/ <factor> ]
```

The counter is either a natural number, a loop counter variable 10-131 or a *ParaVision* parameter. Loop counters are initialized from the parameter L[0-31]. A factor, by which the loop counter variable is rescaled by multiplication or division, is possible.

You should note, that the counter specifies the number of executions of the code between label and `lo to` command. You cannot access the internal counter which is updated during each loop. Also changing the value of a loop counter variable during the execution of the command will not influence the execution of the loop.

Finally it is important to note, that the condition for the loop will be evaluated when the flow of control arrives at the jump label, thus the code between the label and the `lo to` command will not be executed at all, if the counter is 0. The following example illustrates the use of the `lo to` command.

```

start, d0
        lo to start times 0 ; no execution of d0
        d1 p1 ; e.g. 2 pulses if ACQ_size[1] = 4
        lo to start times ACQ_size[1]/2 ; ACQ[1]/2 executions
        lo to start times 10 ; L[0] executions
    
```

The execution of a `lo to` statement or a `goto` statement will not insert a delay.

A further loop counter can be defined from *ParaVision* parameters:

```
define loopcounter <loopname> [ ${<parametername>} ]
```

In analogy lists of loop counters can be defined from an array parameter:

```
define list<loopcounter> <listname> = ${<parametername>}
```

or directly:

```
define list<loopcounter> <listname> = {<list of integers>}
```

User defined loop counters can be used in the same way as built in loop counters.

Note: It is important that pulses specified in the same line with the loop label will not be executed. At least several micro seconds are needed between a loop label and subsequent pulses.

3.2.6.7.3 Statements if and else

The `if` statement is used to make decisions depending on parameter values or external conditions. For a real-time program it makes sense to distinguish between static and dynamic decisions. This is reflected in a subtle difference in the syntax of the `if` statement in *ParaVision* pulse programs.

Static Decisions

In most cases (e.g. use of preparation modules), it is obvious at the beginning of a pulse sequence, whether a certain section of a pulse program is executed or not. Usually, this depends on the value of a parameter. For this purpose an `if/else` statement can be used in combination with an expression testing the value of a parameter:

```
if (condition)
{ ; true case
}
[ else
{ ; false case
} ]
```

The `else` branch may be omitted as indicated by the square brackets. The condition is either a parameter name or a constant or the comparison between parameter or constants:

```
parameter
!parameter
parameter < value
parameter <= value
parameter > value
parameter >= value
parameter == value
parameter != value
```

This condition is evaluated once at the beginning of the execution of the pulse sequence for the entire sequence. Then the code parts for which the condition is not fulfilled will never be executed ignoring possible changing values of the parameter during the progress of the **Experiment**. The following example illustrates the use of these static decisions:

```

if ( L[0] > 0)
{
    p1
}
if (ACQ_scan_type == Scan_Experiment)
{
    d1
}
else
{
    1ms
}

```

For parameter settings `L[0] = 0` and `ACQ_scan_type = Scan_Experiment`, this will result simply in the following pulse program.

```
d1
```

Note that the final closed bracket in an `if/else` clause must be on a separate line.

Dynamic Decisions

The second type of decision is a run time decision which will change the flow of control of the pulse program depending on a condition. A loop statement is a special case of such a decision. In a runtime **Experiment** such a decision will not select a difference code block but cause a jump to another statement in the pulse program. The syntax is

```

30u ; Delay to be given at Avance and AV II spectrometers
if trigp.. goto label
    if "expression" goto label
or
    if "expression"
    {
        [else
        {
        }]
    }

```

No `else` statement exists when a `goto` statement is used. An example illustrating the implementation of a loop is shown below.

```

"10 = 5" ; initialize loop counter
start, d1
"10 = 10 - 1"
if "10 > 0" goto start
; 10 has value 0 now

```

You should note, that in this example, the loop counter `I0` effectively changes its value, unlike the loop statement, where the current loop counter value cannot be accessed. Also, the condition is tested only at the end of the loop body, causing the loop to be evaluated at least once. A test at the beginning of the loop body and a `goto` statement at the end would avoid this.

Testing for Triggers

The timing control unit of an *AVANCE* spectrometer is equipped with four trigger inputs. For more information see *System Manual* (section "Triggered data acquisition"). Conditional program execution includes reacting to the state of these inputs.

The first option is to test for the trigger status. This is done by an `if` statement with a trigger condition. A sufficient delay (ca. 20 ms on Avance spectrometers with TCU boards) must be specified between subsequent trig- events. The syntax is:

```
if trig[p|n]l[1-4] goto label
```

The letter `p` represents a positive, the letter `n` negative level. This will cause the execution of the program to continue at the given label, if the trigger condition is fulfilled.

Another option is to stop pulse program execution until a trigger-condition becomes true. Execution can wait either for a given level (letter `l`) or for a given edge (letter `e`). The syntax is:

```
<delay> trig[p|n] [e|l] [1-4]
```

The following example will wait for the trigger signal on input 1 to switch from negative to positive level and repeat execution as long as the trigger signal on input 2 has negative level:

```
d0 trigp1 ; wait for trigger 1
start, d1
p1 ; repeat until trigger 2
if trignl2 goto start
exit
```

Note: On *Avance III* spectrometers, some restrictions hold. Testing for a trigger level in an `if` statement is only supported for negative level, i.e. a command `if trigpl1 ...` will result in an error message. In general the interpretation for the (electrical) trigger level is different: When no trigger device is connected to the trigger input, we detect a positive level while shortcircuiting the trigger input will result in a negative level. This is opposite to the behavior of earlier versions of the *Avance* spectrometer hardware. Finally, waiting for a trigger level will require synchronization to the gradient clock afterwards: You must add a `GRAD_SYNC` command within a short delay (typically 10u) after each wait statement, e.g.

```
d0 trigpl1
10u GRAD_SYNC
```

3.2.6.7.4 Subroutines

In addition to macro replacement by the C precompiler, a more mighty macro mechanism has been implemented, which allows relocation of loop labels and rudimentary type checking. Subroutines can be defined via the statement:

```
subroutine <name>([<argumentlist>]) {<subroutine statements>}
```

The `<argumentlist>` is a comma separated list of declarations of the form `<type><argumentname>`.

Legal types are `pulse`, `delay`, `loopcounter`, `phase` and `any`. `any` allows replacement of arbitrary text. If labels are defined within the subroutine, they will be valid locally, i.e. a subroutine can be called multiply and loops will retain their local meaning.

Subroutines are executed with the `subr` command:

```
subr <name>([<arguments>])
```

Example:

```

subroutine SP0(pulse px)
{
px:sp0
}
...
subr SP0(p1); will be evaluated to p1:sp0
...

```

Subroutine calls may be nested, but recursion is not legal. In fact subroutines are executed by text replacement (you can check the result in the `pulseprogram` file created during pulse program execution).

3.2.6.7.5 Navigating in User Defined Lists

Many commands may occur in form of user defined lists as e.g. delays, pulse delays, frequency setting commands or power setting commands. These lists are similar in the way in which they are defined and how the list elements can be addressed. Each example below concentrates on one list type however.

List Command and List Index

A list in a pulse program consists of the list entries and an index. If no index is specified explicitly, then the current list entry will be used. At the start of pulse program execution, the list index is initialized to 0. Whenever a list command is executed, the list entry corresponding to the current list index is used.

Changing the List Index

The list index can be changed in a couple of ways. It can be incremented by one by a `.inc` postfix operator, it can be decremented by one by the `.dec` postfix operator and it can be reset to 0 by the `.res` postfix operator. Note, that these postfix operators do not execute a list command, they only change the list index. Because execution of a list command and immediate index increment is the most common case, the caret `^` postfix operator can be used to execute a list command and increment the list entry immediately. The following example illustrates the use of the postfix operators for power lists, its effect is illustrated in Figure [Changing a list index in a power list ▶ 650](#):

```

; the example assumes a 600 Watt amplifier i.e. 600W = -6db
define list<power> pwl = { Watt 0.0003 0.3 600 }
    10u pwl:f1           ; index = 0: 60 db, no index increment
    20up
    10u pwl:f1 pwl.inc ; index = 0: 60 db, index increment
    20up
    10u pwl:f1 pwl.res ; index = 1: 30 db, reset index to 0
    20up
    10u pwl:f1 pwl.dec ; index = 0: 60 db, decrement
    20up           ; index to end of list
    10u pwl^:f1       ; index = 2: -6 db, increment
    20up           ; index to start of list
exit

```

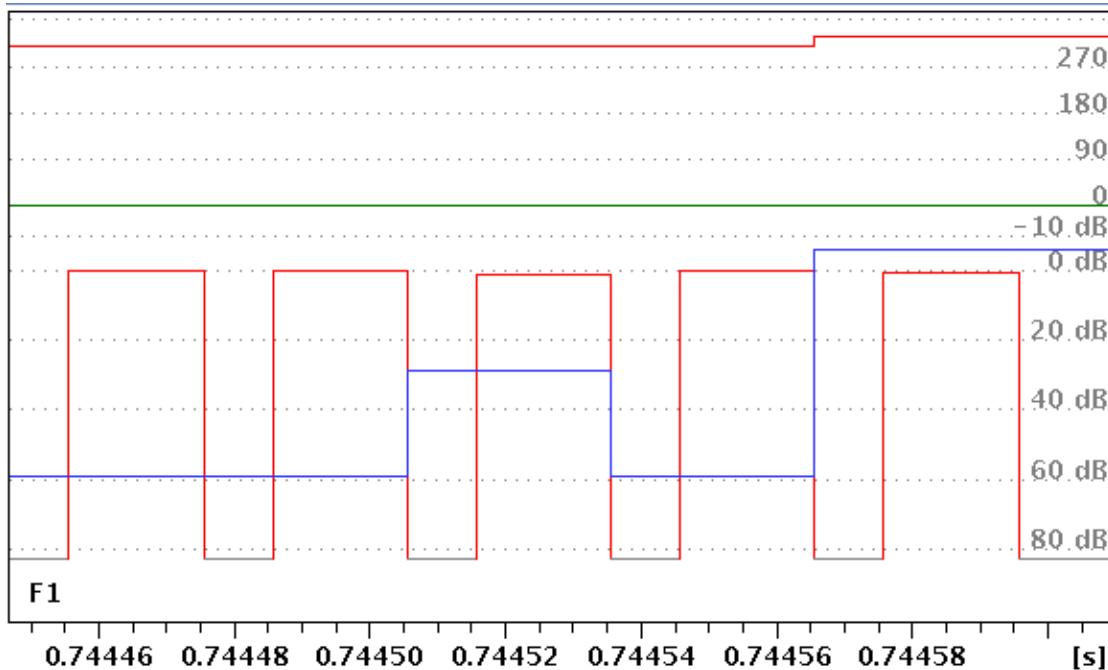


Figure 3.11: Changing a list index in a power list

Finally, the current list index can also be accessed directly for example in an expression. It is addressed by the list name followed by the postfix `.idx`. The length of the list is accessible as read only with the `.len` postfix. The following example shows the access to the list index for a pulse delay list - compare the output illustrated in Figure [Use of index operator in pulse delay lists \[▶ 651\]](#).

```

define list<pulse> pulses = { 40 10 20 }
    pulses      ; first pulse length
    10u
    "pulses.idx = pulses.len / 2" ; set index to 1
    pulses^     ; second pulse length
    10u
    pulses      ; third pulse length

```

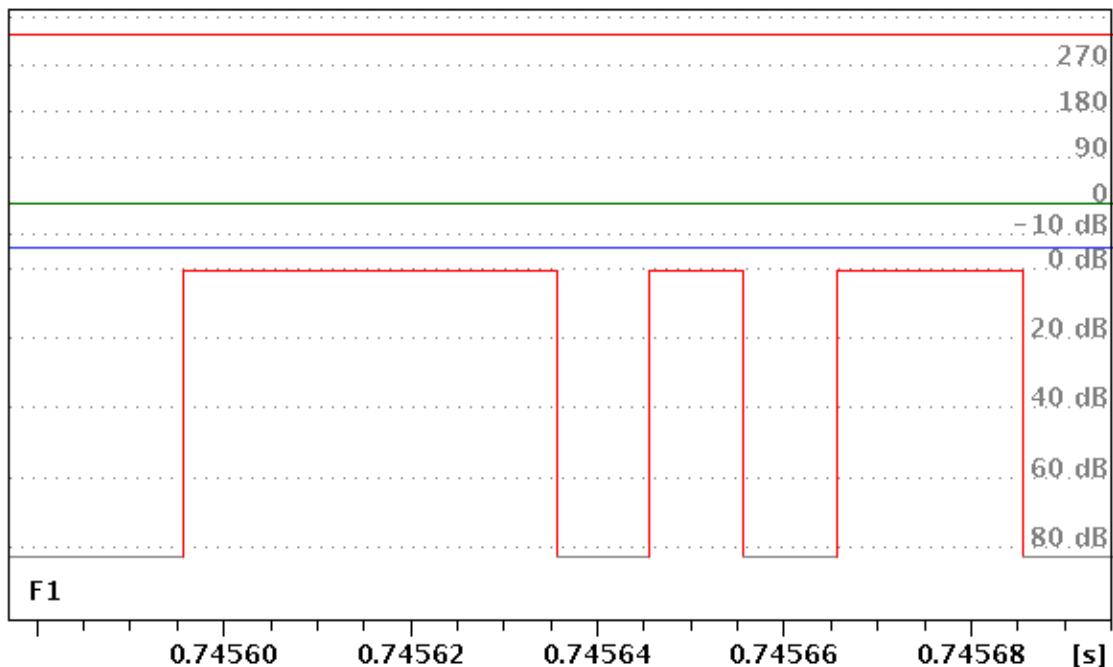


Figure 3.12: Use of index operator in pulse delay lists

Again, all list operations are cyclical, i.e. an increment or decrement behind the end or start of a list will set the index to the start or end respectively.

Direct Access

List entries can be addressed directly by simply adding the index in square brackets after the list name, e.g. `pwl[0]` will address the first entry in a list `pwl`. Indexing ranges from 0 to the length of the list -1, in fact indices will be evaluated modulo the length of the list. Example for modulo: If `pwl` has 3 entries, then `pwl[4]` will be the same as `pwl[1]`. Directly accessing a list entry does not change the list index.

3.2.6.8 Synthesizer Control

3.2.6.8.1 Frequency Setting Lists

The offset frequency of the synthesizers is controlled by frequency list commands. Eight predefined frequency lists `fq1`, ..., `fq8` exist, which can be used within a delay to switch the channel. By default, they are initialized from the parameters `ACQ_O1_list`, ..., `ACQ_O3_list` and `ACQ_O1B_list`. The syntax is

```
<delay> fq1-8:f1-f8
```

Frequency lists have an auto-increment, i.e. each time a frequency setting command is executed, the list index is incremented by 1. User defined frequency lists as defined below do not have this restriction. The minimum execution time of a frequency switch is 2 us.

Apart from the built in frequency lists, further frequency lists can be defined in the same manner as delay list commands. The syntax is

```
define list<frequency> <listname> = { $<ParameterName> }
```

or

```
define list<frequency> <listname> = { <offset list> }
```

User defined frequency list commands can be used in the same way as the built in frequency setting commands, but they do not have a built in increment. In Chapter [Navigating in User Defined Lists \[649\]](#) it is explained how to select specific list entries. Further commands for direct frequency settings exist (rarely used for imaging **Experiments**). See the NMR-SUITE Pulse program Reference Manual chapter 1.5.2.2, Using frequency lists, p.16.

For many imaging **Experiments**, it is essential to switch between transmit and observe frequency and back while maintaining the phase of the transmit signal. This is achieved by providing two independent oscillators on a single SGU unit which may maintain different phases and frequency offsets and can be selected individually. Figure [Frequency switching from the first DDS channel to the second and back \[652\]](#) illustrates the difference between phase coherent and phase continuous frequency switching.

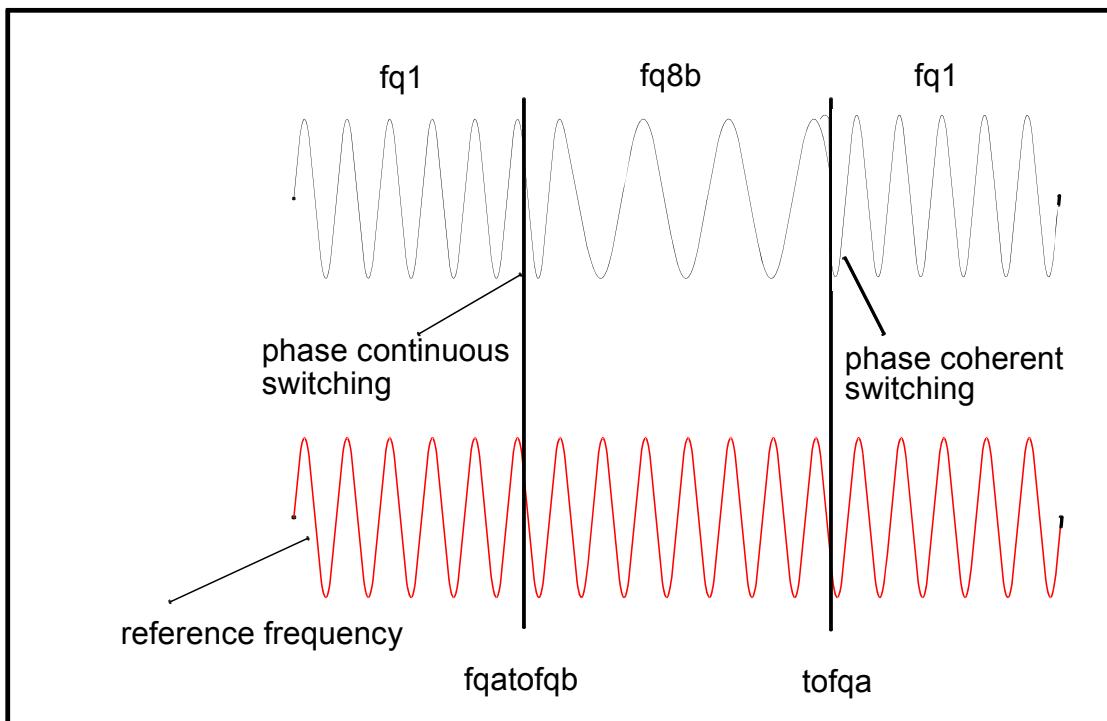


Figure 3.13: Frequency switching from the first DDS channel to the second and back

Frequency setting on the receive synthesizer is done by using frequency lists with the suffix **b** or adding the keyword (**receive**) after frequency switching.

The link between *ParaVision* parameters and built in frequency lists is made via the FQ1LIST - FQ8LIST parameters. They contain as text the name of the corresponding *ParaVision* parameter, from which the corresponding list **fq1-fq8** is initialized. By default, FQ1LIST - FQ3LIST are linked to ACQ_O1_list - ACQ_O3_list and FQ8LIST is linked to ACQ_O1B_list.

3.2.6.8.2 Phase Lists

Phase settings of a synthesizer are implemented by phase lists. There exist 32 predefined phase lists **ph0-ph31** which can be assigned values within the pulse program.

Definition of Phase Lists

The definition of phase lists must be at the end of the pulse program, i.e. after the last delay. The basic syntax is

```
<ph0-31> = [ ( divisor ) ] <phaselist>
```

The divisor is the fraction of the full circle, which is used as a basis for the calculation of phases, i.e. the multiplier for the entries of the phase list is $m = 360/\text{divisor}$. Each entry within the phaselists will be multiplied by the multiplier. The default divisor is 4, i.e. the default multiplier is 90.

Basically, a phaselists is a list of integer numbers, which will be multiplied by the multiplier for the definition of the phase values. A typical example is

```
ph1 = (4) 0 1 2 3
```

This will have phase angles of 0, 90, 180, 270 degrees. Several shortcuts are possible for the definition of complicated lists:

- { }ⁿ: repeat list in braces n-1 times
- { }^m: repeat list in braces m-1 times but shifting each phase once by the multiplier of the list
- For each repetition a subcomponent may also consist of another phase program and subcomponents may be concatenated by a plus sign.

Example:

```
ph0 = 2 3;180 270
ph31 = (12) 4 5;120 150
ph2 ={{1 2}*2}^3 ;90 180 90 180 180 270 180 270 270 0 270 0
ph1 = ph0^2 + ph31*2 ;180 270 270 0 120 150 120 150
```

Remarks:

- Phase list definitions may extend to more than one line - the definition can just be continued in the following line.
- The initialization of a phase list from a *ParaVision* parameter is not possible at the moment.

Definition of Phase Programs Using List Syntax

Instead of setting up ph0-ph31 at the end of the pulse program, a phase program may also be defined by a list definition, which must then occur at the beginning of the pulse program:

```
define list<phase> PhList1 = { 0.0 180.0 90.0 270.0 }
```

This statement defines the phase program PhList1 with phase values of 0°, 180°, 90° and 270°. Note that in contrast to the previously described definitions of phase programs, all angles are written in degree in this syntax. Instead of initializing the phase program directly with {}-brackets, you may also specify a PARX parameter that contains the phase list in {} brackets with a \$ sign before the variable name.

Example:

```
define list<phase> PhList2 = {$PHLIST}
```

Phase setting from user defined phase programs is done in the same way as with the standard phase programs by specifying the phase program after a pulse statement.

Example:

```
(p0:sp0 PhList2):f1
```

After initialization, the current value of a user defined phase program is its first entry. You can access other entries by using the list operations .inc, .dec, or .res to increment, decrement, or to reset the index. By using the caret postfix operator (^) you can combine phase setting with an increment operation, as with other list types or with the standard phase programs. However, in contrast to other list types, you can neither retrieve a particular entry

using the []- bracket notation, nor set the index directly by assigning to `PhList.idx`. Furthermore, no equivalents to the `ipX`, `dpX`, and `rpX` statements available with the standard phase programs `ph0-ph31` exist for user defined phase programs.

Note that user defined phase program names may consist of up to 19 characters, but only the first 15 are interpreted. Up to 32 user defined phase programs may be defined in a single pulse program. It is furthermore possible to define the standard phase programs `ph0` to `ph31` with the above syntax. In this case the phase program base (used for the `ip0-ip31`, and `dp0-dp31` statements) is implicitly 65536 (equivalent to 16 bits). Using an `ipX` command on a standard phase program defined with the above syntax will shift all of its phase entries by $360^\circ/65536 \sim 0.006^\circ$. After 65536 `ipX` statements, the phase program entries would have returned to their initial values.

Phase Switching

The actual setting of the phase is executed by specifying a phase list command within a delay followed by an optional channel specified `f1...f8` after a colon:

```
<delay command> ph0-31[:f1-f8]
```

To switch between the different entries within a phase list, the commands `ipp0-31` and `rpp0-31` can be used to implement the next entry in the list or return to the first entry. Phase lists behave cyclical, i.e. when the end of the list is reached with an `ipp` command, the next `ipp` command will move to the beginning of the list. As a shortcut for the combination `ph0-31 ipp0-31`, a postfix caret operator can be used:

```
ph0-31^ equivalent to ph0-31 ipp0-31
```

The example below illustrates this - its phase output is illustrated in Figure [Phase setting commands in simulator \[654\]](#).

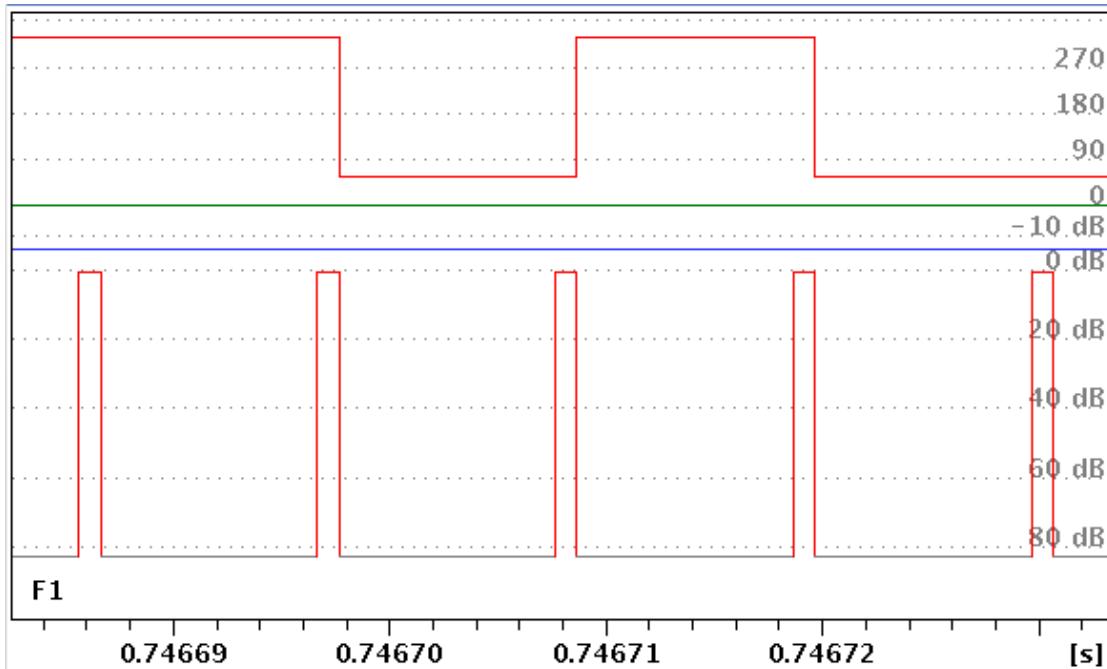


Figure 3.14: Phase setting commands in simulator

```
10u ph0 ipp0 ;set phase 0 deg, switch to next entry
1up
10u ph0 rpp0 ;set phase 270 deg, return to beg. of the list
1up
```

```

10u ph0^      ;set phase 0 deg, switch to next entry
1up
10u ph0 ipp0 ;set phase 270 deg, switch to next entry,
               ;i.e. beg. of the list
1up
...
ph0 = (4) 0 3

```

A typical use of phases is to shift the complete phase cycling for a sequence by 90 degrees for each accumulation. This is done by the `ip0-31` commands not to be mixed up with the `ipp` commands. The `rp0-31` will reset an entire phase list to its initial values. `ip` commands are executed implicitly for all phase lists defined in a pulse program at the end of acquisition (`eoscn`, `rcyc`) - to avoid this, commands exist with the suffix `np`, which have the same functionality but omit phase shifting and thus can be executed in a shorter delay.

Example:

```

10u ph0 ipp0 ; set phase to 90 degrees, next entry
1m ip0 ; add 90 degrees to all list entries: 180 270
10u ph0; set phase to value of second entry, i.e. 270
...
ph0 = 1 2

```

Technical Remarks

- Phase switching for pulse delays is executed before the pulse delay, where it is specified, see NMR-SUITE Pulse program Reference Manual, section 1.5.3.11, “Phase presetting”, p.27.
- The necessary delay to return to phase stability is typically 2 microseconds.

3.2.6.8.3 Power Lists

Power setting for a synthesizer channel is performed with the `p10, ..., p131` commands. These set the power level of the specified channel to the value stored in the parameters `PL[0]` - `PL[31]`. The complete syntax is

```
p10-31[:f1-f8]
```

The values of the parameters `PLW[1]` - `PLW[8]` are the default values for channels 1-8. A pulse will use this value, when the channel is not initialized before. Note that the power level of shaped pulses does not depend on the power level of the channel but on the power level specified in its definition. This default behavior may be overwritten by adding a `(currentpower)` postfix to the shape descriptor in the pulse program.

The power level of a shaped pulse during the runtime of an **Experiment** will not update cortabs and therefore **not compensate for non-linearities** of amplifiers. So it should be used without restrictions only within the linear range of amplifiers.

In addition to the `p10, ..., p131` commands, user defined power lists can be defined which can be used instead of the built in commands. The syntax is:

```
define list<power> <name> = { $<parametername> }
```

or

```
define list<power> <name> = { Watt <power value list> }
```

User defined power lists are used in the same way as the power setting commands. The following example illustrates the use of the different power setting modes, also in combination with shaped pulses - the output of the simulated pulse program is shown in Figure [Power setting commands in simulator \[▶ 656\]](#).

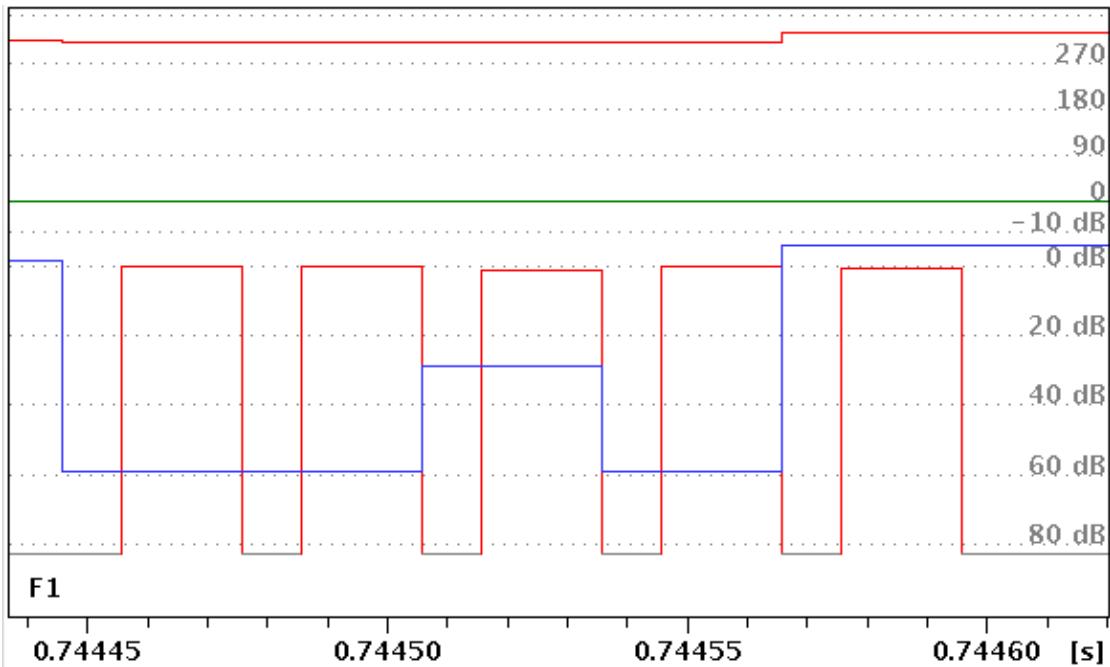


Figure 3.15: Power setting commands in simulator

```

; Assuming maximum power 600W
; display range from 120dB Attenuation to -6dB
; phase and amplitude deviations due to hardware correction
; settings: PLW[1] = 0.3W , i.e. 30dB
; PLW[2] = 30W , i.e. 10dB
; ACQ_RfShapes[0].power = 300W, i.e. 0dB
; ACQ_RfShapes[1].power = 300W, i.e. 0dB
define list<power> pwUsr = { Watt 0.03 } ; 40dB
    120up ; default power level is value of PLW[1], i.e 30dB
    100u p12:f1 ; switch power level of channel 1 to 10dB
    120up ; next blockpulse generated with p12
    100u pwUsr:f1 ; switch power level of channel 1 to 30 dB
    120up:sp0(currentpower) ; pulse at 40 dB
    100u ; after shape return to default power
    120up:sp1 ; use power level defined for shape: 0 dB!
exit

```

The switching time for power setting depends on the available hardware, but is typically 2 microseconds.

3.2.6.8.4 External Hardware Units

External Hardware units can be controlled by a number of TTL outputs. The general syntax for switching these output lines is the `setnmr` command. It has as suffix argument the number of the real time word addressed and a list of bits combined with a | and ^ symbol for setting and blanking of a bit. The labeling of the output connectors depends on the hardware configuration of the *AVANCE* system as well as the internal addresses used in the `setnmr` command.

For this reason, a collection of ppg macros is defined in the `Avance.incl` header file, to switch single TTL-lines to high or low level. You should try to use these macros exclusively in order to produce pulse programs which are independent from the hardware configuration.

The naming for the macros corresponds to the output connectors on recent spectrometers, which are labelled TTL1 - TTL4.

An example for pulling up the TTL1 line for 10u is the following:

```
10u TTL1_HIGH
20u TTL1_LOW
```

The macros `ECG_STAMP_LOW` and `ECG_STAMP_HIGH` are used to switch on a dedicated trigger pulse for the creation of time stamps to be sent to an external trigger device.

The macro `GRAD_SYNC` is a trigger command, which is typically used for exact hardware synchronization with the gradient power supply.

PPG macro name	Labeling at the racks (rear)
TTL1_LOW, TTL1_HIGH	TTL1
TTL2_LOW, TTL2_HIGH	TTL2
TTL3_LOW, TTL3_HIGH	TTL3
TTL4_LOW, TTL4_HIGH	TTL4
ECG_STAMP_LOW, ECG_STAMP_HIGH	ECG
GRAD_SYNC	trigpe3

Table 3.6: PPG macro names and labeling at the racks (rear)

If you need to control several TTL outputs simultaneously, you will have to use the `setnmr` command however. You can derive the correct addresses for the outputs of your system from the `MRI.include` file. Modifications may be necessary, when transferring such a pulse program to different spectrometer hardware. You can find further information on the `setnmr` command in the NMRSUITE Pulse Programming Reference Manual, section 12.5, Real time outputs, p.135.

3.2.6.8.5 Troubleshooting

This section deals with problems typically arising during pulse program development due to technical restrictions.

One Delay - Multiple Actions

Certain actions cannot be performed within the same delay, e.g. only one phase increment command `ip0-31` may occur. On the other hand for phase pointer increments this is not true. The restrictions on possible combination of commands may even depend on the context and for this reason is very hard to explain. For this reason it is recommended, to distribute different actions onto different delays, when an error message occurs. In practice this has not turned out to be a serious problem to date.

Timing Problems - Short Durations

Pulse sequences with short repetition times sometimes drive the sequencer units to their limits. For this reason, here we give a list of measures, which may be necessary to implement shorter events.

preset off - Most imaging sequences use the `preset off` command, to control directly the timing of gating pulses. This should be the first measurement, when optimizing the timing control.

Avoid unnecessary delay commands - Every delay command costs time during execution, even if no actions are performed. Try to avoid unnecessary delays and to combine delays. Time critical BRUKER pulse programs have been optimized in this respect, improving repetition times by up to 20%.

Try to use hardware loops - The innermost loop of an **Experiment** can be executed in a very efficient way on the sequencer unit, when some conditions are fulfilled:

The following list gives some (not comprehensive) examples of pulse programming elements, which will suppress the execution of the pulse program in hardware loop:

- using assignment expressions
- setting the receiver phase
- changing the timing of the sequence

Timing Restraints

When you develop a pulse sequence, you must bear in mind certain restrictions for the timing. The following table gives safe values, which can be used for all hardware configurations. Shorter timing may be possible on certain systems. References to parameters which are typically used to describe corresponding time intervals are given, where they exist:

Pulse program action	Timing	Parameter
Resolution for delays	12.5 ns	-
Minimum length of delay	50 ns	
Minimum length of pulse delay	100 ns	
Time resolution for pulse shapes	100 ns	-
Minimum time between two shaped pulses	4 us	-
Minimum time between a pulse and data acquisition	ca. 6 us	DE
Minimum time between end and start of acquisition	ca. 700 us	-
Minimum time between start and end of scan		DEOSC
Length of Gating pulse: (depends on amplifier)	100 us	D[8]
Time for phase switch to become effective	4 us	
Time for amplitude switch to become effective	2 us	
Time for frequency switch to become effective	2 us	

Table 3.7: Typical timing for pulse program actions

You should note, that timing restraints in most cases are hardware specific.

3.2.6.9 Example of a Complete Pulse Program

The pulse program of the SINGLEPULSE method may serve as an example of an application pulse program. It contains the necessary elements for a simple transmit/receive **Experiment**, sending a pulse and acquiring an fid afterwards. You should note the following characteristics typical for all pulse programs provided by BRUKER:

- Include file `MRI.include` must be included at the beginning of each pulse program. `INIT_DEVICES` must follow after the definitions because it contains a delay.
- Runs in an endless loop for GSP (accomplished by the macro `SETUP_GOTO`)

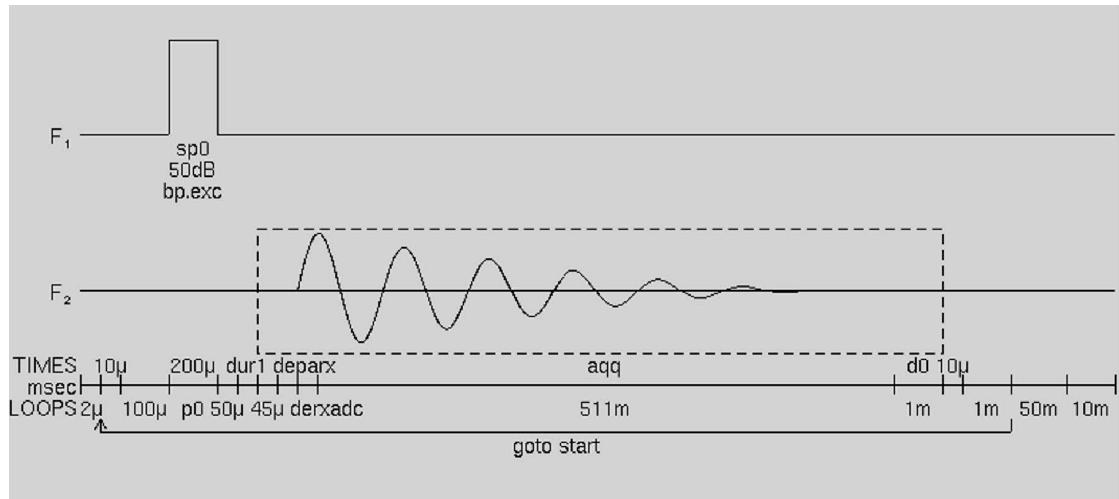


Figure 3.16: SINGLEPULSE pulse sequence

```
;*****
; Copyright (c) 2002 - 2003
; Bruker BioSpin MRI GmbH
; D-76275 Ettlingen, Germany
;
; All Rights Reserved
;
; SINGLEPULSE - non-selective spectroscopy (pulse + acquire)
;
;*****
;
; d0 - TR padding
; d8 - CONFIG_amplifier_enable

#include <MRI.include>
define delay dur1
"dur1=d1-de"
define loopcounter lds={$DS}
preset off
INIT_DEVICES

;-----start of the main loop -----
start, 10u

;-----preparation modules -----
d0
d8      gatepulse 1
(p0:sp0 ph0):f1
```

```
ADC_INIT(ph0, ph1)
aqq      ADC_START
5m
10u      ADC_END
"lds = lds - 1"           ; this makes
if "lds>=0" goto start   ; dummy scans
1m      ipp0
lo to start times NA
2.5u      rpp0
SETUP_GOTO(start)

exit

ph0 = 0 2 1 3
ph1 = 0
```

3.2.6.10 Gradient Commands

3.2.6.10.1 Introduction

In an imaging system, the word **gradients** refers to magnetic fields which are superimposed on the main magnetic field. The superimposed field directions are parallel to the main field, the field strengths vary in the spatial dimensions. In case of linear variations (i.e. constant mathematical gradients) the superimposed gradient fields are termed linear gradients.

Gradient Coordinates

Per default, gradient coordinates refer to the encoding coordinates referring to the directions of data readout (“read”), spatial phase encoding (“phase”) and slice encoding (“slice”).

The transformation matrix ACQ_grad_matrix is used to define the transformation between these encoding coordinates and the subject coordinates, i.e. the main directions of the subjects in the scanner independent from its position (i.e “right”, “posterior”, “head” for a primate). A position matrix describes the transformation to physical coordinates according to the actual position within the scanner.

The physical (x,y,z) gradient values applied can be calculated by the equation:

$$(x, y, z) = (r, p, s) * \text{ACQ_grad_matrix} * \text{Position_Matrix}$$

For all subjects apart from “Material”, the position feet_supine is associated with the identity matrix. For material, no position can be selected, but a constant matrix (-1 0 0 0 1 0 0 0 -1) is used as Position_Matrix, i.e. x and z directions are inverted.

The parameter ACQ_grad_matrix is in fact a nx3x3 three-dimensional array, which can hold a separate orientation for each image object within an experiment.

For certain applications, it is desired to have direct control of the physical gradient channels. Gradient commands can refer to either the object_coord system skipping the gradient matrix or the magnet_coord system skipping both transformations and addressing directly the physical gradients.

Refer to the examples below for further details, how to address specific coordinate systems.

Gradient Strengths / Amplitudes

Gradient strength is given relative to the maximum gradient strength available for a given gradient system. Gradient systems are assumed to be isotropic, i.e. the absolute gradient strength specified in an encoding direction will not depend on the actual orientation selected for the experiment. This said, gradient values range between -100 to + 100 percent. Constant gradient strengths are given as floating point numbers.

The absolute value for the currently installed gradient system can be read from the parameter PVM_GradCalConst, which defines the frequency deviation of the proton resonance frequency per mm, when the maximum gradient is applied. $42.577\text{Hz/mm} = 1\text{mT/m}$.

Using Built in Gradient Amplitudes

For most standard applications, the array ACQ_gradient_amplitudes can be used to specify gradient values. The tokens g0-g99 will then be replaced by the values stored in ACQ_gradient_amplitudes[0-99].

Gradient Amplitude Lists

Alternatively, gradient amplitude lists can be used. Any double valued ParaVision parameter can serve as a gradient amplitude list.

Gradient values can also be defined in a pulse program with the statement

```
define list<grad_scalar> scalar_list = {amplitude1,...,amplitude n}
```

Built in functions can also be used. These function values will have to be rescaled by the desired maximum gradient amplitude

```
define list<grad_scalar,3> sinp
```

Stepping through a list is done by the .inc, .dec, .res commands to increment, decrement or reset a list index. The commands .store and .restore can be used to store and restore the current index.

Ramped Gradients

Physical gradient systems have intrinsic limitations which limit the slew rate which can be used for switching. The physical effect created by a gradient field depends on the time of the applied field and its strength.

The basic way to control gradient fields is to switch them to a desired target value using a linear ramp. The command

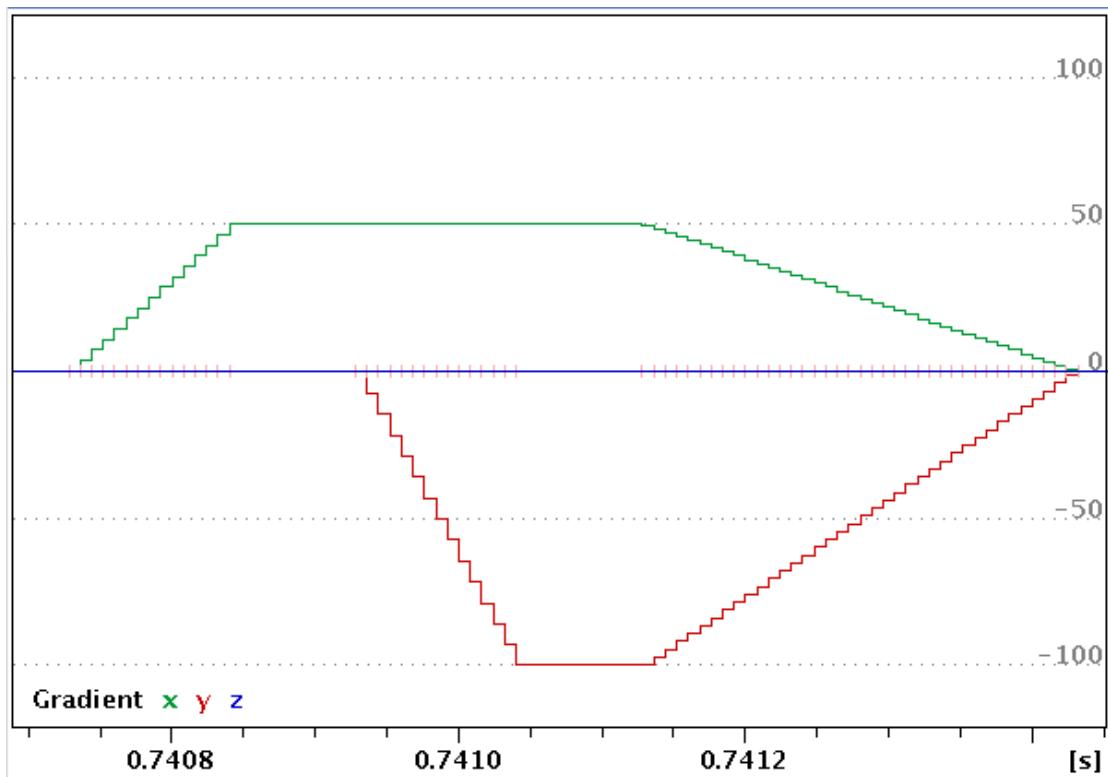
```
grad_ramp{read, phase, slice}
```

switches the gradient system to values $\text{read}/100 * \text{maximum read gradient}$, using a linear ramp of length <RAMPTM> starting with the delay, in which the command is used. The length of this delay is not related to the length of the ramp. It only has to be ensured, that no further gradient command is used, before the gradient ramp has achieved the desired value.

Example

```
1u grad_ramp{100,0,0}; switch read gradient with
                           ; maximum slew rate
d1                         ; wait at least d1 >= RAMPTM - 1u
                           ; until next gradient statement
1u grad_ramp{0,0,0} ; switch gradient fields off -
                           ; ramptime is system ramp
```

Example



```
; gradient ramps
; ACQ_gradient_amplitude[0] = 50
; RAMPTM = 110u
200u grad_ramp{g0,0,0}
200u grad_ramp{g0,100,0}
400u grad_ramp<300u>{0,0,0}
```

The `grad_ramp` command can be called with two optional parameters: A different delay time can be defined as well as a different coordinate system. Both parameters may be appended in `<>` angled brackets at the end of the `grad_ramp` keyword.

```
grad_ramp<ramptime>
or grad_ramp<coordinates>
or grad_ramp<ramptime,coordinates>
```

The `ramptime` may be either a constant (in u) or a delay parameter. The coordinates are given as an index list: When leaving the coordinates out, {r,p,s} will be taken. An index set xyz is defined as well and can be used within the command.

Valid coordinate systems are “`object_coord`” to bypass the rotation defined in `ACQ_grad_matrix` and “`magnet_coord`” to address directly the physical x,y,z gradient.

From the physical considerations above, it is clear that the length of the actually usable ramp delay will depend on the applied gradient settings.

Example

```
1u grad_ramp<120u>{100,0,0} ; leads to a runtime error,
; when the system ramp time is >120u
1u grad_ramp<120u, magnet_coord> {0,-10,0} ; switch y
; direction to -10 percent within 120u
```

For the command `grad_ramp{0,0,0}`, a shortcut `grad_off` can be used.

Shaped Gradients

Instead of the (built in) linear ramp used for interpolation, a different shape can be used to switch gradient values. The command

```
grad_shape{vector of shapes}
```

will use the given shapes to create the gradient form in the output. A shape is an array of floating point values ranging from -1 to 1 which is usually scaled with a gradient amplitude value. Such an array will be identified as a shape form by adding parentheses to its name. The timing of the shape is derived from the delay, for which the gradient command is executed. Please be aware, that a (hardware specific) minimum stepwidth must be observed to avoid runtime errors. The stepwidth is accessible as parameter GRADRES in the configuration.

Example:

```
100u grad_shape{100*shape(), 0, 0}
```

Shapes can be combined with constant values in other directions, which will immediately be selected in these directions.

The timing of a gradient shape can be defined independently from the command delay by adding it in <> to the grad_shape command. Either a constant or parameter delay can be used.

```
1u grad_shape<100u>{100*shape(), 0, 0}
```

When shapes are applied simultaneously on the different channels, they must have the same number of grid points.

Attention: Physical limits also hold for shapes, i.e. slew rate restrictions defined by the RAMPTM must be observed.

Gradient shapes must be defined in advance. This can be done within a pulse program with the following define statement.

```
define list<grad_shape> myshape = { -1, 0, 1 }
```

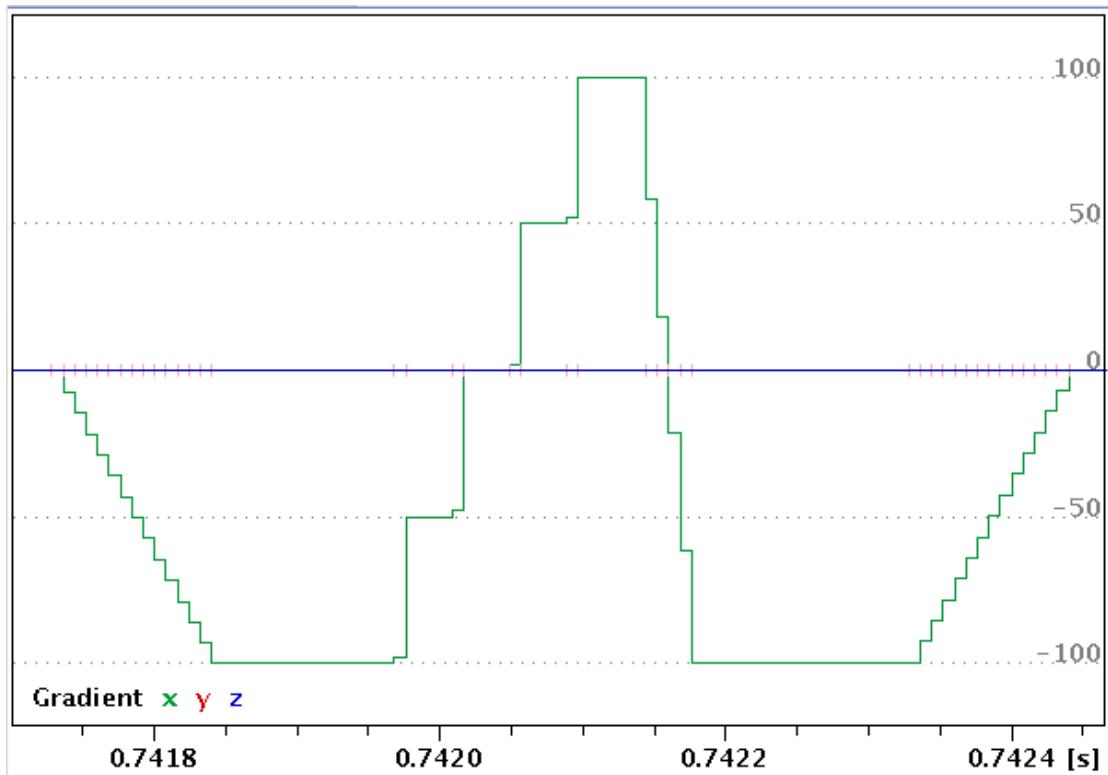
Alternatively, any double valued ParaVision vector can be used for shape description.

Finally, built in functions can also be used as a shape, when the number of grid points is specified in a define statement:

```
define list<grad_shape,100> sin90
```

Built in functions are described below in more detail.

Example:



```
; gradient shapes
; GRADRES = 8.0u
200u grad_ramp{-100,0,0}
200u grad_shape{100*myShape(),0,0}
200u grad_shape<50u>{-100*myShape(),0,0}
200u groff
```

Built in Gradient Functions

The following functions can be used to define gradient shapes and lists.

When requiring n points the functions are applied to the given range in an equidistant way.

sin: sine function from sin(0) to sin((n-1)/n*pi)

sinp: sine function from sin(0) to sin(pi)

sin90: sine function from sin(0) to sin(pi/2)

cos: cosine function from sin(0) to sin((n-1)/n*pi)

cosp: cosine function from sin(0) to sin(pi)

gauss<truncation>: gauss function truncated at given truncation level, e.g. gauss5 truncates at 5%level

plusm: alternating function, switching between +1 and -1 in each step

step: linear ramp from 0 to 1

In earlier releases, the ramp functions r1d, r2d and r3d were defined and implicitly linked to the ACQ_spatial_phase_0-2 parameters. As this link was not straightforward, the build in functions are no longer available. In some pulse programs macros r1d-r3d are defined.

```
#define r1d ACQ_spatial_phase_0
```

They behave similar like the former ramp commands.

Multiple Orientations

Multiple gradient orientations can be used within a single experiment. The parameter ACQ_grad_matrix is a three dimensional array, i.e. it can be regarded as a list of 3x3 orientation matrix. Within a pulse program, it is possible to step through the list with the .inc, .dec, .res commands like in the case of gradient lists. The commands .store and .restore can be used, to store and restore the current list index.

Special Handling in Setup Mode

In order to suppress stepping through gradient lists in setup mode, the statement

```
grad_zero_for_gs<list of gradient list names>
```

can be used. In this case, in 1D setup mode, the value 0 will be assumed for all listed lists.

Control Commands to Reload Gradients

relgrad; reload gradients during Setup if GS_typ = Gradients or Preemphasis

The pulse program should contain only a few gradient commands. Then it is possible to rotate and rescale gradients (e.g. during Preemphasis Adjustment) or to change trim values during GSP.

reload B0; reloads B₀ values

```
12u reload B0 ; reload B0 values
```

With some Preemphasis Units it is possible to control the B₀ field, e.g. to obtain a stable magnet field for long term experiments.

At acquisition start B₀ = 0 is loaded. A pipeline filter may examine the incoming data, derive a new B₀ value and load it into the GCU.

The new B₀ value is activated when the **reload B0** command is executed.

reload shims

On AVIII (HD) Systems the DPP may add the linear shims X,Y,Z,Z0 to the corresponding gradient channels. If the PP contains

```
10u reload shims ; reload shims
```

the shims, previously load into the DPP, are made active at this time, else the shims are made active immediately. But note, the PP should contain at least one gradient command in this case.

reload shims and B0 values

```
10u reload all; reload shim and B0 value
```

ctrlgrad <Data>

On AVIII (HD) systems it is possible to send control information to the Digital Preemphasis Unit.

```
ctrlgrad 1; Blank X Gradient  
ctrlgrad 2; Blank Y Gradient  
ctrlgrad 4; Blank Z Gradient  
ctrlgrad 8; Blank B0 Gradient  
ctrlgrad 15; Blank all Gradients  
ctrlgrad (1*16); resets all gradients immediately to zero
```

```
ctrlgrad (2*16); ramp down all gradients to zero  
ctrlgrad (4*16) ; does the same as the reload B0 command  
ctrlgrad (8*16) ; does the same as the reload shims command
```

The following are commands to active shim sets in a dynamic shim experiment.

```
ctrlgrad (1*256) ; activate first shim set  
ctrlgrad (2*256) ; activate next shim set  
ctrlgrad (3*256) ; activate previous shim set  
ctrlgrad (4*256) ; save index of actual shim set  
ctrlgrad (5*256) ; restore shim set
```

Composite Gradient Command

Gradient Timing can be controlled independent from Pulse Timing. Within a gc_control statement, a sequence of gradient commands including timing can be listed, to compose a complex gradient shape as seen below.

Example:

```
2u gc_control; Begin of gc_control block  
; (delay seen by Timing control)  
{  
    d1 grad_ramp{ 20,0,0}; Gradients statements  
    d2 groff ; within gc_control  
    loop L[10] ; loop within gc_control  
    {  
        d1 grad_ramp{ 10,0,0 }  
        d2 grad_ramp{ -10,0,0 }  
    }  
    if (Spoiler); Conditional compiling  
    { ;is supported  
        d3 grad{ 20, 20, 20 }  
    }  
    groff ; last gradient without delay  
}; End of gc_ control block  
d4 ADC_INIT(ph0, ph1); TCU continues at this point  
; after 2us
```

3.2.7 GOP Simulation Tool (HPDISP)

This tool is available at AV III (HD) spectrometers only. It shows all signals going to spectrometer hardware, the exact timing, phase and amplitude of the rf pulses as well as the amplitude of the gradients.

The GOP Simulation tool can be started in the Examination Card Simulation platform or when selecting a scan in the data browser or workspace explorer by selecting the “Perform GOP Simulation” action. This action is not available for completed data sets.

In a first step a window is opened to select the channels, the simulation should be done (see Figure [Pulse program options \[▶ 667\]](#)).

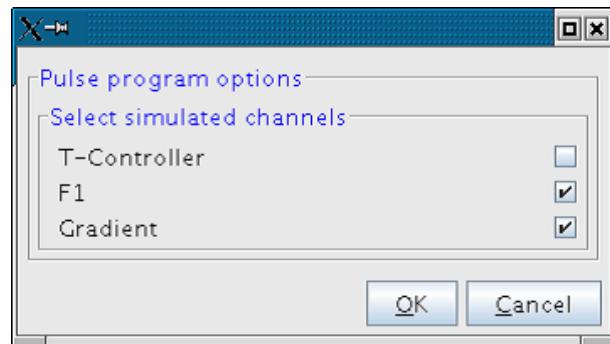


Figure 3.17: Pulse program options

Select the channels you are interested and click **OK**. Then the experiment will be simulated with the same software which runs on the control boards to perform a real experiment. This may lead to a very large number of display events, even for simple experiments. For great experiments it is recommended to reduce the number of repetitions, slices or phase encoding steps, else the simulation may take a lot of time and may even consume the whole disk space.

After simulation the **Hardware pulse program display** window will show the whole experiment within *TopSpin*. There exist buttons to zoom in and out the time axis. You can also zoom by mouse drag. With the compress icon it is possible to compress all intervals without any activity (see Figure [Shows a part of the TRIPilot GE protocol \[▶ 667\]](#)).



Figure 3.18: Shows a part of the TRIPilot GE protocol

The hardware pulse program display window is terminated by clicking the close icon.

3.3 Data Formats

ParaVision stores its image data and description in data files that are located in a path hierarchy reflecting the Study, Examination, Image Series hierarchy. Some information is also stored in the ParaVision database which cannot be accessed from outside the ParaVision graphical user interface. The description of the acquired object, the acquisition process, the reconstruction and the reconstructed data is defined in parameters that are stored in the parameter files.

3.3.1 Data Paths and Files

ParaVision stores its image data and description in data paths and files. They are described in the PDF manual Chapter [Data Paths and Files](#).

The PDF manual contains information that has not or only little changed between ParaVision versions. In addition it contains



- the table of contents for the PDF manual: [Table of Contents](#).
- an index for the PDF manual: [Index](#).
- a parameter index for all parameters described in the PDF manual: [Parameter Index](#).

3.3.2 Mapping of Data Paths to Study, Examination, Image Series.

In the Dataset Browser tabs several categories of information are shown which are mapped to data paths. The general description of data paths can be found in the PDF manual Chapter [Data Paths and Files](#) section D-1.1.

- The Subject and Study is described in the directory `<DataPath>/<study>` where `<study>` is the directory name of one study shown in the study table of the Dataset Browser. Selecting a study and clicking on the **Properties** button shows the study directory in the **Storage Location** row. The Subject information is held in the parameters of every study that belongs to the Subject.
- The Examination is described in the directory `<DataPath>/<study>/<EXPNO>`. `<EXPNO>` is the experiment number which is also shown in the **Exno column** of the Examination table in the Dataset Browser. Selecting an Examination in the Dataset Browser and clicking on the **Properties** button shows the examination directory in the **Storage Location** row.
- The Image Series is described in the directory `<DataPath>/<study>/<EXPNO>/pdata/<PROCNO>`. `<PROCNO>` is the processing number which is also shown in the **Procno column** of the Image Series table in the Dataset Browser. Selecting an Image Series in the Dataset Browser and clicking on the **Properties** button shows the image series directory in the **Storage Location** row.

The Data Paths are hierarchical. This means for example, that the information about an Image Series is only complete if also the corresponding information in the Examination and Study directory is taken into account.

3.3.3 Overview of ParaVision Parameters

ParaVision stores the subject, acquisition, reconstruction and image describing information in Parameters. The acquisition method parameters are described in the Chapter [Method Description \[▶ 240\]](#).

The subject, reconstruction and image parameter are described in the PDF manual Chapter [ParaVision Parameters](#).

3.4 Macros and Automations

3.4.1 Overview

3.4.1.1 Macros

ParaVision consists of different programs that implement commands. Commands can be sent to ParaVision command servers which are the ParaVision processes. They can perform a defined function in the ParaVision process. A command consists of a command identifier and optional / required arguments.

Repetitive operations and batch execution of several ParaVision commands can be implemented using macros. Commands can be sent to a ParaVision program using the utility program pvcmd.



The Macro management is described in the PDF manual Chapter [The Macro Manager](#).



The utility program pvcmd and an introduction into macro programming is given in the PDF manual Chapter [Macro Programming](#).



The PDF manual contains information that has not or only little changed between ParaVision versions. In addition it contains

- the table of contents for the PDF manual: [Table of Contents](#).
- an index for the PDF manual: [Index](#).
- a parameter index for all parameters described in the PDF manual: [Parameter Index](#).

3.4.1.2 Automations

Automations are a possibility to program experiments on a low level. They allow easy and rapid parameter access and changing (e.g. large parameter array redimensioning). They are written in C-language, and are, therefore, convenient for applications involving complicated maths. They can also be used for postprocessing purposes.

A unique feature of ParaVision is the possibility of inserting a user-programmed filter to the acquisition pipeline. Pipeline Filters can process the raw data on their way from the spectrometer to the computer. Pipeline Filters are special types of Automations.



Automations and Pipeline Filters are described in the PDF manual Chapter [Automation Programming](#).



The PDF manual contains information that has not or only little changed between ParaVision versions. In addition it contains

- ▶ the table of contents for the PDF manual: [Table of Contents](#).
- ▶ an index for the PDF manual: [Index](#).
- ▶ a parameter index for all parameters described in the PDF manual: [Parameter Index](#).

3.4.2 Starting Macros

Macros can be started

- in the Macro Manager (see Chapter “Macro Manager”).
- manually for Studies, Examinations, and Image Series (see Chapter [Manual Start of Macros for Studies, Examinations, or Image Series \[▶ 670\]](#)).
- automatically for Studies when the study is completed (see Chapter [Automatic Start of Macro after a Study \[▶ 671\]](#)).
- automatically for Examinations before / after acquisition (see Chapter [Automatic Start of Macro before / after Acquisition \[▶ 671\]](#))
- automatically for Image Series before / after reconstruction is completed see Chapter [Automatic Start of Macro before / after Reconstruction \[▶ 672\]](#).

If the macro is started for Studies, Examinations, or Image Series the corresponding Study, Examination or Image Series path (see Chapter [Mapping of Data Paths to Study, Examination, Image Series. \[▶ 668\]](#)) is the first argument of the macro.

3.4.2.1 Manual Start of Macros for Studies, Examinations, or Image Series

To start a macro manually

1. Select a Study, Examination, or Image Series
 - ▶ in the **Workspace Explorer** below the **Datasets** node by selecting the corresponding node,
 - ▶ in the **Palette Explorer** (only for Image Series),
 - ▶ or in the **Dataset Browser** in the **Study, Examination or Image Series** dataset views.
2. Open the macro selection dialog by
 - ▶ clicking on the **Execute Macros...** context menu entry of the selected element in the **Palette Explorer** or **Workspace Explorer**,
 - ▶ or clicking **Execute Macros...** in a sub-menu of the buttons below the **Study, Examination, or Image Series** view in the **Dataset Browser**. The **Execute Macros...** entry can be found in the sub-menu of the **Properties** button (click on the triangular button).

3. The **Execute Macros** dialog opens where all available macros can be selected. Select a category and the macro. Then click **OK**. For example In Figure [Macro Selection Dialog \[▶ 671\]](#) the macro **Fitinlsa** in the **BRUKER** category is selected.
4. The Macro starts and a progress bar is shown.
5. If the macro finishes with an error code or writes information to standard output or error a dialog opens where this information is displayed.



Figure 3.19: Macro Selection Dialog

3.4.2.2 Automatic Start of Macro after a Study

Macros can be started automatically before (Pre Study Activity) or after (Post Study Activity) a study. The first argument of the macro is then the Study path (see Chapter [Mapping of Data Paths to Study, Examination, Image Series. \[▶ 668\]](#)). If a macro is defined as Pre Study Activity it starts before the first examination is acquired. If it is defined as Post Study Activity the macro starts if the study is set completed (e.g. closing the Exam Card).

To define the automatic macro start before or after a study

1. Open the Examination Card (see Chapter [Opening the Examination Card for an Existing Study \[▶ 24\]](#)).
2. If a Scan Instruction is edited click on **Cancel**.
3. On the right side the lists of **Pre Study Activities** and **Post Study Activities** is displayed. In the corresponding list mark **Execute Macro**.
4. The **Execute Macros** dialog opens where all available macros can be selected. Select a **Category** and the **Macro**. Then click **OK**.

3.4.2.3 Automatic Start of Macro before / after Acquisition

Macros can be started automatically before (Pre Acquisition Activity) or after (Post Acquisition Activity) an acquisition. The first argument of the macro is the Examination path (see Chapter [Mapping of Data Paths to Study, Examination, Image Series. \[▶ 668\]](#)). If the macro starts after acquisition it is guaranteed that the raw data exists. The reconstructed image data does not exist at this moment.

To define the automatic macro start before or after acquisition

1. Edit the Scan Instruction in the Examination card (see Chapter [Editing a Scan Instruction \[▶ 55\]](#)).
2. Select the **Instruction tab** (see Figure [Instruction Parameter Editor \[▶ 672\]](#))
3. In the **Instruction tab** on the right there are lists of **Pre Examination Activities** and **Post Examination Activities**. In the corresponding list mark **Execute Macro**.
4. The **Execute Macros** dialog opens where all available macros can be selected. Select a **Category** and the **Macro**. Then click **OK**.
5. Click the **Apply** button in top of the instruction list to close the **Scan Instruction** editor.

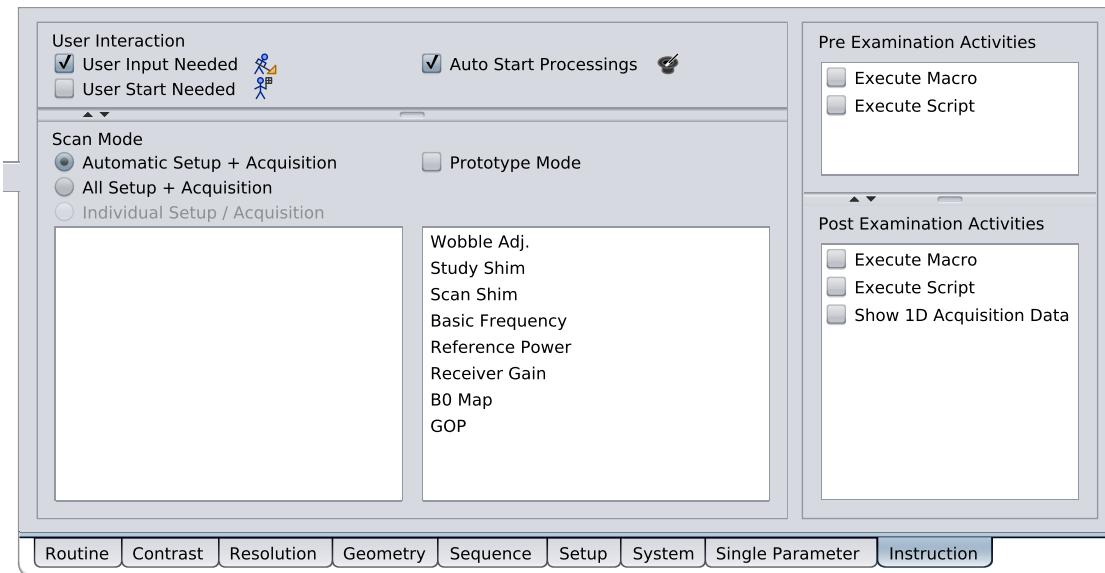


Figure 3.20: Instruction Parameter Editor

3.4.2.4 Automatic Start of Macro before / after Reconstruction

Macros can be started automatically before (Pre Image Series Activity) and after (Post Image Series Activities) a reconstruction process. The first argument of the macro is the Image Series path (see Chapter [Mapping of Data Paths to Study, Examination, Image Series.](#) [▶ 668]). If the macro starts before reconstruction it is guaranteed that the raw data exists. If the macro starts after reconstruction it is guaranteed that the raw data and reconstructed image data exists.

To define the automatic macro start before or after reconstruction

1. Edit the Scan Instruction in the Examination card (see Chapter [Editing a Scan Instruction](#) [▶ 55]).
2. Open the Processing Platform for the edited Scan Instruction (see Chapter [Opening the Processing Platform](#) [▶ 73]).
3. Edit a **Data Reconstruction** instruction (see Chapter [Editing a Processing](#) [▶ 76]).
4. In the opened editor on the right there are lists of Pre Image Series Activities and **Post Image Series Activities** (see Figure [Reco Processing Editor](#) [▶ 673]). In the corresponding list mark **Execute Macro**.
5. The **Execute Macros** dialog opens where all available macros can be selected. Select a **Category** and the **Macro**. Then click **OK**.
6. Click the **Apply** button in top of the instruction list to close the **Data Reconstruction** editor.
7. Click **Back** to change back to the Scan Instruction.

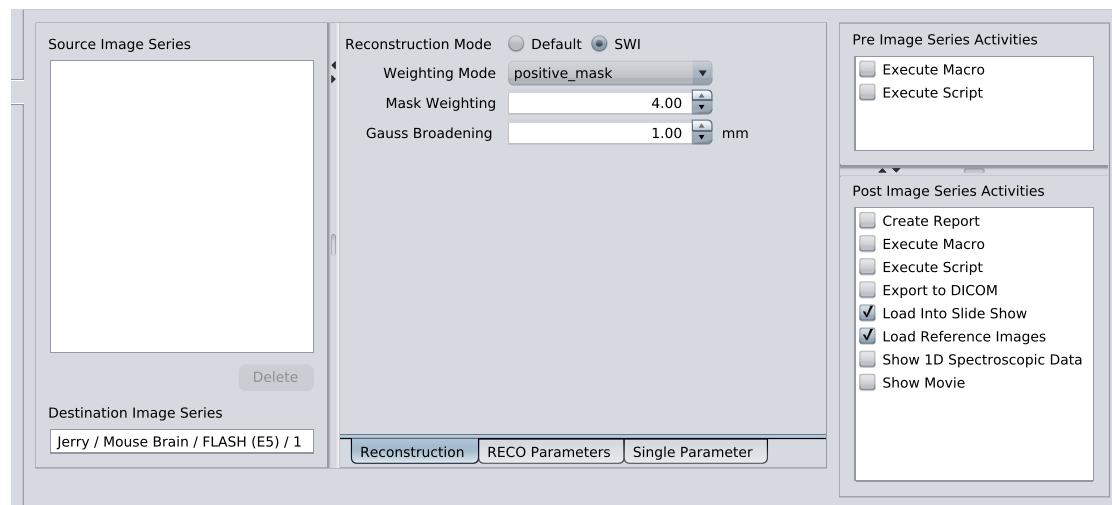


Figure 3.21: Reco Processing Editor

3.4.3 Macro Manager

The Macro Manager program is used to organize, record and start macros.

To start the Macro Manager select the menu entry **Programs > Macro Manager**.



More information about the Macro Manager can be found in the in the PDF manual Chapter [The Macro Manager](#).

3.4.4 Command Sender

The Command Sender program is used to show the available commands in the different ParaVision programs, describes the arguments of the commands. Additionally, the sender can send commands to ParaVision programs and to retrieve the results of the commands.

To start the Command Sender select the menu entry **Programs > Cmd Sender**.



More information about the Command Sender can be found in the in the PDF manual Chapter [Macro Programming](#) section D-3.

3.4.5 Command Observer

The Command Observer program is a tool to help the debugging of macros. It offers the ability to observe the 'engine' (Command Dispatcher) responsible for command dispatching and execution present in each ParaVision server application. The Command Observer is able to attach to any ParaVision server application. Once attached to an application each command dispatched and executed by this program is logged.

To start the Command Observer select the menu entry **Programs > Cmd Observer**.



More information about the Command Observer can be found in the in the PDF manual Chapter [Macro Programming](#) section D-3.

3.4.6 The pvcmd Utility

The pvcmd utility is a command line program that can send command to ParaVision programs. It must be used from a ParaVision shell.

To start a ParaVision shell select the menu entry **Programs > Terminal**.



More information about the pvcmd utility can be found in the in the PDF manual Chapter [Macro Programming](#) section D-3.2.

3.5 Image Sequence Analysis functions

The Image Sequence Analysis tool (ISA) is a part the **Image Display & Processing** program. Its concept is to provide a very general and flexible framework for the visualization and statistical analysis of sequences of images. It is a package intended for any kind of analysis of the type where some values, identically evaluated for each image of a series of images and depending on some parameter as a function, are compared with each other in some predefined manner.



For details about the ISA Tool see the PDF manual Chapter [Image Sequence Analysis](#).



The ISA framework offers the possibility to provide user defined analysis functions. This is described in the PDF manual Chapter [ISA Function Programming](#).



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3.6 The Coil Editor

3.6.1 Overview



⚠ CAUTION

Hardware Damage Possible

This is an expert tool.

False data may damage an RF Coil when it is used for acquisition.

The Coil Editor is an administration tool to register and manage the usage of different RF Coil setups in ParaVision. Every RF Coil connected to the spectrometer must be registered within the editor in order to be usable for study creation and acquisition. A single setup of one or more RF Coils along with their routing through the spectrometer hardware is called **Coil Configuration**.

Common ways to create valid Coil Configurations are

- the import from another ParaVision version, see Chapter [Import of Coil Configurations](#) [▶ 682].
- the import from the ParaVision installation medium (only Micro-Imaging Systems), see Chapter [Configure RF Coil from Installation Medium \(Micro-Imaging only\)](#) [▶ 685].
- using HWIDS detected coils, see Chapter [Using HWIDS Detected Coils](#) [▶ 684].
- using default Coil Configurations created by ParaVision, see Chapter [Using Default Coil Configurations](#) [▶ 686].
- creating Coil Configurations manually from scratch, see Chapter [Create And Edit Coil Configurations From Scratch](#) [▶ 686].

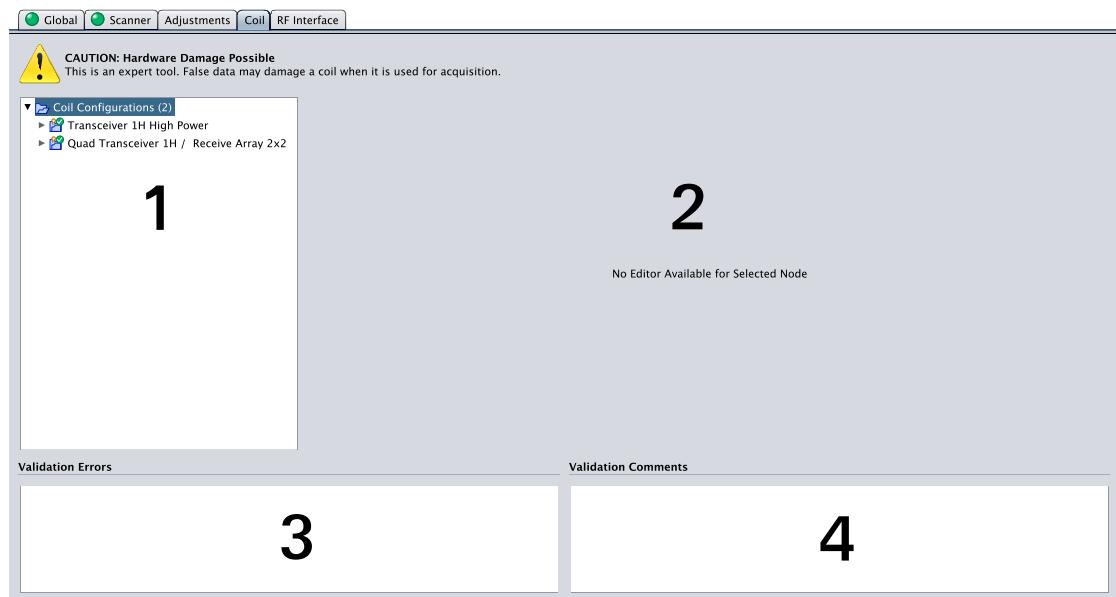


Figure 3.22: Initial View

Figure [Initial View](#) [▶ 675] shows an example view of the Coil Editor. All stored Coil Configurations are shown inside the window to the left (1). Their properties can be observed and changed inside the window to the right (2), when selected. (3) and (4) are used to print comments and errors during validation and saving of configurations, see Chapter [Validating And Saving Coil Configurations](#) [▶ 689].

For reasons of clarity, the following table gives some definitions and explanations of the terminology used in this Chapter.

RF Coil	Physical unit bearing one or more resonant loops
RF Wiring	Map of the hardware wiring of a spectrometer, i.e. all physical connections between devices such as transmitter, preamplifier, receiver, etc.
RF Coil Interface (RF Socket Interface)	Synonym for the (typically four) ODU sockets to plug in RF Coils NOTE: The RF Coil Interface is only available on BioSpec and PharmaScan AV2+, AV3 and AV3HD systems.
Operation Mode	One single routing path through the RF Wiring from signal generation to signal reception, including the connected RF Coil(s)
Coil	ParaVision representation of an RF Coil
Coil Element	ParaVision representation of single resonant loop within an RF Coil
Coil Configuration	A set of Coils and their possible Operation Modes

3.6.2 Coil Configurations

Each Coil Configuration is described by a set of **Coils**, see Chapter [Coils \[▶ 677\]](#), and a set of possible **Operation Modes**, see Chapter [Operation Modes \[▶ 681\]](#).

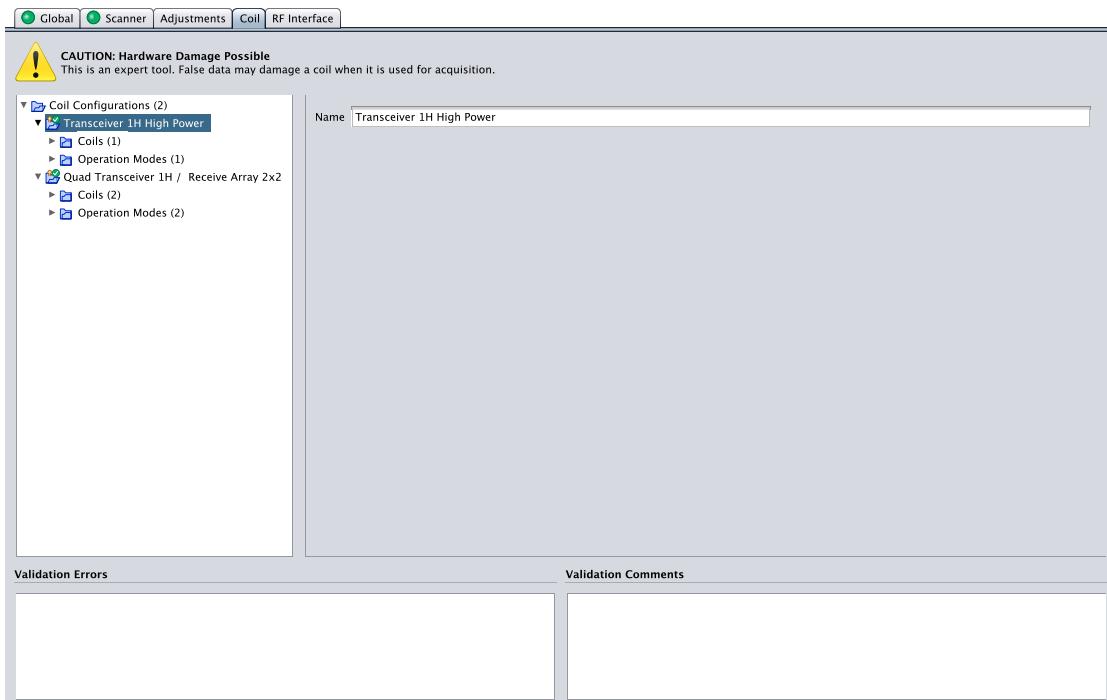


Figure 3.23: Coil Configurations

Selecting a Coil Configuration reveals the **Name** of a configuration as its only property. This can be arbitrarily chosen by the user. A double click on the configuration knot opens a tree view of how many Coils and Operations Modes the configuration contains. Figure [Coil Configurations \[▶ 676\]](#) gives an example for a possible set of Coil Configuration.

3.6.2.1 Coils

A single Coil consists of one or several **Coil Elements**, see Chapter [Coil Elements \[▶ 678\]](#).

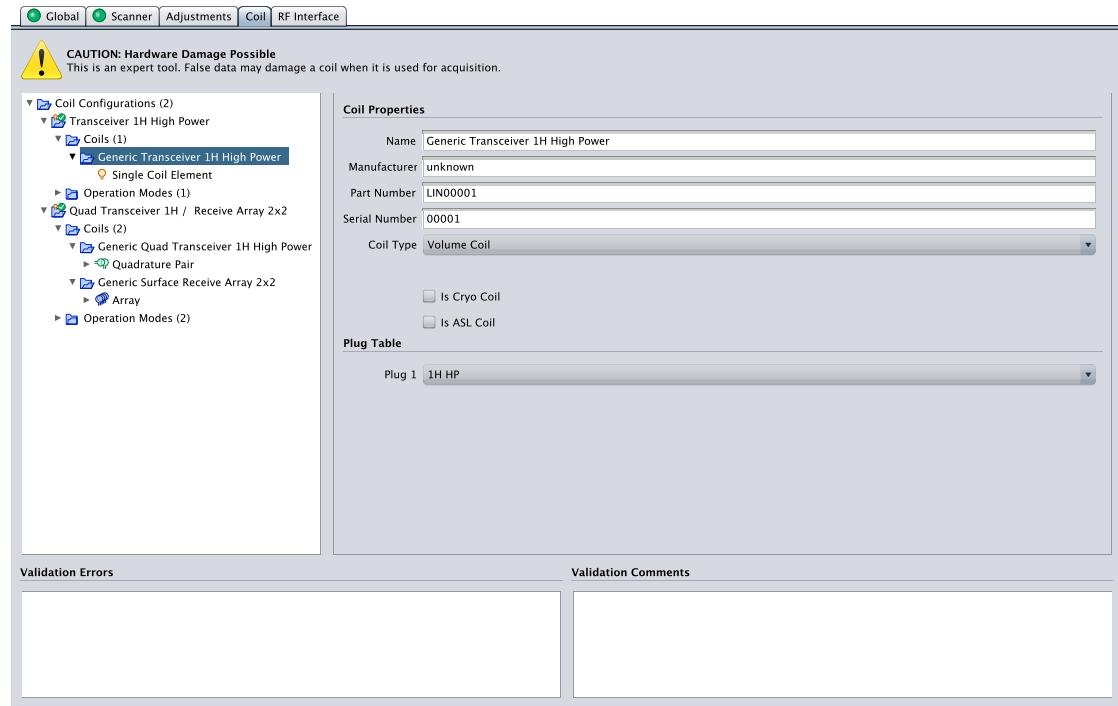


Figure 3.24: Coil Properties

To view the properties of a Coil within a Coil Configuration, open the configuration, double click the knot Coils and select the wanted Coil. Independent from the actual number of Coil Elements, each Coil defines **Coil Properties**:

Name	Descriptive name for this Coil
Manufacturer (o)	Name of the Coils manufacturer
Part Number (o)	Part number of the Coil
Serial Number (o)	Serial number of the Coil
Coil Type	Type of the Coil
Is Cryo Coil	Checked if Coil is a Bruker CryoProbe (CRP)
Is ASL Coil	Checked if Coil is used for Arterial Spin Labeling (ASL)
(o = optional)	

Also a **Plug Table** is given, which defines the mapping of each **Plug** to the **Socket**, where it is plugged in. This entry only exists on systems with an RF Coil Interface. On systems without RF Coil Interface this part is left empty, e. g. on Micro-Imaging systems.

Figure [Coil Properties \[▶ 677\]](#) gives an example how a Coil definition might look like.

3.6.2.1.1 Coil Elements

The Coil Editor distinguishes between the three different Coil Element Groups “Single Coil Elements”, “Quadrature Pairs” and “Arrays”. The latter two are used to encapsulate two or an arbitrary number of Coil Elements respectively. One Coil may contain any subset of those groups.

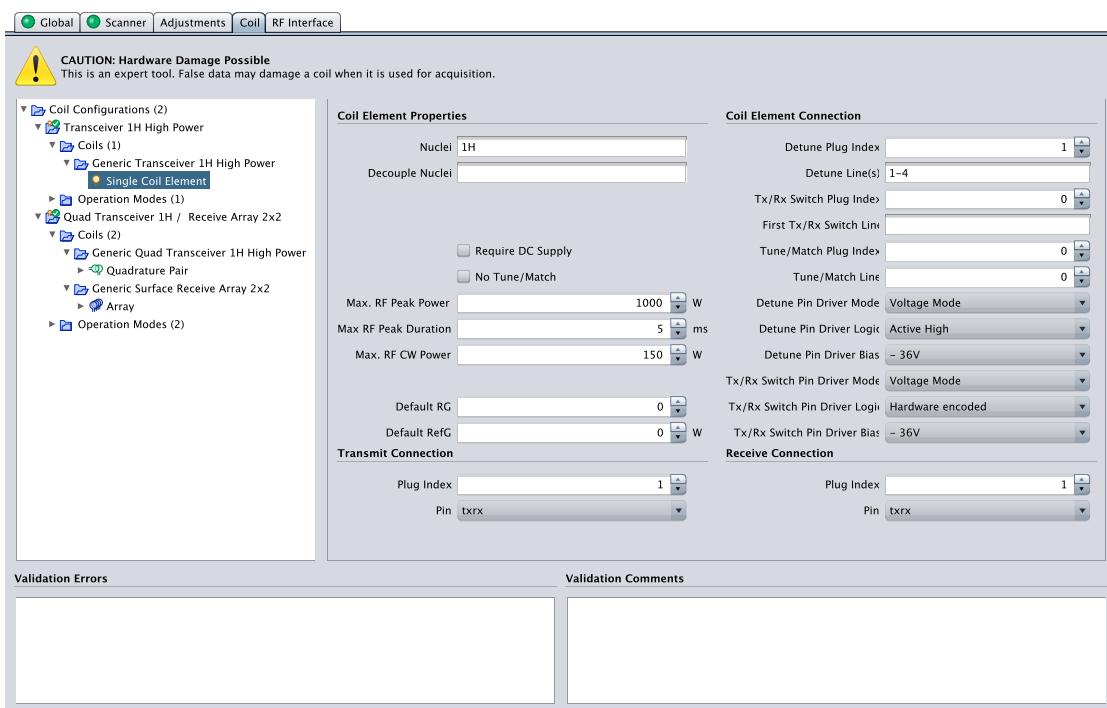


Figure 3.25: Coil Elements

Coil Element Properties

Selecting a Coil Element Group inside the configuration tree shows its Coil Element Properties, which are valid for the whole subset in case of Quadrature Pairs and Arrays, see Figure [Coil Elements \[▶ 678\]](#):

Nuclei	Slash (“/”) separated list of possible nuclei. Use a dash (“-”) between two neighboring nuclei to include a whole nucleus-range. Examples: 1H, 1H-19F, 13C-15N/3H-19F NOTE: The nuclei list is meant to be “either ... or ...” i.e. one Coil Element Group can only be tuned to one of the nuclei at a time. For double tuned coils, create different Coil Elements.
Decouple Nuclei (o)	List of nuclei for which decouple pulses may be transmitted, while the coil is resonant and in receive mode. See Nuclei , for the correct format.
Requires DC Supply (r)	Checked if this Coil Element has an integrated preamplifier that requires an external DC supply voltage from the connected receiver.
No Tune/Match	Checked if this Coil Element does not require tuning and matching.
Max. RF Peak Power (t), Max. RF Peak Duration (t), Max. RF CW Power (t)	Power limits for this Coil Element: Value of the maximum allowed peak power of single pulses this Coil Element can be fed with (Max. RF Peak Power (PP)) and for how long this peak power can be applied (Max. RF Peak Duration (PD)). The maximum power level for continuous wave transmission is described by Max. RF CW Power (CWP), i.e. the maximum power, which can be applied without time limit. NOTE: If a HWIDS detected Coil Element does not specify power limits, the arbitrary values PP = 10000W, PD = 10000ms, CWP = 1000W are used.
Default RG (o, r)	Default value for the receiver gain. It may be used as start value for the receiver gain adjustment.
Default RefPow (o, t)	Default value for the reference gain. It is used to derive a start value for the reference gain adjustment.
(o = optional, t / r = transmit / receive capable Coil Elements only)	

RF Connection

Besides the group specific properties, each single Coil Element defines a **Transmit Connection** and a **Receive Connection**, which indicate the connection points to the spectrometer.

For systems with RF Coil Interface these are given by the respective **Pins** on the ODU socket with the number **Plug Index**, see figure [RF Connection with RF Coil Interface ▶ 680](#). The mapping of the Plug Index to a physical ODU socket is defined by the Coil's Plug Table, see Chapter [Coils ▶ 677](#).



Figure 3.26: RF Connection with RF Coil Interface

On systems without RF Coil Interface the connected transmitter, preamplifier or receiver is selected directly as **Connection Port**, see figure [RF Connection without RF Coil Interface \[680\]](#).



Figure 3.27: RF Connection without RF Coil Interface

Coil Element Connection (Only System with ADM and RF Coil Interface)

Setting the Coil Element Connection, see Figure [Coil Elements \[678\]](#), combines three different features provided by the Active Detuning Module (ADM):

- When using different RF Coils for transmission and reception ("Cross Coil Combination"), only one at a time is allowed to be resonant. Therefore the ADM listens to control signals of the used transmitter and receiver to send **detuning** pulses to RF Coils which are currently not sending/receiving, i.e. making them off-resonant. Each ODU socket of the RF Coil Interface provides four independent pins/lines to route these detuning signals from the ADM to an RF Coil.
- NOTE:** Detuning is essential e. g. to prevent physical damage to the receive RF Coil due to induced power during transmission.
- Some Coil Elements need active **Tx/Rx switching** if they use a single line for transmit and receive. The four possible pins/lines for Tx/Rx switching are identical to those for active detuning. Double seizure is not possible.
- Another ADM functionality is to supply control voltages to variable capacitors ("Varicap") integrated into the resonant circuits of some RF Coils. Such RF Coils can be **tuned and matched** (wobbled) by sweeping through the control voltage range of those Varicaps. The voltages found during wobble are applied whenever the RF Coil is supposed to be resonant.

Plug Index	Index of the RF Coil's plug which is used. Important for multi plug RF Coils.
Line(s)	Index of the used line/pin. If a high current is needed, a range of pins/lines can be specified (not for Tune/Match). Examples: 1, 1-3 NOTE: The two lines for Tune/Match are independent, while Tx/Rx Switch and Detune use the identical four lines. Double seizure is not possible in the latter case.
Pin Driver Mode (p)	Detuning and Tx/Rx switching can either be voltage or current controlled, depending on the RF Coil's specification.

Pin Driver Logic (p) Pin Driver Bias (p)	<p>Selection of the pin logic. Besides active high and low the logic can also be hardware coded. In that case the logic is detected automatically via a special sense line also located within the ODU socket.</p> <p>NOTE: Detuning via an RF Coil Interface Adapter always uses hardware coded logic.</p> <p>Value of the applied negative voltage (-36V or -60V), when the signal level is low (high level is always +5V).</p>
(p = only Detune and Tx/Rx Switch)	

Sensitivity (Only Array Elements)

Each Array Coil Element defines a **Sensitivity** between zero and one, see Figure [Array sensitivity ▶ 681](#). Per default, this weighting factor is used during reconstruction to scale the received signal.

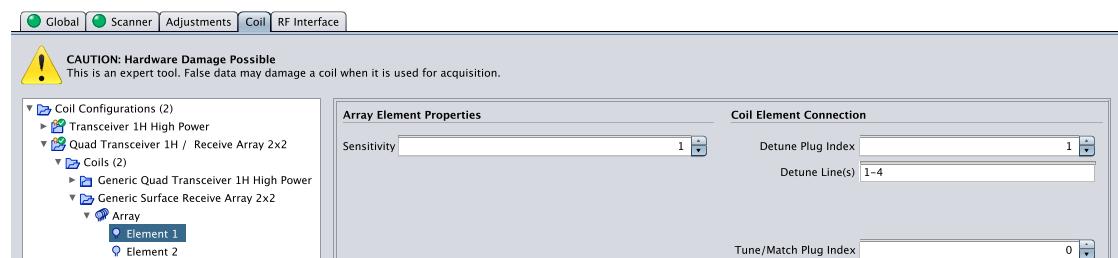


Figure 3.28: Array sensitivity

Integrated Combiner (Only Quadrature Pairs)

The flag **Has Integrated Combiner** indicates whether a Quadrature Pair uses an integrated/pассивный коммутатор for its 0° and 90° signals, see Figure [Combiner for Quadrature Pairs ▶ 681](#).

If unchecked, the **Transmit** and **Receive Connections** of a Quadrature Pair are interpreted as mere 0° and 90° signals. In that case an additional combiner (provided by Bruker) has to be used.

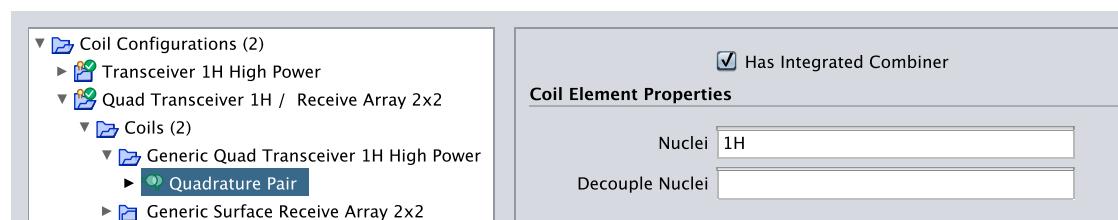


Figure 3.29: Combiner for Quadrature Pairs

3.6.2.2 Operation Modes

One Operation Mode is a representation of the spectrometer's RF Wiring for a given set of RF Coils. Dependent on the RF Coil setup used in a study, several operation modes may be possible. The Operation Mode holds information about the involved hardware modules, when starting acquisition using a specific set of RF Coils.

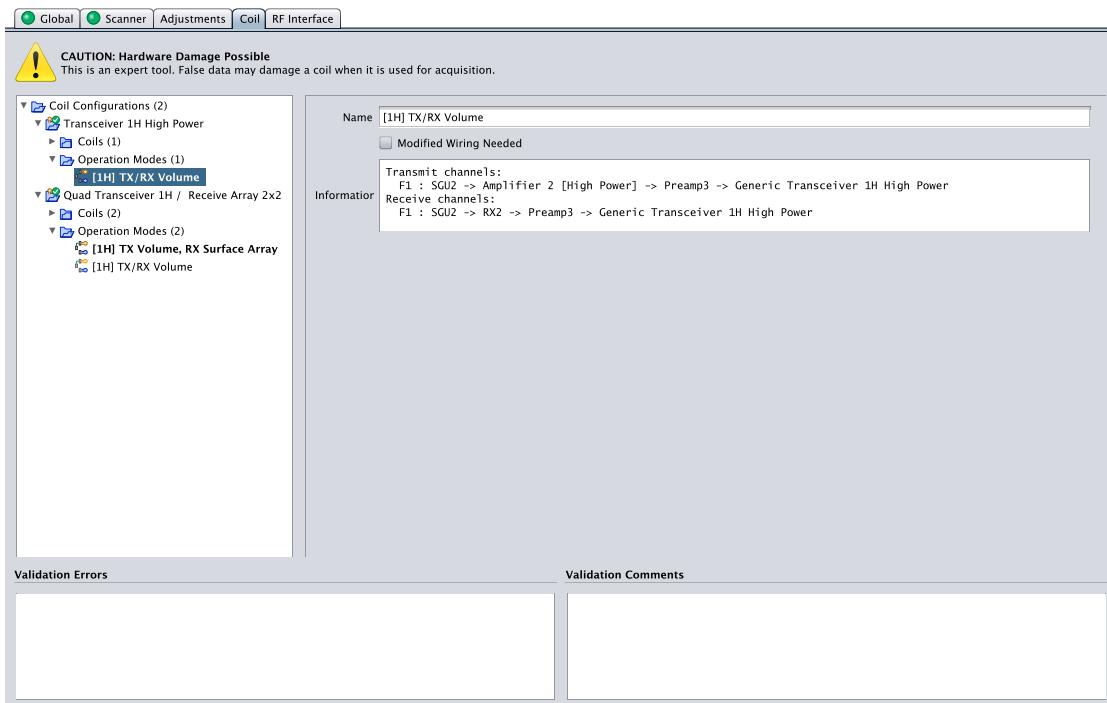


Figure 3.30: Operation Mode

Select an Operation Mode inside the configuration tree to view its **Name** and **Information** text, see Figure [Operation Mode \[▶ 682\]](#). Basically one Operation Mode consists of a transmit and a receive channel. A bold printed name marks the **Default Operation Mode** which is set whenever a study is opened.

The **Modified Wiring Needed** flag indicates, whether the RF Wiring needed by this Operation Mode differs from the global RF Wiring, see Chapter [Coil Configurations With Modified RF-Wiring \[▶ 689\]](#).

3.6.3 Import and Sharing of Coil Configurations

ParaVision stores all Coil Configurations user-specifically, i.e. if one user has created a set of Coil Configurations, they will be invisible for any other user (even for the NMR administrator).

The directory “<PvDir>/share/” plays an important role within the context of import and sharing. It represents the so called **Public Location** of ParaVision.

3.6.3.1 Import of Coil Configurations

One way of creating a valid Coil Configuration is to import an already existing one. This can either be from another ParaVision version or a Coil Configuration shared by another user. In both cases the properties of used Coils and Operation Modes are filled automatically during the import.

To import a Coil Configuration, right-click the knot **Coil Configurations** and select **Import Coil Configuration....**

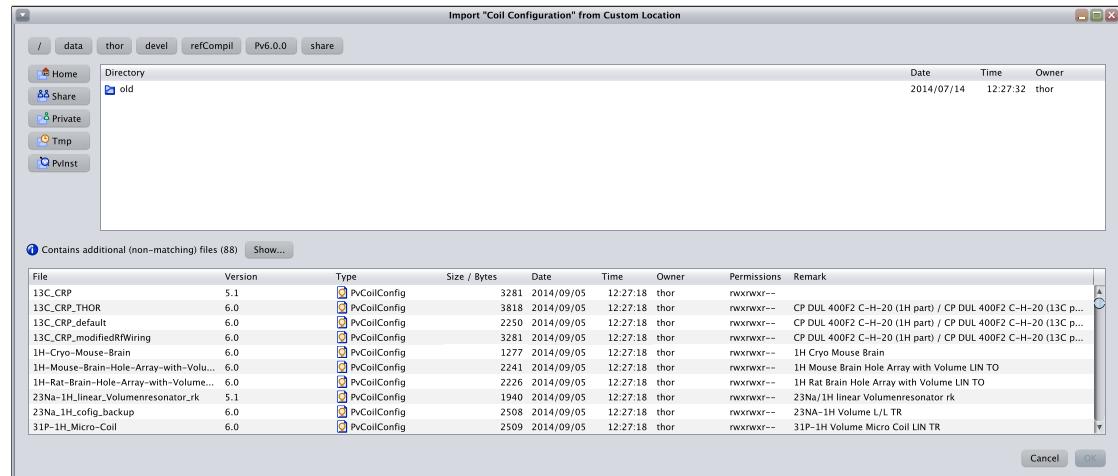


Figure 3.31: Import of a Coil Configuration

The pop-up window **Import “Coil Configuration” from Custom Location** is opened. By browsing through the file system, the user may navigate to any location where existing configuration files are stored, e.g. the Public Location of any ParaVision installation.

A valid Coil Configuration must meet the following requirements:

- **File Name:** Only configuration files named '`*_<PvVersion>.PvCoilConfig`' are listed for import. All other files are not detected as Coil Configuration files. If there are any non matching files inside the Public Location, an information text is shown in the top left corner of the import window. A list of all **Non Matching Files** can then be opened by pressing **Show....**.

Examples of valid names:

'Default_Transceiver_1H_100W_5.1.PvCoilConfig',
'QuadRes_6.Beta.0.30.PvCoilConfig'

- **Matching System Configuration:** The imported Coil Configuration must fit the current system configuration, e.g. the system frequency and the RF Wiring. If there is a conflict, the **Remark** column is left empty. A non-fitting Coil Configuration can be selected, but will produce an error when imported.

If both requirements are met, the Coil Configuration's **Name** is shown in the **Remark** column and it can be imported by selecting it and pressing **OK**, see Figure [Import of a Coil Configuration \[683\]](#).

Multi-selection is possible by holding the 'Ctrl'-key. By holding the 'SHIFT'-key a whole range can be selected.

NOTE: Importing from any custom location only creates a copy of a Coil Configuration's currently stored state inside the user's local directory. If the Coil Configuration inside the original location is updated, it has to be imported again to apply the changes to the user's copy.

3.6.3.1.1 Import from other ParaVision versions

If the current ParaVision version was configured by importing a whole system configuration of another version, included Coil Configurations are automatically copied to the Public Location. I.e. after the import they can be imported from the Public Location using the mechanism described in Chapter [Import of Coil Configurations \[682\]](#).

3.6.3.2 Sharing Coil Configurations

To make a Coil Configuration available to public, the owner of a Coil Configuration has to share it.

Right-click a Coil Configuration and select **Share Coil Configuration....**



Figure 3.32: Sharing a Coil Configuration

The user can define a descriptive name for the stored configuration file and share it by pressing **OK**, see Figure [Sharing a Coil Configuration \[▶ 684\]](#).

A shared Coil Configuration is copied to the public location of ParaVision and from there it can be imported by any other user.

NOTE: Sharing only creates a copy of a Coil Configuration's current state inside the public location. Further changes are not automatically applied to this copy, until the Coil Configuration is shared again.

3.6.4 Using HWIDS Detected Coils

Systems equipped with an RF Coil Interface make use of Bruker's "Hardware Identification System" (HWIDS). HWIDS-capable RF Coils contain a chip where all information about their connections and properties is stored.

If one or more HWIDS detected Coils are plugged into the RF Coil Interface, ParaVision reads out the stored information and automatically generates a Coil Configuration from it. The Coils within this Coil Configuration are marked non-editable, i.e. no properties or connections can be altered by the user, see Figure [Non-editable HWIDS detected RF Coil \[▶ 685\]](#).

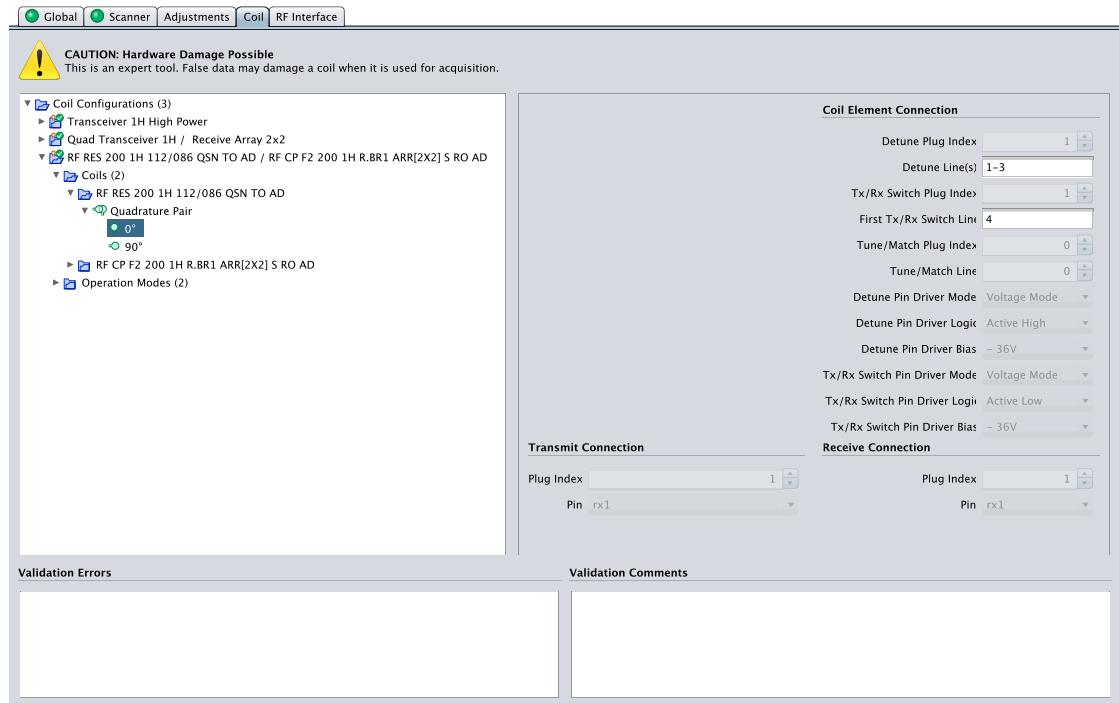


Figure 3.33: Non-editable HWIDS detected RF Coil

Coil Configuration including HWIDS detected RF Coils need to be modified only in the following exceptional cases:

- If a mixed combination of HWIDS and non-HWIDS detected RF Coils is used, see Chapter [Mixed HWIDS/non-HWIDS Coil Configurations \[▶ 688\]](#).
- If a user wants to change some Operation Mode settings for configurations supporting multiple Operation Modes, e.g. change the default Operation Mode, see Chapter [Creating And Editing of Operation Modes \[▶ 687\]](#).
- If a changed RF Wiring is needed, no Operation Modes will be automatically created, when the RF Coil is plugged in. The user has to first change the RF Wiring of the Coil Configuration, see Chapter [Coil Configurations With Modified RF-Wiring \[▶ 689\]](#), and generate the Operation Modes manually, see Chapter [Creating And Editing of Operation Modes \[▶ 687\]](#).

3.6.5 Configure RF Coil from Installation Medium (Micro-Imaging only)

Since Micro-Imaging systems do not use HWIDS detection, ParaVision offers the possibility to create a Coil Configuration by reading in a so called BIS file ("Bruker Information System"), usually shipped along with an RF Coil.

To configure an RF Coil, right-click the knot **Coil Configurations** and select **Configure RF Coil from Installation Medium....**

Browse to the directory of the BIS file, select it and press **Open**. A Coil Configuration is automatically created using the information read from the BIS file.

NOTE: The BIS file itself contains no information about the **Connection Port**, see Chapter [Coil Elements \[▶ 678\]](#). ParaVision just fills in an assumed module the RF Coil could be connected to. Therefore the user is advised to review this entry.

3.6.6 Using Default Coil Configurations

ParaVision can be instructed to generate a set of default Coil Configurations, to avoid a completely manual creation.

To generate default Coil Configurations, right-click the knot **Coil Configurations** and select **Create Default Coil Configurations**.

The user should in any case compare the generated properties of all Coils to those of the actually used RF Coils. In case of differences the Coil Configuration must be adapted manually, see Chapter [Create And Edit Coil Configurations From Scratch \[▶ 686\]](#).

NOTE: A generated set of default Coil Configuration does not meet the claim to cover all combinations of RF Coils which are possible on the given system.

3.6.7 Create And Edit Coil Configurations From Scratch

As a basic recipe of how to create a Coil Configuration from scratch, the following steps should be performed in their stated order (* = optional, may be skipped):

- **Create an empty Coil Configuration:** Right-click the knot **Coil Configurations** and select **New Coil Configuration**. Give the new configuration a descriptive name.
- * **Edit the RF Wiring** (optional), see Chapter [Coil Configurations With Modified RF-Wiring \[▶ 689\]](#).
- **Add Coils**, see Chapter [Creating New Coils \[▶ 686\]](#).
- **Add Coil Elements**, see Chapter [Creating New Coil Elements \[▶ 687\]](#).
- **Add Operation Modes**, see Chapter [Creating And Editing of Operation Modes \[▶ 687\]](#).
- **Save the Coil Configuration**, see Chapter [Validating And Saving Coil Configurations \[▶ 689\]](#).

In some cases only parts of the scratch configuration need to be performed, e.g. when starting off with default Coil Configurations.

NOTE: The idea behind creating a Coil Configuration is to first choose an RF Coil, define where it is connected to the spectrometer and then route the transmit/receive path. Therefore all Coils need to be configured correctly before defining any Operation Modes. Creating Operation Modes first, may lead to errors or inconsistent Coil Configurations.

3.6.7.1 Creating New Coils

To add a new Coil to an existing Coil Configuration, right-click the knot **Coils** and select **New Coil**.

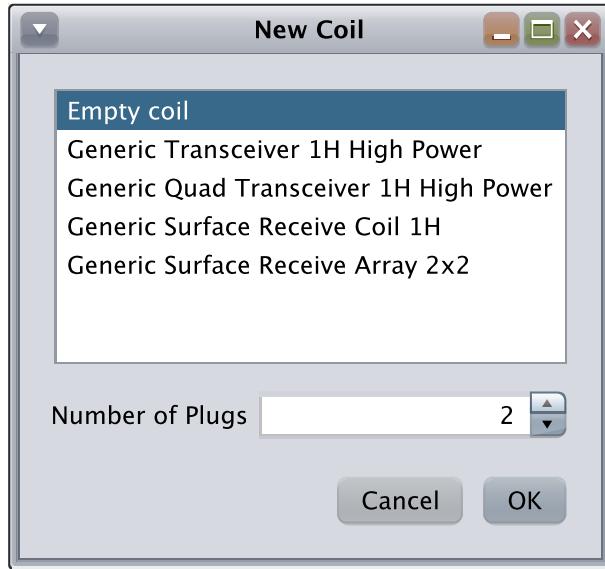


Figure 3.34: Create a new Coil

The user can choose between an Empty Coil or a predefined generic Coil, see Figure [Create a new Coil \[▶ 687\]](#):

- **Empty Coil**

A Coil without any Coil Elements is created. For **Coils using more than one plug**, the **Number of Plugs** has to be defined at this point. A later change is not possible. Such Coils always have to be created using an **Empty Coil**.

- **Generic Coils**

Depending on the system configuration, a set of generic Coils is offered, e.g. Transceiver 1H, Quadrature Transceiver 1H or a Surface Receive Coil 1H. Those Coils should be treated similar as generated default Coil Configurations, see Chapter [Using Default Coil Configurations \[▶ 686\]](#).

After creating a new Coil, its Coil Properties and Plug Table have to be defined, see Chapter [Coils \[▶ 677\]](#).

Any number of Coils can be added to a Coil Configuration.

3.6.7.1.1 Creating New Coil Elements

To add a new group of Coil Elements to an existing Coil, right-click a given Coil and select **New Single Coil Element**, **New Quadrature Pair** or **New Array**. After creating a new Coil Element its Coil Element Properties (and Coil Element Connection) along with its Transmit/Receive Connection has to be defined, see Chapter [Coil Elements \[▶ 678\]](#).

Any number of Coil Elements can be added to a Coil.

3.6.7.2 Creating And Editing of Operation Modes

NOTE: Operation Modes shall not be generated until all Coils are created and validated. Installing Operation Modes with non valid Coils results in a false routing path or may not be possible at all.

If all Coils of a Coil Configuration are defined correctly, ParaVision is able to detect possible Operation Modes automatically. To generate them, right-click the knot **Operation Modes** and select **Create Default Operation Modes**.

Afterwards the user can **Delete** or **Hide** certain Operation Modes or change the **Default Operation Mode**. These options are available via the right-click menu. Hidden Operation Modes are shown greyed and crossed out inside the Coil Editor and are not selectable within a created study, see Figure [Edit Operation Modes \[▶ 688\]](#). Choose **Show Operation Mode** from the right-click menu to make them selectable again.

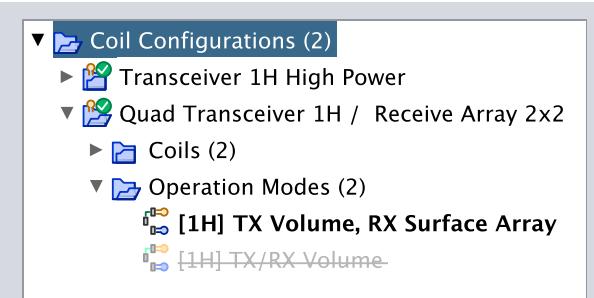


Figure 3.35: Edit Operation Modes

To create and route an Operation Mode manually, right-click the knot **Operation Modes** and select **New Operation Mode**. Another right-click on the Operation Mode itself and selecting **Edit Operation Mode...** opens TopSpin's 'edasp'-window. Here the user can set up an individual routing for a chosen nucleus. Save and close the window when finished.

If an Operation Mode needs a changed RF Wiring, see Chapter [Coil Configurations With Modified RF-Wiring \[▶ 689\]](#).

3.6.7.3 Copy, Paste, Cut and Delete

Coil Configuration, Coils, Coil Elements and Operation Modes can also be created, added, moved or deleted via **Copy**, **Paste**, **Cut** and **Delete**.

- **Copy/Cut:** Right-click an element X inside the Coil Editor and select **Copy X** or **Cut X**.
- **Paste:** Right-click a destination knot inside the Coil Editor and select **Paste X**.
- **Delete:** Right-click the destination and select **Delete X**.

3.6.7.4 Mixed HWIDS/non-HWIDS Coil Configurations

If a HWIDS detected RF Coil is plugged in, ParaVision automatically generates a Coil Configuration. It is then possible to add additional non-HWIDS Coils to it and generate new Operation Modes.

NOTE: For reasons of clarity a copy of the automatically generated Coil Configuration should be made and manually created Coils should only be added to this copy.

To summarize the order of creating a mixed Coil Configuration:

- Plug in the HWIDS detected RF Coil.
- Create a copy of the automatically generated Coil Configuration, see Chapter [Copy, Paste, Cut and Delete \[▶ 688\]](#).
- Open the copied Coil Configuration.
- Add a new Coil entry for each used non-HWIDS RF Coil, as described in Chapter [Creating New Coils \[▶ 686\]](#).
- Generate new Operation Modes, as described in Chapter [Creating And Editing of Operation Modes \[▶ 687\]](#).
- Save the Coil Configuration.

3.6.7.5 Coil Configurations With Modified RF-Wiring

Some RF Coils may require the user to reconnect parts of the spectrometer hardware, e. g. an amplifier has to be connected to a different preamplifier module. In that case the altered RF Wiring can be set locally without changing the global spectrometer setting. The scope of a changed RF Wiring can either be a whole Coil Configuration or a single Operation Mode.

- **RF Wiring of a Coil Configuration:**

Right-click a Coil Configuration knot and select **Edit RF Wiring....**

- **RF Wiring of a single Operation Mode:**

Select an Operation Mode and tick **Modified Wiring Needed**. Right-click the Operation Mode and select **Edit RF Wiring....**

After typing the administrator password, TopSpin's 'edasp'-window will pop up allowing the user to change the RF Wiring as desired.

NOTE: The user has to **make sure the physical hardware connections are installed correctly** in order to avoid unexpected behavior or even hardware damage. ParaVision always gives priority to a local RF Wiring over the global RF Wiring. ParaVision automatically assumes the local RF Wiring, whenever a modified Coil Configuration or Operation Mode is used.

3.6.8 Validating And Saving Coil Configurations

Different states of a Coil Configuration are indicated by font colors, see Figure [Unsaved Coil Configurations \[689\]](#).

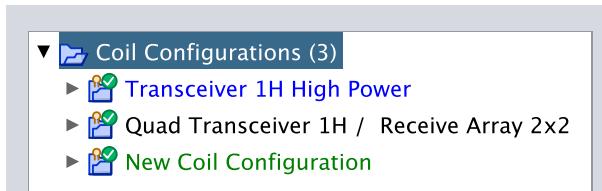


Figure 3.36: Unsaved Coil Configurations

Black	Coil Configuration is saved.
Blue	Coil Configuration is altered and not yet saved. It is set to its last stored state after closing the Coil Editor without saving.
Green	Coil Configuration is new and not yet saved. It is deleted after closing the Coil Editor without saving.

To save an altered or new Coil Configuration right-click it and select **Save Coil Configuration**.

Before a Coil Configuration is saved, ParaVision automatically performs a few validation checks. Some of those checks are mandatory and some optional. If one of them fails, an information output is printed to the respective window:

Validation Errors	A mandatory check failed. Coil Configurations can not be saved until all given errors are resolved.
Validation Comments	An optional check failed. The user is advised to correct the stated issues. Nevertheless, the Coil Configuration can be saved.

The validation check can also be performed manually by right-clicking a Coil Configuration and selecting **Validate Coil Configuration**. A valid Coil Configuration is marked by a green tick above the icon of the Coil Configuration, a non-valid by a red exclamation mark, see Figure [Validation Check \[690\]](#).

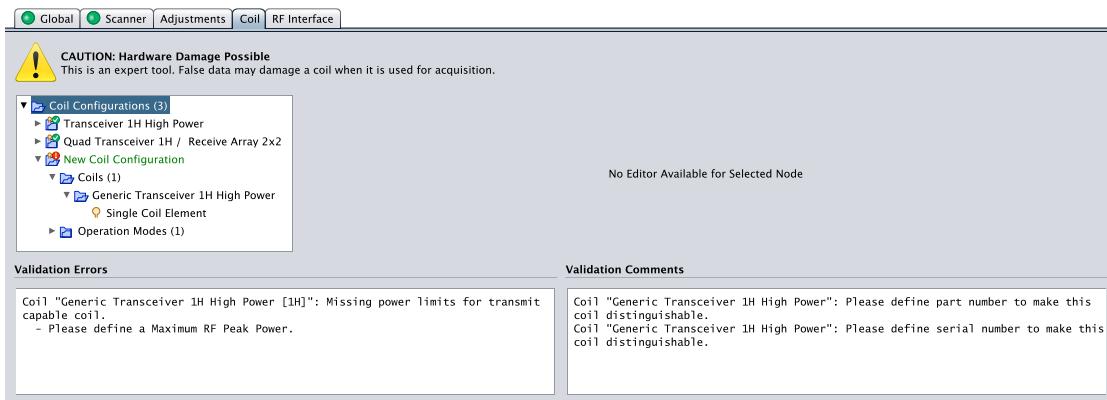


Figure 3.37: Validation Check

3.7 Quality Assurance RF Coils

Quality Assurance of RF coils is typically based on a Signal-to-Noise Ratio (SNR) measurement using a standardized measurement setup, phantom (sample), and measurement protocol. Setup, phantom and protocol may be different for every type of coil and therefore they are defined in the corresponding Coil Specific Information (see accordingly).

Therein, also the QA SNR specification of the RF coil is given.

The QA SNR specification serves as a reference value for quality assurance. In addition, other parameters may be defined. Normal operation of a RF coil with regard to SNR is defined as when the actual measurement is better than or equal to the QA SNR specification. Repeating measurements and recording them over time will enable the operator to establish a site specific value for reproducibility and performance.

Quality Assurance of most Bruker RF Coils is based on the protocol QA SNR located in the Scan Programs & Protocols tree “AnyObjects”, “AnyRegions”, “QualityAssurance”.

This protocol measures and determines automatically the SNR value based on a contour finding algorithm for signal and noise regions. Finally, it normalizes the SNR to a volume of one mm³ (SNR / mm³) which is compared with the QA SNR specification. The results are provided on the Routine Card.

In addition, a QA Test Report (filename QaSnrReport.pdf) is automatically created and saved in the corresponding Dataset in the Procno directory.

Please note that the automatically determined QA SNR value is used to check the normal operation of a coil.

The specification is based on the reproducibility of measurements for a specific coil and setup. It cannot be used to compare SNR values of different types of coils.



For QA SNR measurements, use the phantom and setup as described in the Coil Specific Information and tune/match the coils accordingly.

4 References

- [1] Zhang Y, Hetherington HP, Stokely EM, Mason GF, Twieg DB. A Novel k-space Trajectory Measurement Technique. *Magn. Reson. Med.* 39, 1998; 999-1004.
- [2] Hafner S. Fast imaging in liquids and solids with the back-projection low angle shot (BLAST) technique. *Magn Reson Imag* 12, 1994; 1047-1051.
- [3] Madio DP, Lowe IJ. Ultra-fast imaging using low flip angles and FIDs. *Magn Reson Med* 34, 1995; 525-529.
- [4] Kuethe DO, Caprihan A, Fukushima E, Waggoner RA. Imaging lungs using inert fluorinated gases. *Magn Reson Med* 39, 1998; 85-88.
- [5] Wu Y, Ackerman JL, Chesler DA, Li J, Neer RM, Wang J, Glimcher MJ. Evaluation of bone mineral density using three-dimensional solid state phosphorus- 31 NMR projection imaging. *Calcif Tissue Int* 62, 1998; 512-518.
- [6] Kuethe DO. Transforming NMR data despite missing points. *J Magn Reson* 139, 1999; 18-25.
- [7] Ordidge RJ, Gibbs P, Chapman B, Stehling MK, Mansfield P. High-Speed Multislice T1-Mapping Using Inversion-Recovery Echo-Planar Imaging. *Magn Reson Med.* 16, 1990; 238-245.
- [8] Gowland P, Mansfield P. Accurate Measurement of T1 in Vivo in Less than 3 Seconds Using Echo Planar Imaging. *Magn Reson Med.* 30, Jul 1993; 351-354.
- [9] Freeman AJ, Gowland PA, Mansfield P. Optimization of the ultrafast Look-Locker Echo-Planar Imaging T1 mapping sequence. *Magn Reson Imaging.* 16(7), 1998; 765-772.
- [10] Oshio K, Feinberg DA. GRASE (Gradient- and spin-echo) imaging: a novel fast MRI technique. *Magn Reson Med.* 20(2), 1991 Aug; 344-349.
- [11] Does MD, Gore JC. Rapid acquisition transverse relaxometric imaging. *J Magn Reson.* 147(1), 2000 Nov; 116-120.
- [12] Speck O and Hennig J. Functional imaging by T0- and T2*-parameter mapping using multi-image EPI. *Magn Reson Med.* 40(2), 1998; 243-248.
- [13] Posse S, Wiese S, Gembris D, et al. Enhancement of BOLD-contrast sensitivity by single-shot multi-echo functional MR imaging. *Magn Reson Med.* 42(1), 1999; 87-97.
- [14] Yang QX, Posse S, Le Bihan D, Smith MB. Double-sampled echo-planar imaging at 3 tesla. *J Magn Reson B* 113(2), Nov 1996; 145-50.
- [15] Duyn JH, Yang Y, Frank JA, van der Veen JW. Simple correction method for k-space trajectory deviations in MRI. *JMR* 132, 1998; 150-153.
- [16] Boernert P, Schomberg H, Aldefeld B, Groen J. Improvements in spiral MR imaging. *MAGMA* 9, 1999; 29-41.
- [17] E.O. Stejskal and J.E. Tanner. Spin Diffusion Measurements: Spin Echoes in the Presence of a Time-Dependent Field Gradient. *J. Chem. Phys.* 42(1), 1965; 288-292.
- [18] Kim S.G. and Tsekos N.V. Perfusion imaging by a flow-sensitive alternating inversion recovery (FAIR) technique: application to functional brain imaging. *Magn. Reson. Med.* 37, 1997, 425-435.
- [19] Weiger M, Hennel F, Pruessmann KP. MRI with zero echo time: hard versus sweep pulse excitation. *Magn Reson Med.* 66(3), 2011; 379-389.
- [20] Weiger M, Pruessmann KP, Bracher AK, Köhler S, Lehmann V, Wolfram U, Hennel F, Rasche V. High-resolution ZTE imaging of human teeth. *NMR Biomed.* 25(10), 2012; 1144-1151.

References

- [21] Weiger M, Pruessmann KP. MRI with zero echo time. In: Harris, RK; Wasylissen, RE. Encyclopedia of Magnetic Resonance. John Wiley: Chichester, 2012; 311-321.
- [22] Jones DK. et al. The Effect of Gradient Sampling Schemes on Measures Derived From Diffusion Tensor MRI: A Monte Carlo Study. Magn. Reson. Med. 51, 2004, 807-815.
- [23] Hull WE. NMR Tips for Shimming, Part I, Computerized Shimming with the Tuning Algorithm. SpinReport 152/153, 2003, 53-61.
- [24] Porter T, Duff T. Composing Digital Images. Computer Graphics 18 (3), 1984, 253-259.
- [25] Roméo F, Hoult DI. Magnet field profiling: analysis and correcting coil design. Magn. Reson. Med. 1, 1984, 44-65.

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